THE CONSTRUCTION OF A *GOSSYPIUM* AD-GENOME-WIDE
COMPREHENSIVE REFERENCE MAP
BASED ON DIVERSE DATA RESOURCES

A Dissertation

by

JING YU

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

May 2009

Major Subject: Plant Breeding

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Approved by:

Co-Chairs of Committee,	C. Wayne Smith
	Russell J. Kohel
Committee Members,	Larry J. Grauke
	John Zhihong Yu
Head of Department,	David D. Baltensperger

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ABSTRACT

The Construction of a *Gossypium* AD-genome-wide

Comprehensive Reference Map Based on Diverse Data Resources.

(May 2009)

Jing Yu, B.S., Beijing Normal University, China;

M.S., Cornell University

Co-Chairs of Advisory Committee: Dr. Russell J. Kohel
Dr. C. Wayne Smith

Integration of two or more genomic maps provides a higher density of markers and greater genome coverage than can be obtained with the resources available for a single mapping study. Map integration is important in any species for which an annotated complete genome sequence is not available. For organisms currently being sequenced, a pre-sequence integrated map is essential to provide the "backbone" for assembly of the sequence. Map integration also facilitates the identification and resolution of discrepancies among different maps; mapping of QTLs, ESTs, and BACs; and positioning of candidate genes. However, the inconsistencies in markers and populations used in individual mapping studies limit our ability to fully integrate the available data. By concentrating on marker orders rather than marker distances, one can join together published map data to include a majority of markers with the best estimate of their order in the genome. In this study, a comprehensive reference map was constructed from 28 published cotton AD genome maps. The output reference map contains 7,424 markers and represents over 93% of the combined mapping information from the 28 individual AD genome genetic maps. This study applied the use of bioinformatics and computational biology in cotton genome mapping integration. The output will be stored and displayed through CottonDB (http://www.cottondb.org), a public cotton genome database.

DEDICATION

To the memory of my grandma and primer teacher, Runbo Li, who I wish could share this happiness with me at this moment.

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I would like to express my sincere appreciation to Dr. Russell Kohel, for his encouragement, support, guidance, time, and patience during my entire graduate education at A&M. I would like to express my gratitude to Dr. Wayne Smith, for his encouragement, support, and advice. I am truly fortunate to have them as co-chairs of my committee. Without their invaluable encouragement and support, it is hard to believe that I could make any achievement on my continued education due to the heavy duties of full time work. I would also like to thank Dr. John Yu and Dr. L.J. Grauke, the other members of my committee, for their work and valuable feedback on my aptitude exam, degree proposal defense, and final dissertation defense.

My special thanks goes to Dr. Lori Hinze, a colleague and my first and best friend in College Station, Texas, for her selfless help and time listening, discussing, and sharing comments on my dissertation.

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Most of all, I am grateful to my parents, sister, and son, for their love, support and concern.

NOMENCLATURE

AFLP	Amplified Fragment Length Polymorphism
At or Dt	A or D subgenome of the tetraploid AD genome
BAC	Bacterial Artificial Chromosome
CMap	Comparative Map Viewer
DAG	Directed Acyclic Graph
EST	Expressed Sequence Tag
FISH	Fluorescence In Situ Hybridization
NP	Nondeterministic Polynomial time
NP-hard	at least as hard as any NP problem
PCR	Polymerase Chain Reaction
QTL	Quantitative Trait Locus
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
RH	Radiation Hybrid
SNP	Single Nucleotide Polymorphism
SSR	Simple Sequence Repeat
TSP	The Traveling Salesman Problem

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CHAPTER I

INTRODUCTION

1.1 The Cotton Genus

Cotton (*Gossypium* spp.) is the world's most important textile fiber crop and one of the major oilseed crops. The cotton genus, *Gossypium* spp., belongs to the Malvaceae family and is distributed throughout tropical and subtropical regions of the world. The cotton genus consists of 50 recognized species (Fryxell, 1992), most are diploids with 13-pair chromosomes, but five found in the New World are allotetraploids with 26-pair (13 A- and 13 D-subgenome) chromosomes. Cytological analyses of chromosome size and meiotic affinity revealed that the 13-chromosome diploid genomes could be assigned to genomic groups (A, B, C, D, E, F, G, or K), and that the groups are distributed in a geographically related manner (Beasley 1940, 1942; Phillips and Strickland, 1966; Edwards and Mirza, 1979; Endrizzi et al., 1985; Stewart, 1995; Percival et al., 1999). All of the 52-chromosome species are disomic (Kimber, 1961), have an AD-genome composition, and are hybridized readily to form relatively fertile hybrid progenies (Beasley, 1942; Endrizzi et al., 1985; Percival et al., 1999). Data implicate an origin for *Gossypium* 5–15 million years ago (mya) and a rapid early diversification of the major genome groups. Allopolyploid cottons appear to have arisen within the last n million years, as a

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This dissertation follows the style of *Crop Science*.

consequence of trans-oceanic dispersal of an A-genome taxon to the New World followed by hybridization with an indigenous D-genome diploid (Wendel and Cronn, 2003).

Of the fifty species of cotton, four were independently domesticated and cultivated for their fibers (Brubaker et al., 1999a; Brubaker and Wendel, 1994; Percy and Wendel, 1990; Wendel, 1989; Wendel et al., 1992: Wendel et al., 1999). The two domesticated AD genome species, *G. hirsutum* and *G. barbadense*, were independently domesticated in Mexico and Peru, respectively; while the two domesticated A genome species, *G. arboreum* and *G. herbaceum*, originated in the Indo-Pakistan subcontinent and southern Africa. Due to the specific evolutionary history of cotton, cotton genomes can be used as model system in several biological studies. For example:

(1) A unique aspect in cotton domestication is that it is global in scope, involving ancient human cultures in both the Old and New Worlds and a convergent or parallel plant domestication process from divergent and geographically isolated wild ancestors.

(2) *Gossypium* allopolyploids offer a powerful model for they are in as much as the two genomes are known to be largely co-linear yet differ in genome size by a factor of two. An early suggestion of unequal evolutionary rate for the A- and D-genomes was stimulated by the observation that synthetic A-genome x D-genome hybrids can be

synthesized only with the A-genome parent as female (Wendel and Cronn, 2003).

(3) Due to their economic importance, the cotton genus' diploidized allopolyploid species can be used as a model system to study polyploidization and post-polyploidization of plants (Wendel and Cronn, 2003).

1.2 Cotton Breeding and Genetic Research

"Plant breeding is the art and science of the genetic improvement of crops to produce new varieties that have increased productivity and quality. Genetic variation is the engine that propels breeding to meet future challenges" (Zamir, 2001).

Like other crops, cotton was first domesticated and selected by early man and later improved by modern plant breeders to form the basis of today's sophisticated and highly-productive agricultural economy. In the past 100 years, U.S. cotton production has demonstrated significant advances (Figure 1.1). Major efforts came from cotton breeding programs (improved cotton cultivars or improved genetics), management inputs (new pesticides and herbicides, Boll Weevil Eradication Program) and biotechnology inputs (genetic engineering or transgenic plants) (Marra and Martin, 2007).

Meanwhile, plateaus or even declines (such as that from 1965 to 1980) appear in the chart, which indicates that cotton yield is not continuously increasing. There are several major factors that impact cotton yield. They are weather, management, rise of new pests, and genetic improvement (Meredith, 2000). Among them, the great challenge to cotton breeders is to make progress in cotton breeding for stabilized yield, improved quality and stability of fiber traits, and disease and pest resistance while dealing with a very narrow genetic diversity.

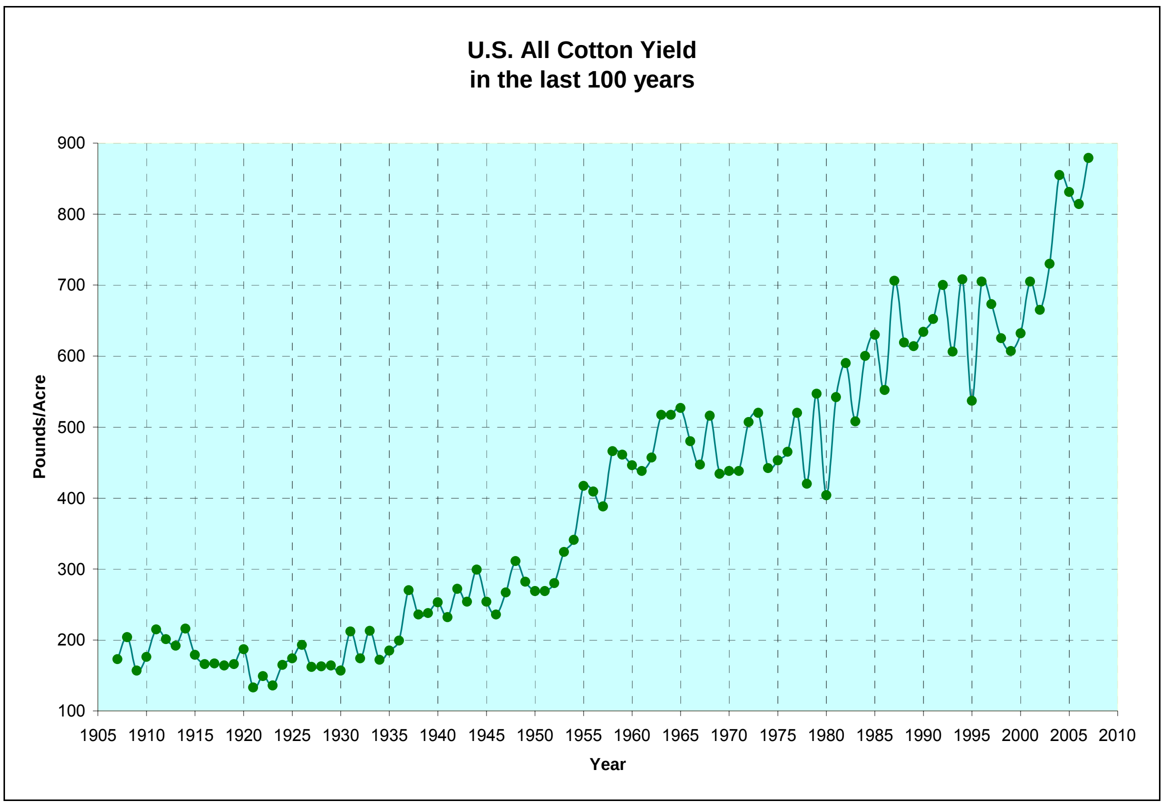


Figure 1.1. Average U.S. cotton yield per acre from 1907 to 2007 (Data source: http://www.nass.usda.gov).

Yield, fiber quality, disease and pest resistance, and abiotic stress responses are cotton plant traits. A trait is a distinct variant of a phenotypic character of an organism whose value may be inherited, environmentally determined or a mixture of genotype and environment effects. The inherited influence on a trait is controlled by gene(s). To introduce new gene(s) or gene combinations into elite cultivars are the main objectives in breeding programs. To identify a new gene that potentially benefits the defined breeding goal(s) depends on new genetic diversity. Therefore the availability of good genetic resources is the basis for developing new varieties.

However, although all four cultivated cotton species have spread far beyond their ancestral homes during the last several millennia, one species, *G. hirsutum*, has come to dominate world cotton commerce. *G. hirsutum* presently is responsible for over 90% of the annual cotton crop internationally. *G. barbadense* accounts for over 5% of world fiber production. The rest of the worldwide fiber production is from two A genome species, *G. arboreum* and *G. herbaceum*. Furthermore, the current genetic base of U.S. commercial cotton cultivars represents less than 1% of U.S. cotton germplasm (Esbroeck and Bowman, 1998).

Over the centuries, farmers have selected improved plant types in their fields, which have arisen through recombination, naturally occurring mutation, and spontaneously outcrossing events with wild relatives (Koornneef and Stam, 2001). While quantitatively inherited traits, like yield and fiber quality, are controlled by multiple genes, such that as the gene number for a trait increases, the probability of finding an individual with beneficial alleles at all of the genetic loci decreases. Such traits do not consistently fall into discrete classes because environmental conditions greatly modify their performance. The identification of genetic factors responsible for such improvement has been difficult, limiting the efficiency of breeding efforts by the traditional approach, which only well-defined characters, usually controlled by a single, dominant gene, can be identified (Kohel, 1999, Tanksley and McCouch, 1997).

The developments in molecular genetics promise to offer plant breeders a rapid and precise alternative approach to conventional selection schemes. The advances in the use of DNA markers for marker-assisted selection (MAS) are promising for streamlining many crop improvement efforts (Burr et al., 1983; Tanksley et al., 1988). DNA-based markers are phenotype-neutral, free of epistatic effects, and have simple Mendelian inheritance. DNA markers are particularly useful in introgression of valuable genes from exotic germplasm (Tanksley and McCouch, 1997) and breeding for traits affected by many quantitative trait loci (QTLs) (Edwards et al., l987; Paterson et al., 1988). Genetic linkage maps based on the DNA markers offer new opportunities in evaluation and characterization of crop germplasm resources for their better utilization (Tanksley and McCouch, 1997).

1.3 Cotton Genome Mapping

The inheritance of specific regions of DNA can be followed by molecular markers that detect DNA sequence polymorphisms. Recombination frequencies between traits and markers reveal their genetic distance, and trait-linked markers can be anchored. Linkage analysis allows us to determine regions of chromosomes that are likely to contain the gene(s) of interest. Genetic mapping provides observed results of genetic markers along with chromosome(s). Construction of a detailed genetic map for cotton will make available precise and vast amounts of information that cotton breeders can use to identify and manipulate traits to their maximum advantage. In addition to genetic maps, physical maps can be developed that mark an estimate of the true distance, in DNA base-pair based measurements, between points of interest, thus allowing a scientist to more easily home in on the location of a gene.

As a consequence of the development in molecular markers, adequate numbers of mapped genetic/physical markers are now available for cotton. As of 2007, over 50 maps derived from 35 different mapping populations were constructed by either genetic linkage analysis, radiation hybrid (RH) (Gao et al., 2004; 2006), or fluorescence in situ hybridization (FISH) (Bie et al., 2004; Ji et al., 1999, 2007; Wang et al., 2001; 2006). Over 30,000 genetic markers and genes were presented on these maps, four genomic groups were involved, AD, A, D, and G, but the large majority were AD genomes. The number of cotton sequences is also increasing rapidly. More than 450,000 *Gossypium* sequences have been deposited in GenBank, of which over 80% are Expressed Sequence Tags (ESTs), 10% bacterial artificial chromosomes (BAC) end sequences, and nearly 10,000 Simple Sequence Repeats (SSRs).

Three recently published articles show the most significant progress in cotton genome research. In 2006, scientists at Nanjing Agricultural University reported that all 26 chromosome/linkage groups of *G. hirsutum* L. were completely assigned by SSR marker-based BAC-FISH (Wang et al., 2006; 2008). In the same year, a global assembly of 185,000 *Gossypium* ESTs from over 30 cotton cDNA libraries of A, D, and AD genomes was reported by scientists at Iowa State University (Udall et al., 2006). Last year, a high density, microsatellite-based, gene-rich linkage map was published, which contains 1,790 loci with average intermarker distance less than 2 cM (Guo et al., 2007).

However, all these types of data resources have caveats and limitations. The first is the assumption that a particular map truly reflects the underlying genome. Genomic duplications, inversions, and other complex rearrangements (which may vary between individuals) can complicate the interpretation of these maps. Sex-specific differences can complicate genetic maps. Any type of statistically based map (whether RH or genetic linkage) should be carefully scrutinized for the likely probability of marker order. There are also gaps in many of the available maps, and DNA fragments may become lost or mistakenly mapped to a wrong position. Meanwhile, individual maps often were created independently by different research groups on diverse mapping populations, and the number of markers on an individual map reflected the genotype of the parents and the progeny and the rate of heterozygosity. Thus each map may contain valuable markers that may not be observable on other maps. In other words, the number of markers that can be mapped on a single combined map is limited.

Cross-referencing different genomic maps enhances the utility of a given map, confirms DNA fragment order, and helps order and orient evolving contigs. To overcome the problems as well as to study the complex genome structure of tetraploid cotton, researchers started to compare maps drawn from different populations of the same or different species (Rong et al., 2004; 2005). Consequently, efforts on merging multi-maps began, based on looking for shared marker orders among the maps. Such efforts included merging several genetic maps into a consensus map, or combining genetic and physical map data. However, as of March 2008 there were only two reports in cotton that reported this kind of merging. One is a study inferring gene order along the chromosomes of the hypothetical ancestor of the A and D genomes of *Gossypium* (Rong et al., 2005), and the other is an integration of cotton genetic and physical maps of homoeologous chromosomes 12 and 26 in the *Gossypium* AD genome (Xu et al., 2008). No AD genome-wide map integrations have been reported. A few cotton research projects have attempted the construction of AD genome consensus maps. However, the constructions have shortcomings since they are based on the sequence homology or marker consistency approach. By use of these approaches, a large number of maps cannot be handled at the same time, and many markers are excluded because of inconsistencies. In many cases, new marker development and linkage analysis will have to be conducted to obtain enough markers on the consensus map to ensure its accuracy.

The genome sequencing project on *Arabidopsis*, a dicot model plant that has a small genome size, was completed nine years ago and the sequenced genome is well characterized. The cotton genomes are presently the nearest relative to *Arabidopsis* outside of the *Brassicaes* (Bowers et al., 2003). Thus, comparative genome analysis between cotton and *Arabidopsis* is possible through the use of comparative maps. Constructed by mapping common sets of gene probes on different genomes, comparative maps allow us to use structural and functional information about the *Arabidopsis* genome to make predictions about cotton genome. In particular, since we know about where and when each gene is expressed and what the consequences are of increasing or decreasing the expression of any gene in *Arabidopsis* genome, direct comparisons of full sequenced portions and alignment of the robust *Arabidopsis* genetic maps with cotton species will allow us to isolate and address agronomically important genes in cotton species rapidly. However, without such an “All-in-One” map that carries the most information from the cotton genome, it is impossible to gain the most benefits from the comparison with the *Arabidopsis* genome.

1.4 Goal of This Research

Computational biology and genome databases play a unique role to overcome problems, as well as to best improve overall mapping accuracy so as to share the maximum useful information of each individual map. The goal of this proposal is to build a *Gossypium* AD-genome-wide comprehensive reference map to incorporate all publicly available genetic information that has been produced in the study of the cotton crop. Gathering and presenting data in one reference map will accelerate the understanding of the cotton genome structure, hence ultimately contributing to agronomic improvement and sustainability. All data that will be used in the comprehensive map construction will be managed and stored in CottonDB, a USDA-ARS cotton genome database. The constructed map will be displayed online through the CottonDB website (http://www.cottondb.org).

This project will aim to construct a “comprehensive map” based on the Genome Database approach and computational algorithms that were used in graph theoretic approach. Computational biology plays a unique and most important role in constructing a comprehensive map based on many datasets from diverse data resources.

1.5 Potential Significance of This Research

1. It is useful to construct maps from multiple populations because no one population can contain polymorphisms for all desired mapping loci,

2. A comprehensive map will be an integration of current cotton genome knowledge, provides the "backbone" for the assembly of the ongoing cotton genome sequencing projects
3. Adoption of necessary genomic information for utilization in cotton improvement, e.g. if tagged to genes or QTLs, the loci contain practical information for molecular marker assisted selection breeding.
4. The complex tetraploid cotton genome offers many challenges and opportunities for genomics research, which will be facilitated by a comprehensive map.
5. Provide a framework to incorporate QTLs, construct cotton-Arabidopsis comparative map, and set pipelines for dynamically updating data from newly published results
6. To improve data management for maps, markers, sequences, QTLs, and trait studies through CottonDB and other data storage systems that exist in the cotton community.

CHAPTER II

LITERATURE REVIEW

2.1 Genetic Markers in Genome Research

Genetic markers are inherited variations. They are genes or DNA segments located on chromosomes. Genetic markers are tools used in marker assisted selection breeding, studies to understand genetic events, quantitative trait studies, taxonomic and evolutionary studies, or to determine the precise inheritance pattern of the gene that has not yet been exactly localized on a chromosome. Genetic markers also play a role in genetic engineering, as they can be used to produce normal, functioning proteins to replace defective ones.

Genetic markers are variations of genes with features such as dominant/recessive inheritance, co-dominance, and epistasis. In general, a good genetic marker will have these conditions (Gupta et. al., 1999):

1) Must be polymorphic

2) Co-dominant inheritance

3) Randomly and frequently distributed throughout the genome

4) Easy and cheap to detect

5) Reproducible

There are three types of genetic markers commonly used in genome research: morphological, biochemical or protein-based and molecular or DNA-based markers.

2.1.1 Morphological Markers

Morphological markers are originating by genes that affect form, coloration, male sterility or resistance etc., which include aspects of the outward appearance (shape, structure, color, and pattern) as well as the form and structure of the internal parts like bones and organs. Morphological markers have been used to understand genetic variation for more than a century since Mendel's discoveries. Advantages of morphological markers are they are cheap and easy to observe. Morphological markers have a long history of being used in traditional plant breeding programs and QTL studies (Sax, 1923). There are about 145 morphological markers identified in cultivated cotton but their utility in breeding programs has remained limited because of their deleterious effect and the difficulties in accumulating multiple markers in a single genotype (Percy and Kohel, 1999).

Morphological markers have restricted uses because first, they are highly dependent on environmental factors. Often the conditions in which a plant is grown can influence the expression of these markers and lead to false determination. Second, these mutant traits often have undesirable features such as dwarfism, albinism, etc. And lastly, performing breeding experiments with these markers is time consuming and labor intensive (Stuber et al., 1992).

2.1.2 Protein-Based Markers

A protein-based marker, also called a biochemical marker, is a gene that encodes a protein that can be extracted and observed. Isozyme markers were first described by Hunter and Markert (1957) who defined them as different variants of the same enzyme having identical functions and present in the same individual. The first to introduce the term biochemical polymorphisms often referred to them as allozyme or isozyme markers. Isozymes are functionally similar forms of enzymes (Murphy et al., 1990), whereas allozymes are differential forms of the same emzyme resulting from allelic variation (Crozier, 1993). Allozymes display differential mobility with electrophoresis techniques and can be detected by staining for enzyme activity (Conkle et al., 1982). The procedures to identify isozyme variation are simple. A crude protein extract is made from some tissue sources, usually leaves. The extracts are next separated by electrophoresis in a starch gel. The gel is then placed in a solution that contains reagents required for the enzymatic activity of the enzyme you are monitoring. In addition, the solution contains a dye that the enzyme can catalyze into a color reagent that stains the protein. In this manner allelic variants of the protein can be visualized in a gel. Isozymes are generally expressed in a co-dominant fashion and rarely exhibit epistatic interaction (Tanksley and Rick, 1980).

Biochemical protein-based markers are generally independent of environmental growth conditions, thus they are considerably more useful than morphological markers. By the early 1980s, biochemical markers had been employed as a general tool in strain or stock identification and taxonomic and evolutionary studies (Moss, 1982; Suiter and Parks, 1984; McAndrew and Majumder, 1983; Bourdon, 1986; Richardson et al., 1986; Basaglia, 1988), and mapping QTL (Weller et al., 1988). In cotton, biochemical markers were used in identification of origin and diversification (Percy and Wendel, 1990) and gene functions (Ni and Trelease, 1991).

However, the number of genetic markers provided by isozyme assays was insufficient in plant breeding applications (Cherry et al., 1972; Tanksley, 1983; Wendel and Weeden, 1989). Electrophoretic analysis of isozymes can be very difficult in plants that contain high levels of phenolic compounds, because these compounds interact with proteins in a variety of ways, causing inhibition of enzyme activities or otherwise in obscuring isozyme banding patterns (Wendel and Parks, 1982). As a result, genetic research on isozymes has been relatively difficult in polyphenolic-rich plants, such as cotton.

2.1.3 DNA-Based Markers

Since the 1980’s, new molecular techniques have made it possible to examine variations at the DNA level, thus providing numerous number of genetic markers. These markers are based on naturally occurring polymorphism in DNA sequences such as base pair deletions, substitutions, additions or patterns (Gupta et al., 1999). DNA-based markers are relatively simple to detect, abundant throughout the genome even in highly inbred cultivars, independent of environmental conditions selection and can be detected neutral at virtually any stage of plant development, thus they can be widely used in modern agriculture. They have been used for genome and comparative mapping, phylogeny and population genetics, parental selection and species identification, association studies and QTL analysis. Using DNA-based markers, Marker-Assisted Selection (MAS) can enhance the speed and effectiveness of plant breeding.

There are various methods to detect and amplify these polymorphisms. The most commonly used DNA-based markers are:

2.1.3.1 RFLP

RFLP (Restriction Fragment Length Polymorphism) was one of the earliest molecular marker identified. An RFLP is a sequence of DNA that has a restriction site on each end with a "target" sequence in between. A target sequence is any segment of DNA that binds to a probe by forming complementary base pairs. A probe is a sequence of single-stranded DNA that has been tagged with radioactivity or an enzyme so that the probe can be detected. When a probe binds with its target, the investigator can detect this binding and know where the target sequence is since the probe is detectable. RFLPs produce a series of bands when a Southern blot (Southern, 1975) is performed with a particular combination of restriction enzyme and probe sequence. RFLP probes are mostly species-specific single locus probes of about 0.5-3.0 kb in size, obtained from a cDNA library or a genomic library. The genomic libraries are easy to construct and almost all sequence types are included; however, a large number of interspersed repeats are found in inserts, which detect a large number of restriction fragments forming complex patterns. In plants, this problem is overcome to some extent by using the methylation-sensitive restriction enzyme PstI. This helps to obtain low copy DNA sequences of small fragment sizes, which are preferred in RFLP analysis (Figdore et al., 1988; Liu and Knapp, 1990; Miller and Tanksley, 1990).

RFLPs are codominant markers that can detect the coupling phase of DNA molecules, as DNA fragments from all homologous chromosomes are detected. They are very reliable markers in linkage analysis and breeding and can easily determine if a linked trait is present in a homozygous or heterozygous state in an individual. This information is highly desirable for recessive traits (Winter and Kahl, 1995). Genome mapping based on RFLP markers has been accomplished in many crop species (O'Brien, 1992). The availability of RFLP-based linkage maps has led to the widespread application of molecular techniques to the genetic studies of crop plants. Examples are: to map genes of economic importance (McCouch et at., 1990; Liu et al., 1992), to detect and analyze quantitatively inherited agronomic traits (Keim et al., 1990; Pearson et al., 1991; Stuber et al., 1992), and to study population diversity and systematics (Wang et al., 1992; Zhang et al., 1993). With RFLP markers, the identification and evaluation germplasm has been greatly enhanced (Dudley et al., 1992; Zhang et al., 1993). RFLPs have been the basic tool for genome mapping and other genetic investigations of plants with complex genomes and/or coupled with low levels of polymorphisms, such as cotton. Several cotton species have been studied in regards to evolution, population genetics, phylogenetic relationships, genome mapping, and QTL analysis (Wendel et al., 1989; Wendel and Albert, 1992; Small and Wendel, 1999; Meredith, 1992; Wang et al., 1992; Stelly, 1993; Cantrell and Davis, 1993; Paterson, 1993; Wing, 1993; Kohel et al., 2001; Reinisch et al., 1994; Brubaker and Wendel, 1994; Shappley et al., 1996; 1998a; 1998b; Yu and Kohel, 1999; Brubaker et al., 1999b; Ulloa et al., 2000; 2005; Jiang et al., 2000; Rong et al., 2004; 2007). However, RFLP use has been hampered due to the large amount of DNA required for restriction digestion and Southern blotting. The requirement of radioactive isotope makes the analysis relatively expensive and hazardous. The assay is time-consuming and labor-intensive and only one out of several markers may be polymorphic, which limits their use especially for crosses between closely-related species. Their inability to detect single base changes restricts their use in detecting point mutations occurring within the regions at which they are detecting polymorphism.

2.1.3.2 RAPD

RAPD (Random Amplified Polymorphic DNA) is the oldest PCR-based technique (Williams et al., 1990). PCR stands for the Polymerase Chain Reaction and is a technique that has been widely used in molecular biology since the PCR process was invented in 1983 (Bartlett and Stirling, 2003). Unlike RFLPs, RAPD markers do not require any specific knowledge of the DNA sequence of the target organism. Instead, identical 10-mer primers are used in the reactions. These primers will or will not amplify a segment of DNA, depending on positions that are complementary to the primers' sequence. For example, no fragment is produced if primers annealed too far apart or 3' ends of the primers are not facing each other. Therefore, if a mutation has occurred in the template DNA at the site that was previously complementary to the primer, a PCR product will not be produced, which results in a different pattern of amplified DNA segments on the gel. RAPD products are usually visualized on agarose gels stained with ethidium bromide.

RAPDs only show dominant relationships, i.e. it is not possible to distinguish whether a DNA segment is amplified from a locus that is heterozygous or homozygous (Williams et al., 1990). RAPD markers do not require specific knowledge of DNA sequences, creation of genomic libraries, time-consuming blotting, or radioactivitiie isotopes. With a little amount of DNA for the reaction, a RAPD marker can detect several loci by a single amplification (Wililiams et al., 1990). RAPD markers provide a powerful tool for the automation of genome mapping, and for extending the power of genetic analysis to plants, such as cotton, which have few phenotypic markers to completely describe the whole genome. RAPD markers can be used as probes for RFLPs after reamplification of the RAPD fragment (Williams et al., 1990). RAPD markers also can be converted into SCARs (Sequence Characterized Amplification Regions) (Michelmore et al., 1992; Paran and Michelmore, 1993) that overcome some of the drawbacks of RAPDs. RAPD markers have been used in genetic mapping in several plant species such as Arabidopsis thaliana (Reiter et al., 1992), pine (Chaparro et al., 1994; Devey et al., 1996), peach (Chaparro et al., 1994), lettuce (Kesseli et al., 1994), cocoa (Lanaud et al., 1995), and tomato (Grandillo and Tanksley, 1996). In cotton, RAPDs have been employed for germplasm evaluations (Multani and Lyon, 1995; Tatineni et al., 1996; Iqbal et al., 1997), analyzing gene functions (Lu and Myers, 1999; Yu and Kohel, 1999), genetic mapping (Yu and Kohel, 1999; Khan et al.,2000; Zhang et al., 2002), and QTL studies (Ulloa et al., 2000; Yu and Kohel, 1999; Khan et al.,2000). However, there is low reproducibility of the RAPD profile within and between different labs. This is because several factors, including DNA concentration, thermocycler, and primer quality can influence the outcomes of a RAPD reaction. Another limitation of RAPD markers is the mismatches between the primer and the template, which may result in the total absence of PCR product as well as in a merely decreased amount of the product. Thus, the RAPD results can be difficult to interpret.

2.1.3.3 AFLP

AFLP stands for Amplified Fragment Length Polymorphism. The technique was developed in the early 1990's by Keygene (http://www.keygene.com), a commercial research company with a strong focus on molecular genetics and biotechnology for the plant breeding industry. As originally described by Vos and Zabeau in 1993, the technique involves digesting DNA with two different restriction enzymes, followed by ligation of adaptors to the sticky ends of the restriction fragments. A subset of the restriction fragments are then amplified using primers complementary to the adaptor and part of the restriction site fragments. The amplified fragments are visualized on denaturing polyacrylamide gels either through autoradiography or fluorescence methodologies (Zabeau and Vos, 1993).

The power of the AFLP procedure is that a large number of mappable loci can be generated in a single amplification, which will help saturate a region of the genome rather quickly. The efficiency of generating AFLP markers leads to a much higher density of markers when compared to RFLP mapping in the same population (Huang et al., 1994) in a similar region covered by RFLP markers (Maheswaran et al., 1997). Like RAPDs, most AFLP markers show dominant relationships (Meksem et al., 1995; Maughan et al., 1996). However, AFLPs provide a higher level of technology which is much more efficient (Sharma et al., 1996). AFLPs not only have higher reproducibility, they have resolution and sensitivity at the whole genome level compared to other techniques (Mueller and Wolfenbarger, 1999). In addition, no prior sequence information is needed for amplification (Meudth and Clarke, 2007). AFLP markers have been widely and successfully used in the studies of plants. In cotton, AFLP markers have been used in estimating genetic diversity (Vroh et al., 1999; Abdalla et al., 2001; Rana and Bhat, 2004; Zhang et al., 2005) and developing linkage maps (Brubaker and Brown, 2003; Lacape et al., 2003; Mei et al., 2004; Zhang, et al., 2005). The drawback of AFLP is that they typically require polyacrylamide gels and the technique is more laborious and time consuming than RAPD methods.

2.1.3.4 SSR

Simple Sequence Repeats (SSRs or microsatellites) are present in the genomes of all eukaryotes and consist of several to over a hundred repeats of a one to six nucleotide motif. SSRs occur frequently in most eukaryote genomes and can be very informative, multiallelic and reproducible (Vos et al., 1995; Senior and Heun, 1993). The application of SSR techniques to plants depends on the availability of suitable microsatellite markers, which have been developed for many species.

Microsatellite primers can be developed by cloning random segments of DNA from the focal species. By screening a clone library with fluorescently-labelled oligonucleotide sequences, positive clones will be obtained if hybridizations happened between the oligonucleotide and a microsatellite repeat. If searching for microsatellite markers in specific regions of a genome; for example within a particular exon of a gene, primers can be designed manually. This involves searching the genomic DNA sequence for microsatellite repeats, which can be done manually or by using automated tools. Once the potentially useful microsatellites are determined (removing non-useful ones such as those with random inserts within the repeat region), the flanking sequences can be used to design oligonucleotide primers which will amplify the specific microsatellite repeat in a PCR reaction.

SSRs are highly reliable (i.e. reproducible), co-dominant in inheritance, relatively simple and cheap to use. They are typically highly polymorphic, robust, and often portable, particularly among different mapping populations or crosses and often to related species. They have been useful in species where low levels of genetic diversity limit the use of other markers. The regions flanking the microsatellites are generally conserved and PCR primers relative to the flanking regions are used to amplify SSR-containing DNA fragments. The length of the amplified fragment will vary according to the number of repeated residues. In cotton, SSRs represent the class of genetic markers which have accelerated cotton genome mapping work. Liu et al. (2000) used 65 SSR primer pairs to amplify 70 marker loci localized to a specific cotton genome. The SSR markers identified in this study provide a framework that can be used with further conventional linkage mapping to other DNA markers to expand the genome-wide coverage of the cotton genetic map. A linkage map was constructed with 199 RAPD and SSR markers to assist in selection for stomatal conductance; two putative QTL for this difficult to measure physiological trait were identified on two cotton linkage groups (Ulloa et al., 2000). Using SSR markers, all 26 chromosomes have been covered with an average inter-loci distance of 1.91 cM (Guo et al., 2007). Recently, much effort has been focused on employing Expressed Sequence Tag (EST) derived-SSRs (EST-SSRs) as putative functional marker loci to easily tag corresponding functional genes (Wang et al., 2006; Guo et al., 2007; 2008).

SSRs have proven to be versatile molecular markers, particularly for population analysis, but they are not without limitations. SSRs developed for particular species can often be applied to closely related species, but the percentage of loci that successfully amplify may decrease with increasing genetic diversity (Jarne and Lagoda, 1996).

2.1.3.5 SNP

Single Nucleotide Polymorphism (SNP) is the most abundant sequence variations encountered in most genomes (Cho et al., 1999; Griffin and Smith, 2000). Various large-scale discovery projects are currently aimed at identifying SNPs from a broad range of organisms, including crop plants. The abundance, ubiquity and interspersed nature of SNPs make them ideal candidates as molecular markers for marker-assisted plant breeding. Various SNP detection methods have been described (Landegren et al., 1998).

The discovery of SNP is useful to breeders because the polymorphisms observed through SNP could be used as simple genetic markers that can be identified in the vicinity of virtually every gene. There also is great potential for the use of SNPs in the detection of associations between allelic forms of a gene and phenotypes, especially common diseases, or cotton fiber quality. The availability of such markers could assist breeders in introducing new germplasm into commercial cotton varieties to improve fiber quality or other traits. SNPs in coding sequences create furthermore the possibility of changes in the amino acid sequence within a protein and might have an effect on protein function and thus monogenic or polygenic traits associated with the expression of such genes In the process of integrating physical maps (which consist of multiple contigs of bacterial artificial chromosome [BAC] clones) with traditional genetic maps, BAC end sequences may be screened for the absence of repetitive elements and then used to identify SNPs that are polymorphic between the mapping parents. Such SNPs are then mapped genetically.

SNP variation analysis and SNP marker development from candidate genes could provide valuable information regarding gene evolution and its effects on complex traits. The anticipated value of SNPs for analysis of candidate gene evolution and their effects on complex traits have stimulated large scale SNP characterization and marker mapping in rice (Feltus et al., 2004), wheat (Mochida et al., 2003; Somers et al., 2003; Zhang et al., 2003; Caldwell et al., 2004), maize (Ching et al., 2002; Batley et al., 2003), soybean

(Zhu et al., 2003; Kim et al., 2005), and barley (Kanazin et al., 2002; Bundock and Henry, 2004). Due to the complexity of the cotton genome, the research on SNP analysis in cotton has been limited. Last year, An and colleagues reported the expression profiles of EXPANSIN transcripts during fiber elongation and the discovery of SNP markers, assessed the SNP characteristics, and localize six EXPANSIN A genes to chromosomes (An et al., 2007). So far, this is the only article reporting the use of SNPs by cotton researchers.

The frequency and nature of SNPs in plants is beginning to receive considerable attention. A number of reports in Arabidopsis thaliana, rice and maize have provided estimates of sequence diversity in these species. In many species, the analysis of DNA sequence variation has been confined to single genes or DNA fragments with the goal of defining gene structure, function or evolutionary relationships. It is known that SNPs are widely distributed throughout genomes, although various studies show that the occurrence and distribution of SNPs differs between species, in particular between inbreeding and outbreeding species, or in those species with a narrow genetic base. It is generally well accepted that some species, for example maize, are highly polymorphic, while others, such as soybean and melon, are less polymorphic. Detailed studies of sequence diversity have now been performed at selected loci for a range of plant species and in plants, the typical frequencies are in the range of 1 SNP every 100–300 bp (Shifman et al., 2002).

2.1.4 Marker Comparisons

Comparisons among different genetic marker types and different DNA-based markers are summarized through Table 2.1 and Table 2.2.

Table 2.1 Comparison of morphological, biochemical and DNA-based genetic markers.

FEATURE	MORPHOLOGICAL	BIOCHEMICAL	DNA-BASED
Inheritance	Recessive / Dominant	Co-dominant	Co-dominant / Dominant
Environment	Sensitive	Less sensitive	Less sensitive
Epistatic	Yes	No	No
DNA	Not require	Not require	Require
Polymorphism	Limit	Limit	Un-limit
Cost	Inexpensive	More expensive	Most expensive
Coding-region	Yes	Yes	Yes / No

Table 2.2 Comparison of common used DNA-based genetic markers.

FEATURE	RFLP	RAPD	AFLP	SSR	SNP
Inheritance	Co-dominant	Dominant	Dominant	Co-dominant	Co-dominant or dominant
Pattern Detected	Single-locus	Multi-Loci	Multi-Loci	Single-locus	Multi-Loci
Cloning	Required	No	No	Required	No
Radioactivity	Required	No	Required	No	No
DNA quantity	Large amount	Small	Moderate	Small	Small
PCR-based	No	Yes	Yes	Yes	Yes
Sequence	No	No	No	Required	Required
Polymorphism	High	High	Higher	Higher	Very High
Ease of use	Not easy	Easy	Easy	Easy	Easy
Reproducibility	High	Unreliable	Moderate	High	High
Cost	High	Low	Moderate	Low	Low

2.2 Genetic Mapping

Genetic mapping - also called linkage mapping – is a tool to make gene hunts faster, cheaper and practical. During reproduction, genes that are on the same chromosome are transmitted to the offspring together or are separated by cross-over events. The farther apart the genes are on the chromosome, the greater the chance they will be separated in segregating populations. By studying how often two genes are transmitted together researchers can estimate how close they are on the chromosome and create what is called a linkage map. The distance between genes is called a genetic map unit (m.u.), or a centimorgan (cM), and is defined as the distance between genes for which one product in 100 meiosis events is recombined. A recombination frequency (RF) of 1 % is equivalent to 1 m.u. A linkage map is created by finding the map distances between several traits that are present on the same chromosome, ideally avoiding having significant gaps between traits to avoid the inaccuracies that will occur due to the possibility of multiple recombination events.

In genetic linkage studies, mapping populations are the tools used to identify the genetic loci controlling measurable phenotypic traits. In plants, F2 populations and recombinant inbred lines (RIL) are used for self-pollinating species; for self-incompatible, highly heterozygous species, Fn populations are mostly the tools of choice. Backcross populations and doubled haploid lines are a possibility for both types of species. Recombination frequencies between traits and markers reveal their genetic distance, and trait-linked markers can be anchored to a more complete genetic map of the species. For map-based cloning of a gene, populations of a large size are needed to provide the resolution required. Summarized information of genetic segregation ratios at a given marker locus in different maker-population combinations is given in Table 2.3.

There are several potential limitations involved in genetic linkage mapping. Many traits of economic interest like disease resistance may be species specific and therefore not detectable or even absent in closely related genomes, marker presence or order may not be conserved (Foote et al., 1997; Han et al., 1998) and marker polymorphism is often limited.

Table 2.3 Genetic segregation ratio at marker locus in different maker-population combinations.

Marker	Inheritance	Population Type				
		F2	RIL	DH	BC1	BC2
RFLP	co-dominant	1:2:1	1:1	1:1	1:1	1:1
RAPD	dominant	3:1	1:1	1:1	0	1:1
AFLP	dominant	3:1	1:1	1:1	0	1:1
SSR	co-dominant	1:2:1	1:1	1:1	1:1	1:1
SNP	co-dominant	1:2:1	1:1	1:1	1:1	1:1

Certain chromosome regions may have been mapped more intensively by one research group than another, because different groups use different mapping populations or map are derived by different methodologies. It is useful to be able to synthesize a single merged map when two or more genomic maps of a chromosomal region are available. Map integrations will summarize the linkage information in an entire genome or particular genomic region by presenting a higher density of markers and greater genome coverage than is possible from a single study.

It is known that multipoint linkage analysis is extremely sensitive to genotyping error and that error rates as small as 1% can significantly decrease the power to detect loci (Douglas et al., 2000; Abecasis et al., 2001). Thus, if an increase in marker density also increases the number of genotyping errors present in the data, the net effect may actually be a decrease in the power to detect linkage (Evans and Cardon, 2004).

2.3 Map Integration

Map integration is a very important activity for any species for which an annotated complete genome sequence is not available. For organisms that are currently being sequenced, a pre-sequence integrated map is essential to provide the ‘‘backbone’’ for assembly of the sequence (Liao et al., 2007). In addition, integrated maps facilitate the identification and resolution of discrepancies (of locus identity and location) among different maps, the mapping of QTLs, ESTs, and BACs, and the identification of positional candidate genes. They also maximize the power of comparative mapping involving non-sequenced species by enabling all known loci in one species to be simultaneously compared with all known loci in another species. Consequently, achievements on map integrations were developed using different approaches:

1. The simplest approach is visually aligning different maps on the basis of common markers to create a “consensus map”, such as that was created

in wheat (Liu, 1998; Nelson et al., 1995a;b;c; Van Deynze et al., 1995; Marino et al., 1996).

2. By computing the average linkage distance from the various map studies, a “composite map” can be created, like that was used in Brassica (Liu 1998; Kianian and Quiros, 1992).
3. An approach of pooling all of the marker data from different mapping populations with similar size and structure, then using MAPMAKER (Lander et al., 1987; Lincoln, et al., 1993) to conduct a “pooled map” was used in maize (Liu, 1998; Beavis and Grant, 1991).
4. The approach used in JoinMap (Stam, 1993; Stam and Ooijen, 1995), the first software to combine primary data from disparate mapping studies, is to weight for population structure and size (Liu, 1998). JoinMap was used to integrate two loblolly pine linkage maps (Sewell et al., 1999) and to merge maps from two pedigrees for sugi (*Cryptomeria japonica*) (Tani et al., 2003).
5. The Genome Database approach creates a “comprehensive map” by designing a standard map then project additional maps onto the standard; this approach was used in the human genome construction (Pearson et al., 1991).
6. A graph theoretic approach, which was adapted from a well studied mathematical graph theory problem -- the traveling salesman problem (TSP) (Lawler et al., 1985) -- uses the pairwise distances between each

marker to find an ordering of them with minimum total length (Goldberg and Lingle, 1985; Liu, 1998). This approach has been applied to the comparison and integration of genetic, physical and sequence-based maps (Lander and Green, 1987; Falk, 1992; Doerge, 1996; Yap et al., 2003; Mester et al., 2003, Mester and Braysy, 2004; Jackson et al., 2008).

2.4 Bioinformatics and Algorithms

2.4.1 Bioinformatics

Bioinformatics is the field of science in which biology, computer science, and information technology merge to form a single discipline. The ultimate goal of the field is to enable the discovery of new biological insights as well as to create a global perspective from which unifying principles in biology can be discerned. At the beginning of the "genomic revolution", a bioinformatics concern was the creation and maintenance of a database to store biological information, such as nucleotide and amino acid sequences. Development of this type of database involved not only design issues but the development of complex interfaces whereby researchers could both access existing data as well as submit new or revised data. Therefore, bioinformatics nowadays entails the creation and advancement of databases, algorithms, computational and statistical techniques, and theory to solve formal and practical problems arising from the management and analysis of biological data.

Bioinformatics has been employed in many major research areas such as sequence analysis, genome annotation, computational evolutionary biology, measuring biodiversity, analysis of gene or protein expression, comparative genomics, modeling biological systems, high-throughput image analysis, software and tool development, web services in bioinformatics, and so on. All these research areas are dealing with huge and complex datasets, hence corresponding algorithms are frequently involved.

2.4.2 Algorithms

An algorithm is a sequence of computational steps that transform the input into the output. It is also can be viewed as a tool for solving a well-specified computational problem. Algorithms that have been used in various bioinformatics tasks can be functionally classified into data analysis algorithms and prediction algorithms. Many algorithms have been used and built in bioinformatics software. Examples are: The BLAST programs (Basic Local Alignment Search Tools) which were introduced in 1990 and are used in identifying sequence similarities using a set of sequence comparison algorithms to search sequence databases for optimal local alignments to a query (Altschul et al., 1990; BLAST); the GDB (Genome Data Base) serves the human genome sequencing project both as a genome database and as a genome database mining tool through a description of loci and probes and given gene orders based on small subsets of the data (Pearson et al., 1991); GENSCAN, which is defined as the process by which an uncharacterized DNA sequence is documented by the location along the DNA sequence of all the genes that are involved in genome functionality (Burge and Karlin, 1997; Burge, 1998; GENSCAN); PHYLIP (the PHYLogeny Inference Package), which includes algorithms like parsimony, distance matrix, and likelihood methods, including bootstrapping and consensus trees (Felsenstein, 1985, 2003; PHYLIP).

To search sequence databases for optimal local alignments to a query (Altschul et al., 1990); the GDB (Genome Data Base) that serves in human genome sequencing project for genome database and genome database mining through emphasized description of loci and probes and given gene orders based on small subsets of the data (Pearson et al., 1991); GENSCAN, which is defined as the process by which an uncharacterized DNA sequence is documented by the location along the DNA sequence of all the genes that are involved in genome functionality (Burge and Karlin, 1997; Burge, 1998; GENSCAN); PHYLIP (the PHYLogeny Inference Package), which includes algorithms like parsimony, distance matrix, and likelihood methods, including bootstrapping and consensus trees (Felsenstein, 1985; 2003).

Different algorithms have been employed in genome mapping and genome mapping data integrations, which are based on different approaches (as listed in session 2.3). The linkage map pooling approach uses the maximum likelihood estimate of the multipoint map distance for the anchored map and can be estimated using an expectation-maximization (EM) algorithm

(Dempster et al., 1977; Lander and Green, 1987) or the least squares method (Jensen and Jorgensen, 1975). This approach requires original phenotypic scores of individuals. In the JoinMap approach (Stam, 1993), a regression mapping algorithm is used. These approaches typically involve the juxtaposition of pictures of two or more partial maps, each still represented in its original units. The CarthaGene package (de Givry et al., 2005; CarthaGene) is increasingly being used to generate actual integrated maps (Demeure et al., 2003; Snelling et al., 2004). This is done by creating maximum likelihood consensus maps from linkage and radiation hybrid raw data.

For species for which a high-resolution physical map exists, linkage maps and cytogenetic maps have been integrated into a physical map by linear interpolation (Nievergelt et al., 2004) and linear programming (Furey and Haussler, 2003), respectively. The graphical strategy (Yap et al., 2003; Jackson et al. 2008) is another approach to integration, although its major aim is to highlight areas of ambiguity and inconsistency among maps rather than try to create a single integrated map (Liao et al., 2007).

CHAPTER III

METHODOLOGY

As described in Chapter I, the goal of this project is to construct a "comprehensive reference map" of genome wide marker order from all available maps including different types of mapping populations, different marker types, and inconsistencies in marker order between different map studies. The major problems that have to be addressed in this project are:

1. Numerous genetic maps.
2. Different types of mapping populations.
3. Inconsistencies in marker order between different map studies.

From reviews described in Chapter II, we know that genetic maps are constructed based on experimental designs with statistical assumptions, and experimental errors exist in the maps. Such errors will be included in the group of inconsistencies among loci orders that are from different maps. Also, differences exist in the accuracy of genetic linkage information which was derived from varying combinations of mapping populations and marker types.

It is easier to just understand an integration of a small number of anchor nodes that were from two different groups. However, when more maps and/or markers join into the integration, the level of difficulty increases in order of magnitude as the map or marker numbers increase.

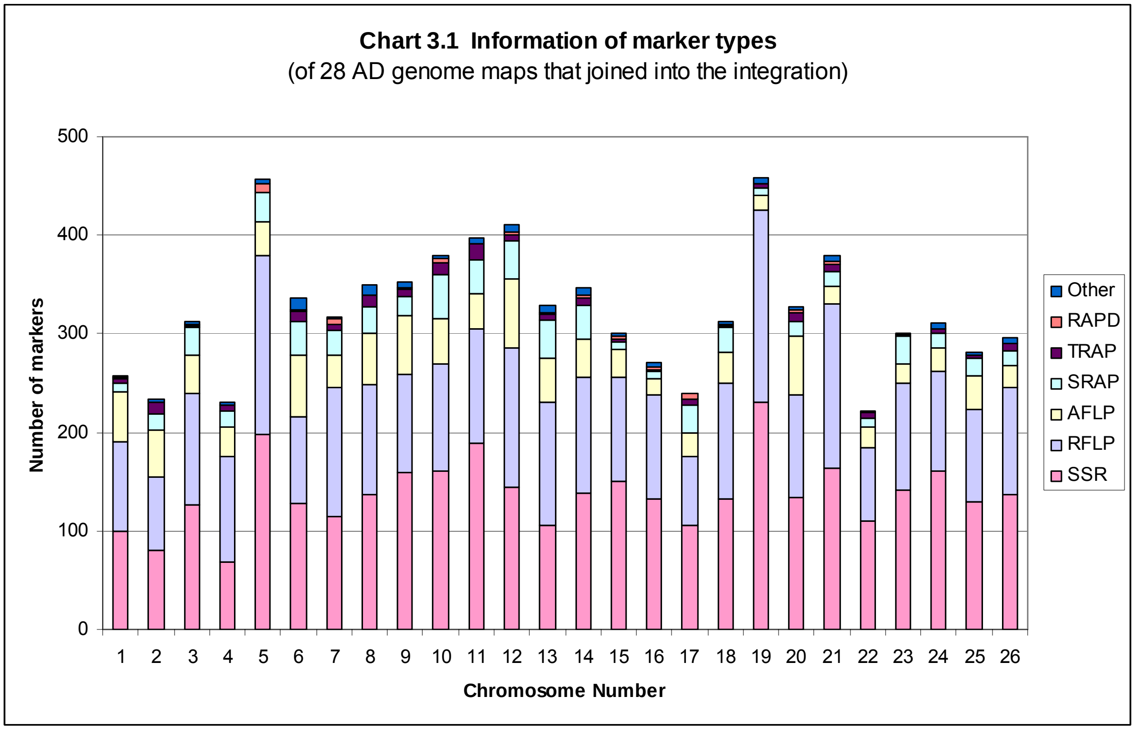
A famous mathematic graphical problem, the Traveling Salesman Problem (TSP), has been intensively studied in optimization mathematical graph theory since 1930. TSP is a problem in combinatorial optimization studied in operations research and theoretical computer science. Given a list of cities and their pairwise distances, the task is to find a shortest possible route that visits each city exactly once (Lawler et al., 1985). The problem of determining the comprehensive order of genetic markers along a linkage group for genetic mapping can be modeled as a special case of the TSP.

3.1 Data Collection, Management, and Pre-Evaluation

Forty *Gossypium* genetic maps including 34 of AD genome, three of A genome, one of D genome, and two of G genome, were collected from publicly available sources. A total of 20,233 loci were included in the forty genetic maps. Table 3.2 (Appendix C) gives general information about the forty maps.

All collected map data were loaded into CottonDB (http://www.cottondb.org), from which they can be conveniently retrieved as well as clearly displayed and compared through Comparative Map Viewer (Fang, et al., 2003). For better management and convenient retrieval of the temporary outputs from computer program runs or calculations, a local MySQL database was also created. The MySQL database also helped to solve the problem of different names representing the same locus, and differences in chromosome nomenclature assigned by different cotton genome researchers from different research groups.

The collected data then was pre-evaluated based on points useful to know in any map integration attempt, such as: What kind of mapping populations are in the dataset? What types of markers are in the dataset? What is the information of mapping coverage and marker density from each map? How many data would be useful in the integration? Since we aim to construct an AD genome wide interspecies reference map, information from maps of the AD genome were a special focus. The output of this evaluation indicates that six of the AD genome maps were constructed by individual marker sets and can not be integrated since they do not share information with any other maps. The remaining 28 AD genome maps were further evaluated. Table 3.3 (Appendix C) summarizes information regarding number of marker and genome coverage from each of the 28 maps. In the table, each map contains two rows; the first row of each map represents map coverage information and the second row gives the number of loci on that map. The six map names listed at the bottom are the maps that do not contain information that can be used in this study. Table 3.4 (Appendix C) provides information on marker types used in the 28 AD genome maps that were joined in this integration and the following Chart 3.1 gives visions on marker proportions by chromosome. Table 3.5 provides the number of loci per map-chromosome, and the number of the number of individual markers of each chromosome.



3.2 Constructing the Backbone Structure for the Reference Map

To construct the backbone structure, conversion to symmetric TSP and related algorithms were used. The descriptions of these algorithms are given below when they are first used in the process.

<u>Step1. Identifying anchor nodes</u>

When the different maps have common markers, these markers will be referred to as anchor nodes. Thus all markers that are shared by more than one of the 28 AD genome maps were identified and then used as anchor nodes to construct the "skeleton" of the reference map.

Step2. Representing anchor nodes in partial orders

Orders of anchor nodes within each map are the components of the order in the ongoing backbone structure and can be seen as sets of partial orders in the skeleton map. These partial orders can be further broken down into the orders between any pair of nodes within any map. These pairwise partial orders can be listed based on the node orders in a particular map.

For example, if nodes a, b, and c are ordered as a->b->c in map A,

The pairwise partial orders within map A will be:

a->b, a->c, b->a, b->c, c->a, c->b

Readers can refer to Appendix A for a more detailed explanation.

Step3. Setting a weighted symmetric order difference matrix for comparing orders

To build a weighted symmetric order difference matrix, the order differences (also known as “Kemeny Distance”; Kemeny, 1959) between each pair of nodes need to be calculated.

Let’s follow the example from above:

The Kemeny distance of a and b within map A is defined as

A(a->b)=(position b in A)-(position a in A)=2-1=1

Similarly,

A(a->c)=3-1=2

A(b->c)=3-2=1

A(b->a)=1-2=-1

… …

Therefore, the Kemeny Distance tells us two things: 1. a negative value indicates a reversed order, and 2. the larger the distance value between the two nodes, the more nodes are present in between.

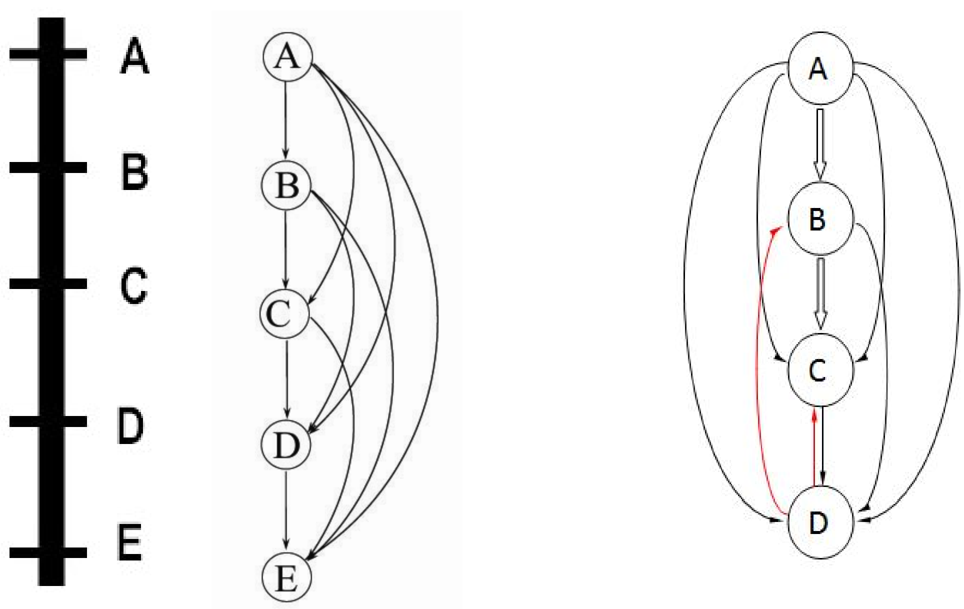
An order difference weight of paired nodes is an aggregated value of the pairwise order differences from different maps. A weighted symmetric order difference matrix is a symmetrical matrix which contains order difference weights of each pair of nodes (see Appendix A for more details).

These weights tell us two things, too: 1. a negative weight indicates the order of the two nodes is globally in a reversed order; 2. the larger the weight value of paired nodes indicates the order between these nodes is globally strongly connected.

Step4. Using maximum acyclic sub-graph for combinatorial optimization.

The simplest way to find the optimal order of a given anchor set extracted from different input map data is to list all combinations of these anchor nodes and identify the one which has the best match with the most anchor node orders derived from different input maps. However, for a number of N anchor nodes extracted from the different input maps, there will have a total number of N! different ways to list their orders (see Appendix B for a detailed explanation). Computational complexity theory has defined such a problem as NP-hard, which means “at least as hard as any NP (Nondeterministic Polynomial time) problem”.

A directed graph will be useful in solving this problem. A directed graph is a set of ordered pairs of vertices, called arcs, directed edges, or arrows. Using a directed graph to represent a single genetic map, all edges will be



(a) (b) (c)

A single map (a) is represented by directed graph, as shown in (b). This is a directed acyclic graph (DAG) because in the graph, all edges of each pair of markers are directed downward.

(c) is a directed graph that can represent the combined node orders of MAP-1 and MAP-2 (as used in Appendix A case 2). This graph is not DAG, because there are three cycles within the graph: B->D->B, C->D->C, and B->C->D->B (See Appendix B for a detailed

Figure 3.1 Using Directed Graphs to represent genetic maps.

directed in a downward manner, i.e. acyclic (Figure 3.1 left). Whereas globally representing the orders of anchor nodes that are integrated from two or more maps, some edges will be in upward orientation; i.e. directed cycles (Figure 3.1 right) exist in the graph.

A single genetic map induces a directed acyclic graph (DAG), whereas an integrated map is not a DAG if there are any inconsistencies within the group of anchor nodes.

The optimal order of anchor nodes should be a combination which represents the most anchor nodes order information derived from different maps. In other words, the most optimized combinatorial order will be the one that matches these conditions:

1. is consistent over the maximum number of anchor nodes
2. has the fewest edges in directed cycles

<u>Step5. Dissecting inconsistencies</u>

From the previous section we learned that cycles in the integrated directed graph indicate an inconsistency in anchor node orders. We wish to eliminate those cycles to obtain a DAG for the purpose of combinatorial optimization of the input anchor nodes.

From the previous section we learned that a weighted order differences matrix represents the accumulated order information of different maps. In graph theory, these aggregated differences values called edges. We also learned that a larger edge value not only reflects the further apart they are, i.e. more nodes present in between, but also reflects stronger evidence that the two nodes are in this particular order (i.e. this particular order of the two markers has been observed in a larger number of map studies). In general, a larger edge value means that the order between the nodes is strongly connected. Oppositely, a small edge value means the order connection is weak. Therefore, the weighted symmetric order difference matrix has helped to eliminate many of the inconsistencies through the aggregated order differences values. Also, based on the directed edges given in such a matrix, the global order list for all anchor nodes in the matrix can be graphically displayed.

It is possible to further eliminate the cycles that remain in the output of the weighted symmetric order differences matrix. We have learned that marker order differences may originate as an error from an individual mapping study. Looking at the matrix, a weak order connection, i.e. an edge with a small value, suggests that an error exists between the paired anchor nodes. Tracing back to their original map data, it is possible to identify and correct these errors to break the cycle caused by the error.

We want to find cycles from a directed graph that represent a weighted symmetric order difference matrix. Because the matrix is symmetrical, the information from the upper right half is the same as the information from the lower left (see Appendix A for details). So only half of the matrix needs to be graphically displayed.

Because a directed graph draws lines for each pair of nodes, a large number of edges exist in the graph, and many of them are not informative, for example, the DAG showed in Figure 3.2 left (b). Therefore, we want to have a simplified version for the directed graph driven from the weighted order difference matrix, so that we can quickly identify cycles remaining in the graph.

Graph algorithms for transitive reduction give assistance in this simplification. The transitive reduction of a graph is sometimes referred to as its minimal representation. In general, if an edge in a directed graph matches the following conditions, this edge then will be removed in its transitive reduction graph:

1. this directed edge can be represented by number of small edges
2. all these small edges have the same direction as the direction of this edge

The following Figure 3.2 displays drawings of graphs corresponding to a directed graph before (on the left) the removal of undesired edges and its transitive reduction (on the right) after the removal (adopted from http://wikipedia.org).

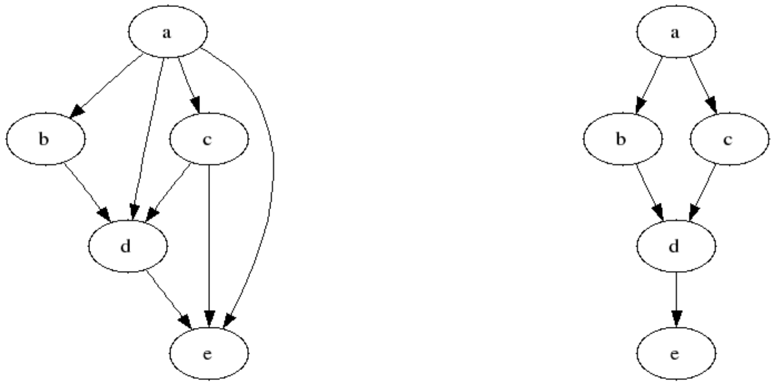


Figure 3.2 A directed graph of non-transitive and transitive reduction. The figure on the left is a directed graph of non-transitive reduction whose transitive reduction is shown on the right, where the edges a->d, a->e, and c->e are not represented.

Now we can quickly identify the nodes and edges which form cycles. Tracing back to the original map data, it is possible to find and manually correct these errors to break more cycles for an optimal anchor nodes order. The optimized order will be used as the backbone structure of the reference map. An example taken from this study is the data of chromosome 17. Graphical displays used in this example were drawn by free software - aiSee (http://www.aisee.com/). The simplified version of the directed graph for the weighted order differences matrix of chromosome 17 is displayed on the left of Figure 3.3. In the graph, red edges indicate they are in fact in upper wand manner, i.e. where cycles are formed. The red color also indicates they are weak edges in cycles. So, it is easy to find that there are two cycles in the

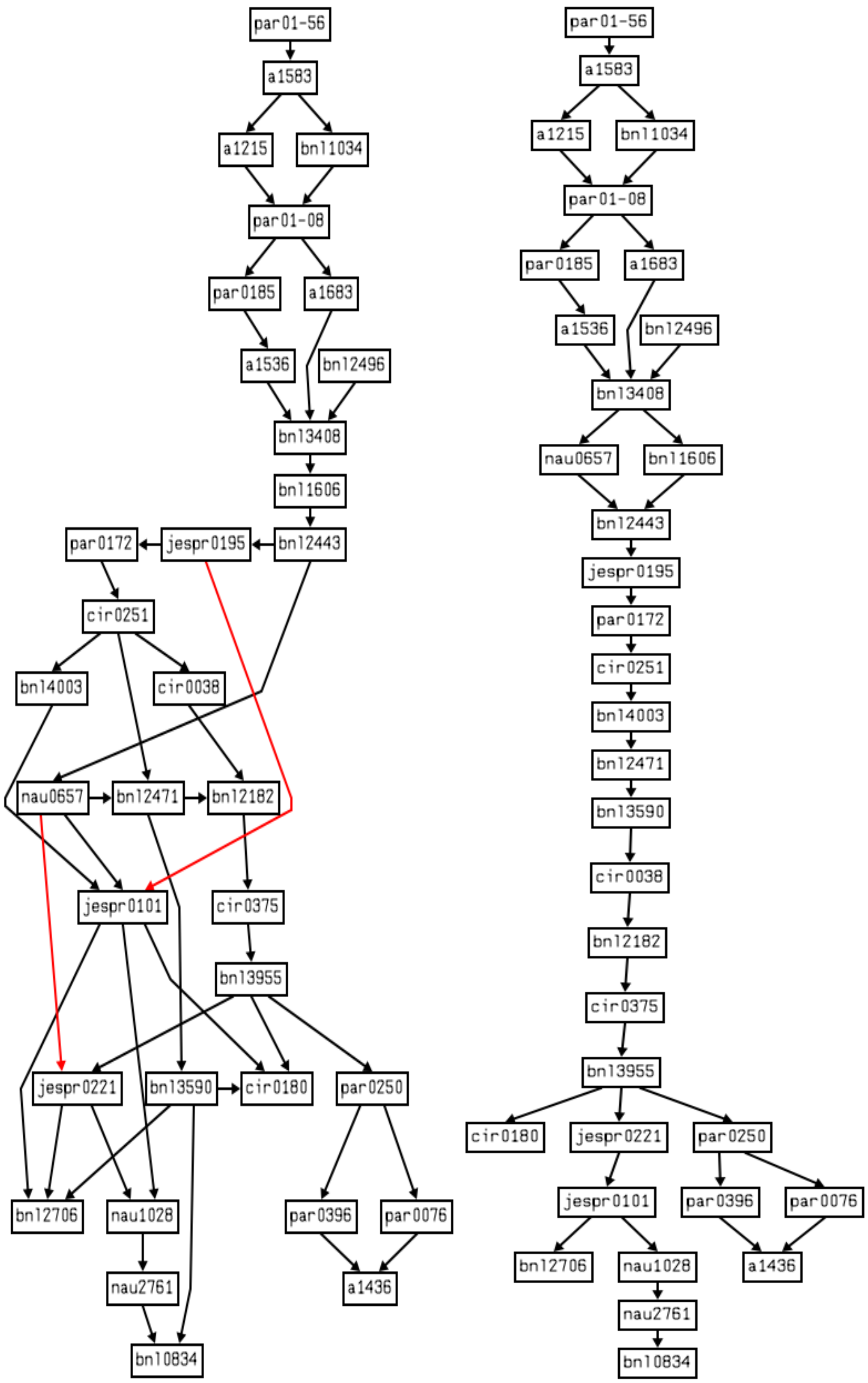


Figure 3.3 Graphs of chr17 before and after manually breaking cycles.

graph that one of the cycles is caused by the order of the paired markers NAU0657<- JESPR0221 and the other is caused by the order of markers JESPR0195<-JESPR0101. Tracing down to the input map data, we find the information shown as below, from where we learn that both pairs of markers have small linkage distance, i.e. 0.7 and 1.6 (Table 3.1).

Table 3.1 The map positions of two pairs of anchor nodes that form cycles in Figure 3.3

Map Origin	Marker name	Position on Map
TH-BC1	NAU0657	54.9
	JESPR0221	54.2
CH-F2	JESPR0195	71.1
	JESPR0101	69.5

As reviewed in genetic linkage study in Chapter II, we know that an increase in marker density also increases the number of errors present in the data. The net effect of more markers may actually be a decrease in the power to detect linkage. When the density of a linkage map increased, the closer the two markers are linked with each other, and the less accurate their order may be. This is because when the map becomes denser, and the recombination rate between adjacent markers decreases to the error rate of about 0.5% ~ 3%, a significant proportion of observed recombination events will be spurious. Considering this together with the fact that the orders of the two paired markers are globally in a weak connection, the orders between the two paired markers are more likely errors from an individual linkage study. After manually broke the cycles and a DAG was derived for an optimal order of chromosome 17 anchor nodes. The DAG is displayed on the right of Figure 3.3.

3.3 Incorporate Remaining Markers into the Skeleton Map

The last step for this integration is to incorporate the remaining markers into the skeleton map. Since we have had DAG graphs, i.e. optimal orders of anchor nodes for each chromosome, a remaining marker will be placed on the skeleton map if it meets one of these cases:

1. remaining marker(s) is between two anchor markers in the local map,
2. remaining marker(s) comes before an anchor marker, and the anchor marker is ordered the first in the backbone structure, and
3. remaining marker(s) is behind an anchor marker where it is ordered as the last in the backbone structure.

When remaining marker(s) meet the conditions of case 1, it will be simply inserted between the two anchor markers. Marker(s) in case 2 or 3 will be attached before or after the anchor marker on the end of the backbone structure.

CHAPTER IV

RESULTS AND DISCUSSION

4.1 Results

The backbone structure of the reference map was constructed from marker order information of all 28 AD-genome genetic input maps. This information produced 2,166 anchor nodes, which is the one-forth of the total 8,407 individual input markers, represented 7,926 loci, which is one half of the total number of 15,969 loci from the 28 input maps (see Table 4.1 and 4.2 in Appendix C for detailed information). From the 2,166 anchor nodes, a set of 26 weighted symmetric anchor order difference matrixes were produced to represent the backbone structure of the 26 individual chromosomes (data not show). The reference map contains 7,424 markers, which is 88.31% of the 8,407 individual markers from the 28 input maps (details are presented in Table 4.3 in Appendix C). The reference map represents 14,868 of the 15,969 original loci, or 93% of the total loci contained in the input map data (details are presented in Table 4.4 in Appendix C). Charts 4.1 and 4.2 show the number of markers and loci represented by the reference map. Since current assigned chromosome numbers were not in AtDt pairs, these numbers were converted into At or Dt paired numbers for use in Charts 4.1 and 4.2 (See Tables 4.5 and 4.6 in Appendix C for detailed information).

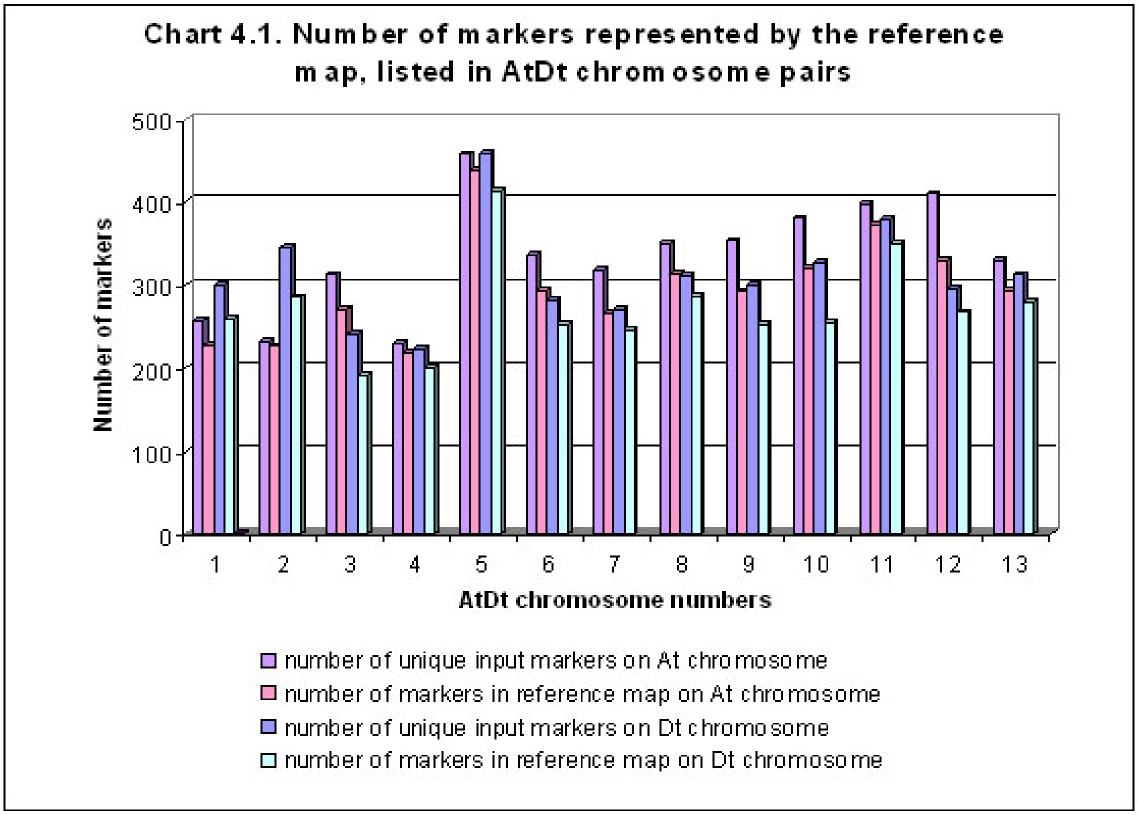


Chart 4.1. Number of markers represented by the reference map, listed in AtDt chromosome pairs
Number of markers
500
400
300
200
100
0
1 2 3 4 5 6 7 8 9 10 11 12 13
AtDt chromosome numbers
number of unique input markers on At chromosome
number of markers in reference map on At chromosome
number of unique input markers on Dt chromosome
number of markers in reference map on Dt chromosome

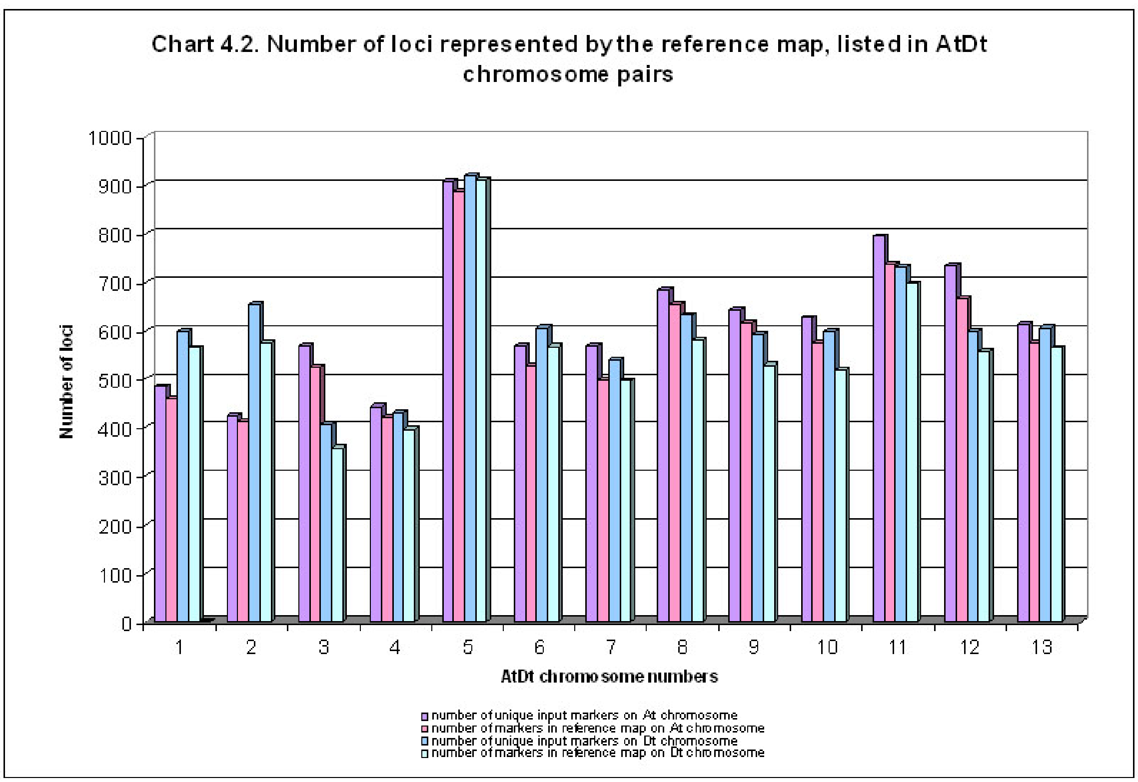


Chart 4.2. Number of loci represented by the reference map, listed in AtDt chromosome pairs
Number of loci
1000
900
800
700
600
500
400
300
200
100
0
1 2 3 4 5 6 7 8 9 10 11 12 13
AtDt chromosome numbers
number of unique input markers on At chromosome
number of markers in reference map on At chromosome
number of unique input markers on Dt chromosome
number of markers in reference map on Dt chromosome

Ideally, the reference map integrates all the maps into a single map in which all of the markers used in the various mapping studies have been placed with respect to one another. However, this was not possible because disagreements in marker orders exist among the input maps. Therefore, the percentage of marker order disagreements between the reference and original maps was calculated. The overall average disagreement is 11.86 percent. The order disagreements of each chromosome fell in the range from 4.458 (chr.12) to 27.22 (chr. 21) percent, while the disagreements with each input map range from 0.5 (7T-RIL) to 35.88 (HP-F2:3) percent. Significant differences exist among the 26 chromosomes and the 28 input maps (See Table 4.7 in Appendix C for detailed information). The significant differences among chromosomes indicate that the orders of anchor markers from different input maps agreed with each other much more on some chromosomes than that on others (4.458% on chromosome 12 *vs* 27.22% on chromosome 21). The significant differences among individual maps indicate that the anchor marker orders from one input map disagreed with the orders from most other input maps. In other words, the order of anchor markers from a particular map contradicts that agreed to by the majority of maps. The HP-F2:3 map has the highest disagreement ratio (35.88%) among the input maps.

The following Charts, 4.3 and 4.4, show the disagreement percentages by either each individual input map or each chromosome. The average

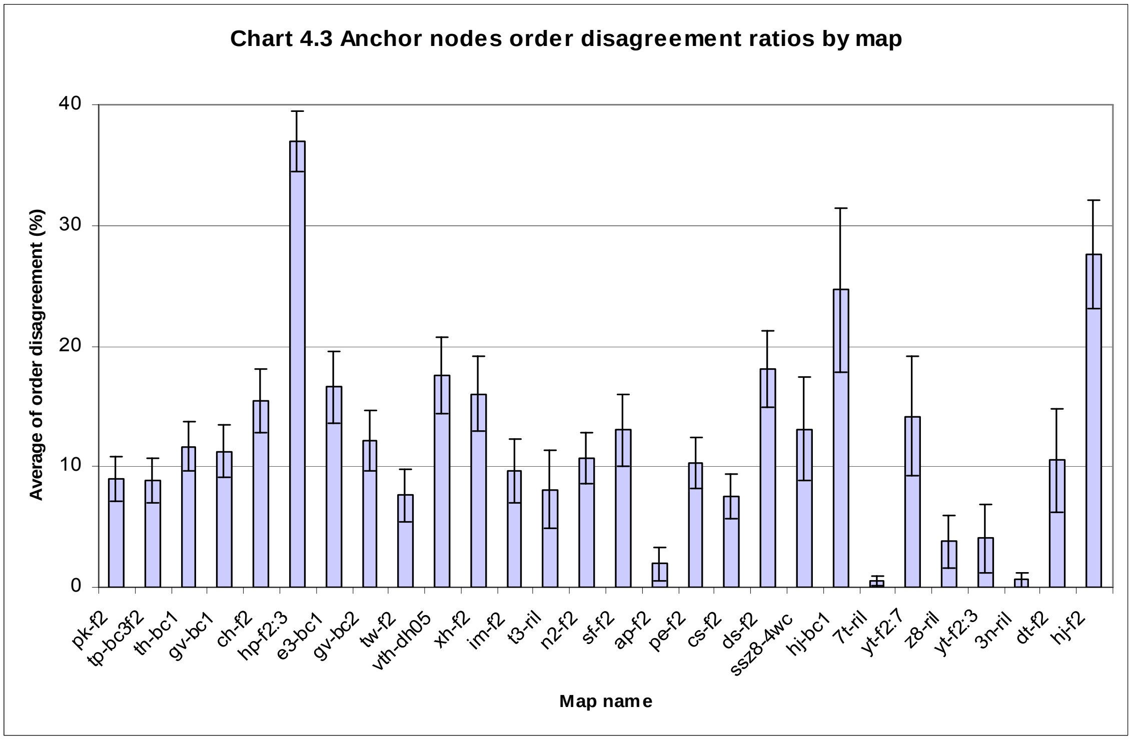


Chart 4.3 Anchor nodes order disagreement ratios by map
Average of order disagreement (%)
0
10
20
30
40
pk-f2
tp-bc3f2
th-bc1
gv-bc1
ch-f2
hp-f2:3
e3-bc1
gv-bc2
tw-f2
vth-dh05
xh-f2
im-f2
t3-ril
n2-f2
sf-f2
ap-f2
pe-f2
cs-f2
ds-f2
ssz8-4wc
hj-bc1
7t-ril
yt-f2:7
z8-ril
yt-f2:3
3n-ril
dt-f2
hj-f2
Map name

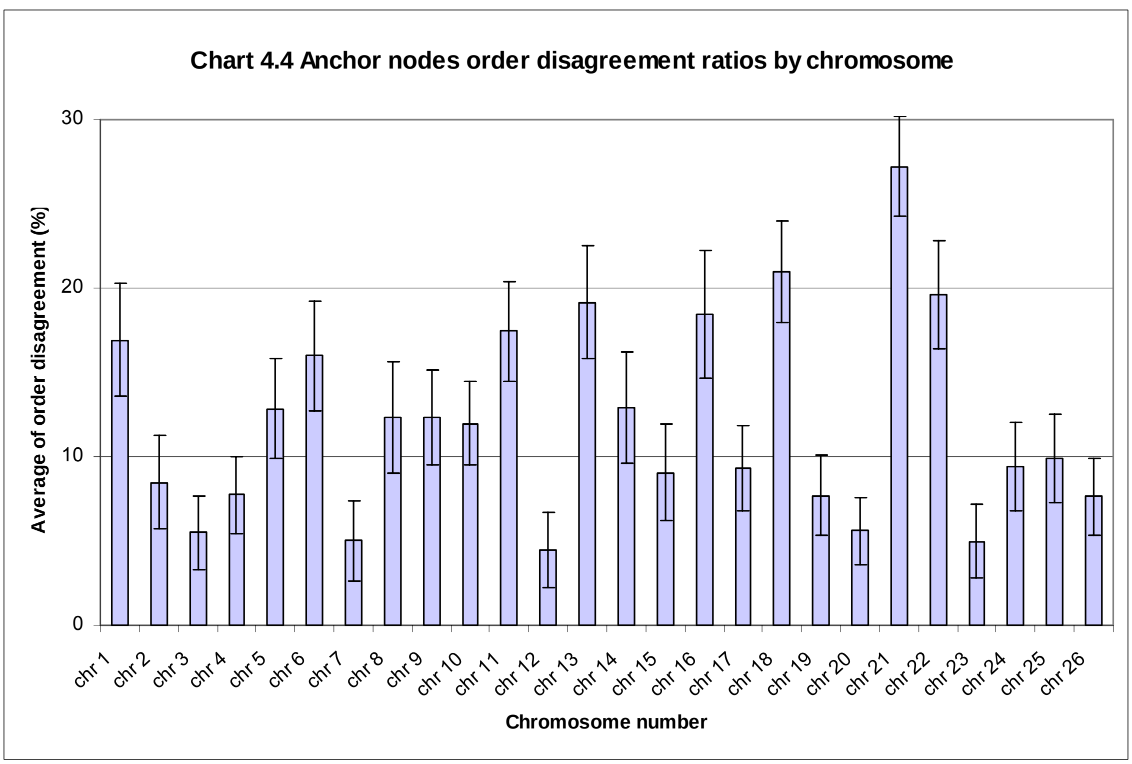


Chart 4.4 Anchor nodes order disagreement ratios by chromosome
Average of order disagreement (%)
0
10
20
30
chr 1
chr 2
chr 3
chr 4
chr 5
chr 6
chr 7
chr 8
chr 9
chr 10
chr 11
chr 12
chr 13
chr 14
chr 15
chr 16
chr 17
chr 18
chr 19
chr 20
chr 21
chr 22
chr 23
chr 24
chr 25
chr 26
Chromosome number

disagreement percentage (shown as vertical bars) and standard error (shown as single line internals) are given in the Charts.

4.2 Discussion

The purpose of genome map integration is to combine individual maps into one map. Therefore, an implicit assumption behind the notion of an integrated map is the view that, for a species as a whole, there is one correct order of markers. Under this assumption, the data from individual mapping studies represent different samplings of the species map. Hence different maps produced by different studies are assumed to sample the same underlying physical order of markers. However, there will invariably be differences in marker order among the different studies. Such differences could be influenced by many factors, such as population type, population size, marker type, statistical confidence level, map density, marker score quality, etc.

It is possible to identify some of the local existing errors that cause the marker order inconsistencies by globally looking at the order of markers. The above assumption indicates that the marker order determined by the majority of individual map studies should be the closest one to the correct order of markers. In other words, if one map has a marker order that shows a significant difference from the order of the majority of input maps, it could be assumed that there is an error in this map.

It has been reported that RAPD markers have low reproducibility and higher frequency of mismatches between the primer and the template. Thus, the RAPD results can be difficult to interpret as well as not being reliable if used in mapping studies. The results of this study show that there is a significant difference in marker order between HP-F2:3 mapping data and that of the remaining maps (Chart 4.3, Table 4.31). Tracing back to the original map information of HP-F2:3, we found that all of the 54 RAPD markers (Table 3.4) were from HP-F2:3, which could explain why the marker orders from this particular mapping data were significantly different from the marker orders of other maps. In addition, about 18% of HP-F2:3 mapped loci are distortions (He et al., 2007). The relatively large proportion of distorted data could be another factor drawing marker orders of this map far away from that of the majority.

Because the approach used in this study was based on the order information from each pair of anchor markers, unlinked small segments from individual input maps can be integrated to the reference map. That is, this approach will help to identify the linkage relationships that could not be accomplished in individual studies. However, this is based on the assumption that each marker was assigned to the correct chromosome in the individual mapping study. Due to the high frequencies of repetitive segments that exist in the *Gossypium* allopolyploid genome, it is not possible to use this approach to identify any small segments that have not been assigned to any chromosome. The high frequencies of repetitive segments on the same chromosome caused problems in the chromosomal integration, too. It has been observed many times that the same marker can appear more than once on the same chromosome within the same map. For example, a SSR marker BNL100 mapped on both Map-A and Map-B has two loci on Map-A and one locus on Map-B, as shown below (x indicates other markers):

Map-A: BNL100a --------- x -----x ------ x ------ BNL100b -------- x ------ x

Map-B: x -----x ---- x --------- BNL100_220 --------- x ----- x ----- x ------- x

Clearly, this generates confusion because two different integration outputs can be derived depending on whether BNL100 on Map-B represents the location of BNL100a or BNL100b on Map-A. Therefore, in this study, any anchor marker that has multiple loci on the same chromosome was removed from the anchor marker group.

Twenty-eight AD genome genetic maps were used in this study. Among them, 15,969 loci represented by 8,407 individual markers were used in the integration. Many of the maps have low marker density and some of them only have partial data available (Table 3.3 and Table 3.5). The lack of uniform mapping information from these maps generates a large diversity of agreements among marker orders from different input maps, just as there will be a large variation when using a small sample set in an experiment. The variation among input maps was reflected by the disagreement percentages between the output reference map and each of the input maps (Table 4.5). Choosing better quality of input maps (such as higher marker density and larger number of mapped loci, relevant equal marker intervals, etc.) to construct the skeleton structure for the reference map can reduce the marker order disagreement between reference map and input maps. However, the total number of integrated markers in the output of the reference map also will be reduced. For example, using the four maps (CH-F2, GV-BC1, PK-F2, and TH-BC1) that have the largest number of mapped loci with higher marker density of (see Table 3.3 for detailed information) in the skeleton structure construction reduced 2.64 percent (from 11.86% to 9.22%) of the overall marker order disagreement between reference map and that of input maps. Meanwhile, the total number of markers in the reference map was reduced from 7,424 to 7,276. With additional cotton genetic mapping studies and the incorporation of physical mapping and sequence information, the reference map will be much improved.

This study presented a use of bioinformatics and computational biology in cotton genome mapping integration. The output reference map contains 7,424 markers and represents over 93% of the combined mapping information of 28 AD genome genetic maps. The output will be stored and displayed through CottonDB (http://www.cottondb.org), a public cotton genome database.

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APPENDIX A

SETTING A WEIGHTED SYMMETRIC ORDER DIFFERENCE MATRIX

Case 1. One-map weighted symmetric order difference matrix.

If nodes a, b, and c are ordered a->b->c in map A,
the set of pairwise partial orders within map A will be:

```
a->b, a->c, b->a, b->c, c->a, c->b
```

The Kemeny distances of a, b and c within map A are:

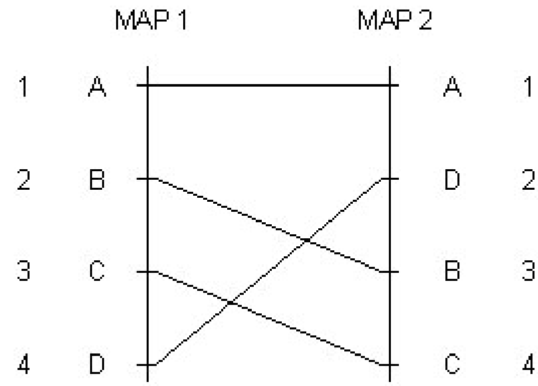
```
A(a->b) = 2-1 = 1
A(a->c) = 3-1 = 2
A(b->a) = 1-2 = -1
A(b->c) = 3-2 = 1
A(c->a) = 1-3 = -2
A(c->b) = 2-3 = -1
```

The weighted symmetric order difference matrix is:

	a	**b**	**c**
a	0	1	2
b	-1	0	1
c	-2	-1	0

Case 2. Two-map weighted symmetric order difference matrix.

First, Converting Kemeny Distance calculations to node order differences Below, nodes A, B, C, and D are in Map-1 and Map-2 in different orders. Orders of each node in each map are labeled beside the nodes' names.



Calculations of order differences of each pair of nodes per map and the accumulations of them are listed in the table below. The combined information of node order differences forms the order differences weights.

Node pairs	Order differences in MAP-1	Order differences in MAP-2	Combined order differences
A→B	1	2	3
A→C	2	3	5
A→D	3	1	4
B→A	-1	-2	-3
B→C	1	1	2
B→D	2	-1	1
C→A	-2	-3	-5
C→B	-1	-1	-2
C→D	1	-2	-1
D→A	-3	-1	-4
D→B	-2	1	-1
D→C	-1	2	1

Second, Filling order difference weights into a matrix containing nodes A, B, C, and D to construct the weighted symmetric order difference matrix.

	A	B	C	D
A	0	3	5	4
B	-3	0	2	1
C	-5	-2	0	-1
D	-4	-1	1	0

Case 3. Setting weighted symmetric order difference matrix for data from this study.

Table A is a sample set of anchor node data.

Anchor Name	Map Name				
	e3-bc1_chr01	ch-f2_chr01	gv-bc2_chr01	gv-bc1_chr01	pk-f2_chr01
bnl1350	81.4			154.1	
bnl1667		97.4			
bnl1693				45.2	
bnl2440		0	0	25.4	9.8
bnl2564	64.3				
bnl2921	62.2	73.6		115.3	100
bnl3085		80.7			
bnl3090	103.3		86.1	168.7	
bnl3580	103.3	113.1	108.7	196.3	
bnl3778		80			
bnl3888	137.4	92.1	96.7	185.5	131.6
cir0018	72.8			185.5	
cir0049	97.7	81.6			

Table B, replacing each node's map position by its order number in the map

Anchor name	Map Name				
	e3-bc1_chr01	ch-f2_chr01	gv-bc2_chr01	gv-bc1_chr01	pk-f2_chr01
bnl1350	4			4	
bnl1667		7			
bnl1693				2	
bnl2440		1	1	1	1
bnl2564	2				
bnl2921	1	2		3	2
bnl3085		4			
bnl3090	6		2	5	
bnl3580	6	8	4	7	
bnl3778		3			
bnl3888	7	6	3	6	3
cir0018	3			6	
cir0049	5	5			

Following the steps in case 2, the matrix was built.

APPENDIX B

USING DIRECTED GRAPH TO REPRESENT GENETIC MAP INFORMATION

Let's use the same sample data used in Example 1, case 2 (Figure A).

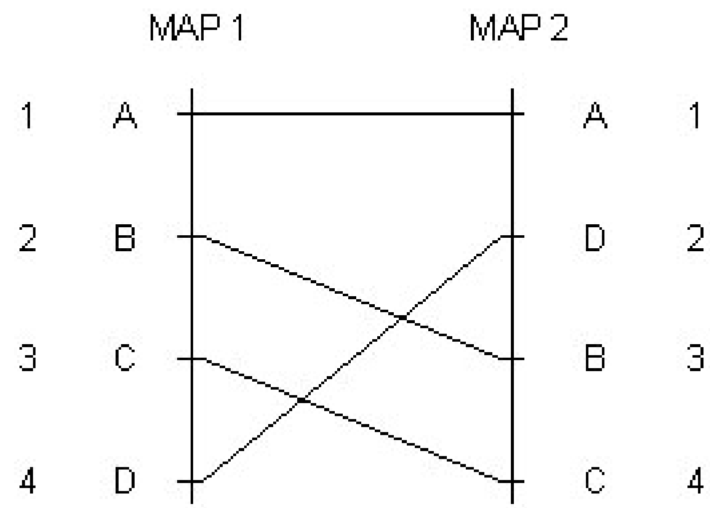


Figure A. Sample input maps, MAP-1 and MAP-2, for integration.

Because the four markers A, B, C, and D present in both MAP-1 and MAP-2, all is anchor node in the integration. Therefore, there are 24 (4!) different combinatorial orders for the integration. Figure B shows all the 24 combinations.

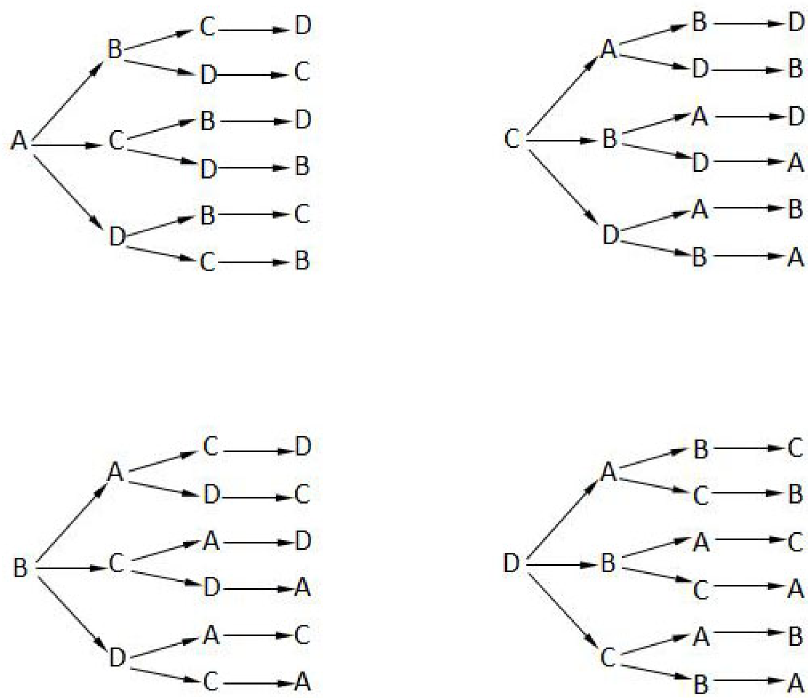


Figure B. Given 4 anchor nodes, their orders can be assigned in 24 different ways (4! = 4*3*2*1 =24) for the integrated map.

Because there are marker order differences between MAP-1 and MAP-2, directed cycles will exist in any of the directed graphs. Two of the 24 different directed graphs are shown in Figure C.

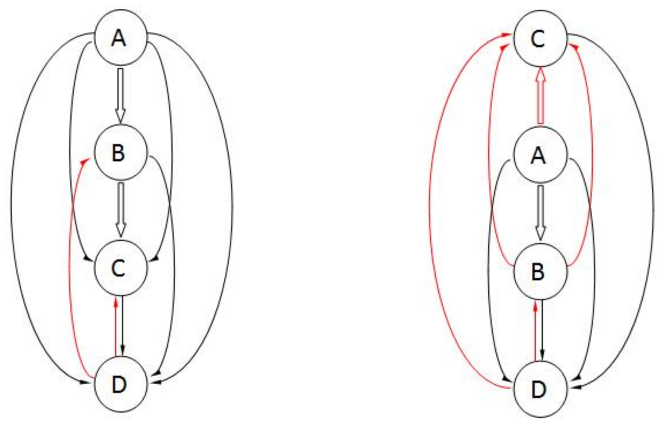


Figure C. Directed cyclic graphs, derived by combined orders A->B->C->D and C->A->B->D. The left side of each graph represents the pairwised anchor order information of MAP-2, while the right side represents the order information of MAP-1. A thicken arrow indicates the order between the two anchor nodes is repeated twice. Upward edges are in red color to help on easier distinguishing them from downward edges.

APPENDIX C

TABLES OF SUPPLEMENT DATA

Table 3.2 General information of collected map data

ID	Map Name	Sp.	Genome	Female Parent	Male Parent	Pop. Type	Pop. Size	Marker Types	# of Loci	Reference
1	7T-RIL	Gh/Gh	AD	7235	TM-1	RIL	258	QTL, RAPD, SSR	156	Shen et al, 2007
2	AP-F2	Gh/Gb	AD	Acala-44	Pima S-7	F2	94	QTL, AFLP, RFLP, SSR,	392	Mei et al. 2004
3	CH-F2	Gh/Gb	AD	CCRI 36	Hai-7124	F2	186	MORPH SSR TRAP SRAP AFLP	1076	Yu et al. 2007
4	GV-BC1	Gh/Gb	AD	Guazuncho-2	VH8-4602	BC1	75	QTL, MORPH AFLP RFLP SSR	1274	Lacape et al. 2003 Nguyen et al. 2004 Lacape et al. 2005
5	GV-BC2	Gh/Gb	AD	Guazuncho-2	VH8-4602	BC2	unknown	AFLP SSR	513	TropGeneDB
6	HP-F2:3	Gh/Gb	AD	Handan-208	Pima-90	F2:3	69	QTL SRAP SSR RAPD	1029	He et al. 2007 Lin et al, 2005 He et al., 2005
7	PE-F2	Gb/Gh	AD	Pima S-7	Empire B2 Empire B3 Empire B2b6 S295	F2	119-150	QTL, RFLP	250	Wright et al. 1998 Wright et al. 1999
8	PK-F2	Gh/Gb	AD	Palmari	K-101	F2	57	QTL, RFLP, SSR, CAP	2636	Rong et al. 2004

9	TH-BC1	Gh/Gb	AD	TM-1	Hai-7124	BC1	138	EST-SSR SSR SRAP seq_BAC_end	1790	Guo et al. 2007
10	TP-BC3F2	Gh/Gb	AD	Tamcot-2111	Pima S-6	BC3F2	22-184	QTL, RFLP	2590	Chee et al. 2005
11	SA-F2	Gar/Ghe	A	SMA-4	A1-97	F2	167	QTL, RFLP	276	Desai et al 2006
12	D	Gt/Gr	D			F2	62	RFLP	763	Rong et al. 2004
13	DT-F2	Gh/Gh	AD	Deltapine-61	Texas 701	F2	251	QTL, MORPH, SSR	73	Guo et al. 2007
14	T3-RIL	Gh/Gb	AD	TM-1	3-79	RIL	183	QTL, SSR, EST-SSR	433	Frelichowski et al. 2006 Park et al. 2005
15	DS-F2	Gh/Gb	AD	Deltapine-61	Sea Island Seaberry	F2	180	QTL RFLP	234	Jiang et al. 2000 Rong et al. 2005
16	CS-F2	Gh/Gb	AD	CAMD-E	Sea Island Seaberry	F2	271	QTL RFLP	254	Jiang et al. 1998 Rong et al. 2005
17	TW-F2	Gh/Gt	AD	TM-1	WT-936	F2	82	QTL, RFLP, SSR, CAP	590	Waghmare et al. 2005
18	SF-F2	Gh/Gb	AD	Sic'on	F-177	F2	406	QTL, RFLP	269	Saranga et al. 2001 Paterson et al. 2003 Saranga et al. 2004
19	im-F2	Gb/Gh	AD	Pima S-7	im	F2	124	QTL, RFLP	364	Rong et al. 2007
20	n2-F2	Gb/Gh	AD	Pima S-7	n2	F2	124	QTL, RFLP	364	Rong et al. 2005.

21	DG-F2	Gh/ Gb	AD	Deltapine	Giza-83	F2	71	QTL RAPD SSR AFLP	140	Adaway et al., 2008
22	XH-F2	Gh/ Gb	AD	Xin-Lu-Zhao 1	Hai-7124	F2:3	76	QTL, SSR	432	Wang et al. 2007
23	AA-F2	Ghe/ Gar	A	A1-97	A2-47	F2	58	RFLP Isozyme	161	Brubaker et al. 1999
24	3N-RIL	Gb/ Gh	AD	3-79	NM 24016	RIL	60	ATG-AFLP	90	Lu et al. 2008
25	JZ-F2	Gar/ Gar	A	Jiang-Ling-Zhong-Mian	Zhe-Jiang-Xiao-Shan-Lu-Shu	F2	189	SSR	267	Ma, et al. 2008
26	E3-BC1	Gh/ Gb	AD	Emian-22	3-79	BC1	141	SSR	917	Zhang et al. 2008
27	GHy-a	Gn/ Gau	G	Gos-5024	Hyb-601-2	F2	94	AFLP	213	Brubaker et al. 2003
28	GHy-n	Gn/ Gau	G	Gos-5024	Hyb-601-2	F2	94	AFLP	176	Brubaker et al. 2003
29	HJ-F2	Gb/ Gh	AD	Hai-7124	Junmian-1	F2	128	QTL SSR	420	Yang et al. 2008
30	HJ-BC1	Gb/ Gh	AD	Hai-7124	Junmian-1	BC1	96?	QTL SSR	219	Yang et al. 2008
31	Z8-RIL	Gh/ Gh	AD	Zhongmia nsuo-12	8891	RIL	180	QTL Gene AFLP, SSR RAPD SRAP	132	Wang et al. 2007
32	VTH-DHv0 5	Gh/ Gb	AD	Vsg	TM-1xHai-7124	DH	73	SSR	444	Song et al. 2005
33	YT-F2:3	Gh/ Gh	AD	Yu-Mian 1	T-586	F2:3	117	QTL, AFLP, SSR, MORPH	70	Zheng et at. 2005
34	VTH-DHv0 2	Gh/ Gb	AD	Vsg	TM-1xHai-7124	DH	58	SSR RAPD	487	Zhang et al. 2002
35	SSZ8-4WC	Gh/ Gh	AD	Simian-3 x Sumian-12	Zhong-4133 x 8891	4WC	280	QTL SSR MORPH	286	Qin et al. 2008
36	MP-F2.3	Gh/ Gh	AD	MD5678n e	Prema	F2.3	119	QTL, RFLP	81	Ulloa et al. 2000 Ulloa et al. 2005

37	HQM-F2.3	Gh/Gh	AD	HQ95–6	MD51ne	F2.3	199	RFLP	83	Ulloa et al. 2005
38	DM-F2.3	Gh/Gh	AD	DES-119-5	MD51ne	F2.3	150	RFLP	56	Ulloa et al. 2005
39	HSM-F2.3	Gh/Gh	AD	HS-46	MARCABUCAG8US-1-88	F2.3	96	QTL, RFLP	120	Shappley et al. 1998 Ulloa et al. 2005
40	YT-F2:7	Gh/Gh	AD	Yu-Mian 1	T-586	F2:7 (RIL)	270	IT-ISJ, SSR, MORPH	113	Zheng et at. 2008

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Table 3.3 Summarizes information on number of loci and genome coverage derived from each of the 28 maps grey cell indicates no information obtained from the map on the chromosome.

ID	Map Name	Chromosome Number*																										Total
		A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	A12	A13	D02	D01	D07	D03	D13	D05	D10	D11	D04	D09	D08	D06	D12	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
24	3N-RIL	22.5	55.3	5.4	3	2.1	30.4		8.5		48.9					120.7					2.4					11.9	61.4	373
		6	6	2	2	2	5		3		6					15					2					4	8	61
1	7T-RIL		0.8	37.4		16.6	5.6	0.5		1.4	18.6	0.1	99.6		72.5	41.5	34.7	0.3		59.9	43.9	13.3		46.4	72.7	188.9		755
			2	6		2	3	2		2	5	3	7		3	7	6	2		6	3	4		8	36	16		123
2	AP-F2	234.3		141.4	93.9		239.9			144.7	65.1	192.3	113.8		141.4		50.4		44.5		170.3		58.1			140.9	112.8	1944
		21		12	10		24			13	5	63	25		12		5		4		23		9			11	14	251
3	CH-F2	128.5	106	133.2	121.9	224.5	169.3	167.5	202.4	235.1	120.6	192.3	230.3	146.2	201	190.7	142.4	166.7	121.9	206.2	141.5	194.3	141	190.5	213.8	113.1	173.7	4374.6
		26	44	31	26	49	54	36	44	56	45	63	55	57	50	40	25	37	34	43	41	37	24	43	42	36	38	1076
4	GV-BC1	216.2	207.2	152.2	197.1	347.8	297.3	212	235.2	316.4	193.7	273.1	189.9	217.4	193.1	198.3	234.1	99.5	158.9	257.5	275.6	292.9	157.3	222.9	171.3	183.4	191.9	5692
		36	49	49	38	61	47	54	65	50	47	71	61	67	48	48	29	33	46	63	47	50	31	47	45	47	40	1269
5	GV-BC2	132.7	108.8	104.5	59.9	181.1	108.7	80.3	99.5	156.7	107	166.6	123.9	133.6	159.6	126.2	82	136.2	100.7	148.3	135.6	143.4	103.9	165	78.5	107.1	63.5	3113
		16	24	19	16	24	26	15	37	24	26	32	26	20	14	14	9	18	20	17	17	18	10	18	18	23	9	510
6	HP-F2:3	69.5	16.3	201.8	105.1	291.2	228.8	146.7	360.9	154	271	332.1	133.5	178	304.2	289.8	113.9	220.9	143.5	414.7	210.2	224.7	202.9	207	169.3	328.1	154.2	5472
		22	6	37	17	60	35	46	46	41	52	55	37	38	47	36	33	54	43	59	42	28	24	55	26	53	37	1029
7	PE-F2	55.9	27.3	108.8	89.5	253.2	88.5	170.2	174.9	38.7	72.7	96.2	75	140.1	98.9	60.9	59.8	65.7	149.3	72.1	66.1	226.3	56.1	81	70.3	76.8	131.2	2606
		9	2	8	8	16	10	16	12	8	5	11	5	8	15	6	6	8	9	23	10	14	6	8	7	10	7	247
8	PK-F2	147.2	147.4	150.8	186.1	239.6	126.7	230.1	177.6	152.5	182.7	198	213.6	173.4	164.8	176.4	149.9	84	192.2	245.4	146	191.1	95.4	172.6	183.8	159.9	164.1	4451
		81	67	96	99	169	74	107	103	96	99	106	127	108	115	98	90	57	114	159	98	135	68	97	94	86	93	2636
9	TH-BC1	99.1	86	146.4	126.4	213.9	156.3	97.9	129.1	134.1	71.2	169.5	112.2	133.7	112.1	124.5	129.1	128.2	118.3	181.9	116.1	184.7	116.1	155.5	111.7	140.5	131.4	3426
		47	40	56	36	102	64	50	69	68	65	88	74	61	75	68	67	51	68	120	67	86	60	60	94	65	89	1790
10	TP-BC3F2	147.2	147.4	150.8	186.1	239.6	126.7	230.1	177.6	152.5	182.7	198	213.6	173.4	164.8	176.4	149.9	84	192.2	242	146	191.1	95.4	172.6	183.8	159.9	164.1	4448
		76	66	95	99	166	72	106	102	95	101	105	122	107	112	96	88	57	111	157	93	133	65	95	94	86	91	2590
13	DT-F2	67.4						12.8		8.1	26.3	5.5	33.4	22		62.5				110.5		103.7		34.4		35.4		522
		4						2		3	5	3	3	4		4				7		12		3		4		54
14	T3-RIL	39.9	59.2	97.5	12.5	65.3	39.8	76.8	104.6	184.8	77.2	115.8	53.4		31.7	13.5	72.3	42.9	113.3	17.2	102.8		80.6	43.4		43.1	35.3	1523
		7	18	26	2	16	20	12	29	23	25	10	13		5	13	14	3	29	5	15		10	8		7	12	322
15	DS-F2	76.8	57.5	96.7	39.4	179.5	168	64.2	265.5	157.2	104.5	236.8	54.5	239.9	179	156.5	116.7	80.4	65.3	349.9	184.1	212.8	89.8	147.1	174.8	157.1	106	3760

		6	6	8	5	11	8	10	12	7	6	11	7	12	10	12	7	6	4	22	20	6	7	9	7	12	6	237
16	CS-F2	102.8	94.3	62.3	67.6	175.9	89.2	155.2	217.8	107.3	162.6	163.5	50.5	192.6	80.7	78.3	169.1	81.3	85.2	291.8	87.7	224.5	80.7	78.3	130.8	161.7	209.6	3401
		10	5	8	6	13	8	17	14	7	8	8	4	13	9	8	12	7	7	17	8	11	4	7	10	12	10	243
17	TW-F2	125.7	71.3	146.4	133.5	133.9	109.3	161.2	92.1	155.6	83	37.2	112.2	130.6	147.3	150.2	208	65.3	105.5	98	182.5	217.4	128.8	150.6	150.5	52.8	199.3	3348
		19	10	25	23	26	13	21	12	15	9	11	12	17	23	24	30	9	17	15	17	30	9	19	20	9	30	465
18	SF-F2	232.3	89.1	119	86	248	187.7	129.7	207.4	177.9	147.2	139.5	44.7	266.3	173	235	181.9	135.3	101.4	218.4	131.2	199.3	204	162.3	163.8	172	186.9	4339
		13	8	8	6	10	10	7	9	7	7	6	3	10	33	14	17	7	7	14	6	6	11	9	24	10	6	268
19	im-F2	149.6	104	113.6	68.1	111.7	115.5	50.2	164.1	56.1	72.9	76.7	256.2	143.5	123.8	49.6	147	60.6	67	194	137.3	242.5	64.5	182.7	67.4	55.8	166.1	3041
		17	11	15	9	13	9	6	17	4	6	11	26	16	9	7	12	6	11	26	16	26	10	12	7	6	17	325
20	n2-F2	146.4	49	120.3	24.3	248.8	68.9	130.5	153.7	43.2	82.7	109.3	163.4	42	47.1	112.6	89.8	202.5	86.4	134.3	159.8	221.1	62.3	82.1	69.7	38	190.3	2879
		15	7	12	7	16	5	13	12	6	6	12	34	9	5	10	11	11	14	14	16	23	9	7	8	5	18	305
22	XH-F2	66.8	168.6	83	59.4		142		112.3	133.7	180.5	159.2	154.3	70.4	96.8	78.9	170.6		154.3	344.1			96	134.3	210.9	159.5	96.2	2872
		14	19	7	5		12		9	18	17	20	19	8	8	21	23		12	38			12	14	21	22	11	330
26	E3-BC1	205.6	148.2	200.9	157	230.3	224.2	101.5	223.1	259.6	152	407	246.9	179.5	133.3	138.7	157.1	111.6	177.3	345.7	195	320.4	137.1	203	232	251.3	185.6	5324
		27	23	27	24	40	34	25	39	43	26	62	40	29	24	42	29	23	25	59	34	48	26	35	41	40	33	898
31	Z8-RIL			1.6		95.3				52.2	40.2	41.7	32.6		34.9		26.8			0.2	39		67.5	83	18.3	34.2	9.8	577
				3		10				8	9	3	4		3		2			7	3		5	10	2	12	2	83
32	VTH-DHv05	117.1	102.2	130.8	57.2	113.7	20.6		15.4	136.3	179.8	148.9	95.5	52.5	157.3	26.8	140.5	50.3	115.6	150.3	115.5	244.9	92.4	53.3	143.3	151.6	146.1	2758
		13	9	14	5	14	6		6	22	17	22	15	13	18	11	19	8	17	19	12	25	13	7	17	21	22	365
33	YT-F23		21.7			51.5	29		35.6	35.4	34.4		10.9	52.5		33.7	20		26.3		34.4	26.3	8.6	35.4	35.4	16	10.9	518
			2			7	6		6	4	3		2	4		3	5		3		3	3	2	4	6	2	2	67
30	HJ-BC1					113.4		171.2	66.8	112.8										116.1		96.4	76.5					753
						28		21	18	17										18		15	12					129
29	HJ-F2					175.6			63.6																			239
						35			14																			49
35	SSZ8-4WC					85.9	66.5				110	70.1	102.7		46.9			30.9	58.1	52.1		19.7	39.4	124.5	77.8			885
						12	12				26	9	9		11			10	5	11		8	4	17	7			141
40	YT-F27			55.6		57.1	37.8	10.7	19.4	46.4		25.5	21.3	31.3	49.5				44		46.3	112.3			75.5	18.6	34.2	686
				4		5	12	2	7	6		9	3	12	5				6		6	13			6	6	4	106
21	DG-F2																											140
34	VTH-DHv02																											487
36	MP-F23																											81
37	HQM-F23																											83

38	DM-F2.3																											56
39	HSM-F2.3																											120

* row 1 gives numbers in pairs of assigned At or Dt sub-genome (reference: Wang et al., 2006)
  row 2 gives the correlated numbers used before the complementment of the assignment.

Gray background indicates data not available. Yellow background indicates the maps that do not contain information that can be used in this study, i.e. marker from each of these maps have not yet mapped on any other maps.

Table 3.4 Information of marker types (of 28 AD genome maps that used in the integration).

chr	AFLP	ISO	IT-ISJ	MORTH	RAPD	REMAP	RFLP	SRAP	SSR	TRAP	Other	No. of Individual Markers
1	50			1	1		92	9	99	5		257
2	48			1			75	16	80	12	1	233
3	40		1		1		113	27	126	2	2	312
4	31		1	1			106	15	69	7		230
5	35			1	10		181	29	198		3	457
6	62		7	1	2	1	88	35	128	10	2	336
7	33		1		5		131	25	114	7	1	317
8	52		5		1	2	111	28	137	11	3	350
9	60		3	1	1	1	100	19	159	7	2	353
10	45				5		110	45	160	12	3	380
11	36	1	2		1		116	34	189	16	2	397
12	69	1	1	1	3		141	39	145	6	4	410
13	46		6	1	1		124	38	106	6	1	329
14	39		1	2	3		118	34	138	8	3	346
15	28			2	2		105	8	151	3	2	301
16	17				4		106	7	132	1	4	271
17	24				6	1	71	27	105	6		240
18	31		1		1		118	26	132	1	2	312
19	15	1					194	8	231	4	6	459
20	60		2		2		104	14	134	10	1	327
21	18		4	1	3		166	15	164	7	1	379
22	20						75	10	110	5	2	222
23	19				1		108	29	142	1	1	301
24	23		4				101	15	161	5	2	311
25	34		1		1		94	19	129	2	1	281
26	23		2				108	15	137	7	4	296
Total	958	3	42	13	54	5	2956	586	3576	161	53	8407

Table 3.5 Number of markers per map-chromosome, and number of individual markers per chromosome.

Map Name	Chromosome Number*																										Total No. of Marker Loci
	1	15	2	14	3	17	4	22	5	19	6	25	7	16	8	24	9	23	10	20	11	21	12	26	13	18	
	A01	D01	A02	D02	A03	D03	A04	D04	A05	D05	A06	D06	A07	D07	A08	D08	A09	D09	A10	D10	A11	D11	A12	D12	A13	D13	
PK-F2	81	98	67	115	96	57	99	68	169	159	74	86	107	90	103	94	96	97	99	98	106	135	127	93	108	114	2636
TP-BC3F2	76	96	66	112	95	57	99	65	166	157	72	86	106	88	102	94	95	95	101	93	105	133	122	91	107	111	2590
TH-BC1	47	68	40	75	56	51	36	60	102	120	64	65	50	67	69	94	68	60	65	67	88	86	74	89	61	68	1790
GV-BC1	36	48	49	48	49	33	38	31	61	63	47	47	54	29	65	45	50	47	47	47	71	50	61	40	67	46	1269
CH-F2	26	40	44	50	31	37	26	24	49	43	54	36	36	25	44	42	56	43	45	41	63	37	55	38	57	34	1076
HP-F2:3	22	36	6	47	37	54	17	24	60	59	35	53	46	33	46	26	41	55	52	42	55	28	37	37	38	43	1029
E3-BC1	27	42	23	24	27	23	24	26	40	59	34	40	25	29	39	41	43	35	26	34	62	48	40	33	29	25	898
GV-BC2	16	14	24	14	19	18	16	10	24	17	26	23	15	9	37	18	24	18	26	17	32	18	26	9	20	20	510
TW-F2	19	24	10	23	25	9	23	9	26	15	13	9	21	30	12	20	15	19	9	17	11	30	12	30	17	17	465
VTH-DH_05	13	11	9	18	14	8	5	13	14	19	6	21		19	6	17	22	7	17	12	22	25	15	22	13	17	365
XH-F2	14	21	19	8	7		5	12		38	12	22		23	9	21	18	14	17		20		19	11	8	12	330
im-F2	17	7	11	9	15	6	9	10	13	26	9	6	6	12	17	7	4	12	6	16	11	26	26	17	16	11	325
T3-RIL	7	13	18	5	26	3	2	10	16	5	20	7	12	14	29		23	8	25	15	10		13	12		29	322
n2-F2	15	10	7	5	12	11	7	9	16	14	5	5	13	11	12	8	6	7	6	16	12	23	34	18	9	14	305
SF-F2	13	14	8	33	8	7	6	11	10	14	10	10	7	17	9	24	7	9	7	6	6	6	3	6	10	7	268
AP-F2	21			12	12		10	9			24	11		5			13		5	23	63		25	14		4	251
PE-F2	9	6	2	15	8	8	8	6	16	23	10	10	16	6	12	7	8	8	5	10	11	14	5	7	8	9	247
CS-F2	10	8	5	9	8	7	6	4	13	17	8	12	17	12	14	10	7	7	8	8	8	11	4	10	13	7	243
DS-F2	6	12	6	10	8	6	5	7	11	22	8	12	10	7	12	7	7	9	6	20	11	6	7	6	12	4	237
SSZ8-4WC				11		10		4	12	11	12					7		17	26		9	8	9			5	141

HJ-BC1								12	28	18			21		18		17					15					129
7T-RIL		7	2	3	6	2			2	6	3	16	2	6		36	2	8	5	3	3	4	7				123
YT-F2:7				5	4				5		12	6	2		7	6	6			6	9	13	3	4	12	6	106
Z8-RIL				3	3			5	10	7		12		2		2	8	10	9	3	3		4	2			83
YT-F2:3		3	2					2	7		6	2		5	6	6	4	4	3	3		3	2	2	4	3	67
3N-RIL	6	15	6		2		2		2		5	4			3				6	2				8			61
DT-F2	4	4								7		4	2				3	3	5		3	12	3		4		54
HJ-F2									35						14												49
Total No. of Loci	485	597	424	654	568	407	443	431	907	919	569	605	568	539	685	632	643	592	626	599	794	731	733	599	613	606	15969
Total No. of Individual Markers	257	301	233	346	312	240	230	222	457	459	336	281	317	271	350	311	353	301	380	327	397	379	410	296	329	312	8407

* row 1 gives numbers in pairs of assigned At or Dt sub-genome (reference: Wang et al., 2006)
row 2 gives the correlated numbers used before the complementment of the assignment.

Table 4.1 Comparisons on number of markers between individual input markers and anchor nodes per chromosome.

Map Name	Chromosome Number*																										Total Number
	A01	D01	A02	D02	A03	D03	A04	D04	A05	D05	A06	D06	A07	D07	A08	D08	A09	D09	A10	D10	A11	D11	A12	D12	A13	D13	
	1	15	2	14	3	17	4	22	5	19	6	25	7	16	8	24	9	23	10	20	11	21	12	26	13	18	
Total No. of Individual markers	257	301	233	346	312	240	230	222	457	459	336	281	317	271	350	311	353	301	380	327	397	379	410	296	329	312	8407
Total No. of Individual anchor nodes (pulled out from 28map)	67	86	59	74	74	49	53	64	139	141	71	86	61	69	113	85	90	71	79	65	113	107	115	86	76	73	2166

* row 1 gives numbers in pairs of assigned At or Dt sub-genome (reference: Wang et al., 2006)
row 2 gives the correlated numbers used before the complementment of the assignment.

Table 4.2 Comparisons on number of loci between the loci represented by anchor nodes and loci from input maps per chromosome.

Map Name	Chromosome Number*																										Total Number
	A01	D01	A02	D02	A03	D03	A04	D04	A05	D05	A06	D06	A07	D07	A08	D08	A09	D09	A10	D10	A11	D11	A12	D12	A13	D13	
	1	15	2	14	3	17	4	22	5	19	6	25	7	16	8	24	9	23	10	20	11	21	12	26	13	18	
Total Loci Eepresented by Input Markers	485	597	424	654	568	407	443	431	907	919	569	605	568	539	685	632	643	592	626	599	794	731	733	599	613	606	15969
Total Loci Represented by Anchor Nodes (pulled out from 28 maps)	251	321	264	277	205	184	187	217	502	537	253	346	209	259	395	318	348	284	263	261	411	363	375	324	285	287	7926

* row 1 gives numbers in pairs of assigned At or Dt sub-genome (reference: Wang et al., 2006)
row 2 gives the correlated numbers used before the complementment of the assignment.

Table 4.3 Number and percentage of individual input markers that are integrated into the reference map.

Chromosome Number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	Total No. of Marker
Total Individual Markers of 28 Maps	257	233	312	230	457	336	317	350	353	380	397	410	329	346	301	271	240	312	459	327	379	222	301	311	281	296	8407
No. of Marker in Reference map	227	227	270	218	438	293	266	306	292	320	373	329	293	285	260	246	222	280	413	255	350	201	253	286	253	268	7424
% of Total Incorporated Markers	0.88	0.97	0.87	0.95	0.96	0.87	0.84	0.87	0.83	0.84	0.94	0.80	0.89	0.82	0.86	0.91	0.93	0.90	0.90	0.78	0.92	0.91	0.84	0.92	0.90	0.91	0.88

Table 4.4 Number and percentage of loci represented by the reference map.

Chromosome Number	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	Total No. of Loci
Total Loci from Input Map Data	485	424	568	443	907	569	568	685	643	626	794	733	613	654	597	539	407	606	919	599	731	431	592	632	605	599	15969
No. of Loci Represented in Ref. Map	461	414	524	422	887	527	499	655	617	576	736	666	573	574	564	496	359	564	910	518	696	396	529	581	567	557	14868
% of Loci Covered by Ref. Map	0.95	0.98	0.92	0.95	0.98	0.93	0.88	0.96	0.96	0.92	0.93	0.91	0.93	0.88	0.94	0.92	0.88	0.93	0.99	0.86	0.95	0.92	0.89	0.92	0.94	0.93	0.93

Table 4.5 Percentage of disagreements between the marker orders of reference and original input maps.

Map	Chromosome Number																										% of Map Overall Disagreements
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	
pk-f2	22.51	3.87	0.92	6.11	2.42	14.11	0.86	0.70	21.29	14.53	17.07	3.10	8.20	5.98	6.38	6.50	1.50	23.05	5.27	0.94	40.00	15.38	0.05	0.89	2.25	2.51	8.71
tp-bc3f2	21.92	3.99	0.94	6.11	2.46	14.59	0.77	0.72	21.76	13.93	16.53	3.10	7.95	5.96	6.24	6.40	1.50	23.00	5.41	0.85	40.45	14.34	0.05	0.89	2.25	2.62	8.64
th-bc1	2.50	1.79	2.24	5.53	8.95	24.85	1.33	0.77	17.96	12.40	17.24	1.78	23.56	6.18	10.62	6.11	4.16	26.95	4.79	5.63	35.76	36.84	1.87	12.90	12.49	6.22	11.21
gv-bc1	26.20	3.57	3.23	2.42	8.69	30.53	0.00	4.22	10.29	13.51	20.08	0.71	24.42	7.54	4.79	1.23	2.65	37.10	3.44	2.68	33.69	18.49	0.83	12.02	1.30	3.72	10.67
ch-f2	3.38	19.60	23.15	24.31	4.70	37.18	0.00	0.74	10.64	15.01	25.76	0.54	28.38	5.27	12.01	41.00	7.56	15.86	6.39	6.34	32.58	48.55	1.95	9.39	7.94	6.61	15.19
hp-f2:3	48.48	50.00	47.62	0.74	18.58	43.37	39.29	43.81	41.13	13.96	33.07	10.71	49.09	50.00	39.17	37.93	11.39	33.57	43.56	28.33	38.96	43.94	48.35	35.90	35.33	46.67	35.88
e3-bc1	0.00	20.95	7.98	3.62	33.33	25.07	0.00	2.02	13.62	9.85	42.96	0.00	33.20	23.39	50.00	29.44	0.00	0.00	4.97	10.87	40.79	32.31	0.28	8.90	11.03	19.12	16.30
gv-bc2	9.17	9.06	8.77	19.17	39.86	34.77	0.00	4.05	5.80	13.85	15.32	0.62	20.53	7.50	4.40	2.78	3.92	32.63	2.21	5.88	39.87	31.11	1.96	3.27	1.98	2.22	12.33
tw-f2	24.26	0.00	5.53	8.57	2.11	0.00	0.95	1.52	6.67	10.71	0.00	0.00	18.10	3.16	0.00	7.12	0.00	35.00	0.00	0.00	41.63	8.33	1.31	4.58	0.00	3.17	7.03
vth-dh05	9.52	0.00	9.09	40.00	12.73	0.00		50.00	30.53	11.67	30.56	50.00	28.21	23.08	0.00	20.00	4.76	33.33	1.31	10.61	15.58	33.33	0.00	7.35	16.96	0.00	17.54
xh-f2	2.20	20.47	0.00	0.00		12.12		0.00	0.00	5.88	24.74	28.89	46.67	14.29	17.89	22.53		27.27	9.75			46.97	0.00	21.90	10.48	23.81	15.99
im-f2	33.33	4.44	0.95	5.56	50.00	4.76	10.00	1.90	0.00	0.00	33.33	1.54	14.10	2.78	0.00	3.64	0.00	17.78	1.58	3.85	22.94	26.67	0.00	0.00	0.00	2.21	9.28
t3-ril	0.00	0.00	2.33	0.00	0.00	0.00	0.00	9.11	7.11	0.00	33.12	0.00		0.00	0.00	50.00	0.00	0.00	0.00	0.00		0.00	0.00		38.10	19.05	6.91
n2-f2	28.57	0.00	0.00	19.05	5.83	33.33	0.00	3.03	33.33	16.67	16.36	4.92	9.52	0.00	27.78	2.22	5.45	24.36	5.13	5.13	0.00	11.11	9.52	6.67	0.00	0.83	10.34
sf-f2	39.74	20.00	3.57	6.67	2.22	8.33	0.00	3.57	4.76	40.00	6.67	0.00	0.00	40.00	1.28	52.38	19.05	23.81	0.00	10.00	13.33	14.29	8.33	0.00	6.67	0.00	12.49
ap-f2	0.00		0.00	0.00		0.00			0.00	0.00		0.00		0.00		0.00		19.05		0.00		0.00			1.82	6.59	1.96
pe-f2	36.11	0.00	0.00	6.67	3.81	6.67	8.97	1.52	7.14	30.00	0.00	0.00	7.14	10.99	6.67	16.67	0.00	25.00	25.00	0.00	27.47	20.00	3.57	0.00	13.33	9.52	10.24
cs-f2	27.78	0.00	0.00	0.00	0.00	38.10	5.13	2.78	0.00	3.57	0.00	0.00	8.97	7.14	4.76	6.06	9.52	13.33	6.59	0.00	16.67	0.00	6.67	5.56	7.58	14.29	7.10
ds-f2	20.00	20.00	3.57	0.00	33.33	42.86	30.00	8.89	0.00	40.00	1.82	0.00	15.15	0.00	7.27	28.57	13.33	50.00	34.56	38.10	33.33	9.52	0.00	33.33	6.06	0.00	18.07
ssz8-4wc					4.55	0.00				33.33	0.00	5.56		33.33			0.00	0.00	4.76		30.00	0.00	19.12	40.00			13.13
hj-bc1					12.17		3.27	49.26	42.86										7.84		40.95	19.70					25.15
7t-ril		0.00	6.67		0.00	0.00	0.00		0.00	0.00	0.00	0.00		0.00	0.00	0.00	0.00		0.00	0.00	0.00		0.00	3.03	0.00		0.51
yt-f2:7			0.00		33.33	0.00	0.00	0.00	0.00		33.33	0.00	40.00	50.00				0.00		0.00	23.08			0.00	46.67	0.00	14.15
z8-ril			0.00		0.00				0.00	0.00	0.00	0.00		0.00		0.00			0.00	0.00		20.00	11.11	0.00	25.76	0.00	3.79

yt-f2:3		0.00			10.00	13.33		0.00	0.00	0.00		0.00	0.00		0.00	50.00		0.00		0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.07
3n-ril	0.00	0.00	0.00	0.00	0.00	0.00		0.00		0.00					0.00					0.00					0.00	7.14	0.60
dt-f2	0.00						0.00		33.33	0.00	33.33	0.00	0.00		0.00	33.33			4.76		31.82		0.00		0.00		10.51
hj-f2					32.02			16.48																			24.25
% of Chr Overall Disagreement	16.94	8.46	5.50	7.73	12.84	16.00	5.03	8.92	12.33	11.95	17.45	4.46	19.16	12.90	9.06	18.43	4.46	20.96	7.71	5.62	27.22	19.60	5.00	9.39	9.92	7.67	11.86

Table 4.6 Chromosomes A01 and D01 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
1	A01	Reference_v1_chr1	cir0009	1
1	A01	Reference_v1_chr1	cir0199	2
1	A01	Reference_v1_chr1	par0658	3
1	A01	Reference_v1_chr1	coau4h11	3
1	A01	Reference_v1_chr1	par06f11	4
1	A01	Reference_v1_chr1	a1126	4
1	A01	Reference_v1_chr1	gate4db12	4
1	A01	Reference_v1_chr1	gate1bc01	5
1	A01	Reference_v1_chr1	par0925	6
1	A01	Reference_v1_chr1	bnl2440	7
1	A01	Reference_v1_chr1	gate4ca01	8
1	A01	Reference_v1_chr1	par0926	9
1	A01	Reference_v1_chr1	e4m6b	10
1	A01	Reference_v1_chr1	mucs0164	11
1	A01	Reference_v1_chr1	nau3254	12
1	A01	Reference_v1_chr1	par03-04	13
1	A01	Reference_v1_chr1	par0121	14
1	A01	Reference_v1_chr1	par0848	14
1	A01	Reference_v1_chr1	gate4ah09	14
1	A01	Reference_v1_chr1	nau2474	15
1	A01	Reference_v1_chr1	nau2095	16
1	A01	Reference_v1_chr1	pgh487	17
1	A01	Reference_v1_chr1	g1051	17
1	A01	Reference_v1_chr1	a1485	17
1	A01	Reference_v1_chr1	jespr0063	18
1	A01	Reference_v1_chr1	coau1i11	19
1	A01	Reference_v1_chr1	nau2741	20
1	A01	Reference_v1_chr1	unig28a09	21
1	A01	Reference_v1_chr1	gate3cc02	22
1	A01	Reference_v1_chr1	nau5411	23
1	A01	Reference_v1_chr1	nau5163	24
1	A01	Reference_v1_chr1	a1475	25
1	A01	Reference_v1_chr1	unig23c08	26
1	A01	Reference_v1_chr1	nau3433	27
1	A01	Reference_v1_chr1	dpl0490	28
1	A01	Reference_v1_chr1	cir0004	29
1	A01	Reference_v1_chr1	a1155	30
1	A01	Reference_v1_chr1	cir0094	31
1	A01	Reference_v1_chr1	nau3690	32
1	A01	Reference_v1_chr1	e2m7a	33
1	A01	Reference_v1_chr1	tmb0142	34
1	A01	Reference_v1_chr1	a1257	35
1	A01	Reference_v1_chr1	pgh624	36
1	A01	Reference_v1_chr1	t16e2c	37

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
15	D01	Reference_v1_chr15	mucs0141	1
15	D01	Reference_v1_chr15	pgh854	2
15	D01	Reference_v1_chr15	mucs0152	3
15	D01	Reference_v1_chr15	mucs0164	4
15	D01	Reference_v1_chr15	cir0009	5
15	D01	Reference_v1_chr15	t25e16	6
15	D01	Reference_v1_chr15	bnl2440	7
15	D01	Reference_v1_chr15	par0941	8
15	D01	Reference_v1_chr15	par01-14	8
15	D01	Reference_v1_chr15	nau1487	9
15	D01	Reference_v1_chr15	nau2437	10
15	D01	Reference_v1_chr15	nau2015	11
15	D01	Reference_v1_chr15	a1126	12
15	D01	Reference_v1_chr15	a1226	13
15	D01	Reference_v1_chr15	g1033	14
15	D01	Reference_v1_chr15	cms0021	15
15	D01	Reference_v1_chr15	gate1dh11	16
15	D01	Reference_v1_chr15	gate4db12	16
15	D01	Reference_v1_chr15	nau5138	17
15	D01	Reference_v1_chr15	nau3922	18
15	D01	Reference_v1_chr15	nau3901	18
15	D01	Reference_v1_chr15	gafb14k15	19
15	D01	Reference_v1_chr15	nau3040	20
15	D01	Reference_v1_chr15	par0784	21
15	D01	Reference_v1_chr15	par1001	21
15	D01	Reference_v1_chr15	nau0461	22
15	D01	Reference_v1_chr15	nau1495	23
15	D01	Reference_v1_chr15	unig25b04	24
15	D01	Reference_v1_chr15	l2-s	25
15	D01	Reference_v1_chr15	jespr0152	26
15	D01	Reference_v1_chr15	gate3bd01	27
15	D01	Reference_v1_chr15	mghes0032	28
15	D01	Reference_v1_chr15	nau5302	29
15	D01	Reference_v1_chr15	gate4ah09	30
15	D01	Reference_v1_chr15	a1485	31
15	D01	Reference_v1_chr15	bnl1693	31
15	D01	Reference_v1_chr15	e7m5_121	31
15	D01	Reference_v1_chr15	nau2814	32
15	D01	Reference_v1_chr15	nau2901	33
15	D01	Reference_v1_chr15	g1051	34
15	D01	Reference_v1_chr15	gate4cd05	35
15	D01	Reference_v1_chr15	par03-04	36
15	D01	Reference_v1_chr15	gate3cc02	37
15	D01	Reference_v1_chr15	par0019	38

1	A01	Reference_v1_chr1	od3od17-250	38
1	A01	Reference_v1_chr1	tmb1421	39
1	A01	Reference_v1_chr1	par0019	40
1	A01	Reference_v1_chr1	tmb1869	41
1	A01	Reference_v1_chr1	mghes0010	42
1	A01	Reference_v1_chr1	bnl2564	42
1	A01	Reference_v1_chr1	jespr0240	42
1	A01	Reference_v1_chr1	a1691	43
1	A01	Reference_v1_chr1	par0705	43
1	A01	Reference_v1_chr1	a1097	43
1	A01	Reference_v1_chr1	p09-54	43
1	A01	Reference_v1_chr1	nau0731	44
1	A01	Reference_v1_chr1	m2e12a	45
1	A01	Reference_v1_chr1	coau4a11	46
1	A01	Reference_v1_chr1	bnl2921	46
1	A01	Reference_v1_chr1	par0226	46
1	A01	Reference_v1_chr1	nau3384	47
1	A01	Reference_v1_chr1	par0957	48
1	A01	Reference_v1_chr1	jespr0289	49
1	A01	Reference_v1_chr1	e8m8_194	50
1	A01	Reference_v1_chr1	t2e5c	51
1	A01	Reference_v1_chr1	e4m6_204	52
1	A01	Reference_v1_chr1	e5m8_560	52
1	A01	Reference_v1_chr1	par09f09	53
1	A01	Reference_v1_chr1	nau0422	54
1	A01	Reference_v1_chr1	bnl3910	55
1	A01	Reference_v1_chr1	e5m7_340	56
1	A01	Reference_v1_chr1	jespr0090	57
1	A01	Reference_v1_chr1	m6e2	58
1	A01	Reference_v1_chr1	e3m4_84	59
1	A01	Reference_v1_chr1	cms0025	60
1	A01	Reference_v1_chr1	pgh468	60
1	A01	Reference_v1_chr1	g1097	60
1	A01	Reference_v1_chr1	g1171	60
1	A01	Reference_v1_chr1	cir0241	61
1	A01	Reference_v1_chr1	gate2be10	62
1	A01	Reference_v1_chr1	bnl2827	63
1	A01	Reference_v1_chr1	nau0719	64
1	A01	Reference_v1_chr1	nau3533	65
1	A01	Reference_v1_chr1	muss0422	66
1	A01	Reference_v1_chr1	a1794	67
1	A01	Reference_v1_chr1	e3m7_420	68
1	A01	Reference_v1_chr1	coau2o20	69
1	A01	Reference_v1_chr1	bnl4095	70
1	A01	Reference_v1_chr1	e1m6_350	71
1	A01	Reference_v1_chr1	nau0680	72
1	A01	Reference_v1_chr1	par08e03	73

15	D01	Reference_v1_chr15	p02-58	38
15	D01	Reference_v1_chr15	unig26g08	38
15	D01	Reference_v1_chr15	pgh549	38
15	D01	Reference_v1_chr15	par0475	38
15	D01	Reference_v1_chr15	pgh624	39
15	D01	Reference_v1_chr15	unig22d04	40
15	D01	Reference_v1_chr15	par01g03	41
15	D01	Reference_v1_chr15	par0775	42
15	D01	Reference_v1_chr15	par0957	42
15	D01	Reference_v1_chr15	par0906	42
15	D01	Reference_v1_chr15	par0237	43
15	D01	Reference_v1_chr15	pgh700	43
15	D01	Reference_v1_chr15	bnl1454	44
15	D01	Reference_v1_chr15	par0183	45
15	D01	Reference_v1_chr15	pbam291	46
15	D01	Reference_v1_chr15	par0405	46
15	D01	Reference_v1_chr15	a1225	47
15	D01	Reference_v1_chr15	par0607	47
15	D01	Reference_v1_chr15	gate1cd07	48
15	D01	Reference_v1_chr15	gate4ah11	48
15	D01	Reference_v1_chr15	bnl2920	49
15	D01	Reference_v1_chr15	cir0234	50
15	D01	Reference_v1_chr15	pgh317	51
15	D01	Reference_v1_chr15	cir0307	52
15	D01	Reference_v1_chr15	e1m1_174	53
15	D01	Reference_v1_chr15	cir0143	53
15	D01	Reference_v1_chr15	tmb0323	54
15	D01	Reference_v1_chr15	pgh248	55
15	D01	Reference_v1_chr15	nau3576	56
15	D01	Reference_v1_chr15	e4m4_335	57
15	D01	Reference_v1_chr15	gh.myb9	58
15	D01	Reference_v1_chr15	jespr0270	59
15	D01	Reference_v1_chr15	tmb0201	60
15	D01	Reference_v1_chr15	nau3882	61
15	D01	Reference_v1_chr15	y1295	62
15	D01	Reference_v1_chr15	muss0440	63
15	D01	Reference_v1_chr15	jespr0205	64
15	D01	Reference_v1_chr15	dpl0615	65
15	D01	Reference_v1_chr15	nau3736	66
15	D01	Reference_v1_chr15	cir0398	67
15	D01	Reference_v1_chr15	nau3433	68
15	D01	Reference_v1_chr15	nau4081	69
15	D01	Reference_v1_chr15	coau2c11	70
15	D01	Reference_v1_chr15	a1686	70
15	D01	Reference_v1_chr15	p05-32	70
15	D01	Reference_v1_chr15	par0088	70
15	D01	Reference_v1_chr15	jespr0180	71

1	A01	Reference_v1_chr1	pgh273	74
1	A01	Reference_v1_chr1	par0132	75
1	A01	Reference_v1_chr1	cir0018	76
1	A01	Reference_v1_chr1	gate1cb06	77
1	A01	Reference_v1_chr1	bnl3778	78
1	A01	Reference_v1_chr1	pxp4-63	79
1	A01	Reference_v1_chr1	bnl3090	80
1	A01	Reference_v1_chr1	a1549	80
1	A01	Reference_v1_chr1	pgh377	80
1	A01	Reference_v1_chr1	pgh618	80
1	A01	Reference_v1_chr1	cms0009	80
1	A01	Reference_v1_chr1	nau5085	81
1	A01	Reference_v1_chr1	nau4891	81
1	A01	Reference_v1_chr1	nau3022	82
1	A01	Reference_v1_chr1	nau3385	83
1	A01	Reference_v1_chr1	nau3135	84
1	A01	Reference_v1_chr1	jespr0056	85
1	A01	Reference_v1_chr1	nau0591	86
1	A01	Reference_v1_chr1	bnl2702	87
1	A01	Reference_v1_chr1	t4e3a	88
1	A01	Reference_v1_chr1	tmb0062	89
1	A01	Reference_v1_chr1	dpl0513	90
1	A01	Reference_v1_chr1	dpl0094	91
1	A01	Reference_v1_chr1	nau2182	92
1	A01	Reference_v1_chr1	t2e4g	93
1	A01	Reference_v1_chr1	cg09	94
1	A01	Reference_v1_chr1	cir0049	95
1	A01	Reference_v1_chr1	a1591	96
1	A01	Reference_v1_chr1	coau2m13	97
1	A01	Reference_v1_chr1	bnl3085	98
1	A01	Reference_v1_chr1	bnl1350	99
1	A01	Reference_v1_chr1	aagctc5	100
1	A01	Reference_v1_chr1	unig25b08	101
1	A01	Reference_v1_chr1	unig22d06	102
1	A01	Reference_v1_chr1	coau3d18	102
1	A01	Reference_v1_chr1	par0883	103
1	A01	Reference_v1_chr1	par08c07	104
1	A01	Reference_v1_chr1	par09b03	104
1	A01	Reference_v1_chr1	pgh431	105
1	A01	Reference_v1_chr1	par0377	106
1	A01	Reference_v1_chr1	cir0089	107
1	A01	Reference_v1_chr1	acactg7	108
1	A01	Reference_v1_chr1	pgh650	109
1	A01	Reference_v1_chr1	gate1bb12	110
1	A01	Reference_v1_chr1	e4m6d	111
1	A01	Reference_v1_chr1	c209	112
1	A01	Reference_v1_chr1	a1204	113

15	D01	Reference_v1_chr15	jespr0102	72
15	D01	Reference_v1_chr15	musb0664	73
15	D01	Reference_v1_chr15	bnl2700	74
15	D01	Reference_v1_chr15	mghes0059	75
15	D01	Reference_v1_chr15	e4m7_540	76
15	D01	Reference_v1_chr15	tmb0301	77
15	D01	Reference_v1_chr15	e2m8_275	78
15	D01	Reference_v1_chr15	jespr0298	79
15	D01	Reference_v1_chr15	p01-03	80
15	D01	Reference_v1_chr15	p05-39	80
15	D01	Reference_v1_chr15	pbam286	81
15	D01	Reference_v1_chr15	a1109	81
15	D01	Reference_v1_chr15	cg10	81
15	D01	Reference_v1_chr15	cir0270	81
15	D01	Reference_v1_chr15	e6m4_392	81
15	D01	Reference_v1_chr15	a1588	81
15	D01	Reference_v1_chr15	a1583	81
15	D01	Reference_v1_chr15	bnl3902	81
15	D01	Reference_v1_chr15	a1738	81
15	D01	Reference_v1_chr15	cir0015	81
15	D01	Reference_v1_chr15	e6m5_113	81
15	D01	Reference_v1_chr15	nau3067	82
15	D01	Reference_v1_chr15	bnl2564	83
15	D01	Reference_v1_chr15	tmb0303	84
15	D01	Reference_v1_chr15	dpl0264	85
15	D01	Reference_v1_chr15	mghes0010	86
15	D01	Reference_v1_chr15	jespr0240	87
15	D01	Reference_v1_chr15	bnl1418	88
15	D01	Reference_v1_chr15	muss0422	89
15	D01	Reference_v1_chr15	mucs0084	89
15	D01	Reference_v1_chr15	musb1267	90
15	D01	Reference_v1_chr15	cir0411	91
15	D01	Reference_v1_chr15	muss0523	92
15	D01	Reference_v1_chr15	tmb1660	93
15	D01	Reference_v1_chr15	coau2e14	94
15	D01	Reference_v1_chr15	nau2985	95
15	D01	Reference_v1_chr15	tmb0375	96
15	D01	Reference_v1_chr15	e1m6_140	97
15	D01	Reference_v1_chr15	e5m8_152	97
15	D01	Reference_v1_chr15	gate3bc09	98
15	D01	Reference_v1_chr15	bnl0162	99
15	D01	Reference_v1_chr15	muss0012	100
15	D01	Reference_v1_chr15	nau2165	100
15	D01	Reference_v1_chr15	nau3680	101
15	D01	Reference_v1_chr15	dpl0300	102
15	D01	Reference_v1_chr15	tmb0180	103
15	D01	Reference_v1_chr15	e6m5c	104

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1	A01	Reference_v1_chr1	gate1dg06	115
1	A01	Reference_v1_chr1	p01-03	116
1	A01	Reference_v1_chr1	tmb0011	117
1	A01	Reference_v1_chr1	e5m6_77	118
1	A01	Reference_v1_chr1	nau1483	119
1	A01	Reference_v1_chr1	cir0055	120
1	A01	Reference_v1_chr1	par0650	121
1	A01	Reference_v1_chr1	a1643	122
1	A01	Reference_v1_chr1	coau1e09	122
1	A01	Reference_v1_chr1	gafb26n16	122
1	A01	Reference_v1_chr1	a1553	123
1	A01	Reference_v1_chr1	bnl1693	124
1	A01	Reference_v1_chr1	a1738	125
1	A01	Reference_v1_chr1	cg08	126
1	A01	Reference_v1_chr1	gate2ac04	127
1	A01	Reference_v1_chr1	e2m7_500	128
1	A01	Reference_v1_chr1	par0274	129
1	A01	Reference_v1_chr1	tmb2544	130
1	A01	Reference_v1_chr1	gafb26n12	131
1	A01	Reference_v1_chr1	gate3ce05	132
1	A01	Reference_v1_chr1	unig24h12	132
1	A01	Reference_v1_chr1	bnl3888	133
1	A01	Reference_v1_chr1	par0099	134
1	A01	Reference_v1_chr1	t41e8b	135
1	A01	Reference_v1_chr1	par0052	136
1	A01	Reference_v1_chr1	tmb0283	137
1	A01	Reference_v1_chr1	e3m4_420	138
1	A01	Reference_v1_chr1	coau2c11	139
1	A01	Reference_v1_chr1	par0450	139
1	A01	Reference_v1_chr1	e4m4_236	140
1	A01	Reference_v1_chr1	bnl1667	141
1	A01	Reference_v1_chr1	tmb0119	142
1	A01	Reference_v1_chr1	jespr0243	143
1	A01	Reference_v1_chr1	actctg3	144
1	A01	Reference_v1_chr1	par0306	145
1	A01	Reference_v1_chr1	tmb1224	146
1	A01	Reference_v1_chr1	nau0708	147
1	A01	Reference_v1_chr1	gate3cc07	148
1	A01	Reference_v1_chr1	accctg1	149
1	A01	Reference_v1_chr1	bnl1355	150
1	A01	Reference_v1_chr1	nau5107	150
1	A01	Reference_v1_chr1	e1m6_207	151
1	A01	Reference_v1_chr1	nau4073	152
1	A01	Reference_v1_chr1	nau1040	153
1	A01	Reference_v1_chr1	nau5100	154
1	A01	Reference_v1_chr1	nau2798	155

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15	D01	Reference_v1_chr15	nau1521	106
15	D01	Reference_v1_chr15	coau2l06	107
15	D01	Reference_v1_chr15	musb0440	108
15	D01	Reference_v1_chr15	mucs0322	109
15	D01	Reference_v1_chr15	nau3496	110
15	D01	Reference_v1_chr15	bnl2646	111
15	D01	Reference_v1_chr15	nau0338	112
15	D01	Reference_v1_chr15	musb1079	113
15	D01	Reference_v1_chr15	bnl4080	114
15	D01	Reference_v1_chr15	bnl3652	115
15	D01	Reference_v1_chr15	nau3178	116
15	D01	Reference_v1_chr15	nau3188	117
15	D01	Reference_v1_chr15	unig27e09	118
15	D01	Reference_v1_chr15	dpl0322	119
15	D01	Reference_v1_chr15	tmb1633	120
15	D01	Reference_v1_chr15	nau3690	121
15	D01	Reference_v1_chr15	bnl4082	122
15	D01	Reference_v1_chr15	nau5402	123
15	D01	Reference_v1_chr15	gate1bb12	124
15	D01	Reference_v1_chr15	bnl1666	125
15	D01	Reference_v1_chr15	par0011	126
15	D01	Reference_v1_chr15	a1720	126
15	D01	Reference_v1_chr15	pvnc094	126
15	D01	Reference_v1_chr15	musb0325	127
15	D01	Reference_v1_chr15	par09b03	128
15	D01	Reference_v1_chr15	bnl3580	129
15	D01	Reference_v1_chr15	par0099	130
15	D01	Reference_v1_chr15	gate4be06	131
15	D01	Reference_v1_chr15	nau3615	132
15	D01	Reference_v1_chr15	pgh273	133
15	D01	Reference_v1_chr15	bnl3848	134
15	D01	Reference_v1_chr15	musb0309	135
15	D01	Reference_v1_chr15	unig25a07	136
15	D01	Reference_v1_chr15	nau5100	137
15	D01	Reference_v1_chr15	m2e5	138
15	D01	Reference_v1_chr15	par0883	139
15	D01	Reference_v1_chr15	od3od22-295	140
15	D01	Reference_v1_chr15	nau3714	141
15	D01	Reference_v1_chr15	unig28e05	142
15	D01	Reference_v1_chr15	cir0370	143
15	D01	Reference_v1_chr15	bnl3090	144
15	D01	Reference_v1_chr15	pvnc142	144
15	D01	Reference_v1_chr15	nau5085	145
15	D01	Reference_v1_chr15	bnl0300	146
15	D01	Reference_v1_chr15	nau5172	147
15	D01	Reference_v1_chr15	musb1064	148

1	A01	Reference_v1_chr1	nau2789	156
1	A01	Reference_v1_chr1	a1593	157
1	A01	Reference_v1_chr1	gate2dg06	157
1	A01	Reference_v1_chr1	gate1ab12	157
1	A01	Reference_v1_chr1	acgtgc8	158
1	A01	Reference_v1_chr1	actctc2	159
1	A01	Reference_v1_chr1	acaagc3	160
1	A01	Reference_v1_chr1	aggcaa7	161
1	A01	Reference_v1_chr1	aggcaa5	162
1	A01	Reference_v1_chr1	nau2722	163
1	A01	Reference_v1_chr1	actacc2	164
1	A01	Reference_v1_chr1	acgcgt2	165
1	A01	Reference_v1_chr1	acgagc2	166
1	A01	Reference_v1_chr1	aaccac2	167
1	A01	Reference_v1_chr1	acccaa5	168
1	A01	Reference_v1_chr1	aagcag7	169
1	A01	Reference_v1_chr1	aggctc1	170
1	A01	Reference_v1_chr1	aggcag5	171
1	A01	Reference_v1_chr1	coau1m07	172
1	A01	Reference_v1_chr1	a1686	172
1	A01	Reference_v1_chr1	bnl3580	173
1	A01	Reference_v1_chr1	cir0114	173
1	A01	Reference_v1_chr1	bnl2599	174
1	A01	Reference_v1_chr1	nau2419	175
1	A01	Reference_v1_chr1	mghes0037	176
1	A01	Reference_v1_chr1	m1e13a	177
1	A01	Reference_v1_chr1	bnl0846	178
1	A01	Reference_v1_chr1	cir0110	179
1	A01	Reference_v1_chr1	e8m3_186	180
1	A01	Reference_v1_chr1	nau2083	181
1	A01	Reference_v1_chr1	e4m4_278	182
1	A01	Reference_v1_chr1	nau3104	183
1	A01	Reference_v1_chr1	nau4044	184
1	A01	Reference_v1_chr1	nau4045	185
1	A01	Reference_v1_chr1	e5m8_228	186
1	A01	Reference_v1_chr1	nau3911	187
1	A01	Reference_v1_chr1	fg	188
1	A01	Reference_v1_chr1	unig27h12	188
1	A01	Reference_v1_chr1	par0077	188
1	A01	Reference_v1_chr1	nau1067	189
1	A01	Reference_v1_chr1	e8m2_74	190
1	A01	Reference_v1_chr1	g1099	191

15	D01	Reference_v1_chr15	bnl0786	149
15	D01	Reference_v1_chr15	tmb0283	149
15	D01	Reference_v1_chr15	t45e11b	150
15	D01	Reference_v1_chr15	e5m6d	151
15	D01	Reference_v1_chr15	tmb1224	152
15	D01	Reference_v1_chr15	nau4073	153
15	D01	Reference_v1_chr15	tmb0119	154
15	D01	Reference_v1_chr15	me2em2-60	155
15	D01	Reference_v1_chr15	cm0035	156
15	D01	Reference_v1_chr15	jespr0243	156
15	D01	Reference_v1_chr15	muss0128	156
15	D01	Reference_v1_chr15	bnl0830	157
15	D01	Reference_v1_chr15	cir0158	158
15	D01	Reference_v1_chr15	nau3057	159
15	D01	Reference_v1_chr15	nau3056	160
15	D01	Reference_v1_chr15	bnl1667	161
15	D01	Reference_v1_chr15	e6m2_144	162
15	D01	Reference_v1_chr15	bnl1350	162
15	D01	Reference_v1_chr15	nau5235	163
15	D01	Reference_v1_chr15	cir0311	164
15	D01	Reference_v1_chr15	m3e3b	165
15	D01	Reference_v1_chr15	gate1ba10	166
15	D01	Reference_v1_chr15	pgh661	167
15	D01	Reference_v1_chr15	a1340	167
15	D01	Reference_v1_chr15	par0274	168
15	D01	Reference_v1_chr15	nau3337	169
15	D01	Reference_v1_chr15	nau2573	170
15	D01	Reference_v1_chr15	e2m3_255	171
15	D01	Reference_v1_chr15	bnl3085	172
15	D01	Reference_v1_chr15	nau0422	173
15	D01	Reference_v1_chr15	bnl4095	174
15	D01	Reference_v1_chr15	a1593	175
15	D01	Reference_v1_chr15	a1553	176
15	D01	Reference_v1_chr15	p05-31	177
15	D01	Reference_v1_chr15	a1643	178
15	D01	Reference_v1_chr15	pgh468	178
15	D01	Reference_v1_chr15	par0077	178
15	D01	Reference_v1_chr15	e2m7_400	178
15	D01	Reference_v1_chr15	par0959	179
15	D01	Reference_v1_chr15	gate4da07	179
15	D01	Reference_v1_chr15	bnl3345	180
15	D01	Reference_v1_chr15	m16-078	181
15	D01	Reference_v1_chr15	gate1ah09	182
15	D01	Reference_v1_chr15	e8m3_132	183
15	D01	Reference_v1_chr15	t24e6	184
15	D01	Reference_v1_chr15	unig26f09	185
15	D01	Reference_v1_chr15	gate2bg02	185

15	D01	Reference_v1_chr15	par0245	186
15	D01	Reference_v1_chr15	coau2m13	187
15	D01	Reference_v1_chr15	coau1m01	187
15	D01	Reference_v1_chr15	gate1ab12	187
15	D01	Reference_v1_chr15	unig25d08	188
15	D01	Reference_v1_chr15	coau1o13	188
15	D01	Reference_v1_chr15	unig24b11	189
15	D01	Reference_v1_chr15	gate1bg09	189
15	D01	Reference_v1_chr15	m4e3a	190
15	D01	Reference_v1_chr15	gate4bd03	191
15	D01	Reference_v1_chr15	unig22c01	192
15	D01	Reference_v1_chr15	par09d01	193
15	D01	Reference_v1_chr15	unig25b08	194
15	D01	Reference_v1_chr15	par0935	194
15	D01	Reference_v1_chr15	pxp3-42	194
15	D01	Reference_v1_chr15	e4m1_81	195
15	D01	Reference_v1_chr15	cir0105	196
15	D01	Reference_v1_chr15	par08e03	197
15	D01	Reference_v1_chr15	par08c07	197
15	D01	Reference_v1_chr15	nau3543	198
15	D01	Reference_v1_chr15	e1m3_182	199
15	D01	Reference_v1_chr15	nau3347	200
15	D01	Reference_v1_chr15	nau3346	201
15	D01	Reference_v1_chr15	nau1067	202
15	D01	Reference_v1_chr15	coau2e03	203
15	D01	Reference_v1_chr15	cir0110	204
15	D01	Reference_v1_chr15	nau0458	205
15	D01	Reference_v1_chr15	bnl1688	206

Table 4.7 Chromosomes A02 and D02 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
2	A02	Reference_v1_chr2	e4m4_350	1
2	A02	Reference_v1_chr2	bnl3424	2
2	A02	Reference_v1_chr2	nau2896	3
2	A02	Reference_v1_chr2	nau1246	4
2	A02	Reference_v1_chr2	nau3775	5
2	A02	Reference_v1_chr2	nau2277	6
2	A02	Reference_v1_chr2	nau2265	7
2	A02	Reference_v1_chr2	nau3419	8
2	A02	Reference_v1_chr2	nau2858	9
2	A02	Reference_v1_chr2	tmb1580	10
2	A02	Reference_v1_chr2	nau0895	11
2	A02	Reference_v1_chr2	nau5383	12
2	A02	Reference_v1_chr2	par0851	13
2	A02	Reference_v1_chr2	e1m8_345	14
2	A02	Reference_v1_chr2	bnl0663	15
2	A02	Reference_v1_chr2	nau0740	16
2	A02	Reference_v1_chr2	nau3684	17
2	A02	Reference_v1_chr2	jespr0304	18
2	A02	Reference_v1_chr2	e4m3_183	19
2	A02	Reference_v1_chr2	e4m4a	20
2	A02	Reference_v1_chr2	nau5384	21
2	A02	Reference_v1_chr2	par09d10	22
2	A02	Reference_v1_chr2	e6m3_103	23
2	A02	Reference_v1_chr2	cir0376	23
2	A02	Reference_v1_chr2	me2em2-265	24
2	A02	Reference_v1_chr2	e7m5_210	25
2	A02	Reference_v1_chr2	p06-25	26
2	A02	Reference_v1_chr2	pgh248	27
2	A02	Reference_v1_chr2	g1128	27
2	A02	Reference_v1_chr2	par01-54	27
2	A02	Reference_v1_chr2	bnl3523	28
2	A02	Reference_v1_chr2	par0957	29
2	A02	Reference_v1_chr2	nau0854	30
2	A02	Reference_v1_chr2	unig25c09	31
2	A02	Reference_v1_chr2	par0851	32
2	A02	Reference_v1_chr2	par04-11	33
2	A02	Reference_v1_chr2	nau0456	34
2	A02	Reference_v1_chr2	gate4cg06	35
2	A02	Reference_v1_chr2	bnl2635	36
2	A02	Reference_v1_chr2	e6m2_249	37
2	A02	Reference_v1_chr2	e2m4_226	38
2	A02	Reference_v1_chr2	musb0749	39
2	A02	Reference_v1_chr2	coau2g03	40
2	A02	Reference_v1_chr2	nau0437	41

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
14	D02	Reference_v1_chr14	par0582	1
14	D02	Reference_v1_chr14	cshe0263	2
14	D02	Reference_v1_chr14	ests152	3
14	D02	Reference_v1_chr14	t29e8	4
14	D02	Reference_v1_chr14	gate2aa09	5
14	D02	Reference_v1_chr14	mucs0582	6
14	D02	Reference_v1_chr14	gate3bf01	7
14	D02	Reference_v1_chr14	gate1ag12	8
14	D02	Reference_v1_chr14	e7m4c	9
14	D02	Reference_v1_chr14	e8m6b	10
14	D02	Reference_v1_chr14	unig28c03	11
14	D02	Reference_v1_chr14	cir0030	12
14	D02	Reference_v1_chr14	cir0246	13
14	D02	Reference_v1_chr14	nau3903	14
14	D02	Reference_v1_chr14	nau3733	15
14	D02	Reference_v1_chr14	nau0645	16
14	D02	Reference_v1_chr14	nau3209	17
14	D02	Reference_v1_chr14	nau3585	18
14	D02	Reference_v1_chr14	nau5499	19
14	D02	Reference_v1_chr14	nau5467	20
14	D02	Reference_v1_chr14	y1806	21
14	D02	Reference_v1_chr14	nau0561	22
14	D02	Reference_v1_chr14	nau5490	23
14	D02	Reference_v1_chr14	nau4009	24
14	D02	Reference_v1_chr14	nau0734	25
14	D02	Reference_v1_chr14	gate1cb10	26
14	D02	Reference_v1_chr14	par0043	26
14	D02	Reference_v1_chr14	bnl2443	27
14	D02	Reference_v1_chr14	nau1529	28
14	D02	Reference_v1_chr14	nau3885	29
14	D02	Reference_v1_chr14	nau3648	30
14	D02	Reference_v1_chr14	t20e5	31
14	D02	Reference_v1_chr14	nau3189	32
14	D02	Reference_v1_chr14	nau2633	33
14	D02	Reference_v1_chr14	gate3ab10	34
14	D02	Reference_v1_chr14	nau5421	35
14	D02	Reference_v1_chr14	par0129	36
14	D02	Reference_v1_chr14	e1m1_213	37
14	D02	Reference_v1_chr14	y1911	38
14	D02	Reference_v1_chr14	g1012	39
14	D02	Reference_v1_chr14	mucs0105	40
14	D02	Reference_v1_chr14	gate3bf06	41
14	D02	Reference_v1_chr14	gate4bd11	41
14	D02	Reference_v1_chr14	par0932	41

2	A02	Reference_v1_chr2	e3m5_103	42
2	A02	Reference_v1_chr2	bnl1410	43
2	A02	Reference_v1_chr2	t3e6	44
2	A02	Reference_v1_chr2	musb0958	45
2	A02	Reference_v1_chr2	od3ga19-180	46
2	A02	Reference_v1_chr2	e3m3_500	47
2	A02	Reference_v1_chr2	bnl2651	48
2	A02	Reference_v1_chr2	e3m7_78	49
2	A02	Reference_v1_chr2	par0316	50
2	A02	Reference_v1_chr2	a1436	51
2	A02	Reference_v1_chr2	e7m6_214	52
2	A02	Reference_v1_chr2	musb1178	53
2	A02	Reference_v1_chr2	unig27g05	54
2	A02	Reference_v1_chr2	musb0888	55
2	A02	Reference_v1_chr2	e8m1_420	56
2	A02	Reference_v1_chr2	e1m6_378	56
2	A02	Reference_v1_chr2	e2m5_129	57
2	A02	Reference_v1_chr2	gate1cb05	58
2	A02	Reference_v1_chr2	coau4h19	58
2	A02	Reference_v1_chr2	e2m6_420	59
2	A02	Reference_v1_chr2	e5m8_460	59
2	A02	Reference_v1_chr2	e3m2_208	59
2	A02	Reference_v1_chr2	e2m6_500	59
2	A02	Reference_v1_chr2	dc1sa21-380	60
2	A02	Reference_v1_chr2	bnl1145	61
2	A02	Reference_v1_chr2	e3m8_470	62
2	A02	Reference_v1_chr2	e2m8_74	62
2	A02	Reference_v1_chr2	e7m1_138	62
2	A02	Reference_v1_chr2	gate3ba04	63
2	A02	Reference_v1_chr2	muss0073	64
2	A02	Reference_v1_chr2	m7e12b	65
2	A02	Reference_v1_chr2	coau1o15	66
2	A02	Reference_v1_chr2	t8e15a	67
2	A02	Reference_v1_chr2	t34e2a	68
2	A02	Reference_v1_chr2	bnl2706	69
2	A02	Reference_v1_chr2	jespr0101	70
2	A02	Reference_v1_chr2	musb0194	71
2	A02	Reference_v1_chr2	e2m6_224	72
2	A02	Reference_v1_chr2	dpl0674	73
2	A02	Reference_v1_chr2	e3m3c	74
2	A02	Reference_v1_chr2	unig27c04	75
2	A02	Reference_v1_chr2	gate4bg11	76
2	A02	Reference_v1_chr2	gate1cb08	76
2	A02	Reference_v1_chr2	gate4ae09	76
2	A02	Reference_v1_chr2	unig24g02	77
2	A02	Reference_v1_chr2	p02-35	78
2	A02	Reference_v1_chr2	par0318	79

14	D02	Reference_v1_chr14	cir0381	41
14	D02	Reference_v1_chr14	e4m2_500	41
14	D02	Reference_v1_chr14	par0723	41
14	D02	Reference_v1_chr14	a1580	42
14	D02	Reference_v1_chr14	coau4n12	42
14	D02	Reference_v1_chr14	par0451	43
14	D02	Reference_v1_chr14	p05-06	43
14	D02	Reference_v1_chr14	c102	43
14	D02	Reference_v1_chr14	at03	43
14	D02	Reference_v1_chr14	gate3cc11	44
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2	A02	Reference_v1_chr2	jespr0250	128
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14	D02	Reference_v1_chr14	gate1cd07	127
14	D02	Reference_v1_chr14	g34a3-3b	127
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14	D02	Reference_v1_chr14	gate4dc02	133
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14	D02	Reference_v1_chr14	aagcat2	143

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2	A02	Reference_v1_chr2	bnl1434	167
2	A02	Reference_v1_chr2	par0723	167
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2	A02	Reference_v1_chr2	coau2i05	172
2	A02	Reference_v1_chr2	unig23g06	173
2	A02	Reference_v1_chr2	cir0381	174
2	A02	Reference_v1_chr2	p05-32	175
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2	A02	Reference_v1_chr2	e4m2c	184

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14	D02	Reference_v1_chr14	g1044	166
14	D02	Reference_v1_chr14	a1727	166
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14	D02	Reference_v1_chr14	p01-45	169
14	D02	Reference_v1_chr14	e3m2_76	170
14	D02	Reference_v1_chr14	gate4da02	171
14	D02	Reference_v1_chr14	g1147	172
14	D02	Reference_v1_chr14	cir0239	173
14	D02	Reference_v1_chr14	bnl3533	174
14	D02	Reference_v1_chr14	m7e2b	175
14	D02	Reference_v1_chr14	ests175	176
14	D02	Reference_v1_chr14	par0955	177
14	D02	Reference_v1_chr14	pgh699	177
14	D02	Reference_v1_chr14	a1167	177
14	D02	Reference_v1_chr14	bnl3034	177
14	D02	Reference_v1_chr14	w07	177
14	D02	Reference_v1_chr14	par0325	178
14	D02	Reference_v1_chr14	pvnc201	179
14	D02	Reference_v1_chr14	par0815	179
14	D02	Reference_v1_chr14	gate2bb02	179

14	D02	Reference_v1_chr14	par0307	179
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14	D02	Reference_v1_chr14	nau5465	205
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14	D02	Reference_v1_chr14	cshe0210	208
14	D02	Reference_v1_chr14	nau2190	209

14	D02	Reference_v1_chr14	nau3820	210
14	D02	Reference_v1_chr14	nau3573	211
14	D02	Reference_v1_chr14	nau1070	212
14	D02	Reference_v1_chr14	nau2960	213
14	D02	Reference_v1_chr14	cir0097	214
14	D02	Reference_v1_chr14	nau3464	215

Table 4.8 Chromosomes A03 and D03 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
3	A03	Reference_v1_chr3	gate4dg02	1
3	A03	Reference_v1_chr3	par0476	1
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3	A03	Reference_v1_chr3	unig25g07	3
3	A03	Reference_v1_chr3	par01-56	3
3	A03	Reference_v1_chr3	gate1af02	3
3	A03	Reference_v1_chr3	nau3083	4
3	A03	Reference_v1_chr3	unig24b07	5
3	A03	Reference_v1_chr3	gate2aa08	5
3	A03	Reference_v1_chr3	nau2836	6
3	A03	Reference_v1_chr3	nau3172	7
3	A03	Reference_v1_chr3	a1748	8
3	A03	Reference_v1_chr3	nau3016	9
3	A03	Reference_v1_chr3	nau5233	10
3	A03	Reference_v1_chr3	nau1167	11
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3	A03	Reference_v1_chr3	gate4ae05	153
3	A03	Reference_v1_chr3	nau0796	154
3	A03	Reference_v1_chr3	coau1l18	155
3	A03	Reference_v1_chr3	nau1070	156
3	A03	Reference_v1_chr3	bnl4017	157
3	A03	Reference_v1_chr3	muss0162	157
3	A03	Reference_v1_chr3	bnl1080	158
3	A03	Reference_v1_chr3	dpl0605	159
3	A03	Reference_v1_chr3	me1em5-155	160
3	A03	Reference_v1_chr3	nau1071	161
3	A03	Reference_v1_chr3	gate3be09	162
3	A03	Reference_v1_chr3	g1126	163
3	A03	Reference_v1_chr3	gate4ab05	164
3	A03	Reference_v1_chr3	par0325	165
3	A03	Reference_v1_chr3	a1418	166
3	A03	Reference_v1_chr3	me5em3-250	167
3	A03	Reference_v1_chr3	dpl0631	168
3	A03	Reference_v1_chr3	cir0332	169
3	A03	Reference_v1_chr3	g1164	169

17	D03	Reference_v1_chr17	nau2908	138
17	D03	Reference_v1_chr17	par01a04	139
17	D03	Reference_v1_chr17	par0396	139
17	D03	Reference_v1_chr17	gate1bc01	139
17	D03	Reference_v1_chr17	par0076	139
17	D03	Reference_v1_chr17	cir0251	140
17	D03	Reference_v1_chr17	nau3349	141
17	D03	Reference_v1_chr17	nau2761	142
17	D03	Reference_v1_chr17	nau1028	143
17	D03	Reference_v1_chr17	nau5386	144
17	D03	Reference_v1_chr17	nau4035	145
17	D03	Reference_v1_chr17	t58e1a	146
17	D03	Reference_v1_chr17	a1258	147
17	D03	Reference_v1_chr17	nau3948	148
17	D03	Reference_v1_chr17	t9e16b	149
17	D03	Reference_v1_chr17	nau0354	150
17	D03	Reference_v1_chr17	nau3257	151
17	D03	Reference_v1_chr17	t2e4b	152
17	D03	Reference_v1_chr17	bnl2706	153
17	D03	Reference_v1_chr17	a1436	154
17	D03	Reference_v1_chr17	e7m1_252	155
17	D03	Reference_v1_chr17	tmb1268	156
17	D03	Reference_v1_chr17	cir0261	157
17	D03	Reference_v1_chr17	nau3292	158
17	D03	Reference_v1_chr17	bnl0834	159
17	D03	Reference_v1_chr17	par0316	160
17	D03	Reference_v1_chr17	nau2859	161
17	D03	Reference_v1_chr17	cshe0059	162
17	D03	Reference_v1_chr17	mucs0537	163
17	D03	Reference_v1_chr17	nau5111	164
17	D03	Reference_v1_chr17	nau2898	165
17	D03	Reference_v1_chr17	m5e3b	166
17	D03	Reference_v1_chr17	gate2cb12	167
17	D03	Reference_v1_chr17	gate3ag04	167
17	D03	Reference_v1_chr17	cir0180	168
17	D03	Reference_v1_chr17	nau0805	169
17	D03	Reference_v1_chr17	bnl3424	170

3	A03	Reference_v1_chr3	gate2cb02	170
3	A03	Reference_v1_chr3	me1ga38-170	171
3	A03	Reference_v1_chr3	cir0263	172
3	A03	Reference_v1_chr3	cir0212	172
3	A03	Reference_v1_chr3	nau0998	173
3	A03	Reference_v1_chr3	pxp3-89	174
3	A03	Reference_v1_chr3	pvnc163	175
3	A03	Reference_v1_chr3	par0815	175
3	A03	Reference_v1_chr3	at18	175
3	A03	Reference_v1_chr3	gate3bf12	176
3	A03	Reference_v1_chr3	gate3bg09	176
3	A03	Reference_v1_chr3	par0764	177
3	A03	Reference_v1_chr3	unig27e01	177
3	A03	Reference_v1_chr3	mghes0066	178
3	A03	Reference_v1_chr3	par0985	179
3	A03	Reference_v1_chr3	coau1m05	180
3	A03	Reference_v1_chr3	g1129	180
3	A03	Reference_v1_chr3	pxp2-60	180
3	A03	Reference_v1_chr3	bnl0891	181
3	A03	Reference_v1_chr3	nau0483	182
3	A03	Reference_v1_chr3	bnl3443	183
3	A03	Reference_v1_chr3	bnl3259	184
3	A03	Reference_v1_chr3	e7m1_172	185
3	A03	Reference_v1_chr3	cir0084	186
3	A03	Reference_v1_chr3	jespr0231	187
3	A03	Reference_v1_chr3	cir0228	188
3	A03	Reference_v1_chr3	cir0133	189
3	A03	Reference_v1_chr3	cshe0116	190
3	A03	Reference_v1_chr3	nau2161	191
3	A03	Reference_v1_chr3	tmb0836	192
3	A03	Reference_v1_chr3	jespr0107	193
3	A03	Reference_v1_chr3	y1026	194
3	A03	Reference_v1_chr3	cir0202	195
3	A03	Reference_v1_chr3	nau0862	196
3	A03	Reference_v1_chr3	nau1081	197
3	A03	Reference_v1_chr3	nau5289	198
3	A03	Reference_v1_chr3	nau0604	199
3	A03	Reference_v1_chr3	gate1bf05	200

Table 4.9 Chromosomes A04 and D04 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
4	A04	Reference_v1_chr4	musb1112	1
4	A04	Reference_v1_chr4	gate4ac11	2
4	A04	Reference_v1_chr4	hau0101	3
4	A04	Reference_v1_chr4	e2m5_74	4
4	A04	Reference_v1_chr4	gate1dg06	5
4	A04	Reference_v1_chr4	unig24c06	6
4	A04	Reference_v1_chr4	dpl0451	7
4	A04	Reference_v1_chr4	hau0036	8
4	A04	Reference_v1_chr4	hau0086	9
4	A04	Reference_v1_chr4	nau1151	10
4	A04	Reference_v1_chr4	w15	11
4	A04	Reference_v1_chr4	par09a08	12
4	A04	Reference_v1_chr4	cir0218	13
4	A04	Reference_v1_chr4	dpl0494	14
4	A04	Reference_v1_chr4	nau3386	15
4	A04	Reference_v1_chr4	nau2235	16
4	A04	Reference_v1_chr4	tmb2483	17
4	A04	Reference_v1_chr4	nau3777	18
4	A04	Reference_v1_chr4	nau5236	19
4	A04	Reference_v1_chr4	nau3791	20
4	A04	Reference_v1_chr4	jespr0223	21
4	A04	Reference_v1_chr4	m6e4b	22
4	A04	Reference_v1_chr4	cir0381	23
4	A04	Reference_v1_chr4	nau3009	24
4	A04	Reference_v1_chr4	bnl2572	25
4	A04	Reference_v1_chr4	unig28d06	25
4	A04	Reference_v1_chr4	cir0122	25
4	A04	Reference_v1_chr4	unig23b03	26
4	A04	Reference_v1_chr4	par0903	27
4	A04	Reference_v1_chr4	pxp4-58	27
4	A04	Reference_v1_chr4	par0380	27
4	A04	Reference_v1_chr4	pgh286	28
4	A04	Reference_v1_chr4	gate3dg11	29
4	A04	Reference_v1_chr4	nau2477	30
4	A04	Reference_v1_chr4	mucs0101	31
4	A04	Reference_v1_chr4	g1045	32
4	A04	Reference_v1_chr4	par0138	33
4	A04	Reference_v1_chr4	pgh374	33
4	A04	Reference_v1_chr4	nau3093	34
4	A04	Reference_v1_chr4	gate1ag03	35
4	A04	Reference_v1_chr4	gate2bf04	36
4	A04	Reference_v1_chr4	g1058	37
4	A04	Reference_v1_chr4	t60e4b	38
4	A04	Reference_v1_chr4	e8m5_350	39

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
22	D04	Reference_v1_chr22	gate1cd11	1
22	D04	Reference_v1_chr22	cir0122	2
22	D04	Reference_v1_chr22	par0380	3
22	D04	Reference_v1_chr22	nau0476	4
22	D04	Reference_v1_chr22	nau3437	5
22	D04	Reference_v1_chr22	nau5392	6
22	D04	Reference_v1_chr22	musb0876	7
22	D04	Reference_v1_chr22	nau3392	8
22	D04	Reference_v1_chr22	nau3791	9
22	D04	Reference_v1_chr22	bnl4030	10
22	D04	Reference_v1_chr22	nau2120	11
22	D04	Reference_v1_chr22	em1od12-130	12
22	D04	Reference_v1_chr22	nau0623	13
22	D04	Reference_v1_chr22	gate1dg02	14
22	D04	Reference_v1_chr22	nau2291	15
22	D04	Reference_v1_chr22	nau2162	16
22	D04	Reference_v1_chr22	dpl0722	17
22	D04	Reference_v1_chr22	hau0066	18
22	D04	Reference_v1_chr22	jespr0231	19
22	D04	Reference_v1_chr22	bnl3324	20
22	D04	Reference_v1_chr22	unig26f05	21
22	D04	Reference_v1_chr22	bnl4049	21
22	D04	Reference_v1_chr22	g1058	21
22	D04	Reference_v1_chr22	unig22c01	21
22	D04	Reference_v1_chr22	cir0183	22
22	D04	Reference_v1_chr22	cir0036	22
22	D04	Reference_v1_chr22	e6m7_167	22
22	D04	Reference_v1_chr22	bnl0358	22
22	D04	Reference_v1_chr22	par0138	23
22	D04	Reference_v1_chr22	gate3dg11	23
22	D04	Reference_v1_chr22	gate4bd10	24
22	D04	Reference_v1_chr22	e8m1_240	25
22	D04	Reference_v1_chr22	em1od32-130	26
22	D04	Reference_v1_chr22	unig06d11	27
22	D04	Reference_v1_chr22	nau4058	28
22	D04	Reference_v1_chr22	gate1aa05	29
22	D04	Reference_v1_chr22	par09a08	30
22	D04	Reference_v1_chr22	nau2026	31
22	D04	Reference_v1_chr22	par01-06	32
22	D04	Reference_v1_chr22	nau2363	33
22	D04	Reference_v1_chr22	jespr0220	34
22	D04	Reference_v1_chr22	par07f11	35
22	D04	Reference_v1_chr22	pgh286	36
22	D04	Reference_v1_chr22	nau5508	37

4	A04	Reference_v1_chr4	unig06b07	40
4	A04	Reference_v1_chr4	bnl4049	41
4	A04	Reference_v1_chr4	gate3de01	42
4	A04	Reference_v1_chr4	bnl3988	43
4	A04	Reference_v1_chr4	em1od30-55	44
4	A04	Reference_v1_chr4	nau2654	45
4	A04	Reference_v1_chr4	nau2363	46
4	A04	Reference_v1_chr4	cir0048	47
4	A04	Reference_v1_chr4	dpl0667	48
4	A04	Reference_v1_chr4	gate1bb01	49
4	A04	Reference_v1_chr4	t60e4d	50
4	A04	Reference_v1_chr4	gate3ba08	51
4	A04	Reference_v1_chr4	bnl3433	51
4	A04	Reference_v1_chr4	gate1ba05	51
4	A04	Reference_v1_chr4	gate1ca01	51
4	A04	Reference_v1_chr4	par0230	52
4	A04	Reference_v1_chr4	e2m6_121	53
4	A04	Reference_v1_chr4	gate3be09	54
4	A04	Reference_v1_chr4	gate3be01	55
4	A04	Reference_v1_chr4	gate3de03	56
4	A04	Reference_v1_chr4	nau0762	57
4	A04	Reference_v1_chr4	gate2cc07	58
4	A04	Reference_v1_chr4	gate4cg05	58
4	A04	Reference_v1_chr4	unig22d08	58
4	A04	Reference_v1_chr4	tmb0446	59
4	A04	Reference_v1_chr4	g1033	60
4	A04	Reference_v1_chr4	par0219	61
4	A04	Reference_v1_chr4	par0986	62
4	A04	Reference_v1_chr4	par0043	62
4	A04	Reference_v1_chr4	par0197	62
4	A04	Reference_v1_chr4	gate3ce04	63
4	A04	Reference_v1_chr4	m4e15a	64
4	A04	Reference_v1_chr4	par0450	65
4	A04	Reference_v1_chr4	gate4ca09	65
4	A04	Reference_v1_chr4	par0412	66
4	A04	Reference_v1_chr4	coau2i05	67
4	A04	Reference_v1_chr4	pvnc058	68
4	A04	Reference_v1_chr4	gate4ae08	68
4	A04	Reference_v1_chr4	pgh442	69
4	A04	Reference_v1_chr4	gafb14k15	70
4	A04	Reference_v1_chr4	par0049	71
4	A04	Reference_v1_chr4	a1172	71
4	A04	Reference_v1_chr4	bnl0530	71
4	A04	Reference_v1_chr4	pgh857	71
4	A04	Reference_v1_chr4	tmb0809	72
4	A04	Reference_v1_chr4	m4e10d	73
4	A04	Reference_v1_chr4	t60e4c	74

22	D04	Reference_v1_chr22	gate2aa09	38
22	D04	Reference_v1_chr22	nau0569	39
22	D04	Reference_v1_chr22	pgh272	40
22	D04	Reference_v1_chr22	par10g09	40
22	D04	Reference_v1_chr22	e6m1a	41
22	D04	Reference_v1_chr22	nau5294	42
22	D04	Reference_v1_chr22	nau5591	43
22	D04	Reference_v1_chr22	nau3781	44
22	D04	Reference_v1_chr22	m7e7e	45
22	D04	Reference_v1_chr22	e3m2a	46
22	D04	Reference_v1_chr22	t4e2a	47
22	D04	Reference_v1_chr22	nau0538	48
22	D04	Reference_v1_chr22	mucs0558	49
22	D04	Reference_v1_chr22	bnl3849	50
22	D04	Reference_v1_chr22	bnl2771	51
22	D04	Reference_v1_chr22	e1m1_171	52
22	D04	Reference_v1_chr22	par0949	53
22	D04	Reference_v1_chr22	gate1ch01	54
22	D04	Reference_v1_chr22	gate2bg01	54
22	D04	Reference_v1_chr22	gate4ba04	54
22	D04	Reference_v1_chr22	cir0218	55
22	D04	Reference_v1_chr22	nau5457	56
22	D04	Reference_v1_chr22	jespr0129	57
22	D04	Reference_v1_chr22	cir0253	58
22	D04	Reference_v1_chr22	e6m8_88	59
22	D04	Reference_v1_chr22	musb1112	60
22	D04	Reference_v1_chr22	bnl0530	61
22	D04	Reference_v1_chr22	nau3546	62
22	D04	Reference_v1_chr22	t27e7	63
22	D04	Reference_v1_chr22	m1e5b	64
22	D04	Reference_v1_chr22	nau2235	65
22	D04	Reference_v1_chr22	bnl3873	66
22	D04	Reference_v1_chr22	gate3bb11	67
22	D04	Reference_v1_chr22	tmb1648	68
22	D04	Reference_v1_chr22	nau2477	69
22	D04	Reference_v1_chr22	bnl0448	70
22	D04	Reference_v1_chr22	bnl3955	71
22	D04	Reference_v1_chr22	gate1ba05	71
22	D04	Reference_v1_chr22	m8e6	72
22	D04	Reference_v1_chr22	cir0048	73
22	D04	Reference_v1_chr22	pvnc146	74
22	D04	Reference_v1_chr22	bnl1045	74
22	D04	Reference_v1_chr22	par04-48	74
22	D04	Reference_v1_chr22	gate4ca01	74
22	D04	Reference_v1_chr22	nau2329	75
22	D04	Reference_v1_chr22	nau3539	76
22	D04	Reference_v1_chr22	dc15a18-205	77

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4	A04	Reference_v1_chr4	m4e15e	76
4	A04	Reference_v1_chr4	t14e15d	77
4	A04	Reference_v1_chr4	cshe0080	78
4	A04	Reference_v1_chr4	t20e7c	79
4	A04	Reference_v1_chr4	coau4e22	80
4	A04	Reference_v1_chr4	par04-48	80
4	A04	Reference_v1_chr4	t2e3c	81
4	A04	Reference_v1_chr4	nau1158	82
4	A04	Reference_v1_chr4	e3m8_185	83
4	A04	Reference_v1_chr4	m7e9-320	84
4	A04	Reference_v1_chr4	nau3205	85
4	A04	Reference_v1_chr4	cg03	86
4	A04	Reference_v1_chr4	e6m8_102	86
4	A04	Reference_v1_chr4	e1m8_246	86
4	A04	Reference_v1_chr4	e3m7_290	86
4	A04	Reference_v1_chr4	cir0291	86
4	A04	Reference_v1_chr4	bnl3835	86
4	A04	Reference_v1_chr4	e4m5_216	86
4	A04	Reference_v1_chr4	e8m1_124	86
4	A04	Reference_v1_chr4	e3m6_95	86
4	A04	Reference_v1_chr4	e1m3_300	86
4	A04	Reference_v1_chr4	e4m2_430	86
4	A04	Reference_v1_chr4	e1m6_150	86
4	A04	Reference_v1_chr4	e5m6_140	86
4	A04	Reference_v1_chr4	m7e9-360	87
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4	A04	Reference_v1_chr4	e2m1_98	89
4	A04	Reference_v1_chr4	e2m1_129	90
4	A04	Reference_v1_chr4	m16-125	91
4	A04	Reference_v1_chr4	coau1m07	91
4	A04	Reference_v1_chr4	a1543	91
4	A04	Reference_v1_chr4	gate2bf01	91
4	A04	Reference_v1_chr4	par0334	91
4	A04	Reference_v1_chr4	unig06g05	91
4	A04	Reference_v1_chr4	unig25d03	92
4	A04	Reference_v1_chr4	cg24	93
4	A04	Reference_v1_chr4	par0966	94
4	A04	Reference_v1_chr4	par10c12	95
4	A04	Reference_v1_chr4	gate4dd06	95
4	A04	Reference_v1_chr4	par0926	96
4	A04	Reference_v1_chr4	par08a12	97
4	A04	Reference_v1_chr4	unig25d11	98
4	A04	Reference_v1_chr4	gate1dc01	99
4	A04	Reference_v1_chr4	unig27b06	99
4	A04	Reference_v1_chr4	unig28h09	99

22	D04	Reference_v1_chr22	par0711	78
22	D04	Reference_v1_chr22	gate4ad10	78
22	D04	Reference_v1_chr22	jespr0230	78
22	D04	Reference_v1_chr22	cir0224	79
22	D04	Reference_v1_chr22	bnl3994	80
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22	D04	Reference_v1_chr22	bnl1061	83
22	D04	Reference_v1_chr22	bnl1047	83
22	D04	Reference_v1_chr22	gate3de03	83
22	D04	Reference_v1_chr22	musb1050	84
22	D04	Reference_v1_chr22	dpl0489	85
22	D04	Reference_v1_chr22	cg01	86
22	D04	Reference_v1_chr22	e3m6_291	86
22	D04	Reference_v1_chr22	cg18	86
22	D04	Reference_v1_chr22	e4m5_75	86
22	D04	Reference_v1_chr22	e6m8_162	86
22	D04	Reference_v1_chr22	nau3557	87
22	D04	Reference_v1_chr22	jespr0221	88
22	D04	Reference_v1_chr22	y12911	89
22	D04	Reference_v1_chr22	nau3758	90
22	D04	Reference_v1_chr22	bnl4092	91
22	D04	Reference_v1_chr22	jespr0065	92
22	D04	Reference_v1_chr22	a1184	93
22	D04	Reference_v1_chr22	gate2cc07	94
22	D04	Reference_v1_chr22	nau3323	95
22	D04	Reference_v1_chr22	gate4ca09	96
22	D04	Reference_v1_chr22	nau2945	97
22	D04	Reference_v1_chr22	li1	98
22	D04	Reference_v1_chr22	coau1j04	98
22	D04	Reference_v1_chr22	t8e9b	99
22	D04	Reference_v1_chr22	t41e8a	99
22	D04	Reference_v1_chr22	nau3633	100
22	D04	Reference_v1_chr22	tmb1919	101
22	D04	Reference_v1_chr22	nau0667	102
22	D04	Reference_v1_chr22	e2m6_192	103
22	D04	Reference_v1_chr22	bnl1673	103
22	D04	Reference_v1_chr22	a1619	103
22	D04	Reference_v1_chr22	par0078	103
22	D04	Reference_v1_chr22	nau0684	104
22	D04	Reference_v1_chr22	nau0576	104
22	D04	Reference_v1_chr22	par08h07	105
22	D04	Reference_v1_chr22	gate4ae10	105

4	A04	Reference_v1_chr4	unig28c06	99
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4	A04	Reference_v1_chr4	unig26d09	101
4	A04	Reference_v1_chr4	a1638	102
4	A04	Reference_v1_chr4	p11-38	102
4	A04	Reference_v1_chr4	gate4ae10	102
4	A04	Reference_v1_chr4	gate4ad10	102
4	A04	Reference_v1_chr4	bnl3994	103
4	A04	Reference_v1_chr4	em1od22-80	104
4	A04	Reference_v1_chr4	dpl0273	105
4	A04	Reference_v1_chr4	dpl0196	106
4	A04	Reference_v1_chr4	m9e3-950	107
4	A04	Reference_v1_chr4	m8e8-740	107
4	A04	Reference_v1_chr4	coau2k12	108
4	A04	Reference_v1_chr4	m6e6-650	109
4	A04	Reference_v1_chr4	m12e9-500	110
4	A04	Reference_v1_chr4	e3m4_275	111
4	A04	Reference_v1_chr4	bnl4047	112
4	A04	Reference_v1_chr4	m12e3-700	113
4	A04	Reference_v1_chr4	unig22c05	114
4	A04	Reference_v1_chr4	nau3491	115
4	A04	Reference_v1_chr4	par0571	116
4	A04	Reference_v1_chr4	a1310	116
4	A04	Reference_v1_chr4	unig06c08	116
4	A04	Reference_v1_chr4	dpl0299	117
4	A04	Reference_v1_chr4	a1763	118
4	A04	Reference_v1_chr4	a1751	118
4	A04	Reference_v1_chr4	nau0869	119
4	A04	Reference_v1_chr4	a1759	120
4	A04	Reference_v1_chr4	nau5180	121
4	A04	Reference_v1_chr4	musb1050	122
4	A04	Reference_v1_chr4	nau0826	123
4	A04	Reference_v1_chr4	a1667	124
4	A04	Reference_v1_chr4	par09f08	124
4	A04	Reference_v1_chr4	a1717	124
4	A04	Reference_v1_chr4	nau3825	125
4	A04	Reference_v1_chr4	par0417	126
4	A04	Reference_v1_chr4	nau1267	127
4	A04	Reference_v1_chr4	m9e3-960	128
4	A04	Reference_v1_chr4	gate2cc08	129
4	A04	Reference_v1_chr4	a1214	129
4	A04	Reference_v1_chr4	par03-46	130
4	A04	Reference_v1_chr4	par03-41	130
4	A04	Reference_v1_chr4	e3m4_210	131
4	A04	Reference_v1_chr4	bnl3255	131
4	A04	Reference_v1_chr4	unig23g08	132
4	A04	Reference_v1_chr4	bnl3886	133

22	D04	Reference_v1_chr22	me8ca5-130	106
22	D04	Reference_v1_chr22	em5dc1-505	107
22	D04	Reference_v1_chr22	tmb0120	108
22	D04	Reference_v1_chr22	par0144	109
22	D04	Reference_v1_chr22	cir0294	109
22	D04	Reference_v1_chr22	gate2bb08	109
22	D04	Reference_v1_chr22	par0206	109
22	D04	Reference_v1_chr22	a1459	110
22	D04	Reference_v1_chr22	unig26b02	110
22	D04	Reference_v1_chr22	a1535	110
22	D04	Reference_v1_chr22	bnl3368	111
22	D04	Reference_v1_chr22	tmb0086	112
22	D04	Reference_v1_chr22	bnl3881	113
22	D04	Reference_v1_chr22	jespr0235	114
22	D04	Reference_v1_chr22	nau2782	115
22	D04	Reference_v1_chr22	nau3825	116
22	D04	Reference_v1_chr22	nau2955	116
22	D04	Reference_v1_chr22	nau5105	116
22	D04	Reference_v1_chr22	bnl3807	117
22	D04	Reference_v1_chr22	mucs0271	118
22	D04	Reference_v1_chr22	y1022	118
22	D04	Reference_v1_chr22	jespr0063	119
22	D04	Reference_v1_chr22	bnl4015	120
22	D04	Reference_v1_chr22	nau3942	121
22	D04	Reference_v1_chr22	nau2783	122
22	D04	Reference_v1_chr22	nau3514	123
22	D04	Reference_v1_chr22	bnl0206	124
22	D04	Reference_v1_chr22	bnl2609	124
22	D04	Reference_v1_chr22	me4od26-205	125
22	D04	Reference_v1_chr22	nau5046	126
22	D04	Reference_v1_chr22	nau2376	127
22	D04	Reference_v1_chr22	t45e13b	128
22	D04	Reference_v1_chr22	nau2471	129
22	D04	Reference_v1_chr22	nau3824	130
22	D04	Reference_v1_chr22	nau5099	131
22	D04	Reference_v1_chr22	nau2302	132
22	D04	Reference_v1_chr22	pvnc218	133
22	D04	Reference_v1_chr22	par0968	134
22	D04	Reference_v1_chr22	p05-06	135
22	D04	Reference_v1_chr22	bnl1318	136
22	D04	Reference_v1_chr22	a1618	137
22	D04	Reference_v1_chr22	nau2634	138
22	D04	Reference_v1_chr22	par023b	139
22	D04	Reference_v1_chr22	par0023	139
22	D04	Reference_v1_chr22	e2m3_191	140
22	D04	Reference_v1_chr22	par0643	141
22	D04	Reference_v1_chr22	musb1093	142

4	A04	Reference_v1_chr4	par04b02	134
4	A04	Reference_v1_chr4	coau2i23	135
4	A04	Reference_v1_chr4	unig28b06	136
4	A04	Reference_v1_chr4	pgh407	137
4	A04	Reference_v1_chr4	cir0222	138
4	A04	Reference_v1_chr4	bnl4015	139
4	A04	Reference_v1_chr4	gate2ad01	140
4	A04	Reference_v1_chr4	cir0249	141
4	A04	Reference_v1_chr4	bnl0625	142
4	A04	Reference_v1_chr4	coau1j18	143
4	A04	Reference_v1_chr4	par0372	143
4	A04	Reference_v1_chr4	e4m5_236	144
4	A04	Reference_v1_chr4	bnl2821	145
4	A04	Reference_v1_chr4	dpl0573	146
4	A04	Reference_v1_chr4	e3m2c	147
4	A04	Reference_v1_chr4	cir0027	148
4	A04	Reference_v1_chr4	par0182	149
4	A04	Reference_v1_chr4	nau1577	150
4	A04	Reference_v1_chr4	nau3469	151
4	A04	Reference_v1_chr4	nau3592	152
4	A04	Reference_v1_chr4	nau3649	153
4	A04	Reference_v1_chr4	nau3127	154
4	A04	Reference_v1_chr4	par0574	155
4	A04	Reference_v1_chr4	e5m3_400	155
4	A04	Reference_v1_chr4	cir0223	156
4	A04	Reference_v1_chr4	cg14	157
4	A04	Reference_v1_chr4	nau2701	158
4	A04	Reference_v1_chr4	pgh559	159
4	A04	Reference_v1_chr4	bnl3089	160
4	A04	Reference_v1_chr4	cir0142	161
4	A04	Reference_v1_chr4	gate3dc07	162
4	A04	Reference_v1_chr4	a1591	162
4	A04	Reference_v1_chr4	gate2ba04	163

22	D04	Reference_v1_chr22	par0977	143
22	D04	Reference_v1_chr22	parc-14	143
22	D04	Reference_v1_chr22	par04-22	144
22	D04	Reference_v1_chr22	e7m2_166	145
22	D04	Reference_v1_chr22	pxp3-60	146
22	D04	Reference_v1_chr22	muss0187	147
22	D04	Reference_v1_chr22	a1528	148
22	D04	Reference_v1_chr22	a1662	149
22	D04	Reference_v1_chr22	par08d12	150
22	D04	Reference_v1_chr22	par04h06	150
22	D04	Reference_v1_chr22	unig22c05	151
22	D04	Reference_v1_chr22	pvnc311	152
22	D04	Reference_v1_chr22	pbam291	153
22	D04	Reference_v1_chr22	gate4cg07	154
22	D04	Reference_v1_chr22	gate4dc01	155
22	D04	Reference_v1_chr22	gate1cb01	156

Table 4.10 Chromosomes A05 and D05 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
5	A05	Reference_v1_chr5	nau1137	1
5	A05	Reference_v1_chr5	nau1605	2
5	A05	Reference_v1_chr5	nau3450	3
5	A05	Reference_v1_chr5	nau3245	4
5	A05	Reference_v1_chr5	tmb1296	5
5	A05	Reference_v1_chr5	m9e13	6
5	A05	Reference_v1_chr5	nau3607	7
5	A05	Reference_v1_chr5	bnl1042	8
5	A05	Reference_v1_chr5	nau4034	9
5	A05	Reference_v1_chr5	nau3405	10
5	A05	Reference_v1_chr5	nau2865	11
5	A05	Reference_v1_chr5	nau3826	12
5	A05	Reference_v1_chr5	nau3828	13
5	A05	Reference_v1_chr5	nau3737	14
5	A05	Reference_v1_chr5	cms0048	15
5	A05	Reference_v1_chr5	bnl3452	16
5	A05	Reference_v1_chr5	cir0376	17
5	A05	Reference_v1_chr5	nau2000	18
5	A05	Reference_v1_chr5	nau5392	19
5	A05	Reference_v1_chr5	nau4031	20
5	A05	Reference_v1_chr5	nau3269	21
5	A05	Reference_v1_chr5	gate2bg07	22
5	A05	Reference_v1_chr5	nau4951	23
5	A05	Reference_v1_chr5	nau4932	24
5	A05	Reference_v1_chr5	nau5077	25
5	A05	Reference_v1_chr5	par0931	26
5	A05	Reference_v1_chr5	s1288	26
5	A05	Reference_v1_chr5	s0309	26
5	A05	Reference_v1_chr5	cir0067	26
5	A05	Reference_v1_chr5	cir0224	26
5	A05	Reference_v1_chr5	m7e2-880	27
5	A05	Reference_v1_chr5	cir0048	28
5	A05	Reference_v1_chr5	bnl3171	29
5	A05	Reference_v1_chr5	pgh530	30
5	A05	Reference_v1_chr5	par0781	30
5	A05	Reference_v1_chr5	cir0102	31
5	A05	Reference_v1_chr5	bnl0206	32
5	A05	Reference_v1_chr5	s0435	32
5	A05	Reference_v1_chr5	m13e10-680	32
5	A05	Reference_v1_chr5	m3e1-900	33
5	A05	Reference_v1_chr5	gafb08c24	34
5	A05	Reference_v1_chr5	unig22f08	34
5	A05	Reference_v1_chr5	a1135	34
5	A05	Reference_v1_chr5	g1137	34

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
19	D05	Reference_v1_chr19	nau1102	1
19	D05	Reference_v1_chr19	e5m6b	2
19	D05	Reference_v1_chr19	dpl0792	3
19	D05	Reference_v1_chr19	gate2bg07	4
19	D05	Reference_v1_chr19	unig24h03	4
19	D05	Reference_v1_chr19	nbs608	4
19	D05	Reference_v1_chr19	par04-32	4
19	D05	Reference_v1_chr19	jespe122	5
19	D05	Reference_v1_chr19	dpl0247	6
19	D05	Reference_v1_chr19	bnl3043	7
19	D05	Reference_v1_chr19	nau3656	8
19	D05	Reference_v1_chr19	tmb0835	9
19	D05	Reference_v1_chr19	cir0415	10
19	D05	Reference_v1_chr19	nau3609	11
19	D05	Reference_v1_chr19	bnl2865	12
19	D05	Reference_v1_chr19	nau3631	13
19	D05	Reference_v1_chr19	nau0617	14
19	D05	Reference_v1_chr19	musb1056	15
19	D05	Reference_v1_chr19	nau1605	16
19	D05	Reference_v1_chr19	nau4092	17
19	D05	Reference_v1_chr19	nau3092	18
19	D05	Reference_v1_chr19	nau5475	19
19	D05	Reference_v1_chr19	a1569	20
19	D05	Reference_v1_chr19	p13-06	20
19	D05	Reference_v1_chr19	p09-32	20
19	D05	Reference_v1_chr19	par03g11	20
19	D05	Reference_v1_chr19	nau2638	21
19	D05	Reference_v1_chr19	nau3405	22
19	D05	Reference_v1_chr19	hau0112	23
19	D05	Reference_v1_chr19	nau3826	24
19	D05	Reference_v1_chr19	nau3828	25
19	D05	Reference_v1_chr19	hau0111	26
19	D05	Reference_v1_chr19	musb1155	27
19	D05	Reference_v1_chr19	cir0165	28
19	D05	Reference_v1_chr19	bnl3400	29
19	D05	Reference_v1_chr19	par01e01	30
19	D05	Reference_v1_chr19	jespr0235	31
19	D05	Reference_v1_chr19	par0060	32
19	D05	Reference_v1_chr19	par0065	32
19	D05	Reference_v1_chr19	m16-045	32
19	D05	Reference_v1_chr19	par0160	32
19	D05	Reference_v1_chr19	par0169	32
19	D05	Reference_v1_chr19	gate2bf02	32
19	D05	Reference_v1_chr19	nau2942	33

5	A05	Reference_v1_chr5	pxp2-84	34
5	A05	Reference_v1_chr5	m8e12-400	35
5	A05	Reference_v1_chr5	nau1200	36
5	A05	Reference_v1_chr5	unig06g09	37
5	A05	Reference_v1_chr5	cshe0040	38
5	A05	Reference_v1_chr5	s0093	39
5	A05	Reference_v1_chr5	par0065	40
5	A05	Reference_v1_chr5	s0287	41
5	A05	Reference_v1_chr5	par0062	42
5	A05	Reference_v1_chr5	unig28f09	42
5	A05	Reference_v1_chr5	m16-085	42
5	A05	Reference_v1_chr5	bnl3881	43
5	A05	Reference_v1_chr5	m16-045	44
5	A05	Reference_v1_chr5	unig23f09	44
5	A05	Reference_v1_chr5	gate3bg11	44
5	A05	Reference_v1_chr5	par0060	45
5	A05	Reference_v1_chr5	a1152	46
5	A05	Reference_v1_chr5	nau3094	47
5	A05	Reference_v1_chr5	bnl4071	48
5	A05	Reference_v1_chr5	coau1i07	49
5	A05	Reference_v1_chr5	par01e01	50
5	A05	Reference_v1_chr5	m10e2-280*	51
5	A05	Reference_v1_chr5	par07g07	52
5	A05	Reference_v1_chr5	pvnc128	53
5	A05	Reference_v1_chr5	pvnc019	53
5	A05	Reference_v1_chr5	nau2494	54
5	A05	Reference_v1_chr5	a1690	55
5	A05	Reference_v1_chr5	p01-33	55
5	A05	Reference_v1_chr5	t5e3	56
5	A05	Reference_v1_chr5	par0543	57
5	A05	Reference_v1_chr5	s0040	58
5	A05	Reference_v1_chr5	unig22c06	59
5	A05	Reference_v1_chr5	bnl3569	60
5	A05	Reference_v1_chr5	e3m5_298	61
5	A05	Reference_v1_chr5	par0527	62
5	A05	Reference_v1_chr5	unig22d05	62
5	A05	Reference_v1_chr5	unig26c08	62
5	A05	Reference_v1_chr5	nau1223	63
5	A05	Reference_v1_chr5	m7e2-820*	64
5	A05	Reference_v1_chr5	par0954	65
5	A05	Reference_v1_chr5	par0597	65
5	A05	Reference_v1_chr5	par0898	65
5	A05	Reference_v1_chr5	par01f02	65
5	A05	Reference_v1_chr5	nau1372	66
5	A05	Reference_v1_chr5	par0279	67
5	A05	Reference_v1_chr5	nau5015	68
5	A05	Reference_v1_chr5	bnl3492	69

19	D05	Reference_v1_chr19	nau2816	34
19	D05	Reference_v1_chr19	unig22b08	35
19	D05	Reference_v1_chr19	gate4aa02	36
19	D05	Reference_v1_chr19	par0998	37
19	D05	Reference_v1_chr19	nau4884	38
19	D05	Reference_v1_chr19	nau1524	39
19	D05	Reference_v1_chr19	par01a01	40
19	D05	Reference_v1_chr19	dpl0140	41
19	D05	Reference_v1_chr19	cir0086	42
19	D05	Reference_v1_chr19	nau2894	43
19	D05	Reference_v1_chr19	nau2217	44
19	D05	Reference_v1_chr19	bnl1706	45
19	D05	Reference_v1_chr19	a1259	46
19	D05	Reference_v1_chr19	nau3823	47
19	D05	Reference_v1_chr19	unig27h11	48
19	D05	Reference_v1_chr19	par0482	49
19	D05	Reference_v1_chr19	nau2560	50
19	D05	Reference_v1_chr19	hau0117	51
19	D05	Reference_v1_chr19	pgh225	52
19	D05	Reference_v1_chr19	p02-03	52
19	D05	Reference_v1_chr19	nau3012	53
19	D05	Reference_v1_chr19	cir0005	54
19	D05	Reference_v1_chr19	gate1cc05	55
19	D05	Reference_v1_chr19	tmb1296	56
19	D05	Reference_v1_chr19	nau2233	57
19	D05	Reference_v1_chr19	gate4ac11	58
19	D05	Reference_v1_chr19	bnl1075	59
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19	D05	Reference_v1_chr19	par0157	64
19	D05	Reference_v1_chr19	p01-33	65
19	D05	Reference_v1_chr19	gate2b-05	66
19	D05	Reference_v1_chr19	par0219	67
19	D05	Reference_v1_chr19	nau3372	68
19	D05	Reference_v1_chr19	e4m3_272	69
19	D05	Reference_v1_chr19	cir0224	69
19	D05	Reference_v1_chr19	cir0242	70
19	D05	Reference_v1_chr19	nau2811	71
19	D05	Reference_v1_chr19	nau2655	72
19	D05	Reference_v1_chr19	pgh474	73
19	D05	Reference_v1_chr19	nau2604	74
19	D05	Reference_v1_chr19	par0954	75
19	D05	Reference_v1_chr19	par0825	75
19	D05	Reference_v1_chr19	par03b09	75
19	D05	Reference_v1_chr19	par01f05	75

5	A05	Reference_v1_chr5	nau3935	70
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5	A05	Reference_v1_chr5	nau3212	73
5	A05	Reference_v1_chr5	par0825	74
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5	A05	Reference_v1_chr5	nau2630	75
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5	A05	Reference_v1_chr5	cir0364	76
5	A05	Reference_v1_chr5	dpl0368	77
5	A05	Reference_v1_chr5	nau0922	78
5	A05	Reference_v1_chr5	a1650	79
5	A05	Reference_v1_chr5	bnl2988	80
5	A05	Reference_v1_chr5	tmb1489	81
5	A05	Reference_v1_chr5	nau1042	82
5	A05	Reference_v1_chr5	par0219	83
5	A05	Reference_v1_chr5	par01-08	84
5	A05	Reference_v1_chr5	bnl0218	85
5	A05	Reference_v1_chr5	muss0099	86
5	A05	Reference_v1_chr5	dpl0156	87
5	A05	Reference_v1_chr5	tmb0193	88
5	A05	Reference_v1_chr5	musb0312	89
5	A05	Reference_v1_chr5	cshe0115	90
5	A05	Reference_v1_chr5	pgh372	91
5	A05	Reference_v1_chr5	g1386	91
5	A05	Reference_v1_chr5	g1080	92
5	A05	Reference_v1_chr5	gate1cc04	93
5	A05	Reference_v1_chr5	g1112	93
5	A05	Reference_v1_chr5	par0388	94
5	A05	Reference_v1_chr5	unig23e11	94
5	A05	Reference_v1_chr5	p06-58	94
5	A05	Reference_v1_chr5	gate4cd08	95
5	A05	Reference_v1_chr5	unig23a04	95
5	A05	Reference_v1_chr5	par1003	95
5	A05	Reference_v1_chr5	a1246	95
5	A05	Reference_v1_chr5	par0112	96
5	A05	Reference_v1_chr5	par0122	96
5	A05	Reference_v1_chr5	a1318	96
5	A05	Reference_v1_chr5	a1751	96
5	A05	Reference_v1_chr5	g1228	96
5	A05	Reference_v1_chr5	p11-63	96
5	A05	Reference_v1_chr5	unig28c07	96
5	A05	Reference_v1_chr5	gafb17n07	97
5	A05	Reference_v1_chr5	p06-26	97
5	A05	Reference_v1_chr5	par0559	97
5	A05	Reference_v1_chr5	unig06c12	97

19	D05	Reference_v1_chr19	unig22d05	75
19	D05	Reference_v1_chr19	par01-52	75
19	D05	Reference_v1_chr19	pgh489	76
19	D05	Reference_v1_chr19	y2446	77
19	D05	Reference_v1_chr19	nau0567	78
19	D05	Reference_v1_chr19	cir0176	79
19	D05	Reference_v1_chr19	cir0212	80
19	D05	Reference_v1_chr19	bnl4071	81
19	D05	Reference_v1_chr19	dpl0594	82
19	D05	Reference_v1_chr19	bnl2715	83
19	D05	Reference_v1_chr19	bnl1681	84
19	D05	Reference_v1_chr19	p02-09	85
19	D05	Reference_v1_chr19	t12e14b	86
19	D05	Reference_v1_chr19	nau4929	87
19	D05	Reference_v1_chr19	jespr0053	88
19	D05	Reference_v1_chr19	nau0561	89
19	D05	Reference_v1_chr19	dpl0169	90
19	D05	Reference_v1_chr19	bnl1690	90
19	D05	Reference_v1_chr19	g1112	91
19	D05	Reference_v1_chr19	gate1bc02	92
19	D05	Reference_v1_chr19	gafb22m15	92
19	D05	Reference_v1_chr19	nau0571	93
19	D05	Reference_v1_chr19	unig23d12	94
19	D05	Reference_v1_chr19	jespr0037	95
19	D05	Reference_v1_chr19	nau0664	96
19	D05	Reference_v1_chr19	par09b07	97
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19	D05	Reference_v1_chr19	m6e13a	262
19	D05	Reference_v1_chr19	coau3c10	263
19	D05	Reference_v1_chr19	pvnc304	264
19	D05	Reference_v1_chr19	par03-37	264
19	D05	Reference_v1_chr19	par0377	264
19	D05	Reference_v1_chr19	par03-46	265
19	D05	Reference_v1_chr19	pvnc060	266

5	A05	Reference_v1_chr5	m6e16d	228
5	A05	Reference_v1_chr5	pgh272	229
5	A05	Reference_v1_chr5	gate4dc12	230
5	A05	Reference_v1_chr5	t5e4b	231
5	A05	Reference_v1_chr5	a1691	232
5	A05	Reference_v1_chr5	e5m5_190	233
5	A05	Reference_v1_chr5	par0042	234
5	A05	Reference_v1_chr5	gate4df07	234
5	A05	Reference_v1_chr5	par0206	234
5	A05	Reference_v1_chr5	t4e2c	235
5	A05	Reference_v1_chr5	m5e1-520	236
5	A05	Reference_v1_chr5	m9e7-260	236
5	A05	Reference_v1_chr5	m2e3-400	236
5	A05	Reference_v1_chr5	coau4k03	237
5	A05	Reference_v1_chr5	t11e11a	238
5	A05	Reference_v1_chr5	t13e13a	239
5	A05	Reference_v1_chr5	t42e10	240
5	A05	Reference_v1_chr5	nau4040	241
5	A05	Reference_v1_chr5	cir0294	242
5	A05	Reference_v1_chr5	cg12	242
5	A05	Reference_v1_chr5	pxp1-77	243
5	A05	Reference_v1_chr5	e4m5_400	244
5	A05	Reference_v1_chr5	e1m4_95	245
5	A05	Reference_v1_chr5	nau3569	246
5	A05	Reference_v1_chr5	e2m1_125	247
5	A05	Reference_v1_chr5	a1459	248
5	A05	Reference_v1_chr5	unig26b02	248
5	A05	Reference_v1_chr5	a1535	248
5	A05	Reference_v1_chr5	gate2ce06	248
5	A05	Reference_v1_chr5	a1483	248
5	A05	Reference_v1_chr5	g1053	248
5	A05	Reference_v1_chr5	unig25d10	248
5	A05	Reference_v1_chr5	gate3cc12	249
5	A05	Reference_v1_chr5	e3m8_328	250
5	A05	Reference_v1_chr5	gate3de01	251
5	A05	Reference_v1_chr5	nau2562	252
5	A05	Reference_v1_chr5	nau3204	253
5	A05	Reference_v1_chr5	e3m1_225	254
5	A05	Reference_v1_chr5	me2em3-180	255
5	A05	Reference_v1_chr5	nau3824	256
5	A05	Reference_v1_chr5	bnl3955	257
5	A05	Reference_v1_chr5	y1808	258
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5	A05	Reference_v1_chr5	par0144	259
5	A05	Reference_v1_chr5	m5e7a	260
5	A05	Reference_v1_chr5	nau1406	261
5	A05	Reference_v1_chr5	dpl0637	262

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19	D05	Reference_v1_chr19	gafb26n16	267
19	D05	Reference_v1_chr19	pvnc173	268
19	D05	Reference_v1_chr19	a1432	268
19	D05	Reference_v1_chr19	par10c12	268
19	D05	Reference_v1_chr19	pgh777	268
19	D05	Reference_v1_chr19	pxp4-49	268
19	D05	Reference_v1_chr19	unig25h06	268
19	D05	Reference_v1_chr19	gate1bf05	269
19	D05	Reference_v1_chr19	par03h07	270
19	D05	Reference_v1_chr19	par0450	271
19	D05	Reference_v1_chr19	unig25g11	272
19	D05	Reference_v1_chr19	coau1a21	273
19	D05	Reference_v1_chr19	r6592a14dl	273
19	D05	Reference_v1_chr19	unig26d03	274
19	D05	Reference_v1_chr19	coau2c01	275
19	D05	Reference_v1_chr19	coau4n12	276
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19	D05	Reference_v1_chr19	unig26c11	278
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19	D05	Reference_v1_chr19	e2m6_103	280
19	D05	Reference_v1_chr19	e3m1_205	281
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19	D05	Reference_v1_chr19	cg18	283
19	D05	Reference_v1_chr19	cg25	283
19	D05	Reference_v1_chr19	cir0255	283
19	D05	Reference_v1_chr19	e4m7_450	284
19	D05	Reference_v1_chr19	e5m5_280	284
19	D05	Reference_v1_chr19	e8m8_124	285
19	D05	Reference_v1_chr19	bnl1671	286
19	D05	Reference_v1_chr19	e1m8_217	287
19	D05	Reference_v1_chr19	e3m3_430	288
19	D05	Reference_v1_chr19	bnl3535	288
19	D05	Reference_v1_chr19	jespr0023	289
19	D05	Reference_v1_chr19	cir0222	290
19	D05	Reference_v1_chr19	bnl2621	291
19	D05	Reference_v1_chr19	tmb1295	292
19	D05	Reference_v1_chr19	jespr0218	293
19	D05	Reference_v1_chr19	bnl3347	294
19	D05	Reference_v1_chr19	cm0003	294
19	D05	Reference_v1_chr19	par03-41	295
19	D05	Reference_v1_chr19	par0417	295
19	D05	Reference_v1_chr19	nau3110	296
19	D05	Reference_v1_chr19	par1005	297
19	D05	Reference_v1_chr19	nau3268	298

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5	A05	Reference_v1_chr5	me3em6-580	264
5	A05	Reference_v1_chr5	nau2561	265
5	A05	Reference_v1_chr5	coau2c01	266
5	A05	Reference_v1_chr5	gate2aa09	267
5	A05	Reference_v1_chr5	e1m4d	268
5	A05	Reference_v1_chr5	em6pm8-85	269
5	A05	Reference_v1_chr5	nau5400	270
5	A05	Reference_v1_chr5	nau4898	271
5	A05	Reference_v1_chr5	nau2001	272
5	A05	Reference_v1_chr5	cir0393	273
5	A05	Reference_v1_chr5	nau3402	274
5	A05	Reference_v1_chr5	t22e3a	275
5	A05	Reference_v1_chr5	jespr0065	276
5	A05	Reference_v1_chr5	e3m6a	277
5	A05	Reference_v1_chr5	em6ga45-80	278
5	A05	Reference_v1_chr5	e6m8_237	279
5	A05	Reference_v1_chr5	jespr0050	280
5	A05	Reference_v1_chr5	nau2376	281
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5	A05	Reference_v1_chr5	bnl4030	283
5	A05	Reference_v1_chr5	cm0065	284
5	A05	Reference_v1_chr5	cir0185	285
5	A05	Reference_v1_chr5	bnl2732	286
5	A05	Reference_v1_chr5	bnl1038	287
5	A05	Reference_v1_chr5	nau0569	288
5	A05	Reference_v1_chr5	nau1151	289
5	A05	Reference_v1_chr5	nau6109	290
5	A05	Reference_v1_chr5	tmb0770	291
5	A05	Reference_v1_chr5	par0333	292
5	A05	Reference_v1_chr5	hau0042	293
5	A05	Reference_v1_chr5	nau3273	294
5	A05	Reference_v1_chr5	a1662	295
5	A05	Reference_v1_chr5	gate4ce05	296
5	A05	Reference_v1_chr5	gate4dc01	297
5	A05	Reference_v1_chr5	par0351	297
5	A05	Reference_v1_chr5	pxp3-07	298
5	A05	Reference_v1_chr5	gate3db06	299
5	A05	Reference_v1_chr5	coau1m05	300
5	A05	Reference_v1_chr5	par0812	301
5	A05	Reference_v1_chr5	unig22c05	302
5	A05	Reference_v1_chr5	par08d12	303
5	A05	Reference_v1_chr5	unig22f03	304
5	A05	Reference_v1_chr5	gate1cb02	305
5	A05	Reference_v1_chr5	pxp4-26	306
5	A05	Reference_v1_chr5	coau3f17	306
5	A05	Reference_v1_chr5	cir0253	307

19	D05	Reference_v1_chr19	nau3344	299
19	D05	Reference_v1_chr19	bnl2821	300
19	D05	Reference_v1_chr19	nau3183	301
19	D05	Reference_v1_chr19	cir0277	302
19	D05	Reference_v1_chr19	e1m6_267	303
19	D05	Reference_v1_chr19	cac278	303
19	D05	Reference_v1_chr19	e3m3_420	303
19	D05	Reference_v1_chr19	e3m4_164	304
19	D05	Reference_v1_chr19	pgh559	305
19	D05	Reference_v1_chr19	cir0344	306
19	D05	Reference_v1_chr19	pgh510	307
19	D05	Reference_v1_chr19	bnl0678	308
19	D05	Reference_v1_chr19	jespr0236	309
19	D05	Reference_v1_chr19	bnl3020	310
19	D05	Reference_v1_chr19	e1m8a	311
19	D05	Reference_v1_chr19	par01g05	312
19	D05	Reference_v1_chr19	pbam291	313
19	D05	Reference_v1_chr19	cms0021	314
19	D05	Reference_v1_chr19	coau2a18	315
19	D05	Reference_v1_chr19	par01d01	315
19	D05	Reference_v1_chr19	a1591	316
19	D05	Reference_v1_chr19	nau3592	317
19	D05	Reference_v1_chr19	mucs0517	318
19	D05	Reference_v1_chr19	nau2232	319
19	D05	Reference_v1_chr19	par09c12	320
19	D05	Reference_v1_chr19	mucs0585	321
19	D05	Reference_v1_chr19	unig25h05	322
19	D05	Reference_v1_chr19	gate3dc07	322
19	D05	Reference_v1_chr19	nau2801	323
19	D05	Reference_v1_chr19	nau2231	324
19	D05	Reference_v1_chr19	par0182	325
19	D05	Reference_v1_chr19	nau3946	326
19	D05	Reference_v1_chr19	opd08.1(bt)	327
19	D05	Reference_v1_chr19	par0574	328
19	D05	Reference_v1_chr19	nau3649	329
19	D05	Reference_v1_chr19	nau2111	330
19	D05	Reference_v1_chr19	nau2503	331
19	D05	Reference_v1_chr19	nau4907	332
19	D05	Reference_v1_chr19	nau0524	333
19	D05	Reference_v1_chr19	nau3095	334

5	A05	Reference_v1_chr5	par023a	308
5	A05	Reference_v1_chr5	par0023	308
5	A05	Reference_v1_chr5	gate1ab04	308
5	A05	Reference_v1_chr5	p1	309
5	A05	Reference_v1_chr5	gate4af11	310
5	A05	Reference_v1_chr5	cir0328	311
5	A05	Reference_v1_chr5	par01c07	312
5	A05	Reference_v1_chr5	nau4058	313
5	A05	Reference_v1_chr5	nau4057	314
5	A05	Reference_v1_chr5	nau2121	315
5	A05	Reference_v1_chr5	nau4030	316
5	A05	Reference_v1_chr5	nau1426	317
5	A05	Reference_v1_chr5	e4m12	318
5	A05	Reference_v1_chr5	e9m14	319
5	A05	Reference_v1_chr5	nau0934	320
5	A05	Reference_v1_chr5	est24	321
5	A05	Reference_v1_chr5	nau3036	322
5	A05	Reference_v1_chr5	muss0219	323

Table 4.11 Chromosomes A06 and D06 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
6	A06	Reference_v1_chr6	nau2714	1
6	A06	Reference_v1_chr6	nau0614	2
6	A06	Reference_v1_chr6	cir0298	3
6	A06	Reference_v1_chr6	cshe0267	4
6	A06	Reference_v1_chr6	cir0267	5
6	A06	Reference_v1_chr6	bnl3359	6
6	A06	Reference_v1_chr6	bnl1902	7
6	A06	Reference_v1_chr6	tmb0154	8
6	A06	Reference_v1_chr6	gafb17h13	9
6	A06	Reference_v1_chr6	pxp4-69	9
6	A06	Reference_v1_chr6	m10e2-670	10
6	A06	Reference_v1_chr6	m7e3-400	10
6	A06	Reference_v1_chr6	m11e7-500	11
6	A06	Reference_v1_chr6	bnl1746	12
6	A06	Reference_v1_chr6	unig28f03	13
6	A06	Reference_v1_chr6	gate4bb01	14
6	A06	Reference_v1_chr6	par0026	15
6	A06	Reference_v1_chr6	par026a	15
6	A06	Reference_v1_chr6	cir0280	16
6	A06	Reference_v1_chr6	dpl0101	17
6	A06	Reference_v1_chr6	dpl0238	18
6	A06	Reference_v1_chr6	m4e1b	19
6	A06	Reference_v1_chr6	par0433	20
6	A06	Reference_v1_chr6	a1550	20
6	A06	Reference_v1_chr6	bnl4004	21
6	A06	Reference_v1_chr6	nau2611	22
6	A06	Reference_v1_chr6	gate3ah06	23
6	A06	Reference_v1_chr6	pxp4-08	24
6	A06	Reference_v1_chr6	nau1151	25
6	A06	Reference_v1_chr6	nau1027	26
6	A06	Reference_v1_chr6	m3e5-550	27
6	A06	Reference_v1_chr6	tmb1530	28
6	A06	Reference_v1_chr6	gate3ag06	29
6	A06	Reference_v1_chr6	nau5270	30
6	A06	Reference_v1_chr6	nau5269	31
6	A06	Reference_v1_chr6	nau0433	32
6	A06	Reference_v1_chr6	nau4969	33
6	A06	Reference_v1_chr6	nau3243	34
6	A06	Reference_v1_chr6	cir0329	35
6	A06	Reference_v1_chr6	t29e7	36
6	A06	Reference_v1_chr6	jespr0273	37
6	A06	Reference_v1_chr6	a1402	38
6	A06	Reference_v1_chr6	e7m1_102	39
6	A06	Reference_v1_chr6	bnl1035	40

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
25	D06	Reference_v1_chr25	jespr0070	1
25	D06	Reference_v1_chr25	e4m3_268	2
25	D06	Reference_v1_chr25	bnl1231	3
25	D06	Reference_v1_chr25	a1686	4
25	D06	Reference_v1_chr25	bnl3359	5
25	D06	Reference_v1_chr25	cshe0267	6
25	D06	Reference_v1_chr25	bnl0584	7
25	D06	Reference_v1_chr25	cir0109	8
25	D06	Reference_v1_chr25	muss0519	9
25	D06	Reference_v1_chr25	bnl0827	10
25	D06	Reference_v1_chr25	cir0267	11
25	D06	Reference_v1_chr25	unig06d09	12
25	D06	Reference_v1_chr25	coau3b05	13
25	D06	Reference_v1_chr25	pxp3-46	13
25	D06	Reference_v1_chr25	a1215	14
25	D06	Reference_v1_chr25	par0366	14
25	D06	Reference_v1_chr25	par0070	15
25	D06	Reference_v1_chr25	par0237	16
25	D06	Reference_v1_chr25	gate2cb08	16
25	D06	Reference_v1_chr25	par04-30	16
25	D06	Reference_v1_chr25	par0445	17
25	D06	Reference_v1_chr25	e4m4_400	18
25	D06	Reference_v1_chr25	nau3502	19
25	D06	Reference_v1_chr25	cir0298	20
25	D06	Reference_v1_chr25	nau2714	21
25	D06	Reference_v1_chr25	nau2713	22
25	D06	Reference_v1_chr25	nau1606	23
25	D06	Reference_v1_chr25	gafb17h13	24
25	D06	Reference_v1_chr25	unig25c07	25
25	D06	Reference_v1_chr25	bnl3436	26
25	D06	Reference_v1_chr25	gate4bb01	27
25	D06	Reference_v1_chr25	m7e3a	28
25	D06	Reference_v1_chr25	gate1ce02	29
25	D06	Reference_v1_chr25	pxp3-56	30
25	D06	Reference_v1_chr25	par0433	31
25	D06	Reference_v1_chr25	bnl2569	32
25	D06	Reference_v1_chr25	pxp4-18	33
25	D06	Reference_v1_chr25	unig06f04	34
25	D06	Reference_v1_chr25	nau2641	35
25	D06	Reference_v1_chr25	bnl1061	36
25	D06	Reference_v1_chr25	bnl1047	37
25	D06	Reference_v1_chr25	par0026	38
25	D06	Reference_v1_chr25	par026b	38
25	D06	Reference_v1_chr25	e3m5_162	39

6	A06	Reference_v1_chr6	nau2278	41
6	A06	Reference_v1_chr6	dpl0080	42
6	A06	Reference_v1_chr6	musb0399	43
6	A06	Reference_v1_chr6	e3m3_82	44
6	A06	Reference_v1_chr6	nau2971	45
6	A06	Reference_v1_chr6	dpl0847	46
6	A06	Reference_v1_chr6	musb0500	47
6	A06	Reference_v1_chr6	e2m1_375	48
6	A06	Reference_v1_chr6	musb0078	49
6	A06	Reference_v1_chr6	bnl1440	50
6	A06	Reference_v1_chr6	coau2e11	51
6	A06	Reference_v1_chr6	gate1cf01	51
6	A06	Reference_v1_chr6	coau1i01	51
6	A06	Reference_v1_chr6	coau4h09	51
6	A06	Reference_v1_chr6	musb0754	52
6	A06	Reference_v1_chr6	par0961	53
6	A06	Reference_v1_chr6	p10-20	54
6	A06	Reference_v1_chr6	par0934	55
6	A06	Reference_v1_chr6	par0485	55
6	A06	Reference_v1_chr6	pgh906	56
6	A06	Reference_v1_chr6	m7e3d	57
6	A06	Reference_v1_chr6	gate3ba05	58
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6	A06	Reference_v1_chr6	nau0905	60
6	A06	Reference_v1_chr6	bnl3955	61
6	A06	Reference_v1_chr6	cir0033	61
6	A06	Reference_v1_chr6	cir0291	61
6	A06	Reference_v1_chr6	a1152	61
6	A06	Reference_v1_chr6	e6m3_240	61
6	A06	Reference_v1_chr6	e4m5_205	61
6	A06	Reference_v1_chr6	e7m7_194	61
6	A06	Reference_v1_chr6	m7e15-680	62
6	A06	Reference_v1_chr6	bnl1153	63
6	A06	Reference_v1_chr6	m8e17-300	64
6	A06	Reference_v1_chr6	m5e7b	65
6	A06	Reference_v1_chr6	m14e5-500	66
6	A06	Reference_v1_chr6	em5ga30-115	67
6	A06	Reference_v1_chr6	me2em3-210	68
6	A06	Reference_v1_chr6	m8e17-250	69
6	A06	Reference_v1_chr6	e6m5b	70
6	A06	Reference_v1_chr6	musb0919	71
6	A06	Reference_v1_chr6	m10e10-430	72
6	A06	Reference_v1_chr6	tmb1484	73
6	A06	Reference_v1_chr6	musb0971	74
6	A06	Reference_v1_chr6	hau0091	75
6	A06	Reference_v1_chr6	m12e9-780	76
6	A06	Reference_v1_chr6	musb0955	77

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25	D06	Reference_v1_chr25	par0969	43
25	D06	Reference_v1_chr25	par0696	43
25	D06	Reference_v1_chr25	cir0280	44
25	D06	Reference_v1_chr25	bnl1404	45
25	D06	Reference_v1_chr25	gate1ca07	45
25	D06	Reference_v1_chr25	m16-119	46
25	D06	Reference_v1_chr25	unig26g04	46
25	D06	Reference_v1_chr25	gafb08c24	47
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25	D06	Reference_v1_chr25	cshe0037	53
25	D06	Reference_v1_chr25	acccaa13	54
25	D06	Reference_v1_chr25	e2m16	55
25	D06	Reference_v1_chr25	em2ga34-155	56
25	D06	Reference_v1_chr25	bnl3806	57
25	D06	Reference_v1_chr25	bnl0272	58
25	D06	Reference_v1_chr25	tmb0313	59
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25	D06	Reference_v1_chr25	bnl3190	61
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25	D06	Reference_v1_chr25	acagcg3	63
25	D06	Reference_v1_chr25	aggcaa4	64
25	D06	Reference_v1_chr25	pgh691	65
25	D06	Reference_v1_chr25	m8e1b	66
25	D06	Reference_v1_chr25	e2m7_89	67
25	D06	Reference_v1_chr25	cir0329	68
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25	D06	Reference_v1_chr25	tmb0573	70
25	D06	Reference_v1_chr25	e6m8a	71
25	D06	Reference_v1_chr25	tmb0436	72
25	D06	Reference_v1_chr25	nau3578	73
25	D06	Reference_v1_chr25	bnl2691	74
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25	D06	Reference_v1_chr25	jespe224	78
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25	D06	Reference_v1_chr25	e1m3_285	80

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6	A06	Reference_v1_chr6	gate1ba09	83
6	A06	Reference_v1_chr6	pxp3-23	83
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6	A06	Reference_v1_chr6	em1od30-230	86
6	A06	Reference_v1_chr6	jespr0194	87
6	A06	Reference_v1_chr6	t2e4f	88
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6	A06	Reference_v1_chr6	bnl2884	89
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6	A06	Reference_v1_chr6	e3m4_410	90
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25	D06	Reference_v1_chr25	g042d01a	126
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25	D06	Reference_v1_chr25	par0364	167
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6	A06	Reference_v1_chr6	tmb1740	241

Table 4.12 Chromosomes A07 and D07 of reference map.

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7	A07	Reference_v1_chr7	p11-72	4
7	A07	Reference_v1_chr7	gafb05f01	5
7	A07	Reference_v1_chr7	par10f12	6
7	A07	Reference_v1_chr7	par0515	6
7	A07	Reference_v1_chr7	gate1cb11	7
7	A07	Reference_v1_chr7	unig26e07	8
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7	A07	Reference_v1_chr7	e8m6_115	161
7	A07	Reference_v1_chr7	pgh408	162
7	A07	Reference_v1_chr7	a1189	162
7	A07	Reference_v1_chr7	coau1c04	162
7	A07	Reference_v1_chr7	bnl1597	162
7	A07	Reference_v1_chr7	par0615	162
7	A07	Reference_v1_chr7	par06a09	162
7	A07	Reference_v1_chr7	par0624	162
7	A07	Reference_v1_chr7	nau2862	163
7	A07	Reference_v1_chr7	nau2657	164
7	A07	Reference_v1_chr7	nau2686	165
7	A07	Reference_v1_chr7	nau2685	166
7	A07	Reference_v1_chr7	nau0474	167
7	A07	Reference_v1_chr7	par07a02	168
7	A07	Reference_v1_chr7	cir0412	169
7	A07	Reference_v1_chr7	a1316	170
7	A07	Reference_v1_chr7	g1185	171
7	A07	Reference_v1_chr7	nau5152	172
7	A07	Reference_v1_chr7	coau4n19	173
7	A07	Reference_v1_chr7	par0564	174

16	D07	Reference_v1_chr16	bnl1604	147
16	D07	Reference_v1_chr16	bnl1122	147
16	D07	Reference_v1_chr16	par0161	148
16	D07	Reference_v1_chr16	par0040	149
16	D07	Reference_v1_chr16	bnl3090	149
16	D07	Reference_v1_chr16	unig23a09	149
16	D07	Reference_v1_chr16	par0173	149
16	D07	Reference_v1_chr16	par040b	149
16	D07	Reference_v1_chr16	par0285	149
16	D07	Reference_v1_chr16	par0291	149
16	D07	Reference_v1_chr16	unig25g01	149
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16	D07	Reference_v1_chr16	par0887	149
16	D07	Reference_v1_chr16	tmb1114	150
16	D07	Reference_v1_chr16	par0231	151
16	D07	Reference_v1_chr16	coau4b05	151
16	D07	Reference_v1_chr16	bnl0391	152
16	D07	Reference_v1_chr16	ests183	153
16	D07	Reference_v1_chr16	bnl3065	154
16	D07	Reference_v1_chr16	s1298	155
16	D07	Reference_v1_chr16	par0048	156
16	D07	Reference_v1_chr16	unig06d05	157
16	D07	Reference_v1_chr16	m16-106	158
16	D07	Reference_v1_chr16	pxp4-52	159
16	D07	Reference_v1_chr16	par0714	160
16	D07	Reference_v1_chr16	e4m7_150	161
16	D07	Reference_v1_chr16	g1271	162
16	D07	Reference_v1_chr16	m12e15-800	163
16	D07	Reference_v1_chr16	bnl3496	164
16	D07	Reference_v1_chr16	bnl3923	165
16	D07	Reference_v1_chr16	par0057	166
16	D07	Reference_v1_chr16	nau3911	167
16	D07	Reference_v1_chr16	par0844	168
16	D07	Reference_v1_chr16	par0544	168
16	D07	Reference_v1_chr16	a1625	169
16	D07	Reference_v1_chr16	par0669	169
16	D07	Reference_v1_chr16	unig25c01	170
16	D07	Reference_v1_chr16	nau2974	171
16	D07	Reference_v1_chr16	unig26e07	172
16	D07	Reference_v1_chr16	nau2733	173
16	D07	Reference_v1_chr16	nau2680	173
16	D07	Reference_v1_chr16	nau2734	174
16	D07	Reference_v1_chr16	gate1cb11	175
16	D07	Reference_v1_chr16	p12-16	176
16	D07	Reference_v1_chr16	cms0026	177
16	D07	Reference_v1_chr16	a1619	178

7	A07	Reference_v1_chr7	nau5303	175
7	A07	Reference_v1_chr7	nau2820	176
7	A07	Reference_v1_chr7	par10f06	177
7	A07	Reference_v1_chr7	gate1db07	177
7	A07	Reference_v1_chr7	gate1bd08	177
7	A07	Reference_v1_chr7	par0048	178
7	A07	Reference_v1_chr7	par0888	179
7	A07	Reference_v1_chr7	a1597	180
7	A07	Reference_v1_chr7	nau2432	181
7	A07	Reference_v1_chr7	unig23c07	182
7	A07	Reference_v1_chr7	par01-25	182
7	A07	Reference_v1_chr7	unig06b10	183
7	A07	Reference_v1_chr7	nau0450	184
7	A07	Reference_v1_chr7	nau3654	185
7	A07	Reference_v1_chr7	e2m4_171	186
7	A07	Reference_v1_chr7	g1158	187
7	A07	Reference_v1_chr7	nau3918	188
7	A07	Reference_v1_chr7	nau3053	189
7	A07	Reference_v1_chr7	nau4030	190
7	A07	Reference_v1_chr7	nau0493	191
7	A07	Reference_v1_chr7	nau2597	192
7	A07	Reference_v1_chr7	cir0320	193
7	A07	Reference_v1_chr7	nau0933	194
7	A07	Reference_v1_chr7	unig28a10	195
7	A07	Reference_v1_chr7	gate4cf04	196
7	A07	Reference_v1_chr7	par0666	197
7	A07	Reference_v1_chr7	par04d08	198
7	A07	Reference_v1_chr7	a1478	199
7	A07	Reference_v1_chr7	a1135	200
7	A07	Reference_v1_chr7	gate1cf06	201
7	A07	Reference_v1_chr7	par0395	201
7	A07	Reference_v1_chr7	gate3df04	202
7	A07	Reference_v1_chr7	pvnc127	203
7	A07	Reference_v1_chr7	coau2c21	204

16	D07	Reference_v1_chr16	p01-24	178
16	D07	Reference_v1_chr16	p11-72	179
16	D07	Reference_v1_chr16	nau2556	180
16	D07	Reference_v1_chr16	pvnc190	181
16	D07	Reference_v1_chr16	par04-09	181
16	D07	Reference_v1_chr16	nau2286	182
16	D07	Reference_v1_chr16	a1826	183
16	D07	Reference_v1_chr16	nau3608	184
16	D07	Reference_v1_chr16	nau3906	185
16	D07	Reference_v1_chr16	nau3678	186
16	D07	Reference_v1_chr16	nau5325	187
16	D07	Reference_v1_chr16	nau0966	188
16	D07	Reference_v1_chr16	nau3279	189
16	D07	Reference_v1_chr16	e5m4_480	190

Table 4.13 Chromosomes A08 and D08 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
8	A08	Reference_v1_chr8	tmb1427	1
8	A08	Reference_v1_chr8	cir0244	2
8	A08	Reference_v1_chr8	musb0812	3
8	A08	Reference_v1_chr8	coau2l09	4
8	A08	Reference_v1_chr8	gate1cf06	5
8	A08	Reference_v1_chr8	mucs0113	6
8	A08	Reference_v1_chr8	muss0500	7
8	A08	Reference_v1_chr8	mucs0021	8
8	A08	Reference_v1_chr8	coau2i12	9
8	A08	Reference_v1_chr8	muss0021	10
8	A08	Reference_v1_chr8	musb0422	11
8	A08	Reference_v1_chr8	musb0175	12
8	A08	Reference_v1_chr8	g1114	13
8	A08	Reference_v1_chr8	par0540	13
8	A08	Reference_v1_chr8	a1783	13
8	A08	Reference_v1_chr8	nau0920	13
8	A08	Reference_v1_chr8	coau1m19	13
8	A08	Reference_v1_chr8	nau3010	14
8	A08	Reference_v1_chr8	nau3482	15
8	A08	Reference_v1_chr8	nau3072	16
8	A08	Reference_v1_chr8	jespr0232	17
8	A08	Reference_v1_chr8	pgh742	18
8	A08	Reference_v1_chr8	p01-08	18
8	A08	Reference_v1_chr8	gate1af08	18
8	A08	Reference_v1_chr8	gate1ce09	19
8	A08	Reference_v1_chr8	bnl2772	20
8	A08	Reference_v1_chr8	par06g04	21
8	A08	Reference_v1_chr8	gate4ch11	21
8	A08	Reference_v1_chr8	par0792	22
8	A08	Reference_v1_chr8	nau1254	23
8	A08	Reference_v1_chr8	a1698	24
8	A08	Reference_v1_chr8	gate2cc06	25
8	A08	Reference_v1_chr8	a1706	26
8	A08	Reference_v1_chr8	a1216	26
8	A08	Reference_v1_chr8	tmb2781	27
8	A08	Reference_v1_chr8	par0968	28
8	A08	Reference_v1_chr8	nau2407	29
8	A08	Reference_v1_chr8	nau1017	30
8	A08	Reference_v1_chr8	nau0789	31
8	A08	Reference_v1_chr8	tmb1702	32
8	A08	Reference_v1_chr8	nau3773	33
8	A08	Reference_v1_chr8	a1488	34
8	A08	Reference_v1_chr8	y12921	35
8	A08	Reference_v1_chr8	nau5128	36

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
24	D08	Reference_v1_chr24	e5m7b	1
24	D08	Reference_v1_chr24	gate4dg08	2
24	D08	Reference_v1_chr24	par0490	3
24	D08	Reference_v1_chr24	a1811	4
24	D08	Reference_v1_chr24	gate3be04	5
24	D08	Reference_v1_chr24	g1276	6
24	D08	Reference_v1_chr24	gate4cb07	7
24	D08	Reference_v1_chr24	gate3ca01	8
24	D08	Reference_v1_chr24	m2e15	9
24	D08	Reference_v1_chr24	jespr0307	10
24	D08	Reference_v1_chr24	parc-04	11
24	D08	Reference_v1_chr24	par01a05	12
24	D08	Reference_v1_chr24	gate2bc08	13
24	D08	Reference_v1_chr24	unig23h12	13
24	D08	Reference_v1_chr24	p07-04	14
24	D08	Reference_v1_chr24	a1658	15
24	D08	Reference_v1_chr24	a1197	15
24	D08	Reference_v1_chr24	par03-23	16
24	D08	Reference_v1_chr24	par0789	17
24	D08	Reference_v1_chr24	gate1ca10	18
24	D08	Reference_v1_chr24	g1010	19
24	D08	Reference_v1_chr24	cir0359	20
24	D08	Reference_v1_chr24	coau2c15	21
24	D08	Reference_v1_chr24	par09h09	21
24	D08	Reference_v1_chr24	par0309	21
24	D08	Reference_v1_chr24	par04-11	21
24	D08	Reference_v1_chr24	gate1ag10	21
24	D08	Reference_v1_chr24	a1348	21
24	D08	Reference_v1_chr24	gate1db08	22
24	D08	Reference_v1_chr24	par0418	22
24	D08	Reference_v1_chr24	par0332	22
24	D08	Reference_v1_chr24	gate1cc03	23
24	D08	Reference_v1_chr24	p05-24	24
24	D08	Reference_v1_chr24	gate2cf02	24
24	D08	Reference_v1_chr24	a1590	24
24	D08	Reference_v1_chr24	g1013	24
24	D08	Reference_v1_chr24	a1168	25
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24	D08	Reference_v1_chr24	a1401	27
24	D08	Reference_v1_chr24	g1272	28
24	D08	Reference_v1_chr24	par0118	29
24	D08	Reference_v1_chr24	a1667	29
24	D08	Reference_v1_chr24	gate2cd01	29

8	A08	Reference_v1_chr8	p06-26	37
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8	A08	Reference_v1_chr8	gate1af01	37
8	A08	Reference_v1_chr8	m16-088	37
8	A08	Reference_v1_chr8	a1679	37
8	A08	Reference_v1_chr8	nau5368	38
8	A08	Reference_v1_chr8	nau5129	39
8	A08	Reference_v1_chr8	nau5357	40
8	A08	Reference_v1_chr8	cir0376	41
8	A08	Reference_v1_chr8	jespr0066	41
8	A08	Reference_v1_chr8	e3m6_149	42
8	A08	Reference_v1_chr8	g029h11a	43
8	A08	Reference_v1_chr8	nau3558	43
8	A08	Reference_v1_chr8	tmb2899	44
8	A08	Reference_v1_chr8	par0571	45
8	A08	Reference_v1_chr8	a1252	45
8	A08	Reference_v1_chr8	gate4cg09	46
8	A08	Reference_v1_chr8	gate1ae07	46
8	A08	Reference_v1_chr8	gafb16d09	46
8	A08	Reference_v1_chr8	gate4cc07	46
8	A08	Reference_v1_chr8	w11	46
8	A08	Reference_v1_chr8	nau1369	47
8	A08	Reference_v1_chr8	bnl0252	48
8	A08	Reference_v1_chr8	par0044	49
8	A08	Reference_v1_chr8	cshe0237	50
8	A08	Reference_v1_chr8	pvnc244	51
8	A08	Reference_v1_chr8	pgh242	52
8	A08	Reference_v1_chr8	cir0237	53
8	A08	Reference_v1_chr8	gate2bf03	54
8	A08	Reference_v1_chr8	mucs0188	55
8	A08	Reference_v1_chr8	cir0119	56
8	A08	Reference_v1_chr8	cir0354	57
8	A08	Reference_v1_chr8	gate4dd02	58
8	A08	Reference_v1_chr8	e2m3_261	59
8	A08	Reference_v1_chr8	bnl3556	59
8	A08	Reference_v1_chr8	e4m7_161	60
8	A08	Reference_v1_chr8	bnl3255	61
8	A08	Reference_v1_chr8	a1412	61
8	A08	Reference_v1_chr8	nau4900	62
8	A08	Reference_v1_chr8	e8m1_138	63
8	A08	Reference_v1_chr8	nau2881	64
8	A08	Reference_v1_chr8	unig22e12	65
8	A08	Reference_v1_chr8	bnl2961	66
8	A08	Reference_v1_chr8	nau1037	67
8	A08	Reference_v1_chr8	pgh244	68
8	A08	Reference_v1_chr8	a1108	68
8	A08	Reference_v1_chr8	fif1-800	69
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24	D08	Reference_v1_chr24	p10-56	30
24	D08	Reference_v1_chr24	par08f09	30
24	D08	Reference_v1_chr24	e2m1_242	31
24	D08	Reference_v1_chr24	coau2a11	32
24	D08	Reference_v1_chr24	unig27f10	32
24	D08	Reference_v1_chr24	gate4ah08	32
24	D08	Reference_v1_chr24	par07d04	33
24	D08	Reference_v1_chr24	gate1bg03	33
24	D08	Reference_v1_chr24	a1108	34
24	D08	Reference_v1_chr24	bnl3089	35
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24	D08	Reference_v1_chr24	dc1od8-250	39
24	D08	Reference_v1_chr24	gate4de09	40
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24	D08	Reference_v1_chr24	cir0278	42
24	D08	Reference_v1_chr24	bnl3627	43
24	D08	Reference_v1_chr24	nau3455	44
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24	D08	Reference_v1_chr24	nau1350	46
24	D08	Reference_v1_chr24	jespr0183	47
24	D08	Reference_v1_chr24	jespr0092	48
24	D08	Reference_v1_chr24	nau3771	49
24	D08	Reference_v1_chr24	t34e2b	50
24	D08	Reference_v1_chr24	nau3910	51
24	D08	Reference_v1_chr24	t21e4	52
24	D08	Reference_v1_chr24	cir0289	53
24	D08	Reference_v1_chr24	e6m5_350	53
24	D08	Reference_v1_chr24	cir0070	53
24	D08	Reference_v1_chr24	bnl0252	54
24	D08	Reference_v1_chr24	nau1088	55
24	D08	Reference_v1_chr24	nau5379	56
24	D08	Reference_v1_chr24	bnl2582	57
24	D08	Reference_v1_chr24	nau2230	58
24	D08	Reference_v1_chr24	nau0435	59
24	D08	Reference_v1_chr24	jespr0127	60
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24	D08	Reference_v1_chr24	muss0255	62
24	D08	Reference_v1_chr24	mghes0022	63
24	D08	Reference_v1_chr24	bnl1017	64

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8	A08	Reference_v1_chr8	unig25b12	71
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8	A08	Reference_v1_chr8	e1m5_85	73
8	A08	Reference_v1_chr8	nau2665	74
8	A08	Reference_v1_chr8	jespr0046	75
8	A08	Reference_v1_chr8	unig24d03	76
8	A08	Reference_v1_chr8	dpl0176	77
8	A08	Reference_v1_chr8	t44e11d	78
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8	A08	Reference_v1_chr8	par0785	79
8	A08	Reference_v1_chr8	unig27g11	79
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8	A08	Reference_v1_chr8	bnl3084	82
8	A08	Reference_v1_chr8	tmb1675	83
8	A08	Reference_v1_chr8	nau3964	84
8	A08	Reference_v1_chr8	e1m3_270	85
8	A08	Reference_v1_chr8	tmb0834	86
8	A08	Reference_v1_chr8	musb0255	87
8	A08	Reference_v1_chr8	em2od13-105	88
8	A08	Reference_v1_chr8	nau2214	89
8	A08	Reference_v1_chr8	tmb2103	90
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8	A08	Reference_v1_chr8	me1em6-80	94
8	A08	Reference_v1_chr8	bnl2993	95
8	A08	Reference_v1_chr8	tmb1330	96
8	A08	Reference_v1_chr8	nau3499	97
8	A08	Reference_v1_chr8	e2m6_322	98
8	A08	Reference_v1_chr8	tmb0181	99
8	A08	Reference_v1_chr8	muss0280	100
8	A08	Reference_v1_chr8	nau1164	101
8	A08	Reference_v1_chr8	nau1336	102
8	A08	Reference_v1_chr8	gate2bc04	103
8	A08	Reference_v1_chr8	nau4010	104
8	A08	Reference_v1_chr8	nau3058	105
8	A08	Reference_v1_chr8	nau5173	106
8	A08	Reference_v1_chr8	musb1188	107
8	A08	Reference_v1_chr8	em5dc1-300	108
8	A08	Reference_v1_chr8	nau3769	109
8	A08	Reference_v1_chr8	nau3199	110
8	A08	Reference_v1_chr8	nau1531	111
8	A08	Reference_v1_chr8	nau2914	112

24	D08	Reference_v1_chr24	cg03	65
24	D08	Reference_v1_chr24	em1od26-500	66
24	D08	Reference_v1_chr24	nau0774	67
24	D08	Reference_v1_chr24	e2m6_77	68
24	D08	Reference_v1_chr24	cir0017	69
24	D08	Reference_v1_chr24	nau5335	70
24	D08	Reference_v1_chr24	nau1575	71
24	D08	Reference_v1_chr24	e4m3_117	72
24	D08	Reference_v1_chr24	nau1546	73
24	D08	Reference_v1_chr24	cir0004	74
24	D08	Reference_v1_chr24	e7m4_287	75
24	D08	Reference_v1_chr24	e5m5_269	75
24	D08	Reference_v1_chr24	e3m7_360	75
24	D08	Reference_v1_chr24	bnl3604	76
24	D08	Reference_v1_chr24	nau1125	77
24	D08	Reference_v1_chr24	nau3773	78
24	D08	Reference_v1_chr24	tmb0010	79
24	D08	Reference_v1_chr24	nau3988	80
24	D08	Reference_v1_chr24	dpl0231	81
24	D08	Reference_v1_chr24	tmb1182	81
24	D08	Reference_v1_chr24	nau3224	82
24	D08	Reference_v1_chr24	nau2240	83
24	D08	Reference_v1_chr24	nau2914	83
24	D08	Reference_v1_chr24	em1dc1-205	84
24	D08	Reference_v1_chr24	nau0827	85
24	D08	Reference_v1_chr24	nau3954	86
24	D08	Reference_v1_chr24	e1m2_360	87
24	D08	Reference_v1_chr24	bnl2568	88
24	D08	Reference_v1_chr24	t2e3d	89
24	D08	Reference_v1_chr24	cir0370	90
24	D08	Reference_v1_chr24	nau2926	91
24	D08	Reference_v1_chr24	m4e9a	92
24	D08	Reference_v1_chr24	nau2631	93
24	D08	Reference_v1_chr24	nau2829	94
24	D08	Reference_v1_chr24	nau1531	95
24	D08	Reference_v1_chr24	bnl2499	96
24	D08	Reference_v1_chr24	t12e13	97
24	D08	Reference_v1_chr24	t4e2b	98
24	D08	Reference_v1_chr24	nau3667	99
24	D08	Reference_v1_chr24	nau1322	100
24	D08	Reference_v1_chr24	nau1262	101
24	D08	Reference_v1_chr24	nau2292	102
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8	A08	Reference_v1_chr8	e7m2_156	140
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8	A08	Reference_v1_chr8	gate3da02	143
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8	A08	Reference_v1_chr8	cir0324	144
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8	A08	Reference_v1_chr8	e6m6_550	145
8	A08	Reference_v1_chr8	t28e7e	146

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24	D08	Reference_v1_chr24	nau3499	135
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24	D08	Reference_v1_chr24	mucs0419	138
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8	A08	Reference_v1_chr8	a1590	147
8	A08	Reference_v1_chr8	gate4da08	147
8	A08	Reference_v1_chr8	pgh318	147
8	A08	Reference_v1_chr8	mucs0148	148
8	A08	Reference_v1_chr8	gate2cd01	149
8	A08	Reference_v1_chr8	e8m3_440	150
8	A08	Reference_v1_chr8	e1m5_167	151
8	A08	Reference_v1_chr8	e7m5_95	151
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8	A08	Reference_v1_chr8	p10-56	153
8	A08	Reference_v1_chr8	e3m6b	154
8	A08	Reference_v1_chr8	pgh422	155
8	A08	Reference_v1_chr8	e3m1_315	156
8	A08	Reference_v1_chr8	e2m7_87	156
8	A08	Reference_v1_chr8	e2m3_198	156
8	A08	Reference_v1_chr8	e8m6_220	157
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8	A08	Reference_v1_chr8	par0973	165
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8	A08	Reference_v1_chr8	e8m7d	170
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8	A08	Reference_v1_chr8	e2m7_78	172

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24	D08	Reference_v1_chr24	nau0478	147
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24	D08	Reference_v1_chr24	l709	166
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24	D08	Reference_v1_chr24	nau1302	167
24	D08	Reference_v1_chr24	nau2434	168
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24	D08	Reference_v1_chr24	p05-04	170
24	D08	Reference_v1_chr24	p05-37	170
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24	D08	Reference_v1_chr24	gate4bg06	171
24	D08	Reference_v1_chr24	bnl2961	171
24	D08	Reference_v1_chr24	bnl2616	172
24	D08	Reference_v1_chr24	gate3ce04	173
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24	D08	Reference_v1_chr24	par0571	175
24	D08	Reference_v1_chr24	gate2ac11	175

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8	A08	Reference_v1_chr8	bnl2527	179
8	A08	Reference_v1_chr8	e2m1_184	180
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8	A08	Reference_v1_chr8	musb1001	183
8	A08	Reference_v1_chr8	par0950	184
8	A08	Reference_v1_chr8	par03-07	184
8	A08	Reference_v1_chr8	p05-18	184
8	A08	Reference_v1_chr8	cg04	184
8	A08	Reference_v1_chr8	par3-07	184
8	A08	Reference_v1_chr8	e3m5c	185
8	A08	Reference_v1_chr8	musb0818	186
8	A08	Reference_v1_chr8	gafb13b07	187
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8	A08	Reference_v1_chr8	unig06g04	189
8	A08	Reference_v1_chr8	gate1bf02	190
8	A08	Reference_v1_chr8	unig25c01	190
8	A08	Reference_v1_chr8	e6m1d	191
8	A08	Reference_v1_chr8	bnl3658	192
8	A08	Reference_v1_chr8	cm0043	193
8	A08	Reference_v1_chr8	tmb1717	194
8	A08	Reference_v1_chr8	gate3ch11	195
8	A08	Reference_v1_chr8	gate1bh09	196
8	A08	Reference_v1_chr8	jespr0230	197
8	A08	Reference_v1_chr8	par04-11	198
8	A08	Reference_v1_chr8	par0789	199
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8	A08	Reference_v1_chr8	nau2293	202
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8	A08	Reference_v1_chr8	cir0343	212
8	A08	Reference_v1_chr8	bnl1646	212
8	A08	Reference_v1_chr8	a1658	212

24	D08	Reference_v1_chr24	par0972	175
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24	D08	Reference_v1_chr24	pvnc244	178
24	D08	Reference_v1_chr24	cir0119	179
24	D08	Reference_v1_chr24	jespr0070.	180
24	D08	Reference_v1_chr24	nau4091	181
24	D08	Reference_v1_chr24	cir0354	182
24	D08	Reference_v1_chr24	par0144	183
24	D08	Reference_v1_chr24	bnl1513	184
24	D08	Reference_v1_chr24	e5m4_345	185
24	D08	Reference_v1_chr24	nau1561	186
24	D08	Reference_v1_chr24	a1107	187
24	D08	Reference_v1_chr24	g1074	187
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24	D08	Reference_v1_chr24	nau1369	189
24	D08	Reference_v1_chr24	nau3221	190
24	D08	Reference_v1_chr24	nau3158	191
24	D08	Reference_v1_chr24	nau5130	192
24	D08	Reference_v1_chr24	jespr0291	193
24	D08	Reference_v1_chr24	unig23g01	194
24	D08	Reference_v1_chr24	nau5312	195
24	D08	Reference_v1_chr24	nau2306	196
24	D08	Reference_v1_chr24	nau3786	197
24	D08	Reference_v1_chr24	nau0816	198
24	D08	Reference_v1_chr24	y1187	199
24	D08	Reference_v1_chr24	nau2876	200
24	D08	Reference_v1_chr24	mghes0029	201
24	D08	Reference_v1_chr24	par0248	202
24	D08	Reference_v1_chr24	nau2934	203
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24	D08	Reference_v1_chr24	jespr0157	205
24	D08	Reference_v1_chr24	jespr0308	206
24	D08	Reference_v1_chr24	jespr0302	207
24	D08	Reference_v1_chr24	nau0738	208
24	D08	Reference_v1_chr24	gate3bf10	209
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24	D08	Reference_v1_chr24	par0503	209
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24	D08	Reference_v1_chr24	par0947	215

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8	A08	Reference_v1_chr8	muss0250	214
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8	A08	Reference_v1_chr8	musb0100	216
8	A08	Reference_v1_chr8	muss0409	217
8	A08	Reference_v1_chr8	nau3793	218
8	A08	Reference_v1_chr8	nau3668	219
8	A08	Reference_v1_chr8	nau3324	220
8	A08	Reference_v1_chr8	e2m6_159	221
8	A08	Reference_v1_chr8	par0978	222
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8	A08	Reference_v1_chr8	unig26g07	228
8	A08	Reference_v1_chr8	gate3ca01	228
8	A08	Reference_v1_chr8	g1078	228
8	A08	Reference_v1_chr8	gate3be04	228
8	A08	Reference_v1_chr8	par0123	229
8	A08	Reference_v1_chr8	gate4dg08	230
8	A08	Reference_v1_chr8	g1276	231
8	A08	Reference_v1_chr8	par0490	231
8	A08	Reference_v1_chr8	cir0028	232
8	A08	Reference_v1_chr8	t6e6b	233

24	D08	Reference_v1_chr24	nau3072	216
24	D08	Reference_v1_chr24	cir0388	217
24	D08	Reference_v1_chr24	nau3010	218
24	D08	Reference_v1_chr24	coau2l09	219
24	D08	Reference_v1_chr24	cir0026	220
24	D08	Reference_v1_chr24	nau1027	221
24	D08	Reference_v1_chr24	bnl2597	222

Table 4.14 Chromosomes A09 and D09 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
9	A09	Reference_v1_chr9	bnl0686	1
9	A09	Reference_v1_chr9	bnl2681	2
9	A09	Reference_v1_chr9	nau5468	3
9	A09	Reference_v1_chr9	tmb0317	4
9	A09	Reference_v1_chr9	t4e4c	5
9	A09	Reference_v1_chr9	nau3888	6
9	A09	Reference_v1_chr9	t31e12	7
9	A09	Reference_v1_chr9	nau3538	8
9	A09	Reference_v1_chr9	bnl1434	9
9	A09	Reference_v1_chr9	e3m5a	10
9	A09	Reference_v1_chr9	cir0077	11
9	A09	Reference_v1_chr9	cir0079	12
9	A09	Reference_v1_chr9	bnl1707	13
9	A09	Reference_v1_chr9	nau0987	14
9	A09	Reference_v1_chr9	bnl3279	15
9	A09	Reference_v1_chr9	pgh743	16
9	A09	Reference_v1_chr9	par0288	17
9	A09	Reference_v1_chr9	dpl0222	18
9	A09	Reference_v1_chr9	e4m5_140	19
9	A09	Reference_v1_chr9	t33e16a	20
9	A09	Reference_v1_chr9	stv0164	21
9	A09	Reference_v1_chr9	gate1ad03	22
9	A09	Reference_v1_chr9	bnl1670	23
9	A09	Reference_v1_chr9	e1m6_292	24
9	A09	Reference_v1_chr9	tmb0177	25
9	A09	Reference_v1_chr9	a1737	26
9	A09	Reference_v1_chr9	m4e12b	27
9	A09	Reference_v1_chr9	dpl0679	28
9	A09	Reference_v1_chr9	it-isj10f51r	29
9	A09	Reference_v1_chr9	e6m8_168	30
9	A09	Reference_v1_chr9	mghes0025	31
9	A09	Reference_v1_chr9	nau3159	32
9	A09	Reference_v1_chr9	it-isj06f42r	33
9	A09	Reference_v1_chr9	tmb0991	34
9	A09	Reference_v1_chr9	bnl4049	35
9	A09	Reference_v1_chr9	bnl3874	36
9	A09	Reference_v1_chr9	pvnc163	37
9	A09	Reference_v1_chr9	it-isj03f51r	38
9	A09	Reference_v1_chr9	e8m8_97	39
9	A09	Reference_v1_chr9	e3m1a	40
9	A09	Reference_v1_chr9	e2m3_90	41
9	A09	Reference_v1_chr9	e17m5	42
9	A09	Reference_v1_chr9	unig25e04	43
9	A09	Reference_v1_chr9	e11m4b	44

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
23	D09	Reference_v1_chr23	g1074	1
23	D09	Reference_v1_chr23	unig06b07	2
23	D09	Reference_v1_chr23	pvnc027	3
23	D09	Reference_v1_chr23	gate1cc04	3
23	D09	Reference_v1_chr23	g1128	3
23	D09	Reference_v1_chr23	r45s	3
23	D09	Reference_v1_chr23	gate4dg03	4
23	D09	Reference_v1_chr23	unig24a10	5
23	D09	Reference_v1_chr23	coau3l05	6
23	D09	Reference_v1_chr23	gate3cb01	7
23	D09	Reference_v1_chr23	gate3be06	7
23	D09	Reference_v1_chr23	unig24f05	8
23	D09	Reference_v1_chr23	unig23g12	8
23	D09	Reference_v1_chr23	gate4ah01	8
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23	D09	Reference_v1_chr23	gate3da04	164
23	D09	Reference_v1_chr23	e5m1_110	165
23	D09	Reference_v1_chr23	coau2a21	166
23	D09	Reference_v1_chr23	bnl1648	167
23	D09	Reference_v1_chr23	jespr114	168
23	D09	Reference_v1_chr23	jespr0114	169
23	D09	Reference_v1_chr23	jespr0101	170
23	D09	Reference_v1_chr23	par0209	171
23	D09	Reference_v1_chr23	par10g06	172
23	D09	Reference_v1_chr23	par0279	172
23	D09	Reference_v1_chr23	gate3cf09	173
23	D09	Reference_v1_chr23	coau4k10	174
23	D09	Reference_v1_chr23	gate4db01	175
23	D09	Reference_v1_chr23	gate1aa09	175
23	D09	Reference_v1_chr23	unig27b04	176
23	D09	Reference_v1_chr23	e7m1_238	177
23	D09	Reference_v1_chr23	nau2689	178
23	D09	Reference_v1_chr23	nau0864	179

9	A09	Reference_v1_chr9	a1572	189
9	A09	Reference_v1_chr9	tmb2551	190
9	A09	Reference_v1_chr9	bnl3582	191
9	A09	Reference_v1_chr9	unig23e08	191
9	A09	Reference_v1_chr9	pgh647	191
9	A09	Reference_v1_chr9	parc-15	192
9	A09	Reference_v1_chr9	gate2ca02	193
9	A09	Reference_v1_chr9	bnl4028	194
9	A09	Reference_v1_chr9	nau0858	195
9	A09	Reference_v1_chr9	nau1046	196
9	A09	Reference_v1_chr9	pxp2-05	197
9	A09	Reference_v1_chr9	a1733	198
9	A09	Reference_v1_chr9	nau2591	199
9	A09	Reference_v1_chr9	par07c01	200
9	A09	Reference_v1_chr9	par0873	201
9	A09	Reference_v1_chr9	gate1cf01	202
9	A09	Reference_v1_chr9	par0624	203
9	A09	Reference_v1_chr9	nau3414	204
9	A09	Reference_v1_chr9	muss0083	205
9	A09	Reference_v1_chr9	gate3cf09	206
9	A09	Reference_v1_chr9	par0240	207
9	A09	Reference_v1_chr9	par07c05	207
9	A09	Reference_v1_chr9	nau0462	208
9	A09	Reference_v1_chr9	nau3061	209
9	A09	Reference_v1_chr9	mghes0002	210
9	A09	Reference_v1_chr9	bnl2590	211
9	A09	Reference_v1_chr9	nau3280	212
9	A09	Reference_v1_chr9	p10-62	213
9	A09	Reference_v1_chr9	coau2n18	213
9	A09	Reference_v1_chr9	bnl0274	214
9	A09	Reference_v1_chr9	e5m5_158	215
9	A09	Reference_v1_chr9	bnl2741	216
9	A09	Reference_v1_chr9	mghes0046	217
9	A09	Reference_v1_chr9	muss0022	218
9	A09	Reference_v1_chr9	dpl0395	219
9	A09	Reference_v1_chr9	bnl4099	220
9	A09	Reference_v1_chr9	e1m3_116	221
9	A09	Reference_v1_chr9	hau0085	222
9	A09	Reference_v1_chr9	bnl0597	223
9	A09	Reference_v1_chr9	bnl2750	224
9	A09	Reference_v1_chr9	muss0298	225
9	A09	Reference_v1_chr9	nau0864	226
9	A09	Reference_v1_chr9	dpl0541	227
9	A09	Reference_v1_chr9	mucs0072	228
9	A09	Reference_v1_chr9	muss0151	229
9	A09	Reference_v1_chr9	muss0189	230
9	A09	Reference_v1_chr9	at60	231

23	D09	Reference_v1_chr23	muss0151	180
23	D09	Reference_v1_chr23	e3m1_310	181
23	D09	Reference_v1_chr23	tmb1758	182
23	D09	Reference_v1_chr23	bnl0597	183
23	D09	Reference_v1_chr23	bnl4053	184
23	D09	Reference_v1_chr23	cshe0118	185
23	D09	Reference_v1_chr23	cm0007	186
23	D09	Reference_v1_chr23	bnl2608	187
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23	D09	Reference_v1_chr23	mucs0006	189
23	D09	Reference_v1_chr23	a1707	190
23	D09	Reference_v1_chr23	dpl0307	191
23	D09	Reference_v1_chr23	bnl3173	192
23	D09	Reference_v1_chr23	a1482	193
23	D09	Reference_v1_chr23	gate3bf10	194
23	D09	Reference_v1_chr23	par0704	194
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23	D09	Reference_v1_chr23	pgh558	194
23	D09	Reference_v1_chr23	a1608	194
23	D09	Reference_v1_chr23	gate4ae03	195
23	D09	Reference_v1_chr23	gate2aa02	195

9	A09	Reference_v1_chr9	nau0595	232
9	A09	Reference_v1_chr9	jespr0095	233
9	A09	Reference_v1_chr9	cg21	234
9	A09	Reference_v1_chr9	pxp3-07	235
9	A09	Reference_v1_chr9	gate3bf10	236
9	A09	Reference_v1_chr9	ne1	236
9	A09	Reference_v1_chr9	bnl4053	236
9	A09	Reference_v1_chr9	coau1h15	236
9	A09	Reference_v1_chr9	a1707	236
9	A09	Reference_v1_chr9	coau2c13	237
9	A09	Reference_v1_chr9	nau2354	238
9	A09	Reference_v1_chr9	bnl3173	239
9	A09	Reference_v1_chr9	nau2723	240

Table 4.15 Chromosomes A10 and D10 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
10	A10	Reference_v1_chr10	od3od17-150	1
10	A10	Reference_v1_chr10	cir0285	2
10	A10	Reference_v1_chr10	nau5166	3
10	A10	Reference_v1_chr10	nau2538	4
10	A10	Reference_v1_chr10	nau2532	4
10	A10	Reference_v1_chr10	nau2534	4
10	A10	Reference_v1_chr10	nau2531	5
10	A10	Reference_v1_chr10	nau3917	6
10	A10	Reference_v1_chr10	par0468	7
10	A10	Reference_v1_chr10	bnl4059	7
10	A10	Reference_v1_chr10	gate3be08	7
10	A10	Reference_v1_chr10	par0101	7
10	A10	Reference_v1_chr10	unig27b09	8
10	A10	Reference_v1_chr10	a1461	9
10	A10	Reference_v1_chr10	unig25h10	10
10	A10	Reference_v1_chr10	nau3454	11
10	A10	Reference_v1_chr10	e6m7_600	12
10	A10	Reference_v1_chr10	a1468	13
10	A10	Reference_v1_chr10	unig26d08	14
10	A10	Reference_v1_chr10	gate4ca05	14
10	A10	Reference_v1_chr10	gate2af06	14
10	A10	Reference_v1_chr10	a1484	15
10	A10	Reference_v1_chr10	pgh295	16
10	A10	Reference_v1_chr10	gate1be03	16
10	A10	Reference_v1_chr10	a1163	16
10	A10	Reference_v1_chr10	cg24	17
10	A10	Reference_v1_chr10	p12-28	18
10	A10	Reference_v1_chr10	g1059	18
10	A10	Reference_v1_chr10	gate3bd09	19
10	A10	Reference_v1_chr10	bnl3499	20
10	A10	Reference_v1_chr10	jespr0152	21
10	A10	Reference_v1_chr10	gate1ab08	22
10	A10	Reference_v1_chr10	cir0009	23
10	A10	Reference_v1_chr10	pvnc106	24
10	A10	Reference_v1_chr10	m5e1-440	25
10	A10	Reference_v1_chr10	pvnc163	26
10	A10	Reference_v1_chr10	e4m6_258	27
10	A10	Reference_v1_chr10	m14e12-580*	28
10	A10	Reference_v1_chr10	e2m5_355	29
10	A10	Reference_v1_chr10	jespr0056	30
10	A10	Reference_v1_chr10	e7m1_204	31
10	A10	Reference_v1_chr10	e7m5_500	32
10	A10	Reference_v1_chr10	e6m6_440	32
10	A10	Reference_v1_chr10	e3m1_259	32

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
20	D10	Reference_v1_chr20	e3m2_172	1
20	D10	Reference_v1_chr20	e3m2_174	2
20	D10	Reference_v1_chr20	par06g09	3
20	D10	Reference_v1_chr20	p12-19	4
20	D10	Reference_v1_chr20	bnl2553	4
20	D10	Reference_v1_chr20	e6m4_148	4
20	D10	Reference_v1_chr20	e4m3_108	5
20	D10	Reference_v1_chr20	bnl3646	5
20	D10	Reference_v1_chr20	unig23e04	6
20	D10	Reference_v1_chr20	g1104	6
20	D10	Reference_v1_chr20	tmb0272	7
20	D10	Reference_v1_chr20	musb1304	8
20	D10	Reference_v1_chr20	g1237	9
20	D10	Reference_v1_chr20	gate4af02	10
20	D10	Reference_v1_chr20	t4e5d	11
20	D10	Reference_v1_chr20	coau2i04	12
20	D10	Reference_v1_chr20	nau0672	13
20	D10	Reference_v1_chr20	gate1bh09	14
20	D10	Reference_v1_chr20	p12-13	14
20	D10	Reference_v1_chr20	g1115	14
20	D10	Reference_v1_chr20	coau1f04	14
20	D10	Reference_v1_chr20	nau3368	15
20	D10	Reference_v1_chr20	bnl3071	16
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20	D10	Reference_v1_chr20	od3od22-205	18
20	D10	Reference_v1_chr20	muss0096	19
20	D10	Reference_v1_chr20	par04a09	20
20	D10	Reference_v1_chr20	gate1ah09	21
20	D10	Reference_v1_chr20	t14e16a	22
20	D10	Reference_v1_chr20	nau1169	23
20	D10	Reference_v1_chr20	jespr0190	24
20	D10	Reference_v1_chr20	nau4921	25
20	D10	Reference_v1_chr20	bnl3280	26
20	D10	Reference_v1_chr20	g1218	27
20	D10	Reference_v1_chr20	nau4881	28
20	D10	Reference_v1_chr20	a1217	29
20	D10	Reference_v1_chr20	dpl0026	30
20	D10	Reference_v1_chr20	nau3813	31
20	D10	Reference_v1_chr20	nau2888	32
20	D10	Reference_v1_chr20	dpl0442	33
20	D10	Reference_v1_chr20	nau3137	34
20	D10	Reference_v1_chr20	tmb1313	35
20	D10	Reference_v1_chr20	unig26g09	36
20	D10	Reference_v1_chr20	nau1280	37

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10	A10	Reference_v1_chr10	e1m6_240	34
10	A10	Reference_v1_chr10	cir0171	35
10	A10	Reference_v1_chr10	tmb1288	36
10	A10	Reference_v1_chr10	t14e15c	37
10	A10	Reference_v1_chr10	t32e12a	38
10	A10	Reference_v1_chr10	nau0456	39
10	A10	Reference_v1_chr10	t28e7d	40
10	A10	Reference_v1_chr10	nau2166	41
10	A10	Reference_v1_chr10	bnl2530	42
10	A10	Reference_v1_chr10	od3ga34-205	43
10	A10	Reference_v1_chr10	gh.annexin	44
10	A10	Reference_v1_chr10	me1ga13-115	45
10	A10	Reference_v1_chr10	me1dc1-260	46
10	A10	Reference_v1_chr10	nau2935	47
10	A10	Reference_v1_chr10	nau3574	48
10	A10	Reference_v1_chr10	e6m8_235	49
10	A10	Reference_v1_chr10	e7m5_510	49
10	A10	Reference_v1_chr10	cir0291	49
10	A10	Reference_v1_chr10	cir0018	49
10	A10	Reference_v1_chr10	gate1cf10	50
10	A10	Reference_v1_chr10	dc1ga5-400	51
10	A10	Reference_v1_chr10	musb0625	52
10	A10	Reference_v1_chr10	e7m5_425	53
10	A10	Reference_v1_chr10	m4e10c	54
10	A10	Reference_v1_chr10	m11e17-680	55
10	A10	Reference_v1_chr10	bnl2449	56
10	A10	Reference_v1_chr10	e8m3_63	56
10	A10	Reference_v1_chr10	me8ga28-225	57
10	A10	Reference_v1_chr10	m3e13a	58
10	A10	Reference_v1_chr10	t37e4b	58
10	A10	Reference_v1_chr10	tmb1806	59
10	A10	Reference_v1_chr10	t50e15b	60
10	A10	Reference_v1_chr10	nau2472	61
10	A10	Reference_v1_chr10	bnl0391	62
10	A10	Reference_v1_chr10	bnl2641	63
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10	A10	Reference_v1_chr10	nau5362	65
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10	A10	Reference_v1_chr10	a1158	67
10	A10	Reference_v1_chr10	unig28c07	67
10	A10	Reference_v1_chr10	unig25a11	68
10	A10	Reference_v1_chr10	cir0400	69
10	A10	Reference_v1_chr10	nau3013	70
10	A10	Reference_v1_chr10	gate1df08	71
10	A10	Reference_v1_chr10	mghes0075	72
10	A10	Reference_v1_chr10	t24e16	73

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20	D10	Reference_v1_chr20	coau2o08	40
20	D10	Reference_v1_chr20	nau4014	41
20	D10	Reference_v1_chr20	nau0922	42
20	D10	Reference_v1_chr20	jespr0235	43
20	D10	Reference_v1_chr20	gate4bc02	44
20	D10	Reference_v1_chr20	par0827	44
20	D10	Reference_v1_chr20	a1183	45
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20	D10	Reference_v1_chr20	bnl0169	49
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20	D10	Reference_v1_chr20	bnl0119	52
20	D10	Reference_v1_chr20	cir0340	53
20	D10	Reference_v1_chr20	cir0020	54
20	D10	Reference_v1_chr20	nau2182	55
20	D10	Reference_v1_chr20	nau2869	56
20	D10	Reference_v1_chr20	cir0043	57
20	D10	Reference_v1_chr20	gate1dg09	57
20	D10	Reference_v1_chr20	nau1297	58
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20	D10	Reference_v1_chr20	nau3404	60
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20	D10	Reference_v1_chr20	nau3665	62
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20	D10	Reference_v1_chr20	tmb0317	64
20	D10	Reference_v1_chr20	par0430	65
20	D10	Reference_v1_chr20	cir0166	66
20	D10	Reference_v1_chr20	gate3bb08	67
20	D10	Reference_v1_chr20	pxp4-15	67
20	D10	Reference_v1_chr20	gate1bc08	67
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20	D10	Reference_v1_chr20	gate1ca06	67
20	D10	Reference_v1_chr20	muss0279	68
20	D10	Reference_v1_chr20	pxp4-75	69
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20	D10	Reference_v1_chr20	p06-47	74

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10	A10	Reference_v1_chr10	nau0708	76
10	A10	Reference_v1_chr10	bnl4016	77
10	A10	Reference_v1_chr10	mucs0494	78
10	A10	Reference_v1_chr10	e8m4_260	79
10	A10	Reference_v1_chr10	e3m2_88	79
10	A10	Reference_v1_chr10	gate3cb09	80
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10	A10	Reference_v1_chr10	pgh588	83
10	A10	Reference_v1_chr10	musb0847	84
10	A10	Reference_v1_chr10	nau3682	85
10	A10	Reference_v1_chr10	a1344	86
10	A10	Reference_v1_chr10	musb0831	87
10	A10	Reference_v1_chr10	gate4df12	88
10	A10	Reference_v1_chr10	cir0372	89
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10	A10	Reference_v1_chr10	unig28g09	94
10	A10	Reference_v1_chr10	unig26e05	94
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10	A10	Reference_v1_chr10	e7m4_88	97
10	A10	Reference_v1_chr10	tmb0858	98
10	A10	Reference_v1_chr10	gate1bf03	99
10	A10	Reference_v1_chr10	nau0440	100
10	A10	Reference_v1_chr10	nau0785	101
10	A10	Reference_v1_chr10	musb0958	102
10	A10	Reference_v1_chr10	nau1066	103
10	A10	Reference_v1_chr10	gafb17n07	104
10	A10	Reference_v1_chr10	gate4dh08	105
10	A10	Reference_v1_chr10	m3e2-670	106
10	A10	Reference_v1_chr10	bnl0256	107
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10	A10	Reference_v1_chr10	mghes0030	109
10	A10	Reference_v1_chr10	pbam250	110
10	A10	Reference_v1_chr10	pgh653	110
10	A10	Reference_v1_chr10	e5m3_108	111

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20	D10	Reference_v1_chr20	bnl0946	77
20	D10	Reference_v1_chr20	dpl0135	78
20	D10	Reference_v1_chr20	e7m7_291	79
20	D10	Reference_v1_chr20	t2e5a	80
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20	D10	Reference_v1_chr20	cir0080	82
20	D10	Reference_v1_chr20	a1695	82
20	D10	Reference_v1_chr20	cir0171	82
20	D10	Reference_v1_chr20	gate4cf10	82
20	D10	Reference_v1_chr20	e6m5_78	82
20	D10	Reference_v1_chr20	bnl3660	83
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20	D10	Reference_v1_chr20	t4e5a	85
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20	D10	Reference_v1_chr20	a1131	87
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20	D10	Reference_v1_chr20	bnl3379	87
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20	D10	Reference_v1_chr20	unig24e01	87
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20	D10	Reference_v1_chr20	cg26	88
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20	D10	Reference_v1_chr20	gate3bd09	93
20	D10	Reference_v1_chr20	gate4af01	93
20	D10	Reference_v1_chr20	unig23d03	93
20	D10	Reference_v1_chr20	tmb0281	94
20	D10	Reference_v1_chr20	nau0654	95
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20	D10	Reference_v1_chr20	cir0305	97
20	D10	Reference_v1_chr20	muss0414	98
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20	D10	Reference_v1_chr20	nau3907	100
20	D10	Reference_v1_chr20	tmb0443	101
20	D10	Reference_v1_chr20	bnl3948	102
20	D10	Reference_v1_chr20	cir0063	103
20	D10	Reference_v1_chr20	e8m8_102	104
20	D10	Reference_v1_chr20	bnl3670	104
20	D10	Reference_v1_chr20	bnl3993	104

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10	A10	Reference_v1_chr10	bnl3895	113
10	A10	Reference_v1_chr10	s0237	114
10	A10	Reference_v1_chr10	coau4j15	115
10	A10	Reference_v1_chr10	8b9	116
10	A10	Reference_v1_chr10	e7m4d	117
10	A10	Reference_v1_chr10	par10a09	118
10	A10	Reference_v1_chr10	e2m6_241	119
10	A10	Reference_v1_chr10	unig26b01	120
10	A10	Reference_v1_chr10	gate4ad08	120
10	A10	Reference_v1_chr10	unig28c09	120
10	A10	Reference_v1_chr10	m4e3-300	121
10	A10	Reference_v1_chr10	gate2cc04	122
10	A10	Reference_v1_chr10	gate2bf02	122
10	A10	Reference_v1_chr10	gate4ae01	122
10	A10	Reference_v1_chr10	bnl1160	123
10	A10	Reference_v1_chr10	bnl3300	124
10	A10	Reference_v1_chr10	s0321	125
10	A10	Reference_v1_chr10	s0465	126
10	A10	Reference_v1_chr10	coau3f17	127
10	A10	Reference_v1_chr10	p06-47	127
10	A10	Reference_v1_chr10	s0435	128
10	A10	Reference_v1_chr10	gate1cb10	129
10	A10	Reference_v1_chr10	gate1bc10	129
10	A10	Reference_v1_chr10	a1695	129
10	A10	Reference_v1_chr10	unig06h02	129
10	A10	Reference_v1_chr10	me8ga2-130	130
10	A10	Reference_v1_chr10	gate4ba10	131
10	A10	Reference_v1_chr10	gate1ce04	131
10	A10	Reference_v1_chr10	gate4ag08	131
10	A10	Reference_v1_chr10	nau0921	132
10	A10	Reference_v1_chr10	y1816	133
10	A10	Reference_v1_chr10	nau0538	134
10	A10	Reference_v1_chr10	cm0027	135
10	A10	Reference_v1_chr10	pgh504	136
10	A10	Reference_v1_chr10	pgh700	137
10	A10	Reference_v1_chr10	gate4ca04	137
10	A10	Reference_v1_chr10	bnl1253	138
10	A10	Reference_v1_chr10	m2e1-700	139
10	A10	Reference_v1_chr10	t43e10	140
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10	A10	Reference_v1_chr10	m12e12-800	142
10	A10	Reference_v1_chr10	m11e12-700	142
10	A10	Reference_v1_chr10	tmb0119	143
10	A10	Reference_v1_chr10	e8m8_490	144
10	A10	Reference_v1_chr10	e7m4_370	144
10	A10	Reference_v1_chr10	par0055	145

20	D10	Reference_v1_chr20	mucs0283	105
20	D10	Reference_v1_chr20	nau0697	106
20	D10	Reference_v1_chr20	nau0538	107
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20	D10	Reference_v1_chr20	musb0831	108
20	D10	Reference_v1_chr20	mucs0332	109
20	D10	Reference_v1_chr20	m7e7b	110
20	D10	Reference_v1_chr20	t11e11b	111
20	D10	Reference_v1_chr20	stv0100	112
20	D10	Reference_v1_chr20	nau5013	113
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20	D10	Reference_v1_chr20	w03	123
20	D10	Reference_v1_chr20	e1m5_175	124
20	D10	Reference_v1_chr20	e2m6_257	124
20	D10	Reference_v1_chr20	bnl3838	124
20	D10	Reference_v1_chr20	jespr0261	124
20	D10	Reference_v1_chr20	e4m5_350	124
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20	D10	Reference_v1_chr20	cir0121	125
20	D10	Reference_v1_chr20	jespr0056	126
20	D10	Reference_v1_chr20	muss0070	127
20	D10	Reference_v1_chr20	e4m2a	128
20	D10	Reference_v1_chr20	pgh298	129
20	D10	Reference_v1_chr20	par0850	129
20	D10	Reference_v1_chr20	a1212	129
20	D10	Reference_v1_chr20	muss0143	130
20	D10	Reference_v1_chr20	t7e8	131
20	D10	Reference_v1_chr20	nau0853	132
20	D10	Reference_v1_chr20	nau3574	133
20	D10	Reference_v1_chr20	nau3070	134
20	D10	Reference_v1_chr20	est8	135
20	D10	Reference_v1_chr20	g073a03a	136
20	D10	Reference_v1_chr20	pgh270	137
20	D10	Reference_v1_chr20	gate1df08	137
20	D10	Reference_v1_chr20	a1548	137
20	D10	Reference_v1_chr20	par0946	137
20	D10	Reference_v1_chr20	unig22b09	137
20	D10	Reference_v1_chr20	gate4dh08	137
20	D10	Reference_v1_chr20	gate2df07	137

10	A10	Reference_v1_chr10	gate3ca08	145
10	A10	Reference_v1_chr10	coau1c21	145
10	A10	Reference_v1_chr10	tmb0380	146
10	A10	Reference_v1_chr10	m2e6-750	147
10	A10	Reference_v1_chr10	musb1064	148
10	A10	Reference_v1_chr10	gate3cb05	149
10	A10	Reference_v1_chr10	gate1af09	149
10	A10	Reference_v1_chr10	gate1ce10	149
10	A10	Reference_v1_chr10	e5m1_169	150
10	A10	Reference_v1_chr10	t6e9c	151
10	A10	Reference_v1_chr10	par02-18	152
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10	A10	Reference_v1_chr10	bnl2705	154
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10	A10	Reference_v1_chr10	m8e2	156
10	A10	Reference_v1_chr10	e6m8_308	157
10	A10	Reference_v1_chr10	e2m8_96	157
10	A10	Reference_v1_chr10	e6m8_336	157
10	A10	Reference_v1_chr10	e2m7_158	157
10	A10	Reference_v1_chr10	cir0104	157
10	A10	Reference_v1_chr10	e7m8_410	157
10	A10	Reference_v1_chr10	tmb0307	158
10	A10	Reference_v1_chr10	musb1168	159
10	A10	Reference_v1_chr10	m3e2-700	160
10	A10	Reference_v1_chr10	e8m1_360	161
10	A10	Reference_v1_chr10	nau2323	162
10	A10	Reference_v1_chr10	bnl1161	163
10	A10	Reference_v1_chr10	nau1041	164
10	A10	Reference_v1_chr10	gate3da08	165
10	A10	Reference_v1_chr10	pxp1-30	166
10	A10	Reference_v1_chr10	coau1e05	166
10	A10	Reference_v1_chr10	muss0082	167
10	A10	Reference_v1_chr10	gate4bc08	168
10	A10	Reference_v1_chr10	a1110	169
10	A10	Reference_v1_chr10	musb1127	170
10	A10	Reference_v1_chr10	bnl3563	171
10	A10	Reference_v1_chr10	e5m6_82	171
10	A10	Reference_v1_chr10	e3m3_360	171
10	A10	Reference_v1_chr10	stv0100	172
10	A10	Reference_v1_chr10	m2e17-570	173
10	A10	Reference_v1_chr10	par09d03	174
10	A10	Reference_v1_chr10	e3m3a	175
10	A10	Reference_v1_chr10	cir0166	176
10	A10	Reference_v1_chr10	tmb0325	177
10	A10	Reference_v1_chr10	me1sa9-400	178
10	A10	Reference_v1_chr10	gate1bc08	179

20	D10	Reference_v1_chr20	tmb1356	138
20	D10	Reference_v1_chr20	gate3bf11	139
20	D10	Reference_v1_chr20	pgh384	139
20	D10	Reference_v1_chr20	muss0135	140
20	D10	Reference_v1_chr20	bnl2570	141
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20	D10	Reference_v1_chr20	coau2g20	143
20	D10	Reference_v1_chr20	t17e2	144
20	D10	Reference_v1_chr20	a1461	145
20	D10	Reference_v1_chr20	pgh418	145
20	D10	Reference_v1_chr20	pgh214	145
20	D10	Reference_v1_chr20	pgh404	145
20	D10	Reference_v1_chr20	a1286	145
20	D10	Reference_v1_chr20	gate3dd01	145
20	D10	Reference_v1_chr20	nau3407	146
20	D10	Reference_v1_chr20	tmb1630	147
20	D10	Reference_v1_chr20	par01d04	148
20	D10	Reference_v1_chr20	nau0440	149
20	D10	Reference_v1_chr20	nau1066	150
20	D10	Reference_v1_chr20	gate1ab02	151
20	D10	Reference_v1_chr20	gate4ag08	151
20	D10	Reference_v1_chr20	e3m7	152
20	D10	Reference_v1_chr20	g1257	153
20	D10	Reference_v1_chr20	t3e5b	154
20	D10	Reference_v1_chr20	nau3297	155
20	D10	Reference_v1_chr20	nau2017	156
20	D10	Reference_v1_chr20	bnl1145	157
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20	D10	Reference_v1_chr20	gate4ba10	158
20	D10	Reference_v1_chr20	pgh295	159
20	D10	Reference_v1_chr20	a1163	159
20	D10	Reference_v1_chr20	musb0338	160
20	D10	Reference_v1_chr20	g1272	161
20	D10	Reference_v1_chr20	cir0094	162
20	D10	Reference_v1_chr20	stv0117	163
20	D10	Reference_v1_chr20	e2m3_292	164
20	D10	Reference_v1_chr20	muss0467	165
20	D10	Reference_v1_chr20	a1158	166
20	D10	Reference_v1_chr20	unig26d08	167
20	D10	Reference_v1_chr20	unig23b04	167
20	D10	Reference_v1_chr20	gate3bf08	168
20	D10	Reference_v1_chr20	gate4ca05	169
20	D10	Reference_v1_chr20	gate2af06	169
20	D10	Reference_v1_chr20	p05-61	170
20	D10	Reference_v1_chr20	e4m5_159	171
20	D10	Reference_v1_chr20	pgh486	172
20	D10	Reference_v1_chr20	e4m5c	173

10	A10	Reference_v1_chr10	t2e5b	180
10	A10	Reference_v1_chr10	t1e9b	181
10	A10	Reference_v1_chr10	nau2869	182
10	A10	Reference_v1_chr10	e1m3_370	183
10	A10	Reference_v1_chr10	e6m6d	184
10	A10	Reference_v1_chr10	pxp1-40	185
10	A10	Reference_v1_chr10	par0675	186
10	A10	Reference_v1_chr10	m7e7-320	187
10	A10	Reference_v1_chr10	e3m5_470	187
10	A10	Reference_v1_chr10	bnl2960	187
10	A10	Reference_v1_chr10	y2423	188
10	A10	Reference_v1_chr10	m4e9-900*	189
10	A10	Reference_v1_chr10	nau2989	190
10	A10	Reference_v1_chr10	bnl2872	191
10	A10	Reference_v1_chr10	m7e7-300	192
10	A10	Reference_v1_chr10	cir0082	193
10	A10	Reference_v1_chr10	t31e14	194
10	A10	Reference_v1_chr10	nau2082	195
10	A10	Reference_v1_chr10	mucs0009	196
10	A10	Reference_v1_chr10	bnl3790	197
10	A10	Reference_v1_chr10	nau5438	198
10	A10	Reference_v1_chr10	muss0068	199
10	A10	Reference_v1_chr10	nau4008	200
10	A10	Reference_v1_chr10	e5m6c	201
10	A10	Reference_v1_chr10	m4e16a	202
10	A10	Reference_v1_chr10	m7e7d	203
10	A10	Reference_v1_chr10	m1e16a	204
10	A10	Reference_v1_chr10	nau3122	205
10	A10	Reference_v1_chr10	od3ga38-220	206
10	A10	Reference_v1_chr10	nau5316	207
10	A10	Reference_v1_chr10	m14e16-300	208
10	A10	Reference_v1_chr10	nau1182	209
10	A10	Reference_v1_chr10	m1e4-700	210
10	A10	Reference_v1_chr10	nau2911	211
10	A10	Reference_v1_chr10	nau1236	212
10	A10	Reference_v1_chr10	muss0096	213
10	A10	Reference_v1_chr10	a1183	214
10	A10	Reference_v1_chr10	bnl0511	215
10	A10	Reference_v1_chr10	par0566	216
10	A10	Reference_v1_chr10	bnl3071	217
10	A10	Reference_v1_chr10	m11e3-500	218
10	A10	Reference_v1_chr10	coau1c12	219
10	A10	Reference_v1_chr10	m4e5-350	220
10	A10	Reference_v1_chr10	m1e11-800	221
10	A10	Reference_v1_chr10	s0458	222
10	A10	Reference_v1_chr10	m2e9-700	223
10	A10	Reference_v1_chr10	dpl0026	224

20	D10	Reference_v1_chr20	nau1290	174
20	D10	Reference_v1_chr20	bnl3482	175
20	D10	Reference_v1_chr20	gate1dg04	176
20	D10	Reference_v1_chr20	nau4071	177
20	D10	Reference_v1_chr20	pvnc024	178
20	D10	Reference_v1_chr20	a1758	179
20	D10	Reference_v1_chr20	par0468	180
20	D10	Reference_v1_chr20	nau5359	181
20	D10	Reference_v1_chr20	gate2ba04	182
20	D10	Reference_v1_chr20	p06-57	182
20	D10	Reference_v1_chr20	cir0187	183
20	D10	Reference_v1_chr20	cms0021	183
20	D10	Reference_v1_chr20	e1m1	184
20	D10	Reference_v1_chr20	nau3916	185
20	D10	Reference_v1_chr20	nau3917	186
20	D10	Reference_v1_chr20	nau5307	187
20	D10	Reference_v1_chr20	nau2544	188
20	D10	Reference_v1_chr20	nau2540	189
20	D10	Reference_v1_chr20	nau2543	190
20	D10	Reference_v1_chr20	nau2549	191
20	D10	Reference_v1_chr20	a1214	192
20	D10	Reference_v1_chr20	nau2776	193
20	D10	Reference_v1_chr20	nau0453	194

10	A10	Reference_v1_chr10	tmb0317	225
10	A10	Reference_v1_chr10	m1e3-580	226
10	A10	Reference_v1_chr10	gate2bh02	227
10	A10	Reference_v1_chr10	od3od17-205	228
10	A10	Reference_v1_chr10	bnl0169	229
10	A10	Reference_v1_chr10	jespr0235	229
10	A10	Reference_v1_chr10	m8e10-820	230
10	A10	Reference_v1_chr10	jespr0171	231
10	A10	Reference_v1_chr10	bnl3660	232
10	A10	Reference_v1_chr10	bnl3993	233
10	A10	Reference_v1_chr10	bnl3948	234
10	A10	Reference_v1_chr10	bnl2597	235
10	A10	Reference_v1_chr10	mucs0023	236
10	A10	Reference_v1_chr10	m4e2-900	237
10	A10	Reference_v1_chr10	par0144	238
10	A10	Reference_v1_chr10	a1708	238
10	A10	Reference_v1_chr10	m12e3-480	239
10	A10	Reference_v1_chr10	m10e3-630	240
10	A10	Reference_v1_chr10	m13e6-600	241
10	A10	Reference_v1_chr10	bnl0580	242
10	A10	Reference_v1_chr10	gate1ah09	243
10	A10	Reference_v1_chr10	gate1dg09	244
10	A10	Reference_v1_chr10	par0812	245
10	A10	Reference_v1_chr10	g1272	246
10	A10	Reference_v1_chr10	gate3be04	247
10	A10	Reference_v1_chr10	cir0305	248
10	A10	Reference_v1_chr10	pxp4-38	249
10	A10	Reference_v1_chr10	pgh597	250
10	A10	Reference_v1_chr10	unig22c10	251
10	A10	Reference_v1_chr10	pvnc149	252
10	A10	Reference_v1_chr10	coau2k21	253
10	A10	Reference_v1_chr10	nau1169	254
10	A10	Reference_v1_chr10	w02	255
10	A10	Reference_v1_chr10	pgh854	256
10	A10	Reference_v1_chr10	g1104	257
10	A10	Reference_v1_chr10	par0572	258
10	A10	Reference_v1_chr10	par0709	258
10	A10	Reference_v1_chr10	gate2ac08	258
10	A10	Reference_v1_chr10	pxp1-26	259
10	A10	Reference_v1_chr10	p12-19	260
10	A10	Reference_v1_chr10	e8m8_66	261

Table 4.16 Chromosomes A11 and D11 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
11	A11	Reference_v1_chr11	cir0316	1
11	A11	Reference_v1_chr11	pvnc149	2
11	A11	Reference_v1_chr11	par0101	3
11	A11	Reference_v1_chr11	m16-040	4
11	A11	Reference_v1_chr11	par0111	5
11	A11	Reference_v1_chr11	pgh648	5
11	A11	Reference_v1_chr11	par0044	6
11	A11	Reference_v1_chr11	musb1076	7
11	A11	Reference_v1_chr11	bnl2741	8
11	A11	Reference_v1_chr11	unig22d03	9
11	A11	Reference_v1_chr11	it-isj01f23r	10
11	A11	Reference_v1_chr11	gate4ac11	11
11	A11	Reference_v1_chr11	bnl1231	12
11	A11	Reference_v1_chr11	unig22h11	13
11	A11	Reference_v1_chr11	m8e6-300*	14
11	A11	Reference_v1_chr11	bnl0836	15
11	A11	Reference_v1_chr11	gate2ac11	16
11	A11	Reference_v1_chr11	nau5505	17
11	A11	Reference_v1_chr11	gate4ag09	18
11	A11	Reference_v1_chr11	bnl1066	19
11	A11	Reference_v1_chr11	par0864	20
11	A11	Reference_v1_chr11	me4ga12-500	21
11	A11	Reference_v1_chr11	nau2599	22
11	A11	Reference_v1_chr11	e8m1_500	23
11	A11	Reference_v1_chr11	e1m2_460	24
11	A11	Reference_v1_chr11	e4m3_97	24
11	A11	Reference_v1_chr11	bnl2895	24
11	A11	Reference_v1_chr11	e1m6_382	24
11	A11	Reference_v1_chr11	cir0207	24
11	A11	Reference_v1_chr11	e7m1_107	24
11	A11	Reference_v1_chr11	e5m5_222	24
11	A11	Reference_v1_chr11	e6m5_106	24
11	A11	Reference_v1_chr11	cir0069	25
11	A11	Reference_v1_chr11	mucs0399	26
11	A11	Reference_v1_chr11	nau0453	27
11	A11	Reference_v1_chr11	tpi1	28
11	A11	Reference_v1_chr11	nau3703	29
11	A11	Reference_v1_chr11	nau2809	30
11	A11	Reference_v1_chr11	t12e14a	31
11	A11	Reference_v1_chr11	nau3115	32
11	A11	Reference_v1_chr11	nau4086	33
11	A11	Reference_v1_chr11	bnl0261	34
11	A11	Reference_v1_chr11	pvnc180	35
11	A11	Reference_v1_chr11	pgh320	36

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
21	D11	Reference_v1_chr21	nau1640	1
21	D11	Reference_v1_chr21	jespr0102	2
21	D11	Reference_v1_chr21	nau3415	3
21	D11	Reference_v1_chr21	tmb0294	4
21	D11	Reference_v1_chr21	unig28f05	5
21	D11	Reference_v1_chr21	nau3740	6
21	D11	Reference_v1_chr21	nau2016	7
21	D11	Reference_v1_chr21	lg-f	8
21	D11	Reference_v1_chr21	nau0429	9
21	D11	Reference_v1_chr21	cir0069	10
21	D11	Reference_v1_chr21	cir0112	10
21	D11	Reference_v1_chr21	cir0316	11
21	D11	Reference_v1_chr21	jespr0065	11
21	D11	Reference_v1_chr21	e7m5_102	12
21	D11	Reference_v1_chr21	pvnc149	13
21	D11	Reference_v1_chr21	cg22	14
21	D11	Reference_v1_chr21	a1188	15
21	D11	Reference_v1_chr21	cir0077	16
21	D11	Reference_v1_chr21	nbs008	17
21	D11	Reference_v1_chr21	par0286	17
21	D11	Reference_v1_chr21	me1sa9-140	18
21	D11	Reference_v1_chr21	par0073	19
21	D11	Reference_v1_chr21	par0044	19
21	D11	Reference_v1_chr21	gate4cd11	19
21	D11	Reference_v1_chr21	par0101	19
21	D11	Reference_v1_chr21	unig22d03	19
21	D11	Reference_v1_chr21	mucs0399	20
21	D11	Reference_v1_chr21	par0576	21
21	D11	Reference_v1_chr21	par0566	21
21	D11	Reference_v1_chr21	pgh767	21
21	D11	Reference_v1_chr21	gate3bb09	22
21	D11	Reference_v1_chr21	par03a11	22
21	D11	Reference_v1_chr21	par0921	22
21	D11	Reference_v1_chr21	pgh743	22
21	D11	Reference_v1_chr21	unig26f09	23
21	D11	Reference_v1_chr21	pvnc021	24
21	D11	Reference_v1_chr21	pgh442	24
21	D11	Reference_v1_chr21	bnl1231	25
21	D11	Reference_v1_chr21	gafb14f08	25
21	D11	Reference_v1_chr21	gate4bd02	25
21	D11	Reference_v1_chr21	pvnc012	25
21	D11	Reference_v1_chr21	pgh650	26
21	D11	Reference_v1_chr21	a1316	27
21	D11	Reference_v1_chr21	gate4bf01	27

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11	A11	Reference_v1_chr11	tmb1915	225
11	A11	Reference_v1_chr11	gate4cc04	226
11	A11	Reference_v1_chr11	gate4cf12	227
11	A11	Reference_v1_chr11	nau5418	228
11	A11	Reference_v1_chr11	unig22b11	229
11	A11	Reference_v1_chr11	dpl0585	230
11	A11	Reference_v1_chr11	unig27h12	231
11	A11	Reference_v1_chr11	p01-24	231
11	A11	Reference_v1_chr11	dpl0675	232
11	A11	Reference_v1_chr11	bnl1404	233
11	A11	Reference_v1_chr11	jespr0135	233
11	A11	Reference_v1_chr11	gate2bc02	234
11	A11	Reference_v1_chr11	coau2e22	234
11	A11	Reference_v1_chr11	par0108	234

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21	D11	Reference_v1_chr21	gate4df12	172
21	D11	Reference_v1_chr21	unig27d07	172
21	D11	Reference_v1_chr21	bnl2812	173
21	D11	Reference_v1_chr21	dc1sa14-140	174
21	D11	Reference_v1_chr21	a1400	175
21	D11	Reference_v1_chr21	par024c	176
21	D11	Reference_v1_chr21	par0024	176
21	D11	Reference_v1_chr21	par0178	176
21	D11	Reference_v1_chr21	par0319	176
21	D11	Reference_v1_chr21	musb0810	177
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21	D11	Reference_v1_chr21	par07e12	178
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21	D11	Reference_v1_chr21	par08c07	197
21	D11	Reference_v1_chr21	par09b03	197
21	D11	Reference_v1_chr21	pgh659	198
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11	A11	Reference_v1_chr11	unig24d01	238
11	A11	Reference_v1_chr11	dpl0701	239
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11	A11	Reference_v1_chr11	pgh819	258
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11	A11	Reference_v1_chr11	par0024	267
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11	A11	Reference_v1_chr11	par04-34	270
21	D11	Reference_v1_chr21	e2m5b	202
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21	D11	Reference_v1_chr21	cir0068	203
21	D11	Reference_v1_chr21	bnl2632	203
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21	D11	Reference_v1_chr21	bnl3976	205
21	D11	Reference_v1_chr21	nau2361	206
21	D11	Reference_v1_chr21	dc1sa21-210	207
21	D11	Reference_v1_chr21	nau0674	208
21	D11	Reference_v1_chr21	bnl0137	209
21	D11	Reference_v1_chr21	tmb0628	210
21	D11	Reference_v1_chr21	nau0698	211
21	D11	Reference_v1_chr21	m16-198	212
21	D11	Reference_v1_chr21	nau3493	213
21	D11	Reference_v1_chr21	a1717	214
21	D11	Reference_v1_chr21	tmb1061	215
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21	D11	Reference_v1_chr21	bnl1053	216
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21	D11	Reference_v1_chr21	nau3889	218
21	D11	Reference_v1_chr21	em6ga28-150	219
21	D11	Reference_v1_chr21	nau3354	220
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21	D11	Reference_v1_chr21	tmb0426	222
21	D11	Reference_v1_chr21	m13e17-730	223
21	D11	Reference_v1_chr21	nau4039	224
21	D11	Reference_v1_chr21	t46e15	225
21	D11	Reference_v1_chr21	e2m5_350	226
21	D11	Reference_v1_chr21	e7m5_160	226
21	D11	Reference_v1_chr21	e2m1_94	226
21	D11	Reference_v1_chr21	e3m2_198	226
21	D11	Reference_v1_chr21	nau0697	227
21	D11	Reference_v1_chr21	coau2m19	228
21	D11	Reference_v1_chr21	coau2m09	228
21	D11	Reference_v1_chr21	em6pm8-255	229
21	D11	Reference_v1_chr21	nau0731	230
21	D11	Reference_v1_chr21	nau3792	231
21	D11	Reference_v1_chr21	cir0275	232
21	D11	Reference_v1_chr21	nau3806	233
21	D11	Reference_v1_chr21	pgh484	234
21	D11	Reference_v1_chr21	tmb1976	235
21	D11	Reference_v1_chr21	musb0823	236
21	D11	Reference_v1_chr21	nau5217	237
21	D11	Reference_v1_chr21	cir0414	238
21	D11	Reference_v1_chr21	par0038	239
21	D11	Reference_v1_chr21	nau1103	240
21	D11	Reference_v1_chr21	em5dc1-425	241

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11	A11	Reference_v1_chr11	e1m1_300	272
11	A11	Reference_v1_chr11	dpl0472	273
11	A11	Reference_v1_chr11	unig06e08	274
11	A11	Reference_v1_chr11	a1345	274
11	A11	Reference_v1_chr11	nau2998	275
11	A11	Reference_v1_chr11	nau3409	276
11	A11	Reference_v1_chr11	nau3695	277
11	A11	Reference_v1_chr11	bnl2589	278
11	A11	Reference_v1_chr11	gate1ba07	278
11	A11	Reference_v1_chr11	e4m7_174	278
11	A11	Reference_v1_chr11	m14e10-600	279
11	A11	Reference_v1_chr11	cir0254	280
11	A11	Reference_v1_chr11	par0570	281
11	A11	Reference_v1_chr11	e6m1_180	281
11	A11	Reference_v1_chr11	pxp3-14	281
11	A11	Reference_v1_chr11	par08b09	281
11	A11	Reference_v1_chr11	stv0176	282
11	A11	Reference_v1_chr11	muss0057	283
11	A11	Reference_v1_chr11	muss0123	284
11	A11	Reference_v1_chr11	tmb1980	285
11	A11	Reference_v1_chr11	par3-26	286
11	A11	Reference_v1_chr11	par03-26	286
11	A11	Reference_v1_chr11	gate4af05	286
11	A11	Reference_v1_chr11	muss0281	287
11	A11	Reference_v1_chr11	dpl0715	288
11	A11	Reference_v1_chr11	g1199	289
11	A11	Reference_v1_chr11	a1214	289
11	A11	Reference_v1_chr11	coau4j11	289
11	A11	Reference_v1_chr11	p06-57	289
11	A11	Reference_v1_chr11	nau3341	290
11	A11	Reference_v1_chr11	dpl0570	291
11	A11	Reference_v1_chr11	nau5192	292
11	A11	Reference_v1_chr11	nau3621	293
11	A11	Reference_v1_chr11	mucs0557	294
11	A11	Reference_v1_chr11	nau5461	295
11	A11	Reference_v1_chr11	nau5064	296
11	A11	Reference_v1_chr11	nau2257	297
11	A11	Reference_v1_chr11	nau3377	298
11	A11	Reference_v1_chr11	nau3008	299
11	A11	Reference_v1_chr11	nau3748	300
11	A11	Reference_v1_chr11	cg23	301
11	A11	Reference_v1_chr11	nau0922	301
11	A11	Reference_v1_chr11	a1700	301
11	A11	Reference_v1_chr11	nau0980	301
11	A11	Reference_v1_chr11	e8m8_500	302
11	A11	Reference_v1_chr11	a1346	303

21	D11	Reference_v1_chr21	nau5418	242
21	D11	Reference_v1_chr21	e4m2_192	243
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21	D11	Reference_v1_chr21	nau0984	245
21	D11	Reference_v1_chr21	par0451	246
21	D11	Reference_v1_chr21	bnl1693	247
21	D11	Reference_v1_chr21	bnl1404	248
21	D11	Reference_v1_chr21	bnl3442	249
21	D11	Reference_v1_chr21	nau3895	250
21	D11	Reference_v1_chr21	bnl1705	251
21	D11	Reference_v1_chr21	gate1af07	252
21	D11	Reference_v1_chr21	tmb1493	253
21	D11	Reference_v1_chr21	bnl0197	254
21	D11	Reference_v1_chr21	a1214	255
21	D11	Reference_v1_chr21	unig22g07	255
21	D11	Reference_v1_chr21	muss0532	256
21	D11	Reference_v1_chr21	nau4865	257
21	D11	Reference_v1_chr21	nau5461	258
21	D11	Reference_v1_chr21	nau3377	259
21	D11	Reference_v1_chr21	nau2653	260
21	D11	Reference_v1_chr21	nau3748	261
21	D11	Reference_v1_chr21	gate4cf12	262
21	D11	Reference_v1_chr21	gate4bg11	263
21	D11	Reference_v1_chr21	gate2cc12	264

Table 4.17 Chromosomes A12 and D12 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
12	A12	Reference_v1_chr12	cshe0012	1
12	A12	Reference_v1_chr12	musb1307	2
12	A12	Reference_v1_chr12	par0101	3
12	A12	Reference_v1_chr12	pvnc280	3
12	A12	Reference_v1_chr12	jespr0300	4
12	A12	Reference_v1_chr12	coau2a18	5
12	A12	Reference_v1_chr12	cir0042	5
12	A12	Reference_v1_chr12	unig23f10	5
12	A12	Reference_v1_chr12	a1614	5
12	A12	Reference_v1_chr12	unig28b12	5
12	A12	Reference_v1_chr12	nau3519	6
12	A12	Reference_v1_chr12	bnl1441	7
12	A12	Reference_v1_chr12	bnl4059	8
12	A12	Reference_v1_chr12	cir0272	8
12	A12	Reference_v1_chr12	pgh711	8
12	A12	Reference_v1_chr12	pxp2-75	8
12	A12	Reference_v1_chr12	nau1301	9
12	A12	Reference_v1_chr12	par0175	10
12	A12	Reference_v1_chr12	nau2030	11
12	A12	Reference_v1_chr12	nau5306	12
12	A12	Reference_v1_chr12	dpl0443	13
12	A12	Reference_v1_chr12	e5m5a	14
12	A12	Reference_v1_chr12	par0006	15
12	A12	Reference_v1_chr12	nau3778	16
12	A12	Reference_v1_chr12	par03-42	17
12	A12	Reference_v1_chr12	pgh829	18
12	A12	Reference_v1_chr12	cir0362	19
12	A12	Reference_v1_chr12	nau3305	20
12	A12	Reference_v1_chr12	pgh492	21
12	A12	Reference_v1_chr12	gate1da06	22
12	A12	Reference_v1_chr12	unig28b06	22
12	A12	Reference_v1_chr12	gate4ca11	22
12	A12	Reference_v1_chr12	bnl3537	23
12	A12	Reference_v1_chr12	nau4905	24
12	A12	Reference_v1_chr12	gate2bg06	25
12	A12	Reference_v1_chr12	par03-21	26
12	A12	Reference_v1_chr12	a1252	26
12	A12	Reference_v1_chr12	coau2i09	27
12	A12	Reference_v1_chr12	nau2251	28
12	A12	Reference_v1_chr12	coau4k03	29
12	A12	Reference_v1_chr12	pvnc098	29
12	A12	Reference_v1_chr12	gate1ce12	29
12	A12	Reference_v1_chr12	a1310	30
12	A12	Reference_v1_chr12	bnl0598	31

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
26	D12	Reference_v1_chr26	gate3bb11	1
26	D12	Reference_v1_chr26	m16-041	2
26	D12	Reference_v1_chr26	nau3271	3
26	D12	Reference_v1_chr26	nau4081	4
26	D12	Reference_v1_chr26	cir0170	5
26	D12	Reference_v1_chr26	nau4925	6
26	D12	Reference_v1_chr26	par0177	7
26	D12	Reference_v1_chr26	gate4cf12	8
26	D12	Reference_v1_chr26	g1045	9
26	D12	Reference_v1_chr26	nau3862	10
26	D12	Reference_v1_chr26	par0764	11
26	D12	Reference_v1_chr26	gate4ah02	11
26	D12	Reference_v1_chr26	pgh331	12
26	D12	Reference_v1_chr26	par03c01	13
26	D12	Reference_v1_chr26	me8ga5-225	14
26	D12	Reference_v1_chr26	a1685	15
26	D12	Reference_v1_chr26	pvnc093	15
26	D12	Reference_v1_chr26	g1005	15
26	D12	Reference_v1_chr26	pgh331	16
26	D12	Reference_v1_chr26	gate1cb02	17
26	D12	Reference_v1_chr26	unig24c07	18
26	D12	Reference_v1_chr26	cir0233	19
26	D12	Reference_v1_chr26	nau4090	20
26	D12	Reference_v1_chr26	at30	21
26	D12	Reference_v1_chr26	nau4089	22
26	D12	Reference_v1_chr26	par01d07	23
26	D12	Reference_v1_chr26	bnl2621	24
26	D12	Reference_v1_chr26	nau1274	25
26	D12	Reference_v1_chr26	me5od12-270	26
26	D12	Reference_v1_chr26	n1m3_350	27
26	D12	Reference_v1_chr26	coau2m07	28
26	D12	Reference_v1_chr26	jespr0295	29
26	D12	Reference_v1_chr26	pgh314	30
26	D12	Reference_v1_chr26	e2m5_240	31
26	D12	Reference_v1_chr26	par0479	32
26	D12	Reference_v1_chr26	nau3865	33
26	D12	Reference_v1_chr26	par0218	34
26	D12	Reference_v1_chr26	cir0167	35
26	D12	Reference_v1_chr26	pgh350	36
26	D12	Reference_v1_chr26	p09-03	36
26	D12	Reference_v1_chr26	a1264	36
26	D12	Reference_v1_chr26	bnl3031	37
26	D12	Reference_v1_chr26	bnl3511	38
26	D12	Reference_v1_chr26	jespr0274	39

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12	A12	Reference_v1_chr12	coau1e07	32
12	A12	Reference_v1_chr12	stv0130	33
12	A12	Reference_v1_chr12	cir0302	34
12	A12	Reference_v1_chr12	mghes0031	35
12	A12	Reference_v1_chr12	unig25d04	36
12	A12	Reference_v1_chr12	e5m3c	37
12	A12	Reference_v1_chr12	bnl3414	38
12	A12	Reference_v1_chr12	nau3860	39
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12	A12	Reference_v1_chr12	pgh785	41
12	A12	Reference_v1_chr12	nau2868	42
12	A12	Reference_v1_chr12	nau2671	42
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12	A12	Reference_v1_chr12	nau2640	44
12	A12	Reference_v1_chr12	nau2672	44
12	A12	Reference_v1_chr12	gate1be09	45
12	A12	Reference_v1_chr12	gate4bg06	45
12	A12	Reference_v1_chr12	gate1dc11	45
12	A12	Reference_v1_chr12	a1111	45
12	A12	Reference_v1_chr12	par04-14	45
12	A12	Reference_v1_chr12	gate1ae09	45
12	A12	Reference_v1_chr12	g1263	45
12	A12	Reference_v1_chr12	nau5079	46
12	A12	Reference_v1_chr12	nau3160	47
12	A12	Reference_v1_chr12	e5m3_81	48
12	A12	Reference_v1_chr12	e5m4_240	48
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12	A12	Reference_v1_chr12	par0229	49
12	A12	Reference_v1_chr12	nau5204	50
12	A12	Reference_v1_chr12	musb0497	51
12	A12	Reference_v1_chr12	cm0068	52
12	A12	Reference_v1_chr12	bnl3404	53
12	A12	Reference_v1_chr12	par0999	54
12	A12	Reference_v1_chr12	cm0085	55
12	A12	Reference_v1_chr12	cir0293	56
12	A12	Reference_v1_chr12	g1071	57
12	A12	Reference_v1_chr12	gate4cg06	58
12	A12	Reference_v1_chr12	cir0081	58
12	A12	Reference_v1_chr12	nau0915	58
12	A12	Reference_v1_chr12	a1210	58
12	A12	Reference_v1_chr12	unig24c11	59
12	A12	Reference_v1_chr12	p11-23	59
12	A12	Reference_v1_chr12	nau3713	60
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26	D12	Reference_v1_chr26	nau3774	209
26	D12	Reference_v1_chr26	gate2bg06	210
26	D12	Reference_v1_chr26	g1037	210
26	D12	Reference_v1_chr26	pgh843	210
26	D12	Reference_v1_chr26	g1099	211
26	D12	Reference_v1_chr26	unig28b06	212
26	D12	Reference_v1_chr26	gate4ca11	212
26	D12	Reference_v1_chr26	bnl3368	213
26	D12	Reference_v1_chr26	pxp1-73	213
26	D12	Reference_v1_chr26	bnl3994	214
26	D12	Reference_v1_chr26	nau3032	215
26	D12	Reference_v1_chr26	cir0272	216
26	D12	Reference_v1_chr26	coau2i09	217
26	D12	Reference_v1_chr26	unig22d07	217
26	D12	Reference_v1_chr26	e3m4_219	218
26	D12	Reference_v1_chr26	unig25h12	219
26	D12	Reference_v1_chr26	pxp2-75	219
26	D12	Reference_v1_chr26	nau3896	220
26	D12	Reference_v1_chr26	fg	221
26	D12	Reference_v1_chr26	jespr0300	221
26	D12	Reference_v1_chr26	par0807	221
26	D12	Reference_v1_chr26	par0101	221
26	D12	Reference_v1_chr26	a1614	222
26	D12	Reference_v1_chr26	nau3465	223
26	D12	Reference_v1_chr26	nau3084	224

12	A12	Reference_v1_chr12	par0265	199
12	A12	Reference_v1_chr12	unig24d12	199
12	A12	Reference_v1_chr12	par0479	199
12	A12	Reference_v1_chr12	par0476	200
12	A12	Reference_v1_chr12	m9e1a	201
12	A12	Reference_v1_chr12	a1780	202
12	A12	Reference_v1_chr12	e5m5d	203
12	A12	Reference_v1_chr12	muss0026	204
12	A12	Reference_v1_chr12	jespr0270	204
12	A12	Reference_v1_chr12	dc1sa14-270	205
12	A12	Reference_v1_chr12	pgh331	206
12	A12	Reference_v1_chr12	gate3cc01	206
12	A12	Reference_v1_chr12	bnl2621	207
12	A12	Reference_v1_chr12	gate2ac07	208
12	A12	Reference_v1_chr12	gate4bc01	209
12	A12	Reference_v1_chr12	bnl2657	210
12	A12	Reference_v1_chr12	unig28b03	211
12	A12	Reference_v1_chr12	a1685	212
12	A12	Reference_v1_chr12	a1807	212
12	A12	Reference_v1_chr12	g1176	212
12	A12	Reference_v1_chr12	gate3bb04	213
12	A12	Reference_v1_chr12	od3od22-550	214
12	A12	Reference_v1_chr12	gate3bf02	215
12	A12	Reference_v1_chr12	unig27f05	215
12	A12	Reference_v1_chr12	gate3cc06	216
12	A12	Reference_v1_chr12	pgh337	217
12	A12	Reference_v1_chr12	g1045	218
12	A12	Reference_v1_chr12	bnl2578	219
12	A12	Reference_v1_chr12	musb1117	220
12	A12	Reference_v1_chr12	par0177	221
12	A12	Reference_v1_chr12	g1209	222
12	A12	Reference_v1_chr12	dc1od8-120	223
12	A12	Reference_v1_chr12	bnl3816	224
12	A12	Reference_v1_chr12	gate4cf12	225
12	A12	Reference_v1_chr12	t8e15b	226
12	A12	Reference_v1_chr12	e4m5_500	227
12	A12	Reference_v1_chr12	bnl3261	228
12	A12	Reference_v1_chr12	nau1274	229
12	A12	Reference_v1_chr12	nau0526	230
12	A12	Reference_v1_chr12	nau2202	231
12	A12	Reference_v1_chr12	bnl4041	232
12	A12	Reference_v1_chr12	me1em3-270	233
12	A12	Reference_v1_chr12	t28e7f	234
12	A12	Reference_v1_chr12	jespr0295	235
12	A12	Reference_v1_chr12	od3ga38-270	236
12	A12	Reference_v1_chr12	e6m5_103	237
12	A12	Reference_v1_chr12	em6pm8-600	238

12	A12	Reference_v1_chr12	t3e8a	239
12	A12	Reference_v1_chr12	tmb0799	240
12	A12	Reference_v1_chr12	e8m7b	241

Table 4.18 Chromosomes A13 and D13 of reference map.

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
13	A13	Reference_v1_chr13	gate2bf11	1
13	A13	Reference_v1_chr13	a1552	2
13	A13	Reference_v1_chr13	a1417	2
13	A13	Reference_v1_chr13	a1345	2
13	A13	Reference_v1_chr13	gate4bc01	3
13	A13	Reference_v1_chr13	pgh639	4
13	A13	Reference_v1_chr13	coau2j11	5
13	A13	Reference_v1_chr13	gate4db12	5
13	A13	Reference_v1_chr13	coau2k07	5
13	A13	Reference_v1_chr13	gate4bf10	6
13	A13	Reference_v1_chr13	gate1cf04	6
13	A13	Reference_v1_chr13	gate1ad04	7
13	A13	Reference_v1_chr13	gafb23b18	8
13	A13	Reference_v1_chr13	g1115	8
13	A13	Reference_v1_chr13	par0601	8
13	A13	Reference_v1_chr13	gate3ah03	8
13	A13	Reference_v1_chr13	e7m3_370	9
13	A13	Reference_v1_chr13	bnl3281	10
13	A13	Reference_v1_chr13	cir0057	11
13	A13	Reference_v1_chr13	cir0095	12
13	A13	Reference_v1_chr13	e7m3b	13
13	A13	Reference_v1_chr13	nau0464	14
13	A13	Reference_v1_chr13	cir0188	15
13	A13	Reference_v1_chr13	nau2285	16
13	A13	Reference_v1_chr13	t47e13b	17
13	A13	Reference_v1_chr13	nau2765	18
13	A13	Reference_v1_chr13	e5m8_400	19
13	A13	Reference_v1_chr13	unig25a05	20
13	A13	Reference_v1_chr13	gate4bc11	20
13	A13	Reference_v1_chr13	unig22b01	20
13	A13	Reference_v1_chr13	gate2bg10	21
13	A13	Reference_v1_chr13	nau2038	22
13	A13	Reference_v1_chr13	pgh690	23
13	A13	Reference_v1_chr13	par0238	23
13	A13	Reference_v1_chr13	coau2l11	24
13	A13	Reference_v1_chr13	a1520	24
13	A13	Reference_v1_chr13	gate1bg08	25
13	A13	Reference_v1_chr13	a1835	26
13	A13	Reference_v1_chr13	unig24b05	27
13	A13	Reference_v1_chr13	par0265	28
13	A13	Reference_v1_chr13	par0788	28
13	A13	Reference_v1_chr13	gate4cg09	28
13	A13	Reference_v1_chr13	w11	28
13	A13	Reference_v1_chr13	gate1ae07	28

AD Chr No.	Chr. Name	map_name	feature_name	Marker Order
18	D13	Reference_v1_chr18	nau2980	1
18	D13	Reference_v1_chr18	nau3991	2
18	D13	Reference_v1_chr18	nau0699	3
18	D13	Reference_v1_chr18	nau2886	4
18	D13	Reference_v1_chr18	nau3447	5
18	D13	Reference_v1_chr18	nau3827	6
18	D13	Reference_v1_chr18	nau3223	7
18	D13	Reference_v1_chr18	nau3843	8
18	D13	Reference_v1_chr18	nau3321	9
18	D13	Reference_v1_chr18	nau3861	10
18	D13	Reference_v1_chr18	nau3161	11
18	D13	Reference_v1_chr18	li2	12
18	D13	Reference_v1_chr18	coau1o05	12
18	D13	Reference_v1_chr18	coau2k07	12
18	D13	Reference_v1_chr18	nau4861	13
18	D13	Reference_v1_chr18	bnl4029	14
18	D13	Reference_v1_chr18	mucs0405	15
18	D13	Reference_v1_chr18	e3m5b	16
18	D13	Reference_v1_chr18	cshe0221	17
18	D13	Reference_v1_chr18	tmb1152	18
18	D13	Reference_v1_chr18	a1552	19
18	D13	Reference_v1_chr18	a1417	19
18	D13	Reference_v1_chr18	cir0099	20
18	D13	Reference_v1_chr18	e3m5_112	21
18	D13	Reference_v1_chr18	tmb1767	22
18	D13	Reference_v1_chr18	acacta5	23
18	D13	Reference_v1_chr18	unig22e01	24
18	D13	Reference_v1_chr18	gate4bf10	24
18	D13	Reference_v1_chr18	nau2488	25
18	D13	Reference_v1_chr18	nau3437	26
18	D13	Reference_v1_chr18	nau2443	27
18	D13	Reference_v1_chr18	jespr0178	28
18	D13	Reference_v1_chr18	bnl1079	29
18	D13	Reference_v1_chr18	e1m2_175	29
18	D13	Reference_v1_chr18	e6m2_79	29
18	D13	Reference_v1_chr18	gate3ah03	29
18	D13	Reference_v1_chr18	y2459	30
18	D13	Reference_v1_chr18	e3m1_115	31
18	D13	Reference_v1_chr18	gate4cd04	32
18	D13	Reference_v1_chr18	par0788	32
18	D13	Reference_v1_chr18	at51	32
18	D13	Reference_v1_chr18	par0028	32
18	D13	Reference_v1_chr18	bnl1555	33
18	D13	Reference_v1_chr18	dpl0049	34

13	A13	Reference_v1_chr13	par0338	28
13	A13	Reference_v1_chr13	t2e4e	29
13	A13	Reference_v1_chr13	t5e4d	30
13	A13	Reference_v1_chr13	nau5345	31
13	A13	Reference_v1_chr13	a1258	32
13	A13	Reference_v1_chr13	a1135	33
13	A13	Reference_v1_chr13	mucs0267	34
13	A13	Reference_v1_chr13	bnl4061	35
13	A13	Reference_v1_chr13	jespr0204	36
13	A13	Reference_v1_chr13	m9e6a	37
13	A13	Reference_v1_chr13	par04e08	38
13	A13	Reference_v1_chr13	bnl2571	38
13	A13	Reference_v1_chr13	unig22c08	38
13	A13	Reference_v1_chr13	par0755	39
13	A13	Reference_v1_chr13	unig25g07	39
13	A13	Reference_v1_chr13	a1208	39
13	A13	Reference_v1_chr13	unig22a02	40
13	A13	Reference_v1_chr13	unig06c10	40
13	A13	Reference_v1_chr13	tmb1767	41
13	A13	Reference_v1_chr13	e4m8_150	42
13	A13	Reference_v1_chr13	gate2ab07	43
13	A13	Reference_v1_chr13	unig22d09	44
13	A13	Reference_v1_chr13	gate1ag05	44
13	A13	Reference_v1_chr13	bnl4064	45
13	A13	Reference_v1_chr13	cir0040	46
13	A13	Reference_v1_chr13	tmb1152	47
13	A13	Reference_v1_chr13	gate3da09	48
13	A13	Reference_v1_chr13	tmb0820	49
13	A13	Reference_v1_chr13	tmb0312	50
13	A13	Reference_v1_chr13	nau3017	51
13	A13	Reference_v1_chr13	m8e5b	52
13	A13	Reference_v1_chr13	par08e06	53
13	A13	Reference_v1_chr13	par01-20	53
13	A13	Reference_v1_chr13	gate3bb11	54
13	A13	Reference_v1_chr13	nau2300	55
13	A13	Reference_v1_chr13	jespr0270	56
13	A13	Reference_v1_chr13	bnl1652	57
13	A13	Reference_v1_chr13	unig26b12	58
13	A13	Reference_v1_chr13	par0274	59
13	A13	Reference_v1_chr13	par0815	60
13	A13	Reference_v1_chr13	mucs0145	61
13	A13	Reference_v1_chr13	dpl0635	62
13	A13	Reference_v1_chr13	nau3468	63
13	A13	Reference_v1_chr13	m2e12b	64
13	A13	Reference_v1_chr13	e7m3_249	65
13	A13	Reference_v1_chr13	gate1bh05	66
13	A13	Reference_v1_chr13	gate3ca11	66

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18	D13	Reference_v1_chr18	bnl0234	37
18	D13	Reference_v1_chr18	t4e1a	38
18	D13	Reference_v1_chr18	coau3d08	39
18	D13	Reference_v1_chr18	nau3534	40
18	D13	Reference_v1_chr18	e8m8a	41
18	D13	Reference_v1_chr18	nau0662	42
18	D13	Reference_v1_chr18	m2e6-450	43
18	D13	Reference_v1_chr18	bnl2895	44
18	D13	Reference_v1_chr18	hau0083	45
18	D13	Reference_v1_chr18	jespr0153	46
18	D13	Reference_v1_chr18	bnl3084	47
18	D13	Reference_v1_chr18	e5m5_98	47
18	D13	Reference_v1_chr18	e6m5_120	47
18	D13	Reference_v1_chr18	e3m4_350	47
18	D13	Reference_v1_chr18	bnl2652	47
18	D13	Reference_v1_chr18	par0574	48
18	D13	Reference_v1_chr18	e2m8_400	49
18	D13	Reference_v1_chr18	e5m3_113	50
18	D13	Reference_v1_chr18	pxp2-25	50
18	D13	Reference_v1_chr18	nau3816	51
18	D13	Reference_v1_chr18	gate4bc10	52
18	D13	Reference_v1_chr18	gate4de08	52
18	D13	Reference_v1_chr18	unig06c10	52
18	D13	Reference_v1_chr18	nau4102	53
18	D13	Reference_v1_chr18	nau2598	54
18	D13	Reference_v1_chr18	a1520	55
18	D13	Reference_v1_chr18	jespr0134	56
18	D13	Reference_v1_chr18	par0964	57
18	D13	Reference_v1_chr18	par0046	57
18	D13	Reference_v1_chr18	gate3db03	57
18	D13	Reference_v1_chr18	a1713	57
18	D13	Reference_v1_chr18	jespr0056	58
18	D13	Reference_v1_chr18	bnl3445	59
18	D13	Reference_v1_chr18	gate4bc01	60
18	D13	Reference_v1_chr18	coau1h06	61
18	D13	Reference_v1_chr18	m3e6-820	62
18	D13	Reference_v1_chr18	tmb0232	63
18	D13	Reference_v1_chr18	m8e17b	64
18	D13	Reference_v1_chr18	pgh690	65
18	D13	Reference_v1_chr18	e6m8_152	66
18	D13	Reference_v1_chr18	e8m8_182	67
18	D13	Reference_v1_chr18	e3m1_154	68
18	D13	Reference_v1_chr18	par0413	69
18	D13	Reference_v1_chr18	jespe178	70
18	D13	Reference_v1_chr18	w13	71

13	A13	Reference_v1_chr13	e1m5_215	67
13	A13	Reference_v1_chr13	e3m4_240	68
13	A13	Reference_v1_chr13	nau3540	69
13	A13	Reference_v1_chr13	bnl4029	70
13	A13	Reference_v1_chr13	bnl1555	71
13	A13	Reference_v1_chr13	e4m6_232	72
13	A13	Reference_v1_chr13	jespr0244	73
13	A13	Reference_v1_chr13	od3od22-215	74
13	A13	Reference_v1_chr13	bnl0569	75
13	A13	Reference_v1_chr13	coau2c17	76
13	A13	Reference_v1_chr13	par0856	76
13	A13	Reference_v1_chr13	pvnc095	76
13	A13	Reference_v1_chr13	m9e16a	77
13	A13	Reference_v1_chr13	gate2cb12	78
13	A13	Reference_v1_chr13	nau3307	79
13	A13	Reference_v1_chr13	nau2938	80
13	A13	Reference_v1_chr13	par0413	81
13	A13	Reference_v1_chr13	pgh576	82
13	A13	Reference_v1_chr13	tmb2904	83
13	A13	Reference_v1_chr13	tmb0635	84
13	A13	Reference_v1_chr13	par0934	85
13	A13	Reference_v1_chr13	y1	86
13	A13	Reference_v1_chr13	nau0660	87
13	A13	Reference_v1_chr13	gate1cd12	88
13	A13	Reference_v1_chr13	gate4cd04	88
13	A13	Reference_v1_chr13	p11-16	88
13	A13	Reference_v1_chr13	par06c06	88
13	A13	Reference_v1_chr13	e6m6c	89
13	A13	Reference_v1_chr13	m2e13b	90
13	A13	Reference_v1_chr13	nau3522	91
13	A13	Reference_v1_chr13	e2m5_269	92
13	A13	Reference_v1_chr13	e3m3_410	93
13	A13	Reference_v1_chr13	mucs0535	94
13	A13	Reference_v1_chr13	par0416	95
13	A13	Reference_v1_chr13	e3m6_240	96
13	A13	Reference_v1_chr13	e6m5_195	96
13	A13	Reference_v1_chr13	e5m1_85	97
13	A13	Reference_v1_chr13	bnl3472	98
13	A13	Reference_v1_chr13	gate2cf08	99
13	A13	Reference_v1_chr13	nau1141	100
13	A13	Reference_v1_chr13	dc1sa18-100	101
13	A13	Reference_v1_chr13	em6pm18-105	102
13	A13	Reference_v1_chr13	par0964	103
13	A13	Reference_v1_chr13	par0958	103
13	A13	Reference_v1_chr13	pvnc256	103
13	A13	Reference_v1_chr13	nau1023	104
13	A13	Reference_v1_chr13	bnl4007	105

18	D13	Reference_v1_chr18	gate4dg12	71
18	D13	Reference_v1_chr18	gate2de11	71
18	D13	Reference_v1_chr18	unig28c01	71
18	D13	Reference_v1_chr18	bnl2571	72
18	D13	Reference_v1_chr18	tmb0114	73
18	D13	Reference_v1_chr18	nau0660	73
18	D13	Reference_v1_chr18	me4em3-380	74
18	D13	Reference_v1_chr18	m5e4e	75
18	D13	Reference_v1_chr18	m5e8-500b	76
18	D13	Reference_v1_chr18	nau4103	77
18	D13	Reference_v1_chr18	m14e12-200	78
18	D13	Reference_v1_chr18	m8e12-750	78
18	D13	Reference_v1_chr18	nau2772	79
18	D13	Reference_v1_chr18	bnl2471	80
18	D13	Reference_v1_chr18	jespr0204	81
18	D13	Reference_v1_chr18	m1e8b	82
18	D13	Reference_v1_chr18	nau4105	83
18	D13	Reference_v1_chr18	cir0216	84
18	D13	Reference_v1_chr18	bnl3911	85
18	D13	Reference_v1_chr18	cm0063	86
18	D13	Reference_v1_chr18	nau3699	87
18	D13	Reference_v1_chr18	muss0603	88
18	D13	Reference_v1_chr18	pxp1-11	89
18	D13	Reference_v1_chr18	nau3211	90
18	D13	Reference_v1_chr18	e6m5_79	91
18	D13	Reference_v1_chr18	a1647	92
18	D13	Reference_v1_chr18	coau2e05	92
18	D13	Reference_v1_chr18	a1591	92
18	D13	Reference_v1_chr18	a1364	92
18	D13	Reference_v1_chr18	unig23b06	92
18	D13	Reference_v1_chr18	nau2138	93
18	D13	Reference_v1_chr18	par0532	94
18	D13	Reference_v1_chr18	m3e3-780	95
18	D13	Reference_v1_chr18	coau1j14	96
18	D13	Reference_v1_chr18	gate4bc11	97
18	D13	Reference_v1_chr18	a1676	97
18	D13	Reference_v1_chr18	cir0040	98
18	D13	Reference_v1_chr18	g1125	98
18	D13	Reference_v1_chr18	nau5275	99
18	D13	Reference_v1_chr18	nau5364	100
18	D13	Reference_v1_chr18	bnl0220	101
18	D13	Reference_v1_chr18	coau2l11	102
18	D13	Reference_v1_chr18	coau1h04	102
18	D13	Reference_v1_chr18	nau4871	103
18	D13	Reference_v1_chr18	tmb0834	104
18	D13	Reference_v1_chr18	gh.cfe	105
18	D13	Reference_v1_chr18	pgh309	106

13	A13	Reference_v1_chr13	e3m7_370	106
13	A13	Reference_v1_chr13	e2m6_70	107
13	A13	Reference_v1_chr13	e3m2_187	107
13	A13	Reference_v1_chr13	e6m5a	108
13	A13	Reference_v1_chr13	unig23e07	109
13	A13	Reference_v1_chr13	gate1ba05	109
13	A13	Reference_v1_chr13	tmb0114	110
13	A13	Reference_v1_chr13	mucs0250	111
13	A13	Reference_v1_chr13	em5dc1-150	112
13	A13	Reference_v1_chr13	tmb0403	113
13	A13	Reference_v1_chr13	cg10	114
13	A13	Reference_v1_chr13	gate4dg12	115
13	A13	Reference_v1_chr13	pxp3-25	115
13	A13	Reference_v1_chr13	m8e5a	116
13	A13	Reference_v1_chr13	e6m8b	117
13	A13	Reference_v1_chr13	e3m3d	118
13	A13	Reference_v1_chr13	bnl1421	119
13	A13	Reference_v1_chr13	bnl1495	119
13	A13	Reference_v1_chr13	bnl3558	120
13	A13	Reference_v1_chr13	e1m5_260	121
13	A13	Reference_v1_chr13	e2m2_450	121
13	A13	Reference_v1_chr13	nau0650	122
13	A13	Reference_v1_chr13	nau1201	123
13	A13	Reference_v1_chr13	gate4be04	124
13	A13	Reference_v1_chr13	y1031	125
13	A13	Reference_v1_chr13	e7m6_129	126
13	A13	Reference_v1_chr13	e5m6_115	126
13	A13	Reference_v1_chr13	e8m4_99	126
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VITA

Jing Yu was born and grew up in Beijing, China, where she received her Bachelor of Science in Mathematics from Beijing Normal University in 1988. The first place she lived outside Beijing was Ithaca, New York, where she received her Master of Science in Plant Breeding and Plant Genetics from Cornell University, Ithaca, New York, in 1997. She continued studying at Cornell on her Ph.D. and finished the courses before moving to Montreal, Canada, in 1999.

Jing Yu has had research experience in particular in Bioinformatics since 1995. She was employed full time as a bioinformatics expert by Texas A&M University and the USDA-ARS Crop Germplasm Research Unit in 2005, assigned to CottonDB, a permanently established USDA-ARS cotton genome database, that serves the whole cotton community, both domestic and international. She finished her Ph.D. degree from Texas A&M University in May 2009.