PHENOTYPIC AND GENOTYPIC CHARACTERIZATION OF PARTIAL RESISTANCE TO BLACK SPOT DISEASE OF DIPLOID *ROSA* SPP.

A Dissertation

by

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ABSTRACT

Black spot disease (*Diplocarpon rosae* (Lib.) Wolf) of rose is the most important leaf disease of garden roses worldwide. Although partial (horizontal) resistance to black spot has been shown to be moderately heritable, the responsible quantitative trait loci (QTL) remain unidentified. The objective of this study was to generate thousands of informative single nucleotide polymorphism (SNP) markers for genetic linkage and QTL mapping.

Five highly black spot resistant breeding lines derived from *R. wichuriana* 'Basye's Thornless', a moderately susceptible cultivar, and four highly susceptible cultivars with excellent ornamental characteristics were used to generate fifteen diploid populations (2n=2x=14) for this study. The disease severity of 812 field-grown seedlings was assessed on the percentage of foliage covered with lesions (PFS) and the size of the lesions (BLS) rating in June, September, October and November of 2016. Lesion size rating was moderately correlated with the amount of foliage with lesions (r = 0.59). The estimated narrow and broad sense heritability of partial resistance was 0.12-0.54 and 0.53, respectively for PFS, and 0.07-0.42 and 0.58, respectively for BLS indicating that partial resistance to black spot is a moderately heritable trait.

By utilizing genotyping by sequencing (GBS) technology, we created a high-density integrated consensus map for diploid roses (ICD) with thousands of informative single nucleotide polymorphism (SNP) markers and known bridge single sequence repeat (SSR) markers. 824 SNPs and 13 SSR bridge markers shared among three individual maps of populations were used to link the three maps to generate the consensus map. As a result, the ICD is composed of 3527 molecular markers covering a total length of 892.2 cM with an average distance between markers of 0.25 cM. The high synteny between the strawberry and diploid rose genome was also clearly demonstrated. One major black spot QTL on LG3 at interval 34-44 cM explaining ~20% of the total phenotypic variance was consistently present in the June, September, October, November and combined analyses. This approach serves as a model study for performing pedigree-based analysis (PBA) on materials with a diverse genetic background. The results will support downstream marker assisted breeding (MAB).

DEDICATION

To my dear mom, Zhengqing Bi, who always shows me love and support. Without her, I could not have accomplished my degree. Also to my father Guozhong Yan and my loving husband Chenyang Zhang, thank you for your understanding and unconditional support.

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Contributors

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CHAPTER I

INTRODUCTION AND LITERATURE REVIEW

The objectives of this dissertation include: 1) to characterize the genetic inheritance of black spot partial resistance of diploid rose populations in the Texas A&M University Rose Breeding Program in College Station, Texas (USA); 2) to generate SNP markers across the rose genome by utilizing a genotyping-by-sequencing (GBS) technique and create a SNP-based consensus map for diploid rose; 3) to identify quantitative trait locus/loci (QTL) for partial resistance to black spot using pedigree-based analysis methodologies.

1.1 Roses and black spot disease

Roses (*Rosa* spp.) are one of the most important and popular ornamental crops in the world today. There are approximately 200 rose species and at least 20,000 commercial rose cultivars. All roses belong to the genus *Rosa L.* of the Rosaceae (Zlesak, 2006). The *Rosa* genus encompasses 130-200 species within four subgenera: *Hulthemia, Platyrhodon, Hesperodos*, and *Rosa*. The subgenus *Rosa* contains over 95% of all rose species and includes ten sections (Akond et al., 2012; Debener and Linde, 2009). *Rosa* together with genera *Fragaria, Rubus, Potentilla,* and *Geum* belong to the Rosoideae subfamily within the family of Rosaceae (Potter et al., 2007). *Rosa* has a basic chromosome number of seven ($x=7$) and ploidy levels ranging from diploid ($2n=2x=14$) to decaploid ($2n=10x=70$) (Jian et al., 2010). The majority of the species are diploid ($2x = 14$), whereas most cultivated roses are either tetraploid ($4x = 28$), triploid ($3x = 21$) or diploid ($2x = 14$) (Ueckert et al., 2015; Zlesak, 2006). Though self-incompatibility is common in diploid rose species, self-fertilization is common for tetraploid and other polyploid species (Gudin, 2000; Rajapakse et al., 2001; Zlesak, 2006). Interspecific hybridization in roses has generated thousands of cultivars, but only eight to ten wild diploid species and some tetraploid species are commonly represented in the pedigrees of modern cultivars, suggesting that breeders were biased when choosing parents and unexploited wild rose species have the potential to broaden the overall gene pool of rose breeding programs in general (Byrne and Crane, 2003; Gudin, 2000). Though the genome size of roses varies among polyploids, sections, subgenera and cultivars, the rose genome size is small within the angiosperms, about 294 Mb/haploid, which is about two times the size of *Arabidopsis thaliana* (L.) Heynh, (Arumuganathan and Earle, 1991; Debener and Linde, 2009; Rajapakse et al., 2001; Yokoya, 2000). This makes rose a possible model plant for ornamental genetic studies.

Black spot (BS) disease of rose is the most important leaf disease of outdoor grown roses in warm humid areas (Debener and Byrne, 2014). Many modern roses are susceptible to this disease (Byrne et al., 2010; Uggla and Carlson-Nilsson, 2005; Zlesak et al., 2010). The causal agent of rose black spot disease is the hemibiotrophic ascomycete fungus *Diplocarpon rosae* (Lib.) Wolf, which is its teleomorph stage, while *Marssonina rosae* (Lib.) Died is the anamorph stage (Horst and Cloyd, 2007). *Diplocarpon rosae* is obligate to the genus *Rosa*, though other *Diplocarpon* fungi are pathogenic to other species in the Rosaceae (Horst and Cloyd, 2007). *D. rosae* is both biotrophic and necrotrophic, but loses pathogenicity over time when grown on artificial media. Free water is necessary for the fungus to germinate and directly penetrate the epidermis of rose leaves and stems, even when the humidity is 100%. The optimal temperature range for conidia germination and disease development is from 18 to 24°C (64-75°F) (Horst and Cloyd, 2007).

Typical symptoms of black spot are circular black spots with irregular margins surrounded by chlorosis. These lesions are mainly found on the upper side of rose leaves. As lesions expand in size, characteristic yellowing of leaf tissue occurs and eventually causes defoliation of the susceptible host (Gachomo et al., 2006). Eleven different physiological races of *D. rosae* have been differentiated across Europe and North America based on eleven unique reactions between hosts and pathogenic races (Whitaker et al., 2010).

Black spot resistance is commonly evaluated in the field for at least 2-3 years to ensure sufficient disease pressure and proper assessment of the plants (Carlson-Nilsson, 2000). However, this approach is costly and can be confounded by concurrent infections with *Cercospora puderi* B.H. Davis which causes similar leaf spot symptoms at an early stage of disease development or other stresses that weaken the plant and increases its susceptibility to disease infection (Horst and Cloyd, 2007).

A wide range of susceptibility and resistance to black spot has been documented in rose (Carlson-Nilsson and Davidson, 2006; von Malek and Debener, 1998; Whitaker et al., 2007; Whitaker et al., 2010; Whitaker and Hokanson, 2009). However, among cultivated roses, the vast majority of cultivars are susceptible to black spot. This situation is not due to the number of different pathogenic races but rather on the low number of resistance genes present in commercial rose germplasm (K. Lühmann et al., 2010). Thus early preselection of resistant germplasm is suggested by spraying conidial suspensions on the seedlings in the greenhouse before they go to the field, in order to save time, money and labor. Because most commercial roses are highly susceptible, the search for new resistance genes focuses on wild rose species (von Malek et al., 2000).

1.2 Resistance to black spot in roses

In rose, complete or vertical resistance which is characterized by a gene-for-gene interaction pattern with pathogenic races of *D. rosae* and susceptible rose cultivars has been reported (von Malek and Debener, 1998; Whitaker et al., 2010). Thus far three major black spot resistance genes – *Rdr1*, *Rdr2* and *Rdr3*, which confer resistance in a dominant fashion have been characterized in both tetraploid and diploid rose populations (Hattendorf et al., 2004; von Malek and Debener, 1998; Whitaker et al., 2010). *Rdr1* (Resistance to *Diplocarpon rosae*), is the first resistance locus identified using the Dort E4 isolate (race 6) (von Malek and Debener, 1998) and the gene has been fully characterized and completely sequenced (Hattendorf et al., 2004). *Rdr2* is later characterized and shown to be linked to *Rdr1* (Debener and Mattiesch, 1999; Hattendorf et al., 2004). Subsequent work on *Rdr1* has identified molecular markers that are tightly linked to the gene (von Malek et al., 2000) and at least nine RGAs (resistance gene analogs) of the TIR-NBS-LRR (Toll/Interleukin receptor-nucleotide binding site-carboxy-terminal leucine-rich repeat) family in the target region around *Rdr1* were discovered (Kaufmann et al., 2010, 2003). The *Rdr1* gene family co-evolved relatively recently in the Rosoideae and is absent in other taxa of the Rosaceae (Debener and Byrne, 2014).

In addition to discovering single R genes, partial resistance has also been discovered in this pathosystem (Shupert, 2005; Whitaker et al., 2007). The quantitative responses are sometimes called quantitative resistance, minor-gene resistance, horizontal resistance, or partial resistance (McDonald and Linde, 2002). Although generally thought to be under quantitative control, partial resistance can also be conferred by single genes in pathosystems such as wheat leaf rust (Rubiales and Niks, 1995) and leaf blast of rice (Zenbayashi et al., 2002). Partial resistance in roses does not prevent infection, but rather, limits the infection process and defends against all pathogenic races, although the degree of resistance may vary when infected with different races of black spot. Partial resistance has been observed as reduced lesion size, reduced sporulation, and/or the delayed onset of infection in both field assessment and in artificial inoculation experiments (Byrne et al., 2010; Dong et al., 2017; Shupert, 2005; Whitaker et al., 2007; Xue and Davidson, 1998). There are five different components that have been used to assess the partial resistance to black spot in both whole plant inoculations and detached leaf assays including incubation period (IP), leaf area with symptoms (LAS), number of lesions (NL), lesion length (LL) and sporulation capacity (SC) (Dong et al., 2017; Xue and Davidson, 1998). However, the various traits may be measuring different mechanisms of partial resistance that may be controlled by separate genes. Although black spot partial resistance has been documented, the responsible QTL remain unidentified and detection can often be very difficult when one of the major resistance genes is present.

Conventional approaches to prevent black spot disease are exclusion, eradication, avoidance, chemical spray and host resistance. The last strategy is to achieve durable resistance by pyramiding several different resistance genes into one genetic background, therefore increasing the resistance spectrum. For plant breeding, the application of molecular markers in the selection of QTL could be a powerful tool to accelerate germplasm improvement. Although the expression of genes is influenced by environment, molecular markers are not. Marker-assisted selection (MAS) will be most cost efficient for traits that require expensive evaluation protocols, traits for which progeny testing is needed to confirm presence of the donor allele (including recessive genes for any trait), and the introgression of simply inherited traits via backcrossing. In the case of backcrossing, selection could be for a desired donor allele and against markers unique to the unwanted genetic background of the donor parent. In other crops, such as common beans, maize, rice, and tomato, QTA (quantitative trait allele) is being routinely used for qualitative trait analysis mostly by the private sector or individuals (Koebner, 2005).

1.3 Genetic mapping of roses

Several groups have conducted mapping studies on diploid and tetraploid roses using AFLP, SSR, protein kinase (PK), RGA, RFLP, SCAR and morphological markers (Byrne, 2009; Moghaddam et al., 2012; Spiller et al., 2011; Yan et al., 2005; Yu et al., 2015). Initially parental linkage maps were created using the pseudo-testcross strategy, and more recently, integrated maps have been possible due to more abundant markers which have led to longer map lengths. Currently, it is possible to sequence the whole plant genome or sample the transcriptomes more thoroughly and cost-efficiently using next generation sequencing (NGS) technologies, such as 454, Illumina, AB SOLiD and PacBio (Myllykangas et al., 2012) than it was a decade ago. Thus SNP markers have become more popular and have been applied on rose as well (Bourke et al., 2017; Vukosavljev et al., 2016). The development of a consensus genetic map in rose will help identify QTL, candidate genes, and markers useful in selection considering the sizes of rose populations are usually too small for a bi-parental QTL analysis. Crespel et al. (2002) used a mapping population of 91 individuals from a cross between a di-haploid rose and a diploid species to identify a major and a minor QTL controlling the quantitative trait thorn density. Later, Yan et al. (2005) identified three QTL for leaf area and two QTL for chlorophyll using 520 AFLP, SSR, PK, RGA, RFLP, SCAR and morphological markers in a cross between two half-sib parents with eighty-eight individuals. Thirteen putative QTL were identified for flower size, days to flowering, leaf size, and resistance to powdery mildew based on a population resulting from a cross between “Blush Noisette” and *Rosa wichuriana.* (Dugo et al., 2005). Linde et al. (2006) identified a QTL for powdery mildew resistance in a cross between a powdery mildew (PM) resistant line (95/13-29) and a susceptible line (82/78-1).

The first unified diploid consensus map for rose, denoted as ICM, was constructed in 2011 (Spiller et al., 2011). This ICM included 597 markers and covered a length of 530 cM on seven linkage groups, QTL for seven different traits were also included on this unified map. Tetraploid rose linkage maps have also been created, and comparisons among diploid roses, autotetraploid roses and strawberry were conducted.

Several macrosynteny studies between the two genera *Fragaria* and *Rosa* revealed that numerous rearrangements have occurred since the genera diverged (Bourke et al., 2017; Gar et al., 2011; Vukosavljev et al., 2016).

1.4 Techniques and methods of QTL analysis

The statistical methods for QTL analysis include simple least squares, weighted least squares, maximum likelihood and Bayesian methods. Single marker analysis is the simplest method to map QTL. It uses a linear regression between a single marker and a phenotypic trait. The disadvantages of this method are the QTL position and effect cannot be fully explained, because it is possible that many markers show linkage to a QTL, and the linked markers may not be allelic to the QTL. Other methods such as interval mapping and composite interval mapping have been developed to take advantage of the genetic map and linked markers with similar results. Interval mapping tests a model for the presence of a QTL at multiple positions between the adjacent (flanking) marker loci, but the effects of additional QTL will cause sampling variance and biased estimates. Composite interval mapping increases accuracy of QTL effects by combining multiple regression and interval mapping methods (Sehgal et al., 2016). Among these methods an effective large mapping population is the limiting factor in mapping the QTL accurately (Linde et al., 2006)

Pedigree based analysis (PBA) under a Bayesian framework has emerged as an alternative strategy to study the genetics of quantitative traits within diverse and highly heterozygous breeding germplasm. This approach has been implemented in the software package FlexQTL™ (Bink et al., 2008) and has been applied on highly heterozygous clonally propagated crops, such as apple, peach, strawberry and sweet cherry (Fresnedo-Ramírez et al., 2016, 2015; Roach et al., 2016; Rosyara et al., 2013). It incorporates multiple populations connected in a pedigree to enhance the identification of important QTL whose alleles segregate for a trait across breeding programs. The PBA analytical approach calculates many genetic parameters, such as heritability, additive and dominance variances and breeding values, and tracks progeny relationships through several generations of the pedigree.

Including a more extensive and diverse genetic background into the QTL mapping populations can increase mapping resolution and enhances the visualization of allele segregation and the detection of QTL for the trait of interest (Fresnedo-Ramírez et al., 2016). Pedigree-based analysis takes both pedigree and marker information into consideration to identify the genetic components of QTL by tracking alleles identical by descent within a Bayesian framework.

1.5 Conclusion

The diseases of roses are now generally controlled by regular fungicide sprays (Debener and Byrne, 2014). However, due to environmental and economic concerns, fungicide application is not desirable. Thus, developing resistant cultivars would be a better approach to control black spot disease (Carlson-Nilsson, 2000). As obtaining reliable field phenotyping data usually takes 2-3 years, molecular markers could accelerate the pace by quickly identifying genotypes containing disease resistance genes. Currently, several markers associated with black spot disease resistance have been reported (Akond et al., 2012; Biber et al., 2010; Debener et al., 2001; Debener and

Mattiesch, 1999; Terefe and Debener, 2011; von Malek et al., 2000; Whitaker et al., 2009; Xu et al., 2005; Yan et al., 2005; Zhang et al., 2006; Zlesak et al., 2015) but not extensively used. With the advent of NGS technology, we have the ability to re-sequence genomes and perform detailed studies of resistance related genes. Additionally, this technology can rapidly generate thousands of markers, allowing for the rapid identification of marker-trait associations (Debener and Byrne, 2014). Our ultimate goal is to accelerate the development of disease resistant cultivars.

CHAPTER II

HERITABILITY OF BLACK SPOT PARTIAL RESISTANCE IN DIPLOID ROSES

2.1 Synopsis

Fifteen diploid rose populations were generated in a partial diallel design by intercrossing five black spot highly resistant breeding lines derived from *R. wichuriana* 'Basye's Thornless' and five moderately to highly susceptible cultivars with excellent ornamental characteristics ('Old Blush', 'Little Chief', 'Red Fairy', 'Sweet Chariot', and 'Vineyard Song'). The disease severity of 812 field-grown seedlings was assessed as the percentage of foliage covered with lesions (PFS) and a rating of the lesion size (BLS) in June, September, October and November of 2016. Lesion size was moderately correlated with amount of foliage with lesions (r = 0.59). Black spot incidence varied among populations and months; and showed a strong population x month interaction effect. The lowest black spot incidence was seen in September which was likely due to hot and dry weather in the previous two months or the disease had not established yet. For PFS, the estimated narrow sense heritability ranged from 0.12 to 0.54 and broad sense heritability was estimated as 0.53 based on the combined analysis. For BLS, the narrow sense heritability ranged from 0.07-0.42 and broad sense heritability was 0.58 according to the combined analysis. In both cases the highest estimate of narrow sense heritability was for the month of June. Moreover, the G x E (interaction between genotype and environment) variance was larger than the total genetic variance emphasizing the importance of the environment in the ability to distinguish among the level of partial resistance among genotypes.

2.2 Introduction

Roses, which have been cultivated for at least 5,000 years, are one of the most important ornamental crops in the world (Gudin, 2000). Black spot disease of rose, caused by the hemibiotrophic ascomycete fungus *Diplocarpon rosae* (Lib.) Wolf is the most prevalent fungal leaf disease of outdoor grown roses in warm humid areas (Debener and Byrne, 2014). This genetically variable fungus which is restricted to *Rosa* has been reported to have eleven physiological races across Germany, UK and North America (Horst and Cloyd, 2007; Whitaker et al., 2010). The optimal temperature for conidia germination and disease development is ~18- 24°C. As free water and high humidity favor infection, the morning dew or rainfall in the field favors black spot development on rose. *Diplocarpon rosae* typically causes circular black spots with irregular margins measuring from 2-12 mm in diameter on rose leaves. With time, the surrounding tissue turns chlorotic and dies leading to defoliation and plant death on highly susceptible roses (Dobbs, 1984; Gachomo et al., 2006). Unfortunately most important commercial rose cultivars are susceptible to black spot (Byrne et al., 2010; Uggla and Carlson-Nilsson, 2005; Zlesak et al., 2010). As disease resistance is the most important trait consumers and industry stakeholders want in a new rose cultivar, many rose breeding programs have the development of black spot resistant rose cultivars as an important breeding objective (Debener and Byrne, 2014).

Both of the major classes of resistance mechanisms (complete and partial) have been reported in roses (Carlson-Nilsson and Davidson, 2006; von Malek and Debener, 1998; Whitaker et al., 2007; Whitaker et al., 2010; Whitaker and Hokanson, 2009;

Zlesak et al., 2010). Complete or vertical resistance is based on pathogen gene for host gene interaction in which resistance prevents the pathogen of reproducing and severely limits fungal growth on the host plant. Complete resistance is generally inherited monogenically and effective against a specific pathogenic race (Trigiano et al., 2004). Three major black spot resistance genes – *Rdr1*, *Rdr2* and *Rdr3* have been characterized in tetraploid and diploid rose populations (Hattendorf et al., 2004; von Malek and Debener, 1998; Whitaker et al., 2010, 2009).

Partial or horizontal resistance has been described in rose as well (Byrne et al., 2010; Carlson-Nilsson and Davidson, 2006; Shupert, 2005; Uggla and Carlson-Nilsson, 2005; Whitaker and Hokanson, 2009; Xue and Davidson, 1998). Partial resistance does not prevent infection, but rather, inhibits fungal growth and reproduction. Partial resistance has been observed as reduced lesion size, reduced sporulation, and/or the delayed onset of infection in both field assessment and in artificial inoculation experiments (Byrne et al., 2010; Dong et al., 2017; Whitaker et al., 2007; Xue and Davidson, 1998). Partial resistance tends to be effective against all strains of a pathogen population but total resistance is rarely observed. It typically takes 2-3 years for the disease pressure to become high and even enough for the field assessment of disease resistance to differentiate the levels of resistance (Carlson-Nilsson, 2000; Debener and Byrne, 2014).

The goals of this study were to evaluate black spot partial resistance in diploid rose germplasm which lacks *Rdr* genes and estimate the heritability to the disease. Two measurements (percentage of the foliage with symptoms and black spot lesion size rating) were conducted to evaluate the partial resistance in fifteen diploid rose populations in a research field. Both narrow and broad sense heritability were estimated for the two parameters, and the correlation between two measurements was calculated.

2.3 Materials and methods

2.3.1 Plant materials

Fifteen diploid rose populations were generated in a partial diallel design by crossing five black spot resistant breeding lines derived from *R. wichuriana* 'Basye's Thornless' [J06-20-14-3 (J14-3), J06-28-4-6 (J4-6), J06-30-3-3 (J3-3), J06-30-3-6 (J3-6) and M4-4], and moderately to highly susceptible cultivars ['Old Blush' (OB), 'Little Chief' (LC), 'Red Fairy' (RF), 'Sweet Chariot' (SC), and 'Vineyard Song' (VS)] with excellent ornamental qualities (Dong et al., 2017). The populations and their sizes are shown in Table 1.

Table 1. Diploid rose populations with parental black spot resistance/susceptibility and population size indicated. S = susceptible, MS = medium susceptible, R = resistant.

Female	Male	Population size
J06-20-14-3 (R)	Little Chief (S)	53
J06-20-14-3 (R)	Red Fairy (S)	152
J06-20-14-3 (R)	Sweet Chariot (S)	60
J06-20-14-3 (R)	Vineyard Song (S)	92
J06-30-3-3 (R)	Red Fairy (S)	28
J06-28-4-6 (R)	Red Fairy (S)	84
M4-4 (R)	Sweet Chariot (S)	19
M4-4 (R)	Vineyard Song (S)	7
Old Blush (MS)	J3-06-30-3-3 (R)	101
Old Blush (MS)	M4-4 (R)	14
Old Blush (MS)	Red Fairy (S)	64
Sweet Chariot (S)	J06-20-14-3 (R)	25
Sweet Chariot (S)	J06-28-4-6 (R)	16
Sweet Chariot (S)	M4-4 (R)	85
Vineyard Song (S)	J06-20-14-3 (R)	12

2.3.2 Field assessment

All progeny were planted in the Texas A&M University Horticulture Farm in College Station, Texas (USA) with weed barrier and drip or overhead irrigation. No fungicides or pesticides were sprayed during the evaluation trial. One plant per seedling was planted in the field. Pruning was only performed to remove dead wood and keep the branches out of the tractor row at the end of winter and beginning of spring in February/March. At the time of evaluation, the plants were at least three years old which allowed sufficient time for uniform inoculum distribution throughout the two fields (Debener and Byrne, 2014). The evaluation for black spot severity was done in the field in June, September, October and November in 2016 with average monthly temperature and rainfall indicated in Table 2 and daily high and low temperature and precipitation in Figure 1 (U.S. climate data, 2016).

Table 2. Climatic records of College Station, TX for 2016 May, June, July, August, September, October and November with average maximum and minimum temperature (high and low °C) and total monthly rainfall (mm).

	Average monthly temperature (°C)		Rainfall
	Maximum	Minimum	(mm)
May	28	18	328
June	33	23	66
July	36	25	6
August	34	24	227
September	33	23	51
October	30	18	55
November	24	13	69

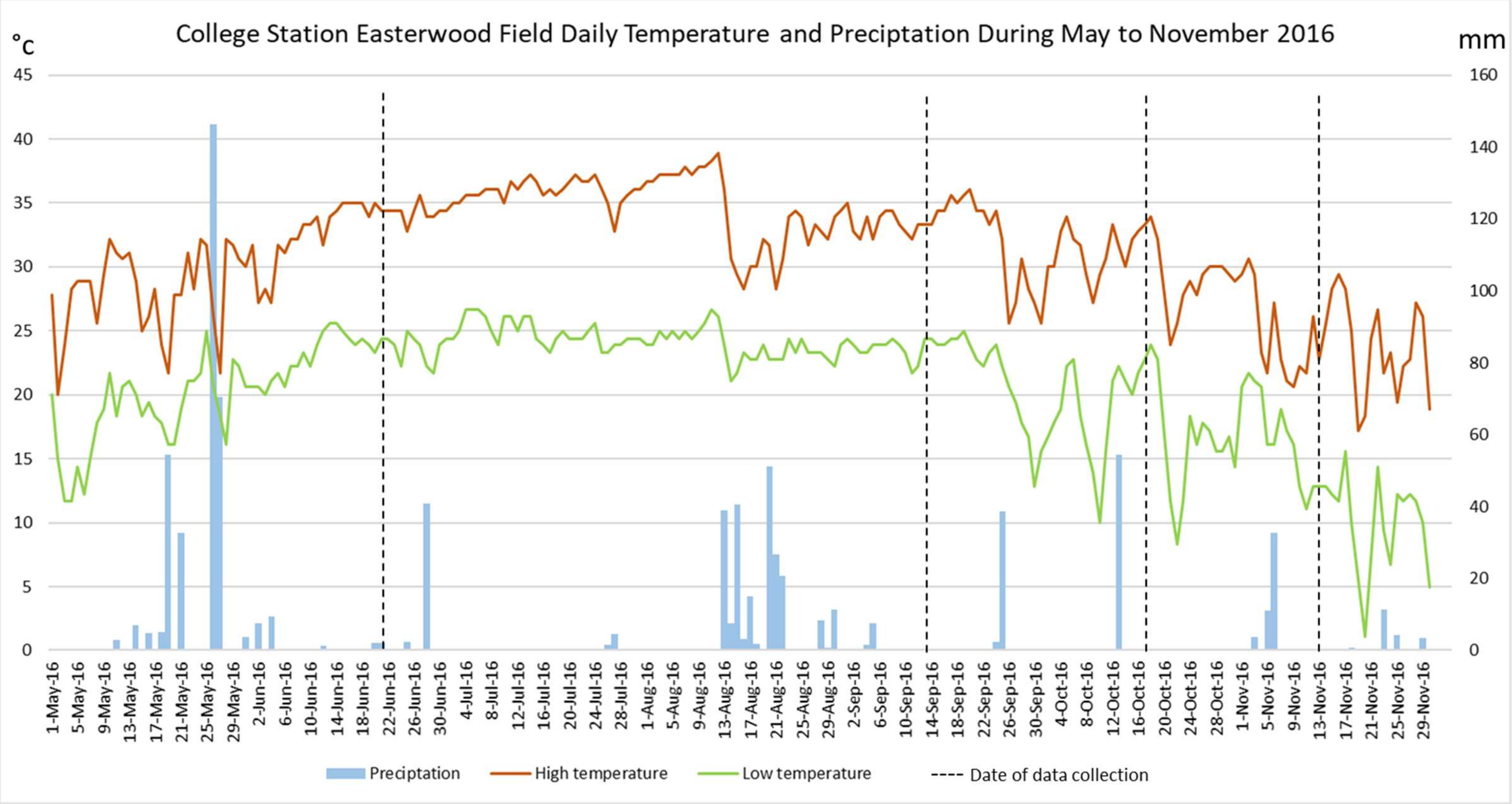


Figure 1. College Station Easterwood Field daily high and low temperatures and precipitation during June, September, October and November 2016 (U.S. climate data, 2016).

Black spot severity was assessed based on the percentage of the foliage with symptoms (PFS). A 0 to 9 scale was used with 0 = no black spot on plants, 1 = one or two isolated spots/infections, 2 = slight infection throughout the plant, 3 to 6 = based on % leaves infected, 7 = most foliage infected except most distal, 8 = all foliage infected, 9 = all foliage infected, heavy defoliation, plant vigor reduced. Black spot lesion size rating (BLS) was rated by naked eye and categorized as small, medium and large based on the whole plant's appearance (if most spots of a plant < 1 mm, the plant BLS was rated as small, spots > 3 mm were rated as large, anything in between would be rated as medium), and numbers 1, 2 and 3 were used to represent each category for the purpose of analysis (Figure 2).

Figure 2. Diagrammatic representation of PFS and BLS. A. Plant representation of PFS at 1, 3, 5, 7, or 9; B. Leaf representation of BLS at 1, 2, or 3 (small, medium, or large).

2.3.3 Statistical analysis

All statistical analysis was performed using JMP Pro Version 12.0.1 SAS Institute Inc. The normality of the population data (original and transformed by taking square root or log10) was analysed by the Shapiro-Wilk test, mean value of four month was analysed as combined data. Two-way factorial ANOVA (analysis of variance) and Student's *t* test were performed to compare means among and between the populations and months. The relationship between black spot partial resistance and lesion size was assessed via Pearson's correlations. The genotypic and phenotypic variances were estimated with a restricted estimated maximum likelihood (REML) model $y = \mu + \sigma_{FP}^2 + \sigma_{MP}^2 + \sigma_{Prog}^2 + \sigma_{month}^2 + \sigma_{Prog\,x\,month}^2 + \sigma_{Error}^2$ (FP = female parent, MP = male parent. Prog = progeny) assuming all effects random. Narrow sense (h^2) and broad (H^2) sense heritability were estimated as follows, $h^2 = V_a/V_P$, $H^2 = \frac{V_a + V_d}{V_P}$, $V_p = V_a + V_d + V_{gxe}/E$ where variances of parents were considered as additive variance (V_a), variance of progeny was considered as non-additive variance (V_d), variance of month/environment was considered as V_e, the interaction between progeny and environment was considered as V_{gxe}, and E represents the number of months/environments of the analysis.

2.4 Results

The mean ratings for both PFS and BLS were the lowest in September indicating less disease pressure than the other three months which reflected the dry hot weather experienced in July and between late August and mid-September (Figure 1 and Table 2) as the pathogen likes a warm (18-24°C) and humid environment (Horst and Cloyd, 2007). Given the lower disease pressure seen in September, the differentiation among susceptible and resistant genotypes was less distinct and the possibility of escapes was higher (Table 3).

Table 3. Mean and range for PFS and BLS evaluations in 2016 June, September, October and November of 812 seedlings from 15 diploid rose populations.

	Mean[z]		Range	
Month	PFS	BLS	PFS	BLS
June	3.54a	1.98c	0-9	0-3
September	2.40b	1.71d	0-7	0-3
October	3.55a	2.27b	0-9	0-3
November	3.40a	2.35a	0-8	0-3

[z]Levels connected by same letter are not significantly different at $\alpha = 0.05$.

2.4.1 Normality test for fifteen populations

As the transformation did not improve the normality of the data, the raw data was used for all statistical analyses (Tables 4 and 5). The results of the Shapiro-Wilk test for the raw data were similar to those obtained with the transformed data (data not shown). All 15 populations showed segregation for disease ratings and more than half of the populations were normally distributed when the four months were combined into one overall PFS rating (mean of four months) suggesting quantitative inheritance of this partial resistance trait (Table 4), whilst BLS did not fit normal distribution well (Table 5).

Table 4. Data transformation and normality test for percent of foliage covered with symptoms for fifteen diploid rose populations. SR: square root transformation.

PFS Shapiro-Wilk test[z]

	June			September			October			November			Combined[y]		
	Raw	SR	log10(1+score)	Raw	SR	log10(1+score)	Raw	SR	log10(1+score)	Raw	SR	log10(1+score)	Raw	SR	log10
J14-3 x LC	***	***	***	**	**	**	*	***	***	***	***	***	NS	NS	NS
J14-3 x RF	***	***	***	***	***	***	***	***	***	***	***	***	*	NS	**
J14-3 x SC	**	***	***	***	***	***	**	***	***	**	***	***	**	NS	NS
J14-3 x VS	***	***	***	***	***	***	***	***	***	***	***	***	***	**	*
J3-3 x RF	**	*	*	*	***	***	*	NS	NS	**	**	**	NS	NS	NS
J4-6 x RF	***	***	***	***	***	***	***	**	***	***	***	***	*	NS	NS
M4-4 x SC	*	**	**	**	***	**	**	**	***	NS	***	***	NS	NS	NS
M4-4 x VS	NS	NS	NS	NS	NS	NS	NS	NS	NS	**	*	*	NS	NS	NS
OB x J3-6	***	***	***	***	***	***	***	***	***	***	***	***	NS	*	***
OB x M4-4	*	*	*	NS	*	*	NS	NS	NS	NS	**	**	NS	NS	*
OB x RF	**	***	***	***	**	***	**	***	***	**	**	**	NS	NS	NS
SC x J14-3	NS	*	*	**	***	**	**	*	*	***	***	***	NS	NS	NS
SC x J4-6	NS	NS	NS	NS	NS	NS	*	*	*	**	***	***	NS	NS	*
SC x M4-4	**	***	***	***	***	***	***	***	***	***	***	***	NS	*	***
VS x J14-3	***	*	*	**	**	**	**	**	**	NS	NS	NS	**	NS	NS

[z] NS, *, **, *** not significant, significant at $p<0.05$, 0.01, and 0.001, respectively.

[y] Combined: Mean value of all three months.

Table 5. Data transformation and normality test for black spot lesion size rating for fifteen diploid rose populations. SR: square root transformation.

BLS Shapiro-Wilk test[z]

	June			September			October			November			Combined[y]		
	Raw	SR	log10(1+score)	Raw	SR	log10(1+score)	Raw	SR	log10(1+score)	Raw	SR	log10(1+score)	Raw	SR	log10
J14-3 x LC	***	***	***	***	***	***	***	***	***	***	***	***	*	**	**
J14-3 x RF	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
J14-3 x SC	***	***	***	***	***	***	***	***	***	***	***	***	*	NS	*
J14-3 x VS	***	***	***	***	***	***	***	***	***	***	***	***	*	**	***
J3-3 x RF	***	***	***	***	***	***	***	***	***	***	***	***	**	**	*
J4-6 x RF	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
M4-4 x SC	***	***	***	**	***	***	***	***	***	***	***	***	NS	NS	NS
M4-4 x VS	***	***	***	N/A[x]	***	***	***	***	***	***	***	***	**	**	**
OB x J3-6	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
OB x M4-4	***	***	***	***	***	***	***	***	***	**	***	***	NS	*	*
OB x RF	***	***	***	***	***	***	***	***	***	***	***	***	*	**	***
SC x J14-3	***	***	***	***	***	***	***	***	***	***	***	***	**	**	**
SC x J4-6	***	***	***	***	***	***	***	***	***	***	***	***	*	*	**
SC x M4-4	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
VS x J14-3	*	**	**	**	**	**	***	**	**	**	***	***	*	*	*

[x] N/A: Only one distinct observation was present, normal distribution does not fit.

[z] NS, *, **, *** not significant, significant at $p<0.05$, 0.01, and 0.001, respectively.

[y] Combined: Mean value of all three months.

2.4.2 Overall disease incidence and correlation between two measurements

Table 6 compares different disease incidences among different months for each population. Disease severity varied among months for some populations but not all of them. Table 7 compares the overall disease levels among populations using combined mean data. Populations SC x M4-4, J4-6 x RF, OB x RF, J3-3 x RF, and J14-3 x RF had the highest PFS rating while J14-3 x VS and VS x J14-3 had the lowest. Populations J14-3 x RF, J3-3 x RF, SC x M4-4, J4-6 x RF, and OB x RF had the biggest lesion size rating and J14-3 x VS had the smallest lesion size rating. Both measurements indicated that J14-3 x RF, J3-3 x RF, SC x M4-4, J4-6 x RF, and OB x RF are more resistant and J14-3 x VS is more susceptible than the rest of the materials.

Table 6. Mean comparison of PFS and BLS for each diploid rose population among June, September, October and November 2016 in College Station, Texas.

	PFS[z]				BLS[y]			
Population	Jun.	Sept.	Oct.	Nov.	Jun.	Sept.	Oct.	Nov.
J14-3 x LC	2.66c	3.49a	3.38ab	2.92bc	1.72b	1.89ab	2.09a	2.06a
J14-3 x RF	3.69a	3.53a	3.74a	3.66a	2.22c	2.26bc	2.35b	2.54a
J14-3 x SC	3.57a	1.59c	3.07ab	2.85b	1.88a	1.18b	1.85a	1.88a
J14-3 x VS	1.73c	0.80d	3.14a	2.13b	1.07b	0.87b	2.02a	1.97a
J3-3 x RF	3.39b	3.11b	4.46a	3.68b	2.11b	2.00b	2.29ab	2.39a
J4-6 x RF	4.40ab	2.10c	4.65a	3.96b	2.04b	1.74c	2.54a	2.67a
M4-4 x SC	3.42ab	2.47c	3.58a	2.68bc	1.95ab	1.74b	2.32a	2.11ab
M4-4 x VS	4.57a	2.57b	3.57ab	3.14ab	2.14a	2.00a	2.14a	2.29a
OB x J3-6	2.99b	2.14c	2.37c	3.40a	2.20b	1.62c	2.28b	2.51a
OB x M4-4	2.79bc	2.00c	3.21ab	4.00a	1.64b	1.57b	2.36a	2.29a
OB x RF	5.38a	2.11d	3.31c	4.20b	2.28b	1.68c	2.33b	2.61a
SC x J14-3	5.36a	2.40b	3.04b	3.12b	2.16ab	1.92b	2.20a	2.12ab
SC x J4-6	3.38ab	2.63b	4.06a	3.81a	1.88a	1.88a	2.19a	2.25a
SC x M4-4	4.18b	2.46c	4.64a	3.91b	2.27b	1.77c	2.56a	2.39ab
VS x J14-3	1.08b	2.33ab	1.83ab	3.00a	1.50a	1.75a	2.17a	2.08a

[y] PFS: percentage of the foliage with symptoms; BLS: black spot lesion size rating; [z] Levels connected by same letter in a row (across months within one population) are not significantly different at $\alpha = 0.05$.

Table 7. Mean comparison of PFS and BLS among 15 diploid rose populations from the 2016 field evaluations.

Population	PFS^z	BLS^y
J14-3 x LC	3.11bc	1.94e
J14-3 x RF	3.66a	2.34a
J14-3 x SC	2.83cd	1.72f
J14-3 x VS	1.95e	1.48g
J3-3 x RF	3.67a	2.2abcd
J4-6 x RF	3.79a	2.25ab
M4-4 x SC	3.04bcd	2.03de
M4-4 x VS	3.46abc	2.14abcde
OB x J3-6	2.73d	2.16bcd
OB x M4-4	3bcd	1.96de
OB x RF	3.76a	2.23bc
SC x J14-3	3.48ab	2.1bcde
SC x J4-6	3.47abc	2.05cde
SC x M4-4	3.8a	2.25ab
VS x J14-3	2.06e	1.88ef

^{y}PFS: percentage of the foliage with symptoms; BLS: black spot lesion size rating; ^{z}Levels connected by same letter within a column (among populations) are not significantly different at $\alpha = 0.05$.

The correlation between foliage covered with symptoms (PFS) and black spot lesion size rating (BLS) was moderate (r = 0.59) in the 2016 field trials (Figure 3). There was a slight tendency showing that PFS and BLS are correlated, the higher the coverage of foliage with symptoms, the larger the lesion size rating tended to be (Figure 3).

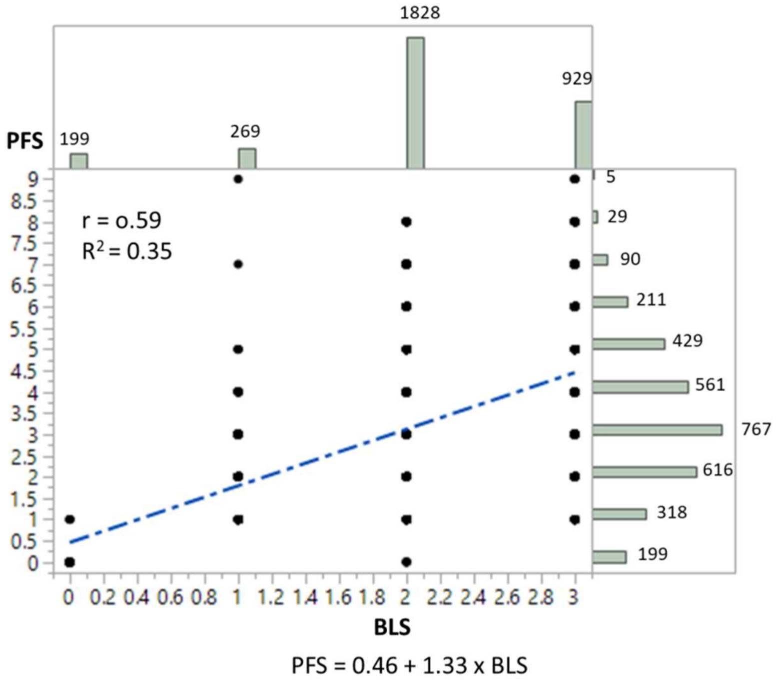


Figure 3. Correlation between % of foliage covered with symptoms (PFS) and black spot lesion size rating (BLS) and the distribution of the progeny of 15 diploid rose populations (812 individuals) in 2016 June, September, October and November field assessments. Dots represent observations per category, numbers of progeny in each category are showed above the histogram bars.

2.4.3 Genetic variance and heritability estimation of black spot partial resistance

In the 2016 black spot partial resistance field trial, narrow sense heritability estimations for PFS and BLS varied from 0.12 to 0.54 and 0.07 to 0.42, respectively when monthly and mean data were evaluated. In both PFS and BLS overall variance analyses, additive variances were larger than non-additive variances, with V_a being 0.40 and 0.11, and V_d being 0.23 and 0.04 for PFS and BLS, respectively. The environmental variance (0.31) was smaller than the additive (0.40) and larger than the non-additive (0.23) variance for PFS, and the environmental variance of BLS (0.08) was smaller than the additive variance (0.11) but larger than the non-additive variance (0.04). The interaction of genetic and environment variance was high for PFS (2.29) and low for BLS (0.44), respectively. The broad sense heritability estimated from the models were moderate (0.53 and 0.58 for PFS and BLS, respectively) indicating that black spot partial resistance is moderately heritable (Table 8 and 9).

Table 8. Mean squares and genetic variances for 2016 PFS field ratings of 15 diploid rose populations by month and for the four months combined.

	Combined	Jun.	Sept.	Oct.	Nov.
	Percentage of total variances				
Female	5.25	34.20	17.12	11.35	1.36
Male	7.25	19.98	25.47	8.89	10.42
Progeny	7.23	45.83	57.41	79.76	88.22
Month	9.61				
Progeny x Month	70.66				
	Genetic variances				
V_a	0.40	2.75	1.62	0.59	0.29
V_d	0.23	2.33	2.19	2.33	2.19
V_g	0.63	5.08	3.81	2.92	2.48
V_p	1.20	5.08	3.81	2.92	2.48
V_{gxe}	2.29				
	Heritability				
h^2	0.33	0.54	0.43	0.20	0.12
H^2	0.53				

Table 9. Mean squares and genetic variances for 2016 BLS field ratings of 15 diploid rose populations by month and for the four months combined.

	Combined	Jun.	Sept.	Oct.	Nov.
	Percentage of total variances				
Female	4.99	11.57	13.99	1.97	1.16
Male	11.19	22.72	22.11	5.28	12.60
Progeny	5.63	65.72	63.89	92.75	86.24
Month	12.67				
Progeny x Month	65.51				
	Genetic variances				
V_a	0.11	0.20	0.36	0.04	0.06
V_d	0.04	0.38	0.64	0.46	0.35
V_g	0.15	0.58	1.00	0.50	0.41
V_p	0.26	0.58	1.00	0.50	0.41
V_{gxe}	0.44				
	Heritability				
h^2	0.42	0.34	0.36	0.07	0.14
H^2	0.58				

2.5 Discussion

Mean disease rating in September was lower than in June, October and November, due to the hot and dry weather in July, mid-late August and early September (Figure 1). Genetic variances of the overall four month combined analyses calculated from the all random restricted maximum likelihood model (REML) showed that the additive variances explained 13% and 16% of the total variance for PFS and BLS, respectively, which were higher than what were explained by the non-additive variances (7% and 6%, respectively). The variance of genotype by environment effect (71% and 66%) explained most of the variance indicating that BS partial resistance was strongly affected by the environment, therefore, it is suggested that selection should be done across different environments (over time and/or locations) rather than in a single environment. The narrow sense heritability estimated from the field assessment ranged from 0.12 to 0.54 and 0.07 to 0.42 for PFS and BLS, respectively, indicating that BS partial disease resistance has low to moderate heritability, which agrees with results obtained using a laboratory-based detached leaf assay (Dong et al., 2017).

The correlation between PFS and BLS was moderate (r = 0.59). Though the correlation was positive, every BLS category (except for the ones with no lesions/black spot) contained the whole range of PFS varying from severe infection to strong resistance (Figure 3), indicating these two measurements should be done separately if both are needed.

Considering black spot partial resistance is moderately heritable as well as selection for non-additive variance is feasible for clonally propagated species, thus it is better to select for the best individual within a specific cross family and followed by the backcrossing to the commercial cultivar to incorporate the resistance into other genetic backgrounds and clonally propagate the new hybrid.

CHAPTER III

A HIGH-DENSITY SNP-BASED CONSENSUS MAP FOR DIPLOID ROSES AND INSIGHTS INTO THE HIGH SYNTENY BETWEEN *FRAGARIA VESCA* AND *ROSA*

3.1 Synopsis

Utilizing genotyping by sequencing technology and the strawberry genome (*Fragaria vesca* v2.0.a1) as a reference, thousands of informative single nucleotide polymorphism (SNP) markers were generated. These SNPs along with known bridge simple sequence repeat (SSR) markers allowed for the creation of the first high-density integrated consensus map for diploid roses. Using the restriction enzyme *Ngo*MIV ($G^{\vee}$CCGGC) to construct the DNA template for three diploid rose populations, 3527 molecular markers were identified to create the consensus map. Individual maps were first created for populations J06-20-14-3 x 'Little Chief' (J14-3 x LC), J06-20-14-3 x 'Vineyard Song' (J14-3 x VS) and 'Old Blush' x 'Red Fairy' (OB x RF) and these maps were linked using 824 SNPs and 13 SSR bridge markers. The anchor SSR markers were used to determine the numbering of the rose linkage groups. The diploid consensus map has seven linkage groups (LGs), a total length of 892.2 cM, and an average distance between markers of 0.25 cM. By combining three individual populations, the marker density and the reliability of the marker order in the consensus map was improved over a single population map. High synteny between the strawberry and diploid rose genomes was observed. This consensus map will serve as the tool for the discovery of marker-trait associations in rose breeding.

3.2 Introduction

Roses (*Rosa* spp.) are one of the most important and popular ornamental crops in the world today. Diverse plant growth types, flower colors, flower size/shapes, and fragrance all contribute to the commercial value of the rose. Besides ornamental uses, roses also have medical, culinary and cosmetic uses (Hummer and Janick, 2009; Zlesak, 2006). Rose is a very important ornamental plant in the US specialty crop market with an annual value of about $400 million (AmericanHort, 2014). There are approximately 200 *Rosa* (Rosaceae) species of which about half of the species are diploid ($2x = 14$). Among the more than 20,000 commercial rose cultivars (Zlesak, 2006), most tested cultivars are either tetraploid ($4x = 28$), triploid ($3x = 21$) or diploid ($2x = 14$) (Ueckert et al. 2015; Zlesak, 2006). Most cultivated roses are hybrids derived from 8 to 10 diploid and tetraploid species (Byrne and Crane, 2003; Gudin, 2000). Though DNA content varies among diploid rose sections, subgenera and cultivars, the diploid rose genome size is small (0.78-1.29 pg/2C) within the angiosperms which is two to four times the size of *Arabidopsis thaliana* (L.) Heynh (Arumuganathan and Earle, 1991; Debener and Linde, 2009; Rajapakse et al., 2001; Yokoya, 2000).

Genetic maps have been constructed in rose using a range of markers including phenotypic (i.e. visible) traits, isozymes, random amplified polymorphic DNA (RAPDs), restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLPs), sequence-tagged sites (STSs), microsatellites or simple sequence repeats (SSR) and single nucleotide polymorphism (SNPs) (Byrne, 2009; Koning-Boucoiran et al., 2012; Yan et al., 2005). For the effective construction of linkage maps, there needs to be polymorphic markers which are evenly distributed across the genome or the region of interest, high marker coverage and a low genotyping error rate (Ball et al., 2010). Mapping work for diploid roses started by creating two parental maps using the pseudo-testcross strategy, one for the female and the other one for the male with rose mapping populations around 100 individuals. The number of markers on the maps varied from less than a hundred to a little less than three hundred covering 300 cM to 500 cM for each parental map (Crespel et al., 2002; Dugo et al., 2005; Yan et al., 2005, 2003). Genetic map construction has also been conducted in tetraploid roses, though populations used for some of the tetraploid mapping were larger than those for most diploid studies, still only two to three hundred molecular markers were successfully mapped into each parental map spanning six hundred to one thousand centi-morgans (cM) for tetraploid rose genome (Gar et al., 2011; Koning-Boucoiran et al., 2012; Yu et al., 2015).

More recently, with more markers available, the integrated map approach has been possible resulting in longer map lengths. Linde et al. (2006) developed an integrated diploid genetic map for rose using 233 markers covering 418 cM of the diploid rose genome. For tetraploid rose, Yu et al. (2015) integrated the homologous linkage groups from both parents with 74 pairs of SSRs and constructed an integrated map with length of 874 cM. Beyond the individual maps, the first unified diploid consensus map for rose (ICM) was constructed in 2011 (Spiller et al., 2011) by using 59 bridge markers to link four diploid populations. This ICM included 597 markers and covered a length of 530 cM on seven linkage groups.

These mapping studies identified QTL associated with horticultural traits such as thorn density, leaf area, chlorophyll content, flower size, days to flowering, leaf size and resistance to powdery mildew. However, some QTL appeared germplasm specific and the same marker could not be used across populations with different genetic background (Byrne, 2009; Debener and Byrne, 2014). With the advance of modern genomic tools, a high-resolution map is possible (Wang et al., 2015), and by integrating several populations, the marker order is more reliable, the genome coverage is improved, and of its usefulness across diverse genetic backgrounds can be improved (Spiller et al., 2011).

Genomic comparative studies within the Rosaceae family has shown that the synteny and collinearity among *Prunus*, *Malus*, *Pyrus*, *Fragaria* and *Rosa* was high (Bourke et al., 2017; Dirlewanger et al., 2004; Gar et al., 2011; Guajardo et al., 2015; Illa et al., 2011; Vilanova et al., 2008; Vukosavljev et al., 2016; Yamamoto et al., 2004). Strawberry and rose both belong to the Rosoideae subfamily of the Rosaceae and have seven as the base chromosome number, they have been shown to have a close genetic relationship as indicated with various molecular markers (Bourke et al., 2017; Gar et al., 2011; Potter et al., 2007; Spiller et al., 2011; Vukosavljev et al., 2016). In 2011, Gar et al. (2011) compared the collinearity among the *Rosa* and *Fragaria* by positioning 70 rose EST markers on the strawberry pseudo-chromosomes. They found most of the markers mapped to one linkage group of *Rosa* were located on one *Fragaria* pseudo-chromosome. It was estimated that four major translocations and six inversions have occurred between *Rosa* and *Fragaria* genome since their divergence from a common ancestor. With the new version of the diploid *Fragaria vesca* genome (Fvb) (Shulaev et al., 2011; Tennessen et al. 2014; Darwish et al. 2015) and improved sequencing technologies, the syteny between *Rosa* and *Fragaria* can now be examined with thousands of markers. In most recent studies, the comprehensive collinearity between strawberry and rose were demonstrated by utilizing the new WagRhSNP 68K Axiom SNP array (Koning-Boucoiran et al., 2015). In both studies the detailed synteny relationship among seven chromosomes between two genera revealed a reciprocal translocation, a major telomeric inversion and a possible inversion between the two genera (Bourke et al., 2017; Vukosavljev et al., 2016).

Currently, it is possible to sequence the whole plant genome or sample the transcriptomes more thoroughly and cost-efficiently using next generation sequencing (NGS) technologies, such as 454, Illumina, PacBio and AB SOLiD (Myllykangas et al., 2012; Varshney et al., 2009). SNP markers generated from genotyping by sequencing (GBS), though due to their biallelic feature contain less information than multi-allelic markers (Ball et al., 2010) are cost effective due to their abundance and the existence of an automated high-throughput genotype calling protocol (Giancola et al., 2006; Rafalski, 2002). This approach has facilitated the genomic study of many plant species, including Thale cress (*Arabidopsis thaliana* L.*)* (Jander et al., 2002), maize (*Zea mays* L.) (Tenaillon et al., 2001), sorghum (*Sorghum bicolor* L.*)* (Morishige et al., 2013), rice (*Oryza sativa* L.) (Caicedo et al., 2007), and barley (*Hordeum vulgare* L.) (Rostoks et al., 2005), as well as many heterozygous horticultural crops such as apple (*Malus x domestica* Borhk) (Bianco et al., 2014), grapevine (*Vitis vinifera* L.) (Hyma et al., 2015), ancestral diploid strawberry (*Fragaria iinumae* Makino) (Mahoney et al., 2016), sweet cherry (*Prunus avium* L.) (Guajardo et al., 2015) and tetraploid cut roses (*Rosa hybrida* L.) (Koning-Boucoiran et al., 2012). Currently, the genome of *Rosa chinensis* 'Old Blush' is being sequenced and some studies have been done using the available RNA seq and expressed sequenced tags (ESTs) (Dubois et al., 2012; Pei et al., 2013; Yan et al., 2014). With more research being done on roses, rose can potentially serve as a model plant for complex ornamental genomes (Debener and Linde, 2009).

The aim of this study was to use previously developed anchor SSRs (Spiller et al., 2011) and SNPs generated from GBS to construct a dense integrated consensus map for several diploid rose populations (ICD). SNPs produced from Illumina HiSeq 2500 platform were used together with the anchor SSRs to construct linkage maps. This consensus map enabled us to visualize the syntenic relationship between strawberry and diploid rose, and compare and validate the marker orders across populations. This was the first SNP based high density consensus map for roses. The development of a high-density consensus genetic map in rose will help identify QTL, candidate genes, and markers associated with traits useful for breeding and will facilitate the synteny comparison among taxonomic groups.

3.3 Materials and methods

3.3.1 Mapping materials

It is critical to select diverse parents to create mapping populations, because the parents' marker profiles must be different to construct a map. In this study, two rose species *Rosa wichuriana* 'Basye's Thornless' (BTh) and *Rosa chinensis* were selected as founder parents because they are divergent in growth habits, horticultural characteristics, and black spot resistance. The black spot resistant breeding line J06-20-14-3 (J14-3) which is derived from BTh, a moderately susceptible line 'Old Blush' (OB) and three susceptible cultivars with excellent ornamental characteristics, 'Little Chief' (LC), 'Red Fairy' (RF), and 'Vineyard Song' (VS) were used to generate three diploid populations (2n = 2x = 14) for this genetic linkage map (Table 10).

Table 10. Diploid rose parents of the three mapping populations and their response to black spot disease. S = susceptible, MS = moderate susceptible, HR = high resistance.

Female parent	**Male parent**	**Number of seedlings**
J06-20-14-3 (HR)	**Little Chief (S)**	69
J06-20-14-3 (HR)	**Vineyard Song (S)**	83
Old Blush (MS)	**Red Fairy (S)**	82

These populations were grown in the field in College Station (30°36'5"N 96°18'52"W, 112 m elevation), TX, USA, a subtropical mild winter, hot summer, humid climate which has an average annual rainfall of 1018 mm, and spring, summer, fall, and winter average temperatures of 20°C, 29°C, 21°C, and 12°C, respectively (http://www.usclimatedata.com/climate/college-station/texas/united-states/ustx2165).

3.3.2 DNA extraction

DNA extraction was performed based on Doyle's (1991) CTAB protocol with some minor modification which can be found in the Appendices 1 and 2. After extraction, DNA samples were incubated with RNase at 37°C for forty to fifty minutes and then the isolated genomic DNA was purified using OneStep™ PCR Inhibitor Removal Kit from Zymo Research (Irvine, CA, USA) according to the manufacturer's protocol. DNA quantification was performed fluorometrically using Qubit Fluorometer (Invitrogen, CA) or AccuBlue™ (Biotium, Hayward, CA, USA) according to the protocol from the manufacturer. All DNA samples were stored at -20°C.

3.3.3 Fluorescence anchor SSR marker

Forty SSRs described by Spiller et al. (2011) as bridge markers were analyzed on the five parental lines: J06-20-14-3 (J14-3), ‘Old Blush’ (OB), ‘Red Fairy’ (RF), ‘Vineyard Song’ (VS) and ‘Little Chief’ (LC). Twenty-six (Table 11) of the 40 SSRs were run on progenies of J14-3 x VS, J14-3 x LC, and OB x RF to determine the linkage groups according to ICM (Spiller et al., 2011) and used as quality control markers. The rest of the markers were not used for further analysis due to the lack of suitable polymorphisms.

The 10 uL PCR reaction mixture contained 2 uL of 2.5 ng/uL genomic DNA, 2 uL 5X GoTaq reaction buffer, 1 uL 25 mM dNTP, 0.8 uL 25 mM $MgCl_2$, 1 uL HEX, TET, FAM, or NED fluorescently labeled forward primer, 1 uL non-fluorescently labeled forward primer, 0.04 uL GoTaq DNA polymerase (Promega Corporation, Madison, WI), and 2.16 uL autoclaved DNase-/RNase-free water. The PCR reactions were performed in GeneAmp® 9700 thermal cycler (Applied Biosystems) programmed for first step of denaturation at 95°C for 2 minutes, followed by 25 cycles of denaturation at 95°C for 45 s, primer annealing at 55°C for 45 s, and primer extension at 72°C for 1 min. The last step of the final extension was done at 72°C for 20 mins, and then held at 4°C. The sets of single fluorescently labeled (HEX, TET, FAM or NED) PCR product (1 uL) were added to 5 uL Hi-Di Formamide and ROX400 master mix (1 mL Hi-Di Formamide + 50 uL ROX400), followed with denaturation at 95°C for 5 min. The mixture was run on the capillary sequencer, ABI3130xl Genetic Analyzer (Applied Biosystems) (Figure 4). The files generated by the ABI3130xl were then analyzed by the GeneMapper v4.0. The allele sizes called from GeneMapper were converted into JoinMap standard codes: abxcd, hkxhk, lmxll and nnxnp.

Table 11. PCR product sizes of twenty-six labeled SSR primers for parents of J14-3 x VS, J14-3 x LC and OB x RF diploid rose populations.

SSR	Primer (5'-3')	Linkage group	J14-3	LC	OB	RF	VS
BFACT47_LG3	F: ATCGTACCTATGCATCATCTGC	LG3	148, 159	-	144, 148	143, 147	147, 165
	R: AGGCAGGACCATCAACTAAGAG						
CL2845_LG5	F: ACAACCCGTAAAACGACCTG	LG5	295, 304	295, 306	295	-	295, 306
	R: ATATGGTGCCTTTGGTGGAA						
CL2980_LG6	F: CCCTATTCGATTTCGAGTGC	LG6	122, 225, 228	122	127, 222	122, 225, 231	125, 223, 235
	R: ACTTGGCTCGACGGATACAC						
CL2996_LG2	F: GCCACCATAGCCAGAGACAT	LG2	-	181, 187	178, 187	178, 184	175, 187
	R: GGGCAGAGAAGAAGTTGACG						
CL3881_LG4	F: GACAACGACCACACCACTTG	LG4	237, 245	238, 240	237, 240	245	232, 249
	R: CCAAAGCAACATTGTCAAAAGA						
CTG21_LG3	F: CACAGTTTCCATTAACACAGCA	LG3	121, 131	-	121, 133	120, 123	124, 133
	R: CAAGAGGAGGCAAGAGGATG						
H5_F12_LG1	F: CACAGAAACGAAGCGCAGTA	LG1	132	132, 141	132, 138	132, 138	132, 141
	R: GCTCGAAGAAGTCCTGGATG						

Table 11. Continued

SSR	Primer (5'-3')	Linkage group	J14-3	LC	OB	RF	VS
Rh48_LG2	F: GATAGTTTCTCTGTACCCCACCTA R: TTGACCAGCTGCAACAAAATTAGA	LG2	105, 118	96, 106, 119	96, 118	97, 117, 144	96, 118, 135
Rh50_LG3	F: TGATGAAATCATCCGAGTGTCAG R: TCACTTTCATTGGAATGCCAGAAT	LG3	96, 310, 337	304	304, 333	304, 310	304, 310
Rh58_LG3	F: ACAATTTAGTGCGGATAGAACAAC R: GGAAAGCCCGAAAGCGTAAGC	LG3	240, 264	289	248, 289	252	248, 289
Rh72_LG7	F: CCAAAAGACGCAACCCTACCATAA R: TCAAAACGCATGATGCTTCCACTG	LG7	263, 269	261, 263	252, 261	261, 269	261, 277
Rh93_LG5	F: GCTTTGCTGCATGGTTAGGTTG R: TTCTTTTTGTCGTTCTGGGATGTG	LG5	129, 190, 243	130, 190	130, 190, 237	130, 190, 243	129, 189, 267
RhAB9-2_LG1	F: GTCAATTTGTGCATAAGCTC R: GTGAGAACAGATGAGAAATG	LG1	95, 97	94, 99	94, 113	95, 101	113
RhABT12_LG4	F: CAAGTTTGTCTCCTTGGACC R: CATAGATGATTATCCTAGAGCC	LG4	162, 198	151, 175	151, 165	151, 202	151, 156
RMS001_LG7	F: TTCAAAATTGCTGCCCCCTTAG R: TACCAGTTGAGTGAGAAATAGTT	LG7	229, 241	226, 229, 231, 233, 234	222, 226, 231, 234	-	229, 232
RMS003_LG7	F: TGGGAAAGGGAAAGCAACA R: AAGGTAGGCAGAAGTGACAGACAT	LG7	160, 163	156, 170	150, 170	160, 174	164, 202

Table 11. Continued

SSR	Primer (5'-3')	Linkage group	J14-3	LC	OB	RF	VS
RMS015_LG1	F: TAATGTAGGCAGATATAAAGGAGT R: GCAGCTGCACAACAAGGAA	LG1	131, 166	132, 154, 172	132, 154, 172	130, 162	131, 164, 182
RMS043_LG7	F: GATCAAAGATGGGTTCTCCTCTC R: AGGGGAATCTTTGAAAGTCGTTC	LG7	130, 205, 220	130, 205	129, 205, 214	129	217
Rw11E5_LG6	F: GATACCGCGAAGGTGTAGT R: GAGTGAAAACTCTGCAATCA	LG6	152, 164, 172, 182	167	154,167, 172, 179	152, 167, 170	139, 168
Rw12J12_LG3	F: CAGTGTCCATGCTGACGAGT R: TGCTCCTGTTTTCTCTTTGCT	LG3	158, 171	170	145, 170	164, 171	160, 164
Rw14H21_LG5	F: ATC ATG TGC AGT CTC CTG GT R: AAT TGT GGG CTG GAA ATA TG	LG5	118, 145	118, 120	118, 123	118, 153	118, 120
Rw22B6_LG7	F: ACAGTGAGTTGTTCGCTTCT R: TTCATTGCTAGGAAGCAGTA	LG7	133, 139	134	131, 133	134	133
Rw34L6_LG1	F: CTCCTTTAGACTCGGGACCA R: CAGGCACGCCATTTCTAACT	LG1	132, 212	130, 209	131, 210?	127, 206	129, 208
Rw35C24_LG3	F: GGCGAATCGAGATTCAGAGA R: GGATTAGCCCAAGTCCAGGT	LG3	254, 258	246, 261	246, 258	248, 250	246, 252
Rw55E12_LG4	F: CGGTGGTTGGACATTAAAGC R: GGAGGCAACAGCACACTCTC	LG4	133, 180	130, 170, 182	130, 165, 182	130, 170, 182	132, 178
Rw5G14_LG7	F: TGGTTTGGGGTTTTGTGTCT R: GCACAGTCTCCACCTGACAA	LG7	234, 250	242, 250	250, 252	227, 238	227, 252

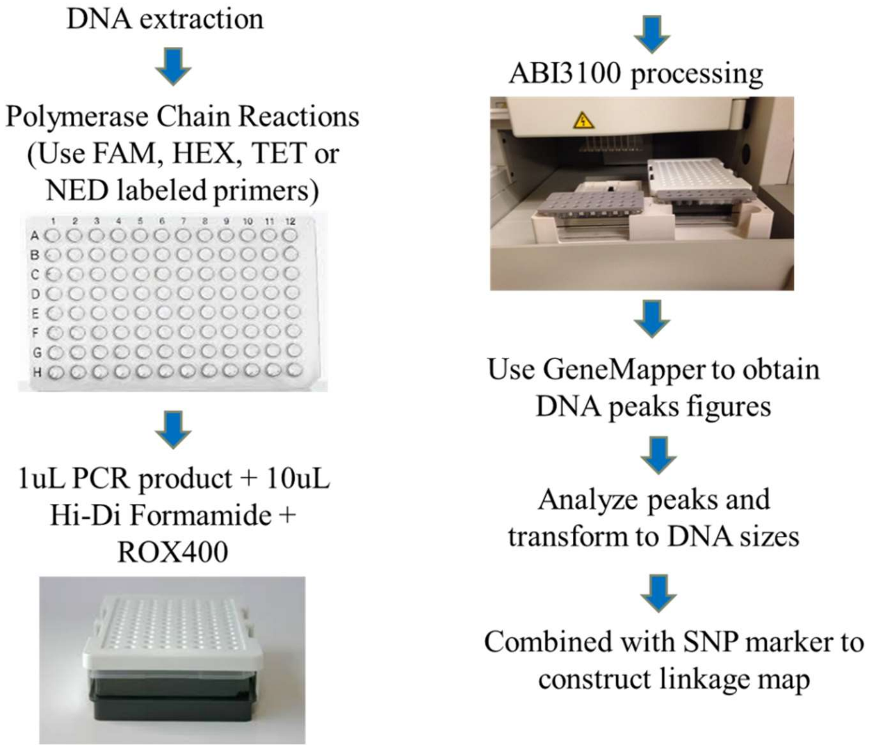


Figure 4. Flowchart of fluorescence anchor SSR analysis performed on an ABI3100 capillary sequencer.

3.3.4 Genotyping by Sequencing

Genotyping by sequencing or digital genotyping uses a restriction enzyme to construct the DNA library for sequencing to generate thousands of SNPs markers. This method was developed and applied on C4 grasses on Illumina GAIIx/HiSeq2500 platforms which read 50 to 300 bp short sequences (Morishige et al., 2013). Two methylation sensitive enzymes (*Fse*I and *Ngo*MIV) and one partially methylation sensitive enzyme *Nhe*I were tested. With a minimum of 250 ng DNA, the DNA library was prepared following the protocol for the Illumina HiSeq 2500 sequencer (Illumina, San Diego). The final DNA pool of 80 individual samples was loaded on one lane of the

Illumina flow cell. 126 cycles of single-end sequencing were completed with the Illumina HiSeq2500 (Figure 5).

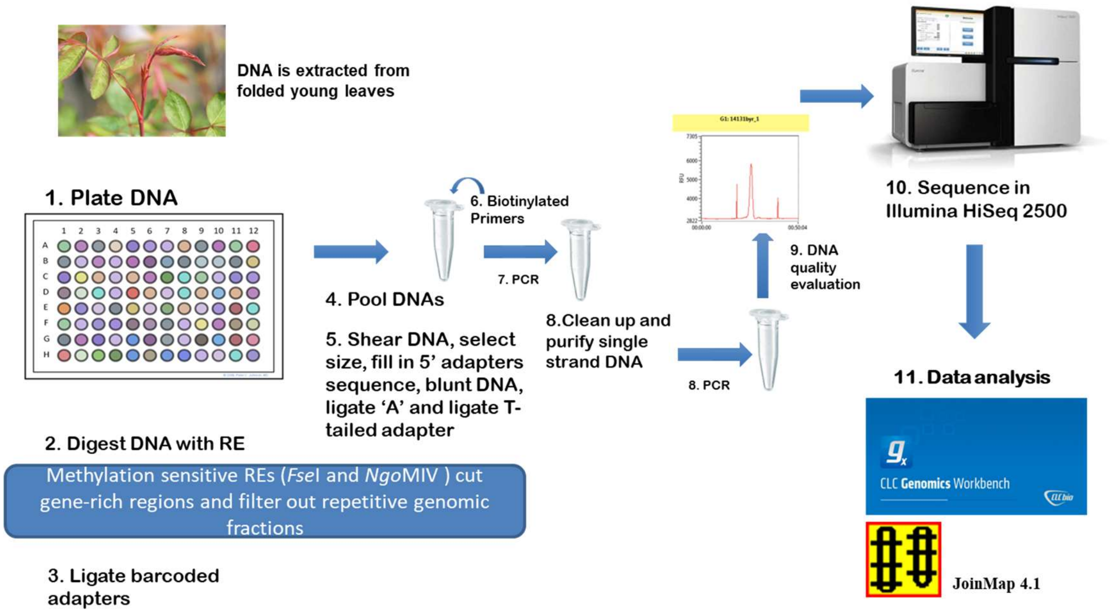


Figure 5. Procedures for genotyping-by-sequencing technology application on rose.

3.3.5 Bioinformatic data processing

After obtaining the FASTQ sequence files from the Illumina HiSeq2500, the distinct 12 bp barcodes on the 5' end were trimmed off the 126 bp long sequences prior to being imported into the CLC Genomics Workbench (Qiagen, Boston, MA). 100% match to both barcodes and partial restriction sites were crucial to retain the sequences. Trimmed reads of rose were mapped to *Fragaria vesca* whole genome v2.0.a1 (Tennessen et al., 2014) and SNPs and INDELs were called from the CLC Bio Genomics Workbench 7.5.1 (https://www.qiagenbioinformatics.com/). Parameters for read alignment were set as mismatch cost = 2, insertion and deletion cost = 3, 50%

minimum read length required to match the reference and a minimum of 75% similarity between the reads and the reference genome. Any reads that failed to align to the reference genome or aligned to more than one position were ignored. After the alignment, variant detection was performed to call SNPs. The parameters for SNP detection in the CLC genomics workbench were: at least 90% probability to detect a variant, a minimum read coverage of 15 to detect a SNP, a minimum count of 3, a neighborhood radius=5, a minimum central quality= 20, a minimum neighborhood quality=15. These parameters were applied to determine legitimate SNPs. The SNP file was exported into SAM and comma-separated-value (.csv) formats respectively. Further SNP call analysis was performed using custom scripts written in python and perl. The reformatted SNP data were filtered in MS-Excel for genetic map construction and SNPs were eliminated if both parents are homozygous, if one or both parents have no-calls, if too many progeny have missing data (>15% of population size), if the segregation ratio is too skewed based on Chi-square test ($p \leq 0.0005$), if any parental genotype does not appear in the JoinMap 4.1 manual (van Ooijen, 2006). SNP markers were named according to their physical position on the *Fragaria vesca* whole genome v2.0.a1 Assembly & Annotation (Fvb) in the GDR database (https://www.rosaceae.org/node/4118857). For example, SNP chr1_19.680628 is located on *Fragaria vesca* pseudo-chromosome 1 at position 19.680628 Mbp. Marker alleles were converted into ab x cd, ef x eg, hk x hk, lm x ll and nn x np according to the CP population segregation type codes in JoinMap.

3.3.6 Individual genetic linkage map construction

Individual linkage maps were first developed from the crosses of J14-3xLC, J14-3xVS and OBxRF independently. Polymorphic markers were kept with less than 15% missing data, and P=0.0005 was used as threshold to filter highly skewed SNP markers based on Chi-square test (χ^2), because highly skewed markers are biologically possible. To facilitate the construction of the consensus rose map, before the map construction, 1014 common markers across three families were all kept even though some had the same segregation patterns within one family. Among the rest of the markers, only one of the co-segregating markers was kept. These 1041 common SNPs were labeled with 'c' at the end. Grouping LOD varies from 5 to 15. Each group was assigned to one of the seven rose chromosomes according to anchor SSR markers whose chromosome positions were known. The maps were constructed with the maximum likelihood mapping function. Cross pollination (CP) population type was chosen in JoinMap® 4.1, because for heterozygous diploid rose, up to four different alleles may be segregating (van Ooijen, 2006). Markers that greatly inflated the linkage group length or cause double recombinations which cannot be solved by moving to other positions were dropped during the mapping process. In addition, individuals with many unexpected alien alleles (>3%) or too many recombination events (either outcrosses or selfed progeny) were dropped before the final mapping. The common markers excluded during the mapping process were pushed back to the map in the final step after ordering all other markers for the purpose of map integration across three families. The final linkage maps were drawn by MapChart 2.3 (Voorrips, 2002). On the final maps, 837 markers were shared between at least two populations and 203 markers were shared across all three populations.

3.3.7 Consensus map construction

A total of 234 F_1 progeny from three populations with 824 common SNPs and 13 common SSRs were used for the final consensus map development. Map integration was first attempted using Joinmap 4.1 “combine groups for map integration” function, however, due to reshuffling of marker order within each individual map and extremely long computational time due to the large number of markers, it hindered the consensus map construction. Therefore, MergeMap (Wu et al., 2011) was used to generate consensus marker order using homologous LGs from individual maps. The integrated consensus map for our diploid materials was designated as ICD.

3.3.8 Genome-wide synteny comparisons between diploid Rosa and F. vesca

The genomic comparative study between diploid rose and *F. vesca* was performed following the map construction of single populations and the consensus map. SNP markers generated based on the Fvb (Tennessen et al., 2014), referred as *Fragaria vesca* whole genome v2.0.a1 Assembly & Annotation (Fvb) in the GDR database (https://www.rosaceae.org/node/4118857) were mapped to the diploid rose LGs by JoinMap 4.1. The visual comparison of these two species was demonstrated by Circos diagrams (Krzywinski et al., 2009) using the ICD result.

3.4 Results

3.4.1 Mapping material

Among all three mapping populations, 19 individuals were excluded during the marker analysis and mapping process due to excessive number of alien alleles (suspicious wrong outcrosses, >3% alleles were not from the parents) or selfing events. As a result, a total of 234 plants plus five parental lines were used to develop the linkage maps (Table 10).

3.4.2 Anchor SSR markers

Twenty-six of 40 tested anchor SSRs were polymorphic and used as quality control markers. On the final individual maps, 14 SSRs were mapped to the J14-3 x LC map, 13 were mapped to the J14-3 x VS map, and 18 were mapped to the OB x RF map (bold and underlined in the maps) (Appendix 3). These SSRs were distributed on all the LGs allowing the proper labeling of the LGs according to the ICM. Other SSR markers were grouped into the expected groups together with SNP markers though they were not included in the final maps. After integrating all three maps, 20 SSR markers were present on the ICD (Table 12 and Appendix 3).

Table 12. Labeled anchor SSR tested on diploid rose mapping populations. SSRs marked with gray color and italicized were grouped into the expected LGs but not mapped to the final map.

Mapping populations	**Number of SSRs**	**Names of SSR**			
J14-3 x LC	15	CL2845_LG5	CL2980_LG6	*CL3881_LG4**	H5_F12_LG1
		Rh48_LG2	Rh72_LG7	RhAB9-2_LG1	RhABT12_LG4
		RMS043_LG7	Rw12J12_LG3	Rw14H21_LG5	Rw22B6_LG7
		Rw34L6_LG1	Rw35C24_LG3	Rw5G14_LG7	
J14-3 x VS	17	CL2845_LG5	CL2980_LG6	*CL3881_LG4*	*CTG21_LG3*
		H5_F12_LG1	Rh48_LG2	*Rh58_LG3*	Rh72_LG7
		RhABT12_LG4	RMS001_LG7	Rw12J12_LG3	Rw14H21_LG5
		Rw22B6_LG7	Rw34L6_LG1	Rw35C24_LG3	*Rw55E12_LG4*
		Rw5G14_LG7			
OB x RF	21	BFACT47_LG3	CL2980_LG6	CL2996_LG2	*CTG21_LG3*
		H5_F12_LG1	Rh48_LG2	Rh50_LG3	Rh72_LG7
		Rh93_LG5	RhAB9-2_LG1	RhABT12_LG4	RMS003_LG7
		RMS015_LG1	RMS043_LG7	*Rw11E5_LG6*	Rw12J12_LG3
		Rw14H21_LG5	Rw22B6_LG7	Rw34L6_LG1	Rw35C24_LG3
		Rw5G14_LG7			

3.4.3 GBS markers

About 90% of the reads were mapped to the raw rose contigs (provided by Thomas Debener) for all three restriction enzymes. The restriction enzyme *Ngo*MIV (G$^{\vee}$CCGCC) was chosen to construct the DNA template for all the populations because it resulted in more reads aligned to the strawberry genome than *Fse*I or *Nhe*I (Table 13). Moreover, due to its sensitivity to methylation, it reduces the involvement of hypermethylated regions which often are associated with highly repetitive DNA near the centromere, pseudogenes, transposons and retrotransposons (Davey et al., 2011). These methylated and repetitive sequences can create challenges during bioinformatic analysis, so the use of a methylation sensitive restriction enzyme such as *Ngo*MIV can facilitate downstream data analysis. Overall, about 50-60% of the rose reads were mapped to the Fvb assemblies. Fvb assemblies were used as the reference genome for this study because only limited information is known for the available rose contigs.

Table 13. Alignment results of three restriction enzymes to the rose contigs and the strawberry genome v2.0.

Enzyme	**% reads mapped to rose contigs**	**% reads mapped to strawberry genome**
***Fse*I**	89-92%	36-37%
***Ngo*MIV**		*59-60%*
***Nhe*I**		33-34%

After calling variants in the CLC Genomics Workbench, I initially obtained more than forty to fifty thousand SNPs for each population. However, after removing SNPs that were monomorphic or missing data in at least one parent (30 000 – 40 000), had too much missing data among progeny (>15% of population size) (~2000), or the marker genotypes were not described in the JoinMap® v4.1 manual (~500), we retained ~7000 SNPs/population. An additional two thousand SNPs were eliminated due to strong segregation distortion ($p<0.0005$) leaving ~5000 candidate SNPs, including 1014 that were common among the three populations for the integration purpose. During the mapping process, ~3500 SNPs were eliminated because of co-segregation or because they failed to fit in the final map. Fourteen to fifteen hundred SNPs were successfully mapped to each population with hundreds of SNPs placed on each LG (Table 14). Among these, 824 SNPs were common in at least two populations (192 common in all three) were retained to aid map integration.

Table 14. Numbers of molecular markers mapped to the LGs of three diploid rose populations and the ICD (integrated consensus map for diploid roses).

Population	J14-3 x LC	J14-3 x VS	OB x RF	ICD
LG1	189	161	103	**348**
LG2	271	297	369	**753**
LG3	196	123	84	**340**
LG4	199	224	221	**520**
LG5	275	226	303	**564**
LG6	220	140	225	**472**
LG7	231	263	246	**530**
Total	1581	1434	1551	**3527**

3.4.4 Individual linkage map construction

Both SSR and SNP markers were used to construct the linkage map. As a result, 14 SSR and 1567 SNP markers were used for J14-3 x LC map covering 464 cM, 13 SSR and 1421 SNP markers were used for J14-3 x VS map covering 517.8 cM, and 18 SSR and 1533 SNP markers were used for OB x RF map spanning 524.1 cM (Appendix 3). Mean distance was calculated using the unique loci, which means the co-segregating markers were considered as one bin marker. The map density and mean distance across all the LGs varied from 1 to 4 markers per cM and 1 to 2.19 cM/bin marker, respectively. The largest gaps ranged from 2.8 cM to 14.7 cM (Table 15). Across the three populations, 837 markers were shared between at least two populations and 203 markers were shared across all three populations. These anchor markers were used to integrate the three individual maps.

Table 15. Statistical summary of the individual diploid rose maps and the integrated map by linkage group (LG).

Population	**Number of progeny**	**Map**	**LG1**	**LG2**	**LG3**	**LG4**	**LG5**	**LG6**	**LG7**	**Overall**
J14-3 x LC	69	Map length (cM)	50.5	74.8	62.1	53	74.3	76.8	72.5	464.0
		Map density (markers/cM)	3.7	3.6	3.2	3.7	3.7	2.9	3.2	3.4
		Mean distance (cM/bin marker)	1.3	1.2	1.3	1.3	1.5	1.7	1.3	1.4
		Largest gap (cM)	3	3.8	4.5	3.8	5.2	13.1	4.3	13.1
J14-3 x VS	83	Map length (cM)	51.8	84.9	79.6	55.4	100.6	67.8	77.7	517.8
		Map density (markers/cM)	3.1	3.5	1.5	4.0	2.2	2.1	3.4	2.8
		Mean distance (cM/bin marker)	1.3	1.1	1.8	1.1	1.8	1.7	1.2	1.4
		Largest gap (cM)	3.8	5.7	8.5	4.2	12.3	5.1	4.4	12.3
OB x RF	82	Map length (cM)	65.5	83.6	67.8	61	80.3	90.2	75.7	524.1
		Map density (markers/cM)	1.6	4.4	1.2	3.6	3.8	2.5	3.2	2.9
		Mean distance (cM/bin marker)	1.4	1.1	2.2	1.0	1.2	1.5	1.7	1.4
		Largest gap (cM)	4.6	4.3	6.9	2.8	3.8	14.7	6.3	14.7
ICD	234	Map length (cM)	94.6	133.0	118.2	117.3	152.7	109.5	166.9	892.2
		Map density (markers/cM)	3.7	5.7	2.9	4.4	3.7	4.3	3.2	3.9
		Mean distance (cM/bin marker)	1.0	0.8	1.3	0.9	1.3	1.0	1.3	1.1
		Largest gap (cM)	3.8	4.5	8.5	4.2	**11.2**	3.6	5.9	11.2

3.4.5 Integrated consensus map for diploid rose (ICD) construction

The ICD was developed with 3 populations, 234 individuals and 837 common markers (13 SSR and 824 SNPs shared between at least two populations serving as bridge markers). The resulting consensus map had 3527 markers and a map length of 892.2 cM (Tables 15 and 16). The largest gap in the ICD map was 11.2 cM on LG5. The

ICD had 3.95 markers every cM, and there was, on average, one bin marker every 1.09 cM (Table 16). The LGs ranged in size (95 to 167 cM) and marker number (300 to 700). The largest group was LG7 (166.87 cM) but LG2 had the highest marker density (5.66 markers/cM) and the least mean distance (0.83 cM/bin marker) among bin markers. Compared to the individual maps, the total map length was increased by nearly 390 cM and the map density and mean distance between markers was improved. The largest gap existing on the map was shortened to 11.2 cM from 14.7 cM as compared to the single maps. The twenty SSR markers mapped on the individual maps were mapped to the ICD to facilitate identification of the linkage groups according to the ICM (Spiller et al., 2011).

Table 16. Numbers of SSR, SNP and bin markers for each LG and diploid rose population. Numbers of distorted markers larger than fifty were bolded and underlined.

LG	Marker Statistics	Population			
		J14-3 x LC	**J14-3 x VS**	**OB x RF**	**ICD**
	SSR no.	3	2	4	4
	SNP no.	186	159	99	344
LG1	**Distorted markers (p<0.05)**	0	**<u>60</u>**	48	-
	Bin marker no.	38	39	48	93
	Total	189	161	103	348
	SSR no.	1	1	2	2
	SNP no.	270	296	367	751
LG2	**Distorted markers (p<0.05)**	**<u>81</u>**	7	**<u>53</u>**	-
	Bin marker no.	60	81	76	161
	Total	271	297	369	753
	SSR no.	2	2	4	4
	SNP no.	194	121	80	336
LG3	**Distorted markers (p<0.05)**	22	27	14	-
	Bin marker no.	49	43	31	91
	Total	196	123	84	340
	SSR no.	1	1	1	1
	SNP no.	198	223	220	519
LG4	**Distorted markers (p<0.05)**	32	4	0	-
	Bin marker no.	40	49	61	120
	Total	199	224	221	520
	SSR no.	2	2	1	2
	SNP no.	273	224	302	562
LG5	**Distorted markers (p<0.05)**	29	**<u>60</u>**	0	-
	Bin marker no.	50	56	64	121
	Total	275	226	303	564
	SSR no.	1	1	1	1
	SNP no.	219	139	224	471
LG6	**Distorted markers (p<0.05)**	**<u>52</u>**	10	**<u>87</u>**	-
	Bin marker no.	45	39	61	109
	Total	220	140	225	472
	SSR no.	4	4	5	6
	SNP no.	227	259	241	524
LG7	**Distorted marker (p<0.05)**	0	32	24	-
	Bin marker no.	54	62	45	125
	Total	231	263	246	530
	SSR no.	14	13	18	20
	SNP no.	1567	1421	1533	3507
Overall	**Distorted markers (p<0.05)**	216	200	226	-
	Bin marker no.	336	369	386	820
	Total	1581	1434	1551	3527

Many markers were mapped to the same locus due to their identical or similar segregation patterns. This happened on every linkage group with as many as 40 markers co-segregating at one position (LGs 2, 4, 7) (Figure 6).

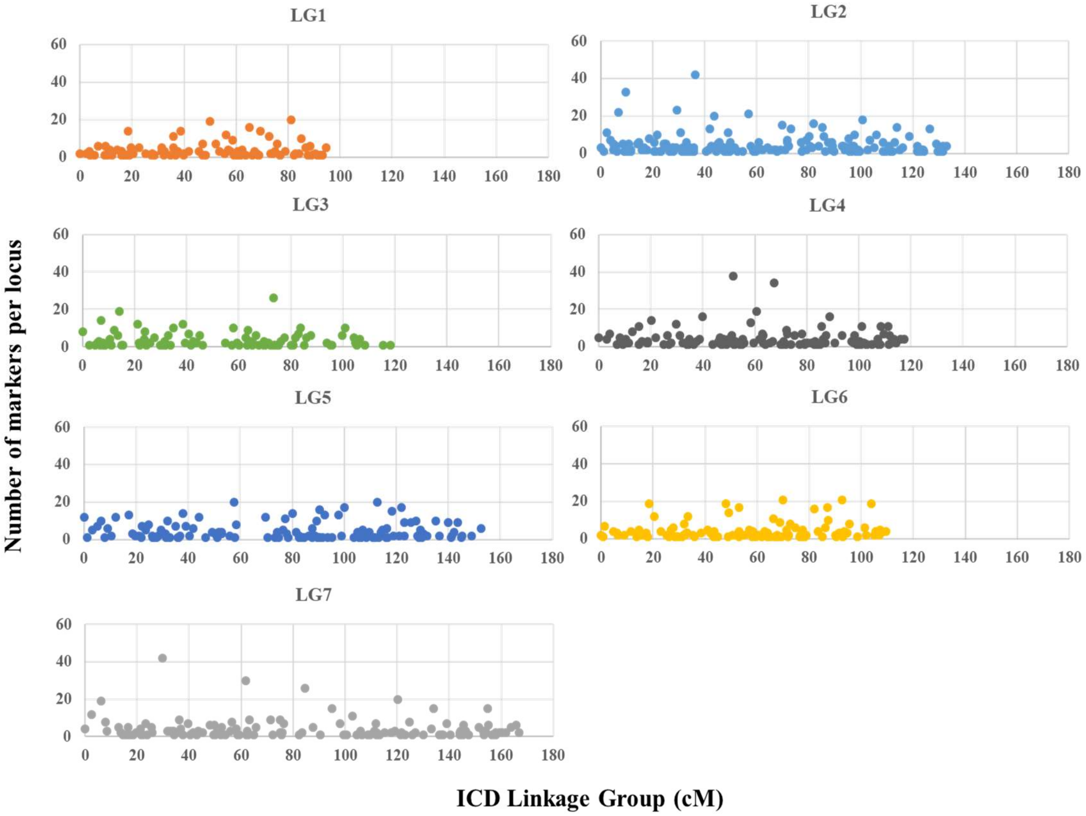


Figure 6. Marker density and distribution along the seven ICD LGs of diploid rose. The X axis is the length (cM) of LGs and Y axis is the number of co-segregating markers per locus.

3.4.6 Marker distortion

When examined, the final maps had ~18% of distorted markers ($0.0005<p<0.05$). The number of distorted markers varied with the LG and the population (Table 16). Significant distortion was predominantly clustered into regions on LG2 and LG6 of J14-3 x LC, LG1 and LG5 of J14-3 x VS, and LG1, LG2 and LG6 of OB x RF (Table 16 and Appendix 3). In total, 19 markers (3 SSR and 16 SNP) showed a significant segregation distortion ($p<0.05$) in two populations and none of the markers showed distortion in all three populations. 206, 187 and 211 markers showed distortion only in J14-3 x LC, J14-3 x VS and OB x RF, respectively. Overall, the majority of the markers on the final maps passed the Goodness-of-fit test favoring the alleles from both parental lines which indicates a good level of cross and self-compatibility among the parental materials (Table 16).

3.4.7 Synteny among individual maps and ICD and Fragaria vesca

The ICD was developed based on three biparental populations. The comparison of the LGs of four different maps shows an excellent collinearity with only a few rearrangements. This indicates the high quality of the maps (Figure 7).

There was a high synteny among the LGs of diploid *Rosa* and strawberry (*Fragaria vesca*). As all of our SNP markers generated from GBS were detected and named based on the strawberry reference genome, when we grouped and mapped the SNP and SSR markers to their location, we found one major translocation between strawberry pseudo-chromosomes 1 and 6 and diploid rose LGs 2 and 3, where LG2 of rose is composed of pseudo-chromosome 1 and half of pseudo-chromosome 6 of strawberry with the other half of the strawberry pseudo-chromosome 6 making up the majority of rose LG3. Pseudo-chromosome 6 of strawberry was reported as one of the largest pseudo-chromosomes in strawberry and pseudo-chromosome 1 was one of the smallest chromosomes (Darwish et al., 2015; Mahoney et al., 2016), so it seems that the large chromosome was broken into two segments and recombined with a small chromosome to form a new plant species during the subfamily divergence. One major inversion was seen between strawberry pseudo-chromosome 5 and rose LG7 near the telomere, and a small inversion between strawberry pseudo-chromosome 2 and rose LG6 was visible at the telomere as well (Table 17 and Figure 8). Overall the *Fragaria* pseudo-chromosomes 7, 3, 2, 4, and 5 correspond to the *Rosa* ICD LGs 1, 5, 6, 4, and 7, respectively, and *Rosa* ICD LGs 2 and 3 were composed of *Fragaria* pseudo-chromosomes 1 and 6, respectively. These patterns were consistent across four maps (Table 17) and agreed with previous studies (Bourke et al., 2017; Vukosavljev et al., 2016).

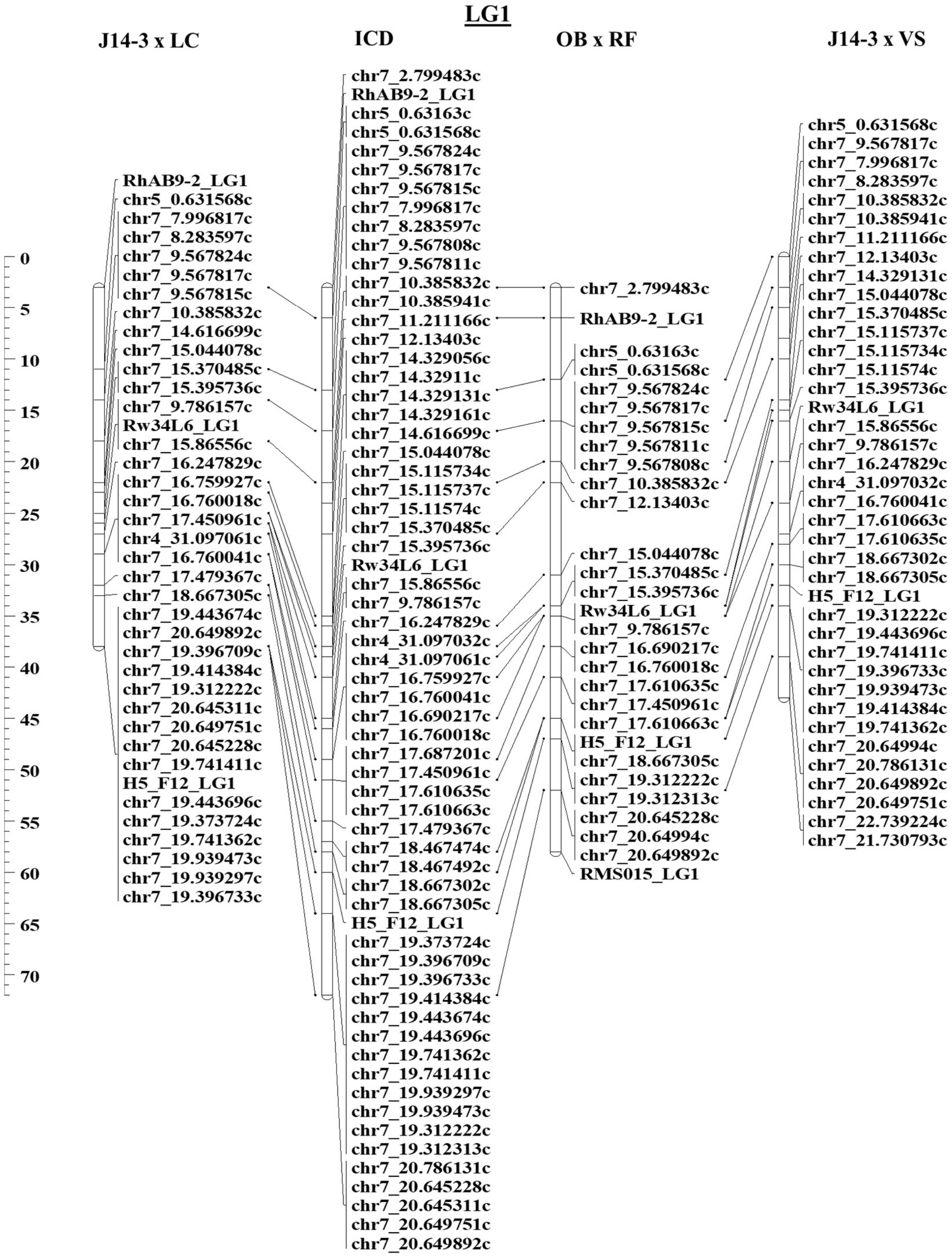


Figure 7. LG1 comparison for J14-3 x LC, J14-3 x VS, OB x RF and ICD of the diploid rose. Full sets of markers can be found in Appendix 3.

Table 17. Synteny comparison between diploid *Rosa* and *Fragaria vesca v2.0.* The number of markers of each diploid rose linkage group and the consensus map that correspond to the *Fragaria* Fvb assemblies are indicated. Marker numbers indicating the macrosynteny between two genera are in bold.

			Fragaria vesca						
	LGs	**Populations**	**1**	**2**	**3**	**4**	**5**	**6**	**7**
Diploid *Rosa*	**1**	J14-3 x LC	2	4	4	4	8	0	**164**
		J14-3 x VS	0	3	1	6	5	0	**144**
		OB x RF	0	3	1	1	2	1	**91**
		ICD	2	8	5	9	10	1	**309**
	2	J14-3 x LC	**136**	0	0	0	0	**134**	0
		J14-3 x VS	**160**	0	0	0	0	**136**	0
		OB x RF	**197**	0	0	0	0	**170**	0
		ICD	**380**	0	0	0	0	**371**	0
	3	J14-3 x LC	14	0	3	4	1	**172**	0
		J14-3 x VS	11	1	4	0	0	**104**	1
		OB x RF	8	1	4	2	1	**64**	0
		ICD	27	2	8	5	1	**292**	1
	4	J14-3 x LC	1	9	9	**173**	2	4	0
		J14-3 x VS	4	3	7	**205**	1	3	0
		OB x RF	6	7	7	**198**	0	2	0
		ICD	11	15	19	**465**	3	6	0
	5	J14-3 x LC	1	6	**235**	16	4	2	9
		J14-3 x VS	2	3	**190**	16	2	3	8
		OB x RF	3	5	**258**	11	9	6	10
		ICD	4	10	**484**	26	15	8	15
	6	J14-3 x LC	1	**210**	4	2	1	0	1
		J14-3 x VS	1	**134**	1	1	0	1	1
		OB x RF	0	**215**	4	1	1	1	2
		ICD	1	**451**	8	4	2	2	3
	7	J14-3 x LC	4	5	1	18	**194**	2	3
		J14-3 x VS	3	6	4	21	**222**	1	2
		OB x RF	1	5	8	16	**210**	1	0
		ICD	7	11	12	25	**460**	4	5

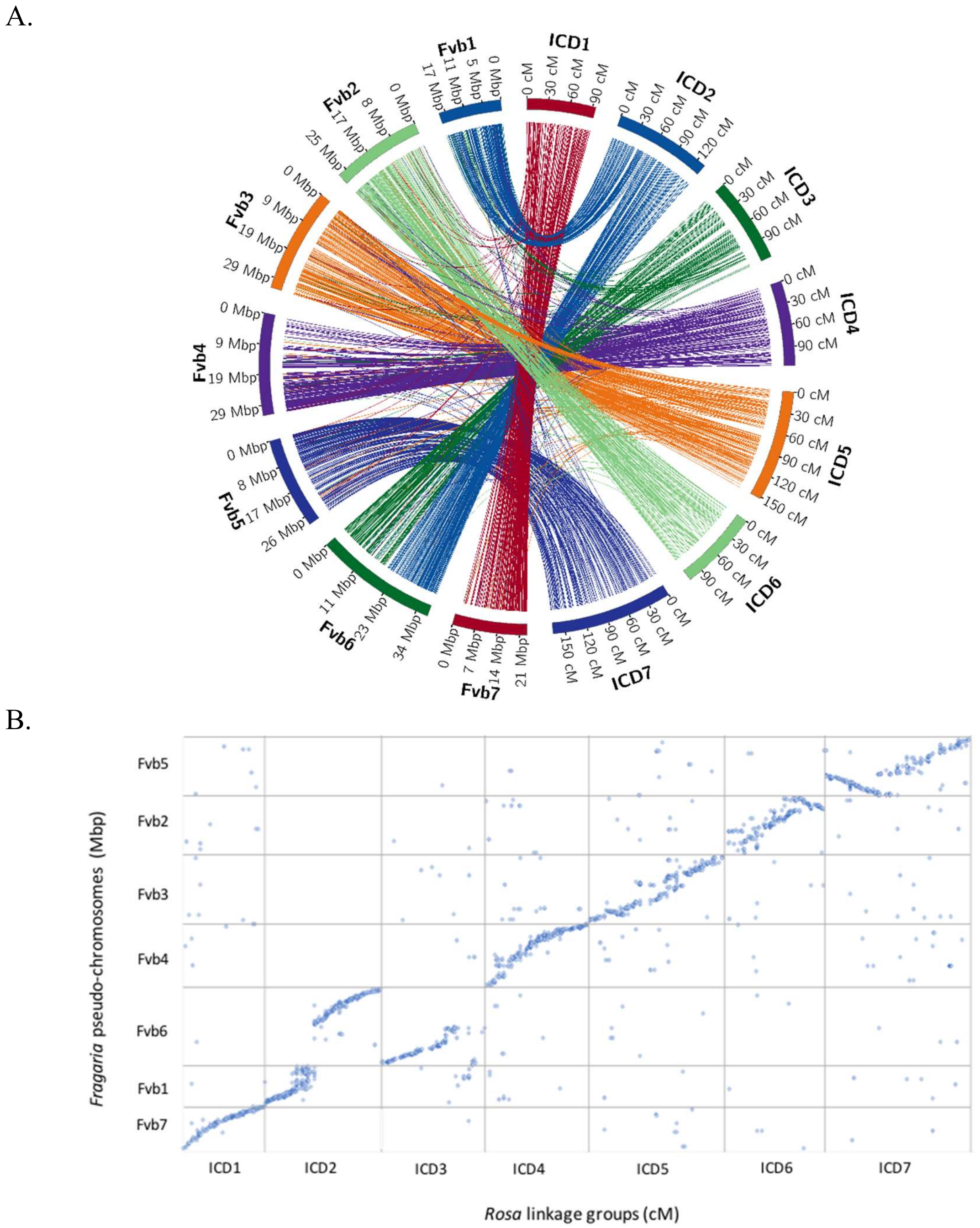


Figure 8. Global synteny and collinearity between diploid *Rosa* and *Fragaria*. A. Circos plot shows that rose LG2 is composed of strawberry chromosomes 1 and 6, and the rest of strawberry chromosome 6 corresponds to rose LG3. Rose and strawberry were designated as ICD (right) and Fvb (left) (by Circos diagrams). The connecting links are color-coded according to the *F. vesca* psedochromosome assemblies (Fvb) to which the rose markers were anchored. B. Comparison between rose LGs (ICD) in cM and Fvb assembly physical positions in Mbp. Each dot represents one SNP marker.

3.5 Discussion

3.5.1 Single map construction

We constructed a saturated integrated consensus map for diploid roses using two half sibs (J14-3 x LC, J14-3 x VS), and one unrelated (OB x RF) highly heterozygous F_1 populations. The pollen parents of the half sib populations are also related as VS has LC as one of its parents. All the maps contained the seven LGs corresponding to the seven base pseudo-chromosomes in rose ($x = 7$). Moreover, an average of 215 markers per LG showed a consistent collinearity among three individual maps, and the ordering of anchor SSR markers on our maps was consistent with the ICM map. All of the above indicated the map quality and marker orders were reliable. Comparing our results to other recent rose maps (Spiller et al., 2011; Vukosavljev et al., 2016; Yu et al., 2015) marker number and density were increased using GBS to generate SNP markers and mapping them to the *F. vesca* genome assembly, but about 20 000 less than the results of Bourke *et al*. (2017). This, in part, is due to the fact that Bourke et al., (2017) did not exclude any co-segregating markers whereas in the present map about half of the co-segregating markers were excluded.

In summary, approximately 7-10% of initial GBS markers were anchored to the single maps for each cross. A total of twenty to thirty thousand putative SNPs were generated by GBS of which six to seven thousand SNPs were saved after eliminating the monomorphic SNPs and ones with more than 15% missing values. Another one to two thousand SNPs were further excluded due to high skewness ($p<0.0005$), and finally three to four thousand informative SNPs were removed from the final map due to co-segregation or difficulties in fitting into the map. Before single map construction, for the purpose of creating a consensus map later, common markers shared among three populations were labeled and kept for further analysis, as a result, all 1041 common markers were saved and other markers with the same segregation patterns were excluded. Seven groups representing seven chromosomes in each population was selected at LOD > 5. To achieve a high-quality map, only polymorphic markers with less than 15% missing data and with acceptable skewness (p>0.0005) were mapped to the final map. Around 1500 markers with excessive numbers of double recombination (DR) events were eliminated as unlikely and probably caused by sequencing error. The exclusion of a large proportion of GBS markers is common in other crops as well, for example, only about 10% GBS SNPs were kept in strawberry mapping (Mahoney et al., 2016), and 4.2% of the starting putative SNPs were retained for grapevine map construction (Hyma et al., 2015). It is also a challenge to fit a high number of markers into small populations. For this same reason, more markers were able to fit in the consensus map by utilizing more individuals across three populations.

The 26 anchor SSR markers from the ICM used in this study all mapped to the expected LGs. Twenty of these anchor SSRs were mapped to the final map with similar mapping positions indicating that our map is reliable. The order of most bridge markers was consistent between our maps and ICM though occasional marker order discrepancies were observed, this may be due to several factors, such as segregation distortion, population size, parental genetic background, and scoring errors (Yu et al., 2015). Distorted markers (~18%) were present for every LG of every population, and clustering of the distorted markers were observed on certain LGs, though the clustering varied among populations, LGs 1, 2, 5 and 6 contained more distorted markers than other LGs. Previous research indicated that 20-22% of the markers on the rose maps showed distortion. This is probably due to the interspecific nature of the crosses and may also be caused by a gametophytic self-incompatibility or genotyping errors (Spiller et al., 2011; Yan et al., 2005; Yu et al., 2015).

We found LG2 was had more markers and a higher density of markers than other LGs, and LG3 was sparser especially for J14-3 x VS and OB x RF. In addition, we observed some large gaps across LGs. The gaps in the populations J14-3 x VS and OB x RF appeared in the same regions on LG3. Several other large gaps were seen in LG5 for J14-3 x VS and LG3 and LG6 for OB x RF. This may be due to the possibility that part of the rose genome is not on the strawberry genome which was used as the reference genome or as a methylation sensitive enzyme was used to digest the genomic DNA, the regions full of repetitive nucleotides might have been missed, or those regions are predominantly homozygous. The *Rosa* LG2 was composed of *Fragaria* pseudo-chromosome 1 and part of *Fragaria* pseudo-chromosome 6 and the *Rosa* LG3 corresponded to the other part of *Fragaria* pseudo-chromosome 6. A possible reason why *Rosa* LG3 had fewer markers could be that part of the *Rosa* LG3 markers were grouped to *Rosa* LG2 because the closeness of the markers, but due to the lack of rose reference genome we cannot test this hypothesis. In apple studies, because there is genome wide duplication (Han et al., 2011), the first step in creating the linkage map is to assign groups manually according to the physical position of the markers (Sun et al., 2015). Hopefully, once the rose whole genome sequence is available, we will be able to more accurately assign markers to the groups, and determine whether the sparseness was due to the genetic nature of rose (e.g. repetitive regions) or the markers grouping issue, which would suggest some markers should be grouped based on the physical positions of the genome. Clustering of markers at the same locus (considered as one bin marker in this study) was observed throughout the LGs across populations, similar segregation patterns among these markers as well as the relatively small population size to number of markers ratio or roses may have low rates of recombination contributed to this phenomenon.

Moreover, a few minor marker inversions on LG1, 2, 4, 6, and 7 were observed among individual maps and the consensus map (Appendix 3). This could be partly explained by the diverse genetic background in the populations. The inconsistency of some markers can be explained by the tight linkage among different markers pairs, inadequate data (missing data), and differences in segregation information among markers and populations (N'Diaye et al., 2008). But overall, no major chromosomal rearrangements were observed across populations because the populations have a similar genetic background.

3.5.2 Consensus map construction

Over six hundred bridge markers linked three individual maps into one integrated map to create a consensus map with 820 bin markers (3507 markers including co-segregating ones) covering 892 cM. The number of recombination events is the key in mapping work, with smaller experimental populations leading to less reliable genetic maps. Thus by combining populations, the number of individuals used for mapping increased and the map quality improved as compared to the inconsistencies in marker orders in single population studies (Doligez et al., 2006; N'Diaye et al., 2008). The final number of individuals used for the consensus map was 234, so more recombination events were taken into consideration than with the individual populations. Because sample bias resulting in the incongruence of marker orders can be attributed to the small population sizes (Doligez et al., 2006), integrating multiple population maps and the consequent larger population size would reduce this issue.

The comparison between the ICD and ICM maps showed all the anchor SSR were mapped to the same linkage group at similar locations. The total map length of ICD was longer and marker number was significantly higher than previous studies (Linde et al., 2006; Spiller et al., 2011; Yan et al., 2005). The genome coverage (LG length) was extended for all the LGs except for LG1 which was the same length as ICM. The ICD had about one bin marker every cM and 0.25 cM/marker taking the co-segregating markers into consideration, which increased the resolution of rose genetic map substantially. Regions missed in some individual maps were covered in the consensus map, such as the lower 15 cM of LG3 and the middle 15 cM of LG5 for J14-3 x VS, the upper 15 cM and lower 20 cM of LG6 for OB x RF, also the sparseness of LG3 was greatly improved. Thus the extended length of the map may reflect an improved coverage for the rose genome as compared to other studies although it is possible that the map length was inflate due to the high numbers of markers fit to the map and the MergeMap program we used (Khan et al., 2012).

Markers with similar segregation patterns were distributed along each LG. The clustering of markers is likely explained by the fact that a large number of markers were mapped on a relatively small number of individuals (Mahoney et al., 2016; Spiller et al., 2011) Few inversions were observed across individual maps and the ICD, and this may be attributed to the small population sizes or the fact that different recombination rates are present among populations (Loridon et al., 2005; N'Diaye et al., 2008) Still, some gaps were evident. As the gaps in LG3 and LG5 were located on the middle of the LG, those gaps may be caused by the lack of markers covering heterochromatic pericentromeric regions (Kirov et al., 2014).

The mapping populations were created by crossing plants with diverse black spot disease response, growth type, plant architecture, horticultural traits, and the progeny showed segregating phenotypes, therefore, the genetic maps created in this study will serve as a tool for QTL analysis for many traits. Marker orders were highly conserved between the integrated consensus map and the individual maps of the three populations, indicating the high quality and value of the consensus map. Minor inconsistencies of marker order are expected when different recombination rates are present among populations (Loridon et al., 2005; N'Diaye et al., 2008).

3.5.3 Synteny between Rosa and Fragaria

Synteny among several *Rosaceae* crops have been revealed in many studies, including among *Prunus* species (almond, peach, apricot and cherry) (Dirlewanger et al., 2004; Guajardo et al., 2015), *Prunus* and *Malus* (apple) comparison (Dirlewanger et al., 2004), *Prunus*, *Fragaria* and *Malus* (Illa et al., 2011), *Fragaria* and *Prunus* (Vilanova et al., 2008), *Malus* and *Pyrus* (Yamamoto et al., 2004), and *Rosa* and *Fragaria* (Bourke et al., 2017; Gar et al., 2011; Vukosavljev et al., 2016). The genome wide comparative analysis with the thousands of markers mapped to the diploid *Rosa* and called based on the physical location on the *F. vesca* (Fvb) genome further confirmed the high level of synteny among the two genomes. *Rosa* LGs 1, 4, 5, 6, 7 correspond to the *Fragaria* pseudo-chromosomes 7, 4, 3, 2 and 5, respectively. In addition, a major translocation and fission/fusion happened between the *Rosa* LGs 2 and 3 and *Fragaria* pseudo-chromosomes 1 and 6, with the *Rosa* LG2 composed of the *Fragaria* pseudo-chromosome 1 plus a part of the *Fragaria* pseudo-chromosome 6, and the rest of the *Fragaria* pseudo-chromosome 6 formed the *Rosa* LG3. The syntenic relationship between *Fragaria* and *Rosa* indicated a hypothetical evolutionary relationship among Rosaceae genome. It is deductive that pseudo-chromosome 6 of strawberry was divided into two segments and forming LGs 2 and 3 in rose during evolution. The detailed comparison in this study further demonstrated a high level of macro-synteny between two genera as well as explored the evolutionary divergence events that occurred in the Rosoideae subfamily (Bourke et al., 2017; Potter et al., 2007; Vukosavljev et al., 2016).

Many genes and QTL traits have been mapped on all seven LGs including recurrent blooming, double flower, powdery mildew resistance, scent metabolites, petal numbers, days to flowering, prickles, and growth vigor (Dugo et al., 2005; Koning-Boucoiran et al., 2012; Linde et al., 2006; Spiller et al., 2011). Beyond the QTL positioned only on one plant species, some QTL were found on multiple Rosaceae species, namely traits of blooming, ripening, fruit quality and disease resistance between

Prunus and *Malus* (Dirlewanger et al., 2004), as well as genes controlling petal colors in *Prunus* and *Rosa* (Gar et al., 2011). The current study will benefit the potential opportunities for additional QTL studies in the Rosaceae family especially in Rosoideae subfamily using the transferable markers.

3.6 Conclusions

By mapping sequence-based co-dominant markers (SSRs and SNPs), we have illustrated the highly conserved synteny between diploid *Rosa* and *Fragaria*, and created a dense SNP-based consensus map for our germplasm. This high synteny will facilitate the ability to study the genetics and QTL between two species and provide a better understanding of the Rosaceae genome. Although we successfully used the *Fragaria* reference genome to find SNPs among *Rosa* sequence data, the accessibility of a rose reference genome which is currently being developed will increase the confidence of the mapping results and provide a better view of QTL positions and likely improve the coverage of the mapped genome.

Phenotypic data of flower intensity, petal number, plant architecture and black spot resistance have been taken for several years, thus the next step will be to perform QTL analysis for these traits starting with the individual populations, and eventually, the consensus map developed in this study will serve as the basic tool for pedigree-based QTL analysis for the germplasm within the TAMU Rose Breeding Program.

Typically, it can take up to 20 years from selection to introduction for a tree cultivar (Bianco et al., 2014). With the help of molecular markers, this process can be accelerated particularly for traits that are hard to phenotype and have low heritability

(Bianco et al. 2014). The high throughput capabilities, whole genome sequencing and lower costs provided by next-generation sequencing (NGS) technology makes whole genome analysis and marker generation affordable as compared to traditional PCR-based markers (Gardner et al., 2014). However, only a very small number of SNP markers that are discovered through GBS (typically 6 -10%) are useful for heterozygous species due to the depth of coverage, missing data and multi-allelic issues (Debener and Byrne, 2014; Gardner et al., 2014; Mahoney et al., 2016).

Another high-throughput genotyping approach that has been widely adopted is the SNP array. The advantages of SNP arrays include providing accurate genotypic information for large numbers of SNP markers, and it can be successfully applied on polyploids, such as tetraploid roses (Bourke et al., 2017; Koning-Boucoiran et al., 2015; Vukosavljev et al., 2016). However, SNP arrays may produce unreliable or meaningless genotyping calls due to the high levels of polymorphism in many heterozygous crops, and are susceptible to ascertainment bias against rare alleles due to the small subset of the individuals on the array in the discovery panel (Bassil et al., 2015; Mahoney et al., 2016; Miller et al., 2013), and may not provide sufficient information for some germplasm with different genetic backgrounds due to the fixed number of markers on the array (Guajardo et al., 2015).

Overall, the high-throughput feature of NGS technology increases the resolution of genetic studies, is more time and labor-efficient than traditional assays with PCR-based markers and opens the possibility of genome-wide association studies (Debener and Byrne, 2014). Though the whole genome sequencing of ‘Old Blush’ is currently in progress, no rose whole genome sequencing data has been released yet. This study applied GBS technology on roses and addresses the possibility of using high-throughput sequencing technology to study rose genetics and genomics. To maximize the utility of GBS in the future, improved computational and statistical tools to obtain more information from the raw data are desired. In conclusion, the high-density consensus map developed here is a reliable tool for multi-population experimental design-based QTL detection and will provide the genetic background effect on QTL expression. Initial studies will examine QTL for black spot partial resistance since the phenotypic data of the germplasm is available.

CHAPTER IV

BLACK SPOT QTL DISCOVERY USING PEDIGREE-BASED ANALYSIS IN FIFTEEN RELATED DIPLOID ROSE POPULATIONS

4.1 Synopsis

Black spot (BS) disease (*Diplocarpon rosae* (Lib.) Wolf) of rose is the most important leaf disease of garden roses in warm humid areas. Although partial (horizontal) resistance to black spot has been shown to be moderately heritable, the responsible quantitative trait loci (QTL) remain unidentified. Due to the interspecific nature and high heterozygosity in commercial roses as well as the diverse genetic and genomic background, the genomic resources for rose are limited, thus the study of the genetic architecture of complex traits is hindered. New high-throughput sequencing technologies and analytical approaches developed during the RosBREED project have made the research more feasible in recent years. In this study, field assessment of black spot severity was done four times (June, September, October and November) in 2016 in College Station for fifteen inter-related diploid rose full-sib families by intercrossing the commercial cultivars ‘Old Blush’, ‘Red Fairy’, ‘Vineyard Song’, ‘Sweet Chariot’ and ‘Little Chief’, and five breeding lines M4-4, J14-3, J3-3, J3-6, and J4-6 developed in the TAMU rose breeding program. A Bayesian QTL discovery based on the pedigree was conducted among these families. One QTL on LG3 within the interval 36-43 cM was consistently visible in the June, September, October, November and combined analyses, which had a 2ln(BF) value larger than 5 (considered as a strong QTL) and explained 20.3% of the total phenotypic variance. Parents J14-3 and J4-6 were estimated as

heterozygous at this QTL location, thus segregating in the corresponding populations. This approach serves as a model study for performing pedigree-based analysis (PBA) on materials with diverse genetic backgrounds and the results support downstream marker-assisted breeding (MAB) in the TAMU rose breeding program. This is the first QTL report on partial black spot resistance of roses.

4.2 Introduction

Roses, which have been cultivated for at least 5,000 years, are one of the most important ornamental crops in the world (Gudin, 2000; Pemberton, 2003). Black spot (BS) disease of rose is the most important leaf disease of outdoor grown roses in warm humid areas causing roses to defoliate (Debener and Byrne, 2014). Many modern roses are susceptible to this disease (Byrne et al., 2010; Uggla and Carlson-Nilsson, 2005; Zlesak et al., 2010). The causal agent of black spot disease of rose is the hemibiotrophic ascomycete fungus *Diplocarpon rosae* (Lib.) Wolf, which is obligate to the *Rosa* genus (Horst and Cloyd, 2007). Eleven physiological races of *D. rosae* have been differentiated across Germany, UK and North America based on eleven unique reactions between hosts and pathogenic races (Whitaker et al., 2010). Typical symptoms of BS are circular black spots with irregular margins measuring from 2-12 mm in diameter and surrounded by chlorosis.

Both complete resistance to a specific race, and partial resistance to BS have been reported in rose (Carlson-Nilsson and Davidson, 2006; von Malek and Debener, 1998; Whitaker et al., 2007; Whitaker et al., 2010; Whitaker and Hokanson, 2009). Complete or vertical resistance corresponds to a gene-for-gene interaction pattern in the

BS infection system in which resistance is generally conditioned by single dominant resistance genes corresponding to specific pathogenic races of *D. rosae* (von Malek and Debener, 1998; Whitaker et al., 2010). Three major black spot resistance genes – *Rdr1*, *Rdr2* and *Rdr3* have been characterized in tetraploid and diploid rose populations (Hattendorf et al., 2004; von Malek and Debener, 1998; Whitaker et al., 2010).

Partial or horizontal resistance has been described in this pathosystem as well (Shupert, 2005; Whitaker et al., 2007). Partial resistance has been observed as reduced lesion size, reduced sporulation, and/or the delayed onset of infection in both field assessment and in artificial inoculation experiments (Dong et al., 2017; Whitaker et al., 2007). Five components including incubation period (IP), leaf area with symptoms (LAS), number of lesions (NL), lesion length (LL) and sporulation capacity (SC) have been used to assess partial resistance to BS in both whole plant inoculations and detached leaf assays (Dong et al., 2017; Xue and Davidson, 1998). This partial resistance tends to be effective against all strains of a pathogen population although total resistance is rarely observed.

Several genes and QTL have been identified in roses including ones associated with horticultural traits (flower size, days to flowering, leaf size) and powdery mildew resistance (Dugo et al., 2005; Linde et al., 2006; Moghaddam et al., 2012). Although BS partial resistance has been documented, the responsible QTL remain unidentified.

A Bayesian approach is very flexible in modeling complex traits, it is very suitable for utilizing data from ongoing breeding programs as it accounts for relationships among all individuals by including the known pedigree information. The

Bayesian approach has been implemented in the software package FlexQTL™ (Bink et al., 2008). The Markov chain Monte Carlo (MCMC) simulation algorithm within the program is applied to simulate posterior samplings, these samples are stored and available for subsequent statistical inference. The determination of the number and magnitude of QTL is based on the statistical evidence, i.e., twice the natural log of Bayes factors (2ln(BF)) (Kass and Raftery, 1995). The values of 2ln(BF) that are >2, 5, and 10 indicate positive, strong, and decisive evidence, respectively. The inferences on QTL positions are based on posterior QTL intensities, and the posterior probabilities of QTL genotypes are also estimated (Bink et al., 2014; Bink et al., 2008). Visual inspection of the trace plots and the assessment of the stability of the genetic models is performed to determine reliable QTL in VisualFlexQTL™ (Bink et al., 2014).

This pedigree-based analysis (PBA) has been done on various tree crops, such as apple, peach and sweet cherry (Allard et al., 2016; Bink et al., 2014; Fresnedo-Ramírez et al., 2016; Rosyara et al., 2013). QTL found in the single bi-parental family are usually not transferrable to a different genetic background (Dong, 2014). This problem can be addressed by analyzing QTL in multi-parental populations which extends the genetic diversity in the population studied, allows for allele comparison in different genetic backgrounds (Huang et al., 2011) and improves the resolution of QTL detection (Bink et al., 2002).

The objective of this study was to identify QTL associated with BS partial resistance by measuring disease severity (percentage of total foliage covered with symptoms) in the field plot. Natural inoculum was relied on in this study. Fifteen families sharing common parents were assessed for disease resistance in June, September, October and November of 2016. This was combined with their genotypic information and analyzed with the pedigree-based QTL analysis software program, FlexQTL™.

4.3 Materials and methods

4.3.1 Plant materials

Fifteen inter-related diploid populations were generated in a partial diallel design by crossing five black spot resistant breeding lines [J06-20-14-3 (J14-3), J06-28-4-6 (J4-6), J06-30-3-3 (J3-3), J06-30-3-6 (J3-6) and M4-4], and moderately to highly susceptible cultivars ['Old Blush' (OB), 'Little Chief' (LC), 'Red Fairy' (RF), 'Sweet Chariot' (SC), and 'Vineyard Song' (VS)] with excellent ornamental qualities to create F_1 populations segregating for black spot partial resistance (Dong et al., 2017). The population sizes varied from 5 to 124 after excluding progeny that were deemed selfs and out crossers based on their genotypic information (Figure 9).

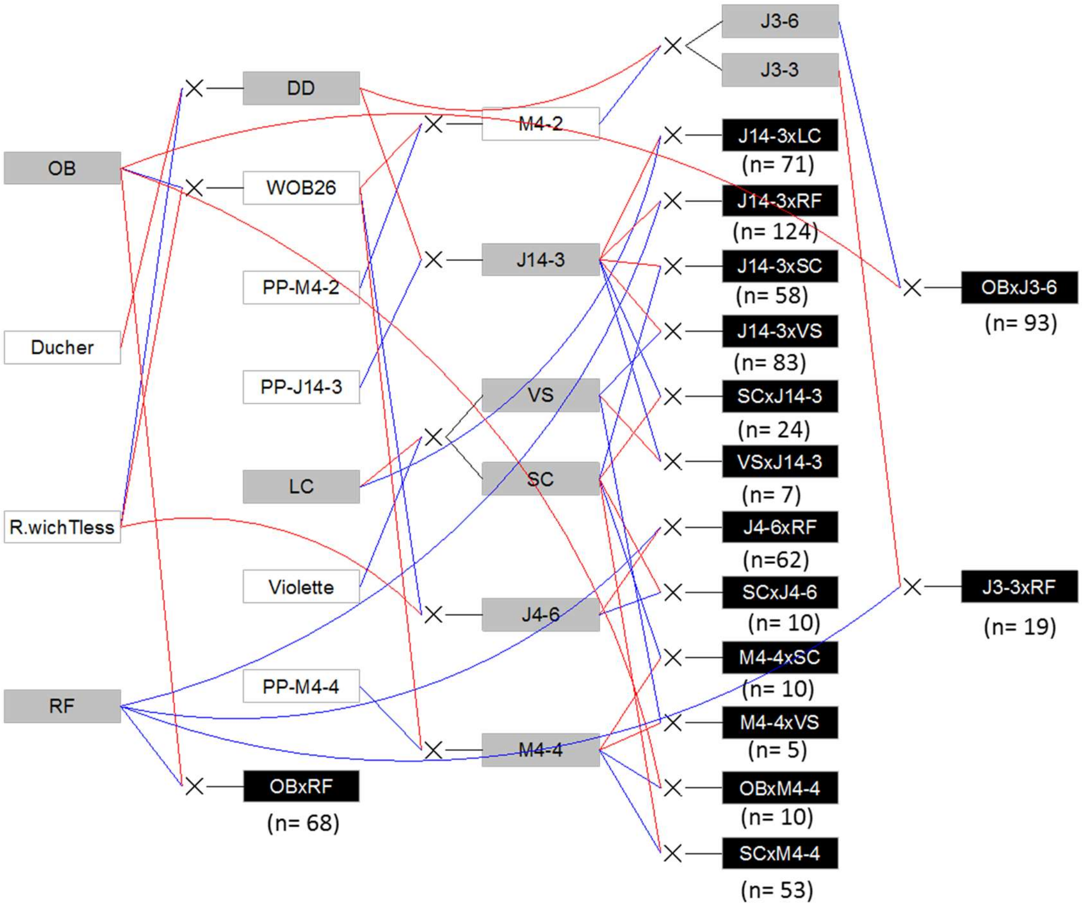


Figure 9: Pedigree of the fifteen diploid rose mapping families and their progeny number. Blue and red lines link progeny to their male and female parents, respectively; white boxes indicate possible founders or intermediate parents with no DNA information nor phenotypic data; gray boxes indicate direct parents of the mapping populations and DD as a grandparent with DNA information; black boxes indicate mapping families used for map construction and QTL discovery.

4.3.2 Phenotypic and SNP information

Partial (horizontal) resistance to black spot fungus was assessed in the research field in College Station, Texas, USA. Field assessments were done in June, September, October and November of 2016 by measuring the percent foliage covered with symptoms (PFS) (Chapter II) (BLS is considered as ordinal data thus does not fit the model and was not analyzed in this chapter). The mean values were used as the overall input for QTL mapping. Raw data of field assessments were used directly because it provided the same conclusions as the transformed data (Chapter II). SNP used in this study were generated by genotyping by sequencing (GBS) as described in Chapter III.

4.3.3 Consensus map development

The initial consensus map based on five families (J14-3 x LC, J14-3 x VS, OB x RF, J4-6 x RF and OB x J3-6) (because their relatively big population sizes and good disease resistance or ornamental characteristics in the paretns) served as the reference for marker order. Linkage maps for J14-3 x LC, J14-3 x VS and OB x RF developed in the initial consensus map study (Chapter III) were used directly in this study after removing the microsatellite markers. Linkage maps for the other two large populations: J4-6 x RF and OB x J3-6 were developed using SNPs generated by GBS and were calculated by JoinMap 4.1 following the same SNP calling and mapping procedures detailed in Chapter III and average numbers of markers removed in each step was close to the numbers in Chapter III. The 1041 common SNPs in Chapter III were kept in these two families at the best effort to facilitate map integration. The cross pollination (CP) population type was chosen in JoinMap® 4.1. Linkage groups were selected with the grouping LOD varying from 5 to 13. Each group was assigned to one of the seven rose linkage groups according to the synteny between diploid rose and strawberry in the previous study (Chapter III) (Bourke et al., 2017; Vukosavljev et al., 2016). The maps were constructed with the maximum likelihood mapping function. Poorly fitting markers and markers that greatly inflated the linkage group length were dropped during the mapping process. Markers which caused gaps larger than 15 cM were examined. If a large gap existed at the end of a LG in a specific map but not in other maps, the associated markers were removed. MergeMap (Wu et al., 2008) was used to integrate LGs from the five populations with equal weight = 1. Markers with conflicting positons were removed by MergeMap. As the genetic distances between markers and the length of LGs were inflated by MergeMap (Khan et al., 2012), a scaling factor was calculated based on the average length of each linkage group across different individual population maps and used to adjust the length of the consensus LGs proportionally (Khan et al., 2012). After combining all five maps, the initial consensus map was composed of 4538 SNP. Next, all the original genotypic data were pulled back from the raw data and input into each family including SNP information failed to fit in one individual map but present on the consensus map and homozygous loci following the order of the initial consensus map. Then VisualFlexQTL (Voorrips et al., 2012)was used to examine the data quality from five families individually to solve the double recombinations based on the expected double recombination information in genomeIM.csv (markers with the sum of both fractions' observed double recombination >20 were removed). Lastly, all five families were combined as one file and imported into FlexQTL for further curation. Markers were eliminated if they had > 10% missing data, inheritance conflicts, or resulted in singletons or suspicious double recombinations due to null alleles or genotyping errors. After that, the remaining ten families were then added to the dataset, and the data was further examined and cleaned to solve inheritance conflicts, singletons and double recombinations. The order and distances of these SNP were based on the initial consensus map.

4.3.4 Bayesian QTL analyses

Using the final consensus map, FlexQTL software was used to test multiple QTL models (Bink et al., 2008). Genome-wide QTL detection was carried out several times with varying chain length, prior QTL number, maximum QTL number and seed numbers to make the effective chain samples (ECS) for the phenotypic mean, variance of the error, number of QTL, and the variance for the number of QTL all above 100 to make valid subsequent inferences and conclusions (Sorensen and Gianola, 2002). The ECS met the criteria when the Markov chain length was 100,000 iterations with 100 thinning which generated 1000 samples for downstream statistical inference. Values of 2ln(BF) greater than 2, 5 and 10 indicate positive, strong and decisive evidence, respectively, for supporting the larger QTL model in the pairwise comparison of different N_{QTL} models. The main criteria to determine major QTL in this study was a 2ln(BF)>5 and consistent detection (colocalized within ±10cM) across the four different environments that were evaluated (i.e. June, September, October, and November 2016). Because a consistent QTL was identified on LG3, it was separated into three segments (3a: 0-10.93cM; 3b: 11.82-31.26cM; 3c: 34.03-51.99cM) based on recombination patterns and reanalyzed. The proportion of phenotypic variance explained (PVE) by a QTL was calculated as: $\mathrm{PVE} = \frac{wAVt}{VP} \times 100$ (Mangandi et al., 2017), where wAVt is the weighted additive variance of the trait, and VP is total variance of the trait.

4.3.5 Haplotype analysis

Nine SNPs in the predicted QTL region spanning the QTL peak were picked to study haplotypes associated with the trait. Manual identifications of non-parental/recombinant haplotypes in the progeny were conducted and only those with at least three neighboring marker calls which differed from the parents were called as recombinant haplotypes. Analysis of variance for different haplotype effects on disease severity and student's t-test on LS means among progeny were conducted using JMP pro 12.2.0. QTL genotype prediction was generated in the FlexQTL program and data at the QTL signal peak in the file "Gtp_Genome.csv" was used for the analyses.

4.4 Results

4.4.1 Black spot field analysis

The field evaluations done in June, September, October and November of 2016 and the overall black spot disease scores (mean of four months' assessments) (Chapter II) were used for QTL analysis (Figure 10). Details can be found in Chapter II.

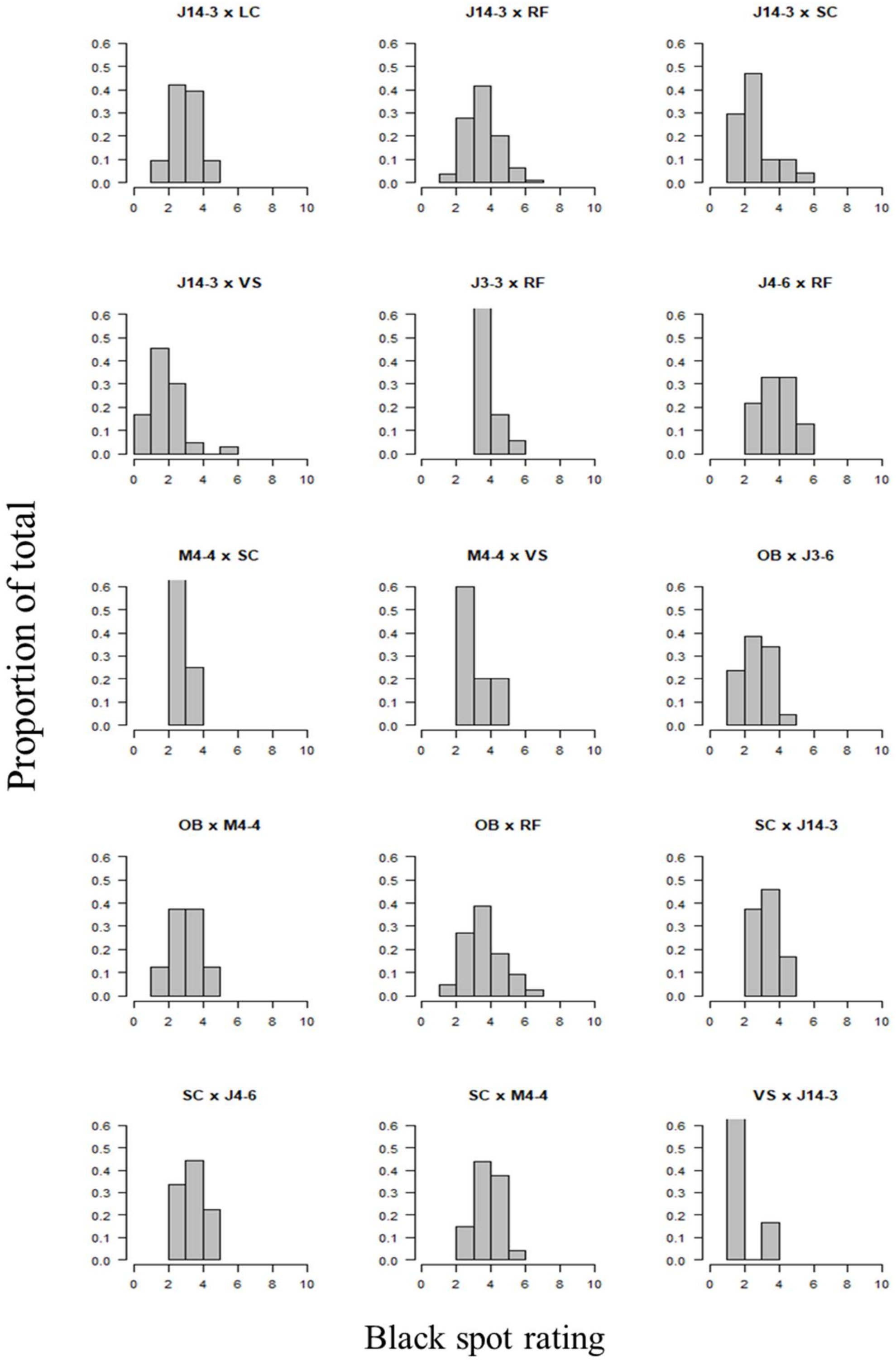


Figure 10. Histograms for the overall black spot PFS field evaluation in 2016 from fifteen diploid rose populations generated by R 3.3.2 (R Core Team, 2016).

4.4.2 Consensus map development

The detailed information about individual genetic maps of J14-3 x LC, J14-3 x VS and OB x RF can be found in Chapter III. Another two individual maps calculated for J4-6 x RF (62 individuals, 1553 SNPs, 438 cM) and OB x J3-6 (93 individuals, 1679 SNPs, 375 cM) (Appendix 3) and the consensus map based on the five families was composed of 4538 SNPs. Individuals used for map development were checked to eliminate any selfs or out crosses. Approximately 11-21% of the total markers were highly distorted ($0.0005 < P < 0.05$; Table 18) which is similar to the ~18% distortion observed in the previous populations. Many markers were mapped to the same locus and they were counted as one bin marker, thus, the mean distance of bin markers ranged from 0.6 - 1 bin marker/cM and there were 2.4 – 6.1 markers/cM if considering the co-segregating markers. The largest gaps varied from 2.9 to 7.9 cM for the seven LGs in the two populations (Table 18). The apparent short length of LG3 (17.1 cM) and LG7 (37.4 cM) in OB x J3-6 may be caused by insufficient genotyping data. LG3 of OB x J3-6 mainly consisted of maternal marker types (lm x ll) with only one bi-parental marker type (hk x hk). MergeMap inflated the map length of the consensus map, thus, the consensus map used for QTL detection was scaled according to the average LG length of individual maps (Khan et al., 2012). The scaling factor was estimated at 0.37±0.04 (mean ± standard deviation) (Table 19). Next, 4538 SNP of the consensus map plus the phenotypes from these five families were imported into FlexQTL for data curation (2318 SNPs had more than 10% missing across ten families, 87 SNPs were removed due to inconsistent inheritance, and 637 SNPs caused double recombination within 10 cM were removed), which resulted in a consensus map with 1496 SNP to initiate the analysis among the first five families. Data curation was further performed after adding an additional ten families (54 SNPs were removed due to inconsistent inheritance, 705 SNPs caused double recombination within 10 cM were removed), leading to the final consensus map with 791 SNP in 407 loci covering 430 cM of the rose genetic map including 4 highly distorted SNPs ($p < 0.01$) (Table 20 and 21). This final consensus map was utilized for QTL analysis in FlexQTL.

Table 18. Map length, number of co-segregating markers, number of bin markers, number of highly distorted markers ($p<0.05$), and the largest gap among markers for diploid rose populations J4-6 x RF and OB x J3-6.

	J4-6 x RF				
LG	**Length (cM)**	**No. of markers**	**No. of distorted markers (P<0.05)**	**No. of bin markers**	**Biggest gap**
1	55.1	132	39	37	5.1
2	88.1	345	107	61	4.4
3	52.2	172	92	46	3.5
4	55.6	185	0	35	7.9
5	69.3	205	0	39	3.3
6	53.3	283	95	43	2.9
7	64.9	231	0	56	3.3
Overall	438.5	1553	333	317	7.9
			OB x J3-6		
1	57.9	223	39	56	4.2
2	66.1	405	46	69	5
3	17.1	65	1	10	7.6
4	59.6	146	83	49	6.3
5	72.6	357	0	68	4.3
6	64	342	12	67	3.1
7	37.4	141	12	34	5.6
Overall	374.7	1679	193	353	7.6

Table 19. Features of the individual diploid rose maps and the consensus diploid rose map: SNP number, length for each LG, the average length by family and for the consensus map and the scaling factors calculated based on the average length of each LG across five maps.

		J4-6 x RF	**J14-3 x LC**	**J14-3 x VS**	**OB x J3-6**	**OB x RF**	**Avg**	**Consensus**	**Scaling factor**
LG1	SNP No.	132	186	159	223	99	159.8	488	-
	Length	55.1	50.5	43.1	57.9	68.2	54.96	145.9	0.38
LG2	SNP No.	345	270	296	405	367	336.6	984	-
	Length	88.1	73.3	75.9	66.1	82.4	77.16	220.8	0.35
LG3	SNP No.	172	193	121	65	78	125.8	416	-
	Length	52.2	62.1	69.8	17.1	58.6	51.96	123.8	0.42
LG4	SNP No.	185	198	223	146	220	194.4	618	-
	Length	55.6	53.1	51.7	59.6	58.3	55.66	148.4	0.38
LG5	SNP No.	205	273	224	357	301	272	706	-
	Length	69.3	74.3	78.4	72.6	85.7	76.06	205.4	0.37
LG6	SNP No.	283	219	139	342	224	241.4	705	-
	Length	53.3	63.5	62.7	64.0	72.1	63.12	151.2	0.42
LG7	SNP No.	231	227	259	141	241	219.8	621	-
	Length	64.9	66.6	56.2	37.4	70.1	59.04	202.2	0.29
Overall	SNP No.	1553	1566	1421	1679	1530	1549.8	4538	0.37±0.04

Table 20. Seven linkage groups of the final diploid rose consensus map generated by JoinMap 4.1.

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr7_5726635	1	0	chr5_19550990	1	27
chr7_23260838	1	0	chr7_18627921	1	27
chr7_23260855	1	0	chr7_18974728	1	27
chr4_10812806	1	1	chr7_19157798	1	28
chr7_7531798	1	1	chr7_19312259	1	28
chr7_7156618	1	2	chr7_19443620	1	28
chr7_9417814	1	4	chr7_19443674	1	28
chr7_9153848	1	5	chr7_19443696	1	28
chr7_9153849	1	5	chr7_19657053	1	28
chr7_11016267	1	5	chr7_19741362	1	29
chr7_8558661	1	5	chr7_19741411	1	29
chr7_11211187	1	6	chr7_19939304	1	29
chr7_12134078	1	9	chr7_20229757	1	30
chr7_12134106	1	9	chr7_20231954	1	30
chr7_13531368	1	10	chr7_20645379	1	31
chr7_13531473	1	11	chr7_19373763	1	31
chr7_15199745	1	11	chr7_19533600	1	31
chr7_14622229	1	12	chr7_20804998	1	31
chr7_15370551	1	13	chr5_11923707	1	36
chr7_15083044	1	13	chr7_21564253	1	36
chr7_15169630	1	13	chr7_21606193	1	36
chr7_15865553	1	14	chr7_21564346	1	37
chr7_15395727	1	16	chr7_21724636	1	37
chr7_15723631	1	16	chr7_22043026	1	38
chr7_16182702	1	16	chr7_22043128	1	38
chr7_16471467	1	16	chr7_22043139	1	38
chr7_17495203	1	18	chr7_22043022	1	39
chr7_16480824	1	18	chr7_22422232	1	41
chr7_16182737	1	18	chr7_22422036	1	41
chr7_16672845	1	19	chr7_22422141	1	41
chr7_16672896	1	19	chr7_22739206	1	41
chr7_16690209	1	19	chr7_23206126	1	46
chr7_16760096	1	19	chr7_23206148	1	49
chr7_17479411	1	22	chr7_23206146	1	49
chr7_17901640	1	22	chr1_1027915	2	0
chr7_18207597	1	22	chr1_141372	2	1
chr7_18627984	1	23	chr1_141437	2	1
chr7_18376963	1	24	chr1_557718	2	1
chr7_18141361	1	25	chr1_1580333	2	1
chr7_18177083	1	25	chr1_1359634	2	2
chr7_18177097	1	25	chr1_1593904	2	2
chr7_18177112	1	25	chr1_1909160	2	2
chr7_18376957	1	25	chr1_1528330	2	2
chr7_18377095	1	26	chr1_1580312	2	3

Table 20. Continued

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr1_2222850	2	5	chr1_5774378	2	18
chr1_2222853	2	5	chr1_6271460	2	18
chr1_2318660	2	5	chr1_6290644	2	18
chr1_2446263	2	6	chr1_6290649	2	18
chr1_2475041	2	6	chr1_5964572	2	19
chr1_2475043	2	6	chr1_5964646	2	19
chr1_2507772	2	6	chr1_6042884	2	21
chr1_2446131	2	6	chr1_6454459	2	21
chr1_2474950	2	6	chr1_6737085	2	21
chr1_2528576	2	7	chr1_10372125	2	25
chr1_2528580	2	7	chr1_10137503	2	26
chr1_2736301	2	7	chr1_10312816	2	26
chr1_2736887	2	7	chr1_10495617	2	26
chr1_2732179	2	7	chr1_10612359	2	26
chr1_2741197	2	7	chr1_10922413	2	26
chr1_2865922	2	9	chr1_11512060	2	26
chr1_2880239	2	9	chr1_11664672	2	26
chr1_2776887	2	9	chr1_11832123	2	26
chr1_2816973	2	9	chr1_15312104	2	26
chr1_4197169	2	11	chr1_16650361	2	26
chr1_4206800	2	11	chr1_18100552	2	26
chr1_4676262	2	12	chr1_18223742	2	26
chr1_3152848	2	12	chr1_7163129	2	26
chr1_4197245	2	13	chr1_7834765	2	26
chr1_4229555	2	13	chr1_7834777	2	26
chr1_3250244	2	13	chr1_9787356	2	26
chr1_3384319	2	13	chr1_10372077	2	26
chr1_4229598	2	13	chr1_9688384	2	26
chr1_4206615	2	14	chr1_11618947	2	28
chr1_4206617	2	14	chr1_17101311	2	30
chr1_4257791	2	16	chr1_17101313	2	30
chr1_4320547	2	16	chr1_17288435	2	30
chr1_4354796	2	16	chr1_19106122	2	30
chr1_5502625	2	17	chr1_15479862	2	31
chr1_5502691	2	17	chr1_14439482	2	32
chr1_5065178	2	17	chr1_16375547	2	32
chr1_5065188	2	17	chr1_16375525	2	35
chr1_5065205	2	17	chr6_20144159	2	35
chr1_5332657	2	17	chr6_19982930	2	35
chr1_5728871	2	17	chr6_19982957	2	35
chr1_5878782	2	17	chr6_20144288	2	35
chr1_5964559	2	17	chr6_20425966	2	35
chr1_5964690	2	17	chr1_6070725	2	36
chr1_5332614	2	18	chr1_6070761	2	36
chr1_5729018	2	18	chr6_21065036	2	36

Table 20. Continued

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr6_21334726	2	37	chr6_29493159	2	57
chr6_21519907	2	38	chr6_29528460	2	57
chr6_22241836	2	39	chr6_29528615	2	57
chr6_22305500	2	40	chr6_29528617	2	57
chr6_22305632	2	40	chr6_32093971	2	59
chr3_16920479	2	40	chr6_32094031	2	59
chr6_22964006	2	41	chr6_31834685	2	59
chr6_23394674	2	44	chr6_31834871	2	59
chr6_24333399	2	44	chr6_32412566	2	59
chr6_24333476	2	44	chr6_32918325	2	60
chr6_23394510	2	44	chr6_33233603	2	60
chr6_23394609	2	44	chr6_33242307	2	60
chr6_23481749	2	44	chr6_32918427	2	60
chr6_24662967	2	45	chr6_32918435	2	60
chr6_24982882	2	46	chr6_32975531	2	60
chr6_24983076	2	46	chr6_33264200	2	61
chr6_25644722	2	46	chr6_32953315	2	61
chr6_25644854	2	46	chr6_32953336	2	61
chr6_25644899	2	46	chr6_33040719	2	61
chr6_25352808	2	47	chr6_33305252	2	61
chr6_25738190	2	47	chr6_33531246	2	61
chr6_25903305	2	47	chr6_33335228	2	61
chr6_26295215	2	47	chr6_34506637	2	62
chr6_26646145	2	47	chr6_34648602	2	62
chr6_27390111	2	51	chr6_34209630	2	62
chr6_27543135	2	51	chr6_34413787	2	63
chr6_27543158	2	51	chr6_34506623	2	64
chr6_28141676	2	51	chr6_34506673	2	64
chr6_27839204	2	51	chr6_34270610	2	65
chr6_27819339	2	51	chr6_34482688	2	65
chr6_29154631	2	52	chr6_34653810	2	65
chr6_29154708	2	52	chr6_34653828	2	65
chr6_29154709	2	52	chr6_34923102	2	65
chr6_29154701	2	52	chr6_35290819	2	65
chr6_29149772	2	53	chr6_35934748	2	67
chr6_30845257	2	54	chr6_36004476	2	67
chr6_31531493	2	55	chr6_35965591	2	67
chr6_28141607	2	55	chr6_36073413	2	67
chr6_15095193	2	55	chr6_35174015	2	67
chr6_30957368	2	55	chr6_35934830	2	68
chr6_31531359	2	56	chr6_35934824	2	68
chr6_15068430	2	57	chr6_35965675	2	68
chr6_15068553	2	57	chr6_36420603	2	69
chr6_15095292	2	57	chr6_36525170	2	69
chr6_15108560	2	57	chr6_36587030	2	70

Table 20. Continued

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr6_36587060	2	70	chr6_7740758	3	29
chr6_36591460	2	70	chr6_8607327	3	30
chr6_36858528	2	70	chr6_8614680	3	30
chr6_36844858	2	71	chr6_8724376	3	30
chr6_36844926	2	71	chr6_8977622	3	31
chr6_9582276	2	73	chr6_8977642	3	31
chr6_9582330	2	73	chr6_8977696	3	31
chr6_9582408	2	73	chr6_8977697	3	31
chr6_37800891	2	74	chr6_10886313	3	34
chr6_38527314	2	75	chr6_10110076	3	37
chr6_37899541	2	75	chr6_10299130	3	37
chr6_37800900	2	76	chr6_17519036	3	40
chr6_38221149	2	76	chr6_17519049	3	41
chr6_38821329	2	77	chr6_17519052	3	41
chr6_106927	3	0	chr6_16820517	3	41
chr6_106933	3	0	chr4_23601458	3	45
chr6_242617	3	3	chr6_13183624	3	45
chr6_811177	3	3	chr4_23601510	3	45
chr6_741884	3	3	chr1_13372495	3	50
chr6_811129	3	3	chr1_23128197	3	52
chr6_811231	3	4	chr3_23543923	3	52
chr6_1425327	3	6	chr3_23543973	3	52
chr6_1425330	3	6	chr4_14903227	3	52
chr6_1425332	3	6	chr4_2910568	4	0
chr6_1974388	3	7	chr4_2910641	4	0
chr6_1974447	3	7	chr1_14815301	4	0
chr6_1974541	3	8	chr4_624747	4	0
chr6_2965689	3	10	chr4_624757	4	0
chr6_2965740	3	10	chr4_1558722	4	0
chr6_3272563	3	11	chr4_1558806	4	0
chr6_2843950	3	11	chr4_1558819	4	1
chr6_2843963	3	11	chr4_1607434	4	1
chr6_2844006	3	11	chr4_13333703	4	2
chr6_3326319	3	12	chr4_13333733	4	2
chr6_3272518	3	12	chr4_13333754	4	2
chr6_3445019	3	12	chr4_10024609	4	9
chr6_3666446	3	13	chr4_10024632	4	9
chr6_3666368	3	13	chr1_2202074	4	10
chr6_4371663	3	15	chr1_2202091	4	10
chr6_4332487	3	16	chr1_2202128	4	10
chr6_4710053	3	16	chr4_10022851	4	10
chr6_4777858	3	19	chr4_10902818	4	10
chr6_5982014	3	22	chr4_4300849	4	10
chr6_5982011	3	23	chr4_6093143	4	10
chr6_5982031	3	25	chr4_9349435	4	11

Table 20. Continued

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr4_13538101	4	12	chr4_26053815	4	30
chr4_15551447	4	12	chr4_17246387	4	31
chr4_15244556	4	13	chr4_17246397	4	31
chr4_15572828	4	13	chr4_17246403	4	31
chr4_15572876	4	13	chr4_27098452	4	34
chr4_15621967	4	14	chr4_27109568	4	34
chr4_16933603	4	14	chr4_27264885	4	34
chr4_16895077	4	15	chr4_27981343	4	34
chr4_16895123	4	15	chr4_28172720	4	34
chr4_16000819	4	16	chr4_29545641	4	38
chr4_16895050	4	16	chr4_27981351	4	41
chr4_19489223	4	17	chr4_29004618	4	41
chr4_20265456	4	17	chr4_29004622	4	41
chr4_20800425	4	18	chr4_29136852	4	42
chr4_20265486	4	19	chr4_29691759	4	46
chr4_20363091	4	19	chr4_29746082	4	46
chr4_22519456	4	19	chr4_29594662	4	46
chr4_22657192	4	19	chr4_29859004	4	46
chr4_20365729	4	19	chr4_30210924	4	48
chr4_20700236	4	19	chr4_30309085	4	49
chr4_20706260	4	19	chr4_30429096	4	49
chr4_22519554	4	19	chr4_30848368	4	51
chr4_20365723	4	19	chr4_30939552	4	51
chr4_20706136	4	19	chr4_30939637	4	51
chr4_23227841	4	21	chr4_31140010	4	51
chr4_23227843	4	21	chr4_31186000	4	51
chr4_20853281	4	22	chr4_30675543	4	52
chr4_23043038	4	22	chr4_30939570	4	52
chr4_23043134	4	22	chr4_30928983	4	52
chr4_25903570	4	23	chr4_30929001	4	52
chr4_23895969	4	23	chr4_31186040	4	53
chr4_25693160	4	24	chr4_31282608	4	53
chr3_6449225	4	29	chr4_31139869	4	53
chr4_24870345	4	29	chr4_31280198	4	53
chr3_6491077	4	29	chr4_31185883	4	53
chr4_25378617	4	29	chr4_31986160	4	53
chr4_24709745	4	29	chr4_31986190	4	53
chr4_24753699	4	29	chr4_32000338	4	53
chr4_24870399	4	29	chr4_31611417	4	54
chr4_25551889	4	29	chr4_31779960	4	54
chr4_24079668	4	30	chr4_31984893	4	55
chr4_24229640	4	30	chr4_31986193	4	55
chr4_26225342	4	30	chr4_32094305	4	55
chr4_24141070	4	30	chr3_405940	5	0
chr4_26044602	4	30	chr3_361363	5	1

Table 20. Continued

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr3_455471	5	1	chr3_18994326	5	33
chr3_426312	5	3	chr3_18615940	5	33
chr3_426387	5	3	chr3_18616047	5	33
chr3_426359	5	3	chr3_8683165	5	33
chr3_426370	5	3	chr3_19014687	5	33
chr3_869268	5	4	chr3_18862082	5	34
chr3_869271	5	4	chr3_18862084	5	34
chr3_869270	5	4	chr3_10598985	5	35
chr3_869272	5	4	chr3_18758276	5	35
chr3_972201	5	4	chr5_23191645	5	36
chr3_869264	5	5	chr3_10598995	5	36
chr3_426408	5	5	chr3_10599066	5	36
chr3_1055824	5	5	chr3_11349294	5	37
chr3_1136064	5	5	chr3_11554020	5	37
chr3_1553932	5	6	chr5_9431825	5	37
chr3_2220732	5	7	chr5_23114511	5	37
chr3_2696516	5	9	chr3_11861432	5	38
chr4_13334563	5	12	chr3_12805107	5	39
chr2_28187001	5	12	chr3_12975438	5	39
chr3_4687361	5	12	chr3_13327220	5	40
chr6_12992660	5	12	chr3_13915841	5	41
chr3_4298301	5	12	chr3_14124476	5	42
chr3_4687313	5	13	chr3_22059885	5	43
chr3_4687322	5	13	chr3_21072830	5	43
chr3_3346242	5	18	chr3_21073097	5	43
chr3_3346244	5	18	chr3_21073123	5	43
chr3_3115275	5	18	chr1_11729744	5	44
chr3_2919821	5	19	chr3_22397858	5	44
chr3_2919718	5	19	chr3_22678527	5	44
chr3_3020856	5	19	chr3_22678583	5	44
chr3_2919720	5	19	chr3_15803015	5	47
chr3_2919722	5	19	chr3_23544333	5	47
chr3_2919842	5	19	chr3_16920619	5	47
chr3_2919798	5	20	chr3_18106402	5	50
chr3_2919827	5	20	chr3_18140795	5	50
chr3_2905097	5	21	chr3_16203146	5	51
chr3_2919840	5	21	chr3_17986965	5	51
chr3_6358107	5	22	chr3_24955036	5	52
chr2_12639441	5	23	chr3_24921938	5	52
chr2_12639449	5	23	chr3_24711579	5	52
chr3_7658006	5	24	chr3_24594162	5	53
chr3_9163581	5	30	chr3_24050323	5	54
chr3_9836060	5	30	chr3_24214576	5	54
chr3_10025041	5	30	chr3_24214642	5	54
chr3_10146850	5	31	chr5_16160301	5	56

Table 20. Continued

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr3_25618143	5	57	chr2_7990292	6	17
chr3_25674418	5	58	chr2_7990325	6	17
chr3_25750115	5	59	chr2_7106324	6	19
chr3_25974470	5	61	chr2_12770187	6	20
chr3_26012934	5	61	chr2_19750229	6	22
chr3_26012985	5	61	chr2_3756853	6	22
chr3_26344419	5	61	chr2_19750265	6	22
chr3_26344376	5	61	chr2_3693948	6	22
chr3_26296132	5	62	chr2_4337490	6	23
chr3_26392692	5	63	chr2_4361539	6	23
chr3_27723279	5	63	chr2_4633530	6	24
chr3_29185653	5	67	chr2_8945508	6	24
chr3_29568573	5	68	chr2_9216348	6	26
chr3_30321480	5	68	chr2_9216428	6	26
chr3_30526930	5	70	chr2_13360973	6	28
chr3_32277762	5	71	chr2_13360912	6	28
chr3_32592274	5	72	chr2_14532723	6	28
chr3_32592277	5	72	chr2_14340569	6	28
chr3_29565427	5	73	chr2_14765803	6	30
chr3_29565460	5	73	chr2_15241175	6	30
chr3_30218792	5	74	chr2_14958810	6	30
chr3_32675821	5	76	chr2_14825076	6	30
chr2_11702810	6	0	chr2_15426851	6	30
chr2_11702858	6	0	chr2_17556844	6	33
chr2_11703045	6	0	chr2_17790181	6	33
chr2_11703057	6	0	chr2_17790190	6	33
chr2_11378807	6	2	chr2_17239977	6	35
chr2_11334944	6	3	chr2_17106347	6	36
chr2_11335023	6	3	chr2_17106440	6	36
chr2_11335090	6	3	chr2_16441108	6	37
chr2_11335101	6	3	chr2_16695551	6	37
chr2_5748052	6	3	chr2_18469715	6	38
chr2_5237009	6	3	chr2_18557623	6	38
chr2_5237183	6	3	chr2_18900138	6	38
chr2_5249624	6	3	chr2_19052872	6	39
chr2_5249636	6	7	chr2_19598786	6	39
chr2_1330104	6	8	chr2_19598858	6	39
chr2_11378810	6	8	chr2_20497450	6	40
chr2_1330184	6	8	chr2_20538051	6	40
chr2_1948952	6	9	chr2_20621917	6	40
chr2_361984	6	11	chr2_20497457	6	40
chr2_293190	6	12	chr2_20497466	6	40
chr2_8832534	6	14	chr2_20497565	6	40
chr2_8832624	6	14	chr2_20697599	6	41
chr5_21721374	6	14	chr2_20775521	6	41

Table 20. Continued

Marker name	Linkage Group	Position cM	Marker name	Linkage Group	Position cM
chr2_27349150	6	41	chr2_24273834	6	58
chr2_27349152	6	41	chr2_24130001	6	59
chr2_20873439	6	41	chr2_24130025	6	59
chr2_21806912	6	42	chr2_24033015	6	59
chr2_21808213	6	42	chr2_23822309	6	60
chr2_21649972	6	42	chr2_24001869	6	60
chr2_21847348	6	46	chr2_23822264	6	60
chr2_21847437	6	46	chr2_23822327	6	61
chr2_22103425	6	46	chr2_23822395	6	61
chr2_21841255	6	47	chr2_23449920	6	61
chr2_28675051	6	49	chr2_23649114	6	61
chr2_28019879	6	50	chr2_23449950	6	61
chr2_28041695	6	50	chr2_22876628	6	62
chr2_28041839	6	50	chr3_18443116	6	62
chr2_28046701	6	50	chr2_23399290	6	63
chr2_27577573	6	51	chr2_22876548	6	63
chr2_27987910	6	51	chr2_23303376	6	63
chr2_27244168	6	51	chr2_23449654	6	63
chr2_27384565	6	51	chr2_23381520	6	63
chr2_25107174	6	52	chr5_9983664	7	0
chr2_25946068	6	52	chr5_9983711	7	0
chr2_26476937	6	52	chr5_9983713	7	0
chr2_26476963	6	52	chr5_23191635	7	1
chr2_26778402	6	52	chr5_9983670	7	1
chr2_27037890	6	53	chr5_10540752	7	1
chr2_26347536	6	53	chr5_10325059	7	2
chr2_25968240	6	54	chr5_10155887	7	2
chr2_24943563	6	55	chr5_9690599	7	4
chr2_25312195	6	55	chr5_23191591	7	5
chr2_25312197	6	55	chr5_23191619	7	5
chr2_25312202	6	55	chr5_8914751	7	6
chr2_25243094	6	56	chr5_8354225	7	7
chr2_25286416	6	56	chr5_7227087	7	10
chr2_25312126	6	56	chr5_8686768	7	10
chr3_27248490	6	56	chr5_8686890	7	10
chr3_27248508	6	56	chr5_7227119	7	10
chr3_27248582	6	56	chr5_6804483	7	11
chr2_25111048	6	57	chr5_7379825	7	11
chr2_25600408	6	57	chr5_8056821	7	11
chr2_25873764	6	57	chr5_7677984	7	13
chr2_24412051	6	58	chr1_13372545	7	13
chr2_24570867	6	58	chr5_6804384	7	13
chr2_24570871	6	58	chr5_4461665	7	13
chr2_24570880	6	58	chr5_4737510	7	13
chr2_24626410	6	58	chr5_4737511	7	13

Table 20. Continued

Marker name	Linkage Group	Position cM
chr5_5379398	7	14
chr5_4243693	7	16
chr5_4306260	7	16
chr5_4766085	7	16
chr5_4785160	7	16
chr5_5061345	7	16
chr5_4489986	7	16
chr5_4737518	7	16
chr5_22550855	7	18
chr5_3180386	7	18
chr5_3495738	7	18
chr5_3349245	7	18
chr5_2909342	7	19
chr5_2909445	7	19
chr5_2069280	7	19
chr5_2069239	7	19
chr5_1881511	7	21
chr5_1881602	7	21
chr5_1881454	7	21
chr5_1825825	7	21
chr5_1861049	7	21
chr5_1860992	7	22
chr5_1861000	7	22
chr5_1861128	7	23
chr5_1861167	7	23
chr5_1861180	7	23
chr5_1131479	7	23
chr5_1131484	7	23
chr5_110605	7	25
chr5_40345	7	25
chr5_110598	7	25
chr5_98049	7	25
chr5_710475	7	25
chr5_722916	7	25
chr5_475269	7	25
chr5_475375	7	25
chr5_363787	7	26
chr5_368219	7	26
chr5_389442	7	26
chr5_240038	7	26
chr5_98223	7	26
chr5_11107612	7	27
chr5_11107679	7	27
chr5_11140558	7	27
chr5_11429377	7	27
chr5_40337	7	30
chr5_12804159	7	34
chr3_18743967	7	37
chr5_11704284	7	37
chr5_16760635	7	38
chr1_12746465	7	40
chr5_19830985	7	40
chr5_20185018	7	42
chr5_20185022	7	42
chr5_20185045	7	42
chr5_23601754	7	45
chr5_22127952	7	45
chr5_24684603	7	45
chr5_24846887	7	45
chr5_26310193	7	45
chr5_26372387	7	45
chr2_12742083	7	47
chr5_26969165	7	47
chr5_27461800	7	47
chr5_26076220	7	48
chr1_9928541	7	49
chr1_9928565	7	49
chr6_10847179	7	51
chr6_10847182	7	51
chr5_26042126	7	52
chr5_28555792	7	55
chr5_28914204	7	56
chr5_24684607	7	58

Table 21. Diploid rose map length, SNP number and maximum gaps between SNP for each LG of the final consensus map utilized for FlexQTL analysis.

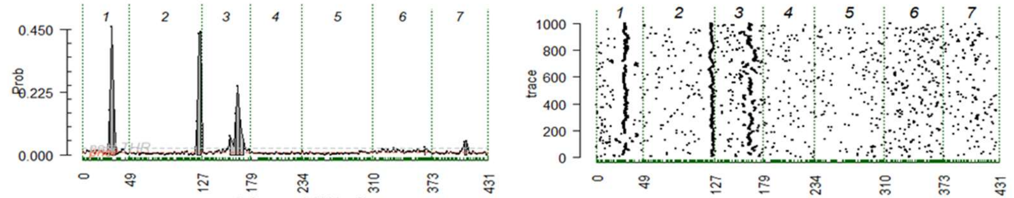
LG	Length	SNP no.	Max gap
1	49	78	4.8
2	77	204	4
3	52	54	5.5
4	55	110	6.6
5	76	114	5.9
6	63	132	4.2
7	58	99	3.8

4.4.3 Pedigree-based QTL analysis

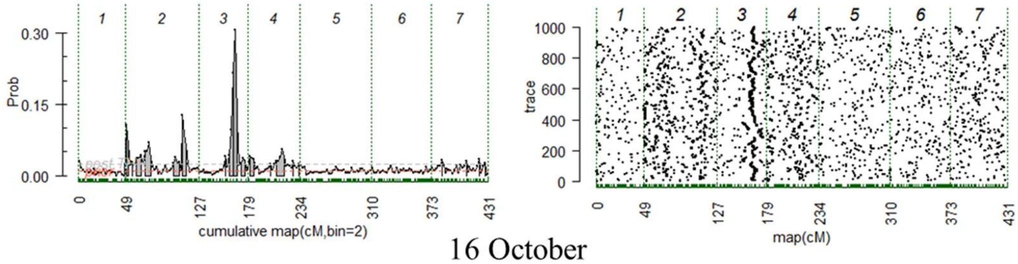
In the preliminary analysis among the first five populations 414 individuals with 1496 SNP, a decisive QTL on LG3 at interval 25-46 cM with 2ln(BF) >10 (decisive) was detected (data not shown). After combining all fifteen families (704 individuals), a strong QTL signal repeatedly appeared in the same region on LG3 in various runs. This QTL was highly consistent across different environments (Figure 11 and Table 22). It was strong in June, September and October (5<2lnBF<10) and decisive in November and overall combined analyses (2lnBF>10). The genome-wide analysis performed with LG3 separated into three parts again indicated a decisive QTL between 35-43 cM with 2lnBF= 32.6 associated with 2016 overall BS field assessment (data not shown). Moreover, the same QTL was discovered as a minor QTL (2lnBF= 2.2, considered as positive) in a 2013 field study in which eight families (J14-3 x SC, J14-3 x VS, J4-6 x RF, M4-4 x SC, OB x J3-6, OB x M4-4, SC x M4-4 and VS x J14-3) were assayed (data not shown). The QTL associated with BS field resistance/susceptibility explained 20.3% of the 2016 field overall phenotypic variance in the diploid rose germplasm under study.

Probable QTL genotypes on LG3 located between 34-44 cM were predicted for the parents and progeny with qq homozygous alleles decreasing disease scores and QQ homozygous alleles increasing disease scores. This QTL was segregating in the black spot resistant parents J4-6 and J14-3 with strong evidence (Figure 12). Unlike J4-6 and J14-3, the QTL genotype prediction for other parents varied among runs and in some cases conflicted with field observations. Some of these parents were only used in a few families or the family size is very small (J3-3 x RF, M4-4 x SC, M4-4 x VS), thus is it likely that there is not enough reliable phenotypic data for these parents to allow clear QTL genotype assignments. Progenies were categorized into qq/QQ/Qq groups according to the predicted QTL genotype at the signal peak on LG3 which was located at 39 cM and the means for the disease ratings were compared using student's t-test in JMP Pro 12.2.0. As expected, group qq had the lowest disease score and group QQ had the highest (Figure 13).

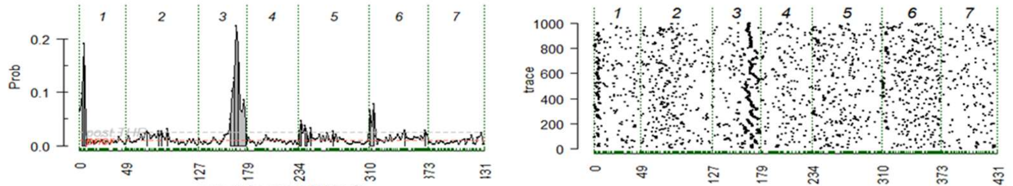
16 June



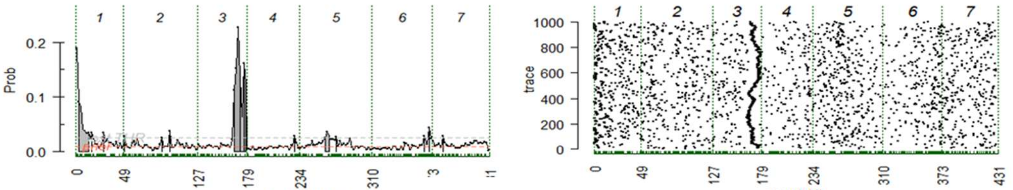
16 September



16 October



16 November



Overall

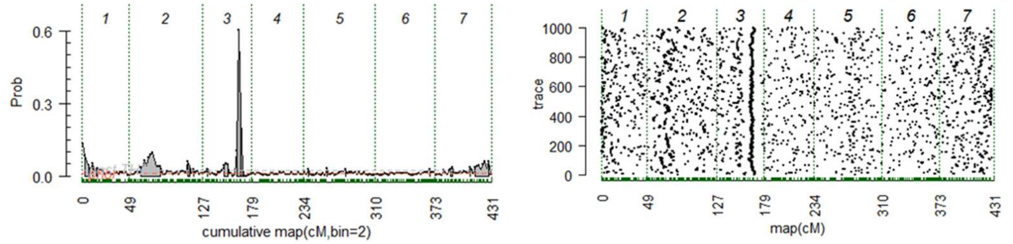


Figure 11. Genome-wide QTL prediction and trace plot outputs from VisualFlexQTL™ software (Bink et al., 2008) for black spot field evaluations in June, September, October, and November of 2016 and for the overall combined mean for 15 diploid rose populations. Each dot in the trace plots represents a QTL model with a subsampling of 1000 out of 100,000 MCMC.

Table 22. Estimations of 2ln(BF) for black spot resistance QTL models in June, September, October, and November of 2016 and for the overall combined mean for 15 diploid rose populations. Only LGs with 2ln(BF) > 2 are shown. Each run assumes a different number of QTL with the number of QTL being compared separated by a slash (/). The interpretation of 2lnBF values are hardly any (0-2); positive (2-5); strong (5-10); and decisive (>10) support for the QTL. Negative values indicate the sparser QTL model was favored. Results of LG3 are in bold.

		June	100,000 MCMC sweeps 100 thinning	
LG	Interval	2ln(BF) 1/0	2ln(BF) 2/1	2ln(BF) 3/2
1		10.2	-0.6	NA
2		29.4	-0.6	-2.3
3	***30-46***	***7.9***	-0.7	NA

		September	100,000 MCMC sweeps 100 thinning	
LG	Interval	2ln(BF) 1/0	2ln(BF) 2/1	2ln(BF) 3/2
2		4.5	2.5	-0.2
3	***28-51***	***8.5***	0.1	-0.4
4		2.8	0.6	NA

		October	100,000 MCMC sweeps 100 thinning	
LG	Interval	2ln(BF) 1/0	2ln(BF) 2/1	2ln(BF) 3/2
1		2.4	0.4	NA
3	***34-52***	***8.3***	0.8	-1.7

		November	100,000 MCMC sweeps 100 thinning	
LG	Interval	2ln(BF) 1/0	2ln(BF) 2/1	2ln(BF) 3/2
1		4.2	1.2	-2.2
3	***38-52***	***14.1***	0.8	-0.8

		Overall	100,000 MCMC sweeps 100 thinning	
LG	Interval	2ln(BF) 1/0	2ln(BF) 2/1	2ln(BF) 3/2
1		3.2	0.7	NA
2		5.1	0.9	-0.2
3	***36-43***	***29.8***	2.4	-0.5
7		3.2	-0.1	NA

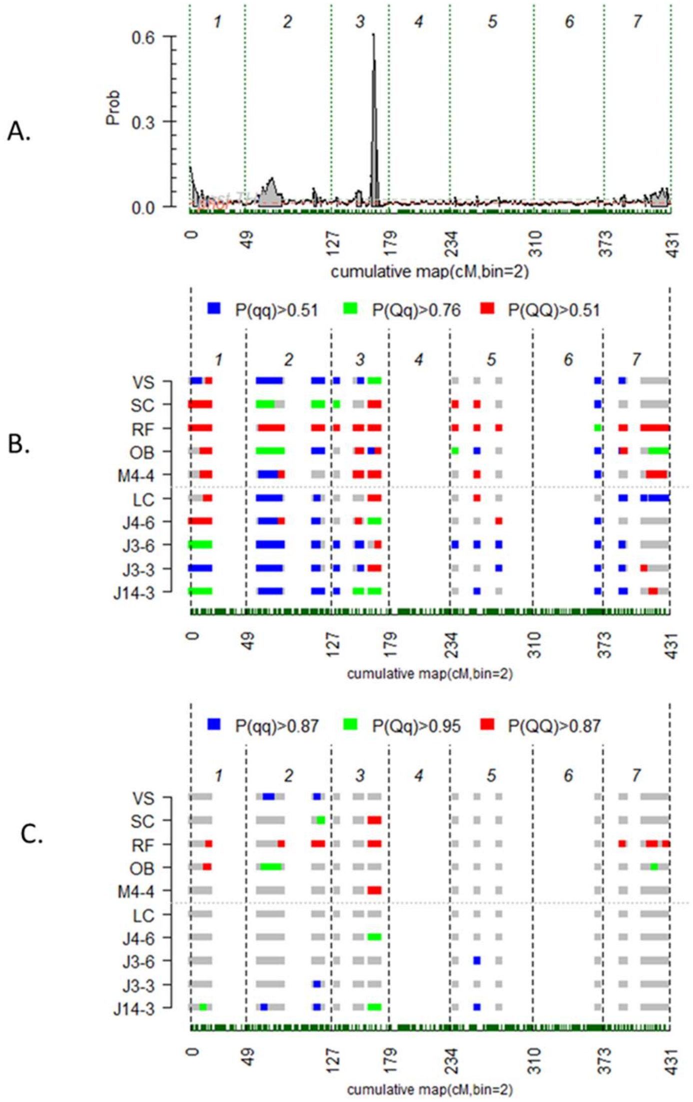


Figure 12. Genome-wide QTL prediction and probable QTL genotypes with positive and strong evidence for the parents of the 15 diploid rose mapping populations as determined in VisualFlexQTL™ (Bink et al., 2008) for the 2016 combined overall BS field evaluations. A. Genome-wide QTL detection in the 2016 overall combined analysis. The QTL was located on LG3 between 34-44 cM; B. Probable QTL genotype with positive evidence. For the predicted QTL genotypes, blue = homozygous qq with >0.51 probability, red = homozygous QQ with >0.51 probability, green = heterozygous Qq with >0.76 probability, and gray indicates the probability is too low to declare a category; C. Probable QTL genotype with strong evidence. For the predicted QTL genotypes, blue = homozygous qq with >0.87 probability, red = homozygous QQ with >0.87 probability, green = heterozygous Qq with >0.95 probability, and gray indicates the probability is too low to declare a category.

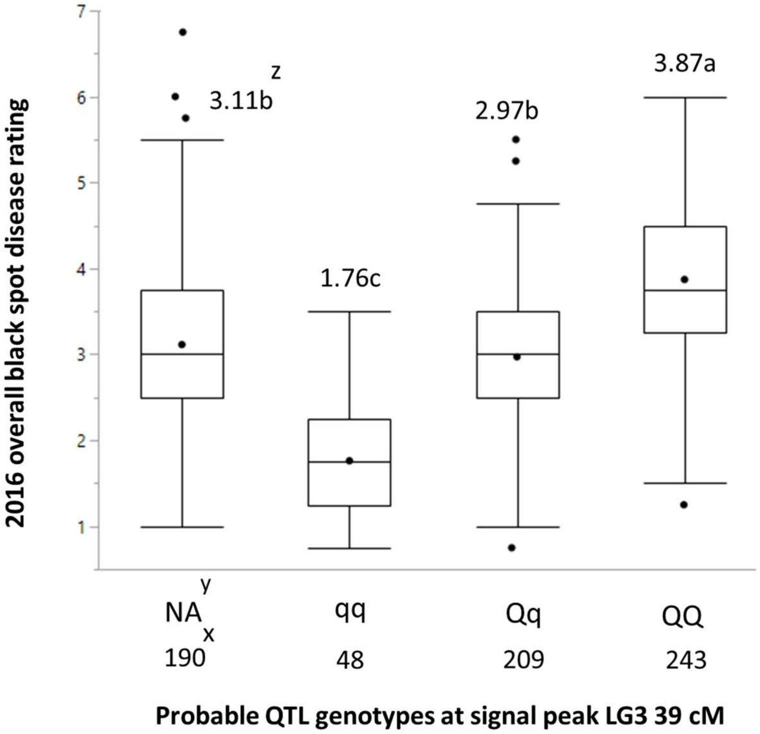


Figure 13. Box and whisker plot of 2016 field overall combined black spot disease rating for the three probable QTL genotypes at signal peak 41cM on LG3 among all diploid rose mapping materials. Dots inside the boxes represent mean of each group and dots outside the maximum and minimum lines are outliers.

[z] Student's t-test mean comparison. Levels not connected by the same letter are significantly different ($\alpha=0.05$)

[y] QTL genotype predicted at LG3 39 cM

[x] Number of progeny in each QTL genotype class

4.4.4 Haplotype analysis

Eighteen haplotypes (9 parental and 9 recombinant) were discovered among eight parents/grandparents: DD, M4-4, OB, J4-6, RF, LC, J14-3, J3-6 and VS, and 369 resulting progenies (Table 23). At least two functional alleles (H3 and H4) with slightly different effects were present in the resistant breeding lines J14-3 and J4-6, respectively. The allelic effects were compared between families J14-3 x RF and J4-6 x RF with RF, a possible homozygous QQ susceptible cultivar, as the common parent (Figure 14). The resistant q allele H3 in J14-3 decreased the overall disease rating by 0.8, while the H4 resistant allele in J4-6 had the effect of decreasing the disease rating by 1.2. However, the box plots showed a poor correlation between genotype and phenotype in both populations with overlapping disease scores of the progenies in two genotypic classes. This could be caused by the difficulty associated with black spot disease phenotyping or due to the fact that only one progeny per seedling was phenotyped demonstrating the need to increase the number of individuals phenotyped in subsequent studies (Figure 14).

The inheritance of the resistance allele was traced in the pedigree, however, due to the lack of data for many progenitors, we were unable to conclusively identify the origin of the resistance. At the time of this study, we were able to conclude that the H3 resistant allele in J14-3 did not come from DD but rather from an unknown source PP-J14-3 (PP: unknown paternal pollen); and the H4 resistant allele likely came from either OB or R.wichThless (*Rosa wichurana* 'Basye's Thornless') (Figure 15).

Table 23. Eighteen haplotypes identified among individuals within the QTL region on LG3 spanning from 34-44 cM. The haplotype is composed of 9 SNP with the QTL peak located at 39 cM.

	SNP	chr6_8977642	chr6_10886313	chr6_10110076	chr6_10299130	chr6_17519036	chr6_17519049	chr6_17519052	chr6_16820517	chr6_13183624
	Position on LG3 (cM)	31.11	34.03	37.06	37.06	39.99	41.09	41.09	41.3	44.88
Haplotypes	H1	C	G	A	G	C	G	A	G	T
	H2	A	A	G	A	C	G	A	A	C
	H3	C	G	G	A	C	T	C	A	C
	H4	A	A	G	A	A	G	A	A	C
	H5	C	A	A	G	C	G	A	G	T
	H6	A	G	G	A	C	G	A	A	C
	H7	C	G	G	A	A	T	C	A	C
	H8	C	G	G	A	C	G	A	A	C
	H9	C	G	G	A	C/-[Z]	T	C	G	C
	H10	C	A	A	G	C	G	A	A	C
	H11	C	A	A	G	A	G	A	A	C
	H12	C	A	G	A	A	G	A	A	C
	H13	C	A	G	A	C	G	A	A	C
	H14	A	G	G	A	C	T	C	A	C
	H15	C	A	A	G	C	G	A	G	C
	H16	A	G	G	A	A	T	C	A	C
	H17	A	A	G	A	C	T	C	A	C
	H18	C	G	G	A	A	G	A	A	C

[z] nucleotide C or missing (represented by "-")

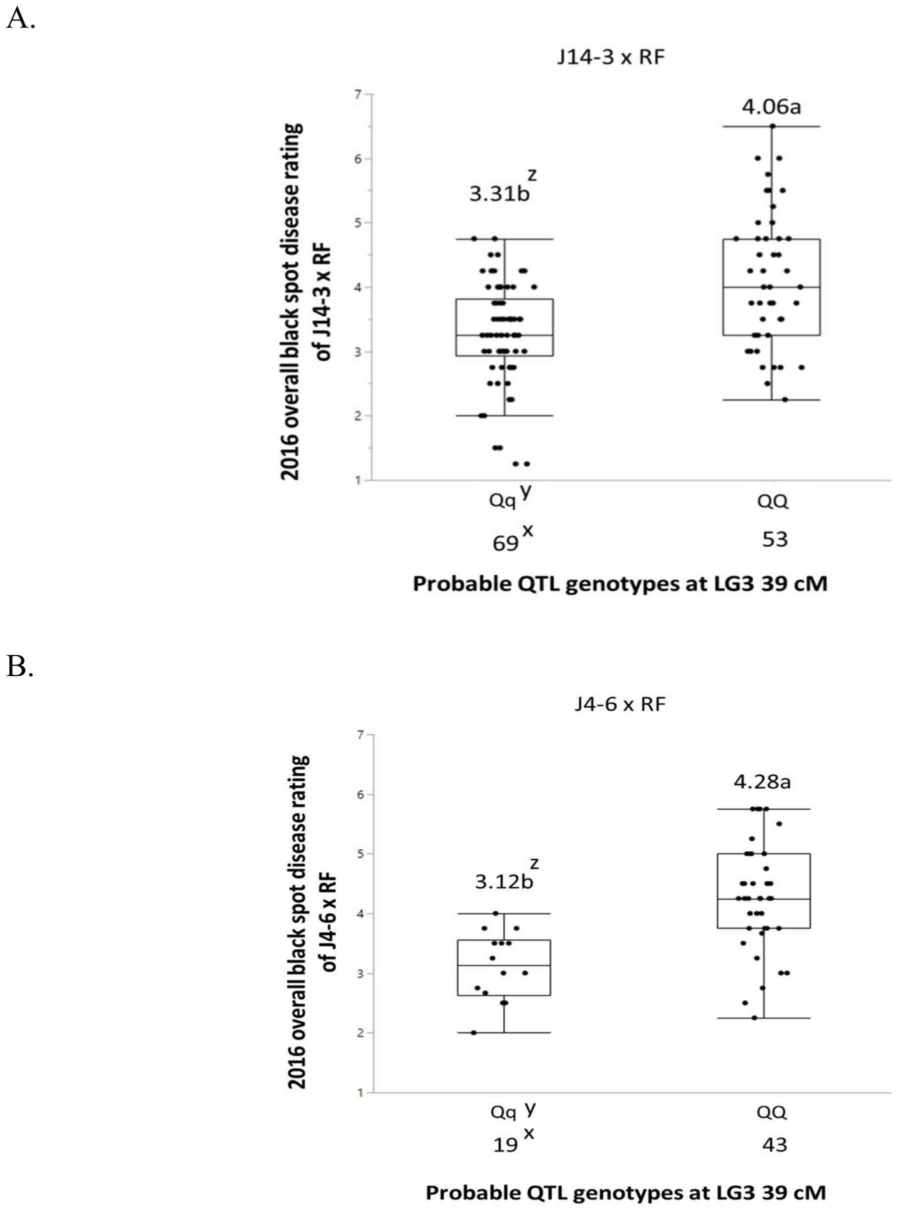


Figure 14. Box and whisker plot examining the effects of two resistant haplotypes in J14-3 and J4-6 within diploid rose families J14-3 x RF and J4-6 x RF on black spot overall combined rating in 2016 within the QTL region. (a.) Comparison of overall combined black spot rating for progeny with or lacking resistant q alleles in J14-3 x RF; (b.) Comparison of overall combined black spot rating for progeny with or lacking resistant q alleles in J4-6xRF. Comparisons of means were conducted by student's t-test at α = 0.05. Dots represent each individual's phenotype.

[z] Levels not connected by the same letter are significantly different (α=0.05)

[y] QTL genotype predicted at LG3 39 cM

[x] Number of progeny in each QTL genotype class

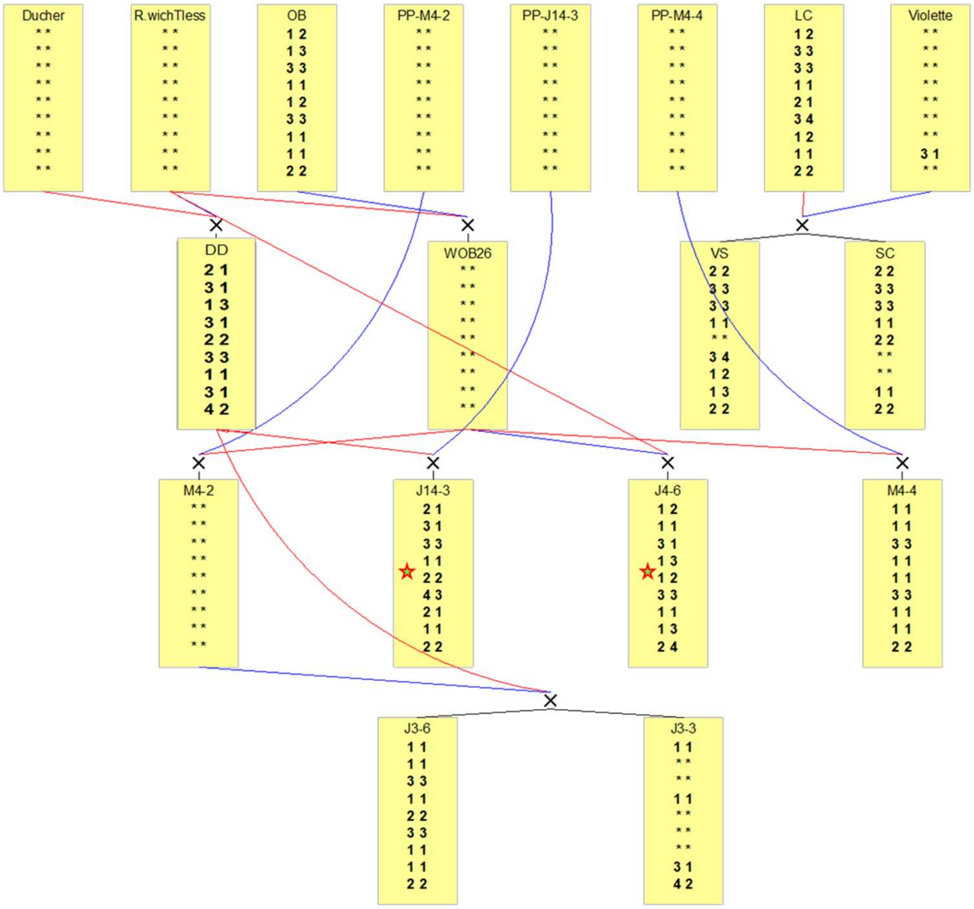


Figure 15. Documented pedigree of nine direct parents of the diploid rose mapping populations generated by Pedimap 1.2. Genotypic data of nine SNP markers in the QTL interval are shown along the pedigree; 1=A, 2=C, 3=G, 4=T, *=missing. Resistant alleles in J14-3 and J4-6 are marked by a red star on the left side. Red and blue lines link to female and male parents, respectively.

4.5 Discussion

Previous work has described the presence of partial resistance to black spot in cultivated roses and have estimated its heritability as low to moderate (Dong et al., 2017; Whitaker et al., 2009; Whitaker and Hokanson, 2009; Xue and Davidson, 1998). The present research extends this work by identifying a QTL that conditions partial resistance to black spot in rose. The strong evidence from the QTL and haplotype analyses, suggests that a major-effect QTL is present at the 1/3 distal end of LG3 (36-43 cM), and that at least two resistance alleles derived from J4-6 and J14-3 are involved in partial black spot resistance. This major QTL explained 20.3% of total phenotypic variance which is comparable to other QTL identified in roses so far, such as for chlorophyll content (25.8%) (Yan et al., 2003) and for powdery mildew resistance (24.9%) (Dugo et al., 2005), as well as the major QTL conferring resistance to *Phytopthora cactorum* in strawberry (20.3-24.2%) (Mangandi et al., 2017). Thus a QTL explaining 20% of phenotypic variance of a moderately heritable trait is significant and can possibly be selected in the breeding program. Annotation of this region based on the sequenced rose genome (work ongoing) would help to provide a better view of this region to see if any resistance associated genes are present, and additional work of fine-mapping and locus function verification could then be performed.

Eighteen unique haplotypes (nine parental and nine recombinant) were identified among eight parents: M4-4, OB, J4-6, RF, LC, J14-3, J3-6 and VS, and 369 resulting progeny. Based on the results obtained with FlexQTL, parents J4-6 and J14-3 were heterozygous at the QTL location carrying the resistant alleles, however, the data did not allow clear QTL conclusions for the remaining parents. QTL genotypes for some parents were variable when data from the different environments (i.e. months) were analyzed, e.g. OB was reported to have a moderate level of partial resistance (Dong et al., 2017), but it was classified as qq in October and QQ in other environments for the QTL on LG3. In a similar fashion, the selections M4-4, J3-3 and J3-6, which were described as resistant lines (Dong et al., 2017) were assigned different QTL genotypes in different environments. Several factors could lead to variable conclusions including the fact that some parents have been used in only 1-2 families, the low reliability of the phenotypic data, the lack of replication in disease screening and an erroneous conclusion on the resistance/susceptibility of a parent. Though J4-6, J14-3 and J3-6 all contain resistant cultivar *Rosa wichuriana* 'Basye's Thornless' (RW) in their pedigree (Dr. Byrne, personal communication), their resistant haplotypes were different: H1 for J4-6, and H3 for J14-3. Currently genotypic information for RW is not available, therefore it is not possible to clarify the source of resistance or verify the pedigree information. Therefore, future studies should focus on pedigree verification and the acquisition of the genotypic data for each of the founder parents. This would allow the clarification of the source of the resistant haplotypes.

VS was predicted to carry resistant haplotype H9 whereas it was rated as a susceptible cultivar. This could be due to inaccurate phenotyping thus leading to the wrong QTL genotype interpretation, or the resistance allele carried in VS may have been inherited recessively, which is a different mechanism from the resistance alleles in J14-3 and J4-6 (rated as heterozygous resistant breeding lines carrying co-dominant resistance alleles). Overall, the sources of resistance are inconclusive and obtaining the missing genotypic information about the founder parents may help clarify this.

The only QTL that was expressed strongly and consistently across all four months was the one on LG3. Since black spot partial disease resistance has been hypothesized as quantitatively inherited, it is possible that more QTL remain undiscovered, however, with the current strategy and populations, it was not possible to identify these QTL with confidence. This could be due to small population sizes, only one replication per seedling, and confounding effects between location and genotype leading to uneven inoculation and biased phenotyping thus affecting downstream QTL genotype prediction.

This study demonstrated the possibility of the application of GBS on pedigree-based QTL analysis, and will serve as the preliminary study for black spot partial resistance. However, with the availability of the new rose WagRhSNP 68K Axiom SNP array (Koning-Boucoiran et al., 2015), more work can be done on rose genetics and genomics, and QTL mapping results may be validated or advanced using other related materials or this SNP array. The genotypes of the parents and founder parents should be more complete in the future which would help to verify the pedigree and the resistance source. The process of marker validation is required to determine the reliability of a marker to predict phenotype (Collard and Mackill, 2008; Langridge et al., 2001). Moreover, the effect of a QTL may differ in different genetic backgrounds due to interactions with other loci or epistasis (Collard and Mackill, 2008). The large-effect QTL on LG3 and associated markers will need to be validated for utilization in a marker-assisted breeding program aimed at developing disease resistant germplasm.

CHAPTER V

CONCLUSIONS

The work presented here demonstrated the heritability of partial resistance to black spot, created a diploid rose consensus map, discovered a major-effect QTL and identified markers associated with partial resistance to black spot in roses.

Fifteen diploid populations generated in a partial diallel design were evaluated for black spot partial resistance in the field and assessed for heritability in Chapter II. Narrow sense heritability estimations varied from 0.12 to 0.54 and 0.07 to 0.42 when individual and overall months' data was analyzed for percentage of foliage with symptoms (PFS) and black spot lesion size ratings (BLS), respectively, indicating that partial resistance to black spot is moderately heritable. Additive variances explained 13% and 16% of the total variance for PFS and BLS, respectively, which were higher than what were explained by the non-additive variances (7% and 6%, respectively). The variance of the genotype by environment effect (71% and 66% for PFS and BLS, respectively) explained most of the total variance indicating that partial resistance was strongly affected by the environment, therefore, it is suggested that selection should be done across different environments (over time and/or locations) rather than in single environment. The correlation between PFS and BLS was moderate ($r = 0.59$) in the 2016 field trial.

While obtaining reliable field phenotyping data usually takes 2-3 years, molecular markers could accelerate the pace by quickly identifying the genotypes with disease resistance alleles. The three populations in Chapter III were used to create a consensus map with bridge SSR and SNP markers to define seven rose linkage groups and visualize the synteny between strawberry and rose. The consensus map in Chapter III had 3527 molecular markers covering a total length of 892.2 cM. The overall collinearity was highly conserved among the consensus map and the individual maps of the three populations, indicating the high quality and value of the consensus map. The genome wide comparative analysis with the markers identified in diploid *Rosa* and mapped to the *F. vesca* (Fvb) pseudo-chromosomes further confirmed the high level of synteny among these two genomes. *Rosa* LGs 1, 4, 5, 6, 7 correspond to *Fragaria* LGs 7, 4, 3, 2 and 5, respectively. In addition, a major translocation and fission/fusion occurred between *Rosa* LGs 2 and 3 and *Fragaria* LGs 1 and 6, with *Rosa* LG2 composed of *Fragaria* LG1 plus a part of *Fragaria* LG6, and the remainder of *Fragaria* LG6 being syntenic with *Rosa* LG3. The syntenic relationship between *Fragaria* and *Rosa* indicated a hypothetical evolutionary relationship among members of the Rosaceae.

Based on the framework in Chapter III, another two populations were added to update the consensus map in Chapter IV. With J4-6 x RF and OB x J3-6 included in consensus map construction, and data curation carried out in VisualFlexQTL, the final consensus map for QTL analysis was composed of 791 SNP markers covering 431 cM. A pedigree-based Bayesian approach testing multiple QTL models implemented with FlexQTL software (Bink *et al.*, 2008) was performed using this final consensus map and phenotypic data from Chapter II. A strong QTL was identified that explained ~20% of the total phenotypic variance. This QTL mapped to LG3 in the region from 36-43 cM and was consistent in various runs and across different environments/months. Parents J14-3 and J4-6 were identified to be heterozygotes carrying two different resistant haplotypes (H3 and H4, respectively). The allelic effects of these two resistant haplotypes were similar. However, due to the lack of data for many progenitors, we were unable to draw conclusions on the origin of the resistance alleles. The H3 resistant allele in J14-3 did not come from DD but from an unknown paternal pollen source (denoted PP-J14-3) and the H4 resistant allele in J4-6 may have come from either OB or R.wichThless (*Rosa wichurana* 'Basye's Thornless') if the pedigree is correct.

This research confirmed the moderately heritable feature of black spot partial resistance and demonstrated the possibility of the application of GBS on pedigree-based QTL analysis. However, the location and genotype effects were confounded in our experiment, and several progenitors in the pedigree were missing. Thus, further work should be performed with replicated individuals in a randomized complete block design to improve the accuracy of the phenotypic data. In addition, the acquisition of the genotypic data of founder parents will be necessary to verify the pedigree and to trace the resistance alleles to the correct founder. QTL mapping results should be validated or confirmed using other related materials. If these results are validated, markers could be developed for use in a marker-assisted breeding program to aid in the development of disease-resistant rose germplasm.

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APPENDIX 1

MODIFIED ROSE DNA EXTRACTION PROCEDURE

1. Harvest new growth tissues (usually 10-15 folded leaves, depends on leaf size) up to 1/3 volume of FastPrep® Lysing Matrix Tubes (Lysing Matrix A catalog # 116910050), immediately place tube in liquid nitrogen to store at -80°C for later use
2. Prepare 2X CTAB buffer according to 'stock solution preparation' document. Add 200 µl β-Mercaptoethanol before use (once added, the buffer can be used for 3-4 days and stored at 4°C). Warm to 65°C prior to use.
3. Add 800 µl of pre-warmed 2X CTAB buffer to Fast Prep tubes arrayed in a 96 well micro tube rack. Make note of the sample names in the proper array.
4. Grind the samples in the Geno Grinder with settings at 1500 rpm for 3 minutes 2- 3 times.
5. Place tubes in water bath for 1-1.5 hours
6. Remove samples from water bath and cool on ice 1-2 minutes.
7. Centrifuge at 13000 rpm for 30 minutes and collect supernatant into new 1.2 ml library tubes in rack – very important to double check the array prior to this transfer step.
8. Add 400 µl of CIA to each tube (working under hood) tightly cap the tubes with strip caps, place in clamp apparatus then invert to mix
9. Centrifuge racks in table top centrifuge at 3500 rpm for 15 minutes
10. Collect top layer and place in a new 1.2 ml library tube in rack – very important to double check the array prior to this transfer step.
11. Add 600 µl of CIA to each tube (working under hood) tightly cap the tubes with strip caps, place in clamp apparatus then invert to mix
12. Centrifuge racks in table top centrifuge at 3500 rpm for 15 minutes
13. Collect top layer and place in a new 1.2 ml library tube in rack – very important to double check the array prior to this transfer step.
14. Add 600 µl of cold isopropanol (-20°C) to each 1.2 ml library tube
15. Mix well by pipetting. DNA may precipitate during this step
16. Place samples in freezer (-20°C) overnight or (-80°C) for 3 hours
17. Centrifuge racks in table top centrifuge at 3500 rpm for 45-60 minutes
18. Carefully remove supernatant with pipet.
19. Wash pellet with 300 µl 70% EtOH (need to wash thoroughly by breaking down the pellet). After washing, centrifuge at 4000 for 5 minutes - repeat until you see the pellet become colorless.
20. Remove EtOH and allow to air dry at room temperature
21. Add 90 µl of TE to each tube, pipet to dissolve the DNA.
22. RNase treat by adding 1 µl Ambion RNase (AM2288), incubate for 1 hour at 37°C
23. Follow Zymo OneStep™ PCR Inhibitor Removal Kit (Catalog #D6035 (96-well)) protocol to clean DNA
24. Store samples at -20°C

Final concentration should be around 100-200 ng/µl

APPENDIX 2

STOCK SOLUTION PREPARATION FOR DNA EXTRACTION

2X CTAB buffer (100 ml):

2% CTAB - 2.00 g
1.4 M NaCl - 8.12 g
20 mM EDTA, pH 8.0 - 4 ml of 0.5 M
100 mM Tris HCl, pH 8.0 - 10 ml of 1.0 M
1% PVP-40 (polyvinylpyrollidone, M.W. 40,000) - 1.00 g
β-Mercaptoethanol - 200 μl (add before use)

Note: CTAB is difficult to dissolve. Do not add β-Mercaptoethanol until ready to use.

0.5M EDTA, pH 8 (1000 ml):

EDTA (Disodium ethylenediaminetetraacetate$\cdot 2H_2O$) - 186.1 g

Preparation: Add 186.1 g of EDTA to 200 ml of water. Stir vigorously on a magnetic stirrer. Adjust the pH to 8 with NaOH (~20 g of NaOH pellets), then adjust volume of the solution to 1000 ml with water.

Note: EDTA will not go into solution until the pH of the solution is adjusted to approximately 8 by the addition of NaOH.

1.0 M Tris HCl, pH 8 (1000 ml):

Tris (Hydroxymethyl) Aminomethane - 121.14 g

Preparation: Dissolve 121.14 g of Tris in 800 ml of water. Adjust the pH to 8 by adding HCl (~42 ml of concentrated HCl). Allow the solution to cool to room temperature before making final adjustment to the pH. Adjust volume of the solution to 1000 mL with water.

TE (100 mL):

10 mM Tris·HCl - 1.0 ml of 1.0 M
1 mM EDTA - 0.5 ml of 0.5 M

Note: Bring solution to 100 ml with nanopure water.

CIA (100 mL):

Chloroform - 96 ml
Isoamyl Alcohol - 4 ml

Note: Store CIA in dark at room temperature.

APPENDIX 3

MARKERS OF THE CONSENSUS MAP (ICD), J14-3 X LC, J14-3 X VS, OB X RF, J4-6 X RF AND OB X J3-6.

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_1.646368	1	0	chr6_10.901867	1	16	chr7_10.930206	1	25
chr7_1.646404	1	0	chr7_5.856314	1	16	chr7_11.211166c	1	25
chr4_20.800379	1	3	chr7_5.856391	1	16	chr7_12.13403c	1	28
chr7_2.370299	1	3	chr7_11.016096	1	16	chr7_11.016267	1	28
chr2_5.970489	1	4	chr7_7.996758	1	17	chr7_11.21128	1	28
chr2_5.970641	1	4	chr7_9.567824c	1	18	chr7_12.365556	1	29
chr7_2.799483c	1	4	chr7_9.567817c	1	18	chr7_12.365489	1	29
chr7_2.241421	1	4	chr7_9.567815c	1	18	chr2_15.167105	1	32
chr7_4.587218	1	5	chr3_3.021324	1	18	chr7_14.32919	1	32
RhAB9-2_LG1	1	7	chr7_7.996817c	1	18	chr7_12.978062	1	32
chr3_3.021336	1	7	chr7_8.283597c	1	18	chr7_12.987868	1	32
chr7_4.146431	1	7	chr7_9.385112	1	18	chr7_13.104348	1	32
chr7_4.240779	1	7	chr7_9.552873	1	18	chr7_12.783112	1	32
chr7_4.24078	1	7	chr7_8.28375	1	18	chr7_12.783197	1	32
chr7_4.3235	1	7	chr7_9.566961	1	18	chr7_12.917504	1	32
chr4_24.537661	1	10	chr7_8.994483	1	18	chr7_12.987811	1	32
chr1_10.368513	1	10	chr7_9.153824	1	18	chr7_12.917681	1	33
chr7_14.651673	1	10	chr7_9.567675	1	18	chr7_12.917696	1	33
chr7_5.726635	1	10	chr7_9.385113	1	18	chr7_13.531368	1	33
chr7_5.856382	1	10	chr7_9.431968	1	18	chr7_13.787815	1	35
chr7_6.019389	1	10	chr7_9.567808c	1	18	chr7_13.104378	1	36
chr7_6.019394	1	10	chr7_9.567811c	1	18	chr7_13.787818	1	36
chr7_5.726746	1	11	chr7_9.785983	1	19	chr7_13.34111	1	36
chr4_10.812788	1	11	chr7_8.76812	1	20	chr7_13.531363	1	36
chr7_5.980514	1	11	chr7_9.153848	1	20	chr7_14.329056c	1	36
chr4_10.812806	1	11	chr7_9.153849	1	20	chr7_14.32911c	1	36
chr7_6.924247	1	11	chr2_1.981716	1	20	chr7_14.329131c	1	36
chr7_6.924305	1	11	chr3_18.737227	1	20	chr7_14.329161c	1	36
chr7_7.531744	1	11	chr7_8.768061	1	20	chr7_14.358688	1	36
chr7_7.531798	1	11	chr2_5.001299	1	20	chr7_13.921956	1	36
chr7_6.373067	1	12	chr2_5.001332	1	20	chr7_15.029067	1	36
chr3_32.662785	1	14	chr7_8.767971	1	21	chr7_12.917607	1	36
chr5_0.63163c	1	14	chr7_8.767988	1	21	chr7_13.10445	1	36
chr5_0.631568c	1	14	chr7_10.385832c	1	23	chr7_13.787704	1	36
chr7_6.500465	1	14	chr7_10.385941c	1	23	chr7_14.616699c	1	36
chr7_7.156618	1	16	chr7_11.608351	1	23	chr7_14.615681	1	36
chr7_7.526217	1	16	chr7_11.905757	1	23	chr7_14.616781	1	37
chr7_7.52622	1	16	chr7_16.540347	1	23	chr7_14.622347	1	37

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_15.044078c	1	37	chr7_16.759927c	1	50	chr7_18.141463	1	57
chr7_14.329158	1	37	chr7_16.760041c	1	50	chr7_18.163184	1	57
chr7_15.142932	1	38	chr7_16.480821	1	50	chr7_18.177114	1	57
chr7_15.151752	1	38	chr7_16.480824	1	50	chr7_18.377104	1	57
chr7_15.199629	1	38	chr7_16.672862	1	50	chr7_18.467474c	1	58
chr7_13.921851	1	39	chr7_16.59818	1	50	chr7_18.467492c	1	58
chr7_15.083224	1	39	chr7_16.623282	1	50	chr7_18.472259	1	58
chr7_15.199669	1	39	chr7_16.623332	1	50	chr7_18.376963	1	59
chr7_15.630095	1	39	chr7_16.672845	1	50	chr7_18.467426	1	59
chr7_14.622202	1	39	chr7_16.672896	1	50	chr7_18.627984	1	59
chr7_14.622264	1	39	chr7_16.690209	1	50	chr7_18.628064	1	59
chr7_15.115734c	1	39	chr7_16.760096	1	50	chr7_18.633285	1	59
chr7_15.115737c	1	39	chr7_17.158766	1	50	chr7_18.633311	1	59
chr7_15.11574c	1	39	chr7_17.61075	1	50	chr7_18.66726	1	59
chr7_15.199566	1	39	chr7_16.690217c	1	50	chr7_18.667302c	1	59
chr7_15.370551	1	39	chr7_16.760018c	1	50	chr7_18.667305c	1	59
chr7_15.169627	1	39	chr7_17.378327	1	52	chr7_18.71384	1	59
chr7_15.370485c	1	39	chr7_17.611923	1	52	H5_F12_LG1	1	61
chr7_15.630106	1	39	chr7_17.687201c	1	52	chr7_18.376957	1	61
chr7_15.865571	1	40	chr7_17.773611	1	52	chr7_18.633293	1	61
chr7_16.411145	1	40	chr7_17.450961c	1	52	chr7_18.974728	1	61
chr7_15.395736c	1	40	chr7_17.610635c	1	52	chr7_18.92274	1	62
Rw34L6_LG1	1	42	chr7_17.610663c	1	52	chr7_18.141394	1	62
chr7_15.395727	1	42	chr7_17.450917	1	54	chr7_18.415494	1	62
chr7_15.395728	1	42	chr7_17.610816	1	54	chr7_18.415579	1	62
chr7_15.865401	1	46	chr7_17.611871	1	54	chr7_18.415693	1	62
chr7_15.86556c	1	46	chr7_18.16492	1	56	chr7_18.971362	1	64
chr7_9.786157c	1	46	chr7_18.922785	1	56	chr7_18.467408	1	65
chr7_16.411142	1	47	chr7_17.479367c	1	56	chr7_19.449169	1	65
chr5_25.5394	1	47	chr7_17.47942	1	56	chr7_20.086801	1	65
chr7_16.247829c	1	47	chr7_17.479411	1	56	chr7_18.472244	1	65
chr7_16.480836	1	47	chr7_17.773514	1	56	chr7_19.373724c	1	65
chr5_25.539452	1	47	chr7_17.773561	1	56	chr7_19.396709c	1	65
chr7_16.540325	1	47	chr7_17.773696	1	56	chr7_19.396733c	1	65
chr7_16.471467	1	47	chr7_17.901675	1	56	chr7_19.414384c	1	65
chr7_16.471613	1	47	chr7_18.141361	1	56	chr7_19.443674c	1	65
chr7_16.690213	1	48	chr7_18.177083	1	56	chr7_19.443696c	1	65
chr4_31.097032c	1	50	chr7_18.177097	1	56	chr7_19.741362c	1	65
chr7_16.855689	1	50	chr7_18.177112	1	56	chr7_19.741411c	1	65
chr4_31.097061c	1	50	chr7_18.207597	1	56	chr7_19.939297c	1	65

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_19.939473c	1	65	chr7_20.904212	1	75	chr7_21.915361	1	85
chr7_19.312222c	1	65	chr7_20.940282	1	75	chr7_21.935157	1	85
chr7_19.312313c	1	65	chr7_20.942895	1	75	chr7_21.935196	1	85
chr7_19.44362	1	66	chr5_24.046184	1	76	chr7_22.043022	1	85
chr7_19.322479	1	67	chr7_20.942885	1	76	chr7_22.043139	1	85
chr7_19.443518	1	67	chr7_21.068143	1	76	chr7_22.043164	1	85
chr7_19.449185	1	67	chr7_21.068173	1	76	chr7_22.422059	1	85
chr7_20.086687	1	68	chr7_20.952222	1	76	chr7_23.206113	1	85
chr7_20.229757	1	68	chr7_21.066544	1	76	chr7_22.042996	1	85
chr7_20.231954	1	68	chr7_21.162249	1	76	chr7_22.043131	1	85
chr7_20.448404	1	69	chr7_21.548604	1	77	RMS015_LG1	1	87
chr3_0.357758	1	69	chr7_21.162281	1	77	chr2_12.63942	1	87
chr5_24.046221	1	69	chr5_11.923669	1	79	chr7_22.316197	1	87
chr7_18.971407	1	69	chr5_11.923707	1	79	chr7_22.422036	1	87
chr7_19.373763	1	69	chr7_21.162359	1	79	chr7_22.422141	1	87
chr7_19.383104	1	69	chr4_32.176374	1	81	chr7_22.316144	1	88
chr7_19.533588	1	69	chr7_21.564424	1	81	chr7_22.556633	1	88
chr7_19.5336	1	69	chr7_21.730793c	1	81	chr7_22.739119	1	88
chr7_20.737535	1	69	chr7_22.739224c	1	81	chr7_23.013171	1	88
chr7_20.786202	1	69	chr7_23.352066	1	81	chr7_23.013217	1	88
chr7_20.904278	1	69	chr7_23.484334	1	81	chr7_23.037789	1	88
chr5_24.046133	1	69	chr4_32.176379	1	81	chr7_22.840457	1	88
chr7_20.086723	1	69	chr7_21.564373	1	81	chr7_23.03772	1	89
chr7_20.728921	1	69	chr7_21.654196	1	81	chr7_22.854125	1	90
chr7_20.804998	1	69	chr7_21.654243	1	81	chr7_22.854141	1	90
chr7_20.523529	1	73	chr7_21.654273	1	81	chr7_23.206148	1	91
chr7_20.523599	1	73	chr7_21.726369	1	81	chr7_23.013203	1	92
chr7_20.544313	1	73	chr7_21.770245	1	81	chr7_23.206146	1	93
chr7_20.645358	1	73	chr7_21.770321	1	81	chr7_23.206126	1	93
chr7_20.737533	1	73	chr7_21.915396	1	81	chr1_10.981881	1	95
chr7_20.786131c	1	73	chr7_20.645239	1	81	chr7_23.351973	1	95
chr7_20.645228c	1	73	chr7_20.728966	1	81	chr7_23.440975	1	95
chr7_20.645311c	1	73	chr7_21.564253	1	81	chr7_23.489476	1	95
chr7_20.649751c	1	73	chr7_21.606193	1	81	chr7_23.602528	1	95
chr7_20.786106	1	73	chr7_21.564376	1	81	chr1_0.141372c	2	0
chr7_20.804926	1	73	chr7_20.737408	1	82	chr1_0.141437	2	0
chr7_20.649892c	1	73	chr4_32.176399	1	83	chr1_0.49595	2	0
chr7_20.64994c	1	73	chr7_21.83418	1	83	chr1_0.824902	2	1
chr7_20.805014	1	74	chr2_12.639586	1	84	chr1_0.553644	2	2
chr7_20.80504	1	74	chr5_4.243711	1	84	chr1_0.821632	2	2

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_1.027988	2	2	chr1_1.937179	2	7	chr1_2.507772	2	10
chr1_1.359534	2	2	chr1_2.002985	2	7	chr1_2.521837c	2	10
chr1_1.452077	2	2	chr1_2.003114	2	7	chr1_2.622826	2	10
chr1_1.452151	2	2	chr1_2.144585c	2	7	chr1_2.732099	2	10
chr1_1.900678	2	2	chr1_2.077827c	2	7	chr1_2.732179	2	10
chr1_1.937062	2	2	chr1_2.077982c	2	7	chr1_2.736262	2	10
chr1_0.974818c	2	2	chr1_2.144306c	2	7	chr1_2.736373	2	10
chr1_1.027812	2	2	chr1_2.144357c	2	7	chr1_2.741197	2	10
chr1_1.39466c	2	2	chr1_2.144735c	2	7	chr1_2.47502	2	10
chr1_1.35928	2	4	chr1_2.14475c	2	7	chr1_3.435523	2	10
chr1_1.359322	2	4	chr1_2.100126	2	9	chr1_3.152825	2	11
chr1_1.359634	2	4	chr1_2.144312	2	9	chr1_3.435488	2	11
chr1_1.394645	2	4	chr1_2.14433	2	9	chr1_3.43551	2	11
chr1_1.580327	2	4	chr1_2.22285	2	9	chr1_2.479221	2	11
chr1_1.593904	2	4	chr1_2.222853	2	9	chr1_2.622883c	2	11
chr1_1.359387	2	4	chr1_2.690475c	2	9	chr1_2.62288c	2	11
chr1_1.580177	2	5	chr1_2.318579	2	10	chr1_2.498949c	2	11
chr1_1.90916	2	5	chr1_2.318639	2	10	chr1_2.695716c	2	11
chr1_1.165438	2	5	chr1_2.521724c	2	10	chr1_2.896456	2	12
chr1_1.394736	2	5	chr1_2.736295c	2	10	chr1_3.549589	2	12
chr1_1.52833	2	5	chr1_2.861731	2	10	chr1_3.549677	2	12
chr1_1.569173	2	5	chr1_2.521723c	2	10	chr1_3.435632	2	14
chr1_1.394796	2	5	chr1_2.521732c	2	10	chr1_3.752717	2	14
chr1_1.528282	2	6	chr1_2.73631c	2	10	chr1_3.75353	2	14
chr1_1.569677	2	6	chr1_2.736407c	2	10	chr1_3.983468	2	14
chr1_1.569737	2	6	chr1_2.776934c	2	10	chr1_3.793777c	2	14
chr1_1.580312	2	6	chr1_2.222813	2	10	chr1_2.340748	2	15
chr1_2.00303	2	6	chr1_2.318574	2	10	chr1_2.776887	2	15
chr1_1.90051	2	7	chr1_2.340835c	2	10	chr1_2.816973	2	15
chr1_2.100003	2	7	chr1_2.475041	2	10	chr1_2.865922	2	15
chr1_2.100006	2	7	chr1_2.475043	2	10	chr1_2.880239	2	15
chr1_2.180944	2	7	chr1_2.686715	2	10	chr1_2.86597	2	15
chr1_2.318584	2	7	chr1_2.736343	2	10	chr1_3.735119	2	16
chr1_1.909106	2	7	chr1_2.776959	2	10	chr1_3.775467	2	16
chr1_1.937087	2	7	chr1_2.896982	2	10	chr1_4.197169	2	17
chr1_1.937134	2	7	chr1_3.034574	2	10	chr1_4.197263	2	17
chr1_1.937206c	2	7	chr1_2.446263	2	10	chr1_4.2068	2	17
chr1_1.938093	2	7	chr1_2.474891	2	10	chr1_3.152817	2	17
chr1_2.003108	2	7	chr1_2.47495	2	10	chr1_3.250202	2	17
chr1_2.077823	2	7	chr1_2.499041	2	10	chr1_3.03039	2	18

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_3.03454	2	18	chr1_4.229562c	2	25	chr1_5.964572	2	31
chr1_3.983543	2	19	chr1_4.253306	2	25	chr1_5.964646	2	31
chr1_4.229559	2	19	chr1_4.206683c	2	27	chr1_6.042884	2	31
chr1_4.197182c	2	19	chr1_5.918619	2	28	chr1_6.18483c	2	31
chr1_4.238907	2	19	chr1_5.964933c	2	28	chr1_6.672308	2	31
chr1_4.257676c	2	19	chr1_5.965028c	2	28	chr1_7.136429c	2	31
chr1_4.197269c	2	19	chr1_4.684296	2	28	chr1_7.150463	2	31
chr1_4.206668c	2	19	chr1_4.684301c	2	28	chr1_15.479951c	2	31
chr1_4.229476	2	19	chr1_4.684358c	2	28	chr1_6.690492c	2	32
chr1_4.354759	2	21	chr1_5.533343c	2	28	chr1_6.907079	2	32
chr1_4.492677	2	21	chr1_6.184806	2	29	chr1_6.907091	2	32
chr1_4.492592	2	21	chr1_6.271493c	2	29	chr1_7.136566	2	32
chr1_4.676262	2	21	chr1_6.290646	2	29	chr1_7.150559	2	32
chr1_4.684316c	2	21	chr1_4.923067	2	29	chr1_15.854827	2	33
chr1_4.684388c	2	21	chr1_5.533339c	2	29	chr1_7.512917	2	33
chr1_3.435634	2	21	chr1_4.996555	2	29	chr1_7.847364	2	33
chr1_3.564995	2	21	chr1_5.065178	2	29	chr1_7.847367	2	33
chr1_3.034634	2	22	chr1_5.065188	2	29	chr1_7.513082	2	33
chr1_3.152827	2	22	chr1_5.065205	2	29	chr1_7.847496	2	33
chr1_3.152848	2	22	chr1_5.332614	2	29	chr1_8.138587c	2	33
chr1_3.246888	2	22	chr1_5.332657	2	29	chr1_5.918602	2	33
chr1_3.250244	2	22	chr1_5.728871	2	29	chr1_6.07063c	2	34
chr1_3.674095	2	22	chr1_5.729018	2	29	chr1_6.184737	2	34
chr1_3.775528	2	22	chr1_5.774378	2	29	chr1_6.18479	2	34
chr1_3.984244	2	22	chr1_5.878782	2	29	chr1_6.737085	2	34
chr1_3.75284c	2	22	chr1_5.964559	2	29	chr1_6.070727	2	35
chr1_3.793592c	2	22	chr1_5.96469	2	29	chr1_6.349745	2	36
chr1_5.396793c	2	23	chr1_5.965097	2	29	chr1_6.405722	2	36
chr1_3.98357	2	23	chr1_6.271448	2	29	chr1_9.459863	2	36
chr1_4.197324	2	24	chr1_6.27146	2	29	chr1_11.644234	2	36
chr1_4.257791	2	24	chr1_6.290644	2	29	chr1_11.575545	2	36
chr1_4.320547	2	24	chr1_6.290649	2	29	Rh48_LG2	2	36
chr1_4.354796	2	24	chr1_5.33267	2	29	chr1_10.053152	2	36
chr1_5.918587	2	24	chr1_5.396723c	2	29	chr1_10.11151	2	36
chr1_5.502625c	2	25	chr1_5.793824c	2	29	chr1_10.137503	2	36
chr1_5.502691c	2	25	chr1_6.042708c	2	29	chr1_10.312816	2	36
chr1_5.533313	2	25	chr1_10.924711	2	31	chr1_10.372077	2	36
chr1_4.197258c	2	25	chr1_6.18475	2	31	chr1_10.495617	2	36
chr1_4.206615	2	25	chr1_6.290499	2	31	chr1_10.612359	2	36
chr1_4.206617	2	25	chr1_6.672413	2	31	chr1_10.922413	2	36

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_11.51206	2	36	chr1_10.775446c	2	42	chr1_19.106101c	2	45
chr1_11.543097	2	36	chr1_15.210714c	2	42	chr1_9.789929	2	45
chr1_11.664672	2	36	chr1_17.069216	2	42	chr1_15.312024c	2	46
chr1_11.748741	2	36	chr1_10.053197c	2	42	chr1_15.312065c	2	46
chr1_11.832123	2	36	chr1_17.069213c	2	42	chr1_15.312027c	2	46
chr1_12.431973	2	36	chr1_10.111581c	2	42	chr1_17.2773	2	46
chr1_15.312104	2	36	chr1_10.495583c	2	42	chr1_17.33801	2	46
chr1_15.571847	2	36	chr1_10.532371	2	42	chr1_17.573105c	2	46
chr1_16.650361	2	36	chr1_10.672126c	2	42	chr1_10.924627	2	46
chr1_17.069182	2	36	chr1_11.664678c	2	43	chr1_15.577885	2	46
chr1_17.101317	2	36	chr1_11.748807c	2	43	chr1_7.507856c	2	46
chr1_17.101319	2	36	chr1_11.74884c	2	43	chr1_15.85486c	2	46
chr1_18.100552	2	36	chr1_11.664852	2	43	chr1_7.150574	2	47
chr1_18.223742	2	36	chr1_12.428288	2	43	chr1_7.507699	2	47
chr1_7.163129	2	36	chr1_7.743341c	2	43	chr1_9.504581	2	47
chr1_7.834765	2	36	chr1_7.847441	2	43	chr1_10.32181	2	48
chr1_7.834777	2	36	chr1_1.661496	2	44	chr1_10.372125	2	48
chr1_9.459833	2	36	chr1_16.994934c	2	44	chr1_10.372167	2	48
chr1_9.688526	2	36	chr1_17.101332	2	44	chr1_11.74876	2	48
chr1_9.787356	2	36	chr1_17.288532c	2	44	chr1_19.10605	2	49
chr1_10.053335	2	36	chr1_17.288562c	2	44	chr1_14.562674	2	49
chr1_10.111551	2	36	chr1_17.28861c	2	44	chr1_14.6501	2	49
chr1_10.137365	2	36	chr1_17.573081c	2	44	chr1_19.227207	2	49
chr1_10.495594	2	36	chr1_17.288427c	2	44	chr1_7.847513c	2	49
chr1_10.495619	2	36	chr1_17.288469c	2	44	chr1_15.479862	2	49
chr1_10.61245	2	36	chr1_17.28847c	2	44	chr1_11.5432	2	49
chr1_10.672086	2	36	chr1_17.28848c	2	44	chr1_11.748681	2	49
chr1_11.050002	2	36	chr1_17.288493c	2	44	chr1_12.336615	2	49
chr1_11.748699	2	36	chr1_17.337983c	2	44	chr1_12.399453	2	49
chr1_16.994883	2	36	chr1_19.106089c	2	44	chr1_18.100665	2	49
chr1_9.790204	2	36	chr1_9.504632c	2	44	chr1_11.748702c	2	49
chr1_19.227311c	2	36	chr1_10.11165c	2	44	chr1_11.748759c	2	49
chr1_10.449852c	2	36	chr1_10.672085c	2	44	chr1_11.832138c	2	49
chr1_7.847544	2	41	chr1_18.100702c	2	44	chr1_12.540578c	2	49
chr1_10.321726	2	41	chr1_18.201755c	2	44	chr1_12.540596c	2	49
chr1_17.573164c	2	41	chr1_18.223722c	2	44	chr1_12.540607c	2	49
chr1_10.053173	2	42	chr1_10.442521c	2	44	chr1_12.33644c	2	50
chr1_10.672072	2	42	chr1_10.321864c	2	45	chr1_14.439401c	2	50
chr1_10.67209c	2	42	chr1_11.424441c	2	45	chr1_11.543007	2	50
chr1_10.67227	2	42	chr1_18.410525	2	45	chr1_15.311956	2	50

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_15.312075	2	50	chr6_22.241836	2	61	chr6_25.644736	2	72
chr1_17.288555c	2	50	chr6_22.3055	2	61	chr6_25.644758	2	72
chr1_18.223819	2	50	chr6_22.305632	2	61	chr6_25.673682	2	72
chr1_19.106105	2	50	chr6_21.334726	2	61	chr6_25.903306	2	72
chr1_16.04228c	2	51	chr6_21.444451	2	61	chr6_25.905732	2	72
chr1_16.466661	2	51	chr6_21.519907	2	61	chr6_25.905902	2	72
chr1_16.46666c	2	51	chr6_22.30561	2	61	chr6_24.717093	2	72
chr1_8.772956c	2	53	chr6_22.020162	2	61	chr6_24.724354	2	72
chr1_16.466634	2	55	chr6_22.020181c	2	61	chr6_25.178794	2	72
CL2996_LG2	2	57	chr6_22.964006	2	62	chr6_25.644759	2	72
chr1_14.439482	2	57	chr6_23.898748c	2	62	chr6_25.644808	2	72
chr1_15.00364	2	57	chr6_18.651732	2	64	chr6_25.644826	2	72
chr1_16.375525	2	57	chr6_22.305666	2	64	chr6_25.905759	2	72
chr1_16.466642	2	57	chr6_22.200336c	2	64	chr6_24.982882	2	72
chr1_18.912286	2	57	chr6_22.020306c	2	65	chr6_24.983076	2	72
chr6_12.894821c	2	57	chr6_22.241879	2	65	chr6_25.644854	2	72
chr6_29.879491	2	57	chr6_22.200502c	2	67	chr6_25.644899	2	72
chr1_12.740688c	2	57	chr6_22.305615c	2	67	chr6_25.73819	2	73
chr6_19.982957c	2	57	chr6_23.454696	2	68	chr6_25.903305	2	73
chr6_19.983023	2	57	chr6_23.59618	2	68	chr6_26.295215	2	73
chr6_20.501779c	2	57	chr6_22.963925c	2	68	chr6_26.646145	2	73
chr6_20.532373	2	57	chr6_24.982865	2	69	chr6_26.118489	2	73
chr6_21.779928c	2	57	chr6_25.012785	2	69	chr6_26.646082	2	73
chr6_20.425868c	2	57	chr6_12.004629	2	70	chr6_26.646092	2	73
chr6_20.486507c	2	57	chr6_24.333528	2	70	chr6_26.646102	2	73
chr6_20.640376c	2	57	chr6_24.717153	2	70	chr6_26.656034c	2	73
chr6_20.640381c	2	57	chr6_24.983034	2	70	chr6_26.689691	2	73
chr6_20.530748	2	57	chr6_25.644821	2	70	chr6_26.877908	2	73
chr6_20.532514	2	57	chr6_25.901543	2	70	chr6_26.914348c	2	73
chr6_21.065036	2	57	chr6_26.877926	2	70	chr6_26.646208c	2	73
chr6_20.144288	2	58	chr6_26.914262	2	70	chr6_26.655966c	2	77
chr6_20.425966	2	58	chr6_23.39451	2	70	chr6_27.767203c	2	77
chr6_20.501838	2	58	chr6_23.394609	2	70	chr6_27.819339	2	77
chr6_20.532456c	2	58	chr6_23.481749	2	70	chr6_28.373698	2	77
chr6_20.14417c	2	58	chr6_23.501483c	2	70	chr6_28.379754	2	77
chr6_20.425967c	2	58	chr6_23.39463	2	70	chr6_29.139394	2	77
chr6_21.444481	2	59	chr6_23.501479c	2	70	chr6_26.656326	2	77
chr6_21.265314	2	60	chr6_23.501482c	2	70	chr6_27.073507	2	78
chr6_21.42716	2	61	chr6_24.333503c	2	71	chr6_27.344809c	2	78
chr6_21.427168	2	61	chr6_24.662967	2	71	chr6_27.390111	2	79

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_27.543135	2	79	chr6_30.271617	2	84	chr6_29.528617	2	89
chr6_27.543158	2	79	chr6_30.27165	2	84	chr6_29.412515	2	89
chr6_28.141676	2	79	chr6_30.271656	2	84	chr6_29.518821c	2	89
chr6_28.141808	2	79	chr6_30.355331	2	84	chr6_29.528584	2	89
chr6_27.819291	2	79	chr6_15.095193	2	85	chr6_30.634536	2	89
chr6_27.839204	2	79	chr6_30.634039	2	85	chr6_30.84518c	2	89
chr6_27.576798	2	79	chr6_30.634496	2	85	chr6_30.845195	2	90
chr6_27.57685	2	79	chr6_30.845198	2	85	chr6_29.266807	2	93
chr6_28.681681	2	80	chr6_30.95729	2	85	chr6_29.412458	2	93
chr6_28.96079	2	80	chr6_31.531493	2	85	chr6_31.954116c	2	93
chr6_29.139503	2	80	chr6_31.699678	2	85	chr6_29.412482	2	93
chr6_29.15463	2	80	chr6_15.095346	2	85	chr6_29.266748	2	94
chr6_29.154631	2	80	chr6_26.118652	2	85	chr6_29.266906	2	94
chr6_29.154708	2	80	chr6_27.390168	2	85	chr6_32.029807	2	94
chr6_29.154709	2	80	chr6_29.107698	2	85	chr6_32.029936	2	94
chr6_28.681842c	2	80	chr6_29.518627	2	85	chr6_31.93804	2	94
chr6_29.154701	2	80	chr6_30.634141	2	85	chr6_31.938048	2	94
chr6_28.141739c	2	81	chr6_30.967032c	2	85	chr6_32.093971	2	94
chr6_28.681778c	2	81	chr6_26.656315	2	86	chr6_32.094031	2	94
chr6_28.141748c	2	81	chr6_27.839739	2	86	chr6_32.141066	2	95
chr6_28.68184c	2	81	chr6_29.0984	2	86	chr6_32.205307	2	95
chr6_29.639698	2	81	chr6_30.957319	2	86	chr6_32.412535	2	95
chr6_29.680111	2	81	chr6_31.625698	2	86	chr6_31.834685	2	95
chr6_30.355325	2	81	chr6_31.625738	2	86	chr6_31.834871	2	95
chr6_28.960886c	2	82	chr6_31.625739	2	86	chr6_32.412566	2	95
chr6_29.098355c	2	82	chr6_31.699646	2	86	chr6_31.805849	2	95
chr6_29.107758	2	82	chr6_29.639695	2	86	chr6_32.344852	2	95
chr6_29.149748	2	82	chr6_31.531428	2	86	chr6_32.344995c	2	95
chr6_29.150396	2	82	chr6_15.06843	2	87	chr6_32.094013c	2	95
chr6_29.639712	2	82	chr6_15.068553	2	87	chr6_32.390975	2	95
chr6_29.139475	2	82	chr6_15.095292	2	87	chr6_32.094109	2	95
chr6_29.149769	2	82	chr6_15.10856	2	87	chr6_32.343667c	2	95
chr6_29.149772	2	82	chr6_31.531359	2	87	chr6_32.343677	2	95
chr6_29.149908	2	82	chr6_15.068559c	2	87	chr6_32.463306	2	96
chr6_29.149967	2	82	chr6_31.219476c	2	89	chr6_32.41241	2	97
chr6_29.680161	2	82	chr6_31.219479c	2	89	chr6_32.461306	2	97
chr6_29.139545	2	82	chr6_14.994698	2	89	chr6_32.461322	2	97
chr6_29.149813	2	82	chr6_29.518701	2	89	chr6_32.756603c	2	97
chr6_29.149836c	2	82	chr6_29.52846	2	89	chr6_32.463148	2	97
chr6_29.154771c	2	82	chr6_29.528615	2	89	chr6_33.233603	2	97

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_33.233689	2	97	chr6_34.506658	2	103	chr6_35.858779	2	114
chr6_33.242307	2	97	chr6_34.506673	2	103	chr6_35.929618	2	114
chr6_33.264286	2	97	chr6_34.546062	2	103	chr6_35.965574	2	114
chr6_32.918299	2	98	chr6_34.876054	2	103	chr6_36.073405	2	114
chr6_32.918422	2	98	chr6_34.87606	2	105	chr6_35.934743c	2	114
chr6_32.918427	2	98	chr6_34.923109	2	105	chr6_35.934809	2	114
chr6_32.975531	2	98	chr6_34.923112	2	105	chr6_35.934821	2	114
chr6_33.026304	2	98	chr6_33.026341	2	106	chr6_35.934829	2	114
chr6_33.051694	2	98	chr6_33.839517c	2	106	chr6_35.93483	2	114
chr6_33.215643	2	98	chr6_34.506637	2	106	chr6_35.934822	2	114
chr6_33.240419	2	98	chr6_34.648606	2	106	chr6_35.934824	2	114
chr6_33.264241c	2	98	chr6_34.712429c	2	106	chr6_36.004464c	2	114
chr6_32.918435	2	98	chr6_34.837756	2	106	chr6_36.004515c	2	114
chr6_33.233579c	2	98	chr6_33.589239c	2	106	chr6_36.073033	2	115
chr6_32.975416	2	99	chr6_33.95328c	2	106	chr6_36.073465	2	115
chr6_33.531387c	2	99	chr6_34.131952	2	106	chr6_36.420608	2	116
chr6_32.461294	2	100	chr6_34.209615	2	106	chr6_36.525111	2	116
chr6_32.953315	2	101	chr6_34.27061	2	108	chr6_36.630288	2	116
chr6_32.953336	2	101	chr6_34.413807	2	108	chr6_36.587015	2	119
chr6_33.040719	2	101	chr6_34.482688	2	108	chr6_36.630291	2	119
chr6_33.305252	2	101	chr6_34.545954	2	108	chr6_36.58703	2	119
chr6_33.335228	2	101	chr6_34.65381	2	108	chr6_36.58706	2	119
chr6_33.335358	2	101	chr6_34.653828	2	108	chr6_36.587183	2	119
chr6_33.525292	2	101	chr6_35.174015	2	108	chr6_36.59146	2	119
chr6_33.526163	2	101	chr6_34.545942	2	110	chr6_36.93301c	2	119
chr6_33.531246	2	101	chr6_34.923102	2	111	chr6_36.858528	2	119
chr6_33.562306	2	101	chr6_35.286285c	2	111	chr6_36.923363	2	119
chr6_33.592703	2	101	chr6_35.290819	2	111	chr6_36.844858c	2	122
chr6_33.953478	2	101	chr6_35.357943	2	111	chr6_36.844926c	2	122
chr6_33.335438	2	101	chr6_34.96216c	2	111	chr6_36.92355	2	122
chr6_33.526076	2	101	chr6_35.072497c	2	111	chr6_36.931765	2	122
chr6_33.53129	2	101	chr6_34.875992	2	111	chr6_36.933091	2	122
chr6_33.525955	2	101	chr6_36.295734c	2	112	chr6_37.539943	2	123
chr6_33.531378	2	101	chr6_35.934748	2	113	chr6_37.028459	2	123
chr6_33.531386c	2	101	chr6_35.965591	2	113	chr6_37.052831	2	123
chr6_34.004709	2	103	chr6_36.004476	2	113	chr6_38.22116	2	124
chr6_34.20963	2	103	chr6_36.073413	2	113	chr6_38.221164	2	124
chr6_34.413787	2	103	chr6_36.295664	2	113	chr6_37.028502	2	124
chr6_34.506503	2	103	chr6_36.633987	2	113	chr6_37.136891	2	127
chr6_34.506623	2	103	chr6_35.67536	2	114	chr6_37.18413	2	127

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_37.184203	2	127	chr6_0.288165	3	6	chr6_1.868958c	3	14
chr6_9.582276	2	127	chr6_0.8391	3	6	chr6_1.974541	3	14
chr6_9.582303	2	127	chr6_0.861928	3	7	chr6_1.816439	3	14
chr6_9.58233	2	127	chr6_0.10684	3	7	chr6_1.816453	3	14
chr6_9.582354	2	127	chr6_0.242617	3	7	chr6_1.816456	3	14
chr6_9.582408	2	127	chr6_0.297877	3	7	chr6_1.816463	3	14
chr6_37.184163	2	127	chr6_0.811177	3	7	chr6_1.826124	3	14
chr6_37.184182	2	127	chr6_0.811222	3	7	chr6_1.826127	3	14
chr6_37.267002	2	127	chr6_0.81124	3	7	chr6_1.868258	3	14
chr6_37.267017	2	127	chr6_0.839095	3	7	chr6_1.868386	3	14
chr6_37.184197	2	127	chr6_0.861947	3	7	chr6_1.86829c	3	14
chr6_37.540081	2	129	chr6_0.537091	3	7	chr6_1.868383	3	14
chr6_37.800891	2	129	chr6_0.594973	3	7	chr6_1.868398	3	14
chr6_37.80096	2	129	chr6_0.741935	3	7	chr6_1.869026	3	14
chr6_38.527314	2	129	chr6_0.741968	3	7	chr6_1.974388	3	14
chr6_38.821311c	2	129	chr6_0.811231	3	7	chr6_1.974447	3	14
chr6_37.266958	2	130	chr6_0.811049	3	7	chr6_1.975171	3	14
chr6_37.8009	2	130	chr6_0.741929	3	7	chr6_2.263093	3	14
chr6_37.539993	2	132	chr6_0.811129	3	8	chr6_2.26311	3	14
chr6_37.800994	2	132	chr6_0.811506	3	8	chr6_2.263134	3	14
chr6_37.801035c	2	132	chr6_1.080281	3	9	chr6_2.263162	3	14
chr6_37.899406	2	132	chr6_1.080135	3	9	chr6_1.868951	3	15
chr6_38.149769c	2	132	chr6_1.350775	3	10	chr6_2.263139	3	16
chr6_38.318259	2	133	chr6_1.350823	3	10	chr6_2.84386	3	21
chr6_38.318325	2	133	chr6_1.350825	3	10	chr6_2.84395	3	21
chr6_38.31838	2	133	chr6_1.350828	3	10	chr6_2.843963	3	21
chr6_38.318397	2	133	chr6_1.482509	3	11	chr6_2.844005	3	21
chr6_0.039488c	3	0	chr6_1.350713	3	12	chr6_2.844006	3	21
chr6_0.106927	3	0	chr6_1.350854	3	12	chr6_2.965657	3	21
chr6_0.288198	3	0	chr6_1.425332	3	12	chr6_2.963191	3	21
chr6_0.861922	3	0	chr6_1.482547	3	12	chr6_2.963197	3	21
chr6_0.861943	3	0	chr6_1.513705	3	12	chr6_2.963267	3	21
chr6_0.106933	3	0	chr6_1.513783	3	12	chr6_2.965689c	3	21
chr6_0.106957c	3	0	chr6_1.425327	3	12	chr6_2.96574c	3	21
chr6_0.242596	3	0	chr6_1.42533	3	12	chr6_2.965734c	3	21
chr6_0.258258	3	2	chr6_1.425389	3	12	chr6_2.963175	3	22
chr6_0.288153c	3	5	chr2_6.356844	3	14	chr6_2.963309	3	22
chr6_0.522755	3	6	chr6_1.816382	3	14	chr6_3.033009	3	22
chr6_0.522773	3	6	chr6_1.816427	3	14	chr3_0.405998	3	24
chr6_0.242599	3	6	chr6_1.868954c	3	14	chr6_3.272563	3	24

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ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_3.272502	3	24	chr6_4.371663	3	34	chr1_18.377545	3	45
chr6_3.326291	3	24	Rw35C24_LG3	3	35	chr3_26.295993c	3	45
chr6_3.272383	3	24	chr6_4.175392	3	35	chr3_26.296016c	3	45
chr6_3.272449	3	24	chr6_4.280806	3	35	chr6_6.482123	3	45
chr6_3.272455	3	24	chr6_4.332487	3	35	chr6_6.7918	3	45
chr6_3.272499	3	24	chr6_4.332489	3	35	chr6_7.070216	3	45
chr6_3.27251	3	24	chr6_4.332525	3	35	chr6_7.274355	3	46
chr6_3.272518	3	24	chr6_4.332563	3	35	Rw12J12_LG3	3	55
chr6_3.326319	3	24	chr6_4.710053	3	35	chr6_7.649678	3	55
chr6_3.581794	3	24	chr6_4.710083	3	35	chr6_7.55052c	3	57
chr6_3.105928	3	24	chr6_4.777858	3	35	Rh50_LG3	3	58
chr6_3.444881	3	24	chr6_4.932935	3	39	chr6_7.702565	3	58
chr6_3.445019	3	25	chr6_4.933007	3	39	chr3_27.736901	3	58
chr6_3.690909	3	25	chr6_5.550275	3	39	chr6_7.214013	3	58
chr6_3.691074	3	25	chr6_5.575539	3	39	chr6_7.399133c	3	58
chr6_3.581779	3	26	chr6_5.982014	3	39	chr6_7.649699c	3	58
chr6_3.666382	3	26	chr6_6.200357	3	39	chr6_7.839982c	3	58
chr6_3.791085	3	26	chr6_6.200484	3	39	chr6_7.399185	3	58
chr6_4.053725	3	26	chr6_6.200511	3	39	chr6_7.702625	3	58
chr6_3.553724	3	26	chr6_5.300251	3	39	chr6_7.781201	3	58
chr6_3.596202	3	26	chr6_5.300276	3	39	chr6_8.607405	3	59
chr6_3.666389	3	26	chr6_5.300289c	3	39	chr6_8.630082	3	59
chr6_3.739383c	3	26	chr6_5.300312c	3	39	chr6_8.724376	3	60
chr6_3.791109	3	28	chr6_5.645322	3	39	chr6_8.724436	3	63
chr6_4.17526	3	28	chr6_5.645458	3	39	chr6_8.951763	3	63
chr6_4.175209	3	28	chr6_5.442559	3	41	chr6_8.977622	3	63
chr6_4.231767	3	28	chr6_6.468231	3	41	chr6_8.977642	3	63
chr6_4.262795	3	28	chr6_6.73794	3	41	chr6_8.977696	3	63
chr6_4.204762	3	30	chr6_6.761155	3	41	chr6_10.916245	3	63
chr6_4.37173	3	30	chr6_6.791664	3	41	chr6_8.607372c	3	64
chr6_4.50671	3	32	chr6_7.073636	3	41	chr6_8.614639c	3	64
chr6_4.506776	3	32	chr6_7.359523	3	41	chr6_8.773447c	3	64
chr6_4.710029	3	32	chr6_5.982011	3	42	chr6_8.951769c	3	64
chr6_4.371733	3	32	chr6_5.982029	3	42	chr6_8.614712c	3	64
chr6_4.332478	3	33	chr6_5.982031	3	42	chr6_8.662506c	3	64
chr6_4.332494	3	33	chr6_6.368022	3	42	chr6_8.662557c	3	64
chr6_4.71008	3	33	chr6_6.468189	3	43	chr6_9.031988	3	64
chr6_4.710212	3	33	chr6_6.468315	3	43	chr6_9.113612	3	64
chr6_4.777808	3	33	chr6_6.737852	3	44	chr6_8.97888c	3	65
chr6_4.777891c	3	33	chr6_6.791673	3	44	chr6_9.032114	3	65

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_9.032051c	3	65	chr6_11.73694	3	73	chr1_14.272655	3	85
chr6_9.354893	3	65	chr6_17.790682	3	73	chr4_23.60151	3	86
chr6_8.978868	3	66	chr6_11.736975	3	73	chr6_13.18357	3	86
chr6_9.176797c	3	66	chr6_11.988579	3	73	chr4_23.601554	3	86
chr3_23.544367	3	67	chr6_12.312783	3	73	chr6_13.183501	3	86
chr6_8.66257	3	67	chr6_14.684969	3	74	chr6_13.183503	3	86
chr6_8.679661	3	67	chr6_14.32699	3	74	chr1_9.306686	3	88
chr6_8.978886	3	67	chr6_18.103511	3	75	chr6_18.243505	3	88
chr6_9.032021	3	67	chr6_17.734756	3	76	chr6_18.24351	3	88
chr6_9.354923	3	67	chr6_17.765146	3	76	chr6_18.270544	3	88
chr6_9.32952	3	68	chr6_17.790678	3	76	chr1_9.306703	3	88
chr5_5.161425	3	70	chr1_0.630283	3	78	chr6_18.243495	3	88
chr6_10.736859c	3	70	chr6_17.519036	3	78	chr1_12.907297	3	94
chr6_10.749852	3	70	chr6_17.519045	3	78	chr1_14.272702	3	94
chr6_11.048559	3	70	chr6_17.765236	3	78	chr1_12.90737	3	95
chr6_10.950386	3	70	chr6_17.519042c	3	78	chr1_13.963736	3	96
chr6_11.409705	3	71	chr6_16.82039	3	80	chr1_13.372495	3	100
chr6_11.451162	3	71	chr6_17.215238	3	81	chr1_13.372615	3	100
chr6_10.807964	3	72	chr6_16.907939	3	82	chr7_15.853166	3	100
BFACT47_LG3	3	73	chr6_17.096838	3	82	chr1_14.303642	3	100
chr6_17.519049	3	73	chr6_17.096856	3	82	chr6_15.486149	3	100
chr6_17.519102	3	73	chr6_17.097003	3	82	chr6_18.270657	3	100
chr6_10.46093	3	73	chr6_17.281238	3	82	chr1_13.372442	3	101
chr6_10.557874	3	73	chr3_3.416949	3	83	chr1_13.372591	3	101
chr6_11.533989	3	73	chr6_15.942954c	3	83	chr1_13.963853	3	101
chr6_11.533993	3	73	chr6_17.070224	3	83	chr1_14.303597	3	101
chr6_11.534	3	73	chr6_17.070391	3	83	chr1_17.717705	3	101
chr6_11.534044	3	73	chr6_17.096884	3	83	chr1_17.893831	3	101
chr6_11.657711	3	73	chr6_17.096951	3	83	chr2_2.65768	3	101
chr6_11.735957	3	73	chr6_18.651777	3	83	chr3_23.543923	3	101
chr6_12.203693	3	73	chr6_15.986821	3	84	chr3_23.543973	3	101
chr6_12.240158	3	73	chr6_15.986928	3	84	chr4_14.903227	3	101
chr6_12.240181	3	73	chr6_18.028824	3	84	chr1_19.762871	3	104
chr6_12.312814	3	73	chr6_18.028841	3	84	chr1_20.19506	3	104
chr6_14.453296	3	73	chr6_18.094742	3	84	chr1_22.015533	3	104
chr6_10.749894	3	73	chr6_18.094787	3	84	chr6_0.346436	3	104
chr6_10.749984	3	73	chr6_18.243462	3	84	chr1_19.762873	3	104
chr6_11.171791	3	73	chr6_18.270642	3	84	chr1_19.762761	3	105
chr6_11.735878	3	73	chr6_18.664101	3	84	chr1_20.616031	3	105
chr6_11.735918	3	73	chr6_18.094868c	3	84	chr1_20.19498	3	105

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_22.885711	3	106	chr4_13.333733	4	13	chr4_6.705474	4	20
chr4_14.90326	3	106	chr4_14.689942	4	13	chr4_6.705482	4	20
chr4_15.377617	3	106	chr4_14.691572	4	13	chr3_18.786682	4	22
chr6_0.346363	3	106	chr4_4.907658	4	13	chr3_18.786699	4	22
chr1_21.072247	3	109	chr6_29.493251	4	13	chr3_18.786716	4	22
chr6_15.94289	3	116	chr4_4.907812c	4	13	chr3_18.786753	4	22
chr6_18.270658	3	118	chr1_2.202074	4	15	chr4_5.442672	4	22
chr2_27.129849	4	0	chr1_2.202091	4	15	chr4_10.378789c	4	25
chr2_27.130002	4	0	chr1_2.202128	4	15	chr1_2.202084	4	26
chr4_0.603715	4	0	chr4_10.022851	4	15	chr4_10.024543	4	26
chr4_0.624912	4	0	chr4_10.378642	4	15	chr4_12.955859	4	26
chr4_0.62493	4	0	chr4_10.902818	4	15	chr4_10.024609c	4	26
chr2_7.10623c	4	3	chr4_13.333919	4	15	chr4_10.024632c	4	26
chr2_7.106241c	4	3	chr4_4.300849	4	15	chr4_13.059825	4	26
chr2_7.10627c	4	3	chr4_4.680704	4	15	chr5_12.69382	4	27
chr2_7.106283c	4	3	chr4_4.871904	4	15	chr3_0.669368c	4	28
chr1_14.815301	4	4	chr4_6.609542	4	15	chr4_13.87273c	4	28
chr1_16.466659	4	4	chr4_4.680702c	4	15	RhABT12_LG4	4	30
chr4_0.624747	4	4	chr4_10.81303c	4	16	chr2_24.584916	4	30
chr4_0.624757	4	4	chr4_10.813041c	4	16	chr2_24.584943	4	30
chr4_0.624824	4	4	chr4_10.813043c	4	16	chr2_24.584953	4	30
chr4_1.558722	4	4	chr4_4.872342c	4	19	chr4_10.902858c	4	30
chr4_1.558806	4	4	chr4_4.872345c	4	19	chr4_10.903029c	4	30
chr4_0.624754	4	7	chr3_0.669406	4	19	chr4_13.579901	4	30
chr4_1.608475	4	8	chr4_13.538034	4	19	chr4_15.244681	4	30
chr4_2.61772c	4	8	chr4_14.26513	4	19	chr4_15.411501	4	30
chr4_2.910568	4	8	chr4_5.442548c	4	19	chr4_9.711998	4	30
chr4_2.910641	4	8	chr6_5.051434c	4	19	chr5_12.693625	4	30
chr4_2.910829	4	8	chr1_2.690519	4	20	chr5_12.693643c	4	30
chr4_3.23362	4	9	chr1_2.690666	4	20	chr2_27.795803c	4	31
chr4_1.608673	4	11	chr1_2.690704	4	20	chr4_13.872754	4	31
chr4_2.13018c	4	11	chr2_24.584994	4	20	chr4_14.019613c	4	31
chr4_2.61771	4	11	chr4_10.378639	4	20	chr3_0.669366c	4	31
chr4_2.643188	4	11	chr1_3.586681c	4	20	chr4_14.265056	4	31
chr4_16.099712	4	11	chr4_4.680678	4	20	chr4_14.265105c	4	31
chr6_29.493328	4	11	chr4_4.680803	4	20	chr3_5.97957	4	32
chr4_10.785089	4	11	chr4_4.87194	4	20	chr4_15.551447	4	32
chr4_13.333904c	4	11	chr4_4.87236c	4	20	chr4_14.967475	4	34
chr4_10.785015	4	13	chr6_5.051381	4	20	chr4_15.244556	4	34
chr4_13.333703	4	13	chr4_4.907813	4	20	chr4_15.244486	4	34

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_15.24411	4	34	chr4_19.261155	4	47	chr4_20.363129c	4	52
chr4_15.572828c	4	34	chr4_19.264845	4	47	chr4_20.363195c	4	52
chr4_13.538038c	4	35	chr4_19.261168	4	47	chr4_20.36565c	4	52
chr4_13.579898	4	35	chr4_19.559636	4	48	chr4_20.365729	4	52
chr4_15.572876c	4	35	chr4_19.559693	4	48	chr4_20.706127	4	52
chr4_15.572861c	4	35	chr4_20.223839	4	48	chr4_20.706199	4	52
chr4_17.257739	4	36	chr4_20.223871	4	48	chr4_20.800257	4	52
chr3_5.979542	4	38	chr4_20.231117	4	49	chr4_20.800284c	4	52
chr4_15.621967	4	38	chr4_20.800395	4	50	chr4_20.932977	4	52
chr4_16.933603	4	38	chr4_20.800425	4	50	chr4_20.98389	4	52
chr2_24.585	4	39	chr4_21.108777	4	50	chr4_22.663824	4	52
chr4_16.895061	4	39	chr4_20.853208	4	50	chr4_20.983941c	4	52
chr4_16.895077	4	39	chr4_20.265456c	4	51	chr4_21.108676c	4	52
chr4_16.895123	4	39	chr4_20.265486c	4	51	chr4_22.384156c	4	52
chr2_24.584797	4	40	chr4_20.2656c	4	51	chr4_25.585298c	4	52
chr3_32.662954	4	40	chr4_22.657176c	4	51	chr4_22.657084	4	52
chr4_16.000819	4	40	chr4_22.664073	4	51	chr4_20.365723c	4	52
chr4_16.000934	4	40	chr4_20.800442	4	51	chr4_20.706136	4	52
chr4_16.140598	4	40	chr4_16.510801	4	52	chr4_23.227857	4	52
chr4_16.666493	4	40	chr4_22.392782c	4	52	chr4_22.650663	4	52
chr4_19.027117	4	40	chr4_22.650647	4	52	chr4_22.650657	4	52
chr3_5.979522	4	40	chr4_19.829848	4	52	chr4_22.384157c	4	52
chr4_14.96765	4	40	chr4_19.82994	4	52	chr4_22.65065	4	52
chr4_15.551408	4	40	chr4_20.265549	4	52	chr4_22.663694	4	52
chr4_16.679351	4	40	chr4_20.324657	4	52	chr4_21.693318	4	54
chr4_20.579566	4	40	chr4_20.363069	4	52	chr2_0.264477	4	55
chr4_13.538025c	4	40	chr4_20.363091	4	52	chr4_22.392716c	4	55
chr4_15.551469c	4	40	chr4_20.700236	4	52	chr4_22.519434	4	55
chr4_16.89505	4	40	chr4_20.70626	4	52	chr4_22.664221	4	55
chr6_34.918843	4	40	chr4_20.800415	4	52	chr4_22.664225	4	55
chr4_17.064622	4	44	chr4_21.108597	4	52	chr4_23.227841c	4	56
chr4_16.510792	4	46	chr4_21.108724	4	52	chr4_23.227843c	4	56
chr4_16.678729	4	46	chr4_21.693218	4	52	chr2_0.264421	4	58
chr4_16.679267c	4	46	chr4_22.519456	4	52	chr4_20.853281	4	58
chr4_16.140549	4	46	chr4_22.519554	4	52	chr4_23.043038	4	58
chr4_16.679197c	4	46	chr4_22.657192	4	52	chr4_23.043134	4	58
chr4_16.140459c	4	47	chr4_22.66421	4	52	chr4_23.12628	4	58
chr4_19.015702	4	47	chr4_23.043013	4	52	chr4_23.227868	4	58
chr4_19.015713c	4	47	chr4_19.838586	4	52	chr4_22.892014c	4	58
chr4_19.015757c	4	47	chr4_20.23112	4	52	chr4_23.043144	4	58

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ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_23.765657	4	58	chr3_6.449223	4	63	chr4_26.760646	4	67
chr4_23.765705	4	58	chr4_23.869726c	4	63	chr4_24.303356	4	67
chr4_23.227904c	4	58	chr4_25.551888	4	63	chr4_26.248412c	4	67
chr3_4.920582c	4	58	chr4_23.7658	4	63	chr4_26.312962	4	67
chr4_22.013886c	4	58	chr4_23.895969	4	63	chr4_26.424639	4	67
chr4_23.357974	4	60	chr4_23.895971	4	63	chr4_26.442628	4	67
chr4_23.766049	4	60	chr4_23.895991c	4	63	chr4_27.992125	4	67
chr4_23.357947	4	61	chr4_23.959349	4	63	chr4_26.344736	4	67
chr4_23.744536	4	61	chr4_25.90357	4	63	chr4_26.347188c	4	67
chr4_23.896043c	4	61	chr4_24.870423	4	64	chr4_26.442568	4	70
chr4_23.896044c	4	61	chr4_26.180019	4	66	chr4_26.442561	4	71
chr4_23.959251c	4	61	chr6_13.037868	4	66	chr4_17.246387	4	71
chr4_24.870522	4	61	chr4_26.235391	4	67	chr4_17.246397	4	71
chr4_23.765388	4	61	chr4_26.760643	4	67	chr4_26.770355c	4	71
chr4_23.869831	4	61	chr4_26.347175c	4	67	chr4_24.107153c	4	71
chr4_23.959241c	4	61	chr3_6.449225	4	67	chr4_24.14093	4	71
chr4_23.959316	4	61	chr3_6.491077	4	67	chr4_26.225406c	4	72
chr4_23.895982c	4	61	chr4_24.079633	4	67	chr4_27.098452	4	72
chr4_25.69303c	4	61	chr4_24.079682	4	67	chr4_27.109568	4	72
chr4_23.959293c	4	61	chr4_24.14099	4	67	chr4_27.11645c	4	72
chr4_23.959311c	4	61	chr4_24.14107	4	67	chr4_27.264868	4	72
chr4_25.693131c	4	61	chr4_24.709745	4	67	chr4_27.264885	4	72
chr4_23.95931c	4	61	chr4_24.753699	4	67	chr4_27.264889	4	72
chr4_25.170109	4	61	chr4_24.870345	4	67	chr4_27.29543	4	72
chr4_25.723911c	4	61	chr4_24.870399	4	67	chr4_27.561547	4	72
chr4_25.72419c	4	61	chr4_25.378617	4	67	chr4_27.681531c	4	72
chr4_25.247845c	4	62	chr4_25.551889	4	67	chr4_26.225259c	4	72
chr4_25.247859c	4	62	chr4_25.551913	4	67	chr4_26.225291c	4	72
chr4_25.247887c	4	62	chr4_25.693012	4	67	chr4_26.225404c	4	72
chr4_25.247853c	4	62	chr4_26.044602	4	67	chr4_26.225403	4	72
chr4_23.687045c	4	63	chr4_26.044632	4	67	chr4_26.225428	4	72
chr4_25.146078	4	63	chr4_26.053815	4	67	chr4_26.225749	4	72
chr4_25.284119	4	63	chr4_26.344803	4	67	chr4_26.235324c	4	72
chr4_25.693034c	4	63	chr4_24.303326	4	67	chr4_25.247964	4	74
chr3_32.662897	4	63	chr4_24.709688c	4	67	chr4_25.247839c	4	75
chr4_24.141004	4	63	chr4_24.753806c	4	67	chr4_25.247851c	4	75
chr4_24.141035	4	63	chr4_26.31286	4	67	chr4_25.247857c	4	75
chr4_25.170089	4	63	chr4_26.314055	4	67	chr4_25.247863c	4	75
chr4_25.29208	4	63	chr4_26.31414c	4	67	chr4_25.247906c	4	75
chr4_25.551891	4	63	chr4_26.760645	4	67	chr4_25.247909c	4	75

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ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_27.264891	4	77	chr4_27.973639	4	87	chr4_29.956145	4	100
chr4_26.225769	4	78	chr4_27.981351	4	87	chr4_29.680221	4	100
chr4_26.844414	4	78	chr4_28.875093	4	87	chr4_29.746051	4	100
chr4_26.84442	4	78	chr4_29.143188	4	87	chr4_29.746049	4	100
chr4_26.900233	4	78	chr4_28.674749	4	89	chr4_29.859004	4	101
chr4_27.109592	4	78	chr4_28.674781	4	89	chr4_29.746187	4	101
chr4_27.264957	4	78	chr4_28.687133	4	89	chr4_30.146063	4	101
chr4_27.265022	4	78	chr4_28.687403c	4	89	chr4_29.956147c	4	101
chr4_27.981343	4	79	chr4_29.082506	4	89	chr4_29.956157	4	101
chr4_26.248417	4	79	chr4_29.3096	4	89	chr4_29.956315	4	101
chr4_26.248425	4	79	chr4_29.590994c	4	89	chr4_29.956428	4	101
chr4_28.17272	4	80	chr4_29.594611	4	89	chr4_30.055069	4	101
chr4_28.548139	4	80	chr4_29.598014	4	89	chr4_30.059204	4	101
chr4_29.121993	4	82	chr4_29.600188	4	89	chr4_30.111326c	4	101
chr4_29.122035	4	82	chr4_29.691626c	4	89	chr4_30.111331c	4	101
chr4_29.482254	4	83	chr4_29.691774c	4	89	chr4_30.111579c	4	101
chr4_26.90022	4	83	chr4_28.687601c	4	89	chr4_29.956251	4	101
chr4_27.0985	4	83	chr4_28.980996	4	89	chr4_30.111387	4	101
chr4_27.445737c	4	83	chr4_29.121976	4	89	chr4_30.111196c	4	102
chr4_29.545641	4	84	chr4_29.136852	4	89	chr4_30.111712c	4	102
chr4_29.600227	4	85	chr4_29.386931	4	91	chr4_30.309085	4	103
chr1_7.834627	4	86	chr4_29.645343	4	91	chr4_30.208266c	4	103
chr4_27.922673	4	86	chr4_29.387028	4	93	chr4_30.429096	4	105
chr4_24.309702	4	86	chr4_29.54552	4	93	chr4_30.210924	4	107
chr4_26.312956	4	86	chr4_29.545529	4	93	chr4_30.229594	4	107
chr4_28.051318	4	86	chr4_29.557967	4	93	chr4_30.584004c	4	107
chr4_27.922625c	4	86	chr4_29.85895	4	93	chr4_30.670637	4	107
chr4_27.922646	4	86	chr4_29.858953	4	93	chr3_5.902116	4	107
chr4_27.922658c	4	86	chr4_29.277525	4	97	chr4_31.14001	4	107
chr4_27.992332c	4	86	chr4_29.422516	4	97	chr4_31.61281	4	107
chr4_27.99233c	4	86	chr4_29.387027c	4	97	chr4_31.186	4	107
chr4_28.051206	4	86	chr4_29.691759	4	98	chr4_30.229548	4	107
chr4_28.156441	4	86	chr4_29.746082	4	98	chr4_30.429149	4	108
chr4_28.674636	4	86	chr4_29.422523	4	98	chr4_30.229574	4	108
chr4_28.674719	4	86	chr4_29.600158	4	98	chr4_30.229584	4	108
chr4_29.082433	4	86	chr4_29.691738	4	98	chr3_5.90206	4	109
chr4_29.004618	4	87	chr4_29.594662	4	98	chr3_5.902101	4	109
chr4_29.004622	4	87	chr4_29.594806	4	98	chr4_30.670628	4	109
chr4_27.29526	4	87	chr4_29.591117	4	98	chr4_30.939637	4	109
chr4_27.29538	4	87	chr4_29.859008	4	99	chr4_31.267132	4	109

Appendix 3. Continued

				ICD				
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_29.849682	4	109	chr4_32.068076c	4	116	chr3_0.869271c	5	7
chr4_30.141904	4	109	chr4_32.06823c	4	116	chr3_1.184312	5	7
chr4_30.142115	4	109	chr4_32.094305	4	116	chr3_0.972201c	5	8
chr4_30.309136	4	109	chr4_31.925842	4	117	chr3_1.055824c	5	9
chr4_30.370151	4	109	chr4_31.984893	4	117	chr3_1.136064c	5	9
chr4_30.584234	4	109	chr4_31.986193	4	117	chr3_1.184325c	5	9
chr4_30.583998	4	110	chr4_32.274135	4	117	chr3_1.553932	5	9
chr4_30.675542	4	110	chr3_0.104302c	5	0	chr3_2.077597	5	9
chr4_30.675543	4	110	chr3_0.361349c	5	0	chr3_2.220732	5	9
chr4_30.67556	4	110	chr3_0.361363	5	0	chr3_1.208568c	5	10
chr4_30.675592	4	110	chr3_0.405875c	5	0	chr3_1.233154c	5	10
chr4_30.584408c	4	110	chr3_0.25191	5	0	chr3_1.553925c	5	12
chr4_30.584409	4	110	chr3_0.455471c	5	0	chr3_2.07766c	5	12
chr4_30.675593	4	111	chr3_0.455473c	5	0	chr4_22.650506c	5	12
chr4_30.704091	4	111	chr3_0.793648c	5	0	chr4_22.650513c	5	12
chr4_30.848341c	4	111	chr3_0.793654c	5	0	chr4_22.650557c	5	12
chr4_30.928863	4	111	chr3_0.479349c	5	0	chr4_22.650563c	5	12
chr4_30.99181	4	111	chr3_0.479389c	5	0	chr4_22.650569c	5	12
chr4_31.065245	4	111	chr3_0.545528c	5	0	chr4_22.650578c	5	12
chr4_30.92891	4	111	chr3_0.669521c	5	1	chr4_22.650584c	5	12
chr4_30.93957	4	111	chr3_0.793645	5	3	chr4_22.65058c	5	12
chr4_30.939643	4	111	chr3_0.869195	5	3	chr4_22.650595c	5	12
chr4_30.928983	4	111	chr3_0.869261	5	3	chr3_1.554004c	5	12
chr4_30.929007c	4	111	chr3_0.793647c	5	3	chr1_2.997769	5	17
chr4_30.929001	4	111	chr3_0.793655c	5	3	chr1_2.997796	5	17
chr4_30.709461	4	112	chr3_0.426312c	5	5	chr3_2.220758	5	17
chr4_31.12036	4	112	chr3_0.426387c	5	5	chr3_2.449563	5	17
chr4_31.139869	4	112	chr3_1.133971c	5	5	chr3_2.449709	5	17
chr4_31.185885	4	112	chr3_0.426359c	5	5	chr3_2.696516	5	17
chr4_31.280198	4	112	chr3_0.42637c	5	5	chr3_2.75611	5	17
chr4_31.282675	4	112	chr3_0.426393c	5	5	chr3_2.756146	5	17
chr4_31.18604	4	112	chr3_0.426408c	5	5	chr7_11.30447	5	17
chr4_31.213549	4	112	chr3_0.793639	5	7	chr1_2.99782c	5	17
chr4_31.588419c	4	114	chr3_0.836698	5	7	chr3_1.553938	5	17
chr4_31.588428c	4	114	chr3_0.869272c	5	7	chr3_2.696615c	5	17
chr4_31.612938	4	114	chr3_0.86927c	5	7	chr4_19.414226c	5	17
chr4_31.675112c	4	114	chr3_0.869296c	5	7	chr3_5.417621	5	19
chr4_31.611417	4	114	chr3_0.972174	5	7	chr4_13.334543c	5	19
chr4_31.77996	4	114	chr3_0.869152c	5	7	chr4_13.33456c	5	19
chr4_31.896395	4	116	chr3_0.869268c	5	7	chr3_5.102709c	5	20

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_9.404351	5	20	chr2_17.431947	5	32	chr3_3.3463	5	39
chr3_4.920592c	5	21	chr3_2.919718c	5	32	chr3_2.919798	5	39
chr3_4.920622c	5	21	chr3_3.020856	5	32	chr3_2.919827c	5	39
chr4_13.334563	5	22	chr3_3.115367	5	32	chr3_2.919842c	5	39
chr2_28.187005	5	22	chr3_3.496012	5	32	chr3_6.029755	5	40
chr3_4.920436	5	22	chr3_3.313779	5	32	chr3_6.491149	5	40
chr4_13.334587	5	22	chr3_3.346134	5	32	chr3_6.123998	5	42
chr3_4.687369	5	22	chr3_3.346242	5	32	chr3_6.376783	5	42
chr3_4.70952	5	22	chr3_3.346244	5	32	chr3_6.600776	5	42
chr3_5.051009c	5	22	chr3_3.497486	5	32	chr3_6.739909	5	42
chr3_5.0538c	5	22	chr3_3.776746	5	32	chr3_6.739921	5	42
chr3_4.298301	5	24	chr3_3.548351	5	33	chr3_6.741723	5	42
chr3_4.300207	5	24	chr3_2.987201	5	35	chr2_12.639441	5	44
chr3_4.68329	5	24	chr3_3.013711	5	35	chr3_6.56816	5	44
chr3_4.687361	5	24	chr3_3.02146c	5	35	chr3_7.657957c	5	44
chr6_12.99266	5	24	chr3_3.362056c	5	35	chr3_7.904143c	5	44
chr3_4.535513c	5	25	chr3_3.362101c	5	35	chr3_8.014088c	5	44
chr3_4.535636c	5	25	chr3_3.369959c	5	35	chr3_5.902028	5	44
chr3_4.606292	5	25	chr3_6.878892c	5	35	chr3_6.355268	5	44
chr3_4.687372	5	25	chr3_5.447599	5	36	chr3_6.358107	5	44
chr3_4.687313c	5	25	chr3_3.013559c	5	36	chr3_6.376784	5	44
chr3_4.687322c	5	25	chr3_3.020797c	5	37	chr3_6.741765	5	44
chr6_18.147322c	5	25	chr3_3.36988	5	37	chr3_6.554197c	5	44
chr3_4.791511c	5	25	chr3_2.905092	5	38	chr3_3.313825c	5	44
chr6_12.992642c	5	26	chr3_2.919821	5	38	chr3_7.249251	5	47
chr6_12.992669	5	26	chr3_3.362055	5	38	chr3_7.647396	5	49
chr6_12.992792	5	26	chr3_3.49741	5	38	chr3_7.647455c	5	49
chr3_4.306393c	5	27	chr6_29.345705	5	38	chr3_7.904074c	5	49
chr3_4.526267	5	27	chr3_2.919721c	5	38	chr3_8.347404	5	49
chr3_5.012772	5	28	chr3_2.919722c	5	38	chr3_6.848796	5	50
chr3_4.298332	5	28	chr3_2.91972c	5	38	chr3_7.647398	5	50
chr3_4.300187c	5	28	chr3_2.9198c	5	38	chr3_7.955774	5	50
chr3_4.166224	5	30	chr3_5.636728c	5	38	chr3_8.190653	5	51
chr3_4.166241	5	30	chr3_5.636736c	5	38	chr3_9.163452	5	52
chr3_4.166274	5	30	chr4_25.395373	5	38	chr3_9.287623	5	52
chr3_4.298369	5	30	chr3_2.919767c	5	38	chr3_9.287642	5	52
chr3_4.306368	5	30	chr3_2.919818c	5	38	chr3_9.743527	5	52
chr3_3.163648	5	31	chr3_2.905095	5	39	chr3_9.163581	5	53
chr3_4.642829	5	31	chr3_2.905097	5	39	chr3_9.597026c	5	53
chr3_4.796164	5	31	chr3_2.987219	5	39	chr3_9.83606	5	53

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_9.597186c	5	53	chr3_18.569408	5	70	chr5_23.114511	5	80
chr3_20.098401c	5	53	chr3_18.786668	5	70	chr5_9.431825	5	80
chr4_29.594789	5	53	chr3_18.786671	5	70	chr3_11.544922c	5	80
chr4_29.594838	5	53	chr3_8.683186	5	70	chr3_11.544963c	5	80
chr3_18.994299	5	56	chr4_8.399065c	5	70	chr3_11.64811c	5	80
chr5_0.053509	5	56	chr4_8.458814c	5	70	chr3_13.154217	5	80
chr3_10.025053	5	58	chr4_8.458825c	5	70	chr4_29.11998c	5	80
chr3_10.146899	5	58	chr4_8.458835	5	71	chr3_11.374317c	5	80
chr3_18.61594	5	58	chr3_18.504736c	5	73	chr3_12.805231	5	81
chr3_18.616047	5	58	chr3_10.598995	5	74	chr3_12.975533c	5	81
chr3_18.629793c	5	58	chr3_10.599066	5	74	chr3_13.559796	5	81
chr3_18.737181c	5	58	chr3_10.599013c	5	74	chr3_13.915841	5	81
chr3_18.737374	5	58	chr3_18.504707c	5	74	chr3_13.327268	5	83
chr3_18.994326	5	58	chr4_8.39899c	5	75	chr3_13.336658c	5	83
chr3_19.957388	5	58	chr7_19.300534c	5	76	chr3_12.176524	5	83
chr3_8.683165	5	58	chr7_19.300555c	5	76	chr5_27.492158c	5	84
chr5_0.053562	5	58	chr7_19.300561c	5	76	chr3_13.889605c	5	85
chr6_3.553754	5	58	chr7_19.300581c	5	76	chr3_14.124454	5	86
chr3_10.149417c	5	58	chr7_19.300596c	5	76	chr3_20.303146	5	86
chr3_18.786629c	5	58	CL2845_LG5	5	77	chr3_14.124476	5	88
chr3_8.332798c	5	58	chr3_10.598993	5	77	chr3_20.303098	5	88
chr3_8.347533c	5	58	chr3_10.606866	5	77	chr3_20.303287	5	88
chr3_8.347534c	5	58	chr3_11.012746	5	77	chr3_21.07283	5	88
chr3_19.783973c	5	58	chr3_11.012872	5	77	chr3_21.073097	5	88
chr3_8.809414c	5	58	chr3_11.104214	5	77	chr3_21.073123	5	88
chr3_8.809417c	5	58	chr5_22.829181c	5	77	chr3_21.073229	5	88
chr2_6.94522	5	58	chr3_11.012869	5	77	chr3_12.413019	5	89
chr3_18.629716c	5	58	chr5_23.114391c	5	77	chr3_13.889638	5	89
chr3_19.482062c	5	58	chr5_23.11445c	5	77	chr3_17.311876c	5	89
chr3_18.737184c	5	58	chr7_18.645068c	5	77	chr3_21.724107	5	89
chr3_18.862082c	5	58	chr3_10.972226c	5	78	chr3_22.007605	5	89
chr3_18.862084c	5	58	chr3_11.01274c	5	78	chr3_22.059596	5	89
chr3_19.144099c	5	58	chr5_23.192046	5	78	chr3_22.059882	5	89
chr3_19.144165	5	58	chr3_11.349301c	5	79	chr3_22.396831	5	89
chr3_19.14409c	5	58	chr3_11.349294	5	80	chr3_22.969602c	5	89
Rw14H21_LG5	5	70	chr3_11.544979	5	80	chr3_22.96961c	5	89
chr3_10.606863	5	70	chr3_11.55402	5	80	chr4_21.23856c	5	89
chr3_10.606876	5	70	chr3_11.648012	5	80	chr3_22.969987	5	89
chr3_10.606961	5	70	chr3_11.861412	5	80	chr3_17.480615c	5	90
chr3_18.44298	5	70	chr3_11.861432	5	80	chr3_22.67851c	5	90

Appendix 3. Continued

			ICD					
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_31.27734	5	90	chr3_17.311735c	5	98	chr3_24.711559	5	110
chr3_22.969965c	5	90	chr3_22.970602c	5	98	chr3_24.711579	5	110
chr2_12.225907c	5	91	chr7_10.273324	5	98	chr7_2.574894	5	110
chr3_23.598381c	5	91	chr3_16.890935c	5	98	chr3_24.531405c	5	111
chr3_16.621877	5	91	chr3_16.920664c	5	98	chr3_24.805637	5	112
chr3_22.678449	5	91	chr3_16.920688c	5	98	chr3_23.876742c	5	113
chr3_22.678527c	5	91	chr3_23.544287	5	98	chr3_23.897624	5	113
chr3_22.678583c	5	91	chr2_12.21935c	5	99	chr3_24.387501	5	113
chr3_22.970556	5	91	chr3_22.824667c	5	99	chr3_24.504684	5	113
chr3_31.33046c	5	91	chr3_16.920496	5	100	chr3_24.955036	5	113
chr3_31.330487	5	91	chr3_17.311759	5	100	chr3_24.955037	5	113
chr3_31.714889	5	91	chr3_17.311898	5	100	chr3_23.876843c	5	113
chr4_12.462544	5	91	chr3_20.30323	5	100	chr3_23.906895	5	113
chr4_12.462564	5	91	chr3_21.072572	5	100	chr3_24.010497	5	113
chr3_22.969637c	5	91	chr3_22.969731	5	100	chr3_24.01077	5	113
chr3_22.971397c	5	91	chr3_22.970551	5	100	chr3_24.050323	5	113
chr3_31.330401c	5	91	chr3_23.544461c	5	100	chr3_24.121044	5	113
chr3_22.397858c	5	91	chr3_17.927866	5	100	chr3_24.214576	5	113
chr3_22.971414c	5	92	chr3_18.140765	5	100	chr3_24.214642	5	113
chr2_12.219439	5	92	chr3_18.14081	5	100	chr3_24.594107	5	113
chr3_22.969603c	5	92	chr3_24.95488	5	100	chr3_24.594162	5	113
chr3_31.277367c	5	92	chr3_22.007514	5	100	chr3_24.031721	5	113
chr2_12.225895c	5	92	chr7_10.22618c	5	100	chr3_24.031731	5	113
chr2_18.464163	5	92	chr3_22.971405c	5	100	chr3_24.214573	5	113
chr3_17.451371	5	92	chr7_14.77686	5	100	chr3_24.387564	5	113
chr3_17.45143c	5	92	chr3_31.277358c	5	100	chr3_24.010726c	5	113
chr3_21.917422c	5	92	chr3_27.830421	5	104	chr3_23.876809c	5	114
chr3_22.059952c	5	92	chr3_18.141427c	5	105	chr3_23.876868c	5	114
chr3_22.39771c	5	92	chr3_18.141429c	5	105	chr3_23.906906c	5	114
chr3_22.397737c	5	92	chr3_18.141457c	5	105	chr3_24.121024c	5	114
chr3_22.397833c	5	92	chr3_18.141449c	5	105	chr3_24.010703c	5	115
chr3_22.397857c	5	92	chr3_18.141451c	5	106	chr5_16.132983	5	115
chr3_22.059723c	5	94	chr3_18.141454c	5	107	chr5_16.160301	5	115
chr3_23.544293c	5	95	chr1_16.650317	5	107	chr5_16.160451	5	115
chr3_15.80301	5	98	chr7_2.574916	5	107	chr5_16.160459	5	115
chr3_15.803015	5	98	chr3_17.986965	5	107	chr3_26.906643c	5	116
chr3_16.890937c	5	98	chr3_18.141431c	5	107	chr3_23.87677	5	116
chr3_23.544333	5	98	chr7_2.574998	5	107	chr3_23.906817	5	116
chr3_16.0145	5	98	chr3_24.921938	5	108	chr3_23.906896	5	116
chr3_16.486868c	5	98	chr3_24.711556	5	110	chr3_23.907006c	5	116

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_24.050328	5	116	chr3_26.20099c	5	123	chr6_25.673668	5	131
chr5_16.174676	5	116	chr3_26.056194	5	123	chr3_27.99615c	5	132
chr3_24.121041	5	117	chr3_26.098431	5	123	chr3_28.897439c	5	132
chr2_27.006425	5	118	chr3_26.056237	5	123	chr3_1.837681	5	135
chr3_25.618143	5	118	chr3_26.098422c	5	123	chr3_29.103306	5	135
chr3_25.618262	5	118	chr3_26.344475	5	123	chr3_29.472835	5	135
chr3_25.750115	5	118	chr3_26.392817	5	123	chr3_29.568573	5	135
chr3_25.782337c	5	118	chr3_26.495694	5	123	chr3_29.719209	5	135
chr3_26.056318	5	118	chr3_27.330373	5	123	chr3_30.32148	5	135
chr7_21.83421	5	118	chr3_27.58572	5	123	chr3_29.236232c	5	135
chr7_21.834239	5	118	chr3_26.296132c	5	126	chr3_29.472699	5	135
chr3_25.333278	5	118	chr3_27.074725	5	126	chr3_30.01321	5	135
chr3_25.674418	5	118	chr3_27.16259	5	126	chr3_30.321402	5	135
chr3_25.988717	5	118	chr3_27.162596	5	126	chr3_29.472774	5	137
chr3_26.097726	5	118	chr3_27.162716	5	126	chr3_29.719252	5	137
chr3_26.09785	5	118	chr3_27.248487	5	126	chr3_30.087184	5	140
chr3_25.782336	5	118	chr3_27.58555	5	126	chr3_30.218924	5	140
chr3_25.915845c	5	118	chr3_27.585556c	5	126	chr3_30.343504	5	140
chr3_25.333306	5	119	chr3_27.074702c	5	126	chr3_30.52693	5	140
chr3_25.618107	5	119	chr3_26.296122c	5	128	chr3_30.526974	5	140
chr3_25.98505	5	121	chr3_27.240247c	5	128	chr3_30.527117	5	140
chr3_25.988638c	5	121	chr3_27.240302c	5	128	chr3_30.527561	5	140
chr3_25.974304	5	122	chr3_27.248581c	5	128	chr3_30.527639	5	140
chr3_25.97447	5	122	chr3_26.392692	5	128	chr3_30.527588c	5	140
chr3_26.012934	5	122	chr3_27.721788	5	128	chr5_12.390497	5	141
chr3_26.012985	5	122	chr3_27.723222	5	128	chr3_29.103285	5	141
chr3_26.033536c	5	122	chr3_27.736828	5	128	chr3_29.185758	5	141
chr3_26.098326c	5	122	chr3_26.495861c	5	128	chr3_32.277741c	5	142
chr3_26.180247	5	122	chr3_29.236292	5	128	chr3_32.277762	5	142
chr3_26.180318	5	122	chr3_27.330448	5	128	chr3_32.27784	5	142
chr3_26.344409	5	122	chr3_27.58571c	5	128	chr3_32.277768c	5	142
chr3_26.344419	5	122	chr3_27.723279	5	129	chr3_30.991683	5	143
chr3_26.392667c	5	122	chr3_27.285255c	5	129	chr3_32.277879c	5	143
chr3_27.285354c	5	122	chr3_27.804249c	5	129	chr3_32.602159	5	143
chr3_27.296046c	5	122	chr3_27.96542	5	129	chr3_32.592274	5	143
chr3_27.330446c	5	122	chr3_27.830538c	5	129	chr3_32.592277	5	143
chr3_27.330486c	5	122	chr3_31.36812	5	129	chr3_32.657737c	5	143
chr3_26.033666c	5	122	chr3_26.200949	5	130	chr3_32.657813c	5	143
chr3_30.321447c	5	122	chr3_30.527495	5	131	chr3_32.847062c	5	143
chr3_26.09832	5	123	chr3_30.527545	5	131	chr3_32.663335c	5	143

Appendix 3. Continued

				ICD				
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_32.602146c	5	145	chr2_11.703057	6	15	chr2_6.304781c	6	20
chr3_29.565427	5	145	chr2_11.703091	6	15	chr2_8.127134	6	23
chr3_29.56546	5	145	chr2_11.177443	6	16	chr2_8.832534	6	23
chr3_30.218792	5	149	chr2_11.334928	6	16	chr2_8.832624	6	23
chr3_30.218807	5	149	chr2_4.827805	6	16	chr5_21.721446	6	23
chr3_32.547276	5	153	chr2_4.92821	6	16	chr2_18.164751	6	25
chr3_32.663302	5	153	chr2_1.948988c	6	17	chr2_8.819145	6	25
chr3_33.10348	5	153	chr2_2.117933	6	17	chr2_7.106386	6	26
chr3_33.103506	5	153	chr2_2.118021	6	17	chr2_7.971989	6	27
chr3_32.602122	5	153	chr2_14.670491	6	18	chr2_7.99021	6	27
chr3_32.675821	5	153	chr2_0.325927c	6	19	chr2_8.164211	6	27
chr2_11.362466	6	0	chr2_0.325936c	6	19	chr2_8.164281	6	27
chr2_5.131921	6	0	chr2_0.325939c	6	19	chr5_21.721374	6	27
chr2_5.74795	6	1	chr2_0.325942c	6	19	chr2_18.164933	6	28
chr1_7.51307	6	1	chr2_0.361985	6	19	chr2_7.990192	6	28
chr2_11.177448c	6	1	chr2_0.367748	6	19	chr2_7.990292	6	28
chr2_11.378663	6	1	chr2_1.948992c	6	19	chr2_7.990325	6	28
chr3_0.836562c	6	1	chr2_0.361984	6	19	chr2_7.95486	6	28
chr2_11.380937	6	1	chr2_0.38754	6	19	chr2_8.003546	6	28
chr3_0.836582c	6	1	chr2_0.387676	6	19	chr2_12.770204	6	28
chr3_0.836585c	6	1	chr2_0.387723	6	19	chr2_7.106382	6	29
chr2_11.378807	6	5	chr2_5.888786	6	19	chr4_14.967591	6	29
chr2_11.37881	6	5	chr2_6.417988	6	19	chr2_12.885057	6	31
chr2_11.378826	6	5	chr2_6.470938	6	19	chr2_10.681617	6	32
chr2_11.380942	6	5	chr2_0.387534	6	19	chr3_1.412857	6	32
chr2_11.33994	6	6	chr2_0.387621	6	19	chr2_10.135844	6	32
chr2_11.340019	6	6	chr2_1.949	6	19	chr2_10.531455	6	32
chr2_11.36242	6	6	chr2_5.94454	6	19	chr2_10.135873	6	32
chr2_4.803325	6	6	chr2_1.948843	6	19	chr2_10.135978	6	32
chr2_4.827898c	6	6	chr2_5.944551	6	20	chr2_10.532927	6	32
chr2_11.953234	6	9	chr2_5.970519	6	20	chr2_9.994994	6	32
chr2_11.953256	6	9	chr2_5.970529	6	20	chr4_7.720808	6	32
chr2_1.330128	6	11	chr2_5.970562	6	20	chr2_10.531353	6	32
chr2_11.010156	6	11	chr2_5.97057	6	20	chr2_3.285053	6	32
chr4_31.779923	6	11	chr2_5.970646	6	20	chr2_7.308774	6	32
chr4_31.779892	6	11	chr2_6.245503	6	20	chr2_2.250349	6	33
chr2_5.249675	6	14	chr2_6.418102	6	20	chr2_2.250487	6	33
chr2_11.702872	6	15	chr2_6.445079	6	20	chr2_3.125281	6	33
chr2_11.702936	6	15	chr2_6.245599	6	20	chr2_3.125832	6	33
chr2_11.702938	6	15	chr2_6.304727	6	20	chr2_3.756898	6	33

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_4.337366	6	33	chr2_14.250229	6	48	chr2_18.952375	6	53
chr2_10.681647	6	33	chr2_14.532731	6	48	chr2_19.052988	6	53
chr2_3.125342	6	33	chr2_14.765857	6	48	chr2_21.390856	6	53
chr2_3.693971	6	33	chr2_14.972715	6	48	chr2_21.693089	6	53
chr2_9.216348	6	33	chr2_14.976726	6	48	chr3_30.378651	6	53
chr2_9.216428	6	33	chr2_14.765773	6	48	chr2_17.556844	6	53
chr6_34.918756	6	33	chr2_14.901787	6	48	chr2_18.047616	6	53
chr2_3.922365	6	33	chr2_15.050654	6	48	chr2_17.790167c	6	53
chr2_9.184282	6	33	chr2_15.051366	6	48	chr2_17.790184c	6	53
chr2_9.486087	6	33	chr2_15.425902c	6	48	chr2_17.7902c	6	53
chr3_9.063234	6	33	chr2_15.426898c	6	48	chr2_17.790205c	6	53
chr2_4.633461c	6	33	chr2_14.972658	6	48	chr2_17.832217	6	53
chr7_10.933577	6	33	chr2_21.84121	6	49	chr2_18.0475c	6	53
chr2_13.119946	6	35	chr2_13.943094	6	49	chr2_15.426889	6	53
chr2_13.494157	6	35	chr2_13.972874	6	49	chr2_21.841208	6	53
chr2_13.249464	6	36	chr2_14.340422	6	49	chr2_17.239957	6	55
chr2_9.184693	6	38	chr2_14.633358	6	49	chr2_17.24005	6	55
chr2_9.486013	6	38	chr2_14.76582	6	49	chr2_17.034695	6	57
chr7_10.93348	6	38	chr2_14.95881	6	49	chr2_17.106194	6	57
chr2_14.785022	6	41	chr2_14.972659	6	49	chr2_17.239954	6	57
chr2_14.78504	6	41	chr2_15.148692	6	49	chr2_17.106326c	6	57
chr2_14.901714	6	41	chr2_15.20857	6	49	chr2_17.106329c	6	57
chr2_14.90176	6	41	chr2_15.426786	6	49	chr2_16.843021	6	58
chr2_15.426851	6	41	chr2_15.426876	6	49	chr2_17.106221	6	58
chr2_13.119851	6	42	chr2_15.590775	6	49	chr2_17.106386	6	58
chr2_13.469506	6	42	chr2_15.656356	6	49	chr2_16.441156	6	58
chr2_13.494187	6	42	chr2_15.425978c	6	49	chr2_16.441018	6	58
chr2_17.859885	6	43	chr2_15.644889	6	51	chr2_16.44103	6	58
chr2_13.488901	6	43	chr2_15.696245	6	51	chr2_16.441108	6	58
chr2_13.97291	6	43	chr2_18.164901c	6	52	chr2_18.267204	6	58
chr2_14.340485	6	43	chr2_18.164943	6	52	chr2_18.294865	6	59
chr2_13.972958	6	43	chr2_17.790181	6	53	chr2_18.469813	6	61
chr2_14.34056	6	45	chr2_17.79019	6	53	chr2_18.55581	6	61
chr2_13.119995	6	48	chr2_17.790252	6	53	chr2_22.17719	6	62
chr2_13.249608	6	48	chr2_17.790193c	6	53	chr2_17.106347	6	63
chr2_13.494133	6	48	chr2_17.790202c	6	53	chr2_17.10644	6	63
chr2_13.675584	6	48	chr2_20.896474	6	53	chr2_17.239977	6	63
chr2_13.675643	6	48	chr2_21.380622	6	53	chr2_17.240048	6	63
chr2_13.943089	6	48	chr2_14.784953	6	53	chr2_16.843031	6	64
chr2_13.972922	6	48	chr2_17.666156	6	53	chr2_16.843067	6	64

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_16.874554	6	64	chr2_21.230882	6	70	chr2_21.843117	6	78
chr2_16.695571c	6	64	chr2_21.231029	6	70	chr2_22.01726	6	78
chr2_28.34139	6	64	chr2_20.497457	6	70	chr2_22.103353	6	78
chr2_28.59198	6	64	chr2_20.497466	6	70	chr2_22.18406	6	78
chr2_24.585006	6	65	chr2_20.497565	6	70	chr2_27.384549	6	78
chr2_18.267205	6	66	chr2_20.697599	6	70	chr2_28.563499	6	78
chr2_18.458047	6	66	chr2_20.775521	6	70	chr2_22.279852	6	78
chr2_18.469778	6	66	chr6_30.858031	6	70	chr2_27.106488	6	78
chr2_18.522509	6	66	chr2_20.53017c	6	70	chr2_27.106572	6	78
chr2_18.900138	6	66	chr2_20.62179	6	70	chr2_27.220657c	6	78
chr2_18.464122	6	66	chr2_20.621921c	6	70	chr2_27.624457	6	79
chr2_18.555884	6	66	chr2_20.621927c	6	70	chr2_27.657306c	6	79
chr2_18.55769	6	66	chr2_20.77553c	6	71	chr2_21.3912	6	82
chr2_18.9002	6	66	chr2_20.880527	6	71	chr2_27.987966	6	82
chr2_18.555809	6	66	chr2_21.207918c	6	71	chr2_28.01983	6	82
chr2_18.557623	6	66	chr2_21.649969	6	71	chr2_28.046836	6	82
chr2_28.056693	6	67	chr2_21.843312c	6	71	chr2_28.465696	6	82
chr2_19.052872	6	68	chr2_21.649972	6	72	chr2_28.6202	6	82
chr2_19.052925	6	68	chr2_27.34915	6	72	chr2_28.658488	6	82
chr2_19.052861c	6	68	chr2_27.349152	6	72	chr2_22.17077	6	82
chr2_28.019885	6	68	chr2_20.873439	6	73	chr2_22.177298	6	82
chr2_19.35846c	6	69	chr2_20.878211	6	73	chr2_27.987994	6	82
chr2_19.534463	6	69	chr2_20.881385	6	73	chr2_28.019879	6	82
chr2_19.598876	6	69	chr2_21.23102	6	73	chr2_28.041467	6	82
chr2_19.605786	6	69	chr2_21.490313	6	73	chr2_28.041695	6	82
chr2_19.750382	6	69	chr2_21.806912	6	73	chr2_28.041839	6	82
chr2_20.26184	6	69	chr2_21.808213	6	73	chr2_28.046701	6	82
chr2_20.296403	6	69	chr2_20.880422c	6	73	chr2_28.046851	6	82
chr2_19.598747c	6	69	chr2_21.380592	6	75	chr2_28.465742c	6	83
chr2_19.598852c	6	69	chr2_21.808225	6	75	chr2_28.592051c	6	83
chr2_19.53446	6	69	chr2_21.80828	6	75	chr2_28.620281	6	83
chr2_19.706908	6	70	chr2_28.658517	6	75	chr2_28.620283	6	83
chr2_19.750277	6	70	chr2_28.620278c	6	75	chr2_27.624581c	6	85
chr2_19.949491	6	70	chr2_21.841224c	6	75	chr2_27.206317	6	86
chr2_20.126052	6	70	chr2_22.177259	6	76	chr2_27.244168	6	86
chr2_20.529991	6	70	chr2_27.206423	6	77	chr2_27.34911	6	86
chr2_20.604056	6	70	chr2_27.22064	6	77	chr2_27.384565	6	86
chr2_20.697564	6	70	chr2_21.841255	6	77	chr2_27.505821	6	86
chr2_20.878249	6	70	chr2_21.848868	6	77	chr2_27.505643c	6	86
chr2_20.87834	6	70	chr2_28.675051	6	77	chr2_26.227822	6	87

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_1.837513	6	87	chr2_25.529379	6	93	chr2_24.799333	6	102
chr2_26.227857	6	87	chr2_25.529398	6	93	CL2980_LG6	6	104
chr2_26.228001	6	87	chr2_25.706236	6	93	chr2_24.501579	6	104
chr2_26.476937	6	87	chr2_25.71126	6	93	chr2_24.591805	6	104
chr2_26.476963	6	87	chr2_25.286319	6	93	chr2_24.646143	6	104
chr2_27.384735	6	87	chr2_25.286422	6	93	chr2_24.001914	6	104
chr2_27.38475c	6	87	chr2_25.600381	6	93	chr2_24.223191	6	104
chr2_27.747281	6	87	chr2_25.306917c	6	93	chr2_24.412118	6	104
chr2_26.77842c	6	87	chr2_25.312193c	6	93	chr2_24.626366	6	104
chr2_27.229587c	6	87	chr2_25.307035	6	93	chr2_24.795128	6	104
chr2_27.229593c	6	87	chr2_25.570601	6	93	chr2_24.223175c	6	104
chr2_27.349189c	6	87	chr2_25.312195c	6	93	chr2_24.223229c	6	104
chr2_27.74727c	6	87	chr2_25.312197c	6	93	chr2_24.626465c	6	104
chr2_27.747377	6	87	chr2_25.30694	6	93	chr2_24.83113	6	104
chr2_27.220718	6	87	chr2_24.412051	6	93	chr2_25.107224	6	104
chr2_27.920995	6	87	chr2_24.591842	6	93	chr2_25.111096c	6	104
chr2_26.345516	6	87	chr2_24.62641	6	93	chr2_24.412081c	6	104
chr2_26.347466	6	87	chr2_24.646116	6	93	chr2_24.626373	6	104
chr2_26.347536	6	87	chr2_24.273834	6	94	chr2_24.626417c	6	104
chr2_26.476926	6	87	chr2_24.273841	6	94	chr2_24.799377	6	104
chr2_26.62235	6	87	chr2_24.27388	6	94	chr2_24.033072	6	105
chr2_26.778402	6	87	chr2_24.033015	6	95	chr2_24.130067	6	105
chr2_26.778409	6	87	chr2_24.130025	6	95	chr2_24.008582c	6	106
chr2_27.03789	6	87	chr2_24.231875	6	95	chr2_24.008603	6	106
chr2_27.038027	6	87	chr2_22.876628	6	95	chr2_24.235513	6	106
chr2_26.345579c	6	87	chr2_23.248213	6	95	chr2_24.927698c	6	106
chr2_25.946191c	6	90	chr2_23.449751	6	95	chr2_23.885495	6	106
chr2_26.005039	6	90	chr2_23.44995	6	95	chr2_24.033014	6	106
chr2_25.96824	6	90	chr2_23.822264	6	95	chr2_24.231811	6	106
chr2_25.57052	6	91	chr2_23.822327	6	95	chr2_23.449792c	6	107
chr2_25.570533	6	91	chr2_23.822395	6	95	chr2_23.44984c	6	107
chr2_25.600576	6	91	chr3_18.443116	6	95	chr2_23.381612c	6	107
chr2_25.111174	6	93	chr2_25.198478c	6	99	chr2_23.39929	6	107
chr2_25.224304	6	93	chr2_25.107069c	6	101	chr2_23.449693c	6	107
chr2_25.224352	6	93	chr2_25.111031c	6	101	chr2_23.449957	6	107
chr2_25.286312	6	93	chr2_25.111182c	6	101	chr2_23.594351	6	107
chr2_25.286467	6	93	chr2_25.111038c	6	101	chr2_0.264419	6	108
chr2_25.312202	6	93	chr2_25.111043c	6	101	chr2_23.303524	6	108
chr2_25.312213	6	93	chr2_25.111084	6	101	chr2_23.38152	6	108
chr2_25.312219	6	93	chr2_24.799219	6	102	chr2_22.876667	6	109

Appendix 3. Continued

ICD								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_18.443098	6	109	chr5_9.370231c	7	8	chr5_7.678127c	7	24
chr2_23.248062c	6	109	chr5_9.433505c	7	8	chr5_6.804396	7	26
chr2_23.248144c	6	109	chr5_8.890938c	7	8	chr5_6.804483	7	26
chr5_23.191635	7	0	chr5_9.387827c	7	8	chr5_7.379825	7	26
chr5_23.191688	7	0	chr5_9.040208c	7	8	chr5_7.677984	7	26
chr5_23.191733	7	0	chr5_9.370183c	7	8	chr5_8.056821	7	26
chr5_23.191701c	7	0	chr5_9.249829c	7	9	chr2_27.350163	7	26
RMS043_LG7	7	2	chr5_9.387917	7	9	chr5_6.848931	7	26
chr5_10.007421c	7	2	chr5_9.387902c	7	9	chr2_27.350177	7	30
chr5_10.00788c	7	2	chr5_9.370173	7	13	chr2_27.350319	7	30
chr5_10.094031	7	2	chr5_9.370225	7	13	chr5_6.672327	7	30
chr5_10.132037c	7	2	chr5_9.387923	7	13	chr5_7.162182	7	30
chr5_10.141077	7	2	chr5_9.431907c	7	13	chr2_27.350248	7	30
chr5_10.682864	7	2	chr5_9.431909c	7	13	chr3_13.73016	7	30
chr5_10.007931	7	2	chr5_9.141231	7	14	chr5_5.379398	7	30
chr5_10.352899	7	2	chr5_9.249778	7	14	chr5_5.678439	7	30
chr5_23.191591	7	2	chr5_8.914843c	7	15	chr5_6.12847c	7	30
chr5_23.191619	7	2	chr5_8.890932	7	16	chr5_6.128499c	7	30
chr5_10.132246c	7	2	chr2_8.848225	7	17	chr5_6.804384	7	30
Rw22B6_LG7	7	6	chr5_8.686755	7	17	chr5_6.804403	7	30
chr5_10.132242c	7	6	chr5_8.626804	7	17	chr5_6.804405	7	30
chr5_8.626905	7	6	chr5_8.672065	7	17	chr5_22.550855	7	30
chr5_8.6719	7	6	chr5_9.061762	7	17	chr5_3.180386	7	30
chr5_8.686768	7	6	chr5_8.708276c	7	17	chr5_3.180388	7	30
chr5_8.68689	7	6	chr5_8.39521	7	19	chr5_3.495738	7	30
chr5_8.890845	7	6	chr5_8.348061	7	20	chr5_4.243693	7	30
chr5_8.908206c	7	6	chr5_8.35421	7	20	chr5_4.30626	7	30
chr5_8.914751	7	6	chr5_7.723511c	7	21	chr5_4.461665	7	30
chr5_9.508023	7	6	chr5_8.056854	7	21	chr5_4.461692	7	30
chr5_9.881391	7	6	chr5_8.21139	7	21	chr5_4.638552	7	30
chr5_9.911991c	7	6	chr5_8.211443c	7	21	chr5_4.73751	7	30
chr5_9.922619	7	6	chr5_7.72349	7	22	chr5_4.737511	7	30
chr5_9.983661	7	6	chr5_6.959854	7	22	chr5_4.766085	7	30
chr5_9.994374c	7	6	chr5_7.227087	7	23	chr5_4.766091	7	30
chr5_9.433571	7	6	chr5_7.723451	7	23	chr5_4.78516	7	30
chr5_9.433601	7	6	chr5_7.227119	7	23	chr5_5.037526	7	30
chr5_9.488542	7	6	chr5_7.379798	7	23	chr5_5.03758	7	30
chr5_9.690679	7	6	chr5_7.707963	7	23	chr5_5.037583	7	30
chr5_8.627009	7	8	chr5_7.379853c	7	23	chr5_5.037586	7	30
chr5_9.17276c	7	8	chr5_7.723982c	7	23	chr5_5.03759	7	30

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_5.061345	7	30	chr5_4.490021c	7	40	chr5_1.861167c	7	56
chr5_5.161795	7	30	chr5_4.766226c	7	40	chr5_1.86118c	7	56
chr5_5.226128	7	30	chr5_4.490059	7	40	chr5_2.003732	7	56
chr5_5.60031	7	30	chr5_4.438173	7	40	chr5_2.018709	7	56
chr5_5.600325	7	30	chr5_3.367913	7	42	chr5_2.411625c	7	56
chr5_5.612412	7	30	chr5_3.558407c	7	42	chr5_3.042214	7	56
chr5_6.066587	7	30	chr5_3.874056	7	43	chr5_0.926925	7	58
chr5_6.513726	7	30	chr4_24.576999c	7	44	chr5_1.202761c	7	58
chr5_6.680437	7	30	chr5_3.623275	7	44	chr5_1.407213c	7	58
chr5_6.71227	7	30	chr5_3.682165	7	44	chr5_1.090909c	7	58
chr5_7.009711	7	32	chr5_2.972791c	7	45	chr5_0.92704	7	59
chr7_6.019372	7	32	chr5_2.97298	7	45	chr5_1.933062c	7	59
chr7_6.019419	7	32	chr3_4.920557c	7	48	chr5_0.05375	7	62
chr5_6.128112c	7	33	chr5_2.727743	7	48	chr5_0.110605	7	62
chr5_6.712208	7	33	chr5_2.972771	7	48	chr5_0.524338c	7	62
chr5_6.804377	7	33	chr5_2.909303	7	48	chr5_0.667359	7	62
chr1_13.372489	7	34	chr5_2.909339	7	48	chr5_0.801544c	7	62
chr5_5.973255	7	34	chr5_3.349344c	7	48	chr5_1.933083c	7	62
chr5_6.066563	7	34	chr5_2.792707c	7	49	chr5_0.110598	7	62
chr1_13.372515	7	34	chr4_10.569954	7	50	chr5_0.259809	7	62
chr5_5.410602c	7	35	chr5_2.018785c	7	50	chr5_0.475189	7	62
chr5_5.600425	7	35	chr5_2.018838c	7	50	chr5_0.475351c	7	62
chr5_4.638577c	7	36	chr5_2.069239	7	50	chr5_0.52447	7	62
chr5_4.739302c	7	36	chr5_2.239591c	7	50	chr5_0.66742	7	62
chr5_4.737501c	7	36	chr5_2.909445	7	50	chr5_0.667556	7	62
chr5_5.244962	7	36	chr5_3.366289	7	50	chr5_0.710475	7	62
chr5_5.612507	7	36	chr5_2.972737c	7	51	chr5_10.963063	7	62
chr5_5.678322	7	36	chr5_3.042158	7	51	chr5_11.080941	7	62
chr5_5.678455	7	36	chr5_2.411627c	7	52	chr5_0.475123c	7	62
chr5_5.037482	7	36	chr5_1.825825	7	53	chr5_0.475269	7	62
chr5_5.410683c	7	36	chr5_1.860992	7	53	chr5_0.626796	7	62
chr5_4.785243	7	37	chr5_1.861	7	53	chr5_0.710184	7	62
chr5_5.161752c	7	37	chr5_1.881454	7	53	chr5_0.722916	7	62
chr5_5.161854c	7	37	chr5_1.861049	7	53	chr5_0.927025	7	62
chr5_5.612502	7	37	chr5_1.932987c	7	54	chr5_1.131479	7	62
chr5_4.739272	7	38	chr5_1.861007c	7	56	chr5_1.131484	7	62
chr5_4.243755	7	40	chr5_1.861115	7	56	chr5_1.202728	7	62
chr5_4.306304	7	40	chr5_1.881442	7	56	chr5_1.476786	7	62
chr5_4.489986	7	40	chr4_10.569959	7	56	chr5_0.626661c	7	62
chr5_5.379243	7	40	chr5_1.861128c	7	56	chr5_0.787991	7	62

Appendix 3. Continued

ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_0.054712c	7	62	chr5_11.140564c	7	75	chr5_15.434358	7	85
chr5_0.110541	7	62	chr5_0.259815c	7	75	chr5_12.804034c	7	85
chr5_0.363666	7	62	chr5_0.295223	7	75	chr3_23.543928	7	88
chr5_10.963069	7	63	chr5_0.054557	7	75	chr3_23.544018	7	88
chr5_0.710208c	7	63	chr5_0.053647	7	76	chr5_11.640243	7	88
chr5_0.801187c	7	63	chr5_0.05471	7	76	chr5_12.390399	7	88
chr5_1.476795	7	63	chr5_0.6267	7	77	chr4_14.967439	7	88
chr5_0.040345	7	63	chr5_10.963072	7	77	chr5_15.295584c	7	90
chr5_10.962992	7	63	chr5_11.08108	7	77	Rw5G14_LG7	7	95
chr5_11.055686	7	63	chr5_11.140567	7	77	chr5_11.64726	7	95
chr6_18.094515	7	63	chr5_11.14057	7	77	chr5_11.704311	7	95
chr5_0.240038	7	63	chr5_11.081096	7	77	chr5_12.067125	7	95
chr5_0.363613	7	63	chr5_11.081111	7	77	chr5_12.067145	7	95
chr5_0.368219	7	63	chr5_12.804039c	7	82	chr5_12.197963	7	95
chr5_0.380629	7	63	chr5_11.429368	7	84	chr5_14.17974	7	95
chr5_0.389442	7	63	chr5_11.429381	7	84	chr5_15.690422	7	95
chr5_0.098223	7	65	chr2_12.639387	7	85	chr5_19.831037	7	95
chr5_11.107612	7	66	chr5_12.731093c	7	85	chr5_20.023494	7	95
chr5_11.107679	7	66	chr5_13.064302	7	85	chr5_20.023579	7	95
chr5_11.141223	7	66	chr2_12.639404c	7	85	chr1_12.746504c	7	95
chr5_11.429377	7	66	chr3_2.011477c	7	85	chr5_18.540035	7	95
chr5_11.140558	7	66	chr5_0.053707	7	85	chr5_14.179643	7	95
chr5_0.054614c	7	71	chr5_11.543543	7	85	chr5_15.295664	7	95
chr5_0.098049	7	71	chr5_11.704197	7	85	chr4_2.910806	7	98
chr5_13.211011c	7	71	chr5_12.696572	7	85	chr4_2.910816	7	98
chr5_0.253532	7	71	chr5_12.731069c	7	85	chr5_14.067751	7	98
chr5_0.295134	7	71	chr5_12.731079c	7	85	chr5_14.191365	7	98
chr5_0.380678	7	71	chr5_12.731085c	7	85	chr5_14.191438	7	98
chr5_0.475009	7	71	chr5_12.731086c	7	85	chr5_11.704284	7	98
chr5_0.47536c	7	71	chr5_12.731087c	7	85	chr5_14.067637c	7	98
chr5_0.475297c	7	71	chr5_12.731108c	7	85	chr5_14.06793	7	99
chr5_0.368279c	7	72	chr5_12.7312c	7	85	chr5_19.391871c	7	101
chr5_0.040337c	7	75	chr5_13.064149c	7	85	chr3_18.743967	7	103
chr5_0.368309	7	75	chr5_14.643872	7	85	chr3_5.979525	7	103
chr5_0.801526	7	75	chr5_14.711678	7	85	chr3_5.979537	7	103
chr5_1.091401	7	75	chr5_15.152198c	7	85	chr4_2.910773	7	103
chr5_11.081098	7	75	chr5_11.55092	7	85	chr5_14.067619	7	103
chr5_0.801171	7	75	chr5_11.704278	7	85	chr5_14.067625	7	103
chr5_11.079223	7	75	chr5_13.0642c	7	85	chr5_14.067757	7	103
chr5_11.107685	7	75	chr5_15.295629c	7	85	chr5_16.951662	7	103

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ICD

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_19.391919	7	103	chr5_20.185009	7	120	chr6_10.847183	7	134
chr5_19.391883	7	103	chr5_20.185014	7	120	chr5_22.321321c	7	134
chr5_19.39188c	7	103	chr5_20.185016	7	120	chr5_22.414727c	7	134
chr5_17.849605c	7	105	chr5_20.185018	7	120	chr5_25.163078c	7	134
chr4_24.271811c	7	106	chr5_20.185022	7	120	chr5_26.310193	7	134
chr5_16.760635	7	106	chr5_20.185025	7	120	chr5_26.372387	7	134
chr5_16.760653c	7	106	chr5_20.185032	7	120	chr5_5.218505c	7	136
chr5_16.951673c	7	106	chr5_20.185045	7	120	chr5_24.225987	7	137
chr5_12.390393	7	109	chr5_20.579721c	7	120	chr5_22.743561c	7	138
chr5_17.261728c	7	109	chr5_20.332037c	7	120	chr5_22.321269c	7	139
chr5_16.555027c	7	111	chr5_20.332095	7	120	chr5_22.414793	7	139
chr5_16.80285c	7	111	chr5_20.746986	7	121	chr5_24.046085	7	139
chr5_19.391751c	7	111	chr3_32.662843c	7	122	chr5_24.168493	7	139
chr5_11.543685	7	112	chr5_20.579745c	7	122	chr5_24.351493c	7	139
chr5_17.586283	7	112	chr5_20.746975c	7	123	chr5_24.168277	7	139
chr5_16.555025c	7	112	chr1_2.622835	7	125	chr5_22.414823c	7	139
chr5_17.521174c	7	112	chr4_20.733934	7	125	RMS003_LG7	7	140
chr5_17.521236c	7	112	chr5_21.864898	7	125	chr4_10.569793c	7	144
chr5_17.586475	7	112	chr7_10.933579	7	125	chr4_10.569787c	7	144
chr5_17.586455c	7	112	chr5_21.864814c	7	125	chr4_10.569749c	7	144
chr5_17.261523c	7	112	chr5_21.86488c	7	125	chr4_10.569723c	7	144
chr1_12.746465	7	112	chr7_10.933525c	7	125	chr4_10.569712c	7	145
chr5_18.155373c	7	112	chr7_10.933544c	7	125	chr4_10.569725c	7	145
chr5_18.539969	7	113	chr4_27.571125	7	126	chr5_24.351542	7	145
Rh72_LG7	7	115	chr4_27.571075	7	127	chr4_10.569785c	7	145
chr3_1.412842	7	115	chr4_27.571114c	7	127	chr4_10.569742c	7	145
chr5_18.28172	7	118	RMS001_LG7	7	130	chr3_2.011494	7	146
chr5_18.540047	7	118	chr5_22.127936c	7	133	chr4_10.569714c	7	146
chr5_19.830985	7	119	chr5_22.12794c	7	133	chr5_24.684607	7	146
chr5_19.83114c	7	119	chr5_23.601754	7	133	chr5_24.714243	7	146
chr5_19.831198c	7	119	chr5_23.60183	7	133	chr5_25.163199c	7	146
chr2_23.649136c	7	120	chr2_22.177116	7	134	chr5_26.07622	7	146
chr5_17.261396	7	120	chr3_2.011499	7	134	chr4_10.569744c	7	146
chr5_17.586256	7	120	chr5_22.127952	7	134	chr4_10.569757c	7	146
chr5_17.586482	7	120	chr5_24.684603	7	134	chr4_10.56977c	7	146
chr5_17.78595	7	120	chr5_24.846887	7	134	chr5_24.226055c	7	148
chr5_18.155355	7	120	chr5_26.042021	7	134	chr1_9.928541	7	151
chr5_19.822917	7	120	chr5_26.310326	7	134	chr1_9.928565	7	151
chr5_20.023504	7	120	chr5_3.04204	7	134	chr5_24.6846	7	151
chr5_20.080087	7	120	chr5_3.042052	7	134	chr5_25.598011	7	151

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ICD

Marker name	Linkage group	position cM
chr5_25.95567	7	151
chr5_26.336713	7	153
chr6_10.847179	7	153
chr6_10.847182	7	153
chr5_25.028373c	7	153
chr5_26.076577	7	154
chr5_26.372423	7	154
chr5_26.372339c	7	154
chr2_12.742083	7	155
chr2_12.742109	7	155
chr5_26.042126	7	155
chr5_26.968991	7	155
chr5_26.372407	7	155
chr5_26.969008c	7	155
chr5_26.969114c	7	155
chr5_27.461714	7	155
chr5_28.886042	7	155
chr5_28.886088	7	155
chr5_26.969165	7	155
chr5_27.040647	7	155
chr5_27.4618	7	155
chr5_27.040702c	7	155
chr5_27.253792	7	155
chr5_26.336871	7	155
chr5_26.968946	7	155
chr5_26.969096	7	155
chr5_26.964228c	7	155
chr5_26.96924c	7	155
chr5_27.25375	7	155
chr5_27.492158c	7	156
chr5_27.735163	7	157
chr5_24.943667c	7	158
chr5_27.990037	7	158
chr5_27.990251	7	158
chr4_24.107276c	7	159
chr5_28.458804	7	159
chr5_27.990199	7	160
chr5_27.990212	7	160
chr5_28.55575	7	162
chr5_6.572694	7	162
chr5_26.003287	7	164
chr5_26.050245	7	164
chr5_28.555792	7	164
chr5_6.572759	7	164
chr5_26.061239	7	164
chr5_28.656597	7	166
chr5_28.902462	7	166
chr5_28.902564c	7	166
chr5_28.902591	7	166
chr5_28.914204	7	166
chr5_28.914328	7	166
chr5_28.914192	7	167
chr5_28.914366c	7	167

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_2.370299	1	0	chr3_18.737227	1	17	chr7_16.759927c	1	30
chr4_20.800379	1	0	chr2_1.981716	1	17	chr7_16.480821	1	30
chr7_2.241421	1	1	chr7_11.905757	1	19	chr7_16.760018c	1	30
chr7_4.587218	1	3	chr7_10.385832c	1	19	chr7_17.450961c	1	30
chr7_4.24078	1	4	chr7_16.540347	1	19	chr7_16.672862	1	30
chr3_3.021336	1	4	chr7_11.608351	1	19	chr7_16.480824	1	30
chr7_4.240779	1	4	chr7_12.365556	1	21	chr4_31.097061c	1	30
chr7_4.3235	1	4	chr7_14.32919	1	22	chr7_16.760041c	1	30
chr7_4.146431	1	4	chr7_12.978062	1	22	chr7_17.610816	1	31
RhAB9-2_LG1	1	4	chr2_15.167105	1	22	chr7_17.611871	1	31
chr1_10.368513	1	7	chr7_13.787818	1	23	chr7_17.450917	1	31
chr7_6.019394	1	7	chr7_13.921956	1	23	chr7_17.479367c	1	33
chr7_5.726635	1	7	chr7_13.104378	1	23	chr7_17.773696	1	33
chr7_6.019389	1	7	chr7_14.615681	1	23	chr7_17.479411	1	33
chr7_14.651673	1	7	chr7_13.10445	1	23	chr7_17.47942	1	33
chr7_5.856382	1	7	chr7_14.616699c	1	23	chr7_17.773514	1	33
chr7_5.856391	1	7	chr7_13.787704	1	23	chr7_17.773561	1	33
chr4_10.812806	1	9	chr7_12.917607	1	23	chr7_17.901675	1	33
chr7_6.924247	1	9	chr7_14.616781	1	24	chr7_18.207597	1	33
chr7_6.924305	1	9	chr7_15.044078c	1	24	chr7_18.71384	1	34
chr7_7.531798	1	9	chr7_14.622347	1	24	chr7_18.376963	1	34
chr7_7.531744	1	9	chr7_14.329158	1	24	chr7_18.667305c	1	34
chr7_6.373067	1	10	chr7_13.921851	1	26	chr7_18.627984	1	34
chr5_0.631568c	1	12	chr7_15.199669	1	26	chr7_18.633285	1	34
chr7_7.52622	1	14	chr7_15.370485c	1	26	chr7_18.628064	1	34
chr7_7.526217	1	14	chr7_15.630095	1	26	chr7_18.467426	1	34
chr7_11.016096	1	14	chr7_15.630106	1	26	chr7_18.141394	1	36
chr7_9.552873	1	15	chr7_15.169627	1	26	chr7_18.415579	1	36
chr7_9.567675	1	15	chr7_15.083224	1	26	chr7_18.415693	1	36
chr7_8.994483	1	15	chr7_15.395736c	1	26	chr7_18.415494	1	36
chr7_7.996817c	1	15	chr7_9.786157c	1	27	chr7_18.971362	1	37
chr7_9.153824	1	15	Rw34L6_LG1	1	27	chr7_20.786202	1	39
chr7_8.283597c	1	15	chr7_15.86556c	1	27	chr7_19.443674c	1	39
chr7_9.385112	1	15	chr7_15.865401	1	27	chr7_19.5336	1	39
chr3_3.021324	1	15	chr5_25.539452	1	28	chr5_24.046133	1	39
chr7_9.567824c	1	15	chr7_16.540325	1	28	chr7_19.383104	1	39
chr7_9.567817c	1	15	chr7_16.480836	1	28	chr7_20.649892c	1	39
chr7_9.567815c	1	15	chr7_16.247829c	1	28	chr7_19.396709c	1	39
chr7_8.768061	1	17	chr7_16.690213	1	28	chr7_20.904278	1	39
chr2_5.001299	1	17	chr5_25.5394	1	28	chr7_19.414384c	1	39

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_20.942895	1	39	chr7_21.770245	1	43	chr1_1.027988	2	0
chr7_20.804926	1	39	chr7_21.654196	1	43	chr1_1.569677	2	1
chr7_20.086723	1	39	chr7_21.770321	1	43	chr1_1.580312	2	1
chr7_19.312222c	1	39	chr4_32.176379	1	43	chr1_1.528282	2	1
chr7_20.645311c	1	39	chr7_22.043139	1	45	chr1_1.569737	2	1
chr3_0.357758	1	39	chr7_21.935196	1	45	chr1_2.077982c	2	2
chr5_24.046221	1	39	chr7_22.422059	1	45	chr1_2.180944	2	2
chr7_18.971407	1	39	chr7_23.206113	1	45	chr1_2.318584	2	2
chr7_20.786106	1	39	chr7_21.915361	1	45	chr1_2.144357c	2	2
chr7_18.472244	1	39	chr7_22.043022	1	45	chr1_2.14475c	2	2
chr7_20.649751c	1	39	chr7_22.043131	1	45	chr1_2.144306c	2	2
chr7_20.645228c	1	39	chr7_22.042996	1	45	chr1_2.100003	2	2
chr7_19.741411c	1	39	chr7_21.935157	1	45	chr1_1.90051	2	2
chr7_19.533588	1	39	chr7_22.043164	1	45	chr1_2.100006	2	2
H5_F12_LG1	1	39	chr7_22.422141	1	46	chr1_2.144735c	2	2
chr7_19.443696c	1	39	chr7_22.422036	1	46	chr1_2.077827c	2	2
chr7_19.373724c	1	39	chr2_12.63942	1	46	chr1_2.776959	2	6
chr7_19.741362c	1	39	chr7_22.316197	1	46	chr1_2.690475c	2	6
chr7_20.737535	1	39	chr7_22.840457	1	49	chr1_2.475041	2	6
chr7_19.939473c	1	39	chr7_23.206126	1	49	chr1_2.776934c	2	6
chr7_19.939297c	1	39	chr7_23.037789	1	49	chr1_2.896982	2	6
chr7_19.373763	1	39	chr7_22.739119	1	49	chr1_3.034574	2	6
chr7_19.396733c	1	39	chr7_23.013217	1	49	chr1_2.736407c	2	6
chr7_21.068173	1	40	chr7_23.013171	1	49	chr1_2.498949c	2	6
chr7_20.942885	1	40	chr7_23.351973	1	50	chr1_2.695716c	2	6
chr7_21.068143	1	40	chr7_23.489476	1	50	chr1_2.736343	2	6
chr5_24.046184	1	40	chr7_23.602528	1	50	chr1_2.521732c	2	6
chr7_21.548604	1	41	chr1_10.981881	1	50	chr1_2.340835c	2	6
chr7_21.564376	1	41	chr7_23.440975	1	50	chr1_2.521723c	2	6
chr5_11.923707	1	41	chr1_1.39466c	2	0	chr1_2.686715	2	6
chr7_21.162359	1	41	chr1_0.821632	2	0	chr1_2.475043	2	6
chr5_11.923669	1	41	chr1_1.394796	2	0	chr1_3.435488	2	9
chr7_21.162281	1	41	chr1_0.974818c	2	0	chr1_3.152825	2	9
chr7_21.564373	1	43	chr1_0.553644	2	0	chr1_2.896456	2	9
chr7_21.726369	1	43	chr1_1.937062	2	0	chr1_2.86597	2	9
chr7_21.606193	1	43	chr1_1.900678	2	0	chr1_3.775467	2	10
chr7_21.654273	1	43	chr1_1.452151	2	0	chr1_3.735119	2	10
chr7_21.915396	1	43	chr1_1.359534	2	0	chr1_3.03454	2	12
chr7_21.564253	1	43	chr1_1.452077	2	0	chr1_3.03039	2	12
chr7_21.654243	1	43	chr1_1.359387	2	0	chr1_4.229476	2	13

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_4.229559	2	13	chr1_15.854827	2	24	chr1_15.85486c	2	26
chr1_4.197269c	2	13	chr1_10.672085c	2	24	chr1_19.10605	2	27
chr1_3.983543	2	13	chr1_7.513082	2	24	chr1_7.847513c	2	27
chr1_4.206668c	2	13	chr1_8.138587c	2	24	Rh48_LG2	2	28
chr1_4.684388c	2	15	chr1_7.847496	2	24	chr1_16.466634	2	31
chr1_4.354759	2	15	chr1_11.575545	2	24	chr1_12.740688c	2	34
chr1_4.492677	2	15	chr1_11.644234	2	24	chr6_20.425868c	2	34
chr1_4.684316c	2	15	chr1_11.74884c	2	25	chr6_20.532514	2	34
chr1_4.206617	2	17	chr1_10.61245	2	25	chr6_20.486507c	2	34
chr1_4.197258c	2	17	chr1_10.672086	2	25	chr6_21.065036	2	34
chr1_4.206615	2	17	chr1_19.227311c	2	25	chr6_20.640376c	2	34
chr1_4.684301c	2	19	chr1_10.495583c	2	25	chr6_20.14417c	2	34
chr1_4.684358c	2	19	chr1_18.201755c	2	25	chr6_20.640381c	2	34
chr1_4.206683c	2	19	chr1_16.994883	2	25	chr6_20.530748	2	34
chr1_5.533343c	2	19	chr1_11.664678c	2	25	chr6_20.532456c	2	34
chr1_5.396793c	2	19	chr1_10.495594	2	25	chr6_21.427168	2	35
chr1_5.502625c	2	19	chr1_10.137365	2	25	chr6_21.42716	2	35
chr1_5.502691c	2	19	chr1_10.321864c	2	25	chr6_21.519907	2	35
chr1_6.042708c	2	20	chr1_10.449852c	2	25	chr6_22.200336c	2	35
chr1_5.793824c	2	20	chr1_10.111581c	2	25	chr6_22.020181c	2	35
chr1_6.07063c	2	20	chr1_10.532371	2	25	chr6_21.444451	2	35
chr1_5.533339c	2	20	chr1_11.748699	2	25	chr6_22.30561	2	35
chr1_4.923067	2	20	chr1_10.053335	2	25	chr6_21.334726	2	35
chr1_5.396723c	2	20	chr1_9.790204	2	25	chr6_22.020306c	2	36
chr1_10.924711	2	22	chr1_10.11165c	2	25	chr6_22.200502c	2	38
chr1_6.290499	2	22	chr1_10.111551	2	25	chr6_22.305615c	2	38
chr1_6.672413	2	22	chr1_18.223722c	2	25	chr6_23.898748c	2	39
chr1_6.18483c	2	22	chr1_10.672126c	2	25	chr6_22.963925c	2	39
chr1_6.672308	2	22	chr1_10.495619	2	25	chr6_24.333528	2	40
chr1_6.18475	2	22	chr1_11.748807c	2	25	chr6_24.333503c	2	40
chr1_15.479951c	2	22	chr1_11.050002	2	25	chr6_26.877926	2	40
chr1_19.106089c	2	22	chr1_17.573105c	2	25	chr6_24.983034	2	40
chr1_9.504632c	2	22	chr1_17.33801	2	25	chr6_25.012785	2	40
chr1_6.907091	2	22	chr1_17.2773	2	25	chr6_23.501479c	2	40
chr1_6.690492c	2	22	chr1_15.312027c	2	25	chr6_23.501482c	2	40
chr1_6.907079	2	22	chr1_15.312024c	2	25	chr6_26.914262	2	40
chr1_10.442521c	2	23	chr1_15.312065c	2	25	chr6_26.646208c	2	40
chr1_7.150559	2	23	chr1_15.577885	2	26	chr6_12.004629	2	40
chr1_7.136566	2	23	chr1_10.924627	2	26	chr6_25.644821	2	40
chr1_18.100702c	2	24	chr1_7.507856c	2	26	chr6_25.901543	2	40

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_24.717153	2	40	chr6_29.266748	2	51	chr6_36.587183	2	64
chr6_28.379754	2	44	chr6_31.938048	2	52	chr6_36.58703	2	64
chr6_27.767203c	2	44	chr6_31.93804	2	52	chr6_36.844926c	2	67
chr6_29.139394	2	44	chr6_32.343667c	2	54	chr6_36.844858c	2	67
chr6_26.655966c	2	44	chr6_32.343677	2	54	chr6_36.931765	2	67
chr6_27.819339	2	44	chr6_32.463148	2	54	chr6_36.92355	2	67
chr6_28.373698	2	44	chr6_32.094109	2	54	chr6_37.184197	2	68
chr6_28.68184c	2	44	chr6_32.094013c	2	54	chr6_37.184163	2	68
chr6_29.098355c	2	47	chr6_32.390975	2	54	chr6_37.267017	2	68
chr6_29.639712	2	47	chr6_32.918427	2	55	chr6_37.184182	2	68
chr6_29.107758	2	47	chr6_32.918422	2	55	chr6_37.267002	2	68
chr6_29.139545	2	47	chr6_32.918435	2	55	chr6_37.266958	2	71
chr6_29.150396	2	47	chr6_33.233579c	2	56	chr6_37.539993	2	73
chr6_29.154771c	2	47	chr6_32.975416	2	57	chr6_37.801035c	2	73
chr6_29.149748	2	47	chr6_33.335438	2	57	chr6_37.800994	2	73
chr6_29.149836c	2	47	chr6_33.53129	2	57	chr6_37.899406	2	73
chr6_29.518627	2	48	chr6_33.531378	2	57	chr6_38.318259	2	75
chr6_29.107698	2	48	chr6_33.526076	2	57	chr6_38.318397	2	75
chr6_27.839204	2	48	chr6_33.531386c	2	57	chr6_38.31838	2	75
chr6_30.967032c	2	48	chr6_33.531387c	2	57	chr6_38.318325	2	75
chr6_26.118652	2	48	chr6_34.20963	2	59	chr6_0.106957c	3	0
chr6_15.095346	2	48	chr6_34.004709	2	59	chr6_0.288153c	3	0
chr6_27.390168	2	48	chr6_34.506658	2	60	chr6_0.242596	3	0
chr6_30.957319	2	48	chr6_34.506623	2	60	chr6_0.861943	3	0
chr6_31.699646	2	48	chr6_34.546062	2	60	chr6_0.106927	3	0
chr6_31.625738	2	48	chr6_34.506673	2	60	chr6_0.861922	3	0
chr6_30.845195	2	48	chr6_34.876054	2	60	chr6_0.288198	3	0
chr6_30.84518c	2	48	chr6_34.413787	2	60	chr6_0.8391	3	1
chr6_31.625698	2	48	chr6_34.506503	2	60	chr6_0.242599	3	1
chr6_31.625739	2	48	chr6_34.875992	2	60	chr6_0.288165	3	1
chr6_27.839739	2	48	chr6_35.934824	2	60	chr6_0.861928	3	2
chr6_29.0984	2	48	chr6_36.004464c	2	60	chr6_0.242617	3	2
chr6_26.656315	2	48	chr6_35.934809	2	60	chr6_0.537091	3	2
chr6_28.681842c	2	48	chr6_35.93483	2	60	chr6_0.81124	3	2
chr6_31.219476c	2	49	chr6_36.004515c	2	60	chr6_0.811177	3	2
chr6_31.219479c	2	49	chr6_35.934821	2	60	chr6_0.10684	3	2
chr6_31.954116c	2	51	chr6_35.934829	2	60	chr6_0.839095	3	2
chr6_29.412482	2	51	chr6_36.58706	2	64	chr6_0.811222	3	2
chr6_29.412458	2	51	chr6_36.587015	2	64	chr6_0.811049	3	2
chr6_29.266807	2	51	chr6_36.630291	2	64	chr6_0.861947	3	2

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_0.297877	3	2	chr6_3.272518	3	19	chr6_7.781201	3	34
chr6_1.080281	3	4	chr6_3.326319	3	19	chr6_7.702625	3	34
chr6_1.080135	3	4	chr6_3.272383	3	19	chr6_7.399185	3	34
chr6_1.482509	3	6	chr6_3.272455	3	19	chr3_27.736901	3	34
chr6_1.513705	3	7	chr6_3.690909	3	20	Rw12J12_LG3	3	34
chr6_1.42533	3	7	chr6_3.691074	3	20	chr6_8.630082	3	36
chr6_1.482547	3	7	chr6_4.053725	3	21	chr6_8.607405	3	36
chr6_1.425327	3	7	chr6_3.791085	3	21	chr6_8.724376	3	36
chr6_1.350713	3	7	chr6_3.739383c	3	21	chr6_8.951763	3	39
chr6_1.425332	3	7	chr6_4.710053	3	24	chr6_8.724436	3	39
chr6_1.350854	3	7	chr6_4.175392	3	24	chr6_8.977622	3	39
chr6_1.513783	3	7	chr6_4.231767	3	24	chr6_8.977696	3	39
chr6_1.868398	3	10	chr6_4.777808	3	24	chr6_8.977642	3	39
chr6_1.86829c	3	10	chr6_4.280806	3	24	chr6_10.916245	3	39
chr6_1.974388	3	10	chr6_4.332563	3	24	chr6_9.032051c	3	40
chr6_1.975171	3	10	chr6_4.332487	3	24	chr6_9.113612	3	40
chr6_2.263162	3	10	chr6_4.332478	3	24	chr6_9.031988	3	40
chr6_2.26311	3	10	chr6_4.332525	3	24	chr6_9.354893	3	40
chr6_1.869026	3	10	chr6_4.710083	3	24	chr6_9.176797c	3	41
chr6_1.868383	3	10	chr6_4.332489	3	24	chr3_23.544367	3	41
chr6_2.263093	3	10	chr6_4.777891c	3	24	chr6_8.607372c	3	41
chr6_1.974447	3	10	Rw35C24_LG3	3	24	chr6_9.354923	3	41
chr6_2.263134	3	10	chr6_5.575539	3	26	chr6_9.32952	3	41
chr6_1.868951	3	11	chr6_5.982014	3	26	chr5_5.161425	3	43
chr6_2.844005	3	16	chr6_5.300312c	3	26	chr6_10.736859c	3	44
chr6_2.84395	3	16	chr6_6.200511	3	26	chr6_10.749852	3	44
chr6_2.844006	3	16	chr6_5.300289c	3	26	chr6_11.048559	3	44
chr6_2.96574c	3	16	chr6_6.200484	3	26	chr6_12.240181	3	46
chr6_2.965734c	3	16	chr6_5.550275	3	26	chr6_11.534	3	46
chr6_2.965689c	3	16	chr6_4.933007	3	26	chr6_12.240158	3	46
chr6_2.965657	3	16	chr6_6.200357	3	26	chr6_11.657711	3	46
chr6_2.843963	3	16	chr6_7.359523	3	29	chr6_10.557874	3	46
chr6_2.84386	3	16	chr6_6.468231	3	29	chr6_11.534044	3	46
chr6_2.963309	3	17	chr6_6.761155	3	29	chr6_14.453296	3	46
chr6_2.963175	3	17	chr6_5.442559	3	29	chr6_11.533993	3	46
chr6_3.033009	3	17	chr6_6.791664	3	29	chr6_11.409705	3	46
chr6_3.27251	3	19	chr6_6.73794	3	29	chr6_11.736975	3	46
chr6_3.581794	3	19	chr6_7.073636	3	29	chr6_11.735957	3	46
chr6_3.272499	3	19	chr6_5.982029	3	32	chr6_12.312783	3	46
chr6_3.272449	3	19	chr6_5.982031	3	32	chr6_10.46093	3	46

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_11.533989	3	46	chr1_13.372495	3	57	chr4_4.87194	4	10
chr6_11.451162	3	46	chr1_9.306703	3	57	chr4_4.872342c	4	10
chr6_12.203693	3	46	chr6_18.243495	3	57	chr4_6.705482	4	10
chr6_12.312814	3	46	chr1_13.372442	3	58	chr4_4.87236c	4	10
chr6_11.988579	3	46	chr1_22.015533	3	61	chr3_18.786753	4	12
chr6_14.684969	3	47	chr1_19.762871	3	61	chr4_5.442672	4	12
chr6_14.32699	3	47	chr1_20.19506	3	61	chr3_18.786682	4	12
chr6_17.734756	3	48	chr6_0.346436	3	61	chr3_18.786716	4	12
chr6_17.790678	3	48	chr1_19.762873	3	61	chr3_18.786699	4	12
chr6_17.765146	3	48	chr1_19.762761	3	61	chr4_13.538038c	4	15
chr6_17.519045	3	49	chr1_20.616031	3	61	chr4_13.87273c	4	15
chr6_17.519042c	3	49	chr1_20.19498	3	62	chr2_24.584943	4	15
chr6_17.519036	3	49	chr1_22.885711	3	62	chr3_0.669368c	4	15
chr6_17.765236	3	49	chr4_14.90326	3	62	chr5_12.693643c	4	15
chr1_0.630283	3	49	chr4_15.377617	3	62	chr4_13.579898	4	15
chr6_17.215238	3	50	chr6_0.346363	3	62	chr4_13.579901	4	15
chr6_17.096856	3	51	chr2_27.129849	4	0	chr4_14.265056	4	15
chr6_17.096838	3	51	chr2_27.130002	4	0	chr4_13.059825	4	15
chr6_17.281238	3	51	chr4_0.62493	4	0	chr5_12.693625	4	15
chr6_16.907939	3	51	chr4_0.603715	4	0	chr4_14.265105c	4	15
chr6_17.097003	3	51	chr4_0.624912	4	0	chr4_15.411501	4	15
chr3_3.416949	3	52	chr2_7.106283c	4	3	chr4_15.572861c	4	15
chr6_18.028841	3	53	chr2_7.10623c	4	3	chr2_24.584953	4	15
chr6_18.094868c	3	53	chr2_7.106241c	4	3	chr3_0.669366c	4	15
chr6_15.986928	3	53	chr2_7.10627c	4	3	chr4_10.903029c	4	15
chr6_18.028824	3	53	chr4_2.910829	4	6	RhABT12_LG4	4	15
chr6_15.986821	3	53	chr4_2.910568	4	6	chr4_15.244681	4	15
chr6_15.94289	3	53	chr4_2.910641	4	6	chr4_10.378789c	4	15
chr6_18.243462	3	53	chr4_2.61772c	4	6	chr4_9.711998	4	15
chr6_18.270642	3	53	chr4_13.333904c	4	9	chr2_24.584916	4	15
chr6_18.094787	3	53	chr4_10.785089	4	9	chr4_10.902858c	4	15
chr6_18.094742	3	53	chr6_5.051381	4	10	chr4_17.257739	4	16
chr6_18.664101	3	53	chr4_4.907812c	4	10	chr6_34.918843	4	18
chr1_14.272655	3	54	chr4_10.785015	4	10	chr4_14.96765	4	18
chr4_23.601554	3	55	chr4_4.680678	4	10	chr4_16.679351	4	18
chr4_23.60151	3	55	chr4_4.680803	4	10	chr4_15.551408	4	18
chr6_13.18357	3	55	chr1_3.586681c	4	10	chr4_16.679197c	4	18
chr1_14.303642	3	57	chr6_5.051434c	4	10	chr3_5.979522	4	18
chr6_18.270657	3	57	chr4_4.872345c	4	10	chr4_20.579566	4	18
chr6_15.486149	3	57	chr4_5.442548c	4	10	chr4_16.89505	4	18

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_20.231117	4	19	chr4_25.247853c	4	25	chr4_28.687601c	4	36
chr4_20.800425	4	20	chr4_25.247887c	4	25	chr4_29.136852	4	36
chr4_20.853208	4	20	chr4_25.247859c	4	25	chr4_29.386931	4	38
chr4_20.800395	4	20	chr3_6.449223	4	28	chr4_29.746049	4	38
chr4_21.108777	4	20	chr6_13.037868	4	31	chr4_29.645343	4	38
chr4_20.983941c	4	21	chr4_26.180019	4	31	chr4_29.557967	4	38
chr4_20.265456c	4	21	chr4_26.225259c	4	32	chr4_29.387028	4	38
chr4_22.013886c	4	21	chr4_26.424639	4	32	chr4_29.858953	4	40
chr4_20.265486c	4	21	chr4_24.303356	4	32	chr4_29.85895	4	40
chr4_21.108676c	4	21	chr4_26.442628	4	32	chr4_29.545529	4	42
chr4_22.384156c	4	21	chr4_26.225291c	4	32	chr4_29.54552	4	42
chr4_22.392782c	4	21	chr4_26.248412c	4	32	chr4_29.600158	4	44
chr4_22.650647	4	21	chr4_27.264891	4	32	chr4_29.691738	4	44
chr3_4.920582c	4	21	chr4_28.051206	4	32	chr4_29.422523	4	44
chr4_20.223871	4	21	chr4_26.347175c	4	32	chr4_29.387027c	4	44
chr4_20.365723c	4	21	chr4_26.312962	4	32	chr4_29.859008	4	45
chr4_16.510801	4	21	chr4_26.225404c	4	32	chr4_29.956145	4	46
chr4_22.650663	4	21	chr4_26.225406c	4	32	chr4_30.055069	4	47
chr4_22.650657	4	21	chr4_27.992125	4	32	chr4_29.956147c	4	47
chr4_22.65065	4	21	chr4_26.347188c	4	32	chr4_29.956315	4	47
chr4_22.384157c	4	21	chr4_26.770355c	4	32	chr4_29.956428	4	47
chr4_22.663694	4	21	chr4_26.225769	4	32	chr4_29.956157	4	47
chr4_22.657084	4	21	chr4_27.445737c	4	33	chr4_29.956251	4	48
chr4_23.765705	4	23	chr4_27.0985	4	33	chr4_30.111387	4	48
chr4_23.227843c	4	23	chr4_26.90022	4	33	chr4_30.309136	4	48
chr4_23.227841c	4	23	chr4_27.922625c	4	34	chr4_30.111196c	4	48
chr4_23.043144	4	23	chr4_28.051318	4	34	chr4_30.111712c	4	48
chr4_23.765657	4	23	chr4_27.99233c	4	34	chr4_30.141904	4	48
chr4_23.959241c	4	24	chr4_26.312956	4	34	chr4_30.208266c	4	48
chr4_23.895982c	4	24	chr4_24.309702	4	34	chr4_30.584234	4	48
chr4_23.959293c	4	24	chr4_27.681531c	4	34	chr4_30.370151	4	48
chr4_23.765388	4	24	chr4_27.992332c	4	34	chr4_30.142115	4	48
chr4_23.869726c	4	24	chr4_28.674719	4	34	chr4_29.849682	4	48
chr4_25.72419c	4	24	chr4_29.082433	4	34	chr4_30.583998	4	49
chr4_25.69303c	4	24	chr4_28.156441	4	34	chr4_30.675592	4	49
chr4_23.869831	4	24	chr4_28.674636	4	34	chr4_30.675543	4	49
chr4_23.959316	4	24	chr4_29.004622	4	35	chr4_30.675542	4	49
chr4_25.693131c	4	24	chr4_29.004618	4	35	chr4_30.67556	4	49
chr4_23.959311c	4	24	chr4_29.121976	4	36	chr4_30.584409	4	49
chr4_25.247845c	4	25	chr4_28.980996	4	36	chr4_30.848341c	4	51

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_31.065245	4	51	chr3_0.793639	5	3	chr3_4.535636c	5	10
chr4_30.704091	4	51	chr3_0.972174	5	3	chr3_4.606292	5	10
chr4_30.675593	4	51	chr3_0.836698	5	3	chr3_4.535513c	5	10
chr4_30.928863	4	51	chr3_1.184312	5	3	chr6_18.147322c	5	10
chr4_30.99181	4	51	chr3_1.233154c	5	4	chr3_4.687313c	5	10
chr4_30.928983	4	51	chr3_1.208568c	5	4	chr3_4.166224	5	13
chr4_30.929001	4	51	chr4_22.650557c	5	6	chr3_4.298369	5	13
chr4_31.280198	4	52	chr4_19.414226c	5	6	chr3_4.300187c	5	13
chr4_31.12036	4	52	chr4_22.650506c	5	6	chr3_4.306368	5	13
chr4_31.185885	4	52	chr3_2.696615c	5	6	chr3_4.166274	5	13
chr4_31.282675	4	52	chr4_22.650578c	5	6	chr3_4.166241	5	13
chr4_30.709461	4	52	chr4_22.650569c	5	6	chr3_3.020856	5	16
chr4_31.139869	4	52	chr4_22.65058c	5	6	chr3_2.919718c	5	16
chr4_31.77996	4	53	chr4_22.650513c	5	6	chr3_2.919818c	5	16
chr4_31.611417	4	53	chr4_22.650563c	5	6	chr3_3.115367	5	16
chr3_0.104302c	5	0	chr4_22.650584c	5	6	chr3_3.496012	5	16
chr3_0.793647c	5	0	chr3_1.553925c	5	6	chr3_2.987201	5	16
chr3_0.793655c	5	0	chr3_2.07766c	5	6	chr3_2.919842c	5	16
chr3_0.455471c	5	0	chr1_2.99782c	5	6	chr3_2.91972c	5	16
chr3_0.793654c	5	0	chr4_22.650595c	5	6	chr3_6.878892c	5	16
chr3_0.669521c	5	0	chr3_1.553938	5	6	chr3_2.919722c	5	16
chr3_0.793648c	5	0	chr4_13.334587	5	7	chr3_5.447599	5	17
chr3_0.455473c	5	0	chr4_13.334563	5	7	chr3_2.919798	5	17
chr3_0.361363	5	0	chr3_4.920436	5	7	chr3_3.013559c	5	18
chr3_0.545528c	5	0	chr3_5.051009c	5	7	chr3_6.554197c	5	18
chr3_0.25191	5	0	chr4_13.33456c	5	7	chr3_6.741765	5	18
chr3_0.405875c	5	0	chr4_13.334543c	5	7	chr3_5.902028	5	18
chr3_0.361349c	5	0	chr3_4.920622c	5	7	chr3_6.355268	5	18
chr3_0.426387c	5	1	chr3_5.0538c	5	7	chr3_6.358107	5	18
chr3_0.426408c	5	1	chr2_28.187005	5	7	chr3_2.919767c	5	18
chr3_0.426312c	5	1	chr3_5.417621	5	7	chr3_6.376784	5	18
chr3_1.133971c	5	1	chr3_4.920592c	5	7	chr3_3.548351	5	18
chr3_0.972201c	5	3	chr6_12.99266	5	9	chr3_2.919827c	5	18
chr3_0.869296c	5	3	chr3_4.298301	5	9	chr3_3.020797c	5	18
chr3_1.136064c	5	3	chr3_4.300207	5	9	chr3_3.313825c	5	18
chr3_0.869272c	5	3	chr3_4.68329	5	9	chr3_2.919721c	5	18
chr3_0.869268c	5	3	chr3_4.687361	5	9	chr3_3.36988	5	18
chr3_1.055824c	5	3	chr3_4.687372	5	10	chr3_7.904074c	5	21
chr3_0.86927c	5	3	chr3_4.791511c	5	10	chr3_8.347404	5	21
chr3_0.869271c	5	3	chr3_4.687322c	5	10	chr5_0.053509	5	26

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_18.994299	5	26	chr3_13.336658c	5	33	chr2_12.21935c	5	44
Rw14H21_LG5	5	28	chr3_12.176524	5	33	chr3_22.824667c	5	44
chr3_10.149417c	5	28	chr3_13.889605c	5	35	chr3_18.141449c	5	45
chr3_8.809414c	5	28	chr3_14.124476	5	38	chr7_10.22618c	5	45
chr3_19.783973c	5	28	chr2_12.225907c	5	41	chr3_22.007514	5	45
chr3_8.809417c	5	28	chr3_23.598381c	5	41	chr3_31.277358c	5	45
chr2_6.94522	5	28	chr4_21.23856c	5	41	chr7_14.77686	5	45
chr3_10.606961	5	29	chr3_22.397858c	5	41	chr3_22.971405c	5	45
chr7_19.300561c	5	29	chr3_22.396831	5	41	chr3_18.141451c	5	47
chr3_10.606863	5	29	chr3_22.96961c	5	41	chr7_2.574998	5	47
chr7_19.300555c	5	29	chr3_21.724107	5	41	chr3_18.141454c	5	47
chr3_18.862082c	5	29	chr3_17.480615c	5	41	chr3_18.141431c	5	47
chr3_18.504707c	5	29	chr3_22.969602c	5	41	chr3_24.387501	5	48
chr7_19.300581c	5	29	chr3_17.311876c	5	41	chr3_24.955037	5	48
chr3_18.737184c	5	29	chr3_22.007605	5	41	chr3_24.504684	5	48
chr7_19.300534c	5	29	chr3_22.059882	5	41	chr3_24.955036	5	48
chr4_8.39899c	5	29	chr3_22.059596	5	41	chr3_23.906906c	5	48
chr3_18.504736c	5	29	chr3_17.451371	5	42	chr3_24.121024c	5	48
chr3_19.482062c	5	29	chr3_22.971414c	5	42	chr3_23.897624	5	48
chr3_19.14409c	5	29	chr2_12.219439	5	42	chr3_24.010703c	5	48
chr7_19.300596c	5	29	chr3_22.969603c	5	42	chr3_23.876742c	5	48
chr3_10.606876	5	29	chr3_31.277367c	5	42	chr3_23.876843c	5	48
chr3_18.862084c	5	29	chr2_12.225895c	5	42	chr3_24.010726c	5	50
chr3_18.629716c	5	29	chr3_16.0145	5	43	chr3_26.906643c	5	50
chr3_11.104214	5	29	chr3_23.544333	5	43	chr3_23.87677	5	50
chr5_22.829181c	5	29	chr3_15.803015	5	43	chr5_16.174676	5	50
chr3_11.012872	5	29	chr3_22.970602c	5	43	chr3_24.050328	5	50
chr3_11.012746	5	29	chr3_22.059723c	5	43	chr3_25.618107	5	50
CL2845_LG5	5	29	chr3_16.486868c	5	43	chr3_25.333306	5	50
chr3_11.012869	5	29	chr3_17.311735c	5	43	chr3_24.121041	5	50
chr5_23.192046	5	30	chr3_22.969637c	5	43	chr3_25.782336	5	52
chr3_11.01274c	5	30	chr3_16.890937c	5	43	chr3_25.915845c	5	52
chr3_11.544922c	5	31	chr7_10.273324	5	43	chr3_26.033666c	5	56
chr3_11.349301c	5	31	chr3_15.80301	5	43	chr3_25.974304	5	56
chr3_11.544963c	5	31	chr3_22.971397c	5	43	chr3_25.97447	5	56
chr3_11.374317c	5	31	chr3_16.920664c	5	43	chr3_26.012985	5	56
chr3_11.64811c	5	31	chr3_16.890935c	5	43	chr3_26.033536c	5	56
chr3_12.805231	5	32	chr3_23.544293c	5	43	chr3_25.98505	5	56
chr3_12.975533c	5	32	chr3_22.969965c	5	43	chr3_26.012934	5	56
chr3_13.327268	5	33	chr3_16.920688c	5	43	chr3_26.056237	5	57

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_26.056194	5	57	chr3_32.592274	5	73	chr2_0.325942c	6	14
chr3_26.098431	5	57	chr3_32.277879c	5	73	chr2_6.304727	6	15
chr3_26.098422c	5	57	chr3_32.602159	5	73	chr2_6.445079	6	15
chr3_27.248487	5	59	chr3_32.657813c	5	73	chr2_6.418102	6	15
chr3_27.074725	5	59	chr3_30.991683	5	73	chr2_6.304781c	6	15
chr3_27.58555	5	59	chr3_32.847062c	5	73	chr2_6.245503	6	15
chr3_27.585556c	5	59	chr3_32.657737c	5	73	chr2_6.245599	6	15
chr3_27.074702c	5	59	chr3_32.602122	5	74	chr2_7.971989	6	18
chr3_27.162716	5	59	chr3_32.602146c	5	74	chr2_7.99021	6	18
chr3_26.296132c	5	59	chr3_32.675821	5	74	chr5_21.721374	6	18
chr3_27.162596	5	59	chr2_11.380937	6	0	chr2_8.164281	6	18
chr3_27.16259	5	59	chr1_7.51307	6	0	chr2_8.164211	6	18
chr3_27.248581c	5	60	chr3_0.836582c	6	0	chr2_7.990325	6	19
chr3_26.495861c	5	60	chr3_0.836585c	6	0	chr2_7.990192	6	19
chr3_29.236292	5	60	chr2_11.177448c	6	0	chr2_7.990292	6	19
chr3_26.296122c	5	60	chr3_0.836562c	6	0	chr2_8.003546	6	19
chr3_27.240302c	5	60	chr2_11.378663	6	0	chr2_18.164933	6	19
chr3_27.240247c	5	60	chr2_4.827898c	6	6	chr2_12.885057	6	22
chr3_27.58571c	5	60	chr2_4.803325	6	6	chr2_10.532927	6	22
chr3_27.330448	5	60	chr4_31.779923	6	9	chr4_7.720808	6	22
chr3_27.96542	5	62	chr2_11.010156	6	9	chr2_10.135978	6	22
chr3_27.99615c	5	62	chr2_1.330128	6	9	chr2_10.531353	6	22
chr3_31.36812	5	62	chr2_11.702938	6	12	chr2_10.135873	6	22
chr3_27.804249c	5	65	chr2_11.702936	6	12	chr2_9.994994	6	22
chr3_27.830538c	5	65	chr2_11.703091	6	12	chr2_7.308774	6	22
chr3_28.897439c	5	65	chr2_11.703057	6	12	chr2_3.285053	6	22
chr3_29.472774	5	68	chr2_11.702872	6	12	chr2_2.250349	6	23
chr3_29.472699	5	68	chr2_11.334928	6	14	chr2_2.250487	6	23
chr3_30.01321	5	68	chr2_11.177443	6	14	chr2_3.125281	6	23
chr3_30.321402	5	68	chr2_1.948988c	6	14	chr2_4.337366	6	23
chr3_30.527117	5	70	chr2_5.94454	6	14	chr2_3.125832	6	23
chr3_30.343504	5	70	chr2_0.367748	6	14	chr2_3.756898	6	23
chr3_30.526974	5	70	chr2_0.387534	6	14	chr2_9.184282	6	23
chr3_30.527639	5	70	chr2_0.325936c	6	14	chr2_9.486087	6	23
chr3_30.527588c	5	70	chr2_1.948992c	6	14	chr2_4.633461c	6	23
chr3_30.527561	5	70	chr2_0.325939c	6	14	chr2_3.922365	6	23
chr3_30.218924	5	70	chr2_0.387621	6	14	chr3_9.063234	6	23
chr3_30.52693	5	70	chr2_0.325927c	6	14	chr7_10.933577	6	23
chr3_30.087184	5	70	chr2_0.361985	6	14	chr2_13.494157	6	25
chr3_30.321447c	5	71	chr2_1.949	6	14	chr2_13.119946	6	25

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_9.184693	6	26	chr2_17.790167c	6	33	chr2_21.841224c	6	44
chr2_9.486013	6	26	chr2_17.24005	6	35	chr2_21.841208	6	44
chr2_13.249608	6	27	chr2_17.239957	6	35	chr2_21.808225	6	44
chr2_13.119995	6	27	chr2_17.106329c	6	37	chr2_28.620278c	6	44
chr2_14.972658	6	27	chr2_17.239954	6	37	chr2_28.658517	6	44
chr2_14.976726	6	27	chr2_17.106326c	6	37	chr2_22.177259	6	46
chr2_14.972715	6	27	chr2_17.106194	6	37	chr2_27.384549	6	47
chr2_13.675643	6	27	chr2_16.843021	6	37	chr2_22.18406	6	47
chr2_13.675584	6	27	chr2_17.106221	6	37	chr2_21.843117	6	47
chr2_14.765857	6	27	chr2_17.106386	6	37	chr2_22.01726	6	47
chr2_14.250229	6	27	chr2_16.441156	6	38	chr2_22.103353	6	47
chr2_14.532731	6	27	chr2_16.695571c	6	38	chr2_27.220657c	6	48
chr2_13.943089	6	27	chr2_16.441018	6	38	chr2_27.657306c	6	49
chr2_13.972922	6	27	chr2_18.267204	6	38	chr2_27.624457	6	49
chr2_13.494133	6	27	chr2_16.441108	6	38	chr2_28.046836	6	52
chr2_15.426786	6	29	chr2_16.44103	6	38	chr2_28.01983	6	52
chr2_15.425978c	6	29	chr2_18.294865	6	39	chr2_28.592051c	6	52
chr2_15.148692	6	29	chr2_18.555809	6	40	chr2_28.658488	6	52
chr2_15.656356	6	29	chr2_19.35846c	6	40	chr2_28.6202	6	52
chr2_15.590775	6	29	chr2_18.555884	6	40	chr2_28.465742c	6	52
chr2_14.76582	6	29	chr2_18.55769	6	40	chr2_27.624581c	6	52
chr2_13.972874	6	29	chr2_18.9002	6	40	chr2_22.17077	6	52
chr2_15.426889	6	29	chr2_18.469813	6	40	chr2_28.465696	6	52
chr2_14.95881	6	29	chr2_18.557623	6	40	chr2_27.987966	6	52
chr2_14.972659	6	29	chr2_18.464122	6	40	chr2_21.3912	6	52
chr2_14.633358	6	29	chr2_18.55581	6	40	chr2_26.345579c	6	54
chr2_13.943094	6	29	chr2_19.750277	6	42	chr2_27.384735	6	54
chr2_15.20857	6	29	chr2_21.230882	6	42	chr2_26.77842c	6	54
chr2_14.340422	6	29	chr2_20.126052	6	42	chr2_26.476963	6	54
chr2_15.426876	6	29	chr2_21.231029	6	42	chr2_27.220718	6	54
chr2_15.696245	6	31	chr2_19.706908	6	42	chr2_26.227857	6	54
chr2_18.164943	6	32	chr2_20.87834	6	42	chr2_27.229587c	6	54
chr2_18.164901c	6	32	chr2_20.604056	6	42	chr2_27.38475c	6	54
chr2_18.047616	6	33	chr2_20.697564	6	42	chr2_26.476937	6	54
chr2_17.790184c	6	33	chr2_20.880422c	6	42	chr2_26.228001	6	54
chr2_17.790202c	6	33	chr2_19.949491	6	42	chr2_27.920995	6	54
chr2_17.556844	6	33	chr2_20.529991	6	42	chr2_27.747281	6	54
chr2_17.790193c	6	33	chr2_20.878249	6	42	chr2_25.312193c	6	56
chr2_17.7902c	6	33	chr2_21.80828	6	44	chr2_25.306917c	6	56
chr2_17.790205c	6	33	chr2_21.380592	6	44	chr2_25.312197c	6	56

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_25.312195c	6	56	chr5_9.370183c	7	4	chr5_5.037482	7	22
chr2_25.570533	6	56	chr5_9.249829c	7	4	chr5_5.678322	7	22
chr2_25.570601	6	56	chr5_9.370225	7	8	chr5_4.638577c	7	22
chr2_25.307035	6	56	chr5_9.431907c	7	8	chr5_5.410602c	7	22
chr2_25.198478c	6	56	chr5_9.370173	7	8	chr5_5.410683c	7	22
chr2_25.57052	6	56	chr5_9.431909c	7	8	chr5_5.678455	7	22
chr2_25.111038c	6	59	chr5_9.387923	7	8	chr5_5.244962	7	22
chr2_24.799333	6	59	chr5_9.249778	7	9	chr5_5.161854c	7	23
chr2_24.799219	6	59	chr5_9.141231	7	9	chr5_5.612502	7	23
chr2_24.799377	6	61	chr5_8.914843c	7	10	chr5_4.785243	7	23
chr2_24.795128	6	61	chr5_8.890932	7	11	chr5_5.161752c	7	23
chr2_24.412081c	6	61	Rw22B6_LG7	7	12	chr5_4.739272	7	24
chr2_24.223191	6	61	chr5_8.626804	7	12	chr5_4.490059	7	26
chr2_24.001914	6	61	chr5_8.708276c	7	12	chr5_4.306304	7	26
chr2_24.412118	6	61	chr5_8.672065	7	12	chr5_4.243755	7	26
chr2_24.626366	6	61	chr5_8.39521	7	13	chr5_3.558407c	7	27
chr2_24.626373	6	61	chr5_8.21139	7	15	chr5_3.367913	7	27
chr2_24.235513	6	62	chr5_8.211443c	7	15	chr5_3.623275	7	28
chr2_24.008603	6	62	chr5_8.056854	7	15	chr4_24.576999c	7	28
chr2_24.927698c	6	62	chr5_7.723511c	7	15	chr5_3.682165	7	28
chr2_24.008582c	6	62	chr5_6.959854	7	16	chr5_2.97298	7	29
chr2_24.033014	6	62	chr5_7.723451	7	17	chr5_2.972791c	7	29
chr2_23.885495	6	62	chr2_27.350177	7	17	chr5_2.727743	7	32
chr2_24.231811	6	62	chr5_7.678127c	7	17	chr5_2.792707c	7	32
chr2_23.449957	6	63	chr5_7.162182	7	17	chr5_2.972771	7	32
chr2_23.594351	6	63	chr5_6.672327	7	17	chr5_2.411627c	7	32
chr2_23.303524	6	64	chr5_7.379853c	7	17	chr5_1.932987c	7	32
chr2_0.264419	6	64	chr2_27.350319	7	17	chr5_1.861115	7	34
chr2_23.38152	6	64	chr5_7.227087	7	17	chr5_1.881442	7	34
CL2980_LG6	6	77	chr5_7.009711	7	19	chr5_1.861007c	7	34
chr5_10.352899	7	0	chr7_6.019372	7	19	chr5_2.018838c	7	35
RMS043_LG7	7	0	chr7_6.019419	7	19	chr5_2.018785c	7	35
chr5_23.191701c	7	0	chr5_6.128112c	7	20	chr4_10.569959	7	35
chr5_23.191619	7	0	chr5_6.804377	7	20	chr5_1.933062c	7	35
chr5_10.007931	7	0	chr5_5.973255	7	21	chr5_2.003732	7	35
chr5_10.132246c	7	0	chr1_13.372489	7	21	chr5_0.52447	7	37
chr5_23.191591	7	0	chr5_6.066563	7	21	chr5_0.667556	7	37
chr5_9.040208c	7	4	chr5_4.739302c	7	22	chr5_0.787991	7	37
chr5_9.387917	7	4	chr5_4.737501c	7	22	chr5_0.66742	7	37
chr5_9.387902c	7	4	chr5_5.612507	7	22	chr5_0.626661c	7	37

Appendix 3. Continued

J14-3 x LC

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_0.475351c	7	37	chr5_11.55092	7	42	chr5_20.332095	7	48
chr5_0.259809	7	37	chr5_15.295629c	7	42	chr5_21.864814c	7	50
chr5_10.963063	7	37	chr5_15.434358	7	42	chr5_21.864898	7	50
chr5_0.098049	7	37	chr5_11.64726	7	42	chr7_10.933579	7	50
chr5_13.211011c	7	37	chr5_20.023579	7	42	chr4_20.733934	7	50
chr5_0.240038	7	37	chr5_11.704311	7	42	chr4_27.571125	7	50
chr5_0.054614c	7	37	chr5_18.540035	7	42	chr5_22.127936c	7	51
chr5_0.110598	7	37	chr5_16.760653c	7	42	chr4_27.571075	7	51
chr5_0.801187c	7	37	Rw5G14_LG7	7	42	chr4_27.571114c	7	51
chr5_11.080941	7	37	chr5_11.704284	7	42	chr5_22.12794c	7	51
chr5_0.710475	7	37	chr5_20.023494	7	42	chr5_22.743561c	7	52
chr5_0.475297c	7	37	chr5_12.067125	7	42	chr5_24.351493c	7	54
chr5_0.475189	7	37	chr5_19.831198c	7	42	chr5_24.168493	7	54
chr5_0.368309	7	38	chr1_12.746504c	7	42	chr5_24.168277	7	54
chr5_0.801526	7	38	chr5_12.067145	7	42	chr5_22.414823c	7	54
chr5_0.368279c	7	38	chr5_15.690422	7	42	chr5_22.414793	7	54
chr5_0.040337c	7	38	chr5_14.17974	7	42	chr5_24.046085	7	54
chr5_1.091401	7	38	chr5_15.295584c	7	42	chr4_10.569785c	7	55
chr5_0.801171	7	38	chr2_12.639404c	7	42	chr4_10.569749c	7	55
chr5_11.140564c	7	38	chr5_13.0642c	7	42	chr4_10.569742c	7	55
chr5_11.081098	7	38	chr5_19.831037	7	42	chr4_10.569712c	7	55
chr5_0.295223	7	38	chr5_16.951673c	7	42	chr4_10.56977c	7	55
chr5_0.259815c	7	38	chr4_24.271811c	7	42	chr4_10.569725c	7	55
chr5_0.054557	7	38	chr5_12.197963	7	42	chr4_10.569757c	7	55
chr5_0.05471	7	39	chr5_14.067637c	7	43	chr4_10.569723c	7	55
chr5_0.053647	7	39	chr5_12.390393	7	44	chr4_10.569744c	7	55
chr5_0.110541	7	39	chr5_16.555027c	7	45	chr4_10.569793c	7	55
chr5_0.054712c	7	39	chr5_19.391751c	7	45	chr5_24.226055c	7	56
chr5_11.140567	7	39	chr5_19.391871c	7	45	chr1_9.928565	7	60
chr5_10.963072	7	39	chr5_17.261728c	7	45	chr1_9.928541	7	60
chr5_11.081096	7	39	chr5_16.80285c	7	45	chr5_25.95567	7	60
chr5_0.710208c	7	39	chr5_11.543685	7	45	chr5_25.598011	7	60
chr5_11.14057	7	39	chr5_17.586455c	7	45	chr5_24.6846	7	60
chr5_11.081111	7	39	chr5_17.586283	7	45	chr5_24.943667c	7	60
chr5_11.08108	7	39	chr5_17.261523c	7	45	chr6_10.847179	7	62
chr5_0.6267	7	39	Rh72_LG7	7	47	chr6_10.847182	7	62
chr5_12.804039c	7	39	chr3_1.412842	7	47	chr5_26.336713	7	62
chr5_11.429368	7	41	chr5_20.332037c	7	48	chr5_26.042126	7	63
chr5_11.429381	7	41	chr5_20.579745c	7	48	chr5_26.968991	7	63
chr5_11.704278	7	42	chr2_23.649136c	7	48	chr5_27.253792	7	63

Appendix 3. Continued

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Marker name	Linkage group	position cM
chr5_27.040702c	7	63
chr2_12.742109	7	63
chr5_26.968946	7	64
chr5_26.969096	7	64
chr5_26.96924c	7	64
chr5_26.964228c	7	64
chr5_26.336871	7	64
chr5_27.492158c	7	65
chr5_27.735163	7	65
chr5_27.990199	7	67
chr5_27.990212	7	67
chr5_28.555792	7	69
chr4_24.107276c	7	69
chr5_6.572759	7	69
chr5_28.902564c	7	73
chr5_28.914204	7	73
chr5_28.914366c	7	73
chr5_28.902462	7	73
chr5_28.902591	7	73
chr5_28.914192	7	73
chr5_28.914328	7	73

Appendix 3. Continued

J14-3 x VS

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_5.980514	1	0	chr7_13.531363	1	15	chr7_17.611923	1	29
chr4_10.812788	1	0	chr7_14.616781	1	15	chr7_18.141463	1	30
chr4_10.812806	1	0	chr7_15.044078c	1	15	chr7_18.163184	1	30
chr7_6.500465	1	1	chr7_14.615681	1	16	chr7_18.177114	1	30
chr5_0.631568c	1	1	chr7_14.622264	1	16	chr7_18.377104	1	30
chr7_7.526217	1	2	chr7_15.370551	1	16	chr7_18.467474c	1	31
chr7_7.156618	1	2	chr7_15.370485c	1	16	chr7_18.467492c	1	31
chr7_9.567817c	1	4	chr7_15.199566	1	16	chr7_18.472259	1	31
chr7_7.996817c	1	4	chr7_15.115737c	1	16	chr7_18.667302c	1	31
chr7_9.567824c	1	4	chr7_15.115734c	1	16	chr7_18.66726	1	31
chr7_9.567815c	1	4	chr7_15.11574c	1	16	chr7_18.633311	1	31
chr7_9.431968	1	4	chr7_15.169627	1	16	chr7_18.667305c	1	31
chr7_9.567808c	1	4	chr7_14.622202	1	16	chr7_18.71384	1	32
chr7_9.567811c	1	4	chr7_16.411145	1	17	H5_F12_LG1	1	33
chr7_9.385113	1	4	chr7_15.865571	1	17	chr7_18.92274	1	35
chr7_9.385112	1	4	chr7_15.395736c	1	17	chr7_19.312222c	1	35
chr7_9.552873	1	4	Rw34L6_LG1	1	21	chr7_19.443696c	1	35
chr7_8.283597c	1	4	chr7_16.480836	1	25	chr7_19.741411c	1	35
chr3_3.021324	1	4	chr7_16.471613	1	25	chr7_19.939297c	1	35
chr2_5.001332	1	5	chr7_16.471467	1	25	chr7_19.396709c	1	35
chr2_5.001299	1	5	chr7_15.86556c	1	25	chr7_19.396733c	1	35
chr7_10.385832c	1	6	chr5_25.5394	1	25	chr7_19.939473c	1	35
chr7_10.385941c	1	6	chr7_9.786157c	1	25	chr7_19.414384c	1	35
chr7_10.930206	1	9	chr7_15.630106	1	25	chr7_19.373724c	1	35
chr7_11.211166c	1	9	chr7_16.247829c	1	25	chr7_19.449169	1	35
chr7_12.13403c	1	11	chr7_16.690213	1	26	chr7_19.443674c	1	35
chr7_12.987868	1	14	chr4_31.097032c	1	28	chr7_18.415494	1	35
chr7_12.978062	1	14	chr7_16.759927c	1	28	chr7_18.415693	1	35
chr7_13.104348	1	14	chr7_16.690217c	1	28	chr7_18.415579	1	35
chr7_12.783112	1	14	chr7_16.760018c	1	28	chr7_18.472244	1	35
chr7_12.917504	1	14	chr4_31.097061c	1	28	chr7_18.467408	1	35
chr7_12.783197	1	14	chr7_16.855689	1	28	chr7_19.312313c	1	35
chr7_12.987811	1	14	chr7_16.760041c	1	28	chr7_19.741362c	1	35
chr7_13.34111	1	15	chr7_17.610663c	1	29	chr7_20.086801	1	35
chr7_14.358688	1	15	chr7_17.610635c	1	29	chr7_19.443518	1	36
chr7_13.921956	1	15	chr7_17.47942	1	29	chr7_19.449185	1	36
chr7_14.329131c	1	15	chr7_17.773611	1	29	chr7_19.322479	1	36
chr7_14.329161c	1	15	chr7_17.687201c	1	29	chr7_20.086723	1	37
chr7_14.329056c	1	15	chr7_17.378327	1	29	chr5_24.046133	1	37
chr7_14.32911c	1	15	chr7_17.479367c	1	29	chr7_20.523599	1	40

Appendix 3. Continued

J14-3 x VS

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_20.64994c	1	40	chr7_23.013203	1	52	chr1_3.983468	2	7
chr7_20.544313	1	40	chr1_1.027812	2	0	chr1_3.250202	2	9
chr7_20.523529	1	40	chr1_1.39466c	2	0	chr1_3.152817	2	9
chr7_20.786131c	1	40	chr1_2.144306c	2	1	chr1_4.257676c	2	10
chr7_20.645358	1	40	chr1_2.144735c	2	1	chr1_4.197269c	2	10
chr7_20.804926	1	40	chr1_2.14475c	2	1	chr1_4.206668c	2	10
chr7_20.786106	1	40	chr1_2.077982c	2	1	chr1_4.229476	2	10
chr7_20.645311c	1	40	chr1_2.144357c	2	1	chr1_4.238907	2	10
chr7_20.737533	1	40	chr1_2.144585c	2	1	chr1_4.197182c	2	10
chr7_20.645228c	1	40	chr1_2.003114	2	1	chr1_4.684316c	2	12
chr7_20.649892c	1	40	chr1_1.937179	2	1	chr1_4.684388c	2	12
chr7_20.649751c	1	40	chr1_2.002985	2	1	chr1_4.492592	2	12
chr7_20.805014	1	41	chr1_2.690475c	2	2	chr1_3.435632	2	12
chr7_20.80504	1	41	chr1_2.318579	2	2	chr1_3.435634	2	12
chr7_20.940282	1	42	chr1_2.736295c	2	2	chr1_3.564995	2	13
chr7_20.904212	1	42	chr1_2.861731	2	2	chr1_3.75284c	2	14
chr7_20.942895	1	42	chr1_2.318639	2	2	chr1_3.793592c	2	14
chr7_21.162249	1	43	chr1_2.73631c	2	2	chr1_5.396793c	2	15
chr7_21.066544	1	43	chr1_2.521723c	2	2	chr1_3.98357	2	15
chr7_21.068143	1	43	chr1_2.521724c	2	2	chr1_5.502625c	2	17
chr7_20.952222	1	43	chr1_2.736407c	2	2	chr1_5.502691c	2	17
chr7_21.068173	1	43	chr1_2.776934c	2	2	chr1_4.197258c	2	17
chr7_21.162281	1	43	chr1_2.521732c	2	2	chr1_4.253306	2	17
chr7_20.942885	1	43	chr1_2.47502	2	2	chr1_4.229562c	2	17
chr7_21.564424	1	44	chr1_2.222813	2	2	chr1_4.206683c	2	17
chr5_11.923707	1	44	chr1_2.318574	2	2	chr1_5.918619	2	18
chr7_21.564253	1	44	chr1_3.435523	2	3	chr1_5.964933c	2	18
chr7_22.739224c	1	44	chr1_3.152825	2	4	chr1_5.965028c	2	18
chr7_21.730793c	1	44	chr1_3.43551	2	4	chr1_4.684296	2	19
chr7_21.564376	1	44	chr1_3.435488	2	4	chr1_4.684301c	2	19
chr4_32.176374	1	44	chr1_2.622883c	2	4	chr1_4.684358c	2	19
chr7_23.352066	1	44	chr1_2.479221	2	4	chr1_6.290646	2	20
chr7_23.484334	1	44	chr1_2.62288c	2	4	chr1_6.18483c	2	20
chr7_21.606193	1	44	chr1_2.498949c	2	4	chr1_6.184806	2	20
chr4_32.176399	1	46	chr1_2.695716c	2	4	chr1_6.271493c	2	20
chr7_21.83418	1	46	chr1_3.549589	2	5	chr1_5.33267	2	20
chr5_4.243711	1	47	chr1_3.549677	2	5	chr1_5.396723c	2	20
chr2_12.639586	1	47	chr1_3.735119	2	7	chr1_7.150463	2	21
chr7_22.854141	1	51	chr1_3.793777c	2	7	chr1_6.690492c	2	21
chr7_22.854125	1	51	chr1_3.75353	2	7	chr1_7.136429c	2	21

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_6.672308	2	21	chr1_7.743341c	2	35	chr1_16.04228c	2	40
chr1_7.847367	2	22	chr1_17.28848c	2	36	chr1_8.772956c	2	42
chr1_7.512917	2	22	chr1_1.661496	2	36	chr6_20.486507c	2	47
chr1_7.847496	2	22	chr1_16.994934c	2	36	chr6_19.982957c	2	47
chr1_8.138587c	2	22	chr1_17.288493c	2	36	chr6_21.779928c	2	47
chr1_7.847364	2	22	chr1_17.573105c	2	36	chr6_20.501779c	2	47
chr1_5.918602	2	22	chr1_18.223722c	2	36	chr6_20.532373	2	47
chr1_5.793824c	2	22	chr1_17.101332	2	36	chr6_20.640381c	2	47
chr1_6.042708c	2	22	chr1_17.288562c	2	36	chr6_20.640376c	2	47
chr1_6.184737	2	23	chr1_10.11165c	2	36	chr6_20.425868c	2	47
chr1_6.07063c	2	23	chr1_12.540596c	2	36	chr6_19.983023	2	47
chr1_6.18479	2	23	chr1_17.573081c	2	36	chr6_20.425967c	2	47
Rh48_LG2	2	29	chr1_17.288427c	2	36	chr6_21.265314	2	50
chr1_7.847544	2	33	chr1_17.28847c	2	36	chr6_22.020181c	2	52
chr1_17.573164c	2	34	chr1_17.288532c	2	36	chr6_22.020162	2	52
chr1_10.321726	2	34	chr1_18.100702c	2	36	chr6_23.898748c	2	53
chr1_10.495583c	2	34	chr1_7.847513c	2	36	chr6_22.305666	2	55
chr1_10.672072	2	34	chr1_19.106089c	2	36	chr6_22.200336c	2	55
chr1_10.111581c	2	34	chr1_9.504632c	2	36	chr6_18.651732	2	55
chr1_10.672126c	2	34	chr1_10.672085c	2	36	chr6_25.012785	2	56
chr1_10.053173	2	34	chr1_12.540578c	2	36	chr6_24.982865	2	56
chr1_10.532371	2	34	chr1_17.337983c	2	36	chr6_24.333503c	2	56
chr1_7.507856c	2	34	chr1_12.540607c	2	36	chr6_23.39463	2	56
chr1_15.210714c	2	34	chr1_18.201755c	2	36	chr6_25.673682	2	57
chr1_17.069216	2	34	chr1_17.28861c	2	36	chr6_25.644758	2	57
chr1_17.069213c	2	34	chr1_17.288469c	2	36	chr6_25.644736	2	57
chr1_10.67227	2	34	chr1_10.442521c	2	37	chr6_25.903306	2	57
chr1_10.053197c	2	34	chr1_15.312024c	2	37	chr6_25.905902	2	57
chr1_10.775446c	2	34	chr1_18.410525	2	37	chr6_25.644826	2	57
chr1_10.67209c	2	34	chr1_11.424441c	2	37	chr6_24.724354	2	57
chr1_11.832138c	2	35	chr1_9.789929	2	37	chr6_25.905759	2	57
chr1_11.664852	2	35	chr1_10.321864c	2	37	chr6_25.178794	2	57
chr1_11.748759c	2	35	chr1_15.312065c	2	37	chr6_24.717093	2	57
chr1_11.664678c	2	35	chr1_19.106101c	2	37	chr6_25.644808	2	57
chr1_11.748702c	2	35	chr1_14.562674	2	39	chr6_25.644759	2	57
chr1_11.748807c	2	35	chr1_19.227207	2	39	chr6_25.905732	2	58
chr1_11.74884c	2	35	chr1_14.6501	2	39	chr6_26.914348c	2	59
chr1_12.428288	2	35	chr1_14.439401c	2	39	chr6_26.646082	2	59
chr1_15.85486c	2	35	chr1_16.46666c	2	40	chr6_26.646102	2	59
chr1_7.847441	2	35	chr1_16.466661	2	40	chr6_26.656034c	2	59

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_27.344809c	2	59	chr6_30.634536	2	67	chr6_36.004515c	2	78
chr6_26.118489	2	59	chr6_30.84518c	2	67	chr6_35.934743c	2	78
chr6_26.646208c	2	59	chr6_29.528584	2	67	chr6_35.858779	2	78
chr6_26.655966c	2	59	chr6_29.518821c	2	67	chr6_36.073405	2	78
chr6_26.646092	2	59	chr6_29.412482	2	68	chr6_35.965574	2	78
chr6_26.689691	2	59	chr6_30.845195	2	68	chr6_35.929618	2	78
chr6_26.877908	2	59	chr6_32.029807	2	69	chr6_35.67536	2	78
chr6_27.819291	2	60	chr6_29.266748	2	69	chr6_36.073465	2	79
chr6_27.576798	2	60	chr6_32.029936	2	69	chr6_36.073033	2	79
chr6_27.57685	2	60	chr6_29.266906	2	69	chr6_36.630288	2	80
chr6_29.139503	2	61	chr6_32.141066	2	69	chr6_36.420608	2	80
chr6_29.154708	2	61	chr6_32.205307	2	69	chr6_36.525111	2	80
chr6_29.15463	2	61	chr6_32.412535	2	69	chr6_36.923363	2	82
chr6_29.154709	2	61	chr6_31.805849	2	70	chr6_36.858528	2	82
chr6_29.154701	2	61	chr6_32.344852	2	70	chr6_36.931765	2	82
chr6_28.96079	2	61	chr6_32.390975	2	70	chr6_37.539943	2	84
chr6_28.681681	2	61	chr6_32.344995c	2	70	chr6_38.221164	2	85
chr6_29.154631	2	61	chr6_32.094013c	2	70	chr6_38.22116	2	85
chr6_28.681842c	2	61	chr6_32.41241	2	71	chr6_0.242596	3	0
chr6_28.68184c	2	61	chr6_32.756603c	2	71	chr6_0.106957c	3	0
chr6_28.141739c	2	61	chr6_32.463148	2	71	chr6_0.288153c	3	0
chr6_28.681778c	2	61	chr6_32.461306	2	71	chr6_0.039488c	3	0
chr6_28.141748c	2	61	chr6_32.461322	2	71	chr6_0.522755	3	1
chr6_29.639698	2	62	chr6_33.531387c	2	73	chr6_0.522773	3	1
chr6_30.355325	2	62	chr6_33.264241c	2	73	chr6_0.811049	3	2
chr6_29.680111	2	62	chr6_32.918299	2	73	chr6_0.811231	3	2
chr6_29.154771c	2	63	chr6_33.531386c	2	73	chr6_0.741968	3	2
chr6_28.960886c	2	63	chr6_32.918435	2	73	chr6_0.741935	3	2
chr6_29.149836c	2	63	chr6_33.525955	2	73	chr6_0.741929	3	2
chr6_29.149813	2	63	chr6_34.712429c	2	73	chr6_1.080135	3	2
chr6_29.139545	2	63	chr6_33.026341	2	73	chr6_1.350828	3	4
chr6_30.634141	2	63	chr6_34.837756	2	73	chr6_1.350825	3	4
chr6_30.967032c	2	63	chr6_33.589239c	2	73	chr6_1.350823	3	4
chr6_29.639695	2	64	chr6_34.648606	2	73	chr6_1.350775	3	4
chr6_29.639712	2	64	chr6_33.95328c	2	73	chr6_1.425389	3	5
chr6_31.531428	2	64	chr6_33.839517c	2	73	chr6_1.425327	3	5
chr6_15.068559c	2	65	chr6_34.506637	2	73	chr6_1.42533	3	5
chr6_31.219476c	2	66	chr6_34.545942	2	74	chr2_6.356844	3	6
chr6_31.219479c	2	66	chr6_35.072497c	2	75	chr6_1.816382	3	6
chr6_29.412515	2	67	chr6_34.96216c	2	75	chr6_1.868954c	3	6

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_1.868958c	3	6	chr6_6.468189	3	36	chr6_17.790682	3	58
chr6_1.974541	3	6	chr6_6.468315	3	36	chr6_10.749894	3	58
chr6_1.816427	3	6	chr6_6.791673	3	37	chr6_17.519042c	3	58
chr6_2.963267	3	9	chr6_6.737852	3	37	chr6_11.73694	3	58
chr6_2.965689c	3	9	chr6_6.482123	3	38	chr6_11.736975	3	58
chr6_2.96574c	3	9	chr3_26.295993c	3	38	chr6_16.82039	3	61
chr6_2.963197	3	9	chr6_6.7918	3	38	chr6_18.243505	3	66
chr6_2.963191	3	9	chr3_26.296016c	3	38	chr1_9.306703	3	66
chr6_3.272563	3	11	chr6_7.070216	3	38	chr6_18.270544	3	66
chr3_0.405998	3	11	chr1_18.377545	3	38	chr6_18.243495	3	66
chr6_3.326291	3	11	chr6_7.274355	3	39	chr6_18.24351	3	66
chr6_3.105928	3	12	Rw12J12_LG3	3	48	chr1_9.306686	3	66
chr6_3.444881	3	12	chr6_7.399133c	3	50	chr1_14.272702	3	72
chr6_3.666382	3	13	chr6_7.214013	3	50	chr1_12.907297	3	72
chr6_3.581779	3	13	chr6_7.55052c	3	50	chr1_14.272655	3	72
chr6_3.596202	3	14	chr6_7.839982c	3	50	chr1_13.963736	3	75
chr6_3.553724	3	14	chr6_7.649699c	3	50	chr1_13.372495	3	78
chr6_4.175209	3	15	chr6_8.773447c	3	53	chr1_13.372615	3	78
chr6_4.231767	3	15	chr6_8.607372c	3	53	chr7_15.853166	3	78
chr6_4.17526	3	15	chr6_8.614712c	3	53	chr1_20.19498	3	80
chr6_3.791109	3	15	chr6_8.662557c	3	53	chr1_19.762873	3	80
chr6_4.204762	3	17	chr6_8.951769c	3	53	chr4_2.61771	4	0
chr6_4.37173	3	18	chr6_8.614639c	3	53	chr4_2.13018c	4	0
chr6_4.50671	3	19	chr6_8.662506c	3	53	chr4_1.608673	4	0
chr6_4.710029	3	19	chr6_9.032051c	3	54	chr4_2.643188	4	0
chr6_4.506776	3	19	chr6_9.032114	3	54	chr4_13.333904c	4	1
chr6_4.371733	3	19	chr6_8.97888c	3	54	chr4_4.907658	4	1
chr6_4.71008	3	20	chr6_9.176797c	3	54	chr6_29.493251	4	1
chr6_4.710212	3	20	chr6_8.978868	3	54	chr4_13.333733	4	1
chr6_4.777891c	3	20	chr6_10.736859c	3	56	chr4_14.691572	4	1
chr6_4.777808	3	20	chr3_23.544367	3	56	chr4_4.680702c	4	1
Rw35C24_LG3	3	24	chr6_11.451162	3	56	chr4_14.689942	4	1
chr6_5.300276	3	31	chr6_11.409705	3	56	chr4_13.333703	4	1
chr6_5.300251	3	31	chr6_10.807964	3	57	chr4_4.907812c	4	1
chr6_5.300289c	3	31	chr6_12.312783	3	58	chr4_10.813043c	4	2
chr6_5.645322	3	32	chr6_11.171791	3	58	chr4_10.81303c	4	2
chr6_5.645458	3	32	chr6_11.988579	3	58	chr4_10.813041c	4	2
chr6_5.982011	3	35	chr6_11.735918	3	58	chr4_4.872345c	4	4
chr6_6.368022	3	35	chr6_11.735878	3	58	chr4_4.872342c	4	4
chr6_5.982029	3	35	chr6_10.749984	3	58	chr6_5.051434c	4	6

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_5.442548c	4	6	chr4_19.015702	4	23	chr4_23.227841c	4	30
chr4_10.378639	4	8	chr4_19.015757c	4	23	chr3_4.920582c	4	32
chr1_2.690666	4	8	chr4_19.261155	4	23	chr4_22.013886c	4	32
chr2_24.584994	4	8	chr4_16.140459c	4	23	chr4_23.227904c	4	32
chr4_10.378789c	4	8	chr4_19.264845	4	24	chr4_22.892014c	4	32
chr1_2.690519	4	8	chr4_19.261168	4	24	chr4_23.959251c	4	35
chr1_2.690704	4	8	chr4_20.223839	4	25	chr4_25.69303c	4	35
chr4_12.955859	4	9	chr4_20.223871	4	25	chr4_24.870522	4	35
chr4_10.024543	4	9	chr4_22.657176c	4	26	chr4_23.896044c	4	35
chr4_6.705482	4	9	chr4_20.800442	4	26	chr4_23.895982c	4	35
chr4_13.059825	4	9	chr4_22.664073	4	26	chr4_25.72419c	4	35
chr4_10.024609c	4	9	chr4_20.231117	4	26	chr4_23.896043c	4	35
chr1_2.202084	4	9	chr4_20.2656c	4	26	chr4_23.744536	4	35
chr4_10.024632c	4	9	chr4_20.265456c	4	26	chr4_23.357947	4	35
chr5_12.69382	4	10	chr4_20.265486c	4	26	chr4_25.146078	4	35
chr4_14.265105c	4	10	chr4_20.363195c	4	26	chr4_25.284119	4	35
chr4_13.87273c	4	11	chr4_20.36565c	4	26	chr4_23.687045c	4	35
chr3_0.669368c	4	11	chr4_20.706127	4	26	chr4_25.693034c	4	35
RhABT12_LG4	4	12	chr4_20.365729	4	26	chr4_25.29208	4	36
chr4_14.019613c	4	14	chr4_22.663824	4	26	chr4_24.141004	4	36
chr4_14.265056	4	14	chr4_22.384157c	4	26	chr3_6.449223	4	36
chr2_27.795803c	4	14	chr4_22.384156c	4	26	chr4_25.170089	4	36
chr3_0.669366c	4	14	chr4_20.800257	4	26	chr4_24.141035	4	36
chr4_13.872754	4	14	chr4_20.365723c	4	26	chr4_25.551891	4	36
chr4_15.572861c	4	16	chr4_21.108676c	4	26	chr3_32.662897	4	36
chr4_15.24411	4	16	chr4_20.363129c	4	26	chr4_23.869726c	4	36
chr4_15.572876c	4	16	chr4_20.706199	4	26	chr4_25.551888	4	36
chr4_15.572828c	4	16	chr4_20.800284c	4	26	chr4_26.760643	4	36
chr4_13.538038c	4	16	chr4_20.98389	4	26	chr4_26.235391	4	36
chr4_13.579898	4	16	chr4_20.23112	4	26	chr4_26.347175c	4	36
chr4_13.538025c	4	16	chr4_20.932977	4	26	chr4_26.31414c	4	37
chr6_34.918843	4	16	chr4_19.838586	4	26	chr4_26.225404c	4	37
chr4_15.551469c	4	16	chr4_25.585298c	4	26	chr4_26.235324c	4	37
chr4_17.064622	4	21	chr4_21.693318	4	28	chr4_26.225406c	4	37
chr4_16.510792	4	23	chr2_0.264477	4	29	chr4_26.225291c	4	37
chr4_16.678729	4	23	chr4_22.664225	4	29	chr4_26.760646	4	37
chr4_16.679267c	4	23	chr4_22.664221	4	29	chr4_26.314055	4	37
chr4_16.679197c	4	23	chr4_22.392716c	4	29	chr4_26.344736	4	37
chr4_16.140549	4	23	chr4_22.519434	4	29	chr4_24.753806c	4	37
chr4_19.015713c	4	23	chr4_23.227843c	4	30	chr4_24.709688c	4	37

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_24.303326	4	37	chr4_29.594611	4	45	chr4_32.068076c	4	54
chr4_26.31286	4	37	chr4_29.691774c	4	45	chr4_31.986193	4	55
chr4_26.760645	4	37	chr4_29.691626c	4	45	chr4_31.925842	4	55
chr4_26.770355c	4	37	chr4_28.674749	4	45	chr4_32.274135	4	55
chr4_25.247964	4	38	chr4_29.082506	4	45	chr4_31.984893	4	55
chr4_25.247909c	4	40	chr4_28.687601c	4	45	chr3_32.847062c	5	0
chr4_25.247857c	4	40	chr4_29.591117	4	45	chr3_32.657813c	5	0
chr4_25.247851c	4	40	chr4_29.746049	4	46	chr3_32.663335c	5	0
chr4_25.247887c	4	40	chr4_29.746051	4	46	chr3_32.657737c	5	0
chr4_25.247863c	4	40	chr4_29.680221	4	46	chr3_32.277768c	5	1
chr4_25.247845c	4	40	chr4_30.208266c	4	47	chr3_30.527588c	5	2
chr4_25.247859c	4	40	chr4_30.111331c	4	47	chr3_29.472774	5	9
chr4_25.247839c	4	40	chr4_30.111712c	4	47	chr3_29.719252	5	9
chr4_25.247906c	4	40	chr4_29.956147c	4	47	chr3_29.236232c	5	10
chr4_27.264957	4	42	chr4_30.111196c	4	47	chr3_1.837681	5	10
chr4_27.098452	4	42	chr4_30.111579c	4	47	chr3_28.897439c	5	13
chr4_27.265022	4	42	chr4_30.059204	4	47	chr3_27.99615c	5	13
chr4_26.84442	4	42	chr4_30.111326c	4	47	chr3_30.527545	5	14
chr4_26.844414	4	42	chr4_30.210924	4	49	chr6_25.673668	5	14
chr4_27.109592	4	42	chr4_30.584004c	4	49	chr3_30.527495	5	14
chr4_26.900233	4	42	chr4_30.229594	4	49	chr3_26.200949	5	15
chr4_27.264891	4	42	chr4_30.670637	4	49	chr3_27.285255c	5	15
chr4_27.922658c	4	43	chr4_30.229548	4	49	chr3_27.96542	5	15
chr4_27.922625c	4	43	chr4_30.229574	4	50	chr3_27.804249c	5	15
chr4_27.922646	4	43	chr4_30.229584	4	50	chr3_27.723279	5	16
chr4_27.445737c	4	43	chr4_30.939637	4	50	chr3_27.330446c	5	16
chr4_27.29526	4	43	chr3_5.90206	4	50	chr3_26.098326c	5	16
chr4_27.29538	4	43	chr4_31.267132	4	50	chr3_27.074702c	5	16
chr4_27.973639	4	43	chr4_30.670628	4	50	chr3_26.180318	5	16
chr4_28.875093	4	43	chr4_30.584234	4	50	chr3_27.285354c	5	16
chr4_29.143188	4	43	chr3_5.902101	4	50	chr3_26.296122c	5	16
chr4_27.981351	4	43	chr4_30.675593	4	50	chr3_26.056237	5	16
chr4_29.3096	4	45	chr4_30.929007c	4	50	chr3_27.330486c	5	16
chr4_29.600188	4	45	chr4_31.588419c	4	52	chr3_27.296046c	5	16
chr4_28.687403c	4	45	chr4_31.588428c	4	52	chr3_27.240247c	5	16
chr4_29.590994c	4	45	chr4_31.675112c	4	52	chr3_27.240302c	5	16
chr4_29.387027c	4	45	chr4_31.612938	4	52	chr3_27.248581c	5	16
chr4_28.674781	4	45	chr4_31.186	4	52	chr3_26.344409	5	16
chr4_28.687133	4	45	chr4_31.896395	4	54	chr3_26.180247	5	16
chr4_29.598014	4	45	chr4_32.06823c	4	54	chr3_26.033666c	5	16

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_27.58571c	5	16	chr3_18.141454c	5	27	chr7_19.300581c	5	42
chr3_26.392667c	5	16	chr3_18.141429c	5	27	chr3_11.349301c	5	42
chr3_26.098422c	5	16	chr3_18.141427c	5	27	chr7_19.300555c	5	42
chr3_26.344419	5	16	chr3_18.141451c	5	27	chr5_23.114391c	5	42
chr3_30.321447c	5	16	chr3_18.14081	5	27	chr7_19.300534c	5	42
chr3_25.98505	5	17	chr3_17.927866	5	27	chr7_19.300561c	5	42
chr3_25.988638c	5	17	chr3_31.330401c	5	30	chr3_11.012869	5	42
chr3_25.618107	5	19	chr3_23.544287	5	30	chr5_23.11445c	5	42
chr3_25.333306	5	19	chr3_16.920688c	5	30	chr3_11.374317c	5	42
chr3_26.097726	5	20	chr3_16.920664c	5	30	chr7_18.645068c	5	42
chr3_25.674418	5	20	chr3_16.890935c	5	30	chr3_18.504736c	5	44
chr3_25.988717	5	20	chr3_31.277358c	5	31	chr4_8.39899c	5	44
chr3_25.333278	5	20	chr7_14.77686	5	32	chr3_18.504707c	5	44
chr3_25.915845c	5	20	chr3_23.544293c	5	32	chr3_10.599013c	5	44
chr3_26.09785	5	20	chr3_22.39771c	5	34	chr4_8.458835	5	47
chr3_26.09832	5	21	chr3_17.45143c	5	34	Rw14H21_LG5	5	48
chr3_23.907006c	5	23	chr3_22.059723c	5	34	chr2_6.94522	5	49
chr3_23.906896	5	23	chr3_22.059952c	5	34	CL2845_LG5	5	56
chr3_24.121024c	5	23	chr3_17.451371	5	34	chr3_8.347533c	5	69
chr3_23.906906c	5	23	chr3_22.397857c	5	34	chr3_8.332798c	5	69
chr3_24.010703c	5	23	chr3_17.480615c	5	34	chr3_18.862082c	5	69
chr3_23.876868c	5	23	chr3_22.397833c	5	34	chr3_18.737184c	5	69
chr3_23.87677	5	23	chr3_21.917422c	5	34	chr3_18.786629c	5	69
chr3_23.906817	5	23	chr3_22.397858c	5	34	chr3_20.098401c	5	69
chr3_23.876809c	5	23	chr3_22.397737c	5	34	chr3_19.14409c	5	69
chr3_24.010726c	5	24	chr2_18.464163	5	34	chr3_8.347534c	5	69
chr3_24.214573	5	24	chr3_22.969987	5	34	chr3_9.597186c	5	69
chr3_24.387564	5	24	chr3_21.073229	5	36	chr3_18.862084c	5	69
chr3_24.031721	5	24	chr3_14.124454	5	37	chr3_10.149417c	5	69
chr3_24.031731	5	24	chr3_20.303146	5	37	chr3_7.647396	5	70
chr3_23.876843c	5	24	chr4_29.11998c	5	39	chr3_7.904074c	5	70
chr3_24.805637	5	25	chr3_13.889605c	5	39	chr3_7.647455c	5	70
chr3_24.531405c	5	26	chr3_11.544922c	5	39	chr3_7.249251	5	72
chr3_18.141431c	5	27	chr3_13.154217	5	39	chr3_6.878892c	5	75
chr1_16.650317	5	27	chr3_11.544963c	5	39	chr3_6.554197c	5	75
chr7_2.574916	5	27	chr3_13.336658c	5	39	chr3_6.029755	5	76
chr3_18.141457c	5	27	chr3_12.975533c	5	39	chr3_6.491149	5	76
chr3_18.140765	5	27	chr3_10.972226c	5	42	chr3_2.919842c	5	77
chr3_18.141449c	5	27	chr3_11.01274c	5	42	chr3_2.91972c	5	77
chr3_24.95488	5	27	chr7_19.300596c	5	42	chr3_5.636736c	5	77

Appendix 3. Continued

J14-3 x VS

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_25.395373	5	77	chr1_2.99782c	5	91	chr2_11.953234	6	4
chr3_2.919827c	5	77	chr4_13.33456c	5	91	chr2_1.330128	6	6
chr3_2.919818c	5	77	chr4_22.650578c	5	96	chr4_31.779892	6	6
chr3_2.919722c	5	77	chr4_22.650506c	5	96	chr2_1.948992c	6	11
chr3_2.9198c	5	77	chr3_1.554004c	5	96	chr2_0.325939c	6	11
chr3_2.919721c	5	77	chr4_22.650569c	5	96	chr2_0.367748	6	11
chr3_2.919767c	5	77	chr4_22.65058c	5	96	chr2_0.325927c	6	11
chr3_2.919718c	5	77	chr3_1.553925c	5	96	chr2_1.948988c	6	11
chr3_5.636728c	5	77	chr4_22.650557c	5	96	chr2_0.361985	6	11
chr3_3.362056c	5	78	chr4_22.650513c	5	96	chr2_0.325942c	6	11
chr3_3.02146c	5	78	chr4_22.650584c	5	96	chr2_1.948843	6	11
chr3_3.020797c	5	78	chr4_22.650563c	5	96	chr2_0.325936c	6	11
chr3_3.36988	5	78	chr3_2.07766c	5	96	chr2_6.304781c	6	14
chr3_3.013559c	5	78	chr4_22.650595c	5	96	chr2_5.970519	6	14
chr3_3.362101c	5	78	chr3_1.184312	5	97	chr2_5.970529	6	14
chr3_3.013711	5	78	chr3_0.426359c	5	98	chr2_5.970562	6	14
chr3_3.369959c	5	78	chr3_0.42637c	5	98	chr2_5.97057	6	14
chr3_3.548351	5	81	chr3_0.426312c	5	98	chr2_5.970646	6	14
chr2_17.431947	5	82	chr3_0.426387c	5	98	chr2_5.944551	6	14
chr3_4.166241	5	85	chr3_0.426408c	5	98	chr2_6.304727	6	14
chr3_4.166224	5	85	chr3_1.133971c	5	98	chr2_8.819145	6	15
chr3_4.166274	5	85	chr3_0.426393c	5	98	chr2_18.164751	6	15
chr3_4.300187c	5	86	chr3_0.793647c	5	99	chr2_8.003546	6	16
chr3_4.298332	5	86	chr3_0.793655c	5	99	chr2_7.95486	6	16
chr3_4.306393c	5	87	chr3_0.405875c	5	101	chr2_7.106382	6	17
chr6_18.147322c	5	88	chr3_0.361349c	5	101	chr2_12.885057	6	18
chr3_4.535513c	5	88	chr3_0.669521c	5	101	chr2_10.531455	6	19
chr3_5.051009c	5	88	chr3_0.104302c	5	101	chr2_10.135844	6	19
chr3_5.0538c	5	88	chr3_0.479349c	5	101	chr2_10.531353	6	19
chr3_4.535636c	5	88	chr3_0.479389c	5	101	chr6_34.918756	6	21
chr6_12.992642c	5	88	chr3_0.361363	5	101	chr2_10.681647	6	21
chr3_4.920622c	5	88	chr2_5.131921	6	0	chr7_10.933577	6	21
chr3_4.920592c	5	88	chr2_11.362466	6	0	chr2_3.693971	6	21
chr3_4.687322c	5	88	chr2_5.74795	6	1	chr2_4.633461c	6	21
chr3_4.687313c	5	88	chr2_11.378663	6	1	chr2_3.125342	6	21
chr3_9.404351	5	89	chr2_4.827898c	6	1	chr2_9.216348	6	21
chr3_5.102709c	5	89	chr3_0.836562c	6	1	chr2_9.216428	6	21
chr4_19.414226c	5	91	chr2_11.177448c	6	1	chr2_13.249464	6	22
chr4_13.334543c	5	91	chr1_7.51307	6	1	chr2_13.972958	6	24
chr3_5.417621	5	91	chr2_11.953256	6	4	chr2_13.488901	6	24

Appendix 3. Continued

J14-3 x VS

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_14.34056	6	25	chr2_20.77553c	6	45	chr2_25.111031c	6	64
chr2_15.051366	6	29	chr2_21.841224c	6	45	chr2_24.223175c	6	64
chr2_15.425902c	6	29	chr2_21.843312c	6	45	chr2_25.107069c	6	64
chr2_14.901787	6	29	chr2_20.880527	6	45	chr2_25.111038c	6	64
chr2_15.426898c	6	29	chr2_21.207918c	6	45	chr2_24.626417c	6	64
chr2_14.972658	6	29	chr2_22.279852	6	46	chr2_25.111096c	6	64
chr2_15.050654	6	29	chr2_22.177298	6	47	chr2_23.449792c	6	67
chr2_15.425978c	6	29	chr2_22.17077	6	47	chr2_23.44984c	6	67
chr2_14.765773	6	29	chr2_28.465742c	6	48	chr2_23.381612c	6	67
chr2_15.644889	6	30	chr2_28.620281	6	48	chr2_23.248144c	6	68
chr2_15.696245	6	30	chr2_28.592051c	6	48	chr2_23.248062c	6	68
chr2_17.790202c	6	32	chr2_28.620278c	6	48	chr5_23.191635	7	0
chr2_18.164943	6	32	chr2_28.620283	6	48	chr5_23.191701c	7	0
chr2_17.790184c	6	32	chr2_26.345579c	6	50	chr5_23.191733	7	0
chr2_17.790205c	6	32	chr2_27.74727c	6	50	chr5_23.191688	7	0
chr2_18.0475c	6	32	chr2_26.77842c	6	50	chr5_10.682864	7	2
chr2_17.790193c	6	32	chr2_27.624581c	6	50	chr5_10.141077	7	2
chr2_17.832217	6	32	chr2_27.229593c	6	50	chr5_10.00788c	7	2
chr2_17.7902c	6	32	chr2_27.505643c	6	50	chr5_10.132037c	7	2
chr2_18.164901c	6	32	chr2_27.747377	6	50	chr5_10.007421c	7	2
chr2_17.790167c	6	32	chr2_27.229587c	6	50	chr5_10.094031	7	2
chr2_17.034695	6	33	chr2_27.349189c	6	50	chr5_10.132246c	7	2
chr2_17.106326c	6	33	chr2_25.946191c	6	54	chr5_9.433601	7	6
chr2_17.106329c	6	33	chr2_25.286422	6	56	Rw22B6_LG7	7	6
chr2_16.441018	6	35	chr2_25.306917c	6	56	chr5_9.433571	7	6
chr2_16.441156	6	35	chr2_25.312193c	6	56	chr5_9.488542	7	6
chr2_18.469813	6	35	chr2_25.312195c	6	56	chr5_9.690679	7	6
chr2_16.695571c	6	36	chr2_25.600381	6	56	chr5_9.370231c	7	8
chr2_18.267205	6	36	chr2_25.286319	6	56	chr5_9.431909c	7	8
chr2_18.555809	6	36	chr2_25.312197c	6	56	chr5_8.914843c	7	8
chr2_19.052861c	6	39	chr2_24.83113	6	57	chr5_8.890938c	7	8
chr2_19.598852c	6	41	chr2_24.626465c	6	57	chr5_9.040208c	7	8
chr2_19.35846c	6	41	chr2_24.412081c	6	57	chr5_8.627009	7	8
chr2_19.598747c	6	41	chr2_24.223229c	6	57	chr5_9.17276c	7	8
chr2_20.621921c	6	44	chr2_24.008582c	6	57	chr5_9.370183c	7	8
chr2_20.62179	6	44	chr2_25.107224	6	57	chr5_9.433505c	7	8
chr2_20.53017c	6	44	chr2_24.799377	6	57	chr5_9.431907c	7	8
chr2_20.621927c	6	44	chr2_25.111182c	6	57	chr5_9.387827c	7	8
chr2_21.649969	6	45	chr2_25.198478c	6	57	chr5_9.387917	7	8
chr2_20.880422c	6	45	CL2980_LG6	6	61	chr5_9.249829c	7	8

Appendix 3. Continued

J14-3 x VS

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_9.387902c	7	8	chr5_3.349344c	7	22	chr5_10.963069	7	27
chr2_8.848225	7	8	chr5_2.909303	7	22	chr5_11.429381	7	27
chr5_8.686755	7	8	chr5_2.909339	7	22	chr5_0.710208c	7	27
chr5_8.35421	7	9	chr3_4.920557c	7	22	chr5_0.040345	7	27
chr5_8.708276c	7	9	chr5_2.792707c	7	22	chr5_12.804039c	7	27
chr5_8.348061	7	9	chr4_10.569954	7	23	chr5_11.055686	7	27
chr5_7.678127c	7	11	chr5_2.018785c	7	23	chr5_10.962992	7	27
chr5_7.723451	7	11	chr5_2.018838c	7	23	chr5_0.040337c	7	27
chr5_7.723511c	7	11	chr5_1.861128c	7	23	chr6_18.094515	7	27
chr5_7.227119	7	11	chr5_1.861007c	7	23	chr5_0.801187c	7	27
chr5_7.227087	7	11	chr5_1.861049	7	23	chr5_13.064149c	7	27
chr5_7.723982c	7	11	chr5_1.861167c	7	23	chr5_11.704278	7	27
chr5_7.379853c	7	11	chr5_2.018709	7	23	chr5_12.7312c	7	27
chr5_6.12847c	7	12	chr5_2.972737c	7	23	chr5_12.731085c	7	27
chr5_6.804384	7	12	chr5_2.411627c	7	23	chr5_14.643872	7	27
chr5_5.410683c	7	12	chr4_10.569959	7	23	chr5_11.543543	7	27
chr5_6.804405	7	12	chr5_3.042214	7	23	chr5_12.731087c	7	27
chr5_5.379398	7	12	chr5_2.411625c	7	23	chr5_12.731108c	7	27
chr3_13.73016	7	12	chr5_1.932987c	7	23	chr5_12.731086c	7	27
chr5_6.804396	7	12	chr5_1.86118c	7	23	chr5_12.731069c	7	27
chr5_6.804403	7	12	chr5_0.926925	7	25	chr2_12.639404c	7	27
chr5_5.678439	7	12	chr5_1.090909c	7	25	chr5_12.731079c	7	27
chr5_6.128499c	7	12	chr5_1.407213c	7	25	chr5_15.295629c	7	27
chr2_27.350248	7	12	chr5_1.202761c	7	25	chr5_11.55092	7	27
chr5_6.804377	7	12	chr5_0.92704	7	25	chr3_2.011477c	7	27
chr5_6.712208	7	12	chr5_0.05375	7	26	chr5_15.434358	7	27
chr1_13.372515	7	14	chr5_0.524338c	7	26	chr5_14.711678	7	27
chr5_5.600425	7	15	chr5_0.626661c	7	26	chr5_15.295584c	7	27
chr5_5.410602c	7	15	chr5_0.295223	7	26	chr5_15.152198c	7	27
chr5_4.489986	7	16	chr5_0.667359	7	26	chr5_0.054614c	7	27
chr5_4.766226c	7	16	chr5_1.933083c	7	26	chr5_0.098049	7	27
chr5_5.037482	7	16	chr5_0.110605	7	26	chr5_11.140564c	7	27
chr5_4.638577c	7	16	chr5_0.110541	7	26	chr5_13.211011c	7	27
chr5_4.739302c	7	16	chr5_0.787991	7	26	chr5_11.140558	7	27
chr5_4.490021c	7	16	chr5_0.259815c	7	26	chr5_0.368279c	7	27
chr5_5.379243	7	16	chr5_0.054712c	7	26	chr5_13.0642c	7	27
chr5_4.438173	7	17	chr5_0.475123c	7	26	chr5_12.804034c	7	27
chr5_3.874056	7	20	chr5_1.933062c	7	26	chr5_0.053707	7	27
chr4_24.576999c	7	21	chr5_0.801544c	7	26	chr5_12.696572	7	27
chr5_2.972791c	7	22	chr5_0.363666	7	26	Rw5G14_LG7	7	32

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_11.704197	7	35	chr2_23.649136c	7	52	chr5_24.168277	7	68
chr5_14.067637c	7	36	chr5_20.579745c	7	52	chr5_24.226055c	7	68
chr5_14.067751	7	36	chr5_20.023504	7	52	chr4_10.569714c	7	68
chr4_2.910816	7	36	chr5_20.579721c	7	52	chr5_24.714243	7	68
chr4_14.967439	7	36	chr5_20.185025	7	52	chr5_25.163199c	7	68
chr5_11.704284	7	36	chr5_20.080087	7	52	chr5_26.07622	7	68
chr5_14.191365	7	36	chr5_20.185045	7	52	chr4_10.56977c	7	70
chr4_2.910806	7	36	chr5_20.185032	7	52	chr4_10.569757c	7	70
chr5_14.191438	7	36	chr4_24.271811c	7	52	chr4_10.569744c	7	70
chr5_14.06793	7	37	chr5_20.185016	7	52	chr5_25.163078c	7	74
chr5_17.849605c	7	39	chr5_20.185022	7	52	chr5_25.028373c	7	74
chr5_17.261523c	7	39	chr5_20.185018	7	52	chr5_26.061239	7	75
chr5_19.391871c	7	39	chr5_20.746975c	7	53	chr5_26.076577	7	75
chr5_19.39188c	7	39	chr7_10.933525c	7	55	chr5_26.372339c	7	75
chr5_19.391883	7	39	chr7_10.933544c	7	55	chr5_26.372423	7	75
chr5_16.760635	7	40	chr5_21.864814c	7	55	chr5_27.25375	7	75
chr5_16.760653c	7	40	chr5_21.86488c	7	55	chr5_28.886042	7	75
chr5_16.951673c	7	40	chr4_27.571075	7	56	chr5_26.969114c	7	75
chr5_17.261728c	7	40	chr4_27.571114c	7	56	chr5_26.969008c	7	75
chr5_17.521174c	7	42	RMS001_LG7	7	59	chr5_27.492158c	7	75
chr5_17.521236c	7	42	chr5_22.127936c	7	62	chr5_26.96924c	7	75
chr5_16.555027c	7	42	chr5_22.12794c	7	62	chr5_26.964228c	7	75
chr5_16.555025c	7	42	chr5_23.601754	7	62	chr5_26.372407	7	75
chr5_16.80285c	7	42	chr5_23.60183	7	62	chr5_26.310193	7	75
chr5_17.586455c	7	42	chr5_22.321321c	7	63	chr4_24.107276c	7	75
chr5_17.586475	7	42	chr5_22.414727c	7	63	chr5_26.372387	7	75
chr1_12.746504c	7	43	chr2_22.177116	7	63	chr5_27.461714	7	75
chr1_12.746465	7	43	chr5_5.218505c	7	65	chr5_27.040702c	7	75
chr5_18.155373c	7	43	chr5_24.225987	7	66	chr2_12.742083	7	75
chr5_18.539969	7	44	chr4_10.569793c	7	67	chr5_28.886088	7	75
Rh72_LG7	7	47	chr5_22.414823c	7	67	chr5_27.990212	7	76
chr5_18.540047	7	49	chr5_22.743561c	7	67	chr5_27.990199	7	76
chr5_18.540035	7	49	chr4_10.569787c	7	67	chr5_28.55575	7	78
chr5_18.28172	7	49	chr4_10.569749c	7	67	chr5_6.572694	7	78
chr5_19.831198c	7	50	chr4_10.569723c	7	67			
chr5_19.830985	7	50	chr4_10.569712c	7	67			
chr5_19.83114c	7	50	chr4_10.569785c	7	67			
chr5_20.185014	7	52	chr4_10.569742c	7	68			
chr5_20.185009	7	52	chr5_24.684607	7	68			
chr5_20.332037c	7	52	chr3_2.011494	7	68			

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_1.646368	1	0	chr7_15.151752	1	34	chr7_20.229757	1	51
chr7_1.646404	1	0	chr7_15.199629	1	34	chr7_20.231954	1	52
chr7_2.799483c	1	4	chr7_15.370485c	1	35	chr7_20.448404	1	52
chr2_5.970489	1	4	chr7_15.395736c	1	35	chr7_20.804998	1	53
chr2_5.970641	1	4	chr7_15.395727	1	36	chr7_20.728921	1	53
RhAB9-2_LG1	1	7	chr7_15.395728	1	36	chr7_20.645228c	1	53
chr4_24.537661	1	10	Rw34L6_LG1	1	36	chr7_20.64994c	1	53
chr7_5.726746	1	11	chr7_9.786157c	1	36	chr7_20.649892c	1	53
chr3_32.662785	1	13	chr7_16.411142	1	37	chr7_21.162359	1	54
chr5_0.63163c	1	13	chr7_16.59818	1	39	chr7_20.728966	1	54
chr5_0.631568c	1	13	chr7_16.623332	1	39	chr7_20.645239	1	54
chr7_5.856314	1	15	chr7_16.690217c	1	39	chr7_20.737408	1	55
chr6_10.901867	1	15	chr7_16.690209	1	39	chr7_22.042996	1	59
chr7_5.856391	1	15	chr7_17.61075	1	39	chr2_12.63942	1	59
chr7_7.996758	1	16	chr7_17.158766	1	39	RMS015_LG1	1	59
chr7_9.567824c	1	17	chr7_16.623282	1	39	chr7_22.043131	1	59
chr7_9.567817c	1	17	chr7_16.760096	1	39	chr7_22.316144	1	60
chr7_9.567815c	1	17	chr7_16.672845	1	39	chr7_22.556633	1	61
chr7_9.567811c	1	17	chr7_16.672896	1	39	chr7_22.840457	1	61
chr7_9.566961	1	17	chr7_16.760018c	1	39	chr7_23.03772	1	61
chr7_9.567808c	1	17	chr7_17.610635c	1	42	chr7_23.206148	1	64
chr7_8.28375	1	17	chr7_17.450961c	1	42	chr7_23.206146	1	65
chr7_9.785983	1	18	chr7_17.610663c	1	42	chr7_23.206126	1	66
chr7_9.153848	1	18	chr7_18.16492	1	46	chr1_0.141372c	2	0
chr7_9.153849	1	18	chr7_18.922785	1	46	chr1_0.141437	2	0
chr7_8.76812	1	18	H5_F12_LG1	1	46	chr1_0.49595	2	0
chr7_8.767971	1	19	chr7_18.667305c	1	46	chr1_0.824902	2	1
chr7_8.767988	1	19	chr7_18.177097	1	46	chr1_0.974818c	2	2
chr7_10.385832c	1	21	chr7_18.177083	1	46	chr1_1.359387	2	4
chr7_12.13403c	1	23	chr7_18.376963	1	46	chr1_1.359322	2	4
chr7_11.016267	1	23	chr7_18.207597	1	46	chr1_1.580327	2	4
chr7_11.21128	1	23	chr7_18.141361	1	46	chr1_1.394645	2	4
chr7_12.365489	1	25	chr7_18.177112	1	46	chr1_1.359634	2	4
chr7_12.917681	1	29	chr7_18.974728	1	47	chr1_1.593904	2	4
chr7_12.917696	1	29	chr7_18.376957	1	47	chr1_1.35928	2	4
chr7_13.531368	1	29	chr7_18.633293	1	47	chr1_1.90916	2	5
chr7_13.787815	1	31	chr7_19.312222c	1	48	chr1_1.580177	2	5
chr7_15.029067	1	32	chr7_19.312313c	1	48	chr1_1.569173	2	5
chr7_15.044078c	1	32	chr7_19.44362	1	49	chr1_1.394796	2	5
chr7_15.142932	1	34	chr7_20.086687	1	51	chr1_1.52833	2	5

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_1.165438	2	5	chr1_2.86597	2	11	chr1_5.965097	2	20
chr1_1.394736	2	5	chr1_2.340748	2	11	chr1_6.271448	2	20
chr1_2.00303	2	5	chr1_2.776887	2	11	chr1_5.332657	2	20
chr1_1.937206c	2	6	chr1_2.865922	2	11	chr1_5.065205	2	20
chr1_2.077982c	2	6	chr1_4.197263	2	12	chr1_6.290649	2	20
chr1_2.077827c	2	6	chr1_4.2068	2	12	chr1_5.96469	2	20
chr1_1.937134	2	6	chr1_4.197169	2	12	chr1_5.728871	2	20
chr1_2.077823	2	6	chr1_4.684388c	2	14	chr1_5.774378	2	20
chr1_1.909106	2	6	chr1_4.676262	2	14	chr1_6.042884	2	21
chr1_1.938093	2	6	chr1_4.684316c	2	14	chr1_5.964933c	2	21
chr1_2.003108	2	6	chr1_3.250244	2	15	chr1_5.964572	2	21
chr1_1.937087	2	6	chr1_3.034634	2	15	chr1_5.965028c	2	21
chr1_2.144312	2	8	chr1_3.674095	2	15	chr1_6.18483c	2	21
chr1_2.22285	2	8	chr1_3.984244	2	15	chr1_5.964646	2	21
chr1_2.222853	2	8	chr1_3.246888	2	15	chr1_6.737085	2	22
chr1_2.14433	2	8	chr1_3.152827	2	15	chr1_6.070727	2	22
chr1_2.100126	2	8	chr1_3.793592c	2	15	chr1_6.405722	2	23
chr1_2.474891	2	9	chr1_3.152848	2	15	chr1_6.349745	2	23
chr1_2.695716c	2	9	chr1_3.549677	2	15	chr1_9.459863	2	23
chr1_2.741197	2	9	chr1_3.775528	2	15	chr1_15.312104	2	24
chr1_2.499041	2	9	chr1_5.396793c	2	16	chr1_11.832123	2	24
chr1_2.736407c	2	9	chr1_4.320547	2	17	Rh48_LG2	2	24
chr1_2.47502	2	9	chr1_5.918587	2	17	chr1_11.664672	2	24
chr1_2.521837c	2	9	chr1_4.257791	2	17	chr1_15.571847	2	24
chr1_2.498949c	2	9	chr1_4.354796	2	17	chr1_10.11165c	2	24
chr1_2.732179	2	9	chr1_4.197324	2	17	chr1_12.431973	2	24
chr1_2.732099	2	9	chr1_5.533313	2	18	chr1_17.069182	2	24
chr1_2.446263	2	9	chr1_5.502625c	2	18	chr1_10.372077	2	24
chr1_2.47495	2	9	chr1_5.502691c	2	18	chr1_17.573164c	2	24
chr1_2.507772	2	9	chr1_6.042708c	2	20	chr1_10.495617	2	24
chr1_2.736373	2	9	chr1_6.27146	2	20	chr1_10.321864c	2	24
chr1_2.73631c	2	9	chr1_6.290644	2	20	chr1_17.069213c	2	24
chr1_2.776934c	2	9	chr1_5.065178	2	20	chr1_10.672085c	2	24
chr1_2.622826	2	9	chr1_4.996555	2	20	chr1_11.748741	2	24
chr1_2.736262	2	9	chr1_5.729018	2	20	chr1_17.101319	2	24
chr1_3.435632	2	10	chr1_5.793824c	2	20	chr1_7.834777	2	24
chr1_3.752717	2	10	chr1_5.332614	2	20	chr1_9.688526	2	24
chr1_3.793777c	2	10	chr1_5.065188	2	20	chr1_17.101317	2	24
chr1_2.880239	2	11	chr1_5.878782	2	20	chr1_11.51206	2	24
chr1_2.816973	2	11	chr1_5.964559	2	20	chr1_18.223742	2	24

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_10.922413	2	24	chr1_12.33644c	2	27	chr6_23.501482c	2	39
chr1_10.053152	2	24	chr1_15.312075	2	28	chr6_23.501483c	2	39
chr1_11.424441c	2	24	chr1_17.28848c	2	28	chr6_23.394609	2	39
chr1_9.459833	2	24	chr1_17.28847c	2	28	chr6_23.39451	2	39
chr1_10.449852c	2	24	chr1_17.288493c	2	28	chr6_23.481749	2	39
chr1_10.442521c	2	24	chr1_11.543007	2	28	chr6_23.501479c	2	39
chr1_16.650361	2	24	chr1_17.288555c	2	28	chr6_24.333503c	2	40
chr1_10.312816	2	24	chr1_17.288427c	2	28	chr6_24.662967	2	40
chr1_9.787356	2	24	chr1_17.288469c	2	28	chr6_25.644899	2	42
chr1_10.137503	2	24	chr1_17.337983c	2	28	chr6_25.644854	2	42
chr1_7.834765	2	24	chr1_15.311956	2	28	chr6_24.982882	2	42
chr1_10.612359	2	24	chr1_19.106105	2	28	chr6_24.983076	2	42
chr1_18.100552	2	24	chr1_18.223819	2	28	chr6_26.646145	2	43
chr1_11.543097	2	24	chr1_16.04228c	2	29	chr6_25.903305	2	43
chr1_7.163129	2	24	chr1_14.439482	2	30	chr6_25.73819	2	43
chr1_10.053197c	2	24	chr1_16.375525	2	30	chr6_26.295215	2	43
chr1_15.85486c	2	24	chr6_12.894821c	2	30	chr6_26.655966c	2	43
chr1_10.11151	2	24	chr1_15.00364	2	30	chr6_26.656326	2	43
chr1_18.100702c	2	24	chr1_16.466642	2	30	chr6_27.073507	2	44
chr1_9.504581	2	25	chr6_29.879491	2	30	chr6_27.344809c	2	44
chr1_7.507699	2	25	CL2996_LG2	2	30	chr6_27.543158	2	45
chr1_7.150574	2	25	chr1_18.912286	2	30	chr6_27.543135	2	45
chr1_11.74876	2	25	chr1_19.227311c	2	30	chr6_27.390111	2	45
chr1_10.372125	2	26	chr1_12.740688c	2	30	chr6_28.141808	2	45
chr1_10.372167	2	26	chr6_20.144288	2	31	chr6_28.141676	2	45
chr1_10.32181	2	26	chr6_20.501838	2	31	chr6_27.819291	2	45
chr1_10.672126c	2	26	chr6_20.425966	2	31	chr6_28.141748c	2	45
chr1_15.479862	2	27	chr6_20.532456c	2	31	chr6_27.839204	2	45
chr1_11.748681	2	27	chr6_20.425967c	2	32	chr6_29.098355c	2	47
chr1_11.832138c	2	27	chr6_20.14417c	2	32	chr6_29.149908	2	47
chr1_18.100665	2	27	chr6_21.444481	2	32	chr6_29.149967	2	47
chr1_12.540607c	2	27	chr6_22.305632	2	34	chr6_29.149769	2	47
chr1_12.399453	2	27	chr6_22.3055	2	34	chr6_29.149836c	2	47
chr1_11.5432	2	27	chr6_22.241836	2	34	chr6_28.960886c	2	47
chr1_11.748702c	2	27	chr6_22.964006	2	35	chr6_29.680161	2	47
chr1_12.540578c	2	27	chr6_23.898748c	2	35	chr6_29.154701	2	47
chr1_12.336615	2	27	chr6_22.020306c	2	37	chr6_29.154771c	2	47
chr1_11.748759c	2	27	chr6_22.241879	2	37	chr6_29.149772	2	47
chr1_12.540596c	2	27	chr6_23.59618	2	38	chr6_29.139475	2	47
chr1_11.664678c	2	27	chr6_23.454696	2	38	chr6_30.271617	2	49

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_30.271656	2	49	chr6_32.461294	2	58	chr6_35.934822	2	69
chr6_30.355331	2	49	chr6_33.040719	2	59	chr6_36.004464c	2	69
chr6_30.27165	2	49	chr6_32.953315	2	59	chr6_35.934824	2	69
chr6_30.845198	2	50	chr6_33.335228	2	59	chr6_36.004515c	2	69
chr6_30.967032c	2	50	chr6_33.335358	2	59	chr6_35.934743c	2	69
chr6_15.095193	2	50	chr6_33.531246	2	59	chr6_36.58703	2	74
chr6_31.531493	2	50	chr6_32.953336	2	59	chr6_36.93301c	2	74
chr6_30.634496	2	50	chr6_33.305252	2	59	chr6_36.844858c	2	74
chr6_30.95729	2	50	chr6_33.526163	2	59	chr6_36.58706	2	74
chr6_30.634039	2	50	chr6_33.531378	2	59	chr6_36.59146	2	74
chr6_31.699678	2	50	chr6_34.413787	2	59	chr6_36.587183	2	74
chr6_15.06843	2	52	chr6_33.525292	2	59	chr6_36.844926c	2	74
chr6_15.095292	2	52	chr6_33.592703	2	59	chr6_36.933091	2	74
chr6_15.068553	2	52	chr6_33.562306	2	59	chr6_37.028459	2	75
chr6_15.10856	2	52	chr6_33.953478	2	59	chr6_37.052831	2	75
chr6_31.531359	2	52	chr6_34.923112	2	60	chr6_37.028502	2	76
chr6_15.068559c	2	52	chr6_34.87606	2	60	chr6_37.136891	2	79
chr6_29.52846	2	53	chr6_34.923109	2	60	chr6_9.582408	2	79
chr6_29.412515	2	53	chr6_34.209615	2	61	chr6_37.184203	2	79
chr6_29.518701	2	53	chr6_34.131952	2	61	chr6_9.582354	2	79
chr6_29.528617	2	53	chr6_33.95328c	2	61	chr6_9.582303	2	79
chr6_14.994698	2	53	chr6_33.589239c	2	61	chr6_9.582276	2	79
chr6_29.528615	2	53	chr6_34.413807	2	64	chr6_9.58233	2	79
chr6_32.093971	2	54	chr6_34.545954	2	64	chr6_37.184197	2	79
chr6_32.094031	2	54	chr6_34.482688	2	64	chr6_37.18413	2	79
chr6_31.834871	2	55	chr6_34.653828	2	64	chr6_37.80096	2	81
chr6_32.412566	2	55	chr6_34.65381	2	64	chr6_37.800891	2	81
chr6_31.834685	2	55	chr6_34.27061	2	64	chr6_38.821311c	2	81
chr6_32.463306	2	55	chr6_35.174015	2	64	chr6_38.527314	2	81
chr6_33.233689	2	57	chr6_35.290819	2	66	chr6_37.540081	2	81
chr6_33.233603	2	57	chr6_34.923102	2	66	chr6_37.8009	2	82
chr6_33.242307	2	57	chr6_35.286285c	2	66	chr6_38.149769c	2	84
chr6_33.264286	2	57	chr6_35.357943	2	66	chr6_0.106933	3	0
chr6_32.975416	2	57	chr6_36.295734c	2	68	chr6_0.106957c	3	0
chr6_33.051694	2	57	chr6_35.965591	2	69	chr6_0.258258	3	2
chr6_33.215643	2	57	chr6_36.073413	2	69	chr6_0.288153c	3	5
chr6_32.975531	2	57	chr6_35.934748	2	69	chr6_0.594973	3	6
chr6_33.240419	2	57	chr6_36.004476	2	69	chr6_0.537091	3	6
chr6_33.026304	2	57	chr6_36.295664	2	69	chr6_0.811129	3	7
chr6_33.264241c	2	57	chr6_36.633987	2	69	chr6_0.811506	3	7

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_1.482509	3	12	chr6_8.679661	3	37	chr4_1.558722	4	1
chr6_1.816463	3	15	chr6_8.614712c	3	37	chr4_0.624757	4	1
chr6_1.816456	3	15	chr6_9.032051c	3	37	chr4_0.624824	4	1
chr6_1.86829c	3	15	chr5_5.161425	3	41	chr4_0.624747	4	1
chr6_1.826124	3	15	chr6_10.950386	3	42	chr1_16.466659	4	1
chr6_1.826127	3	15	BFACT47_LG3	3	46	chr1_14.815301	4	1
chr6_1.816453	3	15	chr6_17.519102	3	46	chr4_1.558806	4	1
chr6_1.816439	3	15	chr6_17.519049	3	46	chr4_0.624754	4	4
chr6_1.868386	3	15	chr6_17.519042c	3	46	chr4_1.608475	4	5
chr6_1.868258	3	15	chr6_18.103511	3	46	chr4_2.61772c	4	5
chr6_2.263139	3	17	chr6_18.651777	3	48	chr4_3.23362	4	6
chr6_2.96574c	3	22	chr6_17.096951	3	48	chr6_29.493328	4	8
chr6_2.965689c	3	22	chr6_17.070224	3	48	chr4_16.099712	4	8
chr6_2.965734c	3	22	chr6_15.942954c	3	48	chr4_10.785015	4	9
chr6_3.272502	3	24	chr6_17.096884	3	48	chr4_13.333919	4	11
chr6_3.326291	3	24	chr3_3.416949	3	48	chr1_2.202128	4	11
chr6_3.445019	3	25	chr6_18.094868c	3	48	chr4_10.378642	4	11
chr6_3.739383c	3	26	chr6_17.070391	3	48	chr1_2.202074	4	11
chr6_3.666389	3	26	chr6_17.734756	3	48	chr4_6.609542	4	11
chr6_4.262795	3	26	chr6_13.183503	3	49	chr4_4.680704	4	11
chr6_4.175209	3	26	chr4_23.601554	3	49	chr4_4.871904	4	11
chr6_4.332478	3	27	chr6_13.183501	3	49	chr1_2.202091	4	11
chr6_4.332494	3	27	chr1_12.90737	3	50	chr4_4.300849	4	11
chr6_4.371663	3	28	chr2_2.65768	3	52	chr4_10.902818	4	11
Rw35C24_LG3	3	29	chr4_14.903227	3	52	chr4_10.022851	4	11
chr6_4.777858	3	29	chr1_17.717705	3	52	chr4_4.680702c	4	11
chr6_4.932935	3	30	chr1_13.372591	3	52	chr3_0.669406	4	13
chr6_5.300312c	3	30	chr1_14.303597	3	52	chr4_13.538034	4	13
chr6_5.300289c	3	30	chr1_13.372442	3	52	chr4_14.26513	4	13
Rw12J12_LG3	3	35	chr1_13.963853	3	52	chr4_5.442548c	4	13
chr6_7.649678	3	35	chr1_17.893831	3	52	chr4_6.705474	4	13
chr6_7.55052c	3	35	chr3_23.543973	3	52	chr4_4.907813	4	13
Rh50_LG3	3	36	chr3_23.543923	3	52	chr6_5.051434c	4	13
chr6_7.702565	3	36	chr1_21.072247	3	58	chr4_10.024609c	4	14
chr3_27.736901	3	36	chr6_15.94289	3	65	chr4_10.024632c	4	14
chr6_9.032021	3	37	chr6_18.270658	3	68	RhABT12_LG4	4	15
chr6_8.662557c	3	37	chr2_7.10623c	4	0	chr4_14.265105c	4	16
chr6_8.662506c	3	37	chr2_7.10627c	4	0	chr4_15.551447	4	17
chr6_8.66257	3	37	chr2_7.106283c	4	0	chr3_5.97957	4	17
chr6_8.978886	3	37	chr2_7.106241c	4	0	chr4_15.244556	4	19

Appendix 3. Continued

OB x RF								
Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_14.967475	4	19	chr4_20.363091	4	27	chr4_25.551913	4	31
chr4_15.244486	4	19	chr4_20.324657	4	27	chr4_24.079682	4	31
chr4_15.572828c	4	20	chr4_22.519456	4	27	chr4_26.044602	4	31
chr4_15.572876c	4	20	chr4_23.043013	4	27	chr4_26.344736	4	31
chr4_15.572861c	4	20	chr4_22.519554	4	27	chr4_25.693012	4	31
chr4_15.621967	4	21	chr4_22.384156c	4	27	chr4_24.14107	4	31
chr4_16.933603	4	21	chr4_20.853208	4	27	chr4_26.344803	4	31
chr3_5.979542	4	21	chr4_20.363069	4	27	chr4_26.044632	4	31
chr2_24.585	4	22	chr4_20.706136	4	27	chr4_25.551889	4	31
chr4_16.895077	4	22	chr4_20.365723c	4	27	chr3_6.491077	4	31
chr4_16.895061	4	22	chr4_23.227857	4	27	chr4_26.053815	4	31
chr4_16.895123	4	22	chr4_23.227843c	4	27	chr4_26.347188c	4	31
chr4_16.89505	4	23	chr4_23.12628	4	27	chr4_24.14099	4	31
chr4_16.679197c	4	23	chr4_22.892014c	4	27	chr4_24.079633	4	31
chr4_19.027117	4	23	chr2_0.264421	4	27	chr4_24.870399	4	31
chr3_32.662954	4	23	chr4_20.853281	4	27	chr3_6.449225	4	31
chr2_24.584797	4	23	chr4_23.043038	4	27	chr4_24.709745	4	31
chr4_16.000934	4	23	chr4_23.043134	4	27	chr4_25.378617	4	31
chr4_16.140598	4	23	chr4_23.227868	4	27	chr4_26.442568	4	34
chr4_16.679267c	4	23	chr4_23.357974	4	29	chr4_26.442561	4	34
chr4_16.666493	4	23	chr4_23.766049	4	29	chr4_17.246397	4	35
chr4_16.000819	4	23	chr4_23.869726c	4	30	chr4_27.445737c	4	35
chr4_20.265456c	4	26	chr4_23.959293c	4	30	chr4_17.246387	4	35
chr4_19.559693	4	26	chr4_25.723911c	4	30	chr4_26.770355c	4	35
chr4_19.559636	4	26	chr4_23.895982c	4	30	chr4_24.107153c	4	35
chr4_21.108597	4	27	chr4_25.693131c	4	30	chr4_24.14093	4	35
chr4_19.82994	4	27	chr4_23.95931c	4	30	chr4_26.225406c	4	36
chr4_20.265549	4	27	chr4_25.170109	4	30	chr4_27.11645c	4	36
chr4_20.800442	4	27	chr4_25.693034c	4	30	chr4_27.098452	4	36
chr4_22.66421	4	27	chr4_23.959311c	4	30	chr4_27.264868	4	36
chr4_20.983941c	4	27	chr4_25.69303c	4	30	chr4_27.29543	4	36
chr4_25.585298c	4	27	chr4_23.895969	4	30	chr4_27.681531c	4	36
chr4_22.657084	4	27	chr4_23.895971	4	30	chr4_27.561547	4	36
chr4_19.829848	4	27	chr4_23.895991c	4	30	chr4_27.264885	4	36
chr4_20.700236	4	27	chr4_23.7658	4	30	chr4_27.109568	4	36
chr4_22.657192	4	27	chr4_25.90357	4	30	chr4_27.264889	4	36
chr4_20.800415	4	27	chr4_23.959349	4	30	chr4_26.225291c	4	36
chr4_21.108724	4	27	chr4_24.870423	4	30	chr4_26.235324c	4	36
chr4_21.693218	4	27	chr4_24.753699	4	31	chr4_26.225404c	4	36
chr4_20.70626	4	27	chr4_24.870345	4	31	chr4_26.225259c	4	36

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_26.225428	4	36	chr4_31.61281	4	53	chr3_1.055824c	5	11
chr4_26.225749	4	36	chr4_31.14001	4	53	chr3_1.553932	5	11
chr4_26.225769	4	36	chr4_30.429149	4	54	chr3_2.696516	5	13
chr4_26.225403	4	36	chr4_30.584409	4	55	chr1_2.99782c	5	13
chr4_27.981343	4	37	chr4_30.584408c	4	55	chr4_13.334543c	5	13
chr4_26.248417	4	37	chr4_30.93957	4	56	chr3_2.449563	5	13
chr4_26.248425	4	37	chr4_30.928983	4	56	chr3_2.696615c	5	13
chr4_28.17272	4	38	chr4_30.929007c	4	56	chr3_2.220758	5	13
chr4_28.548139	4	38	chr4_30.939643	4	56	chr3_2.449709	5	13
chr4_29.121993	4	40	chr4_30.92891	4	56	chr4_13.33456c	5	13
chr4_29.122035	4	40	chr4_31.18604	4	57	chr1_2.997769	5	13
chr4_29.482254	4	41	chr4_31.213549	4	57	chr1_2.997796	5	13
chr4_29.545641	4	42	chr4_31.588428c	4	59	chr3_2.75611	5	13
chr4_29.600227	4	43	chr4_31.588419c	4	59	chr3_2.756146	5	13
chr4_27.99233c	4	44	chr4_32.06823c	4	61	chr7_11.30447	5	13
chr4_27.922673	4	44	chr4_32.094305	4	61	chr3_4.920592c	5	15
chr4_28.687601c	4	44	chr4_32.068076c	4	61	chr3_4.920622c	5	15
chr4_27.992332c	4	44	chr3_0.479349c	5	0	chr4_13.334563	5	16
chr4_28.051206	4	44	chr3_0.479389c	5	0	chr3_4.687322c	5	16
chr1_7.834627	4	44	chr3_0.545528c	5	0	chr6_18.147322c	5	16
chr4_29.422516	4	45	chr3_0.669521c	5	1	chr3_4.687369	5	16
chr4_29.387028	4	45	chr3_0.793647c	5	4	chr3_4.791511c	5	16
chr4_29.387027c	4	45	chr3_0.869195	5	4	chr3_4.70952	5	16
chr4_29.277525	4	45	chr3_0.793645	5	4	chr3_4.687313c	5	16
chr4_29.691759	4	46	chr3_0.869261	5	4	chr6_12.992642c	5	17
chr4_29.746082	4	46	chr3_0.426359c	5	7	chr6_12.992669	5	17
chr4_29.594662	4	46	chr3_0.426312c	5	7	chr6_12.992792	5	18
chr4_29.591117	4	46	chr3_1.133971c	5	7	chr3_4.526267	5	18
chr4_29.594806	4	46	chr3_0.426387c	5	7	chr3_5.012772	5	19
chr4_29.859004	4	47	chr3_0.42637c	5	7	chr3_4.300187c	5	19
chr4_30.111196c	4	47	chr3_0.869268c	5	9	chr3_4.796164	5	22
chr4_29.956147c	4	47	chr3_0.869271c	5	9	chr3_4.642829	5	22
chr4_30.111712c	4	47	chr3_0.869152c	5	9	chr3_3.163648	5	22
chr4_29.746187	4	47	chr3_0.793655c	5	9	chr3_3.313825c	5	22
chr4_30.146063	4	47	chr3_0.972201c	5	10	chr3_3.497486	5	22
chr4_30.309085	4	48	chr3_1.208568c	5	11	chr3_3.346242	5	22
chr4_30.208266c	4	49	chr3_1.136064c	5	11	chr3_3.346244	5	22
chr4_30.429096	4	51	chr3_2.220732	5	11	chr3_3.313779	5	22
chr3_5.902116	4	53	chr3_2.077597	5	11	chr3_3.776746	5	22
chr4_31.186	4	53	chr3_1.184325c	5	11	chr3_3.346134	5	22

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_2.987201	5	23	chr3_9.597186c	5	33	chr7_19.300581c	5	37
chr6_29.345705	5	23	chr4_29.594789	5	33	chr3_11.349301c	5	37
chr3_3.362055	5	23	chr3_20.098401c	5	33	chr3_11.01274c	5	37
chr3_3.49741	5	23	chr4_29.594838	5	33	chr7_19.300561c	5	37
chr3_2.919821	5	23	chr3_18.737374	5	34	chr3_10.598993	5	37
chr3_2.905092	5	23	chr3_18.994326	5	34	chr7_19.300596c	5	37
chr3_2.919767c	5	23	chr3_19.482062c	5	34	chr3_11.544979	5	38
chr3_3.020797c	5	23	chr3_18.616047	5	34	chr3_11.861412	5	38
chr3_2.919818c	5	23	chr3_18.737181c	5	34	chr3_11.349294	5	38
chr3_2.919842c	5	24	chr3_8.683165	5	34	chr3_11.861432	5	38
chr3_3.3463	5	24	chr3_10.025053	5	34	chr5_9.431825	5	38
chr3_2.919798	5	24	chr5_0.053562	5	34	chr3_11.55402	5	38
chr3_2.987219	5	24	chr3_10.146899	5	34	chr3_11.374317c	5	38
chr3_2.919827c	5	24	chr6_3.553754	5	34	chr5_23.114511	5	38
chr3_2.905095	5	24	chr3_18.629716c	5	34	chr3_11.64811c	5	38
chr3_2.905097	5	24	chr3_18.61594	5	34	chr3_11.648012	5	38
chr3_6.123998	5	27	chr3_18.629793c	5	34	chr3_11.544922c	5	38
chr3_6.600776	5	27	chr3_19.957388	5	34	chr3_11.544963c	5	38
chr3_6.739909	5	27	chr3_19.144099c	5	34	chr3_13.915841	5	40
chr3_6.741723	5	27	chr3_19.144165	5	34	chr3_13.559796	5	40
chr3_6.739921	5	27	chr3_19.14409c	5	34	chr3_13.336658c	5	40
chr3_6.376783	5	27	chr3_18.786671	5	35	chr5_27.492158c	5	42
chr2_12.639441	5	29	chr3_18.504736c	5	35	chr3_14.124476	5	45
chr3_7.904143c	5	29	chr3_18.786668	5	35	chr3_21.073123	5	45
chr3_6.56816	5	29	chr3_18.569408	5	35	chr3_21.07283	5	45
chr3_7.647455c	5	29	chr3_8.683186	5	35	chr3_20.303287	5	45
chr3_7.657957c	5	29	chr3_18.44298	5	35	chr3_21.073097	5	45
chr3_8.014088c	5	29	chr4_8.458825c	5	35	chr3_20.303098	5	45
chr3_6.554197c	5	29	Rw14H21_LG5	5	35	chr3_12.413019	5	46
chr3_7.955774	5	31	chr4_8.458814c	5	35	chr3_13.889638	5	46
chr3_6.848796	5	31	chr7_18.645068c	5	35	chr3_17.480615c	5	47
chr3_7.647398	5	31	chr4_8.399065c	5	35	chr3_22.67851c	5	47
chr3_8.190653	5	31	chr3_10.598995	5	36	chr3_31.27734	5	47
chr3_9.287642	5	32	chr3_10.599066	5	36	chr3_22.969965c	5	47
chr3_9.743527	5	32	chr3_10.599013c	5	36	chr3_31.714889	5	48
chr3_9.163452	5	32	chr4_8.39899c	5	37	chr3_22.678583c	5	48
chr3_9.287623	5	32	chr7_19.300555c	5	37	chr3_16.621877	5	48
chr3_9.83606	5	33	chr3_10.972226c	5	37	chr3_22.970556	5	48
chr3_9.163581	5	33	chr3_10.606866	5	37	chr3_31.330401c	5	48
chr3_9.597026c	5	33	chr7_19.300534c	5	37	chr3_31.330487	5	48

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_22.678527c	5	48	chr3_24.711556	5	56	chr3_27.330373	5	62
chr3_22.969637c	5	48	chr3_24.711559	5	56	chr3_26.344475	5	62
chr3_22.971414c	5	48	chr3_24.711579	5	56	chr3_27.074702c	5	62
chr3_31.33046c	5	48	chr3_23.876843c	5	57	chr3_27.58572	5	62
chr3_22.678449	5	48	chr3_23.876868c	5	57	chr3_26.392817	5	62
chr4_12.462564	5	48	chr3_24.010497	5	57	chr3_26.392692	5	65
chr3_22.971397c	5	48	chr3_24.531405c	5	57	chr3_26.495861c	5	65
chr4_12.462544	5	48	chr3_24.214576	5	57	chr3_27.721788	5	65
chr3_22.971405c	5	48	chr3_24.121041	5	57	chr3_27.736828	5	65
chr3_17.311898	5	48	chr3_24.594107	5	57	chr3_27.723222	5	65
chr3_31.277358c	5	48	chr3_24.050323	5	57	chr3_27.830538c	5	65
chr3_23.544461c	5	48	chr3_24.121044	5	57	chr3_29.236232c	5	68
chr2_12.225895c	5	48	chr3_24.594162	5	57	chr3_29.472835	5	68
chr3_16.920664c	5	48	chr3_23.906895	5	57	chr3_30.32148	5	68
chr2_18.464163	5	48	chr3_24.214642	5	57	chr3_29.719209	5	68
chr3_21.072572	5	48	chr3_24.01077	5	57	chr3_29.103306	5	68
chr3_22.969731	5	48	chr3_24.010726c	5	57	chr3_29.719252	5	68
chr3_20.30323	5	48	chr3_24.031721	5	57	chr3_29.568573	5	68
chr3_17.311759	5	48	chr3_23.876809c	5	57	chr3_30.527588c	5	69
chr3_22.970551	5	48	chr5_16.160451	5	58	chr3_30.527495	5	69
chr3_23.544333	5	48	chr5_16.132983	5	58	chr3_30.527545	5	69
chr3_16.890935c	5	48	chr5_16.160459	5	58	chr5_12.390497	5	70
chr3_23.544293c	5	48	chr5_16.160301	5	58	chr3_29.185758	5	70
chr3_15.80301	5	48	chr3_24.010703c	5	58	chr3_29.103285	5	70
chr3_23.598381c	5	48	chr3_26.906643c	5	59	chr3_32.277768c	5	71
chr3_16.920496	5	48	chr2_27.006425	5	60	chr3_32.277762	5	71
chr3_16.890937c	5	48	chr3_25.782337c	5	60	chr3_32.277741c	5	71
chr2_12.225907c	5	48	chr7_21.83421	5	60	chr3_32.27784	5	71
chr3_15.803015	5	48	chr3_26.056318	5	60	chr3_32.592274	5	73
chr3_27.830421	5	52	chr3_25.750115	5	60	chr3_32.592277	5	73
chr3_18.141449c	5	53	chr3_26.033666c	5	60	chr3_32.602146c	5	73
chr3_18.141431c	5	53	chr3_25.618262	5	60	chr3_29.56546	5	73
chr3_17.986965	5	53	chr3_25.915845c	5	60	chr3_29.565427	5	73
chr3_18.141451c	5	53	chr3_25.618143	5	60	chr3_30.218792	5	77
chr3_18.141429c	5	53	chr7_21.834239	5	60	chr3_30.218807	5	77
chr3_18.141454c	5	53	chr3_26.20099c	5	61	chr3_33.10348	5	80
chr3_18.141457c	5	53	chr3_26.09832	5	61	chr3_32.675821	5	80
chr3_18.141427c	5	53	chr3_26.200949	5	61	chr3_32.663302	5	80
chr3_24.921938	5	55	chr3_26.098422c	5	62	chr3_33.103506	5	80
chr7_2.574894	5	56	chr3_26.495694	5	62	chr3_32.547276	5	80

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_11.37881	6	0	chr2_15.426851	6	38	chr2_28.34139	6	46
chr2_11.378807	6	0	chr2_18.164901c	6	39	chr2_28.658488	6	46
chr2_11.380942	6	0	chr2_13.119851	6	40	chr2_28.620278c	6	46
chr2_11.378826	6	0	chr2_13.494187	6	40	chr2_28.59198	6	46
chr2_11.36242	6	1	chr2_13.469506	6	40	chr2_24.585006	6	47
chr2_11.33994	6	1	chr2_17.859885	6	41	chr2_18.557623	6	48
chr2_11.340019	6	1	chr2_13.972958	6	41	chr2_18.522509	6	48
chr2_5.249675	6	6	chr2_13.97291	6	41	chr2_18.900138	6	48
chr2_4.92821	6	9	chr2_14.340485	6	41	chr2_18.469778	6	48
chr2_4.827805	6	9	chr2_21.84121	6	41	chr2_18.458047	6	48
chr2_2.118021	6	10	chr2_17.790181	6	42	chr2_28.056693	6	48
chr2_2.117933	6	10	chr2_17.790252	6	42	chr2_19.052872	6	49
chr2_1.948988c	6	10	chr2_17.790193c	6	42	chr2_19.052925	6	49
chr2_14.670491	6	11	chr2_17.79019	6	42	chr2_28.019885	6	50
chr2_0.387723	6	11	chr2_17.790202c	6	42	chr2_20.26184	6	50
chr2_0.387676	6	11	chr2_20.896474	6	42	chr2_19.598852c	6	50
chr2_0.325936c	6	11	chr2_21.380622	6	42	chr2_19.750382	6	50
chr2_0.325927c	6	11	chr2_17.790205c	6	42	chr2_19.598747c	6	50
chr2_0.325939c	6	11	chr2_15.426889	6	42	chr2_20.296403	6	50
chr2_6.245599	6	11	chr2_21.693089	6	42	chr2_19.605786	6	50
chr2_0.361984	6	11	chr2_18.952375	6	42	chr2_19.35846c	6	50
chr2_5.888786	6	11	chr2_21.390856	6	42	chr2_19.598876	6	50
chr2_0.38754	6	11	chr2_19.706908	6	42	chr2_19.534463	6	50
chr2_6.470938	6	11	chr3_30.378651	6	42	chr2_27.920995	6	51
chr2_6.417988	6	11	chr2_21.841208	6	42	chr2_19.53446	6	51
chr2_8.127134	6	14	chr2_19.052988	6	42	chr2_20.697599	6	51
chr2_8.832624	6	14	chr2_18.55581	6	42	chr2_20.775521	6	51
chr5_21.721446	6	14	chr2_14.784953	6	42	chr6_30.858031	6	51
chr2_8.832534	6	14	chr2_18.267204	6	42	chr2_20.497466	6	51
chr2_7.106386	6	17	chr2_17.666156	6	42	chr2_20.77553c	6	51
chr2_12.770204	6	20	chr2_22.17719	6	43	chr2_20.53017c	6	51
chr4_14.967591	6	21	chr2_17.239977	6	44	chr2_20.497457	6	51
chr2_10.681617	6	24	chr2_17.10644	6	44	chr2_20.497565	6	51
chr3_1.412857	6	24	chr2_17.106347	6	44	chr2_21.649972	6	52
chr7_10.93348	6	36	chr2_17.106329c	6	44	chr2_27.349152	6	52
chr2_9.184693	6	36	chr2_17.106326c	6	44	chr2_27.34915	6	52
chr2_14.785022	6	38	chr2_17.240048	6	44	chr2_21.490313	6	53
chr2_14.90176	6	38	chr2_16.843031	6	45	chr2_21.23102	6	53
chr2_14.78504	6	38	chr2_16.843067	6	45	chr2_21.808213	6	53
chr2_14.901714	6	38	chr2_16.874554	6	45	chr2_20.878211	6	53

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_20.880422c	6	53	chr2_26.347466	6	57	chr2_23.449792c	6	64
chr2_20.873439	6	53	chr2_25.946191c	6	58	chr2_23.822395	6	64
chr2_20.881385	6	53	chr2_26.005039	6	58	chr2_23.44995	6	64
chr2_21.806912	6	53	chr2_25.96824	6	59	chr2_25.111182c	6	68
chr2_27.22064	6	53	chr2_25.57052	6	60	chr2_25.111031c	6	68
chr2_27.206423	6	53	chr2_25.600576	6	60	chr2_25.111084	6	68
chr2_27.220718	6	53	chr2_25.570533	6	60	chr2_25.111038c	6	68
chr2_21.848868	6	54	chr2_25.224304	6	61	chr2_25.111043c	6	68
chr2_21.841255	6	54	chr2_25.224352	6	61	chr2_25.107069c	6	68
chr2_28.675051	6	54	chr2_25.286312	6	61	chr2_24.646143	6	83
chr2_28.563499	6	54	chr2_25.312213	6	61	chr2_24.626373	6	83
chr2_27.106488	6	55	chr2_25.312219	6	61	chr2_24.501579	6	83
chr2_27.106572	6	55	chr2_25.706236	6	61	chr2_24.626417c	6	83
chr2_27.624581c	6	55	chr2_25.529379	6	61	CL2980_LG6	6	83
chr2_27.987994	6	55	chr2_25.312202	6	61	chr2_24.591805	6	83
chr2_28.041839	6	55	chr2_25.312195c	6	61	chr2_24.412081c	6	83
chr2_28.041467	6	55	chr2_24.927698c	6	61	chr2_24.130067	6	84
chr2_28.041695	6	55	chr2_25.71126	6	61	chr2_24.033072	6	84
chr2_28.046851	6	55	chr2_25.312197c	6	61	chr2_23.39929	6	88
chr2_28.019879	6	55	chr2_25.111174	6	61	chr2_23.449957	6	88
chr2_28.046701	6	55	chr2_25.529398	6	61	chr2_23.449693c	6	88
chr2_27.657306c	6	55	chr2_25.286467	6	61	chr2_23.381612c	6	88
chr2_27.384565	6	56	chr2_25.30694	6	61	chr3_18.443098	6	90
chr2_27.244168	6	56	chr2_24.62641	6	62	chr2_22.876667	6	90
chr2_27.505643c	6	56	chr2_24.646116	6	62	chr2_23.248062c	6	90
chr2_27.505821	6	56	chr2_24.591842	6	62	RMS043_LG7	7	0
chr2_27.34911	6	56	chr2_24.412051	6	62	chr5_10.132242c	7	4
chr2_27.206317	6	56	chr2_24.27388	6	62	chr5_8.626905	7	4
chr2_26.227822	6	57	chr2_24.273834	6	62	chr5_8.6719	7	4
chr7_1.837513	6	57	chr2_24.273841	6	62	chr5_8.686768	7	4
chr2_26.77842c	6	57	chr2_24.130025	6	63	chr5_8.68689	7	4
chr2_26.345516	6	57	chr2_24.231875	6	63	chr5_8.890845	7	4
chr2_27.038027	6	57	chr2_24.033015	6	63	chr5_8.890938c	7	4
chr2_26.345579c	6	57	chr2_24.008582c	6	63	chr5_8.908206c	7	4
chr2_26.476926	6	57	chr2_22.876628	6	64	chr5_8.914751	7	4
chr2_26.62235	6	57	chr2_23.449751	6	64	chr5_9.040208c	7	4
chr2_26.778409	6	57	chr2_23.822327	6	64	chr5_9.370183c	7	4
chr2_27.03789	6	57	chr2_23.822264	6	64	chr5_9.387827c	7	4
chr2_26.347536	6	57	chr2_23.248213	6	64	chr5_9.387902c	7	4
chr2_26.778402	6	57	chr3_18.443116	6	64	chr5_9.508023	7	4

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_9.881391	7	4	chr5_5.037526	7	21	chr5_1.860992	7	27
chr5_9.911991c	7	4	chr5_5.03758	7	21	chr5_1.861	7	27
chr5_9.922619	7	4	chr5_5.037583	7	21	chr5_1.861049	7	27
chr5_9.983661	7	4	chr5_5.037586	7	21	chr5_1.881454	7	27
chr5_9.994374c	7	4	chr5_5.03759	7	21	chr5_1.933062c	7	27
Rw22B6_LG7	7	4	chr5_5.061345	7	21	chr5_1.861007c	7	28
chr5_9.061762	7	10	chr5_4.243755	7	21	chr5_1.861115	7	28
chr5_8.890932	7	10	chr5_4.306304	7	21	chr5_1.861128c	7	28
chr5_8.914843c	7	10	chr5_4.739272	7	21	chr5_1.861167c	7	28
chr5_8.39521	7	13	chr5_4.766091	7	21	chr5_1.86118c	7	28
chr5_8.348061	7	14	chr5_4.766226c	7	21	chr5_1.881442	7	28
chr5_7.72349	7	16	chr5_4.785243	7	21	chr5_1.932987c	7	28
chr5_7.379798	7	16	chr5_5.161752c	7	21	chr5_0.475123c	7	29
chr5_7.379853c	7	16	chr5_5.161795	7	21	chr5_0.475269	7	29
chr5_7.707963	7	16	chr5_5.161854c	7	21	chr5_0.710184	7	29
chr5_7.723982c	7	16	chr5_5.410683c	7	21	chr5_0.722916	7	29
chr5_6.804396	7	17	chr5_5.60031	7	21	chr5_0.926925	7	29
chr5_6.804483	7	17	chr5_5.600325	7	21	chr5_1.131484	7	29
chr5_7.379825	7	17	chr5_5.612412	7	21	chr5_1.202728	7	29
chr5_7.677984	7	17	chr5_6.066587	7	21	chr5_0.710208c	7	29
chr5_7.678127c	7	17	chr5_6.128112c	7	21	chr5_0.801187c	7	29
chr5_8.056821	7	17	chr5_6.513726	7	21	chr5_1.202761c	7	29
chr5_6.848931	7	17	chr5_6.680437	7	21	chr5_0.801171	7	29
chr2_27.350163	7	17	chr5_6.71227	7	21	chr5_1.131479	7	29
chr5_22.550855	7	21	chr5_5.226128	7	21	chr5_0.626796	7	29
chr5_3.180386	7	21	chr3_4.920557c	7	22	chr5_1.476786	7	29
chr5_3.180388	7	21	chr5_2.018785c	7	24	chr5_0.927025	7	29
chr5_3.495738	7	21	chr5_2.018838c	7	24	chr5_1.476795	7	29
chr5_4.243693	7	21	chr5_2.069239	7	24	chr5_1.407213c	7	29
chr5_4.30626	7	21	chr5_2.239591c	7	24	chr5_0.240038	7	30
chr5_4.461665	7	21	chr5_2.792707c	7	24	chr5_0.363613	7	30
chr5_4.461692	7	21	chr5_2.909445	7	24	chr5_0.368219	7	30
chr5_4.490021c	7	21	chr5_3.366289	7	24	chr5_0.380629	7	30
chr5_4.638552	7	21	chr5_3.367913	7	24	chr5_0.389442	7	30
chr5_4.638577c	7	21	chr5_3.558407c	7	24	chr5_0.054712c	7	32
chr5_4.73751	7	21	chr5_2.972737c	7	25	chr5_0.098223	7	32
chr5_4.737511	7	21	chr5_2.97298	7	25	chr5_11.140558	7	33
chr5_4.739302c	7	21	chr5_3.042158	7	25	chr5_11.107612	7	33
chr5_4.766085	7	21	chr5_2.411627c	7	26	chr5_11.107679	7	33
chr5_4.78516	7	21	chr5_1.825825	7	27	chr5_11.141223	7	33

Appendix 3. Continued

OB x RF

Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_11.429377	7	33	chr5_19.39188c	7	57	chr4_10.569712c	7	68
chr5_0.47536c	7	38	chr5_19.391919	7	57	chr4_10.569723c	7	68
chr5_0.253532	7	38	chr4_2.910773	7	57	chr4_10.569725c	7	68
chr5_0.295134	7	38	chr2_23.649136c	7	59	chr4_10.569742c	7	68
chr5_0.368279c	7	38	chr4_24.271811c	7	59	chr4_10.569744c	7	68
chr5_0.380678	7	38	chr5_17.261396	7	59	chr4_10.569749c	7	68
chr5_0.475009	7	38	chr5_17.586256	7	59	chr4_10.569757c	7	68
chr5_0.475297c	7	38	chr5_17.586482	7	59	chr4_10.56977c	7	68
chr5_0.040337c	7	41	chr5_17.78595	7	59	chr4_10.569785c	7	68
chr5_0.054614c	7	41	chr5_17.849605c	7	59	chr4_10.569793c	7	68
chr5_11.079223	7	41	chr5_18.155355	7	59	chr5_24.226055c	7	68
chr5_11.081096	7	41	chr5_19.822917	7	59	chr5_24.351542	7	68
chr5_11.081111	7	41	Rh72_LG7	7	59	chr5_26.969165	7	70
chr5_11.107685	7	41	chr5_18.539969	7	59	chr5_27.253792	7	70
chr5_11.140564c	7	41	chr5_20.746986	7	60	chr5_27.040647	7	70
chr2_12.639404c	7	47	chr3_32.662843c	7	60	chr5_27.040702c	7	70
chr5_12.731093c	7	47	chr5_20.579745c	7	60	chr5_27.4618	7	70
chr5_12.804034c	7	47	chr1_2.622835	7	61	chr2_12.742083	7	70
chr5_12.804039c	7	47	chr5_21.864814c	7	61	chr5_27.25375	7	70
chr5_13.064302	7	47	chr5_21.86488c	7	61	chr5_24.943667c	7	71
chr2_12.639387	7	47	chr6_10.847183	7	62	chr5_27.990037	7	71
chr5_13.211011c	7	47	chr5_22.127952	7	62	chr5_27.990251	7	71
chr5_11.640243	7	50	chr5_22.321321c	7	62	chr5_28.458804	7	72
chr5_12.390399	7	50	chr5_22.414727c	7	62	chr4_24.107276c	7	72
chr4_14.967439	7	50	chr5_22.414823c	7	62	chr5_28.656597	7	75
chr3_23.544018	7	50	chr3_2.011499	7	62	chr5_28.914328	7	75
chr3_23.543928	7	50	chr5_24.684603	7	62	chr5_26.003287	7	75
Rw5G14_LG7	7	53	chr5_24.846887	7	62	chr5_26.061239	7	75
chr5_15.295664	7	55	chr5_25.163078c	7	62	chr5_26.050245	7	75
chr5_14.179643	7	55	chr5_26.042021	7	62	chr5_28.914192	7	76
chr5_15.295584c	7	55	chr4_27.571125	7	62	chr5_28.914366c	7	76
chr5_19.391871c	7	55	chr5_26.310193	7	62			
chr4_2.910806	7	55	chr5_26.310326	7	62			
chr3_5.979525	7	57	chr5_26.372339c	7	62			
chr3_18.743967	7	57	chr5_26.372387	7	62			
chr5_14.067619	7	57	chr5_3.04204	7	62			
chr3_5.979537	7	57	chr5_3.042052	7	62			
chr5_14.067625	7	57	chr5_22.321269c	7	63			
chr5_14.067757	7	57	chr5_22.743561c	7	63			
chr5_16.951662	7	57	RMS003_LG7	7	65			

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_1.646404c	1	0	chr7_12.987811c	1	17	chr7_16.760018c	1	24
chr7_2.370361	1	0	chr7_12.365508	1	17	chr7_16.759927c	1	24
chr7_2.370275	1	0	chr7_13.531368c	1	18	chr7_17.90164	1	26
chr7_1.646368c	1	0	chr7_13.787818c	1	19	chr7_18.207597c	1	26
chr7_1.246201	1	0	chr7_13.793629	1	19	chr7_17.773696c	1	26
chr7_4.240786	1	0	chr7_13.787815c	1	19	chr7_18.376963c	1	27
chr7_5.726728	1	5	chr7_15.151752c	1	21	chr7_18.415494c	1	27
chr4_24.537661c	1	5	chr7_14.358652	1	21	chr7_18.377095	1	27
chr5_0.63163c	1	8	chr7_15.199745	1	21	chr7_18.415693c	1	27
chr5_0.631568c	1	8	chr7_13.477166	1	21	chr7_19.117533	1	30
chr7_7.531744c	1	8	chr7_14.616781c	1	21	chr7_18.667185	1	30
chr3_32.663471	1	8	chr7_15.083179	1	21	chr7_19.396709c	1	30
chr7_7.996817c	1	10	chr7_14.329158c	1	21	chr7_18.627921	1	30
chr7_8.283695	1	10	chr7_13.531363c	1	21	chr7_18.467426c	1	30
chr7_9.56769	1	12	chr7_14.358688c	1	21	chr7_18.713959	1	30
chr7_8.218517	1	12	chr7_13.531473	1	21	chr7_19.610745	1	33
chr7_8.28375c	1	12	chr7_15.199566c	1	21	chr7_19.533588c	1	33
chr7_9.566961c	1	12	chr7_15.370485c	1	21	chr7_19.939473c	1	33
chr7_9.153824c	1	13	chr7_15.199669c	1	21	chr7_19.61069	1	33
chr7_8.871442	1	13	chr7_15.199629c	1	21	chr7_19.610622	1	33
chr7_8.744292	1	13	chr7_15.142932c	1	21	chr7_20.086675	1	34
chr7_11.211166c	1	14	chr7_15.395727c	1	22	chr7_20.904212c	1	35
chr7_11.016267c	1	14	chr7_15.865553	1	22	chr7_20.904366	1	37
chr7_11.21128c	1	14	chr7_15.865571c	1	23	chr7_20.786202c	1	37
chr7_10.385832c	1	14	chr7_15.889169	1	23	chr7_20.728966c	1	37
chr7_9.153848c	1	14	chr7_16.182702	1	23	chr7_20.649883	1	38
chr7_8.76812c	1	14	chr7_17.47942c	1	23	chr7_21.162359c	1	38
chr7_10.585111	1	14	chr7_17.479411c	1	23	chr7_20.64994c	1	38
chr7_11.009459	1	14	chr7_16.471587	1	23	chr7_20.649892c	1	40
chr7_12.917504c	1	14	chr7_16.247829c	1	23	chr7_21.730793c	1	40
chr7_11.016243	1	14	chr7_16.471613c	1	23	chr7_21.548481	1	40
chr7_8.558554	1	14	chr7_15.865546	1	23	chr7_20.786131c	1	40
chr7_11.211106	1	14	chr7_17.495203	1	23	chr7_21.548604c	1	40
chr7_8.558541	1	14	chr7_16.480836c	1	23	chr7_21.606218	1	40
chr7_9.153849c	1	14	chr7_15.86556c	1	23	chr2_12.63942c	1	44
chr2_5.001254	1	15	chr7_17.479358	1	24	chr7_22.043139c	1	44
chr7_12.365703	1	15	chr7_16.182737	1	24	chr7_22.043022c	1	44
chr7_12.134186	1	16	chr7_16.760041c	1	24	chr7_23.484274	1	45
chr7_12.13403c	1	16	chr7_16.855748	1	24	chr7_22.854353	1	47
chr7_12.365489c	1	17	chr7_16.690217c	1	24	chr7_23.013171c	1	48

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_22.316144c	1	48	chr1_2.318639c	2	7	chr1_5.965028c	2	25
chr7_23.602528c	1	48	chr1_2.736262c	2	8	chr1_5.964933c	2	25
chr7_23.013217c	1	48	chr1_2.521837c	2	8	chr1_5.918619c	2	28
chr7_22.739224c	1	48	chr1_2.47502c	2	8	chr1_6.184806c	2	28
chr7_23.013203c	1	48	chr1_2.736373c	2	8	chr1_6.070668	2	28
chr7_23.352066c	1	48	chr1_2.521724c	2	8	chr1_5.728886	2	28
chr7_23.037789c	1	48	chr1_2.521732c	2	8	chr1_6.18475c	2	28
chr7_23.03772c	1	48	chr1_2.73631c	2	8	chr1_6.18483c	2	28
chr7_23.206113c	1	52	chr1_2.776934c	2	8	chr1_6.271493c	2	28
chr7_23.206126c	1	52	chr1_2.736407c	2	8	chr1_6.070727c	2	28
chr7_23.351973c	1	52	chr1_2.776874	2	8	chr1_6.042884c	2	28
chr7_23.206148c	1	55	chr1_2.521723c	2	8	chr1_7.150574c	2	28
chr1_1.027915	2	0	chr1_2.690475c	2	8	chr1_6.405722c	2	28
chr1_1.027988c	2	0	chr1_3.435632c	2	12	chr1_6.690492c	2	28
chr1_1.39466c	2	2	chr1_3.250202c	2	12	chr1_6.349737	2	30
chr1_1.027812c	2	2	chr1_3.793777c	2	12	chr1_7.507856c	2	30
chr1_1.394796c	2	2	chr1_3.793768	2	13	chr1_8.138575	2	33
chr1_1.569173c	2	2	chr1_3.752717c	2	13	chr1_8.138587c	2	33
chr1_1.451461	2	2	chr1_4.2068c	2	17	chr1_7.136566c	2	35
chr1_1.580312c	2	2	chr1_4.197269c	2	17	chr1_7.150559c	2	35
chr1_1.165438c	2	2	chr1_4.197182c	2	17	chr1_9.459991	2	36
chr1_1.569737c	2	2	chr1_4.197263c	2	17	chr1_9.504581c	2	36
chr1_1.52833c	2	2	chr1_4.206668c	2	17	chr1_9.504725	2	36
chr1_2.144735c	2	5	chr1_4.197169c	2	17	chr1_9.459863c	2	36
chr1_1.937065	2	5	chr1_4.238907c	2	17	chr1_7.74335	2	38
chr1_2.144585c	2	5	chr1_4.676262c	2	20	chr1_10.495594c	2	38
chr1_2.144357c	2	5	chr1_4.684316c	2	22	chr1_10.495639	2	38
chr1_1.938093c	2	5	chr1_5.533343c	2	22	chr1_9.790204c	2	38
chr1_2.14475c	2	5	chr1_4.960489	2	22	chr1_10.32181c	2	38
chr1_1.937134c	2	5	chr1_5.533313c	2	22	chr1_10.372077c	2	38
chr1_1.938077	2	5	chr1_5.502691c	2	22	chr1_10.372125c	2	38
chr1_2.077982c	2	5	chr1_5.396793c	2	22	chr1_9.662914	2	38
chr1_1.937062c	2	5	chr1_5.533339c	2	22	chr1_10.495583c	2	38
chr1_1.937206c	2	5	chr1_4.684388c	2	22	chr1_10.372167c	2	38
chr1_2.00303c	2	5	chr1_5.502625c	2	22	chr1_10.924711c	2	39
chr1_2.144306c	2	5	chr1_5.918564	2	23	chr1_10.672126c	2	40
chr1_2.077823c	2	5	chr1_5.918624	2	23	chr7_15.889179	2	41
chr1_2.077827c	2	5	chr1_5.964572c	2	25	chr1_11.050002c	2	41
chr1_2.31866	2	7	chr1_5.964609	2	25	chr7_15.889221	2	41
chr1_2.318584c	2	7	chr1_5.964646c	2	25	chr7_15.889235	2	41

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_10.982006	2	41	chr1_18.842012	2	46	chr6_20.501779c	2	49
chr7_15.889247	2	41	chr1_18.841929	2	46	chr6_20.640376c	2	49
chr1_11.644306	2	42	chr4_22.650557c	2	46	chr6_20.14417c	2	49
chr1_17.28847c	2	42	chr1_15.312027c	2	46	chr6_21.334768	2	50
chr1_17.28848c	2	42	chr1_15.312075c	2	46	chr6_20.425868c	2	50
chr1_11.664678c	2	42	chr1_17.288435	2	46	chr6_20.425796	2	50
chr1_11.644234c	2	42	chr1_19.106112	2	46	chr6_21.065036c	2	50
chr1_11.618947	2	42	chr1_17.288555c	2	46	chr6_22.020162c	2	50
chr1_11.5432c	2	43	chr4_22.650563c	2	46	chr6_22.020306c	2	50
chr1_11.543007c	2	43	chr1_17.288566	2	46	chr6_22.200336c	2	50
chr1_17.288562c	2	43	chr4_22.650506c	2	46	chr6_22.241879c	2	50
chr1_18.223722c	2	43	chr1_11.832138c	2	46	chr6_21.427201	2	50
chr1_12.310733	2	43	chr1_17.573105c	2	46	chr6_21.444343	2	50
chr1_11.748807c	2	43	chr1_16.19764	2	46	chr6_21.519898	2	50
chr7_21.80661	2	43	chr1_12.374915	2	46	chr6_21.42716c	2	50
chr4_22.650595c	2	43	chr1_14.439401c	2	46	chr6_22.200502c	2	50
chr1_19.106089c	2	43	chr1_18.100665c	2	46	chr6_22.020181c	2	50
chr4_22.650513c	2	43	chr1_16.197628	2	46	chr3_0.836584	2	52
chr1_11.74884c	2	43	chr1_16.466634c	2	46	chr6_23.59618c	2	52
chr1_11.748759c	2	43	chr1_16.197633	2	46	chr6_23.39463c	2	52
chr1_12.431963	2	43	chr4_22.65058c	2	46	chr6_22.963925c	2	52
chr1_17.288427c	2	44	chr1_12.540607c	2	46	chr6_23.394506	2	53
chr1_19.106105c	2	46	chr1_17.573081c	2	46	chr6_24.954825	2	53
chr1_17.101311	2	46	chr1_16.70819	2	46	chr3_26.098233	2	54
chr4_22.650569c	2	46	chr1_12.428288c	2	46	chr6_24.724226	2	54
chr1_15.311956c	2	46	chr1_16.19763	2	46	chr6_25.901642	2	54
chr1_19.106122	2	46	chr1_16.375547	2	46	chr6_25.644759c	2	54
chr1_17.2773c	2	46	chr1_8.772956c	2	46	chr6_24.717093c	2	54
chr1_12.428887	2	46	chr1_17.288493c	2	46	chr6_24.333528c	2	55
chr1_12.540596c	2	46	chr1_16.197477	2	46	chr6_24.982865c	2	55
chr1_12.540578c	2	46	chr4_22.650584c	2	46	chr6_24.983034c	2	55
chr1_12.399453c	2	46	chr1_18.223819c	2	46	chr6_24.333414	2	55
chr1_17.101313	2	46	chr1_18.201755c	2	46	chr6_24.954924	2	55
chr1_19.10605c	2	46	chr6_29.8795	2	48	chr6_25.352808	2	59
chr1_19.106101c	2	46	chr6_29.879491c	2	48	chr6_25.644821c	2	59
chr1_17.101328	2	46	chr1_12.740688c	2	48	chr3_3.021322	2	60
chr1_17.288469c	2	46	chr6_20.144159	2	48	chr6_25.905739	2	62
chr4_22.650578c	2	46	chr6_20.289633	2	48	chr6_25.905902c	2	62
chr1_15.312024c	2	46	chr6_20.425967c	2	49	chr6_26.656034c	2	62
chr1_17.277362	2	46	chr6_20.640381c	2	49	chr6_26.646092c	2	62

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_26.914262c	2	63	chr6_32.205309	2	66	chr6_34.875959	2	70
chr6_26.646263	2	63	chr6_15.095193c	2	66	chr6_35.174015c	2	71
chr6_26.914348c	2	63	chr6_33.264241c	2	66	chr6_35.895266	2	73
chr6_26.877926c	2	63	chr6_29.412458c	2	66	chr6_36.004515c	2	73
chr6_31.699678c	2	64	chr6_32.094013c	2	66	chr6_35.934824c	2	73
chr6_30.355325c	2	64	chr6_33.026304c	2	66	chr6_36.073441	2	73
chr6_28.141739c	2	64	chr6_33.051694c	2	66	chr6_35.93483c	2	73
chr6_29.107698c	2	64	chr6_32.343667c	2	66	chr6_35.934821c	2	73
chr6_28.960886c	2	64	chr6_33.531378c	2	66	chr6_35.934829c	2	73
chr6_30.634039c	2	64	chr6_33.839517c	2	66	chr6_36.004464c	2	73
chr6_29.149836c	2	64	chr6_33.335358c	2	66	chr6_35.934822c	2	73
chr6_29.680111c	2	64	chr6_14.994587	2	66	chr6_35.934743c	2	73
chr6_27.344842	2	64	chr6_29.518821c	2	66	chr6_37.136891c	2	75
chr6_30.96703	2	64	chr6_33.215661	2	66	chr6_36.59146c	2	75
chr6_29.154701c	2	64	chr6_33.531386c	2	66	chr6_36.591449	2	75
chr6_30.271656c	2	64	chr6_33.264311	2	66	chr6_36.58703c	2	75
chr6_27.344918	2	64	chr6_33.026256	2	66	chr6_36.587183c	2	75
chr6_30.355331c	2	64	chr6_33.215616	2	66	chr6_36.410461	2	75
chr6_27.767203c	2	64	chr6_33.335228c	2	66	chr6_36.630348	2	75
chr6_29.154708c	2	64	chr6_33.531387c	2	66	chr6_36.58706c	2	75
chr6_29.154709c	2	64	chr6_32.756603c	2	66	chr6_36.844858c	2	76
chr6_31.531428c	2	64	chr6_31.954116c	2	66	chr6_36.844926c	2	76
chr6_30.84518c	2	64	chr6_14.994578	2	66	chr6_36.428129	2	77
chr6_30.845172	2	64	chr6_33.215643c	2	66	chr6_36.93301c	2	77
chr6_29.149769c	2	64	chr6_32.975416c	2	66	chr6_37.184203c	2	81
chr6_29.139503c	2	64	chr6_36.295664c	2	68	chr6_37.028502c	2	81
chr6_31.531493c	2	64	chr6_35.290819c	2	68	chr6_37.800891c	2	81
chr6_30.95729c	2	64	chr6_33.953478c	2	68	chr6_37.184293	2	81
chr6_30.845198c	2	64	chr6_34.506503c	2	68	chr6_37.540081c	2	83
chr6_29.150396c	2	65	chr6_34.413787c	2	68	chr6_37.8009c	2	83
chr6_29.139475c	2	65	chr6_33.693417	2	68	chr6_37.800873	2	83
chr6_29.154771c	2	65	chr6_34.712429c	2	68	chr6_38.318397c	2	86
chr6_29.149908c	2	65	chr6_34.837797	2	68	chr6_38.318325c	2	86
chr6_29.139545c	2	65	chr6_34.546062c	2	68	chr6_37.899493	2	86
chr6_28.141607	2	65	chr6_34.506623c	2	68	chr6_38.527313	2	87
chr6_29.639695c	2	66	chr6_34.923112c	2	70	chr6_38.575608	2	87
chr6_33.53129c	2	66	chr6_34.87606c	2	70	chr6_38.821329	2	88
chr6_33.242307c	2	66	chr6_34.876054c	2	70	chr6_0.106957c	3	0
chr6_33.589239c	2	66	chr6_34.923109c	2	70	chr6_0.288165c	3	3
chr6_32.975531c	2	66	chr6_34.875992c	2	70	chr6_0.288198c	3	3

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_0.242596c	3	3	chr6_2.965734c	3	13	chr6_5.442559c	3	26
chr6_0.297877c	3	3	chr6_3.445019c	3	13	chr6_5.575539c	3	26
chr6_0.242599c	3	3	chr6_3.326291c	3	13	chr6_5.496726	3	26
chr6_0.258258c	3	3	chr6_3.444881c	3	13	chr6_7.399133c	3	27
chr6_0.53712	3	4	chr6_3.444903	3	13	chr6_7.386695	3	27
chr6_0.811561	3	5	chr6_3.272434	3	13	chr6_5.982031c	3	27
chr6_0.861947c	3	5	chr6_2.844006c	3	13	chr6_7.55052c	3	29
chr6_0.861922c	3	5	chr6_3.27251c	3	13	chr6_7.702565c	3	29
chr6_0.522755c	3	5	chr6_2.96574c	3	13	chr6_7.649678c	3	29
chr6_0.741884	3	5	chr6_3.272502c	3	13	chr6_7.839982c	3	29
chr6_0.537124	3	5	chr6_3.691074c	3	15	chr6_7.34249	3	31
chr6_0.741929c	3	5	chr6_3.666446	3	15	chr6_6.851571	3	31
chr6_0.811506c	3	5	chr6_3.581837	3	15	chr6_9.582315	3	31
chr6_0.537091c	3	5	chr6_3.666368	3	16	chr6_7.073636c	3	31
chr6_0.741968c	3	5	chr6_3.690909c	3	16	chr6_7.214013c	3	31
chr6_1.080135c	3	5	chr6_3.739403	3	17	chr6_6.200484c	3	31
chr6_0.861943c	3	5	chr6_3.739383c	3	17	chr6_7.342552	3	31
chr6_0.741935c	3	5	chr6_4.332494c	3	18	chr6_7.359523c	3	31
chr6_0.594973c	3	5	chr6_4.17526c	3	18	chr5_10.278451	3	31
chr6_1.816439c	3	7	chr6_4.371663c	3	18	chr6_7.342568	3	32
chr6_1.826124c	3	7	chr6_4.175209c	3	18	chr6_7.740758	3	32
chr6_1.868386c	3	8	chr6_4.053725c	3	20	chr6_7.781201c	3	32
chr6_1.868258c	3	8	chr6_4.175405	3	20	chr6_8.773447c	3	32
chr6_1.869018	3	8	chr6_4.710029c	3	21	chr6_8.66257c	3	32
chr6_1.86829c	3	8	chr6_4.262755	3	21	chr6_8.662557c	3	32
chr6_1.425332c	3	8	chr6_4.280806c	3	21	chr6_8.614639c	3	32
chr6_1.425327c	3	8	chr6_4.37173c	3	21	chr6_8.61468	3	34
chr6_1.42521	3	8	chr6_4.777891c	3	22	chr6_8.607327	3	34
chr6_1.42533c	3	8	chr6_4.897143	3	22	chr6_8.724376c	3	34
chr2_6.356844c	3	10	chr6_4.933007c	3	22	chr6_8.403801	3	34
chr6_1.816427c	3	10	chr6_4.710065	3	22	chr6_8.607405c	3	34
chr6_1.974541c	3	10	chr6_5.300312c	3	22	chr6_8.97776	3	35
chr6_2.263139c	3	12	chr6_4.777858c	3	22	chr6_8.977697	3	35
chr6_2.965657c	3	13	chr6_5.300289c	3	22	chr6_9.113612c	3	35
chr6_2.965708	3	13	chr6_4.777808c	3	23	chr6_8.977696c	3	35
chr6_2.963291	3	13	chr6_5.550275c	3	24	chr6_8.977642c	3	35
chr6_2.963197c	3	13	chr6_4.915567	3	24	chr6_8.977622c	3	35
chr6_2.843963c	3	13	chr6_5.645362	3	25	chr6_9.032021c	3	36
chr6_3.272383c	3	13	chr6_5.873817	3	25	chr6_8.97888c	3	36
chr6_3.272499c	3	13	chr6_5.575564	3	25	chr6_10.916428	3	36

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_5.161425c	3	36	chr1_19.762871c	3	51	chr4_25.585359	4	19
chr6_8.951769c	3	36	chr1_17.893831c	3	51	chr4_31.097061c	4	19
chr6_10.29913	3	37	chr1_21.072247c	3	51	chr4_15.244486c	4	19
chr5_5.161395	3	37	chr1_23.128197	3	51	chr4_19.015713c	4	20
chr6_12.312783c	3	37	chr6_12.757479	3	51	chr4_19.015757c	4	20
chr6_9.32952c	3	37	chr4_14.903227c	3	52	chr4_19.027117c	4	21
chr6_11.988579c	3	37	chr4_14.90326c	3	52	chr4_16.679267c	4	21
chr6_11.533505	3	37	chr3_23.543973c	3	52	chr4_16.89505c	4	21
chr6_11.735849	3	37	chr3_23.543923c	3	52	chr3_32.662954c	4	21
chr6_10.110076	3	37	chr4_2.432586	4	0	chr4_16.679197c	4	21
chr6_14.453296c	3	38	chr4_2.61772c	4	0	chr4_20.223875	4	25
chr6_16.82039c	3	38	chr4_2.13018c	4	0	chr4_20.324714	4	25
chr6_14.32699c	3	38	chr4_2.130177	4	0	chr4_22.66421c	4	25
chr6_14.684969c	3	38	chr4_1.608475c	4	0	chr4_22.657084c	4	25
chr6_17.519036c	3	38	chr4_2.605435	4	0	chr4_20.800395c	4	25
chr6_15.986821c	3	40	chr4_2.64327	4	0	chr4_20.36565c	4	25
chr1_0.630283c	3	41	chr4_4.87236c	4	8	chr4_20.800442c	4	25
chr6_17.519049c	3	41	chr4_4.872345c	4	8	chr4_21.108597c	4	25
chr6_17.519052	3	41	chr4_4.907812c	4	8	chr4_22.657176c	4	25
chr6_17.519045c	3	41	chr4_4.907708	4	8	chr4_20.853208c	4	25
chr6_17.734756c	3	41	chr6_5.051434c	4	8	chr4_20.983941c	4	25
chr6_16.820517	3	42	chr4_4.872342c	4	8	chr4_23.227841c	4	28
chr6_17.244584	3	43	chr4_4.680702c	4	8	chr4_23.227904c	4	28
chr6_13.418541	3	43	chr4_7.93756	4	10	chr4_23.227868c	4	28
chr6_16.820417	3	45	chr4_6.609592	4	12	chr4_22.384157c	4	28
chr6_13.183631	3	48	chr4_6.14539	4	12	chr4_23.227843c	4	28
chr6_13.183658	3	48	chr4_6.705474c	4	12	chr4_22.384131	4	28
chr6_13.183585	3	48	chr4_10.903029c	4	12	chr4_22.892014c	4	28
chr4_23.601458	3	48	chr4_10.378789c	4	12	chr4_23.959311c	4	32
chr6_13.183624	3	48	chr4_10.902858c	4	12	chr4_23.869726c	4	32
chr6_18.103511c	3	48	chr4_14.265105c	4	13	chr4_23.895982c	4	32
chr6_13.183661	3	48	chr4_9.71198	4	13	chr4_24.753806c	4	32
chr4_23.60144	3	48	chr4_10.024632c	4	13	chr4_23.357974c	4	32
chr4_23.601554c	3	48	chr4_10.024609c	4	13	chr4_23.959251c	4	32
chr1_17.717705c	3	49	chr5_12.693643c	4	13	chr4_23.896044c	4	32
chr1_14.272702c	3	49	chr4_13.538025c	4	15	chr4_23.766049c	4	32
chr1_17.893823	3	49	chr4_13.579901c	4	15	chr4_23.896043c	4	32
chr1_13.372615c	3	51	chr4_13.538038c	4	15	chr4_23.959241c	4	32
chr1_13.372442c	3	51	chr4_15.572876c	4	19	chr4_25.723911c	4	32
chr2_2.65768c	3	51	chr4_15.572828c	4	19	chr4_23.959293c	4	32

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_23.959316c	4	32	chr4_27.0985c	4	44	chr4_29.746187c	4	47
chr4_25.693131c	4	32	chr4_26.344736c	4	44	chr4_28.674719c	4	48
chr4_23.95931c	4	32	chr4_24.079682c	4	44	chr4_29.545641c	4	48
chr4_25.170089c	4	34	chr4_27.264872	4	44	chr4_30.370151c	4	48
chr4_25.69303c	4	36	chr4_26.347188c	4	44	chr4_29.600188c	4	48
chr4_25.72419c	4	36	chr4_26.044632c	4	44	chr4_29.600227c	4	48
chr4_23.765951	4	36	chr4_26.770355c	4	44	chr4_30.309085c	4	48
chr4_24.14093c	4	38	chr4_24.14107c	4	44	chr4_30.370115	4	49
chr4_26.053807	4	38	chr4_24.870354	4	44	chr4_28.051318c	4	49
chr4_25.247829	4	38	chr4_27.264889c	4	44	chr4_28.548139c	4	50
chr4_25.247863c	4	39	chr4_28.541018	4	46	chr4_31.267018	4	51
chr4_25.247839c	4	39	chr4_27.922673c	4	46	chr4_31.61281c	4	51
chr4_25.247859c	4	39	chr4_28.051206c	4	46	chr3_5.902101c	4	51
chr4_25.247851c	4	39	chr4_27.992125c	4	46	chr4_32.273246	4	52
chr4_25.247853c	4	39	chr4_27.99233c	4	46	chr4_31.925842c	4	52
chr4_25.247909c	4	39	chr4_29.082506c	4	46	chr4_31.986193c	4	52
chr4_25.247857c	4	39	chr4_29.309608	4	46	chr4_32.094373	4	52
chr4_25.247887c	4	39	chr4_27.922625c	4	46	chr4_31.984893c	4	52
chr4_25.247845c	4	39	chr4_27.922658c	4	46	chr4_30.429149c	4	52
chr4_25.247906c	4	39	chr4_30.055069c	4	47	chr4_30.92891c	4	54
chr4_26.225746	4	40	chr4_27.681531c	4	47	chr4_30.93957c	4	54
chr4_26.313998	4	41	chr4_30.210924c	4	47	chr4_30.584409c	4	54
chr4_26.225404c	4	41	chr4_28.674636c	4	47	chr4_30.928983c	4	54
chr4_26.225749c	4	41	chr4_27.561547c	4	47	chr4_31.18604c	4	54
chr4_26.225259c	4	41	chr4_29.746049c	4	47	chr4_30.848341c	4	54
chr4_26.248425c	4	41	chr4_27.922646c	4	47	chr4_31.213573	4	54
chr4_26.235324c	4	41	chr4_29.591117c	4	47	chr4_30.929001c	4	54
chr4_26.225291c	4	41	chr4_29.594716	4	47	chr4_29.121993c	4	54
chr4_26.248412c	4	41	chr4_29.594662c	4	47	chr4_30.929007c	4	54
chr4_26.225403c	4	41	chr4_29.746051c	4	47	chr4_30.584004c	4	54
chr4_26.248417c	4	41	chr4_29.387027c	4	47	chr4_30.630581	4	54
chr4_27.295353	4	44	chr4_29.387028c	4	47	chr4_30.939643c	4	54
chr4_27.279251	4	44	chr4_30.111196c	4	47	chr4_31.588428c	4	55
chr3_6.449225c	4	44	chr4_30.229548c	4	47	chr4_31.675112c	4	56
chr4_24.709688c	4	44	chr4_29.859004c	4	47	chr3_0.40594	5	0
chr4_27.11645c	4	44	chr4_27.981343c	4	47	chr3_0.545528c	5	2
chr4_27.264868c	4	44	chr4_29.956147c	4	47	chr3_0.455471c	5	2
chr4_27.264891c	4	44	chr4_30.111712c	4	47	chr3_0.405875c	5	2
chr4_27.264885c	4	44	chr4_29.594806c	4	47	chr3_0.479349c	5	2
chr4_24.870345c	4	44	chr4_29.277525c	4	47	chr3_0.361349c	5	2

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_0.479389c	5	2	chr6_12.992792c	5	18	chr3_6.029767	5	25
chr3_0.455473c	5	2	chr3_4.535636c	5	18	chr3_6.376783c	5	25
chr3_0.25191c	5	2	chr4_13.33456c	5	18	chr4_25.395373c	5	25
chr3_0.677893	5	3	chr4_19.414226c	5	18	chr3_6.376784c	5	25
chr3_0.426312c	5	5	chr3_2.696615c	5	18	chr3_6.600776c	5	26
chr3_0.426408c	5	5	chr3_4.216017	5	18	chr3_6.741723c	5	26
chr3_0.869195c	5	5	chr3_4.306393c	5	18	chr3_7.647398c	5	28
chr3_0.793645c	5	5	chr3_2.919718c	5	22	chr3_7.955774c	5	30
chr3_0.869261c	5	5	chr3_3.449668	5	22	chr3_8.347404c	5	33
chr3_0.426393c	5	5	chr3_2.9198c	5	22	chr3_8.085097	5	33
chr3_0.426359c	5	5	chr3_3.362101c	5	22	chr3_8.347534c	5	33
chr3_0.793647c	5	5	chr3_2.919767c	5	22	chr1_2.498976	5	35
chr3_0.426387c	5	5	chr3_3.020797c	5	22	chr3_9.163452c	5	35
chr3_0.793648c	5	5	chr3_3.369959c	5	22	chr3_9.287623c	5	36
chr3_1.133971c	5	5	chr3_3.313779c	5	22	chr3_9.287642c	5	36
chr3_0.869296c	5	5	chr3_3.346134c	5	22	chr3_10.025051	5	38
chr3_0.42637c	5	5	chr3_3.497486c	5	22	chr3_9.836063	5	38
chr3_1.184189	5	10	chr3_2.919721c	5	22	chr3_10.149417c	5	40
chr3_1.23319	5	10	chr3_3.163696	5	22	chr3_19.144165c	5	41
chr3_1.412794	5	12	chr3_3.346244c	5	22	chr3_18.862084c	5	41
chr3_1.590517	5	13	chr3_3.02146c	5	22	chr3_8.683186c	5	41
chr3_2.077489	5	15	chr3_2.919842c	5	22	chr3_18.862082c	5	41
chr3_2.220758c	5	17	chr3_3.346242c	5	22	chr3_19.14409c	5	41
chr3_2.449709c	5	17	chr3_3.496012c	5	22	chr3_20.098401c	5	41
chr3_4.687322c	5	18	chr3_2.905128	5	22	chr3_18.786668c	5	41
chr3_5.102709c	5	18	chr3_3.362056c	5	22	chr3_18.786629c	5	41
chr3_4.306538	5	18	chr3_2.919722c	5	22	chr3_18.737184c	5	41
chr4_13.334587c	5	18	chr3_2.91972c	5	22	chr3_19.783973c	5	41
chr3_4.687369c	5	18	chr3_2.919827c	5	22	chr2_6.94522c	5	43
chr3_5.051009c	5	18	chr3_2.919818c	5	22	chr7_18.645099	5	43
chr3_4.526267c	5	18	chr3_3.013559c	5	22	chr7_19.300534c	5	43
chr4_13.334543c	5	18	chr3_3.313825c	5	22	chr7_19.300561c	5	43
chr3_4.535513c	5	18	chr3_3.36988c	5	22	chr7_19.300596c	5	43
chr6_12.992642c	5	18	chr3_3.346251	5	22	chr3_18.504736c	5	43
chr3_5.0538c	5	18	chr3_5.902028c	5	23	chr4_8.39899c	5	43
chr3_4.687313c	5	18	chr3_5.447744	5	23	chr7_18.645149	5	43
chr6_18.147322c	5	18	chr3_6.029806	5	25	chr7_19.300581c	5	43
chr3_4.920622c	5	18	chr3_6.029764	5	25	chr3_18.504707c	5	43
chr6_12.992669c	5	18	chr3_6.344806	5	25	chr3_18.569408c	5	43
chr3_4.791511c	5	18	chr3_6.116958	5	25	chr7_19.300555c	5	43

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_10.972226c	5	45	chr3_23.876843c	5	56	chr2_23.248062c	6	0
chr3_11.64811c	5	45	chr3_23.907006c	5	56	chr2_23.381612c	6	0
chr3_11.104277	5	45	chr3_23.876809c	5	56	chr2_24.033015c	6	0
chr3_11.012883	5	45	chr3_24.010703c	5	56	chr2_23.449654	6	0
chr5_23.114391c	5	45	chr3_24.531421	5	56	chr2_23.266131	6	0
chr5_23.11445c	5	45	chr3_23.876868c	5	56	chr2_24.008603c	6	0
chr3_11.01274c	5	45	chr3_31.36812c	5	58	chr2_23.39929c	6	0
chr3_11.349301c	5	45	chr3_27.330486c	5	58	chr2_23.266129	6	0
chr5_23.192046c	5	45	chr3_26.495694c	5	58	chr2_22.876628c	6	0
chr3_11.544979c	5	45	chr3_27.296046c	5	58	chr2_23.822327c	6	0
chr3_22.971482	5	48	chr3_27.162596c	5	58	chr2_23.594351c	6	0
chr3_17.311876c	5	48	chr3_26.392667c	5	58	chr2_23.822395c	6	0
chr7_10.22618c	5	48	chr3_27.58572c	5	58	chr2_23.44995c	6	0
chr3_22.970602c	5	48	chr3_27.330373c	5	58	chr3_18.443116c	6	0
chr3_22.969731c	5	48	chr3_25.988638c	5	58	chr2_23.874155	6	1
chr2_18.464163c	5	48	chr3_27.16259c	5	58	chr2_23.449957c	6	1
chr3_17.311898c	5	48	chr3_27.074702c	5	58	chr2_23.449693c	6	1
chr3_31.277367c	5	48	chr3_25.782336c	5	58	chr2_24.129881	6	4
chr3_22.970737	5	48	chr3_27.830538c	5	58	chr2_24.273834c	6	4
chr3_22.970551c	5	48	chr3_27.58571c	5	58	chr2_24.62641c	6	4
chr3_31.277358c	5	48	chr3_26.392817c	5	58	chr2_24.412051c	6	4
chr3_17.311759c	5	48	chr3_26.098422c	5	58	chr2_24.501579c	6	4
chr3_22.969603c	5	48	chr3_27.330446c	5	58	chr2_24.626417c	6	4
chr3_31.27734c	5	48	chr3_27.585556c	5	58	chr2_25.198478c	6	4
chr3_22.969602c	5	48	chr3_27.285255c	5	58	chr2_24.626465c	6	4
chr3_12.975533c	5	50	chr3_27.99615c	5	58	chr2_24.231867	6	4
chr4_29.11998c	5	50	chr3_27.162617	5	58	chr2_24.570881	6	4
chr3_11.861412c	5	50	chr3_27.162716c	5	58	chr2_24.235476	6	4
chr3_20.30323c	5	50	chr3_29.280685	5	59	chr2_24.235453	6	4
chr3_12.413019c	5	50	chr3_29.103285c	5	59	chr2_24.273832	6	4
chr3_21.072572c	5	50	chr3_29.185758c	5	59	chr2_24.130067c	6	4
chr3_12.176524c	5	50	chr3_29.565427c	5	61	chr2_25.111096c	6	4
chr3_13.889638c	5	51	chr3_29.56546c	5	61	chr2_24.646143c	6	4
chr3_16.920664c	5	53	chr3_29.641115	5	63	chr2_24.033014c	6	4
chr4_21.23856c	5	53	chr3_30.218807c	5	64	chr2_24.412081c	6	4
chr3_16.920688c	5	53	chr3_31.20921	5	68	chr2_24.033072c	6	4
chr3_23.906906c	5	56	chr3_33.10348c	5	69	chr2_24.626373c	6	4
chr5_16.160459c	5	56	chr3_32.675821c	5	69	chr2_25.111038c	6	4
chr3_24.805637c	5	56	chr3_32.663302c	5	69	chr2_25.312197c	6	6
chr3_24.121024c	5	56	chr2_23.26609	6	0	chr2_25.312219c	6	6

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_25.312193c	6	6	chr2_27.106488c	6	15	chr2_21.649972c	6	19
chr3_27.248551	6	6	chr2_27.349189c	6	15	chr2_21.23102c	6	19
chr2_25.71126c	6	6	chr2_27.74727c	6	15	chr2_21.808213c	6	19
chr2_25.312202c	6	6	chr2_26.77842c	6	15	chr2_21.808225c	6	19
chr2_25.111174c	6	6	chr2_27.349152c	6	15	chr2_21.231029c	6	19
chr3_27.248569	6	6	chr2_27.34915c	6	15	chr2_19.949491c	6	19
chr3_27.248496	6	6	chr2_27.22064c	6	15	chr2_20.697599c	6	20
chr2_25.312213c	6	6	chr2_27.220718c	6	15	chr2_21.015515	6	20
chr2_25.312195c	6	6	chr2_27.220657c	6	15	chr2_20.775584	6	20
chr2_25.224304c	6	6	chr2_27.505814	6	15	chr2_20.873445	6	20
chr2_24.83113c	6	6	chr2_26.778437	6	15	chr2_20.697564c	6	20
chr3_27.248527	6	6	chr2_28.675051c	6	16	chr2_21.207876	6	20
chr2_25.243185	6	6	chr2_28.019885c	6	17	chr2_20.880422c	6	20
chr2_25.570601c	6	7	chr2_27.920995c	6	17	chr2_20.873439c	6	20
chr2_25.570533c	6	7	chr2_28.465742c	6	17	chr2_17.666156c	6	20
chr2_26.005039c	6	10	chr2_28.620278c	6	17	chr2_15.426889c	6	20
chr2_25.946068	6	10	chr2_28.465696c	6	17	chr2_14.340485c	6	20
chr2_25.96824c	6	10	chr2_28.056693c	6	17	chr2_17.24005c	6	20
chr2_26.778402c	6	10	chr2_14.765884	6	18	chr2_17.7902c	6	20
chr2_26.62235c	6	10	chr2_21.390856c	6	18	chr2_18.557681	6	21
chr2_26.347536c	6	10	chr2_16.695571c	6	18	chr2_16.441018c	6	21
chr2_25.946191c	6	10	chr2_22.103425	6	18	chr2_18.469778c	6	21
chr2_26.005022	6	10	chr6_8.652761	6	18	chr2_20.604056c	6	21
chr2_26.227822c	6	11	chr2_21.843141	6	18	chr2_18.9002c	6	21
chr2_27.34911c	6	12	chr2_21.759036	6	18	chr2_19.052925c	6	21
chr2_27.384735c	6	12	chr2_21.841255c	6	18	chr2_19.052872c	6	21
chr7_1.837513c	6	13	chr2_21.841208c	6	18	chr2_16.44103c	6	21
chr2_26.664116	6	13	chr2_19.867982	6	19	chr2_19.598858	6	21
chr2_27.747384	6	14	chr2_21.693089c	6	19	chr2_18.458047c	6	21
chr2_27.987994c	6	14	chr2_19.052861c	6	19	chr2_19.598777	6	21
chr2_28.046836c	6	14	chr2_19.052988c	6	19	chr2_20.497565c	6	21
chr2_28.041695c	6	14	chr2_22.103353c	6	19	chr2_16.843067c	6	21
chr2_27.747281c	6	14	chr2_20.880521	6	19	chr2_19.598747c	6	21
chr2_28.019879c	6	14	chr2_18.952375c	6	19	chr2_21.80828c	6	21
chr2_27.505821c	6	14	chr2_20.529991c	6	19	chr2_17.106221c	6	21
chr2_28.041839c	6	14	chr2_15.20857c	6	19	chr2_17.106347c	6	22
chr2_27.98791	6	14	chr3_30.378651c	6	19	chr2_17.106329c	6	22
chr2_28.046701c	6	14	chr2_13.494187c	6	19	chr2_17.106194c	6	22
chr2_28.046851c	6	14	chr2_21.806912c	6	19	chr2_14.784953c	6	23
chr2_27.577573	6	14	chr2_21.490313c	6	19	chr2_21.380592c	6	23

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_17.832217c	6	23	chr2_3.125949	6	33	chr2_2.117933c	6	47
chr2_17.79019c	6	23	chr2_3.125348	6	33	chr2_0.361979	6	47
chr2_17.790167c	6	23	chr2_3.285044	6	33	chr2_0.29321	6	47
chr2_17.859885c	6	23	chr2_3.922365c	6	35	chr2_5.97057c	6	47
chr2_21.84121c	6	23	chr2_3.285053c	6	35	chr2_15.16713	6	47
chr2_17.790205c	6	23	chr4_7.720808c	6	35	chr2_0.38754c	6	47
chr2_17.790193c	6	23	chr2_10.531353c	6	35	chr2_0.325942c	6	47
chr2_17.240048c	6	23	chr2_3.756898c	6	35	chr2_0.387676c	6	47
chr2_20.893995	6	23	chr2_12.770187	6	35	chr2_0.387723c	6	47
chr2_21.380622c	6	23	chr2_19.750265	6	35	chr2_0.325936c	6	47
chr2_18.555865	6	23	chr2_3.922347	6	35	chr2_0.325939c	6	47
chr2_21.3912c	6	23	chr2_3.756953	6	35	chr2_0.325927c	6	47
chr2_17.790202c	6	23	chr2_10.135978c	6	35	chr2_2.118021c	6	47
chr2_17.790181c	6	23	chr2_2.630091	6	35	chr2_0.361984c	6	47
chr2_18.522452	6	23	chr2_3.693948	6	35	chr2_14.670491c	6	48
chr2_19.706908c	6	23	chr4_14.967591c	6	36	chr2_14.670495	6	49
chr2_17.239957c	6	23	chr2_12.770204c	6	36	chr2_14.670467	6	49
chr2_14.250229c	6	23	chr2_12.884941	6	36	chr2_5.249549	6	51
chr2_13.469506c	6	26	chr2_7.557305	6	38	chr2_1.330104	6	51
chr2_15.426851c	6	27	chr2_7.990292c	6	38	chr2_4.803325c	6	51
chr2_14.532723	6	27	chr2_7.990325c	6	38	chr2_11.953256c	6	51
chr2_14.340377	6	27	chr2_7.55733	6	38	chr2_5.237114	6	51
chr2_14.340569	6	27	chr2_7.990192c	6	38	chr2_11.953141	6	51
chr2_15.148763	6	27	chr2_8.164281c	6	40	chr2_5.249636	6	51
chr2_15.050654c	6	27	chr2_7.106386c	6	41	chr2_11.378826c	6	51
chr2_15.116567	6	27	chr2_8.382445	6	43	chr2_11.37881c	6	51
chr2_15.590775c	6	27	chr2_8.832433	6	43	chr2_11.340019c	6	51
chr2_9.486087c	6	28	chr2_0.326002	6	46	chr2_4.827682	6	51
chr7_10.93348c	6	28	chr2_6.127613	6	46	chr2_4.827898c	6	52
chr2_13.249464c	6	28	chr2_5.970529c	6	46	chr2_4.827805c	6	52
chr2_9.486166	6	28	chr2_5.970562c	6	46	chr2_11.36242c	6	52
chr2_9.486073	6	28	chr2_1.948952	6	46	chr2_11.378807c	6	52
chr3_10.955571	6	28	chr2_8.832534c	6	46	chr2_11.177575	6	52
chr2_13.360912	6	28	chr2_8.127134c	6	46	chr2_5.249675c	6	52
chr2_9.184633	6	28	chr2_6.445763	6	46	chr2_11.177448c	6	53
chr2_13.119851c	6	28	chr2_8.832624c	6	46	chr2_11.702936c	6	53
chr2_4.217116	6	29	chr2_6.445079c	6	46	chr2_11.703057c	6	53
chr2_4.217066	6	29	chr2_6.470938c	6	46	chr2_11.70281	6	53
chr4_24.537692	6	30	chr2_6.304781c	6	46	chr2_11.177478	6	53
chr3_9.063252	6	30	chr2_7.99021c	6	46	chr2_11.339951	6	53

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_5.74795c	6	53	chr5_7.723511c	7	13	chr5_3.042158c	7	22
chr2_11.33994c	6	53	chr5_7.72349c	7	13	chr5_2.972791c	7	22
chr5_10.094031c	7	0	chr5_7.379853c	7	17	chr5_2.97298c	7	22
chr5_10.007823	7	0	chr5_7.379798c	7	17	chr5_1.881602	7	23
chr5_9.983686	7	0	chr5_7.227119c	7	17	chr5_2.411625c	7	23
chr5_9.885695	7	2	chr2_27.350242	7	17	chr5_1.861007c	7	23
chr5_10.791804	7	2	chr5_7.009711c	7	17	chr5_2.411627c	7	23
chr5_10.282994	7	2	chr5_7.724143	7	17	chr5_1.861128c	7	23
chr5_10.325059	7	2	chr5_7.678127c	7	17	chr5_1.861115c	7	23
chr5_10.155887	7	3	chr5_6.066596	7	18	chr5_1.881511	7	23
chr5_9.986703	7	5	chr1_13.372545	7	18	chr5_2.018785c	7	23
chr5_10.007421c	7	5	chr5_6.513726c	7	18	chr5_1.861167c	7	23
chr5_10.00788c	7	5	chr5_6.128112c	7	18	chr5_1.932987c	7	23
chr5_10.132037c	7	5	chr5_6.12847c	7	18	chr5_1.86118c	7	23
chr5_9.488485	7	7	chr2_27.350294	7	18	chr5_1.881442c	7	23
chr5_9.690599	7	7	chr5_6.128499c	7	18	chr5_0.295134c	7	25
chr5_9.911991c	7	7	chr5_4.243774	7	19	chr5_11.079223c	7	25
chr5_9.431909c	7	8	chr5_5.061515	7	20	chr5_1.407213c	7	25
chr5_9.249829c	7	8	chr5_5.037515	7	20	chr3_23.543928c	7	25
chr5_9.433505c	7	8	chr5_4.739272c	7	20	chr5_0.475297c	7	25
chr5_9.141249	7	8	chr5_5.678322c	7	20	chr5_12.731093c	7	25
chr5_9.387827c	7	8	chr5_5.678439c	7	20	chr5_11.081111c	7	25
chr5_9.17276c	7	8	chr5_5.379398c	7	20	chr5_12.804039c	7	25
chr5_9.141127	7	8	chr5_4.766079	7	20	chr5_0.475351c	7	25
chr5_9.387902c	7	8	chr5_4.766091c	7	20	chr2_12.639387c	7	25
chr5_9.370173c	7	8	chr5_5.161854c	7	20	chr5_1.090909c	7	25
chr5_9.370218	7	8	chr5_4.306304c	7	20	chr5_0.253532c	7	25
chr5_9.431907c	7	9	chr5_5.226128c	7	20	chr5_11.140564c	7	25
chr5_9.061762c	7	9	chr5_3.367913c	7	20	chr5_0.667556c	7	25
chr5_8.914843c	7	10	chr5_5.161795c	7	20	chr5_0.054614c	7	25
chr5_8.890932c	7	11	chr5_3.349344c	7	20	chr5_11.107685c	7	25
chr5_8.348061c	7	12	chr5_3.558407c	7	20	chr5_0.626661c	7	25
chr5_7.723982c	7	12	chr5_4.785243c	7	20	chr5_0.710208c	7	25
chr5_8.686755c	7	13	chr5_4.766226c	7	20	chr5_0.801187c	7	25
chr5_8.795819	7	13	chr5_4.490059c	7	20	chr5_0.47536c	7	25
chr5_8.908206c	7	13	chr5_3.366289c	7	20	chr5_0.66742c	7	25
chr5_8.580964	7	13	chr5_5.161752c	7	20	chr5_11.081096c	7	25
chr5_8.890938c	7	13	chr5_4.490021c	7	22	chr5_0.710184c	7	25
chr5_8.39521c	7	13	chr5_4.739302c	7	22	chr5_0.368279c	7	25
chr5_7.707963c	7	13	chr5_2.972771c	7	22	chr5_13.064302c	7	25

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_0.667359c	7	25	chr3_32.662843c	7	35	chr5_26.96924c	7	45
chr5_12.390399c	7	25	chr5_12.731069c	7	35	chr5_25.95567c	7	45
chr5_1.202653	7	25	chr5_12.731108c	7	35	chr5_15.295657	7	45
chr5_0.040337c	7	25	chr5_12.731079c	7	35	chr5_15.434358c	7	45
chr5_12.804034c	7	25	chr5_12.731087c	7	35	chr5_14.711749	7	45
chr5_13.211011c	7	25	chr5_12.731085c	7	35	chr5_27.492173	7	46
chr5_0.363628	7	26	chr5_13.064307	7	35	chr5_27.735163c	7	48
chr4_14.967439c	7	26	chr5_12.731086c	7	35	chr5_19.391751c	7	50
chr5_11.704311c	7	26	chr5_22.12794c	7	36	chr5_16.555098	7	50
chr5_1.202761c	7	26	chr5_22.127936c	7	36	chr5_16.760635c	7	50
chr5_15.295664c	7	28	chr5_23.604817	7	36	chr5_17.26185	7	52
chr5_14.06793c	7	28	chr5_12.197955	7	37	chr5_17.58627	7	53
chr5_15.295584c	7	28	chr4_10.569712c	7	38	chr5_6.57267	7	55
chr4_2.910773c	7	28	chr4_10.569723c	7	38	chr5_6.572694c	7	55
chr5_15.152198c	7	28	chr5_24.226055c	7	38	chr5_17.78595c	7	55
chr5_13.74982	7	28	chr5_24.351542c	7	38	chr2_23.649135	7	55
chr5_0.52447c	7	28	chr4_10.569742c	7	38	chr5_28.902564c	7	56
chr5_11.08108c	7	29	chr4_10.569793c	7	38	chr4_24.107244	7	56
chr5_16.80285c	7	30	chr4_10.56977c	7	38	chr5_21.864814c	7	58
chr5_17.521174c	7	30	chr5_22.743561c	7	38	chr4_27.571075c	7	60
chr5_16.555027c	7	30	chr5_22.321269c	7	38	chr5_21.135741	7	60
chr5_16.951673c	7	30	chr4_10.569725c	7	38	chr5_22.414823c	7	63
chr5_19.391883c	7	30	chr5_22.743579	7	38	chr5_22.504748	7	63
chr5_16.760653c	7	30	chr4_10.569744c	7	38	chr5_22.414793c	7	63
chr5_17.521236c	7	30	chr4_10.569757c	7	38	chr5_22.321321c	7	63
chr5_11.429381c	7	30	chr4_10.569749c	7	38	chr5_24.351454	7	65
chr5_10.963069c	7	30	chr4_10.569785c	7	38	chr1_9.928541c	7	65
chr5_0.110541c	7	30	chr5_12.067042	7	38	chr5_24.684607c	7	65
chr5_0.110551	7	30	chr5_12.067187	7	38	chr5_24.351493c	7	65
chr5_19.831198c	7	33	chr5_12.067189	7	38	chr5_23.872616	7	65
chr1_12.746504c	7	33	chr5_11.923669c	7	40	chr5_24.046085c	7	65
chr5_18.155373c	7	33	chr5_11.55092c	7	40	chr5_25.163078c	7	65
chr5_19.83114c	7	33	chr5_11.704278c	7	40	chr1_9.928565c	7	65
chr5_20.023579c	7	33	chr5_25.028373c	7	41			
chr5_18.539969c	7	33	chr5_23.718523	7	41			
chr5_19.822822	7	34	chr5_26.050245c	7	43			
chr5_20.332037c	7	35	chr2_19.598796	7	43			
chr5_20.579721c	7	35	chr5_26.061239c	7	45			
chr4_27.571114c	7	35	chr5_26.964228c	7	45			
chr5_20.579745c	7	35	chr5_26.003287c	7	45			

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_0.128195	1	0	chr7_10.385832c	1	21	chr7_15.865546	1	34
chr7_0.563157	1	1	chr7_11.009343	1	21	chr7_16.247844	1	34
chr3_2.455116	1	3	chr7_11.211166c	1	21	chr7_16.247922	1	34
chr4_28.376875	1	4	chr7_11.211187	1	21	chr7_16.247829c	1	34
chr6_3.791049	1	4	chr7_11.211106	1	21	chr7_16.182737	1	34
chr7_4.24078c	1	8	chr7_11.016107	1	21	chr7_17.479358	1	35
chr2_27.244251	1	8	chr7_11.233502	1	21	chr7_17.610717	1	35
chr7_4.746381	1	10	chr7_11.611844	1	22	chr7_17.450917c	1	35
chr7_6.500465c	1	14	chr7_12.365489c	1	22	chr5_25.539351	1	35
chr7_7.996817c	1	14	chr7_11.608351c	1	22	chr7_17.773561c	1	36
chr7_6.924247c	1	14	chr7_12.134106	1	23	chr7_17.773514c	1	36
chr5_0.631568c	1	14	chr7_12.134078	1	23	chr7_17.687201c	1	36
chr7_7.531744c	1	14	chr7_12.365514	1	23	chr7_16.760018c	1	36
chr5_0.63163c	1	14	chr7_12.783197c	1	24	chr7_17.47942c	1	36
chr7_6.212351	1	14	chr7_12.783112c	1	24	chr7_16.672845c	1	36
chr7_23.260862	1	14	chr7_12.917504c	1	24	chr7_16.673033	1	36
chr7_23.260855	1	14	chr7_12.987952	1	25	chr7_16.760096c	1	36
chr1_10.36863	1	14	chr7_12.987811c	1	25	chr7_17.378363	1	36
chr7_23.260838	1	14	chr7_15.044078c	1	27	chr7_16.760041c	1	36
chr7_5.856412	1	14	chr7_14.358011	1	27	chr7_16.540365	1	36
chr7_7.156789	1	14	chr7_13.567074	1	27	chr7_16.672896c	1	36
chr7_5.856391c	1	14	chr7_14.329131c	1	27	chr7_17.773577	1	36
chr7_6.373067c	1	14	chr7_14.329089	1	27	chr7_17.773696c	1	36
chr7_5.856314c	1	14	chr7_14.622229	1	28	chr7_17.610663c	1	36
chr7_9.567811c	1	15	chr7_14.622202c	1	28	chr7_16.612431	1	36
chr7_9.567815c	1	15	chr7_15.16963	1	28	chr7_17.450961c	1	36
chr7_9.567824c	1	15	chr7_15.199669c	1	28	chr7_17.479411c	1	36
chr7_9.567808c	1	15	chr7_15.083179	1	28	chr7_16.690209c	1	36
chr7_9.567817c	1	15	chr7_14.616781c	1	28	chr7_17.773511	1	36
chr7_9.417814	1	16	chr7_15.199566c	1	28	chr7_18.177097c	1	37
chr7_9.153843	1	17	chr7_15.083044	1	28	chr7_18.376957c	1	37
chr7_9.153808	1	17	chr7_15.199641	1	28	chr7_18.177112c	1	37
chr2_1.981638	1	18	chr7_15.083224c	1	28	chr7_11.916467	1	37
chr2_1.981647	1	18	chr7_15.115658	1	28	chr7_18.177083c	1	37
chr7_8.994399	1	18	chr7_9.786157c	1	30	chr7_18.376963c	1	37
chr2_1.981716c	1	18	chr7_15.395736c	1	30	chr7_18.207597c	1	37
chr7_8.558541	1	19	chr7_15.370534	1	31	chr7_18.141346	1	37
chr2_5.001299c	1	19	chr7_15.395727c	1	32	chr7_18.141361c	1	37
chr7_8.558661	1	19	chr7_15.723631	1	34	chr7_18.16492c	1	37
chr6_22.020214	1	21	chr7_16.182702	1	34	chr7_18.141463c	1	37

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr7_21.770273	1	37	chr7_21.099301	1	46	chr2_12.63942c	1	51
chr7_18.472244c	1	39	chr7_20.649883	1	46	chr7_21.654273c	1	51
chr7_18.44858	1	39	chr7_20.805014c	1	46	chr7_22.452437	1	51
chr7_18.971407c	1	39	chr7_20.544256	1	46	chr7_22.42221	1	51
chr3_0.357758c	1	39	chr7_20.645239c	1	46	chr7_22.422141c	1	52
chr7_18.667305c	1	39	chr7_20.737408c	1	46	chr7_22.316193	1	52
chr7_18.467474c	1	39	chr7_20.645379	1	46	chr7_22.316197c	1	52
chr7_18.472259c	1	39	chr7_20.544313c	1	46	chr7_22.422232	1	52
chr3_0.357663	1	39	chr7_20.804998c	1	46	chr7_22.422036c	1	52
chr7_18.467426c	1	39	chr7_20.786127	1	46	chr7_22.739206	1	52
chr7_18.633293c	1	39	chr7_20.649892c	1	46	chr7_22.85435	1	54
chr7_18.627966	1	39	chr7_20.645228c	1	46	chr7_22.840347	1	54
chr5_19.55099	1	40	chr7_20.649751c	1	46	chr7_23.013217c	1	54
chr7_18.974728c	1	40	chr4_3.921965	1	46	chr7_22.739119c	1	54
chr7_18.922785c	1	40	chr7_20.786106c	1	46	chr7_22.840457c	1	54
chr7_19.214587	1	40	chr7_20.645311c	1	46	chr7_22.556633c	1	54
chr7_19.696941	1	41	chr7_20.729119	1	47	chr7_23.013207	1	54
chr7_19.228228	1	41	chr7_20.904212c	1	48	chr7_23.013171c	1	54
chr7_19.396709c	1	41	chr7_20.729117	1	48	chr7_23.206126c	1	55
chr7_19.157798	1	41	chr7_21.066436	1	48	chr7_23.351973c	1	55
chr7_19.414384c	1	41	chr7_20.728921c	1	48	chr7_23.206148c	1	56
chr7_19.312259	1	41	chr7_21.564346	1	48	chr7_23.206113c	1	58
chr7_19.443696c	1	42	chr7_21.654196c	1	48	chr7_23.352066c	1	58
chr7_19.443674c	1	42	chr7_21.770311	1	48	chr1_0.49595c	2	0
chr7_19.657053	1	43	chr7_21.724636	1	48	chr1_0.557718	2	0
chr7_19.741362c	1	43	chr7_22.043128	1	48	chr1_0.141372c	2	0
chr7_19.750895	1	43	chr7_22.043139c	1	48	chr1_0.141437c	2	0
chr7_19.741411c	1	43	chr7_22.043026	1	48	chr1_2.499041c	2	2
chr7_19.939304	1	44	chr7_21.915361c	1	48	chr1_2.144312c	2	2
chr7_20.086687c	1	44	chr7_21.915475	1	48	chr1_2.144357c	2	2
chr7_19.939297c	1	44	chr7_21.162256	1	49	chr1_2.14475c	2	2
chr7_20.374326	1	45	chr7_21.162359c	1	49	chr1_1.580327c	2	2
chr7_20.231954c	1	45	chr7_21.654243c	1	51	chr1_1.937206c	2	2
chr7_20.448404c	1	45	chr7_22.043131c	1	51	chr1_1.580333	2	2
chr7_20.229757c	1	45	chr7_21.726369c	1	51	chr1_2.003108c	2	2
chr7_20.729114	1	46	chr7_21.548615	1	51	chr1_2.144585c	2	2
chr7_20.786202c	1	46	chr7_22.043022c	1	51	chr1_0.974818c	2	2
chr7_20.649832	1	46	chr7_21.548382	1	51	chr1_1.359634c	2	2
chr7_20.942885c	1	46	chr7_21.564424c	1	51	chr1_2.144735c	2	2
chr7_20.64994c	1	46	chr7_21.915396c	1	51	chr1_1.39466c	2	2

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_2.14433c	2	2	chr1_2.86597c	2	6	chr3_1.585287	2	12
chr1_1.937087c	2	2	chr1_4.229555	2	6	chr1_5.396723c	2	12
chr1_1.593904c	2	2	chr1_4.3548	2	6	chr1_5.502646	2	12
chr1_2.100126c	2	2	chr1_4.354759c	2	6	chr1_6.290652	2	12
chr1_1.580177c	2	2	chr1_4.492677c	2	6	chr1_6.290649c	2	12
chr1_1.394796c	2	2	chr1_3.775467c	2	6	chr1_6.907091c	2	16
chr1_1.937134c	2	2	chr1_4.197245	2	6	chr1_6.454432	2	16
chr1_2.22285c	2	3	chr1_3.775528c	2	7	chr1_6.27161	2	16
chr1_2.222853c	2	3	chr1_3.250244c	2	7	chr1_6.290499c	2	16
chr1_2.340835c	2	3	chr1_4.197215	2	7	chr1_6.569897	2	16
chr1_2.521837c	2	4	chr1_4.206683c	2	7	chr1_6.454459	2	16
chr1_2.144306c	2	4	chr1_3.793592c	2	7	chr1_6.737085c	2	16
chr1_2.446263c	2	4	chr1_3.734991	2	7	chr1_18.841986	2	16
chr1_1.394625	2	4	chr1_4.229598	2	7	chr1_16.994883c	2	16
chr1_1.909026	2	4	chr1_3.983468c	2	7	chr1_12.540578c	2	16
chr1_2.446131	2	4	chr1_3.549677c	2	7	chr1_17.2773c	2	16
chr1_2.47495c	2	4	chr1_3.775461	2	7	chr1_6.690444	2	16
chr1_2.521724c	2	4	chr1_3.674095c	2	7	chr1_11.050002c	2	16
chr1_2.498949c	2	4	chr1_3.75284c	2	7	chr1_7.150463c	2	16
chr1_2.474891c	2	4	chr1_3.564995c	2	7	chr1_10.775389	2	17
chr1_2.446085	2	4	chr1_4.197258c	2	7	chr1_11.602453	2	17
chr1_2.736343c	2	4	chr1_3.384319	2	7	chr1_16.650361c	2	17
chr1_2.52858	2	4	chr1_3.549589c	2	7	chr1_17.573164c	2	17
chr1_2.528576	2	4	chr1_4.257791c	2	7	chr1_17.573078	2	17
chr1_2.736301	2	4	chr1_4.271843	2	7	chr1_10.775418	2	17
chr1_2.776887c	2	5	chr1_4.320547c	2	7	chr1_12.540607c	2	17
chr1_2.732179c	2	5	chr1_4.354796c	2	7	chr1_7.512917c	2	17
chr1_2.690707	2	5	chr1_4.316229	2	7	chr1_10.495594c	2	17
chr1_2.736319	2	5	chr1_3.030575	2	7	chr1_10.67227c	2	17
chr1_2.732099c	2	5	chr1_3.03039c	2	7	chr2_15.241292	2	17
chr1_2.662415	2	5	chr1_5.96469c	2	10	chr1_18.841929	2	17
chr1_2.741197c	2	5	chr1_5.728871c	2	10	chr1_11.832138c	2	17
chr1_2.736887	2	5	chr1_5.332657c	2	10	chr1_11.543106	2	17
chr1_2.776835	2	5	chr1_5.065178c	2	10	chr1_10.053173c	2	17
chr1_4.253316	2	6	chr1_5.878782c	2	10	chr1_11.480509	2	17
chr1_2.897077	2	6	chr1_5.065205c	2	10	chr1_11.74876c	2	17
chr1_4.229476c	2	6	chr1_5.065188c	2	10	chr1_15.571847c	2	17
chr1_3.152827c	2	6	chr1_5.964559c	2	10	chr1_7.163129c	2	17
chr1_3.152848c	2	6	chr1_6.271448c	2	12	chr1_18.100552c	2	17
chr1_2.816973c	2	6	chr3_1.585221	2	12	chr1_7.136429c	2	17

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr1_11.748759c	2	17	chr1_10.372077c	2	17	chr6_22.020181c	2	32
chr1_15.312104c	2	17	chr1_11.424441c	2	17	chr6_22.020194	2	32
chr1_11.74884c	2	17	chr1_19.106105c	2	17	chr6_22.241836c	2	33
chr1_18.223742c	2	17	chr1_7.513082c	2	17	chr6_22.200502c	2	33
chr1_10.312816c	2	17	chr1_7.163274	2	17	chr6_22.200411	2	33
chr1_11.832123c	2	17	chr1_10.612359c	2	17	chr6_22.30561c	2	35
chr1_11.748741c	2	17	chr1_9.787356c	2	17	chr6_22.3055c	2	35
chr1_11.575551	2	17	chr1_15.003701	2	17	chr6_22.305632c	2	35
chr1_11.54313	2	17	chr1_11.664672c	2	17	chr3_16.920479	2	36
chr1_11.664852c	2	17	chr1_15.312024c	2	17	chr6_29.412482c	2	38
chr1_17.28861c	2	17	chr1_12.428288c	2	17	chr6_24.333476	2	38
chr1_7.834765c	2	17	chr1_15.854795	2	17	chr3_29.719243	2	38
chr1_10.67209c	2	17	chr1_7.847513c	2	17	chr6_23.898748c	2	38
chr1_18.223722c	2	17	chr1_7.834585	2	17	chr6_23.394506	2	38
chr1_10.449852c	2	17	chr1_10.053152c	2	17	chr3_29.719269	2	38
chr1_7.136566c	2	17	chr1_14.439482c	2	17	chr6_24.333399	2	38
chr1_6.672413c	2	17	chr1_10.11151c	2	17	chr6_22.964006c	2	38
chr1_14.439401c	2	17	chr1_10.922413c	2	17	chr3_29.719205	2	38
chr1_6.672308c	2	17	chr1_7.834777c	2	17	chr6_23.481749c	2	38
chr1_10.495617c	2	17	chr1_15.85486c	2	17	chr6_23.39451c	2	38
chr1_17.288566	2	17	chr1_15.00364c	2	18	chr6_24.717093c	2	38
chr1_10.672086c	2	17	chr1_14.858755	2	18	chr6_23.501482c	2	38
chr1_15.312027c	2	17	chr1_17.288532c	2	18	chr6_24.662967c	2	38
chr1_15.479862c	2	17	chr1_10.775413	2	18	chr6_23.501301	2	38
chr1_15.479951c	2	17	chr1_16.466661c	2	19	chr6_23.394674	2	38
chr1_9.459833c	2	17	chr1_16.466642c	2	20	chr6_23.394609c	2	38
chr1_17.03716	2	17	chr1_16.375525c	2	20	chr6_31.966667	2	40
chr1_11.748807c	2	17	chr6_19.982957c	2	25	chr6_29.266748c	2	40
chr1_17.33801c	2	17	chr6_19.98293	2	25	chr6_24.983076c	2	40
chr1_11.51206c	2	17	chr6_20.501838c	2	27	chr6_24.982882c	2	40
chr1_7.834582	2	17	chr6_20.486513	2	27	chr6_25.178794c	2	40
chr1_9.504632c	2	17	chr1_6.070761	2	27	chr6_25.644766	2	42
chr1_11.748702c	2	17	chr1_6.070725	2	27	chr6_26.646092c	2	42
chr1_10.137365c	2	17	chr6_20.486507c	2	27	chr6_25.644762	2	42
chr1_7.150559c	2	17	chr6_21.334726c	2	29	chr6_26.656034c	2	42
chr1_10.137503c	2	17	chr6_21.444481c	2	32	chr6_25.903305c	2	42
chr6_11.819251	2	17	chr6_21.444421	2	32	chr6_26.656326c	2	42
chr1_7.136467	2	17	chr6_21.779928c	2	32	chr6_25.644899c	2	42
chr1_15.312065c	2	17	chr6_21.519907c	2	32	chr6_25.644759c	2	42
chr1_9.688384	2	17	chr6_22.020223	2	32	chr6_25.644722	2	42

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_25.73819c	2	42	chr6_30.845119	2	46	chr6_32.461205	2	50
chr6_26.646208c	2	42	chr6_30.271617c	2	46	chr6_32.918368	2	51
chr6_25.644859	2	42	chr6_34.291969	2	47	chr6_32.918325	2	51
chr6_26.646145c	2	42	chr6_34.413922	2	47	chr5_5.245014	2	52
chr6_25.905892	2	42	chr6_34.536587	2	47	chr6_33.531246c	2	52
chr6_26.295215c	2	42	chr6_34.875927	2	47	chr6_33.305252c	2	52
chr6_25.644725	2	42	chr6_31.531359c	2	47	chr6_33.335228c	2	52
chr6_25.644818	2	42	chr6_31.531428c	2	47	chr6_33.525951	2	52
chr6_25.644842	2	42	chr6_30.957254	2	47	chr6_33.233603c	2	52
chr6_25.644758c	2	42	chr6_30.957368	2	47	chr6_33.040799	2	52
chr6_25.644854c	2	43	chr6_30.957222	2	47	chr6_33.242307c	2	52
chr2_1.999991	2	43	chr6_30.957308	2	47	chr6_32.953315c	2	52
chr6_26.914348c	2	43	chr6_29.528615c	2	49	chr6_33.2642	2	52
chr6_27.073507c	2	43	chr6_15.068559c	2	49	chr6_33.040719c	2	52
chr6_33.567424	2	43	chr6_29.518701c	2	49	chr6_33.526163c	2	52
chr6_33.526119	2	43	chr6_15.10856c	2	49	chr6_33.525925	2	52
chr6_33.526076c	2	43	chr6_15.06843c	2	49	chr6_33.233579c	2	52
chr6_27.390111c	2	44	chr6_29.528617c	2	49	chr6_32.953336c	2	52
chr6_28.141748c	2	45	chr6_15.068553c	2	49	chr6_34.413809	2	52
chr6_29.139394c	2	45	chr6_29.412515c	2	49	chr6_34.923102c	2	53
chr6_28.681778c	2	45	chr6_15.095292c	2	49	chr6_34.209615c	2	53
chr6_27.819291c	2	45	chr6_29.493159	2	49	chr6_34.482688c	2	53
chr6_29.154701c	2	45	chr6_29.52846c	2	49	chr6_34.875958	2	53
chr6_27.839739c	2	45	chr6_32.461294c	2	50	chr6_34.004714	2	53
chr6_27.543158c	2	45	chr1_3.586681c	2	50	chr6_34.837758	2	53
chr6_28.68184c	2	45	chr6_31.834685c	2	50	chr6_34.27061c	2	53
chr6_28.681842c	2	45	chr6_32.412566c	2	50	chr6_34.875949	2	53
chr6_29.154631c	2	45	chr6_31.834871c	2	50	chr6_34.131847	2	53
chr6_27.731527	2	45	chr6_31.954116c	2	50	chr6_33.953482	2	53
chr6_27.819339c	2	45	chr6_32.344995c	2	50	chr6_34.648602	2	53
chr6_28.141808c	2	45	chr6_32.412597	2	50	chr6_34.545954c	2	53
chr6_27.839204c	2	45	chr6_32.141206	2	50	chr6_34.413811	2	53
chr6_27.543135c	2	45	chr6_32.093971c	2	50	chr6_35.290819c	2	54
chr6_29.15463c	2	45	chr6_32.343667c	2	50	chr6_35.286285c	2	54
chr6_27.767203c	2	45	chr6_32.756603c	2	50	chr6_36.295664c	2	54
chr6_28.141676c	2	45	chr6_32.14051	2	50	chr6_36.004464c	2	55
chr6_29.149772c	2	45	chr6_32.14054	2	50	chr6_36.004515c	2	55
chr6_29.098355c	2	45	chr6_32.094031c	2	50	chr6_36.004485	2	55
chr6_30.845257	2	46	chr6_32.141071	2	50	chr6_35.965675	2	55
chr6_29.810378	2	46	chr6_32.140567	2	50	chr6_36.073087	2	55

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr6_35.965591c	2	55	chr3_0.405986	3	2	chr6_10.916245c	3	5
chr6_36.073413c	2	55	chr6_5.982063	3	3	chr6_8.614639c	3	5
chr6_36.591562	2	57	chr6_5.982031c	3	3	chr6_11.988579c	3	5
chr6_36.630332	2	57	chr6_4.77781	3	3	chr6_12.240158c	3	5
chr6_36.420603	2	58	chr6_5.300251c	3	3	chr6_10.847214	3	5
chr6_36.900904	2	58	chr6_5.575539c	3	3	chr6_10.886402	3	5
chr6_36.489991	2	58	chr6_5.981881	3	3	chr6_11.409739	3	5
chr6_36.52517	2	58	chr6_5.982029c	3	3	chr6_7.702625c	3	5
chr6_37.136891c	2	60	chr6_7.359592	3	4	chr6_10.736859c	3	5
chr6_37.184197c	2	60	chr6_6.46821	3	4	chr6_17.519036c	3	13
chr6_9.582408c	2	60	chr6_6.791673c	3	4	chr6_17.734756c	3	13
chr6_9.582276c	2	60	chr6_6.468189c	3	4	chr6_17.281127	3	14
chr6_37.052758	2	60	chr6_27.7315	3	4	chr6_17.215259	3	17
chr6_9.58233c	2	60	chr6_7.070216c	3	4	chr2_27.129885	4	0
chr6_37.18413c	2	61	chr6_7.399133c	3	5	chr4_0.624824c	4	0
chr6_37.052831c	2	61	chr6_11.735847	3	5	chr2_27.129855	4	0
chr6_37.052757	2	61	chr6_11.048559c	3	5	chr4_0.624754c	4	0
chr6_37.756713	2	62	chr6_7.274229	3	5	chr4_0.603696	4	0
chr6_37.800873	2	63	chr6_8.629801	3	5	chr2_27.129849c	4	0
chr6_37.800891c	2	63	chr6_8.977622c	3	5	chr4_1.020245	4	1
chr6_37.801035c	2	63	chr6_7.656259	3	5	chr4_1.403242	4	1
chr6_37.899541	2	63	chr6_12.312814c	3	5	chr4_1.607434	4	1
chr6_37.80096c	2	63	chr6_11.159677	3	5	chr4_1.558819	4	1
chr6_37.899508	2	63	chr6_8.773447c	3	5	chr4_2.61771c	4	2
chr6_38.527314c	2	63	chr6_11.76202	3	5	chr4_16.099695	4	2
chr6_38.821311c	2	64	chr6_8.977642c	3	5	chr6_29.493328c	4	2
chr6_38.221149	2	66	chr6_8.614712c	3	5	chr4_16.099691	4	2
chr6_38.537253	2	66	chr6_10.886313	3	5	chr4_2.643188c	4	2
chr6_1.868383c	3	0	chr3_27.736903	3	5	chr4_16.099675	4	2
chr6_1.425322	3	0	chr6_12.312783c	3	5	chr4_3.57714	4	2
chr6_1.513783c	3	0	chr6_11.735878c	3	5	chr4_16.0997	4	2
chr6_3.272518c	3	2	chr6_9.032051c	3	5	chr4_2.643257	4	2
chr6_3.272563c	3	2	chr3_27.736838	3	5	chr4_10.785072	4	3
chr6_3.581794c	3	2	chr6_8.662557c	3	5	chr4_10.785169	4	3
chr6_3.691074c	3	2	chr6_9.176797c	3	5	chr4_13.333754	4	3
chr3_0.40602	3	2	chr6_7.839982c	3	5	chr4_13.333769	4	3
chr6_4.053725c	3	2	chr6_11.451162c	3	5	chr4_4.680704c	4	4
chr6_3.272502c	3	2	chr6_11.409705c	3	5	chr4_10.024609c	4	4
chr3_0.405998c	3	2	chr6_7.649699c	3	5	chr4_4.871904c	4	4
chr3_0.406034	3	2	chr6_11.657717	3	5	chr4_4.871949	4	4

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_4.907741	4	5	chr4_20.700236c	4	21	chr4_17.246397c	4	29
chr4_7.937463	4	6	chr4_22.519554c	4	22	chr4_27.681531c	4	29
chr4_6.609542c	4	7	chr4_22.384156c	4	22	chr4_27.109568c	4	29
chr4_10.024632c	4	7	chr4_23.043134c	4	23	chr4_28.17272c	4	30
chr4_10.022851c	4	7	chr4_21.69326	4	23	chr4_28.755197	4	32
chr4_4.87194c	4	7	chr4_23.959349c	4	25	chr4_29.120016	4	36
chr4_6.093143	4	7	chr4_23.896043c	4	25	chr4_29.482254c	4	43
chr4_4.300849c	4	7	chr4_25.90357c	4	25	chr4_29.545641c	4	43
chr4_10.378459	4	7	chr4_23.765298	4	26	chr4_29.746082c	4	46
chr4_5.442548c	4	7	chr4_23.895969c	4	26	chr4_29.888214	4	47
chr4_4.907843	4	7	chr4_23.7445	4	26	chr4_29.859004c	4	48
chr4_10.902818c	4	7	chr4_23.959344	4	26	chr4_30.153339	4	48
chr4_9.170436	4	8	chr4_25.69316	4	26	chr4_30.309085c	4	49
chr4_9.349435	4	8	chr4_23.959251c	4	26	chr4_30.429096c	4	53
chr4_14.265056c	4	8	chr4_23.896044c	4	26	chr4_30.709395	4	55
chr4_14.265213	4	8	chr4_23.686953	4	26	chr4_30.929001c	4	57
chr4_14.019645	4	8	chr4_25.378617c	4	27	chr4_30.939637c	4	57
chr4_13.538034c	4	9	chr4_25.284129	4	27	chr4_30.93969	4	57
chr4_13.538025c	4	9	chr4_25.284084	4	27	chr4_30.848368	4	57
chr4_13.538101	4	9	chr3_6.491077c	4	27	chr4_30.939674	4	57
chr4_13.579919	4	9	chr4_26.225342	4	28	chr4_30.92889	4	57
chr4_13.87273c	4	9	chr4_26.344736c	4	28	chr4_30.939552	4	57
chr4_13.538038c	4	9	chr4_26.044632c	4	28	chr4_31.186c	4	58
chr4_13.537969	4	9	chr4_24.14107c	4	28	chr4_31.14001c	4	58
chr4_15.551408c	4	11	chr4_26.044602c	4	28	chr4_30.99181c	4	58
chr4_31.097061c	4	11	chr4_24.079682c	4	28	chr4_31.282608	4	58
chr4_15.41148	4	11	chr4_26.347188c	4	28	chr4_31.98616	4	59
chr4_15.411501c	4	11	chr4_26.053815c	4	28	chr4_31.98619	4	59
chr4_15.621942	4	12	chr4_24.079668	4	28	chr4_32.000338	4	59
chr4_25.585376	4	12	chr4_24.22964	4	28	chr4_32.000228	4	59
chr4_18.907379	4	15	chr4_17.246387c	4	29	chr4_31.588428c	4	59
chr4_19.489223	4	16	chr4_26.558467	4	29	chr4_32.068076c	4	59
chr4_25.551889c	4	20	chr4_27.264889c	4	29	chr4_32.094373	4	59
chr4_25.551913c	4	20	chr4_27.116559	4	29	chr4_31.675112c	4	59
chr4_25.247853c	4	20	chr4_27.264885c	4	29	chr4_32.06823c	4	59
chr4_24.709688c	4	20	chr4_27.098452c	4	29	chr4_31.986193c	4	59
chr4_20.365723c	4	21	chr4_26.770355c	4	29	chr4_31.784524	4	59
chr4_20.365632	4	21	chr4_17.246403	4	29	chr4_31.185883	4	59
chr4_20.70626c	4	21	chr4_26.442561c	4	29	chr4_31.588419c	4	60
chr4_20.800415c	4	21	chr4_27.264891c	4	29	chr3_0.793654c	5	0

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_0.86927c	5	0	chr3_2.756137	5	11	chr3_2.919821c	5	18
chr3_0.793648c	5	0	chr4_19.414226c	5	12	chr3_2.905097c	5	18
chr3_0.869271c	5	0	chr3_2.75611c	5	12	chr3_2.919842c	5	18
chr3_0.793655c	5	0	chr4_13.334563c	5	13	chr3_2.905265	5	18
chr3_0.677968	5	0	chr3_5.0538c	5	13	chr3_2.91984	5	18
chr3_0.869272c	5	0	chr2_28.187005c	5	13	chr3_2.919798c	5	18
chr3_0.869296c	5	0	chr3_4.776043	5	13	chr3_2.919721c	5	18
chr3_0.869268c	5	0	chr3_4.796164c	5	13	chr3_6.123998c	5	19
chr3_0.869152c	5	0	chr2_28.187001	5	13	chr3_6.124154	5	19
chr3_0.42637c	5	1	chr4_13.334587c	5	13	chr3_6.02976	5	19
chr3_0.972201c	5	1	chr3_4.541542	5	14	chr3_5.9021	5	19
chr3_1.055875	5	2	chr3_4.68329c	5	14	chr3_6.358107c	5	19
chr3_0.413203	5	2	chr3_4.478768	5	14	chr2_12.639449	5	20
chr3_0.426408c	5	2	chr6_12.99266c	5	14	chr2_12.639441c	5	20
chr3_1.136064c	5	2	chr3_4.687361c	5	14	chr2_12.639498	5	20
chr3_1.055824c	5	2	chr3_4.298301c	5	15	chr3_6.56816c	5	20
chr3_1.055935	5	2	chr3_3.362055c	5	15	chr3_6.554128	5	20
chr3_0.869264	5	2	chr3_3.497364	5	15	chr3_7.658006	5	22
chr3_0.413249	5	2	chr3_4.300207c	5	15	chr3_7.249402	5	23
chr3_0.426312c	5	2	chr3_4.306393c	5	15	chr3_7.249251c	5	23
chr3_0.413171	5	2	chr6_29.345705c	5	15	chr1_2.499084	5	25
chr3_0.413162	5	2	chr3_3.369977	5	15	chr3_8.014082	5	25
chr3_0.426387c	5	2	chr2_12.736746	5	16	chr3_9.063239	5	25
chr3_0.413187	5	3	chr3_3.342287	5	16	chr3_9.063233	5	25
chr3_0.479389c	5	3	chr3_3.346269	5	16	chr3_9.163452c	5	25
chr3_0.426366	5	3	chr3_3.346272	5	16	chr3_7.904143c	5	25
chr3_0.479349c	5	3	chr3_3.369923	5	16	chr3_8.347534c	5	25
chr3_0.405875c	5	3	chr3_3.34249	5	16	chr3_9.163581c	5	25
chr3_0.545528c	5	3	chr3_3.346251	5	16	chr3_8.431132	5	25
chr3_0.455473c	5	3	chr3_3.3463c	5	16	chr3_8.347407	5	25
chr3_0.455471c	5	3	chr3_3.163648c	5	18	chr3_7.904164	5	25
chr3_1.553932c	5	7	chr3_3.115275	5	18	chr3_8.332798c	5	25
chr3_1.554004c	5	7	chr3_3.115367c	5	18	chr3_7.904089	5	25
chr3_2.077597c	5	8	chr3_2.91972c	5	18	chr3_8.332671	5	25
chr3_2.220732c	5	8	chr3_2.987219c	5	18	chr3_9.597186c	5	26
chr7_11.30447c	5	10	chr3_2.905092c	5	18	chr3_9.74352	5	26
chr3_2.696516c	5	11	chr3_2.919718c	5	18	chr3_9.597026c	5	26
chr1_2.99782c	5	11	chr3_3.020856c	5	18	chr3_9.83606c	5	26
chr1_2.997796c	5	11	chr3_2.919827c	5	18	chr3_10.025041	5	27
chr3_2.696574	5	11	chr3_2.919722c	5	18	chr3_10.14685	5	29

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr4_29.594838c	5	30	chr3_18.61594c	5	34	chr3_20.303287c	5	48
chr3_10.149417c	5	30	chr5_23.191749	5	34	chr3_21.073123c	5	48
chr6_3.553703	5	30	chr3_18.629793c	5	34	chr3_20.303146c	5	48
chr3_19.144099c	5	31	chr3_18.44298c	5	34	chr3_21.777015	5	48
chr3_19.014687	5	31	chr5_23.191788	5	34	chr1_11.729585	5	49
chr3_19.14409c	5	31	chr3_18.737181c	5	34	chr1_11.729744	5	49
chr3_8.809414c	5	31	chr3_18.786763	5	34	chr3_17.451371c	5	49
chr3_8.809417c	5	31	chr4_8.399065c	5	34	chr1_11.72958	5	49
chr3_10.415648	5	31	chr5_23.11445c	5	35	chr3_22.397858c	5	50
chr3_10.149265	5	31	chr5_23.114391c	5	35	chr3_22.96961c	5	50
chr3_18.862084c	5	32	chr5_9.431825c	5	35	chr2_12.225895c	5	50
chr3_18.786595	5	32	chr3_11.374428	5	35	chr3_22.971414c	5	50
chr3_18.786589	5	32	chr3_11.544979c	5	35	chr3_31.330401c	5	50
chr3_18.862082c	5	32	chr3_11.544963c	5	35	chr3_22.971397c	5	50
chr3_18.786629c	5	32	chr3_11.349294c	5	35	chr3_22.67851c	5	50
chr7_19.300581c	5	33	chr3_11.277971	5	35	chr3_17.451478	5	50
chr7_19.300534c	5	33	chr3_11.544922c	5	35	chr3_22.397833c	5	50
chr3_18.758276	5	33	chr3_11.55402c	5	35	chr3_31.33046c	5	50
chr7_19.300555c	5	33	chr3_11.64811c	5	35	chr3_22.059723c	5	50
chr3_10.598985	5	33	chr3_11.861432c	5	37	chr3_22.969602c	5	50
chr4_8.39899c	5	33	chr3_12.176524c	5	37	chr3_22.678527c	5	50
chr7_19.300596c	5	33	chr3_12.975438	5	38	chr3_17.311735c	5	50
chr7_19.300561c	5	33	chr3_12.805107	5	38	chr3_17.480615c	5	50
chr3_10.598993c	5	33	chr3_13.15429	5	39	chr3_22.971405c	5	50
chr3_19.482062c	5	33	chr3_13.154217c	5	39	chr2_12.225907c	5	50
chr5_0.053562c	5	33	chr3_12.805218	5	40	chr2_12.21935c	5	50
chr3_19.783973c	5	33	chr3_13.336658c	5	40	chr3_21.917616	5	50
chr5_23.191645	5	34	chr3_12.975533c	5	40	chr3_22.678449c	5	50
chr3_10.95563	5	34	chr3_13.32722	5	41	chr3_22.397857c	5	50
chr3_11.012746c	5	34	chr3_13.915765	5	42	chr3_17.45143c	5	50
chr3_10.598995c	5	34	chr4_31.779899	5	42	chr3_22.678583c	5	50
chr3_10.606912	5	34	chr3_13.915841c	5	42	chr3_31.714889c	5	50
chr3_8.683165c	5	34	chr3_14.124454c	5	46	chr3_22.970556c	5	50
chr3_18.737374c	5	34	chr3_22.059885	5	48	chr3_22.969603c	5	50
chr5_23.191785	5	34	chr3_21.764845	5	48	chr3_22.969637c	5	50
chr3_18.616047c	5	34	chr3_21.776972	5	48	chr3_17.084814	5	51
chr3_10.599013c	5	34	chr3_21.917483	5	48	chr3_31.277358c	5	51
chr5_23.191701c	5	34	chr3_21.07283c	5	48	chr3_31.277367c	5	51
chr3_10.599066c	5	34	chr3_20.367676	5	48	chr7_10.22618c	5	51
chr3_18.629716c	5	34	chr3_21.073097c	5	48	chr2_12.219439c	5	51

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr3_22.824702	5	51	chr3_24.050323c	5	59	chr3_27.240302c	5	65
chr3_32.662824	5	52	chr3_24.214642c	5	59	chr3_27.240202	5	65
chr3_15.803015c	5	52	chr3_24.121024c	5	59	chr3_27.330486c	5	65
chr3_15.803004	5	52	chr3_24.214573c	5	59	chr3_26.296132c	5	65
chr3_23.544293c	5	52	chr3_24.010703c	5	59	chr3_27.248631	5	65
chr3_15.80301c	5	52	chr3_23.876868c	5	59	chr3_26.296122c	5	65
chr3_23.598381c	5	53	chr3_23.876843c	5	59	chr3_27.296041	5	65
chr3_16.920619	5	53	chr3_23.907006c	5	59	chr3_26.200949c	5	65
chr3_16.890935c	5	53	chr3_24.01077c	5	60	chr3_27.721788c	5	66
chr3_23.544461c	5	53	chr3_23.876742c	5	61	chr3_27.723279c	5	66
chr3_23.544333c	5	53	chr3_23.906895c	5	61	chr3_27.723222c	5	67
chr3_16.890937c	5	53	chr5_16.132983c	5	62	chr3_27.804249c	5	67
chr3_16.920688c	5	53	chr3_25.333278c	5	62	chr3_1.837681c	5	67
chr3_16.920664c	5	53	chr5_16.160467	5	62	chr3_30.527561c	5	68
chr3_23.543935	5	53	chr3_25.674418c	5	62	chr3_30.321447c	5	68
chr4_21.23856c	5	54	chr5_16.160301c	5	62	chr3_29.472835c	5	68
chr3_18.10647	5	55	chr3_25.750115c	5	63	chr3_29.719209c	5	68
chr3_18.140795	5	55	chr3_25.739275	5	63	chr3_29.568573c	5	68
chr3_18.106402	5	55	chr3_25.915776	5	64	chr3_30.527545c	5	68
chr3_18.141429c	5	57	chr3_25.782532	5	64	chr1_3.586774	5	68
chr3_17.986965c	5	57	chr3_25.915845c	5	64	chr3_29.185653	5	68
chr7_2.574894c	5	57	chr3_26.033666c	5	64	chr3_30.527588c	5	68
chr3_18.141454c	5	57	chr3_26.033536c	5	64	chr3_29.236232c	5	68
chr3_24.805637c	5	57	chr3_26.056318c	5	64	chr3_30.527495c	5	68
chr3_18.141449c	5	57	chr3_25.945324	5	64	chr3_30.527498	5	68
chr3_24.921938c	5	57	chr3_27.58571c	5	65	chr3_30.32148c	5	68
chr3_18.141431c	5	57	chr3_26.392692c	5	65	chr5_12.390497c	5	69
chr3_24.711579c	5	57	chr3_27.240247c	5	65	chr3_32.277879c	5	69
chr3_24.528282	5	57	chr3_27.330366	5	65	chr3_32.27784c	5	69
chr3_16.203146	5	57	chr3_27.285255c	5	65	chr3_32.277741c	5	69
chr3_24.711559c	5	57	chr3_26.344376	5	65	chr3_32.277762c	5	69
chr3_24.711556c	5	57	chr3_27.285429	5	65	chr3_32.657813c	5	73
chr3_18.141427c	5	57	chr3_27.285354c	5	65	chr3_32.663335c	5	73
chr3_24.594184	5	57	chr3_27.572778	5	65	chr3_32.602146c	5	73
chr3_24.594162c	5	57	chr3_26.180318c	5	65	chr3_32.657737c	5	73
chr3_18.141457c	5	57	chr3_26.392667c	5	65	chr3_32.602114	5	73
chr3_24.531405c	5	57	chr3_26.344419c	5	65	chr2_11.703057c	6	0
chr3_18.141451c	5	57	chr3_26.495861c	5	65	chr2_11.703045	6	0
chr3_24.411559	5	58	chr3_27.330446c	5	65	chr2_11.702858	6	0
chr3_24.214576c	5	59	chr3_26.20099c	5	65	chr2_11.70281	6	0

Appendix 3. Continued

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_11.335022	6	3	chr2_6.127662	6	12	chr2_19.750367	6	24
chr2_11.380976	6	3	chr2_0.387534c	6	12	chr2_3.922347	6	24
chr2_11.335024	6	3	chr2_6.445079c	6	12	chr2_3.756853	6	24
chr2_11.339977	6	3	chr2_12.169713	6	12	chr2_19.750229	6	24
chr2_11.362466c	6	3	chr2_6.445745	6	12	chr2_4.33749	6	25
chr2_5.74795c	6	4	chr2_5.94454c	6	12	chr2_4.337394	6	25
chr2_11.334928c	6	4	chr2_0.387681	6	12	chr2_4.361539	6	25
chr2_11.380942c	6	4	chr2_6.417988c	6	12	chr6_34.918756c	6	26
chr2_11.335016	6	5	chr2_6.454242	6	12	chr2_4.633461c	6	26
chr2_11.335021	6	5	chr2_8.83243	6	13	chr2_8.945508	6	26
chr2_11.33509	6	5	chr2_8.832438	6	13	chr2_4.63353	6	26
chr2_11.335075	6	5	chr2_8.164211c	6	14	chr2_9.184262	6	27
chr2_11.335023	6	5	chr2_8.819145c	6	14	chr2_9.184282c	6	27
chr2_11.335101	6	5	chr5_21.721407	6	14	chr2_9.486087c	6	27
chr2_11.334944	6	5	chr2_8.003609	6	14	chr2_9.486013c	6	27
chr2_5.748052	6	6	chr2_7.990333	6	14	chr2_9.48603	6	27
chr2_5.249603	6	6	chr2_7.990325c	6	14	chr2_13.360912	6	28
chr2_4.827898c	6	6	chr2_8.832433	6	14	chr2_13.360973	6	28
chr2_5.237114	6	6	chr5_21.721374c	6	14	chr2_13.972922c	6	28
chr2_5.249624	6	6	chr2_7.954935	6	17	chr2_13.119946c	6	28
chr2_5.23712	6	6	chr2_7.308815	6	17	chr3_10.955495	6	28
chr2_5.249636	6	6	chr2_7.308774c	6	17	chr2_13.249581	6	28
chr2_4.827682	6	6	chr4_14.967591c	6	17	chr2_13.943089c	6	28
chr2_5.001207	6	6	chr2_7.106383	6	17	chr2_13.675584c	6	28
chr2_5.237183	6	6	chr2_7.106382c	6	17	chr2_13.249464c	6	28
chr2_5.237009	6	6	chr2_12.885057c	6	17	chr2_13.675643c	6	28
chr2_11.953141	6	9	chr2_7.106324	6	18	chr2_14.34056c	6	30
chr2_11.897767	6	9	chr2_12.770187	6	19	chr2_14.532731c	6	30
chr2_1.329998	6	9	chr2_10.135978c	6	20	chr2_14.340569	6	30
chr2_1.329992	6	9	chr2_10.13593	6	20	chr2_14.972672	6	32
chr2_1.330184	6	9	chr2_10.135795	6	20	chr2_14.765803	6	32
chr2_11.01021	6	9	chr2_10.53144	6	21	chr2_14.972715c	6	32
chr2_1.948952	6	11	chr2_10.531455c	6	21	chr2_14.765857c	6	32
chr2_1.330128c	6	11	chr2_10.532927c	6	21	chr2_14.972658c	6	32
chr2_12.169688	6	12	chr2_10.531448	6	21	chr2_15.42689	6	32
chr2_0.325927c	6	12	chr2_3.142642	6	24	chr2_15.241175	6	32
chr2_6.304727c	6	12	chr2_3.142633	6	24	chr2_14.785022c	6	33
chr2_0.387621c	6	12	chr4_7.720808c	6	24	chr2_15.426876c	6	33
chr2_6.304781c	6	12	chr2_3.756898c	6	24	chr2_15.425902c	6	33
chr2_0.29319	6	12	chr2_2.630091	6	24	chr2_14.765773c	6	33

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_15.426786c	6	33	chr2_18.900138c	6	42	chr2_22.177259c	6	47
chr2_15.148901	6	33	chr2_18.469778c	6	42	chr2_21.380676	6	47
chr2_15.426898c	6	33	chr2_18.464223	6	42	chr2_21.231029c	6	47
chr2_15.148847	6	33	chr2_18.469715	6	42	chr2_21.207918c	6	47
chr2_15.148758	6	33	chr2_18.557623c	6	42	chr2_21.015319	6	47
chr2_14.78504c	6	33	chr2_19.052872c	6	42	chr2_21.806912c	6	47
chr2_15.426851c	6	33	chr2_19.53446c	6	43	chr2_21.808213c	6	47
chr2_15.425923	6	33	chr2_19.598858	6	43	chr2_21.490313c	6	47
chr2_14.825076	6	33	chr2_19.605895	6	43	chr2_21.847437	6	47
chr2_15.051366c	6	33	chr2_19.35846c	6	43	chr2_21.756527	6	47
chr2_18.164969	6	34	chr2_19.598747c	6	43	chr2_20.880509	6	47
chr2_17.666103	6	36	chr2_19.598786	6	43	chr2_21.841255c	6	47
chr2_17.790193c	6	36	chr2_19.534463c	6	43	chr2_20.873439c	6	47
chr2_17.790184c	6	36	chr2_19.750382c	6	43	chr2_20.775521c	6	47
chr2_17.790202c	6	36	chr2_19.534593	6	43	chr2_20.893995	6	47
chr2_17.790205c	6	37	chr2_19.598852c	6	43	chr2_20.880422c	6	47
chr2_17.790181c	6	37	chr2_19.605786c	6	43	chr2_22.10335	6	47
chr2_17.7902c	6	37	chr2_19.605854	6	43	chr2_22.17077c	6	47
chr2_17.79019c	6	37	chr2_19.358589	6	43	chr2_28.658517c	6	50
chr2_17.666144	6	37	chr2_19.437758	6	43	chr2_28.620283c	6	50
chr2_17.790167c	6	37	chr2_20.26184c	6	45	chr2_28.6202c	6	50
chr2_17.239957c	6	38	chr2_20.497466c	6	45	chr2_28.563607	6	50
chr2_17.239977c	6	38	chr2_20.497444	6	45	chr2_28.041804	6	51
chr2_17.240048c	6	38	chr2_20.49745	6	45	chr2_28.675051c	6	52
chr2_17.106194c	6	40	chr2_20.497565c	6	45	chr2_28.041467c	6	52
chr2_17.106347c	6	40	chr2_20.53017c	6	45	chr2_28.563499c	6	52
chr2_16.695551	6	40	chr2_20.497457c	6	45	chr2_28.041695c	6	52
chr2_16.87447	6	40	chr2_20.621917	6	45	chr2_28.592051c	6	52
chr2_16.695571c	6	40	chr2_20.538051	6	45	chr2_28.046701c	6	52
chr2_16.874554c	6	40	chr2_20.697599c	6	47	chr2_27.505814	6	52
chr2_17.10644c	6	40	chr2_22.17065	6	47	chr2_27.624581c	6	52
chr2_18.557681	6	41	chr2_21.23102c	6	47	chr2_27.505643c	6	52
chr2_18.555884c	6	41	chr2_21.649972c	6	47	chr2_27.987851	6	52
chr2_19.214613	6	41	chr2_21.847348	6	47	chr2_27.657306c	6	52
chr2_18.294865c	6	41	chr2_20.77553c	6	47	chr2_27.415948	6	52
chr2_24.585006c	6	41	chr2_22.17722	6	47	chr2_27.747377c	6	52
chr2_18.522509c	6	42	chr2_21.759036	6	47	chr2_27.577737	6	52
chr2_19.052861c	6	42	chr2_21.841224c	6	47	chr2_28.675057	6	52
chr2_19.052925c	6	42	chr2_20.881385c	6	47	chr5_5.244913	6	52
chr2_18.458047c	6	42	chr2_22.103425	6	47	chr2_28.041839c	6	52

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr2_27.505821c	6	52	chr2_25.312213c	6	56	chr2_23.874155	6	61
chr2_28.019879c	6	52	chr2_25.224352c	6	56	chr2_23.594445	6	61
chr2_27.987994c	6	52	chr3_27.248508	6	56	chr2_24.001869	6	61
chr2_28.465696c	6	52	chr2_25.600564	6	56	chr2_23.449792c	6	62
chr2_27.987966c	6	52	chr2_25.529379c	6	56	chr2_23.44992	6	62
chr2_27.106577	6	53	chr2_25.243094	6	56	chr2_23.44995c	6	62
chr2_25.57052c	6	53	chr3_27.24849	6	56	chr2_23.649114	6	62
chr2_27.384741	6	53	chr2_25.312126	6	56	chr2_23.594351c	6	62
chr2_27.244168c	6	53	chr2_25.286401	6	56	chr2_23.303376	6	64
chr2_27.106467	6	53	chr2_25.286416	6	56	chr2_22.876548	6	64
chr2_27.206471	6	53	chr2_25.30694c	6	56	chr2_23.248144c	6	64
chr2_27.220657c	6	53	chr3_27.248582	6	56	chr2_23.22253	6	64
chr2_27.384693	6	53	chr2_25.306917c	6	56	chr2_23.248171	6	64
chr2_27.384549c	6	53	chr2_25.111048	6	56	chr2_23.38152c	6	64
chr2_25.107174	6	53	chr2_25.198303	6	56	chr2_22.876628c	6	64
chr2_26.005039c	6	53	chr2_25.600408	6	56	chr2_23.222476	6	64
chr2_25.286467c	6	53	chr2_25.061952	6	56	chr2_23.381612c	6	64
chr2_27.384565c	6	53	chr2_25.873764	6	57	chr2_23.303524c	6	64
chr2_27.03789c	6	54	chr2_24.943522	6	57	chr5_9.983713	7	0
chr2_27.206423c	6	54	chr2_24.570871	6	58	chr5_9.983711	7	0
chr2_25.759212	6	55	chr2_24.570867	6	58	chr5_9.983664	7	0
chr2_25.96824c	6	55	chr2_24.62641c	6	58	chr5_9.994374c	7	1
chr2_26.347536c	6	55	chr2_24.626465c	6	58	chr5_9.98367	7	1
chr2_25.968205	6	55	chr2_24.646116c	6	58	chr5_10.540752	7	2
chr2_26.62235c	6	55	chr2_24.57088	6	58	chr5_10.13224	7	2
chr2_25.946203	6	55	chr2_24.273834c	6	59	chr5_9.387827c	7	2
chr2_27.384735c	6	55	chr2_24.223175c	6	59	chr5_9.983708	7	2
chr2_26.345516c	6	55	chr2_24.235476	6	59	chr5_10.132248	7	2
chr2_26.417962	6	55	chr2_24.273841c	6	59	chr5_9.488555	7	2
chr2_26.476926c	6	55	chr2_24.130001	6	59	chr5_9.922499	7	3
chr2_26.228934	6	55	chr2_24.231875c	6	59	chr5_9.387902c	7	3
chr2_25.71126c	6	55	chr2_24.130025c	6	59	chr5_9.885695	7	3
chr2_26.347466c	6	55	chr2_24.27388c	6	59	chr5_10.00788c	7	3
chr2_25.873875	6	55	chr2_24.235457	6	59	chr5_9.249829c	7	3
chr2_25.307035c	6	55	chr2_24.223229c	6	59	chr5_9.141249	7	3
chr2_25.529398c	6	55	chr2_24.033015c	6	60	chr5_9.488371	7	3
chr2_24.943563	6	55	chr2_23.822395c	6	61	chr5_9.488542c	7	3
chr2_25.706236c	6	55	chr2_23.822309	6	61	chr5_9.141127	7	3
chr2_25.706199	6	55	chr2_23.822264c	6	61	chr5_9.387917c	7	3
chr2_25.312202c	6	56	chr2_23.822327c	6	61	chr5_9.690679c	7	3

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Marker name	Linkage group	position cM	Marker name	Linkage group	position cM	Marker name	Linkage group	position cM
chr5_10.132037c	7	3	chr5_5.061345c	7	18	chr5_1.881454c	7	22
chr5_9.881391c	7	3	chr5_5.03758c	7	18	chr5_1.202728c	7	22
chr5_9.911991c	7	3	chr5_5.600325c	7	18	chr5_1.825825c	7	23
chr5_8.908382	7	5	chr5_5.612412c	7	18	chr5_0.801544c	7	23
chr5_8.908206c	7	5	chr5_4.490021c	7	18	chr5_1.202761c	7	23
chr5_8.914751c	7	5	chr5_4.630744	7	18	chr5_1.860992c	7	23
chr4_30.671485	7	5	chr5_4.737518	7	18	chr5_0.475351c	7	23
chr5_9.17276c	7	5	chr5_4.739302c	7	18	chr5_0.475123c	7	23
chr5_8.626804c	7	6	chr5_5.03759c	7	18	chr5_1.861c	7	23
chr5_8.627009c	7	6	chr5_4.490059c	7	18	chr5_0.801526c	7	24
chr5_8.672065c	7	6	chr5_4.78516c	7	18	chr5_0.927025c	7	24
chr5_8.708366	7	6	chr5_5.037583c	7	18	chr5_0.710475c	7	24
chr5_8.580964	7	6	chr5_5.037526c	7	18	chr5_0.722916c	7	24
chr5_8.35421c	7	7	chr5_5.410683c	7	18	chr5_0.6267c	7	24
chr5_8.354225	7	7	chr5_5.161702	7	18	chr5_0.475269c	7	24
chr5_8.500875	7	7	chr5_5.218505c	7	18	chr5_0.475375	7	24
chr5_8.395351	7	7	chr5_5.037586c	7	18	chr5_0.389442c	7	25
chr5_7.379825c	7	12	chr5_4.30626c	7	18	chr5_0.363787	7	25
chr5_6.804483c	7	12	chr5_4.243693c	7	18	chr5_0.368219c	7	25
chr5_8.21139c	7	12	chr5_3.180386c	7	19	chr5_0.368309c	7	25
chr5_6.71227c	7	12	chr5_3.349344c	7	19	chr5_0.163886	7	26
chr5_8.626905c	7	12	chr5_3.495738c	7	19	chr5_0.240038c	7	26
chr5_8.211443c	7	12	chr5_22.550855c	7	19	chr5_0.098223c	7	26
chr5_8.68689c	7	12	chr5_3.349245	7	19	chr5_0.163856	7	26
chr5_6.959854c	7	12	chr2_12.73662	7	20	chr5_11.107679c	7	27
chr5_8.686768c	7	12	chr5_2.909426	7	20	chr5_11.140558c	7	27
chr5_8.708276c	7	12	chr5_2.909445c	7	20	chr5_13.586155	7	28
chr5_8.6719c	7	12	chr5_2.909342	7	20	chr5_11.429377c	7	28
chr5_6.752572	7	12	chr5_2.725186	7	20	chr5_13.001228	7	30
chr5_7.678127c	7	12	chr5_2.792707c	7	20	chr5_13.0642c	7	30
chr5_5.161795c	7	17	chr5_2.411625c	7	20	chr5_12.804159	7	32
chr5_6.804396c	7	17	chr5_2.395694	7	20	chr5_12.7312c	7	33
chr5_6.128499c	7	17	chr5_2.239591c	7	21	chr5_12.731087c	7	33
chr5_7.677984c	7	17	chr5_2.094065	7	21	chr5_12.731085c	7	33
chr5_7.747778	7	17	chr5_2.069239c	7	21	chr5_12.731108c	7	33
chr5_5.161854c	7	17	chr5_2.027555	7	21	chr5_12.731079c	7	33
chr5_6.481734	7	17	chr5_2.06928	7	21	chr5_12.731132	7	33
chr5_7.227119c	7	18	chr5_1.091374	7	22	chr5_12.390424	7	37
chr5_4.766085c	7	18	chr5_1.933062c	7	22	chr5_12.39054	7	37
chr5_5.379398c	7	18	chr5_2.018838c	7	22			