Accelerating domestication and genetic gain in the American cranberry (*Vaccinium macrocarpon* Ait.): new genetic and genomic resources for the cranberry breeders' toolbox

By

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A dissertation submitted in partial fulfillment of

The requirements for the degree of

Doctor of Philosophy

(Plant Breeding and Plant Genetics)

At the

UNIVERSITY OF WISCONSIN-MADISON

2016

Date of final oral examination: 8/12/2016

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Dedication

With praise and thanksgiving to my Lord, Jesus Christ.

Psalm 139: 1-18

[1] For the leader. A psalm of David.

I
LORD, you have probed me, you know me:
[2] you know when I sit and stand;
you understand my thoughts from afar.
[3] You sift through my travels and my rest;
with all my ways you are familiar.
[4] Even before a word is on my tongue,
LORD, you know it all.
[5] Behind and before you encircle me
and rest your hand upon me.
[6] Such knowledge is too wonderful for me,
far too lofty for me to reach.
[7] Where can I go from your spirit?
From your presence, where can I flee?
[8] If I ascend to the heavens, you are there;
if I lie down in Sheol, there you are.
[9] If I take the wings of dawn
and dwell beyond the sea,
[10] Even there your hand guides me,
your right hand holds me fast.
[11] If I say, "Surely darkness shall hide me,
and night shall be my light"—
[12] Darkness is not dark for you,
and night shines as the day.
Darkness and light are but one.

II
[13] You formed my inmost being;
you knit me in my mother's womb.
[14] I praise you, because I am wonderfully made;
wonderful are your works!
My very self you know.
[15] My bones are not hidden from you,
When I was being made in secret,
fashioned in the depths of the earth.
[16] Your eyes saw me unformed;
in your book all are written down;
my days were shaped, before one came to be.

III
[17] How precious to me are your designs, O God;
how vast the sum of them!
[18] Were I to count them, they would outnumber the sands;
when I complete them, still you are with me.

Abstract

The American cranberry (*Vaccinium macrocarpon*) is a recently domesticated fruit crop which has received little attention in the form of genetic research or genetic improvement. Molecular markers and genetic linkage maps, which have traditionally been missing from the cranberry breeders' toolbox, are invaluable for investigating genetic diversity and species relationships, characterizing genomes, and for locating and guiding the selection of candidate genes of economic importance. Leveraging next generation sequencing technologies to identify simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) loci in the cranberry genome could accelerate cranberry domestication and genetic gain by enabling molecular-assisted breeding and allowing exploration of cranberry genomic structure. As such, 697 polymorphic SSR loci were mined from cranberry nuclear contigs and transcriptome sequences and used to explore geographic distributions of cranberry genetic diversity across its native North American range. Using selections of the mined SSRs, multiplexing (4x) panels of the SSR markers were designed to estimate the percentage of self-pollinated seeds in commercial cranberry beds and for use in DNA fingerprinting, paternity analyses, and genetic diversity studies. An additional set of 54 SSR loci were located in the cranberry plastid and mitochondrial genomes, which were found to be cross-transferable and useful for exploring taxonomic relationships between cranberry other *Vaccinium* and Ericaceous species. A total of 541 SSR markers were positioned into 12 linkage groups (LGs), corresponding to the expected haploid chromosomes number, that were used to identify 4 quantitative trait loci (QTL) for mean cranberry fruit weight, 3 QTL for total yield, and QTL related to biennial bearing that colocalized with a yield QTL. Comparative genetic mapping using cross-transferable SSRs revealed perfect synteny and 93% genome-wide collinearity between cranberry and blueberry LGs. Finally, a high-density cranberry composite map containing 6073 markers was constructed using genotyping-by-sequencing for multi-pedigree linkage mapping. Saturation of the cranberry genome allowed for characterization of segregation distortion regions (SDRs) and placement of centromeres onto the 12 LGs. Collectively, these new genetic resources for the cranberry breeders' toolbox will facilitate forthcoming efforts to develop new cultivars through molecular-breeding approaches that meet current and future challenges in the cranberry industry.

Acknowledgements

Thank you Dr. Juan Zalapa for the countless ways you have guided me as my major professor during my studies at UW-Madison. You generously shared your time, your expertise, and your whole self with me. Thank you for giving me this opportunity, for helping me become a scientist, for encouraging me to hold fast to my beliefs and demonstrating to me how to maintain and express those beliefs in an academic setting, and for simply always wanting what was best for me.

Thank you Drs. Shawn Steffan, Michael Havey, Yiqun Weng, Natalia de Leon, and Michael Casler for serving on my examination committee and for your helpful advice during my coursework and research. Thank you also Eric Zeldin; Drs. Nicholai Vorsa, James Polashock, Irwin Goldman, Jeffrey Endelman, Amaya Atucha, Edwin Bingham, Dale Benham, Diego Fajardo, and Massimo Iorizzo; and Holly Ruess for your guidance as teachers and/or mentors.

Thank you Eduardo (Giovanny) Covarrubias-Pazaran and Luis Diaz-Garcia for your patience, understanding, assistance, and for being my most important teachers and companions in this process. Thank you Eric Wiesman, Lorraine Bonilla-Rodriguez, and Dr. Jenny Bolivar for your support in my research and for your friendship. Thank you Walter Salazar, Tierney Bougie, Tiffany Bougie, Laura Salmon, Sarah Hodapp, and Miguel Ochoa-Hernandez for allowing me to serve as your mentor and for helping me with fun tasks, hard tasks, easy tasks, tedious tasks… basically all the tasks.

Thank you to the Wisconsin Cranberry Growers Association for allowing me to participate in meetings and events, to the Frank B. Koller family, and to cranberry growers Nicole Hansen, Ed Grygleski, Bill Hatch, and Mike Moss for generously sharing your time, property, and knowledge of cranberries to support my research endeavors.

Thank you family and friends for your unending support. Thank you Charlie Brunnert for loving me like a grandpa should and for being the source of my love for agriculture and so many of the things that make my life great. Thank you to my wife's family who have accepted me as one of their own. Thank you Nathan, my brother, for being my keeper and for letting me be yours. I love you mom and dad. Thank you for the countless hours and good times that you, Nathan, and I spent together growing up; for teaching and showing me how to live my life well; and for sacrificing your dreams so that I could live mine… for making my dreams yours. Thank you Sophie and Emery for the little smiles, hugs, and the laughter that bring me so much joy. Thank you Malaina for being my love, for saying I do on 12/29/2012, for being a good mom to Sophie and Emery, for listening to my grumbles, for laughing with me and at me, for being so beautiful, for making amazing suppers, for driving me to campus when I was lazy, for letting me go fishing, for following me to far away places like Wisconsin and Kansas, and for striving with me to become the best-versions-of-ourselves.

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General Introduction

"There can be little argument about where this little red berry's place should be in American History, but that of the most American of all fruits and berries" (Eck 1990).

Early in American history, cranberries became a symbol of things uniquely American when they took their seat at the Thanksgiving table. For the first settlers who made their way to the state of Wisconsin, and undoubtedly the Native Americans who had collected the fruits as food and medicine for thousands of years, wild cranberries were an invaluable source of winter vitamins and calories when other fruits and vegetables were no longer available; in fact, they were so important that a law was passed in the state banning the collection of the wild fruits prior to a certain date each fall (Klingbeil and Rawson 1975). The cultivation of the American cranberry (*Vaccinium macrocarpon* Ait.), which is native to the northeastern U.S., began in the early 1800s in the Cape Cod region of Massachusetts, and spread rapidly to Wisconsin, and by 1869, more than 1,000 acres of the fruit were grown with an annual value exceeding $120,000 (Peltier 1970; Klingbeil and Rawson 1975; Eck 1990; Zalapa et al. 2014). Initially, cranberry production involved little more than clearing brush, spreading wild cranberry vines on the soil, and hand harvesting ripened berries (Peltier 1970). Slowly, the inventiveness of cranberry growers and contributions of cranberry researchers in the early 1900s helped to establish a cranberry culture which included the sanding, diking, frost protection, mechanical harvest, fruit sorting, and strict fertilization and integrated pest management regiments typical in modern commercial production (Cole and Gifford 2009). Today almost twice as many cranberries are grown in Wisconsin than any other U.S. state, and anything which has played such an integral role in the natural and agricultural history of the State of Wisconsin is worth knowing about, especially the most American of all fruits and berries, the American Cranberry.

The current cranberry industry is valued at nearly 1 billion U.S. dollars, and while domestic markets remain steady, future growth is expected as foreign export markets expand due to increased recognition and demand for the cranberry fruit (Alston et al. 2014). This increased demand and consumption of juices, sweetened dried cranberries (SDCs), and other cranberry products can be attributed to various reasons, but perhaps the most important is the mounting evidence suggesting various human health benefits provided by the phytochemicals present in the cranberry fruit such as anthocyanins, proanthocyanidins, acids, and other tannins and flavonoids (Duarte et al. 2006; Brown et al. 2012; Feghali et al. 2012). However, while consumer demand continues to grow, cranberry poducers and processors also face an increasing number of economic, social and environmental challenges. New cranberry germplasm, developed with a combination of classical and molecular-assisted breeding methods, is needed to address these issues.

Background

Cranberry Botany and Horticulture

The American cranberry (2n=2x=24) is a long-lived, perennial in the Ericaceae family within the *Vaccinium* section *Oxycoccus* (Hill) Koch (Camp 1945; Vander Kloet 1983). Like other members of the Ericaceae, cranberry thrives in nutrient-poor acidic soils that are generally inhospitable to other non-Ericaceous plants (Roper and Vorsa 1997; Vander Kloet and Avery 2010). Wild cranberries can be found in boggy regions extending from Maine, and some Canadian provinces including Nova Scotia, west to Minnesota, and southward to regions of low elevation in Tennessee and West Virginia (Eck 1990). Parts of *V. macrocarpon's* native range overlap with its only relative within section *Oxycoccus*, *V. oxycoccos,* which has a smaller leaves, flowers and berries, a circumpolar distribution, and is composed of plants in a range of ploidy levels ranging from diploids to hexaploids (Vander Kloet 1983; Eck 1990; Zalapa et al. 2014; Smith et al. 2015). Many questions still remain regarding the speciation and radiation within section *Oxycoccus*; however, fertile interspecific hybrids between *V. macrocarpon* and *V. oxcycoccus* have been generated suggesting that historic gene flow between the species has potentially occurred and still may occur where their ranges intersect (Vorsa and Polashock 2005).

Both *V. macrocarpon* and *V. oxycoccus* are diminutive shrubs consisting of a growth habit that allows for both asexual reproduction through low, horizontal shoots (i.e referred to as runners) which can root along their entire length at leaf nodes, and sexual reproduction through flower bearing vertical branches (referred to as uprights) arising from the runners (Roper and Vorsa 1997). Terminal buds form on each upright which can be vegetative (i.e. referred to as vegetative uprights), containing differentiated tissue for producing new leafy shoot growth, or mixed (i.e. referred to as reproductive uprights), with differentiated tissue for both new shoot growth and the primordia for the cranberry inflorescence, which can produce up to 10 flowers each season though generally only 2 or 3 produce mature, harvestable fruit (Eck 1990; Roper and Vorsa 1997; Vorsa and Johnson-cicalese 2012).

Industry-wide practices such as mechanized water harvest and clonal propagation cause the costs associated with establishing and maintaining a commercial cranberry marsh to be exceedingly high. As a result, the economic livelihood of commercial cranberry growers depends on their ability to manage and produce consistent high yielding crops in individual cranberry beds over multiple decades. Multiple studies have been conducted in cranberry to determine biological and environmental factors affecting annual yield such as geographic location, fruit and flower set, fruit size, fertilizer response, upright density, intra-plant competition for resources, and hormonal signaling (Eady and Eaton 1972; Eaton et al. 1983; McArthur and Eaton 1989; Strik et al. 1991; Davenport 1996; Elle 1996; Roper and

Klueh 1996). Furthermore, much of the fruit in a clonal cranberry bed is likely self-pollinated, due to cranberry's moderate self-compatibility (Sarracino and Vorsa 1991), but no study has been conducted to quantify the amount of self-pollination which occurs nor the effect that self-pollination has on fruit set and yield verses a production system which promotes cross-pollination. Recent studies suggest that year to year production stability in cranberry can be strongly limited by the indeterminate growth of cranberry uprights, which can lead to the phenomena of alternate or biennial bearing (Roper and Patten 1993; Guitton et al. 2012; Devetter et al. 2013).

Biennial bearing is a major economic problem for producing consistent high yielding fruit crops in long-lived perennial species such as cranberries. The reproductive pattern of these perennial species is cyclical in nature with an "on year" characterized by overproduction of fruit and limited vegetative growth followed by an "off year" characterized by vegetative growth and minimal fruit production (Jonkers 1979; Stevenson and Shackel 1998). Biennial bearing results when reproductive uprights fail to form a mixed apical bud capable of flowering and fruiting the next year, referred to as rebud among cranberry growers, during "on years" , and therefore, an "off year" of secondary growth follows (Strik et al. 1991).

Evolutionarily, biennial bearing is hypothesized to be a long-term resource allocation strategy adopted by perennial plants to balance the cost of flower, fruit, and seed production in an "on year" with growth and nutrient acquisition during an "off year"(Goldschmidt *et al.*, 1985; Guitton *et al.*, 2012). This hypothesis arises from observations that the mixed apical bud for the following year begins to form and differentiate while the current year's seed and fruit are still maturing; therefore, they are in competition for nutrients (Eck, 1990). Studies in both apples and cranberries have shown that applications of gibberellic acid, which is a hormone naturally produced by seeds, decreases rebud potential (Eady and Eaton 1972; Guitton et al. 2012). Furthermore, numerous studies in cranberry have shown that available nitrogen and carbohydrates, and even the number of leaves present per upright to produce carbohydrates, are limiting factors in rebud potential (Davenport, 1996; Gifford *et al.*, 1984; Patten & Wang, 1994). Finally, cranberries are known to require a vernalization period to promote flowering, different cultivars display various rates of return bloom across geographic ranges, and photoperiod is likely important in controlling flowering timing in cranberry as has been shown in other species (Strik et al. 1991; Jaeger et al. 2006; Tan and Swain 2006).

Elle (1996) showed that cranberry cultivars consistently display distinct resource allocation strategies and biennial bearing tendencies during reproduction. Specifically, some cultivars produce many fruits with only a few seeds; some produce a few fruits with many seeds; and some produce many fruits with many seeds. Additionally, some early maturing cranberry selections have tendency to rebud, possibly because early fruit maturation allows increased

accumulation of a CONSTANS (CO) like protein in the fall, which in turn, promotes *Flowering Locus T* (*FT*) expression and mediates flowering (Turnbull 2011). Therefore, despite the apparent complexity of time dependent environmental factors like hormonal activity, *FT* expression, or the amount of available nutrients affecting biennial bearing, these observations provide evidence that a selectable genetic component related to rebud tendencies within cranberry cultivars should exist.

Cranberry Breeding History

Cranberry domestication and cultivation began in the mid 1800's with growers making wild selections from native stands, and since then, more than 132 wild selections have been documented (Chandler and Demoranville 1958; Dana 1983; Eck 1990). Historically, many of these wild selections were distributed and shared among growers as named cultivars, but most of them are no longer grown and have unfortunately been lost or forgotten. Until the development of hybrid cultivars in the 1950's, wild selections dominated the cranberry industry as clonally preserved and propagated cultivars (Eck 1990). However, while more than a hundred wild selections were made and documented, the majority of cranberry acres were planted to four wild selections collectively known as "The Big Four" (i.e. McFarlin, Early Black, Searles, and Howes) (Peltier 1970; Eck 1990). Eventually, three additional wild selections (i.e. Ben Lear, Potter's Favorite, and LeMunyon) gained an important number of commercial acres (Peltier 1970; Klingbeil and Rawson 1975; Eck 1990). Collectively, this group of seven wild selections could rightly be referred to as "The Big Seven" due to their contributions to the early success of the cranberry and industry and their important genetic contributions to the development of the cultivars which have gained many of the current commercial acres (Table 1).

The first American cranberry genetic improvement efforts were initiated in the 1930's as a collaboration between the USDA-ARS and the Agricultural Experiment Stations of Massachusetts, New Jersey and Wisconsin. Since then approximately a dozen hybrid cultivars have been developed and released. The first cranberry breeding cycle used crosses between wild selections, all members of "The Big Seven", and resulted in the release of seven first generation artificial hybrid cultivars from 1950 to 1970 (i.e., Beckwith, Bergman, Crowley, Franklin, Pilgrim, Stevens, and Wilcox) (Eck 1990). The second and third breeding cycles generated seven additional cultivars (i.e. HyRed, GH1, DeMoranville, Crimson Queen, Mullica Queen, Sundance and BG) through crosses among first generation hybrids and "The Big Seven" wild selections, which have improved fruit quality (e.g., fruit anthocyanin content) and increased productivity (Fajardo et al. 2012). Cranberry breeding programs have and continue to rely exclusively on phenotypic selection within unreplicated full-sib populations, and have made little use of molecular or quantitative genetics to identify and increase

genetic variance while selecting superior individuals. The reliance on phenotypic selection, combined with its woody perennial habit and a lack of consistent breeding efforts, has caused cranberry genetic improvement to lag behind gains made in other fruit crops. As a result, current commercial production uses only a handful of cultivars whose pedigrees all trace to the original "Big Seven", leaving the industry with a dangerously narrow genetic base (Table 1).

Future Cranberry Breeding Directions

Major challenges in cranberry breeding include: intensive management techniques, the necessity to phenotype large populations in laborious/time expensive methods (i.e. only two cranberry breeding programs with limited funding currently exist and there is limited field space for trials); the lengthy period of juvenility, 2-4 years, from when crosses are made until plants are mature for field evaluation; and the requirement to evaluate yield related traits for 4-5 years to assess biennial bearing. Cranberry breeding efficiency could be improved with techniques that use molecular markers to reduce required population sizes, increase the number of genotypes that can be evaluated, improve the accuracy of selecting the most vigorous/highest yielding genotypes, and morph physical tasks requiring the exertion of many people to computational tasks requiring the mental exertion of single persons.

The breeder's equation is a useful tool when initiating an applied breeding program in perennial fruit crops, whose breeding cycles are extended by long periods of juvenility and the requirement for multi-environment/multi-year trials. A general formula for gain from selection (ΔG) is:

$$\Delta G = \frac{i r_A \sigma_A}{\Delta t} \qquad [1]$$

where i is the selection intensity, r_A is prediction accuracy, σ_A is the square root of the standard deviation of the additive genetic variance (V_A), and Δt is the breeding cycle time. Therefore an ideal breeding strategy in cranberry would be one that increases genetic gain (ΔG) by maintaining or increasing selection intensity (i), prediction accuracy (r_A) and additive genetic variance while decreasing the length of the breeding cycle (Δt) in a manner that is effective and that is not cost-prohibitive (Desta and Ortiz 2014). Molecular markers, such as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs), would be advantageous resources to add to the cranberry breeders' toolbox because of the many ways that they assist breeders during selection by allowing them to "see", quantify, and track genetic

variance (V_G), to connect phenotypic variance (V_P) to V_G for more accurate predictions, and to make decisions about how to best allocate field space and resources.

Increasing variance in breeding populations

Breeders are always interested in the amount and type of variance that is available to them during selection because it is an important component of genetic gain. Phenotypic variance (V_P) can be defined as the total variance in phenotypic values for a trait, and it is the sum of the variation in genotypic values (V_G), the variance of environmental components (V_E), and the interaction between V_G and V_E (V_{GE}) such that $V_P = V_G + V_E + V_{GE}$ (Falconer and Mackay 1996). V_G can be further partitioned into additive variance (V_A), dominance variation (V_D), and epistatic variance (V_I) where V_A is the main cause of resemblance between related plants (Falconer and Mackay 1996); however, both V_D (intra-locus interactions) and V_I (inter-locus interactions) are likely critical in cranberry and can be "captured" through asexually propagated cultivars. V_{GE} exists in the presence of environmental sensitivity, which occurs when some genotypes in a population are affected differently than other genotypes grown in the same environment (Falconer and Mackay 1996). Finally, V_E is the variance that cannot be attributed to genetic causes and resemblance between individuals, such as human induced error during trait measurement (Falconer and Mackay 1996).

Partitioning V_P into the smaller components of variation such as V_G, V_E, and V_{GE} is an important initial step for researchers and breeders trying to understand or improve a trait because it allows them to understand the magnitude by which the variance of that trait is determined by genetic and environmental influences. The amount that V_G influences V_P is known as broad-sense heritability and is calculated as the ratio of V_G/V_p (Falconer and Mackay 1996). Narrow sense heritability (h^2) can be defined as V_A/V_P, which is important because h^2 can be used by breeders too predict the average difference between the parental and selected generations for a trait, the genetic gain or response (R), by multiplying the h^2 by the selection differential (S) (i.e. the difference between the mean of the parent generation and the mean of the plants selected to be parents the following generation); this is exemplified in another version of the breeders equation $R= h^2S$ (Falconer and Mackay 1996).

V_G can be increased in breeding populations in four main ways, the most important, but sometimes overlooked, being sex and recombination which continually generates new variation by breaking apart and/or generating new combinations of genes (Barton and Charlesworth 1998). It is therefore the breeder's job during selection to ensure that sex and recombination occur in a manner leading to the desired outcome, such as generating a combination of genes that results in a cranberry genotype with larger fruit than has previously been known.

Inbreeding, self-fertilization, and pedigree-based selection methods are a second important strategy for maximizing and/or partitioning the selectable V_A in many crop species, especially maize, but it may not be the most effective means of genetic gain in cranberry and other long-lived outcrossing species like cranberry that potentially carry a large genetic load (Williams and Savolainen 1996). However, inbreeding in undomesticated, heterozygous species like cranberry is a potentially valuable means of identifying possible "domestication genes" through exposure of cryptic variation present at extremely low allele frequencies in natural populations (Dehaan and Van Tassel 2014). Recurrent selection using pedigree methods has not yet been attempted in cranberry.

The third method breeders use to increase V_G in their breeding populations is to introduce new variation from outside germplasm sources such as wild relatives of the same species. Most modern crop species have undergone one or more bottlenecks during domestication due to polyploidization, inbreeding, geographic isolation, and artificial selection to the point that it can be difficult to use genes from wild relatives, even when extensive diversity exists in wild populations of the species (Ladizinsky 1985; Cowling et al. 2009). However, because cranberry is a recently domesticated crop, with a moderate portion of commercial cranberry acreage still planted with wild selected cultivars and the remaining cultivars only one or two generations removed from the wild (Fajardo et al. 2012), there is substantial opportunity to utilize diverse, unselected wild germplasm in cranberry breeding without dramatically affecting important yield components and fruit physiology. Unfortunately, little is known about the levels of genetic diversity in cranberry. Bruederle et al. (1996) observed that cranberry populations exhibit low levels of genetic variation and extremely low expected heterozygosity (Ht = 0.048) based on isozymes compared to other species even within the same genera (Bruederle et al. 1994), and hypothesized the cranberry had undergone a bottleneck during the Pleistocene. However, observations of substantial genetic diversity within individual fields presumably planted to the same clone measured by DNA repeat variation (SSRs) versus protein variation (isozymes) suggests that substantial genetic diversity may exist in cranberry (Fajardo et al. 2012), but new methods of detection are needed. Newer molecular marker technologies, such SSRs and SNPs, which capture DNA repeat variation and DNA sequence polymorphism, may be useful tools that improve studies of natural cranberry populations and inferences of past demographic events. Thorough collection and sampling of wild of cranberry germplasm from across its native range, combined with studies cataloging the genetic diversity present using molecular tools, could lead to better understanding of the genetic relationships and geographic barriers to migration which exist among wild cranberry populations. A study of this sort would not only improve the University of Wisconsin and USDA NCGR cranberry collection *ex situ* conservation efforts and provide potential new sources of variation to broaden the genetic base of the commercial cranberry industry, but could also provide valuable

insights about the locations of unique cranberry diversity hotspots which are candidates for *in situ* conservation efforts (Pavek et al. 2003; Meilleur and Hodgkin 2004).

Sometimes the genetic variation desired by the breeder during selection may only exist in his/her imagination (Dehaan and Van Tassel 2014). In this situation, the only way to increase the desired type of V_A is to use foreign sources through a trans genetic approach or through inter-specific hybridization between the crop of interest and members of another species (Zamir 2001). Both trans-genic approaches and inter-specific hybridization can be improved with the aid of molecular and biotechnological tools. Transformation and regeneration protocols have been developed and successfully applied in cranberry, but acceptance of products from trans-genic cranberries by consumers has been questioned and the industry has consciously avoided such strategies (Serres et al. 1992; Serres et al. 1997; Polashock and Vorsa 2002b; Zeldin et al. 2002). Inter-specific hybridization between cranberry and other *Vaccinium* species has been limited due to potential barriers to hybridization (Vorsa and Polashock 2005). Little is known about whether these barriers to hybridization stem from genome divergence, such as major chromosomal rearrangements, problems with endosperm balance number, or are simply pre/post zygotic compatibility barriers. Taxonomic relationships and monophyly of the *Vaccinium* genera has not been completely established, and a molecular tools necessary for phylogenetic reconstruction of the genus are still lacking (Vander Kloet 1988; Kron et al. 1999; Vander Kloet and Avery 2010). Increased understanding of the relatedness and evolutionary distance between cranberry and other *Vaccinium* species made possible with newly developed genetic and genomic resources could help cranberry breeders and geneticists ask new questions and find new answers to overcome barriers to wide-hybridization.

Increasing prediction accuracy

As previously mentioned, the key task for any plant breeder during selection is to ensure that sex and recombination occur in a manner leading to the desired outcome. One problem which has continually affected cranberry breeder's abilities to complete this key task has been the uncertainty about true-to-type cranberry germplasm in controlled crosses. Genetic inconsistencies of named cultivars are common in different growing areas and even within plantings of a single cultivar (Dana 1983; Eck 1990; Fajardo et al. 2012). Most of the potential genetic heterogeneity problem stems from the lack of control by cranberry growers in the preservation, propagation, and distribution of both wild and hybrid cranberry cultivars in a clonally propagated system prior to being utilized by breeders (Fajardo et al. 2012). However, breeders continue to lack confidence in their ability to know the paternity or genetic make-up of germplasm they themselves generate and maintain in their cranberry breeding programs, which likely causes serious

reduction in selection accuracy. Contamination of field genotypes by runners from adjacent plots, which grow across aisles and establish themselves asexually, is a common problem that only serves to compound confusion. Molecular markers serve as simple tools for finger-printing cranberry germplasm to confirm trueness-of-type in plots and to confirm paternity of progeny generated in controlled crosses by acting as an easy to measure "phenotype" whose expression is constant across environments and whose inheritance can be traced from parent to offspring.

After cranberry breeders can confidently establish the pedigree of the germplasm in their breeding program, proper experimental design is essential for accurate estimation of variance components, and for reducing V_E so that it does not inflate estimates V_P. When the same individuals or lines from a population are replicated in multiple environments (e.g. years, locations) and measured for a particular trait, analysis of variance of that trait can be used to accurately estimate the V_G, V_{GE}, and V_E in the population, among families, and within families and predict the breeding values of the parents and progeny in the population for the trait of interest; better estimates lead to a better prediction accuracy (Falconer and Mackay 1996). Particular experimental designs such as random complete block designs (RCBD) can be used to reduce V_E by removing confounding variation such as field spatial effects (Falconer and Mackay 1996). Increasing the number of locations and replications used can increase the precision of estimates and predictions used in selection by reducing the proportion of V_{GE} and V_E present within V_P.

Sometimes, despite having proper experimental design, it is too difficult or too costly for breeders to accurately measure and select the phenotype of interest so they have pursued indirect methods of selection to improve their crops. Indirect selection is accomplished by finding an easier to measure trait, which is genetically correlated with the more difficult to measure trait due to pleiotropy or genetic linkage genes, to assist the breeder in achieving the desired selection accuracy in a more efficient manner (Aastveit and Aastveit 1993). Simple morphological markers such as corolla color or leaf spotting (Bingham et al. 2013) were and continue to be used for this purpose of indirect or marker-assisted selection; however, the term marker-assisted selection has evolved in recent decades to refer specifically to indirect selection using molecular marker data, such as SNP or SSR information. When individuals are genotyped using molecular, or morphological markers, thought to be pleiotropic or closely linked (highly correlated) with expression of the trait of interest, the average effect of allelic substitution (α), defined as the effect of the difference in mean of an individual when changing from one allele at a loci to another at random, can be calculated and used to determine the breeding value of a particular genotype at that locus for more accurate selection (Bernardo 2010).

Molecular markers, specifically DNA repeat variants and sequence polymorphisms, have distinct advantages over morphological markers in marker-assisted/indirect selection for improving selection accuracy: 1) their expression is

constant across environments and plant maturity level; 2) they are naturally abundant and relatively evenly distributed throughout plant genomes (Hamblin et al. 2007; Zalapa et al. 2012; Fugate et al. 2014); 3) they are easy to detect using next-generation sequencing approaches (Elshire et al. 2011; Zalapa et al. 2012) and they can be automated for acquiring substantial amounts of information quickly and accurately (Hayden et al. 2007; Patocchi et al. 2008); 4) their genomic locations relative to other markers and to marker trait loci (MTL) (i.e. simply inherited traits like the morphological markers or causative polymorphisms) can be ascertained through linkage mapping (Bielenberg et al. 2015); and 5) close linkage (a cause of genetic correlation) between marker loci and quantitative trait loci (QTL) involved in the expression of complex traits can be detected using QTL mapping (Jansen et al. 2003; Kenis et al. 2008); and 6) using the QTL and linkage information, many markers can be used at the same time for indirect selection of numerous MTL, QTL, or to select entire chromosomal segments as in marker-assisted backcrossing (Ru et al. 2015; Singh and Singh 2015).

Maintaining selection intensity and decreasing the length of the breeding cycle

Lack of available field space is a limiting factor in cranberry breeding, and as a result, cranberry breeders have sometimes elected to plant large, unreplicated, populations in 4 ft x 4 ft plots evaluated over many years so that they can use relatively high selection intensities without introducing genetic drift into their breeding populations (personal communication, Eric Zeldin). Unfortunately, this strategy has limited the annualized rate of gain in cranberry improvement and has resulted in the evaluation of progeny from only a small number of crosses within "The Big Seven" pedigree. It is likely that a better study is one that performs selection early and often, and provides some mechanism for performing initial selections independent of field evaluations. Molecular markers have the potential to increase the size of the size and number of populations that can be used while maintaining the same stringent selection intensities and decreasing the length of the cranberry breeding cycle through marker-assisted selection in cranberry seedlings and/or genome-assisted prediction (Desta and Ortiz 2014; Ru et al. 2015; Covarrubias-Pazaran 2016). In marker-assisted seedling selection, subsets of molecular markers flanking MTL or large-effect QTL are used to screen large numbers of progeny from controlled crosses to indirectly select for traits of known interest and genomic location, and then those indirectly selected seedlings can be transplanted in the limited field space for more extensive phenotyping (Collard et al. 2008; Ru et al. 2015). The cranberry seedlings transplanted in the field can then undergo the same stringent evaluations of yield stability and fruit quality currently being practiced. The end advantage is that breeding time, field space, and resources are used only on the seedlings predicted to have the best performance based on QTL models, while still maintaining the same selection intensity used in classical cranberry breeding.

In genomic prediction (genomic selection) plants are genotyped with hundreds or thousands of markers, selected based on genomic estimated breeding values (GEBVs) based on models developed from training populations evaluated in field plantings, and then crossed again without the need for lengthy field evaluations (Grattapaglia and Resende 2011; Poland et al. 2012). The generation length is reduced by dramatically decreasing the time required to select parents for the next generation. For this reason, genomic prediction is being increasingly adopted in forest tree genetic improvement and perennial species with long periods of juvenility (Grattapaglia and Resende 2011; Resende et al. 2012). Furthermore, because genomic prediction uses random sets of markers, information from markers with small effects often left out during marker-assisted selection based on QTL models are still incorporated into the model which can result in an increase in prediction accuracy (Dekkers 2007). The utility of genomic selection for fruit crop improvement was recently showcased in apple where researchers found high prediction accuracy (r_A) for complex fruit character traits with low heritability using 2500 SNPs (Kumar et al. 2012). Additionally, it was suggested that genomic prediction could decrease the apple breeding cycle by more than four years (van Nocker and Gardiner 2014), which would almost double annualized genetic gain (ΔG) if prediction accuracy (r_A) is maintained. Informed by the success and potential of genomic selection in apple, analysis of large SNP datasets, mixed-modeling approaches, and genomic-assisted breeding strategies should be assimilated into the existing traditional cranberry breeding programs

Previous applications of molecular technologies in cranberry

Cranberry (2n=2x=24), shares a common base chromosome number and karyotype with other economically important *Vaccinium* species, such as blueberry (*V. angustifolium*, *V. corymbosum*, *V. ashei*, and *V. darrowii*) and lingonberry (*V. vitis-ideae*), consisting of metacentric and submetacentric chromosomes (Hall and Galleta 1971). The cranberry haploid genome is estimated to be around 570 MB, which is roughly 5.5 times large than *Arabidopsis thaliana* (Costich et al. 1993). Research aimed at the discovery and development of genetic and genomic resources in cranberry is lagging behind most crop species of similar importance. For example, upon the initiation of my Ph.D studies at the University of Wisconsin in January 2013, a search of the National Center for Biotechnology (NCBI) would have revealed only 68 sequences in the nucleotide database for *V. macroacarpon.*

In the mid-1990s, cranberry researchers began developing the first DNA markers, Restriction Amplified Polymorphic DNA (RAPDs), to assess genetic diversity and variation within natural populations and grower plantings (Novy et al. 1994; Novy et al. 1996; Stewart and Excoffier 1996). Eventually, Sequence Characterized Amplified Regions (SCAR) markers were derived from the RAPDs for increased marker specificity and reproducibility (Polashock

and Vorsa 2002a). A set of simple sequence repeats designed in blueberry were found to be cross-transferable to cranberry and were useful in distinguishing cranberry cultivars (Rowland et al. 2003; Boches et al. 2005; Bassil et al. 2009).

In the past five years, application of next-generation sequencing technologies in cranberries has increased the availability of sequence data and facilitated assembly of cranberry nuclear contigs for rapid and cost effective SSR discovery (Zalapa et al. 2012). With the assembled contigs, two additional SSR sets, consisting of 32 and 48 markers, respectively, were developed by Georgi et al. (2011) and Zhu et al. (2012), and they were found to be useful in analyzing genetic diversity in Wisconsin native cranberry populations and for confirming parentage of cranberry cultivars (Fajardo et al. 2012; Zalapa et al. 2014). However, none of these advanced DNA sequence datasets have been used to develop a substantial set of codominant markers such as SSR or single nucleotide polymorphism (SNP) for the construction of high-density linkage maps, for performing quantitative trait loci (QTL) studies, and for their subsequent use in marker-assisted selection (MAS) or genomic prediction strategies.

Thesis Objectives

Incorporating molecular-breeding strategies into current selection schemes would be an efficient way to accelerate the rate of domestication and genetic gain in cranberry. However, prerequisites for molecular-assisted breeding strategies, like marker-assisted selection and genomic prediction, include the availability of numerous mapped molecular markers for genome characterization and estimates of recombination, knowledge of associations between molecular markers and traits of interest, available populations with characterized genetic and phenotypic diversity, and efficient high-throughput methodologies which justify the use of molecular-assisted breeding when compared to costs and genetic gain of traditional breeding methods. Upon initiation of my Ph.D thesis, genetic and genomic resources were limited to not available in cranberry. Therefore, the present research was undertaken with the aim of discovering and developing molecular tools to add to the cranberry breeders' tool box and to begin to fulfill the basic requirements for initiating a molecular-assisted breeding program in cranberry at the University of Wisconsin-Madison. The specific objectives of the research were to 1) discover SSR and SNP loci in the cranberry nuclear and organellar genomes and develop markers for the loci to be used in future cranberry breeding and research (Chapters I, II, V, and VI); 2) develop efficient methods, such as multiplex PCR and genotyping-by-sequencing, for gathering genotypic data from large numbers of cranberry samples for DNA fingerprinting and paternity analyses (Chapters III and VI); 3) begin using the markers to develop a more thorough understanding of the genetic diversity in cranberry and of the phylogenetic relationships within the *Vaccinium* genus (Chapters I and II); 4) construct linkage maps for multiple cranberry pedigrees using SSR and SNP markers to begin characterizing the cranberry genome and enabling QTL studies for connecting V_P to V_G (Chapters IV, V, and VI); and 5) explore genomic divergence between cranberry and blueberry through comparative genetic mapping (Chapter IV).

Table 1. Origin, pedigree, and release/selection date for commercial propagated cranberry cultivars. The seven wild selections together make-up "The Big Seven" because of their important role in cranberry production and breeding history.

Cultivar	Type	Origin	Release
McFarlin	wild selection	MA, USA	1874
Searles	wild selection	WI, USA	1893
Howes	wild selection	MA, USA	1843
Early Black	wild selection	MA, USA	1835
LeMunyon	wild selection	NJ, USA	1960
Ben Lear	wild selection	WI, USA	1901
Potter's Favorite	wild selection	WI, USA	1895
Stevens	McFalin x Potter's Favorite	USDA-ARS	1950
Franklin	Early Black x Howes	USDA-ARS	1950
HyRed	Stevens x Ben Lear	UW-Madison	2003
GH1	McFarlin x Searles	Ed Grygleski	2004
Crimson Queen	Stevens x Ben Lear	Rutgers	2006
Demoranville	Franklin x Ben Lear	Rutgers	2006
Mullica Queen	(Howes x Searles) x LeMunyon	Rutgers	2007
Sundance	Stevens x Ben Lear	UW-Madison	2011
BG	(McFarlin x Early Black) x (McFarlin x Searles)	Ed Grygleski	2012

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Chapter I

As published in *Molecules* 2015 20(2):2001-2013; doi:10.3390/molecules20022001.

Development and Validation of 697 Novel Polymorphic Genomic and EST-SSR Markers in the American cranberry (*Vaccinium macrocarpon* Ait.)

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Academic Editor: Derek J. McPhee
Received: 18 December 2014/Accepted: 26 January 2015/ Published: 27 January 2015

Author Contributions

Brandon Schlautman, Diego Fajardo, Shawn Steffan, and Juan Zalapa conceived and designed the experiments; Brandon Schlautman, Eric Wiesman, and Tierney Bougie performed the experiments; Nicholi Vorsa and James Polashock edited the manuscript, performed crosses, and provided cranberry genotypes; Brandon Schlautman and Juan Zalapa analyzed the data and co-wrote the paper.

Abstract

The American cranberry, *Vaccinium macrocarpon* Ait., is an economically important North American fruit crop that is consumed because of its unique flavor and potential health benefits. However, a lack of abundant, genome-wide molecular markers has limited the adoption of modern molecular assisted selection approaches in cranberry breeding programs. To increase the number of available markers in the species, this study identified, tested, and validated microsatellite markers from existing nuclear and transcriptome sequencing data. In total, new primers were designed, synthesized, and tested for 979 SSR loci; 697 of the markers amplified allele patterns consistent with single locus segregation in a diploid organism and were considered polymorphic. Of the 697 polymorphic loci, 507 were selected for additional genetic diversity and segregation analyses in 29 cranberry genotypes. More than 95% of the 507 loci did not display segregation distortion at the $p < 0.05$ level, and contained moderate to high levels of polymorphism with a

polymorphic information content > 0.25. This comprehensive collection of developed and validated microsatellite loci represents a substantial addition to the molecular tools available for geneticists, genomicists, and breeders in cranberry and *Vaccinium*.

Keywords

Microsatellite; SSR Mining; EST; Ericaceae

Introduction

The American cranberry (*Vaccinium macrocarpon* Ait.) is a diploid (2n=2x=24), woody perennial in the family Ericaceae with an estimated genome size of 470Mb (Kron et al. 2002). Like many members of this family, it is uniquely adapted to life in a peat bog and can thrive in acidic, nutrient poor soils (Fajardo et al. 2013). The *Vaccinium* genus includes other important commercial berry species, such as lingonberries, huckleberries, bilberries, and multiple species of blueberries. Together with cranberry, the fruits of these plants are increasing in popularity and consumption because of the potential health benefits provided by their array of phytochemical constituents. For example, various studies have shown that *Vaccinium* fruits contain high concentrations of anthocyanins and other polyphenolic antioxidants (Seeram 2008) and that cranberry fruit proanthocyanidins can help prevent urinary tract infections and various periodontal diseases (Howell et al. 1998; Foo et al. 2000; Feghali et al. 2012).

The growing importance of cranberries and cranberry products has created a demand for new cultivars which meet the economic, social, and environmental demands of cranberry growers, processors, and consumers. The industry currently relies on only a handful of cultivars with a narrow genetic base (Fajardo et al. 2012). Cranberry improvement through classical breeding approaches has been limited but successful; however, most commercial varieties are separated from their wild brethren by only a few breeding and selection cycles (Rodriguez-Saona et al. 2011). Because of the increased demand for new cranberry cultivars, many recent investigations have aimed to increase the genetic resources available for cranberry molecular crop improvement. Multiple sets of microsatellite or short sequence repeat (SSR) markers have been developed in blueberry and transferred to cranberry or have been developed by mining cranberry next generation sequencing data (Georgi et al. 2011; Zhu et al. 2012; Georgi et al. 2013). However, despite these efforts to develop genetic resources, fewer than 200 molecular markers have been tested and validated, and only 136 markers have been added to a cranberry genetic linkage map (Georgi et al. 2013).

Abundant genome-wide molecular markers are a prerequisite for initiating a marker-assisted selection (MAS) program. Therefore, the primary intent of this study was to increase the number of markers available for genetic research in cranberry by testing and validating polymorphic SSR loci in a set of genotypes of diverse, but known origins. The SSR loci developed herein will allow for the identification of quantitative trait loci (QTL) and candidate genes of agronomic importance. This information will be essential for the development of innovative plant breeding systems and MAS programs aimed at generating and releasing new cultivars adapted to meet the current and future challenges of the cranberry industry. Broader implications may follow by adapting these markers for use in comparative genomic and evolutionary studies within the genus *Vaccinium* and the family Ericaceae.

Results and Discussion

SSR Search and Primer Design

Continued advances in Next Generation Sequencing technologies have made genetic research and molecular marker development increasingly available and affordable to "minor" crops (Zalapa et al. 2012; Fugate et al. 2014). As a result, recent efforts have drastically increased the level of organellar (Fajardo et al. 2013), nuclear (Polashock et al. 2014), and transcriptome (Polashock et al. 2014) sequence data existing for *V. macrocarpon*, a species which has traditionally lacked genetic and genomic resources. Furthermore, multiple studies have been conducted characterizing the presence of SSRs within the nuclear genome and transcriptome (Zhu et al. 2012; Polashock et al. 2014); however, these studies have only developed and tested a limited number of these loci. Currently, less than 200 validated nuclear SSR markers are available for cranberry (Georgi et al. 2013), which equates to only one marker for every 3.4Mb of the estimated 470Mb nuclear genome (Polashock et al. 2014). Therefore, this study aimed to increase the number of molecular markers available for conducting comparative genomic analyses, linkage and QTL mapping, genome wide association, and diversity studies in cranberry and the *Vaccinium* genus.

The current SSR search detected 7557 perfect SSRs within an assembly of 237,651 *V. macrocarpon* nuclear scaffolds (Fajardo et al. 2014) using SSR locator (da Maia et al. 2008), which was nearly 90% fewer microsatellites than either of the previous studies discovered (Zhu et al. 2012; Polashock et al. 2014). However, the current investigation employed much stricter parameters (i.e. a minimum of 4 repeat units and a minimum length of 18 bp versus a minimum of 3 repeat units and a minimum length of 12 bp) in order to increase the likelihood of identifying polymorphic loci. The frequency and distribution of SSR motif types were consistent with those found in the most recent SSR characterization (Polashock et al. 2014); the most common motif length within the nuclear scaffolds were di-nucleotides (67.4%) and the GA/TC was the most abundant motif type (28.5%) (Figure 1.1). Requiring tetra-nucleotides to contain a minimum of 5 repeat units caused them to be underrepresented in this study, only 4.6% compared to nearly 20% of the total in past analyses (Zhu et al. 2012; Polashock et al. 2014) (Figure 1.1).

The 7557 microsatellite containing nuclear scaffolds were screened for suitable flanking sites for PCR primer design using WebSat (Martins et al. 2009), and primers were successfully designed for 816 loci. An additional set of 7772 sequences containing EST-SSRs previously identified, but not developed (Polashock et al. 2014) were also screened and 163 primer pairs were designed for di-nucleotide and tri-nucleotide motifs with long repeat lengths. In total, primers were designed and synthesized for 979 new SSR loci; 568 SSRs were from genomic sequences and 129 were from EST sequences.

Validation of Cranberry SSR Loci

Of the 979 designed and tested primer-pairs in this study, 896 (91%) amplified products in an initial polymorphism screen of four cranberry cultivars (Table 1.1; 'Crimson Queen', 'Mullica Queen', 'Stevens', and 'Ben Lear'). A total of 697 (71%) of the 979 developed primer-pairs produced a maximum of two fragments per individual and were considered putative polymorphic loci (Appendix I-1, Appendix I-2, Appendix I-3). The remaining 243 primer-pairs which produced amplicons in the 4 cranberry cultivar either displayed monomorphic allele patterns (9%) or amplified more than two alleles which is not consistent with single locus segregation in a diploid organism (11%). Sequences containing the 697 polymorphic SSR loci validated in this study were deposited in GenBank, and the polymorphic EST-SSR loci were annotated using Blast2Go (Appendix I-1) (Conesa and Götz 2008). About 73% of the polymorphic loci contained alleles which distinguished the cultivars Crimson Queen and Mullica Queen, and these 507 primer-pairs were used in an expanded genetic diversity analysis with 13 cranberry cultivars and a segregation analysis with 16 derived progeny from a 'Crimson Queen' x 'Mullica Queen' cross.

In general, the lack of stuttering in tetra-, penta-, and hexa-nucleotide motifs compared to smaller motif classes makes allele sizing and genotyping more straightforward (Gardner et al. 2011); furthermore, the larger motif classes are sometimes preferred for population genetic studies because they tend to have slower mutation rates and a reduced risk for size homoplasy (Chakraborty et al. 1997). However, in this study, while all of the primers designed for tetra-nucleotide, penta-nucleotide, and hexa-nucleotide SSRs produced amplicons, only 33% of those SSRs were polymorphic suggesting that investigations intending to validate large motif class SSRs should use more lenient parameters and test many more primer-pairs and individuals than were used in the current characterization. Conversely, more than 70% of primer-pairs from both the di-nucleotide and tri-nucleotide motif classes were found to be polymorphic. Therefore, investigations intending to validate markers for direct parentage analysis as in linkage mapping and QTL mapping where size homoplasy due to microsatellite mutation rates are a non-issue should focus their investments on testing primer-pairs designed for lower class SSR loci (i.e. di-nucleotides and tri-nucleotides).

Genetic Diversity and Segregation Analyses

The 507 polymorphic (Appendix I-1, Appendix I-2) SSRs tested on the panel of 13 cranberry cultivars yielded 2278 alleles with an average of 4.49 alleles and a range of 2 to 11 alleles (N_A) per locus (Table 1.2). More than 80% of the 507 polymorphic SSRs tested were di-nucleotides, and the di-nucleotide motif class had greater average number of effective alleles (N_E) (3.24), polymorphic information content (PIC) (0.59), observed heterozygosity (H_O) (0.72), and expected heterozygosity (H_E) (0.63) than the other motif classes (Table 1.2). As in the SSR search, GA/TC was the most common motif type tested in the genetic diversity analysis, and was responsible for 43% of the total alleles detected (Table 1.3).

Nearly 66% of the markers in the genetic diversity study contain high levels of genetic information according to the suggested criterion of high (PIC>0.5), moderate (0.25<PIC<0.5), and low (PIC<0.25) (Kumar Yadav et al. 2010). Of the remaining markers, 31% contain moderate and only 3% contain low levels of genetic information. The large number of alleles possible for each SSR locus allows a single SSR with *k* alleles to achieve the same genetic information content as (*k*-1) biallelic markers such as single nucleotide polymorphisms (SNPs) (Hamblin et al. 2007), and therefore, it can be inferred that these 507 markers may contain an equivalent level of genetic information as more than 1000 SNPs. The 507 polymorphic markers analyzed herein are likely to have broad utility and applicability in various types of *Vaccinium* genetic studies because the relatively even distribution of SSRs throughout nuclear genomes makes them particularly useful for conducting linkage mapping, comparative genomic, and QTL mapping studies (Merdinoglu et al. 2005). Segregation analyses using chi-square tests revealed that only 4% of the 507 markers tested on the 16 'Crimson Queen' x 'Mullica Queen' derived progeny displayed segregation distortion at the $p < 0.05$ level (Appendix I-1, Appendix I-2). The remaining 487 SSR markers are immediately available for resolving the current *V. macrocarpon* linkage map from 13 linkage groups to the true 12 groups and increasing the number of mapped distinct loci from only 136 markers to a number more appropriate for QTL studies (Georgi et al. 2013). The current marker set (up to 697 SSRs) combined with the previous 136 mapped markers could increase the marker density in the cranberry linkage map from an average of one marker every 3.4 Mb to one marker every 0.6 Mb.

The 507 SSR loci were more than sufficient to clearly separate all 29 cranberry genotypes tested in a principle coordinate analysis (PCoA) (Figure 1.2). The first principle coordinate accounted for 30.55% of the total genetic variation and the second principle coordinate accounted for 20.04%. Although the sample size is small, the analysis demonstrates the utility of these markers for inferring genetic and geographic relationships within cranberry. The

second principal coordinate axis separated genotypes based on their geographic origins. All selections east of the Appalachian Mountains and second generation backcrosses to an eastern parent fell below the x axis, and a wild selection from the west and the second generation backcrosses to a western parent fell above the x axis (Table 1.1, Figure 1.2). These markers were also useful for tracking hybrid backgrounds. The first generation hybrids 'Stevens' and 'Demoranville' which lay near the x axis each have pedigrees involving one eastern and one western parent; the 'Ben Lear' x 'Stevens' offspring fall in a cloud between the two parents in the 1st quadrant; and the 'Crimson Queen x Mullica Queen' (50% East/50% West) derived progeny lay in a cloud between the parents in the 2nd and 3rd quadrants (Table 1.1, Figure 1.2). Additional PCoA analyses which included only the 13 cultivars in the genetic diversity panel (Appendix I-4), and a random set of only 50 SSR markers rather than the 507 (Appendix I-4) displayed similar trends and utility for inferring genetic and geographic relationships within cranberry. Expansion of this genetic diversity panel in future studies to include all available cultivars and elite parents from cranberry breeding programs should resolve the parentage composition of several unknown hybrid cultivars, and expanding the panel to include wild selections from across the current *V. macrocarpon* native range will provide insights into cranberry evolutionary history and identify pockets of unsampled genetic diversity for application in future cranberry breeding systems.

Experimental Section

Plant Material

Commercial cranberry production relies on a small number of true-to-type clonal cultivars. Some commercial cultivars are actually clones of native wild selections previously found in North American peat bogs, and the remaining commercial cultivars are either first or second generation artificial hybrids of those native wild selections. In this study, a panel of 13 unique commercial cultivars (Table 1.1) was selected for an analysis of SSR allele diversity and polymorphism screening. In order to perform a simple test of the hypothesis that the Appalachian Mountains may serve as a genetic barrier between extant North American wild cranberries, cultivars with genetic origins from both east and west of the Appalachian Mountains were included. An additional set of 16 progeny from a 'Crimson Queen' x 'Mullica Queen' cross was collected for an analysis of SSR allele segregation. The germplasm for this study was provided by four different sources including: the National Clonal Germplasm Repository in Corvallis, OR; cranberry breeder Edward Grygleski; the Rutgers University cranberry breeding program; and the University of Wisconsin-Madison cranberry

breeding program. Genomic DNA was extracted from lyophilized leaf tissue from individual reproductive stems of each genotype using a Macherey-Nagel (MN) Plant II kit (Düren, Germany) following the manufacturer's instructions.

Detection of Genomic and EST-SSR Markers

SSR markers were mined from a set of nuclear scaffolds greater than 100 bp that were previously reported (Fajardo et al. 2014). Prior to the SSR search, all sequences were mapped against the *V. macrocarpon* plastid and mitochondrial genomes to remove organellar sequences (Fajardo et al. 2013; Fajardo et al. 2014). *In silico* PCR was performed using primers sets for all previously published SSR markers in Geneious 6.1 (Kearse et al. 2012) to locate and remove all scaffolds containing SSRs which had been previously identified and developed (Boches et al. 2005; Georgi et al. 2011; Zhu et al. 2012; Georgi et al. 2013; Liu et al. 2014).

The remaining 237,651 remaining scaffolds were subjected to an SSR search using SSR locator with parameters set to identify motifs with repeat lengths di ≥ 9, tri ≥ 6, tetra ≥ 5, and penta through hexa ≥ 4 (da Maia et al. 2008), which resulted in7557 microsatellite containing scaffolds. WebSat (Martins et al. 2009) was used to design primer pairs for all SSR loci identified above and from an additional set of 7772 EST-SSRs previously identified, but not developed or validated, (Polashock et al. 2014) using. WebSat was used for primer design because it allows the user to visually inspect each loci to ensure that only one SSR primer pair was designed per scaffold; to redesign or discard all primer pairs containing a mononucleotide repeat of 5 or more; and to prevent possible fragment size homoplasy before primer synthesis by discarding all primer pairs with predicted PCR products containing a mononucleotide repeat of 6 or more. Major parameters selected for primer design included primer length of 19 to 25 bp (optimum 22 bp), PCR product length varying between 120 and 325 bp, GC content between 40% and 80%, and an optimum melting temperature of 55ºC. All polymorphic EST-SSRs were annotated using Blast2Go (Conesa and Götz 2008).

PCR Amplification and Fragment Analysis

Prior to synthesis, all SSR forward primers were appended with the M13 sequence (5'-CACGTTGTAAAACGAC-3') to allow for indirect fluorescent labeling of PCR products (Schuelke 2000). The PIG sequence (5'-GTTTCTT-3') was appended to the reverse primers to promote uniform non-templated "A" addition and to facilitate downstream genotyping (Schlautman et al. 2014). PCR reactions were performed in 8ul total volume using 3.5 µl 1x JumpStart REDTaq ReadyMix (Sigma, St. Louis, MO), 1.0 µl of 15 ng/µl DNA, 2.0 µl of ddH_2O, 0.5 µl of 5 µM forward primer, 0.5 µl of 50 µM reverse primer, and 0.5 µl of 0.5 µM M13-FAM, M13-HEX, or M13-NED primer.

Thermocycling conditions included a 3 min melting step of 94ºC, followed by 33 cycles of 94ºC for 15s, 55ºC for 90s, and 72ºC for 2min, and a final extension step of 72ºC for 30 min. 1.0 µl each of FAM, HEX, and NED labeled PCR product was mixed with 10ul formamide and a carboxy-X-rhodamin (ROX) ladder, and the pool-plexed mix was sent to the University of Wisconsin Biotechnology Center DNA Sequencing Facility for fragment analysis using a ABI 3730 fluorescent sequencer (Pop-6 and a 50cm capillary array; Applied Biosystems, Foster City, CA, USA). Allele genotyping was performed using the GeneMarker software v 1.91 (SoftGenetics LLC, State College, PA, USA).

Validation of SSR Polymorphism and Genetic Diversity Analysis

An initial polymorphism screen of all designed primers was performed using four cranberry cultivars ('Crimson Queen', 'Mullica Queen', 'Stevens', and 'Ben Lear'). The 507 primers that amplified allele patterns consistent with single locus segregation and that displayed polymorphism between Crimson Queen and Mullica Queen were used in a subsequent genetic diversity screen which included the remaining 9 cultivars in the study and in a segregation analysis using the 16 experimental hybrids (Table 1.1).

The observed number of alleles (N_A), expected number of alleles (N_E), observed heterozygosity (H_O), and expected heterozygosity (H_e) were calculated for each polymorphic locus in GenAlEx 6.4 (Peakall and Smouse 2006). In addition, the polymorphic information content (PIC) for each locus was calculated using Cervus 3.0 (Slate et al. 2000). Chi-Square tests were used to analyze allele segregation of the 507 loci in a panel of 16 hybrid progenies (Table 1.1). Finally, principal coordinate analysis (PCoA) was performed with all polymorphic loci and all 29 individuals based on pairwise genetic similarity distances, which are equivalent to Euclidean distances, as estimated by the Eigen procedure of GenAlEx 6.4 (Peakall and Smouse 2006).

Conclusions

An extensive number of microsatellite primers located in transcribed and genomic regions were validated for *V. macrocarpon*. The 697 polymorphic loci identified, 507 which were included in genetic diversity and segregation analyses, constitute the most comprehensive set of molecular markers developed in cranberry to date. The collection of microsatellites presented herein is a substantial addition to the various molecular tools previously available. They should have immediate impacts in cranberry breeding programs which use these SSRs and their genomic locations to identify QTL and the genetic architecture of various agronomic traits. However, the long term impact of this research may be

much broader by promoting studies of population genetic structure and comparative genomics within and outside cranberry aimed at increasing knowledge about the evolution and adaptation of unique characteristics in the *Vaccinium* genus and the Ericaceae family.

Acknowledgments

Rom. 8:31-39. This research was supported by funds from the National Science Foundation (DBI-1228280), Wisconsin State Cranberry Growers Association, Cranberry Institute, WI-DATCP (SCBG Project #14-002), and USDA-ARS (project no. 3655-21220-001-00) provided to J.E.Z. and S.A.S.

Table 1.1. Cranberry (*Vaccinium macrocarpon*) genotypes used in the simple sequence repeat (SSR) diversity and SSR segregation analyses, their source, pedigree information, and release data. Pedigree information includes either the genotype's parents if it is a hybrid or the location where the clone was found if it is a native selection. The release date of native selections is the date the clone was found. Native selections are indicated with an "*".

Status	Name	Source	Pedigree	Release Date
Cultivar	Stevens	NCGR (PI 614078)	McFarlin * × Potters Favorite *	1950
Cultivar	GH1	E. Grygleski, Wisconsin	McFarlin * × Searles *	2004
Cultivar	Ben Lear *	NCGR (PI 554983)	Native Selection, WI, USA	1901
Cultivar	Crimson Queen	Rutgers University	Stevens × Ben Lear *	2006
Cultivar	Demoranville	Rutgers University	Franklin × Ben Lear *	2006
Cultivar	Franklin	NCGR (PI 554998)	Early Black * × Howes *	1950
Cultivar	Howes *	NCGR (PI 614076)	Native Selection, MA, USA	1843
Cultivar	Lemunyon *	NCGR (PI 554985)	Native Selection, NJ, USA	1960
Cultivar	Sundance	UW-Madison	Stevens × Ben Lear *	2011
Cultivar	HyRed	UW-Madison	Stevens × Ben Lear *	2003
Cultivar	LoRed	UW-Madison	Stevens × Ben Lear *	Unreleased
Cultivar	Mullica Queen	Rutgers University	(Howes * × Searles *) × LeMunyon *	2007
Cultivar	BG	E. Grygleski, Wisconsin	Beckwith × GH1	2012
Progeny	CNJ02-1-159	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-160	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-161	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-162	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-163	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-164	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-165	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-166	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-168	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-169	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-170	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-173	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-174	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-175	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-176	Rutgers University	Mullica Queen × Crimson Queen	Unreleased
Progeny	CNJ02-1-178	Rutgers University	Mullica Queen × Crimson Queen	Unreleased

Table 1.2. Cranberry (*Vaccinium macrocarpon*) genetic diversity statistics by motif length based on 13 cultivars genotyped using 507 polymorphic simple sequence repeat (SSR) loci.

Motif Length	Number of Loci	Total Na	Average N_A	Average N_E	Average PIC	Average H_O	Average H_E
Dinucleotide	427	1983	4.64	3.24	0.59	0.72	0.63
Trinucleotide	72	272	3.78	2.87	0.51	0.67	0.58
Tetranucleotide	1	5	5.00	2.27	0.51	0.62	0.56
Pentanucleotide	7	18	2.57	1.85	0.37	0.66	0.45
Total	507	2278	4.49	3.17	0.57	0.72	0.62

Note: N_A = number of alleles; N_E = Effective number of alleles; PIC = polymorphic information content; H_O = observed heterozygosity; H_E = expected heterozygosity.

Table 1.3. Cranberry (*Vaccinium macrocarpon*) genetic diversity statistics by motif type based on 13 cultivars genotyped using 507 polymorphic short sequence repeat (SSR) loci.

Motif Type	Number of Loci	Total N_A	Total N_E	Average N_A	Average N_E	Average PIC	Average H_O	Average H_E
AC/GT	30	130	92.76	4.33	3.09	0.57	0.71	0.60
AG/CT	141	650	456.31	4.61	3.24	0.59	0.74	0.64
AT/AT	10	53	38.54	5.30	3.85	0.67	0.61	0.71
CA/TG	38	142	93.89	3.74	2.47	0.46	0.60	0.52
GA/TC	202	979	680.26	4.85	3.37	0.60	0.75	0.65
TA/TA	6	29	23.13	4.83	3.86	0.66	0.73	0.71
AAC/TTG	2	4	3.73	2.00	1.87	0.35	0.54	0.46
AAG/CTT	8	39	27.03	4.88	3.38	0.62	0.71	0.66
AAT/ATT	6	24	18.05	4.00	3.01	0.54	0.66	0.58
ACA/TGT	1	2	1.90	2.00	1.90	0.36	0.46	0.47
AGA/TCT	12	50	42.58	4.17	3.55	0.58	0.80	0.65
AGC/GCT	2	6	3.99	3.00	2.00	0.41	0.64	0.47
AGG/CCT	1	2	1.99	2.00	1.99	0.37	0.77	0.50
CAA/TTG	5	14	10.46	2.80	2.09	0.40	0.66	0.48
CAG/CTG	1	4	2.25	4.00	2.25	0.51	0.62	0.56
ATG/CAT	2	4	3.95	2.00	1.98	0.37	0.85	0.49
CCA/TGG	3	8	5.52	2.67	1.84	0.36	0.43	0.42
CTA/TAG	1	2	2.00	2.00	2.00	0.38	1.00	0.50
GAA/TTC	9	41	30.30	4.56	3.37	0.55	0.57	0.60
CTC/GAG	1	3	2.77	3.00	2.77	0.57	0.92	0.64
ATC/GAT	2	6	5.00	3.00	2.50	0.51	0.85	0.60
GCA/TGC	3	9	6.24	3.00	2.08	0.43	0.54	0.51
GTA/TAC	2	10	8.20	5.00	4.10	0.72	0.85	0.76
CAC/GTG	1	2	1.74	2.00	1.74	0.34	0.31	0.43
TCA/TGA	2	6	4.35	3.00	2.17	0.46	0.65	0.54
GGA/TCC	3	6	5.54	2.00	1.85	0.35	0.53	0.45
TCG/CGA	1	3	1.89	3.00	1.89	0.42	0.62	0.47
TAA/TTA	4	27	17.41	6.75	4.35	0.65	0.65	0.74
TATG/CATA	1	5	2.27	5.00	2.27	0.51	0.62	0.56
AAAAT/ATTTTT	1	3	1.75	3.00	1.75	0.39	0.54	0.43
AAACA/TGTTT	1	3	1.48	3.00	1.48	0.29	0.38	0.32
AAACT/AGTTT	1	2	1.95	2.00	1.95	0.37	0.69	0.49
CACCT/AGGTG	1	3	1.70	3.00	1.70	0.35	0.38	0.41
GTTTG/CAAAC	1	2	2.00	2.00	2.00	0.38	1.00	0.50
TTGGT/ACCAA	1	3	2.05	3.00	2.05	0.46	0.62	0.51
TTTTA/TAAAA	1	2	2.00	2.00	2.00	0.38	1.00	0.50

Note: N_A = number of alleles; N_E = Effective number of alleles; PIC = polymorphic information content; H_O = observed heterozygosity; H_E = expected heterozygosity.

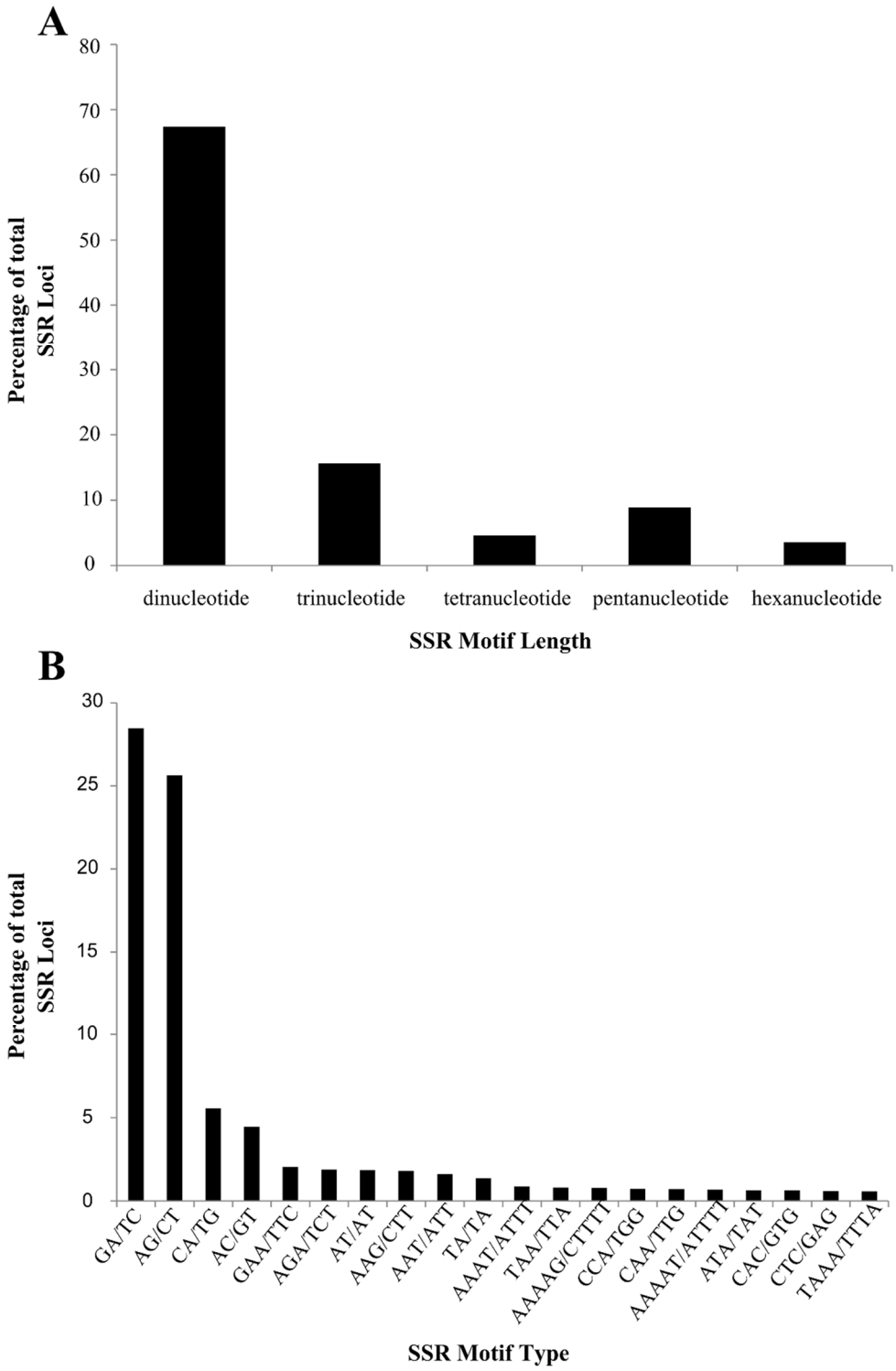

Figure 1.1. (A) The percentage of (*Vaccinium macrocarpon*) simple sequence repeat (SSR) loci identified using SSR locator by motif length and **(B)** by motif type when the motif type represented more than 0.5% of the total detected loci.

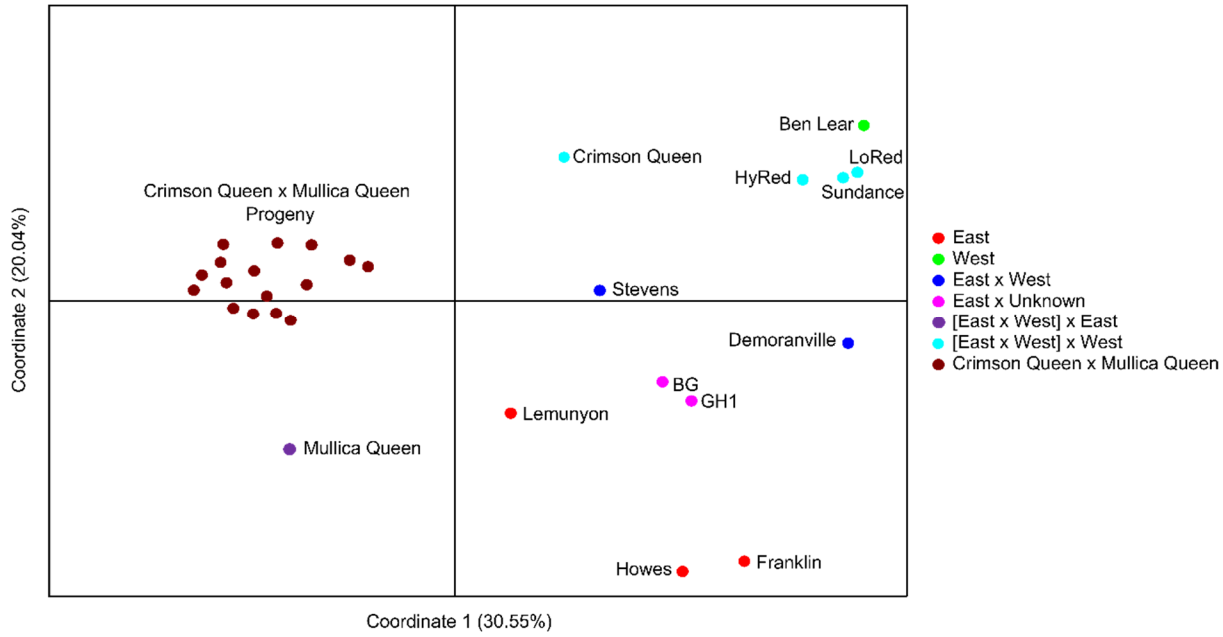

Figure 1.2. Principle Coordinate Analysis (PCoA) based on 507 microsatellite markers tested and validated on a panel of 13 cranberry cultivars and 16 Crimson Queen × Mullica Queen Progeny. Genotypes are color-coded based on the similarity of the geographic origins of their pedigrees (*i.e.*, geographic origins are specified as either east, west, or a combination of east and west of the Appalachian Mountains due to artificial selection).

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Appendix I-1. Primer characteristics, diversity statistics, and segregation analysis statistics of 95 polymorphic EST-SSRs tested on a diversity panel of 13 cranberry cultivars and 16 progeny from a 'Crimson Queen' x 'Mullica Queen' cross.

Primer ID	Motif	Primer Sequences (5'-3')	Allele Range	Description of Putative Function	GenBank Accession Number	Heterozygosity				
						NA	NE	HO	HE	PIC
121633_K63	(CT)18	F:GCAGCTCTCTGTAAATTCCTT R:ATGGTTGAAGATGTTGATGG	288-333	hypothetical protein POPTR_0004s16460g	KP279163	6	4.76	1	0.79	0.76
128239_K63	(GA)19	F:AAATAACGATGGCTACATCC R:GTTTGTTGATGACAATCCTG	185-207	dna-directed rna polymerases iv and v subunit 3-like	KP279164	6	3.52	0.85	0.72	0.67
162108_K70	(GA)15	F:GAAGTCGAAACCCTAGCAG R:GTCCCTCTCAGTCTCTCACTC	285-318		KP279200	7	4.57	0.92	0.78	0.75
16720_K63	(TC)17	F:CTACCTTTCCCTCTCCTTGT R:AGTTGAAGCTGAGAATTGTACC	164-185	cellulose synthase-like protein e1-like	KP279159	6	4.51	0.85	0.78	0.74
172672_K70	(GA)16	F:GATAGTTGTATGCGCTGTAAGA R:GTTACCCGAATGAACAGGT	325-356		KP279201	8	5.83	1	0.83	0.81
187382_K70	(TC)16	F:CCTCCATTCTCTCTCCTACTAA R:CGTTTCTTTTCTTCTCTCTCTC	240-252	probable receptor protein kinase tmk1-like	KP279202	7	5.83	1	0.83	0.81
198358_K70	(AG)14	F:AATCGTCTGTTGCTCAATGT R:AACCATACTTACCACAACCAGT	313-362		KP279203	5	3.05	0.62	0.67	0.62
1TRIMCONTIG175770	(CT)16	F:GTGTAGCTTGGAAAATAGGAGT R:ACTAGGGAGCGAGAGAGAGTA	327-346	tonoplast monosaccharide transporter2 isoform 1	KP279220	6	4.83	1	0.79	0.76
1TRIMCONTIG176042	(AGA)13	F:CCGTTGTTGTTCTTCTGTAGT R:TTCAACCTCTGAAGCCTCT	226-234		KP279221	3	2.18	0.62	0.54	0.46
1TRIMCONTIG176303	(AG)14	F:GCTGATTAGGTTCACTTTCTTC R:TTTCTTCACCTCTTTCTCTCTC	190-196	shock protein src2	KP279222	4	2.99	0.85	0.67	0.6
1TRIMCONTIG176861	(TC)16	F:ATGGATGTATCTTGACAGGC R:CTGCTGTTCATTTCTCTGTG	131-183		KP279223	8	6.26	1	0.84	0.82
1TRIMCONTIG178358*	(GA)15	F:AATTGAACGATCCCTATTCC R:GATTCATCACCCCTTGAAC	224-249		KP279224	7	4.69	0.77	0.79	0.76
1TRIMCONTIG179737	(CT)16	F:CCTCCAACTTCTTCATCTTCT R:ACTGGTAACTCCTCAGAAACAG	204-220	PREDICTED: uncharacterized protein LOC102600962	KP279225	5	4.76	1	0.79	0.76
1TRIMCONTIG182430*	(AG)14	F:GAAGATGGACCTGAGTAAGAAA R:CTACCATTGTGTTCTCAAACTG	184-194		KP279226	4	2.62	0.69	0.62	0.56
1TRIMCONTIG209220	(TC)16	F:GTATTTGTTCACACTCACCAGA R:ACAGTTGTCGAAGCCTCAT	387-421		KP279228	7	4.36	0.92	0.77	0.74
1TRIMCONTIG217158	(GAA)14	F:GGAGTCGGTAAAATCAAGAA R:CCAAATTCAGTAGGAGTACACA	154-169		KP279229	4	3.22	0.46	0.69	0.64
1TRIMCONTIG237406	(GA)15	F:TCTTAGGAAAGACGAGAACATC R:GAAAGGAAGGTATGCTACAGTT	314-342		KP279230	6	3.6	0.67	0.72	0.69
1TRIMCONTIG238080	(AAG)13	F:AGGGGTAATCTTCACACACTTA R:ACAGGCTCTTCTAATCGTTTC	403-423		KP279231	5	4.57	0.69	0.78	0.75
1TRIMCONTIG238343	(TG)15	F:GGTAATAGCTTTGTGATCTTGC R:GATGGTGAATAAATTGCGAC	291-329		KP279232	6	4.07	0.85	0.75	0.72
1TRIMCONTIG238795	(AG)14	F:AGAGGGAGAGAAGAGTATGGTC	262-287		KP279233	4	2.79	0.85	0.64	0.58

1TRIMCONTIG239742*	(GA)19	R:CCGTCAAGATTTGTGAAGAT F:AACAAGAACAACTAAGACCACC	270-290		KP279234	7	4.39	0.85	0.77	0.74
1TRIMCONTIG326802	(AG)14	R:TACAAGTTTCAATCAGCCCT F:TTTTCAGAGCAAGAGGAAAG	201-221	casp-like protein rcom_0464280-like	KP279235	7	5.93	1	0.83	0.81
1TRIMCONTIG328266	(GA)15	R:CTGTCTGTATCATGGAACTCAT F:ACAGATCAAGCGAACACTAAAC	235-274	pto-interacting protein 1	KP279236	6	4.17	0.85	0.76	0.73
1TRIMCONTIG332949	(AG)15	R:CCTGCTCCTGTTATACTACCAA F:ACCCAAACACAAAAGAACAG	306-349		KP279237	7	5.28	0.85	0.81	0.78
1TRIMCONTIG332960	(GA)14	R:GACTGCAAGTGTCTAAATGCT F:GTCAACAGATTCAACACAACAC	242-262		KP279238	5	2.78	0.73	0.64	0.6
1TRIMCONTIG337780	(TC)14	R:CCTGCTTCTCTCTAATGAAGTC F:CTTGATCTTGTCGCTGTAGAC	348-364	udp-d-apiose udp-d-xylose synthase 2	KP279239	6	5.45	1	0.82	0.79
1TRIMCONTIG339726	(GA)17	R:TTCCTTATCGAAATCACGAG F:TACTCATGTCGAAGCAATAGAG	191-199	low quality protein: uncharacterized loc101228446	KP279240	5	2.14	0.54	0.53	0.5
1TRIMCONTIG344502	(AG)16	R:CTTTAGCAGAGGAGAAACAAGT F:TGGAAATGGAAAAGTCTCTG	145-165		KP279241	4	2.91	0.67	0.66	0.6
1TRIMCONTIG351427	(AG)17	R:CACCGTCTACAGTTTAAGAACA F:GACGGCTAAATTGTAACTAACG	220-245		KP279242	7	5.28	0.92	0.81	0.79
1TRIMCONTIG352078	(TC)14	R:AGGGTCCTATCCTATCCTCTAA F:CGTGTTTCTGTTAGATAGCTTG	223-229		KP279243	4	3.65	1	0.73	0.68
1TRIMCONTIG435620	(GA)17	R:CTTGTACGTGAAGATGCAAA F:CAACCAGCCTTACAGTGAATA	235-263	dual specificity protein phosphatase dsp8	KP279244	8	5.54	0.92	0.82	0.8
1TRIMCONTIG436904	(AAT)16	R:GTCCGTTCAATTTCTTTTCC F:TACCAACCACATCACACATC	237-255	thaumatin-like protein	KP279245	5	3.63	0.85	0.72	0.69
1TRIMCONTIG439466	(TC)16	R:CTTATGACGATCCCAGTAGC F:CGAGTGGATAGTGATGATATTG	278-341		KP279246	8	3.35	0.77	0.7	0.66
1TRIMCONTIG439861	(TC)15	R:ACCAAGAGGAACTACAGGTAAA F:CTCCTCTCTCGAATGACACTAC	246-272		KP279247	5	2.84	0.77	0.65	0.61
1TRIMCONTIG440008	(AG)15	R:TTCTTGTTGGCTGGAGATTA F:GCAACAGGGACAGATATTTT	179-195		KP279248	6	3.38	0.69	0.7	0.66
1TRIMCONTIG440230	(AGA)12	R:TACGGACTCATAGAAGGTTAGG F:ACACTTTGTAGGTGGTGGTTAT	235-243		KP279249	4	3.56	0.77	0.72	0.67
1TRIMCONTIG440337*	(TC)15	R:ATTAGCAGTAGTCCAATCGGT F:CTTGGAGTTAGCCTTTTAGTCA	153-182	alpha-galactosidase-like	KP279250	6	4.23	0.85	0.76	0.73
1TRIMCONTIG443603	(GA)15	R:CTGGAAGAGTGAAGATGGAATA F:TGCACCTCCTCTCTCTCTAA	147-151	probable inactive receptor kinase at1g48480	KP279251	3	2.21	0.62	0.55	0.49
1TRIMCONTIG444344	(TC)18	R:GGTTATGATGGTGGGAAAG F:CTGCTAATGTTGTTTGTTGC	253-270		KP279252	6	4.83	1	0.79	0.76
1TRIMCONTIG450309	(TCC)11	R:TATTATCTCCCACCTAATGAGC F:AAAATCAGAGGGAAGAAAGC	144-147	ethylene-responsive transcription factor	KP279253	2	1.99	0.58	0.5	0.37
214102_K63	(TG)15	R:TATTAGCCAGTCCTCCTTTGTA F:GGTAATAGCTTTGTGATCTTGC	219-256		KP279165	5	3.63	0.69	0.72	0.69
242569_K70	(AG)15	R:GATGGTGAATAAATTGCGAC F:GATATGAGAGACGAGGAATCAC R:GTCAGTGGACGGTTTTAAGAT	298-308	octicosapeptide phox bem1p family protein isoform 1	KP279204	6	3.67	1	0.73	0.68

251788_K63	(AG)18	F:GATCTTTACCACTCCCCACT R:GGATTCTCTGTCCATTGTTG	190-208	o-fucosyltransferase family protein isoform 1	KP279166	6	4.69	0.92	0.79	0.76
252600_K70	(AG)14	F:CTAGTTTAGAGTCGTCCCAAAT R:AAGCACCTGAAGATAGTAGGAA	204-212	tetratricopeptide repeat protein 38	KP279205	4	2.23	0.75	0.55	0.51
260167_K70*	(TC)15	F:TCAACATCTTTGGGACTTCT R:GCTTGCCTAATATACTTCCAAC	274-287		KP279206	5	3.45	0.77	0.71	0.66
281884_K70	(AG)17	F:TCCACTATCTTTAGAATCCCAC R:AGAGGATGGAGTTCCTTGATA	330-357	probable u6 snrna-associated sm-like protein lsm1	KP279207	6	3.71	0.85	0.73	0.69
29080_K63	(TC)14	F:ATGAAAACAGGGTAAACTGG R:TCTCAACTCATAGAACTACGGA	384-399	probable gpi-anchored adhesin-like protein pga55 isoform x1	KP279160	6	3.45	0.92	0.71	0.66
297265_K63	(CT)14	F:GATCGTCATAACTAAGCTGGAT R:GTCTCGAATCACAACAGGATA	331-343		KP279167	5	1.98	0.54	0.49	0.47
300409_K63	(CT)16	F:GGGGAATAGCAGGTAGTGAT R:TATTTATCCACCCACTTCACAG	218-235		KP279168	5	4.39	0.77	0.77	0.74
305731_K63	(CT)16	F:GATTTCTTCGTGTTTCTCTCTC R:TGCCTTTCTCTACTCTCTCTTC	379-391		KP279169	7	3.93	0.85	0.75	0.72
307018_K70	(AG)20	F:TAAAACCTTACCTCCTCTTCTG R:TAACCTCGGATCTCCTTATCTA	217-232		KP279208	6	3.6	0.92	0.72	0.69
308539_K70	(GA)14	F:CTAAATTCTCAACATCTCTGGC R:CCAAGAAGCATAAGGGATAGT	304-313	e3 ubiquitin-protein ligase sinat3-like	KP279209	4	3.56	1	0.72	0.67
308812_K70	(TC)15	F:GAAAGGAAGGTATGCTACAGTT R:TCTTAGGAAAGACGAGAACATC	316-344		KP279210	7	5.28	0.92	0.81	0.79
308839_K70	(TC)16	F:ATAATGTGTCCAGTCCCTTTC R:TTCCTTCCTCAATCCACTC	292-313		KP279211	5	3.48	0.85	0.71	0.66
309084_K70	(AG)16	F:CTTCTTTTCCTCTCCACTGATA R:CTCTCCGTTGTCCATTTCT	389-400		KP279212	5	2.91	0.54	0.66	0.61
309124_K70	(GA)15	F:AAAGGTCGTTAAGGCTATCAG R:TGATGACTGCGATATGTACTCT	157-177	nucleic acid binding related	KP279213	8	6.15	1	0.84	0.82
311291_K70	(TC)14	F:CTTGATCTTGTCGCTGTAGAC R:TTCCTTATCGAAATCACGAG	287-303	udp-d-apiose udp-d-xylose synthase 2	KP279214	7	6.04	1	0.83	0.81
313711_K70	(TC)16	F:CGACTTAATCCCTCTCTTTCTA R:CTTTACTTTTCCATCTCCCTC	321-340	beta- -mannosyl-glycoprotein 4-beta-n-acetylglucosaminyltransferase-like isoform x2	KP279215	5	3.98	0.77	0.75	0.71
313928_K70	(GA)15	F:CAATTATCAAGGAGGCAATC R:TCACAAATGAGGATCTACACAC	204-224	photosystem ii 5 kda chloroplastic-like	KP279216	6	3.22	0.85	0.69	0.66
314402_K70	(GA)17	F:TGGAAGAACTCGATACGAAC R:GAGAAGTTGGATACTGGAAATG	154-170	30s ribosomal protein chloroplastic-like	KP279217	6	3.41	0.77	0.71	0.67
314761_K63*	(CT)14	F:ATTGTTGGATACTTCATGGC R:GTTGGTACTGGTAAACCCTAAT	137-197	hypothetical protein VITISV_008952	KP279170	8	5.54	0.85	0.82	0.8
314797_K70	(AC)14	F:CTTGTTCTCCTCCTTTAGTCTG R:CATCTTCATACTCCTATTGTCG	201-217		KP279218	5	3.16	0.85	0.68	0.65
314831_K70	(GA)14	F:ATCTCTCGTGCCTGTCATAC R:CTTTTCGATGTCGTACTTGTC	159-169	syntaxin-71-like	KP279219	4	2.89	0.85	0.65	0.6

1Trimcontig191066	(TCT)13	F:GATATTAGTCCGGTTTACGAGA R:GATACAGGAGTCGAGAATGAAT	290-309		KP279227	5	4.39	0.85	0.77	0.56
319429_K63	(GA)17	F:GGAGATAGGAAGTGTGATGAAC R:TTATTGTGCAAGCATACGAG	180-194		KP279171	6	2.86	0.69	0.65	0.62
354699_K63	(TC)15	F:GAAGCGATTTGGAAGAAAC R:ACACAGAGAGATTACGAACACA	172-191		KP279172	7	5.12	1	0.8	0.78
364103_K63	(TC)17	F:TACAAACCCTAAGCTCTAAACC R:CGACTTGAGTGATACCAAAGA	184-202	nicastrin isoform x2	KP279173	3	2.3	0.85	0.57	0.47
372875_K63	(TC)18	F:CACACACAAATCCCAATTTC R:GATGGTGTTTTCATAGTTCGAC	198-228	pentatricopeptide repeat-containing protein at1g16830	KP279174	6	3.31	0.77	0.7	0.65
407841_K63	(AG)17	F:TTGAGTAGATACATGCTGGCT R:CTCACCCTTTCTCTTGTGATA	274-294	tyrosine-specific transport	KP279175	6	4.76	1	0.79	0.76
408825_K63	(AG)16	F:GTTCTCCTCTTTCATCATTCAG R:AGTCTTGAACTCCTTGTACTCG	262-286	ankyrin repeat-containing	KP279176	6	3.93	0.92	0.75	0.71
409500_K63	(CA)22	F:GATTCCTGGGTGTAGTTCTGT R:CTTAGTCTTTAATGCTGGCTCA	333-395	pentatricopeptide repeat-containing protein at1g08070-like	KP279177	6	3.48	0.85	0.71	0.68
409618_K63	(CT)14	F:CTTCTCCTTCCCTTCACTTTA R:TTAGTGTTAGTGTTGGTGTTGG	249-287		KP279178	6	5.28	0.92	0.81	0.78
411145_K63	(CT)16	F:GGTAGGAATTAAAGTGAAGACG R:ACTAGGGAGCGAGAGAGAGTA	370-389	tonoplast monosaccharide transporter2 isoform 1	KP279179	6	4.83	1	0.79	0.76
411348_K63	(GA)18	F:AATTACCAATGTTCACTCCG R:GTTGATGTAGTTCTGTGGTTGA	266-283		KP279180	9	5.54	0.83	0.82	0.8
411475_K63	(AG)15	F:GCAACAGGGACAGATATTTT R:TACGGACTCATAGAAGGTTAGG	179-199		KP279181	7	4.39	1	0.77	0.74
412234_K63	(AG)17	F:GTGCAAGCCGTTTCTTATG R:ATCGGAGGTTCCATCATTTA	147-155		KP279182	4	3.41	0.92	0.71	0.65
414791_K63	(GA)17	F:ACGACTAGCAGCATTCAGTAA R:CAGGAGATCAGAAAACACAATC	335-362	PREDICTED: uncharacterized protein LOC104588813	KP279183	8	5.73	0.92	0.83	0.81
416275_K63	(TC)15	F:GGTTATGATGGTGGGAAAG R:TGCACCTCCTCTCTCTCTAA	195-197	probable inactive receptor kinase at1g48480	KP279184	2	1.31	0.27	0.24	0.21
416328_K63	(AG)21	F:GTATGCCCAGAATATCCATTAC R:TAGTCACGAGGAAAGCTAAAGT	167-225	chaperonin-like protein	KP279185	7	4.33	0.77	0.77	0.74
416815_K63	(GA)17	F:CGTTTCTTTTCTTCTCTCTCTC R:CCTCCATTCTCTCTCCTACTAA	240-252	probable receptor protein kinase tmk1-like	KP279186	4	3.1	0.55	0.68	0.62
417587_K63	(AG)19	F:TGGGTAGATATTAGATGGCAGT R:CTTCTTCTGGAAATCTGGTTAG	238-275		KP279187	7	6.26	0.85	0.84	0.82
417854_K63	(CT)17	F:AAAAGGAGTCTTGGGAGTAAGT R:TTGAGATGTAACTATGCAGTCC	271-297	50s ribosomal protein chloroplastic-like	KP279188	7	3.48	0.85	0.71	0.68
418294_K63	(AG)18	F:CAAGAACAAGAAGAAGAAGACC R:AGAGACCACCCAAAAGATAAG	336-348		KP279189	6	4.76	1	0.79	0.76
418596_K63	(CT)17	F:CGTGAGTTTGAGTGAGTAATTG R:AGGACATGGTGAGTTGAGAAT	395-401		KP279190	4	3.48	0.69	0.71	0.66
418931_1_K63	(TC)15	F:ATTAGCTCAGTTCCCAGTAACA R:CTTCTTTCTCTTTCTCCTTCCT	165-177	beta-galactosidase 3	KP279191	5	3.28	0.85	0.7	0.64

419834_K63	(TC)16	F:GAAAAGAGAGGAGAAGATGGAT R:TACCAGAACTGTGTGAGATTGT	183-208	probably inactive leucine-rich repeat receptor-like protein kinase at5g48380	KP279192	6	3.52	0.54	0.72	0.67
42710_K70	(AG)16	F:GTTACACACACACCCACAGA R:GAGAGAGGACTAGGTCGTACAG	181-203	wd-40 repeat-containing protein msi2-like	KP279194	4	3.16	0.85	0.68	0.63
47166_K70	(GA)15	F:TATTGAGAGTGTGAGACCGTT R:TGGTAAGTATCGTAGGTCCAAT	310-315		KP279195	3	1.91	0.69	0.48	0.39
482_K70	(CT)15	F:ACAGCGGCATAGTAAAATGA R:GTCACCGAAATCTCACTCAATA	179-192		KP279193	6	5.45	1	0.82	0.79
60699_K70	(CT)19	F:CTTCTCACTGTATTTCTTCGAG R:GGCTACTTTGTTAGGGTAGATT	277-304		KP279196	11	8.05	1	0.88	0.86
71002_K63	(GA)16	F:CTTCAATCCACGAATACCAC R:CAATTATGCAAAGGAGGAAG	235-248		KP279161	8	4.63	0.85	0.78	0.76
76126_K63	(AG)16	F:TTTATTGGAGCGAAAGAGAG R:AAAAGGGGAGGAGAGAGAT	231-242		KP279162	5	3.45	0.77	0.71	0.66
76326_K70	(GA)15	F:AATGTCTTCCAAATCAGGTG R:CAAGAACGAACCCTCTATTTC	279-294		KP279197	6	5.04	0.85	0.8	0.77
80734_K70	(TC)15	F:AGGGAGAACCAATTCCTTAC R:GACCTAACCCTAACCCAGTC	347-373		KP279198	7	5.12	0.92	0.8	0.78
82171_K70	(CT)14	F:TAGTAGAGTTGAAGAGGAGGGA R:CTAGGGTTTAAGCAAGCATAGT	168-185	single-stranded dna-binding mitochondrial	KP279199	6	3.52	0.77	0.72	0.68

Note: * = marker displayed segregation distortion $p < 0.05$

Appendix I-2. Primer characteristics, diversity statistics, and segregation analysis statistics of 412 polymorphic genomic SSRs tested on a diversity panel of 13 cranberry cultivars and 16 progeny from a 'Crimson Queen' x 'Mullica Queen' cross.

Primer ID	Motif	Primer Sequences (5'-3')	Allele Range	GenBank Accession Number	Heterozygosity				
					N_A	N_E	H_O	H_E	PIC
ct106280	(AC)10	F:GCCATAGCTATTTTGTAACGAG R:TATCATGGACTAGGTCTCAACA	216-225	KP279109	3	2.43	0.69	0.59	0.50
ct110752	(TC)14	F:ACACACACTAACGAAATCCTTC R:CTAGCTCCGACATTGTTATCTC	126-141	KP279110	6	4.33	0.85	0.77	0.74
ct115258	(CT)13	F:GTTCGTTGTGGAAGTCACAT R:CAAAATGAGTGCCAGATAGTG	192-207	KP279111	6	4.57	1.00	0.78	0.75
ct116900	(GT)11	F:CTCAAACATACCCTTTGAGC R:GGTATAGCTTAACAACACACCA	166-168	KP279112	4	1.91	0.62	0.48	0.43
ct118602	(TC)9	F:TAGAATGCAGTCGTGAAGTGTA R:ACTAAATGAGGGGTAGTACGTG	152-159	KP279113	3	2.66	0.77	0.62	0.55
ct119523	(AG)11	F:GACTCATGGGAGTGAGGAC R:TGAACTTGTGTAGTCTTTACCG	234-279	KP279114	10	6.63	0.92	0.85	0.83
ct119590	(CT)9	F:ACATGACATCAATTGCCC R:TATCCTACCTCAAAGAGCCTAA	186-189	KP279115	4	2.50	0.67	0.60	0.52
ct120091	(CT)9	F:GTTGAAAGCGACAAGTCTTC R:TAATTTTGCCCTACCCACC	181-183	KP279116	2	1.83	0.39	0.45	0.35
ct121951	(TTGGT)6	F:CATGTAGCCGACTCCAATTA R:TATCCCATTCCGTATAAGGTC	178-193	KP279117	3	2.05	0.62	0.51	0.46
ct124256	(TC)9	F:GCCGTTAGTTCGTGATATGT R:CCTACATGCATACGTAAAACAG	209-214	KP279118	2	1.95	0.69	0.49	0.37
ct129169	(AG)10	F:TAAATCACCTTCTTCCTCCTC R:GGTCCCAAACTTACTACTCAAA	125-133	KP279119	4	3.22	0.77	0.69	0.64
ct129202	(CT)9	F:CGACCTACACGAGATTGTTTAT R:GTTCCAAATCTTCAGTAAGCTG	276-278	KP279120	2	1.99	0.92	0.50	0.37
ct130570	(TTC)6	F:GTTCACAATCTGCATCTCCT R:ACGTAATAGATCAAGAACAGGG	197-200	KP279121	2	1.55	0.31	0.36	0.29
ct132010	(TTTTA)4	F:TACGTGAATTACCCATATCCAC R:CTCACCCTTTACTTCTCTTTGA	203-214	KP279122	2	2.00	1.00	0.50	0.38
ct134336	(TCC)6	F:GAACACTCCTTCTCTAGCTCTG R:CTTTTTAGTCTCCGACAATCTC	195-201	KP279123	2	1.55	0.46	0.36	0.29
ct135942	(TC)12	F:CTACTTGCCTTCCTCTTTGAC R:TAAATAATCCGTCCACGAAC	163-170	KP279124	4	3.43	0.17	0.71	0.66
ct139553	(CT)11	F:GATCAAGCATTGTTCTCTTCC R:AGCTATAGGGCTAGCGATG	123-150	KP279125	5	3.35	0.77	0.70	0.66
ct140233	(GA)14	F:TTACAGAAGGAAGAGAGAGGAA R:ACTGGCTTCTATAGCTCATTTC	224-249	KP279126	7	5.05	0.85	0.80	0.78
ct144370	(TC)11	F:GTAGGAAAAGTTTGAACCGTC R:TCAAAGGTTTCACGTTTCTC	223-237	KP279127	4	3.31	0.77	0.70	0.65

ct144558	(AG)9	F:TCATTACCCCTAACCTCTAAAC R:ATTCGACTAGAGTGGAGAGAAA	223-227	KP279128	3	2.18	0.69	0.54	0.46
ct144936	(AAACT)4	F:AGGTGACTAAGGCAGTGTTC R:CGTGTCTGTTTGGTTAGTAGGT	181-191	KP279129	2	1.95	0.69	0.49	0.37
ct145170	(CTT)12	F:GAATCCTAGCCTATTTCCTTTG R:GAAGCAAACACCACTCAATATC	208-223	KP279130	5	3.38	0.69	0.70	0.66
ct145217	(AT)10	F:CCAGTACTAGATCCACTGCATA R:TGTTCTAGAGAGGATGACATTG	156-165	KP279131	5	3.16	0.77	0.68	0.65
ct145906	(AC)10	F:TCTAGACTTGAGAAGCACTTTG R:AGTTAGAGGAGGTTTCTGTTGA	260-262	KP279132	2	1.55	0.46	0.36	0.29
ct147864	(ATT)6	F:CTCTCTTTACCCTCAATTTCTC R:GGTCTAATATCAATCGATGACC	273-276	KP279133	2	1.26	0.23	0.20	0.18
ct149097	(TCT)6	F:GAACTGACTGAGTCCACAAAAT R:GAACAATAGTAACCCATGCAG	257-263	KP279134	2	2.00	1.00	0.50	0.38
ct152567	(TC)13	F:GTGGCTTTTCTGATCTTGTT R:AAAGTACTCTCAATTGGTACGG	208-226	KP279135	6	4.23	0.85	0.76	0.73
ct153008	(CT)11	F:CTTTCCAAGATCTTCATAGGC R:CGACAGTATAATAGCATGGAGA	257-266	KP279136	3	2.75	0.77	0.64	0.56
ct154206	(CT)14	F:GAGAGCGTACGATACCTAATTC R:CTGGTTAGGAAAACCACTAGAA	198-204	KP279137	4	3.22	0.85	0.69	0.63
ct154615	(CT)9	F:AAAATTGAGCACTGGCTAAG R:CTCATACAAACAATAGGGGG	131-135	KP279138	3	2.00	0.69	0.50	0.41
ct154654	(GA)10	F:GATTTCTAGTGGGAAATGAAGG R:GGTGTATGTGTGTGATTAAGGA	167-171	KP279139	4	2.10	0.62	0.52	0.45
ct155339	(CCA)6	F:AAGTTCCTCTGTTACAAGCTCT R:ATGACGAACTCTTCCTCCTTAT	219-228	KP279140	2	1.99	0.46	0.50	0.37
ct155461	(TG)10	F:GGTTTCAAACTCGAACAAAG R:ATCCTATAACTGGGGATAATGC	258-277	KP279141	4	2.62	0.85	0.62	0.56
ct159707	(CA)9	F:TGTTAGCTCCTTACTTTCCATC R:GTGAAGAGGAAGATGAAGAATG	185-188	KP279142	3	1.59	0.46	0.37	0.32
ct160768	(GTTTG)4	F:GTGTGGTATGTTGGATGTAAAC R:TAAGGGGATTTCATTGGG	139-144	KP279143	2	2.00	1.00	0.50	0.38
ct161908	(TATG)7	F:CCTAGGAGATGGGTCAAGAT R:ACCACTGTCTTCCATATTCACT	156-173	KP279144	5	2.27	0.62	0.56	0.51
ct165512	(CT)9	F:CTTCCTACTCTCTCCCTCTACA R:GTTGGATCTTGATGGGTTTA	128-139	KP279145	3	2.15	0.31	0.54	0.47
ct171223	(TG)9	F:GCGTGTTATTATTCCTCTACCT R:GGTACATTCTTTGACCGAGTAT	152-154	KP279146	2	1.26	0.23	0.20	0.18
ct174735	(TC)14	F:CTTATTTGTATGGCCTTCCT R:GCAGCATATATTGTCCAGTTC	171-194	KP279147	7	5.28	0.92	0.81	0.79
ct188529	(GA)10	F:TTGCAGAATCAATAGTACCTCC R:CCTCATTAGCTATGGTGAAAC	191-232	KP279148	7	2.91	0.85	0.66	0.63
ct89348	(CACCT)4	F:GGCTCAATCTTGTGTAGGTATT R:GAGAAAGTGGAAAGATTGTGTG	184-194	KP279100	3	1.70	0.39	0.41	0.35

ct89379	(TC)10	F:ATGAAGAGCTTGAATGGCTA R:ACACTTTACACCACAACTCGTA	171-183	KP279101	5	4.63	0.85	0.78	0.75
ct89711	(CT)13	F:CTCCACACCCACAATCTG R:CGTCTTATTTTTAGTCACCTGG	137-149	KP279102	5	3.13	0.77	0.68	0.63
ct92708	(TC)10	F:CCCTAGATATTTCTGGAACACT R:AAGATAGAGAGAGACAAAGGAGG	144-152	KP279103	4	3.98	0.77	0.75	0.70
ct93137	(CT)11	F:AAGATTTCCGCTACAGTACCT R:GCTATGGGTGTCTCAAAAAG	177-207	KP279104	5	3.41	0.92	0.71	0.67
ct94504	(AAACA)5	F:CTCTAAAGCTCAAGAAAACGTC R:AGCTGTGACTATAAGGGATTTG	258-268	KP279105	3	1.48	0.39	0.32	0.29
ct95345	(CT)9	F:ACTCTACAAGGGCACGAAC R:ATGGAAGTAAGAAAGTGAGTGG	122-128	KP279106	3	2.09	0.46	0.52	0.44
ct95842	(GA)12	F:GTGGAAAGAGATTGTTGATGTC R:AAAACTAATGGATGACGACG	222-234	KP279107	5	3.22	0.77	0.69	0.64
ct98042	(AAAAT)5	F:CCTTTTAAGTACTTTCCCTTCC R:CCCCTCATCTTTATGTGC	266-272	KP279108	3	1.75	0.54	0.43	0.39
SCF1001	(ACA)7	F:AAACTAGCATATCCCAAGGTAG R:ATATAGCAACAGTGGGCAGT	209-215	KP278595	2	1.90	0.46	0.47	0.36
SCF100820	(TG)10	F:GTAATTCCACTTAACCCACTCA R:GTTGAAGATAAACCACCTTCC	342-353	KP278804	4	2.97	0.62	0.66	0.60
SCF101064	(GT)9	F:CATCAGACAGAAAGCAGTTAAG R:CCCCAAGTATATTAGCAAACAC	296-302	KP278805	3	2.27	0.69	0.56	0.49
SCF101878	(CAA)7	F:GACTCATTGGATACGTGCT R:TCTATGTAGCTTTGAAGTGAGG	343-346	KP278807	2	2.00	0.54	0.50	0.38
SCF101914	(TC)10	F:CTTTGGAGCACAACAACTCTA R:GTGTAAAGACCAGGACCCTT	150-165	KP278806	4	3.17	0.75	0.68	0.62
SCF102347	(AG)12	F:GGTAGTGAGCAACGACATAAC R:CCTGAAGGTAAAGAAAGTAGCA	335-349	KP278808	7	4.94	1.00	0.80	0.77
SCF10459	(TC)11	F:TCTTTGTTTCTGAGGTTGCT R:ATTTGTAGGTACTATGGAAGCC	253-257	KP278631	3	2.36	0.77	0.58	0.50
SCF104688	(GA)10	F:ACAAAGAAATGTATGGCACC R:CTTTTCGTCTCCTCTAATTCC	194-207	KP278809	5	3.27	0.92	0.69	0.49
SCF1047	(AC)10	F:GAGCTTTGGCCTCATATTACT R:CGAATTACTCCAACCAACAT	266-267	KP278596	3	2.27	0.85	0.56	0.49
SCF105092	(AT)11	F:AGGAACTAGGAAGTAGGAAGATG R:GTGCTATACAGGCATACAAGTG	140-176	KP278810	5	3.89	0.31	0.74	0.70
SCF10514	(GA)11	F:GTACTCTTTGTCGGATGTTTTC R:GTTTCACTCCCACCTCTTAAT	240-252	KP278632	4	3.22	1.00	0.69	0.63
SCF105151	(GA)9	F:CAGAATAAGATTGGGTAGAAGG R:TTTGAGAATTACTTGGCACC	284-286	KP278811	2	1.60	0.50	0.38	0.31
SCF105925	(TC)15	F:CCGTGTCAAAAGATCAAGC R:AGTTTGTGCCGTCGTACTC	159-166	KP278812	4	2.70	0.62	0.63	0.57
SCF106182	(GT)11	F:TACCCTTGTGTATCCCTACATT R:GAACAATAGCAGCAACAGAAC	151-153	KP278813	2	1.74	0.46	0.43	0.34

SCF107429	(CT)13	F:ATGTGAGGTGGGATGATATTAG R:ATATGGTGTCAGTGTGGTGTAG	348-378	KP278815	9	7.51	0.92	0.87	0.85
SCF107477	(AG)10	F:GTCTTATTTTCACTGTCGTGTG R:CGGGCATTAACCTTATACCT	190-200	KP278814	5	2.64	0.77	0.62	0.56
SCF107715	(AG)11	F:AAAGCGAGTCAGAAACATAGAC R:CCTATCAGTTCCTTTCCTATTG	244-302	KP278816	7	4.69	0.92	0.79	0.76
SCF10785	(TC)10	F:ACATAAAGGAGAGGGAGTAGAG R:ATACCACTTGATAGATTCCTCC	247-251	KP278633	3	1.49	0.39	0.33	0.30
SCF108252	(TC)10	F:CCTATGTAATTGGATTCTACCC R:GTGTATCAAGGTGGAGAAAGTC	204-208	KP278817	3	2.33	0.77	0.57	0.50
SCF108294	(TC)12	F:GGTAAGATTGAGGTTCTGGTCT R:GGTAGAAGCAAGAAGATGCAC	240-260	KP278818	4	3.05	0.92	0.67	0.62
SCF108454	(TG)9	F:CTAACTAAATGAAGTGTTCCCCT R:ATGTCACGCTCTGAAGTTTG	192-198	KP278819	4	2.50	0.62	0.60	0.52
SCF109269	(TC)11	F:CACTCCTTCCTTATAGATCAGC R:AAGTAGAAGAGCAGCACAAGAG	242-268	KP278820	5	2.27	0.69	0.56	0.51
SCF109660	(GA)9	F:CCCCAAACTGTCGTATAAAA R:TAGAGTACAGGAAAAGCCCTAA	289-291	KP278821	2	2.00	0.54	0.50	0.38
SCF110168	(GA)12	F:AAAGGACTAGAGGGAAGTACAAC R:CTTATTATCCAGAAACTCGTGC	316-347	KP278822	7	4.39	0.92	0.77	0.74
SCF110223	(GA)11	F:GATTCTGTTCCAATAGGCATAC R:GGAGTAGTAGTGAAAGGACCAA	347-371	KP278823	6	5.04	1.00	0.80	0.78
SCF110507	(CT)14	F:GTAGCTGAGGTGGAGGATAAC R:GAGCTGGTGCTGAAATTAAC	221-235	KP278824	5	3.89	0.92	0.74	0.70
SCF11065	(TC)11	F:CTTTGTCCCAACACGTTAAT R:AAGTCTATAAGCATCCTGCAAC	191-193	KP278634	3	1.50	0.40	0.34	0.30
SCF110757	(GA)9	F:TCATATCAACCTAACAATCGG R:CACAAACAAGGAAATTAAGACC	286-342	KP278825	6	1.82	0.46	0.45	0.43
SCF11084	(CT)9	F:GTTGGCTGAGGTAGCTGATAG R:CCTAAAAGGGCTCACAAGTTA	312-316	KP278635	3	1.61	0.46	0.38	0.34
SCF110888	(CA)9	F:CTCCTACCCAAATTCACTTGT R:CCAAAACTAAACCATTTCTCAC	191-193	KP278826	2	1.35	0.31	0.26	0.23
SCF111145	(TA)9	F:TTAGTCTGGCTGGTTTTAGTTT R:TTGTACCTATTGTTGGATTGTG	342-350	KP278827	5	4.08	0.60	0.76	0.72
SCF111370	(AC)14	F:ACCACATCTTCATTTTGAGC R:GTAAAACAATACGGGTCCTTAC	273-284	KP278828	6	3.71	0.92	0.73	0.69
SCF11186	(TCC)9	F:AGAAAGGCTAAAAGGGTATCTC R:GCTCTCAACAACTCGAAAGTA	278-287	KP278636	2	2.00	0.54	0.50	0.38
SCF112295*	(AC)9	F:AACATCTCTACCTCTCACGTTT R:TAGTATTAGTTGATTTGGCGTG	271-273	KP278829	2	1.08	0.08	0.07	0.69
SCF112540	(CT)9	F:CAGTAGTGGTATTTCACAATCG R:TTTAATGCTTTTGGAAGAGG	224-226	KP278830	2	1.26	0.23	0.20	0.69
SCF1128	(AG)13	F:GTTTGTTGTTGTGGTGGTTT R:CCTTACTTGACGCTTACTTCAG	304-322	KP278597	5	3.77	1.00	0.74	0.69

SCF113389	(AC)9	F:GACATCACTCAAGCAAGATAAA R:CCTCGATTCCTCAAGATATG	157-171	KP278831	5	2.70	0.77	0.63	0.58
SCF113558	(TTC)11	F:GAGCTTGATCTGGGTATCTTT R:CAAAATCAGAATCGACTGC	200-206	KP278832	4	2.25	0.39	0.56	0.51
SCF11431	(TC)13	F:GCTGCTGATTTGTTATGTAGAG R:CACTTAGCCCCTTAAACTATTG	306-318	KP278637	5	2.79	0.85	0.64	0.60
SCF116329	(AT)12	F:GAATCCCACATTAGAAGTTGAT R:TTGTATCTTCCCTATTCCTACTG	191-199	KP278833	4	2.62	0.31	0.62	0.56
SCF116485	(CAT)7	F:CAATATAAACGTCAGTCACCAG R:ACTTTTGGTTATGCTGGAAG	226-232	KP278834	2	1.95	0.69	0.49	0.37
SCF116567	(GAT)8	F:GTTGGTCTACAATTCTGTTCCT R:GCCCTTTTAGTTGAAATGC	201-207	KP278835	3	2.75	0.85	0.64	0.56
SCF116864	(AC)9	F:TGCCCCTTGATTCTAATTTT R:ATGCCTCAGATTGATTTACCT	150-154	KP278836	3	2.60	0.77	0.62	0.54
SCF117157	(GA)15	F:GGATAGAAACCTGATACGGAC R:CGTTACCGTCCCAAATATAA	194-204	KP278837	6	5.05	1.00	0.80	0.77
SCF117385	(GA)12	F:TAAGAATCCTCGTCATAGGGT R:CTGTCTTCTCAACTTTCCCTC	145-153	KP278838	4	2.40	0.77	0.58	0.51
SCF117422	(TC)12	F:TTCTGTTTCTTGGCTCTGTATC R:TATTATGCTACATCGGTCGAG	249-275	KP278839	7	3.76	0.77	0.73	0.69
SCF11802	(AAC)8	F:CGAGGAACAAGTTTTATAGGAG R:ACACTCACCTTTATTATGGGAC	290-293	KP278638	2	1.99	0.62	0.50	0.37
SCF118468	(CT)15	F:ATAAGCGGAGCACAGTTACA R:GATAGGATGACCTGTTTTGGT	242-260	KP278840	6	3.49	0.92	0.71	0.67
SCF118608	(TC)14	F:AACTACTCGATCTTCACCCTTA R:AGGAGACCAACACTTAACCTC	239-256	KP278841	6	4.45	0.92	0.78	0.74
SCF118999	(AG)9	F:CTAAACTCCAAAATGCCTAAAC R:AAAGTGGATGGGTTCTAAAAG	272-313	KP278842	5	2.06	0.62	0.52	0.47
SCF120352	(GA)10	F:AGTTCTATGACCCCTAACTGAA R:GAAAGGAAAGAAGCACTATCAC	272-295	KP278843	5	3.89	0.69	0.74	0.70
SCF120937	(GA)13	F:TGTGCAAGAGTCATCTCCTAT R:TATTCCCTTTCATTCTCCTTC	285-305	KP278844	6	4.76	0.92	0.79	0.76
SCF121995	(AC)14	F:TAGTCGTGACCAAGAGTGATTA R:GCCACCGAGTATATTTCTATGT	169-179	KP278845	4	3.63	0.85	0.73	0.67
SCF122746	(TC)13	F:ATTGTATGAAAACCCTAACCC R:GAGACGATTCCAAATATAGCA	191-218	KP278846	7	4.33	0.85	0.77	0.73
SCF123189	(TC)9	F:CCTAGAAATGTTACTCTCCGAC R:TTCACTTCCTTACTCCTTTCAT	191-193	KP278847	2	1.74	0.62	0.43	0.34
SCF124075	(GA)13	F:ATTTTCCCTCCAACCTCTAT R:GGTGCAACCAACTAACATAA	344-362	KP278848	6	4.69	0.85	0.79	0.76
SCF124322	(TC)9	F:TAAAACTGTGAGGTTCAATGTG R:CTTCGTGTCTCAAATTACAAAA	214-235	KP278849	5	4.17	0.92	0.76	0.72
SCF124927	(TG)12	F:CGAGTGTCATTAGCAACAGA R:TATCACTTTAGATCGAGCAGAC	230-236	KP278850	4	2.89	0.85	0.65	0.60

SCF125251	(GA)21	F:TATACAGTCAGATCCAATCCAC R:TGCAGATAAAGTACAAGAGTGC	240-267	KP278851	7	5.28	1.00	0.81	0.79
SCF125667	(CA)10	F:AAGGGAGACATTACACAACAA R:TTCGAGATTGACCAAGTATGT	171-188	KP278852	7	4.45	1.00	0.78	0.74
SCF125889	(GA)17	F:TCTCGTGTATTTTGGAGTGA R:GTTGTATCCTTTGTCGATTCT	175-195	KP278853	6	4.97	0.92	0.80	0.77
SCF126708	(CA)9	F:CGACGAATAAACAAATCAAGTA R:GAGAAGAAGTGAAGGAGAGTTG	315-317	KP278854	2	1.95	0.54	0.49	0.37
SCF127023	(TC)14	F:TATGCTAATCCACTTTGTAGGG R:AATCTGGGTAATTGGGAACT	200-212	KP278855	5	3.67	0.92	0.73	0.69
SCF128015	(TCT)7	F:ACCCACTCTTTCTATTATCTTCC R:GTGAGTTCCAAGTTCCACATA	216-219	KP278856	2	1.90	0.62	0.47	0.36
SCF128307	(TG)14	F:ACTCAGAAGTTGAAGCACAAA R:GTATCAAGTACACCAACACCAG	220-262	KP278857	11	6.15	1.00	0.84	0.82
SCF128992	(TC)11	F:GAGTGTTGAGTTATAGGGGTTT R:TCACAAGAATAGAAGGATGGA	237-239	KP278858	2	1.90	0.31	0.47	0.36
SCF13006	(GCA)7	F:AAAACATAAGAAAGAGCCCC R:GGATGATGATGTATGGGAAT	300-303	KP278639	3	1.81	0.46	0.45	0.38
SCF131915	(AT)9	F:TTTTGTTTCCTTATTTTCGG R:TGTAAGTGCATGAAATCGTAAT	184-223	KP278859	6	4.65	0.83	0.79	0.75
SCF132369*	(TTC)14	F:CTACTTTGGGATGGAGAGAGTA R:AGGTTTAGGTAGTGTTGGATTG	261-292	KP278860	8	5.83	0.85	0.83	0.81
SCF132506	(TCA)10	F:AATGTGCCAAGTTTTGTAGAC R:GTCCCCTATAAGTCATCTGAAA	270-282	KP278862	3	2.30	0.85	0.57	0.47
SCF132532	(AG)12	F:GACTGGATTTTCACGAATCTAC R:CTTCATCTTCCTTGACACTTCT	275-285	KP278861	4	2.30	0.77	0.57	0.50
SCF132595	(AC)13	F:CAAACAAATCTCAACAACACC R:ATTTCAAGATAAGCTCTCCACC	222-277	KP278863	7	4.97	0.92	0.80	0.77
SCF132922	(AT)12	F:TTAGACGCTTTATGTCCATTC R:GAGTGTCCTTGTCTTTGTTGTA	199-256	KP278864	7	4.69	0.62	0.79	0.76
SCF133376	(AAG)9	F:ATTAGCACCGAATTTAACACC R:GATTATGGGTGAGTCTGTGAAT	238-244	KP278865	3	1.62	0.46	0.38	0.35
SCF136207	(CT)9	F:GTCTCTGTAGTCGGTGCTTT R:GATTTCGATTCCTTGACACT	167-171	KP278866	3	2.50	0.77	0.60	0.53
SCF136317	(GA)10	F:GAGAGTTCAAATTACCTGTACCA R:GGAGATTAGGTTGTGGACTAGA	271-277	KP278867	3	1.49	0.39	0.33	0.30
SCF136826	(CA)9	F:GATCTTGATTAGCTCCAACTG R:GCTTACACCAATTCTACAGTCA	267-269	KP278868	2	1.99	0.31	0.50	0.37
SCF13711	(GAG)7	F:GACTTCCTTGGTACTTGGTG R:ACTTTGAGGGTAGGAGTAAACA	348-354	KP278640	3	2.77	0.92	0.64	0.57
SCF137494	(CT)10	F:CCAACATAAAGAGGACTAGAGG R:GACCTAGACTCCAAATCACG	336-397	KP278869	3	1.98	0.31	0.49	0.43
SCF13753	(CT)9	F:AAGTCCTTTCCTTCTTTTGC R:GCTATGTGATGTCGTTCCTAA	195-199	KP278641	3	1.81	0.54	0.45	0.38

SCF13771	(GA)11	F:AGGATGATGAAATCTGCAAG R:ATCAGTTAGGTGGGGTAAGG	171-191	KP278642	6	3.60	0.92	0.72	0.68
SCF138014	(TC)11	F:TTATTCTCTTCGCTTGGGTA R:TCAGATCATGGATTACTGGTT	243-245	KP278870	2	1.45	0.39	0.31	0.26
SCF138394	(GA)11	F:AAGCCCAGAAGAAATAACCTA R:TGCAAATGTTAGGAACTGTGT	218-229	KP278871	4	3.31	0.83	0.70	0.37
SCF138607	(GA)17	F:CATATAGAATACTGGACGGACA R:TTCTGCCATCTCCTTTCTC	203-215	KP278872	4	3.10	0.77	0.68	0.63
SCF138992	(GA)11	F:ATACTTTACCCCACAGAGCTTA R:CCACTCATGCTCACATCAC	227-229	KP278873	2	1.65	0.23	0.39	0.32
SCF139334	(GT)10	F:GAGGGTCTAATATCTGGTTTCA R:GAGAAAAGATGGAGCAAAAG	203-205	KP278874	2	1.08	0.08	0.07	0.07
SCF139660	(GA)12	F:ATAAATCTACGTCCATACAGCC R:GAGTACATACAAATCCTCTTTCG	333-379	KP278875	6	4.45	0.92	0.78	0.74
SCF140628	(GT)10	F:GTGAAATTGGTCAGGTTGAT R:GTCGTCATCATCATCTCCTC	143-154	KP278876	3	2.70	0.77	0.63	0.56
SCF14119	(TC)9	F:TAACAGTACAATGCCTAGTTCG R:GGATTCTCTTGCTTTGGTATAG	243-245	KP278643	2	1.26	0.23	0.20	0.18
SCF141794	(AAG)7	F:CCATCTGCATCTATTGTTTTG R:CATTTGTAGGTCTATCTTTCGC	149-164	KP278877	4	2.27	0.62	0.56	0.47
SCF14189	(TC)9	F:GTCTAGGTGAGGATGGTTGAT R:AAAACAGAGCCCAACAAGT	263-280	KP278644	2	1.35	0.31	0.26	0.23
SCF141985	(AG)11	F:GAATGGTCTTGAGGGATGTAT R:ACTCTGGAAGAAATAAAACGG	180-188	KP278878	5	4.12	0.85	0.76	0.72
SCF142441	(TC)10	F:TTGCGTTTACTATCTAAGGAGG R:CTCAGCCGTCCAAAAGTAT	219-233	KP278879	5	3.63	0.92	0.73	0.68
SCF142664	(AG)9	F:TACTGACGATGAGCTAGAGTTG R:AATGACAAGTGGAATAGTAGGC	247-249	KP278880	3	1.86	0.62	0.46	0.40
SCF142767*	(TC)10	F:ATAGTTGGACGGGTGTAATG R:CTCTCGCAAAGTAGAACAATCT	257-293	KP278881	8	4.51	0.92	0.78	0.75
SCF143035	(AT)15	F:TATTTATAGACGACCAACCTGC R:GTGACCAATATACCAAACCAAG	166-208	KP278882	6	5.28	0.77	0.81	0.78
SCF143318	(GA)12	F:CCGTGCTTAAATTCTGTAGTG R:TCATCCATAGGAGAACATCC	279-300	KP278883	5	3.63	0.92	0.73	0.68
SCF144748	(TC)10	F:ATTTCCAATCCTTTCCTCTC R:CTCTGACACCTTCTGACACATA	151-153	KP278884	2	1.90	0.62	0.47	0.36
SCF145689	(TC)13	F:GGCATAAGAGTAGACCATGAAC R:GTACTATAAAATGCTTCCAGCG	260-277	KP278885	5	2.91	0.69	0.66	0.59
SCF145739	(CT)10	F:AAATCCTCCTGTTTTAGACTCC R:CCTCAAGTCATCATTCCCT	240-242	KP278886	2	1.99	0.46	0.50	0.37
SCF146740	(AC)15	F:ATGGGACTGCTTATTGAACAC R:CAAGTGGTGCATTGTGAGA	202-222	KP278887	6	3.52	0.85	0.72	0.68
SCF147117	(TC)9	F:AGATATGGAGTGGATTAGGTTG R:GTTAGAGTGAAATGAGCCCTAT	240-246	KP278888	3	1.49	0.23	0.33	0.30

SCF147295*	(GA)9	F:ACTGAGGTAAAAGAGGAGTACG R:CCATCAAGGTCTCAATCTGT	199-207	KP278889	3	2.45	0.85	0.59	0.52
SCF147358	(AG)10	F:GTACACTAAACACCTTGCGTTA R:CTCACCTACATCCCTCTAGTTC	211-213	KP278890	2	1.74	0.62	0.43	0.34
SCF149633	(GA)14	F:CCTTAATACCCATCCCATAATC R:CTTCTTTTCATTGTTGTGGC	289-310	KP278891	8	5.54	0.92	0.82	0.80
SCF149976	(TTC)19	F:TATACCCATGTATGTACGCATC R:ACTCTAAGCAGGACAATGCTAT	272-309	KP278893	8	6.26	0.92	0.84	0.82
SCF149989	(AG)11	F:AGTAGGCATTGTTCACTCACTC R:TTTCTCCTAAAGCTAAACTCCC	293-302	KP278892	5	1.98	0.62	0.49	0.47
SCF150173	(AG)12	F:GTGTTGGGAAACAGCAGAT R:TTATTCTCGTTGTCAGCCTT	182-186	KP278894	3	2.07	0.77	0.52	0.42
SCF150898*	(AG)11	F:AAGCTCCATGTATGCGTATC R:ACACTGACTAGCGTTTGTTGT	311-317	KP278895	3	2.05	0.62	0.51	0.46
SCF150919	(AT)10	F:TTGTTAGCACTTAGCATAACCC R:GCTTCATCTCCACCAATACAT	333-363	KP278896	5	4.23	0.85	0.76	0.72
SCF1527	(GA)9	F:TCAAACGGTGACATCTATACAC R:GTATCTACGCCTCTTACTCTCG	241-256	KP278598	4	2.44	1.00	0.59	0.50
SCF153094	(TC)9	F:TGTCATTAGGGTTCCTCAAA R:CACCTAGACAACATCGAAACTA	210-235	KP278897	8	3.45	0.69	0.71	0.69
SCF153636	(TC)14	F:GGTATCAAAGCAAGGTTGAG R:CTCGTTAGAAGTATGTTGGTGA	275-297	KP278898	6	4.57	0.85	0.78	0.75
SCF153722	(TC)11	F:AGTTATGAGGCTTACGAGGAG R:GATGGAACGATGAAACTGAT	263-279	KP278899	4	3.89	0.92	0.74	0.70
SCF154541	(GA)12	F:AGAAAGCACAGTAGGTATGGAG R:CAAGAAACCCTAGAGACCAAT	265-285	KP278900	7	5.12	1.00	0.81	0.78
SCF155637	(AT)13	F:TGTTAGTGTTAGGACCCGTTA R:AAAGTAGGAGTTAGGATGGGAT	206-224	KP278901	6	5.12	0.85	0.81	0.78
SCF155797	(TC)9	F:ATCATTAAGGCTCCCAAAG R:GTACGTCTACTCTGACGGCTA	187-188	KP278902	2	1.83	0.54	0.45	0.35
SCF156807	(CA)9	F:AGGAGGTTTGGACTAGAAGTTT R:CCTGGTTGTCGGATTAGAT	150-161	KP278903	4	2.33	0.31	0.57	0.48
SCF157992	(TTG)9	F:TAGGTTTGTCTCTTATCCATCC R:GAGTTTGTGATTTCTTAGGAGC	266-272	KP278904	3	2.27	0.62	0.56	0.49
SCF158255	(AG)15	F:ATGCGTACACCTCAATCTTT R:GTGGGTACTTGTTTTCAGTTC	300-303	KP278905	4	3.45	0.11	0.71	0.66
SCF15845	(AG)10	F:AGGCTAATGAAGAAGAAGTCTG R:GACCAAGACAAGATGAACAAG	312-328	KP278645	4	2.70	0.77	0.63	0.57
SCF158633	(GA)18	F:AGATGCTGAAGTTTTCCCTT R:TATGTGGATTCTTTGCCTTG	168-195	KP278906	8	4.72	1.00	0.79	0.76
SCF158988	(TC)10	F:CTCTCACCAAAATCACCATTAG R:CAAGTATCAAGTTTTAGACGGG	228-264	KP278907	8	5.45	0.92	0.82	0.79
SCF159195	(CT)9	F:AACAAAGACCCTAATCAGACAC R:ACAATCAAAACACCGTCAG	309-315	KP278908	3	1.91	0.54	0.48	0.39

SCF160647	(GA)10	F:TAACTCAAAGAACCTAACCCC R:TAAAGTGACAGGTAATGTCGTC	162-178	KP278909	5	3.28	0.85	0.70	0.65
SCF160663	(TC)10	F:TTACACCCTATCTCCTGTTTTC R:CAGTTCATCTTGCTAGTTATGC	149-155	KP278910	4	3.05	0.77	0.67	0.62
SCF16166	(AC)15	F:CCTAGTCATTCTTCTACTCCCA R:GGGTTATCTCGTCCATATTGT	307-322	KP278646	7	5.63	0.92	0.82	0.80
SCF161998	(GT)9	F:ATATACCAGTGCTCTTTCCATC R:AGACTTCTTTCTCCAAAGGC	273-275	KP278911	2	1.55	0.31	0.36	0.29
SCF162175	(TC)11	F:ACACGTTGAGGTTCCAAAT R:AGTTTCTGATTGACCTAGATGG	175-179	KP278912	3	2.02	0.54	0.51	0.45
SCF162565	(GTA)10	F:CTTCCGTGATTGTTCTTGTAG R:ACACAGATGGGATGTTGTATC	155-180	KP278913	5	4.23	0.85	0.76	0.73
SCF163134	(AG)12	F:CAGTGCAATTAGTTTCCTATCC R:TTCTTGGGTTGGTTATTCAG	224-233	KP278914	5	2.58	0.62	0.61	0.57
SCF16359	(AG)12	F:GAAGTGCTTTTCTTTCGTAGAG R:AGACAGATTAAGATCCACCTTG	316-328	KP278647	3	2.45	0.54	0.59	0.52
SCF16407	(TC)11	F:GGCAGTGAATTAAAGGTCAAC R:GATGAGAAAGAAGAGTAAGGCA	271-279	KP278648	3	2.09	0.62	0.52	0.35
SCF1648	(TG)10	F:GTTGATCTGAAGGAAACCAA R:TCGTATTAACTCCCCTATTGAC	284-288	KP278599	2	1.83	0.54	0.45	0.35
SCF164915	(AC)12	F:CTCAAAGTATCTCACTCACGC R:ACTGTTGTCCCCTCTGACTAC	191-211	KP278915	6	5.54	0.85	0.82	0.79
SCF167793	(GA)9	F:GTGAAACGACAAGACCAAAT R:AGGACATCCACCTTCAAAT	180-184	KP278916	3	1.59	0.46	0.37	0.32
SCF169090	(TG)10	F:GAGACAAAGTTCAAATAGGGAG R:ATACTGCAACCGATACTGAGA	249-258	KP278917	4	2.94	0.77	0.66	0.60
SCF170213	(TC)13	F:GGGTTTGATGACTTGTTTGTA R:CCTAGAAAATGCAGAAATCG	158-166	KP278918	4	3.07	0.69	0.68	0.61
SCF171621	(CT)12	F:CACCACTCCCCATTTTAAG R:AAGGGACAGAGGAAGTATTTG	196-209	KP278919	6	3.13	0.92	0.68	0.64
SCF172019	(GA)14	F:TGTGAGTAGTTGTTGAAGGGA R:CCTCGAAAATCCGGTAAAT	244-279	KP278920	5	4.39	1.00	0.77	0.74
SCF172027	(CCA)9	F:ACTCCTATTGCCATTCCAC R:CAGTGACAGAGTTGTGGTTAAG	161-173	KP278921	3	1.26	0.22	0.20	0.19
SCF172149	(CT)9	F:GTTAAATGATGCTGTTAGGGAG R:ATGTCCAGTCGTTATCTCTAGG	187-205	KP278922	5	3.41	0.77	0.71	0.67
SCF172906	(GA)10	F:CTGTTCAAGGATTTGTACTGG R:TATTGACATGAGAAGCACGA	167-179	KP278923	3	2.31	0.44	0.57	0.49
SCF173212*	(TC)9	F:TGTAGTGGGAGATGCTGATAC R:AATTGGCGAACTAGAAAGTG	198-206	KP278924	4	2.24	0.69	0.55	0.50
SCF174394	(CT)9	F:GGTGGATGGAATGCTAAATA R:CTTTATTGGTAGTGGATTGGAC	259-263	KP278925	2	1.95	0.54	0.49	0.37
SCF174468	(AG)13	F:CAACATTCTTCGCTCACAA R:CTAAGAGTTGACATGATTGGC	174-178	KP278926	3	2.52	0.77	0.60	0.54

SCF175823	(CT)12	F:AGGGGCAGTTTAGTCCTAGTAT R:GCACGTCTTTTCTGTAGTTCAT	221-231	KP278927	3	2.25	0.85	0.56	0.47
SCF177450	(TC)10	F:TCTAAAACTCTCCTCTCACCTC R:GATAGCAGTGGACTCATGTCT	268-271	KP278928	3	2.17	0.58	0.54	0.77
SCF177451	(AG)10	F:GTACCATATAAGAAAGGGAGCC R:CAATAGAAACCCAAGACAACTC	183-209	KP278929	8	4.76	0.92	0.79	0.77
SCF17979	(TC)17	F:ATATCAGAACAAGGAGATGGTG R:GATACCGAATGAACCAAGAA	210-229	KP278649	6	3.76	0.85	0.73	0.70
SCF180863	(CT)11	F:CCAGTTACAGATCCTTGAGTTG R:GCAATGTTCCCTCGAATTA	169-181	KP278930	4	3.35	0.85	0.70	0.65
SCF181772	(TTA)28	F:AGCAACGTATGGTGGTATC R:CATTTGTTTCCACAGCTTC	129-179	KP278931	9	6.38	0.23	0.84	0.60
SCF181909	(CT)10	F:CTCTCAATCTCTTGTTTTCTCC R:TTCAAACCTCAGCAATCAG	172-176	KP278932	3	2.38	0.75	0.58	0.50
SCF183590	(CT)11	F:TTTGTAGTATGGGGACACTGAT R:AAAGAGGCAGGTCAGAAAAT	168-173	KP278933	3	1.89	0.54	0.47	0.42
SCF18363	(TC)10	F:CAAAGACCGCTAGGTTTACA R:ACTGCTCACTAGACAAGATCG	170-176	KP278650	3	1.89	0.62	0.47	0.42
SCF184873	(TA)11	F:AAGCGTAGAATATGTATGACCC R:GGTAGTCCTCACGGAAGAG	223-239	KP278934	4	2.94	0.70	0.66	0.61
SCF18709	(AC)12	F:GTAATGGTAAGTGTCGAAATCC R:CATAGATGTAACCACGCTTCT	342-350	KP278651	4	3.63	0.85	0.73	0.67
SCF187979	(AG)10	F:AGATAAGGCACCCGATAATAC R:GATCAAGGAACGCAAATCT	201-269	KP278935	6	3.67	0.77	0.73	0.69
SCF189612	(AG)10	F:GAGGATTGTTAATGGTTTCTTT R:TACGCTTCATCTTGTTATTTTC	148-154	KP278936	4	2.89	0.85	0.65	0.59
SCF189657	(AG)10	F:CATCCTTGAAAATAGACAGACC R:CTTAGAAGACCGCACTGAGA	238-240	KP278937	2	1.80	0.67	0.44	0.35
SCF189827	(AG)9	F:TTCATTTCCTTACACTTCCC R:GTTAGCTTCTTCTCCTTCTTCA	184-187	KP278938	3	1.73	0.54	0.42	0.38
SCF191642	(CA)10	F:CTACATCCACTAAATATCAAGGC R:GATCAAGCCAAAGGAAGAA	228-230	KP278939	2	1.17	0.15	0.14	0.13
SCF192074	(TA)9	F:CCTTGGAAAACACCTTTTG R:GCCAAACAATATGGGACAG	187-189	KP278940	2	2.00	0.54	0.50	0.38
SCF192219	(GA)9	F:GAATTTTGTCGTTCCAGAGA R:AAAAGAAGAAGAGGAATGGC	150-158	KP278941	4	2.30	0.62	0.57	0.50
SCF192715	(AG)9	F:CTCTGCCTTGTTCGTCTCT R:AACCAATCGAAGGTGACAA	187-213	KP278942	5	3.45	0.77	0.71	0.67
SCF193103	(GA)11	F:GAGGAGTTGAAACAATTAGTCC R:TACCCACTTTAGTCGAAGGAT	150-168	KP278943	4	2.62	0.69	0.62	0.56
SCF194552	(CT)9	F:CACAGGTGTAGGGTCTTGTT R:AAAAGGAGGCAAGGATAGAG	209-238	KP278944	7	4.23	0.69	0.76	0.73
SCF19565	(CT)13	F:GGGTTTTATGAGTTAGAGTCCC R:GTAGGTTTCTTCGATGGTCTT	287-317	KP278652	4	2.62	0.69	0.62	0.56

SCF197903	(GA)11	F:TCTCGTGAGCGTTACAATATAC R:ATGGAGTCAAGGTAAACCG	147-155	KP278945	5	2.91	0.77	0.66	0.59
SCF199831	(TC)15	F:GTAGGTATCATCGCTGTCTTC R:GTGCATCACATACAAGCTCT	182-201	KP278946	5	3.31	0.77	0.70	0.66
SCF201915	(AC)19	F:ATGCACATCCTGAAGTACCA R:CTGAACACATTGGACGGAT	188-218	KP278947	8	6.26	0.92	0.84	0.82
SCF204332	(TC)9	F:CGTGATCTCCCAGAGTTGT R:CTTTTATTTCCCTATGTGTCCC	169-182	KP278948	4	1.77	0.46	0.44	0.40
SCF204979	(CA)13	F:GGAAAGAGGTAAGAAATGGG R:TAAGAGTTCCCACAACCAAA	149-153	KP278949	3	1.89	0.62	0.47	0.42
SCF20681	(GA)16	F:AGCCTAAACCTCTGTTTGATG R:TTACAATACCTCGCTCCTTAGA	218-233	KP278653	3	1.48	0.39	0.32	0.29
SCF208509*	(GA)14	F:GCTTCACACTTGATAGTAGGTTG R:TACCGCCATTGTAGCAGAT	146-165	KP278950	6	4.83	0.92	0.79	0.76
SCF208875	(CA)10	F:AAGGAGTTCAGATAGTCAAAGG R:AGGAATGAGATGGATATGGA	172-182	KP278951	2	1.95	0.85	0.49	0.37
SCF208883	(GA)9	F:GAGGAGTGAAGAGCCAGTAA R:GACATTTCAAGTCCCACACT	155-163	KP278952	3	2.00	0.54	0.50	0.41
SCF21119	(TA)9	F:GGATTTGAGGACTATACCAAGA R:TTAAAAGGCATACGCTGAC	331-347	KP278654	6	3.84	0.92	0.74	0.70
SCF213102	(CAG)8	F:GTGAAGATACAGTGGAGAGCA R:ATGGTAGTTGTTGACCTGATG	148-160	KP278953	4	2.25	0.62	0.56	0.51
SCF21596	(AC)11	F:ATATACTGGCATAAACACCCTC R:CCTTACTCTTATCATGGCTAGG	303-320	KP278655	8	5.20	0.92	0.81	0.78
SCF22434	(GA)9	F:TATGTATAGTCCCACAACAAGG R:TCCTGTCTATCACTCACATCAC	263-265	KP278656	2	1.74	0.46	0.43	0.34
SCF22442	(CT)11	F:ACAAAGAAAGACACTCCATCTC R:GTATTTGACTTCCATGACCAC	338-348	KP278657	4	2.62	0.77	0.62	0.56
SCF22477	(CT)12	F:CTCTCCCCTACTTTCTTCCTAT R:GCCGCTAACACAATTAACTAAC	243-247	KP278658	3	1.77	0.42	0.43	0.37
SCF2288	(AGA)8	F:CAATAGTAGTTTCGAGCTTTCC R:GTTTCCAATTCAAGCCTCTA	216-230	KP278600	4	3.22	0.85	0.69	0.64
SCF22962	(AC)9	F:GTGCAACAGCTAACAGCATA R:AGGACCAATACTCAGAACAAAC	198-204	KP278659	2	1.95	0.54	0.49	0.37
SCF23210	(TC)11	F:TTGATACTCTCGACCTCTTCTT R:GTGGTGTTCGACATGATTTAC	189-209	KP278660	5	4.28	1.00	0.77	0.73
SCF23339	(GA)15	F:GCAAAACAGAGTTATAGTGGCT R:TAGACAGAAGCACAGATTGGTA	253-270	KP278661	6	4.51	0.85	0.78	0.75
SCF23691	(TCT)13	F:CGGCTTTGTTAGTTGATGTT R:CGATGTTGTACTATTCATGTCC	259-281	KP278662	7	5.12	0.92	0.81	0.78
SCF24087	(CTT)11	F:GTCCCTTTCTCGTGTCTTTAT R:GAGTAGTGACGATGCAACTAGA	191-212	KP278663	4	2.47	0.54	0.60	0.52
SCF2483	(GTG)8	F:TTTCCTTCATAGTGTTGCCT R:GTCTCCCTGTTAAATCCACTC	169-184	KP278601	2	1.74	0.31	0.43	0.34

SCF25221	(CT)10	F:GTATCCCCACACTTACCACTAT R:AGGATTGGACGGTAGCTTA	317-331	KP278664	4	2.75	0.62	0.64	0.66
SCF25446	(CT)9	F:TAGTGTGGACTTAACATGGAGA R:ATCCAACCAAGTATCAGCAA	159-161	KP278665	2	1.99	0.62	0.50	0.66
SCF259	(CT)10	F:TGACAGTACCAATAGCAGGAC R:AACACCCAGTCGTTATACATCT	177-194	KP278591	5	3.49	0.69	0.71	0.66
SCF25944	(GA)10	F:AACTATGCCAGAAGACTCAGAT R:CTTCACAAATCACAACCACTAC	293-321	KP278666	7	4.69	1.00	0.79	0.76
SCF26014	(GA)9	F:GGTCCCAGAATCAATGTCTA R:GAAATCAGAGAAGAAACAGGTC	166-170	KP278667	3	2.89	0.77	0.65	0.58
SCF26049	(TTC)13	F:GTTCAGGTCTGTTGTAAGGAAG R:TTTCTTGTAGGACGAAGTGG	168-187	KP278668	6	4.28	0.85	0.77	0.73
SCF26697	(CT)13	F:TCGTAACTATTCAGTGGGTGT R:GGAGCAGTAGAGATTAAACGAC	272-282	KP278669	5	2.52	0.85	0.60	0.56
SCF2714	(AG)9	F:ACAAGTCTCTGGAAGCTAACAT R:GTTGATTGTTGGGTCTAAGTTC	202-208	KP278602	4	2.60	0.85	0.62	0.54
SCF27510	(GA)13	F:CCTTCAGATTCAACGTATTCTC R:GGTGTATCACATCCCAAAAC	239-284	KP278670	8	5.73	1.00	0.83	0.80
SCF27755	(GA)11	F:GAAGTGAGAGTAGGAATCGAAG R:CCACAACACAAAACCCTAAT	335-357	KP278671	6	3.98	0.92	0.75	0.71
SCF27811*	(TC)10	F:ATGTGACTAGCATGGGACTTA R:TATTTACCTGGATAGGAGAAGG	219-259	KP278672	4	2.97	0.77	0.66	0.61
SCF27934	(AC)9	F:TCCAAATAGCCCAGAATAAG R:GGTACTCCCATGTAATTGTTGT	234-237	KP278673	2	2.00	1.00	0.50	0.38
SCF28100	(TCT)7	F:TAGAAACTAACATGGGAGGTGT R:GCACGCTGTATTGATAGAAGAT	239-295	KP278674	6	5.93	1.00	0.83	0.81
SCF28279	(TC)12	F:GATACTTTACCTCCTCCTCAAG R:TTGTCCTCTATCTCTAACTCCC	231-239	KP278675	4	1.63	0.46	0.39	0.36
SCF28509	(GA)9	F:GCAAACACCACACTATATGAGA R:ATAGAGAACCACAGAACAGGAC	212-221	KP278676	5	2.86	0.77	0.65	0.59
SCF28613	(CAA)16	F:CATTCTTCACTCCAACTTCAG R:CAAGTCCCATCATCATTTTC	182-220	KP278677	5	2.94	0.92	0.66	0.60
SCF28931	(TC)13	F:TCTCATAAGTCAGAACCTCACA R:CTAAACTAAACCTCCTAACCGA	225-229	KP278678	5	4.07	0.69	0.75	0.71
SCF28955	(GT)9	F:TATTCAAAGCCACTAGGCAC R:CAAACCAAATTCTCCTTCTG	235-246	KP278679	5	3.45	0.89	0.71	0.67
SCF29560	(GA)13	F:GTGTGGTGTGGTCTCTACAAT R:ACATCTCTTTGGCTGATACTTC	248-258	KP278680	5	2.41	0.62	0.59	0.53
SCF29735	(TG)16	F:CGTAAAATCTGTTGTCTCTGTG R:TCTCTATGCTCCTTCCACTTAT	263-278	KP278681	5	3.84	0.85	0.74	0.70
SCF30000	(AGA)10	F:GACTCTTCAACTTCCACGTTA R:GAAATCTTAATCTTGCAGCC	161-167	KP278682	3	1.98	0.69	0.49	0.43
SCF30010	(CT)9	F:CTCAAATCAACGATCAAGAC R:GAAAGAGACAACAAAACCCT	302-337	KP278683	8	4.33	0.92	0.77	0.74

SCF30734	(TTA)8	F:GTTGAAAACCCAACTGTGAG R:AGATCCAGTCATGGTACTTTTG	178-240	KP278684	6	2.89	0.69	0.65	0.62
SCF30816*	(TCG)8	F:GTCCAAAATAGCATCGAAAG R:CGCATTACTTCTTCACTATACG	207-216	KP278685	3	1.89	0.62	0.47	0.42
SCF31172	(CT)11	F:ACTGGATCTGGTGTTATTTACC R:GGCTGGAAACAATTCAAAC	161-167	KP278686	3	2.70	0.77	0.63	0.56
SCF31208	(CT)10	F:AACAGCACCACTACAACACTT R:AGAGAACAATCGTCTAATCGTC	306-359	KP278687	5	3.60	0.85	0.72	0.68
SCF31394	(TC)11	F:GTAGCAAAAGAAGAGACACCAT R:CGTTTTCCAGTTCCAGAGTA	273-287	KP278688	5	3.80	0.85	0.74	0.69
SCF3191	(TCT)15	F:GCACTATCAGGAAGAGGAATTA R:GTAACACCAGAAAACAACTGC	238-260	KP278603	5	3.71	0.92	0.73	0.69
SCF3261	(TC)10	F:GTTTACCATATTCACTCCTTCC R:TGAGACAGACCTAACATTTGAC	260-268	KP278604	3	2.77	0.77	0.64	0.57
SCF32727	(TC)18	F:ATGTAACGGTCTCCACTTTCT R:TAGTATCTTCGTGGTCAGAGGT	192-210	KP278689	8	5.45	0.92	0.82	0.79
SCF33047	(GCT)8	F:TAGGGAAGGAGTAGTTATCGAA R:ATGCTGACCTCATCGTCTT	161-173	KP278690	4	2.44	0.82	0.59	0.52
SCF33185	(CT)14	F:AGCACACTACAGACAGGGTAAT R:GTTTTGGCTCTGGCTAAGTAT	198-202	KP278691	3	2.62	0.69	0.62	0.55
SCF33471	(TC)12	F:TTTATTGCACACGAGAACAG R:ATATTTTGTCCACGCTCACT	288-329	KP278692	7	2.70	0.46	0.63	0.61
SCF3362	(TGC)9	F:GTACAGCAAAATTCAGCACA R:GGATTTATCTACAGCCCATTAC	343-372	KP278605	3	2.25	0.46	0.56	0.47
SCF34010	(CA)10	F:GAGAATATGTGATGTTGAGGTG R:CAAGTGTTAGGCTCGTTTAGTT	285-287	KP278693	2	1.35	0.31	0.26	0.23
SCF34071	(TG)10	F:CGTGTGCAGATTTACTTCAG R:AATTCATAGATCCCCATGAC	268-276	KP278694	3	2.94	0.85	0.66	0.59
SCF3427	(CT)11	F:GCAAGACATCATCACAAACA R:CTTATCCCAGTCCTTCAACTTA	347-349	KP278606	2	1.35	0.31	0.26	0.23
SCF34513	(TG)10	F:TACTAATCTTCTGGTTTGGGC R:GTACACCACTCCTGATGGC	228-232	KP278695	2	1.47	0.40	0.32	0.27
SCF34584	(AG)10	F:GTCTGTTTGGAAGAAGAAGGT R:CTGTTCGTCAATCCCTAGC	199-213	KP278696	4	3.49	0.85	0.71	0.66
SCF35507	(GA)9	F:GTCTAATCTAATGCAGAATGCC R:AATGTGGACAACGAGTACATCT	238-240	KP278697	2	1.55	0.46	0.36	0.76
SCF3551	(AC)9	F:CTTCGACGTTTCTGTGACTAT R:AGTTGGTGATTGGAAGAGTAAG	274-289	KP278608	6	4.76	0.92	0.79	0.76
SCF3595	(CA)10	F:AGACTACAGTGAACAAAGACCA R:CTGACTTGGTGTGATTAGTGAG	316-332	KP278607	6	4.90	1.00	0.80	0.77
SCF36745	(TC)14	F:TCCTCATTAAGTATTGGACAGG R:CTGGATTCTTGTTCTTAGCTTC	307-316	KP278698	4	2.94	0.69	0.66	0.60
SCF37023	(AAT)12	F:GAATAGCCTTAACATACGCTGT R:ATTGGAATGGTTTAGTGGTG	332-351	KP278699	3	2.74	0.67	0.64	0.56

SCF37628	(GA)12	F:ACCAGCTCAGATAACAATGC R:GAGTAGGATACCTCCACACCTA	255-263	KP278700	2	1.90	0.62	0.47	0.36
SCF38340	(TC)9	F:CAAACCATTTTAACGGAGAG R:AATCATCGTGCATACCTGTT	336-339	KP278701	3	1.27	0.23	0.21	0.20
SCF38430	(GA)14	F:CAATAGTTAGGAAGTTGGAACC R:CTAAGAACCAAACAGAGCCTTA	156-176	KP278702	3	1.91	0.62	0.48	0.39
SCF38553	(GA)10	F:CTTCTGTTTACTCACTTCCACC R:ATGGTCCCAAGATACTTTAGC	350-358	KP278703	4	2.09	0.46	0.52	0.48
SCF38942	(CT)11	F:CTTGCTATTTGGTACTCGTCTT R:CTTGACAGTTATTTCTCTTCGG	230-240	KP278704	3	2.86	0.69	0.65	0.58
SCF3914	(TAC)13	F:TGTGGAGTTAGAGTGACATACC R:GACAAGAATGATGAGTAGCGT	345-372	KP278609	5	3.98	0.85	0.75	0.71
SCF39242	(TC)14	F:ACTCCTGAAGAAGAAGAACAGA R:AATGAATGCAGACCACAGAT	246-276	KP278705	7	4.76	1.00	0.79	0.76
SCF3932*	(TC)10	F:CAGAGTTTCAGTGGAGCATT R:CTCAGCTTCTGTGTTTTGTGT	311-319	KP278610	5	3.31	0.77	0.70	0.66
SCF39705	(AT)13	F:GCAGGTAAATCCTATCTGGAAT R:GTTGAAGACACCTAGTCCACTC	333-397	KP278706	7	3.08	0.70	0.68	0.64
SCF40517	(CT)12	F:GTAGAATGGCAATAGGGTTT R:GAAGAAGATGACGAAGATCAC	245-259	KP278707	5	3.05	0.92	0.67	0.62
SCF41361	(CA)9	F:AAAATTGCTTGGTCCTCAC R:AAGTGTATAGTCTGGGGTGTTC	231-233	KP278708	3	1.61	0.31	0.38	0.34
SCF41971	(GA)12	F:ATACTTGACCTCTATGGCTTGA R:GTACTTACGTGTTTGGTTCGTT	280-300	KP278709	7	4.83	0.92	0.79	0.77
SCF42332	(CT)10	F:GATAGAATGACGAAACTAACCC R:AGTGGGGAGATAATTGAGAAG	194-208	KP278710	4	2.60	0.92	0.62	0.54
SCF4305	(GA)13	F:AATGAGTGGTTATGTAGGGAGA R:AGATTGGTGAGATATGAGGAAG	179-191	KP278611	5	4.76	0.85	0.79	0.76
SCF43145	(TCT)7	F:TGGTTTTGGATACACACTTG R:AAGAACAAGATCACCACTCTG	235-261	KP278711	7	6.76	0.69	0.85	0.83
SCF43220	(TC)14	F:CTTGTCGAGCATCCTATATTTC R:AAAAGTCATGGGAAGGTGTT	154-159	KP278712	4	2.50	0.69	0.60	0.52
SCF4386	(TTC)9	F:GTTACTCATTTCTTTGCTGAGG R:CCTCTTAGTGTTGGAGTTTCAT	200-203	KP278612	2	1.99	0.62	0.50	0.37
SCF45712	(CA)9	F:GCAGTGTGCTTTTCTTTTCT R:GTTACTAGGGTACTGGGTTTGA	206-210	KP278713	2	1.35	0.31	0.26	0.23
SCF46588	(TG)11	F:ACAAACCTTGAGCCTATTTG R:GTCTGAGTTTCCACTATCGTCT	350-356	KP278714	5	2.06	0.46	0.52	0.47
SCF46739	(TC)10	F:ATGTTAGGTGATGCTGTTGTC R:CAGGTGCTTATTTTCGTTTC	247-249	KP278716	2	1.83	0.69	0.45	0.35
SCF46751	(AG)12	F:ACCAGATGAAGAAGAAGAAGC R:GCCTCTCATTACCATTACAAAC	309-325	KP278715	5	3.07	0.85	0.68	0.63
SCF46824	(ATT)10	F:GGAGATGCTGTAATAACGAAGT R:TTAGTCAATATGCGTGCAAC	193-209	KP278717	5	3.80	0.77	0.74	0.70

SCF46833	(AAC)7	F:GGACCGCCGTATTTAGTTA R:GCCCATACCCCTAGTTATTG	208-211	KP278718	2	1.74	0.46	0.43	0.34
SCF46912	(AG)9	F:GAACAATAAAGAGGCTAGAGGA R:CATAGTTGTAGAGAAGATCGGG	172-182	KP278719	4	2.50	0.69	0.60	0.55
SCF47809	(CAT)10	F:CTTCTACCTTCCAAGATTTGTG R:ATTACTATTCCCAGAGACGACC	289-304	KP278720	2	2.00	1.00	0.50	0.38
SCF48414	(GA)12	F:GTAGGGAAACAAGAATTGGAC R:ACTGTGAGATTGGTGTGATATG	284-286	KP278721	2	1.95	0.69	0.49	0.37
SCF48645	(CT)10	F:AAAATAGGTCCCACATGAGTAG R:GCTAGACGATGACACATTATTC	310-312	KP278722	3	1.37	0.31	0.27	0.25
SCF49598	(TCT)8	F:ATGAGGTTTTCCAACACAAC R:TCAGAGGGAAGTACATGAGAAT	258-261	KP278723	2	1.83	0.69	0.45	0.35
SCF49656	(TC)14	F:ACTCTTACCCTTGAAACCAACT R:TAGGTGCATGAGACTTTTAACC	284-301	KP278724	5	3.71	0.85	0.73	0.69
SCF51810	(TGC)8	F:TATTACTCTGTTGCTGCTGTTG R:ACTAAACCCTAATGTCCCTTCT	189-204	KP278725	3	2.18	0.69	0.54	0.46
SCF53282	(GA)11	F:GACAATCACATACCCATAACAG R:CCACTCTTTCCCTCTATCG	214-234	KP278726	3	1.61	0.46	0.38	0.34
SCF53750	(CA)10	F:GTTTCATAGAGATGGGTTTCTG R:CTTGGTTCCCTAAGCTACATT	316-353	KP278727	6	2.41	0.69	0.59	0.56
SCF54155	(GA)14	F:TCGAAGAAAATGAAGGGAC R:ACAAATGGAGAGGAAAGTGTAG	292-335	KP278728	8	5.54	0.77	0.82	0.80
SCF55511	(GA)9	F:GAAGTGAAAATCTGAACCTCTC R:ACTCTCGAATCTGTCTTCTTGT	178-183	KP278729	2	2.00	1.00	0.50	0.38
SCF55751	(CT)10	F:ACTCACGTCCATTTTCTCAC R:AGCGATATAACAATACCAGAGC	227-239	KP278730	6	4.97	0.62	0.80	0.77
SCF56032	(GAT)11	F:AGAAATGGCGCTCTGTATC R:GAACAGTCTCATCTTCACGAC	195-216	KP278731	3	2.25	0.85	0.56	0.47
SCF56561	(AG)13	F:ATTAGCCATTCGTGATTAGG R:TAAGGAGATACGACCAAGAAAC	218-230	KP278732	4	2.84	1.00	0.65	0.58
SCF56717	(AGG)7	F:GTGTTTGTGTTTGTGTCTGTG R:GATGATTTCACCTACATCGG	199-211	KP278733	2	1.99	0.77	0.50	0.37
SCF56747	(GA)14	F:TTAGAGAAAGGTCCCAACAG R:GAAGAGGCTAAGAGGTCATGT	256-280	KP278734	7	5.54	1.00	0.82	0.80
SCF56816	(AGC)9	F:CGGATTGACTAATTTCTGTCTC R:CTCTTATTCCACCAAACGAA	210-219	KP278735	2	1.55	0.46	0.36	0.29
SCF57479	(CT)10	F:AAGTGCAAGTGTGAGAGTGTAT R:TGATGGGTGTAAGTGTAAAGAG	196-204	KP278736	4	2.50	0.62	0.60	0.52
SCF57497	(TC)10	F:ATCTGTAGGTTGTGTTACCCC R:ATCAACTGTATCTACCCACCAA	239-240	KP278737	2	1.90	0.77	0.47	0.36
SCF58861	(TA)10	F:GTTGACTAAAAGGCATTGGA R:GACTACTATTTTCTGCACAGGG	147-164	KP278738	7	6.15	1.00	0.84	0.82
SCF59035	(TC)16	F:AGATTTTGAACGATGTCTGC R:GATCTATCGCTTATCCAGTACG	301-336	KP278739	5	3.28	0.92	0.70	0.65

SCF59248	(TTA)7	F:TAGTTGAAAATGGAGAGAGAGC R:TTAGATGCCCAACACTACATC	194-204	KP278740	4	2.94	0.77	0.66	0.61
SCF59739	(CT)11	F:GTATGACTGTACCAAACAAACC R:CAGCTTTCCCTTCTAAATGA	334-350	KP278741	5	3.45	0.77	0.71	0.66
SCF60761	(GA)10	F:ACTTAAACATCGGTCCATAGAG R:AGAGTCGTGTCCTTTCTTTTC	259-263	KP278742	3	2.12	0.55	0.53	0.47
SCF61078	(GAA)7	F:GACTCTTCATATAACCCACAGC R:AAAAGTGCTTGATCGTTAGC	252-254	KP278743	2	1.17	0.15	0.14	0.13
SCF61189	(AG)9	F:GCCATAACTCTCACTCAAATCT R:ACCTATTCACCTACATCCAAAG	307-319	KP278744	5	3.49	0.69	0.71	0.66
SCF6195	(AG)14	F:GACTATGAATCTGACGCTCAC R:CCAGTAAATACGTGACTAATCG	340-354	KP278613	5	3.52	0.85	0.72	0.67
SCF64185	(TG)9	F:CACCTCATTTGGTTCATTCT R:CAGATACTAAAGGTTGCCGTA	316-320	KP278745	3	2.43	0.77	0.59	0.50
SCF64632	(CT)12	F:ACCTCCTAAAACACAACCCTA R:CTGAGTAATCTTCGATGTGAGA	149-175	KP278746	7	4.12	0.85	0.76	0.72
SCF64758	(TG)11	F:TAAGAGGGTTTGAGCATTCA R:TTGGGTCATAAACAACCTCA	350-356	KP278747	3	1.90	0.46	0.47	0.43
SCF6530	(CT)9	F:CCCCAAGTATAATGTGTAAAGG R:AGTTCGCATAGAAACTGTAGGA	349-353	KP278614	2	1.95	0.54	0.49	0.37
SCF65999	(CT)11	F:AGGTAGCATTAGACACGAGATT R:GAGGTTTTACATGACCATTACC	288-300	KP278748	2	1.74	0.46	0.43	0.34
SCF66692	(CT)10	F:AAAGTGTATTGGACGGCTG R:TTGTTATGGCCCCTCATTA	245-259	KP278749	7	4.02	0.92	0.75	0.72
SCF68870	(AG)11	F:GTGAATTGTTGCAGAGTACCTA R:TGAGTTGAGTTCATATAGCTGG	166-168	KP278750	2	1.08	0.08	0.07	0.07
SCF6926	(CT)10	F:ACATGCACTTCAAATAGTACCC R:TTACAACTTACACAGGAAGCAG	212-234	KP278615	4	2.09	0.46	0.52	0.48
SCF69698	(TC)9	F:GAGGAGATAAAGGTTTGTTGAG R:CTTTGAGACTTTGAGTGAGACA	297-303	KP278751	3	1.81	0.46	0.45	0.38
SCF69981	(CT)9	F:AGCGTTACCACCGAATATAA R:CGAGATATAGTTAAAAGGACGG	226-244	KP278752	8	6.38	0.92	0.84	0.82
SCF71136	(CAA)7	F:TCTGTTTTCACAGCTATCACAC R:GTTCATCAAAGGCCAGAGT	179-182	KP278753	2	1.26	0.23	0.20	0.18
SCF71184	(ATT)22	F:TCTGTTCAGTTGGGCTTTAT R:GCTCACATTCACCTGTAATTC	200-231	KP278754	7	4.97	0.92	0.80	0.77
SCF7132	(TC)10	F:AAGGGGAAGGACAATAAGAA R:AATTTGATGACTGTTGTGGC	218-236	KP278616	3	1.98	0.54	0.49	0.43
SCF7155	(GT)11	F:GGGATCTATGAGTTGTGGACTA R:CCACGGAATAGTTGTAAGTTGT	168-196	KP278617	4	1.91	0.54	0.48	0.43
SCF72209	(CT)12	F:CTTTACCTTTTCCTTCAGTCGT R:GAGGTTCACCAAATCTTACCA	206-210	KP278755	3	2.94	0.92	0.66	0.59
SCF72229	(CCA)7	F:CAACTTCTACAACCACTCCAC R:GATTTATTGTGCTACACTGGTC	322-334	KP278756	3	2.27	0.60	0.56	0.50

SCF72379	(GA)12	F:TAAGGAGATCGACTAGGGTTT R:CATCAAGATTCAAGACCACAC	202-217	KP278757	5	2.36	0.62	0.58	0.54
SCF73288	(TC)12	F:CAGAGGAACAGCAGACTACAT R:CCTAGTACGTCATTGGACATTA	226-334	KP278758	5	3.89	0.77	0.74	0.70
SCF7357	(CT)9	F:CAGCTTAATCATCAGTTCCAG R:AGTGAGCATCGACTATTTACCT	282-286	KP278618	2	1.65	0.39	0.39	0.32
SCF74458	(CT)10	F:GCAGGAAGCTATGATTAAGGTA R:TTGAATAGTGTCAGTGGAGAAG	222-240	KP278759	4	2.43	0.62	0.59	0.53
SCF74895	(TC)9	F:GTACTCCTCTCCGTCTAGCAT R:GATTTTATGCGTTAGCTCCA	153-219	KP278760	9	6.76	1.00	0.85	0.84
SCF75572	(TGA)7	F:GACAAGTGGTTGGGGATAC R:ACCCTCATCATCACTCCTT	247-265	KP278761	3	2.05	0.46	0.51	0.46
SCF7569	(AC)10	F:CCCAATAACGACTCATATACCT R:ACCCAGTCAAAATCTCCTTT	279-283	KP278619	3	2.25	0.62	0.56	0.47
SCF76310	(TC)11	F:CTGTGTAGAACTGCATCAAAAC R:TCCTAGAGACCAACCCAATAC	220-226	KP278762	4	2.50	0.77	0.60	0.55
SCF77145*	(TG)10	F:TAGAATTAGCCTCCAAGAAGTG R:AGAACTAGAAACACGAGAACGA	314-325	KP278763	3	1.86	0.54	0.46	0.40
SCF77376	(AAG)11	F:CTCATCAAAAGAGAGGAGAACT R:TGTAACCAATCTTCATGCTG	256-273	KP278764	6	4.33	0.85	0.77	0.74
SCF77645*	(TC)10	F:GGTTCTTTCTTCTGGGTTTT R:TCAGACAATGAGCTACTACCCT	298-343	KP278765	7	3.25	0.85	0.69	0.66
SCF78184	(CA)10	F:CACATTTAAGAGCTACCACCTT R:GGTGAAAGAGAAGACTGGATT	260-276	KP278766	5	3.76	0.85	0.73	0.69
SCF7845	(CT)12	F:GTTCTGACTATTGTGATGGGTT R:TGCAATGAATACTGGAAGTG	254-256	KP278620	2	1.90	0.62	0.47	0.36
SCF79014	(CT)10	F:TCTCTGTCTCTGTCTCTGTCTG R:CCAAATCAAGGTCTGTCTATCT	181-183	KP278767	2	1.94	0.46	0.48	0.37
SCF79620	(GA)15	F:TAATAGCCCTTATACCTGCACT R:GAGCATAGACAGCATACAAAAG	187-218	KP278768	8	4.97	0.85	0.80	0.77
SCF804	(GA)15	F:CAGTCAACAGAGAATACACCAC R:TTCCCTATGAAAATCCACAC	221-231	KP278592	4	2.60	0.77	0.62	0.54
SCF80520	(TC)9	F:TAAAGTGTTTTGGACGGCT R:GCACAAATTATCGGAATCG	172-178	KP278769	3	2.30	0.62	0.57	0.47
SCF80703	(AC)17	F:GGTCTTTCTCCTAATCTCCAA R:GGAACCCCTAAATAACATACAG	196-220	KP278770	9	4.69	1.00	0.79	0.77
SCF81294	(CT)9	F:CTATCGACGGCTGAGATTT R:AAAAGGGGAAGATCCTAGAAG	232-238	KP278771	3	2.07	0.69	0.52	0.42
SCF8151	(CTA)7	F:CGTGCTAGAAGACGAGGTAT R:TTAGGGAACAGTAGAAAGGAAG	311-314	KP278621	2	2.00	1.00	0.50	0.38
SCF81732	(AG)9	F:CGAGTATGTGGAGAGGCTTAC R:GTGTATAAAATGGGCATCACAC	295-315	KP278772	3	1.89	0.62	0.47	0.42
SCF81909	(GT)12	F:TAGAGGAATCAGCAACTTCACT R:TTCACACTCACACTCACACG	311-322	KP278773	4	2.58	0.54	0.61	0.55

SCF8223	(AG)11	F:CATTTAGCATCCATCCATTC R:GACTGTGGGTTATTCCTTGTAT	341-355	KP278622	5	2.79	0.69	0.64	0.59
SCF82535	(AG)9	F:TAGAAGAGGAAAACTGACGGA R:TTGATGCAATCTGACAACG	245-253	KP278774	4	2.52	0.69	0.60	0.56
SCF82870	(CTT)8	F:GCTAAAGAACGAACAACAACAC R:GTCCAACGAGTGAGTAGAGAAG	261-314	KP278775	7	4.51	0.92	0.78	0.75
SCF83036	(TC)14	F:CAACAGTCCTCAAAATCACTC R:GTGAACAGAAGTAGAGATCGG	313-323	KP278776	5	4.02	0.85	0.75	0.71
SCF83615	(TTC)11	F:ATTAGTCGATCTCCTTTTCCTC R:AAATTGTAGAGCCAACACTAGG	323-345	KP278777	5	3.76	0.62	0.73	0.69
SCF83971	(TTG)8	F:ATTCTGGTACTGTTTGTTGCTC R:GTTATGTTTCGTGTTCCACTCT	270-347	KP278778	2	2.00	1.00	0.50	0.38
SCF84804	(CA)13	F:CTAGTCTTCTTGTGACCTAGCC R:TATTCTTTTAGTCCGAGCCA	207-213	KP278779	3	1.62	0.46	0.38	0.35
SCF85773	(GA)12	F:TCTTGAACACAGCACAACAT R:ATAAGTTTGCCCCTTTTGTC	281-301	KP278780	8	6.26	0.77	0.84	0.82
SCF85946	(TC)10	F:TGTGAACAGAACCTACCACTAA R:AAAGAGCCCCGTAGATAGAT	324-328	KP278781	3	2.20	0.62	0.54	0.48
SCF86438	(ATT)7	F:CTATTGAAAACAAGGAACGG R:CCTATACAACCTCTTCGGATAA	336-340	KP278782	2	1.65	0.54	0.39	0.32
SCF87990	(TC)10	F:GTGTAGGTGTAAATGTGCTTTG R:GGCGTATAAAAGGATTCAAG	260-262	KP278783	2	2.00	0.54	0.50	0.38
SCF88396	(GA)9	F:ATAGAGGTTAATTGGTCCTCG R:GACGAAGAACGACAGGTAGAT	284-292	KP278784	3	2.30	0.62	0.57	0.47
SCF8850	(GA)10	F:GTGTGATGTATTTAAGGAGTACCAC R:ACAGATAGAGTAGTTACCAAGGGA	344-356	KP278623	6	5.37	0.92	0.81	0.79
SCF88902	(TC)9	F:GTGTTGTAGGATGAACCGAT R:GATTTCCAGCATTTGATCTC	315-368	KP278785	5	4.75	0.91	0.79	0.76
SCF89247	(GA)11	F:TGGAGGAGGTGAAGAATACTAA R:CCCTTTGGACAACAAAATAC	198-218	KP278786	6	4.57	0.85	0.78	0.75
SCF89447	(TC)9	F:TAAATAAGACCTTCTGCTGACC R:AATATGCTCACCACCAGTAAAG	192-196	KP278787	2	1.45	0.39	0.31	0.26
SCF89672	(GA)14	F:CCACTATAATCTACCCCAAAGA R:TACTACTGCCCCATCCTACTAC	194-200	KP278788	3	2.43	0.31	0.59	0.50
SCF89726	(TC)9	F:TTGCTGACTTGCTAACCCT R:ATTTACCGAACGCTACGAGT	327-329	KP278789	2	1.65	0.23	0.39	0.32
SCF89801	(CT)14	F:TAAACCTGTTCCGTCTCTTAGT R:CTTTACTGTTGTGTTGTCTGCT	323-338	KP278790	7	6.48	0.56	0.85	0.68
SCF8987	(CT)11	F:AATCTTTGTCTGAGGTAAGTGG R:AACCAGTGTAGTGCAGTTTATG	150-156	KP278625	4	3.71	0.85	0.73	0.68
SCF90229	(AG)10	F:GTACTTTTGTGGAACTTAACGC R:CTGTCCTTTCACTCCTCTTTT	280-292	KP278791	5	2.79	0.69	0.64	0.59
SCF9068	(TC)14	F:AAATCTAGGTAGGAGCAGGTCT R:ATGGAGGAGGAGATATGTGAT	174-186	KP278624	6	3.89	0.92	0.74	0.71

SCF915	(GA)9	F:TTAGGGTTTGGAGTACCTGA R:ACTACCGTCTTTCTTTATAGCC	265-269	KP278593	3	2.54	0.77	0.61	0.68
SCF9157	(GA)9	F:GGCTTAACAAATTAGCCCTT R:GAGAGGATTTACCGACAAAGTA	301-330	KP278626	5	3.49	0.85	0.71	0.68
SCF91821	(TG)9	F:TTCTGTGTCTGATTCCATCTC R:ACTAGCCCAACAACTTAGACTG	302-304	KP278792	2	1.55	0.31	0.36	0.29
SCF92414	(AG)12	F:GTTATCCTCCCTTTGATATGTG R:AAGAGCAACAAGATGGGTACT	283-287	KP278793	3	2.15	0.54	0.54	0.47
SCF92564	(CTT)9	F:TCATAACTCCCTCGTAATCAAG R:AGGAAGAAGAGAATAAGGTTGG	181-194	KP278794	5	3.89	0.92	0.74	0.70
SCF94237	(TTA)14	F:ATCGCATCAGGTAAGCTAGTAT R:TCGAGTGTCATTGTAATAGGC	330-363	KP278795	8	5.20	0.92	0.81	0.79
SCF95754	(TC)12	F:CAGTGAGACTTCAGCTTGATAC R:ATTGGTGACTTAGGAGTGAGAC	339-366	KP278797	6	3.49	0.85	0.71	0.68
SCF95767	(TA)9	F:TGAGGAGAGGAGTATCCATAAG R:CCTACAAGTCTCGCAATTCTA	270-302	KP278796	5	4.12	0.62	0.76	0.72
SCF95851	(TG)9	F:GACCTTGGAATTTGATGATG R:TGTAGATGGATGTTGTTACCTG	188-190	KP278798	2	2.00	1.00	0.50	0.38
SCF96311	(TC)9	F:TGTATAATCTCAGGGGCATT R:TTTCTCATTTCCTTCCCAC	155-161	KP278799	4	2.18	0.62	0.54	0.79
SCF965	(GA)14	F:GTAAACTAACAAGCAACGATCC R:GATTTAGCTGATGCAGAGTCAT	258-275	KP278594	6	5.37	0.85	0.81	0.79
SCF96539	(TG)9	F:GTAGCATAACCACCTCTTATCC R:ATCTTGATGACTGTGTAAGCTG	259-261	KP278800	2	1.08	0.08	0.07	0.07
SCF9709	(AT)9	F:CCATTAGAAGAGTTTACCGTGT R:TTATCAGTCCCTTACTCAATCC	270-272	KP278627	2	1.84	0.10	0.46	0.35
SCF97378	(CA)14	F:GTAGAGATCGTTGTCGTCATTT R:AACATCGTGGTGTATTGGAT	233-248	KP278801	6	2.77	0.69	0.64	0.60
SCF9815	(GA)11	F:CATAGGAAGATTGCCTTGAG R:GCCTGTTCACATAGATGGAG	186-194	KP278628	2	1.99	0.62	0.50	0.37
SCF98180	(GA)10	F:CTCCTCTGCTTATCTCTTCAAC R:GGTTTTCCCTTCTCAAGATTAC	345-347	KP278802	2	1.45	0.39	0.31	0.26
SCF98686	(TC)11	F:CGTAATTTCACATCCTCGTT R:CATAACCAGATAGCACCTCAAT	236-253	KP278803	4	3.60	0.92	0.72	0.67
SCF9872	(TC)11	F:ATGGGAGTGCATGAATAAAC R:GGAGAATCGTATTTGTGAAGAG	234-238	KP278629	2	1.26	0.23	0.20	0.18
SCF9909	(AG)11	F:CGTAGGTGGATTTCTCTACAAT R:GGCATCTTATTTATCGTCTCTG	134-173	KP278630	6	5.45	0.85	0.82	0.79

Note: * = marker displayed segregation distortion $p < 0.05$

Appendix I-3. Primer characteristics for primer loci tested and validated in 4 craunberry cultivars, but not used in genetic diversity or allele segregation analyses.

SSR ID	Motif	Sequence	GenBank ID
119364_K70	(CT)18	F:ACCACAAAACCCTAGTTCTATC R:TCCATAGTCTTAGCAACAACAG	KP279272
1TRIMCONTIG175833	(TG)14	F:CTCTTTCTGCCTGGTTCTAA R:ACTACTATTGCGTATGGCTCTT	KP279278
1TRIMCONTIG178732	(TC)15	F:ATGGTCCCTGAGTCTAACTTC R:GGATCTCTATTTCAGTGTGTTG	KP279279
1TRIMCONTIG217288	(AG)17	F:ATAACAGAGGACAACGATCTG R:TCACTCTACTTTTACCGAGACA	KP279280
1TRIMCONTIG240704	(GA)16	F:GAGAGAGGGAAGAGTAACAGG R:AAGATGGTCTATTGAGTATGGC	KP279281
1TRIMCONTIG241039	(GAA)11	F:ATAATGGACTGCACGAAACT R:GTAGTAGGGATTTCACAGGCTA	KP279282
1TRIMCONTIG336911	(TC)14	F:CATTTCCTATTTCATCCCCT R:AACAGAGCGAGAGTAATTGAAG	KP279283
1TRIMCONTIG354570	(TG)14	F:ACCTGTTCTGTTGATTACGAGT R:ACAGTATCGCACAATGAGTTC	KP279284
1TRIMCONTIG439506	(AG)18	F:GATTTAGGTTAGGGTATGGGT R:GCTTGTGTTAGGGTTTGTTA	KP279285
1TRIMCONTIG445838	(CT)14	F:GTTTTCCTCTGAATCTCCACTA R:GTCATACACAATACACAGTCGC	KP279286
1TRIMCONTIG448145	(AC)15	F:TGTGATTAGAGGGAGGATTTC R:AAATAAGGGAGTTTGAACCG	KP279287
204816_K70	(AG)14	F:CACTCTAATCACCCTTTCACTC R:CAGAGAGGAATAATACAGGTGC	KP279273
239628_K63	(AG)16	F:CTCTTTCTTGGATGTTGCTACT R:CGAAACTCTCTAACTCTGGTGT	KP279257
247873_K63	(TC)15	F:GATCGGAGAGTTTTCCTCTT R:CAATTTCCTTCCCCAACTAT	KP279258
24956_K70	(GA)14	F:AGAGAGAGGATTGTTATTGCTG R:TGAACCAAGCCCATATAAGT	KP279270
281741_K70	(GA)17	F:GATTTGACTCGTAAAGCAGAC R:GGAAATGGAGATGGATATGTAG	KP279274
284499_K63	(AG)15	F:ATTAGTTCTCCTATGTGGCTTG R:TCAGAGCTTACCCTATTTCAGT	KP279259
289194_K63	(TC)14	F:CTAGCACTGGCTCTTACCAC R:TGTAGGATGTGTATATGGAGCA	KP279260
307461_K70	(TC)17	F:CAGACACTCCACTAACTCAGAA R:GCATCAACAGTACAACAATACC	KP279275
307534_K70	(AG)15	F:ATCGTCTGCTATAAATACTCCG R:GTGTCAACCTTCCTTACAAGAT	KP279276
310238_K70	(AG)17	F:GAGTAACAACAGTGGCAAAAC R:AACTTCCTCATGTACTTTCCC	KP279277
339139_K63	(CT)18	F:CTAATACTTTCATCGTCAACCC R:AGGAGAGAGAGAGGTAGTTTGG	KP279261
346445_K63	(GA)16	F:TAAGGGAAACCTGTAAAGACG R:GATAGCAAAGTGGACGAGTATT	KP279262
35137_K63	(CT)14	F:GGAACATCAAAACTCCCATAC R:GTTCTTCCCCATTTCAGTAAGT	KP279254
36394_K70	(AG)18	F:CAGTGTTTGTTGCTTGGTC R:ATCTCACTCTCTGTTTCCCTC	KP279271
37487_K63	(GA)15	F:CTTTCATTAGAGGAGAGCTTGT R:AGGAAACTAGCAATCAGTCAAC	KP279255
389746_K63	(CT)17	F:TTGTAAACCTCAAGACACACC R:TATCACACAGTTTTGGAGAGAG	KP279263
413893_K63	(TC)21	F:TACTCCATTTCACAACACGA R:ATCTCTGCTTCTTCTACCTCTG	KP279264
418138_K63	(TC)16	F:CCTCTTCTTCATATCATCCAGT R:TTTAGCCCACTTTTATGCAC	KP279265
418192_K63	(GA)18	F:CAGGCAGAAGAAGAAAGAAA R:TGAATTAAGAGAGGAGGAGAGA	KP279266
418730_K63	(CT)17	F:ACAGATCCAGTCTCTTCAAATC R:ATACGGAGTGTAGATGTCTCCT	KP279267
419957_K63	(GA)14	F:AGACTCACCTCTCTTTCTTGTG R:GACTATCTTTCGGTTGACACTT	KP279268
49132_K63	(TC)18	F:AACCCTAGAAATCAATGCAC R:GTTTTCCGTTTTGTTCTGTC	KP279256
9053_K70	(AG)15	F:GCTGATTAGGTTCACTTTCTTC R:TTTCTTCACCTCTTTCTCTCTC	KP279269

ct117109	(TC)9	F:TTGacGTCTTCTCTCTCTTTCT R:CTAGGGTTCATACTTCGAAAAG	KP279151
ct118488	(TC)9	F:GTTCAGGACAAGTGATTTtCTC R:AGCTAAGTGtTTTcCtACTGGa	KP279152
ct131127	(AAT)6	F:GAGTAGTCCcGtAtAtGGAaTg R:GTTCaTTTCCCCATTCTGA	KP279153
ct136900	(AAAAGG)4	F:ACGATATGAGAGAAGAAGAGGA R:CTCTAGTGCATACCAGCACTT	KP279154
ct139597	(GA)11	F:CTTATAGGCAATGCACATAcAC R:GTAACTAATGGGGCTGAACTT	KP279155
ct142970	(ATATA)4	F:AAACCTAAATaCCCGGAATG R:TATAGAcgGCAtATGCAACA	KP279156
ct146598	(AC)13	F:AATCTCATTTTTCCTGggTC R:CTTGATATgCtcTCTTAATGGC	KP279157
ct170930	(AAG)7	F:ACCcGATTCCATAAAAGAAG R:CAAGCTTCTCCTaCCTcca	KP279158
ct89569	(AC)9	F:ACTAATCCCacgAAAACTGA R:aTCTaggCtTTCAAACtAGGGT	KP279149
ct97791	(AC)10	F:GACTTTGTGAGGATAGACCATT R:ATGTAAGATGTGGaCaTaAgGG	KP279150
SCF101363	(TC)9	F:CGATCTGTATCTAGTCGTGATT R:GAGATGTACTATTGGAACTTGG	KP279053
SCF102190	(GA)11	F:GAGGAAAGGGTGAGAGTTTT R:GTTTGACGAAAAGGAGACTG	KP279054
SCF102509	(CT)10	F:ATAGGATTTGTTAGACTTGGGG R:GGAGCTGTTGAAGCTATTGTTA	KP279055
SCF102538	(GA)12	F:TTACTGGGCAATAGAAGGACT R:CACATAAGTTTGGCTACACAAC	KP279056
SCF108101	(TC)14	F:AAATCTTCCATGAGCTTGTC R:TACTGCGGTGTTGAATTAGA	KP279057
SCF113304	(ATA)24	F:CCAGTCAACGAACAAATAGAG R:CCTAAAGGGAAAGAGAAGTGA	KP279058
SCF113895	(AG)10	F:GGAATCACTATGAACATGCAC R:ATCAGAAACGAGTCCAAAGAC	KP279059
SCF115821	(CT)10	F:TCACCACTTACAACATATCCAC R:TTGACACTAGCAAATTCCATC	KP279060
SCF117	(CA)12	F:ATAGCATCTGTCTTATTGGACG R:GTGGGTTTCTGATCTTCATCT	KP278954
SCF118209	(GA)15	F:AGGATTTAGGACGTTGGAA R:GTAACAGAGAAAGCGAGAGC	KP279061
SCF118536	(GA)10	F:GGGTACTATATGAAGGTGCCTA R:CTACCATGTAACCCTTGAAAGT	KP279062
SCF118603	(TCT)13	F:GGACAAACACTAAATAAGCCAC R:CTGCTCACAGAATACCACTAAA	KP279063
SCF119813	(TG)10	F:GTTAGTCGGCTCAAGTTAGTTC R:ATGGACTTCCCATTTCTTTC	KP279064
SCF119984	(GA)10	F:TTAGAATTGCGTTCCATACAG R:GAAAATCAGTTCGATTCAGGT	KP279065
SCF12084	(TC)12	F:CTCTTGTTGGACGGATCTATT R:CCTAACATTTCTCCCACTCA	KP278974
SCF122440	(GA)12	F:CTAATCTTCCTCCTCTTGTTGA R:CGACAAACTAACATATCATCTCC	KP279066
SCF122552	(AC)10	F:TATATCGAGGTCATTGCGA R:GAGTTGTCGTTAAGGTTTTGA	KP279067
SCF123643	(GA)9	F:CAAGAATGAAGAGAAAGATTCC R:CAGGTTTTATTAGCCTGTGTTT	KP279068
SCF125768	(AG)11	F:CTCACTTCTCATACAACATTGG R:CACAACAGAACCATCAGTACAT	KP279069
SCF126993	(AC)11	F:TTATGGCTCTCATTAAGCAAG R:CTTATTTGGGGTTGATGTGTA	KP279070
SCF127382	(TC)10	F:GTCTTTAGTGCTGGGTTAAAAG R:TGATTTCTAGTGTCTCCTCTCA	KP279071
SCF12818	(CT)9	F:GTGAGGGAGAGTGTTAGATAGC R:ACAAGAGAAAGAACGACAAGAC	KP278975
SCF128658	(AG)9	F:ATTATTGATGAGTAGTCCCCAC R:TGGTTGATTTGTGTAGAAAGAA	KP279072
SCF13045	(CA)9	F:TGTCCAGTGCTAATATCTGTGT R:TCCTCCAAATCTATGCAAAC	KP278976
SCF130555	(ATT)8	F:GGGTAAAATAAAAGGTTCTCC R:TCCTTACTTGTCGATTAGGC	KP279073
SCF130642	(GA)9	F:AGGCGGAAGATGAAAGTAAT	KP279074

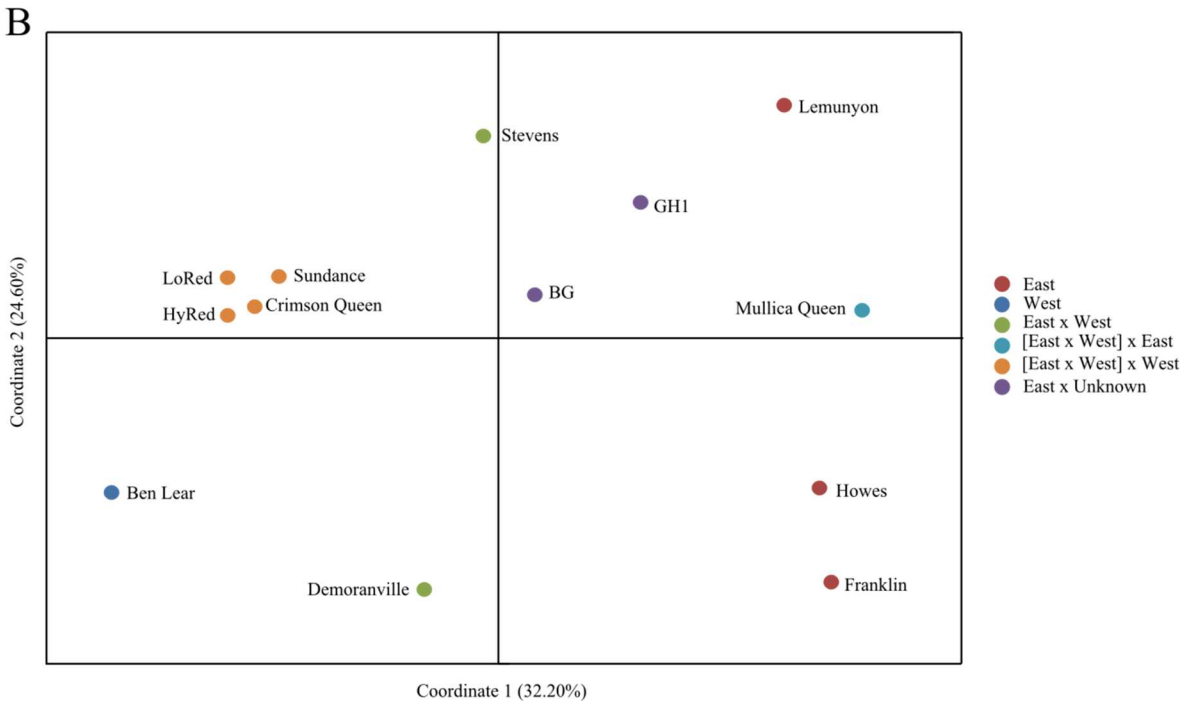
		R:TGTCAACATAAAACGATAGCAG	
SCF132006	(GT)9	F:ATTGAGGTCACTAGGAGGTGTA	KP279075
		R:GAGGAGAGTGTTTATGTTCATGT	
SCF13231	(CT)12	F:GAAACAAAGAGGAGAAGACAAC	KP278977
		R:GTGAAAGGTAAGAGATGGGTAG	
SCF132852	(TC)13	F:TGCTTGTGTTAGGGTTTGTTA	KP279076
		R:GTTAGAGATGATGGCTGAAGAT	
SCF132868	(TG)9	F:CTGATTTGTGTTGATGGATAAG	KP279077
		R:CAGTTAGCACCACCTAGTTAGA	
SCF133587	(AG)10	F:TTAAGCACCAACACTAAATCC	KP279078
		R:AGTTCATGTGACGTTGTATCA	
SCF13393	(AG)16	F:ATATACACAATCGCACGAGAC	KP278978
		R:TCAGCTTACGATCTCACAAA	
SCF134365	(CTT)8	F:GCCTTGTTATGTTACCTGTGA	KP279079
		R:ACAACTATCTGGAAAAGGGTT	
SCF134906	(ATA)7	F:GTATGATTGGTCTTGGTCTGAT	KP279080
		R:GCAACAGCTAGAGATGCTTAAC	
SCF13628	(CT)12	F:AGAGGTCAATAGCTGAAGAAGA	KP278979
		R:AATTCCTGTAGTAAACAGTGGG	
SCF13665	(GT)9	F:TTCTTTACTATACCCACAACCC	KP278980
		R:GTTTCCTAAGAGCATCAACAAC	
SCF136684	(CT)12	F:TCTTATCCTGCTTTCTTACCC	KP279081
		R:ACAGGGTCATTACTGTCTTGTT	
SCF14090	(AC)13	F:GTATTGTCTGGAGATTCCCTAA	KP278981
		R:GCTCTTTGCATCATACTCAA	
SCF142636	(AC)10	F:GGTCATGGTGTCATTCAAG	KP279082
		R:CATGGACAGGTATTGGACA	
SCF142785	(AG)9	F:AGGCTCACATTTCTAACTCAAG	KP279083
		R:ATATCTACCTCCCTAATTTCCG	
SCF14358	(AG)10	F:CCACTAAAACCCTATACTTGGA	KP278982
		R:GTCACTTTTCTATTGCTGGTG	
SCF145195	(GA)14	F:CCACCTTCCATTATACAGCA	KP279084
		R:GAACAAGAGAAGAACCCAGATA	
SCF14690	(CT)9	F:CCTTCCATCTTCTTCTTCAAC	KP278983
		R:AACAAGGTTAGGAAACTAGGGT	
SCF147678	(CT)11	F:ATTCATAGTTTACCCGTCACTC	KP279085
		R:GATTGCTGCTCTTTCAATGT	
SCF14838	(GA)9	F:ATAATTTTGTCCCACACGG	KP278984
		R:TGAGAGTTCAAGGGCAATAA	
SCF14877	(TG)10	F:CCCATGATCCTATGTATGCT	KP278985
		R:AGCTCTGATACCAAACTGTCAT	
SCF148938	(AT)10	F:CTTCTGTCATTTTAGTGTCCTG	KP279086
		R:ACCTTTTGAACACATTGGAC	
SCF149145	(CT)12	F:CTTCAACATATACCCACCCTAT	KP279087
		R:GACCAAAACTAGAAAACTCCCT	
SCF150395	(TC)12	F:CTCTGGTTCATCCCTCTGT	KP279088
		R:CAGACCCTGTCGTTACAAAT	
SCF150410	(TAC)7	F:AACGTAGACACGAAAAGAAGAC	KP279089
		R:GCTAGACATGGTTGGAAGAC	
SCF15112	(GT)12	F:GTATTGTGAGAGGATGACCTG	KP278986
		R:AAGGGCTTTAGTGTTGTTGT	
SCF15143	(AT)10	F:AAAGCCTGCAAATACTCCTA	KP278987
		R:CAAACTAGGTCACAAGCACTTA	
SCF152348	(TC)9	F:AGGAGCAAGAAGAGGTGTTT	KP279090
		R:CCATTGTTTTGCACTTCAG	
SCF1524	(GA)12	F:TAACATACAGTCCTCGACAAGA	KP278957
		R:GATCTAGTTGTTCTTCCGCAT	
SCF15729	(GA)13	F:GAACTGGCTCACTAAAAGAACT	KP278988
		R:GGTGCATAGCGATCTTACTATT	
SCF157301	(AG)10	F:CGTTACATACTCCACCCAAT	KP279091
		R:GATTTCAAGAAGGGTTTGTG	
SCF157676	(TC)10	F:GTCCGCAGTGTCTATGTTT	KP279092
		R:CATACCTTAGATGGTGATTAGG	
SCF16186	(CT)10	F:CTTGTATCAACTTCCATCGTCT	KP278989
		R:CCAAAACCTGAGAAACTTAGAG	
SCF164500	(AG)10	F:AAATCACCATTCTGGAACAC	KP279093
		R:GGTCGGAATACTAAAACAGAGA	
SCF165	(AG)9	F:CCTCCTCAATCTTCTTCTCC	KP278955
		R:TATCTTAAACGGCTGATCTCTG	
SCF171768	(AG)13	F:GTATCCCCTTATACAACCTGC	KP279094
		R:GGCTTCTATTATTCTATTGCCC	

SCF18113	(AG)11	F:GAAGACATCAAAACTGGGACT R:TCAGATCAACACTGGACTAAGA	KP278990
SCF186078	(GAA)10	F:TAGAAAGCAGTAGAGGAGGAAA R:CTTTTCGGATCTGTTTGGT	KP279095
SCF19055	(CA)10	F:AACTCTCACCAAAGGTATTGTC R:GTGACGCTAGATGAGGACTTA	KP278991
SCF195276	(GA)9	F:GTACACTCAAAAGGGAAGAAAC R:TGGCGTATGAGAAGAAGATT	KP279096
SCF197012	(CT)9	F:GTACGATACAACATGGACACA R:ATATAAACAGGGATGCGACT	KP279097
SCF19788	(TC)13	F:TTCTCTGACTTGTCTCGACC R:CATTCCTGAAAACAACTACTCC	KP278992
SCF203038	(TC)12	F:CACTTCTGTACCCTCTTTTACC R:GTCTCATACCTGAATTTTCTGC	KP279098
SCF221037	(TC)9	F:ACACTACAAGCAACAGACAAGT R:TAGTCGAGGTGTGCGTAAG	KP279099
SCF22339	(AG)11	F:CCTCAATCTTATGGATCGAA R:TTGTAGAAGAACCTGTAATGGG	KP278993
SCF2270	(AG)12	F:TTGGTGTAAAGAAGGATAGGAG R:GGCTCCAACTAATGCTATGA	KP278958
SCF22993	(CTT)7	F:GACTGTGCGTAGACTTGATCT R:AAGTATGTGTAGGCCGAAAA	KP278994
SCF24570	(TC)11	F:GGATGCTGTCAAAGATATTG R:TAAACAACTGAGAACTGTAGGC	KP278995
SCF27509	(AG)12	F:ACCAGAAGAACCATGAACTG R:CAAGAAGCCTGATATGTTGTC	KP278996
SCF2942	(GA)11	F:ATAAGATCGGTGAAGGATAGG R:AAGGAGATTAAGAAGGTCCAAG	KP278959
SCF29521	(AG)10	F:CTCAATGCTTCGGAGTAGATA R:CTCCTTGTTTTCACAGGTATG	KP278998
SCF29529	(AG)12	F:AACAGGGAGTTTTCCTACTCTT R:GTATGATGGGAATGGGATAGT	KP278997
SCF30167	(TC)11	F:AGACATACGAAGTCCATGAAAC R:CACCCATAACTCACCTCTAATC	KP278999
SCF30716	(TC)9	F:ATCGGTGACAAAGGTAGATACA R:TGTCTAGGTTGAAAACAAGGAG	KP279000
SCF30747	(AG)10	F:AAGTCAACCAATAGGCATAGAC R:TGTAGTAGCAAGCAAGCTGAT	KP279001
SCF3187	(GA)11	F:CCAGAAAACTACAGATACCCTC R:GTACTTACCGGGACAACTCTTA	KP278960
SCF32389	(AG)10	F:CACTATATCCTACCCCAAAGAG R:TTTGCTGTGACTTGAAAGG	KP279002
SCF32769	(AG)13	F:CTTACTGCCTTACATCCTCTTT R:CTGGCAAATAGCTTACAGAAC	KP279003
SCF33205	(TC)9	F:ATTCTGACTGTTTCATTGCC R:AAATGTATTGGTGGGGAAGT	KP279004
SCF33518	(AG)9	F:GTATTCGTACTCCACACCCTT R:TACAGACAACCATACATTAGCG	KP279005
SCF33654	(CT)11	F:CACAGCCTTAACACAGGATT R:GTGGCTCCTTATCTGGGTA	KP279006
SCF34663	(CT)10	F:GTTTAAGTTCTAGCATAGCCGA R:GTACACAAATACAGAGTGTGGC	KP279007
SCF3507	(CA)9	F:GCTAATAAAGGTTGAAGTCTGG R:CCATGTAGTAGTGAGAGCTGTG	KP278961
SCF35370	(TC)9	F:AATCATGGTCTTCTCACGTT R:GTATAATTGCGTAAGTGCTCG	KP279008
SCF36355	(CT)9	F:GTGAAAGGACTGTTTTACCCTA R:GAGGAGGGGTTTCTCTTTT	KP279009
SCF36716	(TG)9	F:CTAGGCAATGATGACAAAGC R:CCCAATAGTTACCACTAAGCAT	KP279010
SCF36905	(AG)9	F:GATAAGCTGTGCTGAAACATC R:CGATAGGGGATAGAATTAGTCA	KP279011
SCF39229	(TC)12	F:AAAAGCTACGATACGAATGC R:AGAAGGAGATAGTCAACGAATG	KP279012
SCF39691	(AG)9	F:TAAACCATAGTCCTCTCCTCC R:GTCCATAACTCCAAATAAGAGC	KP279013
SCF40225	(GT)11	F:GCTTGACTGGATTAGAACAACT R:CTGGGTATCAACATCAACAGTA	KP279014
SCF41166	(TAA)7	F:TTCTAACTCAAGTAGTCCTCCTG R:AGAAGAACAGCAGATTCCAC	KP279015
SCF41759	(GT)10	F:TTGCCATCTTCTTGTTCTTC	KP279016

		R:ACAACATGCTAATGTGGGTACT	
SCF42256	(GA)9	F:ATACTGCTCAACTGATTTAGGG	KP279017
		R:CGGAGGAAAGTCTGCTATATT	
SCF42549	(CT)10	F:CTCTTCAGCCCTAATCATATTC	KP279018
		R:CAGGACAAACATCTAGGTCAA	
SCF4283	(GAA)7	F:CTTGACTTTGTAGTGGTGTTTG	KP278962
		R:CTCCTCCCCTCTTTTAACTAAT	
SCF43996	(ATT)10	F:ATAGTGTATGTATCAGAGCGGG	KP279019
		R:TATTTACGGGAGGTGTGAACTA	
SCF47689	(CT)12	F:TGTAGATGCCGTCAAAGAAT	KP279020
		R:ACTATAACTCCAAGCGCAGTAT	
SCF48612	(TTC)7	F:GAACACGATTTGACATTTCC	KP279021
		R:CTCCTATGTTGTTTTCGTCTGT	
SCF50668	(AC)11	F:CTTAATATGTCCTAGCCCAAAC	KP279022
		R:GAGGTGTAGAATAGTGAAAGTGG	
SCF51607	(AG)10	F:TTATGTAACTGACGCTGATAGG	KP279023
		R:GTAGATTTGCGATGGTGTATG	
SCF5230	(CT)11	F:TTCAAGATGCCTAAACCAGT	KP278963
		R:GTATAGTGGAGAAGAAGGGTGA	
SCF53058	(TC)11	F:TACCACAGTCTCCTTAACAAAG	KP279024
		R:CATACTCTATAATCCACTTCCG	
SCF54555	(CT)10	F:TTACCAAAGCACCCATTAAC	KP279025
		R:ACGACACATATCTCCAAAGTG	
SCF55619	(CT)9	F:CAAAGAATCAGCAGGAGGT	KP279026
		R:GATGTCTAAGGTACAAGGAAGC	
SCF5899	(GAA)8	F:TAGCCTTGGGTATTAGAACACT	KP278964
		R:GGAAGACAAGACAAGAGGC	
SCF5935	(GA)9	F:CTGAACTGAAACACCAAGAAC	KP278965
		R:AGAAATGAGACCTACACTGCAT	
SCF6050	(TC)9	F:TAACAAAATAGAGACCTCCCTG	KP278966
		R:TTGACTGGTTGATGGTGTATAG	
SCF6053	(CT)13	F:GTTGAAGCATCCTACTCAAAAC	KP278967
		R:CCTAGTGAACAGTCATTTCCTT	
SCF61946	(TG)9	F:GGATAAAAGGGTACTCCATACA	KP279028
		R:GGTTCATAGTGGCGAAATTA	
SCF61972	(GA)9	F:CAGATGAATTTAGACGAGTGG	KP279027
		R:TGCATAGCTCAAATATCCCT	
SCF63953	(GA)9	F:GTTGGTGTGGTTCTCATTATC	KP279029
		R:GTGAGTGCTGATAGGGTAGAGT	
SCF65004	(TTC)9	F:GAATCAATCCAGTCCATAGG	KP279030
		R:CTTACACCACTCTTCCCAAC	
SCF65897	(CT)10	F:CTTATTTTGCTGAACCTTGG	KP279031
		R:CTCTAACTATTCTTGCAGCCTC	
SCF662	(GA)10	F:TTGGACAATCTTACCCATAGAC	KP278956
		R:CTTGGCGTGCATAGAATAA	
SCF66313	(CT)10	F:AATTTGACCCTCTTTCCCT	KP279032
		R:GTCCAAAATACACAAACTAGCC	
SCF68007	(GAG)7	F:CACCCACCACAACATAAAC	KP279033
		R:TCTTCTACTGAACAGCTTCTTG	
SCF6819	(CA)9	F:TCATCATCACTCCAACTACAGA	KP278968
		R:TGTAAATTCTGAGCCCTTGT	
SCF74917	(TA)11	F:AAACATAAAGAGCAGCCAGTAG	KP279034
		R:CTGATAAATAGAGACAGACGGG	
SCF76055	(GT)9	F:GATCGAAATGAGGATTTGTG	KP279035
		R:CTCTTCCACTGTCAACTTTTCT	
SCF77055	(CT)9	F:GAACTGGTAAGGTTTGGAACTA	KP279036
		R:CTTGGAAAGGATTCATACTAGC	
SCF77382	(CA)9	F:GTTTTCCACAAATCTAGTCGTC	KP279037
		R:TGTGAGACCAAAGTGACAAG	
SCF7822	(GA)9	F:GTCACTCATGGTAGTATTGTACG	KP278969
		R:AGTCTTACGTTTGGTGTCG	
SCF80777	(GA)10	F:GAGGCAATGTTAGTCTTTGGT	KP279038
		R:GGATACAACAGCTAGAACCACT	
SCF8189	(GA)10	F:GACAAGGAGGAAGAAATAGTGA	KP278970
		R:ACCAGCAGAAGCAGTTAAAG	
SCF83079	(AC)12	F:GTATTCACCAAATCTACCCAGA	KP279039
		R:GTTAAGGATTGTGTCCCTCA	
SCF83872	(TC)10	F:GGAGCTTGAAAACCTAAACA	KP279040
		R:GTTAGTGAGGAGGGGAGAG	
SCF84796	(TC)10	F:CTACTCTTAGGGCATCTCCA	KP279041
		R:CAACACTACTGACCTTCACAAT	

SCF84921	(TCT)7	F:CTTCATCGTCTTATCAGGTTG R:CCAAGTGAGTCTGTGATTGAT	KP279042
SCF85469	(AC)15	F:CCAGATAAGTAACACAACACCA R:GGGAGTGCTCATTTGTAGTC	KP279043
SCF85776	(AG)9	F:CTAAGTTCCAAACAGAGCCTTA R:AAGTTACCACCGCTAAGAAAC	KP279044
SCF87305	(CT)11	F:AATGCTCTCCAGACTTTTCTAC R:GTGCAGTATCAAATGTAAGACG	KP279045
SCF87786	(CT)11	F:AGGGAGATAGTTGTTCCCAT R:GCCTAAACCTAGTAAACTCTGC	KP279046
SCF9045	(GA)10	F:GCAAATGTCACTGTTAGGATAC R:GAAAGGAAGAGAAGTTAAGCAG	KP278971
SCF9100	(TAT)15	F:TTAGTCCCACTCCTCAATTATC R:GGGCTCACTATCACTACTCATT	KP278972
SCF91560	(AAT)10	F:TATTAAACTCACTGCACCTCTG R:TGACCATCTATGAGAAGCTATG	KP279047
SCF92986	(AC)9	F:AACTAACCCGGACACCTAGTAT R:CGAGGGAGACAATATCAAAGTA	KP279048
SCF9350	(TG)9	F:GGATTTACCACACCATTCTG R:AAGAAATTACCACATGCACC	KP278973
SCF95879	(AT)9	F:TTTTACATGAAGTGGTAGAGGG R:CCAGTTGTATAGATTTTGCTGG	KP279049
SCF96306	(TC)9	F:CCTGTAGTGAGTTACCTTCCAT R:GCTGTCAACCATCCATTATT	KP279050
SCF99113	(GA)9	F:CATGACTTGCTTGTATGGTG R:CACAACTCGCATAACTCTACTC	KP279051
SCF99997	(GA)9	F:ATAGGTCATCTCCTTCTTGTTG R:ACTACTACCGTTGATTGCCTT	KP279052

Appendix I-4. (A) Principle Coordinate Analysis (PCoA) based on 507 microsatellite markers and **(B)** 50 microsatellite markers tested and validated on a panel of 13 cranberry cultivars. Genotypes are color-coded based on the similarity of the geographic origins of their pedigrees (i.e. geographic origins are specified as either east, west, or a combination of east and west of the Appalachian Mountains due to artificial selection.



Chapter II

As published in *Genetic Resources and Crop Evolution* (2016) DOI 10.1007/s10722-016-0371-6

Discriminating power of microsatellites in cranberry organelles for taxonomic studies in *Vaccinium* and Ericaceae

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Received: 29 September 2015/Accepted: 18 January 2016/Published online: 02 February 2016

Author contribution statement

B.S., D.F., S.S., and J.Z. conceived the research and designed experiments. B.S. and D.F. performed SSR mining and primer design. B.S. and G.C-P. performed fragment analyses and Sanger sequencing. B.S. and D.F. performed phylogenetic analyses. B.S. developed multiplexing/poolplexing panels. D.F. and S.S. assisted in analyzing results and developing discussion points. B.S. and J.Z. wrote the paper and oversaw the study.

Abstract

Simple sequence repeats (SSRs) in chloroplast and mitochondrial DNA, which have not been previously developed in the Ericaceae or, more specifically, in the genus *Vaccinium*, can be powerful tools for determining evolutionary relationships among taxa. In this study, 30 chloroplast, 23 mitochondrial, and 1 mitochondrion-like SSRs were identified in cranberry (*V. macrocarpon*), and primer-pairs were developed and tested for each locus. Although no polymorphisms were detected for any of the 54 SSR loci in nine diverse cranberry genotypes, all primers were cross-transferable to some extent to a panel of 12 additional *Vaccinium* taxa and four non-*Vaccinium* Ericaceae species. A Neighbor-Joining tree of the estimated average squared distances resolved the species by genus and by section within *Vaccinium*. Similar topologies with increased branch support were observed in Bayesian inference trees constructed from the DNA sequences of six plastid and two mitochondrial SSR loci. Two multiplexing/poolplexing panels of M13 fluorescently labeled primers, which amplify 24 of the 54 markers, were developed and can serve as an efficient, cost-effective means for characterizing the basic molecular phylogeny of *Vaccinium*. Increased understanding of evolutionary

relationships among *Vaccinium* species should facilitate interspecific hybridization and introgression efforts to improve economically important traits of commercial berry crops.

Keywords

cross-species amplification; mitochondria; organelle markers; plastid; phylogenetic analysis; SSR markers

Introduction

Vaccinium L. is a diverse genus of more than 450 species, displaying a broad range of phenological adaptations, which have allowed them to exist in artic, temperate, and tropical environments (Powell and Kron 2002; Kron et al. 2002b; Vander Kloet and Avery 2010). The genus is distributed worldwide and may be epiphytic, hemi-epiphytic, or terrestrial, usually growing in low nutrient, acidic media (Vander Kloet 1988). The taxonomy of the genus has remained of much debate because of its extensive synonymy (Trehane 2004), and because a thorough molecular phylogeny is still lacking for the genus (or for the Ericaceae) (Vander Kloet and Avery 2010). Preliminary phylogenetic relationships within the genus and family have been studied by using morphological data (Camp 1945; Odell and Vander Kloet 1991; Kron et al. 2002a). Additionally, phylogeny has been explored with *ndhF, rbcL, matK*, nrITS sequences, and nuclear expressed, sequence tag - simple sequence repeat (EST-SSR) markers within and among various Ericaceous genera and *Vaccinium* sections (Kron et al. 2002a, b; Powell and Kron 2002; Rowland et al. 2003; Liu et al. 2014). Monophyly of the Vaccinieae genera and within the sections of the genus *Vaccinium* is still uncertain, and likely requires additional molecular data to be resolved (Kron et al. 1999, 2002b; Powell and Kron 2002). Therefore, additional organellar sequence data and molecular marker sets with proven cross-transferability within and among the Ericaceae and the various *Vaccinium* sections are still needed for researchers exploring the taxonomy, evolution, and domestication of these taxa.

Two sections of the genus, *Cyanococcus* A. Gray and *Oxycoccus* (Hill) Koch, contain economically important terrestrial berry crops (i.e., blueberries and cranberries, respectively) for which numerous genomic resources have been generated to facilitate germplasm improvement. In particular, for the American cranberry (*V. macrocarpon* Ait.), next generation sequencing (NGS) studies have resulted in the reconstruction of its complete mitochondrial and plastid genomes (Fajardo et al. 2013, 2014), a nuclear genome scaffold assembly (Polashock et al. 2014), and a reference transcriptome (Polashock et al. 2014). These cranberry nuclear genomic and transcriptomic resources have been used to develop substantial numbers of nuclear and EST-SSR markers (Georgi et al. 2011; Zhu et al. 2012; Schlautman et al. 2015b) for analyzing genetic diversity and genetic mapping studies within the species (Fajardo et al. 2012; Georgi et al. 2013; Zalapa et al. 2014; Schlautman et al. 2015a). In contrast, development and validation of molecular markers from the cranberry organellar genomes have not been attempted, even though organellar SSRs have been used extensively in genetic diversity and phylogenetic studies in other plant taxa at the inter- and intraspecific levels (Wheeler et al. 2014),

To assess organellar SSR utility in higher order phylogeny in the Ericaceae and within *Vaccinium*, SSR loci within the complete cranberry plastid and mitochondrial genomes were mined and validated in multiple cranberry

cultivars and tested for cross-transferability in various *Vaccinium* and Ericaceae taxa. Sequencing of microsatellite loci was performed to detect the presence of indels occurring in regions surrounding the microsatellite, which may cause size homoplasy in SSR fragment lengths among taxa. We investigated phylogenetic relationships based on organellar SSR fragment lengths and aligned DNA sequences in order to begin developing a molecular phylogeny for *Vaccinium*.

Methods

Plant Materials and Nucleic Acid Extraction

Genomic DNA was extracted from fresh lyophilized leaf tissue from greenhouse plants or herbarium sheets with a Macherey-Nagel (MN) Plant II kit (Düren, Germany) following the manufacturer's instructions. Nineteen representatives (both wild and cultivated) of sections *Oxycoccus* and *Cyanococcus*, single representatives of sections *Vitis-idaea* (Moench) Koch and *Batodendron* (Nutt.) A. Gray, and 4 non-*Vaccinium* species were included in the study (Table 2.1).

SSR mining/Primer Design

The complete cranberry chloroplast genome available in GenBank accession JQ757046 (Fajardo et al. 2013) the complete cranberry mitochondrial genome available in GenBank accession KF386162 (Fajardo et al. 2014), and additional attempted organellar genome assemblies (Fajardo et al. 2014; Polashock et al. 2014) were used as references for organellar SSR mining and development in *V. macrocarpon*. WebSat was used to identify microsatellite loci in the organelles and to design oligonucleotide primers for SSR motifs ranging from 1-10 bp, with repeat lengths of mono ≥ 10, di ≥ 5, tri ≥ 4, and tetra through deca ≥ 3 (Martins et al. 2009). We selected a set of 30 SSR primer pairs from the chloroplast, 23 primer pairs from the mitochondria, and 1 mitochondrion-like sequence based on motif length and repeat number for a survey of polymorphism within *V. macrocarpon* cultivars and cross-transferability within *Vaccinium* and the Ericaceae. Primers were designed following the same parameters as Schlautman et al. (2015b).

Visualization of SSR fragment sizes

Polymerase chain reactions (PCR) were performed as described by Zhu et al. (2012); however, 30 PCR cycles rather than 33 were performed, and the PCR product was diluted with 60 μL ddH_2O before being mixed with 15 μL LHi-Di formamide (Applied Biosystems, Foster City, CA, USA). PCR fragment separation was performed at the

University of Wisconsin Biotechnology Center DNA Sequence Facility with an ABI 3730 fluorescent sequencer (Applied Biosystems). Resulting fragments were visualized and individuals genotyped with GeneMarker software v2.6.3 (SoftGenetics LLC, State College, PA, USA).

Sanger Sequencing of SSR loci

New primer-pairs were developed for selected polymorphic and cross-transferable SSRs in order to amplify a larger region surrounding the microsatellite loci for sequencing (Appendix II-1). PCR reactions were performed according to protocols used in the fragment analysis. ExoSAP was performed by mixing 3 μL of PCR product with 0.2 μL of 20 u/μL ExoI (Thermo Fisher Scientific Inc., Waltham, MA), 1 μL of u/μL SAP (Affymetrix, Santa Clara, CA, USA), and 0.8 μL ddH_20; and then incubating for 25 min at 37 °C followed by 15 min at 80 °C. Big Dye sequencing reactions were executed by using 2.4 μL of DNA template from the ExoSAP, 4.9 μL H_20, 1.5 μL Big Dye Buffer (Applied Biosystems), 0.5 μL of 10 μM forward or reverse primer, and 0.7 μL of Big Dye v3.1 (Applied Biosystems). Big Dye cycling conditions were as follows: 1 min at 96 °C, 10 seconds at 98 °C, then 35 cycles of 5 seconds at 55 °C, 4 min at 62 °C, and 7 min at 72 ° C. Big Dye reactions were purified with a CleanSeq magnetic bead sequencing reaction kit (Agencourt Biosciences, Beverly, MA, USA), and cleaned Big Dye products were sequenced on an Applied Biosystems 3730 fluorescent sequencer. Sequences were manually edited with Geneious 6.1.6 (Kearse et al. 2012) and aligned with MUSCLE (Edgar 2004). Further manual alignments were done in eneious 6.1.6 to minimize gaps, set to prefer transitions over transversions (Kearse et al. 2012). Obtained sequences are available in GenBank.

Phylogenetic Analyses

Pairwise genetic distances based on the fragment analyses were estimated by using the average squared distance (D1) measure, which accounts for possible size homoplasy and is suitable for reconstructing trees that include distantly related taxa (Goldstein et al. 1995). Distances were computed with MICROSAT2 (Minch et al. 1998) with the options of 1000 bootstrap replicates, analysis using nucleotide counts rather than repeat scores, and repeat lengths of one. The genetic distance matrices were imported into PHYLIP 3.695 (Felsenstein 2005), and a Neighbor-Joining tree was constructed by using NEIGHBOUR with 1000 bootstrap replicates and *Rhododendron* as an outgroup. A majority rule consensus tree was calculated with CONSENSE.

Three sequence matrices (mitochondrial, plastid, and combined organellar) were produced within Geneious 6.1.6 (Kearse et al. 2012). The three matrices were gap scored with FastGap v1.2 (Borchsenius 2009), and a presence-absence matrix was concatenated to each matrix that treated indels in complex regions as single mutational events (one character), and which also treated every gain or loss of an SSR repeat as a single mutational event (Bänfer et al. 2006). The optimal evolutionary model was estimated with jModelTest v2.1.5 (Posada 2008) for the aligned loci and concatenated matrices, and all decision theory methods suggested the HKY85 substitution model (Hasegawa et al. 1985).

Bayesian analysis was carried out in Mr.Bayes v3.2.1, with the HKY85 substitution model (Ronquist et al. 2012) run on a total of 1,100,000 generations, with the first 100,000 trees discarded as burn in and trees sampled every 200 generations. A majority rule consensus tree was calculated to generate posterior probabilities (PP) for each node. Maximum likelihood analysis was carried out with PhyML v3.0 (Guindon et al. 2010) also using the HKY85 substitution model and 100 bootstrap replicates. All trees were visualized and edited with FigTree v1.4.2 (Rambaut 2015).

SSR Multiplexing and Poolplexing Panels

Polymorphic SSR markers identified in the fragment analyses were combined into multiple sets of three primer-pairs with non-overlapping allele ranges and tested to determine if they amplified well under normal conditions. PCR reactions and fragment analyses were performed according to Schlautman et al. (2015b), except that 2.0 μL of ddH_2O were replaced with 0.05 μL of forward and 0.5 μL of reverse primer for two additional SSR primer pairs so that the final PCR was a 3× multiplex reaction. Each multiplex reaction was run with either M13-labelled FAM-6, HEX, PET, or NED (Schuelke 2000); and 1ul of all four fluorescently labeled multiplexed PCR reactions were mixed with 15ul of formamide to create a 12× poolplex of SSR loci for fragment analysis with a custom Dy632 ladder (equivalent to the LIZ 500 standard ladder) on the ABI 3730 fluorescent sequencer.

Results and Discussion

Frequency of SSRs in the cranberry plastid and mitochondrial genomes

Detection of SSRs in the cranberry plastid and mitochondrial genomes, by using Websat (Martins et al. 2009), discovered 88 and 121 perfect SSRs (i.e., single motif in an uninterrupted array), respectively (Figure 2.1). The frequency of SSRs in the mitochondrial genome was lower (1 SSR per 3.8 kb) than in the plastid genome (1 SSR per 2.0 kb), which is similar to previous reports in algae and plants (Kuntal et al. 2012; Wang et al. 2012). Microsatellite loci were more frequent in

cranberry plastids than was previously observed in wheat (Tomar et al. 2014), but less than has been detected in soybean (Ozyigit et al. 2015). Mitochondrial SSRs were more frequent in the cranberry genome than in *Oryza* mitochondrial genomes (Nishikawa et al. 2005), but less than *Brassica* species (Filiz 2014). Tetranucleotides were the most common motif length identified in both the cranberry plastid and mitochondrial genomes (32% and 41%, respectively), which has not been a common occurrence in other plant organellar genomes (Von Cräutlein et al. 2014; Tomar et al. 2014). However, poly A/T repeats, the most common class of SSR loci in plant organelles (Islam et al. 2013), were also the most abundant motif type in cranberry organelles.

Interspecific and intraspecific polymorphic SSRs in cranberry, Vaccinium*, and Ericaceae*

Primer-pairs were synthesized for 30 plastid (15 within coding DNA sequences CDS), 23 mitochondrial (2 within CDS), and 1 mitochondrion-like microsatellite loci based on motif length and repeat number (Table 2.2). All markers produced amplification products in a panel of nine cranberry cultivars and five other *Vaccinium* species (Table 2.1). Of the 54 markers, 24 plastid, 23 mitochondrial, and 1 mitochondrion-like SSRs were selected for testing on a larger set of species (Table 2.1, Table 2.2). A combined total of 100 plastid alleles and 50 mitochondrial alleles (including mitochondrion-like alleles) were found within the Ericaceous taxa for 48 organellar loci. Chloroplast SSRs were more cross-transferable and contained a significantly higher number of alleles per locus (3.53) than the mitochondrial SSRs (2.083) ($p < 0.003$). There was no significant difference between the number of observed alleles for SSR loci within plastid genes (3.53) than in the non-coding regions of the chloroplast (3.53). However, cross-amplification (after 2-3 attempts) of several mitochondrial SSRs appeared to be section-specific within *Vaccinium* due to a lack of primer annealing rather than because of a failure of amplification, which suggested that amplification of these loci could function as informative characters for *Vaccinium* sectional phylogeny (i.e., MT9 only amplified in *Vaccinium* sections *Oxycoccus* and *Vitis-idaea*, and MT10 and MT 13 only amplified section *Oxycoccus*). MT19, the mitochondrion-like locus, amplified a monomorphic pattern in cranberry and the other *Vaccinium* and Ericaceae species as is expected for organellar loci. During the assembly of the cranberry mitochondrial genome using total DNA (both nuclear and organellar DNA), the MT19 mitochondrion-like locus was one of the contigs identified with high homology with other mitochondrial genomes at GenBank, but it was not incorporated into the final genome assembly. More research into the origin of this locus is needed to determine if it should have been included in the final genome assembly, if it is potentially evidence of ancient transfer of mitochondrial

DNA to the nuclear or plastid genomes, or if it could be evidence of mitochondrial heteroplasmy in cranberry (Iorizzo et al. 2012; Woloszynska 2009).

Intra- and interspecific polymorphism in organellar SSR loci has been observed and used in genetic diversity studies for numerous species (Arroyo-García et al. 2006; Wheeler et al. 2014). Interestingly, we detected no polymorphisms among the 9 cranberry cultivars or diploid *V. oxycoccos* for any of the 54 SSR markers despite the use of diverse genotypes as determined by previous studies with polymorphic nuclear SSR markers (Zalapa et al. 2014; Schlautman et al. 2015b). The fact that no polymorphism was observed is surprising because of the extensive rearrangements and large numbers of tandem repeats > 150 nt previously reported within the Ericaceae for its plastid genomes when compared to other Ericales and Asterids (Fajardo et al. 2013; Martínez-Alberola et al. 2013). Additionally, gene loss or pseudogenization has been documented within the *V. macrocarpon* mitochondrial genome, which might be expected to lead to the generation of polymorphic loci (Fajardo et al. 2014). However, a previous study (Fajardo et al. 2014) did not find a single nucleotide polymorphism (SNP) within the 54 mitochondrial genes that could be used to distinguish among three cranberry cultivars; rather, polymorphism was only observed in two indels located outside coding regions that were useful for determining that cranberry had a maternal mitochondrial inheritance pattern (Fajardo et al. 2014) Likewise, SNPs were only observed in four of 121 plastid genes for determining that cranberry plastids were maternally inherited (Fajardo et al. 2014). These observations correspond with the lack of polymorphism in organellar SSRs observed in the present study. Whole genome organellar sequencing for studying duplication, rearrangement, tandem repeats, and synteny is needed to improve our current understanding of organelle genome evolution, speciation, and radiation within the Ericaceae and Ericales.

Relationships based on organellar SSR fragment lengths

Relationships of the *Vaccinium* and Ericaceae taxa in this study were explored by using between-individual genetic distance based on fragment lengths from a selection of 27 polymorphic and cross-transferable organellar markers (Table 2.2). Specifically, the average squared distance (D1) measure developed by Goldstein et al. (1995) was estimated in MICROSAT2 (Minch et al. 1998) with 1000 bootstrap replicates to account for possible size homoplasy within the fragment lengths. The Neighbor-Joining tree constructed from the resulting distance matrix showed *Vaccinium* to be monophyletic, with bootstrap support (BS) of 84% (Figure 2.2). The observed monophyly of the Vaccinieae and placement of *Rhododendron* and *Andromeda* outside the Vaccinieae agreed with past reports (Kron et al. 1999; Powell and Kron 2002). The *Vaccinium* clade was further subdivided into four more recent clades, representing previously named

sections of the genus: *Oxycoccus* (BS = 70%), *Cyanococcus* (BS = 76%), *Vitis-idaea*, and *Batodendron* (BS = 76%) in agreement with earlier studies (Kron et al. 1999, 2002b).

Phylogenetic inferences based on DNA sequence data

DNA for six plastid SSRs and two mitochondrial SSRs (Table 2.2; Appendix II-1) were amplified, sequenced, and aligned for 9 *V. macrocarpon* cultivars, 12 additional *Vaccinium* spp., and 4 additional Ericaceae taxa (Table 2.1). No character, indel, or microsatellite differences were observed that allowed the differentiation of the cranberry cultivars, which may reflect slow rates of recombination/mutation in cranberry organelles or indicate a recent genetic bottleneck in cranberry evolutionary history, as previously proposed based on genetic diversity studies (Bruederle et al. 1996). Size homoplasy due to the presence of indels in regions surrounding the microsatellite was not observed within the *Vaccinium* taxa for markers CP8, CP14, and CP16; all variation in fragment length was based on differences in microsatellite repeat number. However, section-specific indels were observed in *Vaccinium* species for loci CP3, CP12, CP17, MT6, and MT24, which could cause size homoplasies in larger panels of taxa.

Three character matrices, with indels and microsatellite differences coded as binary characters concatenated as a separate partition to the end of the matrices, were created in FastGap for use in Bayesian inference and maximum likelihood (ML) analyses. Bayesian trees were generated for the aligned matrices with posterior probabilities (PP) complemented with bootstrap support (BS) from the ML analyses. Nearly congruent topologies were obtained for the plastid and combined datasets based on these two phylogenetic approaches (Appendix II-2; Appendix II-3; Figure 2.3); the Bayesian tree for the mitochondrial partition yielded a similar topology with lower resolution of taxa within the sections of *Vaccinium* (Appendix II-3).

Vaccinium taxa included in this study were separated from the four non-*Vaccinium* species and were monophyletic (PP=1, BS=95%) based on the mitochondrial sequence data for loci MT6 and MT24, the chloroplast sequence data for loci CP3, CP8, CP12, CP14, CP16, and CP17 (PP=1, BS=100%), and the chloroplast and mitochondria combined sequence matrix (PP=1, BS=100%) (Appendix II-2; Appendix II-3; Figure 2.3). *Rhododendron* sp. and *Rhododendron groenlandicum* (Oeder) Kron et Judd grouped together in all three analyses reinforcing the correct placement of *Ledum* as a subgenus within *Rhododendron* (Kron and Judd 1990). We found strong evidence that *Andromeda polifolia* L. var. *glaucophylla* Link f. and *Leucothoe axillaris* (Lam.) D. Don are members of the Vacciniodeae but not members of the genus *Vaccinium* in phylogenetic analyses of our three sequence matrices (Appendix II-2; Appendix II-3;

Figure 2.3), as well as in the Neighbor-Joining analysis (Figure 2.2), which demonstrates that the SSR fragment lengths can be useful for describing the phylogeny of the Ericaceae at the generic and subfamilial levels.

Strong support for the separation of *Vaccinium* section *Oxycoccus* from the other three sections was found for all analyses (PP=1, BS=100% for the combined and plastid data sets; PP=.94, BS =61% for the mitochondrial dataset) (Appendix II-2; Appendix II-3, Figure 2.3). The taxonomy of section *Oxycoccus* has been debated, with most botanists recognizing only two species, *V. macrocarpon* and *V. oxycoccos* L. (Vander Kloet 1983a). However, other treatments of the section have split *V. oxycoccos* into as many as four distinct species based on ploidy levels and morphological differences (Jacquemart 1997; Suda and Lysák 2001), most often with three distinct species (i.e., *V. microcarpum* (2x) Turcz. ex Rupr.) Schmalh., *V. oxycoccos* (4x), and *Vaccinium hageruppii* (6x) (Á. Löve et D. Löve) Ahokas (Ravanko 1990; Suda and Lysák 2001). Bayesian inference and ML of plastid sequence data suggested that *V. oxycoccos* (2x) and *V. oxycoccos* (4x) are distinct species (PP=1, BS=100%), which reinforces the three or more species hypothesis recently supported with allozyme marker data (Smith et al. 2015). However, molecular support for the separation of *V. oxycoccos* (2x) from *V. macrocarpon* was not found in our analyses despite the same genotypes being genetically distinct based on nuclear SSRs (Zalapa et al. 2014).

Vaccinium section *Vitis-idaea* has sometimes been placed closer to section *Oxycoccus* than to sections *Cyanococcus* or *Batodendron* (Kron et al. 2002b), but was not in our current treatment (PP=1, BS=100%) (Appendix II-2; Figure 2.3), which resembled the treatment of *Vaccinium* based on stem characteristics (Odell and Vander Kloet 1991). *Vaccinium vitis-idaea* L. was separated from the *Cyanococcus* and grouped with *V. arboreum* Marshall (PP=1, BS=89%) based on plastid data, but some evidence of separation between sections *Vitis-idaea* and *Batodendron* was still present (PP=.71, BS=53%) (Appendix II-2). *Vaccinium vitis-idaea* was clearly separated from sections *Batodendron* and *Cyanococcus* in the combined data set (PP=1, BS=88%) (Figure 2.3). Section *Batodendron* was placed in a clade with section *Cyanococcus* in the analysis of mitochondrial sequences (Appendix II-3) and was nearer to the *Cyanococcus* than to the *Oxycoccus* in the analysis of the combined dataset (Figure 2.3), which supported report of successful *V. arboreum* × Highbush blueberry hybrids for commercial blueberry germplasm improvement (Lyrene 2011).

Vaccinium section *Cyanococcus* was monopyletic, separate from both sections *Vitis-idaea* and *Batodendron* in the plastid (PP=1, BS=89%) and combined (PP=.74, BS=44%) phylogenetic analyses (Appendix II-2; Figure 2.3). Species boundaries within *Cyanococcus* have been debated, with some botanists recognizing numerous species (Camp 1945) while others have preferred to recognize only a few due to observations of continuous variation in plant morphology (Vander Kloet 1983b). Separation of taxa within *Cyanococcus* was limited in this study; however, inferences about some

phylogenetic relationships could be made, especially based on the Bayesian inference analyses which tend to perform better than does maximum likelihood when distances between branch lengths are short (Alfaro et al. 2003). *Vaccinium darrowii* Camp and *V. myrsinites* Lam. grouped together in their own clade within the combined analysis (Figure 2.3), which agrees with past observations that *V. myrsinites* may have a hybrid origin involving the two diploid species, *V. darrowii* and *V. tenellum* Ait. Also, *V. fuscatum* Ait., sometimes lumped into the species *V. corymbosum* L., grouped in a clade with the diploid *V. corymbosum* and *V. angustifolium* Ait. (Figure 2.3). Placement of southern highbush blueberry cultivar outside the clade containing *V. corymbosum* and *V. angustifolium* highlights the important role of intrasectional interspecific hybridization during the domestication of blueberry and the development of widely adapted commercial cultivars. Crosses and ploidy manipulations between *V. darrowii* and other members of the *Cyanococcus*, such as *V. corymbosum*, were essential to the development of southern highbush blueberry cultivars with reduced chilling requirements (Darrow and Camp 1945; Dweikat and Lyrene 1988; Lyrene et al. 2003). The placement of the half highbush blueberry cultivar, Northcountry, which lacks *V. darrowii* in its pedigree, in a separate clade from the *V. darrowii* clade differentiates it from the southern highbush blueberry cultivar, Sunshine Blue, that does contain *V. darrowii* within its pedigree. (Figure 2.3). Future taxonomic studies of *Vaccinium* section *Cyanococcus* should include hybrid or domesticated individuals such as the southern and half highbush blueberries studied herein, and those taxa with probable hybrid origins in the *Cyanococcus* such as *V. corymbosum, V. myrsinites, V. angustifolium,* but special care should be taken into consideration to recognize how they complicate the resulting phylogenies (Camp 1945; Vander Kloet 1983b; Odell and Vander Kloet 1991).

Intersectional crosses within *Vaccinium* have been reported with less success in cultivar development, but they represent possible means for introgressing taxon-specific traits into and between the commercial berry crop species (Lyrene et al. 2003). Future studies using our organellar SSRs to investigate *Vaccinium* molecular phylogeny more thoroughly, using nuclear SSRs for comparative genetic mapping among economically important species, and using Next Generation Sequencing (NGS)-based, reduced representation genome sequencing strategies to analyze *Vaccinium* genomic structure and evolution could identify "bridge" species that facilitate intersectional hybridization breeding within the arctic, temperate, and tropical *Vaccinium*.

SSR Multiplexing and Poolplexing Panels

Although size homoplasy was observed for 5 of the organellar SSRs developed herein, fragment analysis with D1 distance approaches and Neighbor-Joining trees yielded similar topologies to sequence-based phylogenetic methods.

To facilitate future SSR fragment-based phylogenies, two multiplexing and poolplexing panels were developed from validated polymorphic chloroplast and mitochondrial SSR loci (Appendix II-4). To demonstrate the panels' utility, the cranberry cultivar, 'Stevens', was genotyped with the panels (Appendix II-5), and capillary electrophoresis of the pooled multplex PCR products in two capillaries separated 23 of the 27 organellar SSR loci used in our analysis of genetic distance (Table 2.1, Appendix II-4).

Conclusions

This study mined, tested, and validated 23 mitochondrial, 1 mitochondrion-like, and 30 plastid microsatellite loci from *V. macrocarpon*. The inherent polymorphism and multispecies cross-transferability of these SSR markers, in combination with multiplexing PCR and poolplexing approaches, suggest that they could be useful for quickly generating distance-based molecular phylogenies within *Vaccinium* and the entire Ericaceae. In addition, Bayesian inference and maximum likelihood analyses of aligned DNA sequences of select organellar microsatellite loci revealed monophyly of the genus *Vaccinium* and four of its sections.

Marriage of previous taxonomies based on morphology with future, large-scale phylogenetic studies that utilize these microsatellite loci combined with nrITS and organellar genes to genotype large panels of taxa could resolve the remaining taxonomic questions within the Ericaceae and its numerous genera. Increased understanding of phylogenetic relationships could shed light on the evolution of unique adaptations in the family (e.g., non-green vs. green, parasitic vs. mycotrophic, insectivorous vs. non-insectivorous, heavy metal tolerant vs. hyper-accumulators, different types of specialized and common mycorrhizal associations, etc.), and help implement intersectional hybridization strategies for improving economically important *Vaccinium* berry crops, such as blueberry and cranberry.

Acknowledgements

1 Corinthians 10:31. The authors thank James Polashock, Jennifer Johnson-Cicalese, and Nicholi Vorsa for their contribution of plant materials and comments on this manuscript. This project was supported by USDA-ARS (project no. 3655-21220-001-00 provided to J.Z. and S.S.); WI-DATCP (SCBG Project #14-002); National Science Foundation (DBI-1228280); Ocean Spray Cranberries, Inc.; Wisconsin Cranberry Growers Association; Cranberry Institute; B.S. was supported by the Frank B. Koller Cranberry Fellowship Fund for Graduate Students; G.C.-P. was supported by the Consejo Nacional de Ciencia y Tecnología (CONACYT, Mexico).

Conflicts of interest

The authors declare that there are no conflicts of interest.

Table 2.1. Cranberry (*Vaccinium macrocarpon* Ait.) genotypes and other *Vaccinium* L. and Ericaceae species used in the study of chloroplast and mitochondrial SSR diversity and cross-transferability.

Vaccinium Section and Species	Cultivar or Selection	Voucher Number or Greenhouse id
V. sect. *Oxycoccus* (Hill) Koch		
V. macrocarpon Ait.*	Stevens	UW-WSGH12-45
*V. macrocarpon**	Bergman	UW-WSGH12-83
*V. macrocarpon**	BenLear	UW-WSGH12-86
*V. macrocarpon**	Early Black	UW-WSGH12-87
*V. macrocarpon**	Franklin	UW-WSGH12-88
*V. macrocarpon**	Howes	UW-WSGH12-89
*V. macrocarpon**	Demoranville	UW-WSGH12-315
*V. macrocarpon**	LeMunyon	UW-WSGH12-323
*V. macrocarpon**	Pilgrim	UW-WSGH12-328
V. oxycoccos L. *2x**	wild selection	UW-WSGH12-363
*V. oxycoccos 4x**	wild selection	UW-WSGH12-366
*V. oxycoccos 4x**	wild selection	UW-WSGH12-370
V. section *Cyanococcus* A. Gray		
V. darrowii Camp*	NJ88-9-29	UW-WSGH12-384
Southern Highbush Blueberry Hybrid	Sunshine Blue	UW-WSGH13-370
Half Highbush Blueberry Hybrid	Northcountry	UW-WSGH13-237
Vaccinum angustifolium Ait.*	wild selection	v0135821 wis-
V. corymbosum L.*	wild selection	UW-WSGH12-372
V. fuscatum Ait.	wild selection	UW-WSGH14-197
V. myrsintes Lam.	wild selection	UW-WSGH14-199
V. section *Batodendron* (Nutt.) A. Gray		
V. arboreum Marshall	wild selection	UW-WSGH14-198
V. section *Vitis-idaea* (Moench) Koch		
V. vitis-idaea L.*		UW-WSGH12-382
Non-*Vaccinium*		
Andromeda polifolia var. *glaucophylla* Link f.	wild selection	UW-Birge-73-1
Rhododendron spp. L.	wild selection	UW-Birge-580-1
Rhododendron groenlandicum (Oeder) Kron et Judd	wild selection	UW-Birge-580-3
Leucothe axillaris (Lam.) D. Don	wild selection	UW-WSGH14-196

*Plants used in an initial screen of cranberry organellar SSRs

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Table 2.2. Location, primer sequences, and cross-transferability of 30 chloroplast (CP), 23 mitochondrial (MT), and one mitochondrion-like SSR loci identified in cranberry and amplified in a set of 13 *Vaccinium* and four Ericaceae taxa. The M13 sequence (5'-CACGTTGTAAAACGAC-3') was added to the 5' end of the forward primers to allow indirect fluorescent labeling of PCR products, and the PIG sequence (5'-GTTTCTT-3') was appended to the 5' end of the reverse primer during synthesis (not included in table).

Primer ID	SSR Motif	Cranberry Allele Size	Multi-species Allele	Primer Sequences (5'-3')	Forward Start Position	Reverse End Position	Gene	*Na*	*C-V*	*C-E*
CP1*	(A)10	180	177-180	F:TCTCTATCCTCTCCCTTTCC R:TCGATGTGTAGAAGAAGCAG	2,380	2,534		4	12	4
CP2*	(A)10	290	282-291	F:GTTAGCAACCCGAATCTAAA R:CAGGTAAATGGTGAGTTCGT	2,989	3,255		6	11	4
CP3*	(A)10	204	199-204	F:CAACTCATTCGCTTTCATTC R:CTATAAGAGACCCGCGCT	8,594	8,771		4	12	4
CP4*	(C)10	206	203-206	F:CATGGTATTTGATTCGCC R:GACGGATTCTGCATATTTTC	15,061	15,241		4	12	4
CP5§	(A)11	224	224	F:TACGAAACAACCCTAAAACG R:CCCAAGATTCCAGACATTTA	21,302	21,500	cemA	1	7	n/a
CP6*	(A)10	176	176-187	F:TCTTCTTTTCTGGCTCTGAT R:GTCCTTGGTTGATCTTTAGC	25,593	25,744		7	12	4
CP7*	(T)10	271	269-272	F:CGGAAATCTCTCACATTCAT R:GGGAGTAATCAAGCCTCTCT	62,690	62,934		4	12	4
CP8*ŧ	(A)10	252	252-255	F:AGACCATGAATACGAGCAAT R:GGCGATGAAAGAAATAACC	64,356	64,581	atpA/atpF	3	12	4
CP9*	(A)10	250	247-252	F:TAGGTTGTCGATTCAGCATT R:TCTCTATGAACCAGTAGTGCG	65,290	65,514		6	12	4
CP10 §	(T)12	275	275	F:TATAATGGTAGATGCTCGGG R:GCACTTGGAAGACGAAGTAG	93,207	93,454	rps19/rpI2	1	7	n/a
CP11*	(T)12	258	256-258	F:CGGGAATAGTAGAAGCCATA R:TCTCGTAGAACCCAATCG	7,432	7,663	rps4	2	11	4
CP12*	(T)12	202	197-204	F:GCAATGGCTTCTTTATCTCT R:AACTCTTTCATTTACGGTGG	20,133	20,306	psaI	5	12	2

CP13*	(A)11	232	230-237	F:GCCAATAGTCCAAAGAAATG R:GCAACAAACAAGGTAGTTCAC	65,785	65,992	atpF	6	12	4
CP14*	(T)12	257	254-263	F:ACTTTCGCGTCTCTCTAAAA R:GGCAACCCATTGCTATATT	207	436	psbA	8	12	4
CP15*	(T)14	262	256-262	F:GGCGTATTGCTTGACGTA R:ACGGATTCTTGAACCTCTTT	101,800	102,032	rps7	2	12	4
CP16* ⊦	(AT)5	232	230-250	F:ATAGCCCTTCGTGTTTGTAA R:CCGTTCGTCTTTCTTAATTG	13,262	13,466	trnV-UAC	7	12	4
CP17* ⊦	(TA)5	243	243-283	F:TCCCTACCTATTCCTTCTCC R:GGATTTGAACCTACGACATC	33,713	33,929	trnP-UGG/trnW-	4	12	4
CP18 ⸸	(TA)5	209	209	F:ACAAGAAAGGGATGTAGCAA R:GGGGTGGTGTGACTATGTAA	37,119	37,301		1	7	n/a
CP19*	(AT)5	270	270-270	F:GTACTCCGGCCATAACATAA R:GGTATTTCTGTGAGTCCTCG	72,729	72,973	rpoC2	1	12	4
CP20*	(AAG)4	130	124-132	F:GGTAGAGCCAAAGAGTGTGA R:TACTTCTTAAACGGTGAGGC	30,968	31,074		3	12	4
CP21	(GAA)4	248	248-248	F:TTTTCCTCAACCCTTCTTC R:ATTTGAATCTAGGGCAAGAG	32,652	32,875		1	11	3
CP22 ⸸	(AAT)4	323	323	F:TCTAAATCATGCGAGCAAC R:TGATGGCTCAAGTAGGAAAT	58,228	58,525		1	7	n/a
CP23*	(TTA)4	167	159-167	F:AATATCCCCAGTTTTCTTCC R:AATTTGTGAGGGTCGTTCTA	68,452	68,593	rps2	2	12	4
CP24 ⸸	(CTT)5	252	252	F:AGACGCTCTTGGTAAGTCTG R:ACTAAAAGAAAAGGCAAGGG	45,644	45,868		1		n/a
CP25*	(TTC)5	259	247-262	F:AGCCAAGTGGATAATAAGACC R:TAAACGTCCAAAGAAACCTC	83,800	84,031		4	12	2
CP26*	(ATGG)3	270	258-355	F:GAAAATATGCAGAATCCGTC R:AATTTAGTTGCTACCGTCCA	15,222	15,466		4	11	3
CP27*	(TTCT)3	246	246-268	F:TCACGTAATGAGCGGACT R:TCGAATTGGGTCCTATGTAT	26,902	27,120		3	11	4
CP28 ⸸	(TTCT)3	232	232	F:AACCCTCGGTACAAATAACTC	61,063	6,129	trnS-GCU	1	7	n/a

				R:CCTAACTTTATCGAAACGGA						
CP29	(AATT)3	317	263-317	F:CGGTCAGTATAGTTTCTGTGG	141,299	141,587	ndhF	5	9	1
				R:CTGATAACACCCATTCCATT						
CP30*	(TTTCTT)3	260	259-267	F:GGAACAAAATGGGGTTGA	31,930	32,163	rps18	5	12	3
				R:AATGGAGTGACCGTGAAAC						
MT1	(AGT)4	186	186-186	F:CTTGACCTTATCGTTGTTCTC	22,178	22,339		1	10	3
				R:CTCTTGCCTTTGAAGTAGGA						
MT2	(GA)6	212	212-218	F:ACTACTCCGCTACTGACTGATT	52,000	52,185		2	6	0
				R:GTGATTCTAAAGGAAGCTCTGT						
MT3	(TCC)4	171	171-171	F:GTCACGACTTTCTGTGTCTTT	68,139	68,284		1	9	1
				R:AGTCTATCTCGTATAGCTGCG						
MT4	(TC)5	344	344-344	F:CTGTCTGATCCTTACATCCTCT	91,859	92,174		1	11	1
				R:TTCCTACTTCACTTACCACTCC						
MT5	(AT)5	307	307-312	F:GGCTTTCAGGTATAACACAATC	122,833	123,113		2	7	1
				R:ATATAGTAAGTAGTCCGTGCCG						
MT6*	(TA)5	151	145-151	F:ATATCCCGTGCAATCTATACTC	123,986	124,111		2	12	1
				R:CTAGTTGGAGAAAGGGCTAGT						
MT7	(GAT)5	275	272-275	F:ATGACTTGTCTTCCTTTGAGAC	130,288	130,536		2	12	0
				R:CTCCTTATTGGCCTACTTATTG						
MT8	(AG)5	272	272-272	F:AGAAATAAAAGAGGTAGGAGGG	158,072	158,317		1	10	0
				R:AGCATAGACGATAAGGAGGTAA						
MT9	(TC)5	159	159-159	F:CCTATACCCGTCATTAAAAGG	227,278	227,411		1	4	1
				R:CCTATCTTCTGTCCAAATAAGC						
MT10	(AG)5	356	356-356	F:GATGAGTTAGAGGAGAGTGAGG	221,248	221,575		1	2	0
				R:ACATCTTCTGTTCTGGAAAGTC						
MT11	(TA)5	234	234-234	F:GACACATCACATACAGTGCTAA	269,968	270,174		1	7	1
				R:CTCACAAATGGCTCTACTTTC						
MT12	(A)12	215	215-339	F:GAGCCATTCTAAGTAGTGTCAA	271,721	271,912	atp1	3	5	0
				R:CTCATGTAGTGGAATATGCAGT						

MT13	(TC)5	257	257-257	F:GAGGAAGAGAAGAATAGGGTCT R:AGCTCGGATAAGGAAAGAGTA	277,835	278,064		1	2	0
MT14	(AT)5	367	367-369	F:CTGATAGATGTAACTGCCCTTT R:ATCCACCTTAGTGCTCTCTCTA	296,307	296,646		2	9	1
MT15*	(AG)6	338	333-344	F:ATCTGGAGACATACTGAAAAGC R:GTACAAGTGCTGCGTACAAGT	303,848	304,159	nad4	4	11	4
MT16	(GA)5	358	358-364	F:GGGTCAATTCTAGTTCAGTTTG R:CTGTGGGATATTCAAGGTAGTT	319,858	320,188		2	10	1
MT17	(AG)5	279	279-279	F:CCCCTTATTGTAGTGTTCTAGC R:CTACCTCATTTCCCAAACC	342,016	342,269		1	10	1
MT18*	(T)12	342	342-352	F:ATCTGTTCTAGTCATCCGTTCT R:TCTTAGGGAGTAGGATCTGTTG	347,115	347,427		4	12	3
MT19	(TC)5	183	179-189	F:GAGAATAGCTTCCCCTTCTG R:GCAGATGATTACTTCGATCTCT	Mitochondria-like			3	12	3
MT20*	(TA)5	309	303-309	F:CATGTCTTAGGAAACTCAAAGG R:GTCCAAGCAAGTAGTTCTAACC	436,104	436,387		2	12	2
MT21	(AG)5	247	247-247	F:AGCTATGCTGGTTCTGTAGAGT R:GAGAAGAAAGATGAAGCTGAAG	389,142	389,362		1	12	1
MT22	(TC)5	357	352-357	F:GTGGGCTTATTACCTCTATTTG R:CTTAGCTCAATATCCTTTCACC	365,995	366,324		2	11	1
MT23	(A)12	369	369-379	F:ACTCAGCTTCAGGAAAAGTAAG R:ATAGAAAAGGTTGGAGAGAGTG	353,565	353,906		4	9	2
MT24*	(AGA)4	361	353-366	F:CGTAAGTAATGGTCGAAGTACA R:CAAGCTCAAAAGAAGAGTGAGT	397,805	398,139		6	12	4

Cranberry Allele Size: The fragment length observed in the 9 *V. macrocarpon* accessions
Na: The number of observed alleles within the panel of *Vaccinium* and Ericaceae taxa
C-V: The number of *Vaccinium* taxa to which the SSR marker was cross-transferable
C-E: The number of *Ericaceae* taxa that the SSR marker was cross-transferable
* Used to estimate average square genetic distance (D1) between taxa
ˢ Primers not polymorphic and excluded from additional analyses of cross-transferability
ꟻ Primers used in subsequent Sanger sequencing

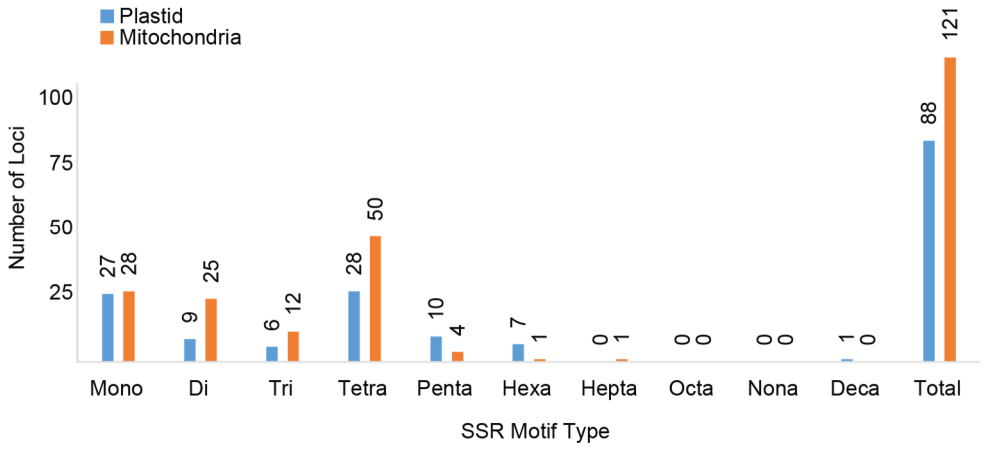

Figure 2.1. The number of SSR loci identified in the cranberry (*Vaccinium macrocarpon*) plastid and mitochondrial genomes sorted by motif length from mononucleotides (Mono) to decanucleotides (Deca).

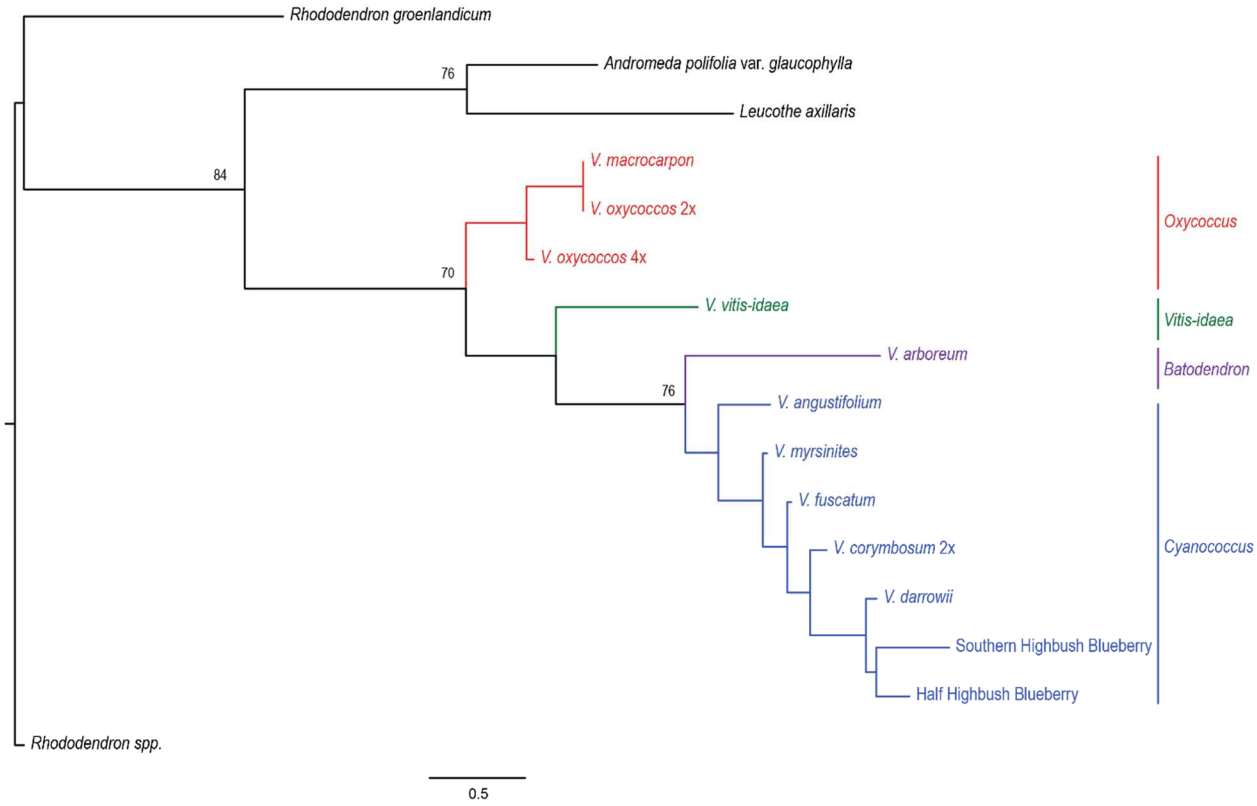

Figure 2.2. Neighbor-Joining tree based on the average squared distances (D1) from Goldstein et al. (1995) using 27 mitochondria or chloroplast SSR loci (Table 2.2) calculated for 13 *Vaccinium* species and 4 non-*Vaccinium* Ericaceae taxa (Table 2.1).

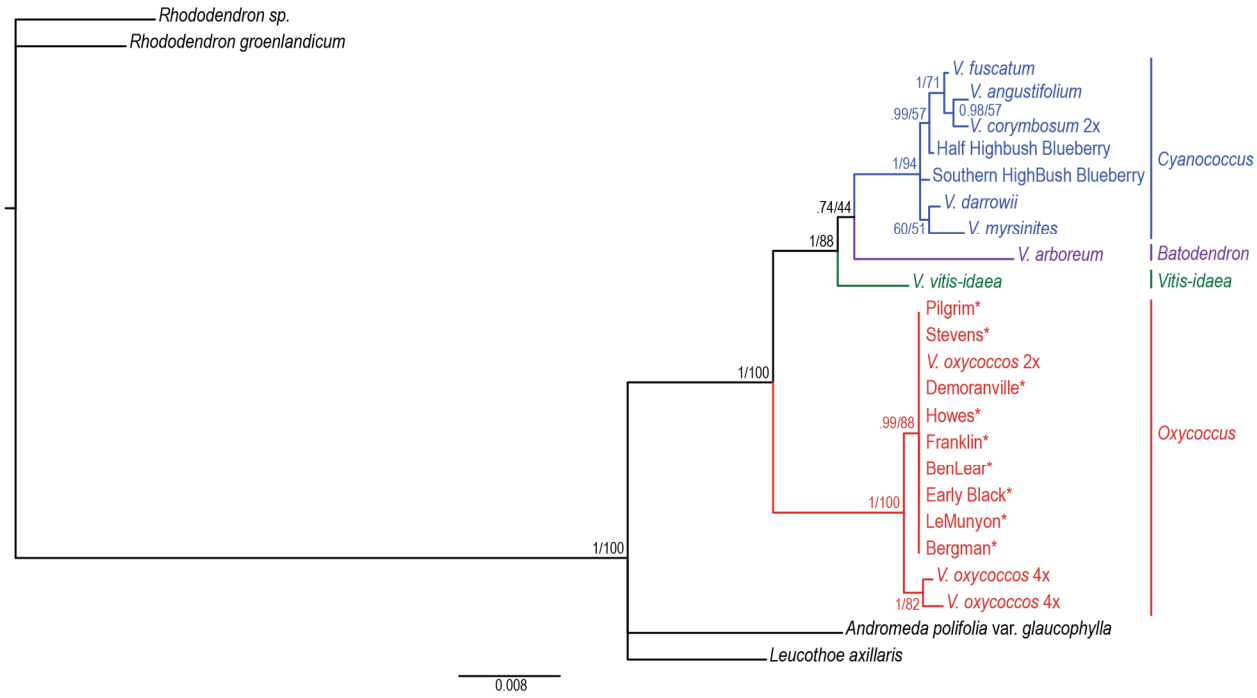

Figure 2.3. Bayesian inference tree of nine cranberry (*V. macrocarpon*); three *V. oxycoccos*; 11 other *Vaccinium* spp. from sections *Cyanococcus*, *Vitis-idaea*, and *Batodendron*; and 4 other Ericaceae species based on aligned nucleotide sequences with indels and microsatellite differences coded as binary characters and concatenated as a separate partition to the end of the aligned sequence matrix for six chloroplast (CP3, CP8, CP12, CP14, CP16, CP17) and two mitochondrial SSR loci (MT6 and MT24). Branch labels are posterior probabilities (PP) from Bayesian inference followed by bootstrap support (BS) by maximum likelihood.

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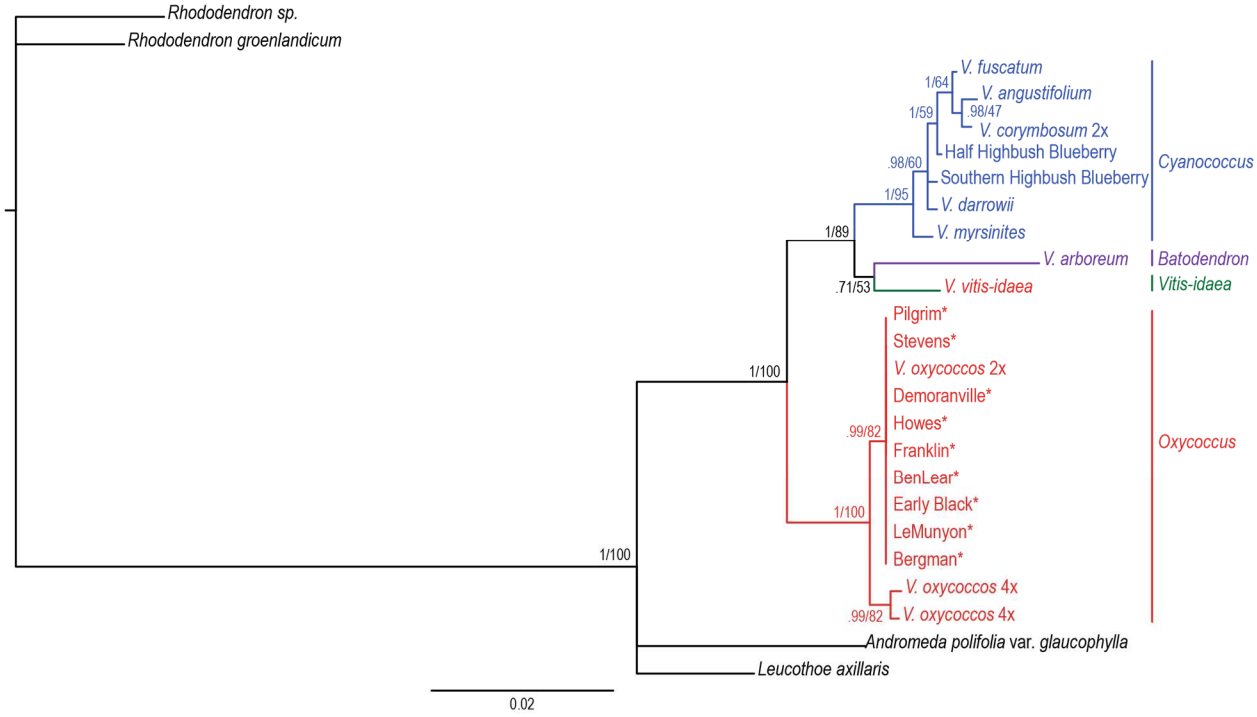
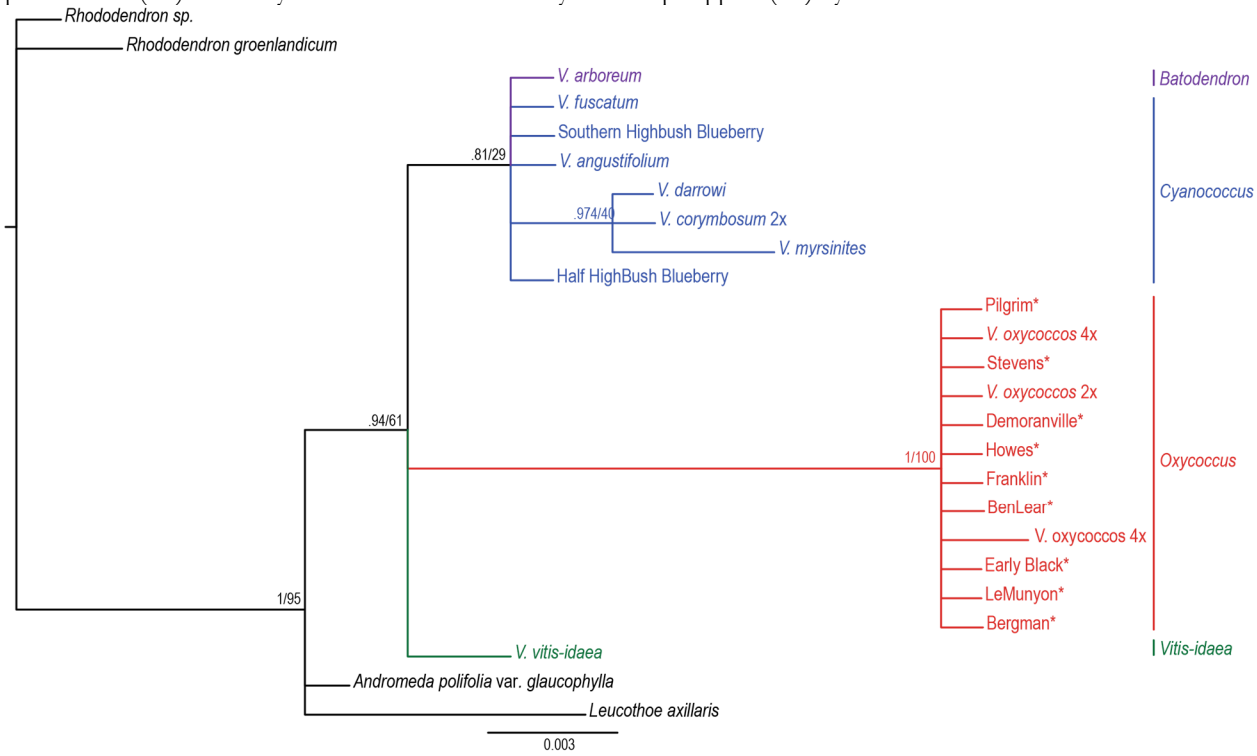
Appendix II-1. Redesigned primers for Sanger sequencing that amplify larger regions surrounding 6 of the polymorphic and cross-transferable SSR loci chosen for sequence-based phylogenetic studies in *Vaccinium* and Ericaceae.

ID	Primer	Genome Start Position	Genome End Position
CP3Seq	F:caactcattcgctttcattc	8594	8613
	R:ttagtaggtttccataccaagg	8754	8771
CP8Seq	F:cttcatcaagaccatgaatacg	64348	64369
	R:attaatcaaatccgacaacgag	64682	64703
CP12Seq	F:tttagtaggcctagtatttccg	20105	20216
	R:tgtgagcctttaggaaaaattc	20492	20513
CP14Seq	F:cacgaataccatcaatatcgac	44	65
	R:aggaaattatctactccatccg	460	481
MT6Seq	F:tgttccgtgtattgtatagagg	123907	123928
	R:aggttgactttgaaaaagatcc	124245	124266
MT24Seq	F:ggtcaataagggtctgtctatc	397851	397872
	R:ccaggatcaaactctgattttg	398333	398354

Appendix II-2. Bayesian inference tree of nine cranberry (*V. macrocarpon*); three *V. oxycoccos*; 11 other *Vaccinium* spp. from sections *Cyanococcus*, *Vitis-idaea*, and *Batodendron*; and 4 other Ericaceae species based on aligned nucelotide sequences with indels and microsatellite differences coded as binary characters and concatenated as a separate partition to the end of the aligned sequence matrix for six chloroplast SSR loci (CP3, CP8, CP12, CP14, CP16, CP17). Branch labels are posterior probabilities (PP) from Bayesian inference followed by bootstrap support (BS) by maximum likelihood.



Appendix II-3. Bayesian inference tree of nine cranberry (*V. macrocarpon*); three *V. oxycoccos*; 11 other *Vaccinium* spp. from sections *Cyanococcus*, *Vitis-idaea*, and *Batodendron*; and four other Ericaceae species based on aligned nucelotide sequences with indels and microsatellite differences coded as binary characters and concatenated as a separate partition to the end of the aligned sequence matrix for two mitochondria SSR loci (MT6 and MT24). Branch labels are posterior probabilities (PP) from Bayesian inference followed by bootstrap support (BS) by maximum likelihood.

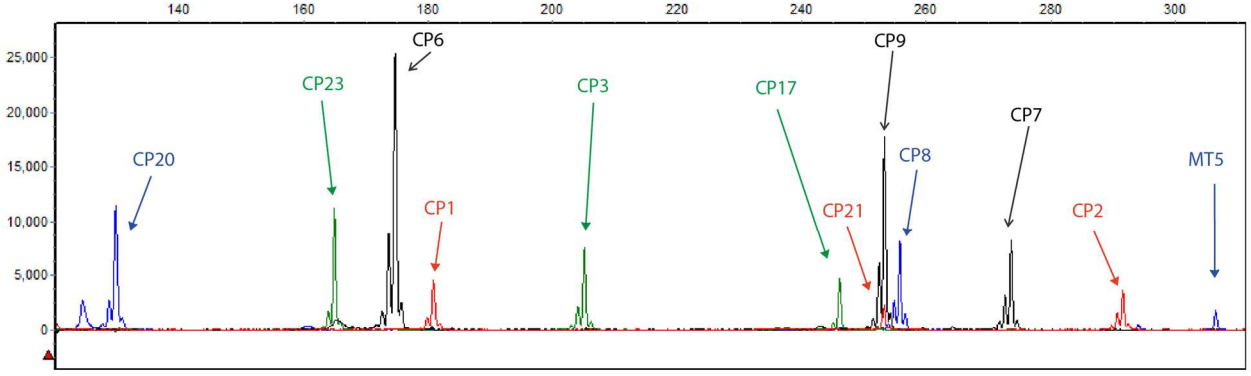


Appendix II-4. Two multiplexing/poolplexing panels designed for 24 organelle SSR loci. Synthesized forward primers contain the M13 sequences (5'-CACGTTGTAAAACGAC-3') to allow indirect fluorescent labeling with FAM, HEX, NED, or PET labeled primers. Multiplexing PCR reactions were run in the presence of a single fluorescently labeled M13 primer with three SSR primer-pairs amplifying non-overlapping allele sizes. The resulting PCR products run with the four different fluorescent dyes (i.e., 12 total SSR markers) are pooled for fragment analysis with a custom Dy632 ladder in a single 50cm capillary on an ABI 3730 fluorescent sequencer.

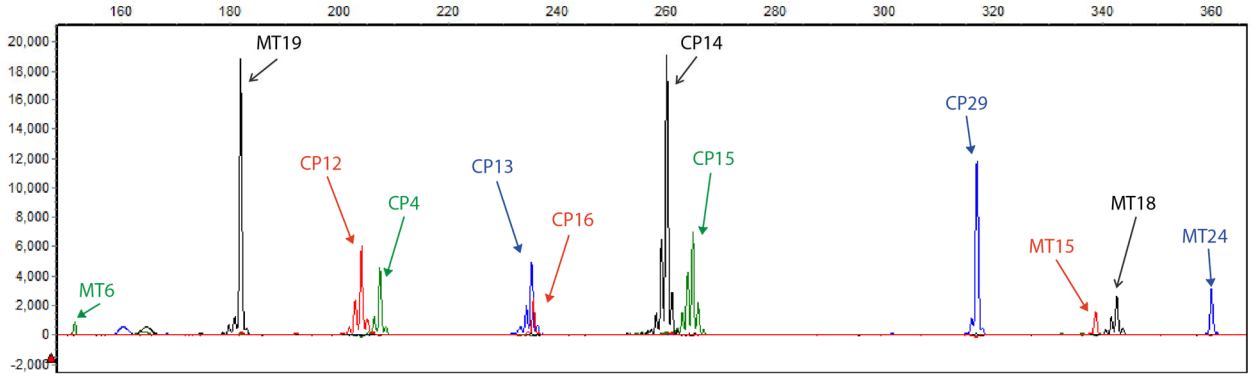
	FAM			HEX			NED			PET		
Panel	Locus 1	Locus 2	Locus 3	Locus 1	Locus 2	Locus 3	Locus 1	Locus 2	Locus 3	Locus 1	Locus 2	Locus 3
Panel 1	CP20	CP8	MT5	CP23	CP3	CP17	CP6	CP9	CP7	CP1	CP21	CP2
Panel 2	CP13	CP29	MT24	MT6	CP4	CP15	MT19	CP14	MT18	CP12	CP16	MT15

Appendix II-5. Visualization of alleles of 24 chloroplast and mitochondrial SSR loci in the cranberry cultivar 'Stevens' amplified in multiplexing/poolplexing panel one (**A**) and panel two (**B**) with M13 FAM (Blue), HEX (Green), NED (Black), or PET (Red) labeled primers.

A)



B)



Chapter III

Cranberry SSR multiplexing panels for DNA horticultural fingerprinting and genetic studies

Abstract

Cranberry (*Vaccinium macrocarpon*) is in need of inexpensive high-throughput DNA fingerprinting methods for genetic research and germplasm purity testing for agricultural purposes. Therefore, we designed and validated 16-multiplexing panels containing 61 evenly distributed simple sequence (SSR) markers, with non-overlapping allele ranges, throughout the 12 cranberry linkage groups. Several important cranberry cultivars and selections (n=18) and a diploid accession of *V. oxycoccos* were genotyped with the multiplexing panels and separated through principal component analysis (PCA) to demonstrate their effectiveness for DNA fingerprinting and genetic diversity analysis. A subset of 3 multiplexing panels containing 12 SSR markers was used to genotype 174 seedlings from fruits collected in a commercial cranberry bed of the cultivar Stevens, and identification of intra-cultivar heterogeneity was investigated in the bed to validate the use of the markers in such future applications. Furthermore, determining the likelihood that each seedling was self- or cross-pollinated provided the first quantitative evidence ($p < 0.0001$) that the majority of seeds within commercial cranberry beds are self-pollinated. These multiplexing panels represent an important, applicable resource for cranberry researchers and farmers of the North American industry. These markers can be used to assess the genetic homogeneity of grower and licensed propagators' cranberry beds, to protect the intellectual property rights of plant breeders, and to enable cranberry researchers to monitor the genetic identity of genotypes within their breeding programs and genetic studies.

Key words

Vaccinium macrocarpon; Microsatellites; Multiplex-PCR; Genetic diversity; Clonal purity; Selfing

Introduction

The American cranberry (*Vaccinium macrocarpon* Ait.) is a low trailing, woody shrub native to North America. It reproduces both sexually through flowers on short vertical branches and asexually through prolific, easily rooting stolons, which allow individual genotypes to form dense mats of vines covering multiple hectares in commercial cranberry beds (Brown and McNeil, 2006). During cranberry domestication in the mid-1800s, growers selected high yielding genotypes from wild stands based on fruit characteristics, and then propagated them as vegetative cuttings in large beds of a presumed single genotype (Peltier, 1970; Fajardo et al., 2012). This process was facilitated by several wild genotypes with unique berry architectural types (e.g., pyriform shaped Ben Lear). A collaborative culture of sharing and selling vines among cranberry producers quickly developed, and more than 100 such wild selections were made, named, clonally preserved, and sold in commercial production during the 19th century (Dana et al., 1983). Today, cranberry remains an asexually propagated crop, and producers still grow, share, and sell vines of some of the same wild selections from the 19th century in addition to newer hybrid cultivars.

Cranberry beds can remain productive for many decades and gradually decrease in genetic homogeneity due to the establishment of selfed or outcrossed seedlings within the bed (Fajardo et al., 2012). Because vine and foliage characteristics vary little between cranberry genotypes (Chandler and Demoranville, 1958), unnoticed genetic diversity within cranberry beds whose vines are mowed, sold, or replanted in combination with human errors in record keeping has resulted in intra-clonal genetic heterogeneity within named wild selections and hybrid cultivars developed during the mid-20th century. Multiple studies have been performed to assess the extent of cultivar misclassification and genetic contamination of cranberry germplasm both in breeding programs and the industry in general using isozymes, random amplified polymorphic DNA (RAPD), sequence characterized amplified regions (SCAR), and simple sequence repeat (SSR) markers (Fajardo et al., 2012; Novy and Vorsa, 1995; Novy et al., 1996; Polashock and Vorsa, 2002; Boches, 2005). Furthermore, since the mid-2000s, a new generation of hybrid cultivars adapted to meet the needs of the modern cranberry farmers have been released (McCown and Zeldin, 2003; Clark and Finn, 2010). Several actions such as plant variety protection, use of licensed propagators for vine sales, and licensing agreements between breeders and growers have been undertaken in an attempt to maintain the genetic purity of these new cultivars. These actions and the royalties required to plant the new hybrid cultivars, combined with large financial input of preparing a cranberry bed to be planted have caused the replacement of existing beds to be a difficult decision and large investment for current grower's in the industry.

Inexpensive and efficient high-throughput DNA fingerprinting technologies using available molecular markers should be an important additional strategy for maintaining the homogeneity of cranberry cultivars. Also, these same DNA fingerprinting technologies could serve as an affordable way for cranberry producers to determine the purity of aged beds when deciding to either replant the bed which has become genetically diverse or to adjust management practices in the bed which is still homogenous. In recent years, multiple studies have generated SSR markers from cranberry next generation sequence data (Schlautman et al., 2015a; Zhu et al., 2012; Georgi et al., 2011), and some of those SSRs have been positioned in genetic linkage maps (Georgi et al. 2013; Schlautman et al., 2015b). However, no standard high-throughput SSR fingerprinting multiplexing panels have been made available to cranberry researchers and industry.

The primary objective of this study was to develop cranberry high-throughput SSR multiplexing panels for inexpensive fingerprinting and testing of genetic diversity in cranberry germplasm. A total of 16 multiplexing panels containing 61 evenly distributed SSR markers, with non-overlapping allele ranges, throughout the 12 cranberry linkage groups were designed and validated in various multiplexing panels combinations to genotype a set of important wild and hybrid cranberry cultivars (Schlautman et al., 2015b). To demonstrate the discriminating power of the SSR multiplexing panels and to test the long-standing hypothesis that the majority of commercial cranberry fruits contain self-pollinated seeds, 3 selected panels, containing 12 SSR combinations, were used to determine whether seedlings from individual fruits collected from a commercial cranberry bed of the cultivar, Stevens, were self-pollinated or were pollinated by cultivars grown in surrounding beds.

Materials and methods

SSR selection, grouping, and PCR conditions

Using only markers with known genomic locations, the SSR primer-pairs were grouped into potential PCR multiplexing combinations of three or four SSRs using the following criteria: the SSRs must have non-overlapping allele ranges according to their previously published fragment length; they must not be linked, they must be located at greater than 10 cM from the tip of each chromosome; they must anneal and amplify PCR products from a single genomic location; and they must not contain any known null alleles based on previous data (Schlautman et al., 2015a; Zhu et al., 2012; Georgi et al., 2011; Georgi et al. 2013; Schlautman et al., 2015b). Throughput potential was increased by pooling 4 PCR multiplex reactions, one for each dye (M13-FAM, HEX, NED, or PET labeled primer) and containing 3-4 SSR markers per dye to be analyzed in a single fragment analysis run.

Forward primers from the selected SSRs were appended with the M13 sequence (5'-CACGTTGTAAAACGAC-3') to allow for indirect fluorescent labeling of PCR products (Schuelke, 2000), and the PIG sequence (5'-GTTTCTT-3') was appended to reverse primers to promote full adenylation of SSR fragments during PCR (Brownstein et al., 1996). Using primers with the M13 sequence in the presence of a universal fluorescently labeled M13-tail is much more economic than direct fluorescent primer labeling (Guichoux et al., 1996); furthermore, it allows the primer-pairs and their multiplexed combinations to be indirectly labeled with any fluorescent type (color) suitable for the intended purpose rather than being limited to a specific dye.

Each multiplex PCR mixture was composed of 3.5 µl 1xJumpstart RedTaq Ready Mix (Sigma, St. Louis, MO, USA), 1.0 µl of 15 ng/µl DNA, 1.5 µl of 5 µM forward primer, 1.5 µl of 50 µM reverse primer, and 0.5 µl of 0.5 µM M13-FAM, HEX, NED, or PET labeled primer. The 1.5 µl of forward and reverse primer was divided by the number of multiplexed SSRs (i.e. 0.5 µl and 0.375 µl of forward and reverse primer from each SSR were added when 3 or 4 markers were multiplexed together, respectively). Thermocycling conditions were identical to those used in Schlautman et al. (2015a). Finally, 1 µl of multiplexed PCR product from each of the four M13 dyes were pooled with 0.125 µl of LIZ500 standard ladder and 14.875 µl formamide to create up to a 16x SSR poolplex. The poolplexed mixture was sent to the University of Wisconsin-Madison Biotechnology Center DNA sequencing facility for fragment analysis using an ABI 3730 fluorescent sequencer (Applied Biosystems, Foster City, CA, USA). Allele genotyping was performed using GeneMarker v2.63 (SoftGenetics LLC, State College, PA, USA).

It should be noted that multiplexing additives, often used to enhance multiplex reactions, were explicitly avoided in order to make DNA fingerprinting simpler and more economic for both cranberry growers and researchers. In addition, no attempt was made to adjust primer concentration during multiplex reactions. The main goal was to identify combinations of markers which could be multiplexed together under a universal protocol without having to use additional costly inputs or to reduce efficiency by using specific primer concentrations or thermocycling conditions for individual markers or marker combinations. Finally, PCR reactions were kept to a small volume (8 µl) to further reduce associated costs, and the selected multiplex combinations worked sufficiently under these conditions. However, doubling each of the reactants to increase the reaction volume, and/or increasing the number of PCR cycles, can improve the quality of the resulting products in the form of more intense fluorescent peaks in the fsa files.

Plant Materials and Statistical Analyses

A total of 18 unique cranberry (*V. macrocarpon*) cultivars, consisting of wild selections from the east coast and from west of the Appalachian Mountains and of hybrids generated from crosses or backcrosses among wild cranberry selections, were genotyped in the initial screen of many different SSR multiplex combinations of three or four markers (Table 3.1). In addition, a diploid *V. oxycoccos* selection, a small-fruited cranberry species closely related to *V. macrocarpon*, was included to assess the transferability of these SSR marker combinations. Principal component analysis (PCA) was performed in R using the *dudi.pca* function in the *ade4* package (Dray and Dufour, 2012). Genotype data for the 18 cranberry cultivars and the single *V. oxycoccos* accession was used to determine the number of alleles and allele ranges observed for each multiplexed marker.

In October 2014, 20 mature cranberry fruits were collected from the center of a flooded commercial cranberry bed planted with the cultivar Stevens. The seeds of these fruits were extracted and 174 seeds (~10 seeds per fruit) were planted in the spring of 2016 after the seeds reached stratification requirements (Appendix III-1). Cranberry is highly self-fertile, therefore, it was hypothesized that most of the seeds within those fruits would be pollinated by flowers within the same bed rather than outcrossed from a cultivar in the adjacent bed (Sarracino and Vorsa, 1991). To test this hypothesis, DNA was extracted from leaf tissue from each seedling, and 3 multiplex panels containing 12 loci were used to genotype the seedlings.

Determination of whether a seedling was self-pollinated or cross-pollinated was performed by classifying progeny as outcrossed when at least one or more alleles within one or more of the 12 loci could not have been inherited from Stevens. The progeny was assumed to be a self when all alleles at all loci were consistent with Stevens' inheritance. Additionally, principal component analysis (PCA) was performed in R using the *dudi.pca* function in the *ade4* package, and individuals were colored within the plot of the first two principle components to visually assess whether progeny classified as selfs or outcross clustered together (Dray and Dufour, 2012). Finally, because some intra-cultivar genetic heterogeneity has previously been observed for multiple cranberry cultivars (Fajardo et al., 2012; Novy et al., 1996), we tested to see if some of the seeds may have arisen from fruits which were from some unknown cultivar rather than Stevens. We determined a seed to have a mother other than Stevens when it did not group with the other seedlings in the PCA, when it did not contain at least one allele from Stevens at every locus, or when one of its sibling seeds from the same fruit did not meet the above criteria.

To test whether the number self-pollinated seeds was equal to the number of cross-pollinated seeds in the Stevens bed, chi-square tests were performed with H_0: proportion of self-pollinated seeds= 0.5, proportion of cross-

pollinated seeds = 0.5 and H_1: H_0 is false. Specifically, we performed $\chi^2 = \sum \frac{(observed\ \#\ of\ selfs - total\ seeds \times 0.5)^2}{(total\ seeds \times 0.5)^2}$ with degrees of freedom equivalent to *k-1=1* where *k* is equal to the number of possible responses. In this case the possible responses were self-pollinated or cross-pollinated seedling and *k* was 2.

Results and Discussion

Effectiveness of SSR multiplexing panels for differentiating important cranberry cultivars and characterizing allelic diversity.

A total of 16 different multiplexing panels containing three or four SSR markers which amplify well together in multiplex PCR reactions were identified (Table 3.2). These 16 multiplexing combinations fulfill the previously described selection and grouping requirements, and the 61 markers they contain span the entire cranberry genome with each of the twelve cranberry linkage groups represented by an average of 5.1 SSR loci (Table 3.2). A total of 388 alleles (an average of 6.4 alleles per locus) were observed across the 61 SSR markers for the 18 cranberry cultivars and the *V. oxycoccos* wild selection used. Because a universal M13 sequence was used for indirect fluorescent labeling, the multiplexing panels can be used with any type of fluorescent label. Therefore, cranberry researchers and industry personnel can select subsets of multiplexing panels which contain the most heterozygous or informative markers for DNA fingerprinting of commercial beds or germplasm of interest.

V. oxycoccos had 27 private alleles not found in any of the cranberry cultivars, which was consistent with previous findings comparing genetic diversity of *V. oxycoccos* and *V. macrocarpon* (Zalapa et al., 2014). The cross-transferability of the markers and multiplexing panels suggests that they can be used to generate the first *V. oxycoccos* linkage map, which would facilitate the comparative genetic study between *V. oxycoccos* and *V. macrocarpon*. Comparative genetic studies between the two closely related species could promote future interspecific hybridization strategies for introgressing commercially important traits from *V. oxycoccos* into *V. macrocarpon* (Vorsa and Polashock, 2005).

PCA using the 61 markers clearly separated all 18 cranberry cultivars and the *V. oxycoccos* selection, even the closely related full-siblings HyRed and LoRed (Figure 3.1). The first principal component (PC) explained 24.31% of the total genetic variation; the second (PC) accounted for 19.79% of the variation. Although the sample size is small, some genetic structure and geographic relationships previously proposed in cranberry were observed (Schlautman et al., 2015a; Nilsen, 1995). Cranberry genotypes selected from east of the Appalachian Mountains tended to group in the bottom right quadrant, while genotypes selected from west of the Appalachian Mountains were located in the top left quadrant. Hybrids and backcrossed genotypes were located in-between as expected (Figure 3.1). Interestingly, *V. oxycoccos* grouped

near the *V. macrocarpon* genotypes selected from east of the Appalachian Mountains, suggesting that some migration could exist between native populations of the two species (Zalapa et al., 2014; Smith et al., 2015). The ability of these markers to distinguish between the cranberry genotypes demonstrates their potential relevance for cultivar discrimination for the protection of patented and released cranberry cultivars (Smith et al., 2015).

Validation of multiplexing panel utility in a population of self-pollinated and cross-pollinated Stevens seedlings.

Cranberry is capable of self-fertilization, therefore, it was hypothesized that the majority of seeds present within individual fruits and within an entire cranberry bed would arise mainly from self- rather than from cross-pollination events since beds are clonally propagated with a single cultivar (Sarracino and Vorsa, 1991). Previous studies have characterized the effect of self- and cross-pollination on the number of seeds per berry for a diverse number of cultivars (Sarracino and Vorsa, 1991; MacKenzie, 1995); however, studies characterizing the extent of self-pollination in a commercial cranberry bed have not been conducted.

DNA fingerprinting analysis using a subset of the SSR multiplexing combos designed herein was used to genotype the 174 seedlings from the 20 fruits collected in a Stevens commercial cranberry bed. A total of 146 of the 174 seedlings did not contain a single allele across the 12 loci amplified that was not inherited from Stevens, and these seedlings were considered to be results of self-pollination. The remaining 28 seedlings contained one or more allele which could not have been inherited from Stevens, and these seedlings were considered to be results of cross-pollination. Interestingly, some of the cross-pollinated seedlings from one of the 20 fruits did not contain a Stevens allele at one or more loci. We interpreted this to mean that the fruit was from an "off genotype" which had germinated and become established in the Stevens bed. This is an example of intra-cultivar genetic heterogeneity, which is fairly common in cranberry (Fajardo et al., 2012; Novy et al., 1996).

PCA performed using the allele scores at 12 loci for the 174 Stevens seedlings revealed a single cluster of seedlings resulting from self-pollination; the remaining outcrossed seedlings were outside the cluster of self-pollinated seedlings and spread across the PCA (Figure 3.2). These PCA results provided further evidence that the seedling pollen source determination based on the presence or absence of Stevens' alleles was accurate. Separation of the cross-pollinated seedlings into two apparent groups by the second principal component (PC) suggests that the foreign pollen which fertilized the cross-pollinated seedlings could have come from two or more sources (Figure 3.2). Additionally, the seedlings which came from the fruit determined to be an "off genotype" rather than a Stevens fruit fell into two distinct groups separated along the first PC. One of the groups contained other outcrossed seedlings whose mother was

Stevens; and therefore, the group could represent a set of full-sib progeny from reciprocal crosses of Stevens and the "off genotype". The other group probably represents a set of progeny whose mother was the "off genotype", and which were either self-pollinated or fertilized by another foreign pollen source.

The ability of these markers to differentiate between the seedlings, even between the self-pollinated seedlings, demonstrates their potential power, precision, and accuracy for high throughput DNA fingerprinting in cranberry. Detecting the "off genotype" in the Stevens bed and the potential full-sibs from reciprocal cross of the "off genotype" and Stevens suggests that the markers can quickly and cheaply be used to assist grower's in determining the genetic purity of existing beds on their property when trueness-to-type is questioned due to observations of unique morphological differences or yield variation between beds of the same cultivar. Furthermore, the markers should allow licensed propagators to monitor the genetic homogeneity of beds used to grow vines for sales and should help breeders maintain the intellectual property rights of hybrid cultivars in cases where license agreements may be violated. Each new cultivar released can have a known genetic fingerprint based on all 61 markers from the 16 multiplexing panels, which can be used for accurate identification by researchers and personnel throughout the industry whenever necessary in the future. Finally, the use of these markers in this small validation study demonstrates their applicability and utility for cranberry researchers and breeders interested in cataloging and maintaining the purity of cranberry lines, assessing cranberry genetic diversity, and designing studies of particular commercial cranberry phenomena such as self-pollination within cranberry beds.

The majority of the seeds present in fruit from a commercial cranberry bed are self-pollinated.

Chi-square tests comparing the number of Stevens seedlings resulting from self-pollination versus cross pollination revealed that there were significantly more self-pollinated seedlings (146 seedlings) than outcrossed seedlings in the bed (18 seedlings) at the $p < 0.0001$ level. Although cranberry growers and researchers assumed that the majority of seeds in cranberry beds were self-pollinated, this is the first quantitative evidence supporting this hypothesis. Although, the ten seedlings from the fruit from an "off genotype" were removed prior to the Chi-square tests, if intra-cultivar heterogeneity did exist within this Stevens bed, the number of outcrossed seedlings may have been inflated by the presence of foreign pollen generated within the bed. When cranberry beds are genetically pure, viable foreign pollen sources can only be adjacent cranberry beds planted to a different cultivar.

The disproportionate number of self- versus cross-pollinated seeds within commercial cranberry beds, while not surprising, suggests that the potential effect of self-pollination on cranberry fruit size and yield is worth studying.

Previous studies of self- and cross-pollinations in a diallel experiment with eight cranberry cultivars (Sarracino and Vorsa, 1991) and with two early selections (MacKenzie, 1995) showed that self-pollination leads to fruits with less seeds compared to fruits with cross-pollinated seeds. Studies in a closely related species to cranberry, high bush blueberry (*V. corymbosum*), also revealed that cross-pollinations favored the development of higher number of seeds (Dogterom et al., 2015; Vander Kloet, 1991). Vander Kloet (1984) also studied the effect of the number of pollen donors in seed production and weight in highbush blueberry and showed that when flowers were pollinated with pollen of three donors, the fruit set, seed number and weight were higher than when pollen of a single donor was used. Therefore, if the same phenomena also occurs in cranberrry, current commercial cranberry cultivation practices of using established beds of a single cultivar may have negative impacts on fruit production and fruit quality. Future research studies should be conducted which study the effect of seed number and pollen source on cranberry fruit set, fruit weight, and yield to determine if cranberry growers could potentially achieve the increases in fruit size and total yield in their cranberry beds by adopting practices which promote cross-pollination on their farms. Such practices could include a variety of strategies including planting adjacent beds in different cultivars, planting a mix of cultivars in a single bed, or choosing active pollinators which move between multiple beds in order to increase the spread of foreign pollen.

Conclusions

This study developed sixteen SSR multiplexing panels which can be used with M13 universal primers for high-throughput DNA fingerprinting in cranberry. The panels contained a total of 61 markers evenly distributed throughout the genome, which easily separated important commercial cranberry cultivars. In addition, a subset of these multiplexing panels were used to genotype seedlings extracted from fruits in a cranberry bed planted to the cultivar Stevens. The seedlings were determined to be either self-pollinated or cross-pollinated using presence/absence of Stevens alleles combined with PCA, and chi-square tests provided the first quantitative evidence that the majority of seeds in commercial cranberries are self-pollinated. Therefore, the efficient and powerful DNA fingerprinting made possible by these multiplexing panels of SSR markers represents an important and applicable resource in the cranberry industry for assessing the purity of grower and licensed propagator cranberry vines, protecting intellectual property rights, assisting growers in determining genetic purity of existing beds, and for enabling genetic research and analysis of genetic diversity in cultivated, breeding and wild cranberry germplasm.

Acknowledgements

J.Z. and B.S. wish to express their gratitude through Mt 10:32. This project was supported by USDA-ARS (project no. 3655-21220-001-00 provided to J.Z.); WI-DATCP (SCBG Project #14-002); National Science Foundation (DBI-1228280); Ocean Spray Cranberries, Inc.; Wisconsin Cranberry Growers Association; Cranberry Institute. B.S. was supported by the Frank B. Koller Cranberry Fellowship for Graduate Students. The authors also thank Nicholi Vorsa, Eric Zeldin, Brent McCown, the Valley Corp., Cranberry Creek Inc., and NCGR for providing cranberry germplasm used in this study. We thank the anonymous reviewers who helped to enhance the quality of this paper.

Table 3.1. Cranberry (*Vaccinium. macrocarpon*) cultivars, breeding selections, and *V. oxycoccos* (diploid) accession genotyped using the 16 SSR multiplex panels.

Cultivar	Pedigree	Accession Origin*
BenLear	Native Selection, WI, USA	Dubay
Bergman	Early Black x Searles	Dubay
Demoranville	Franklin x Ben Lear	Rutgers
Early Black	Native Selection, MA, USA	Dubay
Franklin	Early Black x Howes	Dubay
GH1	McFarlin x Searles	Valley
GH2	McFarlin x Searles	Valley
Howes	Native Selection, MA, USA	Dubay
HyRed	Stevens x Ben Lear	UW
LeMunyon	Native Selection, NJ, USA	Rutgers
LoRed	Stevens x Ben Lear	UW
Pilgrim	McFarlin x Prolific	Rutgers
Potter's Favorite	Native Selection, WI, USA	Dubay
Stevens	McFarlin x Potter's Favorite	PI-614078
V. oxycoccos (diploid)	Native Selection, AK, USA	Rutgers
V07	HyRed x GH1	UW
V11	HyRed x LoRed	UW
Wilcox	Howes x Searles	Dubay
Yellow Bell	Native Selection, ME, USA	PI-555028

*Dubay Cranberries Co., Junction City, WI; PE Marucci Center, New Jersey Agricultural Station, Rutgers University Chatsworth, NJ; University of Wisconsin-Madison; National Clonal Germplasm Repository, Oregon.

Table 3.2. Cranberry (*Vaccinium macrocarpon*) PCR multiplexing panels containing SSR markers with non-overlapping allele ranges. Primer names, NCBI ID, publication origin, and position within the 12 cranberry linkage groups (LGs) (Schlautman et al., 2015b) and allele range (bp) are reported. The subset of multiplexing panels used to genotype self- and cross-pollinated seedlings from the cultivar, Stevens, are indicated.

Multiplexing panel	Primer Name	NCBI ID	LG	Position	Allele range (bp)
Panel 1	ct95345[a]	KP279106	7	30.93	117-128
	SCF124322[a]	KP278849	1	77.97	213-237
	SCF149976[a]	KP278893	5	51.26	273-317
Panel 2	SCF136207[a]	KP278866	9	59.27	161-184
	ct155339[a]	KP279140	3	27.31	221-230
	vm52682[b]	JF834282	4	36.88	271-292
Panel 3†	SCF213102[a]	KP278953	2	37.12	149-159
	SCF71184[a]	KP278754	8	46.00	197-233
	SCF92414[a]	KP278793	6	34.93	285-289
	409500_K63[a]	KP279177	10	53.03	333-393
Panel 4	scf9e[c]	N/A	5	67.28	184-206
	SCF149633[a]	KP278891	1	24.33	292-325
	scf4860[c]	N/A	8	34.85	349-398
	scf439[c]	N/A	9	36.58	513-524
Panel 5	ct89711[a]	KP279102	3	22.42	137-150
	SCF110888[a]	KP278826	3	70.05	179-193
	SCF118999[a]	KP278842	1	78.98	270-309
	SCF72229[a]	KP278756	4	30.61	322-345
Panel 6	1trimcontig344502[a]	KP279241	6	56.80	133-164
	SCF104688[a]	KP278809	10	67.07	200-223
	SCF138014[a]	KP278870	7	37.67	246-248
	SCF21596[a]	KP278655	11	41.89	303-323
Panel 7	scf32j[c]	N/A	9	82.53	132-154
	SCF138394[a]	KP278871	12	29.72	217-244
	SCF82870[a]	KP278775	8	35.70	276-313

	29080_K63[a]	KP279160	2	71.39	383-398
Panel 8	SCF132595[a]	KP278863	5	27.67	227-281
	scf35k[c]	N/A	9	41.03	297-315
	309084_K70[a]	KP279212	12	40.33	389-401
Panel 9†	SCF140628[a]	KP278876	4	33.90	144-169
	SCF59248[a]	KP278740	1	52.75	194-205
	SCF107715[a]	KP278816	10	39.34	247-304
	SCF73288[a]	KP278758	2	65.01	320-334
Panel 10	1trimcontig217158[a]	KP279229	7	52.21	154-174
	SCF27811[a]	KP278672	8	48.08	220-262
	SCF31208[a]	KP278687	5	25.81	306-361
	121633_K63[a]	KP279163	3	76.73	400-426
Panel 11	ct154615[a]	KP279138	6	20.13	131-140
	VCC_J9[d]	AY762683	9	23.36	171-220
	SCF38942[a]	KP278704	12	31.07	233-262
	SCF73288[a]	KP278758	2	65.01	289-333
Panel 12	vm68798[b]	JF834242	11	47.89	152-170
	vm25796[b]	JF834263	10	52.83	197-267
	SCF85773[a]	KP278780	3	34.09	285-304
	SCF18709[a]	KP278651	2	50.35	344-354
Panel 13	vm72062[b]	JF834244	10	41.93	147-170
	SCF20681[a]	KP278653	7	76.07	220-236
	SCF3551[a]	KP278608	1	93.53	264-290
	297265_K63[a]	KP279167	2	48.67	331-343
Panel 14†	SCF113389[a]	KP278831	4	31.54	150-169
	314797_K70[a]	KP279218	8	48.58	202-224
	vm27120[b]	JF834265	6	41.90	255-269
	308539_K70[a]	KP279209	11	54.52	305-315

Panel 15	SCF8987[a]	KP278625	5	51.16	151-157
	372875_K63[a]	KP279174	2	66.03	198-230
	SCF37628[a]	KP278700	12	43.49	258-267
	SCF53750[ia]	KP278727	3	61.68	315-352
Panel 16	SCF7155[a]	KP278617	7	73.80	169-198
	SCF97378[a]	KP278801	5	32.84	238-254
	SCF88396[a]	KP278784	9	62.36	287-296
	SCF59739[a]	KP278741	12	53.07	336-352

† Panel used to genotype self- and cross-pollinated seedlings from the cultivar, Stevens.
[a] Published in Schlautman et al., 2015a.
[b] Published in Zhu et al., 2012.
[c] Published in Georgi et al., 2013.
[d] Published in Boches, 2005.

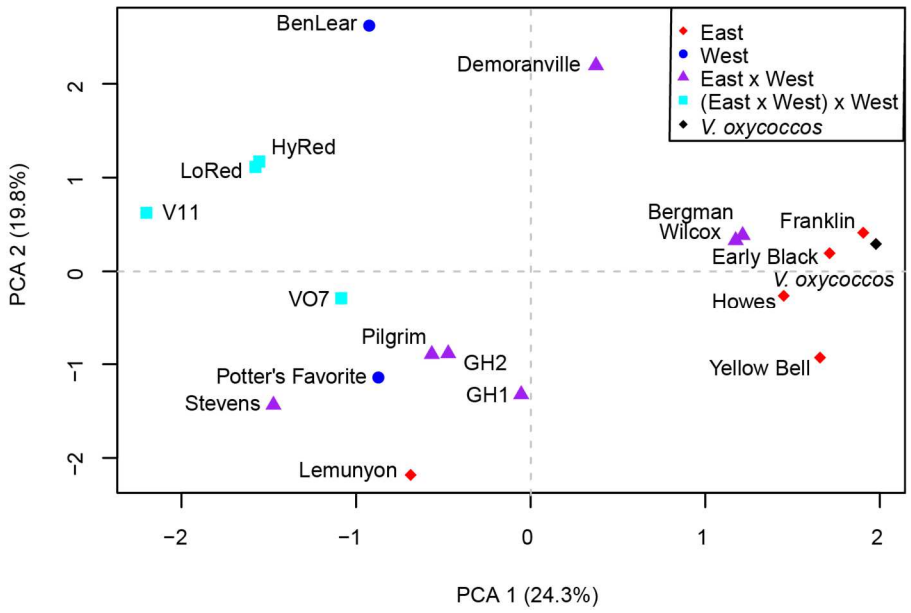
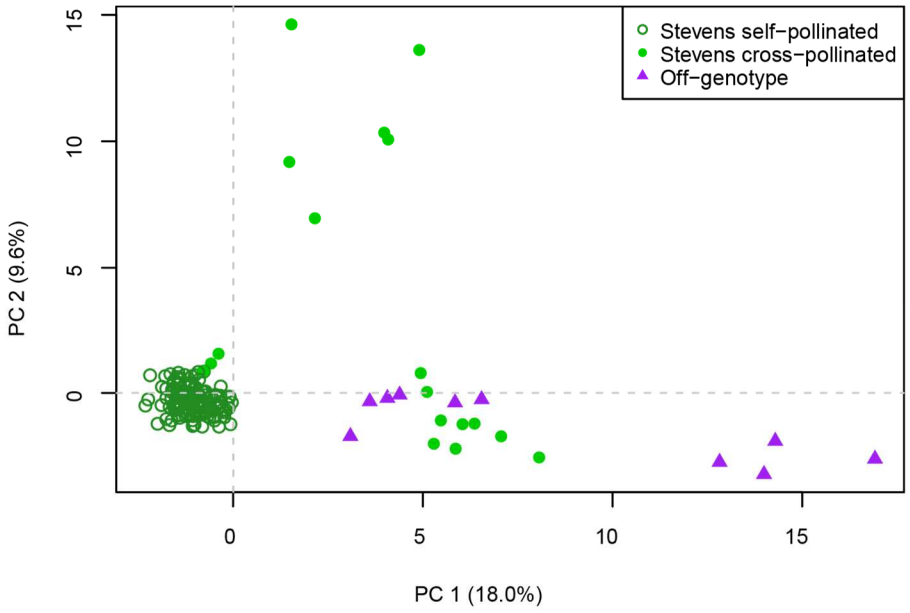


Figure 3.1. Principal component analysis for 18 cranberry (*Vaccinium macrocarpon)* cultivars, breeding selections, and *V. oxycoccos* accession based on genotypic data from 61 short sequence repeats (SSRs) multiplexed in 16 panels. Genotypes are plotted and colored based on their selection origin (either east or west of the Appalachian Mountains) or the selection origin within a specific cultivar's pedigree (i.e. either [east x west] or [[east x west] x west]).

Figure 3.2. Principal component analysis of 174 cranberry (*Vaccinium macrocarpon)* seedlings extracted from 20 fruits collected in a commercial bed of the cultivar Stevens. Seedlings were determined to be either self-pollinated, cross-pollinated by a foreign pollen source, or had a mother which was an "off-genotype" which had somehow established itself in the Stevens bed.



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Appendix III-1. Cranberry (*Vaccinium macrocarpon*) seedlings of the cultivar Stevens, type (self vs. outcrossed), and allele sizes for 12 SSR loci from multiplexing panels 3, 9, and 14.

Seedling	Seedling Type	SCF140628	SCF59248	SCF107715	SCF73288	SCF113389	314797_K70	vm27120	308539_K70	SCF213102	SCF92414	409500_K63	SCF71184
Stevens	parent	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/289	333/367	200/210
St37H1_1	self	144/144	194/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	285/285	333/333	210/210
St37H1_2	self	144/144	194/195	247/247	334/334	156/156	208/210	260/260	307/313	156/156	289/289	367/367	210/210
St37H1_3	self	144/144	194/195	247/247	328/334	156/156	208/210	260/260	307/313	156/156	285/289	367/367	200/210
St37H1_4	self	144/144	194/195	247/249	334/334	156/156	208/210	260/260	307/313	156/156	285/289	333/367	200/210
St37H1_5	self	144/144	194/195	249/249	328/328	156/156	208/210	260/260	307/313	156/156	285/289	333/333	200/210
St37H1_7	self	144/144	194/195	247/249	328/334	156/156	210/210	260/260	NA	156/156	285/289	333/367	210/210
St37H1_8	self	144/144	194/195	247/249	328/334	156/156	210/210	260/260	307/313	156/156	285/285	333/367	210/210
St37H1_9	self	144/144	194/195	249/249	328/334	156/156	210/210	260/260	307/307	156/156	NA	NA	200/210
St37H1_10	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	307/307	156/156	285/289	333/367	200/210
St37H11_1	self	144/144	194/195	247/247	328/334	156/156	208/208	260/260	307/313	156/156	285/289	333/367	210/210
St37H11_2	self	144/144	194/195	247/249	334/334	156/156	208/210	260/260	307/307	156/156	285/289	333/367	200/210
St37H11_3	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/285	333/367	200/210
St37H11_4	self	144/144	194/195	247/247	328/334	156/156	208/208	260/260	307/307	156/156	285/289	367/367	210/210
St37H11_5	self	144/144	195/195	247/249	328/328	156/156	208/208	260/260	307/307	156/156	289/289	333/367	210/210
St37H11_6	self	144/144	195/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	285/285	333/333	200/210
St37H11_7	self	144/144	194/194	249/249	328/328	156/156	208/210	260/260	307/307	156/156	285/285	333/333	200/210
St37H11_8	self	144/144	194/195	249/249	328/328	156/156	208/210	260/260	313/313	156/156	285/285	333/333	200/210
St37H11_9	self	144/144	194/195	247/249	334/334	156/156	208/210	260/260	307/307	156/156	289/289	333/367	210/210
St37H13_1	self	144/144	194/195	249/249	334/334	156/156	208/210	260/260	307/313	156/156	285/289	333/333	200/210
St37H13_2	outcross	144/154	194/195	249/249	323/328	156/165	208/210	260/268	307/313	156/156	285/287	333/377	210/220
St37H13_3	self	144/144	195/195	247/249	328/328	156/156	208/210	260/260	307/307	156/156	285/285	333/333	200/210
St37H13_4	self	144/144	194/195	247/247	328/334	156/156	208/210	260/260	307/313	156/156	285/289	367/367	200/210
St37H13_5	self	144/144	195/195	247/247	328/334	156/156	210/210	260/260	307/307	156/156	285/285	367/367	200/200
St37H13_6	self	144/144	195/195	247/249	334/334	156/156	208/208	260/260	307/313	156/156	289/289	333/367	200/210
St37H13_7	self	144/144	194/195	247/249	328/328	156/156	208/210	260/260	307/313	156/156	285/289	333/367	200/210
St37H13_8	self	144/144	194/195	247/249	328/328	156/156	208/210	260/260	313/313	156/156	285/285	367/367	200/200
St37H13_9	self	144/144	194/194	249/249	328/334	156/156	208/208	260/260	307/313	156/156	285/285	333/333	200/210

St37H13_10	self	144/144	194/194	247/247	328/334	156/156	208/208	260/260	307/313	156/156	289/289	367/367	210/210
St37H15_1	self	144/144	195/195	247/249	328/334	156/156	210/210	260/260	307/313	156/156	285/285	367/367	210/210
St37H15_2	self	144/144	194/195	247/247	334/334	156/156	210/210	260/260	307/307	156/156	289/289	367/367	200/210
St37H15_3	self	144/144	194/194	249/249	334/334	156/156	208/210	260/260	307/307	156/156	289/289	333/333	200/210
St37H15_4	self	144/144	195/195	247/249	328/334	156/156	208/210	260/260	307/307	156/156	285/289	333/367	200/210
St37H15_5	self	144/144	194/194	247/247	328/328	156/156	208/208	260/260	307/313	156/156	285/289	367/367	210/210
St37H15_6	self	144/144	194/194	249/249	328/334	156/156	208/210	260/260	307/313	156/156	285/285	333/333	200/210
St37H15_7	self	144/144	194/195	247/249	334/334	156/156	208/208	260/260	307/313	156/156	285/285	333/367	210/210
St37H15_8	self	144/144	195/195	249/249	328/328	156/156	210/210	260/260	307/307	156/156	285/289	333/333	200/200
St37H15_9	self	144/144	194/194	NA	328/334	156/156	208/208	260/260	307/307	156/156	285/285	333/367	200/210
St37H15_10	self	144/144	194/194	249/249	328/334	156/156	208/208	260/260	307/313	156/156	285/289	333/333	210/210
St37H15_11	self	144/144	195/195	247/247	328/328	156/156	208/210	260/260	307/307	156/156	285/289	367/367	200/210
St37H15_12	self	144/144	195/195	247/247	328/334	156/156	208/210	260/260	313/313	156/156	285/289	367/367	200/210
St37H17_1	outcross	144/154	195/198	247/302	330/334	156/156	NA	260/260	305/307	156/156	285/287	333/367	200/207
St37H17_2	outcross	144/152	195/195	247/277	326/334	156/156	210/210	260/260	307/313	156/156	287/289	333/367	200/207
St37H17_3	outcross	154/154	195/198	277/302	326/330	169/169	202/202	260/260	307/307	156/156	287/289	333/333	224/224
St37H17_4	outcross	144/154	195/198	247/302	328/330	156/169	208/210	260/260	307/307	156/156	285/287	333/367	207/210
St37H17_5	outcross	152/152	195/198	277/277	326/326	161/161	202/210	260/260	305/307	156/156	289/289	333/333	207/224
St37H17_6	outcross	154/154	198/198	277/277	330/330	169/169	202/210	260/260	305/305	156/156	287/287	333/333	207/224
St37H17_7	outcross	154/154	198/198	277/277	326/330	156/169	202/210	260/260	305/307	156/156	287/289	333/333	207/224
St37H17_8	outcross	144/154	195/198	247/247	326/328	156/156	208/210	260/260	307/313	156/156	289/289	333/367	207/210
St37H17_9	outcross	144/154	NA	249/249	NA	156/156	208/210	260/260	305/307	156/156	285/287	333/333	NA
St37H17_10	outcross	144/152	194/198	249/249	330/334	156/156	210/210	260/260	307/313	156/156	287/289	333/333	200/207
St37H18_1	self	144/144	194/194	247/249	328/334	156/156	208/208	260/260	313/313	156/156	285/289	333/367	200/210
St37H18_2	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	313/313	156/156	285/289	367/367	210/210
St37H18_3	self	144/144	194/195	249/249	328/328	156/156	208/210	260/260	313/313	156/156	285/285	333/333	200/210
St37H18_4	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/307	156/156	285/289	333/367	200/210
St37H18_5	self	144/144	194/194	247/247	328/328	156/156	208/210	260/260	307/307	156/156	289/289	333/367	200/210
St37H18_6	self	144/144	194/195	249/249	334/334	156/156	210/210	260/260	307/313	156/156	289/289	333/333	200/200
St37H18_7	self	144/144	195/195	247/249	328/334	156/156	208/210	260/260	307/307	156/156	285/285	333/367	200/210
St37H18_8	self	144/144	194/194	247/249	334/334	156/156	210/210	260/260	307/313	156/156	285/285	367/367	200/200

St37H19_1	self	144/144	194/194	247/249	328/334	156/156	210/210	260/260	307/313	156/156	285/289	367/367	200/200
St37H19_2	self	144/144	195/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	289/289	333/333	200/210
St37H19_3	outcross	144/152	195/198	247/302	326/328	156/156	202/208	260/260	307/313	156/156	285/287	333/367	210/224
St37H19_4	outcross	144/154	195/198	249/277	330/334	156/156	202/210	260/260	305/307	156/156	287/289	333/333	200/224
St37H19_5	self	144/144	195/195	247/247	328/328	156/156	208/208	260/260	313/313	156/156	285/289	367/367	210/210
St37H19_6	outcross	144/146	194/195	249/280	328/336	156/156	210/210	260/268	307/313	156/156	285/285	333/349	NA
St37H19_7	self	144/144	194/195	247/249	328/328	156/156	208/210	260/260	307/313	156/156	285/289	333/367	200/210
St37H19_8	outcross	144/152	195/198	247/277	330/334	156/156	202/208	260/260	305/313	156/156	285/287	333/333	210/224
St37H19_9	self	144/144	194/195	247/249	328/328	156/156	208/208	260/260	307/307	156/156	285/285	367/367	210/210
St37H19_10	self	144/144	194/195	247/249	328/334	156/156	210/210	260/260	307/313	156/156	289/289	333/367	200/200
St37H2_2	self	144/144	194/194	247/249	328/328	156/156	208/210	260/260	307/307	156/156	285/289	333/367	NA
St37H2_3	outcross	144/154	195/195	249/249	328/330	156/169	202/210	260/260	307/307	156/156	289/289	333/333	NA
St37H2_4	self	144/144	194/195	247/249	334/334	156/156	208/208	260/260	307/313	156/156	NA	NA	NA
St37H2_5	self	144/144	194/195	247/249	328/334	156/156	210/210	260/260	307/313	156/156	285/289	333/333	200/200
ST37H2_6	self	144/144	194/194	247/249	328/334	156/156	208/210	260/260	307/313	156/156	289/289	367/367	200/210
St37H2_7	outcross	144/154	194/195	247/277	328/330	156/156	202/210	260/260	305/307	156/156	285/287	333/367	200/224
St37H2_8	self	144/144	195/195	249/249	328/328	156/156	208/210	260/260	313/313	156/156	285/289	333/333	200/210
St37H2_9	self	144/144	194/195	247/249	334/334	156/156	208/210	260/260	313/313	156/156	285/289	333/367	200/210
St37H2_10	outcross	144/152	194/195	249/302	328/330	156/156	202/210	260/260	307/307	156/156	287/289	333/333	NA
St37H3_1	self	144/144	195/195	247/247	328/334	156/156	210/210	260/260	307/307	156/156	289/289	367/367	200/200
St37H3_2	self	144/144	194/195	249/249	328/328	156/156	208/208	260/260	313/313	156/156	285/289	333/333	210/210
St37H3_3	self	144/144	195/195	247/249	328/328	156/156	208/208	260/260	307/313	156/156	285/289	333/367	210/210
St37H3_4	self	144/144	195/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	289/289	333/367	200/210
St37H3_5	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	307/313	156/156	289/289	333/367	210/210
St37H3_6	self	144/144	194/194	247/249	328/334	156/156	208/208	260/260	307/313	156/156	285/289	333/367	210/210
St37H3_7	self	NA	NA	247/249	334/334	156/156	208/208	260/260	307/313	156/156	285/289	333/367	NA
St37H3_8	self	144/144	194/194	247/247	328/334	156/156	208/208	260/260	313/313	156/156	285/289	367/367	200/210
St37H3_9	self	144/144	194/194	247/247	NA	156/156	208/208	NA	307/313	156/156	285/285	367/367	NA
St37H3_10	outcross	NA	195/198	247/277	326/328	156/169	202/208	260/260	307/307	156/156	289/289	333/367	NA
St37H4_1	outcross	144/152	194/198	249/277	326/328	156/156	202/210	260/260	305/313	156/156	289/289	333/333	NA
St37H4_2	self	144/144	195/195	249/249	334/334	156/156	208/210	260/260	313/313	156/156	289/289	333/333	200/210

St37H4_3	self	144/144	194/195	247/249	328/334	156/156	210/210	260/260	307/313	156/156	285/285	333/367	200/200
St37H4_4	self	144/144	195/195	247/249	328/334	156/156	208/210	260/260	313/313	156/156	289/289	333/367	200/210
St37H4_5	self	144/144	195/195	247/247	328/334	156/156	208/210	260/260	307/313	156/156	285/285	367/367	NA
St37H4_6	self	144/144	194/195	247/249	334/334	156/156	208/208	260/260	313/313	156/156	289/289	333/367	200/210
St37H4_7	outcross	144/152	195/198	249/277	326/334	156/161	202/210	260/260	305/313	156/156	289/289	333/333	200/224
St37H4_8	self	144/144	194/195	247/247	328/334	156/156	208/208	260/260	313/313	156/156	285/289	367/367	210/210
St37H4_9	self	144/144	194/194	249/249	328/334	156/156	208/210	260/260	307/307	156/156	285/289	333/333	200/210
St37H4_10	self	144/144	194/194	249/249	328/334	156/156	208/208	260/260	307/307	156/156	289/289	333/333	210/210
StB171_1	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	307/313	156/156	289/289	333/367	210/210
StB171_2	self	144/144	194/195	247/249	328/334	156/156	210/210	260/260	307/307	156/156	285/285	333/367	200/200
StB171_3	self	144/144	194/195	247/247	328/334	156/156	208/210	260/260	307/313	156/156	285/285	367/367	200/210
StB171_4	self	NA	194/195	247/249	334/334	156/156	208/210	260/260	307/313	156/156	285/289	333/333	NA
StB171_5	self	NA	194/195	249/249	NA	156/156	208/210	260/260	307/313	156/156	285/289	333/367	NA
StB171_6	self	NA	194/195	247/249	328/334	156/156	208/210	260/260	313/313	156/156	285/285	333/367	NA
StB1710_1	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/289	333/367	210/210
StB1710_2	outcross	144/152	195/195	249/302	328/332	156/165	208/210	260/262	307/313	156/156	285/287	333/367	200/210
StB1710_3	outcross	144/152	195/195	249/302	328/332	156/165	208/210	260/262	307/313	156/156	285/287	333/367	200/210
StB1710_4	self	144/144	194/194	247/249	328/334	156/156	210/210	260/260	307/313	156/156	289/289	333/367	200/200
StB1710_5	self	144/144	194/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	285/285	333/333	210/210
StB1710_6	self	144/144	194/195	247/247	328/328	156/156	210/210	260/260	307/313	156/156	285/289	367/367	200/200
StB172_1	self	144/144	194/194	247/247	328/328	156/156	210/210	260/260	307/307	156/156	285/289	367/367	NA
StB172_2	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/285	333/367	200/210
StB172_3	self	144/144	194/195	249/249	328/334	156/156	208/208	260/260	307/307	156/156	285/285	333/367	210/210
StB172_4	self	NA	194/194	249/249	NA	156/156	208/210	260/260	307/313	156/156	285/289	333/333	NA
StB172_5	self	144/144	195/195	247/249	334/334	156/156	210/210	260/260	307/313	156/156	285/289	333/367	NA
StB172_8	self	NA	194/194	247/249	334/334	156/156	210/210	260/260	307/307	156/156	285/289	333/367	200/200
StB172_9	outcross	NA	194/195	247/247	332/334	156/156	208/210	260/260	NA	156/156	287/289	367/367	210/217
StB172_10	outcross	NA	195/195	247/247	332/334	156/165	208/210	260/262	307/313	156/156	285/287	367/367	210/217
STB173_2	self	144/144	194/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	285/289	333/333	200/200
StB173_3	self	NA	194/195	247/249	328/328	156/156	208/208	260/260	307/313	156/156	285/289	333/367	210/210
StB173_4	self	144/144	194/195	247/247	328/334	156/156	210/210	260/260	307/307	156/156	NA	NA	NA

StB173_5	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/289	333/367	200/200
StB173_6	outcross	144/144	194/195	249/249	332/334	156/156	208/210	260/260	307/313	156/156	285/289	333/333	200/210
StB173_7	self	144/144	194/195	247/249	328/328	156/156	210/210	260/260	313/313	156/156	285/289	367/367	200/200
StB173_8	self	144/144	194/194	247/247	334/334	156/156	208/208	260/260	307/313	156/156	285/285	367/367	210/210
StB173_9	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/289	333/367	200/210
StB174_1	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/307	156/156	285/289	333/367	NA
StB174_2	self	NA	195/195	247/249	NA	156/156	210/210	260/260	307/313	156/156	285/285	333/367	200/200
StB174_3	self	144/144	194/194	247/247	334/334	156/156	208/208	260/260	307/313	156/156	289/289	367/367	NA
StB174_4	self	144/144	194/195	247/249	328/328	156/156	208/208	260/260	307/307	156/156	285/289	333/367	210/210
StB174_5	self	144/144	194/195	247/249	334/334	156/156	208/210	260/260	307/307	156/156	289/289	333/367	NA
StB174_6	outcross	144/144	194/195	247/249	332/334	156/156	210/210	260/260	307/307	156/156	289/289	333/367	200/200
StB174_7	self	144/144	194/194	249/249	328/334	156/156	208/208	260/260	307/307	156/156	285/289	333/367	NA
StB174_8	self	144/144	194/194	249/249	334/334	156/156	210/210	260/260	307/313	156/156	285/289	333/333	200/200
StB174_10	self	144/144	195/195	249/249	328/334	156/156	208/208	NA	NA	156/156	285/285	333/333	NA
StB175_1	self	144/144	194/195	247/247	328/334	156/156	208/208	260/260	307/313	156/156	NA	NA	NA
StB175_2	self	144/144	195/195	247/249	328/328	156/156	208/210	260/260	313/313	156/156	285/285	333/367	200/210
StB175_3	self	144/144	195/195	247/247	334/334	156/156	208/210	260/260	307/307	156/156	289/289	333/367	200/210
StB175_5	self	144/144	195/195	247/249	334/334	156/156	208/210	260/260	307/307	156/156	289/289	333/367	NA
StB175_6	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/289	333/367	210/210
StB175_7	self	144/144	194/195	247/249	328/328	156/156	208/208	260/260	307/313	156/156	285/289	333/367	200/210
StB175_8	self	144/144	195/195	247/249	328/334	156/156	208/210	260/260	307/307	156/156	285/289	333/367	200/210
StB175_9	self	144/144	195/195	247/249	334/334	156/156	208/210	260/260	313/313	156/156	285/289	333/367	200/210
StB175_10	self	144/144	194/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	289/289	333/333	210/210
StB176_1	self	144/144	194/195	249/249	328/328	156/156	208/210	260/260	307/313	156/156	285/285	333/333	200/210
StB176_2	self	144/144	195/195	247/249	328/328	156/156	208/210	NA	307/313	156/156	289/289	367/367	200/214
StB176_3	self	144/144	194/195	247/249	334/334	156/156	208/210	260/260	307/307	156/156	285/289	333/367	200/214
StB176_4	self	144/144	194/194	247/249	328/334	156/156	208/210	260/260	307/313	156/156	289/289	333/367	200/210
StB176_5	self	144/144	194/195	249/249	328/334	156/156	210/210	260/260	307/307	156/156	285/285	333/333	210/214
StB176_6	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/285	333/367	200/214
StB176_7	self	144/144	194/195	247/247	334/334	156/156	208/210	260/260	307/313	156/156	285/285	367/367	NA
StB176_8	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	313/313	156/156	285/289	333/367	200/210

StB176_9	self	144/144	194/194	247/249	328/334	156/156	210/210	260/260	307/307	156/156	285/289	333/367	200/200
StB178_1	self	144/144	194/195	247/247	334/334	156/156	210/210	260/260	307/307	156/156	285/289	333/367	200/200
StB178_2	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	307/313	156/156	289/289	367/367	210/210
StB178_3	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	307/313	156/156	285/285	333/367	200/200
StB178_4	self	144/144	194/194	247/247	328/334	156/156	208/210	260/260	307/313	156/156	285/285	367/367	200/210
StB178_5	self	144/144	194/195	247/249	328/334	156/156	208/210	260/260	313/313	156/156	289/289	333/367	200/210
StB178_6	self	144/144	194/194	247/249	328/334	156/156	208/210	260/260	313/313	156/156	289/289	333/367	200/210
StB178_7	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	307/313	156/156	289/289	333/367	210/210
StB178_8	self	144/144	195/195	249/249	334/334	156/156	208/210	260/260	307/313	156/156	285/285	333/367	200/210
StB178_9	self	144/144	194/195	249/249	328/334	156/156	208/208	260/260	307/313	156/156	289/289	333/333	210/210
StB178_10	self	144/144	195/195	247/247	334/334	156/156	208/210	260/260	307/307	156/156	285/285	367/367	200/210
StB179_1	self	144/144	195/195	249/249	334/334	156/156	208/208	260/260	307/313	156/156	285/289	333/333	210/210
StB179_2	self	144/144	194/195	247/249	334/334	156/156	208/210	260/260	307/307	156/156	285/289	333/367	200/210
StB179_3	self	144/144	194/194	247/249	328/328	NA	NA	260/260	307/307	156/156	289/289	333/367	200/210
StB179_4	self	144/144	194/195	249/249	328/334	156/156	208/210	260/260	307/307	156/156	285/285	333/333	200/210
StB179_5	outcross	144/152	195/195	NA	334/334	156/156	210/210	260/262	307/313	156/156	285/287	333/393	200/217
StB179_6	self	144/144	194/195	247/249	328/334	156/156	210/210	260/260	307/307	156/156	285/289	333/367	200/200
StB179_7	self	144/144	194/194	247/249	328/328	156/156	208/210	260/260	307/313	156/156	285/285	333/367	200/210
StB179_8	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	313/313	156/156	285/289	333/367	210/210
StB179_9	self	144/144	194/195	247/249	328/328	156/156	208/210	260/260	307/313	156/156	289/289	333/367	200/210
StB179_10	self	144/144	194/194	247/247	328/328	156/156	208/210	260/260	313/313	156/156	285/285	367/367	NA
StB179_11	self	144/144	194/195	247/247	328/334	156/156	210/210	NA	NA	156/156	289/289	367/367	200/200
StB179_12	self	144/144	194/195	247/249	328/334	156/156	208/208	260/260	307/313	156/156	285/289	333/367	200/210

Chapter IV

As published in *Molecular Breeding* (2015) 35:177; DOI 10.1007/s11032-015-0367-5

Development of a High Density Cranberry SSR Linkage Map for Comparative Genetic Analysis and Trait Detection

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Received: 9 June 2015/Accepted: 30 July 2015/Published online: 14 August 2015

Author contribution statement

B.S., M.I., J.P., N.V., S.S., and J.Z. conceived the research and designed the experiments. J.J., J.P., and N.V. developed the full-sib population for linkage mapping and collected the phenotypic data for QTL analysis. B.S., L.R.B., T.B., T.B., and E.W. participated in genotyping the samples. B.S. and G.C.P. performed the statistical analyses of morphological traits. B.S., M.I., and L.D.G. performed the analyses of synteny. B.S. performed most of the experiment including linkage mapping and QTL analyses. B.S., N.V., and J.Z. oversaw the entire study.

Abstract

Since its domestication 200 years ago, breeding of the American cranberry (*Vaccinium macrocarpon*) has relied on phenotypic selection because applicable resources for molecular improvement strategies such as marker-assisted selection (MAS) remain limited. To enable MAS in cranberry, the first high density SSR linkage map with 541 markers representing all 12 cranberry chromosomes was constructed for the CNJ02-1 progeny from a cross of elite cultivars, CNJ97-105-4 and NJ98-23. The population was phenotyped for a three-year period for total yield (TY), mean fruit weight (MFW), and biennial bearing index (BBI) and data were analyzed using mixed models and best linear unbiased predictors (BLUPs). Significant differences between genotypes were observed for all traits. Quantitative trait locus

(QTL) analyses using BLUPs identified 4 MFW QTL on three linkage groups (LGs), 3 TY QTL on 3 LGs, and 1 BBI QTL which co-localized with a TY QTL. Local BLAST of a cranberry nuclear genome assembly identified homologous sequences for the mapped SSRs which were then anchored to 12 pseudo-chromosomes using the linkage map information. Analyses comparing coding regions (CDS) anchored in the cranberry linkage map with grape, kiwifruit, and tomato genomes were performed. Moderate micro-synteny between the cranberry and kiwifruit genomes was detected, although none of the regions overlapped with the QTL identified in this study. The linkage map, QTL, and elite genotypic constitutions identified herein may be applied in subsequent cranberry MAS programs for the development of new cultivars, and potential marker transferability should allow for comparative genomic studies within economically important *Vaccinium* species.

Keywords

Vaccinium macrocarpon, Linkage Map, SSR, QTL

Introduction

The American cranberry, *Vaccinium macrocarpon* Ait. ($2n=2x=24$), is a long-lived woody perennial adapted to moist acidic soils in North America (Roper and Vorsa 1997). *V. macrocarpon* reproduces sexually as well as asexually through stolons. Although cranberry is protandrous which would promote outcrossing, 9th generation selfing lines have been recovered (Vorsa, unpublished data). Cranberry appears to have undergone a genetic 'bottleneck' during the Pleistocene ice age, and relative to blueberry, low genetic diversity among populations across its native range was observed using soluble enzymatic proteins (Bruederle et al. 1996). However, substantial genetic variation has been observed within and among a few small populations of cranberry in Wisconsin using microsatellite markers (Zalapa et al. 2014).

The domestication and commercialization of cranberry began in the mid-1800s in the Cape Cod region of Massachusetts, and spread to New Jersey, the Pacific Northwest, and Wisconsin. Today, the U.S. cranberry industry continues to grow and has an estimated value of nearly 1 billion U.S. dollars (Alston et al. 2014). Popularity of cranberries and cranberry products has increased because of their unique flavor and potential health benefits (Howell et al. 1998; Singh et al. 2009). However, cranberry has undergone relatively little genetic improvement compared to other commercial fruit crops due to its recent domestication and limited private and public breeding programs (Vorsa and Johnson-Cicalese 2012). The cranberry industry currently relies on asexual propagation of a small number of clonal cultivars which are either native selections or 1st, 2nd, or 3rd generation hybrids of those native selections (Fajardo et al. 2012).

To date, cranberry breeding programs have relied solely on phenotypic selection because of the limited molecular resources and information available to facilitate genetic improvement. As a result, these programs require considerable field plot space, expensive and intensive management techniques, and a commitment to phenotypic evaluation over long evaluation periods. Therefore, marker-assisted selection (MAS) strategies that reduce the required time, labor and financial investments should provide for increased breeding efficiency. MAS is especially critical for cranberry because of the long juvenility period, the lengthy phenotyping phase (6-8 years) required for selection for important horticultural traits, e.g., yield, and because dedication of field space for robust experimental designs in cranberry are limiting and financially impractical (Vorsa and Johnson-Cicalese 2012). MAS could also be useful for developing strategies for trait introgression between cranberry and other economically important *Vaccinium* species such as blueberry, lingonberry, *V. oxycoccos*, and bilberry through interspecific hybridization.

High density genetic maps are a prerequisite for the precise identification, dissection, and quantification of individual genetic effects due to quantitative trait loci (QTL) and are useful for MAS (Zalapa et al. 2012). To increase the availability of genetic resources and molecular markers for genetic mapping, DNA sequencing studies have been conducted in cranberry using SOLiD sequencing to develop 32 simple sequence repeat (SSR) markers and 454 GS-FLX sequencing to develop 48 SSR markers, respectively (Georgi et al. 2011; Zhu et al. 2012). Additionally, SSR markers originating in blueberry have been cross amplified or redesigned for use in cranberry (Rowland and Dhanaraj 2003; Boches et al. 2005; Bassil et al. 2009; Georgi et al. 2013). A total of 136 such SSR markers were used to construct the first cranberry genetic linkage map, which yielded 14 linkage groups (LGs) and equated to one molecular marker for every 3.4 million base pairs (Mb) of the estimated 470Mb cranberry genome (Georgi et al. 2013). Although, the marker density could be considered low for localizing genomic regions linked or associated with the inheritance of traits with continuous distributions, QTL were detected for field fruit-rot resistance, sound fruit yield, fruit weight, titratable acidity, and proanthocyanidin content (Georgi et al. 2013). More recently, a transcriptome and genome assembly were published (Polashock et al. 2014), and based on these genetic resources and an additional genome assembly (Fajardo et al. 2014), 697 polymorphic SSRs were designed and validated using a cranberry diversity panel (Schlautman et al. 2015).

The present study was conducted to further molecular crop improvement strategies in cranberry by applying the recently generated genomic resources to improve cranberry genetic linkage and QTL mapping analyses. Specifically, 541 previously published SSR markers were mapped in a bi-parental full-sib population derived from a cross of CNJ97-105 (*Mullica Queen*®) by NJS98-23 (*Crimson Queen*®) to construct an improved high density cranberry genetic linkage map. To determine whether sufficient marker saturation was achieved for investigating the genetic basis of quantitative traits in cranberry, QTL mapping was conducted for total yield, yield stability, and mean fruit weight based on field data from the same segregating progeny. In addition, comparative analyses of sequence order between coding DNA regions (CDS) anchored in the cranberry genetic linkage map and their potential homologs in the grape, tomato, and kiwifruit genomes was performed to explore the levels of macro and micro-synteny between the genomes.

Materials and Methods

Plant Materials and Nucleic Acid Extraction

Mapping was based on a cranberry full-sib breeding population (CNJ02-1) of 221 progeny derived from a cross between the maternal parent, CNJ97-105 (*Mullica Queen*®), by the paternal parent, NJS98-23 (*Crimson Queen*®), from here on referred to as MQ and CQ, respectively. Population CNJ02-1, which is segregating for important horticultural traits,

is particularly suited to linkage and QTL mapping because the bi-parental cross is between two unrelated ancestral lineages derived from four great-grandparents and two grandparents that were selected from native stands across the geographic range of cranberry (Vorsa and Johnson-Cicalese 2012). The parental cultivars and 154 of the CNJ02-1 progeny were planted in 4 rows of 2.25 m^2 square plots at the Rutgers University P.E. Marucci Center, Chatsworth, NJ in 2004, and plots were fully established by 2007. Genomic DNA was extracted from lyophilized leaf tissue from individual reproductive stems of the parentals and their 221 progeny using a Macherey-Nagel (MN) Plant II kit (Düren, Germany) following the manufacturer's instructions.

Molecular Marker Overview

A comprehensive screen of 881 previously published SSR loci for *V. macrocarpon* identified 573 SSR markers segregating in the CNJ02-1 population (Bassil et al. 2009; Georgi et al. 2011; Zhu et al. 2012; Georgi et al. 2013; Schlautman et al. 2015). A complete list of the SSR markers used and their publication origins can be found in Appendix IV-1. The 573 SSR markers were divided into groups of 3 primer-pairs with non-overlapping allele size ranges for use in subsequent multiplex PCR reactions. PCR reactions and fragment analyses were performed according to Schlautman et al. (2015), except the 2.0 µl of ddH_2O were replaced with 0.5 µl of forward and 0.5 µl of reverse primer from two additional SSR primer pairs so that the final PCR was a 3x multiplex reaction.

Map Construction

Linkage analysis was performed using the regression approach implemented for cross-pollinated (CP) populations in JoinMap v4.1 (Van Ooijen 2006). Linkage groups were determined with a LOD threshold > 10.0, and the Kosambi mapping function was used to calculate genetic distances among loci. Markers and genotypes with more than 10% missing data and markers which displayed significant segregation distortion ($P < 0.05$) using Chi-square tests were removed from the analysis. Parental maps were constructed for MQ and CQ using parental specific alleles. Marker order in the parental maps was further interrogated using the *colorize* option for viewing graphical genotypes and the *genotype probabilities* tabsheet in JoinMap v4.1 to identify possible marker inconsistencies or genotyping errors leading to false double recombinations. Markers with 5 or more inconsistencies across the 221 individuals were removed from the analysis before integration. This was repeated until no further instances were detected. An integrated map was constructed for the CNJ02-1 population that included the parental markers plus additional SSRs that did not contain parental specific allele information (i.e. JoinMap hk x hk segregation type). Marker collinearity between the parental

maps, the integrated map, and the previously published cranberry genetic linkage map were visualized and co-aligned to further ensure correct marker order using MapChart v2.2 (Voorrips 2002; Georgi et al. 2013).

The observed genome length (G_O) was calculated by summing the observed map lengths of all linkage groups. The expected length of each linkage group was estimated according to method four of Chakravarti et al. (1991) by inflating the observed map length (cM) by a factor of $(m+1)/(m-1)$ where m is the number of mapped SSR makers in the linkage group. The expected genome length (G_E) was then estimated by summing the estimated linkage group lengths. Observed genome coverage (GC_O) was calculated as the ratio of G_O and G_E (Chancerel et al. 2013).

Evaluation of yield-related traits

Repeated measures of total yield (TY) and mean weight of fruit (MFW) were taken for 154 of the 221 genotypes over a three year (2011-2013) period. TY was determined by harvesting and weighing all of the cranberry fruit within a 0.09 m^2 square, and 100 of the fruits were counted and weighed to calculate MFW as described in Georgi et al. (2013) and Johnson-Cicalese et al. (2015). Two independent 0.09 m^2 samples were taken each year from each 2.25 m^2 plot. Additionally, certain cranberry genotypes can display cyclical rather than static yield patterns due to biennial bearing, a common phenomenon in long-lived woody perennial species (Smith et al. 2004; Vorsa and Johnson-Cicalese 2012; DeVetter et al. 2013). Therefore, the average biennial bearing index (BBI), where $BBI = \left|100 * \frac{difference\ between\ successive\ crops}{sum\ of\ the\ successive\ crops}\right|$, was calculated for each genotype over the three year period based on TY BLUPs as a measure of yield stability (Jonkers 1979).

Statistical analyses were performed in R version 3.1.0 (R Core Team 2014). Because the mapping population was a full-sib family with replication of alleles across genotypes in a uniformly managed cranberry bed, an assumption was made that large blocks of genotypes should resemble one another. A spatial analysis was performed to test this assumption and revealed a gradient of variability along rows for TY and MFW. Therefore, all possible "virtual" blocking designs were applied to the field and their relative efficiencies were analyzed to determine the optimum incomplete blocking design, as is done in a uniformity trial, which accounted for the observed trends in phenotypic spatial variation.

Mixed models were fit for TY and MFW using the restricted maximum likelihood (REML) approach, and the variance components for each trait were estimated using the '*lmer*' function from the lme4 package (Bates et al. 2014). The model for each trait was fit in the form $y = \mu+B+G+Y+G:Y+B:Y+e$ where y is the quantitative measure for MFW or TY, μ is the intercept, B is the effect of the "virtual" block as determined by the spatial analysis, G is the genotype

random effect, *Y* is the year random effect, *G:Y* is the genotype by year interaction, *B:Y* is the block by year interaction, and *e* is the stochastic error associated with the model. *G:Y* obtained from the model was used as a measure of genotype by environment (*GxE*) interactions. In addition, models of the form $y = \mu + B + G + e$ where y is the quantitative measure for MFW or TY, μ is the intercept, *B* is the block effect, and *G* is the genotype effect were fit to be used in a year by year QTL analysis in case of significant *G:Y*. Each component was tested for significance using the Likelihood Ratio Test implemented by the '*update*' and '*anova*' functions in R (Stram and Lee 1994; R Core Team 2014). Best linear unbiased predictors (BLUPs) and standard errors (SE) were computed for MFW and TY for each genotype and parent using the '*lmer*', '*ranef*', and '*se.ranef*' functions in the lme4 R package; genotypes, years, and blocks were treated as random effects (Bates et al. 2014). Additional year-specific BLUPs were estimated for each trait within each year in case of significant *G:Y,* and these BLUPs were noted by the trait name followed by the year (e.g. MFW2011). Prediction intervals (PIs) at the 95% level were constructed for the genotype and parental BLUPs for each trait using the Goldstein method, and the PIs were used to compare genotypic performances. Progeny genotypes were considered to be significantly different from the parents and other siblings at $p < 0.05$ level if the PI limits of the genotypes did not overlap (Goldstein 2011). Broad-sense heritability (H^2) for each trait were calculated as $H^2 = \frac{\sigma^2_{Gen}}{\sigma^2_{Gen} + \frac{\sigma^2_{Gen:Year}}{n} + \frac{\sigma^2_{Res}}{n}}$ where σ^2_{Gen} is the variance due to genotypes, $\sigma^2_{Gen:Year}$ is the genotype by year interaction component, σ^2_{Res} is the residual variance component and *n* is the number of years (Holland et al. 2003).

QTL analyses

QTL analyses were performed in MapQTL v6.0 using BLUPs and year-specific BLUPs estimated for TY and MFW (Van Ooijen 2009). Additionally, BBI calculated using the TY year-specific BLUPs was analyzed as a separate trait. Marker positions were defined by the CNJ02-1 integrated linkage map developed from 221 full-sib progeny, and marker-trait associations were tested using available phenotypic data for 154 individuals.

QTL detection for each trait used a forward selection approach by first detecting QTL using interval mapping (IM). Potential QTL were evaluated if the QTL position was supported by Kruskal-Wallis (KW) non-parametric single locus analysis ($p < 0.001$) and an IM logarithm of odds (LOD) threshold > 2.5 (Khaembah et al. 2013). Potential QTL were further resolved by selecting the nearest markers to set as cofactors, followed by repeated rounds of multiple QTL mapping (MQM) and cofactor reduction or adjustment. Cofactors were only adjusted to marker positions which still fulfilled the conditions outlined above. Potential QTL which met the IM and KW requirements were declared to be true

QTL when the MQM LOD score exceeded the Genome-wide (GW) 90th percentile calculated by permutation tests (10,000 permutations) for each trait.

The BLUP means for the four possible QTL genotypes of the CP population (i.e. *ac, bc, ad, bd*) calculated in MapQTL v6.0 were used to estimate maternal (MQ), paternal (CQ), and interaction allelic effects according to Sewell et al. (2002):

$$Maternal\ effect = (ac + ad) - (bc + bd)$$

$$Paternal\ effect = (ac + bc) - (ad + bd)$$

$$Interaction\ effect = (ac + bd) - (ad + bc)$$

where *a* and *b* are alleles inherited from MQ and *c* and *d* are alleles inherited from CQ.

Comparative Analyses

Comparative analyses of micro-synteny were conducted using positional information of each SSR locus in the linkage map. Specifically, the contig, scaffold, or expressed sequence tag (EST) sequences containing each mapped SSR loci in this study were used in a BLAST search against the recently published cranberry genome assembly (Polashock et al. 2014); a minimum expectation value of 10e^{-06} and a minimum alignment of 70 % of the sequence length (due to the variability in length of the original contig, EST, and scaffold sequences used for SSR design) were used as parameters for identifying SSR sequence location in the genome in an attempt to anchor genomic scaffolds into pseudo-chromosomes. Predicted CDS identified by Polashock et al. (2014) were extracted from the SSR-anchored genomic scaffolds. Basic local alignment search tool (BLAST) searches using the extracted CDS were performed against the grape (NCBI ID 401), tomato (NCBI ID 7), and kiwifruit (NCBI ID 16401) genomes. Parameters used to declare significant BLAST hits included: (i) an alignment score > 150, (ii) an expectation score < 0.001, and (iii) a minimum sequence alignment length > 100bp. Genomic scaffolds or CDS with more than 5 significant hits were removed to avoid potential false positives due to the presence of repetitive regions. When two cranberry scaffolds or predicted CDS were located less than 2 cM apart on a LG and their homologous sequences were within 1.5 Mb in the genome of the local BLAST species, the regions were considered to be putative micro-syntenic blocks.

Results

Map Construction

In total, 221 progeny of the CNJ02-1 population were genotyped using 573 SSR primer pairs (Appendix IV-1). Among these 573 primers, 32 produced markers that displayed significant segregation distortion ($p < 0.05$) or caused potentially false double recombination events in multiple individuals and were therefore excluded from the parental maps and the integrated map. Table 4.1 fully details the marker composition of the 12 LGs.

The linkage analysis in the MQ female parent was based on 436 SSR markers which mapped to 12 LGs with an average of 36 SSRs per LG (Appendix IV-2, Appendix IV-3). The average LG length was 117.4 cM and the total observed genome length (G_O) of MQ was 1330.5 cM, representing an observed genome coverage (GC_O) of 94.5%. The average marker spacing was 3.1 cM, with a maximum gap of 25.6 cM on LG M2.

The linkage analysis of the CQ male parent was based on 426 SSR markers, which mapped to 12 LGs with an average of 35.5 loci per LG (Appendix IV-2, Appendix IV-4). The average LG length was 85.3 cM and the G_O was 94.4%. The average marker interval was 2.4 cM, and the maximum observed marker gap was 24.6 cM on LG C3.

Among the 573 segregating SSR markers, 541 were mapped on 12 LGs in the CNJ02-1 integrated map from here on referred to as MQxCQ (Figure 4.1, Table 4.1). The average number of mapped loci per LG was 45, and ranged from 32 SSRs in LG MC5 to 55 SSRs in LG MC7 (Table 4.1). Although the mean marker interval was relatively dense at 2.2 cM, 3 LGs still had relatively large genomic gaps greater than 15cM (LG MC2, LG MC3, LG MC10), and the largest observed gap was 21.5 cM (LG MC3). Linkage groups were numbered and ordered from longest to shortest observed map lengths, which ranged from 80.3 cM to 116.1 cM with a mean length of 98 cM. The G_O was 1178 cM, the G_E was 1233 cM, and the GC_O was 95.6%.

Analysis of marker collinearity between the MQ, CQ, and MQxCQ maps revealed few marker inconsistencies, and differences in marker order were mainly limited to closely linked markers (< 2 cM) within telomeric regions (Appendix IV-2). Additionally, 73 SSR markers mapped in the previous cranberry linkage map were also positioned in the current MQxCQ map, allowing for map marker collinearity comparisons (Georgi et al. 2013). Of the 14 LGs in the previous map, 13 groups had sufficient markers in common to be anchored into 11 LGs of the current map, and marker order between the two maps was highly collinear (Appendix IV-5).

Evaluation of Yield-Related Traits

Mixed models for TY and MFW containing genotype, year, and block main effects and their interactions were fit in order to estimate the variance components for each trait (Appendix IV-6). Likelihood ratio tests (LRT) revealed that all variance components in the TY were significant at the $p < 0.01$ level, and the genotype and year effects were the main source of variation in the CNJ02-1 population. All main effects were significant in the MFW model according to the LRT analysis; however, no significant genotype x year interactions were observed. Because significant genotype x year interactions were observed for TY, additional mixed models were fit containing only genotype and block main effects for TY and MFW for each year of data separately (Appendix IV-7). The genotype effect was the main source of variance in each of the six models. The block effect was not significant in the models for TY2012, MFW2011, and MFW2013.

Best linear unbiased predictors (BLUPs), standard errors (SE), and 95% prediction intervals were computed for MFW and TY averaged across years and additionally for each trait within each year, and BBI was calculated using the TY BLUPs with each year (Appendix IV-8). Transgressive segregation and significant differences at the 0.05% level in genotypic performance were detected for all traits in all years; a complete summary is presented in Table 4.2. The BLUP values for MFW were consistently lower in MQ than CQ; however, TY BLUPs were not significantly different between the parents. In general, the parental BLUPs were within the range of the F1 progeny; significant differences between the parents and individual genotypes were present. Additionally, the mean MFW and MFW2012 BLUPs of the F_1 population were significantly different than the CQ parent, and the TY2012 mean of the F_1 population was significantly different than MQ. Broad sense heritability for MFW and TY were moderate with values ranging from 0.64 to 0.70 (Table 4.2).

QTL Analyses

Significant associations between SSR markers and yield-related traits were identified in four of the 12 LGs, and at least one QTL was identified for MFW, TY, and BBI (Figure 4.1, Table 4.3). The individual QTL were low to moderate in effect, and explained between 7.6 and 15.3 percent of the total variation; however, the total phenotypic variation explained by all the QTL for each trait ranged from 15.3 to 38.1 percent. Additive allelic effects were observed at all QTL with near complete additivity observed for MFW on LG8 (Table 4.3).

Four significant QTL of nearly equal effect for MFW were found on LG MC6, LG MC10, and LG MC11 which explained 38.1% of the total variance (Figure1, Table 4.3). Additionally, MFW2011 and MFW2012 QTL were found with support intervals overlapping the MFW QTL on LG MC10 and LG MC11; a distinct QTL for MFW2011 on

LG MC11 and MFW2012 on LG MC10 were also found near the MFW QTL regions. Alternative alleles from MQ were most influential for MFW at QTL identified in LG MC6 and LG MC10; CQ alternative alleles were influential at the QTL in LG MC11; and an interaction effect was observed for the MFW QTL on LG MC11 between 78.6 and 82.3 cM (Table 4.3).

Three distinct QTL for TY were found on LG MC4, LG MC6, and LG MC11 which explained 28.0% of the total variance (Figure1, Table 4.3). A TY2012 QTL overlapping the support interval for the TY QTL on LG MC11 was also identified. Alternative alleles from MQ were most influential for the TY QTL on LG MC4, LG MC6, and LG MC11. A BBI QTL which co-localized with the TY QTL on LG MC11 explained 15.3% of the total variance and was also influenced by alternative alleles from MQ.

Comparative Analyses

Of the 541 mapped SSRs, 485 were aligned to 475 corresponding cranberry genomic scaffolds; 185 scaffolds contained a single predicted CDS, 63 contained 2 CDS, and 5 contained 3 CDS (Additional File 1). Comparative analysis with grape, tomato, and kiwifruit was carried out using only scaffolds containing CDS since these are the most conserved portions of a genome. Following this criteria, 77 (30%) of the cranberry scaffolds had 96 hits in the grape genome, 40 (16%) of the cranberry scaffolds had 45 hits in the tomato genome, and 147 (58%) of the cranberry scaffolds had 288 hits in the kiwifruit genome, demonstrating that the cranberry LGs shared the highest number of homologous regions with the kiwifruit genome (Appendix IV-9; Appendix IV-10; Appendix IV-11). The majority of the scaffolds (52%) had multiple hits in the kiwifruit genome. In contrast, most of the cranberry scaffolds that aligned in grape and tomato were homologous to only a single location (Appendix IV-12). Cranberry LGs shared homology with multiple (>7) kiwifruit chromosomes and LG MC7 shared the largest (37 scaffolds) number of sequences in common with the kiwifruit genome, mapping to 11 kiwifruit chromosomes (Figure 4.2). Out of the 22 cranberry scaffolds aligned to the kiwifruit genome that contained two or more CDS, 14 identified corresponding syntenic blocks in the kiwifruit genome while eight were not syntenic, which suggests a moderate level of micro-synteny between the genomes (Figure 4.1). A total of 19 additional micro-syntenic regions which fulfilled the requirements for this study of CDS within 2 cM in a cranberry LG and within 1.5 Mb in the kiwifruit genome were identified (Figure 4.1). None of the potential micro-syntenic regions were located in regions corresponding to the QTL identified in this study, and therefore, they were not useful for candidate gene discovery.

Discussion

This cranberry genetic linkage map is the highest density genetic map to date within the Ericaceae. Lower density genetic maps in *Vaccinium* have been constructed for diploid and tetraploid blueberry species using random amplified polymorphic DNA (RAPD) and sequence characterized amplified region (SCAR) markers (Rowland and Levi 1994; Qu and Hancock 1997) and in cranberry using a combination of 136 SSR and SCAR markers (Georgi et al. 2013). Additionally, a moderate density genetic map spanning 12 LGs was recently published for a population of interspecific blueberry hybrids of *V. darrowii* x *V. corymbosum* using a combination of 265 SNP, SSR, or RAPD markers (Rowland et al. 2014).

The linkage analysis in the CNJ02-1 population positioned 541 SSR loci on 12 LGs in the MQxCQ map which spanned 1177.84 cM and covered 96 percent of the estimated 470Mb cranberry genome. Of the 541 mapped SSRs, 468 have not been included in a previous linkage map. Parental maps constructed for MQ and CQ consisted of 436 SSR loci spanning 1330.55 cM and 426 SSR loci spanning 1023.25 cM, respectively. A comparison of common SSR markers in the parental and MQxCQ maps revealed near complete collinearity between the parental and combined maps and confirmed SSR marker order, and no evidence suggested that the minor differences between parents represented rearrangements rather than lack of recombination between markers or genotyping errors (Appendix IV-2). The linkage groups in the MQ maternal linkage map were consistently longer than the LGs in the CQ paternal map. This may indicate a higher recombination rate for the female parent, which is a phenomenon that has been previously reported for other species such as apple, olive, and grape (Maliepaard et al. 1998; Lowe et al. 2009; Sadok et al. 2013). Tetrad analysis of reciprocal translocation heterozygotes in two cranberry cultivars has previously revealed both genotypic and environmental effects on genetic recombination (Ortiz and Vorsa 1998). Because high levels of segregation distortion have been previously reported in mapping studies for cranberry and blueberry (Georgi et al. 2013; Rowland et al. 2014), extra precautions were taken to ensure correct marker order and to exclude distorted markers using conservative Chi-square tests ($p < 0.05$). Strategies, such as reduced genome representation for developing SNPs, are being conducted to create a high density SSR-backbone/SNP linkage map that will be used to assess the occurrence of segregation distortion along the 12 cranberry LGs with a high degree of precision.

The current study builds on a past linkage mapping effort in cranberry which developed a consensus map for 4 populations (64, 60, 48, and 20 individuals, respectively) that contained 136 positioned loci (Georgi et al. 2013). The current map represents a marked improvement in marker density over the previous map and provides a nearly four-fold increase in marker density with 468 previously unmapped co-dominant markers added. The average marker interval was

reduced from 8.6 to 2.2 cM, with approximately 1 marker for every 0.9 Mb of the estimated 470 Mb of the cranberry genome (Georgi et al. 2013; Polashock et al. 2014). In addition, the newly constructed genetic map more than tripled the average number of markers per linkage group (Table 4.1). More importantly, the higher density of markers achieved in this study consolidated the previous 14 LGs into 12 LGs, which correspond to the expected cranberry karyotype $2n=2x=24$ (Hall and Galleta, 1971; Ortiz and Vorsa, 1998). Two linkage groups from the Georgi et al. (2013) map, specifically Vm 6 and Vm 12 corresponded to a single LG (i.e. LG MC12) of the current map with a 13.52 cM gap between the two groups. Similarly, LG MC3 of the current study consolidated the two small linkage groups denominated Vm7 from the previous map now with a gap of 21.46 cM between the two groups in the current map. The two LGs which corresponded to Vm11 in the previous map were not linked in the current study because one of the groups contained only 4 markers spanning 11 cM, none of which were in common with the MCxCQ map (Appendix IV-5). Interestingly, LG MC10 of the current study, which covers 92 cM and contains 40 SSR markers, was completely unrepresented in the previous map. Even with the notable increase in marker density, the current map still contains gaps of more than 10 cM in 9 of the 12 LGs which could represent centromeric regions lacking recombination. Further marker saturation using SNP markers combined with cytological studies are needed to confirm this hypothesis (Table 4.1). The high density map described here establishes a backbone which will facilitate future gene localization for cranberry. The fact that the SSR marker order between the first genetic map and this high density map demonstrates complete collinearity across 5 diverse populations (Appendix IV-5) supports its broad applicability for future mapping of cranberry traits.

Comparative Genomics in Vaccinium

The genus *Vaccinium* contains multiple berry species in four main sections: *Cyanococcus* (blueberries), *Oxycoccus* (cranberries), *Myrtillus* (bilberries), and *Vitis-idaea* (lingonberries) all of which have biological, environmental, or commercial importance. Interspecific crosses at multiple ploidy levels within the *Vaccinium* sections have been common and important for germplasm enhancement, especially in section *Cyanococcus* where crosses between *V. darrowii* (2n), *V. corymbosum* (4n), and *V. ashei* (6n) were essential to the development of southern highbush blueberry cultivars with reduced chilling requirements (Darrow and Camp 1945; Dweikat and Lyrene 1988; Lyrene et al. 2003). Intersectional hybrids within *Vaccinium* have also been reported, but with various levels of vigor and fertility, and in general, have not been successful for introgressing traits of interest between the more distantly related species (Lyrene et al. 2003).

Comparative genetic and genomic research in *Vaccinium* has remained nonexistent because of insufficient shared mapped molecular markers and the lack of anchored genomic sequences in both cranberry and blueberry. However, multiple studies have analyzed the cross-species transferability of markers within *Vaccinium* and revealed that more than 80% of blueberry EST SSRs and 50% of genomic SSRs produced amplification fragments in related species (Boches et al. 2006; Bassil et al. 2009; Liu et al. 2014). These studies were important sources of genetic resources for the first genetic map in cranberry, which included 33 SSRs derived from blueberry sequences (Georgi et al. 2013), and in the current linkage map which includes 19 of the 33 blueberry SSRs (Appendix IV-1). However, only 4 of these blueberry derived EST-SSRs have been included in a blueberry genetic map (Rowland et al. 2014); and thus, no additional comparative inferences can be made at this time.

Cranberry (*V. macrocarpon*) genetic improvement has relied solely on intraspecific germplasm; however, intrasectional and intersectional hybridization are both possible, but have not been exploited for breeding in the *Oxycoccus* as in the *Cyanococcus* section. For example, no interspecific hybrids of commercial importance between *V. macrocarpon* x *V. oxycoccos* exist, but there is growing interest among cranberry breeders to develop strategies for trait introgression within the *Oxycoccus* section. Specifically, alteration of anthocyanin glycosylation has been accomplished in cranberry through interspecific hybridization to increase glucose-conjugated anthocyanins (Vorsa and Polashock 2005). Additionally, a number of genetic diversity studies of *V. oxycoccos* and *V. macrocarpon* using SCARs, SSRs, and amplified fragment length polymorphisms (AFLPs) have been conducted in order to describe available wild germplasm and to increase understanding of the evolutionary relationships between the two species and various ploidy levels (Polashock and Vorsa 2002; Fajardo et al. 2012; Zalapa et al. 2014; Schlautman et al. 2015). Moreover, 12 SSRs developed for cranberry genetic diversity assessment (Zhu et al. 2012) were all positioned and evenly distributed among 9 linkage groups of the current map, which confirms the validity of recent *V. macrocarpon* and *V. oxycoccos* genetic diversity studies (Fajardo et al. 2012; Zalapa et al. 2014) (Figure 4.1, Appendix IV-1).

The transferability tests of blueberry EST-SSRs performed in cranberry and other species (Boches et al. 2006; Bassil et al. 2009; Liu et al. 2014) suggest that the 85 cranberry EST-SSR markers mapped in the current study could be highly transferable and informative in other *Vaccinium* species. Specifically, these markers could be used to increase marker density in the blueberry genetic map, which still has multiple linkage groups with large gaps and fewer than 15 mapped markers (Rowland et al. 2014), and to develop the first genetic maps for *V. oxycoccos*, bilberry, lingonberry, and other blueberry species. The high SSR marker density in the current cranberry genetic map, combined with the potential EST-SSR transferability, will be essential for future comparative genomic studies in *Vaccinium* leading to the

development of molecular introgression of traits of interest such as reduced chilling requirements into cranberry, blueberry, lingonberry, and other economically important *Vaccinium* crops through interspecific hybridization.

Trait Variation within the mapping population

Substantial continuous variation in total yield (TY) and mean fruit weight (MFW) in the CNJ02-1 population indicated polygenic inheritance for both traits (Table 4.2). In addition, trait variation in the F_1 population extended beyond the means of both parents suggesting transgressive segregation. BLUP estimates were used to adjust parent and progeny means based on the observed field spatial variation (*B*), *Y*, *G:Y*, and *B:Y* effects. Additional year-specific models and year-specific BLUP estimates were also fitted for each trait separately because of significant observed *G:Y* effects in the full models.

The large TY *Y* variance component (41% of total) and *G:Y* variance component (3.5% of total) suggested that yearly environmental conditions have a substantial amount of influence in cranberry yield expression, which was expected for such a complex polygenic trait. Multiple studies have been conducted in cranberry to identify and quantify the biological and environmental factors affecting annual yield such as geographic location, fertilizer response, intra-plant competition for resources, and hormonal signaling (Eady and Eaton 1972; McArthur and Eaton 1989; Strik et al. 1991; Davenport 1996; Roper and Klueh 1996). Other studies have investigated the morphological components of annual cranberry yield such as fruit set, number of reproductive stems, number of flowers per reproductive stem, and mean fruit weight (Eaton and Kyte 1978; Shawa et al. 1981). Additionally, some studies have suggested that cranberry may display an alternate bearing or biennial bearing tendency, and that this tendency is controlled by both environmental and genotypic components (Eaton et al. 1983; Elle 1996; DeVetter et al. 2013). Therefore, a biennial bearing index (BBI) was calculated using the year BLUPs for TY as a measure of yield stability or an indirect measure of *G:Y* for each genotype. Continuous variation and transgressive segregation was observed for BBI. Therefore, the BBI observed for the F_1 population in this study suggests that yield stability across successive years is a heritable trait which is critical for cranberry germplasm improvement.

QTL Analyses

QTL studies in perennial fruit crops are long-term experiments requiring large financial investments. The long interval to establish sufficient biomass and reach reproductive maturity impedes breeding efficiency. The CNJ02-1 mapping population used in this study is the only large (i.e., greater than 100 genotypes) reproductively mature mapping

population with multiple years of phenotypic data that is available to cranberry researchers. Therefore, despite the obvious shortcomings in experimental design in this study, such as the use of a single field location, the results of the trait analyses and QTL studies presented represent the most complete study possible at this time in cranberry. Most importantly, QTL for TY, MFW, and BBI detected in this study at a single location demonstrate that the level of marker saturation achieved in the integrated genetic map is sufficient for marker localization of regions linked or associated with traits with continuous distributions, even if the identified QTL are not necessarily stable in other environments.

The identified QTL were distributed within four of the 12LGs with LG MC11 containing the largest number of QTL. Individual QTL found during this study had relatively small effects and controlled less than 15.5% of the total variance. However, the total amount of variance explained for all the QTL identified for each trait controlled moderate amounts of the phenotypic variance (i.e. up to 38%).

QTL for MFW using whole BLUPs were found on LG MC6, LG MC10, and LG MC11; together they controlled nearly 40% of the MFW phenotypic variance. The MFW QTL identified on LG MC6 and LG MC10 were most affected by substitution of alleles from MQ whose MFW was significantly less than CQ. Conversely, both MFW QTL on LG MC11 were most affected by substitution of CQ alleles, and the QTL near SSR marker SCF118608 suggested a large interaction affect between maternal and paternal alleles. None of the MFW QTL identified in this study were located in genomic regions where MFW QTL were reported in Georgi et al. (2013). However, three of the QTL identified in this study using the whole BLUPs means were also identified using year-specific BLUPs for MFW. Therefore, the MFW QTL identified appear to be stable across years within this specific F_1 population at this location.

Heritability of mean fruit weight in cranberry in a series of second breeding cycle crosses was relatively high ($h>0.8$) and contributed to yield variation across breeding populations (Vorsa and Johnson-Cicalese 2012). Fruit weight QTL have been reported in a variety of other fruit crop species with moderate levels of heritability such as pepper, apple, tomato, and peach (Dirlewanger et al. 1999; Chaim et al. 2001; Lippman and Tanksley 2001; Kenis et al. 2008). MFW has been an important selection criteria in cranberry improvement, and findings here of a heritability of MWF (H^2=0.70) are consistent with Vorsa and Johnson-Cicalese (2012). Because fruit processors continue to increase their desire for larger cranberry fruits for use in specialty products such as sweetened dried cranberries (SDCs), the MFW QTL and heritability identified herein can serve as important resources in deploying marker-assisted selection strategies aimed at developing large-fruited cranberry varieties.

Identification of high-yielding genotypes is a priority of all plant breeding programs, and cranberry breeders have previously used phenotypic selection within individual locations to develop varieties that display increased yield

potential in all commercial environments (McCown and Zeldin 2003; Clark and Finn 2010). Herein, we report the first identification of TY QTL in cranberry in a single environment. The TY QTL are located on three separate linkage groups (i.e. LG MC4, LG MC6, and LG MC11), and explain a combined 28.1% of the total phenotypic variance. Allelic substitution of MQ alleles had the largest effect on mean TY in the F_1 population (Table 4.3). None of the QTL identified for TY overlapped with genomic regions of previously reported QTL (Georgi et al. 2013).

Future studies should attempt to identify QTL for other known yield components such as the number of flowering stems per unit of area, percentage of flowers setting fruit, number of flowers per stem and study their potential yield pleiotropic action (Eaton and MacPherson 1978; Shawa et al. 1981). Moreover, other studies have noted that field fruit rot is one of the most serious threats to annual yield and crop quality in the northeastern U.S. (Oudemans et al. 1998; Tadych et al. 2012). As a result, heritability of fruit rot resistance has already been extensively studied and putative QTL for fruit rot resistance have been identified (Georgi et al 2013; Johnson-Cicalese et al. 2015). Continued analysis of field fruit rot resistance QTL stability across multiple environments and their application in MAS strategies would be beneficial to maintaining consistent annual yields in the cranberry industry.

Finally, cranberry yield stability across years has been noted to be affected by the phenomenon of biennial bearing (Eaton et al. 1983; Vorsa and Johnson-Cicalese 2012; DeVetter et al. 2013). Biennial bearing is a complex problem which affects the economic livelihood of commercial orchards of a variety of fruit crops from diverse taxonomies such as apples, pears, oranges, and pistachios (Jonkers 1979; Smith et al. 2004; Kallsen et al. 2007). As a result, extensive research has been conducted in order to understand the environmental components affecting biennial bearing using BBI (Wilcox 1944; Jonkers 1979; Stevenson and Shackel 1998; Smith and Samach 2013) as well as identifying genotypic variation affecting biennial bearing tendencies using more complex adaptations of BBI (Guitton et al. 2012; Durand et al. 2013). Multiple putative QTL related to biennial bearing have been identified in apple (Guitton et al. 2012).

This is the first study to report of continuous variation and transgressive segregation of BBI in cranberry, and the first to report a BBI QTL related to biennial bearing in cranberry. We identified a BBI QTL located on LG MC11 with support interval overlapping the interval for a TY QTL near SSR locus SCF204332; both QTL were affected by allelic substitution of MQ alleles (Figure 4.1, Table 4.3). The presence of a BBI QTL co-localizing with a TY QTL indicates the QTL may be stable and unaffected by *G:Y* effects and suggests that static yield stability across years and environments, as measured by BBI, may represent an important component in determining annual yield. Successful

mapping of a BBI QTL is the first suggestion of the heritability and selectability of yield stability across successive years in cranberry. QTL for BBI offer the best opportunity to reduce breeding and selection cycle interval.

Comparative Analyses

Comparative genetic mapping can be used to assess genome differentiation by identifying similarities and differences in chromosome organization, and further the transfer of genomic information between taxa through targeted interspecific hybridization. The current study represents the first attempt to anchor cranberry scaffolds from large-scale next generation sequencing (NGS) assemblies (Polashock et al. 2014) into pseudo-chromosomes, and the first comparative analysis with kiwifruit, grape and tomato genomes. Consistent with the closest taxonomic distance, the highest degree of homology was observed between the cranberry integrated linkage map and the kiwifruit genome, both species are members of the Ericales clade and perennial species. It has been proposed that the genomes of perennial species may have a lower divergence rate (Pavy et al. 2012). For example, high synteny was observed between the genomes of spruce and pine, two conifers that diverged more than 100 million years ago (Mya). Despite this hypothesis, the macro-synteny and collinearity between the cranberry map and kiwifruit genome were very low, indicating that the organization of the cranberry-kiwifruit gene space has been largely disrupted over a period dating back about 90 Mya, since the early diversification of the Ericales in the Late Cretaceous (Magallón et al. 2015). In addition, no obvious homeologous chromosomal relationships were identified between cranberry and kiwifruit (Figure 4.2). Different evolutionary mechanisms including large and small-scale duplications may have contributed to the diversification of these two genomes. Whole genome duplication (WGD) represents a major source of genome diversity and diversification. Analysis of the kiwifruit genome revealed that two WGDs occurred about 30 and 70-100 Mya, after the divergence of the Ericales clade from the Asterids (Huang et al. 2013). Although it is still unknown whether the cranberry genome experienced any WGDs in this same evolutionary time period, the kiwifruit lineage specific WGD may have played an important role in the diversification of these two genomes. Estimating the extent of conservation in genome macro-structure was more exhaustive in our study since the high fractionation of the genomes limited small-scale synteny analysis.

Micro-syntenic regions could be lengthened by increasing the number of mapped gene based co-dominant markers such as SNPs through genome reduction strategies such as genotyping-by-sequencing (GBS) (Poland and Rife 2012). Efforts to establish a high resolution cranberry linkage map saturated with SNP markers is currently being undertaken and will provide an opportunity to explore the presence of micro-scale conserved syntenic regions between

cranberry and kiwifruit genomes. An even more effective strategy for lengthening micro-syntenic regions would be to conduct further cranberry genome sequencing efforts in order to increase the average anchored cranberry scaffold length from 6 Kb (CDS per scaffold < 1) to scaffold lengths greater than 50 Kb (CDS per scaffold ≥ 2). Furthermore, the increased scaffold length, and the resulting increase in mapped CDS, would increase the confidence that the identified micro-syntenic blocks represent true syntenic regions. The overall low level of macro-synteny and collinearity observed between the cranberry linkage map and the kiwifruit genome suggests that the genomes of these species are highly divergent, indicating that the transferability of sequence information from the kiwifruit genome to related *Vaccinium* species will likely be limited.

Conclusions

This study has produced a high density SSR linkage map in cranberry which is sufficient for QTL identification of traits with continuous distributions, and the localization of quantitative traits in the cranberry genome. The high inherent polymorphism of SSR loci suggests that the 541 mapped SSRs will be transferable to populations of diverse pedigrees for future QTL studies and in developing innovative MAS strategies for cranberry genetic improvement. Furthermore, the likely transferability of mapped SSR loci originating from cranberry and blueberry EST sequence data within *Vaccinium* should allow for comparative genomic studies and MAS aimed at introgression of species-specific traits through intra and inter-sectional hybridization. This study is the first in cranberry to confirm the existence of heritable genetic variation in yield stability across years as measured by BBI, and the QTL for BBI, TY and MFW identified herein are immediately available for use in cranberry genetic improvement though MAS strategies using MQ, CQ and their progeny. Macro-syntenic relationships between the cranberry and kiwifruit genomes were not observed, however some regions of micro-synteny were identified. Additional genomic sequencing efforts and increased map saturation in cranberry are necessary to further characterize synteny between the genomes.

Acknowledgements

Galatians 6:9. This project was supported by USDA-SRCI under Grant 2008-51180-04878; USDA-NIFA-AFRI Competitive Grant USDA-NIFA-2013-67013-21107; USDA-ARS (project no. 3655-21220-001-00); WI-DATCP (SCBG Project #14-002); National Science Foundation DBI-1228280; Ocean Spray Cranberries, Inc.; NJ Cranberry and Blueberry Research Council; Wisconsin Cranberry Growers Association; Cranberry Institute.

Conflict of interest

The authors declare that they have no conflict of interest.

Table 4.1. Summary statistics, marker composition, and corresponding linkage groups from the Georgi et al. (2013) linkage map for the CNJ02-1 integrated cranberry SSR linkage map (MQxCQ).

Linkage Group	Number of Markers	Observed Length (cM)	Expected Length	Observed coverage (%)	Gaps more than 10cM	Average Spacing	Largest Gap (cM)	Georgi et al. (2013) linkage group
MC1	51	116.15	120.79	96.15	3	2.28	13.99	Vm9
MC2	48	107.83	112.42	95.92	1	2.25	16.10	Vm8
MC3	42	103.52	108.57	95.35	2	2.46	21.46	Vm7 & Vm7b
MC4	54	100.08	103.86	96.36	1	1.85	10.32	Vm2
MC5	32	99.87	106.32	93.94	1	3.12	12.41	Vm10
MC6	41	99.87	104.86	95.24	0	2.44	8.71	Vm5
MC7	55	99.76	103.46	96.43	0	1.81	5.36	Vm3
MC8	40	98.75	103.81	95.12	1	2.47	11.18	Vm4
MC9	49	97.15	101.20	96.00	0	1.98	9.66	Vm1
MC10	40	92.24	96.97	95.12	1	2.31	16.23	None
MC11	38	82.26	86.71	94.87	1	2.16	13.14	Vm11b
MC12	51	80.35	83.56	96.15	1	1.58	13.52	Vm12 & Vm6
Mean	45.08	98.15	102.71	95.55	1	2.23	12.67	
Total	541	1177.84	1232.53	95.56	12			

Table 4.2. Best linear unbiased predictors (BLUPs) and their 95 % prediction intervals for total yield (TY) and mean fruit weight (MFW) for the minimum genotype, maximum genotype, mean of the CNJ02-1 F_1 cranberry mapping population, and the parents based on mixed models fit for 3-year and year-specific models (denoted by trait abbreviation followed by year). Genotypes were considered significantly different when the prediction intervals did not overlap. Prediction intervals are presented as BLUP ± the prediction interval. Broad-sense heritabilities (H^2) were calculated based on the 3-year model.

	F_1 Progeny			Parents		
Trait	Min	Max	Mean	MQ	CQ	H^2
MFW	1.70 ± 0.14^{MC}	2.76 ± 0.14^{MC}	2.12 ± 0.03^{C}	1.99 ± 0.14^{C}	2.33 ± 0.14^{M}	0.70
MFW2011	1.78 ± 0.19^{MC}	3.04 ± 0.19^{MC}	2.30 ± 0.03	2.34 ± 0.19	2.37 ± 0.19	
MFW2012	1.69 ± 0.20^{C}	2.71 ± 0.20^{M}	2.14 ± 0.03^{C}	1.98 ± 0.20^{C}	2.44 ± 0.20^{M}	
MFW2013	1.59 ± 0.18^{C}	2.26 ± 0.18^{M}	1.92 ± 0.02	1.80 ± 0.18	2.02 ± 0.18	
TY	138.63 ± 55.21^{MC}	487.60 ± 54.85^{MC}	313.53 ± 10.53	370.22 ± 55.21	356.00 ± 55.21	0.64
TY2011	260.32 ± 91.79^{MC}	665.46 ± 91.79	453.74 ± 13.03	503.03 ± 91.79	490.39 ± 91.79	
TY2012	99.22 ± 59.63^{MC}	436.71 ± 59.63^{C}	220.18 ± 9.53^{M}	329.09 ± 59.86	303.79 ± 59.86	
TY2013	159.48 ± 67.18	399.84 ± 67.04^{MC}	270.05 ± 8.16	263.46 ± 67.18	264.00 ± 67.18	
BBI	4.66	51.41	25.10	15.99	15.25	

^{M}significantly different from the *Mullica Queen*© parent

^{C}significantly different from the *Crimson Queen*© parent

Table 4.3. Detailed information for mean fruit weight (MFW), total yield (TY), and biennial bearing index (BBI) QTL detected in the CNJ02-1cranberry population based on 3-year best linear unbiased predictors (BLUPs) and year-specific BLUPs.

Trait	LG	Nearest Marker	P/cM[a]	LOD Peak	2-LOD min	2-LOD max	VI%[b]	MQ[c]	CQ[d]	Interaction[e]
MFW	6	SCF171621	17.54	5.16***	12.56	18.54	9.3	-0.25	0.12	-0.01
	10	SCF35507	48.52	5.51***	41.93	48.52	10	0.19	0.08	0.15
	11	SCF122746	12.75	5.24***	11.03	15.75	9.5	-0.05	-0.23	-0.10
	11	SCF118608	82.26	5.15***	78.63	82.26	9.3	0.03	0.05	-0.26
MFW2011	10	SCF35507	48.52	6.07***	41.93	48.52	11.5	0.26	0.10	0.11
	11	SCF21596	41.89	5.08***	37.75	46.89	9.5	0.01	-0.27	0.08
	11	SCF118608	82.26	4.68**	78.63	82.26	8.7	-0.07	0.06	-0.24
MFW2012	10	SCF172906	57.64	4.59**	53.25	57.64	10.6	0.19	0.06	0.12
	11	SCF122746	12.75	3.99*	11.03	15.75	9.2	-0.04	-0.20	-0.09
TY	4	SCF11084	88.99	6.65***	88.82	94.99	11.8	-97.10	-70.88	25.14
	6	1trimcontig344502	56.80	4.29**	53.91	62.80	7.6	73.29	20.36	-6.03
	11	SCF204332	24.18	4.8**	17.73	24.18	8.6	70.68	46.88	-6.12
TY2012	11	SCF204332	24.18	6.79***	17.73	24.18	11.9	82.96	46.09	-10.68
BBI	11	SCF204332	24.18	6.37***	17.73	24.18	15.3	-12.14	-6.27	4.47

[a] QTL position at the peak of LOD

[b] The percent of total phenotypic variance explained by the QTL

[c] The effect of allelic substitution of *Mullica Queen*© alleles

[d] The effect of allelic substitution of *Crimson Queen*© alleles

[e] The interaction effect of *Mullica Queen*© and *Crimson Queen*© alleles

*Genome-wide threshold (GT) of 90%; ** GT of 95%, *** GT of 99%

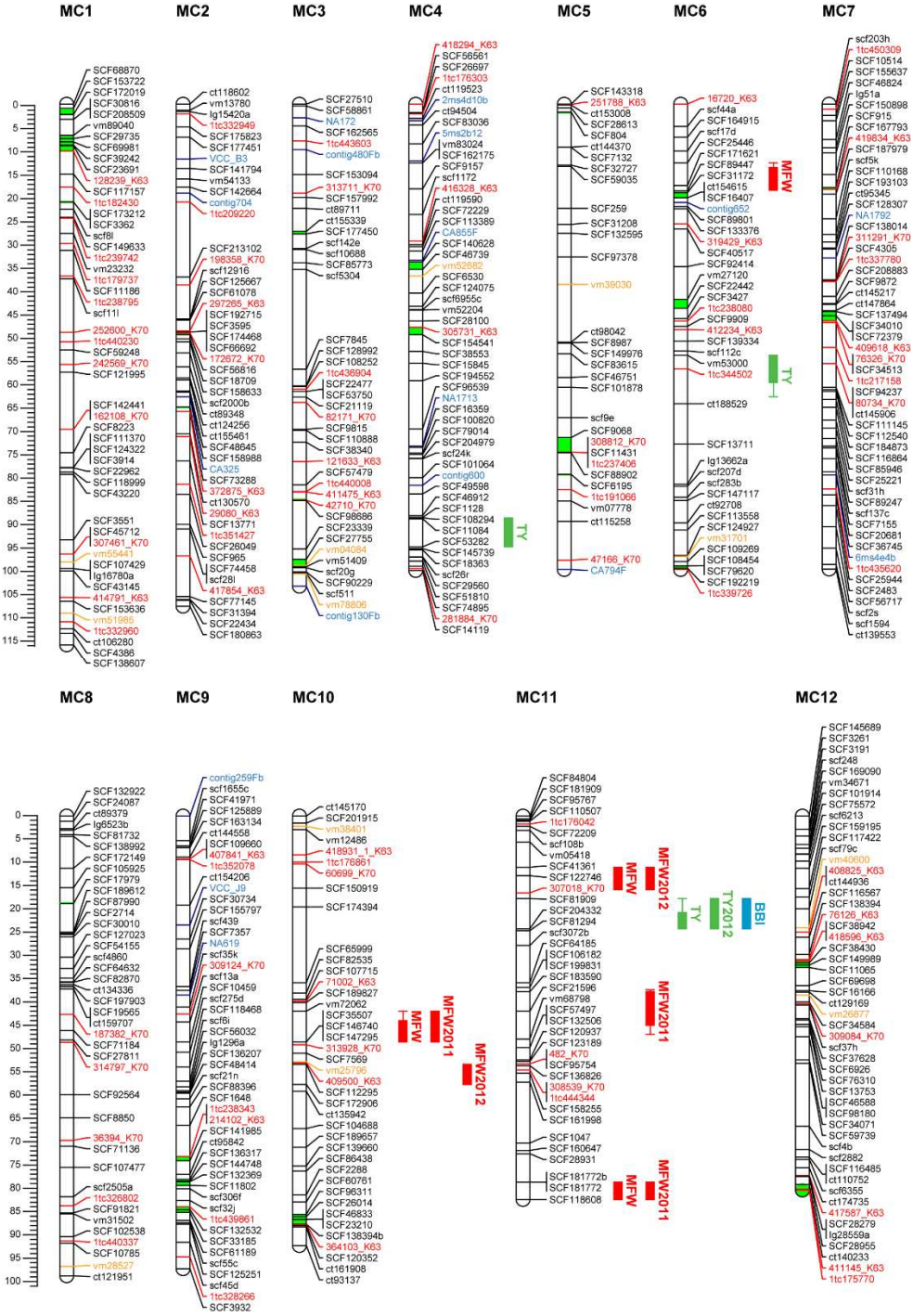

Figure 4.1. The CNJ02-1 integrated cranberry SSR linkage map (MQxCQ). Consisting of 541 markers distributed in 12 linkage groups Loci in blue were developed from blueberry sequence data; loci in red are from cranberry expressed sequence tags (EST); loci in black are from genomic sequences; loci in orange are used extensively in papers evaluating cranberry and *V. oxycoccos* diversity. Quantitative trait loci (QTL) in green are for total yield (TY); red QTL are for mean fruit weight (MFW); and the blue QTL is for biennial bearing index (BBI). QTL for year-specific best linear unbiased predictors (BLUPs) are denoted by the year in which they were identified. Linkage group segments highlighted in light green are putative regions of micro-synteny between the cranberry and kiwifruit genomes. SSR markers with IDs containing "trimcontig" (ESM 1) were shortened to "tc" in the figure.

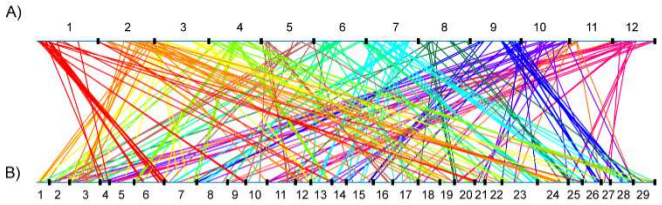

Figure 4.2. Comparative analysis of A) cranberry linkage groups (LGs) and B) kiwifruit genome based on BLAST analyses of the CDS anchored in the CNJ02-1 cranberry integrated map (MQxCQ). Lines connect homologous sequences between the cranberry LGs and the kiwifruit chromosomes, and the lines are colored based on the position of that CDS in the cranberry LGs.

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Appendix IV-1. List of SSR primers, their position in the cranberry integrated map, their publication of origin, their scaffold hit in the cranberry genome, associated predicted coding DNA sequences (CDS), and special features.

Marker ID	NCBI ID	LG	Position (cM)	Marker Origin	Number of Predicted CDS in Genome Scaffold
SCF68870	KP278750.1	1	0	Schlautman et al. (2015)	
SCF153722	KP278899.1	1	0.93	Schlautman et al. (2015)	1
SCF172019	KP278920.1	1	2.193	Schlautman et al. (2015)	1
SCF30816	KP278685.1	1	3.254	Schlautman et al. (2015)	1
SCF208509	KP278950.1	1	3.299	Schlautman et al. (2015)	1
vm89040	JF834248.1	1	6.71	Zhu et al. (2012)	1
SCF29735	KP278681.1	1	7.398	Schlautman et al. (2015)	
SCF69981	KP278752.1	1	8.063	Schlautman et al. (2015)	1
SCF39242	KP278705.1	1	8.812	Schlautman et al. (2015)	
SCF23691	KP278662.1	1	8.911	Schlautman et al. (2015)	1
128239_K63	KP279164.1	1	10.149	Schlautman et al. (2015)	1
SCF117157	KP278837.1	1	15.016	Schlautman et al. (2015)	2
1trimcontig182430	KP279226.1	1	17.803	Schlautman et al. (2015)	
SCF173212	KP278924.1	1	21.039	Schlautman et al. (2015)	3
SCF3362	KP278605.1	1	21.039	Schlautman et al. (2015)	1
scf8l	N/A	1	22.597	Georgi et al. (2013)	
SCF149633	KP278891.1	1	24.334	Schlautman et al. (2015)	2
1trimcontig239742	KP279234.1	1	24.479	Schlautman et al. (2015)	2
vm23232	JF834262.1	1	27.845	Zhu et al. (2012)	
1trimcontig179737	KP279225.1	1	29.907	Schlautman et al. (2015)	
SCF11186	KP278636.1	1	31.432	Schlautman et al. (2015)	1
1trimcontig238795	KP279233.1	1	36.854	Schlautman et al. (2015)	
scf11l	N/A	1	37.457	Georgi et al. (2013)	1
252600_K70	KP279205.1	1	49.043	Schlautman et al. (2015)	1
1trimcontig440230	KP279249.1	1	50.958	Schlautman et al. (2015)	2
SCF59248	KP278740.1	1	52.752	Schlautman et al. (2015)	
242569_K70	KP279204.1	1	55.903	Schlautman et al. (2015)	1
SCF121995	KP278845.1	1	57.454	Schlautman et al. (2015)	2
SCF142441	KP278879.1	1	69.759	Schlautman et al. (2015)	
162108_K70	KP279200.1	1	69.762	Schlautman et al. (2015)	
SCF8223	KP278622.1	1	74.826	Schlautman et al. (2015)	
SCF111370	KP278828.1	1	77.969	Schlautman et al. (2015)	
SCF124322	KP278849.1	1	77.969	Schlautman et al. (2015)	
SCF3914	KP278609.1	1	77.987	Schlautman et al. (2015)	
SCF22962	KP278659.1	1	78.074	Schlautman et al. (2015)	1
SCF118999	KP278842.1	1	78.983	Schlautman et al. (2015)	1
SCF43220	KP278712.1	1	79.544	Schlautman et al. (2015)	
SCF3551	KP278608.1	1	93.532	Schlautman et al. (2015)	1
SCF45712	KP278713.1	1	96.56	Schlautman et al. (2015)	

307461_K70	KP279275.1	1	96.609	Schlautman et al. (2015)	1
vm55441	JF834240.1	1	98.318	Zhu et al. (2012)	
SCF107429	KP278815.1	1	99.655	Schlautman et al. (2015)	
Ig16780a	N/A	1	99.748	Georgi et al. (2013)	
SCF43145	KP278711.1	1	100.179	Schlautman et al. (2015)	1
414791_K63	KP279183.1	1	105.853	Schlautman et al. (2015)	1
SCF153636	KP278898.1	1	106.666	Schlautman et al. (2015)	
vm51985	JF834280.1	1	109.291	Zhu et al. (2012)	
1trimcontig332960	KP279238.1	1	111.099	Schlautman et al. (2015)	
ct106280	KP279109.1	1	112.633	Schlautman et al. (2015)	
SCF4386	KP278612.1	1	113.637	Schlautman et al. (2015)	1
SCF138607	KP278872.1	1	116.146	Schlautman et al. (2015)	1
ct118602	KP279113.1	2	0	Schlautman et al. (2015)	1
vm13780	JF834259.1	2	1.251	Zhu et al. (2012)	
Ig15420a	N/A	2	1.641	Georgi et al. (2013)	
1trimcontig332949	KP279237.1	2	2.144	Schlautman et al. (2015)	2
SCF175823	KP278927.1	2	4.879	Schlautman et al. (2015)	
SCF177451	KP278929.1	2	7.139	Schlautman et al. (2015)	
VCC_B3	N/A	2	11.789	Boches et al.(2005)	
SCF141794	KP278877.1	2	13.842	Schlautman et al. (2015)	2
vm54133	JF834236.1	2	16.059	Zhu et al. (2012)	1
SCF142664	KP278880.1	2	17.826	Schlautman et al. (2015)	1
contig704	N/A	2	19.085	Georgi et al. (2013)	
1trimcontig209220	KP279228.1	2	21.016	Schlautman et al. (2015)	1
SCF213102	KP278953.1	2	37.117	Schlautman et al. (2015)	
198358_K70	KP279203.1	2	38.826	Schlautman et al. (2015)	1
scf12916	N/A	2	46.102	Georgi et al. (2013)	
SCF125667	KP278852.1	2	46.347	Schlautman et al. (2015)	
SCF61078	KP278743.1	2	46.396	Schlautman et al. (2015)	
297265_K63	KP279167.1	2	48.666	Schlautman et al. (2015)	1
SCF192715	KP278942.1	2	48.867	Schlautman et al. (2015)	
SCF3595	KP278607.1	2	48.872	Schlautman et al. (2015)	2
SCF174468	KP278926.1	2	48.872	Schlautman et al. (2015)	
SCF66692	KP278749.1	2	48.919	Schlautman et al. (2015)	
172672_K70	KP279201.1	2	49.073	Schlautman et al. (2015)	
SCF56816	KP278735.1	2	49.48	Schlautman et al. (2015)	1
SCF18709	KP278651.1	2	50.353	Schlautman et al. (2015)	1
SCF158633	KP278906.1	2	50.954	Schlautman et al. (2015)	
scf2000b	N/A	2	53.412	Georgi et al. (2013)	
ct89348	KP279100.1	2	56.376	Schlautman et al. (2015)	
ct124256	KP279118.1	2	58.826	Schlautman et al. (2015)	
ct155461	KP279141.1	2	59.207	Schlautman et al. (2015)	
SCF48645	KP278722.1	2	61.567	Schlautman et al. (2015)	1

SCF158988	KP278907.1	2	61.824	Schlautman et al. (2015)	
CA325	N/A	2	62.781	Georgi et al. (2013)	
SCF73288	KP278758.1	2	65.011	Schlautman et al. (2015)	3
372875_K63	KP279174.1	2	66.029	Schlautman et al. (2015)	2
ct130570	KP279121.1	2	70.749	Schlautman et al. (2015)	1
29080_K63	KP279160.1	2	71.386	Schlautman et al. (2015)	
SCF13771	KP278642.1	2	76.643	Schlautman et al. (2015)	2
1trimcontig351427	KP279242.1	2	81.559	Schlautman et al. (2015)	1
SCF26049	KP278668.1	2	83.78	Schlautman et al. (2015)	2
SCF965	KP278594.1	2	90.246	Schlautman et al. (2015)	1
SCF74458	KP278759.1	2	91.15	Schlautman et al. (2015)	1
scf28l	N/A	2	91.179	Georgi et al. (2013)	
417854_K63	KP279188.1	2	96.984	Schlautman et al. (2015)	1
SCF77145	KP278763.1	2	105.651	Schlautman et al. (2015)	
SCF31394	KP278688.1	2	106.327	Schlautman et al. (2015)	2
SCF22434	KP278656.1	2	106.5	Schlautman et al. (2015)	
SCF180863	KP278930.1	2	107.83	Schlautman et al. (2015)	2
SCF27510	KP278670.1	3	0	Schlautman et al. (2015)	1
SCF58861	KP278738.1	3	0.447	Schlautman et al. (2015)	1
NA172	N/A	3	2.881	Georgi et al. (2013)	
SCF162565	KP278913.1	3	4.653	Schlautman et al. (2015)	1
1trimcontig443603	KP279251.1	3	7.889	Schlautman et al. (2015)	1
contig480Fb	N/A	3	9.843	Georgi et al. (2013)	
SCF153094	KP278897.1	3	15.1	Schlautman et al. (2015)	1
313711_K70	KP279215.1	3	19.06	Schlautman et al. (2015)	1
SCF157992	KP278904.1	3	19.975	Schlautman et al. (2015)	1
ct89711	KP279102.1	3	22.424	Schlautman et al. (2015)	
ct155339	KP279140.1	3	27.314	Schlautman et al. (2015)	1
SCF177450	KP278928.1	3	27.915	Schlautman et al. (2015)	1
scf142e	N/A	3	30.959	Georgi et al. (2013)	
scf10688	N/A	3	31.205	Georgi et al. (2013)	
SCF85773	KP278780.1	3	34.087	Schlautman et al. (2015)	
scf5304	N/A	3	35.477	Georgi et al. (2013)	
SCF7845	KP278620.1	3	56.936	Schlautman et al. (2015)	1
SCF128992	KP278858.1	3	60.513	Schlautman et al. (2015)	
SCF108252	KP278817.1	3	60.647	Schlautman et al. (2015)	
1trimcontig436904	KP279245.1	3	61.188	Schlautman et al. (2015)	1
SCF22477	KP278658.1	3	61.683	Schlautman et al. (2015)	
SCF53750	KP278727.1	3	61.683	Schlautman et al. (2015)	
SCF21119	KP278654.1	3	62.882	Schlautman et al. (2015)	
82171_K70	KP279199.1	3	64.03	Schlautman et al. (2015)	1
SCF9815	KP278628.1	3	69.831	Schlautman et al. (2015)	2
SCF110888	KP278826.1	3	70.049	Schlautman et al. (2015)	

SCF38340	KP278701.1	3	72.589	Schlautman et al. (2015)	1
121633_K63	KP279163.1	3	76.73	Schlautman et al. (2015)	
SCF57479	KP278736.1	3	81.653	Schlautman et al. (2015)	
1trimcontig440008	KP279248.1	3	83.157	Schlautman et al. (2015)	1
411475_K63	KP279181.1	3	83.284	Schlautman et al. (2015)	1
42710_K70	KP279194.1	3	84.988	Schlautman et al. (2015)	2
SCF98686	KP278803.1	3	85.116	Schlautman et al. (2015)	
SCF23339	KP278661.1	3	95.53	Schlautman et al. (2015)	
SCF27755	KP278671.1	3	97.682	Schlautman et al. (2015)	2
vm04084	JF834250.1	3	99.016	Zhu et al. (2012)	2
vm51409	JF834279.1	3	99.338	Zhu et al. (2012)	1
scf20g	N/A	3	99.464	Georgi et al. (2013)	1
SCF90229	KP278791.1	3	100.447	Schlautman et al. (2015)	
scf511	N/A	3	100.594	Georgi et al. (2013)	
vm78806	JF834245.1	3	100.83	Zhu et al. (2012)	
contig130Fb	N/A	3	103.522	Georgi et al. (2013)	
418294_K63	KP279189.1	4	0	Schlautman et al. (2015)	1
SCF56561	KP278732.1	4	1.75	Schlautman et al. (2015)	2
SCF26697	KP278669.1	4	1.99	Schlautman et al. (2015)	1
1trimcontig176303	KP279222.1	4	2.109	Schlautman et al. (2015)	1
ct119523	KP279114.1	4	3.076	Schlautman et al. (2015)	
2ms4d10b	N/A	4	3.595	Georgi et al. (2013)	
ct94504	KP279105.1	4	4.523	Schlautman et al. (2015)	1
SCF83036	KP278776.1	4	8.497	Schlautman et al. (2015)	
5ms2b12	N/A	4	12.247	Georgi et al. (2013)	
vm83024	JF834247.1	4	12.572	Zhu et al. (2012)	1
SCF162175	KP278912.1	4	12.58	Schlautman et al. (2015)	
SCF9157	KP278626.1	4	18.171	Schlautman et al. (2015)	2
scf1172	N/A	4	23.725	Georgi et al. (2013)	
416328_K63	KP279185.1	4	29.449	Schlautman et al. (2015)	1
ct119590	KP279115.1	4	30.209	Schlautman et al. (2015)	
SCF72229	KP278756.1	4	30.611	Schlautman et al. (2015)	
SCF113389	KP278831.1	4	31.538	Schlautman et al. (2015)	2
CA855F	N/A	4	33.539	Boches et al.(2005)	
SCF140628	KP278876.1	4	33.902	Schlautman et al. (2015)	1
SCF46739	KP278716.1	4	35.479	Schlautman et al. (2015)	2
vm52682	JF834282.1	4	36.876	Zhu et al. (2012)	
SCF6530	KP278614.1	4	40.584	Schlautman et al. (2015)	1
SCF124075	KP278848.1	4	43.375	Schlautman et al. (2015)	
scf6955c	N/A	4	44.066	Georgi et al. (2013)	1
vm52204	JF834281.1	4	44.208	Zhu et al. (2012)	
SCF28100	KP278674.1	4	46.61	Schlautman et al. (2015)	
305731_K63	KP279169.1	4	47.911	Schlautman et al. (2015)	1

SCF154541	KP278900.1	4	49.521	Schlautman et al. (2015)	2
SCF38553	KP278703.1	4	53.061	Schlautman et al. (2015)	1
SCF15845	KP278645.1	4	55.569	Schlautman et al. (2015)	1
SCF194552	KP278944.1	4	59.412	Schlautman et al. (2015)	
SCF96539	KP278800.1	4	69.736	Schlautman et al. (2015)	1
NA1713	N/A	4	73.442	Georgi et al. (2013)	
SCF16359	KP278647.1	4	73.729	Schlautman et al. (2015)	1
SCF100820	KP278804.1	4	74.949	Schlautman et al. (2015)	1
SCF79014	KP278767.1	4	75.206	Schlautman et al. (2015)	
SCF204979	KP278949.1	4	76.008	Schlautman et al. (2015)	1
scf24k	JN230516.1	4	76.069	Georgi et al. (2013)	
SCF101064	KP278805.1	4	80.161	Schlautman et al. (2015)	
contig600	N/A	4	81.834	Georgi et al. (2013)	
SCF49598	KP278723.1	4	83.704	Schlautman et al. (2015)	1
SCF46912	KP278719.1	4	88.294	Schlautman et al. (2015)	2
SCF1128	KP278597.1	4	88.693	Schlautman et al. (2015)	
SCF108294	KP278818.1	4	88.818	Schlautman et al. (2015)	2
SCF11084	KP278635.1	4	88.987	Schlautman et al. (2015)	1
SCF53282	KP278726.1	4	95.028	Schlautman et al. (2015)	
SCF145739	KP278886.1	4	95.383	Schlautman et al. (2015)	1
SCF18363	KP278650.1	4	95.707	Schlautman et al. (2015)	
scf26r	N/A	4	97.183	Georgi et al. (2013)	
SCF29560	KP278680.1	4	97.29	Schlautman et al. (2015)	
SCF51810	KP278725.1	4	98.112	Schlautman et al. (2015)	1
SCF74895	KP278760.1	4	99.178	Schlautman et al. (2015)	
281884_K70	KP279207.1	4	99.748	Schlautman et al. (2015)	1
SCF14119	KP278643.1	4	100.079	Schlautman et al. (2015)	
SCF143318	KP278883.1	5	0	Schlautman et al. (2015)	
251788_K63	KP279166.1	5	0.101	Schlautman et al. (2015)	2
ct153008	KP279136.1	5	0.168	Schlautman et al. (2015)	1
SCF28613	KP278677.1	5	0.773	Schlautman et al. (2015)	1
SCF804	KP278592.1	5	1.746	Schlautman et al. (2015)	2
ct144370	KP279127.1	5	9.208	Schlautman et al. (2015)	
SCF7132	KP278616.1	5	9.34	Schlautman et al. (2015)	1
SCF32727	KP278689.1	5	13.069	Schlautman et al. (2015)	
SCF59035	KP278739.1	5	13.377	Schlautman et al. (2015)	1
SCF259	KP278591.1	5	22.375	Schlautman et al. (2015)	
SCF31208	KP278687.1	5	25.806	Schlautman et al. (2015)	
SCF132595	KP278863.1	5	27.67	Schlautman et al. (2015)	
SCF97378	KP278801.1	5	32.843	Schlautman et al. (2015)	
vm39030	JF834273.1	5	38.734	Zhu et al. (2012)	
ct98042	KP279108.1	5	51.143	Schlautman et al. (2015)	1
SCF8987	KP278625.1	5	51.163	Schlautman et al. (2015)	

SCF149976	KP278893.1	5	51.255	Schlautman et al. (2015)	1
SCF83615	KP278777.1	5	53.621	Schlautman et al. (2015)	
SCF46751	KP278715.1	5	58.742	Schlautman et al. (2015)	
SCF101878	KP278807.1	5	60.814	Schlautman et al. (2015)	1
scf9e	N/A	5	67.28	Georgi et al. (2013)	
SCF9068	KP278624.1	5	71.573	Schlautman et al. (2015)	2
308812_K70	KP279210.1	5	74.685	Schlautman et al. (2015)	1
SCF11431	KP278637.1	5	74.685	Schlautman et al. (2015)	1
1trimcontig237406	KP279230.1	5	74.692	Schlautman et al. (2015)	1
SCF88902	KP278785.1	5	74.849	Schlautman et al. (2015)	
SCF6195	KP278613.1	5	79.507	Schlautman et al. (2015)	2
1trimcontig191066	KP279227.1	5	82.657	Schlautman et al. (2015)	
vm07778	JF834253.1	5	85.189	Zhu et al. (2012)	1
ct115258	KP279111.1	5	89.614	Schlautman et al. (2015)	
47166_K70	KP279195.1	5	97.942	Schlautman et al. (2015)	1
CA794F	N/A	5	99.873	Boches et al.(2005)	
16720_K63	KP279159.1	6	0	Schlautman et al. (2015)	1
scf44a	N/A	6	4.811	Georgi et al. (2013)	
SCF164915	KP278915.1	6	7.053	Schlautman et al. (2015)	
scf17d	N/A	6	10.131	Georgi et al. (2013)	
SCF25446	KP278665.1	6	12.559	Schlautman et al. (2015)	2
SCF171621	KP278919.1	6	17.544	Schlautman et al. (2015)	
SCF89447	KP278787.1	6	18.616	Schlautman et al. (2015)	1
SCF31172	KP278686.1	6	19.021	Schlautman et al. (2015)	
ct154615	KP279138.1	6	20.129	Schlautman et al. (2015)	2
SCF16407	KP278648.1	6	20.129	Schlautman et al. (2015)	
contig652	N/A	6	21.08	Georgi et al. (2013)	
SCF89801	KP278790.1	6	22.031	Schlautman et al. (2015)	
SCF133376	KP278865.1	6	22.477	Schlautman et al. (2015)	1
319429_K63	KP279171.1	6	25.659	Schlautman et al. (2015)	
SCF40517	KP278707.1	6	26.835	Schlautman et al. (2015)	
SCF92414	KP278793.1	6	34.936	Schlautman et al. (2015)	1
vm27120	JF834265.1	6	41.895	Zhu et al. (2012)	2
SCF22442	KP278657.1	6	43.808	Schlautman et al. (2015)	1
SCF3427	KP278606.1	6	46.043	Schlautman et al. (2015)	2
1trimcontig238080	KP279231.1	6	46.568	Schlautman et al. (2015)	
SCF9909	KP278630.1	6	47.691	Schlautman et al. (2015)	
412234_K63	KP279182.1	6	48.415	Schlautman et al. (2015)	1
SCF139334	KP278874.1	6	50.87	Schlautman et al. (2015)	1
scf112c	N/A	6	53.021	Georgi et al. (2013)	
vm53000	JF834283.1	6	53.905	Zhu et al. (2012)	2
1trimcontig344502	KP279241.1	6	56.802	Schlautman et al. (2015)	
ct188529	KP279148.1	6	64.275	Schlautman et al. (2015)	1

SCF13711	KP278640.1	6	72.987	Schlautman et al. (2015)	2
Ig13662a	N/A	6	81.556	Georgi et al. (2013)	
scf207d	N/A	6	82.03	Georgi et al. (2013)	
scf283b	N/A	6	84.391	Georgi et al. (2013)	
SCF147117	KP278888.1	6	85.132	Schlautman et al. (2015)	2
ct92708	KP279103.1	6	89.938	Schlautman et al. (2015)	
SCF113558	KP278832.1	6	91.436	Schlautman et al. (2015)	1
SCF124927	KP278850.1	6	96.866	Schlautman et al. (2015)	1
vm31701	JF834268.1	6	97.092	Zhu et al. (2012)	
SCF109269	KP278820.1	6	98.192	Schlautman et al. (2015)	
SCF108454	KP278819.1	6	99.09	Schlautman et al. (2015)	
SCF79620	KP278768.1	6	99.119	Schlautman et al. (2015)	1
SCF192219	KP278941.1	6	99.64	Schlautman et al. (2015)	
1trimcontig339726	KP279240.1	6	99.869	Schlautman et al. (2015)	1
scf203h	N/A	7	0	Georgi et al. (2013)	
1trimcontig450309	KP279253.1	7	1.107	Schlautman et al. (2015)	1
SCF10514	KP278632.1	7	2.396	Schlautman et al. (2015)	1
SCF155637	KP278901.1	7	3.556	Schlautman et al. (2015)	
SCF46824	KP278717.1	7	7.631	Schlautman et al. (2015)	
Ig51a	N/A	7	9.43	Georgi et al. (2013)	
SCF150898	KP278895.1	7	10.518	Schlautman et al. (2015)	1
SCF915	KP278593.1	7	15.099	Schlautman et al. (2015)	1
SCF167793	KP278916.1	7	17.936	Schlautman et al. (2015)	1
419834_K63	KP279192.1	7	18.277	Schlautman et al. (2015)	1
SCF187979	KP278935.1	7	19.281	Schlautman et al. (2015)	
scf5k	N/A	7	24.642	Georgi et al. (2013)	
SCF110168	KP278822.1	7	28	Schlautman et al. (2015)	
SCF193103	KP278943.1	7	29.551	Schlautman et al. (2015)	1
ct95345	KP279106.1	7	30.931	Schlautman et al. (2015)	
SCF128307	KP278857.1	7	31.098	Schlautman et al. (2015)	1
NA1792	N/A	7	33.011	Georgi et al. (2013)	
SCF138014	KP278870.1	7	37.67	Schlautman et al. (2015)	
311291_K70	KP279214.1	7	37.807	Schlautman et al. (2015)	1
SCF4305	KP278611.1	7	37.92	Schlautman et al. (2015)	2
1trimcontig337780	KP279239.1	7	38.079	Schlautman et al. (2015)	1
SCF208883	KP278952.1	7	41.314	Schlautman et al. (2015)	2
SCF9872	KP278629.1	7	42.848	Schlautman et al. (2015)	
ct145217	KP279131.1	7	43.038	Schlautman et al. (2015)	
ct147864	KP279133.1	7	44.269	Schlautman et al. (2015)	1
SCF137494	KP278869.1	7	44.495	Schlautman et al. (2015)	
SCF34010	KP278693.1	7	45.368	Schlautman et al. (2015)	
SCF72379	KP278757.1	7	45.374	Schlautman et al. (2015)	1
409618_K63	KP279178.1	7	46.519	Schlautman et al. (2015)	1

76326_K70	KP279197.1	7	46.895	Schlautman et al. (2015)	1
SCF34513	KP278695.1	7	46.896	Schlautman et al. (2015)	
1trimcontig217158	KP279229.1	7	52.214	Schlautman et al. (2015)	2
SCF94237	KP278795.1	7	55.656	Schlautman et al. (2015)	
80734_K70	KP279198.1	7	55.656	Schlautman et al. (2015)	1
ct145906	KP279132.1	7	55.666	Schlautman et al. (2015)	1
SCF111145	KP278827.1	7	60.801	Schlautman et al. (2015)	
SCF112540	KP278830.1	7	61.325	Schlautman et al. (2015)	2
SCF184873	KP278934.1	7	61.666	Schlautman et al. (2015)	
SCF116864	KP278836.1	7	63.434	Schlautman et al. (2015)	
SCF85946	KP278781.1	7	65.1	Schlautman et al. (2015)	
SCF25221	KP278664.1	7	67.783	Schlautman et al. (2015)	2
scf31h	N/A	7	69.518	Georgi et al. (2013)	
SCF89247	KP278786.1	7	71.802	Schlautman et al. (2015)	1
scf137c	N/A	7	73.443	Georgi et al. (2013)	
SCF7155	KP278617.1	7	73.799	Schlautman et al. (2015)	
SCF20681	KP278653.1	7	76.073	Schlautman et al. (2015)	1
SCF36745	KP278698.1	7	78.883	Schlautman et al. (2015)	1
6ms4e4b	N/A	7	79.622	Georgi et al. (2013)	
1trimcontig435620	KP279244.1	7	82.647	Schlautman et al. (2015)	1
SCF25944	KP278666.1	7	83.943	Schlautman et al. (2015)	1
SCF2483	KP278601.1	7	86.158	Schlautman et al. (2015)	2
SCF56717	KP278733.1	7	90.706	Schlautman et al. (2015)	1
scf2s	N/A	7	95.336	Georgi et al. (2013)	
scf1594	N/A	7	98.833	Georgi et al. (2013)	
ct139553	KP279125.1	7	99.764	Schlautman et al. (2015)	
SCF132922	KP278864.1	8	0	Schlautman et al. (2015)	1
SCF24087	KP278663.1	8	1.08	Schlautman et al. (2015)	1
ct89379	KP279101.1	8	2.697	Schlautman et al. (2015)	2
Ig6523b	N/A	8	2.975	Georgi et al. (2013)	
SCF81732	KP278772.1	8	3.956	Schlautman et al. (2015)	
SCF138992	KP278873.1	8	4.419	Schlautman et al. (2015)	
SCF172149	KP278922.1	8	11.22	Schlautman et al. (2015)	
SCF105925	KP278812.1	8	15.354	Schlautman et al. (2015)	1
SCF17979	KP278649.1	8	18.768	Schlautman et al. (2015)	2
SCF189612	KP278936.1	8	24.943	Schlautman et al. (2015)	
SCF87990	KP278783.1	8	25.164	Schlautman et al. (2015)	
SCF2714	KP278602.1	8	25.354	Schlautman et al. (2015)	1
SCF30010	KP278683.1	8	25.939	Schlautman et al. (2015)	1
SCF127023	KP278855.1	8	30.347	Schlautman et al. (2015)	
SCF54155	KP278728.1	8	32.657	Schlautman et al. (2015)	1
scf4860	N/A	8	34.846	Georgi et al. (2013)	
SCF64632	KP278746.1	8	35.621	Schlautman et al. (2015)	

SCF82870	KP278775.1	8	35.695	Schlautman et al. (2015)	
ct134336	KP279123.1	8	36.203	Schlautman et al. (2015)	1
SCF197903	KP278945.1	8	36.577	Schlautman et al. (2015)	
SCF19565	KP278652.1	8	37.096	Schlautman et al. (2015)	
ct159707	KP279142.1	8	37.096	Schlautman et al. (2015)	
187382_K70	KP279202.1	8	42.581	Schlautman et al. (2015)	1
SCF71184	KP278754.1	8	46.004	Schlautman et al. (2015)	
SCF27811	KP278672.1	8	48.075	Schlautman et al. (2015)	
314797_K70	KP279218.1	8	48.577	Schlautman et al. (2015)	1
SCF92564	KP278794.1	8	59.761	Schlautman et al. (2015)	1
SCF8850	KP278623.1	8	64.791	Schlautman et al. (2015)	1
36394_K70	KP279271.1	8	69.566	Schlautman et al. (2015)	1
SCF71136	KP278753.1	8	70.899	Schlautman et al. (2015)	
SCF107477	KP278814.1	8	75.436	Schlautman et al. (2015)	2
scf2505a	N/A	8	81.748	Georgi et al. (2013)	
1trimcontig326802	KP279235.1	8	83.73	Schlautman et al. (2015)	1
SCF91821	KP278792.1	8	85.187	Schlautman et al. (2015)	1
vm31502	JF834267.1	8	85.39	Zhu et al. (2012)	
SCF102538	KP279056.1	8	90.311	Schlautman et al. (2015)	
1trimcontig440337	KP279250.1	8	91.23	Schlautman et al. (2015)	1
SCF10785	KP278633.1	8	91.716	Schlautman et al. (2015)	
vm28527	JF834266.1	8	96.673	Zhu et al. (2012)	
ct121951	KP279117.1	8	98.746	Schlautman et al. (2015)	
contig259Fb	N/A	9	0	Georgi et al. (2013)	
scf1655c	N/A	9	5.339	Georgi et al. (2013)	1
SCF41971	KP278709.1	9	6.394	Schlautman et al. (2015)	
SCF125889	KP278853.1	9	6.459	Schlautman et al. (2015)	
SCF163134	KP278914.1	9	6.831	Schlautman et al. (2015)	
ct144558	KP279128.1	9	8.831	Schlautman et al. (2015)	
SCF109660	KP278821.1	9	9.17	Schlautman et al. (2015)	1
407841_K63	KP279175.1	9	9.173	Schlautman et al. (2015)	1
1trimcontig352078	KP279243.1	9	9.404	Schlautman et al. (2015)	
ct154206	KP279137.1	9	19.06	Schlautman et al. (2015)	1
VCC_J9	N/A	9	23.358	Boches et al.(2005)	
SCF30734	KP278684.1	9	26.434	Schlautman et al. (2015)	2
SCF155797	KP278902.1	9	28.461	Schlautman et al. (2015)	
scf439	N/A	9	36.577	Georgi et al. (2013)	
SCF7357	KP278618.1	9	37.371	Schlautman et al. (2015)	1
NA619	N/A	9	38.354	Georgi et al. (2013)	
scf35k	N/A	9	41.032	Georgi et al. (2013)	
309124_K70	KP279213.1	9	42.463	Schlautman et al. (2015)	2
scf13a	N/A	9	44.249	Georgi et al. (2013)	
SCF10459	KP278631.1	9	48.472	Schlautman et al. (2015)	

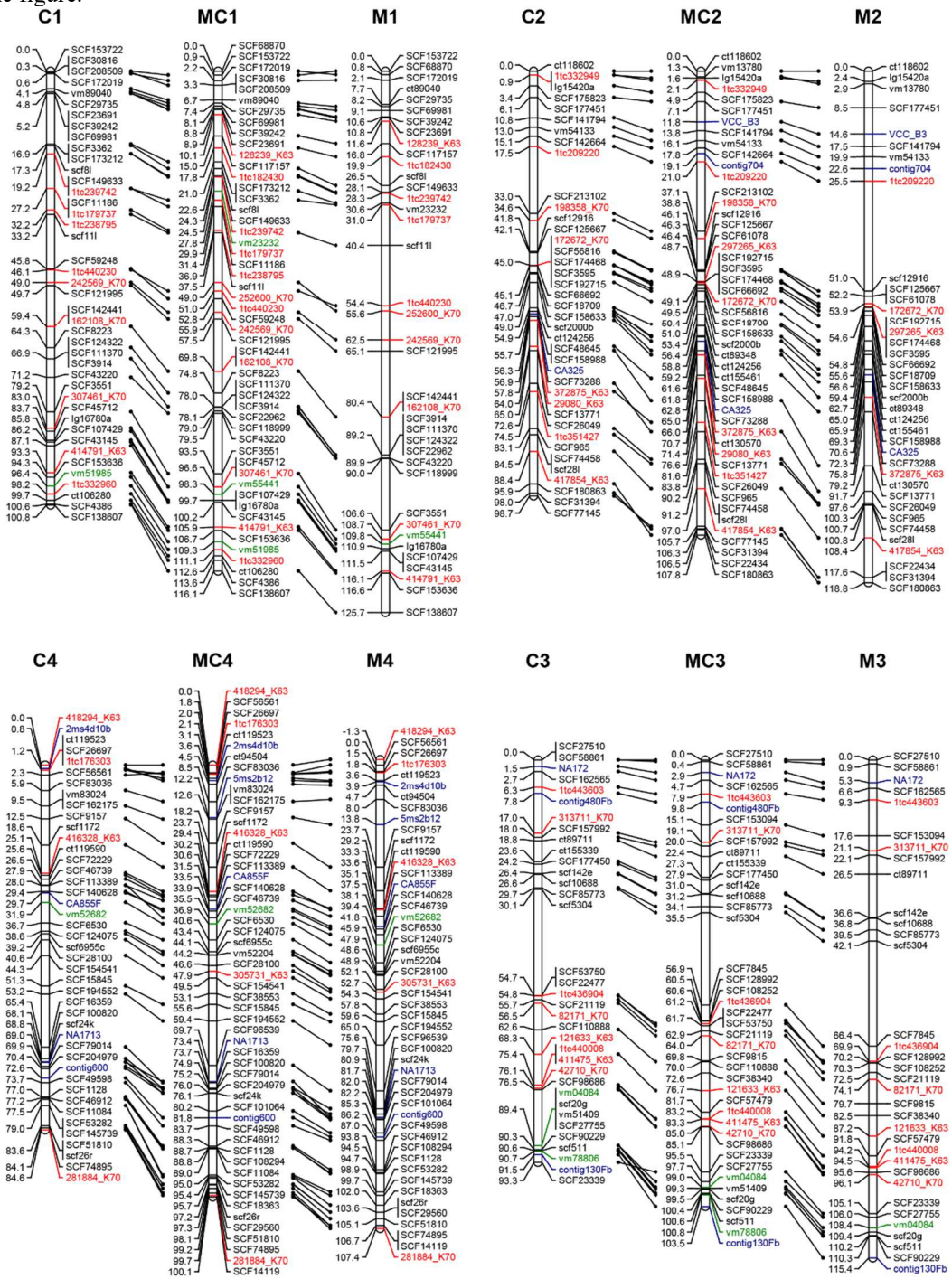
scf275d	N/A	9	50.74	Georgi et al. (2013)	
SCF118468	KP278840.1	9	53.862	Schlautman et al. (2015)	
scf6i	N/A	9	56.94	Georgi et al. (2013)	
SCF56032	KP278731.1	9	58.054	Schlautman et al. (2015)	1
Ig1296a	N/A	9	58.991	Georgi et al. (2013)	
SCF136207	KP278866.1	9	59.268	Schlautman et al. (2015)	2
SCF48414	KP278721.1	9	59.51	Schlautman et al. (2015)	1
scf21n	N/A	9	60.748	Georgi et al. (2013)	
SCF88396	KP278784.1	9	62.364	Schlautman et al. (2015)	1
SCF1648	KP278599.1	9	66.421	Schlautman et al. (2015)	
1trimcontig238343	KP279232.1	9	73.064	Schlautman et al. (2015)	1
214102_K63	KP279165.1	9	73.089	Schlautman et al. (2015)	1
SCF141985	KP278878.1	9	74.046	Schlautman et al. (2015)	2
ct95842	KP279107.1	9	76.948	Schlautman et al. (2015)	
SCF136317	KP278867.1	9	78.012	Schlautman et al. (2015)	1
SCF144748	KP278884.1	9	78.423	Schlautman et al. (2015)	1
SCF132369	KP278860.1	9	78.544	Schlautman et al. (2015)	
SCF11802	KP278638.1	9	79.285	Schlautman et al. (2015)	1
scf306f	N/A	9	79.955	Georgi et al. (2013)	
scf32j	N/A	9	82.526	Georgi et al. (2013)	
1trimcontig439861	KP279247.1	9	83.901	Schlautman et al. (2015)	2
SCF132532	KP278861.1	9	84.503	Schlautman et al. (2015)	2
SCF33185	KP278691.1	9	85.115	Schlautman et al. (2015)	2
SCF61189	KP278744.1	9	86.823	Schlautman et al. (2015)	
scf55c	N/A	9	87.282	Georgi et al. (2013)	
SCF125251	KP278851.1	9	87.602	Schlautman et al. (2015)	
scf45d	N/A	9	91.518	Georgi et al. (2013)	
1trimcontig328266	KP279236.1	9	94.561	Schlautman et al. (2015)	1
SCF3932	KP278610.1	9	97.154	Schlautman et al. (2015)	2
ct145170	KP279130.1	10	0	Schlautman et al. (2015)	1
SCF201915	KP278947.1	10	1.452	Schlautman et al. (2015)	
vm38401	JF834272.1	10	2.156	Zhu et al. (2012)	
vm12486	JF834257.1	10	2.913	Zhu et al. (2012)	
418931_1_K63	KP279191.1	10	8.283	Schlautman et al. (2015)	2
1trimcontig176861	KP279223.1	10	9.914	Schlautman et al. (2015)	
60699_K70	KP279196.1	10	10.333	Schlautman et al. (2015)	2
SCF150919	KP278896.1	10	15.453	Schlautman et al. (2015)	1
SCF174394	KP278925.1	10	19.535	Schlautman et al. (2015)	
SCF65999	KP278748.1	10	35.769	Schlautman et al. (2015)	
SCF82535	KP278774.1	10	37.952	Schlautman et al. (2015)	
SCF107715	KP278816.1	10	39.343	Schlautman et al. (2015)	1
71002_K63	KP279161.1	10	39.651	Schlautman et al. (2015)	1
SCF189827	KP278938.1	10	39.952	Schlautman et al. (2015)	1

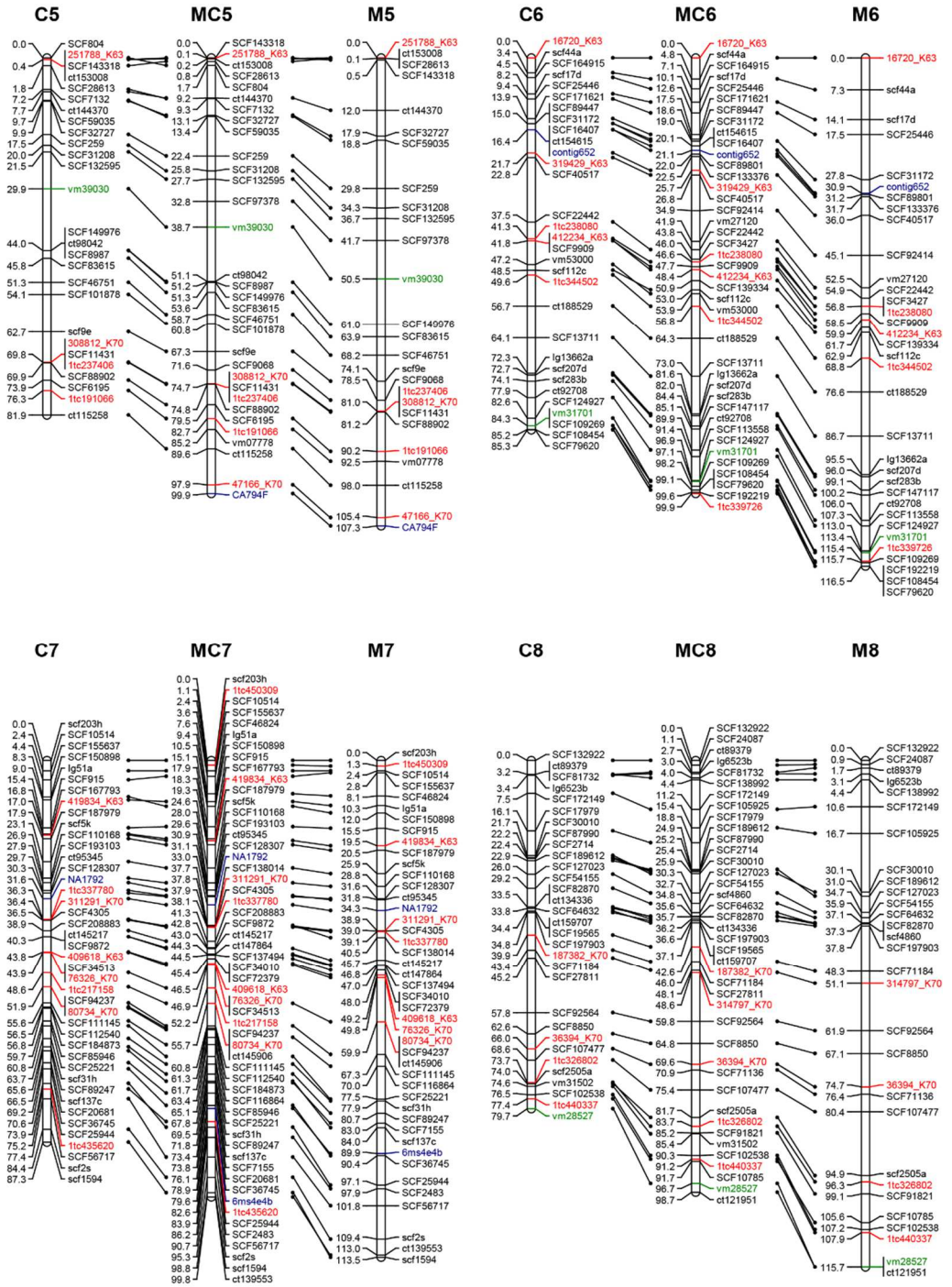
vm72062	JF834244.1	10	41.93	Zhu et al. (2012)	
SCF35507	KP278697.1	10	48.516	Schlautman et al. (2015)	
SCF146740	KP278887.1	10	48.517	Schlautman et al. (2015)	
SCF147295	KP278889.1	10	48.52	Schlautman et al. (2015)	1
313928_K70	KP279216.1	10	49.091	Schlautman et al. (2015)	1
SCF7569	KP278619.1	10	50.877	Schlautman et al. (2015)	
vm25796	JF834263.1	10	52.833	Zhu et al. (2012)	1
409500_K63	KP279177.1	10	53.026	Schlautman et al. (2015)	1
SCF112295	KP278829.1	10	53.25	Schlautman et al. (2015)	
SCF172906	KP278923.1	10	57.64	Schlautman et al. (2015)	
ct135942	KP279124.1	10	59.077	Schlautman et al. (2015)	1
SCF104688	KP278809.1	10	67.074	Schlautman et al. (2015)	1
SCF189657	KP278937.1	10	71.134	Schlautman et al. (2015)	
SCF139660	KP278875.1	10	75.133	Schlautman et al. (2015)	1
SCF86438	KP278782.1	10	76.236	Schlautman et al. (2015)	
SCF2288	KP278600.1	10	81.27	Schlautman et al. (2015)	
SCF60761	KP278742.1	10	82.845	Schlautman et al. (2015)	
SCF96311	KP278799.1	10	85.526	Schlautman et al. (2015)	1
SCF26014	KP278667.1	10	86.005	Schlautman et al. (2015)	
SCF46833	KP278718.1	10	86.571	Schlautman et al. (2015)	3
SCF23210	KP278660.1	10	86.608	Schlautman et al. (2015)	1
SCF138394b	KP278871.1	10	87.619	Schlautman et al. (2015)	3
364103_K63	KP279173.1	10	87.724	Schlautman et al. (2015)	2
SCF120352	KP278843.1	10	87.94	Schlautman et al. (2015)	
ct161908	KP279144.1	10	88.202	Schlautman et al. (2015)	
ct93137	KP279104.1	10	92.243	Schlautman et al. (2015)	1
SCF84804	KP278779.1	11	0	Schlautman et al. (2015)	
SCF181909	KP278932.1	11	0.593	Schlautman et al. (2015)	
SCF95767	KP278796.1	11	0.857	Schlautman et al. (2015)	
SCF110507	KP278824.1	11	1.076	Schlautman et al. (2015)	
1trimcontig176042	KP279221.1	11	1.653	Schlautman et al. (2015)	1
SCF72209	KP278755.1	11	2.222	Schlautman et al. (2015)	1
scf108b	N/A	11	3.114	Georgi et al. (2013)	
vm05418	JF834252.1	11	5.55	Zhu et al. (2012)	2
SCF41361	KP278708.1	11	11.029	Schlautman et al. (2015)	
SCF122746	KP278846.1	11	12.753	Schlautman et al. (2015)	2
307018_K70	KP279208.1	11	16.507	Schlautman et al. (2015)	
SCF81909	KP278773.1	11	17.732	Schlautman et al. (2015)	1
SCF204332	KP278948.1	11	24.184	Schlautman et al. (2015)	
SCF81294	KP278771.1	11	24.591	Schlautman et al. (2015)	
scf3072b	N/A	11	27.795	Georgi et al. (2013)	
SCF64185	KP278745.1	11	35.765	Schlautman et al. (2015)	1
SCF106182	KP278813.1	11	36.774	Schlautman et al. (2015)	

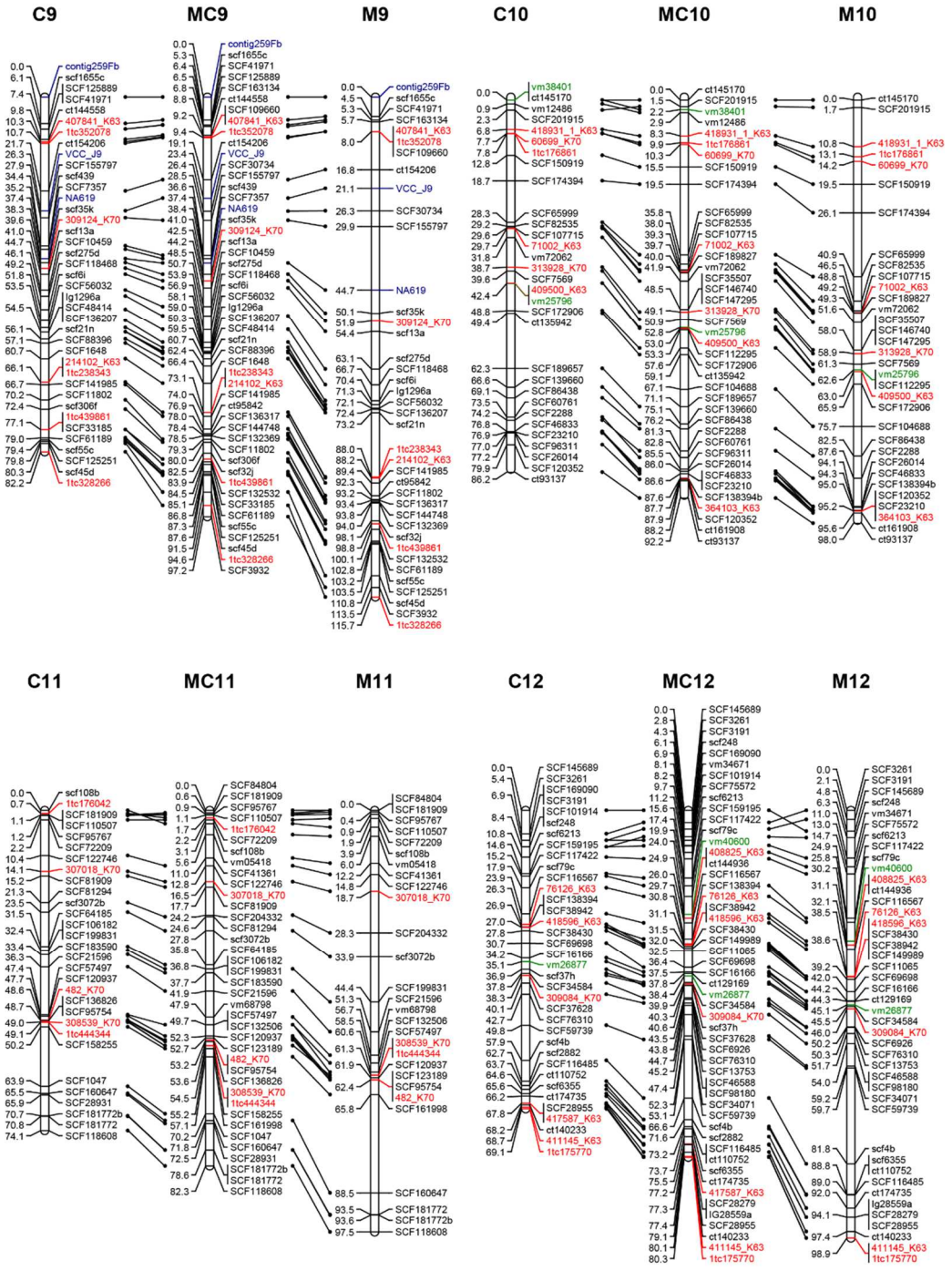
SCF199831	KP278946.1	11	36.826	Schlautman et al. (2015)	
SCF183590	KP278933.1	11	37.749	Schlautman et al. (2015)	1
SCF21596	KP278655.1	11	41.894	Schlautman et al. (2015)	
vm68798	JF834242.1	11	47.889	Zhu et al. (2012)	
SCF57497	KP278737.1	11	49.696	Schlautman et al. (2015)	
SCF132506	KP278862.1	11	49.707	Schlautman et al. (2015)	
SCF120937	KP278844.1	11	52.27	Schlautman et al. (2015)	
SCF123189	KP278847.1	11	52.713	Schlautman et al. (2015)	
482_K70	KP279193.1	11	53.154	Schlautman et al. (2015)	
SCF95754	KP278797.1	11	53.197	Schlautman et al. (2015)	
SCF136826	KP278868.1	11	53.645	Schlautman et al. (2015)	
308539_K70	KP279209.1	11	54.516	Schlautman et al. (2015)	1
1trimcontig444344	KP279252.1	11	54.527	Schlautman et al. (2015)	1
SCF158255	KP278905.1	11	55.151	Schlautman et al. (2015)	
SCF161998	KP278911.1	11	57.075	Schlautman et al. (2015)	
SCF1047	KP278596.1	11	70.214	Schlautman et al. (2015)	1
SCF160647	KP278909.1	11	71.763	Schlautman et al. (2015)	
SCF28931	KP278678.1	11	72.497	Schlautman et al. (2015)	
SCF181772b	KP278931.1	11	78.607	Schlautman et al. (2015)	
SCF181772	KP278931.1	11	78.63	Schlautman et al. (2015)	
SCF118608	KP278841.1	11	82.261	Schlautman et al. (2015)	1
SCF145689	KP278885.1	12	0	Schlautman et al. (2015)	1
SCF3261	KP278604.1	12	2.8	Schlautman et al. (2015)	2
SCF3191	KP278603.1	12	4.251	Schlautman et al. (2015)	1
scf248	N/A	12	6.069	Georgi et al. (2013)	
SCF169090	KP278917.1	12	6.883	Schlautman et al. (2015)	
vm34671	JF834271.1	12	8.128	Zhu et al. (2012)	
SCF101914	KP278806.1	12	8.159	Schlautman et al. (2015)	
SCF75572	KP278761.1	12	9.74	Schlautman et al. (2015)	2
scf6213	N/A	12	11.165	Georgi et al. (2013)	
SCF159195	KP278908.1	12	15.633	Schlautman et al. (2015)	1
SCF117422	KP278839.1	12	17.447	Schlautman et al. (2015)	
scf79c	N/A	12	19.871	Georgi et al. (2013)	
vm40600	JF834274.1	12	23.973	Zhu et al. (2012)	
408825_K63	KP279176.1	12	24.85	Schlautman et al. (2015)	
ct144936	KP279129.1	12	24.868	Schlautman et al. (2015)	
SCF116567	KP278835.1	12	26.047	Schlautman et al. (2015)	
SCF138394	KP278871.1	12	29.722	Schlautman et al. (2015)	
76126_K63	KP279162.1	12	30.778	Schlautman et al. (2015)	1
SCF38942	KP278704.1	12	31.07	Schlautman et al. (2015)	2
418596_K63	KP279190.1	12	31.094	Schlautman et al. (2015)	
SCF38430	KP278702.1	12	31.484	Schlautman et al. (2015)	1
SCF149989	KP278892.1	12	31.955	Schlautman et al. (2015)	

SCF11065	KP278634.1	12	32.483	Schlautman et al. (2015)	3
SCF69698	KP278751.1	12	36.397	Schlautman et al. (2015)	1
SCF16166	KP278646.1	12	37.54	Schlautman et al. (2015)	1
ct129169	KP279119.1	12	37.778	Schlautman et al. (2015)	
vm26877	JF834264.1	12	38.436	Zhu et al. (2012)	
SCF34584	KP278696.1	12	39.893	Schlautman et al. (2015)	1
309084_K70	KP279212.1	12	40.331	Schlautman et al. (2015)	
scf37h	JN230518.1	12	40.575	Georgi et al. (2013)	
SCF37628	KP278700.1	12	43.491	Schlautman et al. (2015)	
SCF6926	KP278615.1	12	43.761	Schlautman et al. (2015)	2
SCF76310	KP278762.1	12	44.654	Schlautman et al. (2015)	
SCF13753	KP278641.1	12	45.215	Schlautman et al. (2015)	1
SCF46588	KP278714.1	12	47.395	Schlautman et al. (2015)	
SCF98180	KP278802.1	12	47.435	Schlautman et al. (2015)	
SCF34071	KP278694.1	12	52.312	Schlautman et al. (2015)	1
SCF59739	KP278741.1	12	53.066	Schlautman et al. (2015)	
scf4b	N/A	12	66.583	Georgi et al. (2013)	
scf2882	N/A	12	71.611	Georgi et al. (2013)	
SCF116485	KP278834.1	12	73.228	Schlautman et al. (2015)	
ct110752	KP279110.1	12	73.241	Schlautman et al. (2015)	1
scf6355	N/A	12	73.722	Georgi et al. (2013)	
ct174735	KP279147.1	12	75.522	Schlautman et al. (2015)	
417587_K63	KP279187.1	12	77.245	Schlautman et al. (2015)	2
SCF28279	KP278675.1	12	77.252	Schlautman et al. (2015)	
Ig28559a	N/A	12	77.252	Georgi et al. (2013)	
SCF28955	KP278679.1	12	77.359	Schlautman et al. (2015)	
ct140233	KP279126.1	12	79.137	Schlautman et al. (2015)	2
411145_K63	KP279179.1	12	80.098	Schlautman et al. (2015)	1
1trimcontig175770	KP279220.1	12	80.349	Schlautman et al. (2015)	1

Appendix IV-2. Analysis of collinearity between the *Crimson Queen*©, *Mullica Queen*©, and CNJ02-1 integrated SSR genetic linkage groups labeled as *C, M,* and *MC* respectively. Line segments between linkage groups identify the position of homologous loci. Loci in blue were developed from blueberry sequence data; loci in red are from cranberry EST sequences; loci in black are from genomic sequences; loci in orange are used extensively in papers evaluating cranberry and *V. oxycoccos* diversity. SSR markers with IDs containing "trimcontig" were shortened to "tc" in the figure.




C5
MC5
M5
C6
MC6
M6
C7
MC7
M7
C8
MC8
M8


C9
MC9
M9
C10
MC10
M10
C11
MC11
M11
C12
MC12
M12

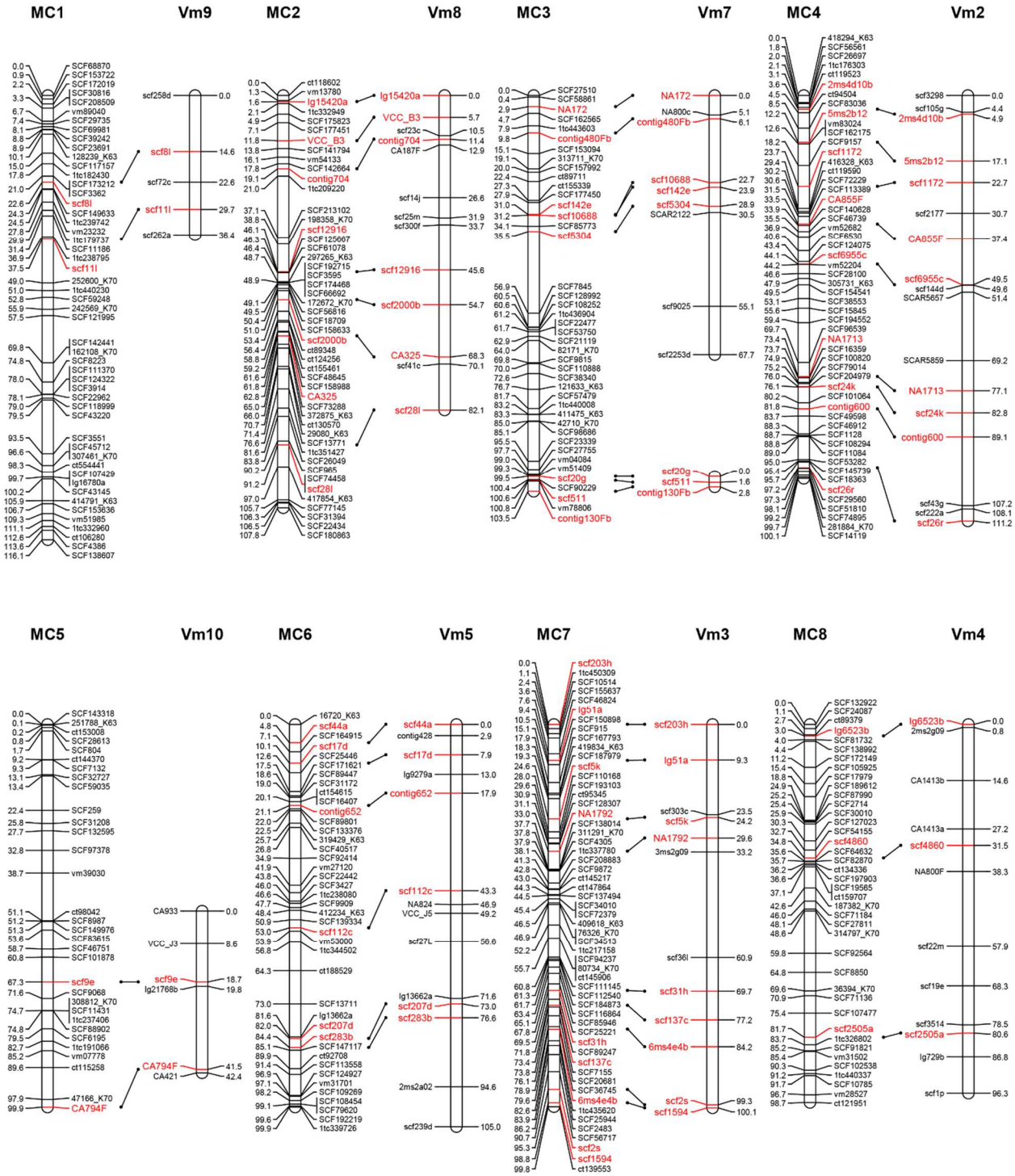
Appendix IV-3. Summary statistics and marker composition of the *Mullica Queen* (M) parental SSR linkage map.

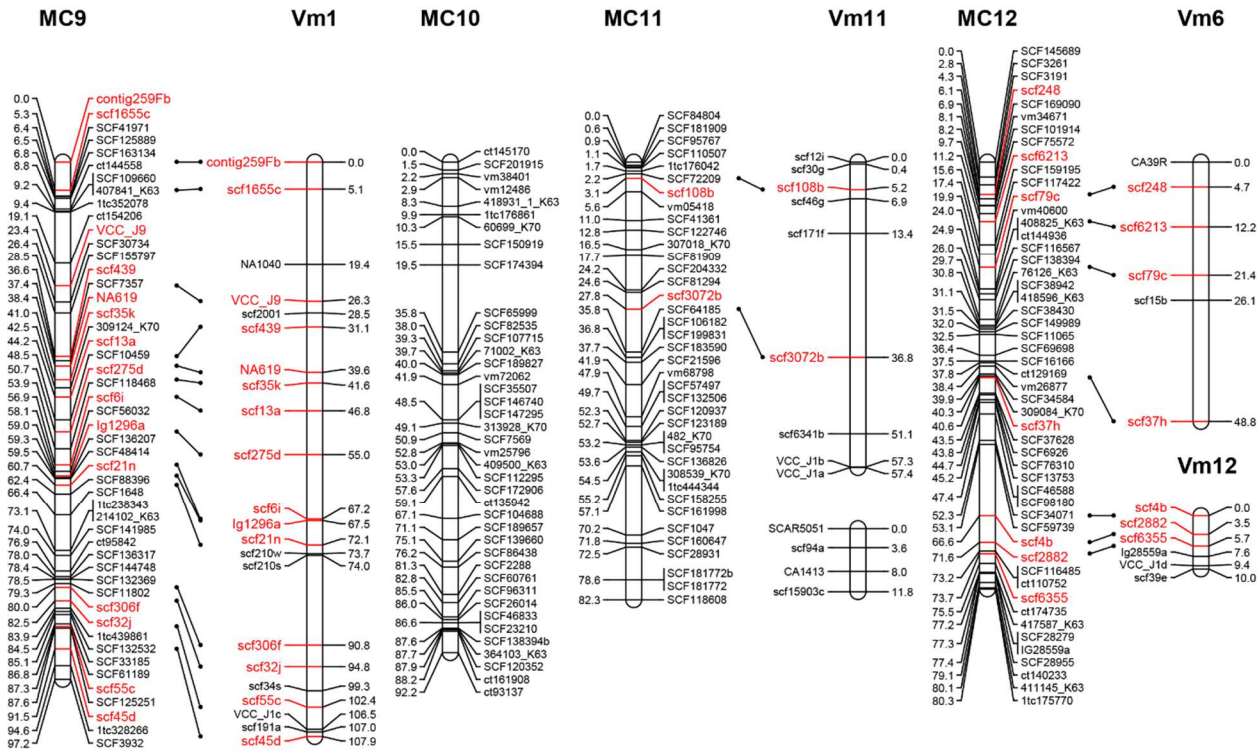
Linkage Group	Number of Markers	Observed Length (cM)	Observed coverage (%)	Expected Length	Gaps more than 10cM	Average Spacing	Largest Gap (cM)
M1	38	125.73	94.87	132.53	3	3.31	16.58
M2	38	118.77	94.87	125.19	2	3.13	25.59
M3	34	115.39	94.29	122.38	2	3.39	24.26
M4	49	107.41	96.00	111.89	1	2.19	10.55
M5	26	107.29	92.59	115.88	3	4.13	11.50
M6	34	116.52	94.29	123.58	2	3.43	10.28
M7	44	113.52	95.56	118.80	1	2.58	10.09
M8	30	115.75	93.55	123.73	4	3.86	14.49
M9	39	115.74	95.00	121.84	2	2.97	14.87
M10	33	97.97	94.12	104.09	1	2.97	14.87
M11	28	97.52	93.10	104.74	2	3.48	22.77
M12	43	98.94	95.45	103.65	2	2.30	22.12
Mean	36.3	110.88	94.47	117.36	2.08	3.14	16.50
Total	436	1330.55	94.48	1408.29	25		

Appendix IV-4. Summary statistics and marker composition of the *Crimson Queen* (C) parental SSR linkage map.

Linkage Group	Number of Markers	Observed Length (cM)	Expected Length	observed coverage (%)	Gaps more than 10cM	Average Spacing	Largest Gap (cM)
1	42	100.79	105.71	95.35	2	2.40	12.57
2	39	98.71	103.90	95.00	1	2.53	15.55
3	35	93.32	98.80	94.44	2	2.67	24.58
4	43	84.63	88.66	95.45	1	1.97	12.29
5	27	81.86	88.16	92.86	1	3.03	14.10
6	31	85.27	90.95	93.75	1	2.75	14.79
7	42	87.35	91.61	95.35	0	2.08	7.03
8	31	79.69	85.01	93.75	1	2.57	12.60
9	39	82.24	86.56	95.00	1	2.11	10.93
10	31	86.16	91.90	93.75	1	2.78	12.88
11	30	74.13	79.24	93.55	2	2.47	13.68
12	36	69.11	73.06	94.59	0	1.92	8.19
Mean	35.5	85.27	90.30	94.40	1	2.44	13.27
Total	426	1023.25	1083.57	94.43	13		

Appendix IV-5. Analysis of collinearity between the CNJ02-1 SSR linkage groups labeled *MC* and the previously published cranberry linkage groups labeled *Vm* (Georgi et al., 2013). Loci in red are those which are present both linkage maps. SSR markers with IDs containing "trimcontig" were shortened to "tc" in the figure.




MC9
Vm1
MC10
MC11
Vm11
MC12
Vm6
Vm12
contig259Fb
scf1655c
VCC_J9
scf439
NA619
scf35k
scf13a
scf275d
scf6i
lg1296a
scf21n
scf306f
scf32j
scf55c
scf45d
scf3072b
scf108b
scf248
scf6213
scf79c
scf37h
scf4b
scf2882
scf6355

Appendix IV-6. Variance components tested using likelihood ratio tests of the mixed models fit for total yield (TY) and mean fruit weight (MFW) in the F_1 population measured over three subsequent years. Both models were of the form $y=\mu+G+B+Y+B:Y+G:Y+e$ where G is the genotypic effect, B is the block effect, Y is the year effect, $B:Y$ is the interaction of block and year, $G:Y$ is the interaction of genotype and year, and e is the stochastic error in the model.

Model	Source of observation	Number of Observations	Variance component	Pr(>Chisq)	Percent of total
TY	*G:Y*	474	1267.06	0.015271***	3.53
	G	158	6022.09	8.09E-26***	16.82
	B:Y	11	1006.89	1.00E-06***	2.81
	B	3	3838.46	0.019389**	10.72
	Y	2	14713.37	0.000629***	41.1
	Residual	299	8947.26		25
	Total	947	35795.12		
MFW	*G:Y*	473	513.13	0.874695 ns	0.27
	G	158	49606.97	8.49E-38 ***	26.21
	B:Y	11	1513.47	0.032468*	0.8
	B	3	38965.41	0.000308***	20.59
	Y	2	36799.34	0.000254***	19.44
	Residual	297	61873.96		32.69
	Total	944	189272.3		

'***' significant at 0.001 level, '**' significant at 0.01 level, '*' significant at 0.05 level, 'ns' not significant

Appendix IV-7. Variance components tested using likelihood ration tests for the year-specific mixed models fit for total yield (TY) and mean fruit weight (MFW) in the CNJ02-1 F_1 population. All models were of the form $y=\mu+G+B+e$ where G is the genotypic effect, B is the block effect, and e is the stochastic error in the model.

Trait	Source of Observation	# of Observations	Variance Component	Chi Square Probability	Percent of total
TY2011	Genotype	158	13695	9.19E-12	34.90
	Block	3	12142	6.06E-06	30.94
	Residuals	157	13408		34.16
	Total	318	39245		
TY2012	Genotype	158	6486.4	5.51E-12	53.31
	Block	3	550.4	0.38	4.52
	Residuals	157	5130.3		42.17
	Total	318	12167.1		
TY2013	Genotype	156	5894	1.07E-07	70.52
	Block	3	1780	0.01072	21.30
	Residuals	152	8358		100.00
	Total	312	16032		
MFW2011	Genotype	158	0.075684	2.20E-16	154.18
	Block	3	0.00659	0.1071	13.42
	Residuals	157	0.049088		100.00
	Total	318	0.131362		
MFW2012	Genotype	158	0.07478	5.91E-13	112.57
	Block	3	0.01932	0.02005	29.08
	Residuals	156	0.06643		100.00
	Total	317	0.16053		
MFW2013	Genotype	155	0.06444	4.17E-10	91.74
	Block	3	0.0174	0.08498	24.77
	Residuals	152	0.07024		100.00
	Total	310	0.15208		216.51

Appendix IV-8. Total Yield (TY) and Mean Fruit Weight (MFW) 3-year and year-specific BLUPs, and biennial bearing index (BBI) for Mullica Queen, Crimson Queen, and their F1 progeny.

	3-Year BLUPs			Year-Specific BLUPs					
				2011		2012		2013	
ID	TY	MFW	BBI	TY	MFW	TY	MFW	TY	MFW
Crimson Queen	356.00	2.33	15.99	490.39	2.37	303.79	2.44	264.00	2.02
Mullica Queen	370.22	1.99	15.25	503.03	2.34	329.09	1.98	263.46	1.80
CNJ02_1_1	313.08	2.15	28.17	415.90	2.23	202.86	2.17	316.75	2.02
CNJ02_1_2	318.58	2.14	36.11	534.75	2.23	202.93	2.20	354.83	1.90
CNJ02_1_3	457.03	2.07	23.11	665.46	2.12	314.28	2.20	255.20	1.92
CNJ02_1_4	326.58	2.21	24.24	508.01	2.34	210.78	2.17	243.12	1.91
CNJ02_1_5	330.10	2.09	31.07	481.74	2.30	230.49	2.04	399.84	1.85
CNJ02_1_6	335.69	2.02	16.00	464.00	2.16	274.27	2.10	311.21	1.83
CNJ02_1_7	237.66	2.03	48.24	353.36	2.23	105.19	2.01	259.82	2.14
CNJ02_1_8	392.06	2.07	33.26	550.91	2.16	199.98	2.10	298.61	2.04
CNJ02_1_9	343.56	2.14	25.75	534.44	2.26	205.16	2.29	178.37	2.06
CNJ02_1_10	254.59	1.80	25.12	368.81	1.97	178.09	1.91	242.71	1.75
CNJ02_1_11	291.07	2.05	16.48	433.53	2.19	223.72	2.06	228.44	1.92
CNJ02_1_12	338.23	1.91	18.90	465.93	2.19	273.77	2.00	215.88	1.73
CNJ02_1_13	265.47	1.90	18.49	387.89	2.19	231.84	1.91	182.93	1.87
CNJ02_1_14	272.03	2.10	18.43	413.20	2.29	201.84	2.15	192.05	1.99
CNJ02_1_15	349.79	2.05	18.81	480.47	2.22	218.54	2.03	219.20	1.82
CNJ02_1_16	368.28	2.27	20.99	528.94	2.58	259.58	2.31	303.61	1.78
CNJ02_1_17	284.92	2.60	30.44	397.17	2.76	181.99	2.37	295.19	1.97
CNJ02_1_19	353.57	1.80	27.10	503.41	1.93	231.88	1.91	328.75	1.99
CNJ02_1_20	408.87	2.17	22.63	584.97	2.29	249.57	2.09	225.45	2.21
CNJ02_1_21	419.91	2.06	26.98	591.35	2.15	239.52	2.03	302.44	1.94
CNJ02_1_22	252.25	2.05	28.22	373.57	2.15	188.30	2.12	303.82	1.94
CNJ02_1_23	372.15	2.71	22.90	498.21	2.73	278.81	2.71	195.53	1.89
CNJ02_1_24	413.33	2.17	14.17	545.49	2.25	344.38	2.28	306.97	2.25
CNJ02_1_25	235.67	2.30	26.77	361.92	2.58	201.73	2.28	337.13	1.97
CNJ02_1_26	421.52	1.97	23.52	655.50	2.18	241.43	1.94	237.25	1.87
CNJ02_1_27	444.01	2.61	17.38	612.85	2.72	311.26	2.46	298.28	1.92
CNJ02_1_28	270.64	2.05	20.61	376.14	2.21	228.16	2.00	319.87	1.82
CNJ02_1_29	410.12	2.08	20.00	581.60	2.29	302.90	2.12	255.49	2.25
CNJ02_1_30	278.03	2.01	24.60	388.50	2.29	211.53	2.03	315.33	1.99
CNJ02_1_31	341.15	2.59	24.88	520.12	2.72	238.07	2.40	306.48	2.09
CNJ02_1_32	342.33	2.17	27.15	483.01	2.32	206.18	2.25	274.01	1.99
CNJ02_1_33	371.61	2.20	26.65	574.72	2.47	195.73	2.09	180.31	1.94
CNJ02_1_34	344.06	2.13	26.83	524.16	2.21	217.74	2.03	279.14	1.61
CNJ02_1_35	199.82	2.26	39.63	334.84	2.54	153.59	2.15	377.41	2.15
CNJ02_1_36	275.40	2.10	24.89	378.39	2.29	185.68	2.09	254.44	1.94
CNJ02_1_37	360.26	2.04	24.60	477.63	2.39	182.32	2.28	199.30	2.04

CNJ02_1_38	359.04	2.76	17.65	539.08	3.04	269.67	2.64	259.14	1.91
CNJ02_1_39	313.83	2.34	26.32	565.16	2.50	188.01	2.45	178.59	1.91
CNJ02_1_40	240.22	2.15	50.13	469.04	2.39	120.51	2.14	289.00	1.94
CNJ02_1_41	302.23	2.05	28.64	448.96	2.25	229.22	2.05	381.08	1.91
CNJ02_1_42	286.81	2.05	35.39	419.42	2.18	162.02	2.11	278.87	1.96
CNJ02_1_43	388.62	1.99	19.76	468.07	2.18	268.13	1.93	343.73	1.96
CNJ02_1_44	331.13	2.11	31.88	503.78	2.32	202.03	2.11	309.50	1.79
CNJ02_1_45	345.94	2.07	30.49	472.80	2.36	194.39	1.93	287.04	2.06
CNJ02_1_46	353.51	2.12	20.19	460.79	2.14	271.39	2.24	363.55	1.82
CNJ02_1_47	419.36	1.99	15.95	603.39	2.10	321.17	2.18	330.07	1.94
CNJ02_1_48	363.95	2.49	45.68	543.72	2.75	140.08	2.42	273.99	1.89
CNJ02_1_49	358.86	1.93	21.75	487.87	2.21	230.08	1.93	267.85	2.03
CNJ02_1_50	316.03	2.21	27.37	493.10	2.61	186.78	2.11	226.81	1.85
CNJ02_1_51	438.60	2.43	21.17	556.51	2.54	282.50	2.48	343.05	1.83
CNJ02_1_52	232.97	1.88	26.62	337.52	2.08	185.61	1.89	304.12	2.02
CNJ02_1_53	422.10	2.06	21.54	549.04	2.26	318.53	2.14	228.25	2.02
CNJ02_1_54	357.62	1.89	29.10	526.84	2.16	217.36	1.89	303.93	2.18
CNJ02_1_55	339.24	2.28	26.79	551.13	2.45	236.63	2.26	311.45	2.14
CNJ02_1_56	306.70	2.40	36.22	446.22	2.77	168.37	2.26	294.32	1.73
CNJ02_1_57	330.28	2.55	26.75	451.57	2.66	216.88	2.47	314.57	1.87
CNJ02_1_58	367.80	2.39	18.94	530.33	2.48	253.50	2.32	266.79	2.09
CNJ02_1_59	422.05	1.89	21.70	571.67	2.19	329.43	1.98	236.06	1.94
CNJ02_1_60	241.89	2.35	33.14	363.70	2.66	169.30	2.14	313.08	1.87
CNJ02_1_61	349.67	2.11	12.75	424.65	2.34	299.40	2.07	254.04	1.71
CNJ02_1_62	254.44	1.87	36.64	340.51	2.12	131.58	1.86	239.21	1.87
CNJ02_1_63	294.89	2.07	11.46	399.37	2.12	250.96	2.26	251.48	1.90
CNJ02_1_64	282.09	1.73	25.47	422.01	1.82	198.45	1.94	268.04	1.71
CNJ02_1_65	283.42	1.80	25.13	430.88	1.97	176.78	1.75	209.43	2.02
CNJ02_1_66	338.51	2.12	28.95	517.20	2.37	210.14	2.09	288.27	1.92
CNJ02_1_67	269.28	1.70	24.42	420.48	1.86	203.01	1.85	268.94	1.92
CNJ02_1_68	391.07	2.36	14.30	511.41	2.44	333.46	2.43	286.75	1.94
CNJ02_1_69	346.19	2.10	30.71	535.51	2.29	209.66	2.09	299.83	1.87
CNJ02_1_70	335.84	2.17	37.66	488.41	2.44	194.47	2.09	379.86	1.59
CNJ02_1_71	330.60	2.05	22.39	467.46	2.58	253.89	1.78	186.98	1.82
CNJ02_1_72	427.23	2.54	19.57	544.69	2.58	279.15	2.55	243.09	2.18
CNJ02_1_74	261.84	1.90	16.97	354.64	1.97	212.85	2.03	254.74	2.23
CNJ02_1_75	348.05	2.35	19.70	466.93	2.22	237.60	2.37	272.55	1.82
CNJ02_1_76	307.83	2.34	16.75	435.64	2.55	233.59	2.37	249.58	1.85
CNJ02_1_77	306.66	2.75	25.99	446.57	2.95	195.91	2.59	254.25	1.97
CNJ02_1_78	269.62	2.05	15.87	334.52	2.21	255.66	2.19	370.82	2.04
CNJ02_1_79	286.44	2.10	23.52	412.94	2.32	209.00	2.19	278.46	2.01
CNJ02_1_80	351.15	2.32	16.95	504.68	2.43	252.78	2.34	249.50	2.01
CNJ02_1_81	382.82	2.37	34.37	619.82	2.54	186.37	2.37	251.99	1.80

CNJ02_1_82	300.04	2.41	29.44	454.28	2.54	206.32	2.43	318.34	1.87
CNJ02_1_83	282.63	2.19	24.06	404.00	2.25	211.36	2.22	296.84	1.94
CNJ02_1_84	302.82	1.86	10.03	347.63	1.96	244.38	2.00	257.53	1.94
CNJ02_1_85	368.22	1.97	20.55	501.56	2.11	279.28	2.03	360.09	1.77
CNJ02_1_86	275.54	2.05	29.94	405.37	2.18	183.63	2.06	288.56	1.97
CNJ02_1_87	429.81	2.02	18.34	573.88	2.11	286.72	2.06	306.37	1.87
CNJ02_1_88	300.80	2.23	40.52	462.90	2.68	149.55	2.25	276.98	1.97
CNJ02_1_89	296.53	2.13	13.96	369.76	2.25	218.08	2.15	227.56	1.94
CNJ02_1_90	285.25	2.09	28.55	428.25	2.29	222.61	2.03	375.03	1.89
CNJ02_1_91	179.30	2.34	44.16	327.02	2.50	109.03	2.43	244.48	1.84
CNJ02_1_92	377.35	2.21	26.37	490.52	2.32	220.51	2.14	296.93	1.86
CNJ02_1_93	280.37	1.99	19.52	404.13	2.25	217.63	1.93	181.49	1.89
CNJ02_1_94	330.77	2.16	22.08	462.87	2.36	223.32	2.30	268.83	1.89
CNJ02_1_95	165.52	1.93	46.32	292.72	1.96	108.54	2.08	298.99	1.89
CNJ02_1_96	271.54	1.99	16.74	370.02	2.14	200.52	2.02	216.24	1.91
CNJ02_1_97	295.63	1.93	21.24	368.96	2.03	228.88	1.99	336.53	2.02
CNJ02_1_98	271.81	2.04	35.52	463.96	2.28	164.18	2.02	264.00	1.80
CNJ02_1_99	387.52	2.18	12.70	439.22	2.21	353.19	2.36	263.46	NA
CNJ02_1_100	313.05	2.12	12.56	426.45	2.21	267.21	2.18	255.91	1.96
CNJ02_1_101	423.62	2.40	12.31	517.97	2.54	390.63	2.39	315.68	2.06
CNJ02_1_102	449.00	2.22	18.09	598.50	2.36	318.66	2.30	356.92	1.94
CNJ02_1_103	275.02	2.16	5.84	325.50	2.28	261.93	2.18	266.49	1.98
CNJ02_1_104	274.86	2.25	35.21	446.84	2.54	155.82	2.08	244.34	2.03
CNJ02_1_105	355.60	2.14	16.83	525.85	2.21	262.65	2.27	264.16	1.91
CNJ02_1_106	287.55	2.00	25.88	378.33	2.41	197.65	1.83	298.86	1.90
CNJ02_1_107	138.63	2.09	33.73	260.32	2.34	99.94	2.07	159.48	1.90
CNJ02_1_108	197.40	2.20	42.59	344.30	2.45	106.15	2.17	207.48	1.94
CNJ02_1_109	231.02	2.18	33.71	385.27	2.30	141.08	2.23	216.25	1.97
CNJ02_1_110	374.28	1.93	19.30	506.14	1.98	269.40	2.04	316.72	1.90
CNJ02_1_111	295.58	2.06	13.04	395.60	2.23	246.98	2.20	261.96	1.83
CNJ02_1_112	300.72	2.00	19.87	443.36	2.23	288.94	2.23	198.11	1.71
CNJ02_1_113	338.18	2.10	22.36	506.74	2.34	231.52	2.17	268.72	1.85
CNJ02_1_114	209.35	2.39	32.89	326.09	2.81	136.11	2.23	225.29	1.99
CNJ02_1_115	377.90	2.15	11.54	475.98	2.37	334.92	2.20	298.91	1.90
CNJ02_1_116	394.45	2.11	22.31	606.50	2.26	307.83	2.20	242.06	1.90
CNJ02_1_117	244.47	2.28	34.49	366.87	2.26	148.28	2.47	255.47	1.97
CNJ02_1_118	353.80	2.18	19.26	531.71	2.48	247.78	2.18	258.41	1.87
CNJ02_1_119	179.34	1.81	39.72	295.72	2.01	119.94	1.88	261.77	1.73
CNJ02_1_120	232.66	2.02	27.05	355.52	2.22	182.34	2.18	284.58	1.87
CNJ02_1_121	342.75	2.05	18.65	438.60	2.15	287.31	2.15	206.07	1.80
CNJ02_1_122	241.75	1.95	26.48	373.07	2.11	184.87	2.06	272.85	1.94
CNJ02_1_124	309.51	2.16	22.64	466.15	2.37	181.69	2.12	186.71	1.99
CNJ02_1_125	211.42	2.10	34.56	351.00	2.33	154.57	2.06	288.78	2.06

CNJ02_1_126	213.73	1.96	42.83	362.43	2.11	145.07	2.15	362.52	1.99
CNJ02_1_127	370.69	2.12	22.53	540.27	2.26	245.76	2.06	286.18	1.78
CNJ02_1_128	376.67	2.46	20.26	478.04	2.55	237.40	2.49	206.85	2.02
CNJ02_1_129	341.06	2.21	30.01	524.21	2.40	186.45	2.15	239.65	1.77
CNJ02_1_130	301.20	2.31	23.61	474.31	2.55	192.11	2.22	211.76	1.97
CNJ02_1_131	200.04	1.86	47.28	352.33	2.36	131.62	1.69	384.07	1.89
CNJ02_1_132	234.72	2.01	39.45	379.26	2.25	159.56	2.00	356.13	1.80
CNJ02_1_133	345.20	2.12	18.23	408.33	2.18	209.41	2.19	228.05	1.94
CNJ02_1_134	391.20	2.04	4.66	419.60	2.25	356.96	2.03	348.07	1.97
CNJ02_1_135	245.66	1.72	30.92	388.84	1.78	158.09	1.85	235.41	1.75
CNJ02_1_136	487.60	2.10	20.62	593.71	2.21	436.71	2.15	256.42	1.75
CNJ02_1_137	266.81	2.16	24.77	409.14	2.32	183.76	2.15	231.63	1.87
CNJ02_1_138	297.78	1.88	31.48	477.41	2.03	166.00	2.06	222.63	1.89
CNJ02_1_139	271.05	1.87	12.56	380.00	2.07	232.10	2.00	236.63	1.63
CNJ02_1_140	301.59	2.12	19.25	453.34	2.39	227.82	2.09	253.81	1.99
CNJ02_1_141	207.14	1.90	51.41	388.75	2.32	99.22	2.04	251.94	2.13
CNJ02_1_142	291.18	2.30	17.59	422.46	2.47	211.91	2.31	203.64	1.86
CNJ02_1_143	303.19	2.04	16.87	426.79	2.03	242.05	2.09	273.61	1.89
CNJ02_1_144	307.99	2.23	28.18	541.00	2.25	190.28	2.15	160.81	1.90
CNJ02_1_145	287.82	2.04	21.58	403.42	2.36	201.83	1.99	245.94	1.94
CNJ02_1_146	283.17	2.14	24.05	491.08	2.47	235.12	2.08	304.47	2.20
CNJ02_1_147	217.73	1.88	27.27	297.92	1.96	162.95	1.99	273.09	1.92
CNJ02_1_148	374.05	2.08	12.75	487.78	2.10	303.68	2.21	317.64	1.79
CNJ02_1_149	320.45	2.37	20.16	430.03	2.43	261.62	2.24	189.58	1.91
CNJ02_1_150	260.67	1.96	20.07	435.70	2.36	198.78	1.90	210.19	1.82
CNJ02_1_151	279.04	2.04	21.51	447.25	2.21	198.47	2.05	217.17	1.84
CNJ02_1_152	343.70	1.92	16.88	527.34	2.14	296.89	1.96	264.32	1.77
CNJ02_1_153	218.87	1.99	29.56	335.21	2.21	161.30	2.05	263.70	2.03
CNJ02_1_154	320.49	1.93	22.36	476.66	2.18	221.44	1.93	260.79	1.82
CNJ02_1_155	256.85	1.89	16.17	350.78	2.07	188.35	2.02	180.19	1.85
CNJ02_1_156	285.76	2.32	32.22	434.42	2.47	178.27	2.30	282.57	2.26
CNJ02_1_157	187.64	2.08	41.99	333.97	2.25	124.72	2.24	279.99	1.99

Appendix IV-9. Local BLAST hits of the SSR containing cranberry genomic scaffolds or predicted CDS in the grape genome.

Marker ID	Cranberry Linkage Group	Map Position	Polashock et al. (2014) Scaffold GenBank ID	Predicted CDS	KEGG KO	Grape Chromosome	Grape Start Position	Grape End Position	Alignment Length
SCF208509	1	3.299	>gi|676411734|gb|JOTO01195049.1|	g4943.t1	K01803	3	1240223	1240057	167
SCF69981	1	8.063	>gi|676437933|gb|JOTO01188880.1|	g12204.t1	None	3	3814024	3813721	304
128239_K63	1	10.149	>gi|676470287|gb|JOTO01177403.1|	g21277.t1	None	3	5985858	5985599	260
SCF117157	1	15.016	>gi|676406871|gb|JOTO01196600.1|	g2380.t1	None	3	9179475	9179097	379
SCF117157	1	15.016	>gi|676406871|gb|JOTO01196600.1|	g2380.t1	None	18	6972745	6972467	279
SCF149633	1	24.334	>gi|676406080|gb|JOTO01197391.1|	g736.t1	None	12	20845710	20845420	291
SCF149633	1	24.334	>gi|676406080|gb|JOTO01197391.1|	g737.t1	K14328	18	22395194	22395572	379
1trimcontig239742	1	24.479	>gi|676406080|gb|JOTO01197391.1|	g736.t1	None	12	20845710	20845420	291
1trimcontig239742	1	24.479	>gi|676406080|gb|JOTO01197391.1|	g737.t1	K14328	18	22395194	22395572	379
SCF22962	1	78.074	>gi|676472469|gb|JOTO01176623.1|	g21764.t1	None	18	3734027	3733920	108
SCF4386	1	113.637	>gi|676437375|gb|JOTO01189078.1|	g12005.t1	K08679	2	4803107	4802529	579
SCF4386	1	113.637	>gi|676437375|gb|JOTO01189078.1|	g12005.t1	K08679	15	14474670	14474015	656
1trimcontig332949	2	2.144	>gi|676407795|gb|JOTO01195709.1|	g3939.t1	None	8	21335288	21335464	177
SCF141794	2	13.842	>gi|676407048|gb|JOTO01196423.1|	g2710.t1	K00705	8	11625372	11625571	200
1trimcontig209220	2	21.016	>gi|676435000|gb|JOTO01189917.1|	g11167.t1	K09835	8	4385937	4385762	176
297265_K63	2	48.666	>gi|676441593|gb|JOTO01187580.1|	g13480.t1	K04733	13	2774291	2774063	229
SCF56816	2	49.48	>gi|676439273|gb|JOTO01188414.1|	g12637.t1	None	13	2173563	2173706	144
372875_K63	2	66.029	>gi|676464116|gb|JOTO01179610.1|	g19780.t1	None	9	21773811	21773946	136
SCF13771	2	76.643	>gi|676406593|gb|JO	g1863.t1	None	19	20133328	20133074	255

			TO01196878.1|					
SCF965	2	90.246	>gi|676407086|gb|JO TO01196385.1|	g2772.t1	None	9	1339663	1339874	212
SCF965	2	90.246	>gi|676407086|gb|JO TO01196385.1|	g2772.t1	None	11	1169460	1169699	240
SCF180863	2	107.83	>gi|676406218|gb|JO TO01197253.1|	g1079.t1	K02941	13	192730	192341	390
SCF27510	3	0	>gi|676510824|gb|JO TO01156073.1|	g30925.t1	None	4	22739436	22739945	510
SCF58861	3	0.447	>gi|676527389|gb|JO TO01147838.1|	g33235.t1	None	4	22359023	22359325	303
313711_K70	3	19.06	>gi|676434909|gb|JO TO01189948.1|	g11134.t1	K00737	14	26871301	26871650	350
SCF157992	3	19.975	>gi|676453945|gb|JO TO01183183.1|	g17154.t1	K02933	4	18395714	18395931	218
SCF177450	3	27.915	>gi|676406891|gb|JO TO01196580.1|	g2420.t1	K10597	14	29977459	29977261	199
1trimcontig4 36904	3	61.188	>gi|676469497|gb|JO TO01177695.1|	g21074.t1	None	17	2254802	2254999	198
SCF9815	3	69.831	>gi|676433932|gb|JO TO01190277.1|	g10799.t1	None	17	7669594	7669425	170
1trimcontig4 40008	3	83.157	>gi|676447975|gb|JO TO01185281.1|	g15485.t1	None	3	1016630	1016071	560
1trimcontig4 40008	3	83.157	>gi|676447975|gb|JO TO01185281.1|	g15485.t1	None	18	12293816	12293392	425
411475_K63	3	83.284	>gi|676447975|gb|JO TO01185281.1|	g15485.t1	None	3	1016630	1016071	560
411475_K63	3	83.284	>gi|676447975|gb|JO TO01185281.1|	g15485.t1	None	18	12293816	12293392	425
42710_K70	3	84.988	>gi|676403321|gb|JO TO01200150.1|	g2299.t1	None	3	1680376	1680631	256
SCF23339	3	95.53	>gi|676444678|gb|JO TO01186424.1|			11	2327033	2327133	101
SCF27755	3	97.682	>gi|676403380|gb|JO TO01200091.1|	g4089.t1	K11434	11	2017472	2017319	154
SCF9157	4	18.171	>gi|676413796|gb|JO TO01194761.1|	g5365.t1	None	5	19609536	19609364	173
scf6955c	4	44.066	>gi|676504289|gb|JO TO01160649.1|	g29364.t1	K02868	10	2923735	2923918	184

scf6955c	4	44.066	>gi|676504289|gb|JOTO01160649.1|	g29364.t1	K02868	12	2419123	2418930	194
vm52204	4	44.208	>gi|676444763|gb|JOTO01186395.1|			10	17291632	17291412	221
305731_K63	4	47.911	>gi|676427836|gb|JOTO01192405.1|	g8493.t1	None	1	22518266	22518506	241
SCF154541	4	49.521	>gi|676406026|gb|JOTO01197445.1|	g593.t1	K06949	1	20693765	20693932	168
SCF38553	4	53.061	>gi|676429255|gb|JOTO01191912.1|	g9026.t1	K09497	1	6764111	6763762	350
SCF38553	4	53.061	>gi|676429255|gb|JOTO01191912.1|	g9026.t1	K09497	12	964515	964166	350
SCF96539	4	69.736	>gi|676407182|gb|JOTO01196289.1|	g2944.t1	None	1	588532	589524	993
SCF100820	4	74.949	>gi|676407124|gb|JOTO01196347.1|	g2835.t1	None	17	4141084	4141751	668
SCF145739	4	95.383	>gi|676476249|gb|JOTO01175297.1|	g22568.t1	None	9	3882914	3883088	175
251788_K63	5	0.101	>gi|676406349|gb|JOTO01197122.1|	g1363.t1	K03691	9	182750	182113	638
SCF804	5	1.746	>gi|676414528|gb|JOTO01194637.1|	g5554.t1	None	9	21917881	21917574	308
SCF804	5	1.746	>gi|676414528|gb|JOTO01194637.1|	g5555.t1	None	4	2403553	2404021	469
SCF804	5	1.746	>gi|676414528|gb|JOTO01194637.1|	g5555.t1	None	11	14181655	14181210	446
SCF7132	5	9.34	>gi|676407470|gb|JOTO01196001.1|	g3469.t1	K17925	9	4041590	4041974	388
SCF132595	5	27.67	>gi|676494321|gb|JOTO01168817.1|			17	12506569	12506750	182
47166_K70	5	97.942	>gi|676427751|gb|JOTO01192434.1|	g8468.t1	None	8	16100734	16100993	260
SCF89447	6	18.616	>gi|676403574|gb|JOTO01199897.1|	g11495.t1	None	12	8064580	8064797	218
ct154615	6	20.129	>gi|676406582|gb|JOTO01196889.1|	g1839.t1	None	12	6693983	6694208	226
vm27120	6	41.895	>gi|676406401|gb|JOTO01197070.1|	g1499.t1	None	8	21787070	21785734	1337
SCF3427	6	46.043	>gi|676406100|gb|JOTO01197371.1|	g805.t1	None	8	19016468	19017057	590

1trimcontig339726	6	99.869	>gi|676413081|gb|JOTO01194864.1|	g5204.t1	None	5	122928	123154	227
SCF167793	7	17.936	>gi|676452550|gb|JOTO01183672.1|	g16794.t1	K16904	5	19192385	19192178	208
311291_K70	7	37.807	>gi|676463311|gb|JOTO01179891.1|	g19596.t1	K12449	3	15559609	15559472	138
1trimcontig337780	7	38.079	>gi|676463311|gb|JOTO01179891.1|	g19596.t1	K12449	3	15559609	15559472	138
76326_K70	7	46.895	>gi|676447212|gb|JOTO01185544.1|	g15248.t1	None	2	7060561	7061093	533
1trimcontig435620	7	82.647	>gi|676455519|gb|JOTO01182635.1|	g17587.t1	None	15	12479614	12479406	209
SCF132922	8	0	>gi|676442563|gb|JOTO01187206.1|	g13837.t1	None	2	1623339	1623544	207
SCF2714	8	25.354	>gi|676405931|gb|JOTO01197540.1|	g312.t1	K02349	4	3319099	3318806	294
SCF30010	8	25.939	>gi|676462108|gb|JOTO01180304.1|	g19310.t1	K11584	4	3645545	3645186	360
ct134336	8	36.203	>gi|676458022|gb|JOTO01181748.1|	g18257.t1	None	10	7854394	7854801	408
187382_K70	8	42.581	>gi|676437464|gb|JOTO01189047.1|	g12024.t1	None	1	5951305	5950696	610
SCF8850	8	64.791	>gi|676403353|gb|JOTO01200118.1|	g3146.t1	K01595	1	2446407	2445655	753
ct154206	9	19.06	>gi|676407058|gb|JOTO01196413.1|	g2727.t1	None	10	1757089	1757471	383
ct154206	9	19.06	>gi|676407058|gb|JOTO01196413.1|	g2727.t1	None	12	3468254	3467960	295
SCF48414	9	59.51	>gi|676429195|gb|JOTO01191932.1|	g9001.t1	None	6	18313235	18313497	263
SCF88396	9	62.364	>gi|676428190|gb|JOTO01192283.1|	g8626.t1	None	6	3542225	3542100	126
1trimcontig238343	9	73.064	>gi|676429479|gb|JOTO01191834.1|	g9106.t1	K11363	6	7679885	7679597	289
214102_K63	9	73.089	>gi|676429479|gb|JOTO01191834.1|	g9106.t1	K11363	6	7679885	7679597	289
SCF141985	9	74.046	>gi|676413149|gb|JOTO01194853.1|	g5222.t1	None	6	7898437	7898295	143
1trimcontig328266	9	94.561	>gi|676426355|gb|JOTO01192926.1|	g7854.t1	K13436	5	2589629	2589900	272

1trimcontig328266	9	94.561	>gi|676426355|gb|JOTO01192926.1|	g7854.t1	K13436	7	4652215	4652486	272
SCF201915	10	1.452	>gi|676456393|gb|JOTO01182315.1|			3	2698766	2698561	206
SCF201915	10	1.452	>gi|676456393|gb|JOTO01182315.1|			18	890283	890492	210
60699_K70	10	10.333	>gi|676406510|gb|JOTO01196961.1|	g1697.t1	None	18	10679599	10679983	385
71002_K63	10	39.651	>gi|676446592|gb|JOTO01185758.1|	g15065.t1	None	10	1024576	1024349	228
ct135942	10	59.077	>gi|676455770|gb|JOTO01182548.1|	g17656.t1	None	1	3557724	3557394	333
SCF104688	10	67.074	>gi|676403646|gb|JOTO01199825.1|	g14494.t1	None	2	866073	866328	256
SCF104688	10	67.074	>gi|676403646|gb|JOTO01199825.1|	g14494.t1	None	14	25069618	25069214	405
SCF104688	10	67.074	>gi|676403646|gb|JOTO01199825.1|	g14494.t1	None	15	18450912	18450629	284
364103_K63	10	87.724	>gi|676406158|gb|JOTO01197313.1|	g931.t1	K17675	14	29313904	29312373	1532
SCF72209	11	2.222	>gi|676436698|gb|JOTO01189321.1|	g11767.t1	None	19	7515513	7515684	172
vm05418	11	5.55	>gi|676429161|gb|JOTO01191944.1|	g8992.t1	None	12	6943755	6944105	351
vm05418	11	5.55	>gi|676429161|gb|JOTO01191944.1|	g8992.t1	None	19	6603485	6603107	379
SCF122746	11	12.753	>gi|676415456|gb|JOTO01194470.1|	g5799.t1	K18482	19	2305727	2305060	668
SCF118608	11	82.261	>gi|676409947|gb|JOTO01195313.1|	g4545.t1	K10838	14	16039358	16039130	229
SCF159195	12	15.633	>gi|676458685|gb|JOTO01181517.1|	g18427.t1	None	14	23018047	23019230	1187
418596_K63	12	31.094	>gi|676442626|gb|JOTO01187183.1|			7	16190645	16190803	159
SCF38430	12	31.484	>gi|676407544|gb|JOTO01195927.1|	g3583.t1	K00924	3	4372594	4372323	272
SCF11065	12	32.483	>gi|676406214|gb|JOTO01197257.1|	g1070.t1	K15029	4	3091791	3092131	341
SCF11065	12	32.483	>gi|676406214|gb|JOTO01197257.1|	g1070.t1	K15029	13	11500140	11499790	351
SCF37628	12	43.491	>gi|676444633|gb|JO			4	7647866	7647697	170

			TO01186439.1|						
411145_K63	12	80.098	>gi|676423301|gb|JO TO01193401.1|	g7253.t1	None	7	18392945	18392446	500
411145_K63	12	80.098	>gi|676423301|gb|JO TO01193401.1|	g7253.t1	None	18	614589	615110	522
1trimcontig1 75770	12	80.349	>gi|676423301|gb|JO TO01193401.1|	g7253.t1	None	7	18392945	18392446	500
1trimcontig1 75770	12	80.349	>gi|676423301|gb|JO TO01193401.1|	g7253.t1	None	18	614589	615110	522

Appendix IV-10. Local BLAST hits of the SSR containing genomic scaffolds or predicted CDS in the tomato genome.

Marker ID	Cranberry Linkage Group	Map Position	Polashock et al. (2014) Scaffold GenBank ID	Predicted CDS	KEGG KO	Tomato Chromosome	Tomato Start Position	Tomato End Position	Alignment Length
SCF149633	1	24.334	>gi|676406080|gb|JOTO01 197391.1|	g736.t1	None	5	4379825	4379559	267
1trimcontig 239742	1	24.479	>gi|676406080|gb|JOTO01 197391.1|	g736.t1	None	5	4379825	4379559	267
SCF4386	1	113.637	>gi|676437375|gb|JOTO01 189078.1|	g12005.t1	K08679	8	60130940	60131325	386
SCF48645	2	61.567	>gi|676494028|gb|JOTO01 168918.1|	g25920.t1	None	6	28438912	28438758	155
SCF965	2	90.246	>gi|676407086|gb|JOTO01 196385.1|	g2772.t1	None	7	49317424	49317204	221
SCF180863	2	107.83	>gi|676406218|gb|JOTO01 197253.1|	g1079.t1	K02941	5	63612466	63612157	310
SCF27510	3	0	>gi|676510824|gb|JOTO01 156073.1|	g30925.t1	None	11	765952	766186	235
SCF157992	3	19.975	>gi|676453945|gb|JOTO01 183183.1|	g17154.t1	K02933	2	42805995	42805687	309
SCF177450	3	27.915	>gi|676406891|gb|JOTO01 196580.1|	g2420.t1	K10597	2	45178441	45178266	176
SCF177450	3	27.915	>gi|676406891|gb|JOTO01 196580.1|	g2420.t1	K10597	6	42708989	42709869	881
SCF9815	3	69.831	>gi|676433932|gb|JOTO01 190277.1|	g10799.t1	None	3	59153967	59154135	170
1trimcontig 440008	3	83.157	>gi|676447975|gb|JOTO01 185281.1|	g15485.t1	None	1	89240636	89240201	436
411475_K63	3	83.284	>gi|676447975|gb|JOTO01 185281.1|	g15485.t1	None	1	89240636	89240201	436
42710_K70	3	84.988	>gi|676403321|gb|JOTO01 200150.1|	g2300.t1	K10752	1	89574280	89574134	147
scf6955c	4	44.066	>gi|676504289|gb|JOTO01 160649.1|	g29364.t1	K02868	2	43541538	43541722	185
scf6955c	4	44.066	>gi|676504289|gb|JOTO01 160649.1|	g29364.t1	K02868	7	60662053	60662237	185
vm52204	4	44.208	>gi|676444763|gb|JOTO01 186395.1|			2	25328072	25328289	218
SCF38553	4	53.061	>gi|676429255|gb|JOTO01 191912.1|	g9026.t1	K09497	5	7494865	7495214	350
251788_K63	5	0.101	>gi|676406349|gb|JOTO01 197122.1|	g1363.t1	K03691	3	64518669	64519097	429

SCF132595	5	27.67	>gi|676494321|gb|JOTO01168817.1|			7	4162957	4163116	160
SCF9068	5	71.573	>gi|676406379|gb|JOTO01197092.1|	g1445.t1	None	11	3202029	3202285	257
47166_K70	5	97.942	>gi|676427751|gb|JOTO01192434.1|	g8468.t1	None	10	59071018	59070756	263
ct154615	6	20.129	>gi|676406582|gb|JOTO01196889.1|	g1839.t1	None	7	59979529	59979755	227
vm27120	6	41.895	>gi|676406401|gb|JOTO01197070.1|	g1499.t1	None	4	5894064	5893746	319
1trimcontig339726	6	99.869	>gi|676413081|gb|JOTO01194864.1|	g5204.t1	None	1	60844056	60843899	158
1trimcontig450309	7	1.107	>gi|676484540|gb|JOTO01172302.1|	g24291.t1	K09286	9	62625398	62625597	200
SCF915	7	15.099	>gi|676447793|gb|JOTO01185345.1|	g15422.t1	None	9	50034042	50034611	570
419834_K63	7	18.277	>gi|676450832|gb|JOTO01184272.1|	g16330.t1	None	6	44837866	44837212	655
76326_K70	7	46.895	>gi|676447212|gb|JOTO01185544.1|	g15248.t1	None	8	58212258	58212864	607
SCF2714	8	25.354	>gi|676405931|gb|JOTO01197540.1|	g312.t1	K02349	8	54408311	54408526	216
187382_K70	8	42.581	>gi|676437464|gb|JOTO01189047.1|	g12024.t1	None	1	87759210	87758633	578
SCF8850	8	64.791	>gi|676403353|gb|JOTO01200118.1|	g3146.t1	K01595	4	664534	664123	412
ct154206	9	19.06	>gi|676407058|gb|JOTO01196413.1|	g2727.t1	None	10	2921198	2920901	298
SCF136207	9	59.268	>gi|676415454|gb|JOTO01194472.1|	g5804.t1	K17795	6	44446960	44446548	413
SCF136207	9	59.268	>gi|676415454|gb|JOTO01194472.1|	g5804.t1	K17795	11	27428612	27429024	413
SCF11802	9	79.285	>gi|676414846|gb|JOTO01194568.1|	g5643.t1	K11835	9	17880195	17880370	176
1trimcontig328266	9	94.561	>gi|676426355|gb|JOTO01192926.1|	g7854.t1	K13436	5	62505854	62505625	230
1trimcontig328266	9	94.561	>gi|676426355|gb|JOTO01192926.1|	g7854.t1	K13436	12	64650609	64650341	269
SCF201915	10	1.452	>gi|676456393|gb|JOTO01182315.1|			4	63725826	63725618	209
SCF107715	10	39.343	>gi|676403729|gb|JOTO01	g17944.t1	K00275	3	57886832	57886663	170

			199742.1|					
364103_K6			>gi|676406158|gb|JOTO01						
3	10	87.724	197313.1|	g931.t1	K17675	11	4515934	4516907	975
			>gi|676429161|gb|JOTO01						
vm05418	11	5.55	191944.1|	g8992.t1	None	7	58186595	58186956	362
			>gi|676429161|gb|JOTO01						
vm05418	11	5.55	191944.1|	g8992.t1	None	12	491912	491562	351
			>gi|676458685|gb|JOTO01						
SCF159195	12	15.633	181517.1|	g18427.t1	None	2	45750373	45749395	979
			>gi|676406356|gb|JOTO01						
SCF38942	12	31.07	197115.1|	g1375.t1	None	10	631011	631499	489
			>gi|676407544|gb|JOTO01						
SCF38430	12	31.484	195927.1|	g3583.t1	K00924	2	30815049	30814772	278
			>gi|676444633|gb|JOTO01						
SCF37628	12	43.491	186439.1|			12	63744529	63744688	160
411145_K6			>gi|676423301|gb|JOTO01						
3	12	80.098	193401.1|	g7253.t1	None	4	63884058	63883711	348
1trimcontig			>gi|676423301|gb|JOTO01						
175770	12	80.349	193401.1|	g7253.t1	None	4	63884058	63883711	348

Appendix IV-11. Local BLAST hits of the SSR containing cranberry genomic scaffolds or predicted CDS in the kiwifruit genome.

Marker ID	Cranberry Linkage Group	Map Position	Polashock et al., 2014 Scaffold GenBankID	Predicted CDS	KEGG KO	Kiwifruit Chromosome	Kiwifruit Start Position	Kiwifruit End Position	Alignment length
SCF153722	1	0.93	>gi|676487255|gb|JOTO01171301.1|	g24765.t1	None	9	11245777	11245939	163
SCF172019	1	2.193	>gi|676403549|gb|JOTO01199922.1|	g10454.t1	K02834	9	10172283	10172106	178
SCF208509	1	3.299	>gi|676411734|gb|JOTO01195049.1|	g4943.t1	K01803	7	846042	846216	175
SCF208509	1	3.299	>gi|676411734|gb|JOTO01195049.1|	g4943.t1	K01803	14	2087975	2088149	175
vm89040	1	6.71	>gi|676440805|gb|JOTO01187868.1|	g13221.t1	None	6	16775875	16775501	375
SCF69981	1	8.063	>gi|676437933|gb|JOTO01188880.1|	g12204.t1	None	6	16299985	16299682	304
SCF23691	1	8.911	>gi|676415019|gb|JOTO01194550.1|	g5679.t1	None	6	16101303	16101449	147
128239_K63	1	10.149	>gi|676470287|gb|JOTO01177403.1|	g21277.t1	None	7	2223492	2223220	273
128239_K63	1	10.149	>gi|676470287|gb|JOTO01177403.1|	g21277.t1	None	6	16115405	16115645	241
SCF117157	1	15.016	>gi|676406871|gb|JOTO01196600.1|	g2380.t1	None	6	15522890	15523261	372
SCF117157	1	15.016	>gi|676406871|gb|JOTO01196600.1|	g2380.t1	None	26	3737960	3737582	379
SCF117157	1	15.016	>gi|676406871|gb|JOTO01196600.1|	g2380.t1	None	4	8528477	8528788	312
SCF117157	1	15.016	>gi|676406871|gb|JOTO01196600.1|	g2380.t1	None	21	9263953	9263642	312
SCF117157	1	15.016	>gi|676406871|gb|JOTO01196600.1|	g2381.t1	None	7	2665523	2665365	159
SCF173212	1	21.039	>gi|676406020|gb|JOTO01197451.1|	g573.t1	None	6	14069886	14071083	1198
SCF173212	1	21.039	>gi|676406020|gb|JOTO01197451.1|	g574.t1	K11548	6	5005495	5005673	179
SCF3362	1	21.039	>gi|676446297|gb|JOTO01185859.1|	g14986.t1	None	6	4950526	4950326	201
SCF149633	1	24.334	>gi|676406080|gb|JOTO01197391.1|	g736.t1	None	6	13572482	13572772	291
SCF149633	1	24.334	>gi|676406080|gb|JOTO0119	g737.t1	K14328	6	5660448	5660066	383

			7391.1|					
1trimcontig239742	1	24.479	>gi|676406080|gb|JOTO01197391.1|	g736.t1	None	6	13572482	13572772	291
1trimcontig239742	1	24.479	>gi|676406080|gb|JOTO01197391.1|	g737.t1	K14328	6	5660448	5660066	383
scf11l	1	37.457	>gi|676488231|gb|JOTO01170961.1|	g24948.t1	None	4	6075084	6074307	778
scf11l	1	37.457	>gi|676488231|gb|JOTO01170961.1|	g24948.t1	None	21	7662344	7661815	530
252600_K70	1	49.043	>gi|676417151|gb|JOTO01194282.1|	g6090.t1	None	13	15428290	15428418	129
SCF22962	1	78.074	>gi|676472469|gb|JOTO01176623.1|	g21764.t1	None	4	10381113	10381236	124
SCF4386	1	113.637	>gi|676437375|gb|JOTO01189078.1|	g12005.t1	K08679	18	14233771	14232739	1033
SCF138607	1	116.146	>gi|676559305|gb|JOTO01133401.1|	g36210.t1	None	14	10050980	10051156	186
vm54133	2	16.059	>gi|676462233|gb|JOTO01180261.1|	g19346.t1	K03327	12	7578374	7578915	542
SCF142664	2	17.826	>gi|676440662|gb|JOTO01187921.1|	g13172.t1	None	20	11929026	11927998	1029
1trimcontig209220	2	21.016	>gi|676435000|gb|JOTO01189917.1|	g11167.t1	K09835	12	6698296	6698504	209
1trimcontig209220	2	21.016	>gi|676435000|gb|JOTO01189917.1|	g11167.t1	K09835	20	11532238	11532351	114
297265_K63	2	48.666	>gi|676441593|gb|JOTO01187580.1|	g13480.t1	K04733	24	11511285	11511507	223
SCF56816	2	49.48	>gi|676439273|gb|JOTO01188414.1|	g12637.t1	None	24	10939216	10939364	149
SCF56816	2	49.48	>gi|676439273|gb|JOTO01188414.1|	g12637.t1	None	3	12535309	12535452	144
SCF18709	2	50.353	>gi|676473717|gb|JOTO01176191.1|	g22049.t1	K13093	22	8411587	8411832	247
SCF48645	2	61.567	>gi|676494028|gb|JOTO01168918.1|	g25920.t1	None	3	10955927	10955770	158
SCF48645	2	61.567	>gi|676494028|gb|JOTO01168918.1|	g25920.t1	None	24	13157282	13157440	159
SCF73288	2	65.011	>gi|676404742|gb|JOTO01198729.1|	g162.t1	None	3	2848946	2849098	153
SCF73288	2	65.011	>gi|676404742|gb|JOTO01198729.1|	g162.t1	None	24	13776268	13776430	163

SCF73288	2	65.011	>gi|676404742|gb|JOTO01198729.1|	g164.t1	None	24	13785926	13786124	199
SCF13771	2	76.643	>gi|676406593|gb|JOTO01196878.1|	g1862.t1	K01728	3	8031576	8031396	181
SCF13771	2	76.643	>gi|676406593|gb|JOTO01196878.1|	g1863.t1	None	17	14204272	14203985	288
1trimcontig351427	2	81.559	>gi|676423463|gb|JOTO01193383.1|	g7274.t1	K08900	3	6902193	6903033	841
1trimcontig351427	2	81.559	>gi|676423463|gb|JOTO01193383.1|	g7274.t1	K08900	18	6083118	6083967	850
SCF965	2	90.246	>gi|676407086|gb|JOTO01196385.1|	g2772.t1	None	1	3096511	3096048	464
SCF965	2	90.246	>gi|676407086|gb|JOTO01196385.1|	g2772.t1	None	19	10511864	10511710	155
SCF965	2	90.246	>gi|676407086|gb|JOTO01196385.1|	g2772.t1	None	10	12122257	12122049	209
SCF965	2	90.246	>gi|676407086|gb|JOTO01196385.1|	g2772.t1	None	23	710518	710666	149
417854_K63	2	96.984	>gi|676442046|gb|JOTO01187405.1|	g13650.t1	K14484	12	10869548	10869763	216
417854_K63	2	96.984	>gi|676442046|gb|JOTO01187405.1|	g13650.t1	K14484	1	7157071	7156944	128
SCF31394	2	106.327	>gi|676438401|gb|JOTO01188720.1|	g12357.t1	None	29	11393400	11393531	132
SCF31394	2	106.327	>gi|676438401|gb|JOTO01188720.1|	g12358.t1	None	1	3525675	3525509	167
SCF31394	2	106.327	>gi|676438401|gb|JOTO01188720.1|	g12358.t1	None	20	10395082	10394915	168
SCF180863	2	107.83	>gi|676406218|gb|JOTO01197253.1|	g1079.t1	K02941	24	12107925	12107526	400
SCF180863	2	107.83	>gi|676406218|gb|JOTO01197253.1|	g1079.t1	K02941	3	11454545	11454901	359
SCF180863	2	107.83	>gi|676406218|gb|JOTO01197253.1|	g1080.t1	K03267	16	575189	575352	164
SCF180863	2	107.83	>gi|676406218|gb|JOTO01197253.1|	g1080.t1	K03267	19	6341685	6341547	139
SCF27510	3	0	>gi|676510824|gb|JOTO01156073.1|	g30925.t1	None	7	14384712	14385629	921
1trimcontig443603	3	7.889	>gi|676464812|gb|JOTO01179358.1|	g19957.t1	None	7	8419464	8419728	266
313711_K7	3	19.06	>gi|676434909|gb|JOTO0118	g11134.t1	K00737	2	13424251	13425328	1078

0			9948.1|						
313711_K70	3	19.06	>gi|676434909|gb|JOTO01189948.1|	g11134.t1	K00737	27	9065370	9064316	1055
313711_K70	3	19.06	>gi|676434909|gb|JOTO01189948.1|	g11134.t1	K00737	5	8765627	8764921	707
SCF157992	3	19.975	>gi|676453945|gb|JOTO01183183.1|	g17154.t1	K02933	1	2010319	2010011	309
SCF157992	3	19.975	>gi|676453945|gb|JOTO01183183.1|	g17154.t1	K02933	25	7754247	7754030	218
SCF157992	3	19.975	>gi|676453945|gb|JOTO01183183.1|	g17154.t1	K02933	13	8662530	8662666	137
SCF157992	3	19.975	>gi|676453945|gb|JOTO01183183.1|	g17154.t1	K02933	24	8184636	8184803	168
ct155339	3	27.314	>gi|676405111|gb|JOTO01198360.1|	g22092.t1	None	2	12210869	12210687	183
SCF177450	3	27.915	>gi|676406891|gb|JOTO01196580.1|	g2420.t1	K10597	2	12040595	12039850	749
SCF177450	3	27.915	>gi|676406891|gb|JOTO01196580.1|	g2420.t1	K10597	3	15599376	15598880	500
SCF9815	3	69.831	>gi|676433932|gb|JOTO01190277.1|	g10799.t1	None	23	4823471	4823303	169
SCF9815	3	69.831	>gi|676433932|gb|JOTO01190277.1|	g10799.t1	None	19	6782160	6782328	169
SCF38340	3	72.589	>gi|676415301|gb|JOTO01194496.1|	g5766.t1	None	26	9733716	9733435	282
42710_K70	3	84.988	>gi|676403321|gb|JOTO01200150.1|	g2299.t1	None	7	574240	573531	710
42710_K70	3	84.988	>gi|676403321|gb|JOTO01200150.1|	g2300.t1	K10752	7	564749	565025	277
SCF27755	3	97.682	>gi|676403380|gb|JOTO01200091.1|	g4089.t1	K11434	12	11553078	11553226	149
SCF27755	3	97.682	>gi|676403380|gb|JOTO01200091.1|	g4090.t1	None	12	11558363	11557903	461
vm51409	3	99.338	>gi|676481557|gb|JOTO01173361.1|	g23687.t1	None	12	11780444	11780149	296
scf20g	3	99.464	>gi|676496795|gb|JOTO01167957.1|	g26390.t1	None	1	3008508	3008062	447
SCF56561	4	1.75	>gi|676408154|gb|JOTO01195597.1|	g4123.t1	K03017	29	9630209	9630047	163
SCF56561	4	1.75	>gi|676408154|gb|JOTO01195597.1|	g4123.t1	K03017	20	9543303	9543470	168

SCF26697	4	1.99	>gi|676455389|gb|JOTO01182679.1|	g17551.t1	None	29	10266781	10266924	144
SCF26697	4	1.99	>gi|676455389|gb|JOTO01182679.1|	g17551.t1	None	20	9077182	9077042	141
SCF9157	4	18.171	>gi|676413796|gb|JOTO01194761.1|	g5365.t1	None	3	3594616	3594436	181
SCF9157	4	18.171	>gi|676413796|gb|JOTO01194761.1|	g5365.t1	None	2	3840366	3840186	181
SCF9157	4	18.171	>gi|676413796|gb|JOTO01194761.1|	g5365.t1	None	19	2388024	2388196	173
SCF140628	4	33.902	>gi|676405271|gb|JOTO01198200.1|	g29465.t1	None	18	4033026	4032898	129
SCF46739	4	35.479	>gi|676406856|gb|JOTO01196615.1|	g2348.t1	None	18	3655180	3655295	116
305731_K63	4	47.911	>gi|676427836|gb|JOTO01192405.1|	g8493.t1	None	6	198714	198209	506
305731_K63	4	47.911	>gi|676427836|gb|JOTO01192405.1|	g8493.t1	None	7	17258219	17257718	502
305731_K63	4	47.911	>gi|676427836|gb|JOTO01192405.1|	g8493.t1	None	29	1827879	1827287	602
305731_K63	4	47.911	>gi|676427836|gb|JOTO01192405.1|	g8493.t1	None	13	13504822	13504245	587
305731_K63	4	47.911	>gi|676427836|gb|JOTO01192405.1|	g8493.t1	None	2	5025826	5026117	292
SCF154541	4	49.521	>gi|676406026|gb|JOTO01197445.1|	g593.t1	K06949	6	948514	948204	311
SCF154541	4	49.521	>gi|676406026|gb|JOTO01197445.1|	g594.t1	K12946	7	18576232	18576511	280
SCF154541	4	49.521	>gi|676406026|gb|JOTO01197445.1|	g594.t1	K12946	6	942530	942810	281
SCF154541	4	49.521	>gi|676406026|gb|JOTO01197445.1|	g594.t1	K12946	13	14153449	14153729	281
SCF154541	4	49.521	>gi|676406026|gb|JOTO01197445.1|	g594.t1	K12946	29	3403920	3404200	281
SCF38553	4	53.061	>gi|676429255|gb|JOTO01191912.1|	g9026.t1	K09497	7	16665800	16666149	350
SCF38553	4	53.061	>gi|676429255|gb|JOTO01191912.1|	g9026.t1	K09497	6	1469213	1468888	326
SCF38553	4	53.061	>gi|676429255|gb|JOTO01191912.1|	g9026.t1	K09497	13	14485280	14484956	325
SCF96539	4	69.736	>gi|676407182|gb|JOTO0119	g2944.t1	None	6	4735979	4736777	799

			6289.1|					
SCF96539	4	69.736	>gi|676407182|gb|JOTO0119 6289.1|	g2944.t1	None	22	2960088	2960893	807
SCF16359	4	73.729	>gi|676518368|gb|JOTO0115 2359.1|	g32063.t1	None	19	5625445	5625604	161
SCF100820	4	74.949	>gi|676407124|gb|JOTO0119 6347.1|	g2835.t1	None	23	5535445	5534702	744
SCF108294	4	88.818	>gi|676470975|gb|JOTO0117 7169.1|	g21440.t1	None	23	2912673	2912838	166
SCF28613	5	0.773	>gi|676437164|gb|JOTO0118 9151.1|	g11937.t1	None	11	14792871	14792300	572
SCF804	5	1.746	>gi|676414528|gb|JOTO0119 4637.1|	g5554.t1	None	16	11288673	11288363	311
SCF804	5	1.746	>gi|676414528|gb|JOTO0119 4637.1|	g5555.t1	None	16	11268589	11267921	669
SCF7132	5	9.34	>gi|676407470|gb|JOTO0119 6001.1|	g3469.t1	K17925	16	9105678	9105288	391
SCF7132	5	9.34	>gi|676407470|gb|JOTO0119 6001.1|	g3469.t1	K17925	11	12711490	12711880	391
SCF7132	5	9.34	>gi|676407470|gb|JOTO0119 6001.1|	g3469.t1	K17925	19	9893001	9892625	377
SCF7132	5	9.34	>gi|676407470|gb|JOTO0119 6001.1|	g3469.t1	K17925	10	7926451	7926586	136
SCF59035	5	13.377	>gi|676432917|gb|JOTO0119 0630.1|	g10443.t1	None	11	12066497	12066274	224
SCF59035	5	13.377	>gi|676432917|gb|JOTO0119 0630.1|	g10443.t1	None	16	8390458	8390235	224
SCF101878	5	60.814	>gi|676433567|gb|JOTO0119 0404.1|	g10671.t1	None	10	343940	343623	318
SCF9068	5	71.573	>gi|676406379|gb|JOTO0119 7092.1|	g1444.t1	None	7	3471664	3472120	463
SCF9068	5	71.573	>gi|676406379|gb|JOTO0119 7092.1|	g1444.t1	None	6	14804332	14804802	471
SCF9068	5	71.573	>gi|676406379|gb|JOTO0119 7092.1|	g1445.t1	None	7	3476945	3476674	272
308812_K70	5	74.685	>gi|676407835|gb|JOTO0119 5687.1|	g3974.t1	None	24	6412892	6413103	212
1trimcontig237406	5	74.692	>gi|676407835|gb|JOTO0119 5687.1|	g3974.t1	None	24	6412892	6413103	212
SCF6195	5	79.507	>gi|676406565|gb|JOTO0119 6906.1|	g1799.t1	None	2	6480610	6480187	424

SCF6195	5	79.507	>gi|676406565|gb|JOTO0119 6906.1|	g1800.t1	None	2	6480474	6480187	288
SCF6195	5	79.507	>gi|676406565|gb|JOTO0119 6906.1|	g1800.t1	None	3	5505373	5505060	314
47166_K70	5	97.942	>gi|676427751|gb|JOTO0119 2434.1|	g8468.t1	None	15	7604480	7604225	256
47166_K70	5	97.942	>gi|676427751|gb|JOTO0119 2434.1|	g8468.t1	None	3	4304746	4305002	257
47166_K70	5	97.942	>gi|676427751|gb|JOTO0119 2434.1|	g8468.t1	None	8	17023854	17023667	188
47166_K70	5	97.942	>gi|676427751|gb|JOTO0119 2434.1|	g8468.t1	None	2	4672249	4672452	204
16720_K63	6	0	>gi|676431573|gb|JOTO0119 1106.1|	g9961.t1	None	23	9128605	9128259	347
SCF89447	6	18.616	>gi|676403574|gb|JOTO0119 9897.1|	g11495.t1	None	13	4024519	4024153	367
ct154615	6	20.129	>gi|676406582|gb|JOTO0119 6889.1|	g1838.t1	None	10	1546056	1546437	382
ct154615	6	20.129	>gi|676406582|gb|JOTO0119 6889.1|	g1839.t1	None	13	3753292	3753637	346
ct154615	6	20.129	>gi|676406582|gb|JOTO0119 6889.1|	g1839.t1	None	23	12385863	12386090	228
ct154615	6	20.129	>gi|676406582|gb|JOTO0119 6889.1|	g1839.t1	None	17	12759063	12758837	227
SCF133376	6	22.477	>gi|676494795|gb|JOTO0116 8655.1|	g26049.t1	None	23	12088908	12089386	479
vm27120	6	41.895	>gi|676406401|gb|JOTO0119 7070.1|	g1499.t1	None	9	1137701	1135372	2330
vm27120	6	41.895	>gi|676406401|gb|JOTO0119 7070.1|	g1499.t1	None	1	4168597	4170482	1886
vm27120	6	41.895	>gi|676406401|gb|JOTO0119 7070.1|	g1500.t1	None	9	1112492	1112824	333
vm27120	6	41.895	>gi|676406401|gb|JOTO0119 7070.1|	g1500.t1	None	1	4182656	4182330	327
SCF22442	6	43.808	>gi|676439114|gb|JOTO0118 8475.1|	g12586.t1	K13495	3	13993457	13994085	629
SCF22442	6	43.808	>gi|676439114|gb|JOTO0118 8475.1|	g12586.t1	K13495	9	1306258	1306601	347
SCF3427	6	46.043	>gi|676406100|gb|JOTO0119 7371.1|	g804.t1	None	12	3297002	3296578	428
SCF3427	6	46.043	>gi|676406100|gb|JOTO0119	g804.t1	None	17	10279683	10280107	428

			7371.1|					
SCF3427	6	46.043	>gi|676406100|gb|JOTO0119 7371.1|	g805.t1	None	3	13473075	13474252	1178
412234_K6 3	6	48.415	>gi|676435395|gb|JOTO0118 9776.1|	g11311.t1	None	3	12975806	12975622	185
vm53000	6	53.905	>gi|676480465|gb|JOTO0117 3761.1|	g23480.t1	None	3	5163530	5162867	665
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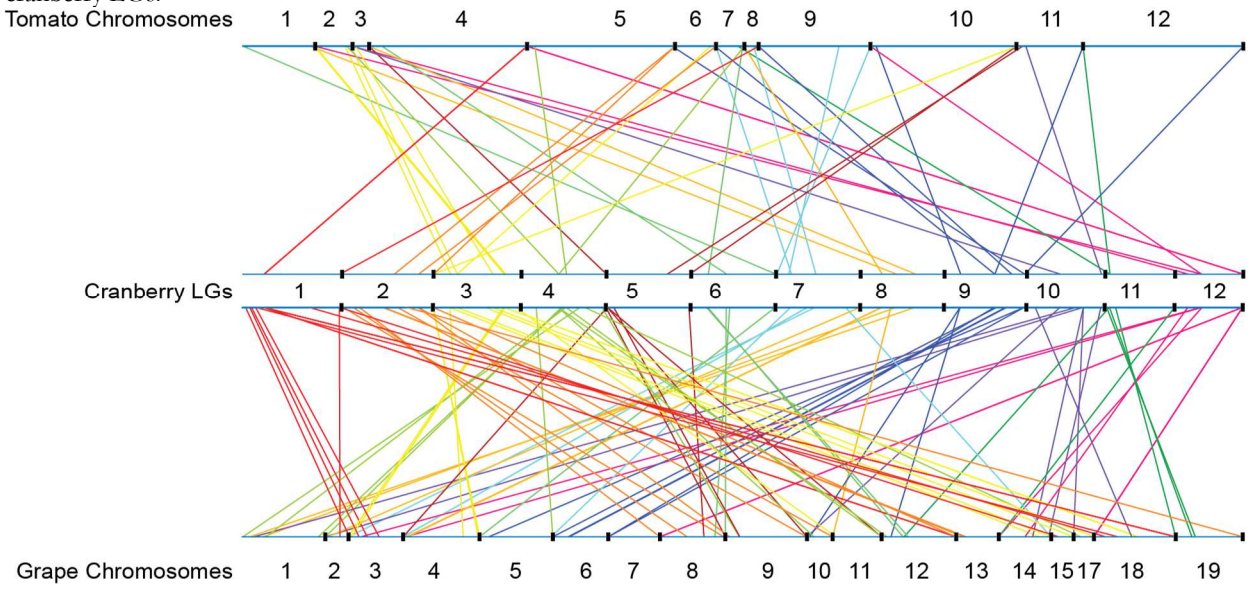
Appendix IV-12. Comparative analysis of the grape chromosomes, tomato chromosomes, and cranberry LGs based on BLAST analyses using the CDS anchored in the cranberry integrated map. Lines connect homologous sequences between the cranberry and the other species genomes, and the lines are colored based on the position of that CDS in the cranberry LGs.



Chapter V

Comparative genetic mapping reveals synteny and collinearity between the American cranberry and diploid blueberry genomes

Abstract

Cranberry (section *Oxcycoccus*) and blueberry (section *Cyanococcus*), are closely related and recently domesticated fruit crops in the genus *Vaccinium* (family Ericaceae). Both the *Oxycoccus* and *Cyanococcus* sections are presumed to have an American origin and likely evolved from a common ancestor; however, the details of species radiation and genomic divergence within and among the two sections and the genus *Vaccinium* are still little understood. Comparative genetic mapping between cranberry and blueberry was therefore conducted to examine the synteny and collinearity of their genomes in an effort to better understand the evolutionary relationships between the two species and sections. A set of common cross-transferable simple sequence repeat (SSR) markers were identified and used to add 43 and 255 SSRs to genetic maps previously constructed for a cranberry mapping population and a interspecific diploid blueberry population ((*V. corymbosum* x *V.darrowii*) x (*V. corymbosum*)), respectively. An exceptionally high degree of macro-synteny and collinearity was detected in comparisons of marker order in the linkage groups (LGs) of the two linkage maps, which are the highest SSR based linkage maps constructed in *Vaccinium*. Approximately 93% of the blueberry linkage map was collinear with the cranberry map while the remaining 7% (66.25 cM) was spread across 15 occurrences of non-collinearity detected in 8 of the 12 LGs. Despite these differences, the high degree of synteny and collinearity observed between cranberry (section *Oxycoccus*) and blueberry (section *Cyanococcus*) suggests that the genomes of these species are highly conserved and that few complicated structural changes such as large-scale rearrangements or chromosome fusion events have occurred during their evolution. Therefore, it is likely that genome sequence information will be highly transferable between species among and within the two sections for genetic research and applied breeding purposes. Finally, the set of cross-transferable SSR markers, and the linkage maps they were used to construct, can serve as a shared resource for the whole *Vaccinium* research community that allows for future comparative genetic mapping studies, identification and transfer of quantitative trait loci and candidate genes between studies and species, and future phylogenetic studies exploring evolutionary relationships in *Vaccinium*.

Introduction

The genus *Vaccinium* L. is a diverse genus comprised of more than 450 species, including economically important berry crops such as the American cranberry (*V. macrocarpon* Ait.) and blueberry (*V. spp.*) (Vander Kloet 1988; Vander Kloet and Avery 2010). The commercially propagated American cranberry is a diploid (2n=2x=24) member of the *Vaccinium* section *Oxycoccus* (Hill) Koch with an estimated genome size of about 470 Mb (Vander Kloet 1983; Polashock et al. 2014), while commercial blueberries are composed of multiple species and their interspecific hybrids from the *Vaccinium* section *Cyanococcus* A. Gray including: *V. darrowii* Camp (2n=2x=24), *V. angustifolium* Ait. (2n=2x=24 or 2n=4x=48), *V. corymbosum* L. (2n=2x=24 or 2n=4x=48), and *V. virgatum* Ait syn. *V. ashei* Reade (2n=6x=72) among others (Brevis et al. 2008). Both cranberries and blueberries are native to North America and were only recently domesticated; cranberry breeding efforts were initiated in 1929 by the USDA in response to outbreaks of cranberry false-blossom disease (Eck 1990) while blueberry breeding began in 1908 by F.V. Coville (Coville 1937). Global export and consumption of blueberries and cranberries is continuing to expand, with a combined 100,000+ hectares in global production valued more than 1.5 billion dollars (FAO 2012). Much of the expansion in global importance of these two berry crops can be attributed to their genetic improvement, which has resulted in new cultivars with larger fruit size, increased concentrations of phytochemicals that are beneficial to human health or that improve flavor, broadened phenological adaptations, such as reduced chilling requirements in blueberries, and yield increases (McCown and Zeldin 2003; Clark and Finn 2010; Schlautman et al. 2015a).

Most cranberry and blueberry breeding programs still rely mainly on phenotypic selection and have yet to incorporate molecular-assisted breeding strategies into their selection regimens; however, knowledge of the genetics of both blueberry and cranberry has greatly improved in the last decade through the development of molecular markers such as randomly amplified polymorphic DNA (RAPDs) (Rowland and Levi 1994; Nilsen 1995; Stewart and Excoffier 1996; Qu and Hancock 1997), PCR markers designed in expressed sequence tags (EST-PCRs) (Rowland et al. 2003a; Rowland et al. 2003b), sequence characterized amplified regions (SCAR) (Polashock and Vorsa 2002), simple sequence repeats (SSRs) (Boches 2005; Boches et al. 2006; Bassil et al. 2009; Georgi et al. 2011; Zhu et al. 2012; Georgi et al. 2013; Liu et al. 2014; Schlautman et al. 2015b), and more recently, single nucleotide polymorphisms (SNPs) (Covarrubias-Pazaran et al. 2016; McCallum et al. 2016). In addition, RNA sequencing and shotgun sequencing of genomic DNA have been used to assemble the cranberry organellar genomes (Fajardo et al. 2013; Fajardo et al. 2014) and to construct transcriptomes and nuclear scaffold assemblies for both species (i.e. 229,745 cranberry scaffolds with N50=4,237 bp and 13,757 blueberry scaffolds with N50 = 145 kb) (Li et al. 2012; Polashock et al. 2014; Gupta et al. 2015).

Construction of genetic maps for cranberries and blueberries using the available molecular markers has begun only recently as an important research goal among *Vaccinium* researchers and geneticists to characterize *Vaccinium* genomes, to anchor *Vaccinium* scaffold sequences into pseudomolecules, and to facilitate quantitative trait locus (QTL) analysis identifying genomic regions controlling traits of economic importance for use in marker-assisted selection and marker-assisted seedling selection of cranberries and blueberries (Ru et al. 2015). To date, two moderate density SSR linkage maps and a single high-density linkage map composed of SNPs and SSRs have been constructed for biparental populations of the American cranberry (Georgi et al. 2013; Schlautman et al. 2015a; Covarrubias-Pazaran et al. 2016); and two RAPD linkage maps, a linkage map composed of RAPDs, SSRs, SNPs, and EST-PCR markers, and a SNP and SSR linkage map have been constructed for diploid and tetraploid blueberry populations of inter- and intra-specific origins which include *V. darrowii*, *V. ashei*, and *V. corymbosum* in their pedigrees (Rowland and Levi 1994; Qu and Hancock 1997; Rowland et al. 2014; McCallum et al. 2016). However, none of these maps contained enough common markers to enable comparative genomic studies to determine the degree of synteny and collinearity between cranberry and blueberry species' genomes.

Taxonomic relationships within *Vaccinium* have been explored using morphological data (Darrow and Camp 1945; Odell and Vander Kloet 1991; Kron et al. 2002a; Kron et al. 2002b) and molecular sequence data (Powell and Kron 2002; Rowland et al. 2003a; Liu et al. 2014; Schlautman et al. 2016). However, a thorough molecular phylogeny for the genus is still lacking and monophyly of the Vaccinieae genera and within the *Vaccinium* sections is still uncertain (Vander Kloet 1988; Vander Kloet and Avery 2010). The substantial set of *Vaccinium* genomic resources, in the form of SNP and microsatellite markers randomly distributed throughout the nuclear genome, is sufficient to expand knowledge about molecular phylogenetic relationships among *Vaccinium* taxa from comparisons at the sequence level to assessments of synteny and differentiation at the genome level. Information related to *Vaccinium* genome organization would not only useful for generating more detailed phylogenies and a more accurate understanding of evolution in the genus, but likely has important future breeding implications. For example, knowledge about the similarities between the cranberry and blueberry genomes could address key questions as to what extent the genomic and transcriptomic sequence datacan be transferred between the two berry crops. Perhaps more importantly, characterizing the genomic features and relationships of cranberry, from the section *Oxycoccus,* and blueberry, from the section *Cyanococcus,* could increase current understanding about the genome evolution and species radiation which has resulted in the surprisingly broad display of phenotypic and phenological adaptations in genus *Vaccinium* (Vander Kloet and Avery 2010).

Therefore, the aim of this present study was to examine genomic differentiation between cranberry and blueberry by conducting a comparative genetic mapping study using microsatellite linkage maps, the first study of its kind in the genus *Vaccinium*. SSR markers previously developed and mapped separately in each species were tested for cross-transferability between the two berry crops. A set of common transferable markers were then used to genotype the same biparental populations used in Schlautman et al. (2015a) and Rowland et al. (2014) and combined with the previous marker data sets to improve the accuracy and density of the current cranberry and blueberry SSR linkage maps and to facilitate genome comparisons. These are the highest density SSR linkage maps constructed to date for both berry species. The results observed herein should accelerate collaborations among the larger community of cranberry, blueberry, and *Vaccinium* breeders and geneticists and facilitate future explorations into genome evolution in the genus.

Methods

Plant Material and DNA Extraction

Two full-sib mapping populations, one each from cranberry and diploid blueberry, were used for comparative genetic mapping in this study. The cranberry population, CNJ02-1, included 222 progeny derived from a cross between the maternal parent, CNJ97-2015 (*Mullica Queen* ®), by the paternal parent, NJS98-23 (*Crimson Queen* ®), from here on referred to as MQ and CQ, respectively. The blueberry population, F_1#10 x W85-23, was an interspecific population that included 86 progeny from a cross between the interspecific maternal parent F_1#10, (*Vaccinium darrowii* selection Fla4B x diploid *V. corymbosum* selection W85-20), and the diploid *V. corymbosum* paternal parent selection W85-23. The CNJ02-1 cranberry population is maintained at the Rutgers University P.E. Marucci Center, Chatsworth, NJ, and the F_1#10 x W85-23 blueberry population is maintained at the Beltsville Agriculture Research Center-West, Beltsville, MD. DNA from the CNJ02-1 progeny and parents was extracted from newly emerged leaves using a Macherey-Nagel (MN) Plant II kit (Düren, Germany) following the manufacturer's instructions. DNA from the F_1#10 x W85-23 progeny, the parents, and grandparents Fla4b and W85-23 was extracted using a modified CTAB procedure previously described in Rowland et al. (2003b).

SSR Genotyping

Linkage maps for the CNJ02-1 cranberry population and the F_1#10 x W85-23 interspecific diploid blueberry population were previously constructed in Schlautman et al. (2015a) and Rowland et al. (2014), respectively. The SSR marker data for the CNJ02-1 population and the EST-PCRs, SSRs, SNPs, and RAPDs for the F_1#10 x W85-23 from

these studies were incorporated into the current study whenever possible. However, many of the SSRs from Rowland et al. (2014) were split into multiple markers (i.e. one per allele), and these SSRs were rescored and formatted as codominant markers for the present study. To facilitate comparisons between the linkage maps for the two species, 788 cranberry SSRs including the 541 markers mapped in Schlautman et al. (2015a), the cranberry SSRs developed and validated in Schlautman et al. (2015b), and a few additional markers mapped in Georgi et al. (2013) or developed in Zhu et al. (2012) were screened for polymorphism in the parents and grandparents of the F_1#10 x W85-23 blueberry population. In addition, the blueberry EST-PCRs and SSRs mapped in Rowland et al. (2014) were screened for polymorphisms between the MQ and CQ parents of the CNJ02 cranberry population. Finally, additional blueberry marker data from SSRs developed and used to genotype the F_1#10 x W85-23 population in Lin (2015) were used to improve the marker density of the resulting blueberry linkage map.

All SSR and EST-PCR forward primers were appended with the M13 sequence (5'-CACGTTGTAAAACGAC-3') to allow for indirect fluorescent labeling of polymerase chain reactions (PCR) products, and reverse primers were appended with the PIG sequence (5'-GTTTCTT-3') (Brownstein et al. 1996; Schuelke 2000). PCRs for SSR marker screens for polymorphism in the cranberry and blueberry parents were performed according to Schlautman et al. (2015b). The mappable SSR loci were then grouped by non-overlapping allele sizes, used in multiplex (3x) PCRs run with M13-labeled FAM-6, HEX, PET, or NED primers, and then pooled for fragment separation on an ABI 3730 fluorescent sequencer with a Dy632 ladder according to Schlautman et al. (2016). Generated .fsa files were viewed in GeneMarker software v1.91 to determine lengths of the resulting fragments (SoftGenetics LLC, State College, PA, USA).

Linkage Map Construction

SSR marker allele sizes for the two biparental populations were formatted and separated into 5 groups (i.e. single cross markers that are heterozygous in a single parent (lm x ll and nn x np) and intercross markers that are heterozygous in both parents (hk x hk, ef x eg, and ab x cd)) according to the pseudo-testcross approach, and all linkage mapping was performed in JoinMap v4.1 (Van Ooijen 2006). Cranberry parental maps were first constructed with the single cross markers and the intercross markers split into two single cross markers using an independent LOD threshold > 5.0 to establish linkage groups (LGs) and the maximum likelihood (ML) algorithm to determine marker order in the LGs (Van Ooijen 2006; Van Ooijen 2011). To ensure an accurate estimation of marker order and distances, markers were removed which were deemed to cause problems due to genotyping errors (i.e. false double recombinations) and/or

were placed far from ends of the LGs using the *colorize* option in JoinMap to view graphical genotypes. Iterative rounds of mapping were then performed removing markers until no markers remained which caused a nearest neighbor stress greater than 0.05. Genetic distances among loci were then recalculated with the regression approach and the Kosambi mapping function using the fixed marker order determined by the ML mapping to facilitate map comparisons between the current parental maps and previous maps.

Only a small number of markers were available for the W85-23 blueberry parental map as a result of selecting markers which were heterozygous in the F1#10 parent and homozygous in the *V. corymbosum* W85-23 parent for the Rowland et al. (2014) linkage mapping study. This made it difficult to perform grouping in the W85-23 parental map using an independent LOD threshold > 4.0 to establish linkage groups, and we could not reduce the number of LGs to less than 17 for the W85-23 parent likely due to large gaps between markers. To overcome this issue, we modified the parental mapping approach used for the cranberry CNJ02-1 population by leaving the intercross formatted markers as intercross markers within the *cp* approach to facilitate better grouping in both parents. We took advantage of the ability JoinMap v4.1 to construct both parental maps and the combined map simultaneously. We still used the ML algorithm and the previously described iterative process of removing markers which caused a nearest neighbor stress greater than 0.05 in either parent. Next, the blueberry intercross markers were split into two single cross markers and combined with the original single cross markers to form two datasets, one for F1#10 and one for W85-23, as was previously done with cranberry. The markers were assigned LGs and positions based on the simultaneously constructed blueberry parental maps.

With the resulting marker positional information, all parental marker data was converted to the same phase using custom R scripts and linkage informed imputation of missing data in the four parental marker sets was performed using the *linkim* R package (R Core Team 2015; Xu and Wu 2015). With the imputed data, the multiple spanning tree (MST) algorithm implemented in the *ASmap* R package was then used to detect genotyping errors and to perform bin mapping (i.e. determining bins of identical markers) for each of the parental maps (Wu et al. 2008; Taylor and Butler 2015). Parental maps were compared to ensure that they were syntenic and collinear, and then a combined consensus map for each population was constructed with the imputed and corrected data from each of the parental marker sets, with the single cross markers converted back to intercross markers, using the regression based approach and the Kosambi mapping function in Joinmap v4.1.

Each marker was tested for significant deviation from the expected Mendelian genotype frequencies using chi-square tests with 1 degree of freedom to detect segregation distortion. Distorted markers were conserved and integrated

into the map, and the χ2 statistic for each locus in each parental map was then plotted along the LGs in Circos to determine if clusters of distorted markers exist in cranberry or blueberry linkage maps (Krzywinski et al. 2009).

Determining Synteny and Collinearity of Linkage Maps

Each LG from the four parental maps and the two combined maps was numbered and oriented according to its homologous/homeologous LG in the Schlautman et al. (2015a) cranberry SSR linkage map. Pair-wise Spearman rank correlations were used to compare collinearity in marker order between the LGs of the four parental maps and the two combined maps. Additionally, synteny and collinearity between the maps was visually assessed by plotting links between homologous markers in the LGs from each of the maps in Circos (Krzywinski et al. 2009), and by plotting the relative position of the common markers in each map on different axes. Synteny and collinearity of the F_1#10 x W85-23 parental and consensus maps were also compared to the previous map for F_1#10 x W85-23 (Rowland et al. 2014). To facilitate comparisons with the maps generated herein, the Rowland et al. (2014) map was modified by deleting identical or nearly identical markers (i.e. less than 2 cM separation or consecutive order in an LG) which were actually 2 separate alleles generated from the same locus/primer-pair. Loci/primer-pairs from Rowland et al. (2014) which contained alleles that mapped more than 15 cM apart or to separate LGs were maintained as two separate markers for subsequent comparisons. Lastly, the Rowland et al. (2014) map was further modified by converting map distances from Haldane to Kosambi distances using the *convert* function from the *qtl* package in R (Broman et al. 2003).

Results

Marker Genotyping and Transferability

In total, 788 cranberry SSR primer-pairs derived from cranberry were used to screen the parents and grandparents of the F_1#10 x W85-23 interspecific diploid blueberry population for transferability and polymorphism discovery. A total of 340 SSRs failed to amplify, 119 amplified a single monomorphic allele, 42 were polymorphic but not mappable because the alleles would not segregate in the F1#10 x W85-23 progeny, and 287 were polymorphic and predicted to segregate in a Mendelian manner (Appendix V-1). The 287 cranberry SSR markers predicted to segregate in the F1#10 x W85-23 progeny were grouped into 96 (3x) combinations for multiplex PCR (Appendix V-2), and the resulting marker data was combined with a marker dataset from the Rowland et al. (2014) linkage map and SSRs used to genotype the F1#10 x W85-23 population in Lin (2015) (Appendix V-1).

Of the 182 blueberry SSR or EST-PCR primer-pairs used to screen the MQ and CQ cranberry parents of the CNJ02-1 population, 119 failed to amplify, 23 amplified a single monomorphic allele for the two parents, 4 were polymorphic but would not segregate in the progeny, and 36 were polymorphic and predicted to segregate in a Mendelian manner (Appendix V-3). The set of 36 blueberry SSR and EST-PCR markers predicted to segregate in the CNJ02-1 population were grouped into 12 (3x) combinations used for multiplex PCR (Appendix V-4), and combined with a marker dataset consisting of 572 cranberry SSRs, of which 539 were mapped in Schlautman et al. (2015a) (Appendix V-3).

Blueberry Map Construction

The number of markers available for parental map construction in the *V. darrowii* x *V. corymbosum* interspecific maternal blueberry parent F_1#10 (i.e. 486 markers) and the paternal *V. corymbosum* blueberry parent W85-23 (i.e. 220 markers) differed considerably because the marker set from Rowland et al. (2014) was composed almost entirely of markers which were heterozygous in F_1#10 and homozygous in W85-23. In total, 356 of the 486 (i.e. 75.1 %) F_1#10 markers, representing 182 unique marker bins, were positioned on 13 LGs in the F_1#10 parental bin map (Appendix V-5; Figure 5.1). Conversely, 198 of the 220 (i.e. 90 %) W85-23 markers, representing 105 unique marker bins, were positioned on 14 LGs in the W85-23 parental bin map (Appendix V-6; Figure 5.1). A greater recombination frequency (0.77 vs. 0.58 recombinations per LG per progeny) was observed in the F_1#10 compared to W85-23, which likely caused the increased total length (1029.15 cM vs. 873.99 cM) and mean LG length (79.17 cM vs. 62.43 cM) in the maternal versus paternal bin maps (Appendix V-5; Appendix V-6; Figure 5.1). On average, there were more bins in the F_1#10 compared to the W85-23 LGs (i.e. 14 vs 7.5 bins), and the average distance between unique marker bins was shorter in the F_1#10 bin map (6.37 cM) than in the W85-23 map (10.15 cM).

There were 154 markers in common shared between F1#10 and W85-23 parental bin maps, and the LGs of both maps were entirely syntenic and almost perfectly collinear (Figure 5.1), except for two local inversions, one each in LGs 1 and 4 (Appendix V-7). The remaining differences in marker order were solely due to markers being in the same bin in one parent while being in two adjacent bins in the other parent. As a result, pair-wise Spearman rank correlations (r) were high for comparisons of marker order in LGs of the two maps (i.e. mean $r = 0.97$) (Table 5.1). LG 5 was split into two separate LGs (LG 5 and LG 5.1) in W85-23; however, marker order in the split LGs were collinear with LG 5 of F1#10 (Figure 5.1; Table 5.1, Figure 5.1). A gap of ~27 cM in LG 5 of the F_1#10 bin map separates the markers on

the distal ends of LGs 5 and 5.1 in the W85-23 bin map, suggesting that there simply were not enough markers in W85-23 to connect the two LGs.

Both the F_1#10 and W85-23 maps contained a moderate, yet similar (i.e. 25 % and 26 %, respectively), proportion of markers with distorted segregation according to $\chi 2$ tests at the $\alpha \leq 0.1$ level (Appendix V-7). Markers displaying significant segregation distortion were distributed on 9 of 13 LGs in the F1#10 maternal parent and 8 of 14 LGs in the W85-23 paternal parent (Appendix V-8; Figure 5.1). Clusters of distorted markers were observed in LGs 2, 3, 5, 9, 10, 11, and 12 of F1#10 and LGs 2, 3, 4, 5, and 9 of W85-23; however, none of the clusters appeared in similar regions of the two blueberry parents (Appendix V-8; Figure 5.1).

After checking the collinearity of the LGs of the F_1#10 and W85-23 bin maps (Figure 5.1) and converting the cleaned and imputed single-cross markers back to intercross markers, a consensus map for the F1#10 x W85-23 interspecific diploid blueberry population was constructed that contained 409 markers (293 unique marker bins) which mapped to 13 LGs spanning 948.21 cM (Table 5.2). The mean LG length was 72.94 cM, and each LG contained an average of 22.54 marker bins with a mean gap of 3.4 cM between bins. The largest gap between marker bins was on LG 12 (i.e. 24.6 cM). Of the 409 markers mapped, 154 were blueberry markers previously mapped in Rowland et al. (2014), 124 were cranberry SSRs previously mapped in Schlautman et al. (2015a), 4 were cranberry SSRs previously mapped in Georgi et al. (2013) but not in Schlautman et al. (2015a), 46 were newly mapped cranberry SSRs, and 81 were newly mapped blueberry SSRs (Appendix V-1; Appendix V-3). Marker order in the consensus map for the F1#10 x W85-23 population was highly collinear with the two blueberry parental maps, with average pair-wise Spearman rank correlations between the LGs of F1#10 and W85-23 compared to the consensus map of $r = 0.97$ and $r = 0.96$ respectively (Table 5.1).

Lack of synteny and collinearity in some LGs was observed between the F1#10 and W85-23 parental bin maps and the blueberry consensus map when compared to the former linkage map constructed for the population in Rowland et al (2014) (Appendix V-9, Figure 5.2). All LGs from Rowland et al. (2014) are from here on denoted as R_LG. In particular LGs 2.1, 3, and 9 in the current parental bin maps and consensus map for the population were syntenic with R_LG1, and a single marker from LG 6 was also found in R_LG1 (Appendix V-13, Figure 5.2). Similarly, R_LG2 was syntenic with LG 1 from the current study, however, R_LG2 also contained a small portion of LG 10 from the current study. R_LG3 was syntenic with LG 11, but contained a single additional marker from LG 5. R_LG8 was syntenic with LG 10, but collinearity between the linkage groups was low ($r = 0.53$) (Figure 5.2; Appendix V-13). R_LG12 was composed of only dominant type markers, and as a result, no markers were found in common with the LG in the

present study. The remaining LGs from Rowland et al. (2014) were syntenic with only a single LG from the current study, and collinearity between these homologous LGs was high (spearman rank correlations $r > 0.9$) (Figure 5.2; Appendix V-9).

Cranberry Map Construction

The parental bin maps for MQ, the maternal parent, and CQ, the paternal parent, contained 466 and 451 markers corresponding to 238 and 210 unique marker bins, respectively (Appendix V-10; Appendix V-11; Figure 5.3). Both maps contained 12 LGs in accordance with the haploid chromosome number of *V. macrocarpon* (Hall and Galleta 1971). The MQ map spanned a total distance of 1189.81 cM with a mean LG length of 99.15 cM, an average of 19.83 bins per LG, a mean interval between bins of 5.37 cM, and an average of 0.97 recombinations per progeny per LG (Appendix V-10). The CQ map was shorter with a total length of 898.54 cM, a mean LG length of 74.88 cM, an average of 17.5 bins per LG, a mean interval between bins of 4.71 cM, and an average of 0.74 recombinations per progeny per LG (Appendix V-11). There were 335 markers in common shared between the MQ and CQ parental bin maps, and analysis of collinearity of the LGs between these two parents revealed nearly identical marker order, with inconsistencies resulting from markers being in a single bin in one parent and in two adjacent bins in the other parent (Figure 5.3). Spearman rank correlations were high for all comparisons performed (i.e. $r \geq 0.99$) (Table 5.3).

The MQ and CQ bin maps contained a smaller percentage of markers with significant segregation distortion (9 % and 11 %, respectively) than the blueberry parental bin maps (Appendix V-12; Figure 5.3). Markers displaying significant segregation distortion according to $\chi 2$ tests at the $\alpha \leq 0.1$ level were located on 5 of 12 LGs in MQ and on 4 of 12 LGs in CQ with clusters appearing in LGs 1, 6, 9, and 10 in MQ and LGs 1, 2, 8, and 12 of CQ (Appendix V-12; Figure 5.3). Common clusters of distorted markers were observed in both MQ and CQ in the first 30 cM of LG 1 (Appendix V-12; Figure 5.3).

After checking the collinearity of the MQ and CQ LGs against themselves and the Schlautman et al. (2015a) cranberry linkage map, a consensus map for the CNJ02-1 cranberry population was constructed that contained 582 markers (565 marker bins) which mapped to 12 LGs spanning 948.21 cM (Table 5.4). The mean LG length was 88.33 cM, and each LG contained an average of 35.58 marker bins with a mean gap of 2.64 cM between bins. The largest gap between marker bins was on LG 3 (24.75 cM) (Table 5.4). Of the 582 SSR markers mapped, 537 were cranberry SSRs previously mapped in Schlautman et al. (2015a), 17 were blueberry markers mapped in Rowland et al. (2014), 2 were cranberry SSRs mapped in Georgi et al. (2013) but not in Schlautman et al. (2015a), and 26 were newly mapped

cranberry SSRs (Appendix V-1; Appendix V-3). Marker order in the consensus map for the CNJ02-1 population was also highly collinear with both parental bin maps with mean correlations across the 12 LGs of 0.997 and 0.995 compared to MQ and CQ, respectively (Table 5.3).

Synteny and Collinearity of Cranberry and Blueberry Linkage Maps

The synteny, collinearity, and similar map lengths within the F1#10 x W85-23 parental bin maps and consensus map and within the CNJ02-1 bin maps and consensus maps suggested that the observed marker orders could be considered representative for cranberry and blueberry and used for inter-specific comparisons. There were 147 markers in common shared between the CNJ02-1 cranberry consensus map and the F1#10 x W85-23 interspecific diploid blueberry parental and consensus maps (Table 5.5; Figure 5.4). Each LG in blueberry was syntenic with only a single LG in cranberry, and therefore, no translocations seem to exist between the cranberry and blueberry LGs (Figure 5.4). LGs 2 and 2.1 from the blueberry consensus map were syntenic with LG 2 of the CNJ02-1 map, with markers from the blueberry LG 2 syntenic for the first 60 cM of cranberry and markers from blueberry LG 2.1 syntenic with cranberry LG 2 from ~90 – 100 cM (Figure 5.4).

Within each LG, marker order was moderately to highly collinear between the blueberry parental and consensus maps compared to the CNJ02-1 consensus map based on pair-wise Spearman rank correlations and visualized in the linear diagonal pattern in scatterplots of marker position in the LGs of both species (Table 5.5; Figure 5.4). However, 15 non-collinear segments displaying rearrangements/local inversions, observed as deviations from the diagonal in the marker position scatterplots, were found in eight LGs in comparisons of the cranberry CNJ02-1 consensus map and the blueberry F_1#10 x W85-23 consensus map (Appendix V-13; Figure 5.4). Seven of the non-collinear segments were small and spanned less than 2 cM in the CNJ02-1 and/or F_1#10 x W85-23 consensus maps, while the eight remaining non-collinear segments spanned at least 2 cM in both consensus maps (Appendix V-13; Figure 5.4). Eight of the 15 non-collinear segments (i.e. inversions 1, 6-10, 12, and 15) observed in comparisons between the two consensus maps also appeared as non-collinear segments in comparisons between the CNJ02-1 cranberry consensus map and the F_1#10 interspecific diploid blueberry parental bin map, but only two non-collinear segments (i.e. inversions 1 and 8) were present in comparisons between the CNJ02-1 consensus map and the W85-23 parental bin map (Figure 5.4; Appendix V-13; Appendix V-14; Appendix V-15; Appendix V-16). The remaining seven non-collinear segments (i.e. inversions 2-5, 11, and 13-14) were not present in either of the blueberry parental bin maps, suggesting that they

could potentially be artifacts of the consensus mapping process (Figure 5.4; Appendix V-13; Appendix V-14; Appendix V-15; Appendix V-16).

Discussion

Marker transferability between cranberry and blueberry

A main objective of this study was to identify a set of common orthologous SSR markers which were transferable between cranberry and blueberry to allow for comparative genetic mapping of the two species. The approach taken was to test previously developed markers in cranberry and blueberry for potential amplification and polymorphism in the parents (and grandparents in blueberry) of the CNJ02-1 cranberry and F_1#10 x W85-23 interspecific diploid blueberry mapping populations. In total, 57 % of the SSR primer pairs designed in cranberry amplified PCR products in the parents and grandparents of the blueberry population, while only 35 % of the SSRs or EST-PCR markers amplified in the parents of the CNJ02-1 cranberry population (Appendix V-1; Appendix V-3). Perhaps one of the reasons fewer blueberry markers amplified in cranberry is that they were simply too specific for blueberry and were designed from regions of ESTs lacking DNA repeat variation in cranberry. Additionally, past blueberry genetic diversity and genetic mapping studies used modified touchdown PCR protocols for the blueberry primers with cycling temperatures which gradually decreased annealing temperatures in progressive cycles (Roux 2009; Rowland et al. 2014). However, PCR optimization was not attempted with the blueberry primers herein out of a desire to develop a set of cross-transferable orthologous SSR? markers which amplify under a universal set of PCR conditions across *Vaccinium* taxa (i.e. annealing temperature of 55°C) and can easily be used by multiple research groups at various multiplexing levels. Of those markers which did cross-amplify, 64% of the cranberry SSRs were polymorphic and segregated appropriately for mapping in the F_1#10 x W85-23 interspecific diploid blueberry population, and similarly, 57% of the blueberry markers were polymorphic and segregated appropriately for mapping in the CNJ02-1 cranberry population. As a result of the cross-transferability study, a set of 323 common, orthologous SSR markers were identified for comparative mapping; moreover, the remaining 188 cross-transferable markers which amplified but were not polymorphic or would not segregate in the progeny could potentially be useful in future comparative analyses in other blueberry and cranberry pedigrees (Appendix V-1; Appendix V-3).

Previous studies of marker transferability between cranberry, blueberry and other *Vaccinium* taxa have found results similar to those observed herein, and in some cases, reported higher levels of cross-transferability. Tests of EST-PCR marker transferability between cranberry and blueberry found that 23 of 26 markers tested (89%) produced

amplification products; however only one of the 23 amplified markers were polymorphic and able to distinguish the two cranberry cultivars (Rowland et al. 2003a). In an additional study, 49 microsatellite markers were tested for transferability from blueberry to cranberry, and found that 77% produced amplification products, but that only 60% of those markers amplified polymorphic fragments that distinguished cranberry genotypes (i.e. 46% of the total) (Bassil et al. 2009). Two other studies showed that EST-SSRs derived from *V. corymbosum* were most transferable to other members from the same section, *Cyanococcus*, and that cross-transferability was still greater to all other sections included in the study (i.e. *Batodendron, Myrtillus, Bracteatum,* and *Ciliata*) than to section *Oxycoccus* which includes cranberry (Boches et al. 2005; Boches et al. 2006). Marker transferability tests in other fruit genera, especially members of genus *Prunus* subgenera *Prunophora* (i.e. plum and apricot) and *Amygdalus*, report levels of SSR cross-transferability between species exceeding 90 % (Foulongne et al. 2003; Dirlewanger et al. 2006; Ogundiwin et al. 2009). However, other studies in *Prunus* have shown that marker transferability between more phylogenetically distant subgenera, such as *Prunophora* or *Amygdalus* and *Cerasus*, *Laurocerasus*, or *Padus* (i.e. cherry and laurel), were more similar to cross-transferability percentages observed herein (Shaw and Small 2004; Dondini et al. 2007; Olmstead et al. 2008). Therefore, it is likely that similar trends of greater marker-transferability within sections than among sections can be expected in *Vaccinium*.

Map construction

The CNJ02-1 cranberry consensus map generated herein, which was built upon a previous cranberry SSR linkage mapping study, contained 582 SSR markers positioned on 12 linkage groups representing the expected haploid chromosome number (Hall and Galleta 1971; Schlautman et al. 2015b), making it the densest SSR linkage map in genus *Vaccinium* and the entire Ericaceae family to date. Even though 43 new SSR markers (17 blueberry markers) were added to the map for the CNJ02-1 population, an 8 % increase in marker density compared to Schlautman et al. (2015a), total map length decreased 10 % from 1177.84 cM to 1059.99 cM (Table 5.4). The decrease in length likely reflects the increased accuracy in estimation of marker order and genetic distances achieved through a combination of the stricter parameters used during map constructions, linkage-informed imputation of missing data, correction of genotyping errors leading to false double recombination events, and parental bin mapping performed using the multiple spanning tree algorithm employed in the ASmap package (Wu et al. 2008; Taylor and Butler 2015). Accuracy of the cranberry linkage map is supported by the near perfect collinearity of the parental bin maps as quantified by Spearman rank correlations, and is especially apparent when the recombination events leading to the linkage group architecture for each progeny are observed in the parental bin maps (Table 5.3, Figure 5.3). The cranberry consensus map compares well with the recent

SNP based linkage map constructed for a cranberry mapping population, which spanned 1112.1 cM in total length and positioned 4849 markers (Covarrubias-Pazaran et al. 2016). Although the Covarrubias-Pazaran et al. (2016) map was likely fully saturated and contained approximately 8 fold more markers than the map developed herein and the Schlautman et al. (2015a) map, comparisons between the Covarrubias-Pazaran et al. (2016) and the Schlautman et al. (2015a) maps suggested that a sufficient number of SSRs had been already anchored to cover the full length of the 12 linkage groups. Therefore, it is likely that the 427 unique marker bins spaced at an average interval of 2.64 cM in the new cranberry SSR consensus map reflect the recombination frequency and history in the CNJ02-1 parents and resulting progeny and the location and distribution of the SSR loci within the cranberry genome (Table 5.4, Figure 5.3, Figure 5.4).

Linkage map construction for the interspecific diploid blueberry mapping population F_1#10 x W85-23 improved upon previous mapping efforts undertaken in Rowland et al. (2014). The number of mapped markers for the population was increased nearly two-fold from 219 to 409 loci and total map length was reduced approximately 60 % to 948.21 cM (Table 5.2) (Rowland et al. 2014). Of the 409 markers mapped herein, only 154 were previously mapped in Rowland et al. (2014) while the remaining 255 markers (i.e. 81 and 174 markers developed in blueberry and cranberry, respectively) were mapped for the first time in blueberry (Appendix V-1; Appendix V-3). Although the Rowland et al. (2014) map consisted of 12 linkage groups (R_LGs), the expected base chromosome number in *Vaccinium*, 13 linkage groups were found in the blueberry consensus map and the F_1#10 parental bin map and 14 LGs were found in the W85-23 parental bin map. R_LG12, was not recovered in the current blueberry mapping study (Figure 5.2). R_LG 1 could not be reconstructed even after selecting groups at multiple LOD scores, instead, it was split into three separate LGs, LGs 2.1, 3, and 9, and contained a single marker from LG 6 (Figure 5.2). Regions of segregation distortion, which are common in interspecific pedigrees (Yin et al. 2004; Semagn et al. 2006; Bodénès 2015), can be another potential source of error that could have effected accurate estimation of marker order and distances in the current study and Rowland et al. (2014). Rowland et al. (2014) reported high levels of segregation distortion in R_LG1, and similarly, regions with significant segregation distortion composed of a combination of both dominant newly mapped codominant markers were observed in this study in LGs 3 and 9 for the F_1#10 interspecific parent (Figure 5.2; Appendix V-8). R_LG2 was syntenic and collinear with the entire LG 1 in the current blueberry mapping study, but included a small additional segment syntenic with the end of LG 10 (Figure 5.2). Each of the remaining R_LGs were syntenic with only a single LG in the consensus blueberry map, except for R_LG3, which was syntenic with LG 11 but included a single marker from LG 5 (Figure 5.2, Appendix V-9). Collinearity between the linkage groups, as measured by Spearman rank correlations,

was high (i.e. $r > 0.9$) for the syntenic LGs and R_LGs, except between R_LG8 and LG 10, where a small segment of markers with a high degree of segregation distortion in parent W85-23 may have interfered with estimation of marker order in both studies (Figure 5.2; Appendix V-8; Appendix V-9).

Despite the observed differences in marker order and linkage group structure between the current blueberry maps and the Rowland et al. (2014) map, multiple precautions were taken and analyses performed that provide confidence in the accuracy of the maps developed herein. Stringent parameters were used to remove markers that were potential sources of error; thus, more than 25% of the markers from the original blueberry dataset were discarded during map construction. Dominant markers from the Rowland et al. (2014) were more likely to be removed during the mapping process, possibly because dominant markers can lead to inconsistent scores across genotypes and errors in estimation of marker order and inflation of marker distances (Ferreira et al. 2006; Cavagnaro et al. 2011). Furthermore, the inaccuracy from potential genotyping errors and missing data, which can lead to incorrect marker ordering in dense regions (Hackett and Broadfoot 2003; Cheema and Dicks 2009), was reduced by linkage-informed imputation and parental bin mapping in the current study. The near complete collinearity between the two blueberry parental bin maps and lack of obvious genotyping errors leading to false double recombination events also suggests that estimation of marker order in the current map has improved compared to Rowland et al. (2014) (Figure 5.1; Table 5.1; Appendix V-7). Interestingly, the only two segments of non-collinearity between the two blueberry parental bin maps overlap with regions of segregation distortion in the paternal parent W85-23 (Figure 5.1; Appendix V-7).

Comparisons between the cranberry and blueberry linkage maps

An exceptionally high degree of macro-synteny and collinearity was detected in the comparative genetic mapping analysis of the cranberry CNJ02-1 population and the interspecific diploid blueberry F_1#10 x W85-23 population. All common markers between the cranberry and blueberry maps were completely syntenic, such that no translocations were observed between the linkage groups of cranberry and blueberry (Table 5.5, Figure 5.4). On a genome-wide basis ~93% of the blueberry F_1#10 x W85-23 map was collinear with the CNJ02-1 map while the remaining ~7% (66.25 cM) was spread across 15 occurrences of non-collinearity detected in 8 of the 12 LGs (Figure 5.4; Appendix V-13). This level of genome-wide collinearity is higher than was observed in comparative genetic mapping of other perennial species of similar relatedness from genera such as in *Helianthus* and *Elaeis* (Barb et al. 2014; Ting et al. 2014), and similar to those observed in comparative mapping studies in *Eucalyptus* and *Prunus* (Foulongne et al. 2003; Dondini et al. 2007; Olmstead et al. 2008; Hudson et al. 2012). The high level of collinearity observed between

blueberry and cranberry suggests that the genomes of the species are highly similar, have undergone little divergence, and that genomic and transcriptomic sequence information is likely highly transferable between these species.

None of these non-collinear regions appeared to be major rearrangements or paracentric inversions, but rather small pericentric inversions (Inv) (Appendix V-13, Figure 5.4). In fact, the majority of the instances of non-collinearity involved only two or three unique marker bins and averaged less than 6 cM and 4.5 cM in length in cranberry and blueberry, respectively (Appendix V-13). A large number of the instances of non-collinearity appear at the tips of the linkage groups, such as Inv 8, which is particularly interesting because it is present in both the blueberry parental bin maps and the blueberry consensus map. It is difficult to determine how many of the regions of non-collinearity between cranberry and blueberry represent true chromosomal rearrangements. It is possible that some could be relics of a lack of power to estimate true marker order due to the small blueberry population size (86 plants) or analytical errors which occurred during the genotyping and map construction despite meticulously inspecting marker-order fit statistics and removing errant markers. For example, of the 15 occurrences of non-collinearity; only 8 are present when comparing either of the blueberry parental bin maps to the cranberry consensus map suggesting that they could be errors introduced during the consensus mapping process (Appendix V-14; Appendix V-15). Future studies using larger population sizes and other marker technologies, combined with cytogenetic and genomic approaches, should be used to validate the observed instances of non-collinear and detect rearrangements which were too small to identify at the marker density achieved in the cranberry and blueberry consensus maps.

Linkage mapping in some interspecific populations from other genera containing woody perennials such as *Eucalyptus* and *Quercus* concluded that mapping markers with distorted segregation ratios, a common phenomenon in wide crosses, had little effect on marker collinearity (Hudson et al. 2012; Bodénès 2015). However, close inspection of regions of non-collinearity between the F1#10 x W85-23 blueberry and CNJ02-1 cranberry maps suggests that segregation distortion was likely an important source of error in estimation of recombination frequency and marker order, particularly in dense map regions (Figure 5.1; Figure 5.4; Appendix V-8; Appendix V-13). Specifically, Inv 1 overlapped with regions of segregation distortion (SDRs) in blueberry parent F_1#10 and cranberry parents MQ and CQ; Inv 2 overlapped and (SDR) in MQ; Inv 6 overlapped an SDR in F_1#10 and W85-23; Inv 10 overlapped an SDR in F_1#10; Inv 12 overlapped an SDR in MQ; and Inv 15 overlapped an SDR in F_1#10 (Appendix 8; Appendix 12; Appendix 13). Segregation distortion regions are frequently identified in interspecific crosses (Lowe and Walker 2006; Wang et al. 2012; Ting et al. 2014), and numerous biological factors such as the pre- and post-reproductive barriers, such as those previously observed in blueberry, have been postulated as potential causes (Vander Kloet and Lyrene 1987;

Krebs and Hancock 1991). For this reason, the SDRs which can affect estimation of marker order in comparative mapping, may actually provide important insights into genomic regions which potentially act as barriers to wide hybridization in natural populations, promoting sympatric evolution, or in artificially selected populations like those developed in crop breeding programs.

Wide-hybridization has been an important mechanism for transferring novel genes between wild species and their domesticated crop relatives, especially in *Vaccinium* section *Cyanococcus*, which includes blueberries (Darrow and Camp 1945; Dweikat and Lyrene 1988; Lyrene et al. 2003; Brevis et al. 2008). Intersectional hybridization in *Vaccinium* between species such as cranberry and blueberry, and intrasectional hybridization within *Vaccinium* section *Oxycoccus* (cranberries), remains an important challenge and goal of breeders in both crops (Lyrene et al. 2003; Vorsa and Polashock 2005; Lyrene 2011). The lack of past success in generating viable/fertile hybrids in crosses between the two sections, *Cyanococcus* and *Oxycoccus*, is somewhat surprising after observing such a high the degree of in this comparative mapping study, which suggests the apparent absence of chromosome structural differentiation potentially acting barriers to gene flow between *Vaccinium* species.

The many comparative mapping studies that have been performed in genera such as *Solanum, Prunus, Helianthus,* and *Eucalyptus* have consistently shown that the genomes with each genera are highly collinear, that genome differentiation with a genus mainly consists of a limited number of chromosome rearrangements, and that the duration of temporal separation between sections/subgenera within a genus is closely related to the degree of non-synteny observed in interspecific comparison (Doganlar et al. 2002; Dirlewanger et al. 2004; Lambert et al. 2004; Dirlewanger et al. 2006; Dondini et al. 2007; Olmstead et al. 2008; Hudson et al. 2012; Iorizzo et al. 2014). Therefore, we can predict that high levels of synteny and collinearity will also be observed in future comparative mapping studies within and among *Vaccinium* sections. This highlights the importance of the set of common orthologous SSR markers identified herein. A major advantage of SSR loci, especially in biparental populations generated from two heterozygous parents, is that they can contain multiple alleles allowing them the potential to be fully informative for both parents and highly transferable across pedigrees and species for map comparisons and map merging (Zalapa et al. 2012; Schlautman et al. 2015b). Additionally, because the SSRs mapped herein are randomly distributed throughout the cranberry and blueberry genomes, have previously been shown to be highly heterozygous (Schlautman et al. 2015b), and are easily grouped into multiplexing panels (Chapter III), they should serve as an important resource which allows cranberry and blueberry breeders to focus on particular genomic regions in a high-throughput, reproducible manner, such as is common in marker-assisted selection, by selecting targeted polymorphic loci (Dekkers 2007; Ru et al. 2015). Finally, the SSR linkage

maps developed herein can serve as a framework *Vaccinium* reference map for the whole *Vaccinium* research community, which could allow for QTLs to be mapped and candidate genes be identified in one species and easily transferred to another by means of the common set of cross-transferable markers.

Table 5.1. Spearman rank correlations (*r*) by linkage group as a measure of collinearity of marker order between the F1#10 and W85-23 blueberry parental bin maps and the blueberry consensus map. The number of common markers involved in each comparison are written in parentheses.

LG	Blueberry consensus vs F1#10	Blueberry consensus vs W85-23	F1#10 vs W85-23
1	0.96 (36)	0.98 (16)	0.97 (15)
2	0.95 (15)	0.99 (16)	0.97 (9)
2.1	0.93 (8)	0.91 (6)	0.8 (5)
3	1.00 (25)	1.00 (17)	0.99 (8)
4	0.99 (33)	1.00 (21)	0.99 (16)
5	0.99 (31)	0.98 (10)	1.00 (8)
5.1†	- (-)	0.97 (5)	0.97 (5)
6	1.00 (33)	0.96 (19)	0.98 (17)
7	1.00 (31)	0.95 (17)	0.97 (12)
8	1.00 (31)	0.99 (14)	0.99 (12)
9	0.97 (35)	0.95 (20)	0.99 (17)
10	0.95 (26)	0.84 (12)	0.98 (8)
11	0.92 (30)	0.93 (7)	0.93 (7)
12	0.99 (31)	0.97 (18)	0.99 (15)
mean *r* (markers)	0.97 (365)	0.96 (198)	0.97 (154)

† LG 5 was split into two LGs (i.e. LG 5 and LG 5.1) in the W85-23 parent while LG 5 was complete in the F_1#10 parent and the consensus map.

Table 5.2. Features of the F1#10 (*V. darrowii x V. corymbosum*) x W85-23 (*V. corymbosum*) interspecific diploid blueberry consensus map including the length of the linkage groups (LG), the total number of markers mapped (No. Markers), the number of simple sequence repeats (SSRs) previously developed in cranberry mapped, the number of markers previously developed in blueberry mapped, the number of unique marker bins (No. Bins), the average gap between unique marker bins, and the largest gap between marker bins.

LG	Length (cM)	No. Markers	Cranberry SSRs	Blueberry Markers	No.Bins	Average gap between bins (cM)	Largest Gap Between Marker Bins (cM)
1	80.88	37	17	20	24	3.52	16.71
2	58.17	22	11	11	15	4.16	24.31
2.1	18.45	9	3	6	8	2.64	6.40
3	94.78	34	15	19	24	4.12	20.49
4	89.11	38	19	19	33	2.78	12.42
5	77.72	33	12	21	23	3.53	14.21
6	85.65	35	17	18	23	3.89	13.75
7	80.12	36	16	20	25	3.34	14.50
8	87.38	33	14	19	23	3.97	18.62
9	59.05	38	16	22	28	2.19	17.39
10	56.10	30	11	19	20	2.95	12.80
11	69.92	30	7	23	22	3.33	13.79
12	90.88	34	17	17	25	3.79	24.60
mean	72.94	31.46	13.46	18	22.54	3.40	16.15
total	948.21	409	175	234	293		

Table 5.3. Spearman rank correlations (*r*) by linkage group as a measure of collinearity of marker order between the CNJ97-2015 *Mullica Queen* ® (MQ) and NJS98-23 Crimson Queen ® (CQ) cranberry parental bin maps) and the consensus map for the CNJ02-1 population. The number of common markers involved in each comparison is written in parentheses.

LG	CNJ02-1 vs MQ	CNJ02-1 vs CQ	MQ vs CQ
1	1.00 (37)	1.00 (45)	0.99 (28)
2	1.00 (43)	1.00 (44)	1.00 (32)
3	1.00 (37)	1.00 (37)	1.00 (29)
4	1.00 (50)	0.99 (34)	0.99 (31)
5	1.00 (27)	0.99 (28)	1.00 (22)
6	1.00 (36)	0.99 (34)	1.00 (25)
7	0.99 (44)	0.99 (43)	1.00 (31)
8	1.00 (37)	1.00 (38)	1.00 (27)
9	1.00 (43)	1.00 (42)	1.00 (32)
10	0.99 (37)	1.00 (37)	0.99 (29)
11	1.00 (30)	0.99 (31)	0.99 (20)
12	0.99 (45)	0.99 (38)	0.99 (29)
mean *r* (markers)	1.00 (466)	1.00 (451)	1.00 (335)

Table 5.4. Features of the CNJ02-1 cranberry consensus map including the length of the linkage groups (LG), the total number of markers mapped (No. Markers), the number of simple sequence repeats (SSRs) previously developed in cranberry mapped, the number of markers previously developed in blueberry mapped, the number of unique marker bins (No. Bins), the average gap between unique marker bins, and the largest gap between marker bins.

LG	Length (cM)	No. Markers	Cranberry SSRs	Blueberry Markers	No.Bins	Average gap between bins (cM)	Largest Gap Between Marker Bins (cM)
1	105.14	54	53	1	38	2.84	13.37
2	102.66	55	52	3	41	2.57	18.10
3	94.44	45	44	1	30	3.26	24.75
4	101.10	53	52	1	40	2.59	22.76
5	75.64	33	33	0	20	3.98	15.81
6	90.75	45	42	3	35	2.67	10.09
7	82.77	56	56	0	41	2.07	8.47
8	94.22	48	46	2	38	2.55	11.06
9	88.04	53	50	3	40	2.26	16.02
10	77.01	45	43	2	34	2.33	10.49
11	75.12	41	40	1	29	2.68	10.74
12	73.10	54	54	0	41	1.83	8.84
mean	88.33	48.5	47.08	1.42	35.58	2.64	14.21
total	1059.99	582	565	17	427		

Table 5.5. Spearman rank correlations (*r*) by linkage group as a measure of collinearity of marker order between the F_1#10 and W85-23 parental bin maps and the blueberry consensus map compared to the CNJ02-1 cranberry consensus map. The number of common markers involved in each comparison is written in parentheses.

LG	CNJ02-1 vs Blueberry consensus	CNJ02-1 vs F1#10	CNJ02-1 vs W85-23
1	0.85 (12)	0.92 (11)	0.87 (7)
2	0.85 (11)	0.84 (9)	0.99 (8)
2.1€	0.87 (3)	1.00 (3)	1.00 (2)
3	0.96 (11)	0.99 (8)	1.00 (6)
4	0.97 (14)	0.99 (12)	0.99 (9)
5	0.94 (6)	0.95 (6)	0.82 (4)
5.1†	- (-)	- (-)	- (1)
6	1.00 (16)	1.00 (15)	0.99 (12)
7	0.99 (14)	0.98 (13)	0.98 (9)
8	0.95 (14)	0.95 (14)	0.94 (10)
9	0.99 (15)	0.98 (14)	0.99 (12)
10	0.93 (13)	0.95 (11)	0.95 (9)
11	0.8 (5)	0.87 (5)	0.87 (3)
12	0.99 (13)	1.00 (11)	0.99 (11)
mean *r* (markers)	0.93 (147)	0.96 (132)	0.95 (103)

€ LG 2 was split into two LGs (i.e LG 2 and 2.1) for the parental bin maps and consensus map of the F_1#10 x W85-23 interspecific diploid blueberry populations. Comparisons with both the LG 2 and LG 2.1 were compared to the homologous chromosome (i.e LG 2) of cranberry.

† LG 5 was split into two LGs (i.e. LG 5 and LG 5.1) in the W85-23 parent while LG 5 was complete in the F_1#10 parent.

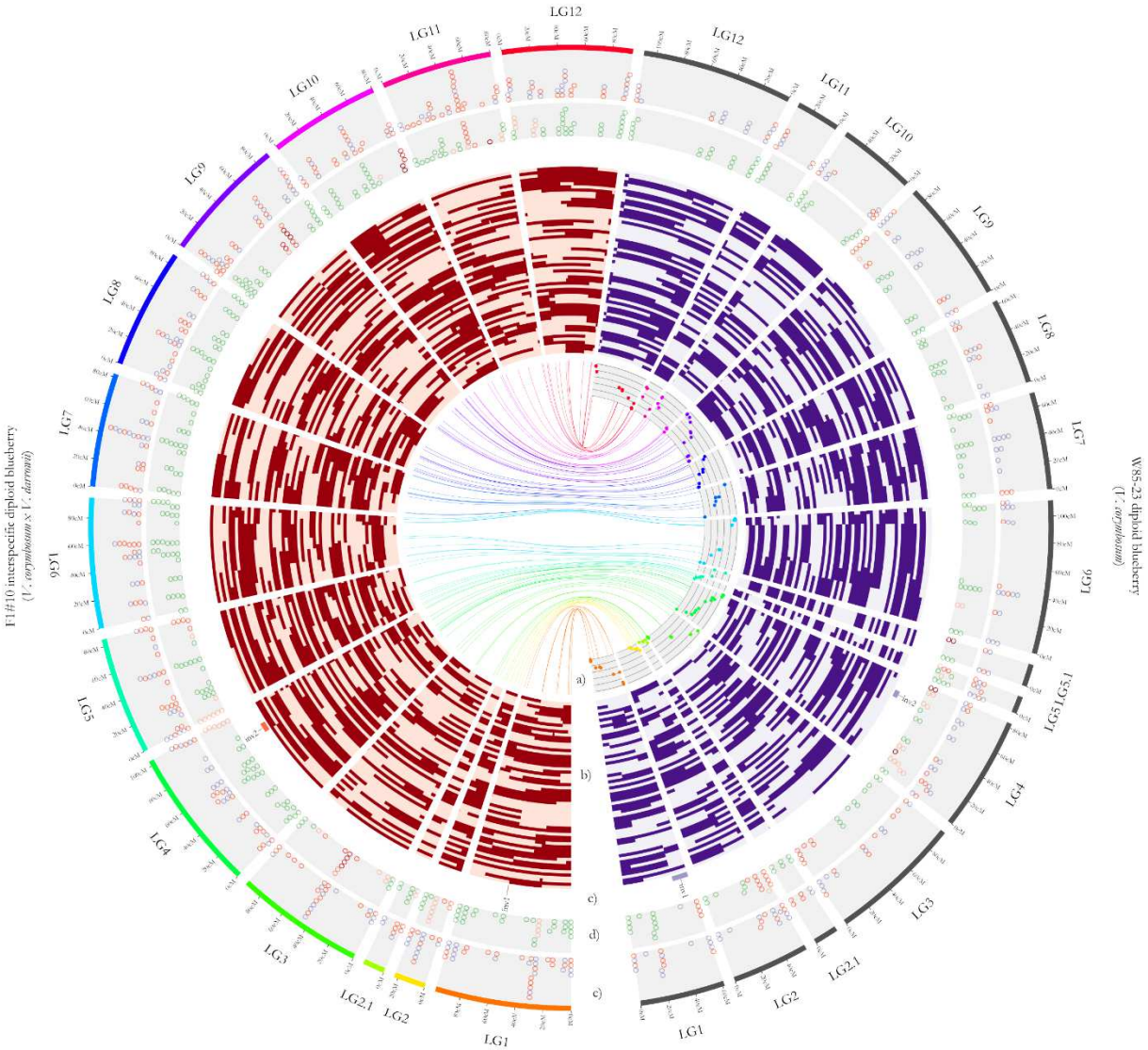


Figure 5.1. Comparison of the LGs of the F_1#10 and W85-23 parental maps based on blueberry and cranberry markers mapped developed in both species. Linkage groups are numbered according to the homologous LGs in the Schlautman et al. (2015a) cranberry map, and links are drawn between common orthologous SSR markers in each of the blueberry parental bin maps. **(a)** Scatterplots of the position of the common markers each of the two maps are shown with intervals between lines representing 20 cM Kosambi map distance. **(b)** Bars show gametic recombination which occurred in both parents for a random subset of 60 progeny. **(c)** Regions of non-collinearity (Inv), and their relative size in cM, observed between the two parental bin maps (Appendix V-7). **(d)** Position of markers in both parental maps colored by the $\chi 2$ p-value from tests for distortion from expected Mendelian segregation rations. Marker colors range from green for markers not showing distortion (i.e. $\chi 2$ $p > 0.1$) to dark red for markers showing highly significant segregation distortion (i.e. $\chi 2$ $p < 0.0001$). **(e)** Position of markers in both parental maps colored by the origin of the marker (i.e. red markers were previously developed in cranberry vs. blue markers were previously developed in blueberry.

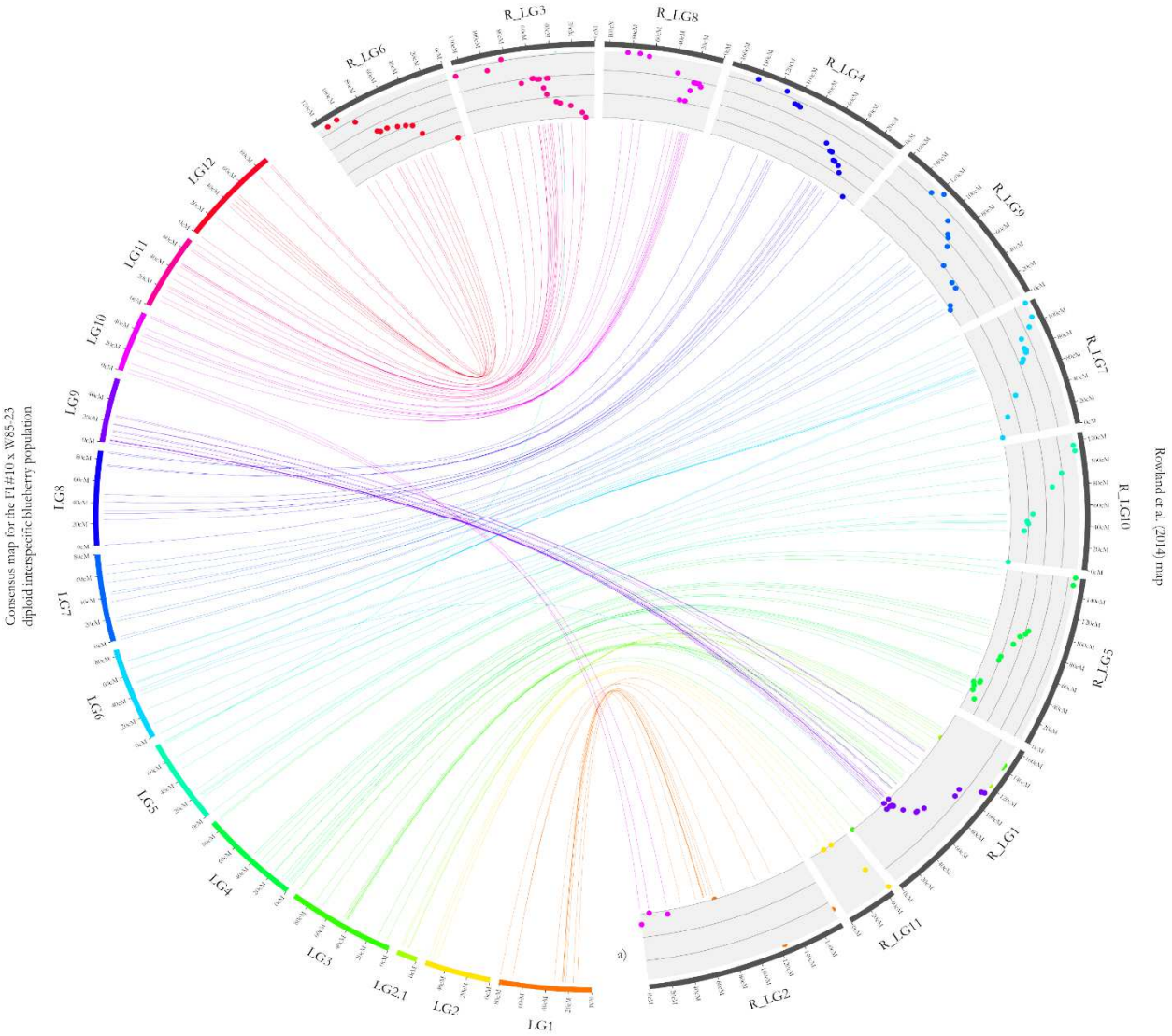


Figure 5.2. Comparison of the LGs of the F1#10 x W85-23 interspecific diploid blueberry consensus map and the former map for the population constructed in Rowland et al. (2014). Linkage groups in the F1#10 x W85-23 interspecific diploid blueberry consensus map are numbered according to the homologous LGs in the Schlautman et al. (2015a) cranberry map while the Rowland et al (2014) LGs (R_LGs) are numbered as they appeared in the publication. Links are drawn between the positions of common orthologous SSR markers in both maps, and **(a)** scatterplots of the position of the common markers in the consensus map vs. Rowland et al (2014) with intervals between lines representing 20 cM Kosambi map distance.

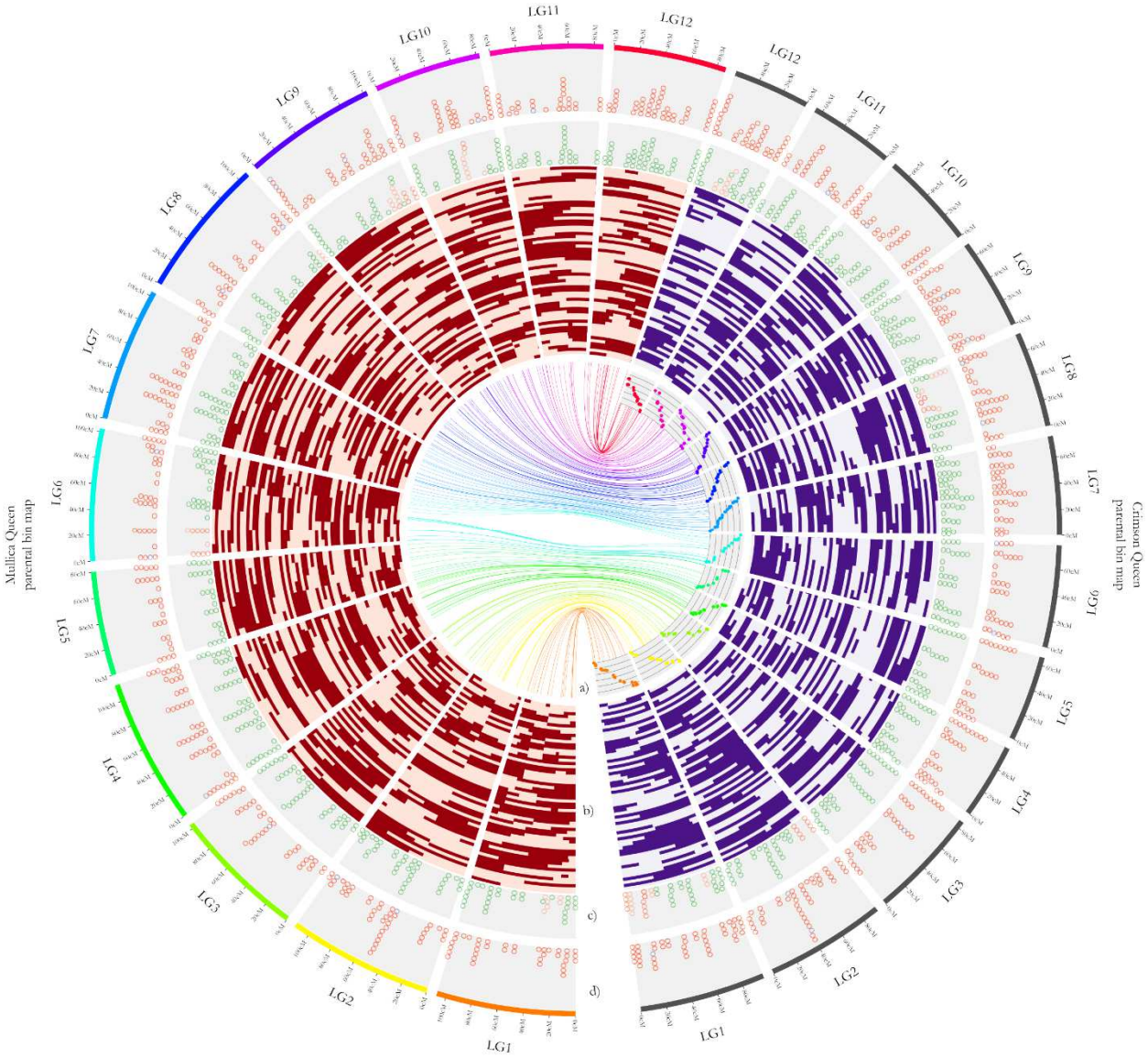


Figure 5.3. Comparison of the LGs of the MQ (left) and CQ (right) parental maps based on blueberry and cranberry markers developed in both species. Linkage groups are numbered according to the homologous LGs in the Schlautman et al. (2015a) cranberry map, and links are drawn between common orthologous SSR markers in each of the blueberry parental bin maps. **(a)** Scatterplots of the position of the common markers each of the two maps are shown with intervals between lines representing 20 cM Kosambi map distance. **(b)** Bars show gametic recombination which occurred in both parents for a random subset of 60 progeny. **(c)** Position of markers in both parental maps colored by the $\chi 2$ p-value from tests for distortion from expected Mendelian segregation rations. Marker colors range from green for markers not showing distortion (i.e. $\chi 2$ $p > 0.1$) to dark red for markers showing highly significant segregation distortion (i.e. $\chi 2$ $p < 0.0001$). **(d)** Position of markers in both parental maps colored by the origin of the marker (i.e. red markers were previously developed in cranberry vs. blue markers were previously developed in blueberry.

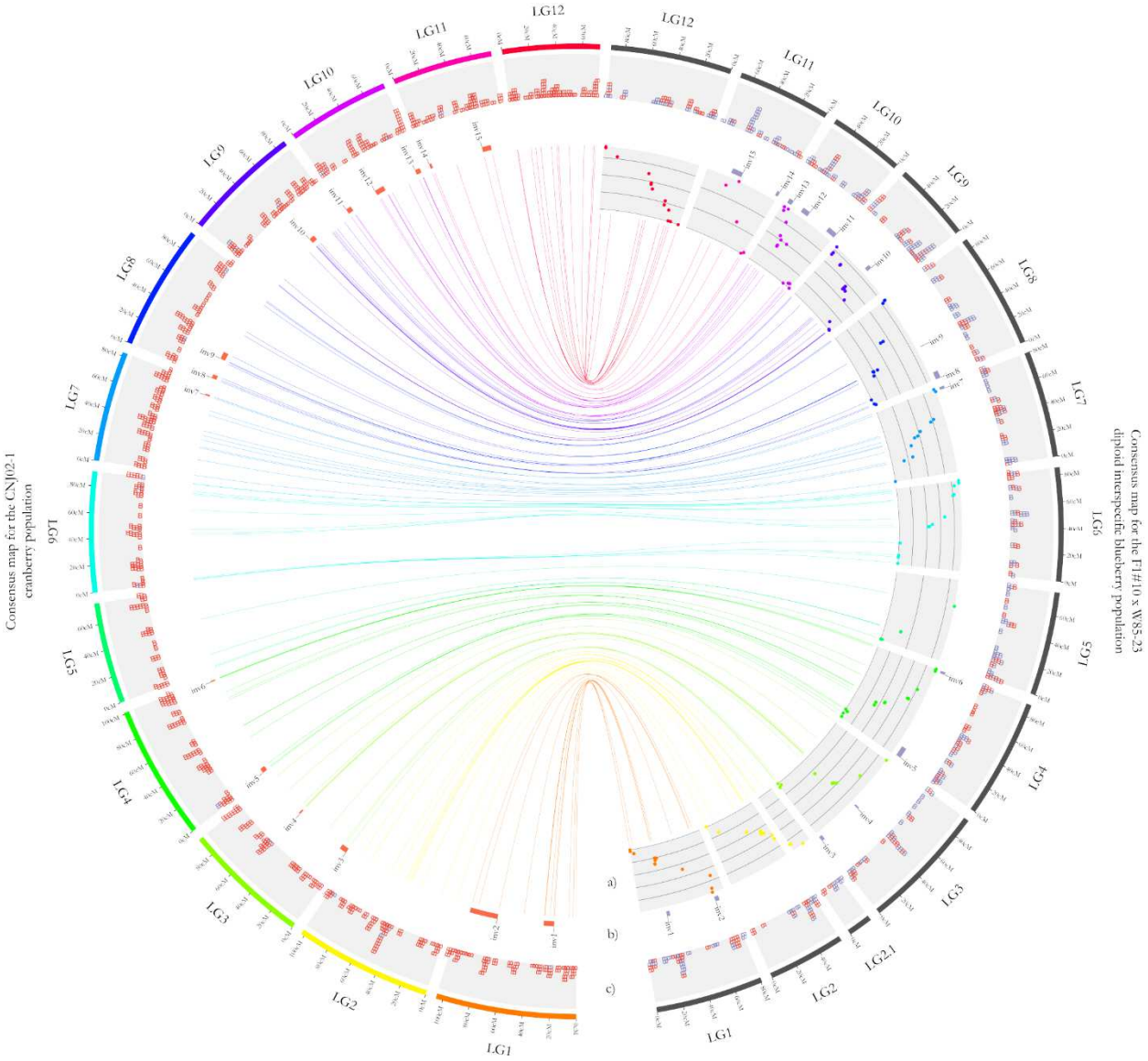


Figure 5.4. Comparison of the LGs of the CNJ02-1 cranberry consensus map and the F1#10 x W85-23 interspecific diploid blueberry consensus map based on blueberry and cranberry markers developed in both species. Linkage groups are numbered according to the homologous LGs in the Schlautman et al. (2015a) cranberry map, and links are drawn between common orthologous SSR markers in each of the blueberry parental bin maps. **(a)** Scatterplots of the position of the common markers each of the two maps are shown with intervals between lines representing 20 cM Kosambi map distance. **(b)** Regions of non-collinearity (Inv), and their relative size in cM, observed between the map (Appendix V-13). **(c)** Position of markers in both parental maps colored by the origin of the marker (i.e. red markers were previously developed in cranberry vs. blue markers were previously developed in blueberry.

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Appendix V-1. Information regarding the SSR primer-pairs designed in cranberry and used in this study including their primer sequences, cross-transferability, publication origin, NCBI ID, and whether they were positioned in linkage maps in this study or the former linkage mapping studies performed in cranberry including Georgi et al. (2013) and Schlautman et al. (2015a).

Locus	NCBI ID	Publication Origin	Forward	Reverse	min	max	Marker Test
ct89348[a,b,c]	KP279100	Schlautman et al. (2015a)	GGCTCAATCTTG TGTAGGTATT	GAGAAAGTGGAA AGATTGTGTG	184	192	polymorphic
ct89379[a,b,c]	KP279101	Schlautman et al. (2015a)	ATGAAGAGCTT GAATGGCTA	ACACTTTACACCA CAACTCGTA	189	255	polymorphic
ct92708[a,b,c]	KP279103	Schlautman et al. (2015a)	CCCTAGATATTT CTGGAACACT	AAGATAGAGAGA GACAAAGGAGG	150	202	polymorphic
ct94504[a,b]	KP279105	Schlautman et al. (2015a)	CTCTAAAGCTCA AGAAAACGTC	AGCTGTGACTATA AGGGATTTG	315	340	polymorphic
ct97791	KP279150	Schlautman et al. (2015a)	GACTTTGTGAG GATAGACCATT	ATGTAAGATGTG GACATAAGGG	316	320	polymorphic
ct110752[a,b,c]	KP279110	Schlautman et al. (2015a)	ACACACACTAAC GAAATCCTTC	CTAGCTCCGACAT TGTTATCTC	118	141	polymorphic
ct129169[a,b]	KP279119	Schlautman et al. (2015a)	TAAATCACCTTC TTCCTCCTC	GGTCCCAAACTTA CTACTCAAA	186	196	polymorphic
ct129202[c]	KP279120	Schlautman et al. (2015a)	CGACCTACACGA GATTGTTTAT	GTTCCAAATCTTC AGTAAGCTG	278	309	polymorphic
ct130570[a,b]	KP279121	Schlautman et al. (2015a)	GTTCACAATCTG CATCTCCT	ACGTAATAGATCA AGAACAGGG	191	197	polymorphic
ct132010	KP279122	Schlautman et al. (2015a)	TACGTGAATTAC CCATATCCAC	CTCACCCTTTACT TCTCTTTGA	173	176	polymorphic
ct134336[a,b]	KP279123	Schlautman et al. (2015a)	GAACACTCCTTC TCTAGCTCTG	CTTTTTAGTCTCC GACAATCTC	191	211	polymorphic
ct140233[a,b,c]	KP279126	Schlautman et al. (2015a)	TTACAGAAGGA AGAGAGAGGAA	ACTGGCTTCTATA GCTCATTTC	218	236	polymorphic
ct145170[a,b,c]	KP279130	Schlautman et al. (2015a)	GAATCCTAGCCT ATTTCCTTTG	GAAGCAAACACC ACTCAATATC	193	226	polymorphic
ct145906[a,b]	KP279132	Schlautman et al. (2015a)	TCTAGACTTGAG AAGCACTTTG	AGTTAGAGGAGG TTTCTGTTGA	264	311	polymorphic
ct147864[a,b]	KP279133	Schlautman et al. (2015a)	CTCTCTTTACCCT CAATTTCTC	GGTCTAATATCAA TCGATGACC	273	279	polymorphic
ct149097	KP279134	Schlautman et al. (2015a)	GAACTGACTGA GTCCACAAAAT	GAACAATAGTAA CCCATGCAG	260	273	polymorphic
ct153008[a,b,c]	KP279136	Schlautman et al. (2015a)	CTTTCCAAGATC TTCATAGGC	CGACAGTATAATA GCATGGAGA	249	272	polymorphic
ct154206[a,b,c]	KP279137	Schlautman et al. (2015a)	GAGAGCGTACG ATACCTAATTC	CTGGTTAGGAAA ACCACTAGAA	205	216	polymorphic
ct154615[a,b]	KP279138	Schlautman et al. (2015a)	AAAATTGAGCAC TGGCTAAG	CTCATACAAACAA TAGGGGG	129	137	polymorphic
ct155339[a,b]	KP279140	Schlautman et al. (2015a)	AAGTTCCTCTGT TACAAGCTCT	ATGACGAACTCTT CCTCCTTAT	219	225	polymorphic
SCF8151[c]	KP278621	Schlautman et al. (2015a)	CGTGCTAGAAG ACGAGGTAT	TTAGGGAACAGT AGAAAGGAAG	314	319	polymorphic
SCF13711[a,b,c]	KP278640	Schlautman et al. (2015a)	GACTTCCTTGGT ACTTGGTG	ACTTTGAGGGTA GGAGTAAACA	342	354	polymorphic
SCF28100[a,b,c]	KP278674	Schlautman et al. (2015a)	TAGAAACTAACA TGGGAGGTGT	GCACGCTGTATT GATAGAAGAT	232	247	polymorphic
SCF84921[c]	KP279042	Schlautman et al. (2015a)	CTTCATCGTCTT ATCAGGTTG	CCAAGTGAGTCT GTGATTGAT	376	397	polymorphic
SCF75572[a,b,c]	KP278761	Schlautman et al. (2015a)	GACAAGTGGTT GGGGATAC	ACCCTCATCATCA CTCCTT	238	240	polymorphic

SCF2288[a,b]	KP278600	Schlautman et al. (2015a)	CAATAGTAGTTT CGAGCTTTCC	GTTTCCAATTCAA GCCTCTA	200	204	polymorphic
SCF134365	KP279079	Schlautman et al. (2015a)	GCCTTGTTATGT TACCTGTGA	ACAACTATCTGGA AAAGGGTT	221	234	polymorphic
SCF30816[a,b,c]	KP278685	Schlautman et al. (2015a)	GTCCAAAATAGC ATCGAAAG	CGCATTACTTCTT CACTATACG	201	210	polymorphic
SCF51810[a,b,c]	KP278725	Schlautman et al. (2015a)	TATTACTCTGTT GCTGCTGTTG	ACTAAACCCTAAT GTCCCTTCT	193	205	polymorphic
SCF30734[a,b]	KP278684	Schlautman et al. (2015a)	GTTGAAAACCCA ACTGTGAG	AGATCCAGTCATG GTACTTTTG	171	176	polymorphic
SCF11186[a,b,c]	KP278636	Schlautman et al. (2015a)	AGAAAGGCTAA AAGGGTATCTC	GCTCTCAACAACT CGAAAGTA	266	278	polymorphic
SCF65004[c]	KP279030	Schlautman et al. (2015a)	GAATCAATCCAG TCCATAGG	CTTACACCACTCT TCCCAAC	166	264	polymorphic
SCF30000[c]	KP278682	Schlautman et al. (2015a)	GACTCTTCAACT TCCACGTTA	GAAATCTTAATCT TGCAGCC	149	161	polymorphic
SCF186078	KP279095	Schlautman et al. (2015a)	TAGAAAGCAGT AGAGGAGGAAA	CTTTTCGGATCTG TTTGGT	149	152	polymorphic
SCF24087[a,b,c]	KP278663	Schlautman et al. (2015a)	GTCCCTTTCTCG TGTCTTTAT	GAGTAGTGACGA TGCAACTAGA	193	200	polymorphic
SCF56032[a,b]	KP278731	Schlautman et al. (2015a)	AGAAATGGCGC TCTGTATC	GAACAGTCTCATC TTCACGAC	200	210	polymorphic
SCF113558[a,b,c]	KP278832	Schlautman et al. (2015a)	GAGCTTGATCTG GGTATCTTT	CAAAATCAGAATC GACTGC	185	210	polymorphic
SCF26049[a,b]	KP278668	Schlautman et al. (2015a)	GTTCAGGTCTGT TGTAAGGAAG	TTTCTTGTAGGAC GAAGTGG	168	174	polymorphic
SCF1527[c]	KP278598	Schlautman et al. (2015a)	TCAAACGGTGAC ATCTATACAC	GTATCTACGCCTC TTACTCTCG	256	303	polymorphic
SCF7357[a,b]	KP278618	Schlautman et al. (2015a)	CAGCTTAATCAT CAGTTCCAG	AGTGAGCATCGA CTATTTACCT	300	319	polymorphic
SCF12818	KP278975	Schlautman et al. (2015a)	GTGAGGGAGAG TGTTAGATAGC	ACAAGAGAAAGA ACGACAAGAC	243	246	polymorphic
SCF30010[a,b,c]	KP278683	Schlautman et al. (2015a)	CTCAAATCAACG ATCAAGAC	GAAAGAGACAAC AAAACCCT	305	315	polymorphic
SCF33205	KP279004	Schlautman et al. (2015a)	ATTCTGACTGTT TCATTGCC	AAATGTATTGGT GGGGAAGT	290	314	polymorphic
SCF36716[c]	KP279010	Schlautman et al. (2015a)	CTAGGCAATGAT GACAAAGC	CCCAATAGTTACC ACTAAGCAT	297	330	polymorphic
SCF39691	KP279013	Schlautman et al. (2015a)	TAAACCATAGTC CTCTCCTCC	GTCCATAACTCCA AATAAGAGC	191	202	polymorphic
SCF42256[c]	KP279017	Schlautman et al. (2015a)	ATACTGCTCAAC TGATTTAGGG	CGGAGGAAAGTC TGCTATATT	217	227	polymorphic
SCF55511[c]	KP278729	Schlautman et al. (2015a)	GAAGTGAAAAT CTGAACCTCTC	ACTCTCGAATCTG TCTTCTTGT	192	221	polymorphic
SCF55619	KP279026	Schlautman et al. (2015a)	CAAAGAATCAGC AGGAGGT	GATGTCTAAGGT ACAAGGAAGC	208	229	polymorphic
SCF61972[c]	KP279027	Schlautman et al. (2015a)	CAGATGAATTTA GACGAGTGG	TGCATAGCTCAAA TATCCCT	295	318	polymorphic
SCF64185[a,b]	KP278745	Schlautman et al. (2015a)	CACCTCATTTGG TTCATTCT	CAGATACTAAAG GTTGCCGTA	236	238	polymorphic
SCF69698[a,b,c]	KP278751	Schlautman et al. (2015a)	GAGGAGATAAA GGTTTGTTGAG	CTTTGAGACTTTG AGTGAGACA	304	322	polymorphic
SCF76055	KP279035	Schlautman et al. (2015a)	GATCGAAATGA GGATTTGTG	CTCTTCCACTGTC AACTTTTCT	259	272	polymorphic
SCF77055[c]	KP279036	Schlautman et al. (2015a)	GAACTGGTAAG GTTTGGAACTA	CTTGGAAAGGAT TCATACTAGC	206	338	polymorphic

SCF81732[a,b,c]	KP278772	Schlautman et al. (2015a)	CGAGTATGTGG AGAGGCTTAC	GTGTATAAAATG GGCATCACAC	213	272	polymorphic
SCF88396[a,b,c]	KP278784	Schlautman et al. (2015a)	ATAGAGGTTAAT TGGTCCTCG	GACGAAGAACGA CAGGTAGAT	294	317	polymorphic
SCF88902[a,b]	KP278785	Schlautman et al. (2015a)	GTGTTGTAGGA TGAACCGAT	GATTTCCAGCATT TGATCTC	142	330	polymorphic
SCF89447[a,b]	KP278787	Schlautman et al. (2015a)	TAAATAAGACCT TCTGCTGACC	AATATGCTCACCA CCAGTAAAG	177	185	polymorphic
SCF89726	KP278789	Schlautman et al. (2015a)	TTGCTGACTTGC TAACCCT	ATTTACCGAACGC TACGAGT	234	344	polymorphic
SCF91821[a,b]	KP278792	Schlautman et al. (2015a)	TTCTGTGTCTGA TTCCATCTC	ACTAGCCCAACAA CTTAGACTG	293	295	polymorphic
SCF92986[c]	KP279048	Schlautman et al. (2015a)	AACTAACCCGGA CACCTAGTAT	CGAGGGAGACAA TATCAAAGTA	196	201	polymorphic
SCF95767[a,b]	KP278796	Schlautman et al. (2015a)	TGAGGAGAGGA GTATCCATAAG	CCTACAAGTCTCG CAATTCTA	294	301	polymorphic
SCF95851[c]	KP278798	Schlautman et al. (2015a)	GACCTTGGAATT TGATGATG	TGTAGATGGATG TTGTTACCTG	177	192	polymorphic
SCF95879	KP279049	Schlautman et al. (2015a)	TTTTACATGAAG TGGTAGAGGG	CCAGTTGTATAGA TTTTGCTGG	253	254	polymorphic
SCF99113[c]	KP279051	Schlautman et al. (2015a)	CATGACTTGCTT GTATGGTG	CACAACTCGCATA ACTCTACTC	246	252	polymorphic
SCF99997	KP279052	Schlautman et al. (2015a)	ATAGGTCATCTC CTTCTTGTTG	ACTACTACCGTTG ATTGCCTT	148	156	polymorphic
SCF101064[a,b]	KP278805	Schlautman et al. (2015a)	CATCAGACAGAA AGCAGTTAAG	CCCCAAGTATATT AGCAAACAC	263	290	polymorphic
SCF101363[c]	KP279053	Schlautman et al. (2015a)	CGATCTGTATCT AGTCGTGATT	GAGATGTACTATT GGAACTTGG	236	272	polymorphic
SCF108454[a,b,c]	KP278819	Schlautman et al. (2015a)	CTAACTAAATGA AGTGTTCCCCT	ATGTCACGCTCTG AAGTTTG	194	206	polymorphic
SCF109660[a,b]	KP278821	Schlautman et al. (2015a)	CCCCAAACTGTC GTATAAAA	TAGAGTACAGGA AAAGCCCTAA	281	294	polymorphic
SCF110757[b,c]	KP278825	Schlautman et al. (2015a)	TCATATCAACCT AACAATCGG	CACAAACAAGGA AATTAAGACC	311	346	polymorphic
SCF110888[a,b,c]	KP278826	Schlautman et al. (2015a)	CTCCTACCCAAA TTCACTTGT	CCAAAACTAAACC ATTTCTCAC	215	239	polymorphic
SCF111145[a,b]	KP278827	Schlautman et al. (2015a)	TTAGTCTGGCTG GTTTTAGTTT	TTGTACCTATTGT TGGATTGTG	336	340	polymorphic
SCF112540[a,b,c]	KP278830	Schlautman et al. (2015a)	CAGTAGTGGTAT TTCACAATCG	TTTAATGCTTTTG GAAGAGG	249	280	polymorphic
SCF116864[a,b]	KP278836	Schlautman et al. (2015a)	TGCCCCTTGATT CTAATTTT	ATGCCTCAGATTG ATTTACCT	138	143	polymorphic
SCF118999[a,b]	KP278842	Schlautman et al. (2015a)	CTAAACTCCAAA ATGCCTAAAC	AAAGTGGATGGG TTCTAAAAG	264	277	polymorphic
SCF132006[c]	KP279075	Schlautman et al. (2015a)	ATTGAGGTCACT AGGAGGTGTA	GAGGAGAGTGTT TATGTTCATGT	281	286	polymorphic
SCF136207[a,b,c]	KP278866	Schlautman et al. (2015a)	GTCTCTGTAGTC GGTGCTTT	GATTTCGATTCCT TGACACT	167	181	polymorphic
SCF147295[a,b,c]	KP278889	Schlautman et al. (2015a)	ACTGAGGTAAA AGAGGAGTACG	CCATCAAGGTCTC AATCTGT	275	286	polymorphic
SCF159195[a,b,c]	KP278908	Schlautman et al. (2015a)	AACAAAGACCCT AATCAGACAC	ACAATCAAAACAC CGTCAG	321	330	polymorphic
SCF167793[a,b,c]	KP278916	Schlautman et al. (2015a)	GTGAAACGACA AGACCAAAT	AGGACATCCACCT TCAAAT	174	188	polymorphic
SCF173212[a,b]	KP278924	Schlautman et al. (2015a)	TGTAGTGGGAG ATGCTGATAC	AATTGGCGAACT AGAAAGTG	209	223	polymorphic

SCF174394[a,b]	KP278925	Schlautman et al. (2015a)	GGTGGATGGAA TGCTAAATA	CTTTATTGGTAGT GGATTGGAC	251	255	polymorphic
SCF192219[a,b]	KP278941	Schlautman et al. (2015a)	GAATTTTGTCGT TCCAGAGA	AAAAGAAGAAGA GGAATGGC	132	146	polymorphic
SCF192715[a,b]	KP278942	Schlautman et al. (2015a)	CTCTGCCTTGTT CGTCTCT	AACCAATCGAAG GTGACAA	179	193	polymorphic
SCF195276	KP279096	Schlautman et al. (2015a)	GTACACTCAAAA GGGAAGAAAC	TGGCGTATGAGA AGAAGATT	179	243	polymorphic
SCF197012	KP279097	Schlautman et al. (2015a)	GTACGATACAAC ATGGACACA	ATATAAACAGGG ATGCGACT	184	201	polymorphic
SCF208883[a,b]	KP278952	Schlautman et al. (2015a)	GAGGAGTGAAG AGCCAGTAA	GACATTTCAAGTC CCACACT	165	225	polymorphic
SCF804[a,b,c]	KP278592	Schlautman et al. (2015a)	CAGTCAACAGA GAATACACCAC	TTCCCTATGAAAA TCCACAC	222	238	polymorphic
SCF965[a,b,c]	KP278594	Schlautman et al. (2015a)	GTAAACTAACAA GCAACGATCC	GATTTAGCTGAT GCAGAGTCAT	253	258	polymorphic
SCF1524[c]	KP278957	Schlautman et al. (2015a)	TAACATACAGTC CTCGACAAGA	GATCTAGTTGTTC TTCCGCAT	257	280	polymorphic
SCF3427[a,b,c]	KP278606	Schlautman et al. (2015a)	GCAAGACATCAT CACAAACA	CTTATCCCAGTCC TTCAACTTA	376	390	polymorphic
SCF3932[a,b,c]	KP278610	Schlautman et al. (2015a)	CAGAGTTTCAGT GGAGCATT	CTCAGCTTCTGTG TTTTGTGT	323	340	polymorphic
SCF4305[a,b,c]	KP278611	Schlautman et al. (2015a)	AATGAGTGGTT ATGTAGGGAGA	AGATTGGTGAGA TATGAGGAAG	181	206	polymorphic
SCF7155[a,b]	KP278617	Schlautman et al. (2015a)	GGGATCTATGA GTTGTGGACTA	CCACGGAATAGTT GTAAGTTGT	159	165	polymorphic
SCF8223[a,b,c]	KP278622	Schlautman et al. (2015a)	CATTTAGCATCC ATCCATTC	GACTGTGGGTTA TTCCTTGTAT	331	353	polymorphic
SCF9045[c]	KP278971	Schlautman et al. (2015a)	GCAAATGTCACT GTTAGGATAC	GAAAGGAAGAGA AGTTAAGCAG	323	346	polymorphic
SCF9872[a,b]	KP278629	Schlautman et al. (2015a)	ATGGGAGTGCA TGAATAAAC	GGAGAATCGTAT TTGTGAAGAG	242	262	polymorphic
SCF10459[a,b,c]	KP278631	Schlautman et al. (2015a)	TCTTTGTTTCTG AGGTTGCT	ATTTGTAGGTACT ATGGAAGCC	253	335	polymorphic
SCF12084	KP278974	Schlautman et al. (2015a)	CTCTTGTTGGAC GGATCTATT	CCTAACATTTCTC CCACTCA	330	332	polymorphic
SCF13231[c]	KP278977	Schlautman et al. (2015a)	GAAACAAAGAG GAGAAGACAAC	GTGAAAGGTAAG AGATGGGTAG	310	321	polymorphic
SCF13393	KP278978	Schlautman et al. (2015a)	ATATACACAATC GCACGAGAC	TCAGCTTACGATC TCACAAA	244	273	polymorphic
SCF14358[c]	KP278982	Schlautman et al. (2015a)	CCACTAAAACCC TATACTTGGA	GTCACTTTTCTAT TGCTGGTG	364	398	polymorphic
SCF14877	KP278985	Schlautman et al. (2015a)	CCCATGATCCTA TGTATGCT	AGCTCTGATACCA AACTGTCAT	306	339	polymorphic
SCF15845[a,b]	KP278645	Schlautman et al. (2015a)	AGGCTAATGAA GAAGAAGTCTG	GACCAAGACAAG ATGAACAAG	348	364	polymorphic
SCF16186	KP278989	Schlautman et al. (2015a)	CTTGTATCAACT TCCATCGTCT	CCAAAACCTGAGA AACTTAGAG	246	268	polymorphic
SCF16359[a,b,c]	KP278647	Schlautman et al. (2015a)	GAAGTGCTTTTC TTTCGTAGAG	AGACAGATTAAG ATCCACCTTG	319	323	polymorphic
SCF17979[a,b,c]	KP278649	Schlautman et al. (2015a)	ATATCAGAACAA GGAGATGGTG	GATACCGAATGA ACCAAGAA	204	216	polymorphic
SCF18363[a,b,c]	KP278650	Schlautman et al. (2015a)	CAAAGACCGCTA GGTTTACA	ACTGCTCACTAGA CAAGATCG	163	166	polymorphic
SCF19055[c]	KP278991	Schlautman et al. (2015a)	AACTCTCACCAA AGGTATTGTC	GTGACGCTAGAT GAGGACTTA	235	244	polymorphic
SCF22339[c]	KP278993	Schlautman	CCTCAATCTTAT GGATCGAA	TTGTAGAAGAAC CTGTAATGGG	220	237	polymorphic

		et al. (2015a)					
SCF27811[a,b]	KP278672	Schlautman et al. (2015a)	ATGTGACTAGCA TGGGACTTA	TATTTACCTGGAT AGGAGAAGG	156	240	polymorphic
SCF28279[a,b,c]	KP278675	Schlautman et al. (2015a)	GATACTTTACCT CCTCCTCAAG	TTGTCCTCTATCT CTAACTCCC	220	304	polymorphic
SCF29529[c]	KP278997	Schlautman et al. (2015a)	AACAGGGAGTT TTCCTACTCTT	GTATGATGGGAA TGGGATAGT	295	344	polymorphic
SCF30747	KP279001	Schlautman et al. (2015a)	AAGTCAACCAAT AGGCATAGAC	TGTAGTAGCAAG CAAGCTGAT	314	334	polymorphic
SCF32389	KP279002	Schlautman et al. (2015a)	CACTATATCCTA CCCCAAAGAG	TTTGCTGTGACTT GAAAGG	263	308	polymorphic
SCF32727[a,b,c]	KP278689	Schlautman et al. (2015a)	ATGTAACGGTCT CCACTTTCT	TAGTATCTTCGTG GTCAGAGGT	142	195	polymorphic
SCF33185[a,b,c]	KP278691	Schlautman et al. (2015a)	AGCACACTACAG ACAGGGTAAT	GTTTTGGCTCTG GCTAAGTAT	194	218	polymorphic
SCF33471	KP278692	Schlautman et al. (2015a)	TTTATTGCACAC GAGAACAG	ATATTTTGTCCAC GCTCACT	280	294	polymorphic
SCF34071[a,b,c]	KP278694	Schlautman et al. (2015a)	CGTGTGCAGATT TACTTCAG	AATTCATAGATCC CCATGAC	242	274	polymorphic
SCF34584[a,b,c]	KP278696	Schlautman et al. (2015a)	GTCTGTTTGGAA GAAGAAGGT	CTGTTCGTCAATC CCTAGC	190	205	polymorphic
SCF34663[c]	KP279007	Schlautman et al. (2015a)	GTTTAAGTTCTA GCATAGCCGA	GTACACAAATACA GAGTGTGGC	251	295	polymorphic
SCF36745[a,b,c]	KP278698	Schlautman et al. (2015a)	TCCTCATTAAGT ATTGGACAGG	CTGGATTCTTGTT CTTAGCTTC	301	311	polymorphic
SCF37628[a,b,c]	KP278700	Schlautman et al. (2015a)	ACCAGCTCAGAT AACAATGC	GAGTAGGATACC TCCACACCTA	255	324	polymorphic
SCF38430[a,b]	KP278702	Schlautman et al. (2015a)	CAATAGTTAGGA AGTTGGAACC	CTAAGAACCAAAC AGAGCCTTA	154	298	polymorphic
SCF39242[a,b]	KP278705	Schlautman et al. (2015a)	ACTCCTGAAGAA GAAGAACAGA	AATGAATGCAGA CCACAGAT	242	248	polymorphic
SCF40225	KP279014	Schlautman et al. (2015a)	GCTTGACTGGAT TAGAACAACT	CTGGGTATCAACA TCAACAGTA	154	389	polymorphic
SCF41759[c]	KP279016	Schlautman et al. (2015a)	TTGCCATCTTCT TGTTCTTC	ACAACATGCTAAT GTGGGTACT	319	328	polymorphic
SCF43220[a,b]	KP278712	Schlautman et al. (2015a)	CTTGTCGAGCAT CCTATATTTC	AAAAGTCATGGG AAGGTGTT	131	155	polymorphic
SCF46751[a,b,c]	KP278715	Schlautman et al. (2015a)	ACCAGATGAAG AAGAAGAAGC	GCCTCTCATTACC ATTACAAAC	313	333	polymorphic
SCF46739[a,b]	KP278716	Schlautman et al. (2015a)	ATGTTAGGTGAT GCTGTTGTC	CAGGTGCTTATTT TCGTTTC	271	294	polymorphic
SCF47689	KP279020	Schlautman et al. (2015a)	TGTAGATGCCGT CAAAGAAT	ACTATAACTCCAA GCGCAGTAT	296	336	polymorphic
SCF48414[a,b,c]	KP278721	Schlautman et al. (2015a)	GTAGGGAAACA AGAATTGGAC	ACTGTGAGATTG GTGTGATATG	294	303	polymorphic
SCF51607[c]	KP279023	Schlautman et al. (2015a)	TTATGTAACTGA CGCTGATAGG	GTAGATTTGCGA TGGTGTATG	160	182	polymorphic
SCF53058	KP279024	Schlautman et al. (2015a)	TACCACAGTCTC CTTAACAAAG	CATACTCTATAAT CCACTTCCG	218	226	polymorphic
SCF54555	KP279025	Schlautman et al. (2015a)	TTACCAAAGCAC CCATTAAC	ACGACACATATCT CCAAAGTG	152	159	polymorphic
SCF58861[a,b,c]	KP278738	Schlautman et al. (2015a)	GTTGACTAAAAG GCATTGGA	GACTACTATTTTC TGCACAGGG	133	139	polymorphic
SCF59035[a,b,c]	KP278739	Schlautman et al. (2015a)	AGATTTTGAACG ATGTCTGC	GATCTATCGCTTA TCCAGTACG	288	291	polymorphic
SCF60761[a,b,c]	KP278742	Schlautman et al. (2015a)	ACTTAAACATCG GTCCATAGAG	AGAGTCGTGTCC TTTCTTTTC	257	263	polymorphic

SCF64632[a,b]	KP278746	Schlautman et al. (2015a)	ACCTCCTAAAAC ACAACCCTA	CTGAGTAATCTTC GATGTGAGA	137	175	polymorphic
SCF65897[c]	KP279031	Schlautman et al. (2015a)	CTTATTTTGCTG AACCTTGG	CTCTAACTATTCT TGCAGCCTC	333	338	polymorphic
SCF65999[a,b,c]	KP278748	Schlautman et al. (2015a)	AGGTAGCATTA GACACGAGATT	GAGGTTTTACAT GACCATTACC	296	298	polymorphic
SCF68870[a,b,c]	KP278750	Schlautman et al. (2015a)	GTGAATTGTTGC AGAGTACCTA	TGAGTTGAGTTC ATATAGCTGG	168	206	polymorphic
SCF72379[a,b]	KP278757	Schlautman et al. (2015a)	TAAGGAGATCG ACTAGGGTTT	CATCAAGATTCAA GACCACAC	189	236	polymorphic
SCF73288[a,b]	KP278758	Schlautman et al. (2015a)	CAGAGGAACAG CAGACTACAT	CCTAGTACGTCAT TGGACATTA	320	334	polymorphic
SCF74458[a,b]	KP278759	Schlautman et al. (2015a)	GCAGGAAGCTA TGATTAAGGTA	TTGAATAGTGTCA GTGGAGAAG	232	264	polymorphic
SCF76310[a,b]	KP278762	Schlautman et al. (2015a)	CTGTGTAGAACT GCATCAAAAC	TCCTAGAGACCAA CCCAATAC	208	277	polymorphic
SCF77645[b,c]		Schlautman et al. (2015a)	GGTTCTTTCTTC TGGGTTTT	TCAGACAATGAG CTACTACCCT	296	312	polymorphic
SCF78184[b,c]	KP278766	Schlautman et al. (2015a)	CACATTTAAGAG CTACCACCTT	GGTGAAAGAGAA GACTGGATT	292	320	polymorphic
SCF80703[b]	KP278770	Schlautman et al. (2015a)	GGTCTTTCTCCT AATCTCCAA	GGAACCCCTAAAT AACATACAG	155	156	polymorphic
SCF83036[a,b,c]	KP278776	Schlautman et al. (2015a)	CAACAGTCCTCA AAATCACTC	GTGAACAGAAGT AGAGATCGG	290	309	polymorphic
SCF84796[c]	KP279041	Schlautman et al. (2015a)	CTACTCTTAGGG CATCTCCA	CAACACTACTGAC CTTCACAAT	302	306	polymorphic
SCF85946[a,b,c]	KP278781	Schlautman et al. (2015a)	TGTGAACAGAAC CTACCACTAA	AAAGAGCCCCGT AGATAGAT	318	347	polymorphic
SCF95754[a,b,c]	KP278797	Schlautman et al. (2015a)	CAGTGAGACTTC AGCTTGATAC	ATTGGTGACTTA GGAGTGAGAC	333	360	polymorphic
SCF97378[a,b]	KP278801	Schlautman et al. (2015a)	GTAGAGATCGTT GTCGTCATTT	AACATCGTGGTG TATTGGAT	200	298	polymorphic
SCF100820[a,b]	KP278804	Schlautman et al. (2015a)	GTAATTCCACTT AACCCACTCA	GTTGAAGATAAA CCACCTTCC	349	365	polymorphic
SCF102190[c]	KP279054	Schlautman et al. (2015a)	GAGGAAAGGGT GAGAGTTTT	GTTTGACGAAAA GGAGACTG	211	221	polymorphic
SCF105925[a,b,c]	KP278812	Schlautman et al. (2015a)	CCGTGTCAAAAG ATCAAGC	AGTTTGTGCCGTC GTACTC	154	166	polymorphic
SCF107715[a,b,c]	KP278816	Schlautman et al. (2015a)	AAAGCGAGTCA GAAACATAGAC	CCTATCAGTTCCT TTCCTATTG	242	295	polymorphic
SCF109269[a,b,c]	KP278820	Schlautman et al. (2015a)	CACTCCTTCCTT ATAGATCAGC	AAGTAGAAGAGC AGCACAAGAG	238	338	polymorphic
SCF110168[a,b,c]	KP278822	Schlautman et al. (2015a)	AAAGGACTAGA GGGAAGTACAA C	CTTATTATCCAGA AACTCGTGC	314	318	polymorphic
SCF110507[a,b,c]	KP278824	Schlautman et al. (2015a)	GTAGCTGAGGT GGAGGATAAC	GAGCTGGTGCTG AAATTAAC	233	249	polymorphic
SCF119984	KP279065	Schlautman et al. (2015a)	TTAGAATTGCGT TCCATACAG	GAAAATCAGTTC GATTCAGGT	323	337	polymorphic
SCF120352[a,b,c]	KP278843	Schlautman et al. (2015a)	AGTTCTATGACC CCTAACTGAA	GAAAGGAAAGAA GCACTATCAC	262	278	polymorphic
SCF122552	KP279067	Schlautman et al. (2015a)	TATATCGAGGTC ATTGCGA	GAGTTGTCGTTA AGGTTTTGA	237	248	polymorphic
SCF124927[a,b,c]	KP278850	Schlautman et al. (2015a)	CGAGTGTCATTA GCAACAGA	TATCACTTTAGAT CGAGCAGAC	236	257	polymorphic
SCF125667[a,b,c]	KP278852	Schlautman et al. (2015a)	AAGGGAGACAT TACACAACAA	TTCGAGATTGACC AAGTATGT	114	165	polymorphic

SCF125768[c]	KP279069	Schlautman et al. (2015a)	CTCACTTCTCAT ACAACATTGG	CACAACAGAACCA TCAGTACAT	134	156	polymorphic
SCF128307[a,b,c]	KP278857	Schlautman et al. (2015a)	ACTCAGAAGTTG AAGCACAAA	GTATCAAGTACAC CAACACCAG	227	268	polymorphic
SCF132532[a,b,c]	KP278861	Schlautman et al. (2015a)	GACTGGATTTTC ACGAATCTAC	CTTCATCTTCCTT GACACTTCT	274	291	polymorphic
SCF138014[a,b]	KP278870	Schlautman et al. (2015a)	TTATTCTCTTCG CTTGGGTA	TCAGATCATGGAT TACTGGTT	244	254	polymorphic
SCF138394[a,b]	KP278871	Schlautman et al. (2015a)	AAGCCCAGAAG AAATAACCTA	TGCAAATGTTAG GAACTGTGT	216	255	polymorphic
SCF138607[a,b]	KP278872	Schlautman et al. (2015a)	CATATAGAATAC TGGACGGACA	TTCTGCCATCTCC TTTCTC	175	204	polymorphic
SCF140628[a,b,c]	KP278876	Schlautman et al. (2015a)	GTGAAATTGGTC AGGTTGAT	GTCGTCATCATCA TCTCCTC	143	160	polymorphic
SCF144748[a,b,c]	KP278884	Schlautman et al. (2015a)	ATTTCCAATCCT TTCCTCTC	CTCTGACACCTTC TGACACATA	142	173	polymorphic
SCF145689[a,b,c]	KP278885	Schlautman et al. (2015a)	GGCATAAGAGT AGACCATGAAC	GTACTATAAAATG CTTCCAGCG	255	261	polymorphic
SCF150395	KP279088	Schlautman et al. (2015a)	CTCTGGTTCATC CCTCTGT	CAGACCCTGTCGT TACAAAT	167	193	polymorphic
SCF150919[a,b]	KP278896	Schlautman et al. (2015a)	TTGTTAGCACTT AGCATAACCC	GCTTCATCTCCAC CAATACAT	203	292	polymorphic
SCF153636[a,b]	KP278898	Schlautman et al. (2015a)	GGTATCAAAGCA AGGTTGAG	CTCGTTAGAAGTA TGTTGGTGA	205	304	polymorphic
SCF203038[c]	KP279098	Schlautman et al. (2015a)	CACTTCTGTACC CTCTTTTACC	GTCTCATACCTGA ATTTTCTGC	168	191	polymorphic
416275_K63	KP279184	Schlautman et al. (2015a)	GGTTATGATGG TGGGAAAG	TGCACCTCCTCTC TCTCTAA	148	184	polymorphic
418931_1_K63[a,b,c]	KP279191	Schlautman et al. (2015a)	ATTAGCTCAGTT CCCAGTAACA	CTTCTTTCTCTTTC TCCTTCCT	155	161	polymorphic
260167_K70[b,c]		Schlautman et al. (2015a)	TCAACATCTTTG GGACTTCT	GCTTGCCTAATAT ACTTCCAAC	274	321	polymorphic
1trimcontig440337[a,b,c]	KP279250	Schlautman et al. (2015a)	CTTGGAGTTAGC CTTTTAGTCA	CTGGAAGAGTGA AGATGGAATA	156	211	polymorphic
239628_K63[c]	KP279257	Schlautman et al. (2015a)	CTCTTTCTTGGA TGTTGCTACT	CGAAACTCTCTAA CTCTGGTGT	237	253	polymorphic
408825_K63[a,b,c]	KP279176	Schlautman et al. (2015a)	GTTCTCCTCTTT CATCATTCAG	AGTCTTGAACTCC TTGTACTCG	252	268	polymorphic
300409_K63[b,c]	KP279168	Schlautman et al. (2015a)	GGGGAATAGCA GGTAGTGAT	TATTTATCCACCC ACTTCACAG	194	196	polymorphic
305731_K63[a,b,c]	KP279169	Schlautman et al. (2015a)	GATTTCTTCGTG TTTCTCTCTC	TGCCTTTCTCTAC TCTCTCTTC	365	366	polymorphic
411145_K63[a,b]	KP279179	Schlautman et al. (2015a)	GGTAGGAATTA AAGTGAAGACG	ACTAGGGAGCGA GAGAGAGTA	359	378	polymorphic
1trimcontig179737[a,b,c]	KP279225	Schlautman et al. (2015a)	CCTCCAACTTCT TCATCTTCT	ACTGGTAACTCCT CAGAAACAG	196	214	polymorphic
346445_K63[c]	KP279262	Schlautman et al. (2015a)	TAAGGGAAACCT GTAAAGACG	GATAGCAAAGTG GACGAGTATT	Inf	-Inf	polymorphic
172672_K70[a,b,c]	KP279201	Schlautman et al. (2015a)	GATAGTTGTATG CGCTGTAAGA	GTTACCCGAATGA ACAGGT	345	381	polymorphic
1trimcontig240704	KP279281	Schlautman et al. (2015a)	GAGAGAGGGAA GAGTAACAGG	AAGATGGTCTATT GAGTATGGC	Inf	-Inf	polymorphic
418138_K63[c]	KP279265	Schlautman et al. (2015a)	CCTCTTCTTCAT ATCATCCAGT	TTTAGCCCACTTT TATGCAC	265	269	polymorphic
313711_K70[a,b]	KP279215	Schlautman et al. (2015a)	CGACTTAATCCC TCTCTTTCTA	CTTTACTTTTCCA TCTCCCTC	326	340	polymorphic

1trimcontig176861[a,b,c]	KP279223	Schlautman et al. (2015a)	ATGGATGTATCT TGACAGGC	CTGCTGTTCATTT CTCTGTG	146	161	polymorphic
1trimcontig439466	KP279246	Schlautman et al. (2015a)	CGAGTGGATAG TGATGATATTG	ACCAAGAGGAAC TACAGGTAAA	274	278	polymorphic
407841_K63[a,b,c]	KP279175	Schlautman et al. (2015a)	TTGAGTAGATAC ATGCTGGCT	CTCACCCTTTCTC TTGTGATA	256	270	polymorphic
412234_K63[a,b,c]	KP279182	Schlautman et al. (2015a)	GTGCAAGCCGTT TCTTATG	ATCGGAGGTTCC ATCATTTA	140	154	polymorphic
281884_K70[a,b]	KP279207	Schlautman et al. (2015a)	TCCACTATCTTT AGAATCCCAC	AGAGGATGGAGT TCCTTGATA	310	334	polymorphic
414791_K63[a,b,c]	KP279183	Schlautman et al. (2015a)	ACGACTAGCAGC ATTCAGTAA	CAGGAGATCAGA AAACACAATC	312	339	polymorphic
281741_K70[c]	KP279274	Schlautman et al. (2015a)	GATTTGACTCGT AAAGCAGAC	GGAAATGGAGAT GGATATGTAG	156	174	polymorphic
314402_K70	KP279217	Schlautman et al. (2015a)	TGGAAGAACTC GATACGAAC	GAGAAGTTGGAT ACTGGAAATG	146	158	polymorphic
1trimcontig339726[a,b,c]	KP279240	Schlautman et al. (2015a)	TACTCATGTCGA AGCAATAGAG	CTTTAGCAGAGG AGAAACAAGT	177	180	polymorphic
16720_K63[a,b,c]	KP279159	Schlautman et al. (2015a)	CTACCTTTCCCTC TCCTTGT	AGTTGAAGCTGA GAATTGTACC	170	199	polymorphic
364103_K63[a,b,c]	KP279173	Schlautman et al. (2015a)	TACAAACCCTAA GCTCTAAACC	CGACTTGAGTGA TACCAAAGA	175	216	polymorphic
307461_K70[a,b,c]	KP279275	Schlautman et al. (2015a)	CAGACACTCCAC TAACTCAGAA	GCATCAACAGTAC AACAATACC	318	341	polymorphic
251788_K63[a,b,c]	KP279166	Schlautman et al. (2015a)	GATCTTTACCAC TCCCCACT	GGATTCTCTGTCC ATTGTTG	197	217	polymorphic
418294_K63[a,b]	KP279189	Schlautman et al. (2015a)	CAAGAACAAGA AGAAGAAGACC	AGAGACCACCCA AAAGATAAG	341	356	polymorphic
36394_K70[a,b]	KP279271	Schlautman et al. (2015a)	CAGTGTTTGTTG CTTGGTC	ATCTCACTCTCTG TTTCCCTC	170	196	polymorphic
1trimcontig439506[c]	KP279285	Schlautman et al. (2015a)	GATTTAGGTTAG GGTATGGGT	GCTTGTGTTAGG GTTTGTTA	298	336	polymorphic
339139_K63[c]	KP279261	Schlautman et al. (2015a)	CTAATACTTTCA TCGTCAACCC	AGGAGAGAGAGA GGTAGTTTGG	221	247	polymorphic
411348_K63[b,c]	KP279180	Schlautman et al. (2015a)	AATTACCAATGT TCACTCCG	GTTGATGTAGTTC TGTGGTTGA	299	362	polymorphic
372875_K63[a,b,c]	KP279174	Schlautman et al. (2015a)	CACACACAAATC CCAATTTC	GATGGTGTTTTCA TAGTTCGAC	186	251	polymorphic
60699_K70[a,b]	KP279196	Schlautman et al. (2015a)	CTTCTCACTGTA TTTCTTCGAG	GGCTACTTTGTTA GGGTAGATT	168	191	polymorphic
1trimcontig239742[a,b,c]	KP279234	Schlautman et al. (2015a)	AACAAGAACAAC TAAGACCACC	TACAAGTTTCAAT CAGCCCT	254	277	polymorphic
409500_K63[a,b,c]	KP279177	Schlautman et al. (2015a)	GATTCCTGGGT GTAGTTCTGT	CTTAGTCTTTAAT GCTGGCTCA	337	343	polymorphic
411475_K63[a,b,c]	KP279181	Schlautman et al. (2015a)	GCAACAGGGAC AGATATTTT	TACGGACTCATAG AAGGTTAGG	166	174	polymorphic
1trimcontig332949[a,b]	KP279237	Schlautman et al. (2015a)	ACCCAAACACAA AAGAACAG	GACTGCAAGTGT CTAAATGCT	295	317	polymorphic
1trimcontig440008[a,b,c]	KP279248	Schlautman et al. (2015a)	GCAACAGGGAC AGATATTTT	TACGGACTCATAG AAGGTTAGG	166	174	polymorphic
76326_K70[a,b,c]	KP279197	Schlautman et al. (2015a)	AATGTCTTCCAA ATCAGGTG	CAAGAACGAACC CTCTATTTC	270	290	polymorphic
309124_K70[a,b]	KP279213	Schlautman et al. (2015a)	AAAGGTCGTTAA GGCTATCAG	TGATGACTGCGA TATGTACTCT	139	144	polymorphic
313928_K70[a,b,c]	KP279216	Schlautman et al. (2015a)	CAATTATCAAGG AGGCAATC	TCACAAATGAGG ATCTACACAC	192	212	polymorphic

1trimcontig443603[a,b,c]	KP279251	Schlautman et al. (2015a)	TGCACCTCCTCTCTCTCTAA	GGTTATGATGGTGGGAAAG	142	178	polymorphic
314797_K70[a,b]	KP279218	Schlautman et al. (2015a)	CTTGTTCTCCTCCTTTAGTCTG	CATCTTCATACTCCTATTGTCG	224	238	polymorphic
198358_K70[a,b,c]	KP279203	Schlautman et al. (2015a)	AATCGTCTGTTGCTCAATGT	AACCATACTTACCACAACCAGT	334	340	polymorphic
1trimcontig326802[a,b,c]	KP279235	Schlautman et al. (2015a)	TTTTCAGAGCAAGAGGAAAG	CTGTCTGTATCATGGAACTCAT	190	200	polymorphic
35137_K63	KP279254	Schlautman et al. (2015a)	GGAACATCAAAACTCCCATAC	GTTCTTCCCCATTTCAGTAAGT	241	305	polymorphic
297265_K63[a,b]	KP279167	Schlautman et al. (2015a)	GATCGTCATAACTAAGCTGGAT	GTCTCGAATCACAACAGGATA	319	333	polymorphic
409618_K63[a,b,c]	KP279178	Schlautman et al. (2015a)	CTTCTCCTTCCCTTCACTTTA	TTAGTGTTAGTGTTGGTGTTGG	263	288	polymorphic
24956_K70	KP279270	Schlautman et al. (2015a)	AGAGAGAGGATTGTTATTGCTG	TGAACCAAGCCCATATAAGT	287	337	polymorphic
314831_K70[b]	KP279219	Schlautman et al. (2015a)	ATCTCTCGTGCCTGTCATAC	CTTTTCGATGTCGTACTTGTC	144	154	polymorphic
289194_K63[c]	KP279260	Schlautman et al. (2015a)	CTAGCACTGGCTCTTACCAC	TGTAGGATGTGTATATGGAGCA	206	228	polymorphic
1trimcontig337780[a,b,c]	KP279239	Schlautman et al. (2015a)	CTTGATCTTGTCGCTGTAGAC	CTGAGCATCTCTCCTTTATCTC	306	323	polymorphic
1trimcontig450309[a,b,c]	KP279253	Schlautman et al. (2015a)	AAAATCAGAGGGAAGAAAGC	TATTAGCCAGTCCTCCTTTGTA	134	140	polymorphic
1trimcontig440230[a,b,c]	KP279249	Schlautman et al. (2015a)	ACACTTTGTAGGTGGTGGTTAT	ATTAGCAGTAGTCCAATCGGT	236	253	polymorphic
1trimcontig176042[a,b,c]	KP279221	Schlautman et al. (2015a)	CCGTTGTTGTTCTTCTGTAGT	TTCAACCTCTGAAGCCTCT	222	226	polymorphic
1trimcontig191066[a,b]	KP279227	Schlautman et al. (2015a)	GATATTAGTCCGGTTTACGAGA	GATACAGGAGTCGAGAATGAAT	299	314	polymorphic
1trimcontig436904[a,b,c]	KP279245	Schlautman et al. (2015a)	TACCAACCACATCACACATC	CTTATGACGATCCCAGTAGC	240	242	polymorphic
scf37h[a,b]	JN230518	Georgi et al. (2013)	TGGACTTTTCTTGCTTGGCT	GGATACACGTGACCGAGCTT	Inf	-Inf	polymorphic
scf43g[c]		Georgi et al. (2013)	ATGGGCTCCATTGTGTTTTG	ATCGCCCCTACCTCGTATCT	169	174	polymorphic
CA421		Boches et al.(2005)	TCAAATTCAAAGCTCAAAATCAA	GTTTAAGGATGATCCCGAAGCTCT	196	228	polymorphic
CA855F[a,b,c]		Boches et al.(2005)	CGCGTGAAAAACGACCTAAT	GTTTACTCGATCCCTCCACCTG	264	278	polymorphic
VCC_B3[a,b]		Boches et al.(2005)	CCTTCGATCTTGTTCCTTGC	GTTTGATGCAATTGAGGTGGAGA	248	258	polymorphic
2ms2g09		Georgi et al. (2013)	GGGGAACTCAGATGGGTTTT	GCTGTCATTTTTCGGAGAGC	253	262	polymorphic
2ms4d10b[a,b,c]		Georgi et al. (2013)	GGAAACGATGCCGTTTTCTA	CAACCCTTCCAGGTCAAAAA	210	245	polymorphic
5ms2b12[a,b,c]		Georgi et al. (2013)	AAAACTGCAACTGGAATCGG	GTCTGCAGGTCACAGGTTCA	284	293	polymorphic
6ms4e4b[a,b,c]		Georgi et al. (2013)	GGCCAAGGTTCTACCCTTTC	CAACTACCCACCACCACCAT	150	192	polymorphic
CA325[a,b,c]		Georgi et al. (2013)	ACCACCCTCCCATTTCAAAC	AGGCGAAAAAGGTGTTGATG	226	254	polymorphic
contig130Fb[a,b,c]		Georgi et al. (2013)	GAGATTCTCGCTTTTTCCCC	ATGCACAGCTGCAACAAAAG	227	237	polymorphic
contig480Fb[a,b]		Georgi et al. (2013)	GATGATGTGGGGCCTAAGAA	CGCATTCGACTCAATGTTGT	283	288	polymorphic

contig600[a,b,c]		Georgi et al. (2013)	GCCAAAGCTGG AGAGAGAAA	GACTTCAGCAGCC AACATCA	156	164	polymorphic
contig652[a,b,c]		Georgi et al. (2013)	AAAACTGTCGGC AGATCCTC	GGGATACCAATG TGGGTCAG	250	256	polymorphic
Ig6523b[a,b]		Georgi et al. (2013)	CCATCTACCACG GCAGAGAT	GCATATTTTGGTT GGATCGG	302	308	polymorphic
Ig9279a[c]		Georgi et al. (2013)	CCACTCATTGCC ATCAAGTC	ACTGGCTCTGAAT GCCATCT	183	198	polymorphic
Ig15420a[a,b]		Georgi et al. (2013)	TGGGGGATTTC TCACAAGAG	AATCCCACTTGAT TAGGCCC	204	227	polymorphic
Ig16780a[a,b]		Georgi et al. (2013)	GTGAGGGGTGC CAAGTAGTC	CCAAAATTGGTG ACCCTTTC	341	342	polymorphic
NA172[a,b,c]		Georgi et al. (2013)	CCTCGTCCTCCT CTTCCTCT	GTTTGACTTTGGA GAAGGCGAAG	329	335	polymorphic
NA1713[a,b,c]		Georgi et al. (2013)	ATTCGCGTATGG AAGGTGAC	CTCACACCACTGT GGCTCAT	305	311	polymorphic
scf6i[a,b]		Georgi et al. (2013)	TTGTTTGGTGCT ACGAGTGC	GGCCTGAACTTTC CTGACTG	216	228	polymorphic
scf17d[a,b]		Georgi et al. (2013)	TCGCTTGAAGCT TACCGAAT	AGAACGAACACCT CGGTCAC	235	304	polymorphic
scf21n[a,b,c]		Georgi et al. (2013)	ACCAATTCCCTC CCAAGTTC	CCCTGGATATTTG CTTGCAT	236	255	polymorphic
scf28l[a,b,c]		Georgi et al. (2013)	AACTCTTCGCTT TGGTTGGA	TCGGTCGTAGAG ACGAGGAT	174	180	polymorphic
scf35k[a,b]		Georgi et al. (2013)	TCACCTTAAACC CTGGCTTG	GTGGAGATGGAT AGCTTGGG	291	297	polymorphic
scf511[a,b]		Georgi et al. (2013)	CTCCCTCCTTCC GATGAAGT	CACAAAGTTCCAC GCAGAAA	204	218	polymorphic
scf1594[a,b,c]		Georgi et al. (2013)	ATGCGAATGGA GAAATCTGG	ATACCGCAAATG GAGTCTGC	178	199	polymorphic
scf2000b[a,b,c]		Georgi et al. (2013)	GGCCCTTTTTAT CCCCAATA	AATCAAAAGCTGC GAGGAAA	300	334	polymorphic
scf8l[a,b,c]		Georgi et al. (2013)	CGAATCCGAAG ATCAGAAGC	GGGATACCAGAG ATTTCCCG	172	320	polymorphic
scf14j		Georgi et al. (2013)	CAGCAGAATTCA GGAAAGCC	AGCTTTCCACACG CTCATTT	171	215	polymorphic
scf26r[a,b,c]		Georgi et al. (2013)	ATGATGTTGGAT GTGCCTCA	TTCCTCAACAAAC CCTCCAC	245	313	polymorphic
scf44a[a,b,c]		Georgi et al. (2013)	ACAAAACCACTG GCGAAAAC	GAGTGACCAGGG GAGATGAA	247	268	polymorphic
scf55c[a,b]		Georgi et al. (2013)	AGCCATTGATCT CCAACCAC	GCGTTTCAATCTT TGGCAAT	168	323	polymorphic
scf79c[a,b,c]		Georgi et al. (2013)	GGTTCTTCGTGG CATGATAGT	CCAAATAACCCAG GAGAGCA	205	253	polymorphic
scf112c[a,b,c]		Georgi et al. (2013)	ATGTGATTCGCG AAGGATTC	GAAATCCGGGGG TGTAAACT	152	168	polymorphic
vm89040[a,b,c]	JF834248	Zhu et al. (2012)	TAGACAGACTTT CATGCTATGG	GAACTGATGAAG GTGGTTTATC	230	238	polymorphic
scf258d[c]		Georgi et al. (2013)	GTAACGCATTG GTCGGCTAT	TAAGCCAAACCCA ATCCAAC	219	224	polymorphic
scf306f[a,b,c]		Georgi et al. (2013)	GGGCAAGGATA AAGGGTTGT	TGCATGCAACTTC CTAGTCCT	306	334	polymorphic
scf10688[a,b,c]		Georgi et al. (2013)	TCACTTTTCTTTC ATGCCCC	GTGCTCCCACTAG CCCATAA	316	316	polymorphic
vm31701[a,b,c]	JF834268	Zhu et al. (2012)	GTCACTGGTAAT GCTATTCTGA	CTTCTTTGTTTCA TCTCCCTAC	280	309	polymorphic

vm39030[a,b]	JF834273	Zhu et al. (2012)	CTGATTACTGAGTCTACTAACACCA	ACAGATTTGTAGTCACGAAGTG	197	223	polymorphic
vm10462[c]		Zhu et al. (2012)	AGATTGACCAGAGATAATCAGG	CCCAGTAGCCTAGTCAGTAGAA	256	268	polymorphic
vm13884[b,c]		Zhu et al. (2012)	TAAAGCTATGTATGAGCCGATG	GTTTTGGCAAATAGACTATCCC	127	139	polymorphic
vm68798[a,b]	JF834242	Zhu et al. (2012)	ATAGAAATCGAGCAAGGAGAG	CAGACCTAAACTCAATTTCTGG	169	181	polymorphic
vm25796[a,b]	JF834263	Zhu et al. (2012)	CACTTACCTGAATCCTCTTAGC	TAGAGGAGCCAAACTGATAACT	201	258	polymorphic
vm13780[a,b,c]	JF834259	Zhu et al. (2012)	CCTTCTGCTGGACACTCATA	ACCCATACCAGAGGAGTACATA	148	180	polymorphic
vm34671[a,b,c]	JF834271	Zhu et al. (2012)	CCATCTCTCTCTTGTTTCTCTC	GCGAAAAATAAGTCTCCACA	274	278	polymorphic
vm52204[a,b]	JF834281	Zhu et al. (2012)	CTATATAACAGACGTCCAACCC	GGGTTGTTTCAGACAAGTAAGT	167	261	polymorphic
vm54133[a,b,c]	JF834236	Zhu et al. (2012)	GTGTAAAATTCCAGGTAGAAGC	ATCAAGCTCTCAGTATCCTCTG	264	327	polymorphic
ct116900[b]	KP279112	Schlautman et al. (2015a)	CTCAAACATACCCTTTGAGC	GGTATAGCTTAACAACACACCA	435	435	Not polymorphic
ct161908[a,b]	KP279144	Schlautman et al. (2015a)	CCTAGGAGATGGGTCAAGAT	ACCACTGTCTTCCATATTCACT	201	211	Not polymorphic
ct165512	KP279145	Schlautman et al. (2015a)	CTTCCTACTCTCTCCCTCTACA	GTTGGATCTTGATGGGTTTA	132	144	Not polymorphic
SCF71136[a,b]	KP278753	Schlautman et al. (2015a)	TCTGTTTTCACAGCTATCACAC	GTTCATCAAAGGCCAGAGT	147	183	Not polymorphic
SCF13006	KP278639	Schlautman et al. (2015a)	AAAACATAAGAAAGAGCCCC	GGATGATGATGTATGGGAAT	300	304	Not polymorphic
SCF3191[a,b]	KP278603	Schlautman et al. (2015a)	GCACTATCAGGAAGAGGAATTA	GTAACACCAGAAAACAACTGC	136	144	Not polymorphic
SCF113304	KP279058	Schlautman et al. (2015a)	CCAGTCAACGAACAAATAGAG	CCTAAAGGGAAAGAGAAGTGA	136	142	Not polymorphic
SCF915[a,b]	KP278593	Schlautman et al. (2015a)	TTAGGGTTTGGAGTACCTGA	ACTACCGTCTTTCTTTATAGCC	149	161	Not polymorphic
SCF33518	KP279005	Schlautman et al. (2015a)	GTATTCGTACTCCACACCCTT	TACAGACAACCATACATTAGCG	190	197	Not polymorphic
SCF96306	KP279050	Schlautman et al. (2015a)	CCTGTAGTGAGTTACCTTCCAT	GCTGTCAACCATCCATTATT	253	318	Not polymorphic
SCF96539[a,b]	KP278800	Schlautman et al. (2015a)	GTAGCATAACCACCTCTTATCC	ATCTTGATGACTGTGTAAGCTG	253	261	Not polymorphic
SCF105151	KP278811	Schlautman et al. (2015a)	CAGAATAAGATTGGGTAGAAGG	TTTGAGAATTACTTGGCACC	302	308	Not polymorphic
SCF123189[a,b]	KP278847	Schlautman et al. (2015a)	CCTAGAAATGTTACTCTCCGAC	TTCACTTCCTTACTCCTTTCAT	201	201	Not polymorphic
SCF128658	KP279072	Schlautman et al. (2015a)	ATTATTGATGAGTAGTCCCCAC	TGGTTGATTTGTGTAGAAAGAA	215	224	Not polymorphic
SCF130642	KP279074	Schlautman et al. (2015a)	AGGCGGAAGATGAAAGTAAT	TGTCAACATAAAACGATAGCAG	179	286	Not polymorphic
SCF131915	KP278859	Schlautman et al. (2015a)	TTTTGTTTCCTTATTTTCGG	TGTAAGTGCATGAAATCGTAAT	184	201	Not polymorphic
SCF132868	KP279077	Schlautman et al. (2015a)	CTGATTTGTGTTGATGGATAAG	CAGTTAGCACCACCTAGTTAGA	180	180	Not polymorphic
SCF142664[a,b]	KP278880	Schlautman et al. (2015a)	TACTGACGATGAGCTAGAGTTG	AATGACAAGTGGAATAGTAGGC	176	181	Not polymorphic
SCF152348	KP279090	Schlautman et al. (2015a)	AGGAGCAAGAAGAGGTGTTT	CCATTGTTTTGCACTTCAG	253	253	Not polymorphic

SCF172149[a,b]	KP278922	Schlautman et al. (2015a)	GTTAAATGATGC TGTTAGGGAG	ATGTCCAGTCGTT ATCTCTAGG	179	194	Not polymorphic
SCF204332[a,b]	KP278948	Schlautman et al. (2015a)	CGTGATCTCCCA GAGTTGT	CTTTTATTTCCCT ATGTGTCCC	156	347	Not polymorphic
SCF221037	KP279099	Schlautman et al. (2015a)	ACACTACAAGCA ACAGACAAGT	TAGTCGAGGTGT GCGTAAG	153	189	Not polymorphic
SCF259[a,b]	KP278591	Schlautman et al. (2015a)	TGACAGTACCAA TAGCAGGAC	AACACCCAGTCGT TATACATCT	252	332	Not polymorphic
SCF6195[a,b]	KP278613	Schlautman et al. (2015a)	GACTATGAATCT GACGCTCAC	CCAGTAAATACGT GACTAATCG	339	359	Not polymorphic
SCF6926[a,b]	KP278615	Schlautman et al. (2015a)	ACATGCACTTCA AATAGTACCC	TTACAACTTACAC AGGAAGCAG	193	201	Not polymorphic
SCF7845[a,b]	KP278620	Schlautman et al. (2015a)	GTTCTGACTATT GTGATGGGTT	TGCAATGAATACT GGAAGTG	234	234	Not polymorphic
SCF9909[a,b]	KP278630	Schlautman et al. (2015a)	CGTAGGTGGAT TTCTCTACAAT	GGCATCTTATTTA TCGTCTCTG	155	179	Not polymorphic
SCF11431[a,b]	KP278637	Schlautman et al. (2015a)	GCTGCTGATTTG TTATGTAGAG	CACTTAGCCCCTT AAACTATTG	261	261	Not polymorphic
SCF55751	KP278730	Schlautman et al. (2015a)	ACTCACGTCCAT TTTCTCAC	AGCGATATAACA ATACCAGAGC	205	280	Not polymorphic
SCF59739[a,b]	KP278741	Schlautman et al. (2015a)	GTATGACTGTAC CAAACAAACC	CAGCTTTCCCTTC TAAATGA	334	342	Not polymorphic
SCF89672	KP278788	Schlautman et al. (2015a)	CCACTATAATCT ACCCCAAAGA	TACTACTGCCCCA TCCTACTAC	183	209	Not polymorphic
SCF108294[a,b]	KP278818	Schlautman et al. (2015a)	GGTAAGATTGA GGTTCTGGTCT	GGTAGAAGCAAG AAGATGCAC	248	286	Not polymorphic
SCF113895	KP279059	Schlautman et al. (2015a)	GGAATCACTATG AACATGCAC	ATCAGAAACGAG TCCAAAGAC	307	382	Not polymorphic
SCF124075[a,b]	KP278848	Schlautman et al. (2015a)	ATTTTCCCTCCA ACCTCTAT	GGTGCAACCAAC TAACATAA	237	248	Not polymorphic
SCF127382	KP279071	Schlautman et al. (2015a)	GTCTTTAGTGCT GGGTTAAAAG	TGATTTCTAGTGT CTCCTCTCA	232	242	Not polymorphic
SCF128992[a,b]	KP278858	Schlautman et al. (2015a)	GAGTGTTGAGT TATAGGGGTTT	TCACAAGAATAG AAGGATGGA	233	241	Not polymorphic
SCF158633[a,b]	KP278906	Schlautman et al. (2015a)	AGATGCTGAAG TTTTCCCTT	TATGTGGATTCTT TGCCTTG	282	286	Not polymorphic
80734_K70[a,b]	KP279198	Schlautman et al. (2015a)	AGGGAGAACCA ATTCCTTAC	GACCTAACCCTAA CCCAGTC	314	362	Not polymorphic
1trimcontig444 344[a,b]	KP279252	Schlautman et al. (2015a)	CTGCTAATGTTG TTTGTTGC	TATTATCTCCCAC CTAATGAGC	243	251	Not polymorphic
scf5304[a,b]		Georgi et al. (2013)	TACACAGCTTCA TTCGGCAA	AAGCTCACCCAAT CGAAAGA	166	346	Not polymorphic
vm26877[a,b]	JF834264	Zhu et al. (2012)	CCCCTTTTGAAC GAAACTATAC	ACATCTCAATTCC GAGCATA	224	226	Not polymorphic
vm38401[a,b]	JF834272	Zhu et al. (2012)	CAATGGGAAGT ACAAAGAGC	CGATGCAATCTTA GTCTTGA	168	185	Not polymorphic
ct98042[a,b]	KP279108	Schlautman et al. (2015a)	CCTTTTAAGTAC TTTCCCTTCC	CCCCTCATCTTTA TGTGC	261	261	Monomorphic
ct106280[a,b]	KP279109	Schlautman et al. (2015a)	GCCATAGCTATT TTGTAACGAG	TATCATGGACTAG GTCTCAACA	200	200	Monomorphic
ct135942[a,b]	KP279124	Schlautman et al. (2015a)	CTACTTGCCTTC CTCTTTGAC	TAAATAATCCGTC CACGAAC	175	175	Monomorphic
ct145217[a,b]	KP279131	Schlautman et al. (2015a)	CCAGTACTAGAT CCACTGCATA	TGTTCTAGAGAG GATGACATTG	147	147	Monomorphic
ct155461[a,b]	KP279141	Schlautman et al. (2015a)	GGTTTCAAACTC GAACAAAG	ATCCTATAACTGG GGATAATGC	254	254	Monomorphic
ct170930	KP279158	Schlautman	ACCCGATTCCAT AAAAGAAG	CAAGCTTCTCCTA CCTCCA	164	164	Monomorphic

		et al. (2015a)					
ct174735[a,b]	KP279147	Schlautman et al. (2015a)	CTTATTTGTATG GCCTTCCT	GCAGCATATATTG TCCAGTTC	161	161	Monomorphic
SCF101878[a,b]	KP278807	Schlautman et al. (2015a)	GACTCATTGGAT ACGTGCT	TCTATGTAGCTTT GAAGTGAGG	335	335	Monomorphic
SCF116485[a,b]	KP278834	Schlautman et al. (2015a)	CAATATAAACGT CAGTCACCAG	ACTTTTGGTTATG CTGGAAG	207	207	Monomorphic
SCF11802[a,b]	KP278638	Schlautman et al. (2015a)	CGAGGAACAAG TTTTATAGGAG	ACACTCACCTTTA TTATGGGAC	260	260	Monomorphic
SCF213102[a,b]	KP278953	Schlautman et al. (2015a)	GTGAAGATACA GTGGAGAGCA	ATGGTAGTTGTT GACCTGATG	151	151	Monomorphic
SCF5899	KP278964	Schlautman et al. (2015a)	TAGCCTTGGGTA TTAGAACACT	GGAAGACAAGAC AAGAGGC	144	144	Monomorphic
SCF116567[a,b]	KP278835	Schlautman et al. (2015a)	GTTGGTCTACAA TTCTGTTCCT	GCCCTTTTAGTTG AAATGC	193	193	Monomorphic
SCF56816[a,b]	KP278735	Schlautman et al. (2015a)	CGGATTGACTAA TTTCTGTCTC	CTCTTATTCCACC AAACGAA	207	207	Monomorphic
SCF92564[a,b]	KP278794	Schlautman et al. (2015a)	TCATAACTCCCT CGTAATCAAG	AGGAAGAAGAGA ATAAGGTTGG	165	165	Monomorphic
SCF3362[a,b]	KP278605	Schlautman et al. (2015a)	GTACAGCAAAAT TCAGCACA	GGATTTATCTACA GCCCATTAC	362	362	Monomorphic
SCF71184[a,b]	KP278754	Schlautman et al. (2015a)	TCTGTTCAGTTG GGCTTTAT	GCTCACATTCACC TGTAATTC	139	139	Monomorphic
SCF43145[a,b]	KP278711	Schlautman et al. (2015a)	TGGTTTTGGATA CACACTTG	AAGAACAAGATC ACCACTCTG	226	226	Monomorphic
SCF2714[a,b]	KP278602	Schlautman et al. (2015a)	ACAAGTCTCTGG AAGCTAACAT	GTTGATTGTTGG GTCTAAGTTC	202	202	Monomorphic
SCF28509[b]	KP278676	Schlautman et al. (2015a)	GCAAACACCACA CTATATGAGA	ATAGAGAACCAC AGAACAGGAC	207	207	Monomorphic
SCF63953	KP279029	Schlautman et al. (2015a)	GTTGGTGTGGT TCTCATTATC	GTGAGTGCTGAT AGGGTAGAGT	347	347	Monomorphic
SCF96311[a,b]	KP278799	Schlautman et al. (2015a)	TGTATAATCTCA GGGGCATT	TTTCTCATTTCCTT CCCAC	155	155	Monomorphic
SCF113389[a,b]	KP278831	Schlautman et al. (2015a)	GACATCACTCAA GCAAGATAAA	CCTCGATTCCTCA AGATATG	151	151	Monomorphic
SCF124322[a,b]	KP278849	Schlautman et al. (2015a)	TAAAACTGTGAG GTTCAATGTG	CTTCGTGTCTCAA ATTACAAAA	142	142	Monomorphic
SCF142785	KP279083	Schlautman et al. (2015a)	AGGCTCACATTT CTAACTCAAG	ATATCTACCTCCC TAATTTCCG	369	369	Monomorphic
SCF161998[a,b]	KP278911	Schlautman et al. (2015a)	ATATACCAGTGC TCTTTCCATC	AGACTTCTTTCTC CAAAGGC	267	267	Monomorphic
SCF194552[a,b]	KP278944	Schlautman et al. (2015a)	CACAGGTGTAG GGTCTTGTT	AAAAGGAGGCAA GGATAGAG	224	224	Monomorphic
SCF1648[a,b]	KP278599	Schlautman et al. (2015a)	GTTGATCTGAAG GAAACCAA	TCGTATTAACTCC CCTATTGAC	258	258	Monomorphic
SCF3187	KP278960	Schlautman et al. (2015a)	CCAGAAAACTAC AGATACCCTC	GTACTTACCGGG ACAACTCTTA	320	320	Monomorphic
SCF7132[a,b]	KP278616	Schlautman et al. (2015a)	AAGGGGAAGGA CAATAAGAA	AATTTGATGACTG TTGTGGC	235	235	Monomorphic
SCF8189	KP278970	Schlautman et al. (2015a)	GACAAGGAGGA AGAAATAGTGA	ACCAGCAGAAGC AGTTAAAG	326	326	Monomorphic
SCF9815[a,b]	KP278628	Schlautman et al. (2015a)	CATAGGAAGATT GCCTTGAG	GCCTGTTCACATA GATGGAG	178	178	Monomorphic
SCF10514[a,b]	KP278632	Schlautman et al. (2015a)	GTACTCTTTGTC GGATGTTTTC	GTTTCACTCCCAC CTCTTAAT	247	247	Monomorphic
SCF11065[a,b]	KP278634	Schlautman et al. (2015a)	CTTTGTCCCAAC ACGTTAAT	AAGTCTATAAGCA TCCTGCAAC	183	183	Monomorphic

SCF13628	KP278979	Schlautman et al. (2015a)	AGAGGTCAATA GCTGAAGAAGA	AATTCCTGTAGTA AACAGTGGG	326	326	Monomorphic
SCF18709[a,b]	KP278651	Schlautman et al. (2015a)	GTAATGGTAAG TGTCGAAATCC	CATAGATGTAACC ACGCTTCT	338	338	Monomorphic
SCF29521	KP278998	Schlautman et al. (2015a)	CTCAATGCTTCG GAGTAGATA	CTCCTTGTTTTCA CAGGTATG	361	361	Monomorphic
SCF39705	KP278706	Schlautman et al. (2015a)	GCAGGTAAATCC TATCTGGAAT	GTTGAAGACACCT AGTCCACTC	362	362	Monomorphic
SCF40517[a,b]	:	Schlautman et al. (2015a)	GTAGAATGGCA ATAGGGTTT	GAAGAAGATGAC GAAGATCAC	249	249	Monomorphic
SCF42332	KP278710	Schlautman et al. (2015a)	GATAGAATGAC GAAACTAACCC	AGTGGGGAGATA ATTGAGAAG	198	198	Monomorphic
SCF42549	KP279018	Schlautman et al. (2015a)	CTCTTCAGCCCT AATCATATTC	CAGGACAAACATC TAGGTCAA	176	176	Monomorphic
SCF46588[a,b]	KP278714	Schlautman et al. (2015a)	ACAAACCTTGAG CCTATTTG	GTCTGAGTTTCCA CTATCGTCT	196	196	Monomorphic
SCF48645[a,b]	KP278722	Schlautman et al. (2015a)	AAAATAGGTCCC ACATGAGTAG	GCTAGACGATGA CACATTATTC	200	200	Monomorphic
SCF49656[b]	KP278724	Schlautman et al. (2015a)	ACTCTTACCCTT GAAACCAACT	TAGGTGCATGAG ACTTTTAACC	281	281	Monomorphic
SCF50668	KP279022	Schlautman et al. (2015a)	CTTAATATGTCC TAGCCCAAAC	GAGGTGTAGAAT AGTGAAAGTGG	326	326	Monomorphic
SCF53282[a,b]	KP278726	Schlautman et al. (2015a)	GACAATCACATA CCCATAACAG	CCACTCTTTCCCT CTATCG	176	176	Monomorphic
SCF54155[a,b]	KP278728	Schlautman et al. (2015a)	TCGAAGAAAAT GAAGGGAC	ACAAATGGAGAG GAAAGTGTAG	299	299	Monomorphic
SCF56561[a,b]	KP278732	Schlautman et al. (2015a)	ATTAGCCATTCG TGATTAGG	TAAGGAGATACG ACCAAGAAAC	217	217	Monomorphic
SCF57479[a,b]	KP278736	Schlautman et al. (2015a)	AAGTGCAAGTG TGAGAGTGTAT	TGATGGGTGTAA GTGTAAAGAG	188	188	Monomorphic
SCF64758	KP278747	Schlautman et al. (2015a)	TAAGAGGGTTT GAGCATTCA	TTGGGTCATAAAC AACCTCA	332	332	Monomorphic
SCF66313	KP279032	Schlautman et al. (2015a)	AATTTGACCCTC TTTCCCT	GTCCAAAATACAC AAACTAGCC	169	169	Monomorphic
SCF66692[a,b]	KP278749	Schlautman et al. (2015a)	AAAGTGTATTG GACGGCTG	TTGTTATGGCCCC TCATTA	151	151	Monomorphic
SCF77145[a,b]	KP278763	Schlautman et al. (2015a)	TAGAATTAGCCT CCAAGAAGTG	AGAACTAGAAAC ACGAGAACGA	Inf	Inf	Monomorphic
SCF79014[a,b]	KP278767	Schlautman et al. (2015a)	TCTCTGTCTCTG TCTCTGTCTG	CCAAATCAAGGTC TGTCTATCT	220	220	Monomorphic
SCF80777	KP279038	Schlautman et al. (2015a)	GAGGCAATGTT AGTCTTTGGT	GGATACAACAGC TAGAACCACT	178	178	Monomorphic
SCF83079	KP279039	Schlautman et al. (2015a)	GTATTCACCAAA TCTACCCAGA	GTTAAGGATTGT GTCCCTCA	237	237	Monomorphic
SCF85773[a,b]	KP278780	Schlautman et al. (2015a)	TCTTGAACACAG CACAACAT	ATAAGTTTGCCCC TTTTGTC	298	298	Monomorphic
SCF92414[a,b]	KP278793	Schlautman et al. (2015a)	GTTATCCTCCCT TTGATATGTG	AAGAGCAACAAG ATGGGTACT	282	282	Monomorphic
SCF102347[b]	KP278808	Schlautman et al. (2015a)	GGTAGTGAGCA ACGACATAAC	CCTGAAGGTAAA GAAAGTAGCA	305	305	Monomorphic
SCF104688[a,b]	KP278809	Schlautman et al. (2015a)	ACAAAGAAATGT ATGGCACC	CTTTTCGTCTCCT CTAATTCC	258	258	Monomorphic
SCF107429[a,b]	KP278815	Schlautman et al. (2015a)	ATGTGAGGTGG GATGATATTAG	ATATGGTGTCAG TGTGGTGTAG	337	337	Monomorphic
SCF110223[b]	KP278823	Schlautman et al. (2015a)	GATTCTGTTCCA ATAGGCATAC	GGAGTAGTAGTG AAAGGACCAA	344	344	Monomorphic
SCF116329	KP278833	Schlautman	GAATCCCACATT AGAAGTTGAT	TTGTATCTTCCCT ATTCCTACTG	161	161	Monomorphic

		et al. (2015a)					
SCF117157[a,b]	KP278837	Schlautman et al. (2015a)	GGATAGAAACCT GATACGGAC	CGTTACCGTCCCA AATATAA	190	190	Monomorphic
SCF117422[a,b]	KP278839	Schlautman et al. (2015a)	TTCTGTTTCTTG GCTCTGTATC	TATTATGCTACAT CGGTCGAG	182	182	Monomorphic
SCF118209	KP279061	Schlautman et al. (2015a)	AGGATTTAGGA CGTTGGAA	GTAACAGAGAAA GCGAGAGC	189	189	Monomorphic
SCF125889[a,b]	KP278853	Schlautman et al. (2015a)	TCTCGTGTATTT TGGAGTGA	GTTGTATCCTTTG TCGATTCT	212	212	Monomorphic
SCF126993	KP279070	Schlautman et al. (2015a)	TTATGGCTCTCA TTAAGCAAG	CTTATTTGGGGTT GATGTGTA	184	184	Monomorphic
SCF132595[a,b]	KP278863	Schlautman et al. (2015a)	CAAACAAATCTC AACAACACC	ATTTCAAGATAAG CTCTCCACC	229	229	Monomorphic
SCF132852	KP279076	Schlautman et al. (2015a)	TGCTTGTGTTAG GGTTTGTTA	GTTAGAGATGAT GGCTGAAGAT	183	183	Monomorphic
SCF132922[a,b]	KP278864	Schlautman et al. (2015a)	TTAGACGCTTTA TGTCCATTC	GAGTGTCCTTGTC TTTGTTGTA	174	174	Monomorphic
SCF139334[a,b]	KP278874	Schlautman et al. (2015a)	GAGGGTCTAAT ATCTGGTTTCA	GAGAAAAGATGG AGCAAAAG	192	192	Monomorphic
SCF141985[a,b]	KP278878	Schlautman et al. (2015a)	GAATGGTCTTGA GGGATGTAT	ACTCTGGAAGAA ATAAAACGG	188	188	Monomorphic
SCF145739[a,b]	KP278886	Schlautman et al. (2015a)	AAATCCTCCTGT TTTAGACTCC	CCTCAAGTCATCA TTCCCT	228	228	Monomorphic
SCF149989[a,b]	KP278892	Schlautman et al. (2015a)	AGTAGGCATTGT TCACTCACTC	TTTCTCCTAAAGC TAAACTCCC	257	257	Monomorphic
SCF157301	KP279091	Schlautman et al. (2015a)	CGTTACATACTC CACCCAAT	GATTTCAAGAAG GGTTTGTG	235	235	Monomorphic
SCF157676	KP279092	Schlautman et al. (2015a)	GTCCGCAGTGTC TATGTTT	CATACCTTAGATG GTGATTAGG	274	274	Monomorphic
SCF175823[a,b]	KP278927	Schlautman et al. (2015a)	AGGGGCAGTTT AGTCCTAGTAT	GCACGTCTTTTCT GTAGTTCAT	278	278	Monomorphic
SCF181909[a,b]	KP278932	Schlautman et al. (2015a)	CTCTCAATCTCT TGTTTTCTCC	TTCAAACCTCAGC AATCAG	276	276	Monomorphic
SCF191642	KP278939	Schlautman et al. (2015a)	CTACATCCACTA AATATCAAGGC	GATCAAGCCAAA GGAAGAA	248	248	Monomorphic
SCF197903[a,b]	KP278945	Schlautman et al. (2015a)	TCTCGTGAGCGT TACAATATAC	ATGGAGTCAAGG TAAACCG	247	247	Monomorphic
SCF199831[a,b]	KP278946	Schlautman et al. (2015a)	GTAGGTATCATC GCTGTCTTC	GTGCATCACATAC AAGCTCT	249	249	Monomorphic
308812_K70[a,b]	KP279210	Schlautman et al. (2015a)	GAAAGGAAGGT ATGCTACAGTT	TCTTAGGAAAGA CGAGAACATC	278	278	Monomorphic
1trimcontig439861[a,b]	KP279247	Schlautman et al. (2015a)	CTCCTCTCTCGA ATGACACTAC	TTCTTGTTGGCTG GAGATTA	248	248	Monomorphic
1trimcontig238343[a,b]	KP279232	Schlautman et al. (2015a)	GGTAATAGCTTT GTGATCTTGC	GATGGTGAATAA ATTGCGAC	276	276	Monomorphic
76126_K63[a,b]	KP279162	Schlautman et al. (2015a)	TTTATTGGAGCG AAAGAGAG	AAAAGGGGAGGA GAGAGAT	228	228	Monomorphic
1trimcontig344502[a,b]	KP279241	Schlautman et al. (2015a)	TGGAAATGGAA AAGTCTCTG	CACCGTCTACAGT TTAAGAACA	120	120	Monomorphic
308839_K70[b]	KP279211	Schlautman et al. (2015a)	ATAATGTGTCCA GTCCCTTTC	TTCCTTCCTCAAT CCACTC	237	237	Monomorphic
1trimcontig435620[a,b]	KP279244	Schlautman et al. (2015a)	CAACCAGCCTTA CAGTGAATA	GTCCGTTCAATTT CTTTTCC	257	257	Monomorphic
121633_K63[a,b]	KP279163	Schlautman et al. (2015a)	GCAGCTCTCTGT AAATTCCTT	ATGGTTGAAGAT GTTGATGG	166	166	Monomorphic
119364_K70	KP279272	Schlautman et al. (2015a)	ACCACAAAACCC TAGTTCTATC	TCCATAGTCTTAG CAACAACAG	361	361	Monomorphic

418192_K63	KP279266	Schlautman et al. (2015a)	CAGGCAGAAGA AGAAAGAAA	TGAATTAAGAGA GGAGGAGAGA	249	249	Monomorphic
416328_K63[a,b]	KP279185	Schlautman et al. (2015a)	GTATGCCCAGAA TATCCATTAC	TAGTCACGAGGA AAGCTAAAGT	144	144	Monomorphic
214102_K63[a,b]	KP279165	Schlautman et al. (2015a)	GGTAATAGCTTT GTGATCTTGC	GGGTAAAATGAC TGCCAAC	203	203	Monomorphic
1trimcontig237406[a,b]	KP279230	Schlautman et al. (2015a)	TCTTAGGAAAGA CGAGAACATC	GAAAGGAAGGTA TGCTACAGTT	277	277	Monomorphic
1trimcontig445838	KP279286	Schlautman et al. (2015a)	GTTTTCCTCTGA ATCTCCACTA	GTCATACACAATA CACAGTCGC	191	191	Monomorphic
419957_K63	KP279268	Schlautman et al. (2015a)	AGACTCACCTCT CTTTCTTGTG	GACTATCTTTCGG TTGACACTT	377	377	Monomorphic
308539_K70[a,b]	KP279209	Schlautman et al. (2015a)	CTAAATTCTCAA CATCTCTGGC	CCAAGAAGCATA AGGGATAGT	301	301	Monomorphic
29080_K63[a,b]	KP279160	Schlautman et al. (2015a)	ATGAAAACAGG GTAAACTGG	TCTCAACTCATAG AACTACGGA	357	357	Monomorphic
311291_K70[a,b]	KP279214	Schlautman et al. (2015a)	CTTGATCTTGTC GCTGTAGAC	TTCCTTATCGAAA TCACGAG	246	246	Monomorphic
scf24k[a,b]	JN230516	Georgi et al. (2013)	ATTGAGCCCCAC ACTACAGG	AGCCATGGAAAT CCAACAAA	294	294	Monomorphic
CA794F[a,b]		Boches et al.(2005)	CGGTTGTCCCAC TTCATCTT	GTTTGAATTTGGC TTCGGATTC	259	259	Monomorphic
VCC_J9[a,b]		Boches et al.(2005)	GCGAAGAACTTC CGTCAAAA	GTGAGGGCACAA AGCTCTC	179	179	Monomorphic
contig259Fb[a,b]		Georgi et al. (2013)	TTGCTGAAGCCC TAAGCAGT	AAACCAGATCTGT TGGACGC	160	160	Monomorphic
contig704[a,b]		Georgi et al. (2013)	AAATGGCAGGA ATCATGGAC	CTGTTGATCAGCA CCACCAC	293	293	Monomorphic
Ig51a[a,b]		Georgi et al. (2013)	TTGGTGCAAGAT CACCACAT	GCACAAACGGAT GTAGCAGA	302	302	Monomorphic
Ig729b		Georgi et al. (2013)	GAAAGAAAGGT AAAGGGCCG	ATCGAAGGCATTT CCATGAG	285	285	Monomorphic
Ig1296a[a,b]		Georgi et al. (2013)	CCCCTGAATTCT TGTTCCAA	GAGTGGAAAACG CAGTGGAT	200	200	Monomorphic
scf248[a,b]		Georgi et al. (2013)	CAACTGGAGGC AAAACAACA	CACGCATTGCAAT TATACCG	Inf	Inf	Monomorphic
scf1p[b]		Georgi et al. (2013)	AGAGTTGCCTCG AAGTAGCG	TGGGTGTGCTGA G	214	214	Monomorphic
scf23c		Georgi et al. (2013)	TCCTCAGCACAC GTCAATTC	GCAGTAAGGACC GAGATCCA	218	218	Monomorphic
scf137c[a,b]		Georgi et al. (2013)	CTCCGGGAACTC TCCATACA	CTTCGTTGTGAAC GCAAAAG	135	135	Monomorphic
vm72062[a,b]	JF834244	Zhu et al. (2012)	CACCCATAAGAG ATAGAACAAG	CTATCAATCATGA TCTTCAGCC	145	145	Monomorphic
scf283b[a,b]		Georgi et al. (2013)	CCCGATCGAAAT AAGGAACA	ATTGACGACCCA GACTCCAC	297	297	Monomorphic
scf6355[a,b]		Georgi et al. (2013)	ACAATGTTGTCA TTCCGACG	CTAGACTCGTCCA AAAGCCC	138	138	Monomorphic
vm05418[a,b]	JF834252	Zhu et al. (2012)	GGGATAAACACT TACAGGAAGA	CTAGCTAGCCGTC AGTTATTTC	251	251	Monomorphic
vm51409[a,b]	JF834279	Zhu et al. (2012)	TCCTAGGTTAAT TCTTCCCATC	GAGGAGAATCAC AAGCTACATT	263	263	Monomorphic
vm40600[a,b]	JF834274	Zhu et al. (2012)	CAAAAGAGCCAT GAAATAGG	TTGGTGAAAACT ATACCTGTCC	140	140	Monomorphic
vm52682[a,b]	JF834282	Zhu et al. (2012)	CTCAGGTTATCA GGCTTATTTC	CAATTAGTGTGTT CCCAACTC	269	269	Monomorphic
ct188529[a,b]	KP279148	Schlautman	TTGCAGAATCAA TAGTACCTCC	CCTCATTAGCTAT GGTGAAAC	-	-	No

		et al. (2015a)					amplification
ct89569	KP279149	Schlautman et al. (2015a)	ACTAATCCCACG AAAACTGA	ATCTAGGCTTTCA AACTAGGGT	-	-	No amplification
ct89711[a,b]	KP279102	Schlautman et al. (2015a)	CTCCACACCCAC AATCTG	CGTCTTATTTTTA GTCACCTGG	-	-	No amplification
ct93137[a,b]	KP279104	Schlautman et al. (2015a)	AAGATTTCCGCT ACAGTACCT	GCTATGGGTGTC TCAAAAAG	-	-	No amplification
ct95345[a,b]	KP279106	Schlautman et al. (2015a)	ACTCTACAAGGG CACGAAC	ATGGAAGTAAGA AAGTGAGTGG	-	-	No amplification
ct95842[a,b]	KP279107	Schlautman et al. (2015a)	GTGGAAAGAGA TTGTTGATGTC	AAAACTAATGGAT GACGACG	-	-	No amplification
ct115258[a,b]	KP279111	Schlautman et al. (2015a)	GTTCGTTGTGG AAGTCACAT	CAAAATGAGTGC CAGATAGTG	-	-	No amplification
ct117109	KP279151	Schlautman et al. (2015a)	TTGACGTCTTCT CTCTCTTTCT	CTAGGGTTCATAC TTCGAAAAG	-	-	No amplification
ct118488	KP279152	Schlautman et al. (2015a)	GTTCAGGACAA GTGATTTTCTC	AGCTAAGTGTTTT CCTACTGGA	-	-	No amplification
ct118602[a,b]	KP279113	Schlautman et al. (2015a)	TAGAATGCAGTC GTGAAGTGTA	ACTAAATGAGGG GTAGTACGTG	-	-	No amplification
ct119523[a,b]	KP279114	Schlautman et al. (2015a)	GACTCATGGGA GTGAGGAC	TGAACTTGTGTA GTCTTTACCG	-	-	No amplification
ct119590[a,b]	KP279115	Schlautman et al. (2015a)	ACATGACATCAA TTGCCC	TATCCTACCTCAA AGAGCCTAA	-	-	No amplification
ct120091	KP279116	Schlautman et al. (2015a)	GTTGAAAGCGA CAAGTCTTC	TAATTTTGCCCTA CCCACC	-	-	No amplification
ct121951[a,b]	KP279117	Schlautman et al. (2015a)	CATGTAGCCGAC TCCAATTA	TATCCCATTCCGT ATAAGGTC	-	-	No amplification
ct124256[a,b]	KP279118	Schlautman et al. (2015a)	GCCGTTAGTTCG TGATATGT	CCTACATGCATAC GTAAAACAG	-	-	No amplification
ct131127	KP279153	Schlautman et al. (2015a)	GAGTAGTCCCGT ATATGGAATG	GTTCATTTCCCCA TTCTGA	-	-	No amplification
ct136900	KP279154	Schlautman et al. (2015a)	ACGATATGAGA GAAGAAGAGGA	CTCTAGTGCATAC CAGCACTT	-	-	No amplification
ct139553[a,b]	KP279125	Schlautman et al. (2015a)	GATCAAGCATTG TTCTCTTCC	AGCTATAGGGCT AGCGATG	-	-	No amplification
ct139597	KP279155	Schlautman et al. (2015a)	CTTATAGGCAAT GCACATACAC	GTAACTAATGGG GCTGAACTT	-	-	No amplification
ct142970	KP279156	Schlautman et al. (2015a)	AAACCTAAATAC CCGGAATG	TATAGACGGCAT ATGCAACA	-	-	No amplification
ct144370[a,b]	KP279127	Schlautman et al. (2015a)	GTAGGAAAAGT TTGAACCGTC	TCAAAGGTTTCAC GTTTCTC	-	-	No amplification
ct144558[a,b]	KP279128	Schlautman et al. (2015a)	TCATTACCCCTA ACCTCTAAAC	ATTCGACTAGAGT GGAGAGAAA	-	-	No amplification
ct146598	KP279157	Schlautman et al. (2015a)	AATCTCATTTTT CCTGGGTC	CTTGATATGCTCT CTTAATGGC	-	-	No amplification
ct152567	KP279135	Schlautman et al. (2015a)	GTGGCTTTTCTG ATCTTGTT	AAAGTACTCTCAA TTGGTACGG	-	-	No amplification
ct154654[b]	KP279139	Schlautman et al. (2015a)	GATTTCTAGTGG GAAATGAAGG	GGTGTATGTGTG TGATTAAGGA	-	-	No amplification
ct159707[a,b]	KP279142	Schlautman et al. (2015a)	TGTTAGCTCCTT ACTTTCCATC	GTGAAGAGGAAG ATGAAGAATG	-	-	No amplification
ct160768	KP279143	Schlautman et al. (2015a)	GTGTGGTATGT TGGATGTAAAC	TAAGGGGATTTC ATTGGG	-	-	No amplification
ct171223	KP279146	Schlautman et al. (2015a)	GCGTGTTATTAT TCCTCTACCT	GGTACATTCTTTG ACCGAGTAT	-	-	No amplification
SCF46833[a,b]	KP278718	Schlautman et al. (2015a)	GGACCGCCGTAT TTAGTTA	GCCCATACCCCTA GTTATTG	-	-	No amplification

SCF141794[a,b]	KP278877	Schlautman et al. (2015a)	CCATCTGCATCT ATTGTTTTG	CATTTGTAGGTCT ATCTTTCGC	-	-	No amplification
SCF56717[a,b]	KP278733	Schlautman et al. (2015a)	GTGTTTGTGTTT GTGTCTGTG	GATGATTTCACCT ACATCGG	-	-	No amplification
SCF134906	KP279080	Schlautman et al. (2015a)	GTATGATTGGTC TTGGTCTGAT	GCAACAGCTAGA GATGCTTAAC	-	-	No amplification
SCF86438[a,b]	KP278782	Schlautman et al. (2015a)	CTATTGAAAACA AGGAACGG	CCTATACAACCTC TTCGGATAA	-	-	No amplification
SCF72229[a,b]	KP278756	Schlautman et al. (2015a)	CAACTTCTACAA CCACTCCAC	GATTTATTGTGCT ACACTGGTC	-	-	No amplification
SCF22993	KP278994	Schlautman et al. (2015a)	GACTGTGCGTA GACTTGATCT	AAGTATGTGTAG GCCGAAAA	-	-	No amplification
SCF68007	KP279033	Schlautman et al. (2015a)	CACCCACCACAA CATAAAC	TCTTCTACTGAAC AGCTTCTTG	-	-	No amplification
SCF41166	KP279015	Schlautman et al. (2015a)	TTCTAACTCAAG TAGTCCTCCTG	AGAAGAACAGCA GATTCCAC	-	-	No amplification
SCF150410	KP279089	Schlautman et al. (2015a)	AACGTAGACAC GAAAAGAAGAC	GCTAGACATGGT TGGAAGAC	-	-	No amplification
SCF48612	KP279021	Schlautman et al. (2015a)	GAACACGATTTG ACATTTCC	CTCCTATGTTGTT TTCGTCTGT	-	-	No amplification
SCF130555	KP279073	Schlautman et al. (2015a)	GGGTAAAATAA AAGGTTCTCC	TCCTTACTTGTCG ATTAGGC	-	-	No amplification
SCF82870[a,b]	KP278775	Schlautman et al. (2015a)	GCTAAAGAACG AACAACAACAC	GTCCAACGAGTG AGTAGAGAAG	-	-	No amplification
SCF2483[a,b]	KP278601	Schlautman et al. (2015a)	TTTCCTTCATAG TGTTGCCT	GTCTCCCTGTTAA ATCCACTC	-	-	No amplification
SCF49598[a,b]	KP278723	Schlautman et al. (2015a)	ATGAGGTTTTCC AACACAAC	TCAGAGGGAAGT ACATGAGAAT	-	-	No amplification
SCF83971	KP278778	Schlautman et al. (2015a)	ATTCTGGTACTG TTTGTTGCTC	GTTATGTTTCGTG TTCCACTCT	-	-	No amplification
SCF133376[a,b]	KP278865	Schlautman et al. (2015a)	ATTAGCACCGAA TTTAACACC	GATTATGGGTGA GTCTGTGAAT	-	-	No amplification
SCF172027	KP278921	Schlautman et al. (2015a)	ACTCCTATTGCC ATTCCAC	CAGTGACAGAGT TGTGGTTAAG	-	-	No amplification
SCF4386[a,b]	KP278612	Schlautman et al. (2015a)	GTTACTCATTTC TTTGCTGAGG	CCTCTTAGTGTTG GAGTTTCAT	-	-	No amplification
SCF157992[a,b]	KP278904	Schlautman et al. (2015a)	TAGGTTTGTCTC TTATCCATCC	GAGTTTGTGATTT CTTAGGAGC	-	-	No amplification
SCF91560	KP279047	Schlautman et al. (2015a)	TATTAAACTCAC TGCACCTCTG	TGACCATCTATGA GAAGCTATG	-	-	No amplification
SCF43996	KP279019	Schlautman et al. (2015a)	ATAGTGTATGTA TCAGAGCGGG	TATTTACGGGAG GTGTGAACTA	-	-	No amplification
SCF162565[a,b]	KP278913	Schlautman et al. (2015a)	CTTCCGTGATTG TTCTTGTAG	ACACAGATGGGA TGTTGTATC	-	-	No amplification
SCF132506[a,b]	KP278862	Schlautman et al. (2015a)	AATGTGCCAAGT TTTGTAGAC	GTCCCCTATAAGT CATCTGAAA	-	-	No amplification
SCF3914[a,b]	KP278609	Schlautman et al. (2015a)	TGTGGAGTTAG AGTGACATACC	GACAAGAATGAT GAGTAGCGT	-	-	No amplification
SCF23691[a,b]	KP278662	Schlautman et al. (2015a)	CGGCTTTGTTAG TTGATGTT	CGATGTTGTACTA TTCATGTCC	-	-	No amplification
SCF118603	KP279063	Schlautman et al. (2015a)	GGACAAACACTA AATAAGCCAC	CTGCTCACAGAAT ACCACTAAA	-	-	No amplification
SCF94237[a,b]	KP278795	Schlautman et al. (2015a)	ATCGCATCAGGT AAGCTAGTAT	TCGAGTGTCATT GTAATAGGC	-	-	No amplification
SCF9100	KP278972	Schlautman et al. (2015a)	TTAGTCCCACTC CTCAATTATC	GGGCTCACTATCA CTACTCATT	-	-	No amplification

SCF149976[a,b]	KP278893	Schlautman et al. (2015a)	TATACCCATGTA TGTACGCATC	ACTCTAAGCAGG ACAATGCTAT	-	-	No amplification
SCF181772[a,b]	KP278931	Schlautman et al. (2015a)	AGCAACGTATG GTGGTATC	CATTTGTTTCCAC AGCTTC	-	-	No amplification
SCF59248[a,b]	KP278740	Schlautman et al. (2015a)	TAGTTGAAAATG GAGAGAGAGC	TTAGATGCCCAAC ACTACATC	-	-	No amplification
SCF77376[b]	KP278764	Schlautman et al. (2015a)	CTCATCAAAAGA GAGGAGAACT	TGTAACCAATCTT CATGCTG	-	-	No amplification
SCF132369[a,b]	KP278860	Schlautman et al. (2015a)	CTACTTTGGGAT GGAGAGAGTA	AGGTTTAGGTAG TGTTGGATTG	-	-	No amplification
SCF165	KP278955	Schlautman et al. (2015a)	CCTCCTCAATCT TCTTCTCC	TATCTTAAACGGC TGATCTCTG	-	-	No amplification
SCF3507	KP278961	Schlautman et al. (2015a)	GCTAATAAAGGT TGAAGTCTGG	CCATGTAGTAGT GAGAGCTGTG	-	-	No amplification
SCF3551[a,b]	KP278608	Schlautman et al. (2015a)	CTTCGACGTTTC TGTGACTAT	AGTTGGTGATTG GAAGAGTAAG	-	-	No amplification
SCF5935	KP278965	Schlautman et al. (2015a)	CTGAACTGAAAC ACCAAGAAC	AGAAATGAGACC TACACTGCAT	-	-	No amplification
SCF6050	KP278966	Schlautman et al. (2015a)	TAACAAAATAGA GACCTCCCTG	TTGACTGGTTGAT GGTGTATAG	-	-	No amplification
SCF6530[a,b]	KP278614	Schlautman et al. (2015a)	CCCCAAGTATAA TGTGTAAAGG	AGTTCGCATAGA AACTGTAGGA	-	-	No amplification
SCF6819	KP278968	Schlautman et al. (2015a)	TCATCATCACTC CAACTACAGA	TGTAAATTCTGAG CCCTTGT	-	-	No amplification
SCF7822	KP278969	Schlautman et al. (2015a)	GTCACTCATGGT AGTATTGTACG	AGTCTTACGTTTG GTGTCG	-	-	No amplification
SCF9157[a,b]	KP278626	Schlautman et al. (2015a)	GGCTTAACAAAT TAGCCCTT	GAGAGGATTTAC CGACAAAGTA	-	-	No amplification
SCF9350	KP278973	Schlautman et al. (2015a)	GGATTTACCACA CCATTCTG	AAGAAATTACCAC ATGCACC	-	-	No amplification
SCF9709	KP278627	Schlautman et al. (2015a)	CCATTAGAAGAG TTTACCGTGT	TTATCAGTCCCTT ACTCAATCC	-	-	No amplification
SCF11084[a,b]	KP278635	Schlautman et al. (2015a)	GTTGGCTGAGG TAGCTGATAG	CCTAAAAGGGCT CACAAGTTA	-	-	No amplification
SCF13045	KP278976	Schlautman et al. (2015a)	TGTCCAGTGCTA ATATCTGTGT	TCCTCCAAATCTA TGCAAAC	-	-	No amplification
SCF13665	KP278980	Schlautman et al. (2015a)	TTCTTTACTATA CCCACAACCC	GTTTCCTAAGAGC ATCAACAAC	-	-	No amplification
SCF13753[a,b]	KP278641	Schlautman et al. (2015a)	AAGTCCTTTCCT TCTTTTGC	GCTATGTGATGT CGTTCCTAA	-	-	No amplification
SCF14119[a,b]	KP278643	Schlautman et al. (2015a)	TAACAGTACAAT GCCTAGTTCG	GGATTCTCTTGCT TTGGTATAG	-	-	No amplification
SCF14690	KP278983	Schlautman et al. (2015a)	CCTTCCATCTTCT TCTTCAAC	AACAAGGTTAGG AAACTAGGGT	-	-	No amplification
SCF14838	KP278984	Schlautman et al. (2015a)	ATAATTTTGTCC CACACGG	TGAGAGTTCAAG GGCAATAA	-	-	No amplification
SCF21119[a,b]	KP278654	Schlautman et al. (2015a)	GGATTTGAGGA CTATACCAAGA	TTAAAAGGCATAC GCTGAC	-	-	No amplification
SCF22434[a,b]	KP278656	Schlautman et al. (2015a)	TATGTATAGTCC CACAACAAGG	TCCTGTCTATCAC TCACATCAC	-	-	No amplification
SCF22962[a,b]	KP278659	Schlautman et al. (2015a)	GTGCAACAGCTA ACAGCATA	AGGACCAATACTC AGAACAAAC	-	-	No amplification
SCF25446[a,b]	KP278665	Schlautman et al. (2015a)	TAGTGTGGACTT AACATGGAGA	ATCCAACCAAGTA TCAGCAA	-	-	No amplification
SCF26014[a,b]	KP278667	Schlautman et al. (2015a)	GGTCCCAGAATC AATGTCTA	GAAATCAGAGAA GAAACAGGTC	-	-	No amplification
SCF27934	KP278673	Schlautman	TCCAAATAGCCC AGAATAAG	GGTACTCCCATGT AATTGTTGT	-	-	No

		et al. (2015a)					amplification
SCF28955[a,b]	KP278679	Schlautman et al. (2015a)	TATTCAAAGCCA CTAGGCAC	CAAACCAAATTCT CCTTCTG	-	-	No amplification
SCF30716	KP279000	Schlautman et al. (2015a)	ATCGGTGACAAA GGTAGATACA	TGTCTAGGTTGA AAACAAGGAG	-	-	No amplification
SCF35370	KP279008	Schlautman et al. (2015a)	AATCATGGTCTT CTCACGTT	GTATAATTGCGTA AGTGCTCG	-	-	No amplification
SCF35507[a,b]	KP278697	Schlautman et al. (2015a)	GTCTAATCTAAT GCAGAATGCC	AATGTGGACAAC GAGTACATCT	-	-	No amplification
SCF36355	KP279009	Schlautman et al. (2015a)	GTGAAAGGACT GTTTTACCCTA	GAGGAGGGGTTT CTCTTTT	-	-	No amplification
SCF36905	KP279011	Schlautman et al. (2015a)	GATAAGCTGTG CTGAAACATC	CGATAGGGGATA GAATTAGTCA	-	-	No amplification
SCF38340[a,b]	KP278701	Schlautman et al. (2015a)	CAAACCATTTTA ACGGAGAG	AATCATCGTGCAT ACCTGTT	-	-	No amplification
SCF41361[a,b]	KP278708	Schlautman et al. (2015a)	AAAATTGCTTGG TCCTCAC	AAGTGTATAGTCT GGGGTGTTC	-	-	No amplification
SCF46912[a,b]	KP278719	Schlautman et al. (2015a)	GAACAATAAAGA GGCTAGAGGA	CATAGTTGTAGA GAAGATCGGG	-	-	No amplification
SCF61189[a,b]	KP278744	Schlautman et al. (2015a)	GCCATAACTCTC ACTCAAATCT	ACCTATTCACCTA CATCCAAAG	-	-	No amplification
SCF61946	KP279028	Schlautman et al. (2015a)	GGATAAAAGGG TACTCCATACA	GGTTCATAGTGG CGAAATTA	-	-	No amplification
SCF69981[a,b]	KP278752	Schlautman et al. (2015a)	AGCGTTACCACC GAATATAA	CGAGATATAGTT AAAAGGACGG	-	-	No amplification
SCF74895[a,b]	KP278760	Schlautman et al. (2015a)	GTACTCCTCTCC GTCTAGCAT	GATTTTATGCGTT AGCTCCA	-	-	No amplification
SCF77382	KP279037	Schlautman et al. (2015a)	GTTTTCCACAAA TCTAGTCGTC	TGTGAGACCAAA GTGACAAG	-	-	No amplification
SCF80520[b]	KP278769	Schlautman et al. (2015a)	TAAAGTGTTTTG GACGGCT	GCACAAATTATCG GAATCG	-	-	No amplification
SCF81294[a,b]	KP278771	Schlautman et al. (2015a)	CTATCGACGGCT GAGATTT	AAAAGGGGAAGA TCCTAGAAG	-	-	No amplification
SCF82535[a,b]	KP278774	Schlautman et al. (2015a)	TAGAAGAGGAA AACTGACGGA	TTGATGCAATCTG ACAACG	-	-	No amplification
SCF85776	KP279044	Schlautman et al. (2015a)	CTAAGTTCCAAA CAGAGCCTTA	AAGTTACCACCGC TAAGAAAC	-	-	No amplification
SCF112295[a,b]	KP278829	Schlautman et al. (2015a)	AACATCTCTACC TCTCACGTTT	TAGTATTAGTTGA TTTGGCGTG	-	-	No amplification
SCF123643	KP279068	Schlautman et al. (2015a)	CAAGAATGAAG AGAAAGATTCC	CAGGTTTTATTAG CCTGTGTTT	-	-	No amplification
SCF126708	KP278854	Schlautman et al. (2015a)	CGACGAATAAAC AAATCAAGTA	GAGAAGAAGTGA AGGAGAGTTG	-	-	No amplification
SCF136826[a,b]	KP278868	Schlautman et al. (2015a)	GATCTTGATTAG CTCCAACTG	GCTTACACCAATT CTACAGTCA	-	-	No amplification
SCF153094[a,b]	KP278897	Schlautman et al. (2015a)	TGTCATTAGGGT TCCTCAAA	CACCTAGACAACA TCGAAACTA	-	-	No amplification
SCF155797[a,b]	KP278902	Schlautman et al. (2015a)	ATCATTAAGGCT CCCAAAG	GTACGTCTACTCT GACGGCTA	-	-	No amplification
SCF156807	KP278903	Schlautman et al. (2015a)	AGGAGGTTTGG ACTAGAAGTTT	CCTGGTTGTCGG ATTAGAT	-	-	No amplification
SCF189827[a,b]	KP278938	Schlautman et al. (2015a)	TTCATTTCCTTAC ACTTCCC	GTTAGCTTCTTCT CCTTCTTCA	-	-	No amplification
SCF192074	KP278940	Schlautman et al. (2015a)	CCTTGGAAAACA CCTTTTG	GCCAAACAATATG GGACAG	-	-	No amplification
SCF117	KP278954	Schlautman et al. (2015a)	ATAGCATCTGTC TTATTGGACG	GTGGGTTTCTGA TCTTCATCT	-	-	No amplification

SCF662	KP278956	Schlautman et al. (2015a)	TTGGACAATCTT ACCCATAGAC	CTTGGCGTGCAT AGAATAA	-	-	No amplification
SCF1047[a,b]	KP278596	Schlautman et al. (2015a)	GAGCTTTGGCCT CATATTACT	CGAATTACTCCAA CCAACAT	-	-	No amplification
SCF1128[a,b]	KP278597	Schlautman et al. (2015a)	GTTTGTTGTTGT GGTGGTTT	CCTTACTTGACGC TTACTTCAG	-	-	No amplification
SCF2270	KP278958	Schlautman et al. (2015a)	TTGGTGTAAAG AAGGATAGGAG	GGCTCCAACTAAT GCTATGA	-	-	No amplification
SCF2942	KP278959	Schlautman et al. (2015a)	ATAAGATCGGT GAAGGATAGG	AAGGAGATTAAG AAGGTCCAAG	-	-	No amplification
SCF3261[a,b]	KP278604	Schlautman et al. (2015a)	GTTTACCATATT CACTCCTTCC	TGAGACAGACCT AACATTTGAC	-	-	No amplification
SCF3595[a,b]	KP278607	Schlautman et al. (2015a)	AGACTACAGTGA ACAAAGACCA	CTGACTTGGTGT GATTAGTGAG	-	-	No amplification
SCF5230	KP278963	Schlautman et al. (2015a)	TTCAAGATGCCT AAACCAGT	GTATAGTGGAGA AGAAGGGTGA	-	-	No amplification
SCF6053	KP278967	Schlautman et al. (2015a)	GTTGAAGCATCC TACTCAAAAC	CCTAGTGAACAGT CATTTCCTT	-	-	No amplification
SCF7569[a,b]	KP278619	Schlautman et al. (2015a)	CCCAATAACGAC TCATATACCT	ACCCAGTCAAAAT CTCCTTT	-	-	No amplification
SCF8850[a,b]	KP278623	Schlautman et al. (2015a)	GTGTGATGTATT TAAGGAGTACCA C	ACAGATAGAGTA GTTACCAAGGGA	-	-	No amplification
SCF9068[a,b]	KP278624	Schlautman et al. (2015a)	AAATCTAGGTAG GAGCAGGTCT	ATGGAGGAGGAG ATATGTGAT	-	-	No amplification
SCF8987[a,b]	KP278625	Schlautman et al. (2015a)	AATCTTTGTCTG AGGTAAGTGG	AACCAGTGTAGT GCAGTTTATG	-	-	No amplification
SCF10785[a,b]	KP278633	Schlautman et al. (2015a)	ACATAAAGGAG AGGGAGTAGAG	ATACCACTTGATA GATTCCTCC	-	-	No amplification
SCF13771[a,b]	KP278642	Schlautman et al. (2015a)	AGGATGATGAA ATCTGCAAG	ATCAGTTAGGTG GGGTAAGG	-	-	No amplification
SCF14090	KP278981	Schlautman et al. (2015a)	GTATTGTCTGGA GATTCCCTAA	GCTCTTTGCATCA TACTCAA	-	-	No amplification
SCF15112	KP278986	Schlautman et al. (2015a)	GTATTGTGAGA GGATGACCTG	AAGGGCTTTAGT GTTGTTGT	-	-	No amplification
SCF15143	KP278987	Schlautman et al. (2015a)	AAAGCCTGCAAA TACTCCTA	CAAACTAGGTCAC AAGCACTTA	-	-	No amplification
SCF15729	KP278988	Schlautman et al. (2015a)	GAACTGGCTCAC TAAAAGAACT	GGTGCATAGCGA TCTTACTATT	-	-	No amplification
SCF16166[a,b]	KP278646	Schlautman et al. (2015a)	CCTAGTCATTCT TCTACTCCCA	GGGTTATCTCGTC CATATTGT	-	-	No amplification
SCF16407[a,b]	KP278648	Schlautman et al. (2015a)	GGCAGTGAATT AAAGGTCAAC	GATGAGAAAGAA GAGTAAGGCA	-	-	No amplification
SCF18113	KP278990	Schlautman et al. (2015a)	GAAGACATCAAA ACTGGGACT	TCAGATCAACACT GGACTAAGA	-	-	No amplification
SCF19565[a,b]	KP278652	Schlautman et al. (2015a)	GGGTTTTATGA GTTAGAGTCCC	GTAGCGATGGTC TT	-	-	No amplification
SCF19788	KP278992	Schlautman et al. (2015a)	TTCTCTGACTTG TCTCGACC	CATTCCTGAAAAC AACTACTCC	-	-	No amplification
SCF20681[a,b]	KP278653	Schlautman et al. (2015a)	AGCCTAAACCTC TGTTTGATG	TTACAATACCTCG CTCCTTAGA	-	-	No amplification
SCF21596[a,b]	KP278655	Schlautman et al. (2015a)	ATATACTGGCAT AAACACCCTC	CCTTACTCTTATC ATGGCTAGG	-	-	No amplification
SCF22442[a,b]	KP278657	Schlautman et al. (2015a)	ACAAAGAAAGA CACTCCATCTC	GTATTTGACTTCC ATGACCAC	-	-	No amplification
SCF22477[a,b]	KP278658	Schlautman et al. (2015a)	CTCTCCCCTACTT TCTTCCTAT	GCCGCTAACACAA TTAACTAAC	-	-	No amplification

SCF28931[a,b]	KP278678	Schlautman et al. (2015a)	TCTCATAAGTCA GAACCTCACA	CTAAACTAAACCT CCTAACCGA	-	-	No amplification
SCF29560[a,b]	KP278680	Schlautman et al. (2015a)	GTGTGGTGTGG TCTCTACAAT	ACATCTCTTTGGC TGATACTTC	-	-	No amplification
SCF29735[a,b]	KP278681	Schlautman et al. (2015a)	CGTAAAATCTGT TGTCTCTGTG	TCTCTATGCTCCT TCCACTTAT	-	-	No amplification
SCF30167	KP278999	Schlautman et al. (2015a)	AGACATACGAA GTCCATGAAAC	CACCCATAACTCA CCTCTAATC	-	-	No amplification
SCF31172[a,b]	KP278686	Schlautman et al. (2015a)	ACTGGATCTGGT GTTATTTACC	GGCTGGAAACAA TTCAAAC	-	-	No amplification
SCF31208[a,b]	KP278687	Schlautman et al. (2015a)	AACAGCACCACT ACAACACTT	AGAGAACAATCG TCTAATCGTC	-	-	No amplification
SCF31394[a,b]	KP278688	Schlautman et al. (2015a)	GTAGCAAAAGA AGAGACACCAT	CGTTTTCCAGTTC CAGAGTA	-	-	No amplification
SCF32769	KP279003	Schlautman et al. (2015a)	CTTACTGCCTTA CATCCTCTTT	CTGGCAAATAGCT TACAGAAC	-	-	No amplification
SCF33654	KP279006	Schlautman et al. (2015a)	CACAGCCTTAAC ACAGGATT	GTGGCTCCTTATC TGGGTA	-	-	No amplification
SCF34010[a,b]	KP278693	Schlautman et al. (2015a)	GAGAATATGTG ATGTTGAGGTG	CAAGTGTTAGGC TCGTTTAGTT	-	-	No amplification
SCF38553[a,b]	KP278703	Schlautman et al. (2015a)	CTTCTGTTTACT CACTTCCACC	ATGGTCCCAAGAT ACTTTAGC	-	-	No amplification
SCF38942[a,b]	KP278704	Schlautman et al. (2015a)	CTTGCTATTTGG TACTCGTCTT	CTTGACAGTTATT TCTCTTCGG	-	-	No amplification
SCF39229	KP279012	Schlautman et al. (2015a)	AAAAGCTACGAT ACGAATGC	AGAAGGAGATAG TCAACGAATG	-	-	No amplification
SCF41971[a,b]	KP278709	Schlautman et al. (2015a)	ATACTTGACCTC TATGGCTTGA	GTACTTACGTGTT TGGTTCGTT	-	-	No amplification
SCF72209[a,b]	KP278755	Schlautman et al. (2015a)	CTTTACCTTTTCC TTCAGTCGT	GAGGTTCACCAA ATCTTACCA	-	-	No amplification
SCF74917	KP279034	Schlautman et al. (2015a)	AAACATAAAGAG CAGCCAGTAG	CTGATAAATAGA GACAGACGGG	-	-	No amplification
SCF79620[a,b]	KP278768	Schlautman et al. (2015a)	TAATAGCCCTTA TACCTGCACT	GAGCATAGACAG CATACAAAAG	-	-	No amplification
SCF8190[9a,b]	KP278773	Schlautman et al. (2015a)	TAGAGGAATCA GCAACTTCACT	TTCACACTCACAC TCACACG	-	-	No amplification
SCF83872	KP279040	Schlautman et al. (2015a)	GGAGCTTGAAA ACCTAAACA	GTTAGTGAGGAG GGGAGAG	-	-	No amplification
SCF84804[a,b]	KP278779	Schlautman et al. (2015a)	CTAGTCTTCTTG TGACCTAGCC	TATTCTTTTAGTC CGAGCCA	-	-	No amplification
SCF85469	KP279043	Schlautman et al. (2015a)	CCAGATAAGTAA CACAACACCA	GGGAGTGCTCAT TTGTAGTC	-	-	No amplification
SCF87305	KP279045	Schlautman et al. (2015a)	AATGCTCTCCAG ACTTTTCTAC	GTGCAGTATCAA ATGTAAGACG	-	-	No amplification
SCF87786	KP279046	Schlautman et al. (2015a)	AGGGAGATAGT TGTTCCCAT	GCCTAAACCTAGT AAACTCTGC	-	-	No amplification
SCF87990[a,b]	KP278783	Schlautman et al. (2015a)	GTGTAGGTGTA AATGTGCTTTG	GGCGTATAAAAG GATTCAAG	-	-	No amplification
SCF89247[a,b]	KP278786	Schlautman et al. (2015a)	TGGAGGAGGTG AAGAATACTAA	CCCTTTGGACAAC AAAATAC	-	-	No amplification
SCF89801[a,b]	KP278790	Schlautman et al. (2015a)	TAAACCTGTTCC GTCTCTTAGT	CTTTACTGTTGTG TTGTCTGCT	-	-	No amplification
SCF90229a,b,	KP278791	Schlautman et al. (2015a)	GTACTTTTGTGG AACTTAACGC	CTGTCCTTTCACT CCTCTTTT	-	-	No amplification
SCF98180[a,b]	KP278802	Schlautman et al. (2015a)	CTCCTCTGCTTA TCTCTTCAAC	GGTTTTCCCTTCT CAAGATTAC	-	-	No amplification

SCF98686[a,b]	KP278803	Schlautman et al. (2015a)	CGTAATTTCACA TCCTCGTT	CATAACCAGATAG CACCTCAAT	-	-	No amplification
SCF101914[a,b]	KP278806	Schlautman et al. (2015a)	CTTTGGAGCACA ACAACTCTA	GTGTAAAGACCA GGACCCTT	-	-	No amplification
SCF102509	KP279055	Schlautman et al. (2015a)	ATAGGATTTGTT AGACTTGGGG	GGAGCTGTTGAA GCTATTGTTA	-	-	No amplification
SCF102538[a,b]	KP279056	Schlautman et al. (2015a)	TTACTGGGCAAT AGAAGGACT	CACATAAGTTTGG CTACACAAC	-	-	No amplification
SCF105092	KP278810	Schlautman et al. (2015a)	AGGAACTAGGA AGTAGGAAGAT G	GTGCTATACAGG CATACAAGTG	-	-	No amplification
SCF106182[a,b]	KP278813	Schlautman et al. (2015a)	TACCCTTGTGTA TCCCTACATT	GAACAATAGCAG CAACAGAAC	-	-	No amplification
SCF107477[a,b]	KP278814	Schlautman et al. (2015a)	GTCTTATTTTCA CTGTCGTGTG	CGGGCATTAACCT TATACCT	-	-	No amplification
SCF108101	KP279057	Schlautman et al. (2015a)	AAATCTTCCATG AGCTTGTC	TACTGCGGTGTT GAATTAGA	-	-	No amplification
SCF108252[a,b]	KP278817	Schlautman et al. (2015a)	CCTATGTAATTG GATTCTACCC	GTGTATCAAGGT GGAGAAAGTC	-	-	No amplification
SCF111370[a,b]	KP278828	Schlautman et al. (2015a)	ACCACATCTTCA TTTTGAGC	GTAAAACAATAC GGGTCCTTAC	-	-	No amplification
SCF115821	KP279060	Schlautman et al. (2015a)	TCACCACTTACA ACATATCCAC	TTGACACTAGCAA ATTCCATC	-	-	No amplification
SCF117385[b]	KP278838	Schlautman et al. (2015a)	TAAGAATCCTCG TCATAGGGT	CTGTCTTCTCAAC TTTCCCTC	-	-	No amplification
SCF118468[a,b]	KP278840	Schlautman et al. (2015a)	ATAAGCGGAGC ACAGTTACA	GATAGGATGACC TGTTTTGGT	-	-	No amplification
SCF118536	KP279062	Schlautman et al. (2015a)	GGGTACTATATG AAGGTGCCTA	CTACCATGTAACC CTTGAAAGT	-	-	No amplification
SCF118608[a,b]	KP278841	Schlautman et al. (2015a)	AACTACTCGATC TTCACCCTTA	AGGAGACCAACA CTTAACCTC	-	-	No amplification
SCF119813	KP279064	Schlautman et al. (2015a)	GTTAGTCGGCTC AAGTTAGTTC	ATGGACTTCCCAT TTCTTTC	-	-	No amplification
SCF120937[a,b]	KP278844	Schlautman et al. (2015a)	TGTGCAAGAGT CATCTCCTAT	TATTCCCTTTCAT TCTCCTTC	-	-	No amplification
SCF121995[a,b]	KP278845	Schlautman et al. (2015a)	TAGTCGTGACCA AGAGTGATTA	GCCACCGAGTAT ATTTCTATGT	-	-	No amplification
SCF122440	KP279066	Schlautman et al. (2015a)	CTAATCTTCCTC CTCTTGTTGA	CGACAAACTAACA TATCATCTCC	-	-	No amplification
SCF122746[a,b]	KP278846	Schlautman et al. (2015a)	ATTGTATGAAAA CCCTAACCC	GAGACGATTCCA AATATAGCA	-	-	No amplification
SCF125251[a,b]	KP278851	Schlautman et al. (2015a)	TATACAGTCAGA TCCAATCCAC	TGCAGATAAAGT ACAAGAGTGC	-	-	No amplification
SCF127023[a,b]	KP278855	Schlautman et al. (2015a)	TATGCTAATCCA CTTTGTAGGG	AATCTGGGTAATT GGGAACT	-	-	No amplification
SCF133587	KP279078	Schlautman et al. (2015a)	TTAAGCACCAAC ACTAAATCC	AGTTCATGTGAC GTTGTATCA	-	-	No amplification
SCF136317[a,b]	KP278867	Schlautman et al. (2015a)	GAGAGTTCAAAT TACCTGTACCA	GGAGATTAGGTT GTGGACTAGA	-	-	No amplification
SCF136684	KP279081	Schlautman et al. (2015a)	TCTTATCCTGCT TTCTTACCC	ACAGGGTCATTAC TGTCTTGTT	-	-	No amplification
SCF137494[a,b]	KP278869	Schlautman et al. (2015a)	CCAACATAAAGA GGACTAGAGG	GACCTAGACTCCA AATCACG	-	-	No amplification
SCF138992[a,b]	KP278873	Schlautman et al. (2015a)	ATACTTTACCCC ACAGAGCTTA	CCACTCATGCTCA CATCAC	-	-	No amplification
SCF139660[a,b]	KP278875	Schlautman et al. (2015a)	ATAAATCTACGT CCATACAGCC	GAGTACATACAA ATCCTCTTTCG	-	-	No amplification

SCF142441[a,b]	KP278879	Schlautman et al. (2015a)	TTGCGTTTACTA TCTAAGGAGG	CTCAGCCGTCCAA AAGTAT	-	-	No amplification
SCF142636	KP279082	Schlautman et al. (2015a)	GGTCATGGTGT CATTCAAG	CATGGACAGGTA TTGGACA	-	-	No amplification
SCF142767[b]		Schlautman et al. (2015a)	ATAGTTGGACG GGTGTAATG	CTCTCGCAAAGTA GAACAATCT	-	-	No amplification
SCF143035	KP278882	Schlautman et al. (2015a)	TATTTATAGACG ACCAACCTGC	GTGACCAATATAC CAAACCAAG	-	-	No amplification
SCF143318[a,b]	KP278883	Schlautman et al. (2015a)	CCGTGCTTAAAT TCTGTAGTG	TCATCCATAGGAG AACATCC	-	-	No amplification
SCF145195	KP279084	Schlautman et al. (2015a)	CCACCTTCCATT ATACAGCA	GAACAAGAGAAG AACCCAGATA	-	-	No amplification
SCF146740[a,b]	KP278887	Schlautman et al. (2015a)	ATGGGACTGCTT ATTGAACAC	CAAGTGGTGCAT TGTGAGA	-	-	No amplification
SCF147358[b]	KP278890	Schlautman et al. (2015a)	GTACACTAAACA CCTTGCGTTA	CTCACCTACATCC CTCTAGTTC	-	-	No amplification
SCF147678	KP279085	Schlautman et al. (2015a)	ATTCATAGTTTA CCCGTCACTC	GATTGCTGCTCTT TCAATGT	-	-	No amplification
SCF148938	KP279086	Schlautman et al. (2015a)	CTTCTGTCATTT TAGTGTCCTG	ACCTTTTGAACAC ATTGGAC	-	-	No amplification
SCF149145	KP279087	Schlautman et al. (2015a)	CTTCAACATATA CCCACCCTAT	GACCAAAACTAG AAAACTCCCT	-	-	No amplification
SCF149633[a,b]	KP278891	Schlautman et al. (2015a)	CCTTAATACCCA TCCCATAATC	CTTCTTTTCATTG TTGTGGC	-	-	No amplification
SCF150173[b]	KP278894	Schlautman et al. (2015a)	GTGTTGGGAAA CAGCAGAT	TTATTCTCGTTGT CAGCCTT	-	-	No amplification
SCF150898[a,b]	KP278895	Schlautman et al. (2015a)	AAGCTCCATGTA TGCGTATC	ACACTGACTAGC GTTTGTTGT	-	-	No amplification
SCF153722[a,b]	KP278899	Schlautman et al. (2015a)	AGTTATGAGGCT TACGAGGAG	GATGGAACGATG AAACTGAT	-	-	No amplification
SCF154541[a,b]	KP278900	Schlautman et al. (2015a)	AGAAAGCACAG TAGGTATGGAG	CAAGAAACCCTAG AGACCAAT	-	-	No amplification
SCF158255[a,b]	KP278905	Schlautman et al. (2015a)	ATGCGTACACCT CAATCTTT	GTGGGTACTTGT TTTCAGTTC	-	-	No amplification
SCF158988[a,b]	KP278907	Schlautman et al. (2015a)	CTCTCACCAAAA TCACCATTAG	CAAGTATCAAGTT TTAGACGGG	-	-	No amplification
SCF160647[a,b]	KP278909	Schlautman et al. (2015a)	TAACTCAAAGAA CCTAACCCC	TAAAGTGACAGG TAATGTCGTC	-	-	No amplification
SCF160663[b]	KP278910	Schlautman et al. (2015a)	TTACACCCTATC TCCTGTTTTC	CAGTTCATCTTGC TAGTTATGC	-	-	No amplification
SCF162175[a]	KP278912	Schlautman et al. (2015a)	ACACGTTGAGG TTCCAAAT	AGTTTCTGATTGA CCTAGATGG	-	-	No amplification
SCF163134[a,b]	KP278914	Schlautman et al. (2015a)	CAGTGCAATTAG TTTCCTATCC	TTCTTGGGTTGG TTATTCAG	-	-	No amplification
SCF164500	KP279093	Schlautman et al. (2015a)	AAATCACCATTC TGGAACAC	GGTCGGAATACT AAAACAGAGA	-	-	No amplification
SCF164915[a,b]	KP278915	Schlautman et al. (2015a)	CTCAAAGTATCT CACTCACGC	ACTGTTGTCCCCT CTGACTAC	-	-	No amplification
SCF169090[a,b]	KP278917	Schlautman et al. (2015a)	GAGACAAAGTTC AAATAGGGAG	ATACTGCAACCGA TACTGAGA	-	-	No amplification
SCF170213	KP278918	Schlautman et al. (2015a)	GGGTTTGATGA CTTGTTTGTA	CCTAGAAAATGCA GAAATCG	-	-	No amplification
SCF171621[a,b]	KP278919	Schlautman et al. (2015a)	CACCACTCCCCA TTTTAAG	AAGGGACAGAGG AAGTATTTG	-	-	No amplification
SCF171768	KP279094	Schlautman et al. (2015a)	GTATCCCCTTAT ACAACCTGC	GGCTTCTATTATT CTATTGCCC	-	-	No amplification

SCF172019[a,b]	KP278920	Schlautman et al. (2015a)	TGTGAGTAGTT GTTGAAGGGA	CCTCGAAAATCCG GTAAAT	-	-	No amplification
SCF172906[a,b]	KP278923	Schlautman et al. (2015a)	CTGTTCAAGGAT TTGTACTGG	TATTGACATGAG AAGCACGA	-	-	No amplification
SCF174468[a,b]	KP278926	Schlautman et al. (2015a)	CAACATTCTTCG CTCACAA	CTAAGAGTTGAC ATGATTGGC	-	-	No amplification
SCF177450[a,b]	KP278928	Schlautman et al. (2015a)	TCTAAAACTCTC CTCTCACCTC	GATAGCAGTGGA CTCATGTCT	-	-	No amplification
SCF177451[a,b]	KP278929	Schlautman et al. (2015a)	GTACCATATAAG AAAGGGAGCC	CAATAGAAACCCA AGACAACTC	-	-	No amplification
SCF180863[a,b]	KP278930	Schlautman et al. (2015a)	CCAGTTACAGAT CCTTGAGTTG	GCAATGTTCCCTC GAATTA	-	-	No amplification
SCF183590[a,b]	KP278933	Schlautman et al. (2015a)	TTTGTAGTATGG GGACACTGAT	AAAGAGGCAGGT CAGAAAAT	-	-	No amplification
SCF184873[a,b]	KP278934	Schlautman et al. (2015a)	AAGCGTAGAAT ATGTATGACCC	GGTAGTCCTCAC GGAAGAG	-	-	No amplification
SCF187979[a,b]	KP278935	Schlautman et al. (2015a)	AGATAAGGCAC CCGATAATAC	GATCAAGGAACG CAAATCT	-	-	No amplification
SCF189612[a,b]	KP278936	Schlautman et al. (2015a)	GAGGATTGTTA ATGGTTTCTTT	TACGCTTCATCTT GTTATTTTC	-	-	No amplification
SCF189657[a,b]	KP278937	Schlautman et al. (2015a)	CATCCTTGAAAA TAGACAGACC	CTTAGAAGACCG CACTGAGA	-	-	No amplification
SCF193103[a,b]	KP278943	Schlautman et al. (2015a)	GAGGAGTTGAA ACAATTAGTCC	TACCCACTTTAGT CGAAGGAT	-	-	No amplification
SCF201915[a,b]	KP278947	Schlautman et al. (2015a)	ATGCACATCCTG AAGTACCA	CTGAACACATTGG ACGGAT	-	-	No amplification
SCF204979[a,b]	KP278949	Schlautman et al. (2015a)	GGAAAGAGGTA AGAAATGGG	TAAGAGTTCCCAC AACCAAA	-	-	No amplification
SCF208509[a,b]	KP278950	Schlautman et al. (2015a)	GCTTCACACTTG ATAGTAGGTTG	TACCGCCATTGTA GCAGAT	-	-	No amplification
247873_K63	KP279258	Schlautman et al. (2015a)	GATCGGAGAGT TTTCCTCTT	CAATTTCCTTCCC CAACTAT	-	-	No amplification
354699_K63[b]	KP279172	Schlautman et al. (2015a)	GAAGCGATTTG GAAGAAAC	ACACAGAGAGAT TACGAACACA	-	-	No amplification
1trimcontig178 732	KP279279	Schlautman et al. (2015a)	ATGGTCCCTGAG TCTAACTTC	GGATCTCTATTTC AGTGTGTTG	-	-	No amplification
42710_K70[a,b]	KP279194	Schlautman et al. (2015a)	GTTACACACACA CCCACAGA	GAGAGAGGACTA GGTCGTACAG	-	-	No amplification
309084_K70[a,b]	KP279212	Schlautman et al. (2015a)	CTTCTTTTCCTCT CCACTGATA	CTCTCCGTTGTCC ATTTCT	-	-	No amplification
1trimcontig175 770[a,b]	KP279220	Schlautman et al. (2015a)	GTGTAGCTTGG AAAATAGGAGT	ACTAGGGAGCGA GAGAGAGTA	-	-	No amplification
71002_K63[a,b]	KP279161	Schlautman et al. (2015a)	CTTCAATCCACG AATACCAC	CAATTATGCAAAG GAGGAAG	-	-	No amplification
419834_K63[a,b]	KP279192	Schlautman et al. (2015a)	GAAAAGAGAGG AGAAGATGGAT	TACCAGAACTGTG TGAGATTGT	-	-	No amplification
187382_K70[a,b]	KP279202	Schlautman et al. (2015a)	CCTCCATTCTCTC TCCTACTAA	CTTCTTCTCTCTCT C	-	-	No amplification
1trimcontig209 220[a,b]	KP279228	Schlautman et al. (2015a)	GTATTTGTTCAC ACTCACCAGA	ACAGTTGTCGAA GCCTCAT	-	-	No amplification
310238_K70	KP279277	Schlautman et al. (2015a)	GAGTAACAACA GTGGCAAAAC	AACTTCCTCATGT ACTTTCCC	-	-	No amplification
1trimcontig217 288	KP279280	Schlautman et al. (2015a)	ATAACAGAGGA CAACGATCTG	TCACTCTACTTTT ACCGAGACA	-	-	No amplification
1trimcontig351 427[a,b]	KP279242	Schlautman et al. (2015a)	GACGGCTAAATT GTAACTAACG	AGGGTCCTATCCT ATCCTCTAA	-	-	No amplification

389746_K63	KP279263	Schlautman et al. (2015a)	TTGTAAACCTCA AGACACACC	TATCACACAGTTT TGGAGAGAG	-	-	No amplification
417854_K63[a,b]	KP279188	Schlautman et al. (2015a)	AAAAGGAGTCTT GGGAGTAAGT	TTGAGATGTAACT ATGCAGTCC	-	-	No amplification
418596_K63[a,b]	KP279190	Schlautman et al. (2015a)	CGTGAGTTTGA GTGAGTAATTG	AGGACATGGTGA GTTGAGAAT	-	-	No amplification
418730_K63	KP279267	Schlautman et al. (2015a)	ACAGATCCAGTC TCTTCAAATC	ATACGGAGTGTA GATGTCTCCT	-	-	No amplification
319429_K63[a,b]	KP279171	Schlautman et al. (2015a)	GGAGATAGGAA GTGTGATGAAC	TTATTGTGCAAGC ATACGAG	-	-	No amplification
416815_K63	KP279186	Schlautman et al. (2015a)	CGTTTCTTTTCTT CTCTCTCTC	CCTCCATTCTCTC TCCTACTAA	-	-	No amplification
49132_K63	KP279256	Schlautman et al. (2015a)	AACCCTAGAAAT CAATGCAC	GTTTTCCGTTTTG TTCTGTC	-	-	No amplification
417587_K63[a,b]	KP279187	Schlautman et al. (2015a)	TGGGTAGATATT AGATGGCAGT	CTTCTTCTGGAAA TCTGGTTAG	-	-	No amplification
128239_K63[a,b]	KP279164	Schlautman et al. (2015a)	AAATAACGATG GCTACATCC	GTTTGTTGATGAC AATCCTG	-	-	No amplification
307018_K70[a,b]	KP279208	Schlautman et al. (2015a)	TAAAACCTTACC TCCTCTTCTG	TAACCTCGGATCT CCTTATCTA	-	-	No amplification
413893_K63	KP279264	Schlautman et al. (2015a)	TACTCCATTTCA CAACACGA	ATCTCTGCTTCTT CTACCTCTG	-	-	No amplification
1trimcontig448145	KP279287	Schlautman et al. (2015a)	TGTGATTAGAG GGAGGATTTC	AAATAAGGGAGT TTGAACCG	-	-	No amplification
284499_K63	KP279259	Schlautman et al. (2015a)	ATTAGTTCTCCT ATGTGGCTTG	TCAGAGCTTACCC TATTTCAGT	-	-	No amplification
9053_K70	KP279269	Schlautman et al. (2015a)	GCTGATTAGGTT CACTTTCTTC	TTTCTTCACCTCTT TCTCTCTC	-	-	No amplification
242569_K70[a,b]	KP279204	Schlautman et al. (2015a)	GATATGAGAGA CGAGGAATCAC	GTCAGTGGACGG TTTTAAGAT	-	-	No amplification
307534_K70	KP279276	Schlautman et al. (2015a)	ATCGTCTGCTAT AAATACTCCG	GTGTCAACCTTCC TTACAAGAT	-	-	No amplification
482_K70[a,b]	KP279193	Schlautman et al. (2015a)	ACAGCGGCATA GTAAAATGA	GTCACCGAAATCT CACTCAATA	-	-	No amplification
37487_K63	KP279255	Schlautman et al. (2015a)	CTTTCATTAGAG GAGAGCTTGT	AGGAAACTAGCA ATCAGTCAAC	-	-	No amplification
47166_K70[a,b]	KP279195	Schlautman et al. (2015a)	TATTGAGAGTGT GAGACCGTT	TGGTAAGTATCG TAGGTCCAAT	-	-	No amplification
162108_K70[a,b]	KP279200	Schlautman et al. (2015a)	GAAGTCGAAAC CCTAGCAG	GTCCCTCTCAGTC TCTCACTC	-	-	No amplification
1trimcontig178358[b]		Schlautman et al. (2015a)	AATTGAACGATC CCTATTCC	GATTCATCACCCC TTGAAC	-	-	No amplification
1trimcontig328266[a,b]	KP279236	Schlautman et al. (2015a)	ACAGATCAAGC GAACACTAAAC	CCTGCTCCTGTTA TACTACCAA	-	-	No amplification
204816_K70	KP279273	Schlautman et al. (2015a)	CACTCTAATCAC CCTTTCACTC	CAGAGAGGAATA ATACAGGTGC	-	-	No amplification
252600_K70[a,b]	KP279205	Schlautman et al. (2015a)	CTAGTTTAGAGT CGTCCCAAAT	AAGCACCTGAAG ATAGTAGGAA	-	-	No amplification
1trimcontig176303[a,b]	KP279222	Schlautman et al. (2015a)	GCTGATTAGGTT CACTTTCTTC	TTTCTTCACCTCTT TCTCTCTC	-	-	No amplification
1trimcontig182430[a,b]	KP279226	Schlautman et al. (2015a)	GAAGATGGACC TGAGTAAGAAA	CTACCATTGTGTT CTCAAACTG	-	-	No amplification
1trimcontig238795[a,b]	KP279233	Schlautman et al. (2015a)	AGAGGGAGAGA AGAGTATGGTC	CCGTCAAGATTTG TGAAGAT	-	-	No amplification
314761_K63[b]		Schlautman et al. (2015a)	ATTGTTGGATAC TTCATGGC	GTTGGTACTGGT AAACCCTAAT	-	-	No amplification

82171_K70[a,b]	KP279199	Schlautman et al. (2015a)	TAGTAGAGTTG AAGAGGAGGGA	CTAGGGTTTAAG CAAGCATAGT	-	-	No amplification
1trimcontig332 960[a,b]	KP279238	Schlautman et al. (2015a)	GTCAACAGATTC AACACAACAC	CCTGCTTCTCTCT AATGAAGTC	-	-	No amplification
1trimcontig336 911	KP279283	Schlautman et al. (2015a)	CATTTCCTATTTC ATCCCCT	AACAGAGCGAGA GTAATTGAAG	-	-	No amplification
1trimcontig352 078[a,b]	KP279243	Schlautman et al. (2015a)	CGTGTTTCTGTT AGATAGCTTG	CTTGTACGTGAA GATGCAAA	-	-	No amplification
1trimcontig175 833	KP279278	Schlautman et al. (2015a)	CTCTTTCTGCCT GGTTCTAA	ACTACTATTGCGT ATGGCTCTT	-	-	No amplification
1trimcontig354 570	KP279284	Schlautman et al. (2015a)	ACCTGTTCTGTT GATTACGAGT	ACAGTATCGCACA ATGAGTTC	-	-	No amplification
1trimcontig238 080[a,b]	KP279231	Schlautman et al. (2015a)	AGGGGTAATCTT CACACACTTA	ACAGGCTCTTCTA ATCGTTTC	-	-	No amplification
1trimcontig217 158[a,b]	KP279229	Schlautman et al. (2015a)	GGAGTCGGTAA AATCAAGAA	CCAAATTCAGTAG GAGTACACA	-	-	No amplification
1trimcontig241 039	KP279282	Schlautman et al. (2015a)	ATAATGGACTGC ACGAAACT	GTAGTAGGGATT TCACAGGCTA	-	-	No amplification
scf2s[a,b]		Georgi et al. (2013)	TGAGACGTACG CACTAGCCA	GTCGATGGTGTT TGTCGATG	-	-	No amplification
scf4b[a,b]		Georgi et al. (2013)	GATACGATACG GATACGCGG	GTCGATCATGGT CGTCAGTG	-	-	No amplification
scf5k[a,b]		Georgi et al. (2013)	GCATTACTAACA GCATCCCAA	GAGCCACTTTTCA CTCCCAA	-	-	No amplification
Ig13662a[a,b]		Georgi et al. (2013)	CATCTAGCCATG CACCATTG	CCAAGTTCGACAT TTTCCGT	-	-	No amplification
Ig28559a[a,b]		Georgi et al. (2013)	CAAGAGTCGCA AATTCCACA	CCTCCTTCTAGAG AGGGCCA	-	-	No amplification
NA619[a,b]		Georgi et al. (2013)	TCACACTACAGG CAGGAGAGA	GAAGCCCCAGTTC TCACAAG	-	-	No amplification
NA1792[a,b]		Georgi et al. (2013)	GCATCATCGCCG TCAAG	TTGACTTCATCGA AAGCACG	-	-	No amplification
scf9e[a,b]		Georgi et al. (2013)	TCACAGCGGAG AAGTTGATG	ATTTGCGAATCAA CCCAAAC	-	-	No amplification
scf11l[a,b]		Georgi et al. (2013)	TAATGAGTGCTG GTTCTGCG	TTCAAATCCACGT CAGCAAA	-	-	No amplification
scf20g[a,b]		Georgi et al. (2013)	TGAGTGCCGAT GAGGTATTG	AGAGGAGGAGAC GTGCATTG	-	-	No amplification
scf31h[a,b]		Georgi et al. (2013)	TGGAACTCCAAA TGTGCGTA	TGGCACCATAAAT AGCACGA	-	-	No amplification
scf439[a,b]		Georgi et al. (2013)	TTGTGTGATCCG CTACTTGG	ATCGTTCAAAACG AAGGGTG	-	-	No amplification
scf1172[a,b]		Georgi et al. (2013)	GGGGTTTGTGT GTTTATCGC	GTATGCGAATTCA AAGCCGT	-	-	No amplification
scf1655c[a,b]		Georgi et al. (2013)	CATCTATTGATC AGCCGCAA	ACGACCATATGA GCCGAGTT	-	-	No amplification
scf13a[a,b]		Georgi et al. (2013)	TAGAGGGCGTT GAAAGGAGA	CCCCAAATTTCTC CCCATTA	-	-	No amplification
scf32j[a,b]		Georgi et al. (2013)	ATCCACCAAACA AGCCACAT	TCAATCAACGCGA TTCCATA	-	-	No amplification
scf45d[a,b]		Georgi et al. (2013)	TTCTTGTGGTTG TGCTGCAT	TAATGGCTGAAA CGCTCACA	-	-	No amplification
scf94ac		Georgi et al. (2013)	ATGATTTCTTCG GTGCGACT	GCATATCTGTCGC CATTGTG	-	-	No amplification
scf108b[a,b]		Georgi et al. (2013)	ACATAAACGGC GATTCCAAC	ATTGCTCGAGGA TTGGACAC	-	-	No amplification
scf142e[a,b]		Georgi et al.	CTACCGAGCTGG TTGAGGAG	CGAGCGCATAAT CATCTTCA	-	-	No

		(2013)					amplification
scf171f		Georgi et al. (2013)	CTTCGCGCTGCT CTCTATCT	ACAAGAGGAAAG CCCTTGGT	-	-	No amplification
scf203h[a,b]		Georgi et al. (2013)	AAGTTACAACGG TTCGTGGC	TGCAACATTGTGA TGGTCCT	-	-	No amplification
scf207d[a,b]		Georgi et al. (2013)	GACACACGTGG TGCACTGTT	GGTTGATCTTAG GAGCTGCG	-	-	No amplification
scf262a		Georgi et al. (2013)	GAGGGGAAAGG AGAACAAGG	CTAGATTGGGCC ATGCAGAT	-	-	No amplification
scf275d[a,b]		Georgi et al. (2013)	GCTTTTCTGAAG CGATTTGC	CCGCATACACGGC GTACTA	-	-	No amplification
scf303c		Georgi et al. (2013)	AACACCGGTCGA TACACCAT	TCCAAACGTGTGA AATGTCC	-	-	No amplification
scf2253d		Georgi et al. (2013)	TGGATTGTAACC AAGGGCTC	GCCCATCAACACG TAAACCT	-	-	No amplification
scf2505a[a,b]		Georgi et al. (2013)	CCAGAGAGAAG GGGGAAATC	TTATCCCGCCGCT TAGTAGA	-	-	No amplification
scf2882[a,b]		Georgi et al. (2013)	CGCTACCATTGT CAGCTTCA	ACACTCAAAAGCA GGTGGCT	-	-	No amplification
scf3072b[a,b]		Georgi et al. (2013)	AGTTTAAGCGG AGCGAATGA	TTTGGCGACATTT TTCTTCC	-	-	No amplification
scf4860[a,b]		Georgi et al. (2013)	TTCGCTCAAGTC AACTGTGG	CCTTGGACATTTT TCTGGGA	-	-	No amplification
scf6213[a,b]		Georgi et al. (2013)	GCTCGCTCTCGC ATATTTTC	CCTAGCCCGTTCA TCATTGT	-	-	No amplification
scf6955c[a,b]		Georgi et al. (2013)	ATGCCTGCCATT CATCATTT	TTTCCGTCATTTC GTCCTTC	-	-	No amplification
scf9025[b]		Georgi et al. (2013)	TGGCTCCTATAG CGTGTCCT	GCACACCAGGTTC CTTGATT	-	-	No amplification
scf12916[a,b]		Georgi et al. (2013)	GGAGATGGATT TGGCAAGAA	ATCCATGTGGCA GCAGTGTA	-	-	No amplification
vm04084[a,b]	JF834250	Zhu et al. (2012)	GGATTCTCACTC TGATACCATT	GAACGATACACA ACGAAGGT	-	-	No amplification
vm51985[a,b]	JF834280	Zhu et al. (2012)	TGCTAGTATTTT GACTCAGGTG	GCCTATATATAAC CAAGCAAGG	-	-	No amplification
vm55441[a,b]	JF834240	Zhu et al. (2012)	AAAAGGAACAC GGATACGAT	GGATTCGAGAAC CTATCTCAT	-	-	No amplification
vm13742		Zhu et al. (2012)	TCTTAACCACTT TCTTTGCC	GTAAGCCAAGCTT GAGAATATG	-	-	No amplification
vm23232[a,b]	JF834262	Zhu et al. (2012)	ACAGAGCTCAAT GGAGAAAA	TTCTGCTGATAGT GTTGGTACA	-	-	No amplification
vm31502[a,b]	JF834267	Zhu et al. (2012)	TTCTTTTGTCCA CCTTGAGT	TCTCTTCACTTAT TACACCTGC	-	-	No amplification
vm53000[a,b]	JF834283	Zhu et al. (2012)	CTCTCTCTAGCC AAGCAGATAC	AAGATGTGAGGA AGCTAGGAG	-	-	No amplification
vm83024[a]	JF834247	Zhu et al. (2012)	TTCGCCTCTCTA GTTTCTAGTC	GTTATATTACCAC AAGCACACG	-	-	No amplification
vm28527[a,b]	JF834266	Zhu et al. (2012)	GGACAAGTGAA ATGCTAGTTG	AGATTGTTCGTA GGTAGAAGTG	-	-	No amplification
vm78806[a,b]	JF834245	Zhu et al. (2012)	CAAAGAAGAGG AGGATTGAGT	GAGCGAGTATTA CAAGTGTTTC	-	-	No amplification
vm07778[a,b]	JF834253	Zhu et al. (2012)	ATATACGTACAC TCACGCACAC	GTTAGGTGCATA ATAACGGTTG	-	-	No amplification
vm12486[a,b]	JF834257	Zhu et al. (2012)	GGTGGAGATGC TCGTAGTATT	CTAAGGGACGTC AAACCTAAC	-	-	No amplification
vm21169		Zhu et al. (2012)	GTAACCAACAGA AAACTCCTCT	TTACAAGTGGAA AAGGGTAGTG	-	-	No amplification

vm27120[a,b]	JF834265	Zhu et al. (2012)	AAGGTCTAAGA GTTATACCGCA	GGGCATAAGTTA AGAGAGCTAA	-	-	No amplification
SCF45712[a,b]	KP278713	Schlautman et al. (2015a)	GCAGTGTGCTTT TCTTTTCT	GTTACTAGGGTA CTGGGTTTGA	-	-	not tested
SCF61078[a,b]	KP278743	Schlautman et al. (2015a)	GACTCTTCATAT AACCCACAGC	AAAAGTGCTTGA TCGTTAGC	-	-	not tested
SCF27510[a,b]	KP278670	Schlautman et al. (2015a)	CCTTCAGATTCA ACGTATTCTC	GGTGTATCACATC CCAAAAC	-	-	not tested
SCF53750[a,b]	KP278727	Schlautman et al. (2015a)	GTTTCATAGAGA TGGGTTTCTG	CTTGGTTCCCTAA GCTACATT	-	-	not tested
SCF23339[a,b]	KP278661	Schlautman et al. (2015a)	GCAAAACAGAG TTATAGTGGCT	TAGACAGAAGCA CAGATTGGTA	-	-	not tested
SCF27755[a,b]	KP278671	Schlautman et al. (2015a)	GAAGTGAGAGT AGGAATCGAAG	CCACAACACAAAA CCCTAAT	-	-	not tested
SCF26697[a,b]	KP278669	Schlautman et al. (2015a)	TCGTAACTATTC AGTGGGTGT	GGAGCAGTAGAG ATTAAACGAC	-	-	not tested
SCF28613[a,b]	KP278677	Schlautman et al. (2015a)	CATTCTTCACTC CAACTTCAG	CAAGTCCCATCAT CATTTTC	-	-	not tested
SCF83615[a,b]	KP278777	Schlautman et al. (2015a)	ATTAGTCGATCT CCTTTTCCTC	AAATTGTAGAGC CAACACTAGG	-	-	not tested
SCF147117[a,b]	KP278888	Schlautman et al. (2015a)	AGATATGGAGT GGATTAGGTTG	GTTAGAGTGAAA TGAGCCCTAT	-	-	not tested
SCF155637[a,b]	KP278901	Schlautman et al. (2015a)	TGTTAGTGTTAG GACCCGTTA	AAAGTAGGAGTT AGGATGGGAT	-	-	not tested
SCF46824[a,b]	KP278717	Schlautman et al. (2015a)	GGAGATGCTGT AATAACGAAGT	TTAGTCAATATGC GTGCAAC	-	-	not tested
SCF34513[a,b]	KP278695	Schlautman et al. (2015a)	TACTAATCTTCT GGTTTGGGC	GTACACCACTCCT GATGGC	-	-	not tested
SCF25221[a,b]	KP278664	Schlautman et al. (2015a)	GTATCCCCACAC TTACCACTAT	AGGATTGGACGG TAGCTTA	-	-	not tested
SCF25944[a,b]	KP278666	Schlautman et al. (2015a)	AACTATGCCAGA AGACTCAGAT	CTTCACAAATCAC AACCACTAC	-	-	not tested
SCF23210[a,b]	KP278660	Schlautman et al. (2015a)	TTGATACTCTCG ACCTCTTCTT	GTGGTGTTCGAC ATGATTTAC	-	-	not tested
SCF57497[a,b]	KP278737	Schlautman et al. (2015a)	ATCTGTAGGTTG TGTTACCCC	ATCAACTGTATCT ACCCACCAA	-	-	not tested
ct144936[a,b]	KP279129	Schlautman et al. (2015a)	AGGTGACTAAG GCAGTGTTC	CGTGTCTGTTTG GTTAGTAGGT	-	-	not tested

[a] Marker mapped in Schlautman et al. (2015a)

[b] Marker mapped in the current cranberry consensus map

[c] Marker mapped in the current interspecific diploid blueberry consensus

Appendix V-2. Multiplexing combinations (3x) of cranberry simple sequence repeat (SSR) loci used to genotype the F_1#10 x W85-23 interspecific diploid blueberry population for linkage map construction.

Multiplex PCR Combos	Locus1	Locus2	Locus3
multiplex1	ct110752	SCF39691	SCF3427
multiplex2	ct154615	SCF56032	SCF84921
multiplex3	SCF43220	SCF2288	SCF109269
multiplex4	SCF58861	SCF30816	SCF150919
multiplex5	vm13884	1trimcontig179737	scf26r
multiplex6	1trimcontig450309	ct154206	SCF107715
multiplex7	SCF116864	SCF17979	SCF37628
multiplex8	309124_K70	scf6i	vm54133
multiplex9	SCF192219	289194_K63	ct145906
multiplex10	ct92708	scf511	SCF32389
multiplex11	SCF140628	ct140233	409618_K63
multiplex12	SCF99997	SCF65004	76326_K70
multiplex13	SCF186078	SCF55619	SCF46739
multiplex14	314831_K70	SCF173212	35137_K63
multiplex15	412234_K63	SCF195276	scf17d
multiplex16	SCF125768	SCF22339	SCF147295
multiplex17	SCF80703	ct155339	260167_K70
multiplex18	314402_K70	SCF53058	ct129202
multiplex19	SCF54555	1trimcontig176042	vm31701
multiplex20	SCF30000	Ig15420a	SCF109660
multiplex21	1trimcontig176861	SCF42256	contig480Fb
multiplex22	418931_1_K63	CA421	5ms2b12
multiplex23	contig600	vm25796	SCF59035
multiplex24	SCF125667	SCF102190	SCF83036
multiplex25	SCF7155	339139_K63	SCF33205
multiplex26	SCF18363	SCF134365	SCF88396
multiplex27	SCF105925	SCF804	SCF95767
multiplex28	SCF26049	vm89040	SCF78184
multiplex29	scf112c	314797_K70	SCF48414
multiplex30	SCF68870	SCF64185	SCF29529
multiplex31	281741_K70	SCF110888	SCF91821
multiplex32	SCF144748	SCF75572	scf35k
multiplex33	vm68798	1trimcontig436904	SCF47689
multiplex34	scf43g	SCF19055	SCF65999
multiplex35	411475_K63	2ms4d10b	1trimcontig332949
multiplex36	1trimcontig440008	SCF12818	SCF77645
multiplex37	SCF64632	SCF28100	411348_K63
multiplex38	ct132010	SCF39242	1trimcontig191066
multiplex39	SCF30734	SCF122552	SCF7357
multiplex40	1trimcontig443603	SCF110507	SCF36745
multiplex41	vm13780	SCF174394	scf55c
multiplex42	scf8l	contig652	SCF84796
multiplex43	scf28l	SCF99113	SCF69698
multiplex44	1trimcontig339726	1trimcontig440230	scf2000b
multiplex45	SCF136207	scf79c	SCF30010
multiplex46	SCF51607	408825_K63	NA1713

multiplex47	SCF150395	239628_K63	SCF77055
multiplex48	416275_K63	SCF95879	SCF14877
multiplex49	SCF167793	CA325	Ig6523b
multiplex50	SCF203038	SCF138014	scf306f
multiplex51	60699_K70	scf21n	1trimcontig337780
multiplex52	SCF95851	ct89379	SCF13231
multiplex53	6ms4e4b	SCF138394	281884_K70
multiplex54	ct89348	SCF124927	SCF110757
multiplex55	SCF192715	SCF33471	414791_K63
multiplex56	SCF32727	SCF965	24956_K70
multiplex57	ct129169	VCC_B3	SCF110168
multiplex58	372875_K63	SCF60761	1trimcontig439506
multiplex59	SCF51810	scf44a	SCF8151
multiplex60	300409_K63	SCF145689	SCF30747
multiplex61	364103_K63	vm52204	ct94504
multiplex62	36394_K70	2ms2g09	ct97791
multiplex63	ct130570	SCF9872	SCF46751
multiplex64	SCF108454	SCF74458	307461_K70
multiplex65	Ig9279a	SCF34071	SCF61972
multiplex66	16720_K63	SCF16186	SCF85946
multiplex67	scf1594	vm10462	SCF16359
multiplex68	SCF24087	SCF128307	scf94a
multiplex69	1trimcontig326802	CA855f	scf10688
multiplex70	SCF197012	SCF120352	SCF73288
multiplex71	SCF92986	SCF101064	SCF132532
multiplex72	SCF38430	418138_K63	305731_K63
multiplex73	SCF72379	407841_K63	SCF119984
multiplex74	SCF138607	ct149097	SCF9045
multiplex75	SCF34584	SCF11186	313711_K70
multiplex76	SCF4305	ct153008	SCF3932
multiplex77	SCF113558	SCF81732	NA172
multiplex78	ct134336	SCF76055	SCF12084
multiplex79	ct145170	SCF101363	SCF65897
multiplex80	1trimcontig440337	SCF13393	SCF95754
multiplex81	313928_K70	1trimcontig239742	198358_K70
multiplex82	scf14j	1trimcontig239742	SCF111145
multiplex83	251788_K63	SCF118999	SCF89726
multiplex84	SCF33185	ct147864	409500_K63
multiplex85	SCF55511	1trimcontig439466	418294_K63
multiplex86	SCF55511	SCF76310	Ig16780a
multiplex87	vm39030	vm34671	SCF13711
multiplex88	SCF208883	SCF34663	172672_K70
multiplex89	SCF27811	SCF10459	SCF15845
multiplex90	scf258d	SCF112540	SCF8223
multiplex91	contig130Fb	SCF1524	SCF100820
multiplex92	SCF97378	SCF36716	411145_K63
multiplex93	SCF88902	SCF1527	SCF14358
multiplex94	SCF40225	SCF132006	SCF159195
multiplex95	SCF153636	297265_K63	346445_K63

multiplex96	SCF28279	SCF41759	1trimcontig240704

Appendix V-3. Information regarding the markers designed in blueberry and used in this study including their primer sequences, cross-transferability, publication origin, NCBI ID, and whether they were positioned in linkage maps in this study or the former linkage mapping studies performed in blueberry including Rowland et al. (2014) and Lin et al. (2015).

Locus	Forward	Reverse	Marker Type	min allele	max allele	Amplification in Cranberry
KAN-16471[a,b]	GGGGTCGGCTAGAAAGAAAC	TGGTTATATGGCCAACTGCAT	SSR	196	207	polymorphic
berc128a[a,b]	CGATAATGATCCAGCAACCA	CCCCTCTCTCGCTCTCTCTA	EST-PCR	NA	NA	did not amplify
pink-00254a	GGACAAAGAGGCCAGAGAGA	ACGCTGTTAGTCGGCAAGTT	EST-PCR	NA	NA	did not amplify
berc263ca	TTGAGCCCAAAAGGATCAAC	CGAAATTTTGGGAAATTGGA	EST-PCR	NA	NA	NA
CA169[a,b]	TAGTGGAGGGTTTTGCTTGG	TCTAAATAAAGGGGCCAAAGG	EST-PCR	NA	NA	did not amplify
bud397-01134[a,b]	GCCTCAACAATGGCTCTCTC	TGCACGCAAAATCCATCATA	EST-PCR	NA	NA	did not amplify
berc136[a,b]	TGTTACGTTGCTTTGGCAGA	CATATACGGCATCGAAACGA	EST-PCR	NA	NA	did not amplify
KAN-2328[a,b]	AGAGATTGCCAACACTGGCT	AAAGTTAGCCCAGCCTCCTC	SSR	244	304	polymorphic
GVC-V61g11[a,b]	CATGGATTGGAGATCCTGCT	AAATGGCACGGAAGTGAGAG	SSR	270	270	monomorphic
OPC-09a[a,b]	CTCACCGTCC	0	RAPD	NA	NA	NA
CA243[a,b]	CAAGCTCAAGTTCCCGTCAT	GATTCCCAGAACACCTTCCA	EST-PCR	506	507	did not segregate
Pr031818815[a,b]	TGCCAGAAGTGTGTTGCTTA	TCCAAACACTACCCAAAGGA	SSR	NA	NA	did not amplify
ripe-00787[a,b]	TCGACCAAATTGGAACCCTA	GGCAATTTGAGTTTGTTTTCC	EST-PCR	NA	NA	did not amplify
berc229[a,b]	CAACATCTTAGCGGGTTGGT	TGCACTGTACACCGAGGAAG	EST-PCR	NA	NA	did not amplify
VCB-BH-1DVIYK[a,b]	CTTCAAACTCCTCTCTCCTCCA	ACTTCTCGACGTGCCTTACTTC	SSR	NA	NA	did not amplify
all03191[a,b]	AAGATTGCCGGTGTCAAAAC	CCAACAGCTTCAGTCCCATT	EST-PCR1	NA	NA	did not amplify
SL192a	ATTGAAGGCCTGAAATTGGA	TTGCCCTATTGAGGATTTGG	EST-PCR	NA	NA	did not amplify
all11619a	TTCAGGCTTTGGCTGAGAAT	ATCAGTGGGAGGTGTGCTCT	EST-PCR	452	452	monomorphic
KAN-11057[a,b]	TTGCCAGCTTTTTATCCTGC	CGTGCTGAAATGCAAAAAGA	SSR	298	298	monomorphic
berc51b[a,b]	GAACAAAATCGGAGGCCATA	TCTCAAGCAACACCAACACC	EST-PCR	NA	NA	NA
VCB-C09527[a,b]	TATGCAGCTTGGGGTTCTTAAT	CAACCTAGAAAAATGCGCCTAC	SSR	228	228	monomorphic
berc396[a,b]	TCGAGGAAGAGTTTCCCAAA	CTTGATTACGATGCCAACCA	EST-PCR	NA	NA	did not amplify
OPC-02aa	GTGAGGCGTC	0	RAPD	NA	NA	NA
berc351a	CCAGTTCAAAGCCCCTTACA	CCTCTGGAGAGCGAGAGAAA	EST-PCR	NA	NA	did not amplify
berc647a	TTAATGGCTGGGATGTGTTG	CCTCAAATGGCCAATCCATA	EST-PCR	NA	NA	did not amplify
berc102[a,b]	CAAAGCAGTCACATTCTCACG	ATAATGTGGCAGACGCAAGG	EST-PCR	NA	NA	did not amplify
SL172aa	CAAGCTTGATTTCCCTTTCG	TATCAAGGAGGGGGAGAGGT	EST-PCR	344	346	polymorphic
OPAO-02b[a,b]	AATCCGCTGG	0	RAPD	NA	NA	NA
berc60a	CCTTCCCCTCCACACATAAA	GGGTTTGGGTCAAAAACTGA	EST-PCR	NA	NA	did not amplify
KAN-11260[a,b]	ATGCAAATGCAGCCTCTCTT	TGAGGAAAGGGGAACTGTTG	SSR	296	296	monomorphic
berc104[a,b]	GGCTGAAGAGTTGGCTGAAG	AGACAATTCCCCCAATGGTT	EST-PCR	NA	NA	did not amplify
OPC-09b[a,b]	CTCACCGTCC	0	RAPD	NA	NA	NA
Pr031818818[a,b]	CGAACGGCCACTTTT	CCCATCAGTGCAGA	SSR	NA	NA	did not amplify

OPU-06aa	AGAGA ACCTTTGCGG	AGGAA 0	RAPD	NA	NA	NA
berc781a[a,b]	TAGCGTGAGACAAA GGCAAA	AAGCAACCGCAACT ACAGGT	EST-PCR	NA	NA	did not amplify
SL161a	CCCATTACAAAAAGC CGTGT	CCCCCTTTCCACCTT AAAAA	EST-PCR	NA	NA	did not amplify
Pr031818813[a,b]	CCGATCCAAATCCAT GTCTA	CCCATCAGTCCTTCA CTTCA	SSR	NA	NA	did not amplify
berc203[a,b]	CCCGTGTCCCATATA AATTGTT	AACTCTCCCCAACCT TCACC	EST-PCR	NA	NA	did not amplify
GVC-C102[a,b]	GGAACCTGCACAGA GCTACA	GAAATTCGACGACT TCTCCG	SSR	245	245	monomorphic
berc345a	CATTTTCGGGTCTCA ACCAT	GTCGGTTTCCGACA TGTTTT	EST-PCR	NA	NA	did not amplify
berc301da	ATGATGAAGACCTG GGTGGT	TGAGGTGTTGTTTG CCCATA	EST-PCR	NA	NA	did not amplify
KAN-11348[a,b]	TATCTCCGATCTGTT TCCCG	GCCCTGATCTGAAA GTCACC	SSR	409	409	monomorphic
KAN-0009C[a,b]	TTGTTTTGTGTCAAA CAATGTACG	AGATCTGCAGCTCA CGTCCT	SSR	NA	NA	did not amplify
berc301ca	ATGATGAAGACCTG GGTGGT	TGAGGTGTTGTTTG CCCATA	EST-PCR	NA	NA	NA
2ms2-g08[a,b]	CCAGCCCTTCCTTTCT TTCT	GCTGTTGGCAAAGA TTCCAT	SSR	241	245	polymorphic
bud0-00161a	TACAAACGCAGAGTG CCATT	CGCAGATAATGCAA CCAAAA	EST-PCR	NA	NA	did not amplify
CA221aa	GATTAAAAGCGCTTA TCGGAAG	AACTCCTGCAGGGA CTTTAGG	EST-PCR	NA	NA	did not amplify
OPB-05ba	TGCGCCCTTC	0	RAPD	NA	NA	NA
VCB-C12195[a,b]	TCCTGGTCGGAGTA GTTTGATT	CAGCAACAGCAGAT GTATTTCC	SSR	393	413	polymorphic
VCB-C08295[a,b]	CAGCTGCTATCTGGT TCACATC	AACTCTGCAGTCTG CTCACAAC	SSR	278	278	monomorphic
berc369[a,b]	TTGCAGAAACCACAC TCAGG	CGAAAAGACCAGTG CCTCTC	EST-PCR	NA	NA	did not amplify
GVC-V23g01[a,b]	TCTTGACGTATGATG GCGAG	ATGCCTGATGCTGT ACTCCC	SSR	NA	NA	did not amplify
KAN-11200[a,b]	CGTGCCCTGAAAAAG GAGTA	GGTTGTGCGTTTGG AGAAAT	SSR	157	157	monomorphic
berc542aa	CTCAGAAGAGCCACC ACCTC	TATTGCAGACCCCA GAATCC	EST-PCR	NA	NA	NA
berc279[a,b]	ATTCTTCTCGATGGG GATCA	CCGGGAGATGAACA AAGTCT	EST-PCR	NA	NA	did not amplify
leaf-00186a	TGTATAATAATTTGA TCCTTTCTGCAA	TCTAGACAGAGAGA GCGAGGAGA	EST-PCR	NA	NA	did not amplify
berc536a	AGCAGGCCACAATAC TCCAT	CTATTGGCCCAGTT GAAGGA	EST-PCR	196	196	monomorphic
berc542b[a,b]	CTCAGAAGAGCCACC ACCTC	TATTGCAGACCCCA GAATCC	EST-PCR	NA	NA	did not amplify
SL172ba	CAAGCTTGATTTCCC TTTCG	TATCAAGGAGGGG GAGAGGT	EST-PCR	NA	NA	NA
OPAG-14aa	CTCTCGGCGA	0	RAPD	NA	NA	NA
berc341[a,b]	ATTGCCTTCCTTTCCA TTCC	CCGGCAAGCAAAAA TATCAG	EST-PCR	NA	NA	did not amplify
OPAA-15aa	ACGGAAGCCC	0	RAPD	NA	NA	NA
SL309a	AGGTCCGGGCAGGT ACTTT	CGTAGAGCAGGAG GAGGACA	EST-PCR	NA	NA	did not amplify
IP5PII-2[a,b]	ATGGAGTACCAAGG AAAAACGA	CCATTTTTATCGGG GTGAGTAA	SSR	NA	NA	did not amplify
OPC-02ba	GTGAGGCGTC	0	RAPD	NA	NA	NA
berc401[a,b]	TCCGAAGAGTCCCAA ACATC	TGCTTTCCAATGCTT TCCTT	EST-PCR	NA	NA	did not amplify
berc98a[a,b]	CGTGGCTGAATTCTT TGGTT	TGTGAAGAATGGGA GTTCAGG	EST-PCR	NA	NA	did not amplify
berc98ba	CGTGGCTGAATTCTT TGGTT	TGTGAAGAATGGGA GTTCAGG	EST-PCR	NA	NA	NA
green-00012a	ATCTCCGAAGAGGCA GTGAA	AGCCTGCCATAGAC CCTCTT	EST-PCR	NA	NA	did not amplify
OPV-08c[a,b]	GGACGGCGTT	0	RAPD	NA	NA	NA
GVC-C066a[a,b]	TAAACACACACCATG	ATGGAGTAGGTGAC	SSR	136	459	polymorphic

Pr031818816[a,b]	CCCTC CCTCACGAATCATCC ATCTC	GCCAAG GGATGTGATTGGG GTTGAG	SSR	208	208	polymorphic
leaf-00158a[a,b]	ATCCTCCAGCAGGCA TTCA	GAATTATAGTGGCG GTGGTCA	EST-PCR	NA	NA	did not amplify
berc218a	TCTTCTTCCTCCACCA CTCC	GCTTTGGCCCCCAT ATTATT	EST-PCR	NA	NA	did not amplify
OPU-01b[a,b]	ACGGACGTCA	0	RAPD	NA	NA	NA
berc54b[a,b]	CTCTTCCGCCCTCTCT CTCT	CCCAATAACGGGAG CTACAA	EST-PCR	NA	NA	NA
OPB-04a[a,b]	GGACTGGAGT	0	RAPD	NA	NA	NA
UBC211b[a,b]	GAAGCGCGAT	0	RAPD	NA	NA	NA
ripe-01939[a,b]	TGGTGCTTCTTTCCT TGACC	TACCTTTTGCATCCC ACCAC	EST-PCR	NA	NA	did not amplify
OPAR-19[a,b]	CTGATCGCGG	0	RAPD	NA	NA	NA
berc97a	GAGAAGAGTGGGAC GTGGAG	GGATCCCAAAACAA GCTTCA	EST-PCR	NA	NA	did not amplify
KAN-2459[a,b]	CCTGCATTTGGTTTT GGTTT	GGCTGGTTTAGGTA CGGTGA	SSR	159	160	did not segregate
VCB-C06669[a,b]	CATGAGTGGGGTAA GAAGAAGG	CCCTACAGCATAAAC GGGTTAG	SSR	330	330	monomorphic
CA1785S[a,b]	AATCCAGCACCTGTG ATTCC	CAATTCCGGTCAGG TCTTGT	EST-PCR	408	408	monomorphic
berc222a	CTGGGTCCTGCTTAA TTTCG	TCCCTCCATCCTCTC TCTCA	EST-PCR	492	492	polymorphic
berc56b[a,b]	CAACGTTTCCCCAAA TTTCA	TTTTGTTGCTGGTC ATTCCA	EST-PCR	NA	NA	NA
green-00058a	GGGGACACAAGCTA CAACCA	GAAGTATAACATCA TGTCACAATAGCC	EST-PCR	NA	NA	did not amplify
berc539a	TGGTTGTGTGTTTGG TGCTT	CAGGTTCTCTACCCC CAATG	EST-PCR	NA	NA	did not amplify
berc149b[a,b]	CGGATTAGTCCTCCC TCCTC	CCAGAGCAAACGAA AGAGTG	EST-PCR	NA	NA	NA
GVC-V62a08[a,b]	TTACGGTTTGGTCTT TTGGC	AAATTACAGAAGTG CAGCCCA	SSR	NA	NA	did not amplify
bud789-00617ba	TCAAACACCTTGAGC CATCA	TCGAAAGGTGGGAA AAAGAA	EST-PCR	NA	NA	did not amplify
CA636S[a,b]	AAACTACCCGATGTC GATGC	TCCATCGATGACGA TGAAAA	EST-PCR	NA	NA	did not amplify
bud0-00191a	TCAAAATGCACTTGG AGACAA	TTCTCTCTCCTCTCT CCCACTC	EST-PCR	NA	NA	did not amplify
OPAR-14a[a,b]	CTCACAGCAC	0	RAPD	NA	NA	NA
Pr031818822a	TTTCTCTCTCCTCCCC TTCC	AACAAGGTTCGCGG GATT	SSR	211	211	monomorphic
SL256[a,b]	GCGGCCGAGGTACT TTTT	GGCAATGGAAAAAT GAGAGG	EST-PCR	323	331	polymorphic
OPP-12b[a,b]	AAGGGCGAGT	0	RAPD	NA	NA	NA
OPAR-12b[a,b]	GGATCGTCGG	0	RAPD	NA	NA	NA
berc230[a,b]	AGGGATTTCGATGG GCTATT	TGGGGAGAATCACT CTGCAT	EST-PCR	NA	NA	did not amplify
leaf-00248[a,b]	ATTACGGCCGGGACT GTGT	TTATCATCAAATGAA AGCCAGGA	EST-PCR	NA	NA	did not amplify
leaf-00158b[a,b]	ATCCTCCAGCAGGCA TTCA	GAATTATAGTGGCG GTGGTCA	EST-PCR	NA	NA	NA
OPU-01ca	ACGGACGTCA	0	RAPD	NA	NA	NA
GVC-C703aa	TCTCTCTCCAAAGCCC AGAA	GAAAAATGGAAAGG CATGGA	SSR	263	267	polymorphic
berc890a	AGCAGCAGTCCCAGC AAC	CATACAACCCTGTAC CAACGTC	EST-PCR	NA	NA	did not amplify
berc85[a,b]	GTGTTCGAAGCTGTT CGGTA	GGGGACATTTCACA AACCAT	EST-PCR	NA	NA	did not amplify
berc56a[a,b]	CAACGTTTCCCCAAA TTTCA	TTTTGTTGCTGGTC ATTCCA	EST-PCR	NA	NA	did not amplify
CA1105[a,b]	TGGTGCTTTCATCCT GCTAA	GCTTGCTTCTTGGG TGACTC	EST-PCR	NA	NA	did not amplify
berc209ba	AAGCTGCTGGCATGT TTTCT	AACAAACGTCCTGC CAAAAC	EST-PCR	NA	NA	NA
berc209a[a,b]	AAGCTGCTGGCATGT TTTCT	AACAAACGTCCTGC CAAAAC	EST-PCR	NA	NA	did not amplify

OPU-03ba	CTATGCCGAC	0	RAPD	NA	NA	NA
ANPER00666-2a	CCGTTTCGATCTCTCTCTCAGT	CATCCCTAGATCTGACACCACA	SSR	NA	NA	did not amplify
CA278a	CACCACCACCACTCAGTCAC	CTCGCAGAAACAGTCCATCA	EST-PCR	NA	NA	did not amplify
GVC-NA721[a,b]	CAGATTTTGAGGAGCGCATT	ATTGGAACTTCGGGGTTCTT	SSR	192	192	monomorphic
NA1304+[a,b]	GGACGGTAAGGAGGAGGAAG	GCAAATCTCCCATTCCACAT	EST-PCR	490	500	polymorphic
OPAA-17b[a,b]	GAGCCCGACT	0	RAPD	NA	NA	NA
berc24[a,b]	TCAAGTGAATAGACATCAGGTCTTG	TTGAGAAAACAACCGTGAAGG	EST-PCR	529	529	monomorphic
berc2[a,b]	GCGCTGCAACTCTTCTCTCT	TTGGAACCTTCCTCATTCCA	EST-PCR	NA	NA	did not amplify
berc363a	GCCGAGGTACATACCCAGAA	CACACCTATGGCTTTCAGCA	EST-PCR	NA	NA	did not amplify
berc482a	TGTGATGAAATTGGATTTTGGA	TGCATTCAAAACAGAGTGCAA	EST-PCR	NA	NA	did not amplify
GVC-NA113[a,b]	TACAACATGCCCCACAAGAA	GCAAAATACTTGCACACCGA	HRM SNP Marker	NA	NA	NA
GVC-V41c07[a,b]	CACAGGTGGCGAATAGACCT	TTCTTAGTTTCGCTTCGTTCG	SSR	190	190	polymorphic
UBC34ca	CCGGCCCCAA	0	RAPD	NA	NA	NA
VCB-C09467[a,b]	ATCAAGTACATCATCACAGCCG	CGAACCATCCTTGTTGTACTCA	SSR	NA	NA	did not amplify
CA344[a,b]	TTACCAAAACGCCTCTCCAC	CTTCCTTACGCCCCTGAAAT	EST-PCR	NA	NA	did not amplify
KAN-11118[a,b]	ACGACCAGTAATCATTCGCC	GGCACAACCCGATCTCTTTA	SSR	252	252	monomorphic
CA54[a,b]	CCGGTGAACTTCCACTTGTT	AGATACTACTGGGGGTGGGG	EST-PCR	NA	NA	did not amplify
GVC-C71a	NA	NA	NA	330	330	monomorphic
SL151a	AAAGACCGGGACACGACAC	TTGGGCCCATATGGTTTTT	EST-PCR	NA	NA	did not amplify
berc243ba	CGAGCATTCAGACAGCATAGA	CCGGTATCTGGAAATCATGG	EST-PCR	NA	NA	did not amplify
SL40a	TCTGCAGAATTCCACCACAC	CCGCCCATTACGTCAATAA	EST-PCR	NA	NA	did not amplify
Pr031818820[a,b]	TCCCACACCTTATCCCTCTT	GAGAGAAGCCCTTTTGTTTG	SSR	NA	NA	did not amplify
berc62[a,b]	GCACACACAAAAACACGCATA	GCCAAGATCAACCATGGAGT	EST-PCR	NA	NA	did not amplify
berc54aa	CTCTTCCGCCCTCTCTCTCT	CCCAATAACGGGAGCTACAA	EST-PCR	NA	NA	did not amplify
GVC-C608[a,b]	GATATGACCTGCCAGACCGT	TCGGTCACGTTGAAGCATTA	HRM SNP Marker	NA	NA	NA
GVC-C625a	CCCAAGTCGAAACAAAAAGC	TTTCCCATCTGTGGTGCATA	HRM SNP Marker	NA	NA	NA
KAN-11482[a,b]	TGTGGTTTGAGGAATGGTGA	TTATTCAGAGCCCCTAGGCA	SSR	NA	NA	did not amplify
GVC-C322[a,b]	CTCGGCTCTGACTTTGAAGC	AACATCGGACTTGGGAGTTG	SSR	181	181	polymorphic
berc133a	AAACAATCCACCAATCAACTTGT	CCTCTCCACAGTCCGATCAA	EST-PCR	NA	NA	did not amplify
CA1343[a,b]	CACGAGTGGCGTCGTAGTTA	GGTACCGGGCTTAATCAACA	EST-PCR	NA	NA	did not amplify
CA1049[a,b]	GTCACAGCTTGGCAATTGAA	CGGCTGCTTTCTGATCTACC	EST-PCR	NA	NA	did not amplify
berc123a	TAAGTGCCACCTCAACGACA	GGAAGGGAACAGGGAGTTTC	EST-PCR	NA	NA	did not amplify
SL42[a,b]	AAAATGGCATCAGTCCATGC	GGGTGGGTGGGGGTAAAC	EST-PCR	NA	NA	did not amplify
berc187ba	TCCTTTCTTCTCGTGGTGCT	TGGCACAGTATGGAAGTGGA	EST-PCR	NA	NA	did not amplify
GVC-V64f07[a,b]	TTGAGCTGCATCACAAGACC	AACTTGTGCAGCCAAAGGAT	SSR	261	261	polymorphic
SL186aa	CACAACACGACACATGTCCA	GAGCGGAGGGGATAAAAAGA	EST-PCR	NA	NA	did not amplify

berc523[a,b]	TTGTCAGGTTTCAGC CAGTG	GCTTTCAACACCCTA GACATCC	EST-PCR	NA	NA	did not amplify
berc138a	GGTAAAGCAAATTCC GGTGA	CATAAACGGAAGCC AACACA	EST-PCR	NA	NA	did not amplify
OPP-16a[a,b]	CCAAGCTGCC	0	RAPD	NA	NA	NA
berc485[a,b]	GTCGCCCATTACCAC CTCT	CAAAAGAGTGAGCA ACAACG	EST-PCR	NA	NA	did not amplify
berc366a	AGTTTGACCGAACTG CCAAT	TCACCTGCATTTTTG CTCTG	EST-PCR	NA	NA	did not amplify
berc51aa	GAACAAAATCGGAG GCCATA	TCTCAAGCAACACCA ACACC	EST-PCR	NA	NA	did not amplify
berc826a	CCTTCTCCTCCTCAAC TTTGG	CGAGATGGAAAGCA CACAAA	EST-PCR	NA	NA	did not amplify
OPP-09b[a,b]	GTGGTCCGCA	0	RAPD	NA	NA	NA
OPB-05aa	TGCGCCCTTC	0	RAPD	NA	NA	NA
berc268[a,b]	GGCATTGCTCTGGG ATAAAA	AAATACACACGGGC ATCACA	EST-PCR	NA	NA	did not amplify
KAN-11199[a,b]	TTATGCCCTTTGATA TGCCC	CGAGAATCTGACAA CGGTGA	SSR	NA	NA	did not amplify
CA191a	GCCTGGTGTTTGGG AATATG	TGTACAGTTCGCTC GGTGAG	EST-PCR	NA	NA	did not amplify
berc263aa	TTGAGCCCAAAAGGA TCAAC	CGAAATTTTGGGAA ATTGGA	EST-PCR	NA	NA	did not amplify
berc472aa	GATCGACCCCGAGG AACT	TCCCCTCTGAGAAC ACAGACT	EST-PCR	NA	NA	did not amplify
berc618a	GGTATGATGACCGAC CTCGT	GTGGGTTTGTCAAG CCAGTT	EST-PCR	521	522	did not segregate
VCB-C00694[a,b]	GTGCCAAAGTTCAAA ATTCTCC	GATGTTGAAACAGG ATTAGGGC	SSR	316	316	monomorphic
Pr031818819[a,b]	TCTCTTTCCCTTTTCA AGTGG	ATGATGGAATTCCG AGTTTG	SSR	NA	NA	did not amplify
berc488b[a,b]	GGACTCCGACAAGG AAATGA	TTGAAAAGAGTGGG CAAAGG	EST-PCR	NA	NA	NA
Pr031818811[a,b]	AAATGCCCCAACAGT CTTCT	CCGGTCCTCCTAAA AGTAATC	SSR	277	278	polymorphic
OPAO-19a[a,b]	GTTCTCGGAC	0	RAPD	NA	NA	NA
CA66[a,b]	TTCCTTTAGTCGCGT CATCA	ACTAAAACGCCGAC AGTGGA	EST-PCR	NA	NA	did not amplify
berc895[a,b]	CGTTGCTGGTTTGTA GCTGA	GCAAGGAAACAACA ACATGC	EST-PCR	NA	NA	did not amplify
VCB-C04624[a,b]	GTTCATCCCAATGCA GAAGAAG	CCTCTTGTGGGTTA GGGTTTCT	SSR	NA	NA	did not amplify
OPAQ-01c[a,b]	GGCAGGTGGA	0	RAPD	NA	NA	NA
OPV-08aa	GGACGGCGTT	0	RAPD	NA	NA	NA
OPP-12c[a,b]	AAGGGCGAGT	0	RAPD	NA	NA	NA
NA292Sa[a,b]	CAAGGGCTGATATTG GAGGA	ATGGCCGTGGACTT TCATAG	EST-PCR	NA	NA	did not amplify
berc5[a,b]	TGCTGCCATGATTTT TGTTC	AGAGAACGGCATTA GGCTGA	EST-PCR	NA	NA	did not amplify
ripe-00122a	GCTAGCCTGCATTTT CCATT	AATGATCCAATCCTC GCAAA	EST-PCR	NA	NA	did not amplify
berc210[a,b]	CGGCCCTAGTTCTCT CACAG	CAACGGAAGACCAA ACCAGT	EST-PCR	NA	NA	did not amplify
berc149aa	CGGATTAGTCCTCCC TCCTC	CCAGAGCAAACGAA AGAGTG	EST-PCR	NA	NA	did not amplify
OPV-08da	GGACGGCGTT	0	RAPD	NA	NA	NA
OPP-14d[a,b]	CCAGCCGAAC	0	RAPD	NA	NA	NA
berc893[a,b]	AGAAAACAGTCCCGG AAAAA	TCTCTCTACCTCTCC ACAACAGC	EST-PCR	NA	NA	did not amplify
GVC-C136[a,b]	TCTGTCTCAGCTGCT TCATCA	AAATTCGTTGAAAC TGCGCT	SSR	NA	NA	did not amplify
KAN-11109[a,b]	AAAACAACCCACAAT CCAGG	CATCGACTTCAGCCT GTTCA	SSR	162	162	monomorphic
GVC-C089[a,b]	CCCTAGATGTGTTTC CTGGG	GAGCAAATCCAAAA ACTCCG	HRM SNP Marker	NA	NA	NA
berc496[a,b]	AGGATGTGCCTGAG TTACCG	GGATGGGAAAAACT CGACTG	EST-PCR	NA	NA	did not amplify
OPV-08b[a,b]	GGACGGCGTT	0	RAPD	NA	NA	NA

berc824[a,b]	GACAAAGCTTCGGCCTACAC	TGGATACGAAGATTTGCTTGG	EST-PCR	NA	NA	did not amplify
SL188a	GAACATCGCCCTTTCGAG	AAATTTACGGGGGTTCCTTG	EST-PCR	NA	NA	did not amplify
UBC854ba	TCTCTCTCTCTCTCTCRG	0	RAPD	NA	NA	NA
berc836a	AGAGCCAAGCGGATCTGTTA	CCCTTCAACTCACTTTCTCTCTC	EST-PCR	NA	NA	did not amplify
OPP-14b[a,b]	CCAGCCGAAC	0	RAPD	NA	NA	NA
berc798[a,b]	GACGACGACAACCCTCTCTC	TGAGATTCAAGCAAACCATCA	EST-PCR	NA	NA	did not amplify
berc143[a,b]	GGTTCTTCTCCCCATCCTCT	AGGCCGAAACAACAACAAAC	EST-PCR	NA	NA	did not amplify
berc555[a,b]	CCCATGCTCATCACCAGATA	TGGTGTCTGCAACAGGAAAG	EST-PCR	NA	NA	did not amplify
bud789-02577ca	GAGGACGGAAGAACCCTAGC	GTCAAATTCGACCACAACCA	EST-PCR	442	442	monomorphic
GVC-C179[a,b]	CGTCGTGGAGGCTTAGAAAG	TTCAAAATCACCAGCACCAA	SSR	NA	NA	did not amplify
berc680a	TGCTGGTTCTCAGTCACCAA	CTGGAAAGTCCACCACCACT	EST-PCR	NA	NA	did not amplify
GVC-V32g09[a,b]	CCTAAATTGCAGCCACTGGT	ACGGCAAGACAACGTTCATT	SSR	315	315	monomorphic
GVC-C725[a,b]	TCCACCCACTTCACAGTTCA	ATTGGGAGGGAATTGGAAAC	SSR	208	211	did not segregate
OPAR-13c[a,b]	GGGTCGGCTT	0	RAPD	NA	NA	NA
OPAQ-11b[a,b]	GACGCCTCCA	0	RAPD	NA	NA	NA
berc53aa	AGGGGTCTGAGCCTCTGAAT	AACTGGCATTTGCATCCATT	EST-PCR	NA	NA	did not amplify
berc196[a,b]	TTCCAGTTAGGGTTTCTCCTG	CCCAAATAACAAAGCGGAAG	EST-PCR	NA	NA	did not amplify
pink-00018aa	TAAAAATGCAGCCTCCATCC	GCCGGACAAAACTTGGATAA	EST-PCR	NA	NA	did not amplify
ripe-00162a[a,b]	0	0	0	NA	NA	NA
VCB-BH-1C6ZD8a	TTGTGAGTTGACTCATGCTTCC	CCTTGGAATTAGAATTCGGACA	SSR	NA	NA	did not amplify
Pr031818826a	AAGCTCCGTCCTCGCATTT	TGATCCATACCCTGGTGGAG	HRM SNP Marker	NA	NA	NA
NA186[a,b]	ACCCTGACATGAGCTTCTCG	ACCCAAATCTCTGCTTGCTG	EST-PCR	NA	NA	did not amplify
GVC-C613[a,b]	CAAATCCACCACAAAAGCCT	TTCCTTGTTTGGAAGATGGC	HRM SNP Marker	NA	NA	NA
GVC-NA146[a,b]	AGGTGGATGTTTGCAAGGAC	ACTTCCAACAATTGGGCAAA	HRM SNP Marker	NA	NA	NA
GVC-C455[a,b]	GACTTGAGCTGTGGAGAGGG	GGTCCTTGCATCCTTTGGTA	HRM SNP Marker	NA	NA	NA
OPAG-03ba	TGCGGGAGTG	0	RAPD	NA	NA	NA
berc130[a,b]	ACGGCTGATACACGTATGGA	ATGGCAAAATTGGCTTTTGA	EST-PCR	451	452	monomorphic
Pr031818812[a,b]	CAAATCGACCGAATTCAGAG	ACGGAATCGTAATCATTGCT	SSR	205	205	polymorphic
Pr031818825[a,b]	ACAGTGAGGGAGGAGACAAG	ACCAAAAGTGAAGCTAACGA	SSR	215	215	monomorphic
berc292[a,b]	GGGCAGTCATACACCCAAAA	TTTTGCAGGGGAAATTCATC	EST-PCR	488	489	polymorphic
GVC-C634_272a	GAGTGCATCCAGAATGAGCA	TTGGCCAATATGTCTAGGGC	SSR	303	306	polymorphic
berc198a	CTTCTCCTCGCACGACCTAC	GGGAGGGAAACAATTTCACA	EST-PCR	NA	NA	did not amplify
berc48[a,b]	CACCTCCTCAATTTCCCTGA	AACAATGGGATTGTGGAACG	EST-PCR	NA	NA	did not amplify
SL413[a,b]	TGACATCACGCACACTACCA	TGGGGTAAAGGAGGTTTTCC	EST-PCR	NA	NA	did not amplify
OPAA-11aa	ACCCGACCTG	0	RAPD	NA	NA	NA
AOMT01781-1a	GGCGACTGTGTCTTTCAGTAAA	TAGGATTTCGAGGAGGAGAGGT	SSR	NA	NA	did not amplify

OPP-14aa	CCAGCCGAAC	0	RAPD	NA	NA	NA
berc488aa	GGACTCCGACAAGGAAATGA	TTGAAAAGAGTGGGCAAAGG	EST-PCR	NA	NA	did not amplify
OPP-12aa	AAGGGCGAGT	0	RAPD	NA	NA	NA
berc781ba	TAGCGTGAGACAAAGGCAAA	AAGCAACCGCAACTACAGGT	EST-PCR	NA	NA	NA
CA1545F2[b]	CGTGAGTGACTACCCCATTG	GCCAAACCAACAGAG AGGTC	EST-PCR	NA	NA	did not amplify
ANPER01018C[b]	GAGCTACTGTGAGGACTTCCGT	TCATTTGCTCCTTAAGTTGGGT	SSR	NA	NA	NA
AOMT00011B	CAAGAAACCTGGGATTTGAGTC	GAAACTACACCCACATCTGCAA	SSR	NA	NA	NA
AOMT00197A[b]	GAACCAGAACCAGATCCAGAAG	CAAGGAAAATAGCAAAGTTGGG	SSR	NA	NA	NA
CHI01251A[b]	GGTTGCCAACTAAGGACGTATC	CATCACGAAGTTGTTCCTTGAA	SSR	NA	NA	NA
CHI01251B[b]	ATATACGGATTGCCAAAGAGGA	TCACGTTATAGTGCATGTCGAA	SSR	NA	NA	NA
CHS00014B	CACCATTCTTATTTAATCGCCC	GTAAGCGAGAGAGGGAAGTTCA	SSR	NA	NA	NA
CHS00491A	CTGGAAACATAAGAAACCTGGG	GTAGCAGAAACTGCTCCCACAT	SSR	NA	NA	NA
CHS00491B[b]	AATGAAGCAAAGGCATAAGACC	GAAGTTCCTCTCCGAACTTTGA	SSR	NA	NA	NA
CHS00519A[b]	AGCCTAGAAGCAGCAACACTCT	GGTACTTCGATCAACACCCTCT	SSR	NA	NA	NA
DFR00528A[b]	CACGAAAGTAGACGCTGTGAAA	ATTTGAGCTGTCCAAAACACG	SSR	NA	NA	NA
F3'H00479C	AACAAATCAACTTCGGTGGAGT	TCTGACAATGAGCGACTGTCTT	SSR	NA	NA	NA
F3'H01438B	ATCCGATCGTCACATAGTTCCT	TTGAGCTTCTCTCTTTTGCCTT	SSR	NA	NA	NA
KAN-11106	CTCTGCACTCATCAATCCCA	GCCGAGAAGATTTTCGATCA	SSR	NA	NA	NA
KAN-11205	GCCAATTGGTACGGAAGCTA	TAGTTGGGGGACACCTCATT	SSR	NA	NA	NA
KAN-11381	AGCGTATGGAAGAGGAAGCA	CCCAGTATGCTAGCAAAGCAA	SSR	NA	NA	NA
KAN-11408[b]	CCGCCTCTTGTGTCTGAAAT	ATGGACGGTACCTATTCCCC	SSR	NA	NA	NA
KAN-11799	AGCCTTAACTGGCTTCCGTT	AGACTCACCGAATCCCATTG	SSR	NA	NA	NA
KAN-12244	GCGTTTGAATAATTTTGGGC	CATTCTTGCATTGCTGGCTA	SSR	NA	NA	NA
KAN-12346	GAAATGGGCGTTATTCG	GCTTGACCTTTCCCACCATA	SSR	NA	NA	NA
KAN-129	GCAACTTGTGGAGTGGTAACAA	CAATGAAGGCACAAGCACAT	SSR	NA	NA	NA
KAN-13486	CTCCTTGAAGCCAAAGCAAC	AGTACCAAAGCGCTGCAAAT	SSR	NA	NA	NA
KAN-15306	AGCAGCTGCCTAAACCGTAA	CCCATTTTGAACAAACAGCA	SSR	NA	NA	NA
KAN-16539	TGAACAGTTCGGATCGTCAA	GTCTTCCTTAACGCGTGCAT	SSR	NA	NA	NA
KAN-17147[b]	AGGAGCAATTTGTTGGTTCG	GGGCTATGCAAGCTAACAGC	SSR	NA	NA	NA
KAN-1853	CTCAATCCCAGGTCAATGGT	ATTCGTTGGCATCGAGAATC	SSR	NA	NA	NA
KAN-1875[b]	GTTGCTTAATGGTGGTGGCT	GGAAGCGAGAAGAAGAGGGT	SSR	NA	NA	NA
KAN-20177[b]	ACGTCATTTATCTCGGACGC	AGGAGCAAAGGAGATGGGTT	SSR	NA	NA	NA
KAN-2237[b]	TTGGGTACGGGATTCTTCCT	AGCTGATGGGCTTTGGTCTA	SSR	NA	NA	NA
KAN-2260[b]	ACTCAAACTGGACCAAACCG	AGAGAGGAGTTGGATCGGGT	SSR	NA	NA	NA
KAN-23334[b]	TCCAAACCTCCAATTTGTCC	GGCTATCGATCCAATCCAAA	SSR	NA	NA	NA
KAN-23741[b]	CATGGATCTTGGGCTAGAAAA	CGGTTATGGGATTGGCATAC	SSR	NA	NA	NA

KAN-24307	GGGGTCAAAGGGTTTCATTT	AAACGGCTGAGAAATGGATG	SSR	NA	NA	NA
KAN-24523	TTTATTCTCCACACGCTCCC	AAAAGGTGCTGCCTTTTTCA	SSR	NA	NA	NA
KAN-24598[b]	CAACAGCTGCCCCTATTTGT	TCTGATCTGAGGGAGGATGG	SSR	NA	NA	NA
KAN-24806	CTTTCGGGTGTGTGTTGGTT	GAGATTGGGCAAATGCAAGT	SSR	NA	NA	NA
KAN-24885[b]	AACCGTGATACTACGTCGGC	GGCTCTGTTTGACTTTTCCG	SSR	NA	NA	NA
KAN-24973[b]	CACTCACGGGACAGTAGCAA	GGCCGAGAAAGGTATCAGGT	SSR	NA	NA	NA
KAN-25281[b]	GCACTCATACTCCCCACACA	ACCCCAAATGGAAATCAACA	SSR	NA	NA	NA
KAN-27020	CAAAGCCCAAACAATCAACA	GCCCAGGTGATCTCTCACTC	SSR	NA	NA	NA
KAN-27179[b]	TATGTCTGTGGTGGTGGTGG	CGGAGTGCAGAGTCAAGTCA	SSR	NA	NA	NA
KAN-27356[b]	TGGAAGCCGTTCAACTTCTC	CATTGGCGTAGGGTTTGATT	SSR	NA	NA	NA
KAN-27743[b]	ATTTACCCAAGGCCCAAAAA	TGTTCCTCGAGTTAATGGGG	SSR	NA	NA	NA
KAN-29551	TGAACGGATTGTACCCTTCC	TGCTGTGTTTGAGTCTTCCG	SSR	NA	NA	NA
KAN-3462[b]	TCTCTTCACGACTCCTCCGT	TCACAACATCTGTGCCAACA	SSR	NA	NA	NA
KAN-40732	AAAACGCGATGAATGGAGAG	TGCGCCAAATTATGAATGAA	SSR	NA	NA	NA
KAN-41355	AGGTTGGGAAGGCACTTTTT	TGAATACATCGAGCACACGC	SSR	NA	NA	NA
KAN-41365[b]	GTCGCCTTCTTCCTCTTCCT	CCCACCTCAAGACTTACCCA	SSR	NA	NA	NA
KAN-41661[b]	TCCAAGGGTTCCAAACAAAG	CAATTCTGCAGGTTCGTTCA	SSR	NA	NA	NA
KAN-42567	CCAACCACAAGTGAGCAGAA	TGGTAAGCCTCCAACGGTTA	SSR	NA	NA	NA
KAN-43117	AGGCTGTTGCTGGAACATTT	AAACATTGGCAAACAGAGGC	SSR	NA	NA	NA
KAN-43405	GAACGAAAGTGGTCCGTTTG	GTTTTGCGGGACCTATTTGA	SSR	NA	NA	NA
KAN-711	CCAGTGGCAACTCCAAGACT	GCATTGAGACTACCTAACAACGC	SSR	NA	NA	NA
KAN-79[b]	TCCCGTGTTATGGTCCTTGT	GCCAGGTTTCTCTTTCCCTC	SSR	NA	NA	NA
scaf00001-3	AATCTTTCAAACCCTGAAGCAC	GAAGGGAAAGATATTCCCAAGG	SSR	NA	NA	NA
scaf00001-4	CTGTCAACATGATGTGCAACTT	TGAATACAAAAGGACTTCACCG	SSR	NA	NA	NA
scaf00004-3[b]	CTTCATAGAAGGAAATGTCCCG	TTCATCTTCATCTTCCTCGTCA	SSR	NA	NA	NA
scaf00004-4	CTCGGCTCGTTGACTAAAACTT	AGCCCTAATAATTCCCAGAAGC	SSR	NA	NA	NA
scaf00004-6[b]	TAATAGGTAGCTGGGCCATGAG	CGTTCCATCTCCTTAATCCTTG	SSR	NA	NA	NA
scaf00007-2[b]	TGAACATGGGGAAGACAAAAG	CCAACCTCGTTTAGGTCAAGAA	SSR	NA	NA	NA
scaf00009-4[b]	CGCTGTTGTCCAAATCTTCATA	TCCTTAGCTGAGCTCGGAGTTA	SSR	NA	NA	NA
scaf00013	CACAAAGTGAGGTAATCGTCCA	GCGAAAACTACAGGATGCTAGG	SSR	NA	NA	NA
scaf00021[b]	GCCCACTTCATAAGATGGCTAC	CTGCTACTTGTAGGGCTAGGGA	SSR	NA	NA	NA
scaf00033	TATGATCTCGTTTCGTGCTGAC	ACTCTAGCCAGAGAACGCAAAA	SSR	NA	NA	NA
scaf00062[b]	CAACATGAGCTCCGAAAACTCT	AGAGAGAAGCAAATATCGACGG	SSR	NA	NA	NA
scaf00069[b]	TTTCACTTGAATGGTTGGTCAG	GATCAGCCAGTCCTACCTTTTG	SSR	NA	NA	NA
scaf00074	GGGTTGGAATCTGATAACCTCA	ATCTTTGTCGTGGGTAGTTGGT	SSR	NA	NA	NA
scaf00090	GTTTGAACCTTGGTTGAGCTTC	AATGACCAAACCAGGTGTCTTT	SSR	NA	NA	NA

scaf00100	GGACTGCGTTTTAGGGTACTTG	GCGACTATGATTTCGGTACCTC	SSR	NA	NA	NA
scaf00113	ACCATTGTCACCACCCTTACTC	ACCACGACGTTTAAGGCTATGT	SSR	NA	NA	NA
scaf00125	CTAAAAAGCCAGCTTTAGCAGC	ACGATTGAGCCTTTTTGCTAAG	SSR	NA	NA	NA
scaf00137	ATTGTCCGAAACGGACTAGAAA	TTCGACAGATGATATGAAACGC	SSR	NA	NA	NA
scaf00155	GAAAACCGTCAAAACCAGTAGC	GGCAGTGGATCAAAAAGAAAGA	SSR	NA	NA	NA
scaf00156	CCATCATCACTACCACCATCAC	AGGCAGGGAGAGAGAAATACTG	SSR	NA	NA	NA
scaf00169[b]	TGAGTAGGGCCAATATGATGTG	TGGTCATACGACTTTCAAGGTG	SSR	NA	NA	NA
scaf00206	TAACGCCCCTAATTTTGAGAAC	AGAGAAACCGTAGCCTACCTGA	SSR	NA	NA	NA
scaf00216	CCGTTCATTTTGTTAGCCTCAT	AGGAGATTGTTAGGGTTCCGTT	SSR	NA	NA	NA
scaf00223	GCAATCGATGATTCACAAGAAG	CTTTCCCTTTCATTTCTCTCCA	SSR	NA	NA	NA
scaf00246	TAAGAAAAGGAGAAGCACAGGC	CATCACACTAGCAGAAGGCATC	SSR	NA	NA	NA
scaf00267	TCTCCCCTGTCAACTACACCTT	AAGCTCGTGGAGGTGATTAGAG	SSR	NA	NA	NA
scaf00281	TGCTCCCGAATCAAATAAGACT	TCATTGTTTTTGCAGCTACACC	SSR	NA	NA	NA
scaf00293	AAGTGCTCTCCAACTCATCTCC	CAATTGTGCCATCATAGCTGTT	SSR	NA	NA	NA
scaf00295	TCCGTGTCCGTGCTACATATAC	TCTCTCTCATTACCATGACCCA	SSR	NA	NA	NA
scaf00306	GCAATATTTTGAGGAGGAGGTG	CATGTACGTTTGAGTCGATGGT	SSR	NA	NA	NA
scaf00346	AGGGGCAGACTCATACAGTCAT	CGAAGTGAGTTCCCTTGAGAGT	SSR	NA	NA	NA
scaf00369[b]	AATAGTGCCTCTTCCCCAGATT	GGGACTCCACCACTACTACTGC	SSR	NA	NA	NA
scaf00392[b]	TCATCGTTAATACATGGTGGGA	CAGACCATTCACATCGGAACTA	SSR	NA	NA	NA
OPC-07NA[b]	NA	NA	NA	NA	NA	NA
Vac127278NA[b]	NA	NA	NA	NA	NA	NA
KAN-11388NA[b]	NA	NA	NA	NA	NA	NA
MAH1-00236-2NA[b]	NA	NA	NA	NA	NA	NA
KAN-3736NA[b]	NA	NA	NA	NA	NA	NA
KAN-11261NA[b]	NA	NA	NA	NA	NA	NA
F3'H00479ANA[b]	NA	NA	NA	NA	NA	NA
KAN-4854NA[b]	NA	NA	NA	NA	NA	NA
NA1707NA[b]	NA	NA	NA	NA	NA	NA
CA106NA[b]	NA	NA	NA	NA	NA	NA
VcMyb10ANA[b]	NA	NA	NA	NA	NA	NA
Contig547NA[b]	NA	NA	NA	NA	NA	NA
KAN-16879NA[b]	NA	NA	NA	NA	NA	NA
BH2FXQ1UFNA[b]	NA	NA	NA	NA	NA	NA
KAN-11107NA[b]	NA	NA	NA	NA	NA	NA
VCB-C02477NA[b]	NA	NA	NA	NA	NA	NA
NZSSR50936NA[b]	NA	NA	NA	NA	NA	NA
NA1224NA[b]	NA	NA	NA	NA	NA	NA

scaf00336NA[b]	NA	NA	NA	NA	NA	NA
Contig264NA[b]	NA	NA	NA	NA	NA	NA
IPK2a-2NA[b]	NA	NA	NA	NA	NA	NA
CA933NA[b]	NA	NA	NA	NA	NA	NA
KAN-17000NA[b]	NA	NA	NA	NA	NA	NA
KAN-11202NA[b]	NA	NA	NA	NA	NA	NA
berc44aNA[b]	NA	NA	NA	NA	NA	NA
NZSSR81215NA[b]	NA	NA	NA	NA	NA	NA
Vac287779NA[b]	NA	NA	NA	NA	NA	NA
KAN-11105NA[b]	NA	NA	NA	NA	NA	NA
berc94NA[b]	NA	NA	NA	NA	NA	NA
Vac110686NA[b]	NA	NA	NA	NA	NA	NA
Vac124324NA[b]	NA	NA	NA	NA	NA	NA
CTPP-02378-1NA[b]	NA	NA	NA	NA	NA	NA
AOMT00197BNA[b]	NA	NA	NA	NA	NA	NA
vcs655902NA[b]	NA	NA	NA	NA	NA	NA
scaf00002-5NA[b]	NA	NA	NA	NA	NA	NA
6ms2-h04NA[b]	NA	NA	NA	NA	NA	NA
OPV-14aNA[b]	NA	NA	NA	NA	NA	NA
berc108NA[b]	NA	NA	NA	NA	NA	NA
scf15903cNA[b]	NA	NA	NA	NA	NA	NA
scaf00305NA[b]	NA	NA	NA	NA	NA	NA
scaf00208NA[b]	NA	NA	NA	NA	NA	NA
UBC615bNA[b]	NA	NA	NA	NA	NA	NA
NZSSR97646NA[b]	NA	NA	NA	NA	NA	NA
scaf00183NA[b]	NA	NA	NA	NA	NA	NA
SIZ1-2[a,b,c]	ATTGCAATCTTGCACAGAGAGA	CTACATAGGATACGCATTGGCA	SSR	104	123	polymorphic
KAN-11281[a,b,c]	GGGGTAACATTGACCATTCG	AAATCCCTCAATCCAAAGGG	SSR	177	209	polymorphic
KAN-11440[a,b,c]	CCAGTAACAATGAGCTGCCA	GATCGTTGCTGAAGGGTTGT	SSR	323	346	polymorphic
Pr031818814[a,b,c]	CTCACCCATCCTTCTCCTCT	CGGTGTTGATGTCATGCTT	SSR	210	213	polymorphic
GVC-C722[a,b,c]	AAGTGGATTTCGATTCGGTG	TAATCCCCATCACCGTCATT	SSR	224	227	polymorphic
KAN-11049[a,b,c]	CTGGCTCTGTAGACCTTGCC	AACGGATTATACTGCCACGC	SSR	243	249	polymorphic
GVC-C347[a,b,c]	GGAGAAGATGACCCAAACGA	AGTCCCTTTGGACCATACCC	SSR	410	411	polymorphic
Pr031818821[a,b,c]	TCTAGGGTTTTGGCGCTTC	TCCTTGAGAACAAGTACAGGTGAG	SSR	211	220	polymorphic
Pr031818828[a,b,c]	TCGTTCTATTCCTCCCGAAT	ATAGAAACTCGCCGTCTCCT	SSR	181	197	polymorphic
KAN-11325[a,b,c]	CAACATTCCCGAAAACCAGT	ACCCTTCACCTGACACCATC	SSR	187	210	polymorphic
GVC-V24d10b[a,b,c]	GGAAACGATGCCGTTTTCTA	CAACCCTTCCAGGTCAAAAA	SSR	220	244	polymorphic
Pr031818823[a,b,c]	AATCTCTGTCGCCCATTTTG	TTCCCCTGCTTCTGCTGTT	SSR	185	203	polymorphic
GVC-V22a02ac	ACCGCAAGAGAGAGATTCCA	GTTTGATGATCACGGTGGTG	SSR	186	219	polymorphic
GVC-V31e03[a,b,c]	GGCACCGACGTACCCAC	GGGTGAGTAAAGGACGGTGA	SSR	248	260	polymorphic

Pr031818817[a,b,c]	CGTATTTAGGGATG GAGGGAGT	CGAGGACATCATCT GGCTCT	SSR	304	322	polymorphic
VCB-C03938[a,b,c]	CCTCAGATAACTGAA ACCCGTC	CCTCTCTATTTTCGG TTTCCCT	SSR	332	336	polymorphic
CHI03186-1[a,b,c]	TACATCTTGAGGGGC AGTTTTT	GTGGAGTGTGGGA TATGGATTT	SSR	152	157	polymorphic

[a] Mapped in Rowland et al (2014)
[b] Mapped in current interspecific diploid blueberry consensus map
[c] Mapped in current cranberry consensus map

Appendix V-4. Multiplexing combinations (3x) of blueberry simple sequence repeat (SSR) loci used to genotype the CNJ02-1 cranberry population for linkage map construction.

Multiplex PCR Combos	Locus1	Locus2	Locus3
multiplex1	SIZ1-2	Pr031818816	Pr031818811
multiplex2	GVC-C066a	Pr031818814	GVC-C634_272
multiplex3	CHI03186-1	Pr031818821	Pr031818817
multiplex4	KAN-11281	GVC-V24d10b	KAN-11440
multiplex5	Pr031818828	GVC-C722	SL256
multiplex6	GVC-C322	2ms2-g08	VCB-C03938
multiplex7	Pr031818823	KAN-11049	SL172a
multiplex8	GVC-V22a02	KAN-2328	VCB-C12195
multiplex9	KAN-11325	GVC-V31e03	GVC-C347
multiplex10	GVC-V41c07	CA325	berc292
multiplex11	KAN-16471	GVC-V64f07	NA1304+
multiplex12	Pr031818812	GVC-C703a	berc222

Appendix V-5. Features of the F_1#10 interspecific diploid (*V. corybosum* x *V. darrowii*) blueberry parental map including the length of the linkage groups (LG), the total number of markers mapped (No. Markers), the number of simple sequence repeats (SSRs) previously developed in cranberry mapped, the number of markers previously developed in blueberry mapped, the number of unique marker bins (No. Bins), the average interval or gap between unique marker bins, and the average number of recombination events per individual (Aver. No. Rec. Ind).

LG	Length (cM)	No. Markers	Cranberry SSRs	Blueberry Markers	No. Bins	Average gap between bins (cM)	Aver. No. Rec. Ind
1	98.31	36	16	20	17	6.14	0.95
2	23.00	15	8	7	5	5.75	0.23
2.1	15.85	8	3	5	3	7.93	0.16
3	93.30	25	10	15	12	8.48	0.90
4	103.60	33	17	16	20	5.45	1.01
5	85.30	31	12	19	15	6.09	0.84
6	94.59	33	16	17	15	6.76	0.93
7	82.40	31	15	16	17	5.15	0.81
8	87.26	31	14	17	17	5.45	0.86
9	90.38	35	15	20	17	5.65	0.87
10	80.47	26	9	17	10	8.94	0.78
11	80.20	30	7	23	18	4.72	0.80
12	94.49	31	15	16	16	6.30	0.92
mean	79.17	28	12	16	14	6.37	0.77
total	1029.15	365	157	208	182		

Appendix V-6. Features of the W85-20 diploid *V. corybosum* blueberry parental including the length of the linkage groups (LG), the total number of markers mapped (No. Markers), the number of simple sequence repeats (SSRs) previously developed in cranberry mapped, the number of markers previously developed in blueberry mapped, the number of unique marker bins (No. Bins), the average interval or gap between unique marker bins, and the average number of recombination events per individual (Aver. No. Rec. Ind).

LG	Length (cM)	No. Markers	Cranberry SSRs	Blueberry Markers	No. Bins	Average gap between bins (cM)	Aver. No. Rec. Ind
1	61.51	16	10	6	6	12.30	0.59
2	55.93	16	10	6	8	7.99	0.54
2.1	17.54	6	2	4	5	4.39	0.17
3	95.81	17	9	8	12	8.71	0.92
4	83.15	21	13	8	12	7.56	0.81
5.1	16.20	5	3	2	2	16.20	0.16
5	12.56	10	5	5	6	2.51	0.12
6	111.37	19	14	5	9	13.92	0.96
7	70.23	17	10	7	9	8.78	0.69
8	62.79	14	9	5	8	8.97	0.60
9	89.46	20	15	5	10	9.94	0.84
10	56.30	12	7	5	6	11.26	0.48
11	31.88	7	3	4	3	15.94	0.29
12	109.26	18	13	5	9	13.66	0.90
mean	62.43	14.14	8.79	5	7.5	10.15	0.58
total	873.99	198	123	75	105		

Appendix V-7. Local inversions in the F_1#10 interspecific diploid blueberry (*V. corymbosum* x *V. darrowii*) maternal bin map compared to the W85-23 (*V. corymbosum*) blueberry paternal bin map.

LG	Locus	F_1#10 parental bin map				W85-23 parental bin map			
		Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)	Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)
1	KAN-1875	59.30	0.55	59.30	59.85	61.51	14.85	46.66	61.51
	1trimcontig440230	59.85				46.66			
4	SCF61972	75.16	8.57	75.16	83.73	67.99	6.40	61.59	67.99
	contig600	75.28				61.59			
	ct129202	83.73				67.05			

Appendix V-8. Marker location and segregation distortion in the consensus and parental bin maps for the F_1#10 (P1) x W85-23 (P2) interspecific diploid blueberry population.

Locus	Con-sensus	LG	P1 LG	P1 Position	P1 Chi-Square	P1 *p*-value	P2 LG	P2 Position	P2 Chi-Square	P2 *p*-value
OPC-07	0.0	1	1	0.0	0.98	-	NA	NA	NA	NA
SCF68870	0.0	1	1	0.0	0.98	-	NA	NA	NA	NA
SCF30816	0.0	1	1	0.0	0.98	-	NA	NA	NA	NA
CHS00491B	1.1	1	1	0.0	0.98	-	1	0.0	0.11	-
SCF125768	3.2	1	1	6.1	0.59	-	1	0.0	0.11	-
vm89040	3.6	1	1	4.8	0.3	-	1	0.0	0.11	-
Vac127278	3.6	1	1	4.8	0.3	-	1	0.0	0.11	-
KAN-11388	12.6	1	1	14.6	0.98	-	NA	NA	NA	NA
KAN-11200	12.6	1	1	14.6	0.98	-	NA	NA	NA	NA
GVC-V23g01	16.4	1	1	18.2	1.46	-	NA	NA	NA	NA
scf258d	20.4	1	1	27.9	2.71	*	1	9.8	0.11	-
berc369	22.7	1	1	27.9	2.71	*	NA	NA	NA	NA
1trimcontig179737	23.6	1	1	27.9	2.71	*	1	19.5	0.30	-
SCF11186	23.6	1	1	27.9	2.71	*	1	19.5	0.30	-
VCB-C08295	24.7	1	1	30.3	1.46	-	NA	NA	NA	NA
GVC-C347	24.7	1	1	30.3	1.46	-	NA	NA	NA	NA
1trimcontig239742	24.7	1	1	30.3	1.46	-	NA	NA	NA	NA
KAN-24885	25.6	1	1	30.3	1.46	-	1	21.9	0.01	-
2ms2-g08	25.6	1	1	30.3	1.46	-	1	21.9	0.01	-
VCB-C12195	25.6	1	1	30.3	1.46	-	1	21.9	0.01	-
NA292Sa	25.9	1	1	31.5	0.98	-	NA	NA	NA	NA
scf8l	26.5	1	NA	NA	NA	NA	1	21.9	0.01	-
SCF14358	27.1	1	1	33.0	0.59	-	NA	NA	NA	NA
berc279	32.9	1	1	39.1	0.11	-	NA	NA	NA	NA
1trimcontig440230	49.6	1	1	59.9	0.98	-	1	46.7	0.59	-
CHS00519A	54.5	1	1	66.2	0.59	-	NA	NA	NA	NA
KAN-1875	56.9	1	1	59.3	0.98	-	1	61.5	4.35	**
414791_K63	69.8	1	1	98.3	0.3	-	NA	NA	NA	NA
IP5PII-2	69.8	1	1	98.3	0.3	-	NA	NA	NA	NA
berc341	69.8	1	1	98.3	0.3	-	NA	NA	NA	NA
307461_K70	70.6	1	1	98.3	0.3	-	1	61.5	4.35	**
1trimcontig439506	73.5	1	1	92.3	0.11	-	1	61.5	4.35	**
SCF8223	73.5	1	1	92.3	0.11	-	1	61.5	4.35	**
SCF1527	74.4	1	1	92.3	0.11	-	NA	NA	NA	NA
SCF95851	74.4	1	1	92.3	0.11	-	NA	NA	NA	NA
MAH1-00236-2	80.1	1	1	83.7	0.11	-	NA	NA	NA	NA
berc542b	80.9	1	1	85.0	0.3	-	NA	NA	NA	NA
SCF203038	0.0	2	NA	NA	NA	NA	2	0.0	0.30	-
vm13780	0.0	2	NA	NA	NA	NA	2	0.0	0.30	-
vm54133	10.0	2	NA	NA	NA	NA	2	9.8	0.11	-
KAN-3736	34.3	2	NA	NA	NA	NA	2	32.8	1.46	-
KAN-11261	36.1	2	2	0.0	13.12	******	NA	NA	NA	NA
198358_K70	36.4	2	2	0.0	13.12	******	2	35.4	1.46	-
F3'H00479A	36.8	2	NA	NA	NA	NA	2	35.4	1.46	-
KAN-4854	41.9	2	2	6.1	6.37	**	2	40.2	4.35	**
NA1707	48.2	2	NA	NA	NA	NA	2	47.5	4.35	**
172672_K70	48.7	2	2	13.3	2.71	*	2	47.5	4.35	**
346445_K63	48.7	2	2	13.3	2.71	*	2	47.5	4.35	**

scf2000b	48.7	2	2	13.3	2.71	*	2	47.5	4.35	**
SCF125667	49.3	2	2	13.3	2.71	*	NA	NA	NA	NA
VCB-C03938	49.3	2	2	13.3	2.71	*	NA	NA	NA	NA
CHI03186-1	49.3	2	2	13.3	2.71	*	NA	NA	NA	NA
ct89348	50.9	2	2	13.3	2.71	*	2	52.3	2.71	*
SL413	53.9	2	2	18.2	1.46	-	NA	NA	NA	NA
ANPER01018C	55.5	2	NA	NA	NA	NA	2	55.9	5.31	**
CA106	57.0	2	2	23.0	0.59	-	2	55.9	5.31	**
372875_K63	57.0	2	2	23.0	0.59	-	2	55.9	5.31	**
CA325	57.0	2	2	23.0	0.59	-	2	55.9	5.31	**
CA1545F2	58.2	2	2	23.0	0.59	-	NA	NA	NA	NA
scaf00021	0.0	2.1	NA	NA	NA	NA	2.1	0.2	0.98	-
Pr031818818	1.1	2.1	2.1	0.0	2.71	*	2.1	0.0	0.98	-
OPC-09b	2.8	2.1	2.1	0.0	2.71	*	NA	NA	NA	NA
KAN-23741	7.5	2.1	2.1	4.8	1.46	-	2.1	8.9	0.59	-
GVC-C722	7.5	2.1	2.1	4.8	1.46	-	2.1	9.3	0.59	-
Pr031818813	8.2	2.1	2.1	4.8	1.46	-	NA	NA	NA	NA
339139_K63	11.0	2.1	2.1	4.8	1.46	-	2.1	17.5	0.11	-
SCF965	17.4	2.1	2.1	15.9	2.04	-	2.1	17.5	0.11	-
scf28l	18.5	2.1	2.1	15.9	2.04	-	NA	NA	NA	NA
KAN-41365	0.0	3	3	0.0	0.98	-	NA	NA	NA	NA
1trimcontig443603	0.0	3	3	0.0	0.98	-	NA	NA	NA	NA
SCF58861	0.8	3	3	0.0	0.98	-	3	0.0	5.31	**
KAN-41661	1.7	3	NA	NA	NA	NA	3	0.0	5.31	**
NA172	2.9	3	NA	NA	NA	NA	3	1.2	4.35	**
SCF41759	3.8	3	3	4.8	3.48	*	3	1.2	4.35	**
KAN-16471	4.6	3	3	4.8	3.48	*	NA	NA	NA	NA
SCF51607	10.3	3	NA	NA	NA	NA	3	8.5	6.37	**
berc128a	13.3	3	3	13.5	2.71	*	NA	NA	NA	NA
VcMyb10A	17.7	3	NA	NA	NA	NA	3	15.8	4.35	**
SCF22339	17.7	3	NA	NA	NA	NA	3	15.8	4.35	**
scf10688	38.2	3	3	36.3	8.78	****	NA	NA	NA	NA
berc229	43.6	3	3	43.7	11.58	*****	NA	NA	NA	NA
berc51b	43.6	3	3	43.7	11.58	*****	NA	NA	NA	NA
SCF78184	43.6	3	3	43.7	11.58	*****	NA	NA	NA	NA
all03191	43.6	3	3	43.7	11.58	*****	NA	NA	NA	NA
KAN-11057	44.6	3	3	44.9	13.12	******	NA	NA	NA	NA
SCF8151	44.6	3	3	44.9	13.12	******	NA	NA	NA	NA
1trimcontig436904	44.6	3	3	44.9	13.12	******	NA	NA	NA	NA
KAN-11440	45.0	3	3	44.9	13.12	******	3	45.2	0.59	-
SCF84796	45.0	3	3	44.9	13.12	******	3	45.4	0.59	-
VCB-C09527	46.6	3	3	47.3	10.13	****	3	45.7	0.59	-
SCF110888	47.0	3	3	47.3	10.13	****	NA	NA	NA	NA
berc396	48.2	3	3	48.5	8.78	****	NA	NA	NA	NA
Contig547	59.9	3	NA	NA	NA	NA	3	58.8	0.30	-

1trimcontig440008	67.6	3	NA	NA	NA	NA	3	66.4	0.30	-
411475_K63	67.6	3	NA	NA	NA	NA	3	66.4	0.30	-
berc104	69.3	3	3	70.3	5.31	**	NA	NA	NA	NA
berc781a	77.1	3	3	77.5	3.48	*	NA	NA	NA	NA
KAN-16879	82.4	3	3	83.6	0.59	-	3	80.0	0.30	-
BH2FXQ1UF	87.3	3	NA	NA	NA	NA	3	86.1	0.11	-
berc203	94.0	3	3	93.3	0.11	-	NA	NA	NA	NA
GVC-C102	94.8	3	3	93.3	0.11	-	3	95.8	0.01	-
contig130Fb	94.8	3	3	93.3	0.11	-	3	95.8	0.01	-
OPAA-17b	0.0	4	4	9.7	0.3	-	NA	NA	NA	NA
SCF83036	1.3	4	4	6.0	0.11	-	NA	NA	NA	NA
NA1304+	2.5	4	4	2.4	0.3	-	NA	NA	NA	NA
KAN-11107	2.5	4	4	2.4	0.3	-	NA	NA	NA	NA
GVC-NA721	4.0	4	4	0.0	0.3	-	NA	NA	NA	NA
2ms4d10b	5.4	4	4	0.0	0.3	-	4	0.0	0.01	-
berc24	7.7	4	4	13.5	1.46	-	NA	NA	NA	NA
berc2	7.7	4	4	13.8	1.46	-	NA	NA	NA	NA
5ms2b12	9.3	4	4	17.3	0.98	-	NA	NA	NA	NA
GVC-V24d10b	10.8	4	NA	NA	NA	NA	4	0.0	0.01	-
GVC-NA113	19.3	4	4	29.5	0.3	-	NA	NA	NA	NA
GVC-V41c07	19.9	4	4	29.5	0.3	-	4	8.5	2.71	*
SCF99113	19.9	4	4	29.5	0.3	-	4	8.5	2.71	*
VCB-C02477	26.9	4	NA	NA	NA	NA	4	12.1	3.48	*
VCB-C09467	30.0	4	4	47.0	0.11	-	4	12.1	3.48	*
CA855F	30.6	4	4	48.2	0.3	-	4	12.1	3.48	*
SCF140628	33.9	4	4	48.2	0.3	-	NA	NA	NA	NA
CA344	35.1	4	4	50.6	0.3	-	4	19.4	7.53	***
SCF28100	37.8	4	4	50.6	0.3	-	4	25.5	2.71	*
305731_K63	38.5	4	NA	NA	NA	NA	4	25.5	2.71	*
KAN-11118	41.0	4	4	54.3	0.59	-	NA	NA	NA	NA
281741_K70	42.7	4	4	54.3	0.59	-	4	32.7	0.59	-
scaf00004-3	43.7	4	4	56.7	0.59	-	NA	NA	NA	NA
CA54	43.7	4	4	56.7	0.59	-	NA	NA	NA	NA
NZSSR50936	44.3	4	NA	NA	NA	NA	4	32.7	0.59	-
SCF13231	49.5	4	4	61.5	0.11	-	NA	NA	NA	NA
NA1713	52.6	4	4	61.5	0.11	-	4	53.1	0.01	-
SCF16359	52.6	4	4	61.5	0.11	-	4	53.1	0.01	-
contig600	64.2	4	4	75.3	0.59	-	4	61.6	0.59	-
SCF61972	66.6	4	4	75.2	0.59	-	4	68.0	2.71	*
ct129202	70.9	4	4	83.7	0.3	-	4	67.1	2.71	*
scf43g	83.4	4	NA	NA	NA	NA	4	78.3	3.48	*
NA1224	85.5	4	4	101.2	3.48	*	4	78.3	3.48	*
SCF18363	86.7	4	4	101.2	3.48	*	NA	NA	NA	NA
Pr031818820	87.6	4	4	101.2	3.48	*	4	83.2	7.53	***
scf26r	87.9	4	4	102.4	2.71	*	NA	NA	NA	NA
SCF51810	89.0	4	4	103.6	3.48	*	4	83.2	7.53	***
berc62	89.1	4	4	103.6	3.48	*	NA	NA	NA	NA
berc48	0.0	5	5	0.0	3.48	*	NA	NA	NA	NA
SCF30000	0.0	5	5	0.0	3.48	*	NA	NA	NA	NA
251788_K63	0.8	5	5	0.0	3.48	*	5	0.0	0.98	-
ct153008	0.8	5	5	0.0	3.48	*	5	0.0	0.98	-
KAN-27743	0.8	5	5	0.0	3.48	*	5	0.0	0.98	-
SCF804	0.8	5	5	0.0	3.48	*	5	0.0	0.98	-
KAN-27356	3.5	5	5	3.6	4.35	**	NA	NA	NA	NA
scaf00336	5.1	5	5	3.6	4.35	**	5	4.8	3.48	*

scaf00004-6	10.5	5	NA	NA	NA	NA	5	8.1	2.04	-
SCF34663	10.7	5	5	12.1	3.48	*	5	7.6	2.04	-
Contig264	14.6	5	NA	NA	NA	NA	5	11.4	4.35	**
SCF32727	15.0	5	5	17.0	2.04	-	5	11.4	4.35	**
berc292	15.3	5	5	17.0	2.04	-	NA	NA	NA	NA
SCF59035	15.3	5	5	17.0	2.04	-	NA	NA	NA	NA
Pr031818812	18.3	5	5	21.8	2.04	-	5	12.6	3.48	*
Pr031818825	19.8	5	5	21.8	2.04	-	NA	NA	NA	NA
IPK2a-2	19.8	5	5	21.8	2.04	-	NA	NA	NA	NA
KAN-3462	21.1	5	5	23.3	1.46	-	NA	NA	NA	NA
berc130	24.8	5	5	26.9	0.98	-	NA	NA	NA	NA
KAN-2237	39.1	5	5	40.2	0.01	-	NA	NA	NA	NA
KAN-27179	46.0	5	5	48.7	0.01	-	5.1	0.0	0.59	-
CA933	46.0	5	5	48.7	0.01	-	5.1	0.0	0.59	-
289194_K63	46.0	5	5	48.7	0.01	-	5.1	0.0	0.59	-
GVC-C455	47.8	5	5	48.7	0.01	-	NA	NA	NA	NA
KAN-17147	47.8	5	5	48.7	0.01	-	NA	NA	NA	NA
SCF46751	52.7	5	5	49.9	0.01	-	5.1	16.2	7.53	***
GVC-NA146	59.6	5	5	63.5	0.98	-	NA	NA	NA	NA
418138_K63	64.5	5	5	69.5	2.71	*	NA	NA	NA	NA
KAN-17000	70.5	5	5	76.8	4.35	**	NA	NA	NA	NA
Pr031818816	75.2	5	5	85.3	5.31	**	5.1	16.2	7.53	***
NA186	76.9	5	5	85.3	5.31	**	NA	NA	NA	NA
vm10462	76.9	5	5	85.3	5.31	**	NA	NA	NA	NA
GVC-C613	77.7	5	5	84.0	4.35	**	NA	NA	NA	NA
berc268	0.0	6	6	0.0	0.98	-	NA	NA	NA	NA
16720_K63	1.4	6	6	0.0	0.98	-	6	0.0	2.04	-
scf44a	8.2	6	6	12.2	0.3	-	6	0.0	2.04	-
SCF77055	8.9	6	6	13.5	0.59	-	6	0.0	2.04	-
KAN-11202	10.4	6	6	13.5	0.59	-	NA	NA	NA	NA
Pr031818823	10.4	6	6	13.5	0.59	-	NA	NA	NA	NA
contig652	24.1	6	6	28.4	0.01	-	NA	NA	NA	NA
KAN-11199	24.8	6	6	28.4	0.01	-	6	23.2	3.48	*
Ig9279a	24.8	6	6	28.4	0.01	-	6	23.2	3.48	*
berc44a	37.7	6	6	44.1	0.3	-	NA	NA	NA	NA
CA169	39.5	6	NA	NA	NA	NA	6	44.5	1.46	-
412234_K63	42.9	6	6	49.4	0.98	-	6	39.4	1.46	-
SCF3427	42.9	6	6	49.4	0.98	-	6	39.4	1.46	-
VCB-C00694	42.9	6	6	49.4	0.98	-	6	39.4	1.46	-
SCF132006	42.9	6	6	49.3	0.98	-	6	39.4	1.46	-
scf112c	45.0	6	6	53.0	1.46	-	6	39.4	1.46	-
Pr031818819	45.5	6	6	53.0	1.46	-	NA	NA	NA	NA
CA66	51.0	6	6	59.0	0.3	-	NA	NA	NA	NA
Pr031818811	51.0	6	6	59.0	0.3	-	NA	NA	NA	NA
berc488b	51.0	6	6	59.0	0.3	-	NA	NA	NA	NA
berc895	52.1	6	6	60.2	0.11	-	NA	NA	NA	NA
OPAO-19a	52.1	6	6	60.2	0.11	-	NA	NA	NA	NA
SCF13711	52.1	6	6	60.2	0.11	-	NA	NA	NA	NA
VCB-C04624	65.2	6	6	76.4	0.3	-	NA	NA	NA	NA
ct92708	71.9	6	6	83.7	0.11	-	6	95.0	0.30	-
OPAQ-01c	72.4	6	6	83.7	0.11	-	NA	NA	NA	NA
GVC-V31e03	73.1	6	6	84.9	0.01	-	6	96.3	0.11	-
SCF113558	73.1	6	6	84.9	0.01	-	6	95.7	0.11	-
vm31701	81.2	6	6	91.0	0.01	-	6	107.8	0.30	-
SCF124927	81.2	6	6	91.0	0.01	-	6	107.8	0.30	-
SCF109269	83.1	6	6	94.6	0.11	-	6	107.8	0.30	-
NZSSR81215	83.9	6	6	94.6	0.11	-	NA	NA	NA	NA

SCF108454	83.9	6	6	94.6	0.11	-	NA	NA	NA	NA
KAN-20177	84.9	6	6	94.6	0.11	-	6	111.4	0.59	-
1trimcontig339726	85.6	6	NA	NA	NA	NA	6	111.4	0.59	-
1trimcontig450309	0.0	7	7	0.0	0.11	-	NA	NA	NA	NA
OPP-14b	0.0	7	7	0.0	0.11	-	NA	NA	NA	NA
KAN-79	1.6	7	7	1.2	0.3	-	7	0.0	0.01	-
KAN-24973	2.1	7	NA	NA	NA	NA	7	0.0	0.01	-
scaf00069	2.3	7	7	2.4	0.59	-	7	0.0	0.01	-
berc798	2.4	7	7	2.4	0.59	-	NA	NA	NA	NA
berc555	16.9	7	7	17.2	0.59	-	NA	NA	NA	NA
berc143	16.9	7	7	17.2	0.59	-	NA	NA	NA	NA
GVC-C179	20.6	7	7	20.8	0.01	-	NA	NA	NA	NA
SCF167793	20.6	7	7	20.8	0.01	-	NA	NA	NA	NA
SCF110168	22.7	7	NA	NA	NA	NA	7	17.6	2.04	-
SCF128307	34.3	7	7	35.7	0.98	-	7	26.1	0.11	-
GVC-V32g09	35.7	7	7	35.7	0.98	-	NA	NA	NA	NA
SCF4305	41.3	7	7	41.8	0.11	-	7	34.6	0.01	-
1trimcontig337780	41.3	7	7	41.8	0.11	-	7	34.5	0.01	-
GVC-C725	42.2	7	7	41.8	0.11	-	NA	NA	NA	NA
300409_K63	42.2	7	7	41.8	0.11	-	NA	NA	NA	NA
SCF65897	43.5	7	7	43.0	0.3	-	NA	NA	NA	NA
KAN-24598	43.5	7	7	43.0	0.3	-	NA	NA	NA	NA
OPAR-13c	44.4	7	7	44.2	0.59	-	NA	NA	NA	NA
SCF9045	45.4	7	7	43.0	0.3	-	7	43.2	0.11	-
76326_K70	46.0	7	7	44.2	0.59	-	7	43.2	0.11	-
409618_K63	46.0	7	7	44.2	0.59	-	7	43.2	0.11	-
SCF112540	51.9	7	7	54.0	0.59	-	7	43.2	0.11	-
SCF85946	53.5	7	7	54.2	0.59	-	NA	NA	NA	NA
OPAQ-11b	53.5	7	7	53.7	0.59	-	NA	NA	NA	NA
ripe-00162a	61.8	7	7	63.1	0.98	-	NA	NA	NA	NA
Vac287779	66.0	7	NA	NA	NA	NA	7	58.1	0.11	-
berc196	69.3	7	7	71.1	1.46	-	NA	NA	NA	NA
scaf00392	75.0	7	NA	NA	NA	NA	7	70.2	0.59	-
KAN-11105	75.0	7	NA	NA	NA	NA	7	70.2	0.59	-
SCF36745	77.7	7	7	80.0	0.98	-	7	66.6	0.30	-
6ms4e4b	77.7	7	7	80.0	0.98	-	7	66.6	0.30	-
scaf00369	78.3	7	7	81.2	1.46	-	7	66.6	0.30	-
scf1594	80.1	7	7	82.4	0.98	-	NA	NA	NA	NA
AOMT00197A	80.1	7	7	82.4	0.98	-	NA	NA	NA	NA
SCF81732	0.0	8	8	0.0	0.98	-	8	0.0	0.01	-
OPAR-14a	0.2	8	8	0.0	0.98	-	NA	NA	NA	NA
ct89379	1.4	8	8	2.4	0.98	-	8	0.0	0.01	-
berc94	6.7	8	8	5.7	1.46	-	NA	NA	NA	NA
SCF24087	6.8	8	8	6.2	1.46	-	8	8.5	0.59	-
SCF92986	12.0	8	8	11.3	0.11	-	NA	NA	NA	NA
Vac110686	20.7	8	8	16.2	0.59	-	8	30.1	0.11	-
SL256	23.5	8	8	22.3	0.01	-	NA	NA	NA	NA
411348_K63	29.1	8	8	29.6	0.11	-	8	31.4	0.30	-
SCF105925	29.1	8	8	29.6	0.11	-	8	31.4	0.30	-
OPP-12b	30.6	8	8	29.6	0.11	-	NA	NA	NA	NA
Vac124324	32.6	8	NA	NA	NA	NA	8	37.5	0.11	-
Pr031818828	33.0	8	8	32.0	0.11	-	8	37.5	0.11	-
SCF30010	33.1	8	8	32.0	0.11	-	NA	NA	NA	NA

OPAR-12b	33.1	8	8	32.0	0.11	-	NA	NA	NA	NA
SCF17979	33.5	8	8	33.2	0.01	-	8	37.5	0.11	-
vm13884	33.5	8	8	33.2	0.01	-	8	37.5	0.11	-
berc230	41.2	8	8	41.7	0.01	-	NA	NA	NA	NA
leaf-00248	41.2	8	8	41.7	0.01	-	NA	NA	NA	NA
CTPP-02378-1	47.9	8	8	47.8	0.11	-	NA	NA	NA	NA
leaf-00158b	47.9	8	8	47.8	0.11	-	NA	NA	NA	NA
CHI01251A	49.1	8	8	47.8	0.11	-	8	57.8	0.11	-
CHI01251B	50.2	8	NA	NA	NA	NA	8	57.8	0.11	-
SCF77645	55.4	8	8	55.1	0.59	-	8	62.3	0.11	-
260167_K70	55.4	8	8	55.1	0.59	-	8	62.8	0.11	-
berc85	74.0	8	8	73.8	0.3	-	NA	NA	NA	NA
SCF42256	74.0	8	8	73.8	0.3	-	NA	NA	NA	NA
berc56a	75.1	8	8	72.6	0.59	-	NA	NA	NA	NA
CA1105	75.1	8	8	72.6	0.59	-	NA	NA	NA	NA
berc209a	86.1	8	8	86.1	0.3	-	NA	NA	NA	NA
1trimcontig326802	86.1	8	8	86.1	0.3	-	NA	NA	NA	NA
KAN-11325	87.4	8	8	87.3	0.59	-	NA	NA	NA	NA
1trimcontig440337	87.4	8	8	87.3	0.59	-	NA	NA	NA	NA
OPC-09a	0.0	9	9	0.0	2.04	-	NA	NA	NA	NA
berc136	0.0	9	9	0.0	2.04	-	NA	NA	NA	NA
SCF29529	1.4	9	9	24.3	2.04	-	9	45.3	0.59	-
bud397-01134	2.4	9	9	3.6	1.46	-	NA	NA	NA	NA
SIZ1-2	2.4	9	9	3.6	1.46	-	NA	NA	NA	NA
407841_K63	2.7	9	9	4.8	2.04	-	9	0.0	0.98	-
KAN-2328	2.7	9	9	4.8	2.04	-	9	0.0	0.98	-
KAN-11281	3.3	9	9	4.8	2.04	-	NA	NA	NA	NA
SCF84921	3.3	9	9	4.8	2.04	-	NA	NA	NA	NA
GVC-V61g11	3.3	9	9	4.8	2.04	-	NA	NA	NA	NA
SCF101363	4.3	9	9	7.2	2.04	-	9	0.0	0.98	-
CA243	7.0	9	9	8.4	1.46	-	NA	NA	NA	NA
ct154206	9.4	9	9	8.4	1.46	-	9	12.2	0.98	-
Pr031818815	11.2	9	NA	NA	NA	NA	9	12.5	0.98	-
ripe-00787	11.2	9	9	13.3	0.59	-	NA	NA	NA	NA
scaf00062	12.0	9	9	13.3	0.59	-	9	12.3	0.98	-
VCB-BH-1DVIYK	12.4	9	9	24.3	2.04	-	NA	NA	NA	NA
AOMT00197B	12.4	9	9	24.3	2.04	-	NA	NA	NA	NA
SCF10459	16.9	9	9	51.8	11.58	*****	9	45.3	0.59	-
OPAO-02b	17.7	9	9	51.2	11.58	*****	NA	NA	NA	NA
berc102	18.1	9	9	50.5	13.12	******	NA	NA	NA	NA
SCF136207	23.0	9	NA	NA	NA	NA	9	53.8	0.98	-
SCF48414	24.7	9	9	59.5	8.78	****	9	53.8	0.98	-
KAN-11260	25.1	9	9	59.5	8.78	****	NA	NA	NA	NA
Pr031818814	26.3	9	9	60.7	7.53	***	NA	NA	NA	NA
SCF88396	26.4	9	9	60.7	7.53	***	9	56.2	0.98	-
scf21n	26.4	9	9	60.7	7.53	***	9	56.2	0.98	-
scaf00007-2	27.6	9	9	62.0	6.37	**	NA	NA	NA	NA
scf306f	45.0	9	9	79.5	1.46	-	9	72.4	4.35	**
SCF144748	45.0	9	9	79.5	1.46	-	9	72.4	4.35	**
KAN-2260	53.8	9	9	88.0	0.98	-	9	80.9	3.48	*
SCF33185	57.9	9	9	88.0	0.98	-	9	89.5	4.35	**
SCF132532	57.9	9	9	88.0	0.98	-	9	89.5	4.35	**
239628_K63	58.4	9	9	89.2	1.46	-	9	89.5	4.35	**

vcs655902	58.7	9	9	90.4	2.04	-	NA	NA	NA	NA
scaf00002-5	58.7	9	9	90.4	2.04	-	NA	NA	NA	NA
6ms2-h04	58.9	9	NA	NA	NA	NA	9	89.5	4.35	**
SCF3932	59.0	9	9	90.4	2.04	-	9	89.5	4.35	**
KAN-11348	0.0	10	10	0.0	0.01	-	NA	NA	NA	NA
ct145170	0.0	10	10	0.0	0.01	-	NA	NA	NA	NA
1trimcontig176861	2.8	10	10	13.5	0.59	-	10	3.6	0.98	-
DFR00528A	2.8	10	10	13.5	0.59	-	10	3.6	0.98	-
KAN-0009C	3.4	10	10	13.5	0.59	-	NA	NA	NA	NA
scaf00009-4	4.3	10	10	12.3	0.3	-	NA	NA	NA	NA
418931_1_K63	4.4	10	10	12.3	0.3	-	10	1.2	2.04	-
KAN-11408	7.2	10	NA	NA	NA	NA	10	0.0	1.46	-
KAN-11049	8.9	10	10	0.0	0.01	-	10	0.0	1.46	-
berc893	21.7	10	10	29.6	0.59	-	NA	NA	NA	NA
OPP-14d	21.7	10	10	29.6	0.59	-	NA	NA	NA	NA
SCF147295	31.2	10	10	39.4	0.98	-	NA	NA	NA	NA
GVC-C136	31.2	10	10	39.4	0.98	-	NA	NA	NA	NA
berc824	36.3	10	10	51.8	2.04	-	NA	NA	NA	NA
SCF107715	38.3	10	10	46.7	0.98	-	10	49.0	0.01	-
OPV-08b	38.4	10	10	46.7	0.98	-	NA	NA	NA	NA
SCF65999	38.4	10	10	46.7	0.98	-	NA	NA	NA	NA
KAN-11109	38.4	10	10	46.7	0.98	-	NA	NA	NA	NA
GVC-C089	38.4	10	10	46.7	0.98	-	NA	NA	NA	NA
berc496	38.4	10	10	46.7	0.98	-	NA	NA	NA	NA
313928_K70	38.4	10	10	46.7	0.98	-	NA	NA	NA	NA
KAN-23334	40.0	10	NA	NA	NA	NA	10	46.3	0.11	-
409500_K63	41.4	10	NA	NA	NA	NA	10	49.0	0.01	-
Pr031818817	44.1	10	10	55.3	2.71	*	10	56.3	0.98	-
SCF120352	49.3	10	NA	NA	NA	NA	10	56.3	0.98	-
SCF60761	52.3	10	10	76.9	7.53	***	10	56.3	0.98	-
364103_K63	53.5	10	10	80.5	11.58	*****	10	56.3	0.98	-
berc210	54.5	10	10	76.9	7.53	***	NA	NA	NA	NA
OPP-12c	56.1	10	10	80.5	11.58	*****	NA	NA	NA	NA
berc5	56.1	10	10	80.5	11.58	*****	NA	NA	NA	NA
1trimcontig176042	0.0	11	11	0.0	0.59	-	NA	NA	NA	NA
SCF110507	2.4	11	11	0.0	0.59	-	11	0.0	0.30	-
OPV-14a	4.1	11	11	4.8	1.46	-	NA	NA	NA	NA
berc401	8.3	11	11	9.7	0.59	-	NA	NA	NA	NA
berc98a	12.8	11	11	14.5	0.59	-	NA	NA	NA	NA
SCF1524	16.1	11	11	18.1	0.01	-	NA	NA	NA	NA
OPV-08c	19.6	11	11	21.7	0.59	-	NA	NA	NA	NA
SCF65004	21.8	11	11	24.2	0.59	-	NA	NA	NA	NA
Pr031818821	22.5	11	11	26.6	0.59	-	11	0.0	0.30	-
leaf-00158a	24.1	11	11	26.6	0.59	-	NA	NA	NA	NA
GVC-C066a	24.1	11	11	26.6	0.59	-	NA	NA	NA	NA
OPB-04a	31.6	11	11	33.8	2.71	*	NA	NA	NA	NA
SCF110757	37.9	11	11	39.9	2.04	-	NA	NA	NA	NA
UBC211b	37.9	11	11	39.9	2.04	-	NA	NA	NA	NA
berc56b	44.7	11	11	53.2	6.37	**	NA	NA	NA	NA
berc108	46.0	11	11	51.0	4.35	**	NA	NA	NA	NA
berc54b	46.6	11	11	49.6	3.48	*	NA	NA	NA	NA
OPAR-19	46.6	11	11	49.6	3.48	*	NA	NA	NA	NA
OPU-01b	46.6	11	11	49.6	3.48	*	NA	NA	NA	NA
ripe-01939	46.6	11	11	47.2	3.48	*	NA	NA	NA	NA

CA1785S	47.7	11	11	48.4	4.35	**	NA	NA	NA	NA
VCB-C06669	47.7	11	11	48.4	4.35	**	NA	NA	NA	NA
KAN-2459	47.8	11	11	48.4	4.35	**	11	29.5	0.30	-
SCF95754	47.8	11	11	48.4	4.35	**	11	29.5	0.30	-
KAN-25281	47.8	11	11	48.4	4.35	**	11	29.5	0.30	-
scf94a	61.6	11	11	77.8	2.71	*	11	29.5	0.30	-
GVC-V62a08	62.0	11	11	77.8	2.71	*	NA	NA	NA	NA
scf15903c	63.9	11	11	80.2	1.46	-	11	31.9	0.30	-
CA636S	64.0	11	11	80.2	1.46	-	NA	NA	NA	NA
berc149b	69.9	11	11	66.8	7.53	***	NA	NA	NA	NA
scaf00305	0.0	12	12	2.4	2.71	*	NA	NA	NA	NA
OPP-09b	0.0	12	12	2.4	2.71	*	NA	NA	NA	NA
SCF145689	1.4	12	12	2.4	2.71	*	12	1.2	1.46	-
scaf00169	2.2	12	12	0.0	1.46	-	12	1.2	1.46	-
SCF102190	2.7	12	12	0.0	1.46	-	12	0.0	0.98	-
scaf00208	4.3	12	NA	NA	NA	NA	12	0.0	0.98	-
vm34671	10.5	12	12	17.2	2.71	*	12	1.2	1.46	-
SCF75572	13.2	12	12	17.2	2.71	*	NA	NA	NA	NA
UBC615b	15.9	12	12	19.6	2.71	*	NA	NA	NA	NA
SCF159195	15.9	12	12	19.6	2.71	*	NA	NA	NA	NA
scf79c	22.1	12	NA	NA	NA	NA	12	18.7	0.01	-
408825_K63	22.1	12	NA	NA	NA	NA	12	18.7	0.01	-
SCF19055	22.5	12	12	25.7	2.04	-	12	18.7	0.01	-
berc485	22.6	12	12	25.7	2.04	-	NA	NA	NA	NA
OPP-16a	37.4	12	12	39.2	0.01	-	NA	NA	NA	NA
SCF69698	38.0	12	12	39.2	0.01	-	12	39.0	0.01	-
SCF37628	40.3	12	12	42.9	0.11	-	12	39.9	0.01	-
SCF34584	40.3	12	12	42.9	0.11	-	12	39.3	0.01	-
berc523	41.2	12	12	42.9	0.11	-	NA	NA	NA	NA
SCF55511	43.7	12	12	45.3	0.59	-	NA	NA	NA	NA
GVC-V64f07	44.7	12	12	45.3	0.59	-	12	48.1	0.11	-
SCF34071	44.7	12	12	45.3	0.59	-	12	48.1	0.11	-
SL42	48.7	12	12	50.1	0.59	-	NA	NA	NA	NA
CA1049	48.7	12	12	50.1	0.59	-	NA	NA	NA	NA
CA1343	51.1	12	12	52.5	0.59	-	NA	NA	NA	NA
NZSSR97646	75.7	12	12	75.7	0.59	-	NA	NA	NA	NA
GVC-C322	75.7	12	12	75.8	0.59	-	NA	NA	NA	NA
ct110752	77.4	12	12	76.0	0.59	-	12	105.7	0.59	-
scaf00183	88.3	12	12	92.1	0.98	-	12	109.3	0.30	-
ct140233	89.0	12	12	93.3	0.59	-	12	109.3	0.30	-
GVC-C608	89.0	12	12	93.3	0.59	-	12	109.3	0.30	-
SCF28279	89.0	12	12	93.3	0.59	-	12	109.3	0.30	-
SCF36716	89.8	12	12	93.3	0.59	-	NA	NA	NA	NA
KAN-11482	90.9	12	12	94.5	0.98	-	NA	NA	NA	NA

- = $p > 0.1$, * = $p < 0.1$, ** = $p < 0.05$, *** = $p < 0.01$, **** = $p < 0.005$, ***** = $p < 0.001$, ****** = $p < 0.0005$, ******* = $p < 0.0001$

Appendix V-9. Spearman correlations between marker order in the Rowland et al. (2014) linkage groups (LGs) compared to the LGs from the F_1#10 parental bin map, the W85-20 parental bin map, and the consensus map for the F_1#10 x W85-20 interspecific diploid blueberry population.

Rowland et al. (2014) LG	New Map	New Map LG	Markers in Common	Spearman Correlation
R_LG1	F1#10 x W85-20	LG2.1	4	0.6
		LG3	13	0.96
		LG6	1	-
		LG9	15	0.92
	F1#10	LG2.1	4	0.89
		LG3	13	0.96
		LG9	14	0.91
	W85-20	LG2.1	2	-
		LG3	3	-
		LG6	1	-
		LG9	2	-
R_LG2	F1#10 x W85-20	LG10	3	0.5
		LG1	12	0.42
	F1#10	LG1	12	0.47
		LG10	3	0.87
	W85-20	LG1	2	-
		LG10	1	-
R_LG3	F1#10 x W85-20	LG11	18	0.89
		LG5	1	-
	F1#10	LG5	1	-
		LG11	18	0.86
	W85-20	LG5.1	1	-
		LG11	2	-
R_LG4	F1#10 x W85-20	LG8	13	1
	F1#10	LG8	13	0.98
	W85-20	LG8	1	-
R_LG5	F1#10 x W85-20	LG1	1	-
		LG4	14	0.92
	F1#10	LG1	1	-
		LG4	13	1
	W85-20	LG4	5	1
R_LG6	F1#10 x W85-20	LG12	11	0.99
	F1#10	LG12	11	0.99
	W85-20	LG12	2	-
R_LG7	F1#10 x W85-20	LG6	13	0.98
	F1#10	LG6	13	0.98
	W85-20	LG6	3	1
R_LG8	F1#10 x W85-20	LG10	12	0.53
		LG1	1	-
	F1#10	LG1	1	-
		LG10	12	0.46
	W85-20	LG10	1	-
R_LG9	F1#10 x W85-20	LG7	11	0.99
	F1#10	LG7	11	0.99
	W85-20	-	-	-
R_LG10	F1#10 x W85-20	LG5	10	0.94
	F1#10	LG5	10	0.99
	W85-20	LG5	1	-
		LG5.1	1	-
R_LG11	F1#10 x W85-20	LG2	4	0.95
	F1#10	LG2	4	0.95
	W85-20	LG2	1	-

Appendix V-10. Features of the CNJ97-2015 (*Mullica Queen* ®) cranberry parental map including the length of the linkage groups (LG), the total number of markers mapped (No. Markers), the number of simple sequence repeats (SSRs) previously developed in cranberry mapped, the number of markers previously developed in blueberry mapped, the number of unique marker bins (No. Bins), the average interval or gap between unique marker bins, and the average number of recombination events per individual (Aver. No. Rec. Ind).

LG	Length (cM)	No. Markers	Cranberry SSRs	Blueberry Markers	No. Bins	Average gap between bins (cM)	Aver. No. Rec. Ind
1	107.40	37	37	0	20	5.65	1.05
2	112.26	43	41	2	25	4.68	1.08
3	103.29	37	36	1	22	4.92	0.99
4	112.95	50	49	1	25	4.71	1.11
5	80.42	27	27	0	13	6.70	0.79
6	102.44	36	34	2	20	5.39	1.01
7	103.50	44	44	0	21	5.18	1.02
8	107.61	37	35	2	20	5.66	1.05
9	102.84	43	40	3	22	4.90	1
10	82.69	37	35	2	16	5.51	0.81
11	87.35	30	29	1	15	6.24	0.85
12	87.06	45	45	0	19	4.84	0.85
mean	99.15	38.83	37.67	1.17	19.83	5.37	0.97
total	1189.81	466	452	14	238		

Appendix V-11. Features of the NJS98-23 (*Crimson Que*en ®) cranberry parental map including the length of the linkage groups (LG), the total number of markers mapped (No. Markers), the number of simple sequence repeats (SSRs) previously developed in cranberry mapped, the number of markers previously developed in blueberry mapped, the number of unique marker bins (No. Bins), the average interval or gap between unique marker bins, and the average number of recombination events per individual (Aver. No. Rec. Ind).

LG	Length (cM)	No. Markers	Cranberry SSRs	Blueberry Markers	No. Bins	Average gap between bins (cM)	Aver. No. Rec. Ind
1	97.22	45	44	1	18.0	5.72	0.96
2	92.73	44	42	2	20.0	4.88	0.91
3	85.49	37	36	1	17.0	5.34	0.83
4	58.07	34	34	0	17.0	3.63	0.57
5	66.28	28	28	0	11.0	6.63	0.64
6	78.65	34	32	2	16.0	5.24	0.77
7	76.57	43	43	0	21.0	3.83	0.76
8	73.99	38	36	2	22.0	3.52	0.74
9	70.66	42	40	2	21.0	3.53	0.70
10	74.32	37	35	2	16.0	4.95	0.73
11	65.43	31	30	1	12.0	5.95	0.64
12	59.13	38	38	0	19.0	3.29	0.58
mean	74.88	37.58	36.5	1.08	17.5	4.71	0.74
total	898.54	451	438	13	210		

Appendix V-12. Marker location and segregation distortion in the consensus and parental bin maps for the Mullica Queen (P1) x Crimson Queen (P2) CNJ02-1 cranberry population.

Locus	Con-sensus	LG	P1 LG	P1 Position	P1 Chi Square	P1 *p*-value	P2 LG	P2 Position	P2 Chi Square	P2 *p*-value
SCF68870	0.0	1	1	0.0	0.55	-	NA	NA	NA	NA
SCF153722	1.1	1	1	0.0	0.55	-	1	0.0	4.97	**
SCF172019	1.1	1	1	0.0	0.55	-	1	0.0	4.97	**
SCF208509	2.6	1	NA	NA	NA	NA	1	0.0	4.97	**
SCF30816	2.6	1	NA	NA	NA	NA	1	0.0	4.97	**
vm89040	6.7	1	1	7.3	1.65	-	1	4.1	3.33	*
SCF29735	6.9	1	1	7.3	1.65	-	1	4.6	3.84	*
SCF69981	7.4	1	1	8.3	1.65	-	1	4.6	3.84	*
SCF23691	8.4	1	1	10.1	1.65	-	1	4.6	3.84	*
SCF39242	8.4	1	1	10.1	1.65	-	1	4.6	3.84	*
128239_K63	9.2	1	1	10.1	1.65	-	NA	NA	NA	NA
SCF117157	13.7	1	1	14.7	3.33	*	NA	NA	NA	NA
1trimcontig182430	14.1	1	1	15.2	2.85	*	NA	NA	NA	NA
GVC-C347	20.2	1	NA	NA	NA	NA	1	16.7	4.97	**
SCF173212	20.2	1	NA	NA	NA	NA	1	16.7	4.97	**
SCF3362	20.2	1	NA	NA	NA	NA	1	16.7	4.97	**
scf8l	21.1	1	1	23.4	1.32	-	1	16.7	4.97	**
1trimcontig239742	24.2	1	1	27.5	3.33	*	1	19.0	6.95	***
SCF149633	24.2	1	1	27.5	3.33	*	1	19.0	6.95	***
vm23232	28.9	1	1	30.2	3.33	*	NA	NA	NA	NA
1trimcontig179737	29.2	1	1	30.2	3.33	*	1	26.3	3.33	*
SCF11186	29.7	1	NA	NA	NA	NA	1	26.3	3.33	*
scf11l	32.4	1	1	32.2	2.42	-	1	31.4	1.32	-
1trimcontig238795	34.8	1	NA	NA	NA	NA	1	31.4	1.32	-
252600_K70	48.2	1	1	53.4	0.22	-	NA	NA	NA	NA
1trimcontig440230	48.8	1	1	53.4	0.22	-	1	43.9	0.22	-
SCF102347	49.9	1	NA	NA	NA	NA	1	43.9	0.22	-
SCF59248	49.9	1	NA	NA	NA	NA	1	43.9	0.22	-
242569_K70	53.6	1	1	61.8	0.11	-	1	46.2	0.37	-
SCF121995	53.6	1	1	61.5	0.11	-	1	46.2	0.37	-
162108_K70	66.2	1	1	77.5	0.77	-	1	56.4	0	-
SCF142441	66.2	1	1	77.5	0.77	-	1	56.4	0	-
ct116900	72.3	1	NA	NA	NA	NA	1	63.3	0.37	-
SCF8223	72.3	1	NA	NA	NA	NA	1	63.3	0.37	-
SCF111370	73.5	1	1	85.3	0.55	-	1	63.3	0.37	-
SCF124322	73.5	1	1	85.3	0.55	-	1	63.3	0.37	-
SCF3914	73.5	1	1	85.3	0.55	-	1	63.3	0.37	-
SCF43220	74.3	1	1	85.8	0.77	-	1	64.7	0.55	-
SCF22962	74.8	1	1	85.3	0.55	-	NA	NA	NA	NA
SCF118999	75.2	1	1	85.8	0.77	-	NA	NA	NA	NA
SCF3551	86.8	1	1	94.1	0.77	-	1	81.2	3.84	*
SCF45712	89.2	1	NA	NA	NA	NA	1	81.2	3.84	*
307461_K70	91.8	1	1	106.0	1.32	-	1	81.2	3.84	*
Ig16780a	93.9	1	1	99.1	1.65	-	1	88.1	2.42	-
vm55441	95.7	1	1	106.0	1.32	-	NA	NA	NA	NA
SCF107429	96.9	1	1	107.4	1.03	-	1	88.1	2.42	-
SCF43145	96.9	1	1	107.4	1.03	-	1	88.1	2.42	-
414791_K63	98.1	1	1	107.4	1.03	-	1	90.4	2.01	-
SCF153636	98.1	1	1	107.4	1.03	-	1	90.4	2.01	-
vm51985	101.0	1	NA	NA	NA	NA	1	93.1	2.01	-
1trimcontig332960	102.8	1	NA	NA	NA	NA	1	94.9	0.77	-
ct106280	105.1	1	NA	NA	NA	NA	1	97.2	0.55	-
SCF138607	105.1	1	NA	NA	NA	NA	1	97.2	0.55	-

SCF4386	105.1	1	NA	NA	NA	NA	1	97.2	0.55	-
vm13780	0.0	2	2	0.0	0	-	NA	NA	NA	NA
ct118602	1.3	2	2	0.0	0	-	2	0.0	0.37	-
Ig15420a	1.3	2	2	0.0	0	-	2	0.0	0.37	-
1trimcontig332949	2.9	2	NA	NA	NA	NA	2	0.0	0.37	-
SCF175823	2.9	2	NA	NA	NA	NA	2	0.0	0.37	-
SCF177451	6.2	2	2	6.0	0	-	2	3.7	0.37	-
VCC_B3	13.3	2	2	14.6	0	-	NA	NA	NA	NA
SCF141794	14.6	2	2	16.2	0.22	-	2	9.6	0.04	-
vm54133	15.1	2	2	17.4	0.55	-	2	9.6	0.04	-
contig704	16.4	2	2	17.9	0.37	-	NA	NA	NA	NA
1trimcontig209220	16.7	2	2	17.7	0.37	-	2	12.3	0.11	-
SCF142664	16.8	2	NA	NA	NA	NA	2	12.3	0.11	-
198358_K70	34.9	2	NA	NA	NA	NA	2	29.5	0.55	-
SCF213102	34.9	2	NA	NA	NA	NA	2	30.1	0.55	-
SCF80703	43.6	2	2	46.4	2.01	-	2	37.8	0.22	-
CHI03186-1	44.8	2	2	46.4	2.01	-	2	40.1	0.77	-
SCF125667	45.9	2	2	48.7	1.65	-	2	40.1	0.77	-
scf12916	45.9	2	2	48.7	1.65	-	2	40.1	0.77	-
SCF61078	45.9	2	2	48.7	1.65	-	NA	NA	NA	NA
SCF56816	47.4	2	NA	NA	NA	NA	2	41.5	0.55	-
VCB-C03938	47.4	2	NA	NA	NA	NA	2	41.5	0.55	-
172672_K70	47.4	2	2	50.5	2.42	-	2	41.5	0.55	-
SCF174468	47.4	2	2	50.5	2.42	-	2	41.5	0.55	-
SCF192715	47.4	2	2	50.5	2.42	-	2	41.5	0.55	-
SCF3595	47.4	2	2	50.5	2.42	-	2	41.5	0.55	-
SCF66692	47.4	2	2	50.5	2.42	-	2	41.5	0.55	-
297265_K63	47.6	2	2	50.5	2.42	-	NA	NA	NA	NA
SCF18709	48.2	2	2	50.5	2.42	-	2	43.3	1.03	-
SCF158633	48.7	2	2	51.6	1.65	-	2	43.3	1.03	-
scf2000b	49.4	2	2	52.6	1.03	-	2	44.3	1.03	-
ct89348	50.6	2	2	53.7	1.32	-	NA	NA	NA	NA
ct155461	57.7	2	2	61.5	0.22	-	NA	NA	NA	NA
ct124256	58.3	2	2	61.5	0.22	-	2	53.0	0.37	-
SCF48645	59.2	2	NA	NA	NA	NA	2	53.0	0.37	-
CA325	59.6	2	2	64.3	0.04	-	2	53.0	0.37	-
SCF158988	59.6	2	2	64.3	0.04	-	2	53.0	0.37	-
SCF73288	59.8	2	2	64.3	0.04	-	2	53.5	0.22	-
372875_K63	66.4	2	2	72.1	0.11	-	2	59.5	0.11	-
ct130570	66.7	2	2	72.1	0.11	-	NA	NA	NA	NA
29080_K63	73.1	2	NA	NA	NA	NA	2	64.5	0.22	-
SCF13771	77.2	2	2	90.7	0.11	-	2	64.5	0.22	-
1trimcontig351427	78.5	2	NA	NA	NA	NA	2	70.0	1.65	-
SCF77376	78.5	2	NA	NA	NA	NA	2	70.0	1.65	-
SCF26049	79.9	2	2	91.7	0.11	-	2	68.2	1.03	-
314761_K63	81.1	2	2	91.5	0.11	-	NA	NA	NA	NA
scf28l	87.4	2	2	95.8	0.11	-	2	79.2	4.39	**
SCF74458	87.4	2	2	95.8	0.11	-	2	79.2	4.39	**
SCF965	87.4	2	2	95.8	0.11	-	2	79.2	4.39	**
417854_K63	89.8	2	2	100.4	0	-	2	79.2	4.39	**
GVC-C722	97.6	2	2	106.8	0.11	-	NA	NA	NA	NA
1trimcontig178358	99.9	2	2	107.8	0	-	2	92.3	5.59	**
SCF180863	99.9	2	2	107.3	0	-	2	92.3	5.59	**
SCF77145	101.6	2	NA	NA	NA	NA	2	92.7	6.25	**
SCF31394	102.3	2	2	112.3	0.11	-	2	92.7	6.25	**
SCF22434	102.7	2	2	112.3	0.11	-	NA	NA	NA	NA
SCF27510	0.0	3	3	0.0	0.55	-	3	0.0	0.22	-

SCF58861	0.0	3	3	0.0	0.55	-	3	0.0	0.22	-
NA172	4.8	3	3	10.2	0.55	-	3	0.0	0.22	-
SCF162565	4.8	3	3	10.2	0.55	-	3	0.0	0.22	-
contig480Fb	6.1	3	NA	NA	NA	NA	3	3.7	0.22	-
1trimcontig443603	6.6	3	3	10.2	0.55	-	3	3.7	0.22	-
SCF153094	11.9	3	3	14.8	0.55	-	NA	NA	NA	NA
313711_K70	15.5	3	3	17.1	0.37	-	3	14.3	0.37	-
SCF157992	15.5	3	3	17.1	0.37	-	3	14.3	0.37	-
ct89711	15.8	3	3	17.5	0.22	-	3	14.3	0.37	-
ct155339	22.9	3	NA	NA	NA	NA	3	20.3	0.22	-
SCF177450	22.9	3	NA	NA	NA	NA	3	20.3	0.22	-
scf10688	25.9	3	3	29.6	0.77	-	3	22.6	0.37	-
scf142e	25.9	3	3	29.6	0.77	-	3	22.6	0.37	-
scf5304	28.9	3	3	31.9	1.65	-	3	26.2	0.37	-
SCF85773	28.9	3	3	31.9	1.65	-	3	26.2	0.37	-
SCF7845	53.7	3	3	59.5	0.77	-	NA	NA	NA	NA
SCF78184	54.6	3	3	60.4	0.77	-	NA	NA	NA	NA
SCF108252	54.9	3	3	61.3	0.77	-	NA	NA	NA	NA
SCF128992	54.9	3	3	61.3	0.77	-	NA	NA	NA	NA
scf9025	55.3	3	3	60.4	0.77	-	3	50.3	0	-
KAN-11440	55.5	3	3	60.4	0.77	-	3	50.8	0	-
1trimcontig436904	55.9	3	3	61.3	0.77	-	3	50.8	0	-
SCF22477	56.9	3	NA	NA	NA	NA	3	50.8	0	-
SCF53750	56.9	3	NA	NA	NA	NA	3	50.8	0	-
82171_K70	57.8	3	3	64.1	1.32	-	3	51.7	0.11	-
SCF21119	57.8	3	3	64.1	1.32	-	3	51.7	0.11	-
SCF110888	59.1	3	NA	NA	NA	NA	3	52.9	0.37	-
SCF38340	64.4	3	3	71.8	0.11	-	NA	NA	NA	NA
SCF9815	64.4	3	3	72.3	0.11	-	NA	NA	NA	NA
121633_K63	66.1	3	3	78.9	0.11	-	3	54.4	0.11	-
SCF57479	77.6	3	3	85.7	1.03	-	NA	NA	NA	NA
1trimcontig440008	77.8	3	3	85.9	1.03	-	3	69.5	0.37	-
411475_K63	77.8	3	3	86.1	1.03	-	3	69.5	0.37	-
42710_K70	79.3	3	3	87.3	1.32	-	3	70.9	0.22	-
SCF98686	79.3	3	3	87.3	1.32	-	3	70.6	0.22	-
SCF23339	92.3	3	3	100.2	0.22	-	3	84.1	0.04	-
SCF27755	92.5	3	3	100.0	0.22	-	3	84.6	0.11	-
vm51409	93.1	3	NA	NA	NA	NA	3	84.6	0.11	-
scf20g	93.6	3	3	102.4	0.77	-	3	84.6	0.11	-
vm04084	93.6	3	3	102.4	0.77	-	3	84.6	0.11	-
vm78806	94.0	3	NA	NA	NA	NA	3	85.5	0.11	-
contig130Fb	94.4	3	3	103.3	0.77	-	3	85.5	0.11	-
scf511	94.4	3	3	103.3	0.77	-	3	85.5	0.11	-
SCF90229	94.4	3	3	103.3	0.77	-	3	85.5	0.11	-
418294_K63	0.0	4	4	0.0	0.37	-	NA	NA	NA	NA
SCF56561	0.0	4	4	0.0	0.37	-	NA	NA	NA	NA
1trimcontig176303	0.9	4	4	0.9	0.11	-	NA	NA	NA	NA
SCF26697	0.9	4	4	0.9	0.11	-	NA	NA	NA	NA
2ms4d10b	2.4	4	4	2.7	0.11	-	NA	NA	NA	NA
ct119523	2.4	4	4	2.7	0.11	-	NA	NA	NA	NA
ct94504	2.4	4	4	2.7	0.11	-	NA	NA	NA	NA
GVC-V24d10b	2.4	4	4	2.7	0.11	-	NA	NA	NA	NA
SCF83036	3.4	4	4	4.2	0.55	-	NA	NA	NA	NA
5ms2b12	6.6	4	4	7.5	0.37	-	NA	NA	NA	NA
scf1172	29.4	4	4	27.5	0.22	-	4	0.0	0.55	-
SCF9157	29.4	4	4	27.5	0.22	-	4	0.0	0.55	-
SCF72229	32.0	4	NA	NA	NA	NA	4	0.5	0.37	-

416328_K63	32.7	4	4	34.4	0.04	-	4	0.0	0.55	-
ct119590	32.9	4	4	34.4	0.04	-	4	0.5	0.37	-
SCF113389	34.5	4	4	34.4	0.04	-	4	3.7	0.22	-
SCF46739	35.2	4	4	35.7	0.04	-	4	3.7	0.22	-
CA855F	36.2	4	4	35.7	0.04	-	4	5.5	0.22	-
SCF140628	36.2	4	4	35.7	0.04	-	4	5.5	0.22	-
vm52682	38.9	4	4	41.2	0.55	-	4	5.5	0.22	-
SCF6530	46.5	4	4	49.5	0.22	-	4	11.9	1.03	-
vm52204	48.1	4	4	49.5	0.22	-	NA	NA	NA	NA
SCF124075	48.4	4	4	49.5	0.22	-	4	16.0	0.37	-
SCF28100	48.4	4	4	49.5	0.22	-	4	16.0	0.37	-
scf6955c	48.4	4	4	49.5	0.22	-	4	16.0	0.37	-
305731_K63	48.6	4	4	50.0	0.37	-	NA	NA	NA	NA
SCF154541	49.1	4	4	50.5	0.22	-	4	16.5	0.22	-
SCF38553	54.5	4	4	55.9	0.04	-	NA	NA	NA	NA
SCF15845	55.7	4	4	55.9	0.04	-	4	24.6	0.77	-
SCF194552	56.7	4	4	57.8	0	-	4	24.4	0.77	-
SCF96539	74.8	4	4	77.4	0.04	-	NA	NA	NA	NA
NA1713	75.9	4	4	78.4	0.04	-	4	42.0	0.55	-
scf24k	75.9	4	4	78.4	0.04	-	4	42.0	0.55	-
SCF100820	75.9	4	4	77.9	0.11	-	4	42.0	0.55	-
SCF79014	76.1	4	4	77.9	0.11	-	4	42.4	0.77	-
SCF204979	76.4	4	4	79.3	0.04	-	4	42.4	0.77	-
SCF16359	77.9	4	NA	NA	NA	NA	4	41.0	0.55	-
contig600	83.7	4	4	89.5	0	-	4	47.0	2.01	-
SCF101064	84.0	4	4	89.5	0	-	NA	NA	NA	NA
SCF49598	84.4	4	4	89.5	0	-	4	48.4	1.03	-
SCF108294	93.1	4	4	101.1	0.55	-	NA	NA	NA	NA
SCF1128	93.8	4	4	101.1	0.55	-	4	56.2	2.01	-
SCF46912	93.8	4	4	101.1	0.55	-	4	56.2	2.01	-
SCF11084	94.8	4	NA	NA	NA	NA	4	56.2	2.01	-
SCF145739	95.0	4	4	106.6	0.22	-	4	56.2	2.01	-
SCF53282	95.4	4	4	103.8	0.04	-	4	56.2	2.01	-
scf26r	97.6	4	4	109.8	0.11	-	4	57.6	2.42	-
SCF18363	98.2	4	4	109.8	0.11	-	NA	NA	NA	NA
SCF29560	98.2	4	4	109.8	0.11	-	NA	NA	NA	NA
SCF51810	98.5	4	4	111.6	0	-	4	57.6	2.42	-
281884_K70	99.4	4	4	113.0	0	-	4	58.1	2.01	-
SCF74895	99.4	4	4	113.0	0	-	4	58.1	2.01	-
SCF14119	101.1	4	4	113.0	0	-	NA	NA	NA	NA
251788_K63	0.0	5	5	0.0	0.04	-	5	0.0	0.11	-
ct153008	0.0	5	5	0.0	0.04	-	5	0.0	0.11	-
SCF143318	0.0	5	5	0.0	0.04	-	5	0.0	0.11	-
SCF28613	0.0	5	5	0.0	0.04	-	5	0.0	0.11	-
SCF804	1.2	5	NA	NA	NA	NA	5	0.0	0.11	-
308839_K70	6.0	5	5	6.4	0.55	-	5	5.9	0.11	-
SCF7132	8.1	5	NA	NA	NA	NA	5	6.5	0.04	-
ct144370	8.4	5	5	11.5	0.11	-	5	6.3	0.04	-
SCF32727	12.5	5	5	17.0	0.22	-	5	9.8	0.11	-
SCF59035	12.5	5	5	16.9	0.22	-	5	9.8	0.11	-
SCF132595	23.1	5	5	30.7	0.77	-	5	18.5	0	-
SCF259	23.1	5	5	30.7	0.77	-	5	18.5	0	-
SCF31208	23.1	5	5	30.7	0.77	-	5	18.5	0	-
SCF97378	31.0	5	5	37.6	0.55	-	NA	NA	NA	NA
vm39030	35.2	5	5	44.9	0.22	-	5	27.8	0.37	-
ct98042	44.2	5	NA	NA	NA	NA	5	40.4	0.55	-
SCF8987	44.2	5	NA	NA	NA	NA	5	40.4	0.55	-

SCF149976	44.6	5	5	50.4	0.22	-	5	40.4	0.55	-
SCF83615	44.6	5	5	50.4	0.22	-	5	40.4	0.55	-
SCF46751	46.4	5	5	50.4	0.22	-	5	43.6	0.77	-
SCF101878	47.2	5	NA	NA	NA	NA	5	43.6	0.77	-
scf9e	63.0	5	5	60.6	0	-	5	65.4	1.65	-
SCF9068	66.3	5	5	69.3	1.65	-	NA	NA	NA	NA
1trimcontig237406	67.0	5	5	69.3	1.65	-	5	65.4	1.65	-
308812_K70	67.0	5	5	69.3	1.65	-	5	65.4	1.65	-
SCF11431	67.0	5	5	69.3	1.65	-	5	65.4	1.65	-
SCF88902	67.0	5	5	69.3	1.65	-	5	65.4	1.65	-
SCF6195	67.2	5	NA	NA	NA	NA	5	65.4	1.65	-
1trimcontig191066	72.7	5	5	79.5	0.55	-	5	66.3	2.42	-
ct115258	72.7	5	5	79.5	0.55	-	5	66.3	2.42	-
vm07778	74.7	5	5	79.5	0.55	-	NA	NA	NA	NA
47166_K70	75.6	5	5	80.4	0.55	-	NA	NA	NA	NA
CA794F	75.6	5	5	80.4	0.55	-	NA	NA	NA	NA
16720_K63	0.0	6	6	0.0	5.59	**	6	0.0	0.77	-
scf44a	0.0	6	6	0.0	5.59	**	6	0.0	0.77	-
Pr031818823	0.5	6	6	0.0	5.59	**	6	0.9	1.32	-
contig652	1.5	6	6	0.5	6.25	**	6	2.7	0.77	-
SCF164915	2.6	6	NA	NA	NA	NA	6	0.9	1.32	-
SCF25446	5.5	6	6	9.2	3.33	*	6	2.7	0.77	-
SCF171621	13.9	6	NA	NA	NA	NA	6	11.0	0.77	-
SCF89447	13.9	6	NA	NA	NA	NA	6	11.0	0.77	-
ct154615	15.0	6	NA	NA	NA	NA	6	12.4	1.03	-
SCF16407	15.0	6	NA	NA	NA	NA	6	12.4	1.03	-
SCF31172	16.1	6	6	23.3	4.39	**	6	11.0	0.77	-
scf17d	16.7	6	6	23.3	4.39	**	6	12.4	1.03	-
SCF133376	17.7	6	6	23.3	4.39	**	NA	NA	NA	NA
SCF89801	17.7	6	6	23.3	4.39	**	NA	NA	NA	NA
SCF40517	20.0	6	6	23.8	3.84	*	6	17.7	0.22	-
319429_K63	21.1	6	NA	NA	NA	NA	6	18.0	0.22	-
SCF92414	31.2	6	6	36.8	0.37	-	NA	NA	NA	NA
vm27120	40.1	6	6	45.5	0	-	NA	NA	NA	NA
SCF22442	41.8	6	6	47.3	0.11	-	6	36.4	0.37	-
SCF3427	41.9	6	6	47.3	0.11	-	NA	NA	NA	NA
1trimcontig238080	42.0	6	6	47.3	0.11	-	6	36.8	0.55	-
SCF9909	42.9	6	6	49.2	0	-	6	36.8	0.55	-
412234_K63	43.6	6	6	50.5	0.04	-	6	36.8	0.55	-
SCF139334	46.8	6	6	52.4	0.22	-	NA	NA	NA	NA
scf112c	48.0	6	6	52.4	0.22	-	6	44.1	1.03	-
1trimcontig344502	48.2	6	6	53.3	0.55	-	6	44.1	1.03	-
vm53000	49.2	6	NA	NA	NA	NA	6	43.2	1.03	-
314831_K70	49.6	6	NA	NA	NA	NA	6	44.1	1.03	-
ct188529	58.2	6	6	65.9	0.77	-	6	51.0	0.11	-
SCF13711	66.3	6	6	73.7	2.42	-	6	58.4	0.77	-
Ig13662a	75.1	6	6	82.5	0.77	-	6	67.1	0.22	-
scf207d	75.1	6	6	82.5	0.77	-	6	67.1	0.22	-
SCF147117	76.8	6	6	86.4	0	-	NA	NA	NA	NA
scf283b	77.2	6	6	86.7	0	-	6	67.1	0.22	-
ct92708	80.3	6	6	92.8	0.04	-	6	67.1	0.22	-
GVC-V31e03	81.6	6	6	92.8	0.04	-	NA	NA	NA	NA
SCF113558	81.6	6	6	92.8	0.04	-	NA	NA	NA	NA
SCF124927	83.5	6	6	96.5	0.11	-	6	69.9	0.04	-
vm31701	83.5	6	6	96.5	0.11	-	6	69.9	0.04	-
GVC-V22a02	89.9	6	NA	NA	NA	NA	6	78.7	0.04	-
SCF108454	90.6	6	6	102.4	0.04	-	6	78.7	0.04	-

SCF109269	90.6	6	6	102.4	0.04	-	6	78.7	0.04	-
SCF79620	90.6	6	6	102.4	0.04	-	6	78.7	0.04	-
1trimcontig339726	90.8	6	6	102.4	0.04	-	NA	NA	NA	NA
SCF192219	90.8	6	6	102.4	0.04	-	NA	NA	NA	NA
1trimcontig450309	0.0	7	7	0.0	0.55	-	NA	NA	NA	NA
SCF10514	0.2	7	7	0.0	0.55	-	7	0.0	0.55	-
scf203h	0.2	7	7	0.0	0.55	-	7	0.0	0.55	-
SCF155637	1.1	7	7	0.0	0.55	-	7	1.8	1.65	-
SCF46824	4.4	7	7	5.0	1.32	-	NA	NA	NA	NA
Ig51a	5.9	7	7	6.9	1.32	-	7	4.5	1.03	-
SCF150898	5.9	7	7	6.9	1.32	-	7	4.5	1.03	-
SCF915	14.4	7	7	16.1	2.01	-	7	12.4	0.77	-
SCF167793	14.8	7	NA	NA	NA	NA	7	12.4	0.77	-
419834_K63	18.5	7	7	23.9	1.03	-	7	13.8	1.03	-
SCF187979	18.5	7	7	23.9	1.03	-	7	13.8	1.03	-
scf5k	23.2	7	7	26.2	0.77	-	7	21.1	0.55	-
SCF110168	25.9	7	7	26.2	0.77	-	7	26.2	0.77	-
ct95345	27.2	7	7	27.1	0.77	-	7	28.4	1.03	-
NA1792	27.2	7	7	27.1	0.77	-	7	28.4	1.03	-
SCF128307	27.2	7	7	27.1	0.77	-	7	28.4	1.03	-
SCF193103	27.7	7	NA	NA	NA	NA	7	26.2	0.77	-
SCF138014	32.3	7	7	34.0	0.22	-	NA	NA	NA	NA
1trimcontig337780	33.6	7	7	34.0	0.22	-	7	34.4	0.77	-
311291_K70	33.6	7	7	34.0	0.22	-	7	34.4	0.77	-
SCF4305	33.6	7	7	34.0	0.22	-	7	34.4	0.77	-
SCF208883	37.8	7	NA	NA	NA	NA	7	36.7	0.55	-
SCF9872	37.8	7	NA	NA	NA	NA	7	36.7	0.55	-
300409_K63	37.8	7	NA	NA	NA	NA	7	36.6	0.55	-
ct145217	38.4	7	7	41.4	0.22	-	7	36.7	0.55	-
ct147864	39.1	7	7	41.4	0.22	-	NA	NA	NA	NA
SCF137494	39.1	7	7	41.4	0.22	-	NA	NA	NA	NA
SCF34010	40.0	7	7	42.3	0.55	-	NA	NA	NA	NA
SCF72379	40.0	7	7	42.3	0.55	-	NA	NA	NA	NA
409618_K63	42.1	7	7	43.2	1.03	-	7	42.2	1.03	-
76326_K70	42.1	7	7	43.2	1.03	-	7	42.2	1.03	-
SCF34513	43.7	7	NA	NA	NA	NA	7	42.2	1.03	-
1trimcontig217158	48.5	7	NA	NA	NA	NA	7	46.3	2.01	-
ct145906	49.7	7	7	53.4	0.55	-	NA	NA	NA	NA
80734_K70	50.6	7	7	53.4	0.55	-	7	49.5	2.42	-
SCF94237	50.6	7	7	53.4	0.55	-	7	49.5	2.42	-
SCF116864	55.4	7	7	60.9	0.11	-	NA	NA	NA	NA
SCF111145	56.2	7	7	61.9	0.11	-	7	54.6	2.01	-
SCF112540	57.6	7	NA	NA	NA	NA	7	54.6	2.01	-
SCF184873	57.6	7	NA	NA	NA	NA	7	54.6	2.01	-
SCF85946	61.7	7	NA	NA	NA	NA	7	58.2	0.77	-
SCF25221	62.0	7	7	70.4	0.37	-	7	58.2	0.77	-
scf31h	63.2	7	7	70.4	0.37	-	7	60.4	1.65	-
SCF89247	64.5	7	7	73.1	0.11	-	7	60.6	1.65	-
scf137c	65.6	7	7	75.4	0.04	-	7	60.6	1.65	-
SCF7155	66.7	7	7	75.4	0.04	-	NA	NA	NA	NA
scf1594	74.0	7	7	103.5	0	-	7	76.6	0.37	-
scf2s	74.0	7	7	103.5	0	-	7	76.6	0.37	-
SCF20681	74.7	7	NA	NA	NA	NA	7	68.4	0.77	-
SCF36745	75.2	7	7	85.2	0	-	7	68.4	0.77	-
6ms4e4b	75.3	7	7	85.2	0	-	NA	NA	NA	NA
1trimcontig435620	76.9	7	NA	NA	NA	NA	7	70.1	0.37	-
SCF25944	78.0	7	7	89.3	0.11	-	7	70.1	0.37	-

SCF2483	78.6	7	7	89.3	0.11	-	NA	NA	NA	NA
SCF56717	80.6	7	7	97.1	0	-	7	70.1	0.37	-
ct139553	82.8	7	7	103.5	0	-	NA	NA	NA	NA
SCF24087	0.0	8	8	0.0	0.22	-	NA	NA	NA	NA
ct89379	1.5	8	8	0.0	0.22	-	8	0.0	0.22	-
SCF132922	1.5	8	8	0.0	0.22	-	8	0.0	0.22	-
SCF138992	2.9	8	8	3.2	0.37	-	NA	NA	NA	NA
Ig6523b	3.1	8	8	3.2	0.37	-	8	0.0	0.22	-
SCF81732	3.4	8	NA	NA	NA	NA	8	0.0	0.22	-
SCF172149	10.1	8	8	12.0	0.11	-	8	4.7	0.22	-
411348_K63	17.6	8	8	18.8	0.04	-	NA	NA	NA	NA
SCF105925	17.6	8	8	18.8	0.04	-	NA	NA	NA	NA
SCF17979	19.3	8	NA	NA	NA	NA	8	14.8	1.03	-
Pr031818828	19.9	8	8	22.5	0.55	-	8	14.8	1.03	-
vm13884	19.9	8	8	22.5	0.55	-	8	14.8	1.03	-
SCF189612	25.9	8	8	27.3	0.04	-	8	22.1	2.42	-
SCF30010	25.9	8	8	27.5	0.04	-	8	22.1	2.42	-
SCF2714	27.0	8	NA	NA	NA	NA	8	22.6	2.01	-
SCF87990	27.0	8	NA	NA	NA	NA	8	22.6	2.01	-
SCF127023	29.4	8	8	34.2	0.11	-	8	22.6	2.01	-
SCF54155	31.4	8	8	34.2	0.11	-	8	26.2	2.01	-
scf4860	32.8	8	8	34.7	0.04	-	NA	NA	NA	NA
SCF64632	33.8	8	8	34.7	0.04	-	8	30.4	2.42	-
SCF82870	33.8	8	8	34.7	0.04	-	8	30.4	2.42	-
SCF197903	34.2	8	8	34.7	0.04	-	8	31.3	1.65	-
SCF142767	34.6	8	8	35.2	0.11	-	8	31.7	2.01	-
ct134336	35.1	8	NA	NA	NA	NA	8	30.4	2.42	-
ct159707	35.5	8	NA	NA	NA	NA	8	31.3	1.65	-
SCF19565	35.5	8	NA	NA	NA	NA	8	31.3	1.65	-
187382_K70	42.8	8	NA	NA	NA	NA	8	38.6	3.33	*
SCF71184	46.0	8	8	49.2	0.55	-	8	40.9	4.97	**
SCF27811	46.8	8	NA	NA	NA	NA	8	42.3	4.39	**
314797_K70	47.0	8	8	49.2	0.55	-	NA	NA	NA	NA
260167_K70	48.1	8	8	51.9	0.55	-	8	42.3	4.39	**
SCF77645	52.3	8	8	51.9	0.55	-	8	50.1	7.68	***
SCF92564	57.1	8	8	57.9	0.11	-	8	53.3	6.95	***
SCF8850	61.5	8	8	62.5	0.37	-	8	57.4	4.97	**
36394_K70	68.2	8	8	72.2	1.03	-	8	60.6	3.33	*
SCF71136	68.9	8	8	72.2	1.03	-	NA	NA	NA	NA
SCF107477	70.0	8	8	72.2	1.03	-	8	64.3	1.65	-
SCF91821	81.1	8	8	91.8	2.42	-	NA	NA	NA	NA
1trimcontig326802	81.9	8	8	92.4	2.42	-	8	69.8	3.33	*
scf2505a	82.9	8	NA	NA	NA	NA	8	70.2	3.84	*
vm31502	82.9	8	NA	NA	NA	NA	8	70.2	3.84	*
KAN-11325	85.7	8	8	98.9	1.32	-	8	70.2	3.84	*
1trimcontig440337	86.8	8	8	99.8	2.01	-	8	71.7	2.42	-
SCF102538	86.8	8	8	99.8	2.01	-	8	71.8	2.42	-
SCF10785	87.1	8	8	98.9	1.32	-	NA	NA	NA	NA
scf1p	92.1	8	8	107.6	3.33	*	8	74.0	1.32	-
vm28527	92.1	8	8	107.6	3.33	*	8	74.0	1.32	-
ct121951	94.2	8	8	107.6	3.33	*	NA	NA	NA	NA
contig259Fb	0.0	9	9	0.0	0.04	-	9	0.0	0.11	-
scf1655c	0.0	9	9	0.0	0.04	-	9	0.0	0.11	-
SCF41971	0.7	9	9	0.0	0.04	-	9	1.4	0.04	-
SCF125889	1.0	9	NA	NA	NA	NA	9	1.4	0.04	-
SCF163134	1.3	9	9	0.9	0	-	NA	NA	NA	NA
ct154654	2.2	9	9	0.0	0.04	-	9	4.1	0.11	-

SCF109660	2.7	9	9	2.3	0	-	NA	NA	NA	NA
SIZ1-2	2.7	9	9	2.3	0	-	NA	NA	NA	NA
1trimcontig352078	3.3	9	9	1.8	0	-	9	4.6	0.04	-
407841_K63	3.3	9	9	1.8	0	-	9	4.6	0.04	-
KAN-11281	3.3	9	9	1.8	0	-	9	4.6	0.04	-
ct144558	4.3	9	NA	NA	NA	NA	9	4.6	0.04	-
ct154206	10.6	9	9	10.6	0.11	-	9	10.5	0	-
VCC_J9	13.2	9	9	13.8	0.22	-	9	12.4	0.37	-
SCF155797	15.6	9	9	18.4	0.22	-	9	12.4	0.37	-
SCF30734	17.2	9	9	18.4	0.22	-	NA	NA	NA	NA
scf439	33.2	9	NA	NA	NA	NA	9	27.4	1.32	-
SCF7357	33.2	9	NA	NA	NA	NA	9	27.4	1.32	-
NA619	36.5	9	9	43.6	0.11	-	9	30.1	1.32	-
scf35k	36.7	9	9	44.0	0.22	-	9	30.1	1.32	-
309124_K70	37.5	9	9	44.0	0.22	-	9	31.5	1.65	-
scf13a	37.5	9	9	44.0	0.22	-	9	31.5	1.65	-
scf275d	44.3	9	9	51.9	0.37	-	9	37.3	0.37	-
SCF10459	45.0	9	NA	NA	NA	NA	9	37.6	0.37	-
SCF118468	47.0	9	9	55.1	0.55	-	9	40.0	0.22	-
scf6i	50.5	9	9	60.6	1.65	-	9	41.8	0.04	-
SCF56032	51.8	9	9	60.6	1.65	-	9	44.1	0	-
Ig1296a	53.0	9	9	60.6	1.65	-	9	46.4	0.04	-
Pr031818814	53.2	9	9	61.2	2.01	-	9	46.4	0.04	-
SCF136207	53.6	9	9	61.9	2.01	-	9	46.4	0.04	-
SCF48414	54.3	9	NA	NA	NA	NA	9	46.4	0.04	-
SCF88396	55.9	9	NA	NA	NA	NA	9	47.8	0.11	-
scf21n	58.2	9	9	70.7	1.65	-	9	47.8	0.11	-
SCF1648	63.0	9	NA	NA	NA	NA	9	54.2	1.32	-
1trimcontig238343	64.8	9	9	77.6	2.85	*	9	54.2	1.32	-
214102_K63	64.8	9	9	77.6	2.85	*	9	54.2	1.32	-
SCF141985	64.8	9	9	77.6	2.85	*	9	54.2	1.32	-
SCF11802	71.4	9	9	85.4	3.33	*	9	59.7	2.01	-
ct95842	72.1	9	9	83.4	4.39	**	NA	NA	NA	NA
SCF132369	73.0	9	9	85.4	3.33	*	NA	NA	NA	NA
SCF136317	73.0	9	9	85.4	3.33	*	NA	NA	NA	NA
SCF144748	73.0	9	9	85.4	3.33	*	NA	NA	NA	NA
scf306f	74.1	9	NA	NA	NA	NA	9	63.8	0.55	-
scf32j	75.2	9	9	87.7	2.01	-	NA	NA	NA	NA
SCF132532	75.9	9	9	88.6	2.01	-	NA	NA	NA	NA
1trimcontig439861	77.2	9	9	88.6	2.01	-	9	68.4	0.22	-
SCF33185	78.9	9	NA	NA	NA	NA	9	68.4	0.22	-
SCF125251	80.7	9	9	93.1	4.97	**	9	70.7	1.32	-
scf55c	80.7	9	9	93.1	4.97	**	9	70.7	1.32	-
SCF61189	80.7	9	9	93.1	4.97	**	9	70.7	1.32	-
1trimcontig328266	85.3	9	9	102.8	4.39	**	9	70.7	1.32	-
scf45d	85.3	9	9	102.8	4.39	**	9	70.7	1.32	-
SCF3932	88.0	9	9	102.8	4.39	**	NA	NA	NA	NA
ct145170	0.0	10	10	0.0	0.55	-	10	0.0	0.04	-
KAN-11049	0.0	10	10	0.0	0.55	-	10	0.0	0.04	-
SCF201915	0.4	10	10	0.0	0.55	-	10	1.0	0.04	-
vm12486	0.9	10	NA	NA	NA	NA	10	0.0	0.04	-
vm38401	0.9	10	NA	NA	NA	NA	10	0.0	0.04	-
418931_1_K63	4.0	10	10	0.0	0.55	-	10	7.8	0.11	-
1trimcontig176861	4.8	10	10	1.8	0.22	-	10	7.8	0.11	-
60699_K70	4.8	10	10	1.8	0.22	-	10	7.8	0.11	-
SCF150919	5.2	10	10	2.4	0.11	-	10	8.3	0.22	-
SCF49656	10.8	10	10	14.3	0	-	10	8.3	0.22	-

SCF174394	11.0	10	10	14.5	0	-	10	8.7	0.37	-
SCF80520	21.5	10	10	35.7	2.01	-	10	8.7	0.37	-
SCF189827	30.6	10	10	38.4	2.01	-	NA	NA	NA	NA
SCF107715	31.2	10	10	38.0	1.65	-	10	28.4	0.11	-
SCF117385	31.2	10	10	38.0	1.65	-	10	28.4	0.11	-
SCF82535	31.2	10	10	38.0	1.65	-	10	28.4	0.11	-
71002_K63	31.4	10	10	38.4	2.01	-	10	28.4	0.11	-
vm72062	32.3	10	10	38.4	2.01	-	10	30.2	0.11	-
SCF65999	32.8	10	NA	NA	NA	NA	10	30.2	0.11	-
SCF146740	40.0	10	10	47.6	3.84	*	NA	NA	NA	NA
SCF147295	40.0	10	10	47.6	3.84	*	NA	NA	NA	NA
SCF35507	40.0	10	10	47.6	3.84	*	NA	NA	NA	NA
313928_K70	40.4	10	10	47.6	3.84	*	10	37.6	0.37	-
SCF147358	40.4	10	10	47.6	3.84	*	10	37.6	0.37	-
SCF7569	41.9	10	10	50.4	3.84	*	10	37.6	0.37	-
409500_K63	44.3	10	10	51.8	5.59	**	10	41.2	1.32	-
vm25796	44.3	10	10	51.8	5.59	**	10	41.2	1.32	-
SCF112295	44.4	10	10	51.8	5.59	**	NA	NA	NA	NA
SCF172906	47.5	10	10	51.8	5.59	**	10	47.6	0.37	-
ct135942	50.0	10	NA	NA	NA	NA	10	47.6	0.37	-
SCF104688	57.4	10	10	64.3	2.85	*	NA	NA	NA	NA
SCF189657	59.7	10	NA	NA	NA	NA	10	56.9	0.37	-
SCF139660	60.2	10	NA	NA	NA	NA	10	57.3	0.55	-
Pr031818817	61.7	10	10	70.3	1.65	-	10	57.3	0.55	-
SCF86438	64.1	10	10	70.3	1.65	-	10	61.5	0.37	-
SCF2288	71.3	10	10	75.8	0.22	-	10	69.7	0.77	-
SCF60761	72.3	10	NA	NA	NA	NA	10	69.7	0.77	-
SCF96311	76.0	10	NA	NA	NA	NA	10	73.4	0.37	-
SCF23210	76.3	10	10	82.2	0.55	-	10	73.4	0.37	-
SCF26014	76.3	10	10	82.2	0.55	-	10	73.4	0.37	-
SCF46833	76.3	10	10	82.2	0.55	-	10	73.4	0.37	-
364103_K63	76.5	10	10	82.2	0.55	-	NA	NA	NA	NA
SCF120352	76.8	10	10	82.2	0.55	-	10	74.3	0.37	-
ct161908	77.0	10	10	82.7	0.37	-	NA	NA	NA	NA
ct93137	77.0	10	10	82.7	0.37	-	10	74.3	0.37	-
SCF84804	0.0	11	11	0.0	0.04	-	NA	NA	NA	NA
SCF110507	1.2	11	11	0.0	0.04	-	11	0.0	0	-
SCF181909	1.2	11	11	0.0	0.04	-	11	0.0	0	-
SCF95767	1.2	11	11	0.0	0.04	-	11	0.0	0	-
SCF72209	1.5	11	11	0.5	0.11	-	11	0.5	0.04	-
1trimcontig176042	3.2	11	NA	NA	NA	NA	11	0.0	0	-
scf108b	5.0	11	11	7.3	0.11	-	11	0.0	0	-
vm05418	9.6	11	11	10.5	0	-	NA	NA	NA	NA
SCF41361	12.6	11	11	13.7	0.04	-	NA	NA	NA	NA
SCF122746	14.0	11	11	16.1	0	-	11	9.2	0	-
307018_K70	16.3	11	11	16.1	0	-	11	13.9	0.22	-
SCF81909	17.9	11	NA	NA	NA	NA	11	13.7	0.22	-
SCF81294	24.3	11	NA	NA	NA	NA	11	19.5	0.55	-
Pr031818821	25.0	11	11	28.6	0.37	-	11	19.5	0.55	-
scf3072b	25.0	11	11	28.6	0.37	-	11	19.5	0.55	-
SCF204332	25.7	11	11	28.6	0.37	-	NA	NA	NA	NA
SCF199831	36.5	11	11	39.8	0.77	-	11	31.1	1.32	-
SCF106182	37.9	11	NA	NA	NA	NA	11	31.1	1.32	-
SCF183590	37.9	11	NA	NA	NA	NA	11	31.1	1.32	-
SCF64185	37.9	11	NA	NA	NA	NA	11	31.1	1.32	-
SCF21596	42.5	11	11	51.3	0.55	-	11	31.6	1.65	-
SCF132506	47.3	11	11	52.7	0.37	-	NA	NA	NA	NA

vm68798	47.3	11	11	52.7	0.37	-	NA	NA	NA	NA
SCF123189	50.1	11	11	55.5	0.11	-	NA	NA	NA	NA
SCF57497	50.7	11	11	55.0	0.22	-	11	45.1	0.77	-
SCF120937	50.8	11	11	55.5	0.11	-	11	45.1	0.77	-
482_K70	51.7	11	11	55.5	0.11	-	11	46.9	0.77	-
SCF95754	51.7	11	11	55.5	0.11	-	11	46.9	0.77	-
1trimcontig444344	54.1	11	11	60.1	0.11	-	11	46.9	0.77	-
308539_K70	54.1	11	11	60.1	0.11	-	11	46.9	0.77	-
SCF136826	54.1	11	NA	NA	NA	NA	11	46.9	0.77	-
SCF158255	54.1	11	NA	NA	NA	NA	11	46.9	0.77	-
SCF161998	54.4	11	11	60.1	0.11	-	NA	NA	NA	NA
SCF110757	59.8	11	11	66.1	0.22	-	NA	NA	NA	NA
SCF150173	59.8	11	11	66.1	0.22	-	NA	NA	NA	NA
SCF1047	63.4	11	NA	NA	NA	NA	11	54.3	1.32	-
SCF28931	63.4	11	NA	NA	NA	NA	11	54.3	1.32	-
SCF160647	68.6	11	11	87.3	1.32	-	11	54.3	1.32	-
SCF28509	75.0	11	NA	NA	NA	NA	11	65.4	0.11	-
SCF118608	75.1	11	11	87.3	1.32	-	11	65.4	0.11	-
SCF181772	75.1	11	11	87.3	1.32	-	11	65.4	0.11	-
SCF145689	0.0	12	12	4.1	2.01	-	NA	NA	NA	NA
SCF75572	0.7	12	12	5.0	1.32	-	NA	NA	NA	NA
vm34671	0.7	12	12	5.0	1.32	-	NA	NA	NA	NA
scf248	2.6	12	12	5.0	1.32	-	12	0.9	0	-
scf6213	2.6	12	12	5.0	1.32	-	12	0.9	0	-
SCF3191	4.0	12	12	0.0	2.42	-	12	0.0	0	-
SCF3261	4.0	12	12	0.0	2.42	-	12	0.0	0	-
SCF169090	5.4	12	NA	NA	NA	NA	12	0.0	0	-
SCF101914	5.8	12	NA	NA	NA	NA	12	0.9	0	-
SCF159195	13.0	12	NA	NA	NA	NA	12	6.9	0.04	-
SCF117422	15.0	12	12	22.9	0.77	-	12	6.9	0.04	-
SCF110223	16.9	12	12	21.4	1.03	-	12	11.0	0	-
scf79c	17.4	12	12	22.9	0.77	-	12	11.0	0	-
408825_K63	22.3	12	12	28.0	0.22	-	NA	NA	NA	NA
ct144936	22.3	12	12	28.0	0.22	-	NA	NA	NA	NA
vm40600	22.3	12	12	28.0	0.22	-	NA	NA	NA	NA
SCF116567	24.3	12	12	28.0	0.22	-	12	19.8	1.03	-
SCF138394	26.7	12	NA	NA	NA	NA	12	19.8	1.03	-
SCF38430	27.6	12	12	34.4	0.55	-	12	19.8	1.03	-
SCF38942	27.6	12	12	34.4	0.55	-	12	19.8	1.03	-
418596_K63	28.0	12	12	35.8	0.37	-	12	19.8	1.03	-
76126_K63	28.0	12	12	35.8	0.37	-	12	19.8	1.03	-
SCF11065	28.4	12	12	34.4	0.55	-	NA	NA	NA	NA
SCF149989	29.1	12	12	35.8	0.37	-	NA	NA	NA	NA
SCF69698	32.1	12	12	39.9	0.22	-	12	23.9	2.01	-
354699_K63	32.8	12	12	39.9	0.22	-	12	25.2	2.42	-
ct129169	34.7	12	12	41.7	1.03	-	NA	NA	NA	NA
SCF16166	35.0	12	12	41.7	1.03	-	12	28.0	3.33	*
vm26877	35.4	12	12	42.6	1.65	-	12	28.0	3.33	*
SCF34584	37.2	12	12	43.1	1.32	-	12	31.2	2.85	*
309084_K70	37.2	12	12	43.1	1.32	-	12	31.0	2.85	*
scf37h	38.3	12	NA	NA	NA	NA	12	30.7	2.42	-
SCF37628	38.7	12	NA	NA	NA	NA	12	31.4	2.85	*
SCF76310	40.1	12	12	47.7	0.77	-	12	32.9	3.33	*
SCF6926	40.2	12	12	47.7	0.77	-	NA	NA	NA	NA
SCF13753	42.3	12	12	50.0	1.65	-	NA	NA	NA	NA
SCF46588	44.3	12	12	52.2	1.32	-	NA	NA	NA	NA
SCF98180	44.3	12	12	52.2	1.32	-	NA	NA	NA	NA

SCF59739	47.6	12	12	56.8	0.77	-	12	38.2	2.42	-
SCF34071	48.9	12	12	56.8	0.77	-	NA	NA	NA	NA
scf2882	49.8	12	NA	NA	NA	NA	12	41.0	3.33	*
scf4b	52.8	12	12	64.6	0.22	-	12	41.0	3.33	*
SCF116485	61.7	12	12	67.4	0.22	-	12	54.9	0.22	-
ct110752	62.5	12	12	67.4	0.22	-	12	56.8	0.22	-
scf6355	62.8	12	12	67.4	0.22	-	12	57.3	0.11	-
SCF160663	66.2	12	NA	NA	NA	NA	12	57.3	0.11	-
417587_K63	67.4	12	NA	NA	NA	NA	12	59.1	0.37	-
ct174735	71.2	12	12	87.1	0	-	12	57.3	0.11	-
1trimcontig175770	71.8	12	12	87.1	0	-	12	59.1	0.37	-
411145_K63	71.8	12	12	87.1	0	-	12	59.1	0.37	-
ct140233	71.8	12	12	87.1	0	-	12	59.1	0.37	-
SCF28955	71.8	12	12	87.1	0	-	12	59.1	0.37	-
Ig28559a	73.1	12	12	87.1	0	-	NA	NA	NA	NA
SCF28279	73.1	12	12	87.1	0	-	NA	NA	NA	NA

- = $p > 0.1$, * = $p < 0.1$, ** = $p < 0.05$, *** = $p < 0.01$, **** = $p < 0.005$, ***** = $p < 0.001$, ****** = $p < 0.0005$, ******* = $p < 0.0001$

Appendix V-13. Rearrangements/local inversions in the cranberry CNJ02-1 consensus map compared to the F_1#10 x W85-23 interspecific diploid blueberry consensus map.

Inversion	LG	Locus	CNJ02-1 consensus map				F_1#10 x W85-20 consensus map			
			Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)	Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)
1	1	GVC-C347	20.23	9.44	20.23	29.67	24.67	1.83	23.61	26.50
		scf8l	21.08				26.50			
		1trimcontig239742	24.23				24.67			
		1trimcontig179737	29.23				23.61			
		SCF11186	29.67				23.61			
2	1	SCF8223	72.31	25.80	72.31	98.11	73.54	3.73	69.81	73.54
		307461_K70	91.82				70.63			
		414791_K63	98.11				69.81			
3	3	SCF58861	0.00	6.65	0.00	6.65	0.83	2.94	0.00	2.94
		NA172	4.81				2.94			
		1trimcontig443603	6.65				0.00			
4	3	SCF78184	54.58	1.32	54.58	55.90	43.63	1.40	43.63	45.03
		KAN-11440	55.54				45.03			
		1trimcontig436904	55.90				44.62			
5	4	2ms4d10b	2.37	4.25	2.37	6.61	5.35	9.51	1.27	10.78
		GVC-V24d10b	2.37				10.78			
		SCF83036	3.37				1.27			
		5ms2b12	6.61				9.30			
6	4	scf26r	97.55	0.63	97.55	98.18	87.92	1.20	86.72	87.92
		SCF18363	98.18				86.72			
7	7	scf1594	73.98	1.31	73.98	75.29	80.12	2.44	77.68	80.12
		SCF36745	75.21				77.68			
		6ms4e4b	75.29				77.68			
8	8	SCF24087	0.00	3.45	0.00	3.45	6.81	6.81	0.00	6.81
		ct89379	1.45				1.41			
		SCF81732	3.45				0.00			
9	8	SCF17979	19.26	6.69	19.26	25.95	33.50	0.51	32.99	33.50
		Pr031818828	19.94				32.99			
		vm13884	19.94				33.50			
		SCF30010	25.95				33.07			
10	9	Pr031818814	53.24	1.09	53.24	54.33	26.35	3.30	23.05	26.35
		SCF136207	53.65				23.05			
		SCF48414	54.33				24.66			
11	10	ct145170	0.00	4.77	0.00	4.77	0.00	8.94	0.00	8.94
		KAN-11049	0.00				8.94			

		418931_1_K63	3.98				4.43			
		1trimcontig176861	4.77				2.84			
12	10	SCF107715	31.24	8.71	31.24	39.95	38.33	7.12	31.24	38.36
		SCF65999	32.78				38.36			
		SCF147295	39.95				31.24			
13	10	SCF60761	72.29	4.49	72.29	76.78	52.30	4.15	49.35	53.50
		364103_K63	76.51				53.50			
		SCF120352	76.78				49.35			
14	11	SCF110507	1.20	1.99	1.20	3.18	2.43	2.43	0.00	2.43
		1trimcontig176042	3.18				0.00			
15	11	SCF95754	51.73	8.11	51.73	59.84	47.84	9.94	37.91	47.84
		SCF110757	59.84				37.91			

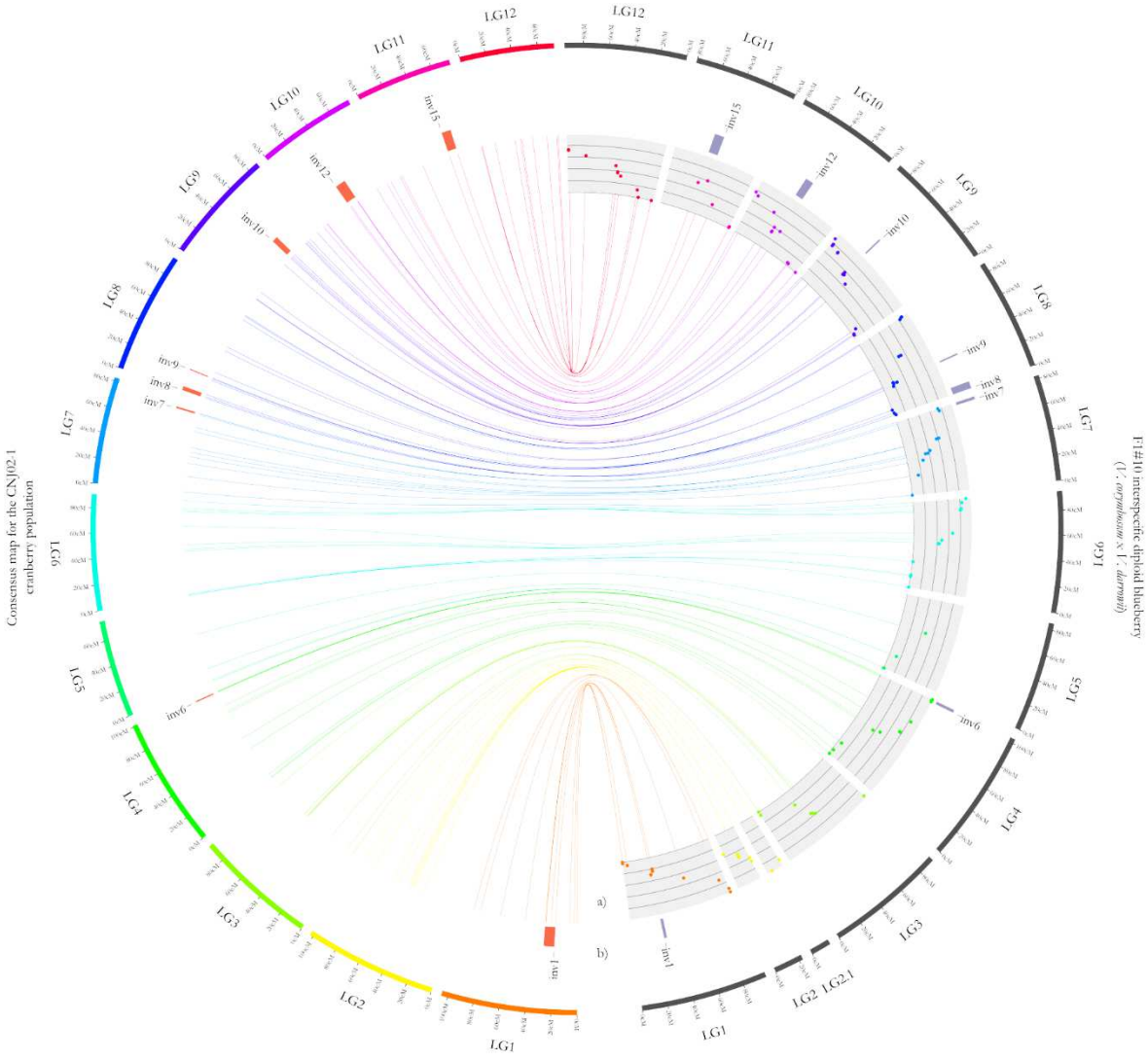
Appendix V-14. Non-collinear segments (i.e. local inversions) in the cranberry CNJ02-1 consensus map compared to the F_1#10 interspecific diploid blueberry (*V. corymbosum* x *V.darrowii*) maternal bin map. Inversions are numbered according to the non-collinear segments observed in comparisons between the CNJ02-1 and F_1#10 x W85-23 consensus maps (Figure 5.4; Appendix V-13).

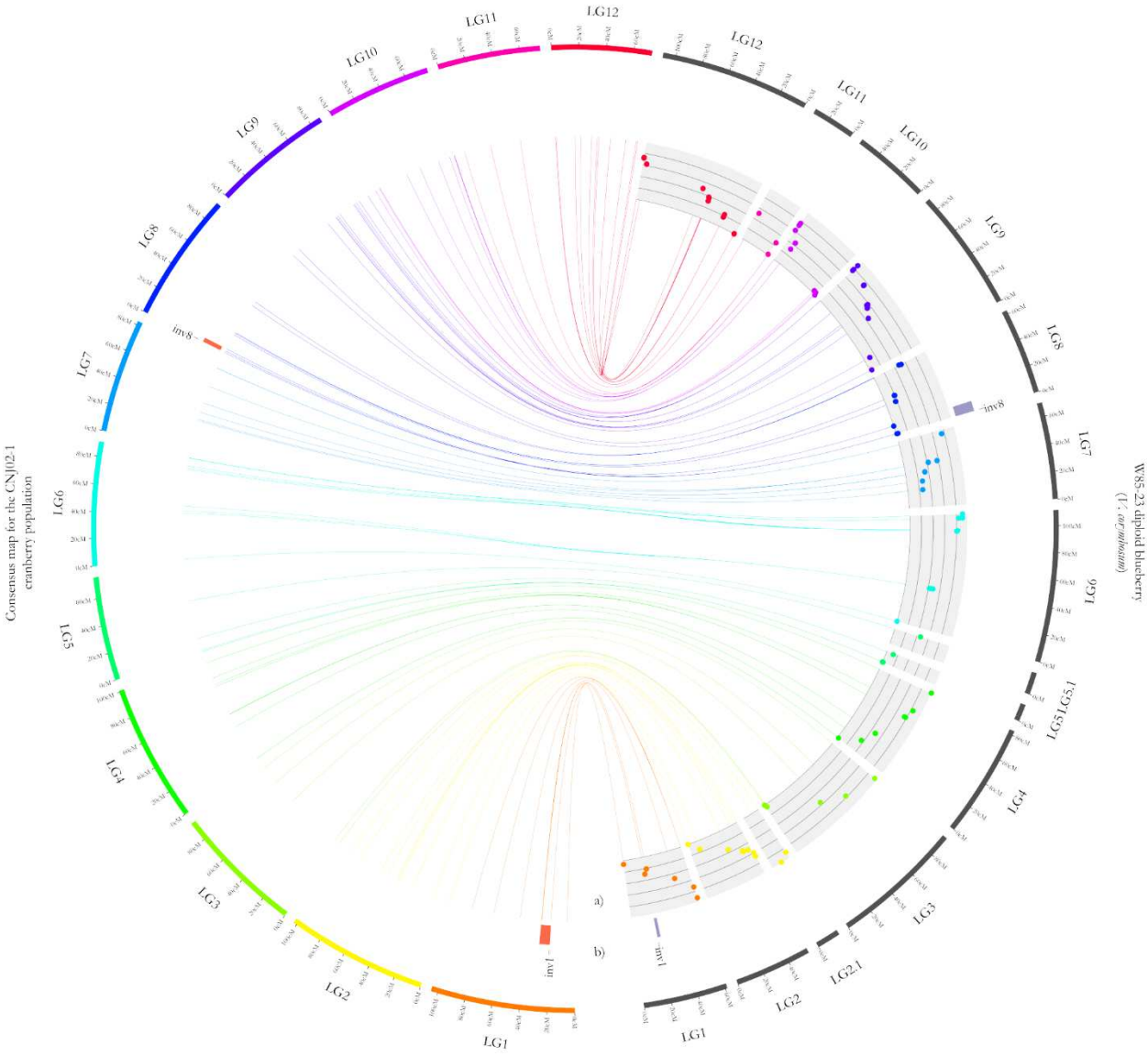
Inversion	LG	Locus	CNJ02-1 consensus map				F_1#10 parental bin map			
			Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)	Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)
1	1	GVC-C347	20.23	9.44	20.23	29.67	30.35	2.41	27.93	30.35
		1trimcontig239742	24.23				30.35			
		1trimcontig179737	29.23				27.93			
		SCF11186	29.67				27.93			
6	4	scf26r	97.55	0.63	97.55	98.18	102.40	1.21	101.19	102.4
		SCF18363	98.18				101.19			
7	7	scf1594	73.98	1.31	73.98	75.29	82.40	2.41	79.99	82.40
		SCF36745	75.21				79.99			
		6ms4e4b	75.29				79.99			
8	8	SCF24087	0.00	3.45	0.00	3.45	6.19	6.19	0.00	6.19
		ct89379	1.45				2.42			
		SCF81732	3.45				0.00			
9	8	SCF17979	19.26	0.68	19.26	19.94	33.21	1.21	32.01	33.21
		Pr031818828	19.94				32.01			
		vm13884	19.94				33.21			
10	9	Pr031818814	53.24	4.96	53.24	58.20	60.71	1.21	59.50	60.71
		SCF48414	54.33				59.50			
		SCF88396	55.93				60.71			
		scf21n	58.20				60.71			
12	10	SCF107715	31.24	9.16	31.24	40.39	46.68	7.28	39.40	46.68
		SCF65999	32.78				46.68			
		SCF147295	39.95				39.40			
		313928_K70	40.39				46.68			
15	11	SCF95754	51.73	8.11	51.73	59.84	48.38	8.48	39.89	48.38
		SCF110757	59.84				39.89			

Appendix V-15. Non-collinear segments (i.e. local inversions) in the cranberry CNJ02-1 consensus map compared to the W85-23 (*V. corymbosum*) blueberry paternal bin map. Inversions are numbered according to the non-collinear segments observed in comparisons between the CNJ02-1 and F_1#10 x W85-23 consensus maps (Figure 5.4; Appendix V-13).

Inversion	LG	Locus	F_1#10 parental bin map.				W85-20 parental bin map			
			Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)	Locus Position (cM)	Inversion Length (cM)	Start position (cM)	End position (cM)
1	1	scf8l	21.08	8.58	21.08	29.67	21.93	2.41	19.52	21.93
		1trimcontig179737	29.23				19.52			
		SCF11186	29.67				19.52			
8	8	SCF24087	0	3.45	0	3.45	8.52	8.52	0	8.52
		ct89379	1.45				0			
		SCF81732	3.45				0			

Appendix V-16. Comparisons between the CNJ02-1 linkage groups and the linkage groups from (A) the F1#10 interspecific diploid blueberry bin map and (B) the W85-23 parental bin map. **(a)** Scatterplots of the position of the common markers each of the two maps are shown with intervals between lines representing 20 cM Kosambi map distance. **(b)** Regions of non-collinearity (Inv), and there relative size in cM, observed between the two maps (Appendix V-14; Appendix V-15).




Consensus map for the CNJ02-1
cranberry population
W85-23 diploid blueberry
(V. corymbosum)
LG12
LG11
LG10
LG9
LG8
LG7
LG6
LG5
LG4
LG3
LG2
LG1
LG5.1
LG2.1
inv8
inv1
a)
b)

Chapter VI

Construction of a high-density cranberry composite map using genotyping-by-sequencing for multi-pedigree linkage mapping

Abstract

The American cranberry (*Vaccinium macrocarpon* Ait.) is a recently domesticated, but economically important, fruit crop. Molecular resources for the species remain limited compared to other crops of similar commercial importance, and as a result, cranberry genetic improvement continues to rely on phenotypic selection. Adding new genetic tools to the cranberry breeders' toolbox could accelerate the domestication and genetic gain in cranberry through characterization of its genomic structure and by enabling molecular-assisted breeding strategies. To increase the availability of cranberry genomic resources, the genotyping-by-sequencing (GBS) approach was used to simultaneously discover and genotype thousands of single nucleotide polymorphisms (SNPs) within three inter-related cranberry full-sib populations, whose pedigrees trace to seven wild cranberry selections that together represent the entire genetic base of the commercial cranberry industry. Additional SSR loci were added to the SNP datasets to construct bin maps for the parents of the three populations, which were than merged to create the first high-density cranberry composite map containing 6073 markers (5437 SNPs and 636 SSRs) in 12 linkage groups (LGs) spanning 1124 cM. The large number of markers in common (i.e. an average of 57.3) and high degree of observed collinearity (i.e. mean Pair-wise Spearman Rank Correlations > 0.99) between the LGs of the 6 parental component maps demonstrates the utility of the genotyping-by-sequencing approach in cranberry for identifying polymorphic SNP loci that are transferable between pedigrees and populations in future quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS). Furthermore, the high-density of markers anchored within the component maps allowed characterization of the cranberry genome through exploration and identification of segregation distortion regions (SDRs) and the placement of centromeres on each of the 12 LGs. Collectively, the results presented herein represent an important contribution to the current understanding of cranberry genomic structure and to the availability of molecular tools for future genetic research and breeding efforts in cranberry.

Key words

Composite Map, Bin Map, Single Nucleotide Polymorphism, Genotyping-By-Sequencing, Centromere

Introduction

The American cranberry (*Vaccinium macrocarpon* Ait.) is a diploid woody perennial in the Ericaceae family, and like other Ericaceous species, it grows well in acidic, nutrient poor soils (Vander Kloet 1983a; Kron et al. 2002; Vander Kloet and Avery 2010). Cranberry, from the section *Oxycoccus* (Hill) Koch, shares a common base chromosome number (i.e. 12), karyotype (i.e. relatively uniformly sized metacentric and submetacentric chromosomes), estimated genome size (i.e. 450-600 Mb) with another economically important *Vaccinium* species, blueberry, from the section *Cyanococcus* A. Gray (Camp 1945; Hall and Galleta 1971; Vander Kloet 1983a; Vander Kloet 1983b; Costich et al. 1993). Both crops are growing in popularity and commercial importance, likely because of their status as "super fruits" due to the numerous health benefits attributed to their phytochemical constituents (Howell et al. 1998; Foo et al. 2000; R.L. et al. 2001; Duarte et al. 2006; Feghali et al. 2012). However, cranberry genetic improvement has lagged behind its blueberry brethren for various reasons including; the lack of continued breeding efforts, the limited number of breeding programs in existence, the long breeding cycle due to lengthy establishment periods (2-4 years) followed by long evaluation periods (4-5 years) required to measure biennial bearing (Eaton et al. 1983; Elle 1996; Vorsa and Johnson-cicalese 2012; Schlautman et al. 2015a), and a lack of adoption of molecular-assisted breeding strategies which could increase the rate of domestication and genetic gain in cranberry.

Prerequisites to marker-assisted breeding strategies, such as molecular-assisted seedling selection and/or genomic prediction (Ru et al. 2015; Covarrubias-Pazaran 2016), include the availability of numerous molecular markers distributed throughout the genome for haplotype estimation, knowledge of associations between markers and traits of interest, available populations with characterized genetic and phenotypic diversity, and high-throughput marker genotyping methodologies that justify the costs associated with molecular-assisted breeding compared to classical breeding methods. Large-scale exploration and development of genetic and genomic resources in cranberry has only begun recently with the advent of next generation sequencing technologies. For example, NGS technologies such as pyrosequencing (i.e., 454), sequencing by oligonucleotide ligation and detection (SOLiD), and Illumina have been useful in assembling both the plastid and mitochondrial genomes (Fajardo et al. 2013; Fajardo et al. 2014), a transcriptome (Polashock et al. 2014), and a nuclear scaffold assembly (i.e. 229,745 scaffolds; N50 = 4,237 bp) (Polashock et al. 2014). SSR mining of the reads, contigs, and scaffolds from those assemblies resulted in the development of SSR markers sets consisting of 32, 48, 91, 54, and 697 polymorphic SSRs (Georgi et al. 2011; Zhu et al. 2012; Georgi et al. 2013; Schlautman et al. 2015b; Schlautman et al. 2016), and 136 and 541 of those SSRs were placed in cranberry SSR linkage maps by Georgi et al. (2013) and Schlautman et al. (2015a), respectively. However, means for gathering SSR genotype

information in an efficient, cost-effective manner at a breeding program scale have not been achieved in cranberry, and uncertainty remains about whether the available set of cranberry SSRs is large enough to saturate the genome.

Covarrubias-Pazaran et al. (2016) recently demonstrated the potential for genotyping-by-sequencing in cranberry to serve as a high-throughput platform that integrates single nucleotide polymorphism (SNP) marker discovery and genotyping into a single procedure (Elshire et al. 2011). The Covarrubias-Pazaran et al. (2016) study increased the availability of cranberry DNA markers 10-fold and used them to construct the first high-density SNP cranberry linkage map. Therefore, in an effort to further saturate the cranberry genome with SNP markers and to test the utility of genotyping-by-sequencing to detect SNPs that are polymorphic across multiple populations, an experiment was designed to develop a cranberry composite map using genotyping-by-sequencing for multi-pedigree linkage mapping. Saturated bin maps were constructed for 5 parental genomes with progeny from three inter-related cranberry populations, whose ancestry trace back to seven historically important cranberry wild selections. The high-density of SNPs identified and placed in the composite map allowed for further genome characterization such as identification of segregation distortion regions, centromere placement, and anchoring of cranberry nuclear scaffolds containing predicted coding DNA sequences.

Materials and Methods

Plant Material and DNA extraction

Three full-sib linkage mapping populations (i.e. CNJ02, CNJ04, and Grygleski) were derived from crosses between five inter-related cranberry parental genotypes (Figure 1). The CNJ02 population included 168 progeny from a cross the between maternal parent, CNJ97-105 (*Mullica Queen*®), and paternal parent, NJS98-23 (*Crimson Queen*®); the CNJ04 population included 67 progeny from a reciprocal cross between CNJ97-105 (*Mullica Queen*®) and Stevens; and the Grygleski population included 352 progeny from a cross between the maternal parent, [BGx(BLxNL)]95, and the paternal parent, GH1x35 (Figure 6.1). The CNJ02 and CNJ04 populations were generated and are maintained at the Rutgers University P.E. Marucci Center in Chatsworth, NJ and were planted in separate unreplicated, completely randomized designs. The Grygleski population was generated and is maintained by the Valley Corporation in Tomah, WI. Genomic DNA from all parents and progeny was extracted from newly emerged leaves, which were flash frozen in liquid nitrogen, using a Macherey-Nagel (MN) Plant II kit (Düren, Germany) following the manufacturer's instructions.

SSR and SNP Genotyping

Linkage maps for the CNJ02 (541 SSRs) and Grygleski (201 SSRs and 4648 SNPs) populations were previously constructed (Schlautman et al. 2015a; Covarrubias-Pazaran et al. 2016), and the SSR marker data from these studies was incorporated into the current study. A subset of the previously mapped and unmapped SSR markers were used to genotype the CNJ04 progeny and its parents in this study (Schlautman et al. 2015a; Schlautman et al. 2015b). In addition, SSRs previously developed and mapped in blueberry (Rowland et al. 2014) and newly developed SSR primer pairs were used to genotyped the CNJ02 progeny. Multiplex (3x) Polymerase Chain Reactions (PCR) and fragment analysis for SSR genotyping were performed according to (Schlautman et al. 2015a).

EcoT221-associated DNA fragments for the progeny and parents of the three mapping populations were generated and sequenced according to the genotyping-by-sequencing (GBS) approach described by Elshire et al. (2011). During library construction, adapters containing unique barcodes were ligated to restriction-digested DNA for the 235 progeny from the CNJ02 and CNJ04 populations and their 3 parental genotypes and then were pooled into three 96-plex sequencing libraries. To guarantee higher sequencing coverage in the parental genotypes, the parents for the CNJ02 and CNJ04 populations were represented by six samples each, and the resulting libraries were sequenced (single-end) on the Illumina HiSeq® 2000 platform in the Cornell University Biotechnology Resource Center (BRC) Genomics Facility. Library preparation and sequencing for the Grygleski population (352 progeny) was performed previously following the same methodology described herein, except the 2 parental genotypes were represented by four samples each. This sequence data, used in a previous publication (Covarrubias-Pazaran et al. 2016), was reprocessed and incorporated into the current study to increase the density and accuracy of the final composite map by ensuring that the linkage maps for all three populations were constructed according to the same standard set of parameters.

The reference-based Tassel v3.0.166 GBS analysis pipeline was used to filter and process the resulting sequence reads, align and merge sequence tags by genotype, and to call SNPs in the resulting data set using the parameters outlined in (Glaubitz et al. 2014) (Appendix VI-1). The reference genome used during SNP discovery and genotyping with the Tassel pipeline was created by concatenating the 229,745 scaffold cranberry genome assembly (N50=4,237 bp) produced by (Polashock et al. 2014) into "pseudochromosomes". After generating the filtered HapMap, the SNP marker data was further processed by removing SNPs separately from each of the three populations which had greater than 20 percent missing data, had a minor allele frequency (MAF) of less than 10 percent, or had severely distorted segregation ratios.

Parental Component Map Construction

Using the pseudo-testcross method, markers were formatted and separated into uniparental markers heterozygous in only a single parent (lm x ll and nn x np) and biparental markers heterozygous in both parents (hk x hk, ef x eg, and ab x cd)) (Van Ooijen 2006; Van Ooijen 2011). Linkage analysis was performed using JoinMap v4.1 and linkage groups were determined with a LOD threshold > 5.0 (Van Ooijen 2006). Marker order was determined using the maximum likelihood (ML) algorithm (Van Ooijen 2011). Preferring an accurate estimation of marker order and marker distances over total number of markers included in the maps, a strict approach was used to determine which markers caused problems in marker ordering or inflation of map distances. First, markers were removed which obviously caused problems and/or were placed far from the ends of the linkage groups (LGs) when visualizing the LGs using the *colorize* option to view graphical genotypes. Next iterative rounds of mapping were performed removing markers until no remaining markers caused a nearest neighbor fit (cM) greater than 2 cM, a nearest neighbor stress greater than 0.035, or a nearest neighbor stress (cM) greater than 3.5 cM.

Linkage mapping proceeded by first constructing component parental maps for each population (6 total) using only the uniparental markers (i.e. lm x ll or nn x np) and removing all markers causing problems in map order and distance according to the guidelines outlined above. Using the resulting marker positional information, linkage-informed imputation was performed using the *linkim* package in R to impute missing marker information in the dataset (R Core Team 2015; Xu and Wu 2015). The multiple spanning tree (MST) algorithm implemented in the *ASMap* R package was then used to detect genotyping errors leading to potentially false double recombination events and to create bins of identical markers for each of the parental maps using the Kosambi mapping function to estimate map distances (Wu et al. 2008; Taylor and Butler 2015).

Next, for each population, a single uniparental marker from each bin of each parental map was added to the remaining biparental makers (i.e hk x hk, ef x eg, and ab x cd markers) and linkage mapping was performed using the before-mentioned guidelines with the *cp* approach in JoinMap v4.1. The resulting marker positional and phase information was used to convert the hk x hk markers to ab x cd format by linkage-informed imputation of the hk genotypes using functions from the *sommer* R package (Covarrubias-Pazaran 2016). Each biparental marker was then split into two uniparental markers (either lm x ll for alleles from the maternal parent or nn x np for alleles from the paternal parent) to create a new dataset for each parent containing all possible markers and the MST algorithm was used once again to detect genotyping errors and to create bins for each of the parental maps using the Kosambi mapping function to estimate map distances (Wu et al. 2008; Taylor and Butler 2015). Pair-wise Spearman rank correlations comparing marker order in the LGs of the six parental component bin maps were estimated to ensure that they were

syntenic and collinear and could be used in composite map construction. Additionally, collinearity between LGs was visually assessed in Circos by plotting the links between homologous markers in the LGs of the parental bin maps in each of the three populations (Krzywinski et al. 2009).

Composite Map Construction and Map Comparisons

A synthetic composite map for the six parental maps was constructed with the *LPmerge* package in R which uses linear programming to minimize the mean absolute error between marker intervals in the parental maps and the composite map (Endelman and Plomion 2014). During composite mapping, iterations of the maximum interval size (*k*) ranging from $k = 1$ to $k = 10$ were tested for each linkage group (LG), and the *k* which minimized the root mean square error (RMSE) when comparing the position of makers in the composite LG to the 6 parental LGs was chosen for construction of the final composite LG. Spearman rank correlations and visual assessment in Circos were used to determine the collinearity of the composite map with each of the 6 component maps, with the previous SSR map constructed map for the CNJ02 population used in a comparative genetic analyses with diploid blueberry (Chapter V), and with the first GBS-based SNP map developed previously for the Grygleski population (Covarrubias-Pazaran et al. 2016). Cranberry scaffolds containing predicted coding DNA sequences (CDS) from the Polashock et al. (2014) cranberry genome assembly containing SSRs or SNPs mapped in this study were anchored and oriented using the markers' position in the composite map.

Genome-wide segregation distortion and centromere placement

Segregation distortion in observed genotype ratios for each mapped marker in parental bin maps was analyzed using chi-square tests (χ^2) with one degree of freedom for codominant markers as implemented in JoinMap v4.1. The χ^2 *p*-value for each locus in each parental component map was then plotted in a heatmap to examine patterns of segregation distortion and to determine if segregation distortion regions existed in any LGs.

Centromeric regions in the cranberry linkage groups (LGs) of the component bin maps were explored and identified following the methodology of Limborg et al. (2016). Recombination frequencies (RF_M) were estimated from phased genotype data by recording the proportion of offspring with an observed recombination (i.e. change of phase) in each interval between the terminal marker (m_0) and every subsequent marker (m_n) in both directions along the 12 cranberry LGs. For metacentric or submetacentric LGs, centromeric regions in the LGs were defined as the region from

the point of intersection between the RF_M estimates made from each terminal marker extending outwards until reaching the first marker interval with an $RF_M = 0.45$ in both directions (Limborg et al. 2016).

Results

SSR and SNP Genotyping

Differing sizes of SSR marker datasets were available for mapping in each of the three populations. The CNJ02 population, which was used in the first high density SSR linkage mapping and a recent SSR-based comparative genetic mapping study, had the largest amount of SSR data (629 SSRs) available for linkage mapping (Table 6.1; Appendix VI-2) (Schlautman et al. 2015a; Chapter V). The Grygleski population, which was used in the first cranberry SNP genotyping study (Covarrubias-Pazaran et al. 2016), had a similar amount of SSR data compared to the CNJ04 population with 189 and 221 SSR markers, respectively (Table 6.1; Appendix VI-2). The CNJ04 population has never been used in a peer-reviewed study, and all SSR and SNP marker data for that population was generated herein using multiplex (3x) PCR reactions.

After using the Tassel v3.0.166 GBS analysis pipeline to filter and process the sequence reads from *Eco*T221 digested DNA, to align and merge sequence tags by genotype, to call SNPs in the resulting genotyping-by-sequencing datasets, and to create HapMaps for the three populations, a total of 18499, 15197, and 15224 SNPs with good sequence tag coverage were detected that were polymorphic in the Grygleski, CNJ02, and CNJ04 populations, respectively (Table 6.1). Further filtering using custom R scripts was performed to exclude SNP loci from each population separately that had greater than 20 % missingness, a minor allele frequency (MAF) less than 10 %, or extreme segregation distortion with $\chi 2$ p-values less than 0.00001. As a result, the 5150, 6193, and 4787 SNPs were combined with the SSR marker datasets so that 5339, 6194, and 4787 markers were available for linkage mapping in the Grygleski, CNJ02, and CNJ04 populations, respectively (Table 6.1).

Parental Component Bin Map Construction

Using the uniparental markers, and biparental markers split into uniparental markers with linkage-informed imputation of the hk x hk type markers, parental linkage maps were generated using strict parameters in JoinMap v4.1 followed by bin mapping using the minimum spanning tree (MST) algorithm in ASmap (Van Ooijen 2006; Wu et al. 2008; Taylor and Butler 2015). An average of 2080 markers were mapped in each of the 6 parental component bin maps ranging from 1774 markers for the MQ parent in the CNJ04 population to 2487 markers for the CQ parent in the

CNJ02 population (Appendix VI-3; Appendix VI-4; Appendix VI-5). The number of SNPs mapped in the three populations was very similar; however, the CNJ02 population had more total markers mapped because of its larger SSR dataset (Appendix VI-6). Twelve linkage groups (LGs), corresponding to the expected haploid chromosome number in cranberry (2n=2x=24) (Hall and Galleta 1971), were retrieved for each of the cranberry parents, and total length of those twelve linkage groups varied from 845.21 cM for ST in CNJ04 to 1296.47 cM for MQ in CNJ02 (Appendix VI-3; Appendix VI-4; Appendix VI-5). On average, the linkage groups in the six parental bin maps spanned 89.4 cM and contained 173.3 markers placed in 34.7 unique bins (Appendix VI-3; Appendix VI-4; Appendix VI-5); however, notable exceptions were present in the component maps. For example, linkage group 5 from the [BGx(BLxNL)]95 component map only contained 34 markers placed in 10 marker bins spanning 61 cM (Appendix VI-3). Population size appeared to have some effect on the average number of bin per LG, a reflection of the number of observed recombination events per LG in the population of parental gametes that fused to form the progeny, such that fewer marker bins were present in the LGs of parents from the CNJ04 population, which was approximately 1/3 and 1/5 the size of the CNJ02 and Grygleski populations, respectively (Figure 6.2). However, there was no obvious difference in number of bins per LG in the CNJ02 and Grygleski parents despite the CNJ02 population containing only half as many progeny (Figure 6.2).

Pair-wise Spearman rank correlations comparing marker order revealed exceptionally high levels of synteny and collinearity between the LGs in the six parental component bin maps (Table 6.2). An average of 57.3 markers were used in each of the 180 pair-wise comparisons of linkage groups, and a mean Spearman rank correlation of 0.993 was observed across all comparisons (Table 6.2). The minimum Spearman rank correlation ($r = 0.92$) was observed in comparison of LG 9 between [BGx(BLxNL)]95 and ST (Table 6.2). The majority of the differences in marker order between linkage groups were due to markers being in a single marker bin in one parent while being in adjacent marker bins in the other parent. The high degree of synteny and collinearity among LGs in the component maps was also visually observed in alignments of the linkage maps of the parents in each of the three cranberry populations in Circos and in scatterplots of the relative position of the common markers in each map on different axes (Appendix VI-7, Appendix VI-8, Appendix VI-9).

Composite Map Construction

The high degree of collinearity between the component maps allowed for the construction of a cranberry composite map with *LPmerge* by retaining the synthetic composite map for each LG computed with the maximum interval size, *k*, which minimized the RMSE (Endelman and Plomion 2014). The composite map contained 6073

markers (636 SSRs and 5437 SNPs) spanning 1124.29 cM (Table 6.3; Figure 6.3; Appendix VI-10). The 12 LGs of the composite map ranged from 84.11 cM to 115.88 cM in length, and each LG contained an average of 506 (453 SNPs and 53 SSRs) markers (Table 6.3). The 6073 markers in the composite map corresponded to 1560 unique marker positions (bins), with an average gap of 0.74 cM between unique marker positions (Table 6.3). The largest gap in the composite map was on LG10 and spanned 6.64 cM; however, there were only 3 gaps more than 5 cM and 9 gaps more than 4 cM in the entire composite map (Appendix VI-11). The composite map anchored a total of 3989 cranberry scaffolds from the Polashock et al. (2014) assembly totaling 21.8 Mb (4.6%) of the predicted 470 Mb cranberry genome (Appendix VI-12). Of the 3989 anchored scaffolds, 1654 contained predicted CDS, whose positions in the composite map were plotted in Figure 6.3.

Collinearity between the cranberry composite map and the 6 component parental bin maps was high; the mean Spearman correlation across the 72 pairwise-comparisons of marker order was $r = 0.997$ (Table 6.4). Collinearity between the parents of the two larger populations (i.e. CNJ02 and Grygleski) and the composite map were slightly higher (i.e. $r \geq 0.999$) than the CNJ04 parents (i.e. $r = 0.995$ and 0.991) (Table 6.4). Marker order variation between the composite and six component maps was highest in LG12, with perfect correlation observed only between the [BGx(BLxNL)]95 component map and the composite map (Table 6.4). Spearman rank correlations comparing the LGs of the composite map to the 12 LGs from the Covarrubias-Pazaran et al.(2016) SNP-SSR map and the Schlautman et al. (2015a) SSR map were also high (i.e. $r = 0.976$ and $r = 0.996$, respectively) (Appendix VI-13).

Genome-wide segregation distortion and centromere placement

Approximately 8 % of the markers in the six parental component bin maps displayed significant segregation distortion (SD) at the χ^2 $p \leq 0.1$ level (Figure 6.4, Appendix VI-14). SD was not randomly distributed across the linkage groups or populations. The GH1x35 parental map contained a much higher proportion of markers displaying segregation distortion (i.e 26 %) compared to the other five parents, with as many as 81% of all markers in LG 6 displaying distortion (Figure 6.4, Appendix VI-14). Segregation distortion regions (SDRs) were observed in LGs of each of the six parental bin maps, and some SDRs, such as the SDR on LG 9, appeared to be present in multiple parental genomes (Figure 6.4, Appendix VI-14).

Phasing the genotype data and estimating RF_M for each marker interval from the terminal markers in both directions allowed for centromere placed on each of the 12 LGs of the component maps using the method developed in Limborg et al. (2016) (Table 6.5, Figure 6.5). The recombination phasing method allows for distinguishing between

metacentric and acrocentric linkage groups. All cranberry linkage groups appeared to be metacentric or submetacentric, which was consistent with the karyotype for cranberry and diploid *Vacciniums* observed in Hall and Galleta (1971), and centromere spans averaged 18.6 cM across the 12 LGs of the 6 component maps (Table 6.5; Figure 6.5).

Discussion

Genotyping-by-sequencing is an effective strategy for simultaneous SNP discovery and genotyping in cranberry, and was used to identify thousands of polymorphic SNP loci which were transferable between inter-related full-sib mapping populations. A composite map was developed by merging the 6 bin maps constructed for the parents of each full-sib family, which allowed for exploration of segregation distortion regions (SDRs) and centromere placement. The map will serve as framework for future genomics studies to identify QTL regions of interest and for the continued investigation of genome organization and evolution in the genus *Vaccinium*. Furthermore, the cranberry genomic scaffolds and predicted CDS anchored in the composite map demonstrate its utility in future efforts to anchor physical maps and assist in the assembly of cranberry and *Vaccinium* genome sequences.

Map construction

The use of three full-sibling populations of diverse genetic backgrounds facilitated an increase in the number of mapped markers (SNPs and SSRs) and resulting genome coverage in the cranberry composite map that has not been possible in past studies using single populations (Georgi et al. 2013; Schlautman et al. 2015a; Covarrubias-Pazaran et al. 2016). More importantly, the pedigrees of the three full-sibling populations all trace their ancestry to the seven wild cranberry selections, "The Big Seven", made in the 19th and 20th centuries, which collectively account for the entire genetic base of the modern cranberry industry (Figure 1) (Eck 1990; Clark and Finn 2010; Fajardo et al. 2012; General Introduction). Therefore, the composite cranberry map affords the ideal opportunity for exploring and connecting the genetic diversity to the phenotypic diversity that has been responsible for the historical success of cranberry production. A key use for the composite map will be to allow for concurrent identification and integration of quantitative trait loci (QTL) and marker trait loci (MTL) which colocalize across populations, across environments, and across phenotypes within and among future linkage mapping, QTL mapping, and genome-wide association studies (GWAS).

The composite map will be most useful for studies within section *Oxycoccus*, and it may aid in future targeted introgression of genomic regions involved in the expression of unique metabolic pathways or disease resistance genes from the small-fruited cranberry, *V. oxycoccos*, to the American cranberry, *V. macrocarpon* (Vorsa and Polashock 2005).

However, due to the high level of synteny and collinearity detected between cranberry and blueberry using cross-transferable SSRs (Chapter V), information from the composite map should also be applicable to many other commercially important *Vacciniums* including blueberry (*Vaccinium* section *Cyanococcus*) and closely related sections lingonberry (*Vaccinium* section *Vitis-Idaea*) and sparkle berry (*Vaccinium* section *Batodendron*) (Lyrene 2011; Schlautman et al. 2016). Unfortunately, despite the recent publication of a high density SSR-SNP linkage map for tetraploid high bush blueberry (McCallum et al. 2016), *V. corymbosum*, comparative genomic analyses were not possible using the present cranberry composite map because neither the blueberry genome scaffolds anchored in the blueberry SNP map nor previous blueberry SSR maps have been made publically available (Rowland et al. 2014; McCallum et al. 2016).

Two methods are commonly employed for integration of independent linkage maps. The first method uses pooled segregation and recombination information from independent maps; however, this method is computationally unfeasible for integration of high-density linkage maps containing thousands of loci (Van Ooijen 2011; Endelman and Plomion 2014; Bodénès 2015). The second method, which was used in the present study and other recent composite mapping studies in pine and oak (Chancerel et al. 2013; Bodénès 2015), performs map integration based on marker position rather than observed recombination such as is proposed and implemented in the *LPmerge* package (Endelman and Plomion 2014). Using *LPmerge*, the six parental component bin maps, each containing an average of 2080 markers (Appendix VI-3; Appendix VI-4; Appendix VI-5), were merged to obtain a synthetic composite map that included 6073 loci (1560 unique marker positions) covering 1124 cM on 12 LGs, making it the highest-density map in the *Vaccinium* genus and the entire Ericaceae family (Table 6.3). This map achieved considerably higher marker saturation (i.e. 0.74 cM mean interval between unique marker positions) than previous published cranberry linkage maps based on SSR and SNP markers (Georgi et al. 2013; Schlautman et al. 2015a; Covarrubias-Pazaran et al. 2016), while decreasing the total map length by 50 cM compared to the highest-density cranberry SSR map and increasing total map length by only 13 cM compared to the first cranberry SNP map (Table 6.3) (Schlautman et al. 2015a; Covarrubias-Pazaran et al. 2016).

The similarity in total map lengths between the current and former maps is a reflection of the robust marker-ordering and marker distance estimation achieved in construction of the 6 individual component maps herein using stringent parameters and the bin mapping strategy. Comparison of marker order in the synthetic composite map against each of the individual component maps provided further indication of the composite map quality. For example, Spearman rank correlations (r) exceeded 0.95 for all 72 pair-wise comparisons of marker order in the LGs of the component map compared to the LGs of each of the component parental bin maps and exceeded 0.99 for 58 (80 %) of the comparisons (Table 6.4). Spearman rank correlations comparing the LGs of the composite map to LGs from the

Covarrubias-Pazaran et al.(2016) SNP-SSR map and the Schlautman et al. (2015a) SSR map were also high (i.e. $r = 0.976$ and $r = 0.996$, respectively) (Appendix VI-13).

Previous high-density linkage mapping studies in outcrossing populations have often excluded the biparental markers (i.e. hk x hk segregation) because of difficulties they cause during mapping and because of assumptions that they are less informative for linkage mapping (Ward et al. 2013; Bodénès 2015); however, including the biparental SNPs in this study significantly increased the number of total markers mapped and the number of markers in common between component maps. All genetic maps (i.e. composite and component maps) in this study could be directly compared because of the high frequency of transferability of SNP markers across parents and populations. A total, 2921 (54%) of the SNPs in the composite map were mapped in two or more populations and 1040 (19%) of the SNPs were mapped in all three populations (Appendix VI-6). The number of markers in common between linkage groups in the parental maps appeared to be correlated ($r = 0.74$) with the degree of shared ancestry between the parents. For example, the average number of markers in common per LG for parents with a coefficient of coancestry greater than 0.1 was 80.1, while parents with a coefficient of coancestry less than 0.1 had an average of 49 markers in common per LG (Table 6.2, Figure 6.1). A high degree of synteny and collinearity was visually observed in alignments of the parental maps in each population (Appendix VI-7, Appendix VI-8, Appendix VI-9), and the mean Spearman rank correlation of 0.993 in comparisons of marker order, based on an average of 57.3 markers per LG, across all 180 pairwise comparisons of LGs in the component maps was remarkably high (Table 6.2). The observed transferability of SNP markers across the 5 cranberry parents from three populations, and the high collinearity between LGs in the component maps, suggests that genotyping-by-sequencing will be an effective marker discovery and genotyping platform for exploring cranberry genetic diversity and population structure, and aided by the placement of more than 5000 SNPs in the composite map, will be useful in estimating linkage disequilibrium (LD) in cranberry diversity panels for genome-wide association studies (GWAS).

The 636 SSR loci positioned in the composite map represent an important genetic resource for future cranberry breeding efforts (Table 6.3). Of the 1540 unique marker positions in the composite map, 27% include one or more SSR markers (Table 6.3; Figure 6.4). Within the Mullica Queen and Crimson Queen parental bin maps for the CNJ02 population, an average of 53% of the unique marker bins include an SSR marker suggesting that a larger number of marker positions could have been represented had more SSR data been available for the other two full-sib populations (Appendix VI-4). The large number of positioned SSRs, and their apparent distribution throughout the entire cranberry genome, should allow them to be useful in marker-assisted seedling selection of marker trait loci (MTL)

in cranberry using multiplexing panels similar to those developed in Chapter III. Despite the obvious benefits of simultaneous marker discovery and genotyping afforded by genotyping-by-sequencing, the high cost per sample does not yet justify its use for large-scale genotyping of thousands of seedlings for selection of a few MTL in a specialty crop such as cranberry. A better way to allocate resource will be to utilize the SSRs, which are likely to be polymorphic in much more diverse backgrounds than SNPs (Hamblin et al. 2007), to select for must-have MTL in large populations for simple traits, and then use genotyping-by-sequencing to further explore the genetic diversity or perform genomic selection in the selected individuals (Dekkers 2007; Collard et al. 2008; Singh and Singh 2015).

There were a couple interesting differences between the number of marker bins and rates of recombination in the five parental genomes that may have important implications for cranberry breeding. First, the average number of marker bins per linkage group, which is a reflection of the number of unique recombination events in the parental gametes, was less in the parents of the CNJ04 population (23 bins per parent per LG), than in the Grygleski and CNJ02 populations (38 bins and 43.5 bins per parent per LG, respectively) (Appendix 3; Appendix 4; Appendix 5; Figure 6.2). The fewer bins observed in the parents of the CNJ04 population was expected and is likely due to its small size (i.e. 67 progeny), suggesting that breeders may need less genetic data (i.e. DNA markers) to capture all the recombination history in small biparental breeding populations. Genotyping-by-sequencing can be performed at various plexing levels by ligating unique barcodes to restriction digested DNA from many genotypes (Elshire et al. 2011; Poland et al. 2012). In the current study, digested DNA from 96 genotypes were pooled per Illumina lane; however, only 283 and 258 unique marker bins were recovered in the parents of the CNJ04 population even though 1774 and 1806 markers were mapped in the Mullica Queen and Stevens bin maps, respectively (Appendix VI-5). Therefore, cranberry breeders can likely better allocate their resources by using higher plexing levels (e.g. 384 plex) when using genotyping-by-sequencing to genotype smaller populations. In fact, even in the larger CNJ02 and Grygleski populations, there were only ¼ as many marker bins as total mapped markers so 384 plex should be sufficient for larger cranberry populations (Appendix VI-3; Appendix VI-4). Unexpectedly, there was no difference in the number of marker bins per LG in the CNJ02 and Grygleski populations; therefore, there may not be an added advantage to working with large populations like Grygleski (i.e. 352 progeny) compared to populations of about 200 plants (CNJ02 included 168 progeny).

The second interesting observation is that the paternal linkage groups were consistently shorter than the maternal linkage groups, and there were fewer phase changes (i.e. recombinations) per LG per parental gamete in the paternal gametes than in the maternal gametes (Appendix VI-3; Appendix VI-4; Appendix VI-5). Sex-specific differences in recombination rates have previously been observed in cranberry (Schlautman et al. 2015a; Covarrubias-

Pazaran et al. 2016), blueberry (Chapter V), apple (Maliepaard et al. 1998), and olive (Sadok et al. 2013). It is uncertain whether these observed differences in recombination rates between sexes are more than coincidental differences in patterns and rates of recombination in the five cranberry parents. However, we hypothesize that the differential recombination rates in male and female gametes observed in *Vaccinium* linkage mapping studies may be a true consequence resulting from a combination of common practices employed by cranberry and blueberry breeders during population development, differences in microsporogenesis and megasporogenesis, and the unique pollen morphology of the *Vaccinium* genus.

During megasporogenesis, three of the four megaspores disintegrate, and only one megaspore survives; conversely, all four microspores survive during microsporogenesis (Fehr 1991). *Vaccinium* pollen, rather than being shed as single grains which is common in flowering plants, are shed as groups of four pollen grains (i.e. the four microspores) called tetrads which are derived from the same meiotic division (Eck 1990; Roper and Vorsa 1997). This has important consequences considering that, during meiosis, chiasma almost always only occur between only two of the four chromatids on each side of the centromere (Roeder 1997). Therefore, assuming *Vaccinium* chromosomes are metacentric (Hall and Galleta 1971), for any single chromosome in a *Vaccinium* pollen tetrad (i.e. a total of eight chromosome arms), four of the eight chromosome arms in the four haploid gametes (i.e. four microspores) represent meiotic recombinants, but in reality, there are only two unique positions of recombination because the reflection of each recombinant chromosome arm exists as one of the three remaining recombinant chromosome arms in the pollen tetrad.

Pollen germination studies in both cranberry and blueberry have revealed that all four pollen grains are viable in the majority of *Vaccinium* pollen tetrads (Huang and Johnson 1996; Cane 2009), and that fruit set does not increase after loading more than 8 tetrads on a cranberry stigma which contain an average of 32 ± 4 ovules (Sarracino and Vorsa 1991; Cane and Schiffhauer 2003). Consequently, it is highly likely that any seed within a *Vaccinium* fruit shares a paternal meiotic history with one or more seeds in the same fruit; however, because of the disintegration of three of the four megaspores, no seed in a fruit shares a maternal meiotic history with any other seed in the same fruit. The result of this phenomena of high *Vaccinium* microspore fertility combined with pollen shed as tetrads is that, because *Vaccinium* breeders and geneticists generally only make a few crosses (i.e. harvest seeds from a few fruits) to generate breeding and/or linkage mapping populations, there is a potential reduction in the number of chromosome arms in paternal gametes that represent unique meiotic recombinants, which could have led to the observed decrease in LG length and recombination rate in the paternal versus maternal maps in this study. Specifically, in a population of 40 cranberry full-sib progeny with a meiotic history tracing to 10 cranberry pollen tetrads (i.e. 40 haploid paternal gametes), assuming

strong cross-over interference, a maximum of 20 unique recombinant chromosome arms out of 80 could be observed for any single paternal metacentric chromosome in the full-sib progeny; conversely, a maximum of 80 out of 80 unique recombinant chromosome arms could be observed for the same maternal metacentric chromosome in the full-sib progeny.

It may be beneficial for *Vaccinium* breeders and geneticists to consider harvesting seeds from as many crosses as possible (i.e. more fruits) during population development to ensure equal representation of recombination in both the maternal and paternal genomes by removing the effect of pollen tetrad formation. Although pollen tetrad could be a challenge in *Vaccinium* breeding and genetics; pollen tetrad analysis, which not feasible in most higher Eukaryotes, has been highly advantageous and used extensively in genetic studies of fungi, algae, and *Arabidopsis* mutants to detect every genetic change between chromatids, to simplify genetic map construction, to define centromere positions, and to quantify crossover and chromatid interference (Preuss et al. 1994; Copenhaver et al. 2002; Brieuc et al. 2014). Furthermore, it has already been useful in detecting chromosomal rearrangements, specifically reciprocal translocations, in cranberry cultivars (Ortiz and Vorsa 2004).

Genome characterization

SNP and SSR loci present within nuclear genome scaffolds from the Polashock et al. (2014) assembly were used anchor 3989 nuclear scaffolds containing 21.8 Mb (4.6%) of the predicted 470 Mb cranberry genome in the composite map (Appendix VI-12). Although the present composite map anchored 1500 more nuclear scaffolds than the previous SNP linkage map, those 1500 scaffolds only represented a 1.9% increase in the total Mb of cranberry genome anchored (Covarrubias-Pazaran et al. 2016). This is reflective of the sheer number of scaffolds (i.e. 229,745 scaffolds) and their size (i.e. N50 = 4,237 bp); and suggests the need for a higher quality cranberry genome assembly (Polashock et al. 2014).

Deviations from expected Mendelian inheritance were widespread throughout the cranberry genome, and ~8 % of the markers positioned in the parental component maps displayed significant segregation distortion (i.e. $p < 0.1$) according to chi-square tests (χ^2) with one degree of freedom (Figure 6.4, Appendix VI-14). Previous high-density linkage mapping studies have sometimes observed that distorted markers are not always randomly distributed, but rather, are grouped together in segregation distortion regions (SDRs) (Yin et al. 2004; Wang et al. 2012a; Bodénès 2015; Covarrubias-Pazaran et al. 2016). Likewise, apparent SDRs were observed in the present study in all six of the parental component maps (Figure 6.4, Appendix VI-14). Many of the SDRs are unique to each parental cranberry genome, as

was previously observed in oak and palm (Ting et al. 2014; Bodénès 2015). However, there is apparent overlapping between some SDRs in the six parents (e.g. SDR in LG9 for the [BGx(BLxNL)]95 and Stevens parents, and SDR in LG8 for the [BGx(BLxNL)]95 and Crimson Queen parents), which could represent biologically significant phenomena such as gametic competition, gametophytic selection, or sterility (Wang et al. 2005; Bloom and Holland 2012; Xu et al. 2013).

There have been minimal efforts to characterize chromosomal structures, such as centromeres, in cranberry, and modern cytogenetic approaches such as fluorescent in situ hybridization (FISH) have not yet been attempted. Centromeres are central components of chromosome architecture that play fundamental roles in the regulation and crossover formation during meiosis (Roeder 1997; Zickler and Kleckner 1999); and therefore, knowledge of centromere location is critically important in attempts to manage the occurrence of meiotic recombination in plant breeding (Wijnker and de Jong 2008). However, many high-density linkage mapping studies in cranberry and other commercially important crops have not attempted or failed to place centromeres onto the linkage groups (Wang et al. 2012b; Castro et al. 2013; Ting et al. 2014; Bodénès 2015; Covarrubias-Pazaran et al. 2016), which could limit their future applicability in interpretations of genome organization, genome divergence, and of the genomic architecture of adaptive or economically important traits (Limborg et al. 2016). Therefore, we utilized the recombination phasing method outlined in Limborg et al. (2016) and effectively applied in Mckinney et al. (2016) to define centromere regions in the cranberry linkage groups (Table 6.5; Figure 6.5).

In general, the Limborg et al. (2016) recombination phasing method appeared to work well in cranberry. Centromeres were placed on all twelve cranberry linkage groups in each of the six parental component maps (Table 6.5; Figure 6.5). All linkage groups were identified as metacentric, consistent with a previous cranberry karyotype presented in Hall and Galleta (1971). The centromere regions in the parental linkage groups, although sometimes large (i.e. an average of 18.6 cM across LGs), were similar in size to those observed in (Mckinney et al. 2016). The centromere regions appeared to have the same general location across linkage groups in the parental maps, providing further confidence in the estimation of their positions. Interestingly, observed marker densities were often higher in centromere regions and had reduced recombination rates (i.e. recombination "coldspots") compared to the rest of the respective linkage groups (Figure 6.5). The knowledge of centromere location generated herein should facilitate future meiotic studies in cranberry exploring crossover interference and recombination "hotspots" and "coldspots", and could potentially be useful for developing cranberry crop improvement strategies for managing meiotic recombination and for overcoming barriers to recombination in cranberry chromosomes (Martinez-Perez and Moore 2008).

In conclusion, genotyping-by-sequencing has been shown to be a highly efficient means for SNP marker discovery and genotyping in cranberry. A large proportion of the genotyping-by-sequencing based SNP loci were polymorphic and transferable between three full-sib cranberry populations, which allowed for the construction of the first a high-density composite linkage map in cranberry composed of both SNP and SSR markers. The stringent parameters used during component map construction, and the remarkable collinearity observed between the six component maps and the composite map suggests that estimation of marker position and distance was performed in an accurate, reproducible manner. The large number of cross-transferable allowed for characterization of cranberry genomic architecture such as the detection of centromeric regions, and we foresee that the composite map and the marker data will be used extensively for future QTL detection, genome-wide association studies, and development of molecular-assisted breeding strategies in cranberry.

Table 6.1. Simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) genotying results and markers available for linkage mapping in the Grygleski, CNJ02, and CNJ04 cranberry populations following marker filtering steps and merging with previous marker datasets generated in Schlautman et al. (2015a) and Covarrubias-Pazaran et al. (2016).

Population	HapMap filtered SNPs	SNPs after missingness[a]	SNPs after MAF[b]	SNPs after SD[c]	SSRs	Total Mappable Markers
Grygleski	18499	18374	8345	5150	189	5339
CNJ02	15197	15028	8721	5564	629	6193
CNJ04	15224	14818	8566	4566	221	4787

[a] SNP loci with more than 20 % missingness were excluded.
[b] SNP loci with a MAF less than 10 % were excluded.
[c] SNP loci with extreme segregation distortion were excluded.

Table 6.2. Pair-wise Spearman rank correlations between the linkage groups (LGs) of the 6 parental component maps constructed for the parents (P) of the Grygleski (i.e. P1 = [BG(BLxNL)]95 and P2 = GH1x35), CNJ02 (P3 = MQ and P4 = CQ), and CNJ04 (P5 = MQ and P6 = ST) full-sib cranberry populations. Coefficients of Coancestry (CoA), or kinship coefficients, were calculated for the parents involved in each pairwise comparison. The number of common markers available and used in each comparison is listed in parenthesis.

LG	P1xP2	P1xP3	P1xP4	P1xP5	P1xP6	P2xP3	P2xP4	P2xP5	P2xP6	P3xP4	P3xP5	P3xP6	P4xP5	P4xP6	P5xP6
1	1.00 (91)	1.00 (78)	1.00 (100)	1.00 (56)	1.00 (75)	1.00 (95)	1.00 (85)	1.00 (81)	0.99 (71)	1.00 (96)	1.00 (119)	1.00 (59)	1.00 (52)	0.99 (69)	1.00 (87)
2	1.00 (42)	1.00 (50)	1.00 (100)	1.00 (46)	1.00 (43)	1.00 (37)	1.00 (50)	1.00 (29)	1.00 (30)	1.00 (89)	1.00 (135)	1.00 (32)	1.00 (49)	1.00 (55)	1.00 (51)
3	1.00 (41)	0.99 (42)	1.00 (56)	0.97 (27)	0.98 (24)	1.00 (91)	1.00 (37)	0.97 (56)	0.98 (32)	1.00 (77)	0.99 (97)	0.99 (37)	0.98 (25)	0.99 (64)	0.99 (44)
4	1.00 (49)	1.00 (66)	1.00 (47)	0.99 (39)	0.99 (32)	1.00 (68)	1.00 (46)	1.00 (42)	1.00 (37)	1.00 (96)	1.00 (102)	0.99 (23)	0.99 (31)	0.99 (62)	0.99 (29)
5	0.99 (15)	0.98 (16)	0.98 (19)	0.95 (11)	0.93 (8)	1.00 (85)	1.00 (86)	1.00 (48)	0.99 (34)	1.00 (85)	1.00 (93)	1.00 (15)	0.99 (35)	1.00 (56)	1.00 (19)
6	1.00 (70)	1.00 (57)	1.00 (86)	0.99 (43)	1.00 (49)	1.00 (96)	1.00 (51)	0.99 (83)	0.99 (42)	1.00 (80)	0.99 (143)	0.99 (49)	1.00 (52)	1.00 (89)	0.99 (55)
7	1.00 (45)	1.00 (54)	1.00 (50)	0.99 (37)	0.99 (22)	1.00 (99)	1.00 (44)	0.99 (68)	0.99 (14)	1.00 (91)	1.00 (122)	0.98 (29)	0.99 (42)	1.00 (48)	0.98 (34)
8	0.99 (32)	0.99 (29)	0.99 (41)	0.99 (26)	0.99 (24)	1.00 (35)	1.00 (36)	1.00 (31)	1.00 (15)	1.00 (83)	1.00 (97)	1.00 (21)	0.99 (46)	0.99 (55)	1.00 (25)
9	1.00 (84)	1.00 (67)	1.00 (70)	0.99 (49)	0.92 (54)	1.00 (83)	1.00 (57)	0.99 (56)	0.98 (37)	1.00 (93)	0.99 (141)	0.97 (31)	1.00 (39)	0.98 (46)	0.98 (36)
10	1.00 (48)	1.00 (34)	1.00 (46)	1.00 (31)	0.99 (69)	1.00 (79)	0.98 (53)	1.00 (59)	0.99 (33)	1.00 (82)	1.00 (100)	0.98 (27)	0.99 (29)	0.99 (64)	0.99 (31)
11	1.00 (56)	1.00 (66)	1.00 (77)	0.99 (49)	0.99 (32)	1.00 (114)	1.00 (69)	0.99 (94)	0.99 (28)	1.00 (97)	1.00 (159)	0.99 (34)	1.00 (61)	0.99 (47)	0.98 (43)
12	1.00 (66)	0.99 (48)	1.00 (77)	0.98 (40)	0.98 (46)	0.99 (85)	1.00 (57)	0.99 (64)	0.97 (37)	0.99 (77)	0.99 (127)	0.98 (32)	0.99 (39)	0.97 (75)	0.98 (45)
CoA[a]	0.094	0.078	0.094	0.078	0.063	0.156	0.031	0.156	0.063	0.000	0.500[c]	0.000	0.000	0.250	0.000
Mean	1.00 (53.25)	1.00 (50.58)	1.00 (64.08)	0.99 (37.83)	0.98 (39.83)	1.00 (80.58)	1.00 (55.92)	0.99 (59.25)	0.99 (34.17)	1.00 (87.17)	1.00 (119.58)	0.99 (32.42)	0.99 (41.67)	0.99 (60.83)	0.99 (41.58)
Total[b]	639	607	769	454	478	967	671	711	410	1046	1435	389	500	730	499

[a] Coefficient of Coancestry

[b] Total markers in common between the compared parental bin maps.

[c] self-Coancestry is 0.5 assuming no prior inbreeding

Table 6.3. Features of the cranberry composite map, constructed using the six parental component bin maps for the parents of the CNJ02, CNJ04, and Grygleski populations, including the length of the linkage groups (LG), the total number of simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers mapped, the number of unique marker positions, the number of unique marker positions containing an SSR, and the mean gap distance (cM) between unique positions.

LG	Length (cM)	SNPs	SSRs	Markers	Unique Marker Positions	Positions with an SSR	Mean Gap (cM)
LG1	115.88	588	50	638	158	37	0.74
LG2	100.75	416	63	479	152	45	0.67
LG3	92.4	407	54	461	99	34	0.94
LG4	86.35	423	61	484	110	36	0.79
LG5	93.09	405	35	440	110	24	0.85
LG6	93.77	473	50	523	157	37	0.6
LG7	97.03	418	59	477	158	47	0.62
LG8	85.2	370	54	424	128	35	0.67
LG9	89.86	532	54	586	112	33	0.81
LG10	84.11	378	51	429	115	32	0.74
LG11	95.25	499	42	541	152	30	0.63
LG12	90.6	528	63	591	109	32	0.84
Mean	93.69	453	53	506	130	35	0.74
Total	1124.29	5437	636	6073	1560		

Table 6.4. Pair-wise Spearman rank correlations between the linkage groups (LGs) of the 6 parental component maps constructed for the parents of the Grygleski ([BG(BLxNL)]95 and GH1x35), CNJ02 (MQ and CQ), and CNJ04 (MQ and ST) full-sib cranberry populations compared to the LGs of the cranberry composite map.

LG	[BGx(BLxNL)]95	GH1x35	MQ-CNJ02	CQ	MQ-CNJ04	ST
LG1	1.00	1.00	1.00	1.00	1.00	1.00
LG2	1.00	1.00	1.00	1.00	1.00	1.00
LG3	1.00	1.00	1.00	1.00	0.99	0.99
LG4	1.00	1.00	1.00	1.00	1.00	0.99
LG5	1.00	1.00	1.00	1.00	1.00	0.97
LG6	1.00	1.00	1.00	1.00	1.00	1.00
LG7	1.00	1.00	1.00	1.00	1.00	1.00
LG8	1.00	1.00	1.00	1.00	1.00	1.00
LG9	1.00	1.00	1.00	1.00	0.99	0.97
LG10	1.00	1.00	1.00	1.00	1.00	1.00
LG11	1.00	1.00	1.00	1.00	1.00	0.99
LG12	1.00	0.99	0.99	0.99	0.96	0.98
mean	1.000	0.999	0.999	0.999	0.995	0.991

Table 6.5. Centromere spans placed on the 12 linkage groups (LGs) of the cranberry parental component bin maps constructed for the parents of the CNJ04 population, Mullica Queen (MQ) and Stevens (ST); the CNJ02 population, MQ and Crimson Queen (CQ); and the Grygleski population, [BGx(BLxNL)]95 (BGBLNL95) and GH1x35 using the method developed in Limborg et al. (2016). Centromeric spans (*x* cM – *y* cM) in the LGs were defined as the range from the intersection between the recombination frequency (RF_M) estimates between each marker and the terminal marker on both ends of the LG extending outwards until reaching the first marker with an $RF_M = 0.45$ in both directions. The intersection point (cM) of RF_M estimates in each LG is provided in parentheses.

Parent	LG											
	1	2	3	4	5	6	7	8	9	10	11	12
MQ-CNJ04	44.3-55.0 (44.3)	24.2-42.1 (28.2)	20.8-58.6 (41.1)	29.9-58.7 (36.9)	47.1-58.5 (47.7)	38.1-43.8 (43.5)	42.3-49.6 (45.4)	13.9-41.1 (23.9)	43.8-55.3 (44.6)	15.0-61.5 (36.6)	46.9-53.0 (50.2)	24.9-64.7 (49.9)
ST	38.0-62.8 (55)	28.2-59.2 (50.2)	20.8-69.9 (45.5)	4.2-79.0 (43.9)	44.7-56.1 (48.3)	21.0-49.8 (34.2)	24.3-57.6 (42.3)	20.0-62.4 (41.7)	25.9-62.7 (38.1)	31.7-52.8 (43.4)	6.6-66.3 (38.1)	35.4-60.1 (43.7)
MQ-CNJ02	68.8-68.8 (68.8)	47.8-47.8 (47.8)	42.9-42.9 (42.9)	33.9-33.9 (33.9)	42.4-44.7 (42.4)	48.9-48.9 (48.9)	42.3-45.4 (42.3)	36.2-36.2 (36.2)	49.3-49.3 (49.3)	39.0-54.2 (44.0)	38.7-38.7 (38.7)	48.0-52.9 (48)
CQ	46.1-85.2 (67.8)	49.3-49.3 (49.3)	33.4-47.0 (37.1)	28.7-43.9 (33.9)	44.7-56.1 (48.3)	40.4-65.4 (45.9)	38.3-53.5 (44.8)	36.2-58.8 (49.4)	38.1-73.2 (52.5)	21.2-45.3 (36)	38.1-53.6 (43.5)	9.8-66.4 (55.3)
BGBLNL95	53.9-53.9 (53.9)	50.0-52.5 (50.3)	36.5-39.3 (36.5)	35.6-50.1 (41.5)	9.8-61.0 (22.4)	44.1-44.1 (44.1)	49.9-49.9 (49.9)	14.7-50.2 (32.1)	52.5-57.2 (52.5)	37.1-44.4 (39.0)	50.2-50.2 (50.2)	49.6-49.6 (49.6)
GH1x35	58.1-58.1 (58.1)	37.4-54.5 (50.2)	26.0-61.0 (42.9)	34.9-55.9 (46.7)	26.4-46.7 (41.8)	37.2-55.3 (45.9)	35.7-52.9 (45.4)	30.9-58.1 (44.7)	31.0-56.3 (43.8)	29.8-52.7 (39.9)	44.6-53.6 (44.6)	34.9-54.7 (46.3)
mean	51.5-64.0 (58.0)	39.5-50.9 (46.0)	30-53.1 (41.0)	27.9-53.6 (39.4)	35.9-53.9 (41.8)	38.3-51.2 (43.7)	38.8-51.5 (45.0)	25.3-51.1 (38.0)	40.1-59 (46.8)	29.0-51.8 (39.8)	37.5-52.6 (44.2)	33.8-58.1 (48.8)

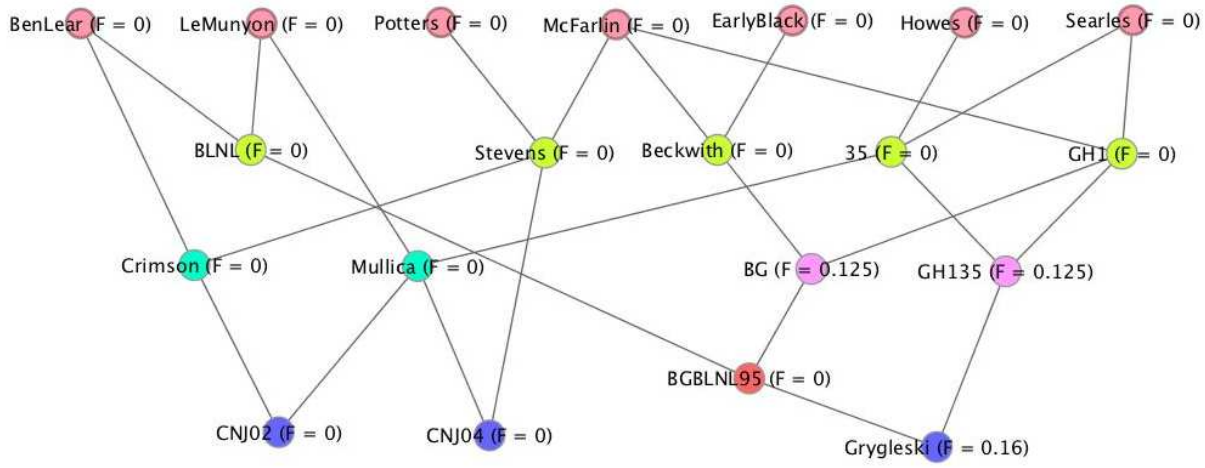


Figure 6.1. Description of the pedigrees of the three mapping populations (blue), CNJ02, CNJ04, and Grygleski, derived from crosses between five inter-related cranberry parental genotypes (i.e. CNJ97-105 (*Mullica Queen*®), NJS98-23 (*Crimson Queen*®), Stevens, [BGx(BLxNL)]95, and GH1x35). All pedigrees trace to "The Big Seven" native cranberry selections (red), which have played important roles in the cranberry production and breeding history. The pedigree contains five first generation hybrid genotypes resulting from crosses between two wild selections (yellow), two genotypes (green) resulting from crosses between and a first generation hybrid (yellow) and a wild selection (red), two genotypes (pink) resulting from crosses between two first generation hybrids (yellow, and a single genotype (orange) resulting from crosses between a first generation hybrid (yellow) and a second generation hybrid (pink). Inbreeding coefficients (F) calculated for each genotype and for each of the three populations are provided.

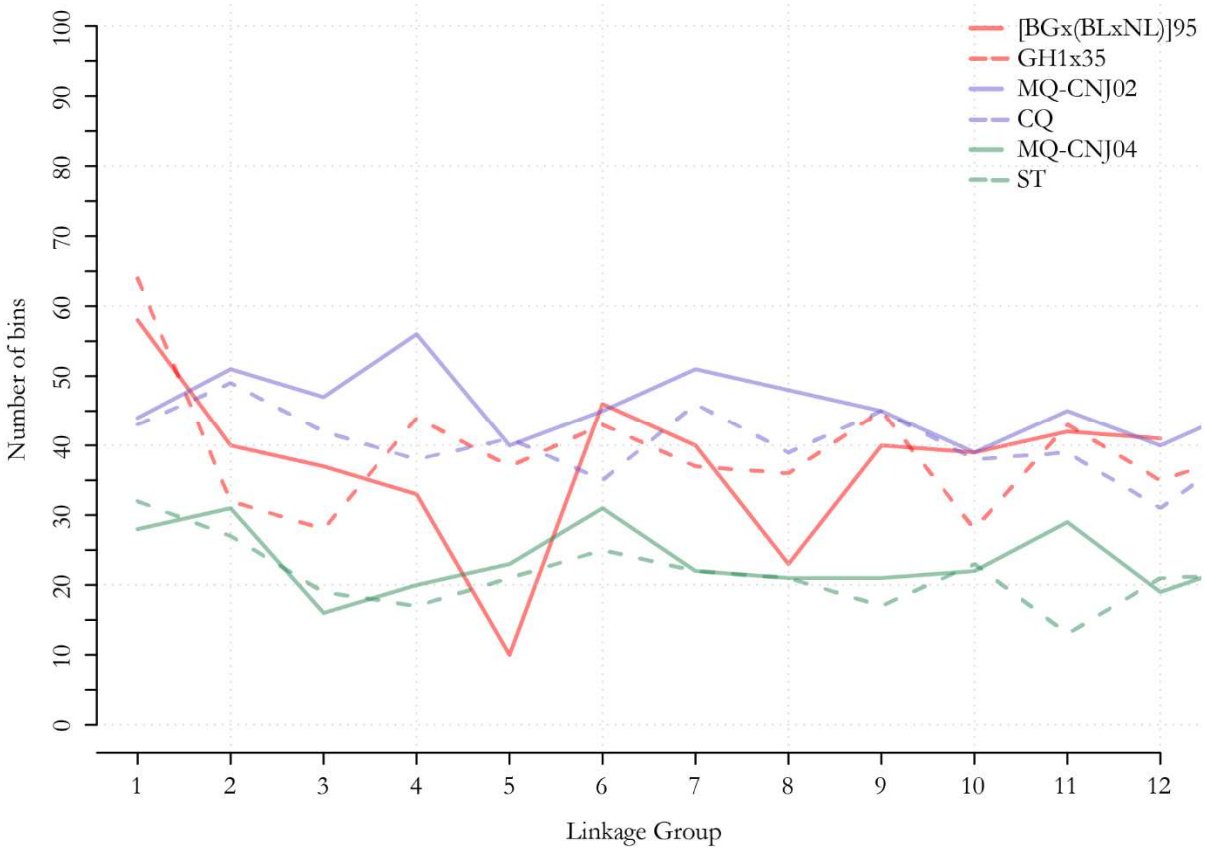


Figure 6.2. The number of recombination bins, estimated using the multiple spanning tree algorithm implemented in ASMap (Wu et al. 2008; Taylor and Butler 2015), for each of the 6 parental component bin maps constructed from progeny from the three cranberry full-sib populations: Grygleski (i.e. [BGx(BLxNL)]95 x GH1x35), CNJ02 (i.e. MQ x CQ), and CNJ04 (i.e. MQ x ST). The Grygleski population (red) included 352 progeny; the CNJ02 population (blue) included 168 progeny, and the CNJ04 population (green) included 67 progeny.

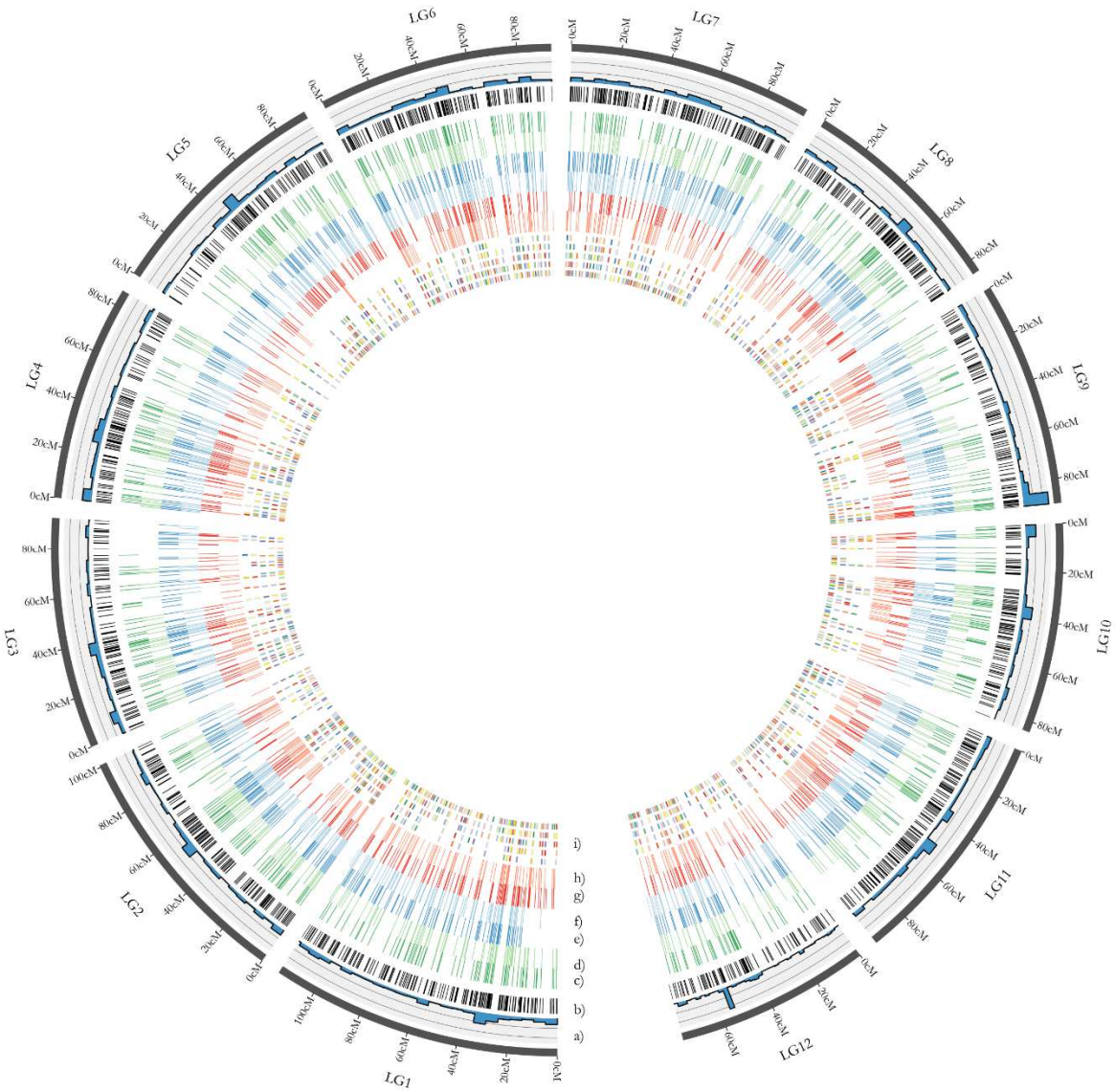


Figure 6.3. (a) Histograms of marker density and **(b)** heatmaps of the unique marker positions within the 12 linkage groups (LGs) of the cranberry composite map. Additional heatmaps display the markers that were present in the **(c)** [BGx(BLxNL)]95, **(d)** GH1x35, **(e)** Mullica Queen, **(f)** Crimson Queen, **(g)** Mullica Queen, **(h)** and Stevens parental component bin maps used to construct the cranberry composite map. **(f)** The distribution of scaffolds from the (Polashock et al. 2014) assembly that contained predicted coding DNA sequences (CDS) and that were anchored with single nucleotide polymorphism (SNP) or simple sequence repeat (SSR) markers in the composite map.

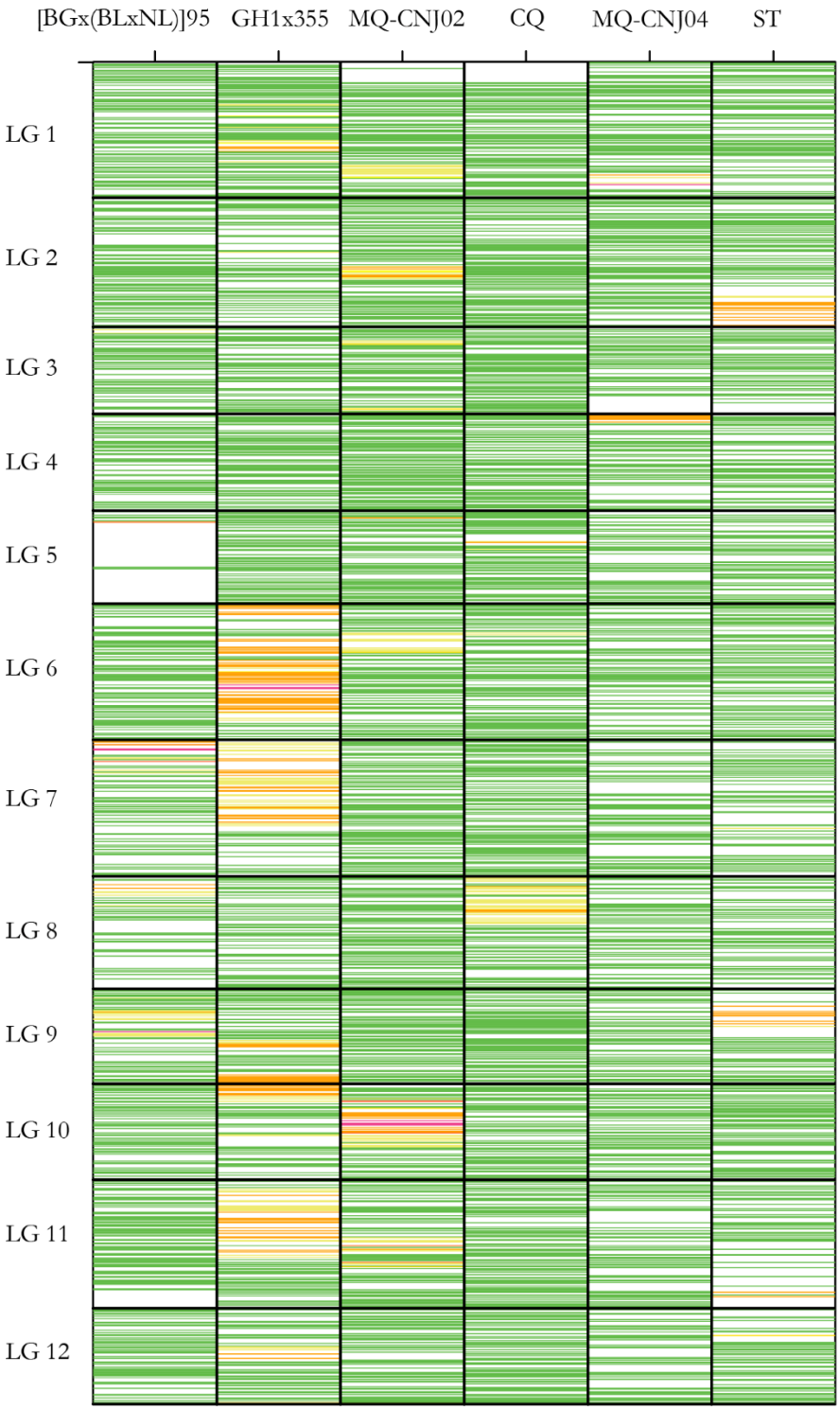


Figure 6.4. Position of markers in the linkage groups (LGs) of the 6 parental component maps (i.e. [BGx(BLxNL)]95, GH1x35, Mullica Queen (MQ), Crimson Queen (CQ), and Stevens (ST) from the Grygleski, CNJ02, and CNJ04 populations). Marker colors range from green for markers not showing distortion (i.e. $\chi 2$ $p > 0.1$) to dark red for markers showing highly significant segregation distortion (i.e. $\chi 2$ $p < 0.0001$) in $\chi 2$ tests of the expected Mendelian genotype ratios.

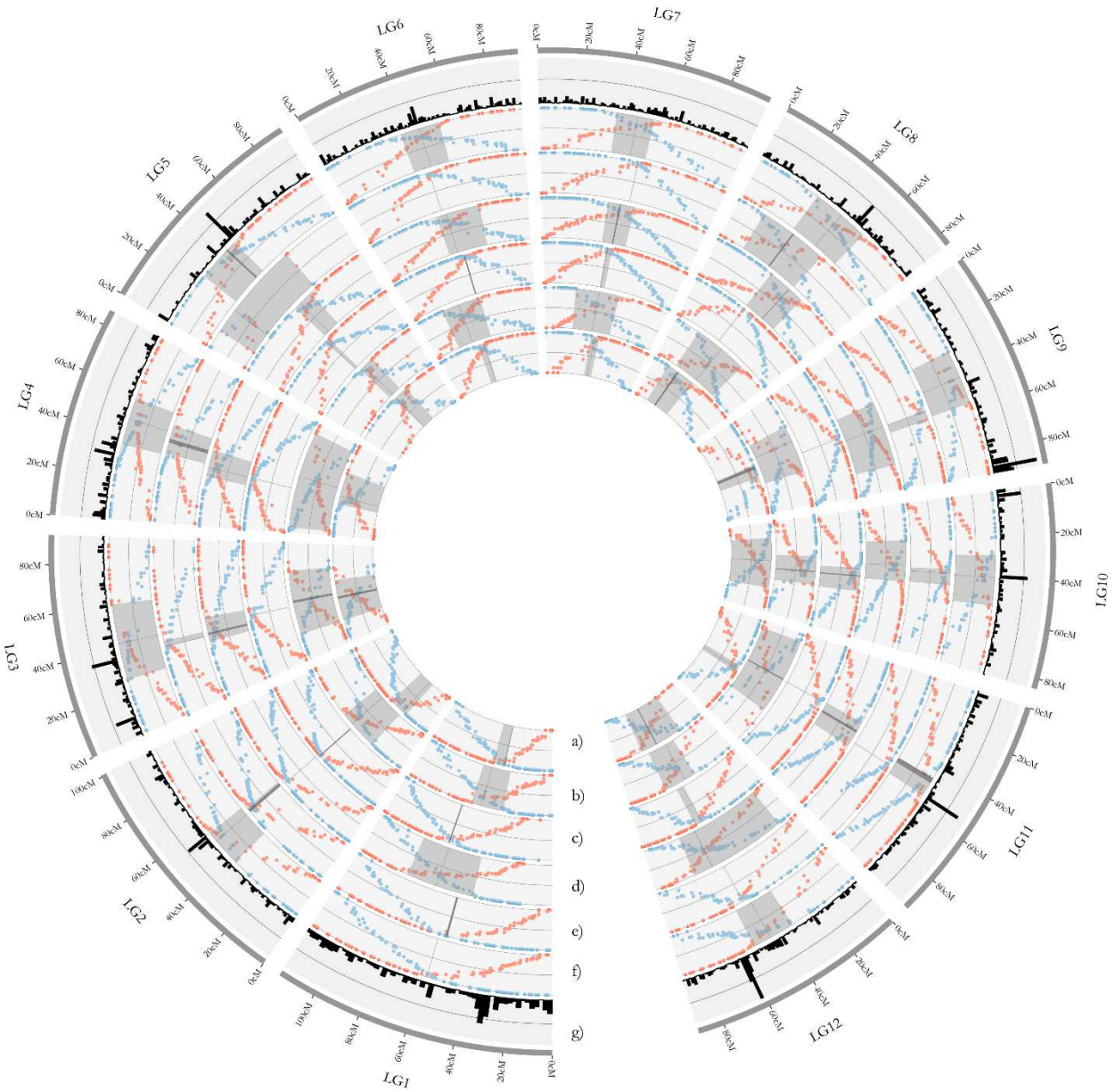


Figure 6.5. Plots of recombination frequency (RF_M) estimated from phased genotype by starting at the terminal markers at the beginning (red points) and end (bluepoints) of each linkage and recording the proportion of offspring with an observed recombination (i.e change of phase) in the interval between the terminal marker (m_0) and each subsequent marker (m_n) for the 12 cranberry LGs. Centromere spans (gray regions) were placed on the 12 linkage groups (LGs) of the cranberry parental component bin maps constructed for the parents of the CNJ04 population, Mullica Queen **(a)** and Stevens **(b)**; the CNJ02 population, Mullica Queen **(c)** and Crimson Queen **(d)**; and the Grygleski population, [BGx(BLxNL)]95 **(e)** and GH1x35 **(f)** using the method developed in Limborg et al. (2016). Centromeric spans in the LGs were defined as the range (cM) extending from the intersection (dark lines) of the recombination frequency (RF_M) estimates made from the both ends of the LG outwards until reaching the first marker with an $RF_M = 0.45$ in both directions. **(g)** Marker density in the cranberry composite map is shown to explore the relationship between marker density and centromere position.

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Appendix VI-1. Parameters used in the Tassel v3.0.166 reference-based genotyping-by-sequencing (GBS) pipeline for processing raw sequence data and calling SNPs in the resulting sequence data generated for the parents and progeny of the CNJ02, CNJ04, and Grygleski cranberry populations.

Plugin	Option	Value	Description
FastqToTagCountPlugin	c	1	Minimum number of times a tag must be present to be output. Default: 1
FastqToTagCountPlugin	s	300000000	Max good reads per lane. (Optional. Default is 300000000).
MergeMultipleTagCountPlugin	c	3	Minimum number of times a tag must be present to be output. Default: 1
TagCountToFastqPlugin	c	1	Minimum count of reads for a tag to be output (default: 1)
SeqToTBTHDF5Plugin	m	internal/04_topm/cranberry_UWisc_Pazaran.topm.bin	TagsOnPhysicalMap (.topm) file containing tags of interest. The -m option i smutually exclusive with the -t option
SeqToTBTHDF5Plugin	s	500000000	Max good reads per lane. (Optional. Default is 500
TagsToSNPByAlignmentPlugin	y	-y	Use byte-formatted TBT file (*.tbt.byte)
TagsToSNPByAlignmentPlugin	errRate	0.01	Average sequencing error rate per base (used to decide between heterozygous and homozygous calls) (default: 0.01)
TagsToSNPByAlignmentPlugin	mnLCov	0.1	Minimum locus coverage i.e. the proportion of taxa with at least one tag at the locus. Default: 0.1
TagsToSNPByAlignmentPlugin	mxSites	2000000	The maximum number of SNPs per chromosome for hapmap files (default = 2000000)
TagsToSNPByAlignmentPlugin	mnMAC	999	Minimum minor allele count. Defaults to 10. SNPs that pass either the specificed minimum minor allele count (mnMAC) or frequency (mnMAF) will be output.
TagsToSNPByAlignmentPlugin	mnMAF	0.01	Minimum minor allele frequency. Defaults to 0.01. SNPs that pass either the specifice dminimum minor allele

			frequency (mnMAF) or count (mnMAC) will be output.
MergeDuplicateSNPsPlugin	misMat	0.05	Threshold mismatch rate above which the duplicate SNPs won't be merged. Default: 0.05.
MergeDuplicateSNPsPlugin	callHets	-callHets	When two genotypes at a replicate SNP disagree for a taxon call it a heterozygote. Defaults to false (=set to missing)
MergeIdenticalTaxaPlugin	hetFreq	0.8	cutoff frequency between het vs. homozygote calls (default = 0.8)
FastqToTBTPlugin	y	-y	output to tagsByTaxaByte (tag counts per taxon from 0 to 127) instead of tagsByTaxaBit (0 or 1)
FastqToTBTPlugin	c	1	Minimum taxa count within a qseq file for a tag to be output. Default: 1
MergeTagsByTaxaFilesPlugin	s	300000000	Maximum number of tags the TBT can hold while merging (default: 200000000)
tbt2vcfPlugin	ak	3	Maximum number of alleles that are kept for each marker across the population default: 3
tbt2vcfPlugin	mnLCov	0.0	Minimum locus coverage (proportion of Taxa with a genotype) (default: 0.0)
tbt2vcfPlugin	mnMAF	0.0	Minimum minor allele frequency (default: 0.0)
MergeDuplicateSNP_vcf_Plugin	ak	3	Maximum number of alleles that are kept for each marker across the population default: 3
GBSHapMapFiltersPlugin	mnSCov	0.8	Minimum site coverage (default: no filter)
GBSHapMapFiltersPlugin	mxMAF	1	Maximum minor allele frequency (default: 1.0 = no filter)
GBSHapMapFiltersPlugin	mnTCov	0.1	Minimum taxa coverage (default: no filter)
GBSHapMapFiltersPlugin	mnMAF	0.01	Minimum minor allele frequency (default: 0.0 = no filter)

Appendix VI-2. Simple sequence repeat (SSR) markers used to genotype the parents and progeny of the CNJ02, CNJ04, and Grygleski full-sib cranberry populations in this study, their primer sequences, their publication of origin, their NCBI ID, and there position (cM) in the linkage groups (LG) of the cranberry composite map constructed herein.

Locus	LG	Position (cM)	NCBI	Origin	Forward	Reverse
SCF138607	1	0.45	KP278872	Schlautman et al. (2015)	CATATAGAATACTGGACGGACA	TTCTGCCATCTCCTTTCTC
SCF4386	1	2.9	KP278612	Schlautman et al. (2015)	GTTACTCATTTCTTTGCTGAGG	CCTCTTAGTGTTGGAGTTTCAT
vm51985	1	9.43	JF834280	Zhu et al. (2012)	TGCTAGTATTTTGACTCAGGTG	GCCTATATATAACCAAGCAAGG
vm55441	1	12.85	JF834240	Zhu et al. (2012)	AAAAGGAACACGGATACGAT	GGATTCGAGAACCTATCTCAT
SCF3551	1	18.41	KP278608	Schlautman et al. (2015)	CTTCGACGTTTCTGTGACTAT	AGTTGGTGATTGGAAGAGTAAG
ct116900	1	30.57	KP279112	Schlautman et al. (2015)	CTCAAACATACCCTTTGAGC	GGTATAGCTTAACAACACACCA
SCF118999	1	30.57	KP278842	Schlautman et al. (2015)	CTAAACTCCAAAATGCCTAAAC	AAAGTGGATGGGTTCTAAAAG
SCF43220	1	30.57	KP278712	Schlautman et al. (2015)	CTTGTCGAGCATCCTATATTTC	AAAAGTCATGGGAAGGTGTT
SCF111370	1	31.68	KP278828	Schlautman et al. (2015)	ACCACATCTTCATTTTGAGC	GTAAAACAATACGGGTCCTTAC
SCF124322	1	31.68	KP278849	Schlautman et al. (2015)	TAAAACTGTGAGGTTCAATGTG	CTTCGTGTCTCAAATTACAAAA
SCF22962	1	31.68	KP278659	Schlautman et al. (2015)	GTGCAACAGCTAACAGCATA	AGGACCAATACTCAGAACAAAC
SCF3914	1	31.68	KP278609	Schlautman et al. (2015)	TGTGGAGTTAGAGTGACATACC	GACAAGAATGATGAGTAGCGT
SCF8223	1	32.27	KP278622	Schlautman et al. (2015)	CATTTAGCATCCATCCATTC	GACTGTGGGTTATTCCTTGTAT
scaffold_71150	1	34.07		Herein	GCTTGTGTTCTCTATCCTCTTT	CCTAATACTAACCCCATCCTTT
SCF142441	1	40.43	KP278879	Schlautman et al. (2015)	TTGCGTTTACTATCTAAGGAGG	CTCAGCCGTCCAAAAGTAT
162108_K70	1	40.72	KP279200	Schlautman et al. (2015)	GAAGTCGAAACCCTAGCAG	GTCCCTCTCAGTCTCTCACTC
scaffold_18824	1	50.87		Herein	TGTTCTTAGGGAGTTGAGAGAT	TTACCTCAGTCATTCCTCTAGC
scaffold_18380	1	52.06		Herein	CAACCACATAACGCACTACTAT	TGGAGTGATACTTGGTCTCC
SCF121995	1	55.02	KP278845	Schlautman et al. (2015)	TAGTCGTGACCAAGAGTGATTA	GCCACCGAGTATATTTCTATGT
242569_K70	1	55.3	KP279204	Schlautman et al. (2015)	GATATGAGAGACGAGGAATCAC	GTCAGTGGACGGTTTTAAGAT
1trimcontig440230	1	62.75	KP279249	Schlautman et al. (2015)	ACACTTTGTAGGTGGTGGTTAT	ATTAGCAGTAGTCCAATCGGT
SCF59248	1	62.99	KP278740	Schlautman et al. (2015)	TAGTTGAAAATGGAGAGAGAGC	TTAGATGCCCAACACTACATC
SCF102347	1	64.25	KP278808	Schlautman et al. (2015)	GGTAGTGAGCAACGACATAAC	CCTGAAGGTAAAGAAAGTAGCA
scf11l	1	76.17		Georgi et al. (2013)	TAATGAGTGCTGGTTCTGCG	TTCAAATCCACGTCAGCAAA
scaffold_26291	1	76.43		Herein	GCCTGTACGATCTTTATCTTCT	TAAAACACTCACCACCCTCTA
1trimcontig238795	1	77.27	KP279233	Schlautman et al. (2015)	AGAGGGAGAGAAGAGTATGGTC	CCGTCAAGATTTGTGAAGAT
SCF11186	1	85.23	KP278636	Schlautman	AGAAAGGCTAAAAG	GCTCTCAACAACTCGAA

				et al. (2015)	GGTATCTC	AGTA
1trimcontig179737	1	85.57	KP279225	Schlautman et al. (2015)	CCTCCAACTTCTTCATCTTCT	ACTGGTAACTCCTCAGAAACAG
vm23232	1	88.91	JF834262	Zhu et al. (2012)	ACAGAGCTCAATGGAGAAAA	TTCTGCTGATAGTGTTGGTACA
1trimcontig239742	1	92.89	KP279234	Schlautman et al. (2015)	AACAAGAACAACTAAGACCACC	TACAAGTTTCAATCAGCCCT
SCF149633	1	92.89	KP278891	Schlautman et al. (2015)	CCTTAATACCCATCCCATAATC	CTTCTTTTCATTGTTGTGGC
GVC-C347	1	94.75		Blueberry Markers	GGAGAAGATGACCCAAACGA	AGTCCCTTTGGACCATACCC
scf8l	1	94.75		Georgi et al. (2013)	CGAATCCGAAGATCAGAAGC	GGGATACCAGAGATTTCCCG
SCF3362	1	94.93	KP278605	Schlautman et al. (2015)	GTACAGCAAAATTCAGCACA	GGATTTATCTACAGCCCATTAC
SCF173212	1	95.35	KP278924	Schlautman et al. (2015)	TGTAGTGGGAGATGCTGATAC	AATTGGCGAACTAGAAAGTG
SCF30816	1	96.39	KP278685	Schlautman et al. (2015)	GTCCAAAATAGCATCGAAAG	CGCATTACTTCTTCACTATACG
1trimcontig182430	1	100.35	KP279226	Schlautman et al. (2015)	GAAGATGGACCTGAGTAAGAAA	CTACCATTGTGTTCTCAAACTG
SCF117157	1	102.73	KP278837	Schlautman et al. (2015)	GGATAGAAACCTGATACGGAC	CGTTACCGTCCCAAATATAA
SCF23691	1	106.91	KP278662	Schlautman et al. (2015)	CGGCTTTGTTAGTTGATGTT	CGATGTTGTACTATTCATGTCC
SCF39242	1	106.91	KP278705	Schlautman et al. (2015)	ACTCCTGAAGAAGAAGAACAGA	AATGAATGCAGACCACAGAT
SCF69981	1	106.91	KP278752	Schlautman et al. (2015)	AGCGTTACCACCGAATATAA	CGAGATATAGTTAAAAGGACGG
SCF29735	1	108.1	KP278681	Schlautman et al. (2015)	CGTAAAATCTGTTGTCTCTGTG	TCTCTATGCTCCTTCCACTTAT
vm89040	1	108.1	JF834248	Zhu et al. (2012)	TAGACAGACTTTCATGCTATGG	GAACTGATGAAGGTGGTTTATC
SCF125768	1	110.2	KP279069	Schlautman et al. (2015)	CTCACTTCTCATACAACATTGG	CACAACAGAACCATCAGTACAT
SCF142785	1	110.2	KP279083	Schlautman et al. (2015)	AGGCTCACATTTCTAACTCAAG	ATATCTACCTCCCTAATTTCCG
SCF42549	1	110.2	KP279018	Schlautman et al. (2015)	CTCTTCAGCCCTAATCATATTC	CAGGACAAACATCTAGGTCAA
SCF208509	1	111.98	KP278950	Schlautman et al. (2015)	GCTTCACACTTGATAGTAGGTTG	TACCGCCATTGTAGCAGAT
SCF153722	1	113.92	KP278899	Schlautman et al. (2015)	AGTTATGAGGCTTACGAGGAG	GATGGAACGATGAAACTGAT
SCF172019	1	113.92	KP278920	Schlautman et al. (2015)	TGTGAGTAGTTGTTGAAGGGA	CCTCGAAAATCCGGTAAAT
SCF68870	1	115.88	KP278750	Schlautman et al. (2015)	GTGAATTGTTGCAGAGTACCTA	TGAGTTGAGTTCATATAGCTGG
SCF31394	2	0	KP278688	Schlautman et al. (2015)	GTAGCAAAAGAAGAGACACCAT	CGTTTTCCAGTTCCAGAGTA
SCF77145	2	0	KP278763	Schlautman et al. (2015)	TAGAATTAGCCTCCAAGAAGTG	AGAACTAGAAACACGAGAACGA
SCF180863	2	1.11E-16	KP278930	Schlautman et al. (2015)	CCAGTTACAGATCCTTGAGTTG	GCAATGTTCCCTCGAATTA
1trimcontig178358	2	1.79		Herein	AATTGAACGATCCCTATTCC	GATTCATCACCCCTTGAAC
SCF22434	2	1.79	KP278656	Schlautman et al. (2015)	TATGTATAGTCCCACAACAAGG	TCCTGTCTATCACTCACATCAC
GVC-C722	2	2.98		Blueberry	AAGTGGATTTCGATT	TAATCCCCATCACCGTCA

				Markers	CGGTG	TT
SCF127382	2	2.98	KP279071	Schlautman et al. (2015)	GTCTTTAGTGCTGG GTTAAAAG	TGATTTCTAGTGTCTCCT CTCA
scf28l	2	11.31		Georgi et al. (2013)	AACTCTTCGCTTTGG TTGGA	TCGGTCGTAGAGACGA GGAT
SCF74458	2	11.31	KP278759	Schlautman et al. (2015)	GCAGGAAGCTATGA TTAAGGTA	TTGAATAGTGTCAGTGG AGAAG
SCF965	2	11.86	KP278594	Schlautman et al. (2015)	GTAAACTAACAAGCA ACGATCC	GATTTAGCTGATGCAGA GTCAT
SCF26049	2	13.99	KP278668	Schlautman et al. (2015)	GTTCAGGTCTGTTGT AAGGAAG	TTTCTTGTAGGACGAAG TGG
SCF77376	2	13.99	KP278764	Schlautman et al. (2015)	CTCATCAAAAGAGAG GAGAACT	TGTAACCAATCTTCATG CTG
1trimcontig351427	2	14.28	KP279242	Schlautman et al. (2015)	GACGGCTAAATTGTA ACTAACG	AGGGTCCTATCCTATCC TCTAA
314761_K63	2	14.83		Herein	ATTGTTGGATACTTC ATGGC	GTTGGTACTGGTAAACC CTAAT
SCF13771	2	22.53	KP278642	Schlautman et al. (2015)	AGGATGATGAAATCT GCAAG	ATCAGTTAGGTGGGGT AAGG
29080_K63	2	23.92	KP279160	Schlautman et al. (2015)	ATGAAAACAGGGTA AACTGG	TCTCAACTCATAGAACTA CGGA
scaffold_38278	2	28.18		Herein	TGTATCTTTGATCTG TACGGG	TTCGGGTTAGAGTTTAG TAGGA
SCF83079	2	28.18	KP279039	Schlautman et al. (2015)	GTATTCACCAAATCT ACCCAGA	GTTAAGGATTGTGTCCC TCA
ct130570	2	29.37	KP279121	Schlautman et al. (2015)	GTTCACAATCTGCAT CTCCT	ACGTAATAGATCAAGAA CAGGG
372875_K63	2	34.75	KP279174	Schlautman et al. (2015)	CACACACAAATCCCA ATTTC	GATGGTGTTTTCATAGT TCGAC
SCF73288	2	37.13	KP278758	Schlautman et al. (2015)	CAGAGGAACAGCAG ACTACAT	CCTAGTACGTCATTGGA CATTA
CA325	2	39.13		Georgi et al. (2013)	ACCACCCTCCCATTTC AAAC	AGGCGAAAAAGGTGTT GATG
CA325_205	2	39.13		Blueberry Markers	ACCACCCTCCCATTTC AAAC	AGGCGAAAAAGGTGTT GATG
SCF130642	2	39.13	KP279074	Schlautman et al. (2015)	AGGCGGAAGATGAA AGTAAT	TGTCAACATAAAACGAT AGCAG
SCF158988	2	39.72	KP278907	Schlautman et al. (2015)	CTCTCACCAAAATCA CCATTAG	CAAGTATCAAGTTTTAG ACGGG
SCF48645	2	40.85	KP278722	Schlautman et al. (2015)	AAAATAGGTCCCACA TGAGTAG	GCTAGACGATGACACAT TATTC
ct124256	2	43.3	KP279118	Schlautman et al. (2015)	GCCGTTAGTTCGTGA TATGT	CCTACATGCATACGTAA AACAG
ct155461	2	43.42	KP279141	Schlautman et al. (2015)	GGTTTCAAACTCGAA CAAAG	ATCCTATAACTGGGGAT AATGC
ct89348	2	47.79	KP279100	Schlautman et al. (2015)	GGCTCAATCTTGTGT AGGTATT	GAGAAAGTGGAAAGAT TGTGTG
scf2000b	2	50.21		Georgi et al. (2013)	GGCCCTTTTTATCCC CAATA	AATCAAAAGCTGCGAGG AAA
SCF158633	2	52.97	KP278906	Schlautman et al. (2015)	AGATGCTGAAGTTTT CCCTT	TATGTGGATTCTTTGCC TTG
VCB-C03938	2	53.56		Blueberry Markers	CCTCAGATAACTGAA ACCCGTC	CCTCTCTATTTTCGGTTT CCCT
SCF18709	2	54.15	KP278651	Schlautman et al. (2015)	GTAATGGTAAGTGT CGAAATCC	CATAGATGTAACCACGC TTCT
35137_K63	2	54.47	KP279254	Schlautman et al. (2015)	GGAACATCAAAACTC CCATAC	GTTCTTCCCCATTTCAGT AAGT
172672_K70	2	54.75	KP279201	Schlautman	GATAGTTGTATGCGC	GTTACCCGAATGAACAG

				et al. (2015)	TGTAAGA	GT
297265_K63	2	54.75	KP279167	Schlautman et al. (2015)	GATCGTCATAACTAAGCTGGAT	GTCTCGAATCACAACAGGATA
SCF174468	2	54.75	KP278926	Schlautman et al. (2015)	CAACATTCTTCGCTCACAA	CTAAGAGTTGACATGATTGGC
SCF192715	2	54.75	KP278942	Schlautman et al. (2015)	CTCTGCCTTGTTCGTCTCT	AACCAATCGAAGGTGACAA
SCF3595	2	54.75	KP278607	Schlautman et al. (2015)	AGACTACAGTGAACAAAGACCA	CTGACTTGGTGTGATTAGTGAG
SCF56816	2	54.75	KP278735	Schlautman et al. (2015)	CGGATTGACTAATTTCTGTCTC	CTCTTATTCCACCAAACGAA
SCF66692	2	54.75	KP278749	Schlautman et al. (2015)	AAAGTGTATTGGACGGCTG	TTGTTATGGCCCCTCATTA
SCF125667	2	57.45	KP278852	Schlautman et al. (2015)	AAGGGAGACATTACACAACAA	TTCGAGATTGACCAAGTATGT
scf12916	2	57.59		Georgi et al. (2013)	GGAGATGGATTTGGCAAGAA	ATCCATGTGGCAGCAGTGTA
SCF61078	2	57.59	KP278743	Schlautman et al. (2015)	GACTCTTCATATAACCCACAGC	AAAAGTGCTTGATCGTTAGC
CHI03186-1	2	58.09		Blueberry Markers	TACATCTTGAGGGGCAGTTTTT	GTGGAGTGTGGGATATGGATTT
SCF80703	2	60.43	KP278770	Schlautman et al. (2015)	GGTCTTTCTCCTAATCTCCAA	GGAACCCCTAAATAACATACAG
198358_K70	2	63.49	KP279203	Schlautman et al. (2015)	AATCGTCTGTTGCTCAATGT	AACCATACTTACCACAACCAGT
SCF213102	2	63.49	KP278953	Schlautman et al. (2015)	GTGAAGATACAGTGGAGAGCA	ATGGTAGTTGTTGACCTGATG
1trimcontig209220	2	84.19	KP279228	Schlautman et al. (2015)	GTATTTGTTCACACTCACCAGA	ACAGTTGTCGAAGCCTCAT
SCF142664	2	85.97	KP278880	Schlautman et al. (2015)	TACTGACGATGAGCTAGAGTTG	AATGACAAGTGGAATAGTAGGC
contig704	2	85.98		Georgi et al. (2013)	AAATGGCAGGAATCATGGAC	CTGTTGATCAGCACCACCAC
vm54133	2	87.76	JF834236	Zhu et al. (2012)	GTGTAAAATTCCAGGTAGAAGC	ATCAAGCTCTCAGTATCCTCTG
SCF122552	2	88.54	KP279067	Schlautman et al. (2015)	TATATCGAGGTCATTGCGA	GAGTTGTCGTTAAGGTTTTGA
SCF203038	2	88.54	KP279098	Schlautman et al. (2015)	CACTTCTGTACCCTCTTTTACC	GTCTCATACCTGAATTTTCTGC
SCF141794	2	89.43	KP278877	Schlautman et al. (2015)	CCATCTGCATCTATTGTTTTG	CATTTGTAGGTCTATCTTTCGC
VCC_B3	2	90.92		Boches et al.(2005)	CCTTCGATCTTGTTCCTTGC	GTTTGATGCAATTGAGGTGGAGA
scaffold_7191	2	91.81		Herein	ATATAGATGTGTGTGATCGCTG	CTCTCTCCATTTTCCACTAAAC
SCF177451	2	94.19	KP278929	Schlautman et al. (2015)	GTACCATATAAGAAAGGGAGCC	CAATAGAAACCCAAGACAACTC
SCF175823	2	97.18	KP278927	Schlautman et al. (2015)	AGGGGCAGTTTAGTCCTAGTAT	GCACGTCTTTTCTGTAGTTCAT
1trimcontig332949	2	99.56	KP279237	Schlautman et al. (2015)	ACCCAAACACAAAAGAACAG	GACTGCAAGTGTCTAAATGCT
ct118602	2	99.56	KP279113	Schlautman et al. (2015)	TAGAATGCAGTCGTGAAGTGTA	ACTAAATGAGGGGTAGTACGTG
Ig15420a	2	99.56		Georgi et al. (2013)	TGGGGGATTTCTCACAAGAG	AATCCCACTTGATTAGGCCC
vm13780	2	100.75	JF834259	Zhu et al. (2012)	CCTTCTGCTGGACACTCATA	ACCCATACCAGAGGAGTACATA
contig130Fb	3	1.16		Georgi et	GAGATTCTCGCTTTT	ATGCACAGCTGCAACAA

				al. (2013)	TCCCC	AAG
vm78806	3	1.16	JF834245	Zhu et al. (2012)	CAAAGAAGAGGAGGATTGAGT	GAGCGAGTATTACAAGTGTTTC
scf511	3	4.56		Georgi et al. (2013)	CTCCCTCCTTCCGATGAAGT	CACAAAGTTCCACGCAGAAA
SCF90229	3	5.33	KP278791	Schlautman et al. (2015)	GTACTTTTGTGGAACTTAACGC	CTGTCCTTTCACTCCTCTTTT
2ms2a02	3	6.52		Georgi et al. (2013)	ACCGCAAGAGAGAGATTCCA	GTTTGATGATCACGGTGGTG
scf20g	3	6.52		Georgi et al. (2013)	TGAGTGCCGATGAGGTATTG	AGAGGAGGAGACGTGCATTG
vm04084	3	6.52	JF834250	Zhu et al. (2012)	GGATTCTCACTCTGATACCATT	GAACGATACACAACGAAGGT
vm51409	3	6.52	JF834279	Zhu et al. (2012)	TCCTAGGTTAATTCTTCCCATC	GAGGAGAATCACAAGCTACATT
SCF23339	3	8.22	KP278661	Schlautman et al. (2015)	GCAAAACAGAGTTATAGTGGCT	TAGACAGAAGCACAGATTGGTA
SCF27755	3	8.22	KP278671	Schlautman et al. (2015)	GAAGTGAGAGTAGGAATCGAAG	CCACAACACAAAACCCTAAT
SCF47809	3	10.77	KP278720	Schlautman et al. (2015)	CTTCTACCTTCCAAGATTTGTG	ATTACTATTCCCAGAGACGACC
SCF98686	3	17.2	KP278803	Schlautman et al. (2015)	CGTAATTTCACATCCTCGTT	CATAACCAGATAGCACCTCAAT
411475_K63	3	17.52	KP279181	Schlautman et al. (2015)	GCAACAGGGACAGATATTTT	TACGGACTCATAGAAGGTTAGG
42710_K70	3	17.52	KP279194	Schlautman et al. (2015)	GTTACACACACACCCACAGA	GAGAGAGGACTAGGTCGTACAG
1trimcontig440008	3	17.71	KP279248	Schlautman et al. (2015)	GCAACAGGGACAGATATTTT	TACGGACTCATAGAAGGTTAGG
SCF57479	3	19.56	KP278736	Schlautman et al. (2015)	AAGTGCAAGTGTGAGAGTGTAT	TGATGGGTGTAAGTGTAAAGAG
121633_K63	3	23.59	KP279163	Schlautman et al. (2015)	GCAGCTCTCTGTAAATTCCTT	ATGGTTGAAGATGTTGATGG
SCF38340	3	25.97	KP278701	Schlautman et al. (2015)	CAAACCATTTTAACGGAGAG	AATCATCGTGCATACCTGTT
1trimcontig439466	3	26.57	KP279246	Schlautman et al. (2015)	CGAGTGGATAGTGATGATATTG	ACCAAGAGGAACTACAGGTAAA
SCF9815	3	26.57	KP278628	Schlautman et al. (2015)	CATAGGAAGATTGCCTTGAG	GCCTGTTCACATAGATGGAG
SCF110888	3	28.64	KP278826	Schlautman et al. (2015)	CTCCTACCCAAATTCACTTGT	CCAAAACTAAACCATTTCTCAC
scaffold_37951	3	30.23		Herein	TTCTGGGTTCCATTACCATA	CTTGTTCTCTATCCTCTTCAGC
82171_K70	3	33.36	KP279199	Schlautman et al. (2015)	TAGTAGAGTTGAAGAGGAGGGA	CTAGGGTTTAAGCAAGCATAGT
SCF21119	3	34.75	KP278654	Schlautman et al. (2015)	GGATTTGAGGACTATACCAAGA	TTAAAAGGCATACGCTGAC
1trimcontig436904	3	35.34	KP279245	Schlautman et al. (2015)	TACCAACCACATCACACATC	CTTATGACGATCCCAGTAGC
KAN-11440	3	35.34		Blueberry Markers	CCAGTAACAATGAGCTGCCA	GATCGTTGCTGAAGGGTTGT
SCF108252	3	35.34	KP278817	Schlautman et al. (2015)	CCTATGTAATTGGATTCTACCC	GTGTATCAAGGTGGAGAAAGTC
SCF128992	3	35.34	KP278858	Schlautman et al. (2015)	GAGTGTTGAGTTATAGGGGTTT	TCACAAGAATAGAAGGATGGA
SCF22477	3	35.34	KP278658	Schlautman et al. (2015)	CTCTCCCCTACTTTCTTCCTAT	GCCGCTAACACAATTAACTAAC
SCF53750	3	35.34	KP278727	Schlautman	GTTTCATAGAGATG	CTTGGTTCCCTAAGCTA

				et al. (2015)	GGTTTCTG	CATT
SCF78184	3	35.34	KP278766	Schlautman et al. (2015)	CACATTTAAGAGCTACCACCTT	GGTGAAAGAGAAGACTGGATT
scf9025	3	36.53		Georgi et al. (2013)	TGGCTCCTATAGCGTGTCCT	GCACACCAGGTTCCTTGATT
SCF7845	3	38.92	KP278620	Schlautman et al. (2015)	GTTCTGACTATTGTGATGGGTT	TGCAATGAATACTGGAAGTG
SCF149145	3	54.52	KP279087	Schlautman et al. (2015)	CTTCAACATATACCCACCCTAT	GACCAAAACTAGAAAACTCCCT
scf5304	3	56.18		Georgi et al. (2013)	TACACAGCTTCATTCGGCAA	AAGCTCACCCAATCGAAAGA
SCF85773	3	58.58	KP278780	Schlautman et al. (2015)	TCTTGAACACAGCACAACAT	ATAAGTTTGCCCCTTTTGTC
scaffold_13275	3	60.96		Herein	AGGAAGAGTGATATTAGCGGT	GAGTATGTGTTTTGGTTGTGG
scaffold_31246	3	60.96		Herein	GGGATATTACACACACACACAC	AGGAGAGAGAGTACCAGTCTTTT
scf10688	3	60.96		Georgi et al. (2013)	TCACTTTTCTTTCATGCCCC	GTGCTCCCACTAGCCCATAA
scf142e	3	60.96		Georgi et al. (2013)	CTACCGAGCTGGTTGAGGAG	CGAGCGCATAATCATCTTCA
ct155339	3	62.75	KP279140	Schlautman et al. (2015)	AAGTTCCTCTGTTACAAGCTCT	ATGACGAACTCTTCCTCCTTAT
SCF177450	3	62.75	KP278928	Schlautman et al. (2015)	TCTAAAACTCTCCTCTCACCTC	GATAGCAGTGGACTCATGTCT
313711_K70	3	68.63	KP279215	Schlautman et al. (2015)	CGACTTAATCCCTCTCTTTCTA	CTTTACTTTTCCATCTCCCTC
ct89711	3	70.52	KP279102	Schlautman et al. (2015)	CTCCACACCCACAATCTG	CGTCTTATTTTTAGTCACCTGG
SCF157992	3	70.52	KP278904	Schlautman et al. (2015)	TAGGTTTGTCTCTTATCCATCC	GAGTTTGTGATTTCTTAGGAGC
scaffold_19017	3	74.7		Herein	GACTACTCTTGTCTTCGATTGG	GTATCAAAATCTCTCTTGGGC
SCF153094	3	74.7	KP278897	Schlautman et al. (2015)	TGTCATTAGGGTTCCTCAAA	CACCTAGACAACATCGAAACTA
contig480Fb	3	82.61		Georgi et al. (2013)	GATGATGTGGGGCCTAAGAA	CGCATTCGACTCAATGTTGT
1trimcontig443603	3	83.66	KP279251	Schlautman et al. (2015)	TGCACCTCCTCTCTCTCTAA	GGTTATGATGGTGGGAAAG
SCF162565	3	85.17	KP278913	Schlautman et al. (2015)	CTTCCGTGATTGTTCTTGTAG	ACACAGATGGGATGTTGTATC
NA172	3	87.55		Georgi et al. (2013)	CCTCGTCCTCCTCTTCCTCT	GTTTGACTTTGGAGAAGGCGAAG
scaffold_35862	3	87.55		Herein	GGAAGATAGAAAACACGACAAG	GATGATTACCCTCCTCTCTCAT
SCF58861	3	88.74	KP278738	Schlautman et al. (2015)	GTTGACTAAAAGGCATTGGA	GACTACTATTTTCTGCACAGGG
SCF27510	3	92.4	KP278670	Schlautman et al. (2015)	CCTTCAGATTCAACGTATTCTC	GGTGTATCACATCCCAAAAC
418294_K63	4	0	KP279189	Schlautman et al. (2015)	CAAGAACAAGAAGAAGAAGACC	AGAGACCACCCAAAAGATAAG
SCF56561	4	0	KP278732	Schlautman et al. (2015)	ATTAGCCATTCGTGATTAGG	TAAGGAGATACGACCAAGAAAC
1trimcontig176303	4	0.59	KP279222	Schlautman et al. (2015)	GCTGATTAGGTTCACTTTCTTC	TTTCTTCACCTCTTTCTCTCTC
SCF26697	4	0.59	KP278669	Schlautman et al. (2015)	TCGTAACTATTCAGTGGGTGT	GGAGCAGTAGAGATTAAACGAC
2ms4d10b	4	1.19		Georgi et al. (2013)	GGAAACGATGCCGTTTTCTA	CAACCCTTCCAGGTCAAAAA

ct119523	4	1.19	KP279114	Schlautman et al. (2015)	GACTCATGGGAGTGAGGAC	TGAACTTGTGTAGTCTTTACCG
ct94504	4	1.19	KP279105	Schlautman et al. (2015)	CTCTAAAGCTCAAGAAAACGTC	AGCTGTGACTATAAGGGATTTG
GVC-V24d10b	4	1.19		Blueberry Markers	GGAAACGATGCCGTTTTCTA	CAACCCTTCCAGGTCAAAAA
SCF83036	4	1.34	KP278776	Schlautman et al. (2015)	CAACAGTCCTCAAAATCACTC	GTGAACAGAAGTAGAGATCGG
scf105g	4	2.39		Georgi et al. (2013)	TCTGTACCTCCCCATTCCTG	CCAAACACGCCGTTAATCTT
vm83024	4	4.18	JF834247	Zhu et al. (2012)	TTCGCCTCTCTAGTTTCTAGTC	GTTATATTACCACAAGCACACG
SCF162175	4	7.16	KP278912	Schlautman et al. (2015)	ACACGTTGAGGTTCCAAAT	AGTTTCTGATTGACCTAGATGG
SCF9157	4	7.16	KP278626	Schlautman et al. (2015)	GGCTTAACAAATTAGCCCTT	GAGAGGATTTACCGACAAAGTA
scf1172	4	10.82		Georgi et al. (2013)	GGGGTTTGTGTGTTTATCGC	GTATGCGAATTCAAAGCCGT
416328_K63	4	15.6	KP279185	Schlautman et al. (2015)	GTATGCCCAGAATATCCATTAC	TAGTCACGAGGAAAGCTAAAGT
ct119590	4	15.6	KP279115	Schlautman et al. (2015)	ACATGACATCAATTGCCC	TATCCTACCTCAAAGAGCCTAA
SCF113389	4	17.98	KP278831	Schlautman et al. (2015)	GACATCACTCAAGCAAGATAAA	CCTCGATTCCTCAAGATATG
SCF72229	4	17.98	KP278756	Schlautman et al. (2015)	CAACTTCTACAACCACTCCAC	GATTTATTGTGCTACACTGGTC
5ms2b12	4	18.45		Georgi et al. (2013)	AAAACTGCAACTGGAATCGG	GTCTGCAGGTCACAGGTTCA
CA855F	4	20.23		Boches et al.(2005)	CGCGTGAAAAACGACCTAAT	GTTTACTCGATCCCTCCACCTG
SCF140628	4	20.23	KP278876	Schlautman et al. (2015)	GTGAAATTGGTCAGGTTGAT	GTCGTCATCATCATCTCCTC
SCF46739	4	20.36	KP278716	Schlautman et al. (2015)	ATGTTAGGTGATGCTGTTGTC	CAGGTGCTTATTTTCGTTTC
vm52682	4	23.94	JF834282	Zhu et al. (2012)	CTCAGGTTATCAGGCTTATTTC	CAATTAGTGTGTTCCCAACTC
SCF6530	4	26.79	KP278614	Schlautman et al. (2015)	CCCCAAGTATAATGTGTAAAGG	AGTTCGCATAGAAACTGTAGGA
SCF124075	4	29.33	KP278848	Schlautman et al. (2015)	ATTTTCCCTCCAACCTCTAT	GGTGCAACCAACTAACATAA
scf6955c	4	29.89		Georgi et al. (2013)	ATGCCTGCCATTCATCATTT	TTTCCGTCATTTCGTCCTTC
vm52204	4	29.89	JF834281	Zhu et al. (2012)	CTATATAACAGACGTCCAACCC	GGGTTGTTTCAGACAAGTAAGT
305731_K63	4	32.32	KP279169	Schlautman et al. (2015)	GATTTCTTCGTGTTTCTCTCTC	TGCCTTTCTCTACTCTCTCTTC
scaffold_24341	4	32.32		Herein	CTGTTTCAGGTTAGCATTGAG	GAGTTTTGCAGTAGCTCTAGGT
SCF28100	4	32.32	KP278674	Schlautman et al. (2015)	TAGAAACTAACATGGGAGGTGT	GCACGCTGTATTGATAGAAGAT
scaffold_120214	4	32.91		Herein	GTGGACCTCGACTATCATTATT	TTCAAATACTCCTGCTGACTAC
SCF154541	4	35.64	KP278900	Schlautman et al. (2015)	AGAAAGCACAGTAGGTATGGAG	CAAGAAACCCTAGAGACCAAT
SCF38553	4	39.4	KP278703	Schlautman et al. (2015)	CTTCTGTTTACTCACTTCCACC	ATGGTCCCAAGATACTTTAGC
SCF15845	4	41.47	KP278645	Schlautman et al. (2015)	AGGCTAATGAAGAAGAAGTCTG	GACCAAGACAAGATGAACAAG

SCF194552	4	45.88	KP278944	Schlautman et al. (2015)	CACAGGTGTAGGGTCTTGTT	AAAAGGAGGCAAGGATAGAG
SCF16359	4	56.42	KP278647	Schlautman et al. (2015)	GAAGTGCTTTTCTTTCGTAGAG	AGACAGATTAAGATCCACCTTG
SCF96539	4	56.9	KP278800	Schlautman et al. (2015)	GTAGCATAACCACCTCTTATCC	ATCTTGATGACTGTGTAAGCTG
NA1713	4	59.88		Georgi et al. (2013)	ATTCGCGTATGGAAGGTGAC	CTCACACCACTGTGGCTCAT
SCF100820	4	59.88	KP278804	Schlautman et al. (2015)	GTAATTCCACTTAACCCACTCA	GTTGAAGATAAACCACCTTCC
scaffold_3314	4	62.26		Herein	CAGATTAAGGAAAAGGAGAAGG	AAAGACCAACCTAGTCCACATA
scaffold_51535	4	62.26		Herein	GACCAATCAGAATTAGACAACG	GTTCGTGAAAATAGGAGTACGA
scaffold_5180	4	62.26		Herein	CTCTCTTACTTTCCACTGTTCC	CTCTATCCTCTTCAACACCACT
SCF204979	4	62.26	KP278949	Schlautman et al. (2015)	GGAAAGAGGTAAGAAATGGG	TAAGAGTTCCCACAACCAAA
scf24k	4	62.26	JN230516	Georgi et al. (2013)	ATTGAGCCCCACACTACAGG	AGCCATGGAAATCCAACAAA
SCF79014	4	62.26	KP278767	Schlautman et al. (2015)	TCTCTGTCTCTGTCTCTGTCTG	CCAAATCAAGGTCTGTCTATCT
SCF101064	4	62.31	KP278805	Schlautman et al. (2015)	CATCAGACAGAAAGCAGTTAAG	CCCCAAGTATATTAGCAAACAC
contig600	4	69.82		Georgi et al. (2013)	GCCAAAGCTGGAGAGAGAAA	GACTTCAGCAGCCAACATCA
SCF49598	4	70.59	KP278723	Schlautman et al. (2015)	ATGAGGTTTTCCAACACAAC	TCAGAGGGAAGTACATGAGAAT
SCF108294	4	77.19	KP278818	Schlautman et al. (2015)	GGTAAGATTGAGGTTCTGGTCT	GGTAGAAGCAAGAAGATGCAC
SCF11084	4	77.19	KP278635	Schlautman et al. (2015)	GTTGGCTGAGGTAGCTGATAG	CCTAAAAGGGCTCACAAGTTA
SCF1128	4	77.19	KP278597	Schlautman et al. (2015)	GTTTGTTGTTGTGGTGGTTT	CCTTACTTGACGCTTACTTCAG
SCF46912	4	77.19	KP278719	Schlautman et al. (2015)	GAACAATAAAGAGGCTAGAGGA	CATAGTTGTAGAGAAGATCGGG
SCF53282	4	83.32	KP278726	Schlautman et al. (2015)	GACAATCACATACCCATAACAG	CCACTCTTTCCCTCTATCG
SCF18363	4	84.57	KP278650	Schlautman et al. (2015)	CAAAGACCGCTAGGTTTACA	ACTGCTCACTAGACAAGATCG
SCF145739	4	85.1	KP278886	Schlautman et al. (2015)	AAATCCTCCTGTTTTAGACTCC	CCTCAAGTCATCATTCCCT
281884_K70	4	85.7	KP279207	Schlautman et al. (2015)	TCCACTATCTTTAGAATCCCAC	AGAGGATGGAGTTCCTTGATA
scf26r	4	85.7		Georgi et al. (2013)	ATGATGTTGGATGTGCCTCA	TTCCTCAACAAACCCTCCAC
SCF29560	4	85.7	KP278680	Schlautman et al. (2015)	GTGTGGTGTGGTCTCTACAAT	ACATCTCTTTGGCTGATACTTC
SCF74895	4	85.7	KP278760	Schlautman et al. (2015)	GTACTCCTCTCCGTCTAGCAT	GATTTTATGCGTTAGCTCCA
SCF14119	4	86.35	KP278643	Schlautman et al. (2015)	TAACAGTACAATGCCTAGTTCG	GGATTCTCTTGCTTTGGTATAG
SCF51810	4	86.35	KP278725	Schlautman et al. (2015)	TATTACTCTGTTGCTGCTGTTG	ACTAAACCCTAATGTCCCTTCT
251788_K63	5	0	KP279166	Schlautman et al. (2015)	GATCTTTACCACTCCCCACT	GGATTCTCTGTCCATTGTTG
ct153008	5	0	KP279136	Schlautman et al. (2015)	CTTTCCAAGATCTTCATAGGC	CGACAGTATAATAGCATGGAGA

SCF143318	5	0	KP278883	Schlautman et al. (2015)	CCGTGCTTAAATTCTGTAGTG	TCATCCATAGGAGAACATCC
SCF28613	5	0	KP278677	Schlautman et al. (2015)	CATTCTTCACTCCAACTTCAG	CAAGTCCCATCATCATTTTC
SCF804	5	0	KP278592	Schlautman et al. (2015)	CAGTCAACAGAGAATACACCAC	TTCCCTATGAAAATCCACAC
308839_K70	5	0.29	KP279211	Schlautman et al. (2015)	ATAATGTGTCCAGTCCCTTTC	TTCCTTCCTCAATCCACTC
SCF7132	5	8.58	KP278616	Schlautman et al. (2015)	AAGGGGAAGGACAATAAGAA	AATTTGATGACTGTTGTGGC
ct144370	5	9.77	KP279127	Schlautman et al. (2015)	GTAGGAAAAGTTTGAACCGTC	TCAAAGGTTTCACGTTTCTC
SCF32727	5	12.51	KP278689	Schlautman et al. (2015)	ATGTAACGGTCTCCACTTTCT	TAGTATCTTCGTGGTCAGAGGT
SCF59035	5	15.21	KP278739	Schlautman et al. (2015)	AGATTTTGAACGATGTCTGC	GATCTATCGCTTATCCAGTACG
SCF259	5	23.41	KP278591	Schlautman et al. (2015)	TGACAGTACCAATAGCAGGAC	AACACCCAGTCGTTATACATCT
SCF31208	5	25.19	KP278687	Schlautman et al. (2015)	AACAGCACCACTACAACACTT	AGAGAACAATCGTCTAATCGTC
SCF132595	5	25.48	KP278863	Schlautman et al. (2015)	CAAACAAATCTCAACAACACC	ATTTCAAGATAAGCTCTCCACC
SCF97378	5	31.09	KP278801	Schlautman et al. (2015)	GTAGAGATCGTTGTCGTCATTT	AACATCGTGGTGTATTGGAT
3ms2g09	5	37.05		Georgi et al. (2013)	CCTAAATTGCAGCCACTGGT	ACGGCAAGACAACGTTCATT
vm39030	5	37.05	JF834273	Zhu et al. (2012)	CTGATTACTGAGTCTACTAACACCA	ACAGATTTGTAGTCACGAAGTG
ct98042	5	47.12	KP279108	Schlautman et al. (2015)	CCTTTTAAGTACTTTCCCTTCC	CCCCTCATCTTTATGTGC
scaffold_29411	5	47.12		Herein	TCTTACTGAATGCTCTTAGGGT	CTCATTACATCAGCTTGTTAGC
SCF149976	5	47.12	KP278893	Schlautman et al. (2015)	TATACCCATGTATGTACGCATC	ACTCTAAGCAGGACAATGCTAT
SCF8987	5	47.12	KP278625	Schlautman et al. (2015)	AATCTTTGTCTGAGGTAAGTGG	AACCAGTGTAGTGCAGTTTATG
SCF83615	5	48.65	KP278777	Schlautman et al. (2015)	ATTAGTCGATCTCCTTTTCCTC	AAATTGTAGAGCCAACACTAGG
SCF46751	5	51.89	KP278715	Schlautman et al. (2015)	ACCAGATGAAGAAGAAGAAGC	GCCTCTCATTACCATTACAAAC
SCF101878	5	54.27	KP278807	Schlautman et al. (2015)	GACTCATTGGATACGTGCT	TCTATGTAGCTTTGAAGTGAGG
scf9e	5	58.41		Georgi et al. (2013)	TCACAGCGGAGAAGTTGATG	ATTTGCGAATCAACCCAAAC
SCF9068	5	61.82	KP278624	Schlautman et al. (2015)	AAATCTAGGTAGGAGCAGGTCT	ATGGAGGAGGAGATATGTGAT
1trimcontig237406	5	63.17	KP279230	Schlautman et al. (2015)	TCTTAGGAAAGACGAGAACATC	GAAAGGAAGGTATGCTACAGTT
308812_K70	5	63.17	KP279210	Schlautman et al. (2015)	GAAAGGAAGGTATGCTACAGTT	TCTTAGGAAAGACGAGAACATC
SCF11431	5	63.17	KP278637	Schlautman et al. (2015)	GCTGCTGATTTGTTATGTAGAG	CACTTAGCCCCTTAAACTATTG
SCF88902	5	63.17	KP278785	Schlautman et al. (2015)	GTGTTGTAGGATGAACCGAT	GATTTCCAGCATTTGATCTC
SCF6195	5	68.53	KP278613	Schlautman et al. (2015)	GACTATGAATCTGACGCTCAC	CCAGTAAATACGTGACTAATCG
1trimcontig191066	5	73.72	KP279227	Schlautman et al. (2015)	GATATTAGTCCGGTTTACGAGA	GATACAGGAGTCGAGAATGAAT

vm07778	5	75.97	JF834253	Zhu et al. (2012)	ATATACGTACACTCACGCACAC	GTTAGGTGCATAATAACGGTTG
ct115258	5	79.37	KP279111	Schlautman et al. (2015)	GTTCGTTGTGGAAGTCACAT	CAAAATGAGTGCCAGATAGTG
47166_K70	5	88.31	KP279195	Schlautman et al. (2015)	TATTGAGAGTGTGAGACCGTT	TGGTAAGTATCGTAGGTCCAAT
CA794F	5	88.31		Boches et al.(2005)	CGGTTGTCCCACTTCATCTT	GTTTGAATTTGGCTTCGGATTC
SCF108454	6	0.9	KP278819	Schlautman et al. (2015)	CTAACTAAATGAAGTGTTCCCCT	ATGTCACGCTCTGAAGTTTG
SCF192219	6	0.9	KP278941	Schlautman et al. (2015)	GAATTTTGTCGTTCCAGAGA	AAAAGAAGAAGAGGAATGGC
SCF79620	6	0.9	KP278768	Schlautman et al. (2015)	TAATAGCCCTTATACCTGCACT	GAGCATAGACAGCATACAAAAG
1trimcontig339726	6	2.19	KP279240	Schlautman et al. (2015)	TACTCATGTCGAAGCAATAGAG	CTTTAGCAGAGGAGAAACAAGT
SCF109269	6	2.19	KP278820	Schlautman et al. (2015)	CACTCCTTCCTTATAGATCAGC	AAGTAGAAGAGCAGCACAAGAG
vm31701	6	2.78	JF834268	Zhu et al. (2012)	GTCACTGGTAATGCTATTCTGA	CTTCTTTGTTTCATCTCCCTAC
SCF124927	6	3.02	KP278850	Schlautman et al. (2015)	CGAGTGTCATTAGCAACAGA	TATCACTTTAGATCGAGCAGAC
GVC-V22a02	6	3.38		Blueberry Markers	ACCGCAAGAGAGAGATTCCA	GTTTGATGATCACGGTGGTG
ct92708	6	11.05	KP279103	Schlautman et al. (2015)	CCCTAGATATTTCTGGAACACT	AAGATAGAGAGAGACAAAGGAGG
GVC-V31e03	6	11.05		Blueberry Markers	GGCACCGACGTACCCAC	GGGTGAGTAAAGGACGGTGA
SCF113558	6	11.05	KP278832	Schlautman et al. (2015)	GAGCTTGATCTGGGTATCTTT	CAAAATCAGAATCGACTGC
SCF147117	6	16.85	KP278888	Schlautman et al. (2015)	AGATATGGAGTGGATTAGGTTG	GTTAGAGTGAAATGAGCCCTAT
scf283b	6	16.85		Georgi et al. (2013)	CCCGATCGAAATAAGGAACA	ATTGACGACCCAGACTCCAC
Ig13662a	6	19.74		Georgi et al. (2013)	CATCTAGCCATGCACCATTG	CCAAGTTCGACATTTTCCGT
scf207d	6	19.74		Georgi et al. (2013)	GACACACGTGGTGCACTGTT	GGTTGATCTTAGGAGCTGCG
SCF13711	6	28.08	KP278640	Schlautman et al. (2015)	GACTTCCTTGGTACTTGGTG	ACTTTGAGGGTAGGAGTAAACA
ct188529	6	34.29	KP279148	Schlautman et al. (2015)	TTGCAGAATCAATAGTACCTCC	CCTCATTAGCTATGGTGAAAC
scaffold_63419	6	37.84		Herein	TTTAGTCGTGTGGAGGAAAA	GACATTGAAGAGAGAGGAATTG
1trimcontig344502	6	42.97	KP279241	Schlautman et al. (2015)	TGGAAATGGAAAAGTCTCTG	CACCGTCTACAGTTTAAGAACA
NA824	6	43.53		Boches et al.(2005)	AAATCGTTGGTTTGGCTCTG	GTTTGGGCCGAAAAGAAATCGTAT
314831_K70	6	43.82	KP279219	Schlautman et al. (2015)	ATCTCTCGTGCCTGTCATAC	CTTTTCGATGTCGTACTTGTC
vm53000	6	45.8	JF834283	Zhu et al. (2012)	CTCTCTCTAGCCAAGCAGATAC	AAGATGTGAGGAAGCTAGGAG
scf112c	6	45.88		Georgi et al. (2013)	ATGTGATTCGCGAAGGATTC	GAAATCCGGGGGTGTAAACT
SCF139334	6	47.23	KP278874	Schlautman et al. (2015)	GAGGGTCTAATATCTGGTTTCA	GAGAAAAGATGGAGCAAAAG
412234_K63	6	49.7	KP279182	Schlautman et al. (2015)	GTGCAAGCCGTTTCTTATG	ATCGGAGGTTCCATCATTTA

SCF9909	6	49.79	KP278630	Schlautman et al. (2015)	CGTAGGTGGATTTCTCTACAAT	GGCATCTTATTTATCGTCTCTG
1trimcontig238080	6	51.28	KP279231	Schlautman et al. (2015)	AGGGGTAATCTTCACACACTTA	ACAGGCTCTTCTAATCGTTTC
SCF3427	6	51.28	KP278606	Schlautman et al. (2015)	GCAAGACATCATCACAAACA	CTTATCCCAGTCCTTCAACTTA
SCF22442	6	53.07	KP278657	Schlautman et al. (2015)	ACAAAGAAAGACACTCCATCTC	GTATTTGACTTCCATGACCAC
vm27120	6	55.34	JF834265	Zhu et al. (2012)	AAGGTCTAAGAGTTATACCGCA	GGGCATAAGTTAAGAGAGCTAA
SCF92414	6	58.66	KP278793	Schlautman et al. (2015)	GTTATCCTCCCTTTGATATGTG	AAGAGCAACAAGATGGGTACT
SCF40517	6	66.18	:	Schlautman et al. (2015)	GTAGAATGGCAATAGGGTTT	GAAGAAGATGACGAAGATCAC
319429_K63	6	66.77	KP279171	Schlautman et al. (2015)	GGAGATAGGAAGTGTGATGAAC	TTATTGTGCAAGCATACGAG
SCF133376	6	68.59	KP278865	Schlautman et al. (2015)	ATTAGCACCGAATTTAACACC	GATTATGGGTGAGTCTGTGAAT
SCF89801	6	69.16	KP278790	Schlautman et al. (2015)	TAAACCTGTTCCGTCTCTTAGT	CTTTACTGTTGTGTTGTCTGCT
ct154615	6	70.35	KP279138	Schlautman et al. (2015)	AAAATTGAGCACTGGCTAAG	CTCATACAAACAATAGGGGG
scaffold_4374	6	70.35		Herein	TCACTCAACACCAACACTAAAC	CATTGTTTTCCCTATCTCTCTC
scf17d	6	70.35		Georgi et al. (2013)	TCGCTTGAAGCTTACCGAAT	AGAACGAACACCTCGGTCAC
SCF31172	6	70.35	KP278686	Schlautman et al. (2015)	ACTGGATCTGGTGTTATTTACC	GGCTGGAAACAATTCAAAC
SCF16407	6	73.28	KP278648	Schlautman et al. (2015)	GGCAGTGAATTAAAGGTCAAC	GATGAGAAAGAAGAGTAAGGCA
SCF171621	6	74.47	KP278919	Schlautman et al. (2015)	CACCACTCCCCATTTTAAG	AAGGGACAGAGGAAGTATTTG
SCF89447	6	74.47	KP278787	Schlautman et al. (2015)	TAAATAAGACCTTCTGCTGACC	AATATGCTCACCACCAGTAAAG
SCF25446	6	79.54	KP278665	Schlautman et al. (2015)	TAGTGTGGACTTAACATGGAGA	ATCCAACCAAGTATCAGCAA
contig652	6	80.75		Georgi et al. (2013)	AAAACTGTCGGCAGATCCTC	GGGATACCAATGTGGGTCAG
Pr031818823	6	83.12		Blueberry Markers	AATCTCTGTCGCCCATTTTG	TTCCCCTGCTTCTGCTGTT
SCF164915	6	83.12	KP278915	Schlautman et al. (2015)	CTCAAAGTATCTCACTCACGC	ACTGTTGTCCCCTCTGACTAC
SCF54555	6	83.12	KP279025	Schlautman et al. (2015)	TTACCAAAGCACCCATTAAC	ACGACACATATCTCCAAAGTG
scf44a	6	87.4		Georgi et al. (2013)	ACAAAACCACTGGCGAAAAC	GAGTGACCAGGGGAGATGAA
SCF126708	6	87.61	KP278854	Schlautman et al. (2015)	CGACGAATAAACAAATCAAGTA	GAGAAGAAGTGAAGGAGAGTTG
16720_K63	6	88.38	KP279159	Schlautman et al. (2015)	CTACCTTTCCCTCTCCTTGT	AGTTGAAGCTGAGAATTGTACC
ct139553	7	0	KP279125	Schlautman et al. (2015)	GATCAAGCATTGTTCTCTTCC	AGCTATAGGGCTAGCGATG
scf1594	7	0		Georgi et al. (2013)	ATGCGAATGGAGAAATCTGG	ATACCGCAAATGGAGTCTGC
scf2s	7	2.38		Georgi et al. (2013)	TGAGACGTACGCACTAGCCA	GTCGATGGTGTTTGTCGATG
scaffold_11617	7	4.76		Herein	TCTCTCTTCTCTCTCACTTTCC	TATCCGCTATCTCATCCTTTAG

scaffold_20967	7	4.76		Herein	TTCGTTTTAGAGAGAGAAGG	GGAAGCAGTGAATATGGAGTAT
SCF56717	7	7.16	KP278733	Schlautman et al. (2015)	GTGTTTGTGTTTGTGTCTGTG	GATGATTTCACCTACATCGG
SCF2483	7	11.64	KP278601	Schlautman et al. (2015)	TTTCCTTCATAGTGTTGCCT	GTCTCCCTGTTAAATCCACTC
SCF25944	7	11.64	KP278666	Schlautman et al. (2015)	AACTATGCCAGAAGACTCAGAT	CTTCACAAATCACAACCACTAC
1trimcontig435620	7	12.29	KP279244	Schlautman et al. (2015)	CAACCAGCCTTACAGTGAATA	GTCCGTTCAATTTCTTTTCC
6ms4e4b	7	15.75		Georgi et al. (2013)	GGCCAAGGTTCTACCCTTTC	CAACTACCCACCACCACCAT
SCF20681	7	16.77	KP278653	Schlautman et al. (2015)	AGCCTAAACCTCTGTTTGATG	TTACAATACCTCGCTCCTTAGA
SCF36745	7	16.77	KP278698	Schlautman et al. (2015)	TCCTCATTAAGTATTGGACAGG	CTGGATTCTTGTTCTTAGCTTC
scf137c	7	19.56		Georgi et al. (2013)	CTCCGGGAACTCTCCATACA	CTTCGTTGTGAACGCAAAAG
SCF7155	7	19.78	KP278617	Schlautman et al. (2015)	GGGATCTATGAGTTGTGGACTA	CCACGGAATAGTTGTAAGTTGT
SCF89247	7	21.95	KP278786	Schlautman et al. (2015)	TGGAGGAGGTGAAGAATACTAA	CCCTTTGGACAACAAAATAC
scf31h	7	24.33		Georgi et al. (2013)	TGGAACTCCAAATGTGCGTA	TGGCACCATAAATAGCACGA
SCF25221	7	25.82	KP278664	Schlautman et al. (2015)	GTATCCCCACACTTACCACTAT	AGGATTGGACGGTAGCTTA
SCF85946	7	29.45	KP278781	Schlautman et al. (2015)	TGTGAACAGAACCTACCACTAA	AAAGAGCCCCGTAGATAGAT
SCF184873	7	32.42	KP278934	Schlautman et al. (2015)	AAGCGTAGAATATGTATGACCC	GGTAGTCCTCACGGAAGAG
SCF116864	7	32.73	KP278836	Schlautman et al. (2015)	TGCCCCTTGATTCTAATTTT	ATGCCTCAGATTGATTTACCT
SCF112540	7	34.8	KP278830	Schlautman et al. (2015)	CAGTAGTGGTATTTCACAATCG	TTTAATGCTTTTGGAAGAGG
SCF111145	7	35.19	KP278827	Schlautman et al. (2015)	TTAGTCTGGCTGGTTTTAGTTT	TTGTACCTATTGTTGGATTGTG
80734_K70	7	41.83	KP279198	Schlautman et al. (2015)	AGGGAGAACCAATTCCTTAC	GACCTAACCCTAACCCAGTC
ct145906	7	41.83	KP279132	Schlautman et al. (2015)	TCTAGACTTGAGAAGCACTTTG	AGTTAGAGGAGGTTTCTGTTGA
SCF94237	7	41.83	KP278795	Schlautman et al. (2015)	ATCGCATCAGGTAAGCTAGTAT	TCGAGTGTCATTGTAATAGGC
1trimcontig217158	7	44.8	KP279229	Schlautman et al. (2015)	GGAGTCGGTAAAATCAAGAA	CCAAATTCAGTAGGAGTACACA
76326_K70	7	49.58	KP279197	Schlautman et al. (2015)	AATGTCTTCCAAATCAGGTG	CAAGAACGAACCCTCTATTTC
SCF34513	7	49.58	KP278695	Schlautman et al. (2015)	TACTAATCTTCTGGTTTGGGC	GTACACCACTCCTGATGGC
409618_K63	7	50.01	KP279178	Schlautman et al. (2015)	CTTCTCCTTCCCTTCACTTTA	TTAGTGTTAGTGTTGGTGTTGG
SCF13006	7	50.21	KP278639	Schlautman et al. (2015)	AAAACATAAGAAAGAGCCCC	GGATGATGATGTATGGGAAT
SCF72379	7	51.93	KP278757	Schlautman et al. (2015)	TAAGGAGATCGACTAGGGTTT	CATCAAGATTCAAGACCACAC
SCF34010	7	52.2	KP278693	Schlautman et al. (2015)	GAGAATATGTGATGTTGAGGTG	CAAGTGTTAGGCTCGTTTAGTT
ct147864	7	52.4	KP279133	Schlautman et al. (2015)	CTCTCTTTACCCTCAATTTCTC	GGTCTAATATCAATCGATGACC

SCF137494	7	52.4	KP278869	Schlautman et al. (2015)	CCAACATAAAGAGGACTAGAGG	GACCTAGACTCCAAATCACG
ct145217	7	54.32	KP279131	Schlautman et al. (2015)	CCAGTACTAGATCCACTGCATA	TGTTCTAGAGAGGATGACATTG
SCF208883	7	54.35	KP278952	Schlautman et al. (2015)	GAGGAGTGAAGAGCCAGTAA	GACATTTCAAGTCCCACACT
SCF9872	7	54.35	KP278629	Schlautman et al. (2015)	ATGGGAGTGCATGAATAAAC	GGAGAATCGTATTTGTGAAGAG
SCF138014	7	56.06	KP278870	Schlautman et al. (2015)	TTATTCTCTTCGCTTGGGTA	TCAGATCATGGATTACTGGTT
300409_K63	7	56.13	KP279168	Schlautman et al. (2015)	GGGGAATAGCAGGTAGTGAT	TATTTATCCACCCACTTCACAG
1trimcontig337780	7	59	KP279239	Schlautman et al. (2015)	CTTGATCTTGTCGCTGTAGAC	CTGAGCATCTCTCCTTTATCTC
311291_K70	7	59	KP279214	Schlautman et al. (2015)	CTTGATCTTGTCGCTGTAGAC	TTCCTTATCGAAATCACGAG
SCF4305	7	59	KP278611	Schlautman et al. (2015)	AATGAGTGGTTATGTAGGGAGA	AGATTGGTGAGATATGAGGAAG
SCF128015	7	62.02	KP278856	Schlautman et al. (2015)	ACCCACTCTTTCTATTATCTTCC	GTGAGTTCCAAGTTCCACATA
NA1792	7	64.37		Georgi et al. (2013)	GCATCATCGCCGTCAAG	TTGACTTCATCGAAAGCACG
ct95345	7	64.69	KP279106	Schlautman et al. (2015)	ACTCTACAAGGGCACGAAC	ATGGAAGTAAGAAAGTGAGTGG
SCF128307	7	65.87	KP278857	Schlautman et al. (2015)	ACTCAGAAGTTGAAGCACAAA	GTATCAAGTACACCAACACCAG
SCF193103	7	67.35	KP278943	Schlautman et al. (2015)	GAGGAGTTGAAACAATTAGTCC	TACCCACTTTAGTCGAAGGAT
SCF110168	7	68.54	KP278822	Schlautman et al. (2015)	AAAGGACTAGAGGGAAGTACAAC	CTTATTATCCAGAAACTCGTGC
scf5k	7	70.33		Georgi et al. (2013)	GCATTACTAACAGCATCCCAA	GAGCCACTTTTCACTCCCAA
SCF187979	7	76.89	KP278935	Schlautman et al. (2015)	AGATAAGGCACCCGATAATAC	GATCAAGGAACGCAAATCT
419834_K63	7	77.73	KP279192	Schlautman et al. (2015)	GAAAAGAGAGGAGAAGATGGAT	TACCAGAACTGTGTGAGATTGT
SCF167793	7	79.27	KP278916	Schlautman et al. (2015)	GTGAAACGACAAGACCAAAT	AGGACATCCACCTTCAAAT
SCF915	7	80.46	KP278593	Schlautman et al. (2015)	TTAGGGTTTGGAGTACCTGA	ACTACCGTCTTTCTTTATAGCC
Ig51a	7	85.62		Georgi et al. (2013)	TTGGTGCAAGATCACCACAT	GCACAAACGGATGTAGCAGA
SCF46824	7	89.89	KP278717	Schlautman et al. (2015)	GGAGATGCTGTAATAACGAAGT	TTAGTCAATATGCGTGCAAC
SCF10514	7	90.38	KP278632	Schlautman et al. (2015)	GTACTCTTTGTCGGATGTTTTC	GTTTCACTCCCACCTCTTAAT
SCF155637	7	90.38	KP278901	Schlautman et al. (2015)	TGTTAGTGTTAGGACCCGTTA	AAAGTAGGAGTTAGGATGGGAT
1trimcontig450309	7	90.7	KP279253	Schlautman et al. (2015)	AAAATCAGAGGGAAGAAAGC	TATTAGCCAGTCCTCCTTTGTA
scf203h	7	95.5		Georgi et al. (2013)	AAGTTACAACGGTTCGTGGC	TGCAACATTGTGATGGTCCT
ct121951	8	0	KP279117	Schlautman et al. (2015)	CATGTAGCCGACTCCAATTA	TATCCCATTCCGTATAAGGTC
2ms2g09	8	1.78		Georgi et al. (2013)	GGGGAACTCAGATGGGTTTT	GCTGTCATTTTTCGGAGAGC
scf1p	8	1.78		Georgi et	AGAGTTGCCTCGAAGTAGCG	TGGGTGTGCTGAG

				al. (2013)		
1trimcontig440337	8	1.79	KP279250	Schlautman et al. (2015)	CTTGGAGTTAGCCTTTTAGTCA	CTGGAAGAGTGAAGATGGAATA
SCF10785	8	1.79	KP278633	Schlautman et al. (2015)	ACATAAAGGAGAGGGAGTAGAG	ATACCACTTGATAGATTCCTCC
vm28527	8	1.79	JF834266	Zhu et al. (2012)	GGACAAGTGAAATGCTAGTTG	AGATTGTTCGTAGGTAGAAGTG
KAN-11325	8	2.38		Blueberry Markers	CAACATTCCCGAAAACCAGT	ACCCTTCACCTGACACCATC
SCF102538	8	2.38	KP279056	Schlautman et al. (2015)	TTACTGGGCAATAGAAGGACT	CACATAAGTTTGGCTACACAAC
vm31502	8	5.31	JF834267	Zhu et al. (2012)	TTCTTTTGTCCACCTTGAGT	TCTCTTCACTTATTACACCTGC
1trimcontig326802	8	6.5	KP279235	Schlautman et al. (2015)	TTTTCAGAGCAAGAGGAAAG	CTGTCTGTATCATGGAACTCAT
SCF91821	8	6.5	KP278792	Schlautman et al. (2015)	TTCTGTGTCTGATTCCATCTC	ACTAGCCCAACAACTTAGACTG
scf2505a	8	10.91		Georgi et al. (2013)	CCAGAGAGAAGGGGGAAATC	TTATCCCGCCGCTTAGTAGA
SCF107477	8	14.65	KP278814	Schlautman et al. (2015)	GTCTTATTTTCACTGTCGTGTG	CGGGCATTAACCTTATACCT
scaffold_37046	8	17.03		Herein	AACACATCTCTTATTACTCGCC	CCTCCTCTCTTGAAAACATCT
scaffold_54259	8	17.03		Herein	ATAAGTTGGGCTAGTAAAGGG	GATGGTCCCCTAAGAATATAGA
SCF71136	8	17.46	KP278753	Schlautman et al. (2015)	TCTGTTTTCACAGCTATCACAC	GTTCATCAAAGGCCAGAGT
36394_K70	8	20.98	KP279271	Schlautman et al. (2015)	CAGTGTTTGTTGCTTGGTC	ATCTCACTCTCTGTTTCCCTC
SCF8850	8	25.19	KP278623	Schlautman et al. (2015)	GTGTGATGTATTTAAGGAGTACCAC	ACAGATAGAGTAGTTACCAAGGGA
SCF92564	8	28.75	KP278794	Schlautman et al. (2015)	TCATAACTCCCTCGTAATCAAG	AGGAAGAAGAGAATAAGGTTGG
SCF77645	8	36.23		Herein	GGTTCTTTCTTCTGGGTTTT	TCAGACAATGAGCTACTACCCT
418192_K63	8	39.74	KP279266	Schlautman et al. (2015)	CAGGCAGAAGAAGAAAGAAA	TGAATTAAGAGAGGAGGAGAGA
260167_K70	8	41.09		Herein	TCAACATCTTTGGGACTTCT	GCTTGCCTAATATACTTCCAAC
314797_K70	8	41.09	KP279218	Schlautman et al. (2015)	CTTGTTCTCCTCCTTTAGTCTG	CATCTTCATACTCCTATTGTCG
SCF27811	8	41.09	KP278672	Schlautman et al. (2015)	ATGTGACTAGCATGGGACTTA	TATTTACCTGGATAGGAGAAGG
SCF71184	8	43.47	KP278754	Schlautman et al. (2015)	TCTGTTCAGTTGGGCTTTAT	GCTCACATTCACCTGTAATTC
187382_K70	8	46.38	KP279202	Schlautman et al. (2015)	CCTCCATTCTCTCTCCTACTAA	CTTCTTCTCTCTCTC
ct159707	8	51.74	KP279142	Schlautman et al. (2015)	TGTTAGCTCCTTACTTTCCATC	GTGAAGAGGAAGATGAAGAATG
scaffold_50168	8	51.74		Herein	CGTTCCAAAATAAGCGTCT	CATCTGCCTAATATAACTGGGT
scaffold_48237	8	51.81		Herein	CTCTCTGCTGTTTTCATCAAC	GCTATTAAGGAAGGGTCAAAC
SCF197903	8	51.81	KP278945	Schlautman et al. (2015)	TCTCGTGAGCGTTACAATATAC	ATGGAGTCAAGGTAAACCG
ct134336	8	52.33	KP279123	Schlautman et al. (2015)	GAACACTCCTTCTCTAGCTCTG	CTTTTTAGTCTCCGACAATCTC
SCF142767	8	52.33		Herein	ATAGTTGGACGGGTGTAATG	CTCTCGCAAAGTAGAACAATCT
SCF19565	8	52.33	KP278652	Schlautman	GGGTTTTATGAGTTA	GTAGCGATGGTCTT

				et al. (2015)	GAGTCCC	
scf4860	8	52.93		Georgi et al. (2013)	TTCGCTCAAGTCAACTGTGG	CCTTGGACATTTTTCTGGGA
SCF64632	8	52.93	KP278746	Schlautman et al. (2015)	ACCTCCTAAAACACAACCCTA	CTGAGTAATCTTCGATGTGAGA
SCF82870	8	52.93	KP278775	Schlautman et al. (2015)	GCTAAAGAACGAACAACAAC	GTCCAACGAGTGAGTAGAGAAG
SCF127023	8	54.64	KP278855	Schlautman et al. (2015)	TATGCTAATCCACTTTGTAGGG	AATCTGGGTAATTGGGAACT
SCF54155	8	54.64	KP278728	Schlautman et al. (2015)	TCGAAGAAAATGAAGGGAC	ACAAATGGAGAGGAAAGTGTAG
SCF87990	8	58.84	KP278783	Schlautman et al. (2015)	GTGTAGGTGTAAATGTGCTTTG	GGCGTATAAAAGGATTCAAG
SCF30010	8	58.86	KP278683	Schlautman et al. (2015)	CTCAAATCAACGATCAAGAC	GAAAGAGACAACAAAACCCT
SCF2714	8	60.93	KP278602	Schlautman et al. (2015)	ACAAGTCTCTGGAAGCTAACAT	GTTGATTGTTGGGTCTAAGTTC
SCF189612	8	62.21	KP278936	Schlautman et al. (2015)	GAGGATTGTTAATGGTTTCTTT	TACGCTTCATCTTGTTATTTTC
Pr031818828	8	64.22		Blueberry Markers	TCGTTCTATTCCTCCCGAAT	ATAGAAACTCGCCGTCTCCT
vm13884	8	64.22		Zhu et al. (2012)	TAAAGCTATGTATGAGCCGATG	GTTTTGGCAAATAGACTATCCC
SCF17979	8	66	KP278649	Schlautman et al. (2015)	ATATCAGAACAAGGAGATGGTG	GATACCGAATGAACCAAGAA
411348_K63	8	69.16	KP279180	Schlautman et al. (2015)	AATTACCAATGTTCACTCCG	GTTGATGTAGTTCTGTGGTTGA
SCF105925	8	70.35	KP278812	Schlautman et al. (2015)	CCGTGTCAAAAGATCAAGC	AGTTTGTGCCGTCGTACTC
SCF172149	8	76.65	KP278922	Schlautman et al. (2015)	GTTAAATGATGCTGTTAGGGAG	ATGTCCAGTCGTTATCTCTAGG
SCF81732	8	80.22	KP278772	Schlautman et al. (2015)	CGAGTATGTGGAGAGGCTTAC	GTGTATAAAATGGGCATCACAC
SCF132922	8	81.37	KP278864	Schlautman et al. (2015)	TTAGACGCTTTATGTCCATTC	GAGTGTCCTTGTCTTTGTTGTA
ct89379	8	84.69	KP279101	Schlautman et al. (2015)	ATGAAGAGCTTGAATGGCTA	ACACTTTACACCACAACTCGTA
Ig6523b	8	84.69		Georgi et al. (2013)	CCATCTACCACGGCAGAGAT	GCATATTTTGGTTGGATCGG
SCF138992	8	84.69	KP278873	Schlautman et al. (2015)	ATACTTTACCCCACAGAGCTTA	CCACTCATGCTCACATCAC
SCF24087	8	84.69	KP278663	Schlautman et al. (2015)	GTCCCTTTCTCGTGTCTTTAT	GAGTAGTGACGATGCAACTAGA
1trimcontig328266	9	1.13	KP279236	Schlautman et al. (2015)	ACAGATCAAGCGAACACTAAAC	CCTGCTCCTGTTATACTACCAA
SCF3932	9	1.13	KP278610	Schlautman et al. (2015)	CAGAGTTTCAGTGGAGCATT	CTCAGCTTCTGTGTTTTGTGT
scf45d	9	1.13		Georgi et al. (2013)	TTCTTGTGGTTGTGCTGCAT	TAATGGCTGAAACGCTCACA
SCF125251	9	3.37	KP278851	Schlautman et al. (2015)	TATACAGTCAGATCCAATCCAC	TGCAGATAAAGTACAAGAGTGC
SCF61189	9	3.37	KP278744	Schlautman et al. (2015)	GCCATAACTCTCACTCAAATCT	ACCTATTCACCTACATCCAAAG
scf55c	9	4.55		Georgi et al. (2013)	AGCCATTGATCTCCAACCAC	GCGTTTCAATCTTTGGCAAT
1trimcontig439861	9	7.53	KP279247	Schlautman et al. (2015)	CTCCTCTCTCGAATGACACTAC	TTCTTGTTGGCTGGAGATTA

SCF132532	9	7.53	KP278861	Schlautman et al. (2015)	GACTGGATTTTCACGAATCTAC	CTTCATCTTCCTTGACACTTCT
scf32j	9	8.81		Georgi et al. (2013)	ATCCACCAAACAAGCCACAT	TCAATCAACGCGATTCCATA
SCF11802	9	11.64	KP278638	Schlautman et al. (2015)	CGAGGAACAAGTTTTATAGGAG	ACACTCACCTTTATTATGGGAC
SCF33185	9	11.64	KP278691	Schlautman et al. (2015)	AGCACACTACAGACAGGGTAAT	GTTTTGGCTCTGGCTAAGTAT
SCF132369	9	12.24	KP278860	Schlautman et al. (2015)	CTACTTTGGGATGGAGAGAGTA	AGGTTTAGGTAGTGTTGGATTG
SCF136317	9	12.24	KP278867	Schlautman et al. (2015)	GAGAGTTCAAATTACCTGTACCA	GGAGATTAGGTTGTGGACTAGA
SCF144748	9	12.24	KP278884	Schlautman et al. (2015)	ATTTCCAATCCTTTCCTCTC	CTCTGACACCTTCTGACACATA
scf306f	9	13.31		Georgi et al. (2013)	GGGCAAGGATAAAGGGTTGT	TGCATGCAACTTCCTAGTCCT
ct95842	9	13.66	KP279107	Schlautman et al. (2015)	GTGGAAAGAGATTGTTGATGTC	AAAACTAATGGATGACGACG
1trimcontig238343	9	21.73	KP279232	Schlautman et al. (2015)	GGTAATAGCTTTGTGATCTTGC	GATGGTGAATAAATTGCGAC
214102_K63	9	21.73	KP279165	Schlautman et al. (2015)	GGTAATAGCTTTGTGATCTTGC	GGGTAAAATGACTGCCAAC
SCF141985	9	21.73	KP278878	Schlautman et al. (2015)	GAATGGTCTTGAGGGATGTAT	ACTCTGGAAGAAATAAAACGG
SCF1648	9	25.15	KP278599	Schlautman et al. (2015)	GTTGATCTGAAGGAAACCAA	TCGTATTAACTCCCCTATTGAC
SCF88396	9	30.92	KP278784	Schlautman et al. (2015)	ATAGAGGTTAATTGGTCCTCG	GACGAAGAACGACAGGTAGAT
scf21n	9	31.29		Georgi et al. (2013)	ACCAATTCCCTCCCAAGTTC	CCCTGGATATTTGCTTGCAT
Pr031818814	9	32.8		Blueberry Markers	CTCACCCATCCTTCTCCTCT	CGGTGTTGATGTCATGCTT
Ig1296a	9	37.47		Georgi et al. (2013)	CCCCTGAATTCTTGTTCCAA	GAGTGGAAAACGCAGTGGAT
SCF136207	9	37.47	KP278866	Schlautman et al. (2015)	GTCTCTGTAGTCGGTGCTTT	GATTTCGATTCCTTGACACT
SCF48414	9	37.47	KP278721	Schlautman et al. (2015)	GTAGGGAAACAAGAATTGGAC	ACTGTGAGATTGGTGTGATATG
SCF56032	9	38.06	KP278731	Schlautman et al. (2015)	AGAAATGGCGCTCTGTATC	GAACAGTCTCATCTTCACGAC
scf6i	9	38.06		Georgi et al. (2013)	TTGTTTGGTGCTACGAGTGC	GGCCTGAACTTTCCTGACTG
SCF118468	9	44.63	KP278840	Schlautman et al. (2015)	ATAAGCGGAGCACAGTTACA	GATAGGATGACCTGTTTTGGT
SCF10459	9	47.18	KP278631	Schlautman et al. (2015)	TCTTTGTTTCTGAGGTTGCT	ATTTGTAGGTACTATGGAAGCC
scf275d	9	47.18		Georgi et al. (2013)	GCTTTTCTGAAGCGATTTGC	CCGCATACACGGCGTACTA
scf13a	9	56.29		Georgi et al. (2013)	TAGAGGGCGTTGAAAGGAGA	CCCCAAATTTCTCCCCATTA
309124_K70	9	56.79	KP279213	Schlautman et al. (2015)	AAAGGTCGTTAAGGCTATCAG	TGATGACTGCGATATGTACTCT
scf35k	9	57.18		Georgi et al. (2013)	TCACCTTAAACCCTGGCTTG	GTGGAGATGGATAGCTTGGG
NA619	9	59.09		Georgi et al. (2013)	TCACACTACAGGCAGGAGAGA	GAAGCCCCAGTTCTCACAAG
scf439	9	62.74		Georgi et	TTGTGTGATCCGCTACTTGG	ATCGTTCAAAACGAAGGGTG

				al. (2013)		
SCF7357	9	62.74	KP278618	Schlautman et al. (2015)	CAGCTTAATCATCAG TTCCAG	AGTGAGCATCGACTATT TACCT
SCF155797	9	71.69	KP278902	Schlautman et al. (2015)	ATCATTAAGGCTCCC AAAG	GTACGTCTACTCTGACG GCTA
SCF30734	9	75.17	KP278684	Schlautman et al. (2015)	GTTGAAAACCCAACT GTGAG	AGATCCAGTCATGGTAC TTTTG
VCC_J9	9	75.26		Boches et al.(2005)	GCGAAGAACTTCCGT CAAAA	GTGAGGGCACAAAGCT CTC
ct154206	9	80.04	KP279137	Schlautman et al. (2015)	GAGAGCGTACGATA CCTAATTC	CTGGTTAGGAAAACCAC TAGAA
1trimcontig352078	9	87.09	KP279243	Schlautman et al. (2015)	CGTGTTTCTGTTAGA TAGCTTG	CTTGTACGTGAAGATGC AAA
407841_K63	9	87.09	KP279175	Schlautman et al. (2015)	TTGAGTAGATACATG CTGGCT	CTCACCCTTTCTCTTGTG ATA
ct144558	9	87.09	KP279128	Schlautman et al. (2015)	TCATTACCCCTAACCT CTAAAC	ATTCGACTAGAGTGGAG AGAAA
KAN-11281	9	87.09		Blueberry Markers	GGGGTAACATTGAC CATTCG	AAATCCCTCAATCCAAA GGG
SCF109660	9	87.09	KP278821	Schlautman et al. (2015)	CCCCAAACTGTCGTA TAAAA	TAGAGTACAGGAAAAG CCCTAA
SIZ1	9	87.09		Blueberry Markers	ATTGCAATCTTGCAC AGAGAGA	CTACATAGGATACGCAT TGGCA
ct154654	9	87.34	KP279139	Herein	GATTTCTAGTGGGA AATGAAGG	GGTGTATGTGTGTGATT AAGGA
SCF191642	9	87.38	KP278939	Schlautman et al. (2015)	CTACATCCACTAAAT ATCAAGGC	GATCAAGCCAAAGGAA GAA
SCF125889	9	87.94	KP278853	Schlautman et al. (2015)	TCTCGTGTATTTTGG AGTGA	GTTGTATCCTTTGTCGA TTCT
SCF163134	9	88.51	KP278914	Schlautman et al. (2015)	CAGTGCAATTAGTTT CCTATCC	TTCTTGGGTTGGTTATT CAG
scf1655c	9	88.51		Georgi et al. (2013)	CATCTATTGATCAGC CGCAA	ACGACCATATGAGCCGA GTT
SCF41971	9	88.51	KP278709	Schlautman et al. (2015)	ATACTTGACCTCTAT GGCTTGA	GTACTTACGTGTTTGGT TCGTT
contig259Fb	9	89.86		Georgi et al. (2013)	TTGCTGAAGCCCTAA GCAGT	AAACCAGATCTGTTGGA CGC
SCF22993	10	0	KP278994	Schlautman et al. (2015)	GACTGTGCGTAGAC TTGATCT	AAGTATGTGTAGGCCGA AAA
ct93137	10	2.96	KP279104	Schlautman et al. (2015)	AAGATTTCCGCTACA GTACCT	GCTATGGGTGTCTCAAA AAG
SCF56747	10	2.96	KP278734	Schlautman et al. (2015)	TTAGAGAAAGGTCCC AACAG	GAAGAGGCTAAGAGGT CATGT
364103_K63	10	2.99	KP279173	Schlautman et al. (2015)	TACAAACCCTAAGCT CTAAACC	CGACTTGAGTGATACCA AAGA
ct161908	10	2.99	KP279144	Schlautman et al. (2015)	CCTAGGAGATGGGT CAAGAT	ACCACTGTCTTCCATATT CACT
SCF105151	10	2.99	KP278811	Schlautman et al. (2015)	CAGAATAAGATTGG GTAGAAGG	TTTGAGAATTACTTGGC ACC
SCF120352	10	2.99	KP278843	Schlautman et al. (2015)	AGTTCTATGACCCCT AACTGAA	GAAAGGAAAGAAGCAC TATCAC
SCF46833	10	2.99	KP278718	Schlautman et al. (2015)	GGACCGCCGTATTTA GTTA	GCCCATACCCCTAGTTA TTG
SCF23210	10	3.59	KP278660	Schlautman et al. (2015)	TTGATACTCTCGACC TCTTCTT	GTGGTGTTCGACATGAT TTAC
SCF26014	10	4.18	KP278667	Schlautman et al. (2015)	GGTCCCAGAATCAAT GTCTA	GAAATCAGAGAAGAAAC AGGTC
SCF60761	10	4.18	KP278742	Schlautman	ACTTAAACATCGGTC	AGAGTCGTGTCCTTTCT

				et al. (2015)	CATAGAG	TTTC
SCF96311	10	4.18	KP278799	Schlautman et al. (2015)	TGTATAATCTCAGGGGCATT	TTTCTCATTTCCTTCCCAC
SCF2288	10	9.55	KP278600	Schlautman et al. (2015)	CAATAGTAGTTTCGAGCTTTCC	GTTTCCAATTCAAGCCTCTA
SCF86438	10	14.96	KP278782	Schlautman et al. (2015)	CTATTGAAAACAAGGAACGG	CCTATACAACCTCTTCGGATAA
Pr031818817	10	15.56		Blueberry Markers	CGTATTTAGGGATGGAGGGAGT	CGAGGACATCATCTGGCTCT
SCF139660	10	16.15	KP278875	Schlautman et al. (2015)	ATAAATCTACGTCCATACAGCC	GAGTACATACAAATCCTCTTTCG
SCF189657	10	19.72	KP278937	Schlautman et al. (2015)	CATCCTTGAAAATAGACAGACC	CTTAGAAGACCGCACTGAGA
SCF104688	10	21.21	KP278809	Schlautman et al. (2015)	ACAAAGAAATGTATGGCACC	CTTTTCGTCTCCTCTAATTCC
scaffold_84092	10	28.27		Herein	CACAAACAGGCAGATTACTTTC	AACCGAAAACGAGAAATACC
SCF172906	10	31.73	KP278923	Schlautman et al. (2015)	CTGTTCAAGGATTTGTACTGG	TATTGACATGAGAAGCACGA
ct135942	10	31.85	KP279124	Schlautman et al. (2015)	CTACTTGCCTTCCTCTTTGAC	TAAATAATCCGTCCACGAAC
SCF112295	10	34.87	KP278829	Schlautman et al. (2015)	AACATCTCTACCTCTCACGTTT	TAGTATTAGTTGATTTGGCGTG
409500_K63	10	35.42	KP279177	Schlautman et al. (2015)	GATTCCTGGGTGTAGTTCTGT	CTTAGTCTTTAATGCTGGCTCA
vm25796	10	35.42	JF834263	Zhu et al. (2012)	CACTTACCTGAATCCTCTTAGC	TAGAGGAGCCAAACTGATAACT
SCF7569	10	37.25	KP278619	Schlautman et al. (2015)	CCCAATAACGACTCATATACCT	ACCCAGTCAAAATCTCCTTT
313928_K70	10	38.44	KP279216	Schlautman et al. (2015)	CAATTATCAAGGAGGCAATC	TCACAAATGAGGATCTACACAC
SCF146740	10	39.03	KP278887	Schlautman et al. (2015)	ATGGGACTGCTTATTGAACAC	CAAGTGGTGCATTGTGAGA
SCF147295	10	39.03	KP278889	Schlautman et al. (2015)	ACTGAGGTAAAAGAGGAGTACG	CCATCAAGGTCTCAATCTGT
SCF35507	10	39.03	KP278697	Schlautman et al. (2015)	GTCTAATCTAATGCAGAATGCC	AATGTGGACAACGAGTACATCT
SCF36905	10	44.43	KP279011	Schlautman et al. (2015)	GATAAGCTGTGCTGAAACATC	CGATAGGGGATAGAATTAGTCA
vm72062	10	44.99	JF834244	Zhu et al. (2012)	CACCCATAAGAGATAGAACAAG	CTATCAATCATGATCTTCAGCC
71002_K63	10	45.75	KP279161	Schlautman et al. (2015)	CTTCAATCCACGAATACCAC	CAATTATGCAAAGGAGGAAG
SCF107715	10	45.75	KP278816	Schlautman et al. (2015)	AAAGCGAGTCAGAAACATAGAC	CCTATCAGTTCCTTTCCTATTG
SCF189827	10	45.75	KP278938	Schlautman et al. (2015)	TTCATTTCCTTACACTTCCC	GTTAGCTTCTTCTCCTTCTTCA
SCF82535	10	47.54	KP278774	Schlautman et al. (2015)	TAGAAGAGGAAAACTGACGGA	TTGATGCAATCTGACAACG
scaffold_21777	10	50		Herein	GATGCTCTCTCTTTCAATTAGG	TTTAGGTCTTGGGTAGCACTAT
SCF65999	10	50	KP278748	Schlautman et al. (2015)	AGGTAGCATTAGACACGAGATT	GAGGTTTTACATGACCATTACC
SCF80520	10	54.17	KP278769	Herein	TAAAGTGTTTTGGACGGCT	GCACAAATTATCGGAATCG
SCF174394	10	61.46	KP278925	Schlautman et al. (2015)	GGTGGATGGAATGCTAAATA	CTTTATTGGTAGTGGATTGGAC
SCF49656	10	61.46	KP278724	Schlautman	ACTCTTACCCTTGAAACCAACT	TAGGTGCATGAGACTTTTAACC

				et al. (2015)		
SCF150919	10	66.9	KP278896	Schlautman et al. (2015)	TTGTTAGCACTTAGCATAACCC	GCTTCATCTCCACCAATACAT
1trimcontig176861	10	71.39	KP279223	Schlautman et al. (2015)	ATGGATGTATCTTGACAGGC	CTGCTGTTCATTTCTCTGTG
60699_K70	10	71.39	KP279196	Schlautman et al. (2015)	CTTCTCACTGTATTTCTTCGAG	GGCTACTTTGTTAGGGTAGATT
418931_1_K63	10	72.58	KP279191	Schlautman et al. (2015)	ATTAGCTCAGTTCCCAGTAACA	CTTCTTTCTCTTTCTCCTTCCT
scaffold_11771	10	72.58		Herein	GAGATCAGAGAGGAGTAGTTGG	ATAAGGGAGAGTTGGTATAGGA
scaffold_71386	10	72.58		Herein	GAAGTAGCTGGACTGATGTATTC	CTCTCTCTTCCCCTTTTACTCT
vm38401	10	77.28	JF834272	Zhu et al. (2012)	CAATGGGAAGTACAAAGAGC	CGATGCAATCTTAGTCTTGA
SCF201915	10	79.07	KP278947	Schlautman et al. (2015)	ATGCACATCCTGAAGTACCA	CTGAACACATTGGACGGAT
vm12486	10	79.07	JF834257	Zhu et al. (2012)	GGTGGAGATGCTCGTAGTATT	CTAAGGGACGTCAAACCTAAC
ct145170	10	79.75	KP279130	Schlautman et al. (2015)	GAATCCTAGCCTATTTCCTTTG	GAAGCAAACACCACTCAATATC
KAN-11049	10	79.75		Blueberry Markers	CTGGCTCTGTAGACCTTGCC	AACGGATTATACTGCCACGC
SCF84804	11	0	KP278779	Schlautman et al. (2015)	CTAGTCTTCTTGTGACCTAGCC	TATTCTTTTAGTCCGAGCCA
SCF110507	11	1.19	KP278824	Schlautman et al. (2015)	GTAGCTGAGGTGGAGGATAAC	GAGCTGGTGCTGAAATTAAC
SCF181909	11	1.19	KP278932	Schlautman et al. (2015)	CTCTCAATCTCTTGTTTTCTCC	TTCAAACCTCAGCAATCAG
SCF72209	11	1.19	KP278755	Schlautman et al. (2015)	CTTTACCTTTTCCTTCAGTCGT	GAGGTTCACCAAATCTTACCA
SCF95767	11	1.19	KP278796	Schlautman et al. (2015)	TGAGGAGAGGAGTATCCATAAG	CCTACAAGTCTCGCAATTCTA
scf108b	11	2.38		Georgi et al. (2013)	ACATAAACGGCGATTCCAAC	ATTGCTCGAGGATTGGACAC
1trimcontig176042	11	4.39	KP279221	Schlautman et al. (2015)	CCGTTGTTGTTCTTCTGTAGT	TTCAACCTCTGAAGCCTCT
vm05418	11	6.87	JF834252	Zhu et al. (2012)	GGGATAAACACTTACAGGAAGA	CTAGCTAGCCGTCAGTTATTTC
SCF41361	11	8.3	KP278708	Schlautman et al. (2015)	AAAATTGCTTGGTCCTCAC	AAGTGTATAGTCTGGGGTGTTC
SCF122746	11	11.07	KP278846	Schlautman et al. (2015)	ATTGTATGAAAACCCTAACCC	GAGACGATTCCAAATATAGCA
307018_K70	11	14.05	KP279208	Schlautman et al. (2015)	TAAAACCTTACCTCCTCTTCTG	TAACCTCGGATCTCCTTATCTA
SCF81909	11	14.62	KP278773	Schlautman et al. (2015)	TAGAGGAATCAGCAACTTCACT	TTCACACTCACACTCACACG
SCF204332	11	23.86	KP278948	Schlautman et al. (2015)	CGTGATCTCCCAGAGTTGT	CTTTTATTTCCCTATGTGTCCC
Pr031818821	11	26.07		Blueberry Markers	TCTAGGGTTTTGGCGCTTC	TCCTTGAGAACAAGTACAGGTGAG
scf3072b	11	26.67		Georgi et al. (2013)	AGTTTAAGCGGAGCGAATGA	TTTGGCGACATTTTTCTTCC
SCF81294	11	26.67	KP278771	Schlautman et al. (2015)	CTATCGACGGCTGAGATTT	AAAAGGGGAAGATCCTAGAAG
SCF106182	11	36.88	KP278813	Schlautman et al. (2015)	TACCCTTGTGTATCCCTACATT	GAACAATAGCAGCAACAGAAC
SCF199831	11	36.88	KP278946	Schlautman	GTAGGTATCATCGCT	GTGCATCACATACAAGC

				et al. (2015)	GTCTTC	TCT
SCF64185	11	36.88	KP278745	Schlautman et al. (2015)	CACCTCATTTGGTTC ATTCT	CAGATACTAAAGGTTGC CGTA
SCF183590	11	37.5	KP278933	Schlautman et al. (2015)	TTTGTAGTATGGGG ACACTGAT	AAAGAGGCAGGTCAGA AAAT
SCF21596	11	39.89	KP278655	Schlautman et al. (2015)	ATATACTGGCATAAA CACCCTC	CCTTACTCTTATCATGGC TAGG
vm68798	11	47.62	JF834242	Zhu et al. (2012)	ATAGAAATCGAGCAA GGAGAG	CAGACCTAAACTCAATTT CTGG
SCF132506	11	50.06	KP278862	Schlautman et al. (2015)	AATGTGCCAAGTTTT GTAGAC	GTCCCCTATAAGTCATCT GAAA
SCF57497	11	50.63	KP278737	Schlautman et al. (2015)	ATCTGTAGGTTGTGT TACCCC	ATCAACTGTATCTACCCA CCAA
SCF120937	11	53	KP278844	Schlautman et al. (2015)	TGTGCAAGAGTCATC TCCTAT	TATTCCCTTTCATTCTCC TTC
482_K70	11	53.59	KP279193	Schlautman et al. (2015)	ACAGCGGCATAGTA AAATGA	GTCACCGAAATCTCACT CAATA
SCF123189	11	53.59	KP278847	Schlautman et al. (2015)	CCTAGAAATGTTACT CTCCGAC	TTCACTTCCTTACTCCTT TCAT
SCF136826	11	53.59	KP278868	Schlautman et al. (2015)	GATCTTGATTAGCTC CAACTG	GCTTACACCAATTCTACA GTCA
SCF158255	11	53.59	KP278905	Schlautman et al. (2015)	ATGCGTACACCTCAA TCTTT	GTGGGTACTTGTTTTCA GTTC
SCF66313	11	53.59	KP279032	Schlautman et al. (2015)	AATTTGACCCTCTTT CCCT	GTCCAAAATACACAAAC TAGCC
SCF95754	11	53.59	KP278797	Schlautman et al. (2015)	CAGTGAGACTTCAGC TTGATAC	ATTGGTGACTTAGGAGT GAGAC
1trimcontig444344	11	54.19	KP279252	Schlautman et al. (2015)	CTGCTAATGTTGTTT GTTGC	TATTATCTCCCACCTAAT GAGC
308539_K70	11	54.19	KP279209	Schlautman et al. (2015)	CTAAATTCTCAACAT CTCTGGC	CCAAGAAGCATAAGGG ATAGT
SCF161998	11	57.76	KP278911	Schlautman et al. (2015)	ATATACCAGTGCTCT TTCCATC	AGACTTCTTTCTCCAAA GGC
SCF150173	11	64.54	KP278894	Schlautman et al. (2015)	GTGTTGGGAAACAG CAGAT	TTATTCTCGTTGTCAGCC TT
SCF110757	11	66.26	KP278825	Schlautman et al. (2015)	TCATATCAACCTAAC AATCGG	CACAAACAAGGAAATTA AGACC
SCF1047	11	72.22	KP278596	Schlautman et al. (2015)	GAGCTTTGGCCTCAT ATTACT	CGAATTACTCCAACCAA CAT
SCF28931	11	73.75	KP278678	Schlautman et al. (2015)	TCTCATAAGTCAGAA CCTCACA	CTAAACTAAACCTCCTAA CCGA
SCF160647	11	77.45	KP278909	Schlautman et al. (2015)	TAACTCAAAGAACCT AACCCC	TAAAGTGACAGGTAATG TCGTC
SCF181772	11	81.02	KP278931	Schlautman et al. (2015)	AGCAACGTATGGTG GTATC	CATTTGTTTCCACAGCTT C
SCF118608	11	84.31	KP278841	Schlautman et al. (2015)	AACTACTCGATCTTC ACCCTTA	AGGAGACCAACACTTAA CCTC
SCF28509	11	93.27	KP278676	Schlautman et al. (2015)	GCAAACACCACACTA TATGAGA	ATAGAGAACCACAGAAC AGGAC
1trimcontig175770	12	2.84	KP279220	Schlautman et al. (2015)	GTGTAGCTTGGAAA ATAGGAGT	ACTAGGGAGCGAGAGA GAGTA
411145_K63	12	2.84	KP279179	Schlautman et al. (2015)	GGTAGGAATTAAAG TGAAGACG	ACTAGGGAGCGAGAGA GAGTA
ct140233	12	2.84	KP279126	Schlautman et al. (2015)	TTACAGAAGGAAGA GAGAGGAA	ACTGGCTTCTATAGCTC ATTTC
Ig28559a	12	2.84		Georgi et al. (2013)	CAAGAGTCGCAAATT CCACA	CCTCCTTCTAGAGAGGG CCA

SCF28279	12	2.84	KP278675	Schlautman et al. (2015)	GATACTTTACCTCCTCCTCAAG	TTGTCCTCTATCTCTAACTCCC
417587_K63	12	5.82	KP279187	Schlautman et al. (2015)	TGGGTAGATATTAGATGGCAGT	CTTCTTCTGGAAATCTGGTTAG
SCF28955	12	5.82	KP278679	Schlautman et al. (2015)	TATTCAAAGCCACTAGGCAC	CAAACCAAATTCTCCTTCTG
ct174735	12	6.26	KP279147	Schlautman et al. (2015)	CTTATTTGTATGGCCTTCCT	GCAGCATATATTGTCCAGTTC
SCF160663	12	6.85	KP278910	Herein	TTACACCCTATCTCCTGTTTTC	CAGTTCATCTTGCTAGTTATGC
ct110752	12	8.25	KP279110	Schlautman et al. (2015)	ACACACACTAACGAAATCCTTC	CTAGCTCCGACATTGTTATCTC
SCF116485	12	8.25	KP278834	Schlautman et al. (2015)	CAATATAAACGTCAGTCACCAG	ACTTTTGGTTATGCTGGAAG
scf6355	12	8.25		Georgi et al. (2013)	ACAATGTTGTCATTCCGACG	CTAGACTCGTCCAAAAGCCC
scaffold_111040	12	9.82		Herein	ACACAGTTTATGCAGAGCTTAC	ATCTCTCTCTCTCTCTTTGAGC
scf2882	12	9.82		Georgi et al. (2013)	CGCTACCATTGTCAGCTTCA	ACACTCAAAAGCAGGTGGCT
scf4b	12	14.77		Georgi et al. (2013)	GATACGATACGGATACGCGG	GTCGATCATGGTCGTCAGTG
scaffold_42843	12	17.15		Herein	TTTCTCCATCTCTCTCTTATCC	ACTCACTGTTCACCTTCTCTG
scaffold01187	12	17.15		Blueberry Flowering Gene	AATGTTTTGTGTCTCCCAATCC	CATTATTTAGCACCAGCGTTGT
SCF122440	12	24.86	KP279066	Schlautman et al. (2015)	CTAATCTTCCTCCTCTTGTTGA	CGACAAACTAACATATCATCTCC
SCF34071	12	35.42	KP278694	Schlautman et al. (2015)	CGTGTGCAGATTTACTTCAG	AATTCATAGATCCCCATGAC
SCF59739	12	38.3	KP278741	Schlautman et al. (2015)	GTATGACTGTACCAAACAAACC	CAGCTTTCCCTTCTAAATGA
SCF190609	12	43.72		Herein	TAACGGAAAGAGTTAAAGGAC	TTGTATCAGAGAAGAAGGAGG
SCF46588	12	43.72	KP278714	Schlautman et al. (2015)	ACAAACCTTGAGCCTATTTG	GTCTGAGTTTCCACTATCGTCT
SCF98180	12	43.72	KP278802	Schlautman et al. (2015)	CTCCTCTGCTTATCTCTTCAAC	GGTTTTCCCTTCTCAAGATTAC
SCF13753	12	47.95	KP278641	Schlautman et al. (2015)	AAGTCCTTTCCTTCTTTTGC	GCTATGTGATGTCGTTCCTAA
SCF14189	12	47.95	KP278644	Schlautman et al. (2015)	GTCTAGGTGAGGATGGTTGAT	AAAACAGAGCCCAACAAGT
SCF6926	12	47.95	KP278615	Schlautman et al. (2015)	ACATGCACTTCAAATAGTACCC	TTACAACTTACACAGGAAGCAG
SCF76310	12	47.95	KP278762	Schlautman et al. (2015)	CTGTGTAGAACTGCATCAAAAC	TCCTAGAGACCAACCCAATAC
SCF96306	12	49.26	KP279050	Schlautman et al. (2015)	CCTGTAGTGAGTTACCTTCCAT	GCTGTCAACCATCCATTATT
SCF37628	12	49.43	KP278700	Schlautman et al. (2015)	ACCAGCTCAGATAACAATGC	GAGTAGGATACCTCCACACCTA
scf37h	12	51.8	JN230518	Georgi et al. (2013)	TGGACTTTTCTTGCTTGGCT	GGATACACGTGACCGAGCTT
309084_K70	12	52.87	KP279212	Schlautman et al. (2015)	CTTCTTTTCCTCTCCACTGATA	CTCTCCGTTGTCCATTTCT
SCF34584	12	52.87	KP278696	Schlautman et al. (2015)	GTCTGTTTGGAAGAAGAAGGT	CTGTTCGTCAATCCCTAGC
vm26877	12	55.31	JF834264	Zhu et al. (2012)	CCCCTTTTGAACGAAACTATAC	ACATCTCAATTCCGAGCATA

ct129169	12	56.43	KP279119	Schlautman et al. (2015)	TAAATCACCTTCTTCCTCCTC	GGTCCCAAACTTACTACTCAAA
SCF16166	12	56.43	KP278646	Schlautman et al. (2015)	CCTAGTCATTCTTCTACTCCCA	GGGTTATCTCGTCCATATTGT
354699_K63	12	59.41	KP279172	Schlautman et al. (2015)	GAAGCGATTTGGAAGAAAC	ACACAGAGAGATTACGAACACA
SCF69698	12	59.41	KP278751	Schlautman et al. (2015)	GAGGAGATAAAGGTTTGTTGAG	CTTTGAGACTTTGAGTGAGACA
SCF11065	12	61.26	KP278634	Schlautman et al. (2015)	CTTTGTCCCAACACGTTAAT	AAGTCTATAAGCATCCTGCAAC
SCF149989	12	61.26	KP278892	Schlautman et al. (2015)	AGTAGGCATTGTTCACTCACTC	TTTCTCCTAAAGCTAAACTCCC
SCF38430	12	61.26	KP278702	Schlautman et al. (2015)	CAATAGTTAGGAAGTTGGAACC	CTAAGAACCAAACAGAGCCTTA
76126_K63	12	61.79	KP279162	Schlautman et al. (2015)	TTTATTGGAGCGAAAGAGAG	AAAAGGGGAGGAGAGAGAT
SCF138394	12	61.79	KP278871	Schlautman et al. (2015)	AAGCCCAGAAGAAATAACCTA	TGCAAATGTTAGGAACTGTGT
418596_K63	12	62.39	KP279190	Schlautman et al. (2015)	CGTGAGTTTGAGTGAGTAATTG	AGGACATGGTGAGTTGAGAAT
scf15b	12	62.39		Georgi et al. (2013)	CTGCCTTGTTTCCCTCTCTG	GGATTGGTTTGTTGGTCGTC
SCF38942	12	62.39	KP278704	Schlautman et al. (2015)	CTTGCTATTTGGTACTCGTCTT	CTTGACAGTTATTTCTCTTCGG
SCF116567	12	64.09	KP278835	Schlautman et al. (2015)	GTTGGTCTACAATTCTGTTCCT	GCCCTTTTAGTTGAAATGC
408825_K63	12	65.37	KP279176	Schlautman et al. (2015)	GTTCTCCTCTTTCATCATTCAG	AGTCTTGAACTCCTTGTACTCG
ct144936	12	65.37	KP279129	Schlautman et al. (2015)	AGGTGACTAAGGCAGTGTTC	CGTGTCTGTTTGGTTAGTAGGT
vm40600	12	65.37	JF834274	Zhu et al. (2012)	CAAAAGAGCCATGAAATAGG	TTGGTGAAAACTATACCTGTCC
scf79c	12	66.36		Georgi et al. (2013)	GGTTCTTCGTGGCATGATAGT	CCAAATAACCCAGGAGAGCA
SCF117422	12	72.34	KP278839	Schlautman et al. (2015)	TTCTGTTTCTTGGCTCTGTATC	TATTATGCTACATCGGTCGAG
SCF159195	12	72.34	KP278908	Schlautman et al. (2015)	AACAAAGACCCTAATCAGACAC	ACAATCAAAACACCGTCAG
scf6213	12	77.11		Georgi et al. (2013)	GCTCGCTCTCGCATATTTTC	CCTAGCCCGTTCATCATTGT
SCF75572	12	77.11	KP278761	Schlautman et al. (2015)	GACAAGTGGTTGGGGATAC	ACCCTCATCATCACTCCTT
vm34671	12	79.7	JF834271	Zhu et al. (2012)	CCATCTCTCTCTTGTTTCTCTC	GCGAAAAATAAGTCTCCACA
SCF101914	12	85.12	KP278806	Schlautman et al. (2015)	CTTTGGAGCACAACAACTCTA	GTGTAAAGACCAGGACCCTT
SCF145689	12	85.12	KP278885	Schlautman et al. (2015)	GGCATAAGAGTAGACCATGAAC	GTACTATAAAATGCTTCCAGCG
SCF169090	12	85.12	KP278917	Schlautman et al. (2015)	GAGACAAAGTTCAAATAGGGAG	ATACTGCAACCGATACTGAGA
scf248	12	85.12		Georgi et al. (2013)	CAACTGGAGGCAAAACAACA	CACGCATTGCAATTATACCG
SCF102190	12	86.61	KP279054	Schlautman et al. (2015)	GAGGAAAGGGTGAGAGTTTT	GTTTGACGAAAAGGAGACTG
SCF3191	12	86.61	KP278603	Schlautman et al. (2015)	GCACTATCAGGAAGAGGAATTA	GTAACACCAGAAAACAACTGC
SCF3261	12	86.61	KP278604	Schlautman	GTTTACCATATTCACTCCTTCC	TGAGACAGACCTAACATTTGAC

scaffold_84992	12	90.6	et al. (2015) Herein	TATACAGTTTGCTCG TTGGAC	CGATCCACTAACACAAA AGAAC

Appendix VI-3. Features of the parental bin maps and linkage groups (LGs) constructed for the maternal parent (M), [BGx(BLxNL)]95, and the paternal parent (P), GH1x35, for the Grygleski full-sib mapping population using simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs).

LG	Length (cM)		SNPs		SSRs		Markers[a]		Bins[b]		Bins with SSRs[c]		Mean Gap[d]		Mean Recombination[e]	
	M	P	M	P	M	P	M	P	M	P	M	P	M	P	M	P
LG1	126.1	111.0	227	254	5	6	232	260	58	64	5	5	2.2	1.8	1.3	1.1
LG2	95.0	90.6	160	125	4	1	164	126	40	32	4	1	2.4	2.9	0.9	0.9
LG3	102.8	86.4	130	139	5	10	135	149	37	28	5	8	2.9	3.2	1.0	0.9
LG4	90.9	85.2	132	150	11	12	143	162	33	44	10	11	2.8	2.0	0.9	0.9
LG5	61.8	88.0	30	162	4	13	34	175	10	37	4	10	6.9	2.4	0.6	0.9
LG6	110.7	84.2	173	184	8	5	181	189	46	43	7	3	2.5	2.0	1.1	0.8
LG7	106.1	85.4	135	132	10	6	145	138	40	37	8	4	2.7	2.4	1.1	0.8
LG8	73.7	79.5	95	106	6	3	101	109	23	36	4	3	3.4	2.3	0.7	0.8
LG9	97.6	89.9	197	194	6	3	203	197	40	45	6	3	2.5	2.0	1.0	0.9
LG10	93.5	77.3	128	159	5	3	133	162	39	28	5	1	2.5	2.9	0.9	0.8
LG11	111.0	94.1	162	213	7	6	169	219	42	43	6	6	2.7	2.2	1.1	0.9
LG12	99.4	88.8	180	198	11	13	191	211	41	35	7	10	2.5	2.6	1.0	0.9
Mean	97.4	88.4	146	168	7	7	153	175	37	39	6	5	3.0	2.4	1.0	0.9
Total	1168.6	1060.4	1749	2016	82	81	1831	2097	449	472	71	65				

[a] Total number of SNPs and SSRs mapped

[b] Total number of unique marker bins estimated using the ASMap package in R (Taylor and Butler 2015).

[c] Number of unique marker bins that contained at least one SSR

[d] Mean distance between unique marker bins

[e] Mean number of recombination events per progeny per parental LG

Appendix VI-4. Features of the parental bin maps and linkage groups (LGs) constructed for the maternal parent (M), Mullica Queen, and the paternal parent (P), Crimson Queen, for the CNJ02 full-sib mapping population using simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs).

LG	Length (cM)		SNPs		SSRs		Markers[a]		Bins[b]		Bins with SSRs[c]		Mean Gap[d]		Mean Recombination[e]	
	M	P	M	P	M	P	M	P	M	P	M	P	M	P	M	P
LG1	107.0	79.3	202	198	31	35	233	233	44	43	18	17	2.5	1.9	1.1	0.8
LG2	113.8	100.2	161	156	45	45	206	201	51	49	26	30	2.3	2.1	1.1	1.0
LG3	111.8	87.8	152	161	41	39	193	200	47	42	23	22	2.4	2.1	1.1	0.9
LG4	115.7	81.0	150	138	54	49	204	187	56	38	31	25	2.1	2.2	1.2	0.8
LG5	105.0	88.9	141	179	27	29	168	208	40	41	19	16	2.7	2.2	1.1	0.9
LG6	111.4	82.5	172	177	38	36	210	213	45	35	24	23	2.5	2.4	1.1	0.8
LG7	108.2	87.6	182	165	46	45	228	210	51	46	31	29	2.2	2.0	1.1	0.9
LG8	112.1	74.7	133	147	40	41	173	188	48	39	23	24	2.4	2.0	1.1	0.7
LG9	107.9	73.3	200	185	42	41	242	226	45	45	19	21	2.5	1.7	1.1	0.7
LG10	91.4	76.3	140	144	39	38	179	182	39	38	23	19	2.4	2.1	0.9	0.8
LG11	105.7	87.2	206	193	31	31	237	224	45	39	23	17	2.4	2.3	1.1	0.9
LG12	106.5	60.9	163	177	48	38	211	215	40	31	26	20	2.7	2.0	1.1	0.6
Mean	108.0	81.6	167	168	40	39	207	207	46	41	24	22	2.4	2.1	1.1	0.8
Total	1296.5	979.7	2002	2020	482	467	2484	2487	551	486	286	263				

[a] Total number of SNPs and SSRs mapped

[b] Total number of unique marker bins estimated using the ASMap package in R (Taylor and Butler 2015).

[c] Number of unique marker bins that contained at least one SSR

[d] Mean distance between unique marker bins

[e] Mean number of recombination events per progeny per parental LG

Appendix VI-5. Features of the parental bin maps and linkage groups (LGs) constructed for the maternal parent (M), Mullica Queen, and the paternal parent (P), Stevens, for the CNJ04 full-sib mapping population using simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs).

LG	Length (cM)		SNPs		SSRs		Markers[a]		Bins[b]		Bins with SSRs[c]		Mean Gap[d]		Mean Recombination[e]	
	M	P	M	P	M	P	M	P	M	P	M	P	M	P	M	P
LG1	117.1	89.9	171	197	6	9	177	206	28	32	6	6	4.3	2.9	1.2	0.9
LG2	103.4	78.3	158	122	16	16	174	138	31	27	10	12	3.5	3.0	1.0	0.8
LG3	61.7	59.9	114	138	8	9	122	147	16	19	5	7	4.1	3.3	0.6	0.6
LG4	83.0	55.6	114	152	8	11	122	163	20	17	7	10	4.4	3.5	0.8	0.6
LG5	88.6	85.1	106	145	7	3	113	148	23	21	5	3	4.0	4.3	0.9	0.8
LG6	98.9	77.8	161	166	10	15	171	181	31	25	9	13	3.3	3.2	1.0	0.8
LG7	108.0	72.1	128	111	8	6	136	117	22	22	7	4	5.1	3.4	1.1	0.7
LG8	88.6	56.9	115	101	8	11	123	112	21	21	6	9	4.4	2.8	0.9	0.6
LG9	97.5	69.5	146	141	13	12	159	153	21	17	11	9	4.9	4.3	1.0	0.7
LG10	70.9	75.1	101	139	14	15	115	154	22	23	10	9	3.4	3.4	0.7	0.8
LG11	99.5	55.8	188	95	8	9	196	104	29	13	7	5	3.6	4.7	1.0	0.6
LG12	69.2	69.2	152	168	14	15	166	183	19	21	10	11	3.9	3.5	0.7	0.7
Mean	90.5	70.4	138	140	10	11	148	151	24	22	8	8	4.1	3.5	0.9	0.7
Total	1086.4	845.2	1654	1675	120	131	1774	1806	283	258	93	98				

[a] Total number of SNPs and SSRs mapped

[b] Total number of unique marker bins estimated using the ASMap package in R (Taylor and Butler 2015).

[c] Number of unique marker bins that contained at least one SSR

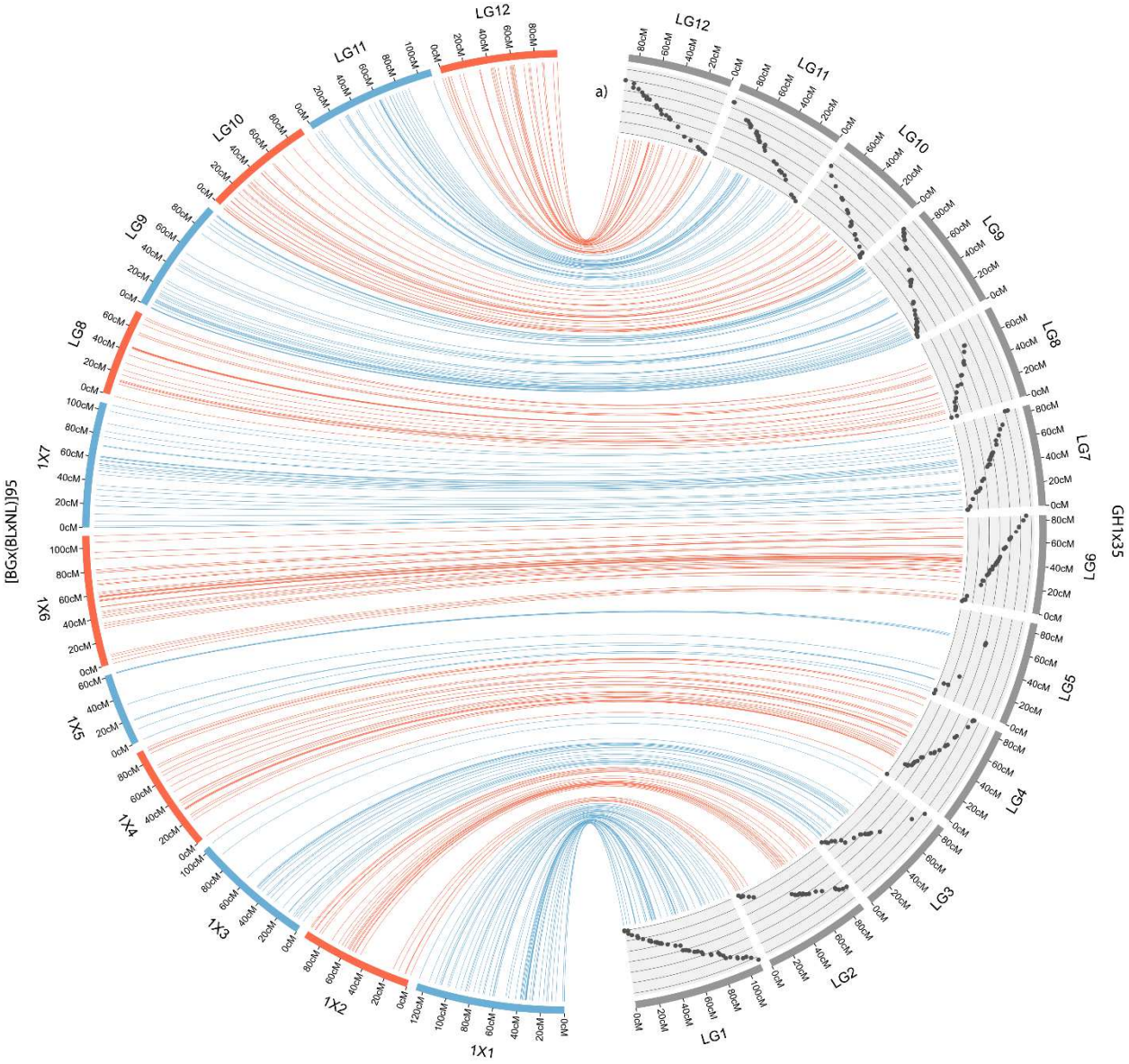
[d] Mean distance between unique marker bins

[e] Mean number of recombination events per progeny per parental LG

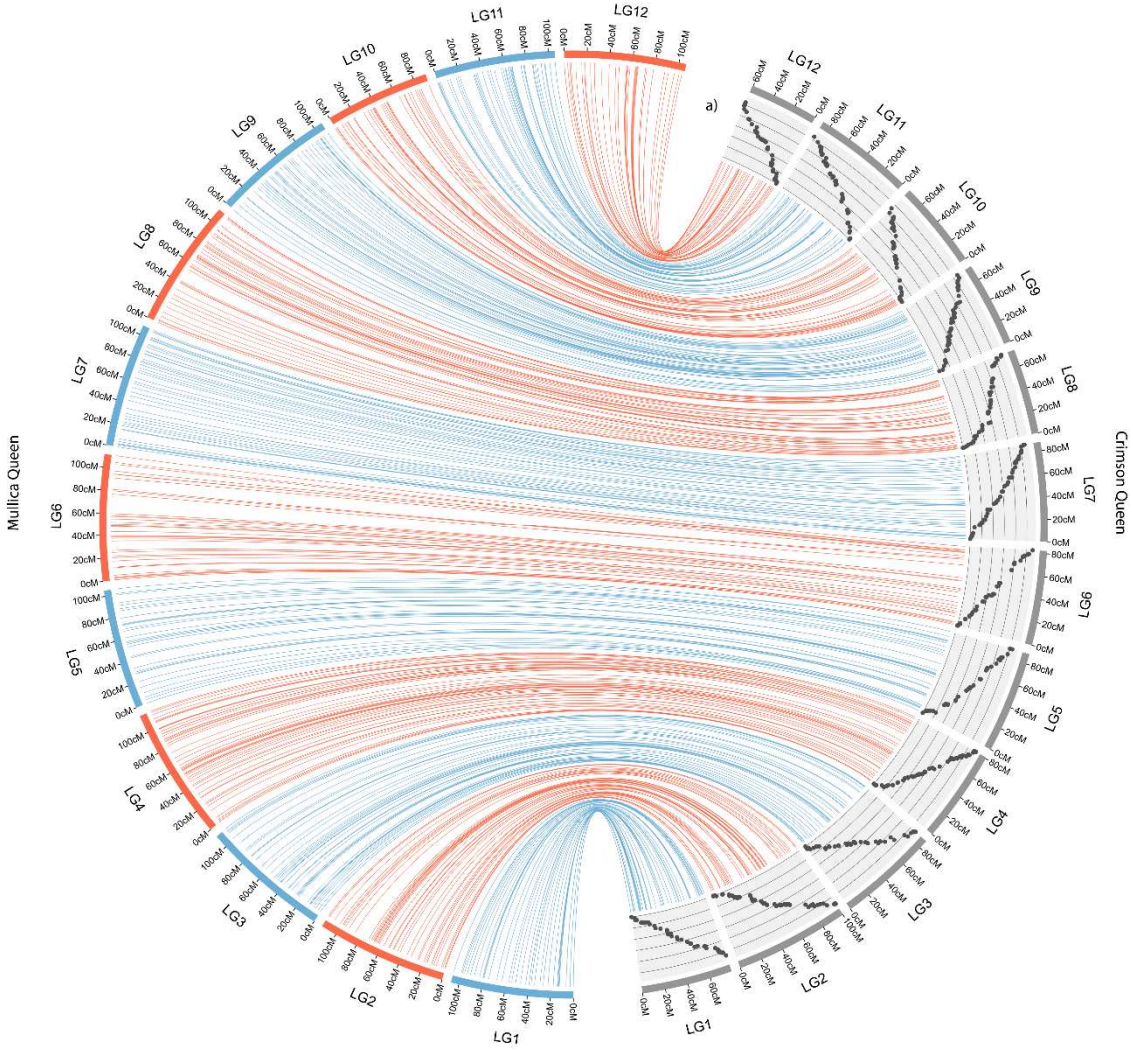
Appendix VI-6. Total number of markers, by linkage group (LG), mapped in the parental component bin maps for each of the three cranberry full-sib populations (i.e. Grygleski, CNJ02, and CNJ04).

LG	SNPs			SSRs			Total Markers		
	Grygleski	CNJ02	CNJ04	Grygleski	CNJ02	CNJ04	Grygleski	CNJ02	CNJ04
LG1	391	327	286	10	43	10	401	370	296
LG2	243	261	240	5	57	21	248	318	261
LG3	231	265	213	12	51	12	243	316	225
LG4	239	236	243	17	59	13	256	295	256
LG5	181	257	235	13	34	7	194	291	242
LG6	291	296	281	9	47	16	300	343	297
LG7	223	289	211	15	58	8	238	347	219
LG8	169	226	198	9	52	12	178	278	210
LG9	308	323	262	8	52	14	316	375	276
LG10	241	232	219	6	47	19	247	279	238
LG11	322	323	246	10	41	11	332	364	257
LG12	319	291	280	17	58	24	336	349	304
Mean	263	277	243	11	50	14	274	327	257
Total	3158	3326	2914	131	599	167	3289	3925	3081

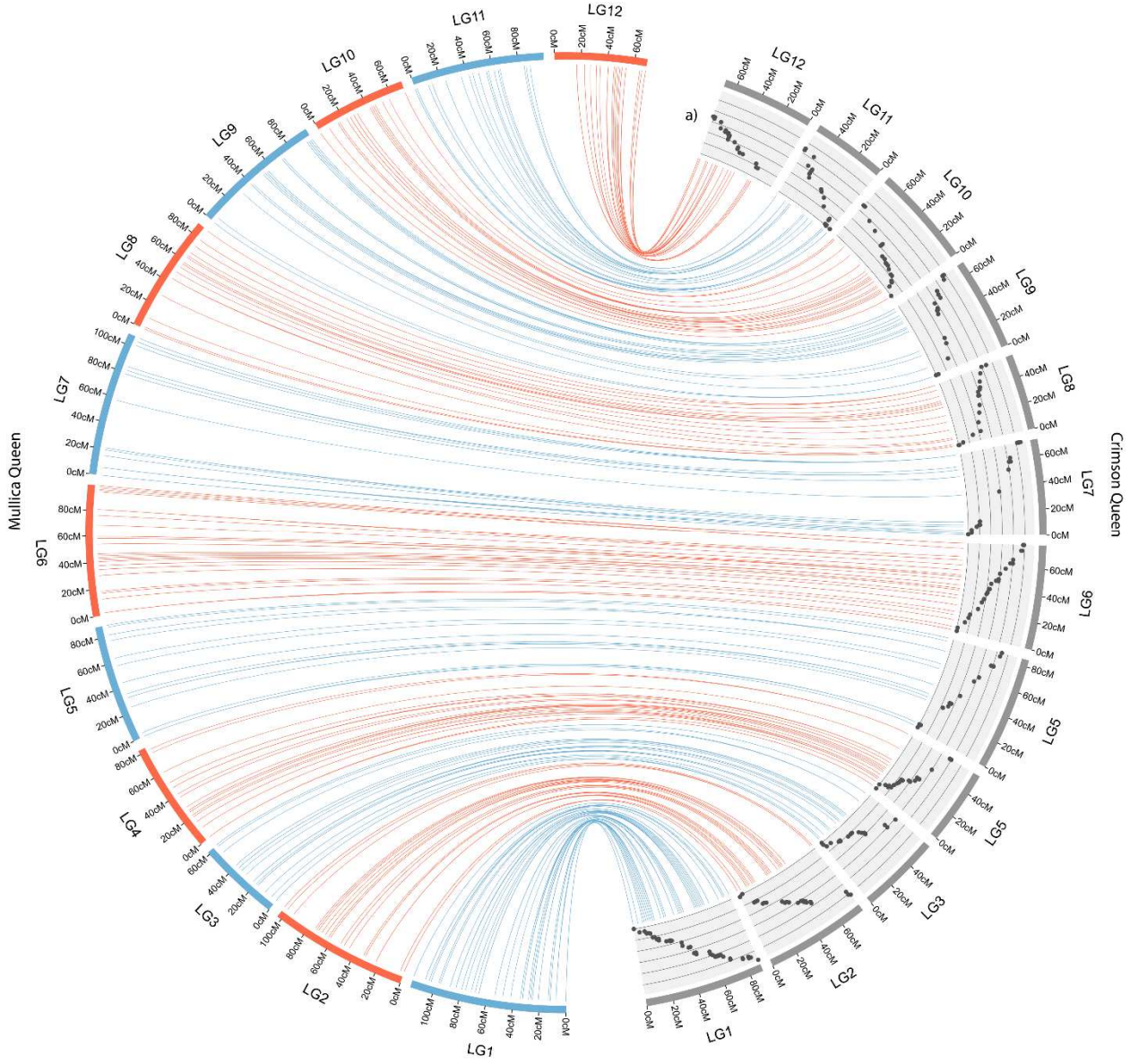
Appendix VI-7. Comparison of the LGs of the [BGx(BLxNL)]95 and GH1x35 parental bin maps constructed with progeny from the Grygleski full-sib cranberry population. Links are drawn between common orthologous markers in each of parental bin maps. **(a)** Scatterplots of the position of the common markers each of the two maps are shown with intervals between lines representing 20 cM Kosambi map distance.



Appendix VI-8. Comparison of the LGs of the Mullica Queen and Crimson Queen parental bin maps constructed with progeny from the CNJ02 full-sib cranberry population. Links are drawn between common orthologous markers in each of parental bin maps. **(a)** Scatterplots of the position of the common markers each of the two maps are shown with intervals between lines representing 20 cM Kosambi map distance.



Appendix VI-9. Comparison of the LGs of the Mullica Queen and Stevens parental bin maps constructed with progeny from the CNJ04 full-sib cranberry population. Links are drawn between common orthologous markers in each of parental bin maps. **(a)** Scatterplots of the position of the common markers each of the two maps are shown with intervals between lines representing 20 cM Kosambi map distance.



Appendix VI-10. Statistic generate during composite map construction with the six parental component bin maps from the cranberry Grygleski, CNJ02, and CNJ04 populations using LPmerge (Endelman and Plomion 2014). The max interval size, *k*, which minimized the root mean square error (RMSE) is displayed along with the corresponding RMSE and standard deviation (SD).

LG	Max Interval (*k*)	Number of Loci	Map Length	RMSE	SD
1	5	638	115.88	10.8	7.99
2	9	479	100.75	6.68	3.37
3	4	461	92.4	8.66	4.94
4	4	484	86.35	8.53	7.99
5	9	440	93.09	6.45	3.68
6	10	523	93.77	7.58	3.27
7	10	477	97.03	7.79	3.99
8	10	424	85.2	10.06	4.64
9	4	586	89.86	9.14	6.54
10	6	429	84.11	3.25	1.35
11	10	541	95.25	6.17	3.57
12	5	591	90.6	9.27	3.49

Appendix VI-11. The number of gaps between unique marker positions in the cranberry consensus map exceeding 1, 2, 3, 4, and 5 cM in length by linkage group (LG).

LG	Gap Size				
	1 cM	2 cM	3 cM	4 cM	5 cM
LG1	40	9	2	0	0
LG2	28	12	3	1	1
LG3	35	13	4	0	0
LG4	28	6	3	2	1
LG5	31	10	5	1	0
LG6	31	7	2	1	0
LG7	29	7	1	0	0
LG8	28	8	2	0	0
LG9	31	9	2	1	0
LG10	27	7	3	2	1
LG11	37	5	0	0	0
LG12	40	11	2	1	0
mean	32.1	8.7	2.4	0.8	0.3
total	385	104	29	9	3

Appendix VI-12. Total number of cranberry scaffold, by linkage group (LG), from the Polashock et al. (2014) assembly containing SNPs or SSRs that were anchored in the cranberry composite map. The number of anchored scaffolds containing predicted coding DNA sequences (CDS) and total number of base pairs (bp) contained within those scaffolds is also provided.

LG	Anchored scaffolds	Length of anchored scaffolds (bp)	Anchored scaffolds containing CDS
LG1	431	2407463	186
LG2	325	1840095	147
LG3	299	1535779	118
LG4	326	1815950	140
LG5	289	1542819	125
LG6	345	2014976	155
LG7	305	1672098	129
LG8	284	1576566	112
LG9	384	2032876	149
LG10	281	1517934	110
LG11	349	1845278	126
LG12	365	2006173	157
mean	332	1817334	138
total	3983	21808007	1654

Appendix VI-13. Pair-wise Spearman rank correlations between the linkage groups (LGs) the cranberry composite map and previous cranberry linkage maps (Schlautman et al. 2015; Covarrubias-Pazaran et al. 2016).

LG	Composite vs. Schlautman et al. (2015a)	Composite vs. Covarrubias-Pazaran et al. (2015a)
LG1	0.99	0.99
LG2	1	1
LG3	1	0.96
LG4	0.99	1
LG5	1	1
LG6	1	0.99
LG7	0.99	0.99
LG8	1	0.97
LG9	1	0.93
LG10	1	0.98
LG11	0.99	0.94
LG12	0.99	0.96
mean	0.996	0.976

Appendix VI-14. Proportion of markers in the linkage groups (LGs) of the 6 parental component maps (i.e. [BGx(BLxNL)]95, GH1x35, Mullica Queen (MQ), Crimson Queen (CQ), and Stevens (ST) from the Grygleski, CNJ02, and CNJ04 populations) that display significant segregation distortion from the expected Mendelian genotype rations according to $\chi 2$ tests at the $p < 0.1$ level.

LG	[BGx(BLxNL)]95	GH1x35	MQ-CNJ02	CQ	MQ-CNJ04	ST
LG1	0	0.21	0.1	0	0.06	0
LG2	0	0.01	0.21	0	0	0.17
LG3	0.06	0	0.05	0	0	0
LG4	0	0	0	0	0.13	0
LG5	0.06	0	0.01	0.07	0	0
LG6	0	0.81	0.13	0.06	0	0
LG7	0.13	0.72	0	0	0	0.03
LG8	0.14	0	0	0.37	0	0
LG9	0.13	0.37	0	0	0	0.1
LG10	0.02	0.3	0.35	0	0	0
LG11	0	0.5	0.09	0	0	0.32
LG12	0	0.16	0.03	0.01	0	0.02
total proportion of distorted markers	0.04	0.26	0.08	0.04	0.02	0.05
total number of distorted markers	71	575	196	100	26	78

General Summary and Conclusions

The future of applied cranberry breeding and cultivar development lies at the intersection of classical breeding and innovative marker-assisted breeding (MAB) strategies. Classical breeding methods and phenotypic selection at public institutions, such as the University of Wisconsin and Rutgers University, have generated many important cultivars in recent decades, and such proven techniques will continue to be essential for crop improvement and for studying the inheritance of simple and complex traits in the future. However, the advent of next generation sequencing (NGS) has made marker development, validation, and quantitative trail loci (QTL)/association studies financially and computationally feasible, even in recently domesticated fruit crops like cranberry. As such, the main goal of this thesis research has been to enable molecular-assisted breeding in cranberry by generating molecular resources to study and better utilize cranberry genetic diversity in selection, to characterize cranberry genomic structure, and to investigate the molecular inheritance of simple and complex traits.

Using nuclear genome scaffold assemblies and a set of expressed sequence tags (Polashock et al. 2014; Fajardo et al. 2014), 697 polymorphic SSR markers were mined, developed, and validated in a core set of elite cranberry cultivars (Schlautman et al. 2015b). This was one of the largest single SSR marker discovery and development projects ever conducted in a fruit crop, and the SSRs were used in attempts to understand the geographic distribution of cranberry diversity across its native range (Schlautman et al. 2015b). Using selections of those nuclear SSRs, multiplexing combinations (4x) were designed to estimate the percentage of self-pollinated seeds within commercial cranberry production; for efficient, high-throughput DNA fingerprinting resources to examine the clonal heterogeneity in growers' beds, in cranberry breeding populations, and in elite parents; and for future application in marker-assisted seedling selection (MASS) (Chapter III; Ru et al. 2015).

To begin characterizing the cranberry genome, the cranberry SSRs that were previously validated (Schlautman et al. 2015b), as well as SSR markers from the first cranberry linkage map (Georgi et al. 2013), were screened for polymorphism in a full-sib mapping population. Using the polymorphic SSRs, a high-density cranberry SSR linkage map was constructed for the population that contained 541 SSRs, which was then used to explore macro-synteny between the cranberry, grape, and kiwifruit genomes (Schlautman et al. 2015a). The map was the densest in the *Vaccinium* genus at the time, and most importantly, it consolidated the previous 14 linkage groups (LGs) (Georgi et al. 2013) into the 12 LGs corresponding to the expected cranberry karyotype (2n=2x=24) (Hall and Galleta 1971) and reduced the average marker interval from 8.6 to 2.2 cM (Schlautman et al. 2015a). The resulting SSR map was useful in exploring marker-trait associations in cranberry. For example, four QTL for mean fruit weight and three QTL for total yield were

identified in cranberry. More importantly, the first cranberry QTL related to biennial bearing, a barrier to consistent annual yields in a large number of woody fruit crop species, was discovered and which colocalized with one of the three identified total yield QTL (Schlautman et al. 2015a).

In addition to being useful in cranberry genetic diversity, linkage mapping, and QTL mapping studies in cranberry, the cranberry SSRs were also useful in exploring and describing evolutionary relationships and genome divergence in the genus *Vaccinium* and the Ericaceae family. Using the published plastid (Fajardo et al. 2013) and mitochondrial (Fajardo et al. 2014) genomes, primers flanking 54 SSR loci were designed and exploited to begin obtaining a molecular phylogeny for the *Vaccinium* genus, and monophyly was found within and among the four *Vaccinium* sections represented (i.e. *Oxycoccus, Cyanococcus, Batodendron,* and *Vitis-Idaea*) compared to the Ericaceous outgroups in the study (Schlautman et al. 2016). In addition, 175 cranberry nuclear SSRs were transferred to an interspecific ((*V. corymbosum* x *V. darrowii*) x *V. corymbosum*) diploid blueberry mapping population and 17 blueberry nuclear SSRs were transferred to the cranberry population used to develop the first high-density cranberry SSR linkage map. The cross-transferability of these markers were useful in revising and further saturating the blueberry genetic map and facilitated a comparative genetic mapping study for exploring genome divergence between cranberry and blueberry. A remarkably high degree of synteny and collinearity between the two species genomes was observed, suggesting that major chromosomal rearrangements or chromosome fusion events have not occurred during the evolutionary history of cranberry and blueberry (Chapter V). The existence of these genetic maps and the knowledge of the similarity between the cranberry and blueberry genomes should promote future collaboration among *Vaccinium* breeders and geneticists and allow for simultaneous studies identifying cross-species marker-trait-loci.

To further characterize the genome and to determine the practicality of the genotyping-by-sequencing approach for simultaneous single nucleotide polymorphism (SNP) marker discovery and genotyping during cranberry breeding efforts, a multi-pedigree linkage mapping study using three inter-related cranberry populations was initiated. In total, 6073 cranberry markers (636 SSRs and 5437 SNPs) were positioned in a cranberry composite map. More than 53 % of the SNPs in the composite map were mapped in parental component maps for at least two of the three full-sib populations, suggesting that genotyping-by-sequencing approach is highly effective means for in detecting SNP polymorphisms that are transferable across cranberry populations and genetic studies. Furthermore, centromere regions were identified that may be useful in the development of future strategies that manage meiotic recombination for cranberry genetic improvement.

As cranberry geneticists continue to use the genetic resources developed herein to identify genomic regions linked or associated with monogenic or near monogenic traits, adoption of marker-assisted seedling selection (MASS) using efficient SSR multiplexing PCR strategies will be increasingly possible (Ru et al. 2015). By using MASS to select or pyramid must-have monogenic traits (loci) based on the genotypes of seedlings instead of the phenotypes of physiologically mature plants, fruit breeders can increase their efficiency, better allocate resources, and focus selection efforts on other more complex characters. Finally, advances in whole genome prediction can be incorporated into breeding programs to further increase selection efficiency of complex traits by predicting the general performance of parents in crosses not made and the specific performance of progeny not evaluated. The establishment of these innovative molecular-assisted breeding strategies, made possible through the discovery and development of genetic and genomic resources herein, should accelerate domestication and genetic gain in cranberry to meet current and future social, economic, and environmental demands through genetic improvement and cultivar release.

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