Second Generation of Catfish Genetic Linkage Map and Integration of Catfish Genetic Linkage and Physical Maps using BAC-Anchored Microsatellites

by

Parichart Ninwichian

A dissertation submitted to the Graduate Faculty of
Auburn University
in partial fulfillment of the
requirements for the Degree of
Doctor of Philosophy

Auburn, Alabama
August 4, 2012

Keywords: Map integration; channel catfish; genetic linkage map; BES; physical map

Approved by

Zhanjiang Liu, Chair, Alumni Professor of Fisheries and Allied Aquacultures
Eric Peatman, Assistant Professor of Fisheries and Allied Aquacultures
Jeffery Terhune, Associate Professor of Fisheries and Allied Aquacultures
Huseyin Kucuktas, Research Fellow IV of Fisheries and Allied Aquacultures
Nannan Liu, Professor of Entomology and Plant Pathology

Abstract

Integration of physical and linkage maps is a critical step in building necessary genome resources for fine mapping of QTL, comparative genomics, and accurate and efficient whole genome assembly. Previously, we have established both linkage maps and a physical map for channel catfish, *Ictalurus punctatus*, the dominant aquaculture species in the U.S. Here we added 2,030 BAC-end sequence-derived microsatellites from 1,481 physical map contigs to a high-density linkage map also containing singleton BES, EST, and anonymous microsatellite markers as well as SNPs. Average marker density across the 29 linkage groups reached 1.4 cM/marker. The increased marker density highlighted variations in recombination rates within and among catfish chromosomes. Several hundred physical map contigs were anchored to the linkage group with two or more BES markers, providing a reasonably accurate basis for determination of ratios of physical to genetic map distances. These ratios ranged from 4 kb/cM to 4,830 kb/cM with an average of 455 kb/cM. The work effectively anchored close to 50% of the catfish BAC physical map contigs (~51% of the genome) to genetic linkage groups enabling future comparative studies with teleost model species as well as providing a framework for ordering and assembly of whole genome scaffolds.

Acknowledgements

I would like to express my deep and sincere gratitude to my major professor, Dr. Zhanjiang (John) Liu, for his guidance throughout my degree program. I also would like to express my gratitude to all of my committee members and my outside reader for their time and directions of my dissertation work. I would like to extend my appreciation to many people who have taught and helped me during my graduate education including Benjaporn Somridhivej, , Atra Chaimongkol, Puttitorn Saengrungruang, Ping Li, Hong Liu, Ludmilla Kaltenboeck, Yanliang Jiang, Shaolin Wang, Jason Abernathy, Shikai Liu, Jianguo Lu, Zhenxia *Sha, Wenqi Wang, Fei Chen,* Yoona Lee and Lilian Wong. Finally, I would like to thank my parents and all my family members for their love, understanding and support.

Table of contents

List of Tables

List of Figures

Introduction

Channel catfish is the leading aquaculture species in the United States and an important research model for neurobiology, ecotoxicology, and immunology (Hansen *et al.* 2003; Booth & Bilodeau-Bourgeois 2009; Jemal *et al.* 2010). With the need to increase product quality and quantities, efforts over the last decade have focused on developing genomic resources for channel catfish for utilization in genetic improvement programs and functional studies (reviewed by Liu 2011), concurrent with the generation of microsatellite-based linkage maps for catfish (Waldbieser *et al.* 2001; Kucuktas *et al.* 2009) and catfish physical maps (Quiniou *et al.* 2007; Xu *et al.* 2007). However, these genomic resources have not been integrated yet because all genetic markers from previous studies coming from anonymous and gene-associated markers in which the location on the physical map is not known.

Map integration aims to place a shared set of markers on both genetic linkage and physical maps such that one can relate genetic map positions and physical sequence. A high density of a genetic linkage map integrated with a physical map spanning across the whole genome provided a valuable resource for fine mapping of QTL and development of marker-assisted selection (MAS) programs, positional cloning of important genes, comparative genome analysis with similar species, and as a framework map for whole genome assembly (Palti *et al.* 2011; Palti *et al.* 2012).

Several methods have been used previously for the integration of the physical and genetic maps including: 1) *in silico* comparison of marker sequences to a whole genome sequence; 2) BAC pooling and PCR screening; 3) hybridization using overgo probes; and 4) mapping of molecular markers from BAC end sequences (Yuan *et al.* 2000; Coimbra *et al.* 2003; Romanov *et al.* 2003; Yim *et al.* 2007). In the last method, the most widely exploited markers have been microsatellites, which can be found in BES and used for genetic mapping to anchor BACs to linkage maps (Córdoba *et al.* 2010). Integration of linkage maps with BAC-based physical maps has been carried out in some fish species including medaka (*Oryzias latipes*) (Matsuda *et al.* 2002), barramundi (*Lates calcarifer*) (Wang *et al.* 2008), Atlantic salmon (*Salmo salar*) *(*Lorenz *et al.* 2010), and rainbow trout (*Onchorhynchus mykiss*) (Palti *et al.* 2011; Palti *et al.* 2012), although the extent of integration varies among species.

BAC end sequencing was carried out on the majority of the channel catfish physical map clones (Xu *et al.* 2006; Wang *et al.* 2007; Liu *et al.* 2009). The BES collection established a resource for mining polymorphic microsatellites which could serve as a connecting point between catfish genetic and physical maps. In catfish, 17.5% of BAC-end sequences (63,387) were found to contain microsatellites (Xu *et al.* 2006). Here, we have constructed the second generation of genetic linkage map using microsatellites and SNPs especially, utilized the BES resource for marker development and genotyping of BES microsatellites for the genetic linkage map construction and map integration. The integration of genetic linkage and physical maps of channel catfish using microsatellites derived from BAC-end sequencing will generate a strong foundation for comparative and functional genomics in catfish and a framework for forthcoming reference genome sequence assemblies.

Literature Review

Fish and channel catfish

Fish can be generally defined as craniates without cervical vertebrae. This characteristic is primary used for distinguish the different between fish and other vertebrates. Fish are extremely diverse when compared with other groups of vertebrates. There are approximately 32,000 species, and they are divided into 4 groups which are the hagfish (Myxini), the lampreys (Cephalaspidomorphi), cartilaginous fish (Chondrichthyes), and bony fish (Osteichthyes). The most common group is the bony fish constituting more than 95 percent of the world's fish species (Schultz 2004; Eschmeyer & Fong 2012).

The superclass Osteichthyes is divided into two classes, the ray-finned fish (Actinopterygii) and lobe-finned fish (Sarcopterygii). Actinopterygii is the dominant class of vertebrates, comprising nearly 96% of the 32,000 species of fish. They are ubiquitous throughout fresh water and marine environments from the deep sea to the highest mountain streams. Actinopterygii has three subclasses (Chondrostei, Neopterygii, and Cladistia). The subclass Neopterygii has two infraclasses: Holostei and Teleostei. Holostei are bony fish that show primitive characteristics. There are eight species divided among two orders, the Amiiformes represented by a single living species, the bowfin (*Amia calva*), and the Lepisosteiformes, the gars. There are more species to be found in the fossil record. Teleostei includes 20,000 extant species in about 40 orders; most living fishes are members of this group.

Channel catfish (*Ictalurus punctatus*) belongs to Order Siluriformes, or the catfishes. It is the leading aquaculture freshwater species in the United States. It belongs to the family Ictaluridae. The distribution of channel catfish was originally in the Gulf States and the Mississippi Valley north to the prairie provinces of Canada and Mexico, but they were not found in the Atlantic coastal plain or west of the Rocky Mountains. Currently, channel catfish have been found to be widely distributed throughout the United States and the world. One obvious physical characteristic of catfish is the presence of barbels around the mouth, four under the jaw and one on each tip of the upper jaw. The body is cylindrical in cross-section and no scales. Fin rays are soft except for the anterior dorsal and pectoral fin rays, which are sharp and hard spines. An adipose fin, lacking rays, is located on the back between dorsal and caudal fins. Irregular spots are on the sides of the body of young channel catfish. However, spots will disappear when the fish become adults. Channel catfish use their sense of taste to locate their food. Taste buds play an important role in finding food. They are usually found over the entire external surface, especially in barbels and gill arches, and inside the mouth. Olfactory organs, the organ of smell, also work along with taste buds for finding their food particularly in turbid water.

Temperatures about 85° F (29.4° C) are the optimum for the best growth of channel catfish and the temperatures between 75°and 85° F (23° to 30° C) are suitable for spawning. Channel catfish usually become sexually mature at 3-4 years of age. However, some may spawn at the age of two years (Wellborn 1988). In 2009, catfish has been ranked at number six in most popular fish or seafood consumed in the United States. The average consumption of catfish in United States is 0.849 pounds per person (National Fisheries Institute, 2010).

Genetic variations

Genetic variations are the variations of genome between individuals within a species or between groups of species. Two factors are involved in the uniqueness between individuals within species: one is deoxyribonucleic acid (DNA) and the other is sexual reproduction. These two factors are important to generate and control the genetic diversity within a species. In cases of DNA factor, genetic variation is the result of the DNA replication process. Although, proofreading mechanisms take place during DNA replication events, a few mistakes are unavoidable when such high numbers of bases are copied by adding the incorrect insertion of bases. These mistakes are called point mutations. Mutations can be induced in much higher rates with certain chemicals and radioactivity. With the nonexistence of such errors, no genetic variations would take place at the DNA level. These are affected to the adaptation of organisms if environment is changed. On the other hand, if these errors occur too much, organisms may not be viable and they can become extinct. In addition to variation at the DNA level, sexual reproduction can cause the genetic variation in organisms due to the shuffling of gene during meiosis in which recombination and independent assortment take place among chromosomes. These processes indicated that no gametes are identical to neither parent chromosomes nor one another. Besides, variations at the DNA level and the shuffling of genes during meiosis, genetic variations also occur at the chromosome level due to chromosome rearrangements. However, such variations are not very useful for developing genetic markers in aquaculture species, but they played a very important role in evolution (Beaumont *et al.* 2010).

Types of genetic markers

The differences of genetic variation between individuals can be measured and quantified by several methods such as the directed sequencing of DNA fragments, measuring the differences between sizes of DNA fragments, identifying phenotypic differences (Beaumont *et al.* 2010). However, the most common methods to measure the genome variations were genetic markers. Some commonly used types of genetic markers are described as following (see Liu 2007)

Allozymes

Allozymes are the different forms of protein products of genes that are encoded at a single gene locus. Allozymes are considered to be Type I markers because they illustrate genes of known function (Liu & Cordes 2004). Allozymes polymorphisms are the result of point mutations, insertions, or deletions. Genetic variation of allozymes can be detected by electrophoresis. The applications of allozymes in fisheries and aquaculture are used for population analysis, stock identification, hybrid identification, parentage analysis, inbreeding analysis and limited genetic mapping (Liu & Cordes 2004). The advantages of allozymes are very cheap and technically easy. However, the major drawbacks of allozymes are that they require a large amount of fresh or frozen samples and in most cases the sampling for allozymes analysis is lethal. Additionally, the number of polymorphic loci is limited because of a very small portion of genetic variation, making the low polymorphic rate in allozymes.

Restriction Fragment Length Polymorphism (RFLP)

RFLP is based on DNA fragment length differences after digesting genomic DNA with one or more restriction enzymes and separated on an agarose gel. Then, the DNA in the gel must be transferred to a solid support such as nitrocellulose or nylon membranes. The specific DNA locus of interest was hybridized with a specific probe, a radioactively labeled DNA or ribonucleic acid (RNA) molecule with sequence similarities to the locus of interest. After hybridization, the nonspecific probes must be wash away leaving only hybridized probe to the specific locus. The membrane is then exposed to the X-ray film for autoradiography to visualize the DNA bands. In addition to hybridization, another approach used for RFLP analysis is the use of polymerase chain reaction (PCR). This approach can replace the tedious Southern blot analysis because the RFLP region is directly amplified via PCR, and the PCR products can be directly digested with restriction enzymes. Then, the DNA bands can be visualized by simple staining with ethidium bromide. In cases where the size shift is small, polyacrylamide or sequencing gels should be considered instead of agarose gel. The molecular basis of RFLP polymorphism is based on insertions and deletions of large shifts in DNA fragment sizes and the gain or loss of the restriction sites. The major strength of RFLP is codominant markers. However, the weaknesses of RFLP are that it cannot detect the vast majority of point mutations and small sizes of insertions or deletions because of the low resolution of agarose gel electrophoresis. Thus, the polymorphic rates are very low in most loci. Moreover, RFLP detects genetic variation at one locus at a time as well as genetic sequence information is required. Therefore, it is difficult and time-consuming to develop markers in species lacking known genetic information.

Mitochondrial DNA (mtDNA)

Mitochondrial DNA is double stranded circular DNA that is around 16 kb in length. In most cases, the offspring usually inherits mtDNA from its mother. However, some aquaculture species such as mussel, *Mytilus* spp., receive mtDNA from both parents. In animals, mtDNA has no introns, no junk DNA or repetitive sequences. Moreover, recombination is a rare event in mtDNA. Mitochondrial DNA was used as a genetic marker because the rate of mutation is higher than the normal nuclear DNA by about 5-10 times, and it represents significant variation among individuals. The rates of polymorphism are usually high in control region (D loop region), making this region highly useful for population genetic studies. Mitochondrial DNA can be analyzed using RFLP followed by gel electrophoresis. Mitochondrial DNA polymorphisms are caused by the loss or gain of restriction sites and also insertions or deletions. The major drawbacks of mtDNA are that it inherits in a non-Mendelian fashion. A total of genetic variation is from mtDNA alone. These features of mtDNA cause limitation for genome research studies.

Randomly Amplified Polymorphic DNA (RAPD)

RAPD is a PCR based multilocus DNA fingerprint technique. RAPD using the single short PCR primers (8-10 base pair [bp] in length to randomly amplify anonymous segments of nuclear DNA. Because the primers are short and low annealing temperatures are used. Thus, increasing in binding sites which distribute throughout the genome and generate a large numbers of amplification products in which each product represents different locus. Genetic variations are assessed by the presence or absence of each product. Base substitutions at the primer binding sites or the insertions or deletions within RAPD regions cause polymorphisms in RAPDs. The polymorphism rates of RAPDs are relatively high because multiple sets of random primers can be used to scan the entire genome and generate multiple RAPD bands. However, polymorphic information content values (PIC) of RAPDs are lower than microsatellites and single nucleotide polymorphisms (SNP), and they are less informative than amplified fragment length polymorphisms (AFLP) because fewer loci are generated at the same time. Strengths of RAPDs are no need of prior knowledge of target DNA sequence and a large number of loci and individuals can be screened. Therefore, RAPDs are useful to differentiate various species, strains, lines, and populations. However, RAPDs are likely to have low levels of polymorphism among individuals of the same population and therefore they are not useful for parentage analysis. The major weaknesses of RAPDs are the low reproducibility due to the use of low annealing temperatures and the dominant nature of inheritance as well as the presences of paralogous PCR products from different DNA regions causing the bands appearing as a single locus. These limited the use of this marker system.

Amplified Fragment Length Polymorphism (AFLP)

AFLP allow rapid generation of large amounts of genetic information. Fingerprints can be used as a tool to identify a specific DNA sample or to assess the relatedness between samples. Conserved common bands refer to relatedness, whereas polymorphic bands refer to differentiation in phylogenetic and population genetic analyses. AFLP technology combines the advantages of RFLP and RAPD. It is based on the selective amplification of a subset of genomic restriction fragments using PCR. DNA is digested with restriction enzymes, and double-stranded DNA adaptors are ligated to the ends of the DNA fragments to generate primer-binding sites for PCR amplification. The sequence of the adaptors and the adjacent restriction site serve as primer binding sites for subsequent amplification of the restriction fragments by PCR. Selective nucleotides extending into the restriction sites are added to 3'ends of the PCR primers in such a way that only a subset of the restriction fragments will be recognized. Only restriction fragments in which the nucleotides flanking the restriction site match the selective nucleotides will be amplified. Then, the subset of amplified fragments is analyzed by denaturing polyacrylamide gel electrophoresis to generate the fingerprints. The molecular basis of AFLP polymorphism is the same with RFLP which refer to insertions and deletions of large shift in DNA fragment sizes and the gain or loss of the restriction sites. The major strengths of AFLP are that it does not require prior genetic sequence information and it can generate a large number of polymorphism. Moreover, it provides robustness, reliability, reproducibility and efficiency. The weaknesses of AFLP markers are the dominant nature of inheritance, the difficulty of transferring the data among laboratories, and requiring a lot of technical demanding and special equipment such as automated DNA sequencers.

Microsatellites

Microsatellites comprise of multiple copies of tandem simple sequence repeats (SSR) ranging in size from 1-6 base pairs (bp) (Tautz 1989). Based on the number of repeats, microsatellites can be classified into mono, di, tri, tetra, penta, hexanucleotide microsatellites. When considered the types of repeats, microsatellites can be categorized into two types called simple microsatellites (AT)7 and composite microsatellite (CA)7(AG)9. Microsatellites are widely used as molecular markers because they are co-dominant markers (can tell homozygous or heterozygous and can tell allele frequencies), highly abundant, highly polymorphic, evenly distributed throughout the genome, and small locus size facilitating PCR genotyping.

Additionally, data can be used across the lab and sometime data can be used across species boarders. However, the disadvantages of microsatellites are the necessity to know sequence information, and the method is labor intensive to develop and has a high cost. Microsatellite polymorphisms are the results of the differences in number of repeat units between individuals. These variations produce the length variation of a given locus and variation can be detected by amplified locus using PCR followed by gel electrophoresis. Chistiakov *et al.* 2005 *et al*. (2005) suggested that two mechanisms might be involved in the change of the number of repeat units. The first mechanism is the interference during recombination events and the second mechanism is the replication slippage. Microsatellites with a larger number of repeats are likely to be more polymorphic. With as few as five repeats, polymorphism has been observed in microsatellites (Karsi *et al.* 2002).

Because the large number of alleles per locus in microsatellites causes high heterozygosity and polymorphic information content (PIC) values, microsatellites became a widely used marker type in a wide variety of genetic research such as genome mapping, population genetics, parentage and kinship analysis, stock discriminations etc. than other markers. Since RFLPs, RAPDs, AFLPs, and SNPs are considered as biallelic markers, because of co-dominant their nature, microsatellites are considered as the most informative genetic markers. Microsatellites can be mined from bacteria artificial chromosomes (BAC) end sequences and they are usually type II markers because of more than 90% represented in non-coding regions. However, microsatellites can be developed as type I markers if they are developed from ESTs. Type I markers are very important because they are associated with genes of known functions. The most effective way to produce microsatellite type I markers is from cDNA libraries. However, some considerations should be given to mined microsatellites from

ESTs such as the presence of introns, the exon-intron boundaries, and 5' and 3' UTR regions. These make the flanking sequences are not suitable for PCR primer designs. Even through introns are not the problems for primer design of BAC end sequencing, the sequencing reactions often terminate after microsatellite repeats, also making the flanking sequences not suitable for PCR primer design.

Single Nucleotide Polymorphism (SNP)

SNPs are the most abundant form of polymorphisms caused by point mutation at a single nucleotide position in the genome. SNPs are inherited as co-dominant markers in a Mendelian fashion. SNPs can be categorized into 2 types: transitions and transversions. A transition is a change between two purines or between two pyrimidines. A transversion is a change between a purine and a pyrimidine. Transitions can be found more often than transversions. SNPs are biallelic markers, because in most cases only two alleles are observed for each locus, but, in theory, one SNP can have up to four alleles (Beaumont *et al.* 2010).

In recent years, many researchers used SNPs as alternative markers despite the fact that they can be observed only as two possible alleles per locus (biallelic marker). This is because, compared to microsatellites, SNPs provide the cost savings, require short running time, has the advantage of high throughput screening, low genotyping error, ease in scoring, and speed in data collection as well as transferable data among laboratories. Moreover, SNPs present high abundant across the genome in both coding and non coding regions, and their mutation mechanisms are simpler than microsatellites. Most of SNPs are linked with coding regions that might be more useful in functional genetic studies than random genetic markers (Ryynänen *et al.* 2007). Since SNPs are biallelic markers representing the relatively low amount of information per marker, a considerable amount of screening effort is required and a large amount of markers are needed to substantially develop and access large portions of genome. The drawbacks of biallelic markers of SNPs are likely to be the limitation in the non-model species because of the difficulty to obtain large scale species specific DNA sequences, therefore, much effort needs to be made through laboratories to discover and develop polymorphic markers instead of quickly scanning through polymorphic sites performed via computer (Morin *et al.* 2004). Another important issue when using SNPs to study population genetics in non-model organisms is the choice of a suitable platform that can be used for genotyping as many high throughput methods require expensive and specialized instruments not commonly found in non-model organism laboratories (Ryynänen *et al.* 2007). Thus, when considering SNP as a marker of choice for genetic research in non-model species, the investment in marker development, genotyping costs, and feasibility needs to be considered deliberately (Schlötterer 2004). Furthermore, if SNPs are identified from small panels of a few individuals, rare SNPs will be under represented, resulting in some sort of bias (Nielsen 2000). However, SNPs also have some advantages over microsatellites as described above and with recent SNP genotyping technologies, allowing the detection of polymorphism from very small fragment sizes (Chen & Sullivan 2003).

Genetic linkage map

Genetic linkage maps are linear arrangements of genes or genetic markers on chromosomes, obtained by recombination (Liu 1998). They are valuable resource tools especially in detection of quantitative trait loci (QTL) for marker assisted selection (MAS). MAS can improve the production traits efficiently through the use of traits linked DNA markers and enhance accuracy in selection of desired traits. MAS was successfully implemented in many economically important farmed animals, such as cattle (Maillard *et al.* 2003), swine (Rothschild 2003), poultry (Malek & Lamont 2003) and sheep (Notter & Cockett 2005). In aquatic species, MAS has not been implemented for the most part, although examples of successful marker-assisted selection have been reported (Fuji *et al.* 2007).

In order to apply MAS as a tool for genetic improvement, a large number of polymorphic molecular markers are needed to construct genetic maps, and some of the markers should be linked to or are part of a gene associated with a desirable characteristic, such as growth rate or disease resistance. Genetic linkage maps have been constructed for a number of aquaculture species, such as tilapia (*Oreochromis* spp.) (Kocher *et al.* 1998; Agresti *et al.* 2000; McConnell *et al.* 2000; Lee *et al.* 2005), channel catfish (*Ictalurus punctatus*) (Waldbieser *et al.* 2001; Liu *et al.* 2003; Kucuktas *et al.* 2009), giant tiger prawn (*Penaeus monodon*) (Wilson *et al.* 2002), kuruma prawn (*Penaeus japonicus*) (Li *et al.* 2003), Japanese flounder (*Paralichthys olivaceus*) (Coimbra *et al.* 2003), rainbow trout (*Oncorhynchus mykiss*) (Young *et al.* 1998; Sakamoto *et al.* 2000; Nichols *et al.* 2003) and Atlantic salmon (*Salmo salar*) (Gilbey *et al.* 2004; Moen *et al.* 2004; Lorenz *et al.* 2010). However, the marker densities on these genetic maps are still too low to implement MAS. Due to low numbers of available molecular markers in many aquaculture species, MAS has not been extensively used in fish breeding schemes today (Sonesson *et al.* 2007). The only successful example is the MAS program in Japanese flounder for the selection of resistance against lymphocystis disease (Fuji *et al.* 2007). The major reason for the successful application of MAS in this species is because of the simple Mendelian inheritance of the resistance against the virus, while in most other situations, disease resistance is controlled by a large number of QTLs, and fully understanding of such complex traits requires a comprehensive genetic linkage map.

Although several types of molecular markers are currently available in genetic research, microsatellites are the most common markers that are used to construct genetic linkage maps and QTL maps in economically important species. Microsatellites are the most preferred markers because of their abundance in genomes, relatively even distribution, small locus size facilitating PCR-based genotyping, codominant nature of Mendelian inheritance, and high levels of polymorphism. In addition, microsatellites are sequence-tagged markers that can be used as probes for integration of different maps such as linkage and physical maps. Microsatellite markers can be easily transferred across the laboratories, and can be used across related species if flanking sequences are conserved (FitzSimmons *et al.* 1995; Rico *et al.* 1996; Cairney *et al.* 2000). In channel catfish, microsatellites represent 2.58% of the catfish genome (Xu *et al.* 2006).

Microsatellite-based linkage maps have been constructed in some economically important aquaculture species such as Arctic charr (*Salvelinus alpinus*) (Woram *et al.* 2004), Atlantic salmon (Moen *et al.* 2004; Lorenz *et al.* 2010), channel catfish (*Ictalurus punctatus*) (Waldbieser *et al.* 2001; Liu *et al.* 2003; Kucuktas *et al.* 2009), Yellowtail (*Seriola* sp.) (Ohara *et al.* 2005), three-spined stickleback (*Gasterosteus aculeatus*) (Peichel *et al.* 2001), Nile tilapia (*Oreochromis niloticus*) (Kocher *et al.* 1998; Agresti *et al.* 2000), hybrid *O. aureus*×*O. niloticus* (Lee *et al.* 2005), rainbow trout (Sakamoto *et al.* 2000; Nichols *et al.* 2003), European sea bass (*Dicentrachus labrax*) (Chistiakov *et al.* 2005), zebrafish (*Danio rerio*) (Knapik *et al.* 1996; Knapik *et al.* 1998; Shimoda *et al.* 1999; Woods *et al.* 2000; Singer *et al.* 2002), Japanese flounder (*Paralichthys olivaceus*) (Coimbra *et al.* 2003), ayu (*Plecoglossus altivelis*) (Watanabe *et al.* 2004), Pacific oyster (*Crassostrea gigas*) (Hubert & Hedgecock 2004), Eastern oyster

(*Crassostrea virginica*) (Yu & Guo 2003) and common carp (*Cyprinus carpio*) (Sun & Liang 2004), cichlid fish (*Astatotilapia burtoni*) (Sanetra *et al.* 2009).

In aquaculture species, genetic linkage maps have been used to undertake comparative genome analysis using conserved syntenic blocks corresponding to the model species thereby transferring important genome information (Kucuktas *et al.* 2009; Phillips *et al.* 2009). However, the major problem of map integration between species is colinearity because, during evolution, many of genes or makers can be rearranged and the evolutionary syntenic conservation, such as in catfish, is relatively low when compared with model fish species (Kucuktas *et al.* 2009).

Physical map

Physical maps are the linear order of genes or DNA fragments containing the order of overlapping cloned DNA fragments, usually obtained from restriction enzyme digestion (Liu *et al.* 1998). In order to understand the physical organization of the genome, most studies often study genomes through physical mapping using BAC libraries. BAC-end sequences provide the abundant information that can be used for physical mapping, comparative genome analysis and map integration (Xu *et al.* 2006) and also provide an unbiased survey of genomic sequences as well as relative abundance of polymorphic microsatellites in an organism. Currently, the physical maps of several important aquaculture species have been constructed. In channel catfish, a BAC contig-based physical map was generated using four-color fluorescence-based fingerprints. A total of 3,307 contigs, based on 30,582 BAC clones, were assembled by FingerPrinted Contigs software (FPC) using a cutoff value of 1×10^{-20}. Each contig contains an average of 9.25 clones with an average size of 292 kb. When combined contig sizes from all contigs, the genome size of the channel catfish was approximately 0.965 Gb, (Xu *et al.* 2007).

Map integration

Map integration is to place the same set of markers on both genetic linkage and physical maps such that one can relate the relative relationships of the linkage map and the physical map. Different methods have been used for the integration of the physical and genetic maps. They can be categorized as following: 1) *in silico* comparison of marker sequences to a whole genome sequence 2) BAC pooling and PCR screening 3) hybridization using overgo probes and 4) mapping of molecular markers from BAC-end sequences. In the last method, the most common and useful genetic markers have been microsatellites, which can be found in BAC-end sequences and used for genetic mapping to link BACs from a physical map (Córdoba *et al.* 2010**)**. In channel catfish, 17.5% of BAC-end sequences contain microsatellites (Xu *et al.* 2006) making it a valuable source of markers that can be used to construct genetic maps.

BAC-anchored microsatellites are a valuable resource for genetic and physical map integration because they are identified through BAC-end sequencing and their location can be identified by BAC contig construction. After they are mapped onto the genetic linkage map, they allow integration of linkage map and the BAC-based physical maps. The map integration will be a possible framework for catfish whole genome sequence assembly, population and comparative genetic studies as well as catfish breeding programs. Integration of linkage maps with BAC cloned physical maps has been done in some fish species such as medaka (*Oryzias latipes*) (Matsuda *et al.* 2002), Barramundi (*Lates calcarifer*) (Wang *et al.* 2008), Atlantic salmon (*Salmo salar*) (Lorenz *et al.* 2010), and rainbow trout (*Onchorhynchus mykiss*) (Palti *et al.* 2011).

This study uses BAC anchored microsatellites as a majority of markers to construct genetic linkage maps because of their high level of polymorphism, high abundance, small locus size, highly distributed nature throughout the genome, co-dominance of inheritance, and sequence-tagged markers from BAC clones in physical map. Therefore, integration of the genetic map with the physical map is feasible. Additionally, microsatellites can be used for comparative genome analysis if they can be tagged to genome sequences, particularly within coding sequences as genes are well conserved through evolution.

Objectives

The objectives of my dissertation are to construct the genetic linkage map using microsatellites and SNPs, especially BAC-anchored microsatellite markers to integrate the genetic and physical maps of channel catfish. The construction of the linkage maps with a high density of markers should enhance and increase the usefulness of the linkage map; integration of the physical map with genetic linkage maps should allow verification of the correctness of the physical map, clarification of the sequence assembly in the problematic regions, generation of the high quality genome sequences, comparative genomic studies with other teleosts and with model fish species, fine mapping of QTL, positional cloning, the development of a marker-assisted selection program and also increasing the potential as a research fish model species in teleosts. The inclusive integrated maps provide a minimal tiling path for genome sequencing and a whole genome sequence assembly in catfish. Therefore, the results from this project will be one step further to develop a marker-assisted selection and enhance genetic improvement program in catfish.

Materials and Methods

Resource Family

The resource family for BES markers used in this study was previously described (Liu *et al.* 2003). In brief, an F_1 interspecific hybrid catfish was generated from the most informative mating of a channel catfish female and a blue catfish male. In 1997, backcross families were made using F_1 fish mating with channel catfish (channel catfish backcross). A specific family, F_1-2 x Channel catfish-6, was used for this project. Blood samples were collected from this specific family for genotyping. Heat brands were applied on each individual fish used for genotyping for future identification.

Genomic DNA Isolation

DNA was extracted from 64 samples plus their two parents from resource family F_1-2 x Channel catfish-6. Blood samples (0.5 to 1 ml) were collected in a 1-ml syringe and immediately expelled into a 50-ml tube containing 20-ml of DNA extraction buffer (100 mM NaCl, 10 mM Tris, pH 8, 25 mM EDTA, 0.5% SDS, and freshly added proteinase K 0.1 mg/ml), and DNA was isolated by using the Puregene DNA Isolation Kit (Gentra Systems, Minneapolis, MN) following the manufacturer's instructions.

Identification of Microsatellites, Primers and PCR Amplification

Catfish BAC end sequences were generated by Xu *et al.* (2006). BAC end sequences (BES) stored in a local database at the Fish Molecular Genetics and Biotechnology Laboratory and available publicly in the NCBI GSS database and in the cBARBEL database (Lu *et al.* 2011) were used for microsatellite mining. The channel catfish BAC-based physical map, web FPC viewer version 2.1: AU 02-20 (http://titan.biotec.uiuc.edu/webAGCOL/AU02-20/webFPC) was used to obtain clones containing microsatellites which were previously identified by the *Msatfinder* program (Somridhivej *et al.* 2008).

BES-containing microsatellites with at least 50 bp of flanking sequences on either side of microsatellites were used for primer design by *Msatfinder*. Primers were designed to amplify product sizes between 100-250 bp. However, in some instances, longer PCR products were accepted. A 19-bp tail sequence (GAGTTTTCCCAGTCACGAC) was added to the 5' end of the upper primer (Oetting *et al.* 1995). A primer whose sequence is complementary to the tail sequence is used as the label (labeled with infrared dye (IRD)-IRD700 or IRD800 from LI-COR Biosciences, Lincoln, NE). All primer pairs and the labeled primer were ordered from Invitrogen (Carlsbad, CA).

PCR reactions were performed on a Mastercycler (Eppendorf NA, NY) or on a DNA Engine Thermocycler PTC 200 (Bio-Rad Hercules, CA) using the following amplification profiles: PCR was performed in a 5 µl reaction mixture containing 1 µl of 50 ng/µl genomic DNA (Gentra Puregene kit), 0.5 µl of 10X PCR buffer, 0.2 µl of 50mM $MgCl_2$, 0.4 µl of 2.5 mM dNTP's, 0.2 µl of 10 pmol/µl upper primer (with tailed primer $5'$GAGTTTTCCCAGTCACGAC$3'$ added at $5'$ end), 0.3 µl of 10 pmol/µl lower primer, 0.1 µl of 1 pmol/µl primer label IRD700 or IRD800 and 0.05 µl of 5 U/µl of Platinum Taq polymerase.

PCR amplifications were conducted using 384 well plates to reduce the variation as much as possible. Two-step PCR profiles were used for amplification. An initial denaturation step at 94°C for 3.5 min was followed by a first denaturation at 94°C for 30 seconds, first annealing step at 57°C for 30 s, and a first extension at 72°C for 30 s. This first step was repeated for 20 cycles followed by 15 cycles of a second step with the following parameters: denaturation at 94°C for 30 s, annealing at 53°C for 30 s, and extension at 72°C for 30 s followed by a final extension step at 72°C for 15 min. The samples were held at 4°C for 15 min. In this two-step PCR profile, the annealing temperature window was accommodated to determine the best T_m for the primer pairs. PCR products were analyzed on a 7% polyacrylamide gel using a LICOR 4300 DNA Analyzer (LICOR Biosciences, Lincoln, NE).

Genotyping

After gel electrophoresis, the polymorphic microsatellite bands were scored and genotyped based on the allele segregation within the resource family. A Chi-square goodness-of-fit test was used to assess the Mendelian segregation patterns. Genotype configurations of markers can be categorized into three expected segregation patterns when null-allele segregation was allowed: 1:1:1:1-ratio type (♀ x ♂: AB x CD or AB x AC), 1:1 ♀ type (AB x AA or CC), and 1:1 ♂ type (AA or CC x AB). All linkage analyses were made using JoinMap version 4.0 software (Van Ooijen 2006).

Microsatellite markers, type I microsatellites, microsatellites derived from next generation sequencing, and SNP markers

Locus identifications and genotyping of anonymous microsatellites, type I EST and SNP markers were previously described in Waldbieser *et al.* 2001 and Kucuktas *et al.* 2009, respectively. Identification of microsatellites by next-generation sequencing (NGS) of the catfish genome was used for generating several NGS markers.

Linkage Analysis

Linkage between markers was examined by estimating LOD scores for recombination rate (Θ) and map distances were calculated using the Kosambi mapping function. Significance between linkage groups was determined using a LOD threshold of 14.0 and a threshold Θ of 0.6 was set to detect suspect linkage possibly resulting from allele-coding errors.

Markers were linearly aligned in each linkage group, converting recombination rates into Kosambi's map distance (centimorgans). The position of markers was explored on the basis of the sequential buildup of the map (Stam 1993). First, the most informative pair of markers was selected, followed by sequential addition of other markers. The ripple, the action that prevented the adding locus to become trapped in the local optimum of goodness-of-fit, was performed each time after adding one marker. The best fitting position of an added marker was searched on the basis of the goodness-of-fit test (chi-square) for the resulting map. When a marker generated a negative map distance in the map or a large jump value in goodness-of-fit, which is the normalized difference in chi-square value before and after adding the marker, the marker was removed, and map calculation was continued to construct a first-round map. After the first-round marker ordering, the previously removed markers were added to the first-round map and again subjected to the goodness-of-fit testing. In this manner, the marker ordering was continued up to the third round until an optimum order of markers was found.

Results

Development of polymorphic microsatellite markers from physical map-associated BES markers

We screened 30,582 BAC end sequences (BES) from BAC clones on the catfish physical map for microsatellites useful for map integration. The catfish physical map derived from fluorescent fingerprinting of the CHORI-212 BAC library contains 3,307 contigs (Xu *et al.* 2007). Ideally, at least one microsatellite from each of the 3,307 contigs, possibly more than one microsatellite for large contigs, is needed to fully anchor the physical map contigs to the linkage map. Our screening identified high quality microsatellites in BES associated with 2,128 of the physical contigs. The remaining physical map contigs could not be targeted by this approach, either due to lack of BES-associated microsatellites or microsatellites lacking sufficient flanking regions for primer design. A total of 3,846 microsatellites from the targeted physical map contigs were selected for PCR optimization and genotyping. Of these, 2,116 BES microsatellites from 1,534 unique physical map contigs amplified a single product of expected size and could be resolved and unambiguously scored (Table 1). These potential BES microsatellite markers were carried forward for use in construction of the genetic linkage map.

Linkage Mapping

To construct a high-density genetic linkage map incorporating the BES markers, we combined the 2,116 BES microsatellites derived from the physical map contigs with 77 BES markers from BAC singletons as well as 100 SNP markers, 283 EST markers, 147 markers from a previous linkage map (Waldbieser *et al.* 2001), and 17 microsatellites derived from next-generation sequencing for mapping on our interspecific hybrid resource family, F_1-2 x Channel-6, using the Joinmap 4.0 program. The majority of the EST and SNP markers were utilized in an earlier linkage map genotyped on the same resource family (Waldbieser *et al.* 2001; Kucuktas *et al.* 2009). To start the linkage analysis of the sex averaged map, the LOD score was set at 14.0 in order to generate the linkage groups based on the segregation data. Among 2,740 polymorphic markers, 2,557 markers, including 2,099 BES-based microsatellites, 235 EST-derived microsatellites, 127 anonymous microsatellites, 17 next generation sequencing-based microsatellites and 79 SNPs, were mapped and assigned to 29 linkage groups. A total of 93.3% of genotyped markers could be successfully mapped (Table 2 and Supplemental Figure 1). The remaining 183 markers were not mapped because of significant segregation distortion, unlinked markers or other mapping abnormalities.

Marker Distribution and Map Characteristics

In the resulting genetic linkage map, markers were distributed across all 29 linkage groups with a minimum of 46 markers/LG (LG29; see Figure 1 for a representative LG). Similarly, the linked physical map contigs were distributed across linkage groups, ranging from 33 to 77 contigs/LG (Table 3). However, distribution of markers was uneven, likely reflecting differences in recombination frequency along the length of the catfish chromosomes

(Supplemental Figure 1). Clustered marker regions were observed in every linkage group of the sex-averaged linkage map, especially in positions close to the centromeres and, more infrequently, at the telomeres.

In order to characterize marker clustering, we tabulated the number of markers sharing an identical genetic map position with other markers as well as the number of map positions where markers were stacked or redundant (Table 3). Linkage group 17 had the highest percentage (72%) of markers placed at the same location, whereas linkage group 19 had only 14.5% of its markers at stacked map positions (Table 3, Figure 1). In order to obtain a more accurate evaluation of marker distribution and map density, we calculated the number of unique markers per linkage group by subtracting the markers at stacked positions (identical cM location) and adding back the number of stacked marker positions (to account for one unique marker per stacked position). A total of 1,836 unique marker positions remained. We then utilized unique marker counts for each linkage group along with estimated linkage group sizes (with corrections for telomere ends) to calculate an average LG density (cM/marker). Densities ranged from 0.5 cM/marker in LG17 to 2.6 cM/marker in LG29, with an average of 1.4 cM/marker. Of note, LG17 represented the skewed corrected map size at only 16.8 cM, likely reflecting the severe shortage of recombination events observed in this linkage group. In contrast, the telomere-corrected average size of the 29 catfish linkage groups was 87.8 cM (Table 4).

The sum of intervals from all loci of the sex-averaged map after excluding stacked markers was 2,467.9 cM (Kosambi). To correct the chromosome ends (telomeric regions), the estimated total map size was calculated by adding 2x, where x is the average space between adjacent markers, to all map sizes of each linkage group (Fishman *et al.* 2001). Therefore, the estimated corrected map size of the sex-averaged map was 2,546.2 cM. The average number of mapped markers per LG was 63 markers, and ranged from 31-87 markers. Inter-marker distance varied from 0 to 43.7 cM (Table 4).

Evaluation of Map Integration

Of the 1,534 physical map contigs with at least one successfully genotyped BES marker (Table 1), 1,481 physical map contigs, approximately 69.6% of physical map contigs with microsatellites, were successfully integrated with the linkage map (Table 5). Due to multiple BES markers being successfully mapped from some physical map contigs, a total of 2,030 contig-based BES were placed in the linkage map. Detailed information regarding mapped contig identities, estimated physical contig sizes, corresponding linkage groups, and genetic map positions is listed in Supplemental Table 1. In terms of the physical coverage of the integrated genetic map, the integrated physical map contigs include a total of 17,972 individual BAC clones.

Fifty-four physical map contigs, each with at least two BES markers, were mapped to multiple linkage groups based on conflicting assignments of individual BES markers, suggesting that these physical map contigs may be erroneously constructed or that they fall within duplicated regions of the genome (Table 5). An example of a linkage group with physical map contig information integrated based on marker position is illustrated in Figure 2.

Given an estimated haploid genome size of channel catfish of $1X10^9$ bp (Tiersch *et al.* 1990; Tiersch & Goudie 1993), and a total corrected map size of 2,546.2 cM, we calculated the relationship between physical and genetic map distances to be approximately 393 kb/cM. Additionally, the combined estimated physical length of the 1,481 anchored physical map contigs was equal to 510,074 Kb (Table 5), the integrated map covered ~ 45% of the physical map contigs and ~51% of the estimated catfish genome. Anchored contigs varied in size from 88 Kb to 2,206 Kb with an average size of 344 Kb (Supplemental Table 1). A total of 322 contigs were mapped with multiple markers and observed recombination between at least one pair of markers, allowing contig-based estimations of ratios of physical to genetic distance (Supplemental Table 2). Physical distances were estimated based on position of the BES markers within each contig. Multiple marker contigs were distributed across all 29 LGs. Ratios ranged from 4 kb/cM to 7,704 kb/cM with an average of 485 kb/cM.

Discussion

The aim of this study was to integrate a BAC-based physical map of channel catfish with genetic linkage maps by genetic mapping of large numbers of BES-associated microsatellites. In this process, we also sought to increase the marker density and utility of the catfish genetic linkage map for genomic studies. Here we mapped 2,030 BES markers from 1,481 physical map contigs to integrate a substantial portion of the physical map and to boost average marker density to 1.4 cM/marker.

Map integration is a critical component of efforts aimed at marker-assisted selection in aquaculture species. Fine-mapping of QTL is often thwarted by an inability to identify genomic regions containing causative genes and/or additional markers in linkage disequilibrium with the locus of interest. With an integrated map, markers of interest can be related to BAC contigs which can then be quickly sequenced using next-generation sequencing approaches to obtain the genic content and structural organization. Additionally, whole genome assembly can be significantly enhanced using an integrated map to orient and order sequence scaffolds along the length of linkage groups based on their matches with BES. Significant gaps revealed during this process can be filled by targeting BAC clones within the gaps for further sequencing. Furthermore, prior to whole genome assembly, information captured through ordering of physical map BES can be used for comparative genomics studies (Yu *et al.* 2009; Palti *et al.* 2012). Assembly of catfish genome sequence scaffolds is currently underway and will utilize the map integration data presented here.

The utility of genetic and integrated maps is directly correlated with the even distribution of markers across linkage groups. Clustered markers in areas of minimal recombination, while allowing general linkage group assignment, often cannot be used for definitive fine mapping and positional cloning. Physical map contigs placed within these regions similarly cannot be ordered and oriented in relation to other nearby contigs. In fish, clustering of DNA markers on genetic linkage maps has been observed in medaka (Naruse *et al.* 2000), rainbow trout (Robison *et al.* 2001), tilapia (Kocher *et al.* 1998), channel catfish (Liu *et al.* 2003), and Atlantic salmon (Lorenz *et al.* 2010). While, potential explanations for high levels of marker clustering are not completely understood (Watanabe *et al.* 2005), most are based on dead zones of recombination. Numerous studies have reported large disparities between genetic map and physical map distances (e.g. Young & Tanksley 1989; Gustafson *et al.* 1990; Gustafson & Dille 1992; Espeso *et al.* 2005). This phenomenon is often attributed to differences in genic content across chromosomes, with recombination decreasing in chromosomal regions containing heterochromatin, large areas of repetitive DNA, and in regions around centromeres and/or telomeres. The catfish genome is known to have long repetitive regions including Xba elements and abundant transposable elements that likely interfere with recombination (Liu *et al.* 1998; Xu *et al.* 2006; Nandi *et al.* 2007; Jiang *et al.* 2011). We observed significant clusters of markers on the majority of the catfish linkage groups. However, some linkage groups were clearly more impacted by this phenomenon than others. For example, linkage group 17 had 67 markers (out of 93 in total) in 5 stacked marker positions, while linkage group 19 had only 8 markers (of 55 in total) in 5 stacked positions. It will be of interest to characterize the repetitive content levels in linkage groups with differing rates of recombination as genome assemblies become available. Of note, a previous EST-based linkage map genotyped on the same resource family had far fewer stacked marker positions (Kucuktas *et al.* 2009). While marker number in the previous map was lower, selection of markers from coding sequences likely helped to avoid highly repetitive genome regions.

Several other potential reasons for low recombination in these regions deserve exploration. The number of genotyped progeny may impact rates of observed recombination between genetic markers. We examined whether the use of 64 fish for genotyping provided insufficient power to detect rare recombinants. We genotyped 128 fish (64 original plus 64 additional family members) for 93 BES markers found within highly clustered map regions. Recombination rates rarely increased substantially from those seen using 64 fish (data not shown), indicating that progeny number was not limiting in these cases.

It has also been long noted that recombination is reduced in hybrids due to decreases in homology and reduced pairing of chromosomes during meiosis (Young & Tanksley 1989; Kreike & Stiekema 1997). This leads in turn to linkage drag where large, non-recombining fragments are retained in backcrosses, an issue long confronted by plant breeders (Rhyne 1962). The use of a hybrid backcross family in the present study, therefore, may have increased the extent and size of cold zones of recombination. In the future, genotyping of clustered markers on an intra-species mapping panel may increase resolution within at least some of the low recombination regions. The clustered BES markers, while of minimal utility in fine ordering of physical map contigs for QTL analysis within these regions or assisting in whole genome assembly, do provide gross assignment of physical map contigs to linkage group regions.

The ratio of physical to genetic linkage distances varied substantially across the 29 linkage groups and between markers within the same physical map contig, again illustrating differing rates of recombination across the catfish genome, as seen in other vertebrate genomes

(Nachman 2002; Nievergelt *et al.* 2004; Quiniou *et al.* 2007; Groenen *et al.* 2009). Ratios calculated on a linkage group level are impacted by the presence of non-BES markers in the analysis. These markers (ESTs, SNPs, and others) contribute to the genetic map distance, but are not part of the physical distance estimation based on contig lengths and thereby skew the calculated ratios. To avoid this issue, we focused on physical to genetic distance ratios based on multiple markers mapped from the same contigs (Supplemental Table 2). Ratios ranged from 4 kb/cM, potentially indicating hyper-recombination, to 7,704 kb/cM, indicating suppressed recombination. Several contigs showed no recombination between markers.

A combination of approaches will be utilized for integration of the remaining 1,826 contigs not integrated in the present study because of lack of sufficient microsatellite sequences or insufficient polymorphism in existing microsatellites. For some contigs, we are in the process of identifying SNPs within BES regions (Lorenz *et al.* 2010) for mapping. Other contigs will be integrated through connection of BES sequences with SNP-containing genomic regions via initial catfish genome assemblies (Liu *et al.* 2011). These SNPs in turn will be genotyped on large reference families utilizing a high-density Affymetrix SNP chip. As the catfish genome assemblies improve, additional contigs will be integrated through the physical sequence connection of genotyped markers and contig BES. Recent rapid improvement in both sequencing and SNP genotyping technologies presents many new options for achieving full integration of the catfish genome resources (Baird *et al.* 2008; Davey *et al.* 2011; Van Oeveren *et al.* 2011; Scaglione *et al.* 2012).

Although variation in recombination frequencies complicates the relationship between genetic and physical distance, integrated maps are valuable for checking for errors in individual map assemblies. The majority of contigs with multiple markers were placed into a single linkage group. However, 54 anchored contigs were mapped to multiple linkage groups. This could indicate FPC assembly error during physical map construction resulting in mis-assembly of genomic regions. Increasing stringency of assembly of these regions may resolve the issue. However, in some cases, these contigs may be the result of assembly of duplicated regions of the catfish genome which share high levels of sequence similarity (Xu *et al.* 2007). The breaking of these contigs during linkage mapping is of great utility in highlighting these potentially duplicated regions. We examined whether increasing stringency for FPC construction of the physical map could resolve the assembly in problematic contigs. We have increased the cutoff values for the contig assembly to 1×10^{-25} and 1×10^{-30}, respectively. The majority of problematic contigs (37 out of 54) were split from the original contigs into different contigs or singletons when increasing the threshold, while 17 of 54 contigs remained in the same physical map contigs. Whether a BAC contig is to be split into different contigs when assembly stringency is increased depend on the level of overlapping segments generated from restriction fingerprinting. Apparently, the 17 contigs that remain in the same contigs with increased assembly stringency indicated that long stretches of duplicated genome segments may have been involved in these contigs. Such information will be important for the assembly of whole genome sequences. Additionally, in a few instances, contigs whose BES markers span an unexpectedly large genetic map distance (>10 cM), may also indicate mis-assembly, or intra-chromosomal duplications. Such large discrepancy between linkage map and physical map distances could also come from genome variations as the resource family used for genetic linkage map is not related with the fish used for physical mapping. Given the large variation in recombination ratios across the catfish linkage groups, however, these determinations will be more difficult to make at the present time with the available genome resources.

Conclusions

The catfish integrated map presented here substantially increases linkage marker density available for QTL studies as well as connecting the majority of the catfish genetic markers to physical sequence BAC contigs through the use of BES microsatellites. The integrated map will allow trait-based studies (e.g. Ninwichian *et al.* 2012) to expand beyond linkage analysis to fine mapping and selection of important candidate genes for further research. The integrated map will also be a valuable asset in improving and validating the catfish whole genome assembly currently underway.

Table 1. Development of physical map contig-specific microsatellites from BAC end sequences.

Number of contigs	3,307
Number of contigs with microsatellites	2,128
Number of contigs with polymorphic microsatellites	1,534
Number of polymorphic microsatellites in the 1,534 contigs	2,116
Number of contigs with two or more polymorphic microsatellites	385

Table 2. A summary of markers used for construction of genetic linkage map.

Marker type	Attempted	Polymorphic	Mapped
Microsatellites from BES	3,846	2,193	2,099
SNPs	384	100	79
Microsatellites from EST	1,025	283	235
Anonymous (IpCG)	268	147	127
Microsatellites from NGS	20	17	17
Total	5,543	2,740	2,557

Table 3. Characteristics of marker distribution among 29 linkage groups.

Linkage Group	Mapped markers	Contigs	Stacked markers	Stacked marker positions	Unique marker positions
1	113	77	56	15	72
2	84	49	19	7	72
3	107	74	41	14	80
4	104	70	48	11	67
5	98	59	33	10	75
6	126	74	89	13	50
7	89	47	44	12	57
8	119	75	55	16	80
9	91	50	43	11	59
10	68	36	11	5	62
11	89	60	36	9	62
12	101	58	29	8	80
13	100	57	32	10	78
14	81	43	18	7	70
15	101	52	33	12	80
16	98	55	32	10	76
17	93	52	67	5	31
18	71	45	25	6	52
19	55	41	8	4	51
20	121	73	44	10	87
21	74	43	15	6	65
22	80	50	39	8	49
23	78	52	32	9	55
24	60	38	22	5	43
25	87	57	31	8	64
26	76	42	27	10	59
27	65	35	21	8	52
28	82	47	21	10	71
29	46	33	14	5	37
Total	2,557		985	264	1,836

Table 4. Characteristics of the catfish genetic map with a total of 2,557 markers at 1,836 unique map positions among the 29 linkage groups.

Linkage group	Unique markers	Map size (cM)	Total map size (cM)	Average marker density (cM)	Range of intermarker spacing (cM)
1	72	76.6	79.3	1.1	0-12.9
2	72	79.9	82.6	1.1	0-6.6
3	80	99.9	102.6	1.2	0-14.9
4	67	88.3	91.0	1.3	0-17.1
5	75	70.0	72.7	0.9	0-6.6
6	50	71.6	74.3	1.4	0-17.6
7	57	78.3	81.0	1.4	0-15.9
8	80	127.8	130.5	1.6	0-43.7
9	59	70.3	73.0	1.2	0-13.0
10	62	98.0	100.7	1.6	0-13.2
11	62	83.9	86.6	1.4	0-22.6
12	80	94.5	97.2	1.2	0-10.0
13	78	114.2	116.9	1.5	0-11.7
14	70	87.0	89.7	1.2	0-13.0
15	80	93.7	96.4	1.2	0-12.6
16	76	111.6	114.3	1.5	0-11.4
17	31	14.1	16.8	0.5	0-2.0
18	52	73.6	76.3	1.4	0-21.8
19	51	90.9	93.6	1.8	0-10.9
20	87	91.0	93.7	1.0	0-13.5
21	65	73.2	75.9	1.1	0-8.9
22	49	89.2	91.9	1.8	0-15.1
23	55	87.7	90.4	1.6	0-12.6
24	43	69.2	71.9	1.6	0-15.7
25	64	84.5	87.2	1.3	0-7.4
26	59	57.5	60.2	1.0	0-5.2
27	52	100.8	103.5	1.9	0-6.0
28	71	93.4	96.1	1.3	0-8.8
29	37	97.2	99.9	2.6	0-18.3
Total	1,836	2,467.9	2,546.2	1.4	-

Table 5. Assessment of integration of the catfish physical and linkage maps.

Number of contigs with polymorphic microsatellites	1,534
Contigs mapped to linkage map	1,481
Number of BES microsatellite markers mapped from the 1,481 contigs	2,030
Contigs mapped with only one microsatellite marker	1,096
Contigs with two or more microsatellites mapped	385
Contigs with two or more microsatellites mapped at the same position	191
Contigs with two or more microsatellites mapped at adjacent map positions	140
Contigs with two or more microsatellites mapped in different linkage groups	54
Average length of integrated physical map contigs (kb)	344
Number of BAC clones contained in the 1,481 contigs	17,972
Total number of BAC clones on the catfish physical map of 3,307 contigs	30,582
% of BAC clones on the physical map integrated with linkage map	58.8%
Total length of integrated physical map contigs (kb)	510,074

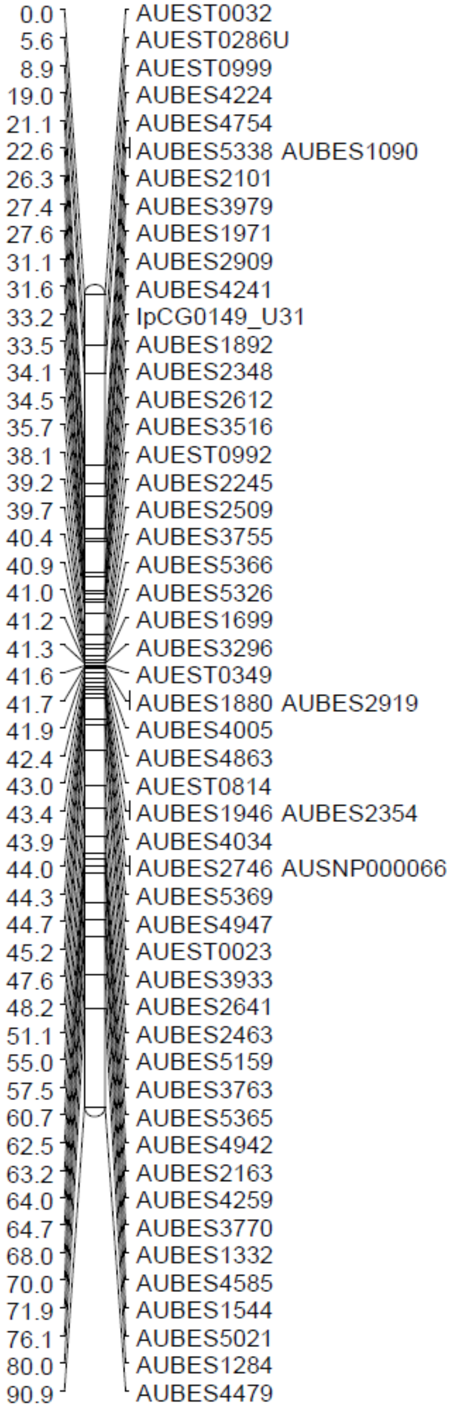


Figure 1. An example linkage group (LG19) from the genetic linkage map of channel catfish. Genetic map distance is given in centimorgans (Kosambi's mapping function) to the left of the markers positions. The vertical straight lines indicate markers placed at the same position.

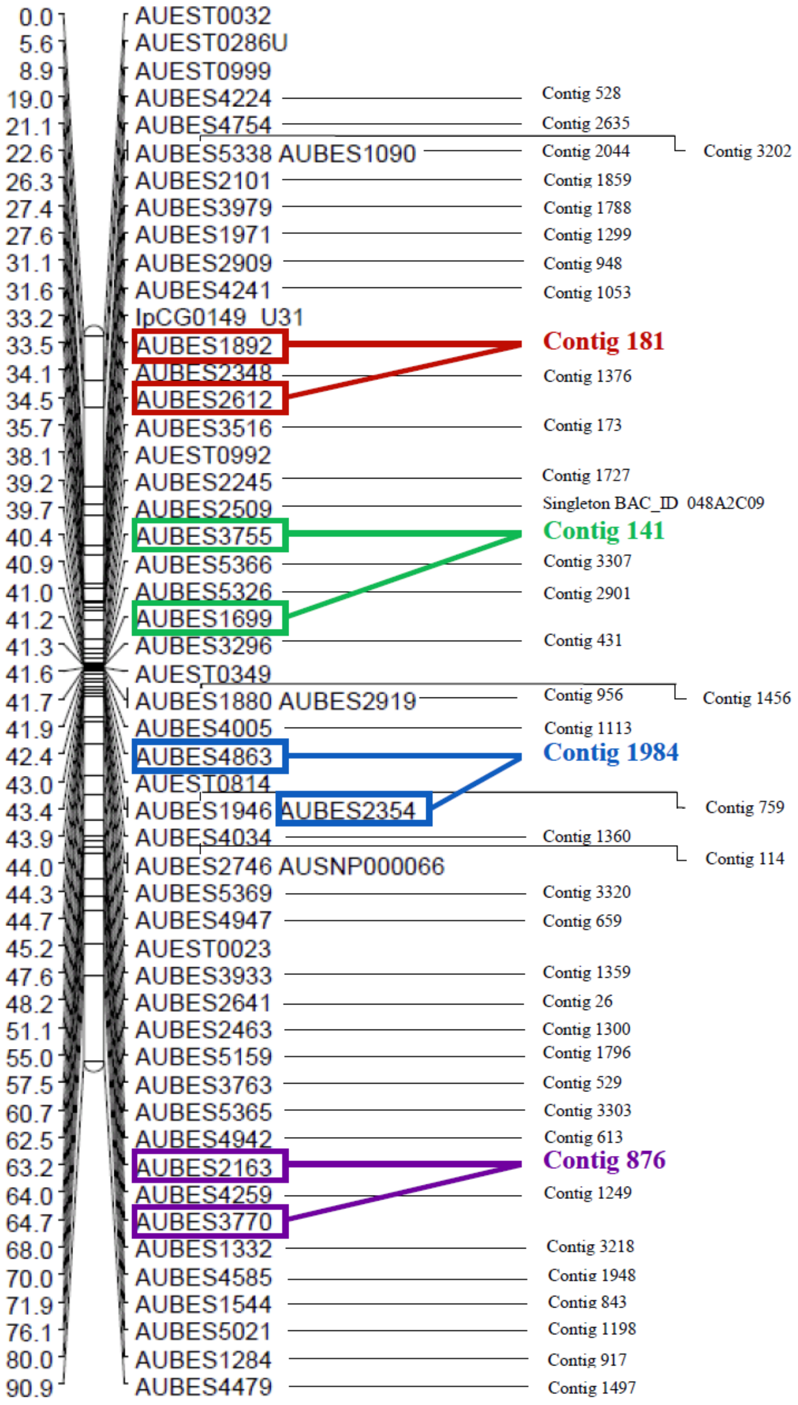
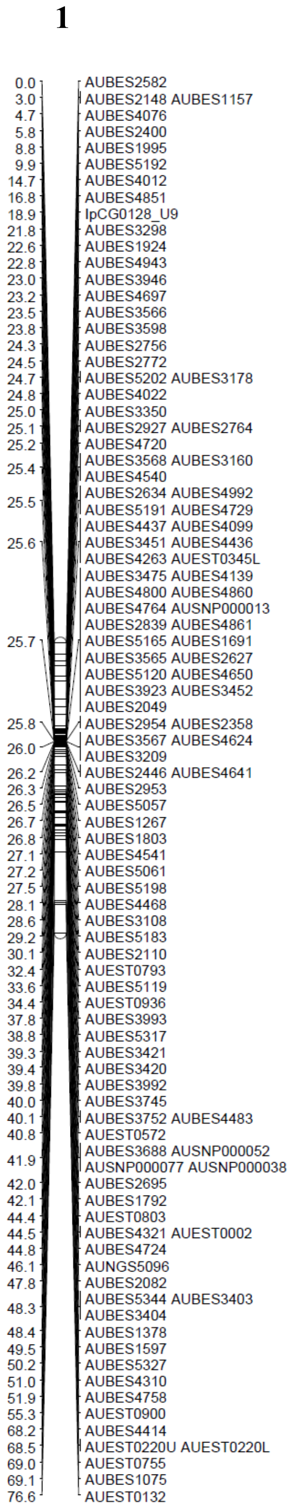
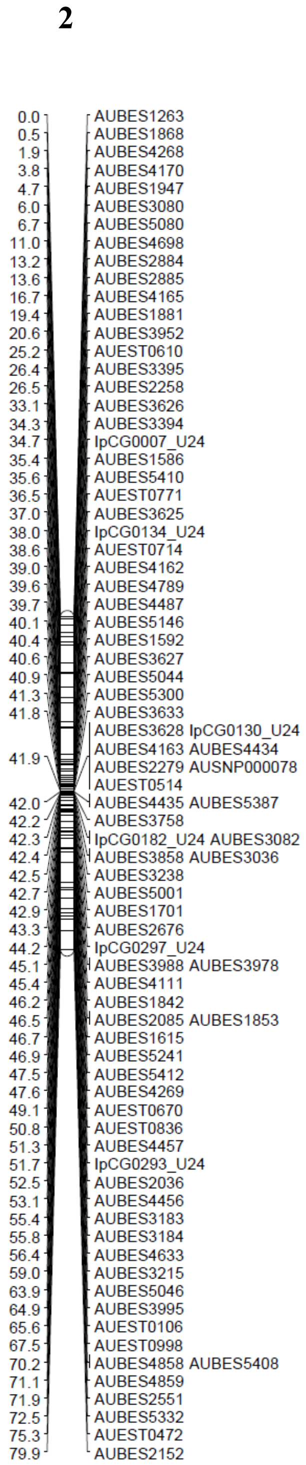


Figure 2. An example linkage group with physical map contig identities integrated (LG19) via their BES markers. Square boxes of the same color indicate markers mapped from the same contig.

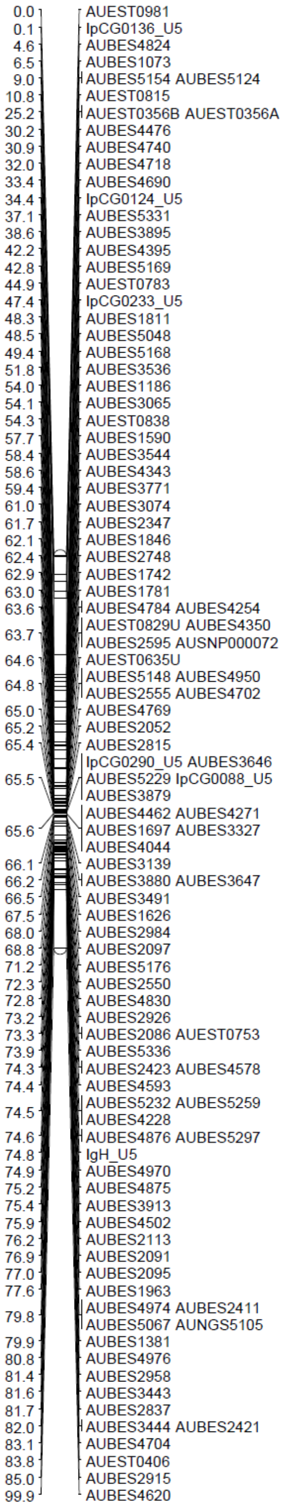


Supplemental Figure 1. A sex-averaged linkage map of channel catfish. Genetic map distance was given in centimorgans (Kosambi's mapping function) to the left of the markers positions. The vertical straight lines indicated markers placed at the same positions.



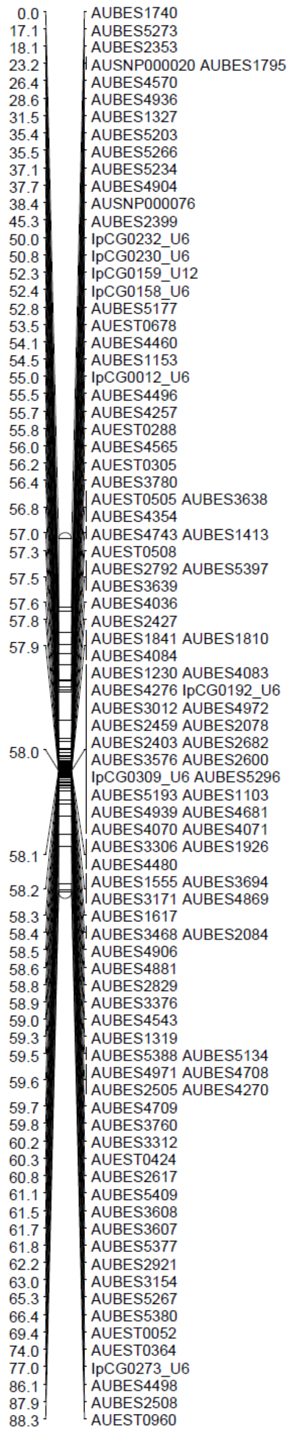
Supplemental Figure 1. Continued.

3



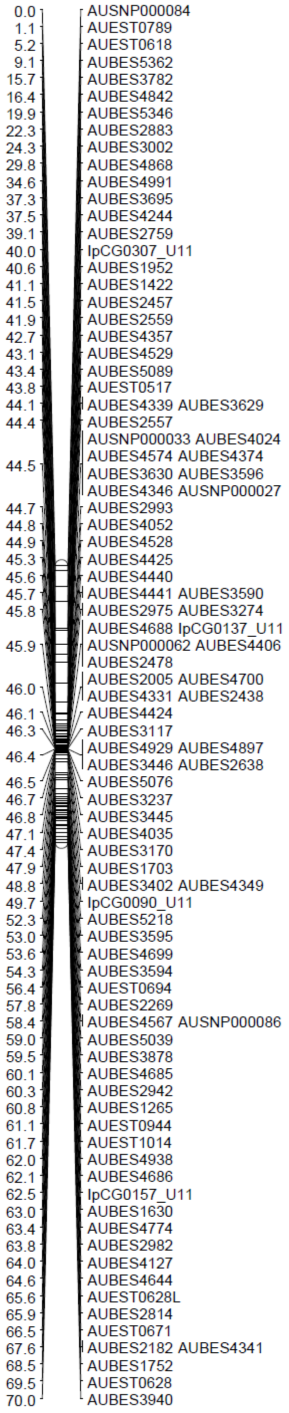
Supplemental Figure 1. Continued.

4

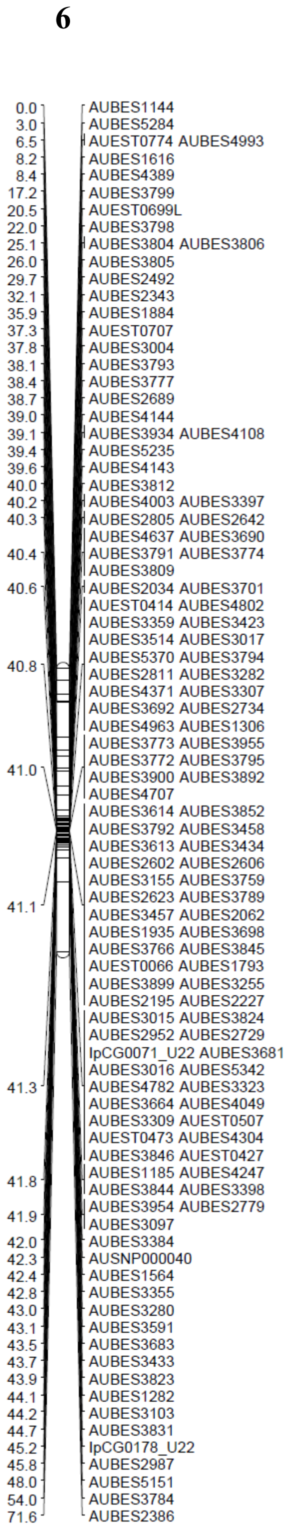


Supplemental Figure 1. Continued.

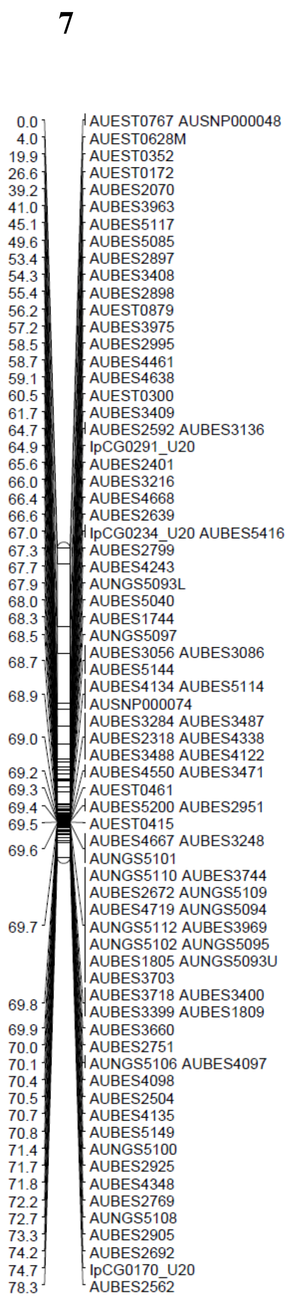
5



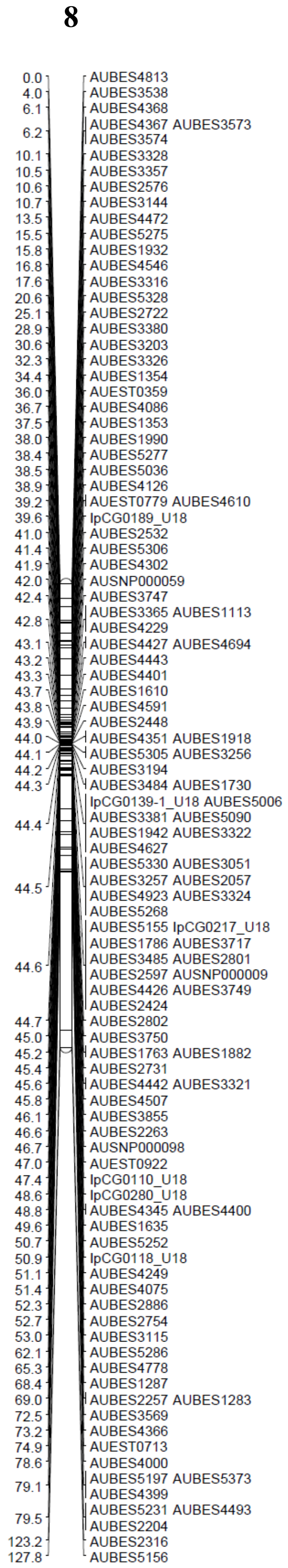
Supplemental Figure 1. Continued.



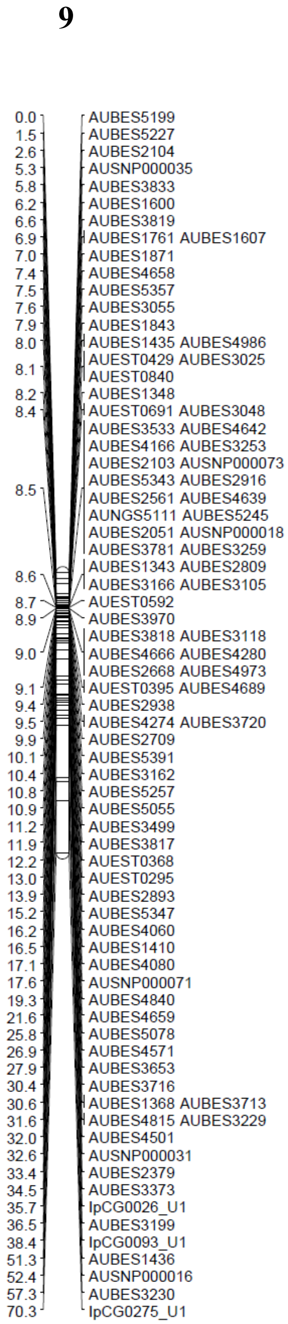
Supplemental Figure 1. Continued.



Supplemental Figure 1. Continued.

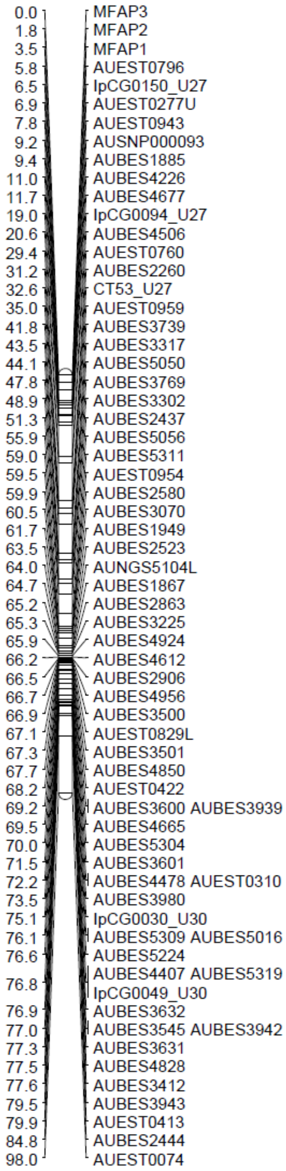


Supplemental Figure 1. Continued.



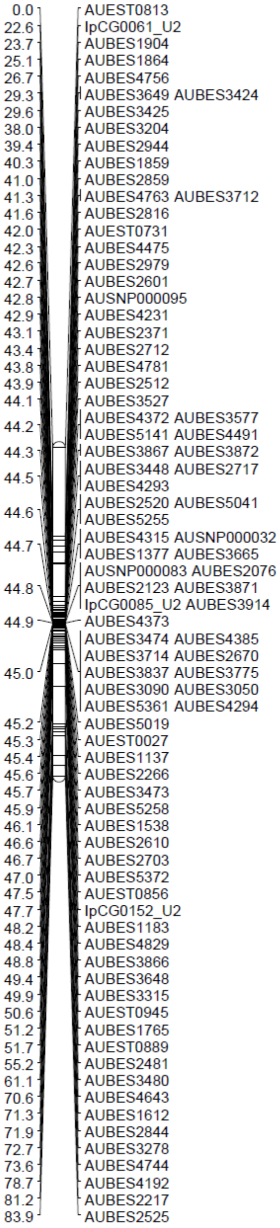
Supplemental Figure 1. Continued.

10



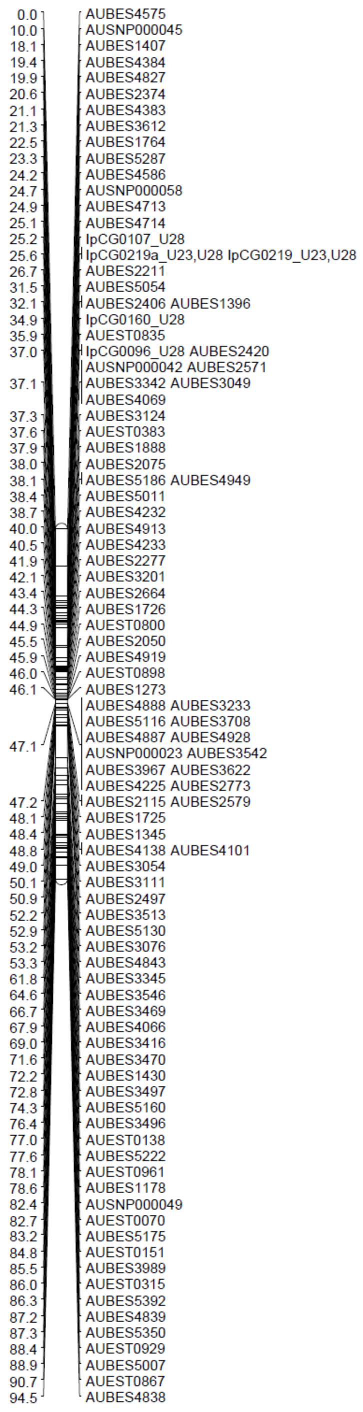
Supplemental Figure 1. Continued.

11



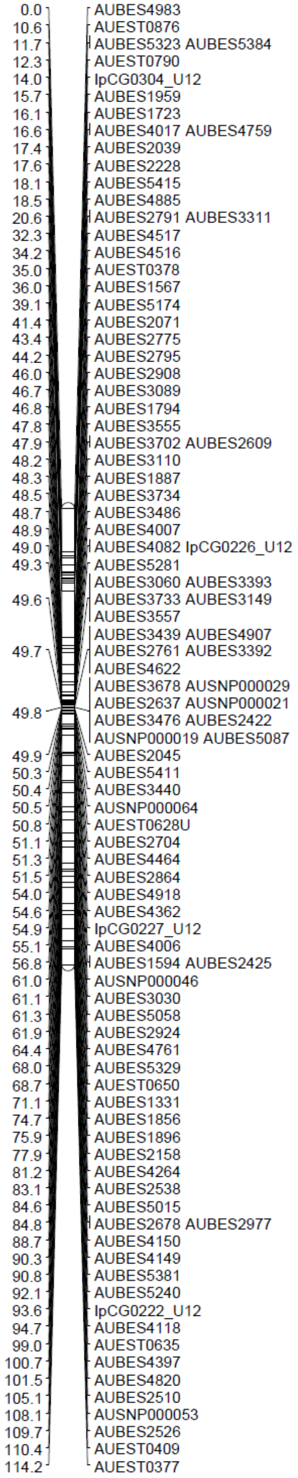
Supplemental Figure 1. Continued.

12



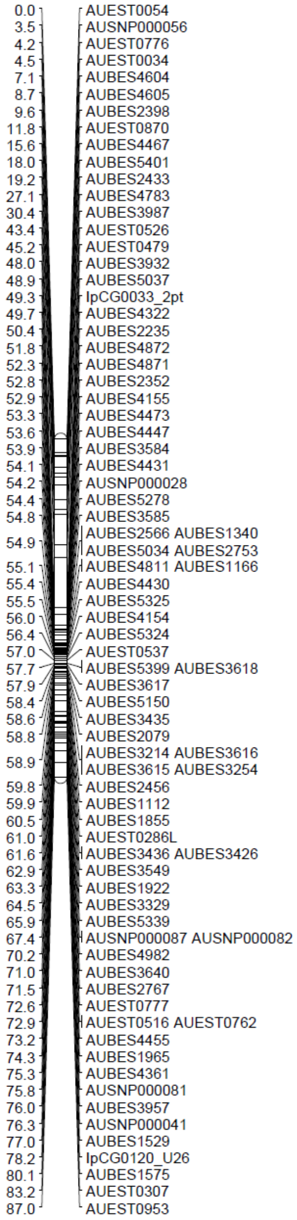
Supplemental Figure 1. Continued.

13



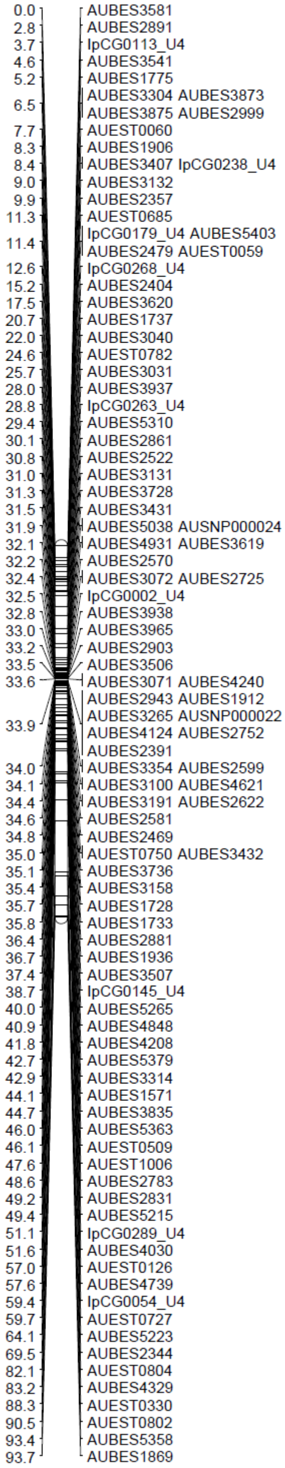
Supplemental Figure 1. Continued.

14



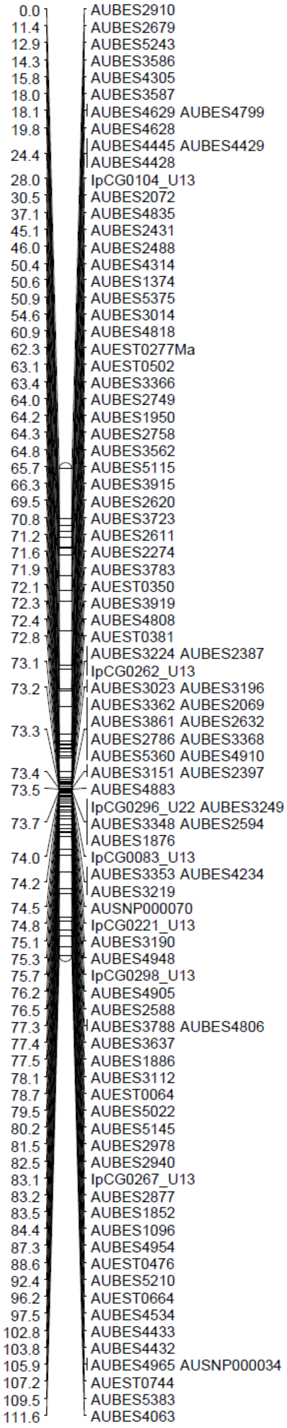
Supplemental Figure 1. Continued.

15



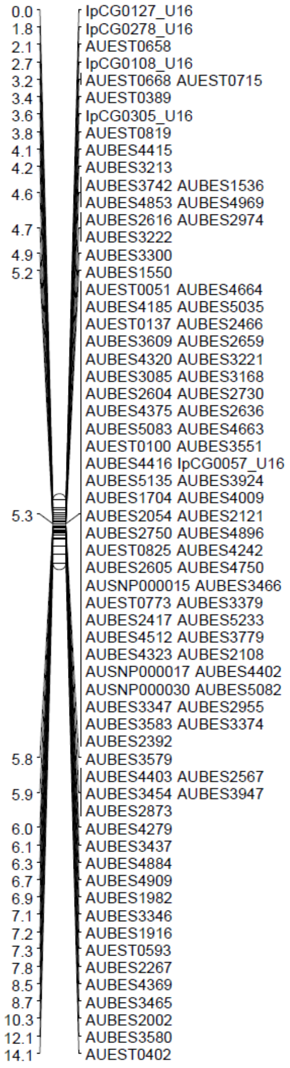
Supplemental Figure 1. Continued.

16



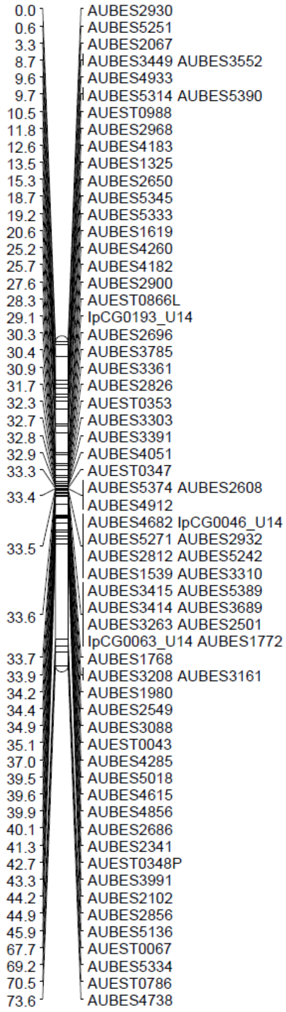
Supplemental Figure 1. Continued.

17



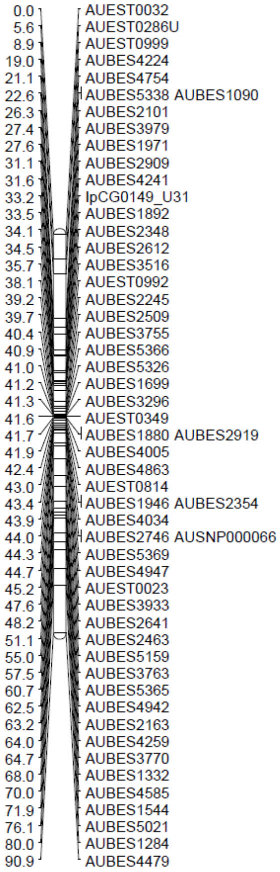
Supplemental Figure 1. Continued.

18



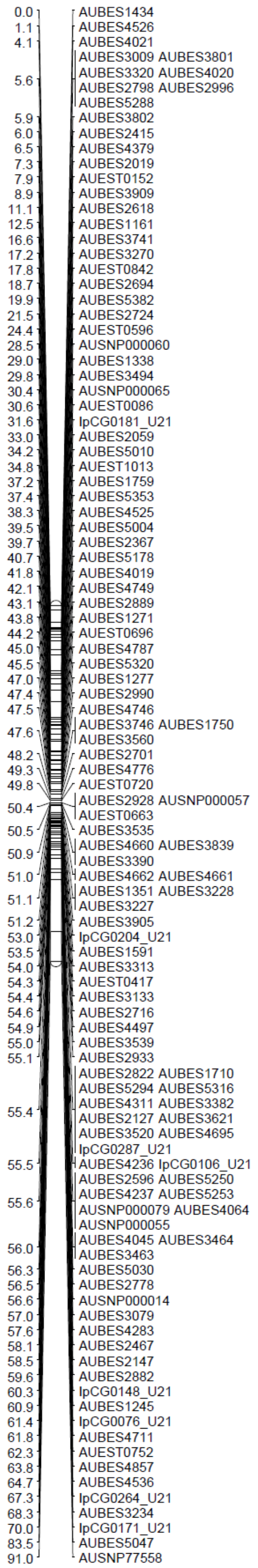
Supplemental Figure 1. Continued.

19



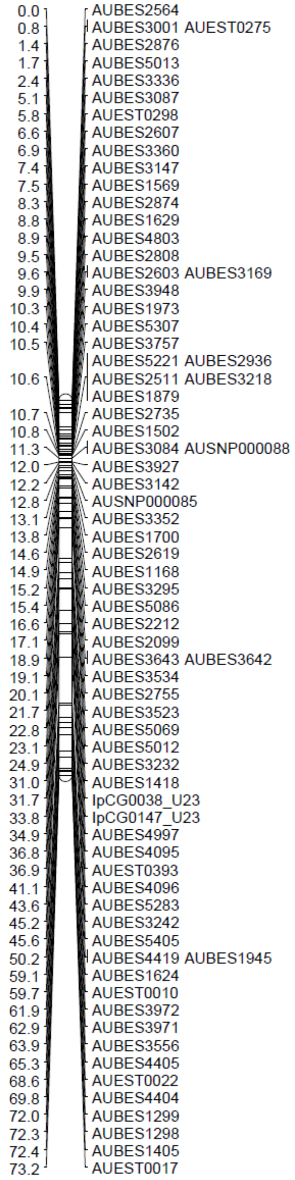
Supplemental Figure 1. Continued.

20



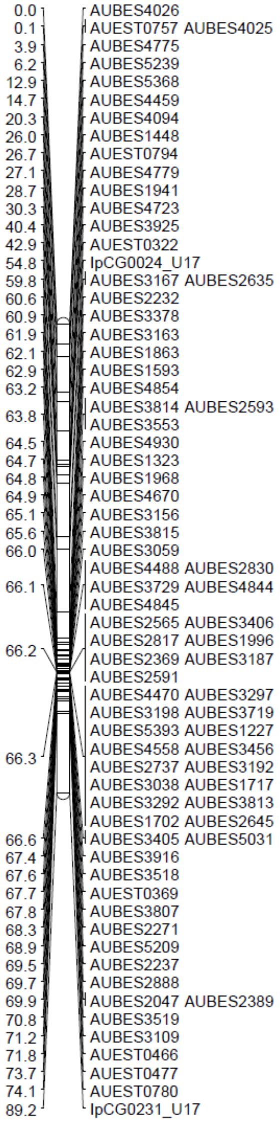
Supplemental Figure 1. Continued.

21



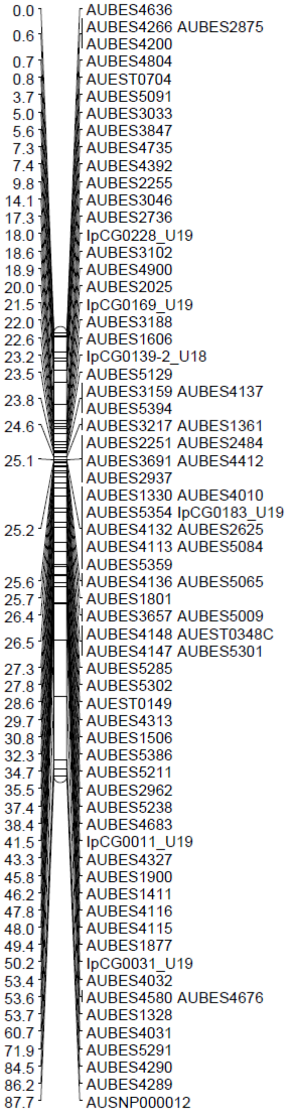
Supplemental Figure 1. Continued.

22



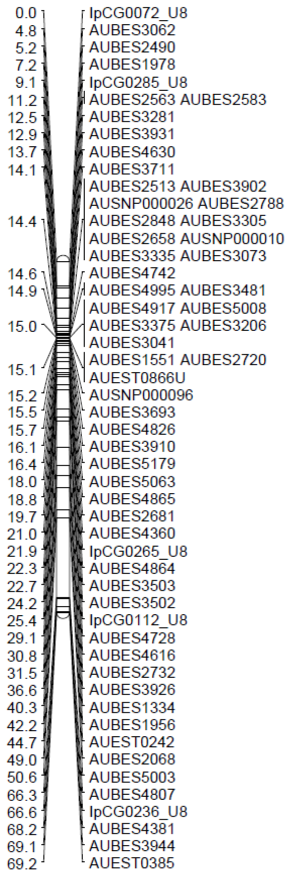
Supplemental Figure 1. Continued.

23



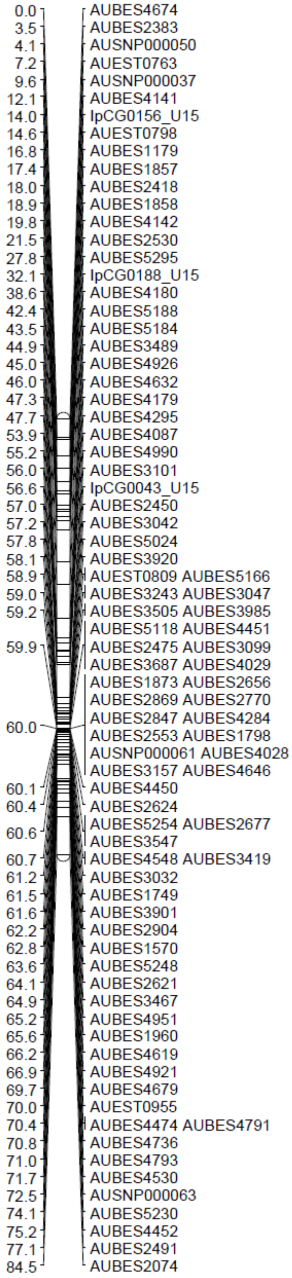
Supplemental Figure 1. Continued.

24



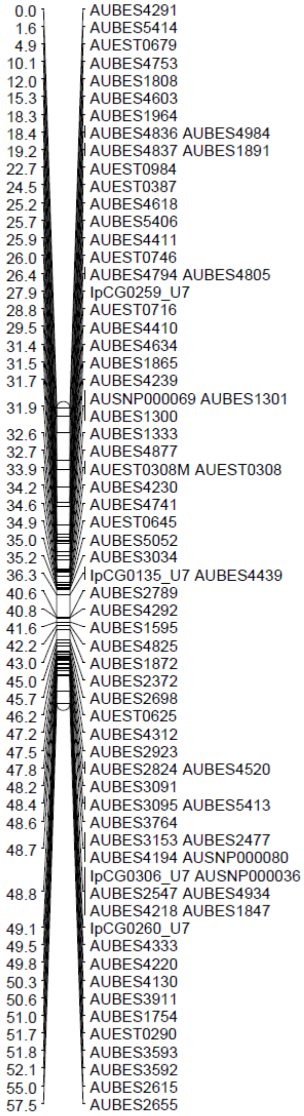
Supplemental Figure 1. Continued.

25



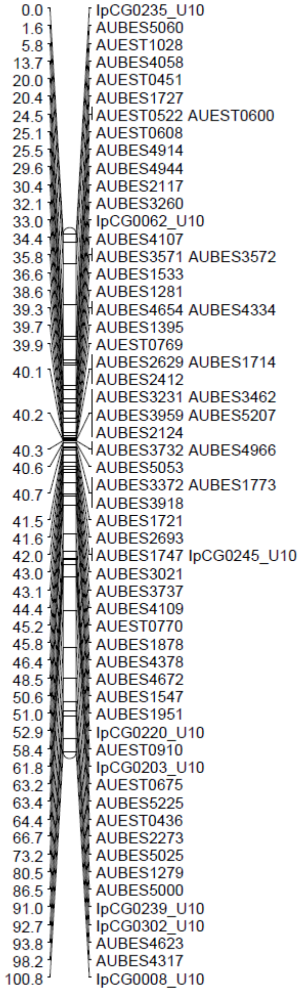
Supplemental Figure 1. Continued.

26



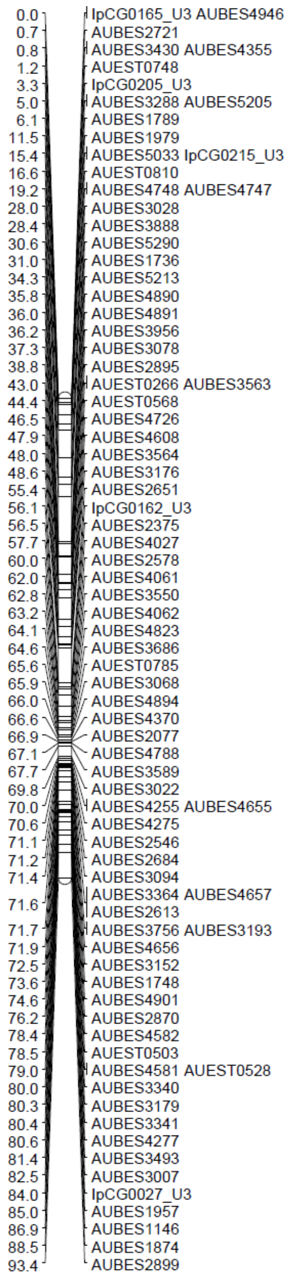
Supplemental Figure 1. Continued.

27



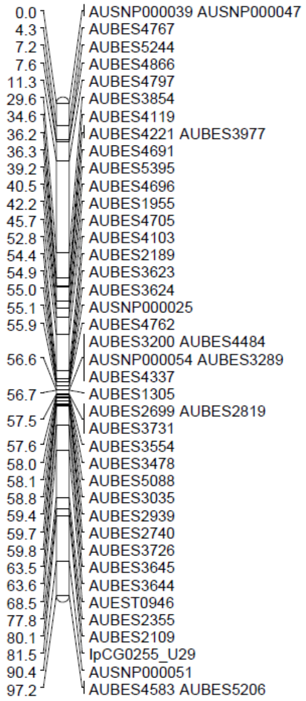
Supplemental Figure 1. Continued.

28



Supplemental Figure 1. Continued.

29



Supplemental Figure 1. Continued.

Supplemental Table 1. Detailed information regarding contig identities, estimated physical contig sizes, corresponding linkage groups, and genetic map positions.

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2582	34	490	1	0.0	GCATGGGAGGCATATCTCAG	CTGACCTTCCTGGCTGTTCT	067B2C11
AUBES1157	536	430	1	3.0	ACACACACTCAGCCTGTTGG	TGGAGCCACTGTACTCGTGC	008A1F09
AUBES2148	1702	183	1	3.0	AAACATTGCGTGAGAGACCA	ACGGATGTGGTGAGCTTCTC	022B2A04
AUBES4076	716	418	1	4.7	CACGCTTACTTCGGACAGTG	AAATCTCTCCTCGCCTCCAC	060B1H12
AUBES2400	1702	183	1	5.8	TGCAGTAATCAGTTGTGGGAAT	GCCAAGACTTTTGCACCCTA	045A1G01
AUBES1995	1970	225	1	8.8	ACCCATACCTTGTGCTGACA	ACCCGGACAACATGACAGAT	027A1G08
AUBES5192	2099	352	1	9.9	AAAGGTTTGCTCTCCCATTG	TGCACAAAGACAGACTGACACA	110A2A11
AUBES4012	1191	267	1	14.7	TGTAAGCTCCATCCCCAGAG	TCAGATGAATGGACGAGTGC	042A1C05
AUBES4851	1749	348	1	16.8	AATCATTGAGCTGGCAAAGC	TGTCTGCACTGTTTTTCATGC	084B2H08
AUBES3298	478	289	1	21.8	TCAAAAGCTGGGAGGTGAAC	TCTTGCAATTACGCTTGCAC	054A1A03
AUBES1924	42	1038	1	22.6	GGAAACGAATGGAAAGCAAA	GTGAATTCGCCTCTCTCCAA	036A2D04
AUBES4943	636	377	1	22.8	GATGAAGCAATGCTGCTTGT	GTCCTGGCCTGGTACAACAT	049B1B01
AUBES3946	150	362	1	23.0	CCAAAAGGCGTTCTAAGCTG	CCCTCCAAAAACATTGGAAC	014A1G10
AUBES4697	3006	230	1	23.2	CATGGCCGAAATTTGTATTTG	CACCGTGGCATTCATTACAG	003A1H09
AUBES3566	767	254	1	23.5	CCGAAAGTGGACCTTTCAAC	CAAATATGGAAAGGAGGCTGT	044A1G01
AUBES3598	1289	683	1	23.8	AGCACAAAACTGTGCAGGTG	TCGGATTCTCCAGTAACTCCA	029B1G06
AUBES2756	249	365	1	24.3	CCAATCTTCCATGCAAGTCA	GAACAGGGATGTGAGGGAGA	019B2A08
AUBES2772	597	654	1	24.5	GGAAGGCAGCGTCTAGAGAA	CCTTCTCTGAACCTCTGAACC	020A2F03
AUBES5202	2155	249	1	24.7	AGTTTGGAGAGACGGAGCTG	TTCCGATTTTGAGCACACAG	074A1C08
AUBES3178	316	775	1	24.7	GTGACAGGAAATGCAGCAGA	CACTACTGTTTGTCGCCAGAAT	053B1E04
AUBES4022	1283	359	1	24.8	GAGCCTATCCCAGGGAACTG	TTACGGGGTTTACCTTGTGC	091B1F06
AUBES3350	149	714	1	25.0	GTACCGATGCCACCAAAAGT	GTGTGCGTTTAGGAATGCAG	034A1H08
AUBES2927	1258	359	1	25.1	TCCACAAAGGCTCTAAGCAC	CTGAAGCCCTGAACCAAAGT	032B2B08
AUBES2764	428	516	1	25.1	TGGGACAAGCAGATTGTGTG	GGATAACCGCATGAATGAGC	048B2F11
AUBES4720	3271	166	1	25.2	ACACATGGGGACATTTGGTT	TTCCTCCTTTGCGCAATAAC	018B2H06

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3568	772	311	1	25.4	ACTTCAGCCATTGAGGAGGA	CCATCTCACATGTTGCTTCC	003A2C01
AUBES3160	370	891	1	25.4	TCATGTCATGGAGGGTTTTT	CTCCACTCAGACATGGGACA	060A2E06
AUBES4540	2276	235	1	25.4	GTGGCTTTACCTCTGGGACA	GAGCTCATTCAACCGACTTG	078B2H04
AUBES2634	42	1038	1	25.5	TCCTGAGCTGCTGTGAGTTG	TGGTGTCCAGGAAGTGTTCA	064B2B12
AUBES4992	1011	345	1	25.5	GGCAACAATGTTTGATTTGC	CCAGGCAAGACTGGAGTAGC	050A1E07
AUBES5191	2097	194	1	25.5	ATCGGTGGTAGTTTCCAAGC	GTGCCAGTTTGTTGCGTACA	008B2A11
AUBES4729	2071	216	1	25.5	TTTTTCCACCAATATGACATGA	TAAGTGGGTGGGAAATGACA	033A2G08
AUBES4437	1272	216	1	25.6	GCACAATAATGTGGTGGGAAA	CGCTTTCTCTTTGTCCTGCT	087B2H07
AUBES4099	1037	227	1	25.6	GCACTGAGGTTTCAGTGAGC	TCTCTGCCTCAGACCGACTT	011A2A05
AUBES3451	949	384	1	25.6	GCATAAAGGAACAGAAAATTACCC	TCTGTTGAATACAGCACCAGAA	066A2H10
AUBES4436	1272	216	1	25.6	GACAGCAGAGGTGGCCAATA	AACAGCACTCTTGCTTGTGC	023A1C09
AUBES4263	1331	355	1	25.6	TGATGGACACTCCTCATGAAC	TGCATGTCTGTCAGAGCAAGTAT	013B2H05
AUBES2839	167	313	1	25.7	TTCTGACCCTGAGCCATTCT	GGTGCACTCATCTCTGTTGC	031A2G09
AUBES3475	251	257	1	25.7	AGTCTCCAGTGCCAGTGCTT	CCTTCACCAGCCTTTCTTGT	062B2G06
AUBES4139	1122	186	1	25.7	CCCCACTTCCAGACTATTCCT	ACCATGATGAAGCGCTAATG	075A2E08
AUBES4860	1940	230	1	25.7	CTTGTTGTGAGTGGGTGTGC	TGCATTACCCTGTGTTTATGTT	030A1A10
AUBES4764	2719	262	1	25.7	GAAGGAGTCTCCGGTGTCAG	CGGTCATTCTTTCACCAACC	041B2F02
AUBES4800	3020	183	1	25.7	AAGGAGTCTTGAGTGTCAGTGC	TGATAGGGCCTGATGGAAAG	001B2G04
AUBES5165	1839	181	1	25.7	CCTACAATTGTTGATGTGGTGAA	GTCTCTACCCACCCAATCCA	026A1C04
AUBES4861	1940	230	1	25.7	GGGACTCCCATCAGAAACAA	TGCCTGTTGTTCAATCTCAA	087A1D01
AUBES1691	350	318	1	25.7	TGTCATGTACAAGAGCAACCTC	CACTCCTCCCTCTGCAACTC	034B2C08
AUBES2627	370	891	1	25.7	CCATACCCAGATGTCTGCAA	ATTGGCCCTGGTTATGAATG	035A2A01
AUBES3565	767	254	1	25.7	CCCATGATTGGCTAATGTCTCT	CGGGACTCCATGAGCACTA	014A2B10
AUBES5120	1561	266	1	25.7	GCAGGATGAGGCTCAGTGTT	GACATTGTGGGTGTACTTATATACCTT	036B1B08
AUBES4650	718	306	1	25.7	GCCTGTCTGTTGGTCTTGGT	AGACAGGCAGAAAACATACAAGAA	029A1A02
AUBES3923	1163	365	1	25.7	TGTCAGCAAAGCCAGATGTC	TATGGGGTGGGGTGTAGAGA	075A2E03
AUBES3452	949	384	1	25.7	TGGTAAGCCTCTGTTGAGTGA	GGTGTAGGCAGTTCCAGCTT	087B2E05
AUBES2049	2717	149	1	25.7	AGGATCACCCAGCTGTCCTA	TGCATCCTACACACGCTCTC	039A1F06
AUBES2954	633	311	1	25.8	CACACAGCGTTAAGCACACA	TGTGCAGAAAACTGTGCTGTC	024A1H01

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2358	597	654	1	25.8	AAGGCTGTGTCACCATCACA	GCATGAGCGACATGAACTTG	047A2H03
AUBES3567	772	311	1	26.0	ACTTCAGCCATTGAGGAGGA	CCATCTCACATGTTGCTTCC	007A2E09
AUBES4624	2169	215	1	26.0	CCCGTTTTCTTTTTATGCTTGT	ACACTGATCCCCAAGTTGCT	107A1F01
AUBES3209	316	775	1	26.0	CATGAATGAGAGGGCATCAG	GATGCCAATCAAAGCAGGAT	032B2G10
AUBES2446	2106	184	1	26.2	AAATTCGGCCAATGCTACAG	CTTCCAGAACACAGCCACAA	040B1A04
AUBES4641	448	245	1	26.2	CCTCCCATAGCGTGGATCT	CTTGGGAAGCTGCATCAAAT	004A1H02
AUBES2953	568	514	1	26.3	TGTGCCAACAGACCTCACTC	CTGGGCTCTTGGATTTGACT	051B1G11
AUBES5057	1352	240	1	26.5	CTCCAAATGCACATTGCTGA	CAGTTATTAATTAGTTTGGCGTGTG	014A1F03
AUBES1267	1612	227	1	26.7	TGCCAACATAAAGAGAAGCTGG	CTCCGCCGTTCAGTGCGAGG	001B2H05
AUBES1803	597	654	1	26.8	AAGGCTGTGTCACCATCACA	GCAGTACGACATCCACCTGA	034B1F10
AUBES4541	2276	235	1	27.1	CTCCAACCTCATCAGGCATT	TGCAAACACAAAACAGGTGTG	088A1C07
AUBES5061	1368	335	1	27.2	TTCAGGGCACAGCTTAATTG	CAACCCATGGATATGCTCCT	108A1H04
AUBES5198	2135	266	1	27.5	CAGGATGAATATGGCGAGAG	CACCTGTACTCACCTGCCATT	076A1E10
AUBES4468	1153	181	1	28.1	CATTAGGCCTAGGGGATGGT	CGTGTCCAAAGGGTCCATAG	106B2C06
AUBES3108	42	1038	1	28.6	GCATGGGCTGCGTAGTTTA	ACCCGTGTTTTCCGATACAG	029B1H10
AUBES5183	2000	255	1	29.2	CCCATAACGACAACGTGAAA	GCGACAGTCAAAGTCTCCAG	107A2C09
AUBES2110	singleton		1	30.1	TTCAATTCCATCCGATGTTG	CAGCTCTTCAGTCTGCTCCA	041B2B05
AUBES5119	1560	249	1	33.6	GCTGTTAACGTTAGAATTTGATTTT	TCATCTTCGTGTGCTGCTTC	005B1A12
AUBES3993	2142	352	1	37.8	CCAATCAGGACATCCACCAT	GACGCCCGCAAATCATATAC	087B2A02
AUBES5317	2745	200	1	38.8	TGCTTTCTGTACCGGTTTCAC	GTATGAGTTTCGGGCTTGCT	038A1H12
AUBES3421	468	348	1	39.3	TTCTTCATGCCTTGCTCTAAG	GGGCATGCCTTGGTTATATG	077B1H08
AUBES3420	468	348	1	39.4	GCGCTTAAAAGCAAATAGATTG	GGGCATGCCTTGGTTATATG	007B1H07
AUBES3992	2142	352	1	39.8	CCAGCCATAATCACTGTGGA	AGGGAACACCATGATCAGTACC	008B1G02
AUBES3745	2239	617	1	40.0	ACACCCCTGCTCTGTCACAT	TGAAATTCCACAATCCCACA	092B1A12
AUBES3752	2239	617	1	40.1	ACACCCCTGCTCTGTCACAT	TGAAATTCCACAATCCCACA	108B1E11
AUBES4483	1542	171	1	40.1	TGTAGACTGAGCTTTGTGGTTCA	CATTGCTGTAGGGCTCTTTACAT	055B2D03
AUBES3688	504	311	1	41.9	CCCACCATTACAACACAGCA	ATCTGGCTCCCTCCTACCTC	048B1B04
AUBES2695	690	524	1	42.0	ATGGAGCGCTCATCCAGA	TCGGTGGGTCTGTTTGTATTC	013B1C09
AUBES1792	2734	259	1	42.1	TATGCACACCCAAGGTGGTA	CACCGGGTTTTCTGTCTCAT	033B2A01

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4321	2019	238	1	44.5	GGAGTGTCCAGTGTCAGCAG	GTGGAACTGATTGTTGGAAGC	106B2A07
AUBES4724	3364	166	1	44.8	GCATTAAGCTTTCAGCTGTGG	TTCACGCAAACATACATTCG	074B1C06
AUBES2082	1924	198	1	47.8	AGCTGGGGGAAAAGAAGAAG	TATTCCCTCGGACACAAAGC	041A1A08
AUBES3403	351	299	1	48.3	GCCGTTGGAGTCTTTGACAT	CCCTTTGCTTTCTCTCTCCA	007B1F09
AUBES3404	351	299	1	48.3	AACGCTGCAATGTGGATTTT	CGGTGTTCTTTATGTCCACCA	039A1A04
AUBES5344	3228	271	1	48.3	GCTCCAGCAAGAGACTGTCC	GCTCAGGTCGCTCATACGAT	019A2B12
AUBES1378	2666	205	1	48.4	CCAGTGGACAAAGCCTGC	CAGTCCTGACTTGCCAGG	034A1G06
AUBES1597	2328	455	1	49.5	TGGAGCAAACAACGTTTGAG	AAAGCGATTCCCCATCATC	023A1A10
AUBES5327	2928	208	1	50.2	CGACTTTCGGCCAATAAAAC	CAGGTAAGGCCCAGTGAGTT	014A2D09
AUBES4310	1934	337	1	51.0	CGTTAAGGCTGCTCCAGATT	AGGGAAAGCACACGACAGTT	104B1G04
AUBES4758	2670	154	1	51.9	TGTTTGATGGACGTTGATGG	CACATGGGTATGCCAATCAC	060B2D12
AUBES4414	2439	381	1	68.2	CAGGACCTTCTGCTCACCAT	GCACTCGTCTTTCAGCCTCT	102B1B04
AUBES1075	2439	381	1	69.1	AAGCAAGCCTGGACCATGAC	GTGCTCTGTTAGCTGGAGTG	010A2A02
AUBES1263	singleton		2	0.0	AGACGTATGGGCGAGATCAG	CTGACCTGAGCACTGGTGTG	033A2D02
AUBES1868	singleton		2	0.5	GTTCTCCAGGCCCAGTCAT	TCCTCTCCTGAGATCCTTAACA	024B1A09
AUBES4268	1378	418	2	1.9	GTGCACTATCTGCCAGCATC	CGTCACTCGTCACACTTAGC	001B1F02
AUBES4170	1693	496	2	3.8	AAATCGGTCGGTTCACTGAG	GGGCGAAAGACGTAAAGGAG	110A1D08
AUBES1947	1693	496	2	4.7	CAGATCCTGATCCCTGATGG	TGGACTCTGCCTTTTGATCC	019A2D06
AUBES3080	236	795	2	6.0	TCCTCTGGAAGGCTCTCAAC	TTCTGCTTGCACCAAATCAG	092B1H10
AUBES5080	1448	289	2	6.7	CAATAATGCGATGGATGGAT	CGCAGACGTTCTGTGACATT	012B1G04
AUBES4698	3007	178	2	11.0	ACCACTGGGTGCTTTCTGTC	TCCAGAAGCGTGTCACTGTC	072A2G03
AUBES2884	343	661	2	13.2	TCACTTTCCTATGGCCTTGTG	ATCCACTCTGTGGTCGGTTC	028A1A11
AUBES2885	371	409	2	13.6	GCTGTTAAACCATTGCCTGA	ACCCTGCCTGCTTAGTGAAC	074A2G06
AUBES4165	1514	445	2	16.7	GCTGCTGCCAGTTTATGGAT	CCTTCATGCCTCATCACGTA	109A2F02
AUBES1881	3007	178	2	19.4	TGTCACTTAAATCACGGAGGTT	ATCGGGCCTTGAGGTAGATT	027B2B03
AUBES3952	343	661	2	20.6	AGCGGATGGAAAGCTCTAGG	GGTCCGATAAATAGCCAACG	096A2E11
AUBES3395	145	352	2	26.4	GCCAAAATGTCTTTGGAGGA	CTACGGTGACATTTGGGTCA	042A2B09
AUBES2258	145	352	2	26.5	TGGAGCAAAACATCCAACAA	GTGACGGGAGAGGATCTCAA	042B2F02
AUBES3626	337	250	2	33.1	ATGCATGCAATTTACCCACA	CCCTAAGGCTCCAATAAGTGC	055B1C09

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3394	145	352	2	34.3	GTGTTGACGCTGTAACACACA	AGCGAATTTATCTGGGGCTA	063A1F02
AUBES1586	1524	296	2	35.4	TCCTCTCATCATCACCACAGT	CAAAACGCCAATGACATGAT	019B1G08
AUBES5410	3534	166	2	35.6	TGAGCTTCTACTCAGCTGTTGG	ATCACGCAGCTGCCTAAGTT	096A1A11
AUBES3625	337	250	2	37.0	CAGAGCTACGAGCAGAGCAT	CCGTACTGGAGCGGAGTAAG	073A1C09
AUBES4162	1513	450	2	39.0	GTGCCCTTTGGAAAACTGG	CACATGTTGGAAGCAGACCA	045A2F12
AUBES4789	2915	242	2	39.6	CGAACACACTTGATCGGCTA	TCCCTTTGGTGAACAGGAGT	062B2A07
AUBES4487	1572	205	2	39.7	TGGCAACTGGAACAGTGGTA	CGGGTGATGGATAGATGGAT	075A2G11
AUBES5146	1690	188	2	40.1	GCACGCTTTTAGTCTGCAAAT	TGAACTCGCACCACACATCT	030B1D11
AUBES1592	2904	125	2	40.4	CCCTTTAAAGAGGGCTTTTCC	GGTGCGTTCAAGAGAAAGGA	029B1A08
AUBES3627	407	294	2	40.6	AGTCTGGTGAACGGGTTTGA	CAACACCTACCATTAGCCACCT	049A1A10
AUBES5044	1296	194	2	40.9	TGGCACGAGTGTGGTTTCTA	TGCCAGAATGAACACTTCAACT	053A2F10
AUBES5300	2659	232	2	41.3	CCGGAAGTATTTGGTTGCAG	TGAAACCGTGTGTCTGTGCT	061A1C12
AUBES3633	544	293	2	41.8	GTCGGGTTCCTCTCAAGGTT	TTGCAAACACAACACAGTGC	006A2E07
AUBES3628	407	294	2	41.9	AGCCAATGTTTCTGGACTCG	CTGGAAACAGACTCCACACTGA	020B2G10
AUBES4163	1513	450	2	41.9	TACATGTGGCTGGAATGCAC	CCTGTGTCCAGGTTCTCCAG	046A2D02
AUBES4434	998	200	2	41.9	GTTCGAATTCGCCTGCTATC	GCACAAGGAGTTGTGGGAAA	063B1G01
AUBES2279	2365	266	2	41.9	TCTGCAGAGGTCAGGTAAGGA	CTGCAACGTTCTAGGGAGGT	043B2A03
AUBES4435	998	200	2	42.0	CGAATTCGCCTGCTATCTGT	GCACAAGGAGTTGTGGGAAA	090B1A08
AUBES5387	3406	198	2	42.0	AGTCAGTGCAGCTGGTTCAA	GGCCATTTGCCTTAATGTCT	038A2H03
AUBES3758	373	266	2	42.2	CCGAATCATTCTCGGATCAC	TTCGACTCTTTGAGCCGATT	032B2A11
AUBES3082	68	668	2	42.3	TACACACAGCCTTCCCATCA	TGAACATCCAGCCCAGTTATC	003B2A10
AUBES3858	71	468	2	42.4	AACAAAGCTGGCTGGGTATC	TGATGAGTGGGCCACATAAA	084B2D07
AUBES3036	456	445	2	42.4	GGATAAGAGGGAAGAGATGAGC	TACGCAGCACAATGGACAAT	058B1H03
AUBES3238	14	404	2	42.5	CGTTGATTCCTTTCATTTGG	TGGCTGCCCTATGAAGTTAAA	081B1C05
AUBES5001	1082	337	2	42.7	TCCTCACGCTTGCCTATTTT	CCAGTTTTCAAACAGTCAGTCC	072A2D11
AUBES1701	1745	167	2	42.9	CAGCAAGAGAGGGCACTACC	GCGCCTGTACATAACTGCAA	034A1C10
AUBES2676	14	404	2	43.3	GCTGGAACGTTTCTGGCTAA	ATCGCTCGCTCTCTGTCTGT	003A1F03
AUBES3988	1998	284	2	45.1	GGCTAGGCCCAAATAAAAGG	TCAGCAGGGGATCAAATACT	052B1H07
AUBES3978	1777	323	2	45.1	AGAACAACGACCAGGGACTC	TGTGGACTTGTCTTGCGAAT	001A1G07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4111	1386	318	2	45.4	TTTGCGTTACAGCAACATGA	TAATGCAGCCCAAATGTGAT	065A2D06
AUBES1842	singleton		2	46.2	CCACCTTCCACTCAGGAGAC	GAACATATCTGGGCCTTCCA	036B1H10
AUBES2085	570	533	2	46.5	TGGAGACGTGCTCTAAAACTCA	CAGACTGAGCCACAGGACAG	041A1C09
AUBES1853	singleton		2	46.5	CTGGAGAAAGAGAATGGAGCA	CTCCCATTCCCCACACAG	036B2A12
AUBES1615	570	533	2	46.7	TGATGCCTGGCTGAGAGATA	TCCCTTAAAGCCCTCAATCA	024B1H04
AUBES5241	2393	188	2	46.9	CAAACCGGAAGTTCTGGAAA	GCACTTCCAGGCAAGACACT	080B2E08
AUBES5412	3537	164	2	47.5	GGAGCTGCAATAGGGCTTT	TTGAAGTCTGAATTTGCTGCAC	085B1C11
AUBES4269	1414	423	2	47.6	AGTGACGTCATGCTCCGAGT	ATGCCCCCATTACTGTGAAC	051A2A09
AUBES4457	1706	233	2	51.3	TTTCACTGCAGAACCTGCATA	TGTAACTTGTCGATGGCGAAT	078A1F03
AUBES2036	803	259	2	52.5	AACGCCGGATAGTGTGAAAG	CGAGTGCGTCTTTGTAATGG	038B1G11
AUBES4456	1706	233	2	53.1	CAGCAAGCTAACGGTGATGA	GCCCAGGAACAAAAACTGAA	072A1E03
AUBES3183	55	614	2	55.4	GAAGCATTGTGGTGCATTGT	CCAGTGTTTTCCAGGGTCAT	107A1H11
AUBES3184	121	956	2	55.8	TGGGAGTTAACCAGGGAAAG	GAGGTTTTTCTCCCCAGTTG	058B1C03
AUBES4633	2173	352	2	56.4	CACGTTTCGAAAATAATATCAGGA	GTTTTGCTCCTCCTTCCAAA	035A1F05
AUBES3215	121	956	2	59.0	TGTGTAGCCAGAAATACAGATGC	GACAGCCAGGCACAGAGATA	014A1E01
AUBES5046	1311	353	2	63.9	CAGAACTCAACAGCAGTGTGG	GATCGTCCAATTCAGCATCA	086B1D08
AUBES3995	2151	269	2	64.9	TCTTTTCGTAATAGTTGCGTCCT	AAAGAATGAATTGGGGTCCA	053A2F06
AUBES4858	1930	430	2	70.2	CTGTCGATGATGTCCTCGTG	GCTGCAGTCCCTCACTACATC	108A2C12
AUBES5408	3523	173	2	70.2	AACTTCCAAGCAGTGCGGTA	CGAGAGCACTTAAACCCTGAA	063A2A08
AUBES4859	1930	430	2	71.1	CAGCACGCAGAATCCTGTTA	GTGCGATCAGTCGAGGATTAC	084A2A07
AUBES2551	singleton		2	71.9	GGTCCTAATGAACACGACGAA	CTTTGCCGCTAAGTCATGGT	049B2H01
AUBES5332	3096	198	2	72.5	GCGTCCTTGAATGACCAGTT	GTCACGTACGAGGAACGATG	061A2D09
AUBES2152	737	731	2	79.9	CGGCTGACTGAGGATTTGA	AATCGCAAGCTGGAGAATCA	023A2A10
AUBES4824	3154	129	3	4.6	TTTCTCATTGCAGTGGATGC	CATTTTCAATGTGGTCTCAGACAT	062B1B04
AUBES1073	2216	107	3	6.5	ACCAAAATGTGAAGGGTGTTCTC	TGCTACTCTGTTGGTGCCAG	010A1A06
AUBES5124	1601	282	3	9.0	GTTTGTGGTGCCATGTCAGA	TGAGGATGACTTTGAGCCTTT	080A2D03
AUBES5154	1746	218	3	9.0	ACTAAACACTGGGCCCCTTT	TGAATGCAGGAGCACAATTT	039A2C05
AUBES4476	1408	274	3	30.2	ACCTGTACGGTCGTCACTCC	TTAAGCTATTGCTCCGTCCA	090B1F08
AUBES4740	2401	211	3	30.9	TAGGGGTTCAAGCAAAATGG	TTCTTCCTCGAATCCCTGTTT	104B1C05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4718	3240	276	3	32.0	CAGAGTCTGTGAGCGGTCTG	CCAAAAAGTTTGAACTGAATCG	090B2G03
AUBES4690	2892	266	3	33.4	AAATCACGCTGGAGGGTTC	ACCAGCCACAACTCAGATCC	070A2B03
AUBES5331	3076	213	3	37.1	TCCATGTCATATCGTCCACCT	TCAAGCTCACTCCAACATGC	038A2D11
AUBES3895	1604	223	3	38.6	TAAATGCAGGTGTGGACTCG	AAGCGACAAACTAGCAAGTGAA	038B2A08
AUBES4395	1869	237	3	42.2	CTCAGGCATTACAGCAGCAG	AGCCCTGTGACCTAGTGAGG	109A1C12
AUBES5169	1882	174	3	42.8	TGGACGAGTCATGAATTAGGC	CAGACAGTGTCCTTCTGCTTG	012A1C09
AUBES1811	3484	238	3	48.3	CCTGAACTCACACTGGCAAA	TTCCGTATTCTGGGGTGTGT	033B1A08
AUBES5048	1326	272	3	48.5	ATCACCACCGTCTGACCAAT	CCTGTTGAGGAGAGCCAATG	087A1A04
AUBES5168	1867	301	3	49.4	GGGTTGCCAGATCAGAACAG	TGTGTTGGTCCATGATCGTT	012A2C03
AUBES3536	227	475	3	51.8	CATTCCCTTGCTCCTTCATC	TTGAAATGGATTTCCCATAGC	052B1H01
AUBES1186	2527	129	3	54.0	GATTAGGGCACTGAAGTCACG	AGACCCCAGCCAAGCTGTCC	011B2C12
AUBES3065	227	475	3	54.1	TGTTGAGGTGTCTAGGATGCTG	AAAAGGGCCTGGCTAATTGT	058A2C07
AUBES1590	684	387	3	57.7	TGTCAACTTGGACCTAATGTGC	CGCTTTCATTCGAAGCAACT	023B2G12
AUBES3544	377	340	3	58.4	GGGAAATATCACAGCCAGGA	AACGTTCATCCCATGTCTCC	011A1C06
AUBES4343	97	599	3	58.6	GGTGGGTTGCTCACAAGTTT	CAAATGCCGGTATGTGGATT	053B2A05
AUBES3771	919	276	3	59.4	TAGCATTCAAACGCCCTTGT	TTTGGGCTCAAACTATCTCCA	079B1B12
AUBES3074	97	599	3	61.0	GGAAGTTACCTGCAAAACACC	TGCTTTCAACAGTGTTTCCAAC	033B1A12
AUBES2347	335	744	3	61.7	AGTCAAGCAAAGACGTGTGC	GAGGCCGAAGTGTCTCTGTC	047A1F03
AUBES1846	477	330	3	62.1	GTCACGCTGATGACTCTCCA	CACTCATTCAGTGACAGGAACTT	036A1C10
AUBES2748	128	416	3	62.4	ACAGTTTTCCGCCATGGTAA	ACCACTGTTGGGCAGCTAAC	001B2A09
AUBES1742	486	440	3	62.9	GCCCAGGGGTCCAATTAC	TGCGTAGGTCAGATCCCTCT	020A1A02
AUBES1781	62	318	3	63.0	CGAGGCGAGCTGGTTTAATA	TTTACCTCTTTTCCCGCTCA	033A1A07
AUBES4784	2884	167	3	63.6	TCATGAAAAGGCAGGTGTTG	GAGGTAGCATTCATGCACAA	112A2H10
AUBES4254	1186	286	3	63.6	CTTATGTTGCTGAGGAGTCTGG	TTGGTTAGGGGAGGTTAGCA	031A1G04
AUBES4350	377	340	3	63.7	TGCCCTAAAAAGCTTTCCCTA	CATTATGGGTGCTGTTCACCT	063A1B05
AUBES2595	335	744	3	63.7	CCGGGTCTCTCAGTCTCTCA	GTGCAGACATCTCCAACACC	009B2C08
AUBES5148	1705	457	3	64.8	TCCTAGTGCCAGGCTCCTAA	GTGGTCAATCACCCACCTG	088B1D05
AUBES4950	683	200	3	64.8	TGACATTTATTCCCCCACTGA	TTCCAAACAACCAAGAGGAAA	076B1D08
AUBES2555	480	709	3	64.8	ACTGTTGTTGCTGTTGTTGTTG	GCACAAACTGACAAACAGATTCA	022A2G04

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4702	3060	198	3	64.8	TGTGATTGAACCCTTCAGACC	CTCAGTGGCTTGCTCAGTTG	064B2E11
AUBES4769	2793	123	3	65.0	TGTGGATTATGGGATGGATG	CCCATTCAAACAGACTTAGGTG	009A1D07
AUBES2052	819	409	3	65.2	GAAAAGCCTCCCTCATACCC	CAGCCCAACTACAATGAGCA	039A1H03
AUBES2815	307	320	3	65.4	GCACGACTCAAAAAGCCACT	GCATCAGCCAAATGAACAAA	027A1E08
AUBES3646	789	279	3	65.5	TGTAACGGCAACGGTTTGTA	GCTATGGTTAACGAGCTGGA	086B2A10
AUBES5229	2353	281	3	65.5	GGATTTCATCCATTCCAGCA	CTGGGAAAGTTCAAGGGTCA	109B2F09
AUBES3879	919	276	3	65.5	GCGACTGAGGGGAATAATGA	ACACACACACACATGCTCGT	045B1E12
AUBES4462	888	201	3	65.6	ACATGTTTGCAATGCCACTC	TGGCAGCTCTGCTACCACT	034A2F08
AUBES3327	480	709	3	65.6	GCCCGTAAAGGATTTGTTCA	ACGATCCCATCCACACTGAG	070A1D09
AUBES4271	1438	365	3	65.6	GGTGAAGGCATGGAGGTTAC	GACCTCTGCACCTTCCTCCT	014B1D11
AUBES1697	1459	335	3	65.6	CAGCACACGAAATTGTCCAG	TGGAGAACACAGAAAATCTTGC	033A2C01
AUBES4044	1504	331	3	65.6	TGTGTCATGGCTCACACTATG	GTTTCTTTGAGGAGCGCTTG	086B1H07
AUBES3139	335	744	3	66.1	TCATGATCAGGGTTCATCACA	GTGTCCGCTTAGTGGGTTTC	107A1C03
AUBES3880	919	276	3	66.2	CAGCACTCTGCTCTCGTGAA	GCCCCCTCACCTCAATAAA	096A1A03
AUBES3647	789	279	3	66.2	TCTTGAGCATTTCCCAGGAT	CGACACACATGGCATACACA	100B2D04
AUBES3491	477	330	3	66.5	CACCTGAAGGATGAGCGAAC	TGTCACAGTAAGCCTCCGGTA	021A1E05
AUBES1626	singleton		3	67.5	AGTGATTGCACATTCACAAGG	TGGTACACGATCATCTTCCTGA	027A2E03
AUBES2984	305	470	3	68.0	CAATCTCTGCACAGCCACAT	GCTTGTTGGTTAGCTCATTCA	106B1A08
AUBES2097	1192	216	3	68.8	GCATCCTTGAGTTCTGGAAAA	AGTCTGCTGTGGGGAACACT	041A2F01
AUBES5176	1937	186	3	71.2	GTCATGCAGCTGAAGAGGAA	AACCTTCAGGCCATTTCTGA	109A1E06
AUBES2550	988	382	3	72.3	CACCTCCTTAAGGTGCATTGA	TGTAGACTTGGCCAGAAAGGA	049B2G08
AUBES4830	3185	223	3	72.8	AGATTTTCTCATGGGGAGCA	CATTCCTGCAATCTGCCAGT	013B1G04
AUBES2926	1205	340	3	73.2	ATGGTGATGTGGTGGATACC	TTGGCCCAAGGTACAGACTC	048A2H02
AUBES2086	571	589	3	73.3	CCACCCCCACCTCTATCTCT	CTCTTTCCCCTGATATTCAAGC	041A1C12
AUBES5336	3198	413	3	73.9	TCTGGGAAATTGCACAGGAT	AATAGCTGCAGGGGAAAATG	090A2B05
AUBES2423	136	514	3	74.3	TTATCCCTATACACGAGCACATAA	TCCTTGGCATCCATATTTCC	045B2G01
AUBES4578	1893	189	3	74.3	TGGAAGCAGGAAGAGTGACC	ACTGGGTCAGCTGGAGTACC	085A2G03
AUBES4593	1893	189	3	74.4	TGGAAGCAGGAAGAGTGACC	ACTGGGTCAGCTGGAGTACC	085A2G03
AUBES4228	679	266	3	74.5	GAGCTGTCTGCACCTAAAGGA	TGGTGAGACAATTCGCAAAG	108A2D09

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5232	2363	191	3	74.5	GCTTCGGTACAAATGCATGA	GCACAGTAACTGGACAATTGGA	045A1H04
AUBES5259	2489	140	3	74.5	AATACGATGGTGATATTCAAACG	CAGAACAGCCTTTCACATCG	010A1G02
AUBES4876	2932	328	3	74.6	TCTGGCCCTTTGACATCTTC	TACCCGCATTCTCATGTCTG	051B2G06
AUBES5297	2650	210	3	74.6	GCAACCCTGTTATGCAATGA	CAGCAATTTAAGCACTGGGAAT	096B1E07
AUBES4970	859	326	3	74.9	GCATCTGACCGAACAACAAC	TATAGGAATGCCCACCTGGA	080A1H02
AUBES4875	2932	328	3	75.2	CGTAAGATAACCAGTGAATGTGATG	AGCTCCTTCCTTGTGTGTCC	001B2A11
AUBES3913	1070	255	3	75.4	CAGGAGTGCTGGGTATGAGG	TCTCCCCGGGTTTTCTCTAT	062B1F09
AUBES4502	2532	274	3	75.9	TTAACTCTGCCTCGCCCTTA	CATAGCCACCCTAGCCAGAT	100B1B09
AUBES2113	2292	147	3	76.2	TTGGCCTATCAAAGCACAAA	GCTTCATGCAAGGTTTCCTC	041B2C10
AUBES2091	1211	259	3	76.9	GCTGTGTGTGCCCTCATCTA	ATGACCACACCCTTCTGACC	041A1H09
AUBES2095	1776	573	3	77.0	CTCTGCCCTGTGGAAGTTGT	CAGCAGCAGGTGATTTTGAG	041A2D04
AUBES1963	412	272	3	77.6	TCCTGCTCTTGCTGTCTTGA	GAATACTTTCCGGATGCACTG	026B1C03
AUBES4974	882	316	3	79.8	AACGGAGTTGCATTATGCTG	GATGTGCACCCTTATCGTCA	072A1A04
AUBES2411	1128	516	3	79.8	ACCCTGACACAAGCTCAAAT	GAGTGACATCTGCTGGTGGA	045A2F07
AUBES5067	1393	288	3	79.8	CGCAGAATAAAATGCGCTCT	ACTTCTAGGAACGCGCACAC	035A2D12
AUBES1381	476	460	3	79.9	AGTTCAGTTCCGCAAGCTG	ACCTGAATTAGGAGGCTACCTG	023B1F03
AUBES4976	889	475	3	80.8	GTCGTTCGTGCACTTGTCTG	TCAGTCGCAGTCTGTCATCC	101A1H05
AUBES2958	827	587	3	81.4	GTGTGAGGCGAACAACTAAGC	CGTCAAATCTGGGTACTGTCG	013A2B07
AUBES3443	702	379	3	81.6	CAACCTGCAGCACAAACATT	AACAGGCAGCTGCATTCAT	065B1H10
AUBES2837	127	359	3	81.7	ACGGCATGTAACGAAGGTTT	CATTTGTATTTAAAGCAGCACATCA	020A1B08
AUBES3444	702	379	3	82.0	TGGAAGCGGTAACGAAACTT	CGTGAACTGAGGAGTGGCTA	110B1F11
AUBES2421	702	379	3	82.0	ATAAGCGGCAGAACAACAGC	AGGAGATCCGTATGGGTTTT	045B2F09
AUBES4704	3085	142	3	83.1	TGCCGGTAGGTGCCTAAAAT	CGGTTAAGGCACATTGGACT	102B2G01
AUBES2915	852	411	3	85.0	CTGACAAAATGCACACCATTC	CTTCAGCGAAAGCTCGTCTT	007A2E03
AUBES4620	2153	269	3	99.9	CCTGTCAAATCGGAGACGTT	CGACAGGGGCTTTGAATATCT	079B2B08
AUBES1740	3	397	4	0.0	AACCCTGAACTTAAAACCCTGA	CAGTGTCAGCATCCAAGAGG	032B2G01
AUBES5273	2543	222	4	17.1	CGTCGAACATGAGGACAGC	CCTTGATTTCGCTGCTGATT	083A1F07
AUBES2353	singleton		4	18.1	TTCCTTTAGTTCCTGGAAACG	GCGTTCTTATCAGCGGTCTT	047A2B08
AUBES1795	670	228	4	23.2	GCCGGATCACCATCAAATA	CCACACACTCAGTTGGCAGT	033B1C07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4570	1803	222	4	26.4	TTCTTCCCTTCCTTCCTTCC	ATGCAGGGAATTGGTGAGAG	072A1E08
AUBES4936	578	347	4	28.6	CAGACGTTTGGACCCCACTA	CGCGCTACATCACCAAGATT	111B1C01
AUBES1327	1302	254	4	31.5	AGGGTCCTCCAACAGGCTCG	CTCGCATCAGCACCATCTCG	031A1C08
AUBES5203	2162	213	4	35.4	CAGGGTTTATTGGAGCTCGT	CAGCCAATCAGAAATTCAGAAG	028B2F04
AUBES5266	2521	196	4	35.5	CTCGGCAAGTGACATGGAT	TGTCAAGCTTTACTGAGCATCTG	006A1D06
AUBES5234	2374	122	4	37.1	CCCCCATCCTCATACTGATT	CACACTGCTACCATTCATCTCA	051A2G06
AUBES4904	234	301	4	37.7	CTCATCCGCGCAGAAATTA	GCACACATATTCAAAGCGTGA	060B1C02
AUBES2399	singleton		4	45.3	TGAAAGAATGATGCTTGTGTGA	GCTTGTGGCGTTAAAAGAGG	045A1E11
AUBES5177	1950	352	4	52.8	AATTGGGCAAACAGGACAAA	TGGTGTCCTTGCTTTAGGTG	064B1D06
AUBES4460	792	169	4	54.1	AGCTCAGCCAGTCACTCCTT	CAGCAGTCACCATTTACACTCA	104B1A09
AUBES1153	1323	342	4	54.5	GTTTATGGGTAACCCTGTCAAGG	AAGGAGCTGTCCTGTTCACC	007B2A11
AUBES4496	2356	220	4	55.5	TTGCTTTAGTGTTTCGTGAATTG	GCAGATCCCACCCTAACTTG	030B1H04
AUBES4257	1223	413	4	55.7	CCACTCACCTGTGCCTGAAT	CTCCACGCACACAGAATATGA	030A1C12
AUBES4565	1756	222	4	56.0	TCAGTTGACTTTGGGGGAAA	TTGTGCTATTGTGACCTGCTG	111A1F11
AUBES3780	1491	325	4	56.4	GCCTGCATAATGGATGGAAG	AACCCAGCTCATAAGCCAAG	027A1C04
AUBES4354	544	293	4	56.8	GTTAGCTGCAAGGGAATCAA	TCCATGAAATGTCCGCATAA	046B2C04
AUBES3638	676	387	4	56.8	CAGCTTGTTGCTTTCCCTTC	GCGGCTGTATCATTTCAGAG	086A2D04
AUBES4743	2501	250	4	57.0	ATGACCCTGACCAGGAAATG	TCATAGCCCTAGCACAAGCA	053A1C04
AUBES1413	2046	299	4	57.0	CCCACGACCCTGTAGGATAA	CGTGGATACTGCTCTGCGTA	026A1C02
AUBES2792	703	250	4	57.5	ATACGATTGGGCTGCTTTTG	CCCTGTAGCCATCAACTTGC	050B2C01
AUBES5397	3463	206	4	57.5	GGATCCTGCACTCAGTCGTT	CAAGAGCATCCACTCACCAA	045B2D11
AUBES3639	676	387	4	57.5	CAGCTCAAGGGTTGTCATCA	ACGGTGACAGGAAAGAGGTG	044B2B04
AUBES4036	1415	291	4	57.6	CCTCTTTCTCAAGTTGGTTGG	CGAAGTCAGGGACCAGAAAC	045B2A08
AUBES2427	94	462	4	57.8	TCCCCTCTGTTTCCTGTCTG	TGACAGACCCATGCATTTAATC	040A1D04
AUBES1841	911	509	4	57.9	TCAAGGACTTTCCGTTCCTG	TTTGGTGAGAACCCCTGAAG	036B1C01
AUBES1810	1597	553	4	57.9	TGTGCAAAACCAGCACTTTC	TTGCATTTGGCCATGAATAA	033B1A06
AUBES4084	787	171	4	57.9	GACAAGACGATTTAACGCAGTG	CCTCACACTCACCACTCAGC	061A1D12
AUBES1230	1721	284	4	58.0	TGTGCTCCCGTGGACCTCAG	CCAACAGTCATCTGTCTGAGC	022B2E01
AUBES4083	787	171	4	58.0	GACAAGACGATTTAACGCAGTG	CCTCACACTCACCACTCAGC	036A2F12

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4276	1591	274	4	58.0	GAGTGTTCTTTGCTGCCGTA	ACATTCTTTCAAGGGCTCCA	098B1F05
AUBES2600	68	668	4	58.0	CATAAGTCAAACACCCTGTCCA	GGGCAATGAATTTCCACAAA	025B2C08
AUBES3012	94	462	4	58.0	TCCCCTCTGTTTCCTGTCTG	TGACAGACCCATGCATTTAATC	040A1D04
AUBES1103	185	512	4	58.0	TGGCAAAGTAGCACTGTGTC	GGAGTGAGCTGTGTGCCCTG	010A2A08
AUBES2682	419	524	4	58.0	TGAAGCAGTATTCCCGACTTG	TTGCCTTATAAGCAGCAGAGG	006B1E01
AUBES2403	802	484	4	58.0	TTGCTTTTGTTATACGTTGCATTT	AATCTACTCCTGGCGCATTG	045A2A03
AUBES4972	877	311	4	58.0	TCTGTTAATGTCTCCAAGACCAAA	CACAATGTGAGGCATCATTTACA	011B2H03
AUBES3576	939	247	4	58.0	CCACCATCCCGTACAGTTTC	TGTCGCATTTGGATAAGACG	106B2G01
AUBES2078	1876	299	4	58.0	CCACATCAACATTGGACAGG	GGTTGACATTTGGCCTCATA	039B2F01
AUBES5193	2120	200	4	58.0	CTTGTGTCCTTTGGCAAATTC	GCCAGGAAGGGAGAAAAACT	011A1D07
AUBES5296	2644	279	4	58.0	CACTCTGTTTGACCTTGTCAGG	GCAATGTGCGCTATGGATT	014A1D04
AUBES2459	singleton		4	58.0	CGAGCGTGAGGTTCTTTTTC	CGGCACTTCTATGATGAGCA	040B1G12
AUBES4939	598	445	4	58.0	CAAGAGTCAACCAAATGAATGAA	GGATCTGCCCAGACATCATC	098B1A10
AUBES4681	2832	159	4	58.0	TCCGAATGTTATGGCAGGA	GGTCAGGAAGAAAACGATGC	108A2B06
AUBES4070	557	365	4	58.0	GGTGTCGTCCAGAAACGAG	GTCCCAACTTCCTGTTTTGC	006B1G04
AUBES4071	557	365	4	58.0	GGTGTCGTCCAGAAACGAG	GTCCCAACTTCCTGTTTTGC	058B1E04
AUBES3306	623	391	4	58.1	CAATCACACTGAGGAATGCAC	GATCGCAAAGGCTGAATCAT	074B2H10
AUBES1926	787	171	4	58.1	CGATTTAACGCAGTGTAATGGA	CACTCACCACTCAGCACAGG	036A2F12
AUBES4480	1506	245	4	58.1	CGTGTTGGGTTTCATTTTGTT	GCAGCATGTCATGGCTTTAG	090A2A05
AUBES1555	2233	401	4	58.2	GGTGGATTCATTGGGTTTGA	GGGGACAGCAAATTTACACTG	023A1C07
AUBES3171	9	2006	4	58.2	GGAAAAAGTGAAGCACTGTGAA	CCAGCTGTCTTCGGTCAAAT	054B1D08
AUBES3694	1023	387	4	58.2	TTTGCATCATTTTGCAACTTC	ACAAGAGCTGGCAAACCATC	031A1A11
AUBES4869	2233	401	4	58.2	GGTGGATTCATTGGGTTTGA	GGGGACAGCAAATTTACACTG	023A1C07
AUBES1617	3092	181	4	58.3	GCGCTCCTCAGTCTCTCATT	AAACTGCGTCGAGTTCCACT	026A1G03
AUBES3468	1598	433	4	58.4	TCCCAACATTCCGTAGTAGACC	CAAATTGTGTGAGGGAGAACAA	006B2F03
AUBES2084	935	413	4	58.4	ACCCGGAAGAGAAGTGAACA	GTGGACCCAAAAAGGTTACG	041A1B06
AUBES4906	238	244	4	58.5	ATCATGGCCATTCCAAAAGA	CGAATGAATTGTCCTTGCTG	107A2A04
AUBES4881	647	266	4	58.6	GAGCGTGGAACCTACCTTGT	CTGCGTCAGGACACCGATA	057A2G02
AUBES2829	623	391	4	58.8	CAGGGGCAGATATGGATGAG	GCGGCAATAAAAATCTGTCAA	020B2E10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3376	170	1074	4	58.9	CATGAGCTGCACACACTCG	TGTCAAACCCCAATACTGAGAG	090A1H09
AUBES4543	2306	186	4	59.0	TGCGGGTTTTGTTTTTCTTC	CGAACGTGCTAACCACTAAGC	086B1F03
AUBES1319	860	264	4	59.3	GTGTTTTCTGAGCCAGGAGG	AGAGAAACCCTAAACTCACAGTCC	018A1E08
AUBES5388	3409	211	4	59.5	ATGGAGGCACAAAAAGCACT	GCGCAAACTTTCAGTACCAC	076B1B02
AUBES5134	1640	252	4	59.5	CGACTCACGCACCCTAAGA	GACCCACTATCTGCAGGGATAC	055A1E03
AUBES4971	863	266	4	59.6	TTTAGGGAAGGCCCACCTAT	GTGCTGGATCACTTCCTGGT	067B2F02
AUBES4708	3120	181	4	59.6	ACAAGGCTCCGAAAGACAGA	ACAGTGAGTGGGCTTTACGG	082B2F07
AUBES2505	1431	445	4	59.6	TTCCAAACACACAAACTCACC	AAAGTGAGGGCGTGTCACTAA	048A2A05
AUBES4270	1431	445	4	59.6	CAAACCTGTGTGACTGTGAGC	GAAAGTGAGGGCGTGTCACTA	048A2A05
AUBES4709	3120	181	4	59.7	CTCCCAAAATTCCCTTAGCC	TTTTAAGCTTCCGGTTTAAGTG	093A2E02
AUBES3760	426	350	4	59.8	CAAGCAGCAAAGTCTGTGGA	CCACATGGACCTTGGAACAC	061B1G06
AUBES3312	703	250	4	60.2	ACAATACGATTGGGCTGCTT	CCCTGTAGCCATCAACTTGC	042B1C08
AUBES2617	442	915	4	60.8	GGGTCACTAACTCAGGTGTGG	AGGTACAAAATGCCTTGACG	053B2B04
AUBES5409	3528	179	4	61.1	AGTGGCACACTGCACAAGAC	TGGGAGGAAACAGTGTCAAA	074B2B01
AUBES3608	1487	546	4	61.5	TCTGCAAATCCAGTTCACCA	AACCTTTTCTGGCTCTGGAA	029A1H01
AUBES3607	1487	546	4	61.7	CATGCGACCCTTTGTAGGAT	TCAGCCAAAGGAAAATGTCA	041B2C01
AUBES5377	3363	235	4	61.8	TTGCAAACAGCTGAAAGTCTG	CGCAAGGTCACAAATGAAGA	054B2A11
AUBES2921	1069	267	4	62.2	GGGACAGAGGACTTTTCTGCT	AAGTTACAACTAATTCTGGAGGTGAA	036B2D05
AUBES3154	442	915	4	63.0	CGGACGTCACAGAACTCAAG	GCTTAGACGCGCAGAGTGAT	011A1B06
AUBES5267	2524	232	4	65.3	GGCGTTACAGTTCCGAGACA	TCGGTCTCCCCCTTACTTCT	003A1F11
AUBES5380	3381	194	4	66.4	TACTGCCACTTGAGCGACTG	GCGTCTGAAACAGAAGCAGA	025B2A09
AUBES4498	2424	289	4	86.1	TCAGATCACGTCGCTACTGG	CTCCATTGATGCAGTGAAGC	096A2D04
AUBES2508	1653	394	4	87.9	ATTGCAAGGACTGTTGGACA	CACAGGTTGCAAAGTGACTGA	048A2C04
AUBES5362	3292	205	5	9.1	CTGGACGAGCTCCAGGTAAC	TCGCTCACCTTGATCTATGC	070A2A08
AUBES3782	1716	580	5	15.7	CCTTGAGCTCTGGAAAGGTG	TTTGTCACGTCAGCACCAGT	038A1A01
AUBES4842	1613	325	5	16.4	GTCAGACGGTGTCGGTTAGC	CGTCTCCTTACAGAAAACTTCACC	074A2E04
AUBES5346	3233	183	5	19.9	CATATTTGGCGATGTTTCCA	TGGGAAATTCCTCCTCTCCT	103A2A09
AUBES2883	341	651	5	22.3	GGCATCATGAGAAGCAGAGC	GCCAAACTCACCACACTGTCT	054B1B08
AUBES3002	341	651	5	24.3	GGTTTGCCCACATTTTTGTT	GGGCATTTGTGCTTGTAGGT	055A2G09

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4868	2185	271	5	29.8	GTTCATCTGCCGCGACTATT	CCCCTCAGAGAAAGAGAGAGC	070A1E04
AUBES4991	1003	264	5	34.6	TGTGGCATGATTAACGTTCTG	CCCTATGTCACTGTGCAACC	082A2G03
AUBES3695	1044	223	5	37.3	CTGTGCATGAGGCAGACATT	GGCTCCATCCATCCAGTTAT	047A2H08
AUBES4244	1044	223	5	37.5	CTGTGCATGAGGCAGACATT	ATGGCTCCATCCATCCAGTT	047A2H08
AUBES2759	338	599	5	39.1	GGTTGAACCTGAAAAGATTGGA	CATGTAACACTGGCAGTTATGGA	054A2B11
AUBES1952	1110	512	5	40.6	CCCTGTTGCTACCCGTGTT	GCGAACGTGCTAACCACTAA	021A1B04
AUBES1422	494	370	5	41.1	CCATAACGCTTCCAGAGTGAC	GACTGCTGAATTTAAGTGAGGGAG	018B2E07
AUBES2457	1137	242	5	41.5	CGCTCCGTCTTCACTTCTTC	GTTCCCTTAAGCCAACACCA	040B1G05
AUBES2559	15	539	5	41.9	ACATTTCATGCAGGAGCAGTT	TAATTGCAGGGAATGGAAGG	031A2E11
AUBES4357	653	288	5	42.7	GAGTGGTCCTGAGAGGTGGA	TGCTATGCTGCAAAGACAATG	001B1F04
AUBES4529	1002	238	5	43.1	CGGAGCAATACATCACTGGA	TCTCCACCACTCACATGCAC	006B2B03
AUBES5089	1505	245	5	43.4	GCGAGAGAGTGTGTGCATGT	AGCTGGTGAATCGTGTGTTG	072A2G07
AUBES4339	2266	171	5	44.1	AGGAAACAGGCCAGACTGAA	GAAGATGGATGGATGGGAGT	008A2C10
AUBES3629	427	306	5	44.1	CCAGGCCACCTCAATATGAT	AAGGAACTTACACAAACAACTTTGC	109B1E11
AUBES2557	190	529	5	44.4	CGTGTTTGTGTAAATGCGTGT	ATTGCAACTGGGTGAATGTG	003A1F02
AUBES4346	190	529	5	44.5	CGTGTTTGTGTAAATGCGTGT	GGGTGAATGTGCTTTATGCTC	003A1F02
AUBES3630	427	306	5	44.5	CCTGAGTTTTGGGTGCAAAG	AACAAAAGCCCCTCACACAC	085A1H07
AUBES4374	1234	424	5	44.5	CTGGAGTGCGATCTGTGAAG	CAGGGTTCAGTGACGTAGAGC	086A1C02
AUBES3596	1234	424	5	44.5	CTTGCAGTTTTGCAGCAATC	GCTACAGCCTGCACCATTCT	112A1F10
AUBES4024	1291	279	5	44.5	ATCCAGAGGCAGTCCTGGTA	TCTGGTTTCCTCCCAGTGTC	076A2A11
AUBES4574	1863	211	5	44.5	TGAATCCATGGAGCAACATC	TGTGATGGGGAAAAGTGGAT	038A1A04
AUBES2993	1110	512	5	44.7	AGCATTCTTTGGATGGGTAA	GCTTCAGTTTGTCCCTCTGG	082B1H09
AUBES4052	137	298	5	44.8	ATTGGCATTTTGAGCCATTC	CAATGCCCAATTTGTACGAC	104B2A05
AUBES4528	1002	238	5	44.9	GACCTTGCCATTCCAACAGT	TCTGTCATGTGTTGGGCTTT	002B1G04
AUBES4425	2839	245	5	45.3	GATCCATTGGAACACACGAA	ATTACCTGGATGTGGCTTCC	028A1E01
AUBES4440	2839	245	5	45.6	GCATAAACGTTGGGTTCAGG	GTCTGCGCAAGTGTGAATGT	002B2B02
AUBES4441	2839	245	5	45.7	GATCCATTGGAACACACGAA	AATTACCTGGATGTGGCTTCC	028A1E01
AUBES3590	1090	289	5	45.7	CGCTTTGTACATGCAGTGTTG	CATCCTGATTAGGGCTGTGG	042B2A06
AUBES2975	1714	504	5	45.8	CTCTGTCTTCCGGGTTTGG	CAAATTCTCCTTGGCTCCTG	060A1C06

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3274	1135	573	5	45.8	TCTGTTGCAGCAAATCCAAG	TGCAATTCCCTCATTTCAGAC	047B1G09
AUBES4406	2112	232	5	45.9	GGTTATCGGTATCGGCTGAG	CAGTGTTGTCGCATGAACAG	030B2G03
AUBES4688	2864	169	5	45.9	TCAGCAGGTTCTCCCATTTC	GGCTGCTGGGAACTGTAGTC	093A2D02
AUBES2478	534	1072	5	45.9	CAGCCTGAGGAGACTTGTGA	GGGCACAGCAAAGATTGTATT	046A1E08
AUBES2005	3037	306	5	46.0	CAGCGAGTCTTGCCTCATTT	TGTGGCTGAATTCTGCTGAT	029A1G07
AUBES4700	3037	306	5	46.0	CCTCATTTTCCCTCATGTCG	TGTGGCTGAATTCTGCTGAT	058B1F01
AUBES4331	2182	210	5	46.0	AGTGGTCCTATGGGGTTCCT	GCACTGCAGCTGGAAATACC	078B1E03
AUBES2438	1742	244	5	46.0	TGTTTTTGGGAGGTGAGAGG	CCCTCTGCAAGCCATGATTA	040A2E04
AUBES4424	2839	245	5	46.1	GCATAAACGTTGGGTTCAGG	GTCTGCGCAAGTGTGAATGT	002B2B02
AUBES3117	495	866	5	46.3	TACACTGGCAGATGCCTTCA	TGTGTTTCTTGCATGACGTGT	036A1G09
AUBES4929	527	309	5	46.4	GACCCGTACTGAATTGAATGG	AGAAATGGAGCGAGCACTGT	028B2D05
AUBES4897	54	364	5	46.4	GCATGACTGTGCTGGCTAGA	CAGGTGGTTAGTGGCAGGTT	035B1D06
AUBES2638	534	1072	5	46.4	CTGCTTGGACTGTGTTGCAT	GCACTCCAGCCAGCTTAGTC	023B2H03
AUBES3446	853	403	5	46.4	GCACACTCCTACCAGCCCTA	GTAATGCAACGCAATGTTCG	106B1B02
AUBES5076	1426	184	5	46.5	TTTGAAATGCAGCTGGTTAAA	CCAAAGAAGCCGTGATGTTT	007A2B05
AUBES3237	534	1072	5	46.7	GTGCAGATCCACATAAGTCCA	GGATAAACCCGTGTTGTGGT	023B2G10
AUBES3445	853	403	5	46.8	CCTGGAATACTGGGCTCAAA	CGATAAGCAAATGACAGTACAACA	023A1A02
AUBES4035	1402	274	5	47.1	CCACTCTGACATTCCCACAG	TGGGTTTGGTTTGACCAGAG	058A2F06
AUBES3170	534	1072	5	47.4	CCCATTGCCAGTATTGGTATC	CGGTGACCCTGTGTAGGATAA	086B1B08
AUBES1703	413	381	5	47.9	TCCAAGCTCACATTCAGCAC	GCCCCAATTCACTAACAACC	033A2F02
AUBES3402	339	348	5	48.8	CTCGGTCAGCTGATGGGTAG	TTCTCCCAATCTGACGTGCT	096A1E09
AUBES4349	339	348	5	48.8	CTCGGTCAGCTGATGGGTAG	TTCTCCCAATCTGACGTGCT	096B1B05
AUBES5218	2269	345	5	52.3	TGCAGGAGTTCTTCCAGGAG	CCTTGGGCAAGACACTGAAC	109B1D08
AUBES3595	1209	470	5	53.0	AACACCCGACTCTCCATCAG	GCACTGGGCTACCTACTTGC	013B2B01
AUBES4699	3019	262	5	53.6	TTTAGTGGCTGGGAGGTTTG	CTCATTCACAGTGTTGCACGTA	077B2D05
AUBES3594	1209	470	5	54.3	CCACCAATAGGGCAAGTCTG	CTCCGAATCTGGTGACGATT	044B1E02
AUBES2269	319	423	5	57.8	CCGACATACACGACTTTTGC	GGGGACAGCAAATTTACACTG	043A2F09
AUBES4567	1786	196	5	58.4	ACCTGCAGGATTCAGGAGTG	AGGGGGTGAACTTTCAGTGAC	054A1B03
AUBES5039	1269	480	5	59.0	TATGCTTGCCTGCATCTTTG	GCACAACATGTCTTTCTTGGA	070A1C06

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3878	913	424	5	59.5	CCATGGAGCTCTGGATCTGT	CCGTTTTAACATTGCAAGACA	062A2C10
AUBES4685	2861	166	5	60.1	TGAATCACATGTAAATGAATCATACG	GCAATTTCCAAACAACAGAAGG	014A2F11
AUBES2942	226	377	5	60.3	CATGGAGGGCAAATGATAGG	ATGTGACCCTCATCCATCAC	023A2F09
AUBES1265	singleton		5	60.8	TGTACGTTGGCTCGTTGACC	ACACACGGAGGGGTCAGAGG	033A2D11
AUBES4938	587	381	5	62.0	TTGACGTGTCCAAAGTGTCC	TGGCTGTGTCTATGGTGTCAA	085A1A07
AUBES4686	2861	166	5	62.1	TTCTTGGGAAGAGCTGGAGA	TGAAGAGTCCCCAAAACAGG	065A2C09
AUBES1630	3093	288	5	63.0	GAGCGCGAAGGTAAGAGTTG	TTCCCTGTCTGAGCGAGTCT	032A1H08
AUBES4774	2814	218	5	63.4	TGAGAGAGACGGAGGGAGAA	AGATGGAGCTGCCAGAACAC	042B2E06
AUBES2982	95	365	5	63.8	TCACTGGCATTGTTTTCATCA	GCCACAGTACCCTCCACATC	108B1C03
AUBES4127	961	250	5	64.0	GGGGACTTCTTATGGCCTTC	AAATAGTGAGATAATCACCTGAACAC	023B1H07
AUBES4644	520	161	5	64.6	ACCTGCTGCTGTCTGTGTCA	TCTGCTGGACTGGAGAATCC	047A1H06
AUBES2814	268	309	5	65.9	AACTGACGGAAGCAATGTCC	CAGGTTCAAAATGAGAGGGAAC	012A2D08
AUBES2182	961	250	5	67.6	CACACTACAGTGGAGCGACAG	TTAAAAGGGGGCAGAAGGTC	027A2A08
AUBES4341	2277	247	5	67.6	ACCTCCCTCCCTGACGTAAC	ATGGCAACCAGCTGAAAAAC	006A2B04
AUBES1752	1339	403	5	68.5	GGGAGTACAGTAAACCACTTGC	CTCTTCCCCACCTCCAAGTA	018A1A09
AUBES3940	95	365	5	70.0	TCTGGAACACTCTGCCATACA	ATGTCCGAGGACTCATTTGC	019A1F04
AUBES1144	2380	238	6	0.0	TCACAGCAACTTGCCAAAGAG	ACATCAGCAAAGGCTTGACAG	007A2D08
AUBES5284	2599	223	6	3.0	TTATGGCGTTCTGGGGATTA	GTTGAACCAGTGTGCCGTTT	079B1G03
AUBES4993	1020	357	6	6.5	CATCTGTGCAGTCTGATGGAA	CCGTACGCTACATCCACCTT	053B1E03
AUBES1616	singleton		6	8.2	ATGGATCTGGCACAATGGAT	TGGATCAAAGTCCCCAATTC	026A1G06
AUBES4389	1842	218	6	8.4	GGCTGCACATTCTAACAAGG	GATGCCATCCAGTGCATTTA	031B2D11
AUBES3799	974	260	6	17.2	CAGGAACTTGTATTGCGGAAG	TGTTACCACCCCGGAAATAA	020A2D03
AUBES3798	974	260	6	22.0	ACCAAGCCAACAGAGCAAAT	TGATGTCGCGGTGATTATTG	002B1F04
AUBES3804	1058	367	6	25.1	CCTGGGTTTAGACTGGAGGA	TAAATCTGCGCTCGGCTAAT	046B1D06
AUBES3806	1058	367	6	25.1	TGTGACCCTTTTAGAACGATG	AAAAACAAACCCAACAAGCA	102A2D06
AUBES3805	1058	367	6	26.0	TTTTCTCCCACCTGCTGAAG	AGTGAGTGAGTGGGCTTCGT	071B2E09
AUBES2492	singleton		6	29.7	TGCGTTTTGCAACACAGTAAC	GTGCCACTTTTCAAGGGTTT	046B2A07
AUBES2343	215	249	6	32.1	CGCACCCCTCTTTACAGAAA	TTTGAAAGAGCAGCCACTGT	047A1D11
AUBES1884	80	311	6	35.9	CCCAGAAAAGGGATCTTGGT	CCCGTGACCCTGTACGATAA	028B1H01

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3004	530	489	6	37.8	ATTTTGTTGACACGCCCAGT	GGGTTTAGGCAGCAAAAGAC	074A1A10
AUBES3793	786	240	6	38.1	TTCAGGATGGAGGACTTTGC	TTGTGGATTCCCCAGAAGTT	074A1G05
AUBES3777	1369	326	6	38.4	CCTGAAATTCCCAGGTAATGA	GCACCAACAACCATGCTACA	023A2H09
AUBES2689	766	506	6	38.7	AGAAATCCAGCCACGGAATA	TGCCAGCTTTAAGCCTCTGT	011B1H02
AUBES4144	1182	303	6	39.0	GGATATCTTTGAGCAGCAGGA	GAATTGCCGAACAAATCTGG	101A1B11
AUBES3934	1362	232	6	39.1	TCAGGCTGCCTTTGTTTTATG	GCATGATGAAAAAGTGGGTTG	026A1F04
AUBES4108	1369	326	6	39.1	ATCCCGCAGACACAGAGAAT	CTACAGACATGCCGGTCTCA	078A1C02
AUBES5235	2376	462	6	39.4	CAAGCACGTGTCCACAAACT	GCTGAAATTGGTGAAACTGACA	109B1B05
AUBES4143	1182	303	6	39.6	TTGGTTTCAAGCCGCTTAGT	AGAACAGATGGGGTGGTCCT	094A2A04
AUBES3812	1468	411	6	40.0	GCCTGCTGAGGGATATTCAC	GGCAAATGGGAAGTGAGAAA	027B1A08
AUBES4003	1098	282	6	40.2	TGACCTTTTCATTTGTGATGATG	CTCCTGAGCCTTGACTCCTG	075A2B05
AUBES3397	229	316	6	40.2	GAGGCCACTGCTTAGTGACG	CACGGAATTCCAGCATTCTT	020A2H12
AUBES2805	93	205	6	40.3	TCCCCACTGTAAGAACCATGA	TCTTCCGGGTTGGTGTTATG	058A2C03
AUBES2642	64	306	6	40.3	AGCATCACGGAATTCAGCA	TCACAGGCTTCTCTCCGATA	008B2E09
AUBES4637	362	215	6	40.4	AACAGGAGGTTCCGAAATATCA	GACGGGGGATCAATAACAGA	024B2D09
AUBES3690	776	455	6	40.4	GTCCCCAGCAAGTGAAACAT	ACACATCCACGCCCTAGAGA	096A2F06
AUBES3791	645	445	6	40.4	TGCATTGATTCACTGTGGTTT	ATCCACACACCGCCTGTAA	070A2B08
AUBES3774	1109	389	6	40.4	TGATCATGGCAGCTTCTGAG	CTGTGCACAAATCATTCATGG	035A1B03
AUBES3809	1310	240	6	40.4	CGAATAAGTAACATTTTACACGTATGG	TTGGTTGGTGAGTTTCTACCTG	109A1E10
AUBES2034	1264	424	6	40.6	CATGTGAGTGAGATGGGCTCT	GCCTGGAGCTTGTGTTTGTA	038B1E03
AUBES3701	1894	330	6	40.6	AGGTGTGAGGTGTGAACGTG	TCTGTCCATTCCCCAGAGAC	052B2C07
AUBES3359	29	847	6	40.8	AGAAGGGCAATTTGTGCAAT	CAGCAGACCTGTTTGGAGGT	088B1C05
AUBES3423	470	360	6	40.8	TCGCACTCTCATAAGGACCA	CACTCAGCCCCAGTCCTAAC	081A2C11
AUBES4802	3026	225	6	40.8	GCGAGAGGGAATAAATGCAG	GTTTGAGCAAAGCCTGATGG	085B1F06
AUBES3514	171	526	6	40.8	TGGCCAGGCATAGTGAAGTA	GCTTCTGCATGCAATCATGT	078B1A04
AUBES3017	502	494	6	40.8	TGTGTGGTTTCCCTCTCTCC	TGCCTTTTCAGGGTGTAAGC	041B2G02
AUBES5370	3321	88	6	40.8	TCAGGGACTTCCACTCAAAAG	AGATTCTTGGACCCCACTGT	101A2D01
AUBES3794	786	240	6	40.8	TTCAGGATGGAGGACTTTGC	TGTTGTGGATTCCCCAGAAG	074B1G05
AUBES2811	196	276	6	40.8	ATGCGGCATTTCTCATGTCT	CCCACCATTCAGAAGCTGAT	006B2A07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3282	196	276	6	40.8	CCGTTTTTCTAAGAGGCTGCT	TCAAAGGTTATTGCGTTGCT	098A2B12
AUBES2734	466	460	6	40.8	GGCGCGTATAAATCACCAGT	CCACTGCACCCATTAGAGTG	026A1G01
AUBES3307	637	259	6	40.8	CCGAGCAAAATTGTGTATGC	AGCAGGGGGAAGTTTCTTTC	087B2G01
AUBES4963	807	267	6	40.8	CCGGTCTAAAATATTTAATGGTGA	GGCTGTTTTAAGGAAAAATTCAGA	042B1B04
AUBES3692	830	675	6	40.8	GAGGGCCGTTGGATTACTTT	CTTGCAAACGGTCCATAACA	095B2D08
AUBES4371	1090	289	6	40.8	GAGGCGTGTGTGGTTATGTTT	TCCCAACAGTCAGTGATTCAG	101A1E06
AUBES1306	766	506	6	40.8	CACTCCCGGAATACACGCAG	TCAGCTCCAGCGCAACGAGG	019B2H05
AUBES3773	1059	450	6	41.0	AGCCAACAATTTCCATGAGG	TTCATGTCAGCGGTTCACTC	020A1H08
AUBES3955	530	489	6	41.0	TTCTGTGCACACGATACCATC	TCACATTGCACAGATGCTCA	014B2B08
AUBES3772	994	340	6	41.0	GGGCACTAATGAGCACACAA	TGTTAAGCCTCAGCCTTTCAT	066A1A07
AUBES3795	808	171	6	41.0	TGACCTCAACAATGTATGCTCA	TTCTGACATGCCGATCTTTT	073B1E11
AUBES3900	2630	205	6	41.0	AGCAGCAGCACAATGCATAA	TCCATAATCCCCCATTTCTTC	100B1B06
AUBES3892	1455	338	6	41.0	TGATAGAACTGGAACACACAAATG	CTCAAAAGCAGGATCCGAGA	106A1A08
AUBES4707	3110	191	6	41.0	TTATTTTTGCCAGGGGTTGT	TTCTCACCACTTGGGGTCTG	070B1H10
AUBES3434	590	381	6	41.1	AGCCGCAGTGTATCCAGACT	CTGCTTCATCGCTCTGTCAA	098A2H11
AUBES3792	786	240	6	41.1	TAACTCCGCGTTCCTAAAGC	GATGCTGGTGGTAGAGAGTGC	045B2D04
AUBES3458	1031	259	6	41.1	TGGTGTCCCAGATAGGGTGT	CTTAAACCCCTGGACCCACT	109B1C05
AUBES3614	1635	411	6	41.1	GGTCGCTAATACCCTCATCG	CTGGAAAATCACGAATTGGA	111A2A03
AUBES3613	1635	411	6	41.1	ACGGCAAAAGGAAACTGATG	GCCAGCTAACGCATTCTCAC	096A1A01
AUBES3852	3026	225	6	41.1	GCGAGAGGGAATAAATGCAG	GTTTGAGCAAAGCCTGATGG	085B1F06
AUBES2606	29	847	6	41.1	GATCTTTTTCGGTCTCCCATC	GTCTGCCAACAGGAGTGTCA	060B2H03
AUBES2623	37	572	6	41.1	ACCTAGCGTGGATTCAGCAC	CTGCTTCCGTCCACTCCTT	038B2C08
AUBES3155	193	868	6	41.1	AAGGCTGGCTCAGAAAAGTG	CTACCAGCTTGCTCCTCTGC	072B2F02
AUBES2602	278	511	6	41.1	GCGCAATGACAGCTTAAACA	TTACACCTGGCGGCATATTT	020B2B02
AUBES3759	374	244	6	41.1	AACCAGCGGAGTTTGTGTCT	CGATCGTCTGTCATCCATTG	087B1H04
AUBES3789	645	445	6	41.1	TCCCCTGTGAGACAGAAAGG	GCCCAAAAGTGGATTATCAAA	018B1G04
AUBES3457	1031	259	6	41.1	TGAACACCAGGACAACATGAA	GGTAACCACTACGCCACCAT	072A1G08
AUBES2062	1098	282	6	41.1	CCTATCCTCAAGGCAAGCAT	GCAAGAATCTGCAAAAGAAGC	039A2G08
AUBES1935	466	460	6	41.1	AGCCATGACACCTGCTGATT	TGTTGCCAGCACCTATCATC	036A1D01

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3766	552	424	6	41.1	CGCTTGCCAGCCTAAATTAT	CACTCGAATAGCGAATAGTTGG	078A1A02
AUBES3698	1455	338	6	41.1	CATGATAGAACTGGAACACACAAA	CTCAAAAGCAGGATCCGAGA	106A1A08
AUBES3845	2533	159	6	41.1	CATTTCGATCCAGGGTGTTT	CAAATCTGTCGGGCTTGACT	111B2D04
AUBES1793	singleton		6	41.1	TTCACCCTATCAGCCCATTC	CAGAGAGAAGCTTTTTGGTGTG	034B1G12
AUBES3899	2630	205	6	41.1	CTGTGCAGCCCAACATGA	GGGACAGAGAGGCAGAGAGA	068A2D11
AUBES3255	346	457	6	41.1	GGCCTTGCATTTGAGAATTT	GGCAAACACAAGTGAAGCTG	070A1H08
AUBES2195	1182	303	6	41.1	GTCTCCCCCACCTTATCCTG	GGGGGTTTAGTTGCAAAAGG	028B1C10
AUBES2227	196	276	6	41.1	AGGCTGAGAGTCTGTGGTCAG	TCTCTGGCTTCCCTCGTTTA	042A1C09
AUBES2952	555	321	6	41.3	TCCAGTCGTGTTGACACAGG	ACACCCACACAATGCACATC	003B2E04
AUBES3015	769	485	6	41.3	TTCTGTTGGTGGAAAGATCTGA	TGACCATAATCCAACTCTTCAAT	040B2G07
AUBES3824	1816	279	6	41.3	TTTTTGGAGTAGCTTCTTAGGATATGA	TTCCACCCAAATGAGACACA	013B2B04
AUBES2729	8	279	6	41.3	AGATGAGACAGGTAAGCAAGTACA	AGCTCAAAGCAGCTCCAGTC	018B1D06
AUBES3681	171	526	6	41.3	TGAAAACACAAATGCATCCAA	AGGCAAACAAGGATGTAGCAC	071A2C10
AUBES3016	466	460	6	41.3	CCATGGCTCCTGGATTTAAG	CCAGCCAGCAAACATGAATA	041A1D03
AUBES3664	590	381	6	41.3	GGATGGACGCACACAGATAA	AAGGGCGTGTGTAAAGTTCG	051A2C05
AUBES4049	1522	254	6	41.3	CCATGCTGACATCACAGGAG	TCAAAGCAGTCGGTCTGATG	038A2D07
AUBES3323	1776	573	6	41.3	TGCCTACCTGCAGTATTTTCAA	CAGTTTGCAGGACAAGAACG	090A1C05
AUBES4782	2880	178	6	41.3	TTGGACAAAAGTCCTTCATCG	TGTCATGATCTCTGACCACCA	007A2H06
AUBES5342	3216	161	6	41.3	ACGGCCGGCTTTAATCTAAT	GACATCGTAGCGCACAACAG	039B2F12
AUBES3309	666	353	6	41.3	TTCCAAAGGATTGCAAGGAG	CAGGCTAACTGGGGACACTG	084B1A10
AUBES4304	1885	249	6	41.3	TCCTGACTGCCAACAGAGATT	CCACCATGCATTTTGTTTTG	027B2C02
AUBES3846	2654	369	6	41.3	CATTGCCAGAACCTCACAGA	GCAATTGTGCATTGATCAGC	042B2D03
AUBES1185	37	572	6	41.8	TGTTTACCGGCTGTGCGAGC	TCATGCCATTTAGCGGCCTG	011B1H04
AUBES4247	1127	347	6	41.8	CAGTCATGTCAGGAGGGTGA	CTTTGATGTCCAATGCACCA	011A2C06
AUBES3844	2533	159	6	41.8	GGATAAGGACGTCTGCCAAC	GGTGCAAGGAAAATGACAGG	024A1A04
AUBES3398	229	316	6	41.8	CACGGAATTCCAGCATTCTT	TGTAGTTTGAGGCCACAGCTT	060B1H01
AUBES3954	530	489	6	41.9	AATGGCATCTTCTCCATGCT	GGATGCATTTGCACAGTGTC	003A1C12
AUBES2779	776	455	6	41.9	CCAAAAATTGCCAAAGCATC	TGTCCTACACTGGCACCTTG	006B2B08
AUBES3097	193	868	6	41.9	AAGCATTGTGAGTCCCTAGCTC	TGCATTGCTCAACTCTAATACAC	023A2A01

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3384	278	511	6	42.0	CGAATTGCACCTACAGAGATGA	CGTGCACCTGAAACGTAATTT	072B2B09
AUBES1564	singleton		6	42.4	GCCTCGTAGAAACCAAGGTG	TGCACGTTGTTCCTTTCATT	021A1A06
AUBES3355	278	511	6	42.8	GGATGTGTAAAGCCCCAGTG	ACTGGTGCTCCCAACTTCAA	078A1A09
AUBES3280	93	205	6	43.0	CCCCACTGTAAGAACCATGA	ACGTAAGAGCTCTGGCCACT	083A2G05
AUBES3591	1090	289	6	43.1	CAAATCTGGGCCAAATGAAG	GAGGAGTTGCCTCAGGAAGA	050B1B01
AUBES3683	297	252	6	43.5	TGGATGACCTCCTCCTTCTC	GCGGCATTTTTCAACCTAAA	046A1F10
AUBES3433	590	381	6	43.7	GTGGGGGAGAAAATCCATTC	ACAAGCACACATTCCCTCGT	026A1A03
AUBES3823	1802	244	6	43.9	GCTCGATATGACTGACTGGATG	TTTCAGGAACAGCTGAAAAATG	026A2D06
AUBES1282	2833	352	6	44.1	TCATTCTGCCACCTGCTGAC	CTGTGACTCCCTCAGACTGC	002A1H01
AUBES3103	370	891	6	44.2	GTGTTCAGATGGTGGTCCAA	GTTTGAAGGCAACTGCACCT	093A2C08
AUBES3831	1881	316	6	44.7	GGTGGAGACTGAGAGGCAAG	CACCTGAGGCAAACACCTCT	003B2D11
AUBES2987	346	457	6	45.8	TTCTCGTCAGAAACCTTTGGA	TGTTTCTGAGATTGGCTCTGG	090A2A03
AUBES5151	1710	254	6	48.0	CATGAACCTCCACTGACGTG	CCTATGGGTCAAAGGTCAGC	060A2B06
AUBES3784	1894	330	6	54.0	AGGTGTGAGGTGTGAACGTG	TCTGTCCATTCCCCAGAGAC	052B2C07
AUBES2386	560	675	6	71.6	GGCGCCTTCAATAAATCAAA	TACCGGTATATCGCAAACGA	044B1G11
AUBES2070	singleton		7	39.2	TTGCAGGTGTGACTGGATTT	TCCACTCAGATTCCTTGCAG	039B1F05
AUBES3963	1528	281	7	41.0	TCTGTGAATGATCCCCATCC	TACAGACTCGATCCCCTTCG	053A2F07
AUBES5117	1540	252	7	45.1	AAAGAAGGTTGCTCCTGCAC	GTAATGTGTGGCGCGTATGT	042B1D08
AUBES5085	1476	206	7	49.6	TGGCACCCTTGGTAAGTATG	CACCACATTTCAGGTGGAACT	111A1B08
AUBES2897	608	490	7	53.4	CCCCTTTTGTGTGGGATTTA	CCGAAGGGCACTAATTAGGAT	052A1E06
AUBES3408	369	492	7	54.3	CAGAAATATGCGTGCAAACC	GCGCCCTAAATATGGGAGAT	008B2C12
AUBES2898	608	490	7	55.4	CCCATCCAGGGTTCTTGAAT	TGAATTACCTGAAGGTGGCATT	074B1D07
AUBES3975	1731	227	7	57.2	CAATGTCTCATTTGCACAGC	TTTGGTCAAGTCAAAATGATGAG	077A1E08
AUBES2995	1461	409	7	58.5	CCCTCCTCTGCCCTTTTAAT	CCTCCCCCATACACACAAAC	107B2E02
AUBES4461	805	194	7	58.7	AGATGTAGCGCATCCACCTC	GGTCCTGTAAGTAGGGACCAGT	108A1B09
AUBES4638	380	200	7	59.1	GCTTGGACCCCTAACAACAA	GTGTTTGTGGCTGTTCCAGA	029B2F11
AUBES3409	369	492	7	61.7	CACCTGAGGTCAAATCACCA	GTGCGTTTGGGCTATAAAGTG	078A2H10
AUBES2592	216	727	7	64.7	GGAGCATAATCCCAGAGCAC	TGTTCACCTTTATACTTCCATCTTATT	014B1D07
AUBES3136	216	727	7	64.7	GCCCATGCCTAAGAGGATTA	CCACAGCCCTGTGTAGGATA	107B1G02

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2401	452	330	7	65.6	GCAAGCACGTGACTGATTTG	TGACCTTGCTTTCTCTTCATCTC	045A1H07
AUBES3216	404	868	7	66.0	GTGAGGCGGAAATGCTACTT	AATGCCTTGACAGCATGTTC	047A2G05
AUBES4668	963	392	7	66.4	TTAAGATGTGGCAACGGATG	AAGCACATAATCTCAGTTCACACC	020B2H09
AUBES2639	9	2006	7	66.6	AACCCTCACTAATGGCTAATGC	TAGCAGCAGTGGTTGAATGG	021B2C03
AUBES5416	3545	173	7	67.0	TTGTGTCTTGTGGGCTATGTG	AAGGTGGGTGAAAGAGTAGTTACAG	057B1E05
AUBES2799	1085	347	7	67.3	GCGGTACTGTACTTCCATCCA	GATGACCTTCCATGCCTGTC	029B2A11
AUBES4243	1014	408	7	67.7	GATCCGCTCTTAGACACGAGA	TTGACAGTGCGGTAAGATGC	025B2G11
AUBES5040	1271	245	7	68.0	CTGCGCTTTCATCTTCTCTG	ACGTTTCAGTCGAGTGTCCA	059B1E02
AUBES1744	1428	227	7	68.3	TTTGATGCTGCTTTCACCTG	CATCCTTCCTTTCCTTCACG	020A1F05
AUBES3056	275	822	7	68.7	CATGAAAGCAGGAAAGTCAGG	CAAGCAAACATCAGGCTCTTC	038B2B05
AUBES3086	726	746	7	68.7	ACCCTGTGCAGGATAAGCAG	GCCAGCTTGTCTCACATCAA	046A2E09
AUBES5144	1687	198	7	68.7	GCAGGCTTGTGAGGTTAGTGT	CAGGATTAACCATGATACCAGGA	100B2H04
AUBES4134	986	254	7	68.9	CAGAGACCAGCACAAAGACG	CAGAGGCAGACCCATAACCA	011A1A05
AUBES5114	1531	538	7	68.9	TTGAAGCTTGAAATTAGTCAAAAGAA	GCATGTTTCCAGGGAGAAAAA	006A1D01
AUBES3284	223	320	7	69.0	AGGTGAAATTCGGCACAATC	TCCCTTTCTGCATTTTAGACC	083A1E07
AUBES3487	429	301	7	69.0	TCTCCCTCTTGGACATCTGC	GCAGTCCAAGGACAAACCAT	083A2E10
AUBES2318	690	524	7	69.0	CTGTCAATGTGTGGCTCACC	GGCAACCATCTGTGTTTGGT	026B2C07
AUBES3488	429	301	7	69.0	CTGAGGATGGTGGTTTTTGC	AAGTGGCGGTGGATATGGT	040A2H11
AUBES4338	2245	291	7	69.0	AGGCCCAGTTGGTATTGGAT	CAATGATTCTCATCCCCAAA	055B2F03
AUBES4122	83	223	7	69.0	GCTTTACATTGACCTCGCTTG	TGCCCTTACTCACTGAAGTGTC	078B1G02
AUBES4550	2951	232	7	69.2	AGGCCAGATGCCTACCATAG	CCAGTGCACCAGTGTTATCTG	010A1F01
AUBES3471	57	245	7	69.2	TCCCCGTGAAGTCTGTGATA	GCAAGCTTGGCTTGTTGATT	082A1A12
AUBES5200	2145	220	7	69.4	TCTTTGCCTAAGCCCTTGAC	CTGTGATTTGCCTAGCAACTGT	004B2F07
AUBES2951	531	281	7	69.4	TGCTACAGCTGTGAGGTCCA	GTTGGGGAATTGGGTGAGAG	026A2D08
AUBES4667	963	392	7	69.6	CCATGGCTGCCAAATGTATAG	GTGACCTGGGGAAATGTTCA	006A1C07
AUBES3248	152	357	7	69.6	TTGCTGTGATAAATGTGCGTAGT	CAAATGAGCAGGGAATAAAACA	109A2B04
AUBES3744	9	2006	7	69.7	TGAGCCATGCTCTGGATACTT	TCAGAGCAACTCCTGAAGCA	088B2D11
AUBES2672	1018	304	7	69.7	ACATTGCCGTATCCACACAG	AATGCCTGATGAGGTTGGAG	053A2H09
AUBES4719	3251	164	7	69.7	GCCAAAACAGCAATAAGGTGA	TCTGAGGTTGAGGAACTGTAGGA	021A2A03

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3969	1657	279	7	69.7	GCAGGGAGCATGTTGCTAA	TCGCTACAGCTCAGAACGAA	112B2F07
AUBES1805	328	392	7	69.7	ACAGTGCTGGTGATGCTGTC	AGCCTTCAGAGCCATGCTAC	033B2G02
AUBES3703	9	2006	7	69.7	GGTTCCGAGGTTGAAGATTG	CATGCCCACAAGTTTCCTTT	005B2G07
AUBES3400	267	364	7	69.8	CTAGCAGCACAATTGGCATT	TTCCCTGTGACCCTGAAAAG	067B2H09
AUBES3399	267	364	7	69.8	TTGTCCCGACCTTACCATTC	ATGAGCAAGCGGTAATGGAG	010B2E12
AUBES3718	328	392	7	69.8	GGACATTTGGTCCCATCAAG	CACGAGCTGATTTGCAAGAG	035B2E01
AUBES1809	963	392	7	69.8	TCATGTCATCCGGTTTGTGT	CGAATGATCCAAAGCCCTAA	033B2D06
AUBES3660	400	257	7	69.9	TACTAAGGAGCCCTGCGATG	CATGAATGTGTGGTTCTGTGG	034B2E02
AUBES2751	162	492	7	70.0	TCACACCACAGAACTGACAGC	CAAGCATGCCTATGTTTGTAGG	038A1E05
AUBES4097	1016	404	7	70.1	GCCACTTTCTGATGGGACAT	TGTCATGCACAATGTGTCAACT	034B2B11
AUBES4098	1016	404	7	70.4	TGAACTGAACCCCCAGAGAG	TGAACAGGGAGCTGAACTGA	052A1H01
AUBES2504	825	340	7	70.5	TATGAGCGTGTGGTGGGTTT	CACAATGAACTGCCCTTTTG	048A1H02
AUBES4135	986	254	7	70.7	TTTGTCTTGGTCGTCTTGGTC	CCAGTGTTAAAGACAATGTTGACG	076A2H10
AUBES5149	1707	235	7	70.8	TTTGTGCAAAATGAAACTTGCT	CTGAGATCTGGGGAATTTGG	024B1E03
AUBES2925	1120	452	7	71.7	TGAGTGCATTTTGCAGTTGG	ATCACCAGGTAATGCCGAAG	031A1C12
AUBES4348	267	364	7	71.8	GCAGCACAATTGGCATTATT	TTCCCTGTGACCCTGAAAAG	067B2H09
AUBES2769	488	636	7	72.2	CCCGTTCAGAGATGTTACGC	GCTGGAAAGATTCAATGTCCA	072B2E03
AUBES2905	690	524	7	73.3	GTCATGTGTGGCTCCCAAGT	GAGGGGGAAGAGGAAAACAT	053B1E10
AUBES2692	410	450	7	74.2	ATGCACCCGAGGTTTTAATG	ACCCCTTCATGACAACGGTA	012A1G11
AUBES2562	275	822	7	78.3	ATTAGTGGTCTGGGCGCTTT	GAACAGCAAAATGTCACCAAA	050B1H02
AUBES4813	3091	205	8	0.0	TGCCCCCAATGTCTGAATAC	TCTCGTCTTCCTGGTGCTCT	104A1H02
AUBES3538	181	695	8	4.0	CAATTGGGCGTTTTATTTGG	ATGAAGCGTTGGATGGATTC	090A1H01
AUBES4368	895	359	8	6.1	GACACCCAGTCAGTTGTGGA	CAGTGTTTGGTAGGGTTGCAT	109B1A01
AUBES4367	895	359	8	6.2	CCTCTGTGGCTTTTCAAAGAA	AAATCCATGTTAGCGGCTTT	074A1D08
AUBES3573	895	359	8	6.2	GACACCCAGTCAGTTGTGGA	CAGTGTTTGGTAGGGTTGCAT	027B2G08
AUBES3574	895	359	8	6.2	TGTTTGTCCCGGTACTATGTTG	CCTTCATGAACCATGATCTGC	008A1F10
AUBES3328	480	709	8	10.1	AAGGAGTCTCCAGTGTCAGCA	TGAGGAACATCCAAGAGTTTCA	081A2B06
AUBES3357	455	727	8	10.5	TGGCTGAGGAGCTAGAGCAT	GAAGTCCCATCACCAGCAAT	059B1C02
AUBES2576	206	658	8	10.6	CATGGTCTGAGCCTGAAGGT	ATATTGCCCAGCCCTAATCC	038B1B08

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3144	455	727	8	10.7	TGGCTGAGGAGCTAGAGCAT	GAAGTCCCATCACCAGCAAT	093A2F06
AUBES4472	1270	238	8	13.5	TCAGGACGGTTCGGAAACTA	AAGCAACGGTGGGAGAATTA	107A1C07
AUBES5275	2555	169	8	15.5	CCCCCTTCACATTCACCATA	CACATCCGCTGACTCACTGT	011A2D09
AUBES1932	singleton		8	15.8	TGTCATTGAGAAACCCTCCA	TTGCTGGTGTTAGATGTGGTG	036A1A09
AUBES4546	2810	352	8	16.8	GCCTAAGAGACTGGCTGTGG	CGGAGAAATCATGTCCTGGT	073B2G07
AUBES3316	774	381	8	17.6	TTCAACATTAAAGCCTACACCTG	TTCACCTCCGGAATATGGTT	085B2H11
AUBES5328	2982	228	8	20.6	AGCTTATTTGTAGGTGGTAATAGTAGG	CGAGCATAACTGCTTTGCTACA	010B2B01
AUBES2722	506	533	8	25.1	GGTGGCGACGTGATCTCTAC	CGCTGTCTTTTCTCCTGTGG	012A1H06
AUBES3380	189	622	8	28.9	CTGACATGTTTCTGATGGATACAA	CGCATCTGCATTACACAAAC	095B2D07
AUBES3203	189	622	8	30.6	GCTGGGTACTCTGGTTACACAA	AACAGCTTTAACCCCGATGA	057A2F09
AUBES3326	189	622	8	32.3	GTTAGAGGCCAAGGCGAAAT	GGATTTGCATGTCCAAAATG	092B2B07
AUBES1354	378	276	8	34.4	ACACTGAAGCGGAACGATGG	ACAACGCTCAGTTGCTGGAC	032A2H07
AUBES4086	812	470	8	36.7	CCTGGTTTTAAAAGCGCAAC	TCATTACAACGCCATCCTGA	088A1E08
AUBES1353	2128	205	8	37.5	GTCCTCCTGAAGTCCAGACG	TCACCAGCTTGCTCTGAGAC	021B2H09
AUBES1990	2128	205	8	38.0	TGATGTAGAAGACCCCCATGT	TGCAGCTCCTAGTGGTATGC	025B2E12
AUBES5277	2559	208	8	38.4	GCTAATCCCTCACAGGCAAG	GATTTCCAGAAAGGCTCCATC	088B1B05
AUBES5036	1265	203	8	38.5	GGCGCAGTCACAAAGATGTA	GCGAGATGCTGATGGTACTG	013B1C07
AUBES4126	905	370	8	38.9	TCTGCTTTGTTGGTGGTAAGG	TGCCACAAAAACACATCCAT	107A2G07
AUBES4610	2054	240	8	39.2	CGTCTCTCACCCATCAGCTC	ACATCATCGATTCGCTGTAGA	064A2H12
AUBES2532	1056	210	8	41.0	TCGGATTCCTCATCATCCAC	ACGGCCAAAGAAACAAACAA	049A1E10
AUBES5306	2693	122	8	41.4	CTGTGAGTGGAAAGTGAAGCA	TATGGGCAGTAGGTGGCACT	021B1G05
AUBES4302	1845	238	8	41.9	TCGGTTAACATGCATCCGTA	GAGCTGACAGAGGGGAAAGG	005B1D04
AUBES3747	375	401	8	42.4	AGAAGGGAGTGCAGAAGACG	CTCAGACCTGGAGGCCAGTA	102A1B06
AUBES3365	885	1133	8	42.8	TCAAATGATGCCCAGGAAAT	GGCCTGCCAGAATCTACTGA	074A2E10
AUBES1113	201	330	8	42.8	GCAAAGTGTCATTTCTTCAGTGTCG	GCCATGTTCAGGTAACGTGG	012B2G07
AUBES4229	743	259	8	42.8	GACTGCATCTGCACCAGCTA	TCTCGATACTTTCTCTTTTGCTCTC	023A1C08
AUBES4427	2866	193	8	43.1	TGCATGTTTACCATTGCATC	TGAGAGGTGCTTCCCATAGC	078B2A05
AUBES4694	2946	149	8	43.1	ATGCGCACACCCTCATACTC	CGGGGGAAATGTTAAAATCA	083A2E06
AUBES4443	2866	193	8	43.2	TGCATGTTTACCATTGCATC	TGAGAGGTGCTTCCCATAGC	078B2A05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4401	1907	281	8	43.3	GACACCCTGAGTAAAAGGCTTG	AACACGTTTGGTCGTTAGCA	090B2F12
AUBES1610	314	556	8	43.7	ACTCGCTGAAGAAGGCATTT	CGCTCACTACATAGGGCATGA	021B1A10
AUBES4591	1868	255	8	43.8	ACACTACCGCTTACCCGAAA	TGCAACCTTTATGCTCCTCA	010B2B03
AUBES2448	2632	255	8	43.9	TCCTCACTCAATTTTCCTCCA	TTTCTCGGATCCATCTGTCC	040B1B11
AUBES4351	408	720	8	44.0	CTGCATAATACCAAGCAACTTGT	TGTGCAGTCGTGAGATGTGA	058A1A02
AUBES1918	2101	419	8	44.0	CCTGTAGGTGGTCACCCTTG	TCTTCCATGGTTTCTGTCCA	036A1B06
AUBES5305	2687	169	8	44.1	TGACCCTTCAACTGGAGGAC	CCCATGCTGGATTATTTGCT	106B1D03
AUBES3256	376	392	8	44.1	TTCAGCTTCCACACAGCATC	TGTCACTATGCTGCCCATGT	054A1D12
AUBES3194	885	1133	8	44.2	TCCTAACATGATTTCCACTGAGG	GTAACCAAGGGCTGGATGTG	048B1B11
AUBES3484	388	274	8	44.3	AACAGCATGGGTGATCATAGG	GCACAGGTGCCTGTCAGTAA	031B2A04
AUBES1730	1909	203	8	44.3	TCAAACCAGTGTGCTTTCTCC	CAGCCAGGAGTCCAAACTGT	026A1G04
AUBES3381	207	502	8	44.4	GACCCTGAGGACTTGGATTG	TCCCCAGTAATCCACACTCTG	111B1C04
AUBES1942	302	313	8	44.4	GGCTCCAGAGCTCATACAGG	CCTCCCACTTTCCAAAAACA	036B2H09
AUBES5006	1114	288	8	44.4	TCCACAGCATTGAGGTGTGT	AGGGTTCAGCAGCAGTTCAT	058A2E02
AUBES3322	1353	392	8	44.4	GCAGGAGAAAGCATCCTGAG	ACCCCATGTTTGGGTAATGA	065B1H12
AUBES5090	1515	169	8	44.4	CGTAGCGAAAGTGGTCACATC	TGGAAACTGAGGGTGCTTGT	107A1F05
AUBES4627	2248	156	8	44.4	CAGCAAGCAACCATCAAACA	TGCATCACACGTTGACACAT	041B1C12
AUBES3257	376	392	8	44.5	CCTCTTGCGTTCTGTGTCCT	TCCTCTTTTTCTAATAACTTCCTTTC	083A2D06
AUBES3051	443	582	8	44.5	TTCACTGCTTTCCTCCAACC	GCCACATAACAGGACCAGTG	052B2D06
AUBES5330	3027	345	8	44.5	TGAGAGCCCAGGTAGTCCAT	AGCTCAGACAAGCCAAGAGC	006A1C06
AUBES2057	1909	203	8	44.5	TCAAACCAGTGTGCTTTCTCC	CAGCCAGGAGTCCAAACTGT	039A2D12
AUBES4923	440	489	8	44.5	CAGTGGAGGGCTACAGGAAA	TTGATCGATACTCCACCATCC	086B1H11
AUBES3324	443	582	8	44.5	TGCAAATTGCCCCAAGTAGT	CCCTGGGATAGGTTCCAGTT	059B2F10
AUBES5268	2525	161	8	44.5	GCACAACATGCACTTCCAGT	AGCCGGTGGTGTGTGAAT	027B1B07
AUBES5155	1750	372	8	44.6	CTGCCTTAGAGCTGGATGGA	AATGGCCAGTCCGTGTAAAG	054A1G02
AUBES3717	236	795	8	44.6	AGCAGCAGCTCCAGAAAGAG	CTCACCGTTCTCTGCATCCT	034B1C11
AUBES2597	236	795	8	44.6	CAGCAGCTCCAGAAAGAGGT	TCGGCATGCTGCTAAAAAC	034B1A11
AUBES1786	376	392	8	44.6	ATCACGGAACACACGTGAAA	TTCAGTCCCATTACACCGATT	034B2C01
AUBES3485	388	274	8	44.6	GCACCTGGAGTGAACTGAATG	TTTCCATTGCATCTGTTCGT	018A2D09

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2801	1208	353	8	44.6	TGCCACCCATGCATTTAATA	ACAGTGTGCAGTGTACCTTGTG	040B2A04
AUBES4426	2866	193	8	44.6	CCTGGCATTAAGAGGCGTTA	TTGAGGTTGTGTTCACAGTGC	012B1B09
AUBES3749	236	795	8	44.6	TGGCAAAAGGTCTTGTTCTTC	TCTGCTGAACTCTCCGATGA	103A1E11
AUBES2424	2058	196	8	44.6	ATGGTCCCCTGCAGTATCAC	TCCCCTTGGCAGGTAACTAA	045B2H06
AUBES2802	1353	392	8	44.7	TTGGCATCCTTGGTAAATCTG	GCAAAGGGAGGTAGCATTGA	022B1B08
AUBES3750	375	401	8	45.0	TGAATTCTTTGGCACCACAT	TCCTCACACAGTGGCATGAT	106A2F11
AUBES1763	236	795	8	45.2	CTGCATGTATGTGGCTCCAG	TCATGGCATGCATACTAACACA	032A2G02
AUBES1882	singleton		8	45.2	AACAAAGCTTGGCCTTATGC	TTGATGATGGTGCTGGAGAA	028A1F11
AUBES2731	33	396	8	45.4	GCCATGCTTTCATCTCTATCC	GGTGTCTGGCTTGCTTATGTC	022A1H02
AUBES4442	2866	193	8	45.6	CCTGGCATTAAGAGGCGTTA	TTGAGGTTGTGTTCACAGTGC	012B1B09
AUBES3321	1208	353	8	45.6	TGCCACCCATGCATTTAATA	CAGTGTGCAGTGTACCTTGTGT	040B2A04
AUBES4507	2914	210	8	45.8	TACAGCTCCCTGCATTCCTC	GGCTGTCTGCTTGGTCTTGT	028B2D02
AUBES3855	3491	159	8	46.1	CAGTTTGCCTGTTGCTTTCA	TTTTTGGATCCCCACTCAGA	018A1B08
AUBES2263	1931	419	8	46.6	TGCAGGAATCATGAAATGGA	CCACATACAAGGCTGCACAC	043A1F07
AUBES4345	159	450	8	48.8	AGTTGGCCATCAAAAACCAG	CAGGAAGCGTTTTGACTTGA	085B1F05
AUBES4400	1907	281	8	48.8	TCACCATGCTCAATGAAATGT	GCTTGCTCAATGGCTACAAA	028A2C01
AUBES1635	314	556	8	49.6	ACTGTGTTTGCCCAGGTGTC	CAGTGGAATGTCCTCACAAGG	023A1B02
AUBES5252	2440	188	8	50.7	TGTCCATTTTCCCCCTCTATT	CCAAATTCCCTCTTTGCGTA	047B2A06
AUBES4249	1156	291	8	51.1	CTTACGAAGCAGGCGAGAGT	TGCACGAGACTACAGGAGGA	080B1D05
AUBES4075	689	279	8	51.4	AGTGGGGAGTCCGAGAGTTT	GCTGCTGATTAGCATATCACTTG	077B2B10
AUBES2886	376	392	8	52.3	CGCTAAATTGCCCCTAGATG	CTCTTTGTTCCCATCTCAATCA	054A1D12
AUBES2754	233	424	8	52.7	AATCAATGAAGGGCCTATCG	TTGGTGCACTAAGGGGAGAG	029A1C05
AUBES3115	159	450	8	53.0	TAACCCAGCACTGCCTTTG	GCAAGATCTTCACATGAGAAACATAA	029A1D06
AUBES5286	2605	315	8	62.1	GTCGAAATCCTTCAGGCGTA	CGAATGGTGCTGCAGAGTT	090B2H06
AUBES4778	2851	269	8	65.3	GGTGCCATTCCTTCCATTAC	TGGAAGTGCTTTGGGTTAGG	074A2G08
AUBES1287	780	233	8	68.4	GGGCGGATCAGAACCGTCTC	TTGGGTCAGTTGACGCCTGG	028A1C10
AUBES2257	9	2006	8	69.0	CGGAAGCACTAAAACCCAAG	CCCCAAATCAAGTACAGGAAA	042B2D10
AUBES1283	780	233	8	69.0	ACAAAACGCAGTGGGGTCTG	TTGGAGGACTGTTGGGTCAG	006B1B04
AUBES3569	780	233	8	72.5	GATCATTTTCCGGAAGGACA	GGGAGCATGTCACCAATCAT	018A2H02

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4366	780	233	8	73.2	GATCATTTTCCGGAAGGACA	GGGAGCATGTCACCAATCAT	030A1C08
AUBES4000	1080	345	8	78.6	TTGTGACCTTAATCCACACTGC	CAGACCTCAGAGACCAGCAA	084B1F07
AUBES5197	2134	272	8	79.1	GAACAGCTATGGGTGGAAGG	CATGGTCAGATGGTGCTGTC	104A2H04
AUBES5373	3349	230	8	79.1	TTGGATTTGCTTGCCTACCT	GGAGCAAGTGGAGGAGTTGA	011B2F10
AUBES4399	1903	262	8	79.1	TCGAAGACGAGTGATCCTGTT	GGAAAGTGAAAATCAAAAGAAAAT	011A2H01
AUBES5231	2359	337	8	79.5	GACATGTATCTGCCGATTTCAA	TAATGCCTGCATGGTTTTCA	084B2G10
AUBES4493	1660	203	8	79.5	TCTGATTGTCATCTCATTGCTTG	TCGAATTTTGGAGGATTTGC	075B1G06
AUBES2204	1345	198	8	79.5	TGTGCTCAGTGGGTTTCACT	GCATTCATTGATTCCATGTCC	030A1D11
AUBES2316	2068	254	8	123.2	CAAATGTCCACAGGGAGCTA	ACACAGGCATGGTCAGTTCA	026B1B11
AUBES5156	1752	142	8	127.8	CACAGGAATCACAACGTGGA	TCTCTGGACATGGTGTGGAA	014A2H10
AUBES5199	2139	220	9	0.0	CTGCTCACCTGATTGCACAC	TCGTAGCGTTCAGGGAAAAA	072A2G11
AUBES5227	2331	193	9	1.5	GGGGCTGTTTGGTTAGTTTG	CTTTCCCGTGTCATTCCACT	107A2G11
AUBES2104	920	306	9	2.6	TGGAATGATACCAGCAAACA	GGGGGAATCATGACAGCTAA	041B1E01
AUBES3833	1881	316	9	5.8	AAAAACCCCCACAACAACAG	GTCCAGCTCAACTGCAGGAT	076A2H04
AUBES1600	singleton		9	6.2	CTCCCTTCACAAGCTGTTCA	CCGGGGCTTCTATAGCACAT	024A1A03
AUBES3819	1684	391	9	6.6	CCCACATTATGCCTTCACG	TAAACTCTGCAGCCTTCCAA	105A2E09
AUBES1761	981	693	9	6.9	GAAACACTGGGGATGAGGTG	GCTGCATGTTCCTGAGGAGT	028B1D05
AUBES1607	1299	298	9	6.9	CCACCATGTGCCCAGTCTAT	CCAGTCCGACATAGTGAGGA	032B1F02
AUBES1871	singleton		9	7.0	TTGGATAGCTCACGGTGTATG	CATGGACGCATTGTAGTGTTG	025A2E02
AUBES4658	176	330	9	7.4	GCCTAGTGGCACTCACATTG	CTCCTCCCAAATGCTGAAAC	058B1F03
AUBES5357	3276	244	9	7.5	CACATTCATGCAGTGTTTGG	CCTTGCTTCCCTGTTCAGAC	079B1C08
AUBES3055	490	753	9	7.6	ACTGAACACCAGTCCGTTCC	CACACTTCCATCTGAAAGACACA	072B2G01
AUBES1843	176	330	9	7.9	GCGAGTTGGAGACCACATC	ACTTCGTTTTCCCCCAGAAG	036A1C08
AUBES1435	singleton		9	8.0	GTGACATGGCTCTGCTAGGC	GCTGATGCCATGCTAGTGTT	020A2C05
AUBES4986	991	227	9	8.0	AATCGGTCAGATGTGGAGGA	TGCCTGTCTGTATCTGTCTGTG	020A2F07
AUBES3025	502	494	9	8.1	TGAGTGGGAAAAGTATGTGAACC	GCATCTGTCACATTGCGTGA	052A1G09
AUBES1348	814	516	9	8.2	CCCATTCACCTCGACATGG	GCGCAAGTTTAAGGATGTGTGC	006A1C09
AUBES3048	985	573	9	8.4	AACAACAGAGTGTCTTCCCTCA	AGATTCAGGATTTTCCGTTCA	075A2G03
AUBES3533	981	693	9	8.5	ATCATCTGCCTGAGGGTGAA	GTGCTGCTGAAGTGGACTGA	100B2G05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4642	465	249	9	8.5	AATAAGGCAGCCAACAGTCG	AAAACAGGAAGTAGAGTGATTTTCA	028B1D06
AUBES4166	1532	450	9	8.5	CGCACATTTTGAAATCTCTCC	TTTAATCGTGTGTATTTGAGTATCG	058B1A07
AUBES3253	300	428	9	8.5	GACCGTGGCAGGTATCAAAC	GCAGCTGTCTAGCGATACCC	078B1A08
AUBES4639	390	252	9	8.5	GCAGAGCGATATCAAGCAGA	ACGAAAGACCCACCTCTTCA	072A1C12
AUBES3259	419	524	9	8.5	CGAATTCTGGATTGTCATGC	CATCGTGGTCGACATACTGG	068B2D08
AUBES2561	490	753	9	8.5	TCGAGGTGTCCAACAGTGAG	ACAAGAAGTGATGCGCTCTG	025A1E06
AUBES2916	879	345	9	8.5	CACATCATGCAAAAGCCTTC	AGAAAAACGAGAACAGACAGTGG	005B1E04
AUBES2051	985	573	9	8.5	AGTCAGGGCTAAAGCTGCAA	ATATCAGCTCTTTCACCAGCTT	039A1H02
AUBES2103	1401	624	9	8.5	TCTGAGCTCTGACCCCAACT	TTTTACACGTGACCAACCTCA	041B1D07
AUBES3781	1684	391	9	8.5	CCCACATTATGCCTTCACG	TAAACTCTGCAGCCTTCCAA	105A2E09
AUBES5245	2416	222	9	8.5	TGAGCAAAGAAGGCTGTGAA	GGTAGCTGGCATGGCATT	044B2H09
AUBES5343	3221	144	9	8.5	GTGCATCTCAGGACAACGAA	CGTTCAAAAGGATTGTGCAG	074B1G04
AUBES2809	176	330	9	8.6	ATTTACCAACCGCCAGATTG	TTACTTCGTTTTCCCCCAGA	036A1C08
AUBES1343	1884	230	9	8.6	CAGCATAGGCGTCTGGCAGG	AACATGGCCCTGTGGTCAGG	006B2C09
AUBES3166	42	1038	9	8.6	GTCTCGAGCAGGTGATAGCC	AGACGTCCTGTCTCGGAAAA	055A2C08
AUBES3105	154	1130	9	8.6	GAGCTCTGGAAAGGCCCTA	AAAACGCTTGCAGACCAATC	064B1H04
AUBES3970	1686	162	9	8.9	CCTGCAATGCTACAATACCG	TCCAAATGAATGGATGGATG	005B2E10
AUBES3818	1684	391	9	9.0	TGTTTAAAGTTGAAGTGAATGGAG	CCCAAAGACTACGTGCAAGA	038B2B01
AUBES3118	490	753	9	9.0	CGGGGCAATTAGTTTTCACA	TTTGGATAAACCCGTGTTCTG	048B1B12
AUBES4666	680	348	9	9.0	TGCAATCGAGCCAGTTACTC	GGTGTGAGGCAAGTGTGCTA	088B1B06
AUBES4280	1684	391	9	9.0	TGTTTAAAGTTGAAGTGAATGGAG	TCCCAAAGACTACGTGCAAGA	038B2B01
AUBES2668	751	391	9	9.0	CCTGCAGTGGAAAGGTGTCT	TGTGGCTGATGTCTCCTTTT	064B2F12
AUBES4973	881	271	9	9.0	GCTTAACTGTCAGTGGCATTC	CCTTTGGTTCTGGTAAGGTTG	079B1B03
AUBES4689	2889	167	9	9.1	TTTTGACAAAGCATGGCAAG	TGACAGAGAATCAATGGACTCATAC	010B2D03
AUBES2938	124	262	9	9.4	TGCCCTATAGCCAAACACAA	TTCCTGTGGACATTCAGCAA	009A2H08
AUBES4274	1565	311	9	9.5	CAGTGGTACTCAAAGTGGGATG	GCTGCCATAGACACCCTAGC	001B1D09
AUBES3720	1401	624	9	9.5	AAGCTCTCCTGGGCGTTTAC	GTGCTGCTGGTTTGTTTGTG	046A2D01
AUBES2709	1401	624	9	9.9	GCCCGACTATGGAAATAACG	TTAACTGCCAAGCCACCACT	006A1D02
AUBES5391	3421	188	9	10.1	AGGCATTTCCTTCACTGTGTC	CGACAGTTAGCCAGCTCAAA	090B1C02

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3162	154	1130	9	10.4	ACACTGCGTGCTGAACAGAG	TTGCCCACGTGACATTTAGT	103B2A01
AUBES5257	2483	188	9	10.8	TCTTCTGCTATGGTGGAACTGA	TTGTCAGAGGAACCAGCTCA	096A1G02
AUBES5055	1337	340	9	10.9	GCGTCTCGTGGAGTTCACTT	GCGAGACTGCCGATACAAAC	050B2G09
AUBES3499	618	264	9	11.2	ACACACAGCCCACCTCTTTC	GTTATGCAAATTGGCCCTGA	045B1C11
AUBES3817	1584	269	9	11.9	GAGCAAAGGACAGACACACA	GCTTGAAAGTGTCAATGCAAA	048B2E07
AUBES2893	539	614	9	13.9	CTGACCGGAGAACCCATATC	TATGAACATGCGTGGCTGAT	058A1G07
AUBES5347	3242	218	9	15.2	TAACAAATGAATGGGCGAAC	GATCCCTGGGGAGAAACACT	083A1E10
AUBES4060	409	421	9	16.2	GCTTCTCAAACACTCCTCAGC	AGGGAATCGTTACGTGCTGT	023B2G08
AUBES1410	409	421	9	16.5	AGACCAGATGCATAGGTGAGC	GGGAATCGTTACGTGCTGTT	023B2G08
AUBES4080	765	311	9	17.1	CACCATCAAACACTGGCATC	CCTCATGCCCTGAAATATGC	003B1C01
AUBES4840	1554	353	9	19.3	GGCGAGGATTAATCGTGATG	ATCTTTTGAGGCCAAACAGC	027B1A02
AUBES4659	176	330	9	21.6	CGACAGAGCTGGAGGGTAAG	TGTGTCCCATAGCAGGTCAG	063B1E07
AUBES5078	1433	296	9	25.8	ACCGTGCAACAATACAATGC	TGTATGATCTGCGTGCTGTG	001B1G10
AUBES4571	1817	252	9	26.9	TGCCATAGAGTGAGCCGAGT	GGGGAACCTTTGTGAACCTT	070A1A06
AUBES3653	72	1338	9	27.9	GCACCTCCTGGTGACGATA	CCGAAGGCCTTACAGAACTC	062A2A11
AUBES3716	72	1338	9	30.4	GAAATCCAGTCAGGGTCGTC	TGTTGAATGAGGCTGTCGTG	030B1G12
AUBES1368	1484	350	9	30.6	GAAATCCAGTCAGGGTCGTC	TGTTGAATGAGGCTGTCGTG	030B2G12
AUBES3713	72	1338	9	30.6	CCCAGAACCCCCACTAGAAC	GGAATGATCAAGTGCACCAC	028B2A05
AUBES4815	3100	223	9	31.6	ACCAAAAGGCCAGGCTAATC	CCACGATGTCGTCCTCTAGC	031B1E06
AUBES3229	72	1338	9	31.6	ACCGCTCCTCCACAGACTAA	CCCAGTTCCTGTAGGTTTGC	011B1A04
AUBES4501	2513	304	9	32.0	CACACCATTCCGTACACGTC	AGCAGAGGAAGAGTCGAAGG	072A2F05
AUBES2379	72	1338	9	33.4	TGAGTAGCTCCCAACGATGA	TGCGTACAAGGCCAATTATG	108B1C02
AUBES3373	72	1338	9	34.5	TCGTTCCTCTCCTCCATCTG	CAGATCAGATTCCCCGTCTC	096A2F05
AUBES3199	72	1338	9	36.5	CGCTGTATCTGAGCGATGAC	AGTTGGGGGACACCCTAGAC	049B1F09
AUBES1436	205	465	9	51.3	GAACCACTGTCTTGCAATGTG	CCCCTAGGGAACCTGAACAT	020B1C12
AUBES3230	72	1338	9	57.3	GTGTCTGAAGGGCCAAAGAG	CGCTAATCAGTCTAAATGCTTTC	055B1F02
AUBES1885	singleton		10	9.4	ATCCACCCCCTTGTCTGACT	CATCAGGCTTTGAGCAACTG	028B1H10
AUBES4226	660	260	10	11.0	CTGCTGGAAGATCCAACCAC	GCAGACCACCATGACATCAC	023A1B10
AUBES4677	2807	198	10	11.7	TTTGGTGAACGGTGTGACTC	TTCCAGTGTGTGGTTTTCCA	024A1D02

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4506	2804	430	10	20.6	CTGTTCCAGCACATTCGAGA	CGGATATGAATACGAGGAGGA	007B2F04
AUBES2260	1261	382	10	31.2	ATTCATCTCGCAGGAAGCAG	TGCTCTGCACTTTTGTTCCA	043A1B01
AUBES3739	904	342	10	41.8	CAGCTCACTCGGTTCTGTCA	CAGCAACGCCTATCACACAG	082B1D07
AUBES3317	904	342	10	43.5	AACCCCTGAGCATTAGTCCA	TCTGGGTATCTGGACAGCAC	059A2C11
AUBES5050	1329	196	10	44.1	GCCAGCAAAAATGGATCTACA	CCAGAGATCGCACTTCCATTA	071B1G07
AUBES3769	661	638	10	47.8	CCTTTATGGATCCGGTAAAACA	TCAGTCTCCCCACTCACCTC	077B2C04
AUBES3302	559	326	10	48.9	TACGGGGTCAACCTCTTCAT	ACGTTTGAGAACCCCTGGTC	088A1D06
AUBES2437	559	326	10	51.3	AGACCAGGGGTTCTCAAACG	GCCTCTAATCCGAGGAGCTT	040A2B12
AUBES5056	1346	266	10	55.9	CAAGAACCAGTTGGGTGTCA	CACGTTTACACTGTGGCTGAA	045A2B08
AUBES5311	2735	296	10	59.0	ATTGAAAGGCAGTGCAGGAG	CGTCAAATAGTACTGAAGCAAAGC	060B2C05
AUBES2580	436	854	10	59.9	TGACATCAAAGATGCCCTCA	CAAGGCGTCAAAGAGGATTC	072A1A03
AUBES3070	436	854	10	60.5	GCACATCCCAGAACAACCT	ACTGTGCCCTGTAGTTTTGGA	111A1F02
AUBES1949	327	463	10	61.7	AGACCTCCATAGGCCACGTC	CATGCTGCTGATACGACTCC	020B1E12
AUBES2523	48	269	10	63.5	GAGAGCACACAGACACATGC	AGACTCCTGCCTAGCACCTG	048B2B06
AUBES1867	37	572	10	64.7	TGTTCACACACATTGCTGACA	TCTGGCAACTTTTACAGTGCAT	023B1E10
AUBES2863	89	387	10	65.2	CCAGGATTGCACATTGTTGA	GCTCGAGTGCACACTGTCAT	030B2G11
AUBES3225	37	572	10	65.3	TGAACCTTGCTAACAAAACGAA	CTTAAGCTGTATTGCAAAAATAGGA	020B2A05
AUBES4924	457	343	10	65.9	GGACAATTAAACGCAAAATGC	GTTCCGATACGTGCAGCAG	012A1H04
AUBES4612	2063	222	10	66.2	AGACGGTGGACGTAATCGAG	CATGCACGGCCACATACTT	112B1D12
AUBES2906	820	605	10	66.5	CTGAGGGAATCTCTGCAAGC	GCAGTGAAGCCGATGATACA	077A2G06
AUBES4956	729	316	10	66.7	GATGGACTGGCACCCTGT	GGCCACTCCACATAAACCAA	112A1E05
AUBES3500	625	326	10	66.9	GCACGCACACATACAAACCT	TGGGATTCTGGGAGCATTTA	096A2B11
AUBES3501	625	326	10	67.3	CATTCATCAATGCAGCCAGT	TGTCATTGTTGCTGCCATTT	104B2E02
AUBES4850	1748	592	10	67.7	CACAAAAGGGCAGACAACAG	TTAGTTCCTGGTGGCAAACT	035B2F04
AUBES3600	1315	389	10	69.2	GGTCTCGCTCCCAAATGTAA	TGGAAGATTTTAAGGCAGTGG	066A2D06
AUBES3939	89	387	10	69.2	AAAAAGAAGGGTGCTAAATGGA	ATGCGCATAGGACATTGACA	069B2D05
AUBES4665	611	372	10	69.5	ACATGGACAGCTGCTGAGTCT	GAACAAAACAAAAACGCCATT	100A2A11
AUBES5304	2680	282	10	70.0	CGAGGTTGTAGTCGCTCGTC	GAGTGATGAGCTCCGCCTAT	052B2E01
AUBES3601	1315	389	10	71.5	GGTTGGATTCTCTGCTGGAC	TTGCAAGGACCTGATTTATCG	043A1A07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4478	1495	250	10	72.2	TTGCAGGGAGGAAAAGTGAC	TCTCTCCATCTCTCCCTGTCTC	029B2F06
AUBES3980	1798	433	10	73.5	GAGGTTCCACACTGGCATTA	ATGCCTAGCCTTTCACTCCA	079B2C09
AUBES5016	1174	260	10	76.1	TTTGTCAGTGGGCAAACGTA	TGTTTCACGGACATTTCCAA	063B2D09
AUBES5309	2721	107	10	76.1	GGTTTGCAGTATTCAGGTGTGA	TTGCATTTGACTGCTGATGTC	060B1C06
AUBES5224	2318	249	10	76.6	GGTGAAAGTCAAACACGTACAAA	ACTGGAGGGTTGATCCACAA	109B1B04
AUBES4407	2112	232	10	76.8	TGTAGCTTGTCCTGTAATATGCAC	GCTGCAATTATCCAAGATGG	045A2D03
AUBES5319	2766	288	10	76.8	CCTACCTCAAGGCACAAGGA	TTGCAGCAAAGGACAGACAC	080B2D11
AUBES3632	458	318	10	76.9	CGTGGTGGTTGAGCAGATTT	ATCGAGACGATCTTGCCACT	081A2B09
AUBES3942	111	462	10	77.0	TGTTGGTGGTGCTAGAAGGA	TTCTTGGGGGATTGTTCTTG	075A2E01
AUBES3545	381	267	10	77.0	CTGCGTCACATTTTCAGCAC	CTGACACCTGCCATCAAAAA	044A2D08
AUBES3631	458	318	10	77.3	CCATTGGGATAACGTGGTCT	GAGATAGCCGGTGGCACTT	032B2A03
AUBES4828	3173	169	10	77.5	AATAAGGCGTCTTTTTGTTTCG	CCACGTGTGACTGGCATCTA	107B2B04
AUBES3412	381	267	10	77.6	TTATTCCAAAAGGCCTGGTC	CAGTTGATTGCTGATGCCTTC	032A1E06
AUBES3943	111	462	10	79.5	GTTAATGCCGACGCTGTTG	TTTTAAAGTTTGAAGAATTTACTGCTG	029A2G06
AUBES2444	3325	353	10	84.8	CCATGTTTGAACCACAAGTTTC	ACCGGACGAGTGGACTGTAG	040A2H09
AUBES1904	384	269	11	23.7	CAAGCAGGAATTGTCCATGA	TCCTTCATTCCTCGTGTGC	036A2D12
AUBES1864	77	499	11	25.1	CGGTCCACAAGTGGTAAAGAA	TTCCCCGTATGAGTGTAGGC	022B1A02
AUBES4756	2642	210	11	26.7	GGGCTTCACATCTGACCAAT	GAAAGAATGGAAGGGTGTGG	061B1H10
AUBES3424	471	458	11	29.3	TACAAAATGGTGCCCACAGA	CGAGCTACAAATTGGGGTGA	112B1C10
AUBES3649	793	279	11	29.3	CCAGCAAATGTCAGGGGTTA	CTGTGAATGGGCTGTTGCTA	007A2E07
AUBES3425	471	458	11	29.6	CAGCTTTCCCGAAACGTAAA	GTGCATTGAGAAAGGCACAG	056A1A06
AUBES3204	266	482	11	38.0	GTTTCCTCCCACAGTCCAAA	GTGAAATCCTGGAGGGACTG	083B1C10
AUBES2944	313	330	11	39.4	TGTAAGTGAGCACCGTGAGC	CGTGTTCTGGGTGAGTCTGA	041B1F03
AUBES1859	20	693	11	40.3	TCACACCATGTGCTTCAACA	TCTGATGCCAGAACTTGTGC	019B1B01
AUBES2859	41	502	11	41.0	TGGCAGTGATCCATTCACAT	AAATCCCGTGGTTTTGAGTG	056B2G06
AUBES4763	2714	222	11	41.3	CCTCAACAATTCGGTGTGC	TCCCCCTTCTGCAAGATGT	054A1B01
AUBES3712	682	474	11	41.3	CCAAGGGACATTAACCCTGA	CCCAGATTTTCAGCCTTCCT	023B1B12
AUBES2816	367	272	11	41.6	CCCTGGGAGACATGAAAGAC	ACAATGGCCTCTGGTGAGAC	057A2F10
AUBES4475	1330	205	11	42.3	AATACGTGCGACTTGTCCAG	CAAAGGGTTTCCTTGTCGAG	098B1C10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2979	41	502	11	42.6	TTGTCAGGTGTCCACATGCT	GGCTTTCCAAAATGTTGATGA	106A1A05
AUBES2601	20	693	11	42.7	TTCCGAAGGAGTCTCCAGTG	GGTTGCAACAGCTACGAACA	053A1A05
AUBES4231	826	370	11	42.9	TTCTTTCTCTCGCAATCTTCCT	ATTGTCCTCGCTTTGGAAAA	058B1B06
AUBES2371	626	712	11	43.1	TACACGACACACGGCTATGG	CACTTTCTCAATCTCTCTCTTTCG	044A1B02
AUBES2712	594	477	11	43.4	CCCACGGACACACAAATAGA	GCAATGACTGTTTTGCACCA	008A1F01
AUBES4781	2876	161	11	43.8	TGGCTGTTTGATGGATTCTG	TGTGTGTGCATGCTCTGTGT	054B1B06
AUBES2512	1716	580	11	43.9	CTTTGGGGGAACGTCTCACT	TACAGCTCCGGTAGGCAATC	048A2E05
AUBES3527	646	524	11	44.1	CACGCCCTGTCGTATATCCT	AACTGATGAGCACGGGTAGG	042A2D10
AUBES3577	941	281	11	44.2	TTGTCTCAGCCAAGAACAGG	GGGACCAGGGTAAAGCAGTT	077B2D01
AUBES4372	1178	316	11	44.2	AGCTCCATGGATGGAATTTG	AACGTCAGTTGCTGGGATTT	038B1G07
AUBES5141	1681	227	11	44.2	CAGGCTCCCTGCAATAAGTG	GCATCCATCCATCCAATCAT	083B1B09
AUBES4491	1655	211	11	44.2	AACAATTTCCATGGCGTGTA	AAGTGGCACAGGGAAAAGAG	100A2D10
AUBES3867	801	558	11	44.3	CTGTTACAGCTGCGAGATGC	TGCTGCCTACAAGTGACAAAA	032A2E08
AUBES3872	801	558	11	44.3	TCAGGCCAAGGTTACCAGTC	TCCAAACAGAGGAGGCAGTT	090B2G11
AUBES3448	875	347	11	44.5	GCTGCTGAGAGTGGTGGTAA	AAAAATGTGAGGGGTGTACTCA	008A1D08
AUBES2717	503	597	11	44.5	TGTGGTGAGAGGCATATGGA	CGCTCTCAAAGCAGAAGACA	011A1C02
AUBES4293	1743	235	11	44.5	TGGTGAACAATGAGTGTCAGG	ATAGCCGGTTGTGCTTCTTG	002B2A09
AUBES2520	303	279	11	44.6	TTCTCAGCAAGATCCAAACAGA	TGGACATTGTCAAAAAGCAG	048B1E02
AUBES5041	1277	235	11	44.6	TGGGCACTTTAGGAAGATAAGG	CCAGTGGCCACAGAGGTAAT	024B2H11
AUBES5255	2471	169	11	44.6	GATCCAGTGACCCAGTGAGAG	CCTGTTGCGTATAGCAGTTCA	082B1F09
AUBES4315	1958	151	11	44.7	CCATTCTCATGCACAAAAGC	AACCGAATATGTGACCCACAA	030B2E08
AUBES3665	646	524	11	44.7	CACGCCCTGTCGTATATCCT	AACTGATGAGCACGGGTAGG	042A2D10
AUBES1377	1525	660	11	44.7	CAGTTACAAGGGGTTTCCCAG	CACATACACACCTCCATGAGC	025B2F07
AUBES2123	646	524	11	44.8	CAGAGATGACACTATTGACTTAAAGC	GTCGACTGGAAGAACCCTGA	018B2A11
AUBES2076	2771	233	11	44.8	TTCCCGTGTGTGTTATTCCA	TCCTATCTCGGCAAGAGTCG	039B2D11
AUBES3871	801	558	11	44.8	ACATGCCGACAATTATTCCAG	GCTTATCACACGCGCTCTTT	090B1A10
AUBES3914	1075	230	11	44.8	TGATCACTGCAAAAACTGTTCC	TGAAGGCTGAGTTGGTTTCC	005A1G12
AUBES4373	1178	316	11	44.9	AGCTCCATGGATGGAATTTG	AACGTCAGTTGCTGGGATTT	077B1D02
AUBES3474	225	267	11	45.0	GCGCTGAACAGAACTGGATT	CCCAAGAACCACTGAGGAAA	008A2G10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3090	161	626	11	45.0	GAAATTGAAACGGCTCTTGC	GATGCTTTGCCATGCTTTAAC	020A1H02
AUBES3050	561	533	11	45.0	GCTGCACATAATGCAACCTG	TGCTGAACAATCCTTTGCTG	077A2E08
AUBES3714	709	387	11	45.0	GGAACCGGCTGAACATAAAC	TGGCACTGATTTGGCTAATG	029A2D03
AUBES2670	831	413	11	45.0	TGACAGAACACAAGGCCAAG	CATAAAATGTCTTGGTGTCATCCGC	045B2C10
AUBES3775	1168	281	11	45.0	CCACCACCATGTCCCTTTAG	TGTGAGATTGGAAACGGTTG	078A1C07
AUBES4385	1698	260	11	45.0	GTTTACCACATTCATGCCAGAG	TGATGTGAGTCTTGCCAATCA	026A1F10
AUBES3837	1975	194	11	45.0	GAGTGCACCCGGCTTTAGTA	TTGGCTCTTAATGCTCTGTCC	090B1G09
AUBES5361	3288	235	11	45.0	CGAGGGGGAGAGACACATAC	CCGTTCTGCCTGTTTTGAGT	095B2F10
AUBES4294	1743	235	11	45.0	TCACATGTAGGGCATGTGGT	TCTGGTGAAAATGTCCTCATTG	106B2G02
AUBES5019	1187	267	11	45.2	TGTCCAAAACTTCACCAGCA	TTCTCTGTGCAACCCTCAGA	012B1D05
AUBES1137	515	414	11	45.4	ACATACCTGACAGGTGAGTTCC	ACTGAAAGCATCTGTTGCACG	007A2E10
AUBES2266	singleton		11	45.6	CACATGAGTGAAACAGCGAGA	TGTCCCACCTTGTTGTATGG	043A2D07
AUBES3473	225	267	11	45.7	GGCCCTGTTTCAAAGATGAT	GGGGGTGAGCAATACGACTA	073A1F08
AUBES5258	2486	191	11	45.9	CAGACATAAATGCTTCGAGTGC	TTGCTGGATTTCCTCTTCACT	003A2C08
AUBES1538	425	228	11	46.1	TTGCATCGGTGCATCTCTAA	TGAGGGGTGTACTCACTTTTG	030B1G03
AUBES2610	161	626	11	46.6	AACCAATAGACCAAACAAATCAG	GGCACCAATGCCAGTCTATC	006A1G10
AUBES2703	17	543	11	46.7	GCAACTGAAGTTTGCCTGAA	GCAACAAAGAGAGTAAGGGTTAAG	026B2C08
AUBES5372	3336	112	11	47.0	CTTGAAGTTGGTGGAAAACAA	AAGTTCATGGCACTTGCTACA	020B2E06
AUBES1183	2034	213	11	48.2	TTATTTGGGGAACGGCAGTG	TGACGTATGGTTGGCAACAC	011B1C04
AUBES4829	3181	318	11	48.4	CAATCGTTGCATTTATGTAGCA	CAATGGAGAAAGGGTTGGTG	073B2F11
AUBES3866	677	360	11	48.8	CCCCACAGTTGGTACCTTTG	TGGCTCTCAACGAGAACTTG	082A2E11
AUBES3648	793	279	11	49.4	ATCAGATTGGCGAGGTGAAC	CAATTCGACCCCTGTAAAGC	051A2H09
AUBES3315	724	431	11	49.9	GCCCTTGGTCAGTTTATCCA	ACCAAAAGGTTTCTTTGAACTAACA	078A2F05
AUBES1765	941	281	11	51.2	GCCCTTGTTTGTTCATGTCC	GGGACCAGGGTAAAGCAGTT	032B2H02
AUBES2481	248	712	11	55.2	GCGATTCCATGTTGTCTTGG	CCTGCCAAACATGACACAAA	046A2C04
AUBES3480	282	408	11	61.1	TCCACTCCAGCATGTTTCAT	GCCGTGTATTGGTGGAATGT	096A2G11
AUBES4643	472	222	11	70.6	CTGGCACGTGTCCAATCTT	TGGAAGTGTGAGCATGATGG	023A1E02
AUBES1612	singleton		11	71.3	TACCAGCCTTCCAAGCATTC	GTCTCTTTTCGGTCCAGACG	024A2B01
AUBES2844	360	416	11	71.9	CCCTATTCATGTGCGAGTCA	GCCATTTAAGAGCAGCGAAC	003A2D05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3278	47	315	11	72.7	GCGATACCCATGATCAGCTC	AAAAGCAAACTAACAGGCAAAGA	090A1C02
AUBES4744	2509	167	11	73.6	AGCTGCAAGCCAAAGACTGT	GGCAGTGCGGAGTCTGATA	030B1H07
AUBES4192	360	416	11	78.7	TTCCCATGAAGGTGACTCGT	CGCAGCTGGAGTAGTTCCTT	013B1A04
AUBES2217	360	416	11	81.2	AAAGAGAGAGACCGGGAATG	GTCTCACTCTCTCTCCCCATC	032B1D10
AUBES2525	1630	157	11	83.9	GCCGTGCCTCTTCTTACTTT	ACACACCCGCAATCTTTTCT	048B2C01
AUBES4575	1865	191	12	0.0	CGCTAAGTTCCTGCCTTTTG	CCTTACACCAACGGTCACAC	106A1H11
AUBES1407	1197	206	12	18.1	CAACCCCTCATTCACGAGAT	TCAGGTTTGCACATCACTCTG	022A2B12
AUBES4384	1646	235	12	19.4	GCTGCAATTCGGAGCATAAT	GGGTACTGGAGTCCCACAGA	108B1F10
AUBES4827	3171	223	12	19.9	GCTGAACTGATCGTTGTTTTTG	TCAAAATGCCATGTCTGACC	109B2C10
AUBES2374	3376	240	12	20.6	TTGAAAATGTATTCCAAATAAGGAC	TTGACCATGAATCTCATTTTGC	044A1D03
AUBES4383	1646	235	12	21.1	GCTGCAATTCGGAGCATAAT	GGGTACTGGAGTCCCACAGA	011A2D06
AUBES3612	1592	460	12	21.3	GAGGATGCCTTGTCCTAACAT	TGGCATTTTGCTGCTGAATA	013A1A01
AUBES1764	2495	264	12	22.5	CAATGTCGAGGCCAATCTG	AGCACGGAATGACTGCTTTT	032B1H08
AUBES5287	2606	181	12	23.3	GCGACCTGCCGCTTTATTAT	GAAAGCGTGCTAATGCTGCT	030B2D09
AUBES4586	1965	194	12	24.2	GGCTTGTGCAGTGTTGATTG	TGCAGTTCCTGACTGCTGAA	108B2H08
AUBES4713	3196	301	12	24.9	CCAGAGACCCCTGCTAATGA	AGGGAGCTTGAGTGTCATCG	049A1D08
AUBES4714	3196	301	12	25.1	GAAGGCAGATCCCATCTCTG	TAGACAAGAATGCCCGAGGA	079A1C11
AUBES2211	1435	203	12	26.7	GGTACCACCTTTTCGCCATA	GATATTTCAGCAGGGCAGGA	031B1D12
AUBES5054	1336	353	12	31.5	TCGCGGTCCTCTCTTATTCT	ATCCCTCCAGACTCGCACTA	034B1D07
AUBES2406	singleton		12	32.1	TCTCGTGTTATCGCAGCTACA	CCACACCAAATTGGCAATAA	045A2C09
AUBES1396	singleton		12	32.1	GCTGCTACTCTCGCATGAC	TGTAACCCTAGCCAGCTACAG	018A1D08
AUBES2420	518	531	12	37.0	GGCAGGAGGATAGCAGAACTC	GGTCACATTGTTTGAGCCAGA	045B2F06
AUBES3342	194	595	12	37.1	GCCATTTACCGAGAGTGGAG	ATTCCCGTACAGCAGAGCAC	068B2C04
AUBES3049	271	555	12	37.1	TTCCAGACTACTTTATCACCAGAA	ACACAGGCCTCGGGAGTAG	076B2D04
AUBES2571	518	531	12	37.1	GACTGGTGATGGAAAAGCTG	GTGGAGATTCACCCCTTCTT	010A2H08
AUBES4069	546	367	12	37.1	AGTGAATCCTCAGGCCCATA	TTGGGGTTGTAATTGTCAGC	111A2D04
AUBES3124	518	531	12	37.3	TTGAATGCCGTGAAAATGTC	GCAACTGGCCCATTATCCT	034B1B11
AUBES1888	271	555	12	37.9	CCTGTTCCCAGATCAGAAGC	GTGACGGAGCCTGTCTCTCT	029B1H08
AUBES2075	194	595	12	38.0	TGACCCTGTTTTCCAGCTCT	AGGGTCACATGCCACAAAG	039B2C06

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5186	2025	184	12	38.1	TGCCGAGTCCAGAGAAAGTT	GCGACCAGTGCCAATATGT	004B2D02
AUBES4949	669	309	12	38.1	TCGCAATGGCGCATATATTA	TCAGCGTCTGGTGGAAGTAA	004B2A09
AUBES5011	1138	244	12	38.4	ACTCATTTCCGTCTGGCTTG	TGATGCCGCAGTCACAAC	048B1C06
AUBES4232	828	211	12	38.7	GCATGTTCCTTTCAGCCTTC	CTTACAGCCCTCCAGCAGAG	107A1G04
AUBES4913	334	228	12	40.0	TATGTGACTGCCGGTGGTAG	CTGTTCCCCTTTGCAGAAAC	083B2G11
AUBES4233	828	211	12	40.5	TTCGTGACTTGAAAAACAGCA	AATTTCGTGCGAAGCCTTTA	107A1G04
AUBES2277	27	430	12	41.9	GGCTGCTGGGAACTGTAGTC	CAGATGCTCGATGAGCTGAA	043B1G03
AUBES3201	166	890	12	42.1	CCTCCAGGAGCTTGAGATTG	GGCCATAGCGATAAGAGCAC	053B2D03
AUBES2664	533	477	12	43.4	GAATGGTGACCAGCTTCACA	GTCCTCATCTCTGGCCTTTG	022A1B10
AUBES1726	609	502	12	44.3	GGTACACCAGTCCATTGCAG	CAGTAGGTGGAATGGCCAAA	023A1F08
AUBES2050	169	715	12	45.5	CAACTGCCATTCTGGGAAAT	AAGTGTTGTGGCTTGAGTGAGA	039A1G05
AUBES4919	422	203	12	45.9	GGAAGCTTTTGGTTGCAGTT	CAGCATTCGGTTATCGGTACT	108B1G04
AUBES1273	3217	157	12	46.1	TCGTAGATGGAGGCTCCGAG	TGTGAGAACAGTGACCGTGC	028B1C09
AUBES3542	217	289	12	47.1	CTTCTGAGCCCATGTCACCT	GCCTGTCTCTCTTCAAAAGCA	071A2E10
AUBES4928	524	337	12	47.1	TGCCAAAGGTATGCTCCCTA	CACCAGTAAATGCACCCAAT	025B2G06
AUBES3708	601	386	12	47.1	CCCTTAATTCTGGCTGGTTG	CAATTCTCCGAACATGAGCA	019A1B02
AUBES3233	609	502	12	47.1	CTGCTTGAAAAGCAAGATGAAA	GACACCCATGATTGCGTCTA	091A1C08
AUBES4888	897	274	12	47.1	GAGAGGGACATCCGGTCTCT	GCGCATAGATTTCCAGTTGC	054A1H05
AUBES4887	897	274	12	47.1	TTGAGTGCGAGTGTGAATGAG	CCGTGGGGATTTACAGATCA	005A1D11
AUBES5116	1539	198	12	47.1	TGCACTTTGCACATATCAGG	CACCAACCCATCATGGAATA	026B1A09
AUBES3967	1673	497	12	47.1	CACCAGCACAAACAGAGCTT	TTTTGGCCTGGTTAAAAGACA	087A2C07
AUBES3622	228	279	12	47.1	GGTGCTTTTTGTGCATCCAT	TCAGGCACCATCAGACAAAG	110A2H03
AUBES4225	629	277	12	47.1	CTGGAAGATAATGGCCGAAG	AAACACAGCATCTGCATTTGA	005B1G10
AUBES2773	601	386	12	47.1	CCATGTCCCTACAATTGCTGT	ATCCATCCATCCATCCACTC	013B1G07
AUBES2115	singleton		12	47.2	TGACCCTCAGGTCAGTCACA	CACCGAGGATATGTTCGAGA	041B2G01
AUBES2579	609	502	12	47.2	CAGGTCCTGGGTGGAATGTA	CAAACAAGCCCAGAACCAGT	012A2E09
AUBES1725	217	289	12	48.1	CCATGTATCAGGTTTGCACATT	TGTCATGTCAGTTGGAAGCA	022A2H05
AUBES1345	singleton		12	48.4	GCTCATTCACAGGGACTTCAC	TGGATCAATCTCAATCAGGTCAGG	002B1E01
AUBES4138	1073	227	12	48.8	TTCTCACAGCCTTCTTTGCTC	CAGCTCCAGTTTCCTGGTTC	023A2D06

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4101	1073	227	12	48.8	TTCTCACAGCCTTCTTTGCTC	CAGCTCCAGTTTCCTGGTTC	023A2D06
AUBES3054	15	539	12	49.0	AAATGGGAATTCGGTACGTG	GTGGTGTCGAATCAACATGG	112A2C06
AUBES3111	534	1072	12	50.1	CAGAAATACACCCTGGAGCTG	CCCATGGCTCAGCTTGTAA	013A2A03
AUBES2497	213	318	12	50.9	CACCTGACTACATGCACACG	CTCCATCATCCTTCCACAGA	046B2C11
AUBES3513	113	460	12	52.2	GCCTATTTAGATTGGCCTTGG	CAGAGGTTCAGCTCAGCAGT	110A1A08
AUBES5130	1623	340	12	52.9	TAAACCGTTGTTCCCTCACC	CATGGATCCTCCTGCCTCTA	088A1C05
AUBES3076	216	727	12	53.2	GGAGCAATGCAAACGAAATC	CAGGCTGGGCTAAGTCTGTT	029B1G01
AUBES4843	1619	350	12	53.3	ACATAGCCTGCCTCTTCACC	TCCAAAAATGCCTTTTGTCTG	075B1E02
AUBES3345	169	715	12	61.8	CCGCACCTTAGTAGCAGTGT	TGGGCATTTTGATGAAACCT	106A1D05
AUBES3546	441	338	12	64.6	CCACTGCATGGTCAAGTTTT	CATGGACAGCTCATTGCCTA	056A1G08
AUBES3469	1800	379	12	66.7	TGGTCGGAAGGTGTTCCTAT	CGACGCAGCATTCTGTAAAA	061A2F02
AUBES4066	492	220	12	67.9	CGCTATTTGAGTGGCCAAAG	TGGCCCAGTGAAAAACTCTT	084B2G01
AUBES3416	441	338	12	69.0	CTGCAGGTTGCTGAGACTGT	AGGTGCGCATAGACACACTG	028A1A07
AUBES3470	1800	379	12	71.6	GCACGCTCATGTGAAAACAC	TCACACTGTCCGACGTGACT	044A1B01
AUBES1430	82	536	12	72.2	GGTTCTGTGTGCCTGTCAGA	TCAAGCACTGGTAAAGAACTGG	032A2C10
AUBES3497	596	418	12	72.8	AGGGTGTGAACGACTGTGTTT	GAATTCATCGAGGTGCCAAT	056A1A10
AUBES5160	1804	269	12	74.3	TGGAGTGGGTGTTTGTCTTG	CATGGGAAGTCAGGTGAGGT	107B2C09
AUBES3496	596	418	12	76.4	CGTCTCCGAGAAACACCGTA	CCATTAGGTGGCGGTAACAC	040B1H03
AUBES5222	2302	181	12	77.6	GGAAAAGCACAATGCTGTGA	GTCACATGGGTGAAAGGTGTT	058A1D05
AUBES1178	1664	269	12	78.6	TCCGGCCAGCGCCATAGACG	TCCTGGTCAGGGTTGTGGTG	011A1B12
AUBES5175	1932	176	12	83.2	GTTATCGCCCTGTTCGTGAC	CGTGTCAGGACCTCATCAAC	034B2E03
AUBES3989	2051	413	12	85.5	GATCCGAGAGAGGGAAAAGC	TAGCGCTGGAGCTAACACTG	024B2A01
AUBES5392	3427	91	12	86.3	CGAGGAACAATTCGGGTCTT	TCCCTGCCACTTCAGAAGATA	092A2C01
AUBES4839	1552	252	12	87.2	AGGCTAAATTCGAGCCAACA	ACAGGAACAATGCACCATCC	083A2F06
AUBES5350	3248	132	12	87.3	TAACCTGGTCCCAGATTTGC	TTGAGTAGTAATGTTGAGTAATGCTGA	008B2F07
AUBES5007	1126	331	12	88.9	CTGGGAATTGTGATGTTCCA	TGTGAGGCGTTTCATTTTGA	052B2A03
AUBES4838	1552	252	12	94.5	ATTCGAGCCAACAAGACCTG	GGTCAGCGGACAAACAAGT	003A2C05
AUBES4983	971	338	13	0.0	CCGGTTCCTTCAGTTCTTTTC	GCCCGTTTCAAGTTTCTTCA	022A1B03
AUBES5323	2849	413	13	11.7	ATTCTTGGAACTCCCCTGGA	TGGACGGATTACACGGTCTT	065A2F08

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5384	3399	211	13	11.7	TACAGGTGAGGGGGTGCTTA	CATATTAACCAAGGGTGCCAAT	046B1A12
AUBES1959	singleton		13	15.7	GCAGCTGCCTATCTGCATTT	GCGATGTTCTTCTGGGTTTC	022B2B02
AUBES1723	3335	309	13	16.1	CGGACGCTCCACATAATCTA	CATGAGCCTGACACTGGAGA	020A1C03
AUBES4017	1221	313	13	16.6	GCCGTCTCTGGTTTTATTGC	AGCAAGACCACATGTGCAAG	040A2H02
AUBES4759	2673	266	13	16.6	GGACGTTTTTCAGTGCTGGT	CACCCTTGAGTGGCTTATCG	066A1E05
AUBES2039	1221	313	13	17.4	CGTTTTCCGTCATTAGACGA	TCGCCAACCCTCTCTTTTTA	038B1H03
AUBES2228	172	406	13	17.6	CCTGTTTGTTTACCTCATCGAA	AGGGCTCTGAAAGAGTGCAA	042A1D05
AUBES5415	3544	162	13	18.1	GATGACGACGCTCTGGAAAT	GGAATGAAAGACAGAGCGAGA	035A1G08
AUBES4885	741	277	13	18.5	AGTGGGTGGTGCAAAAGTTC	TTTGGTGGAAGAGTTTGTGG	043A1E08
AUBES2791	700	545	13	20.6	CCTGTGGCTAGATAAACAGAGGT	GGGTTTCAGCAAGAACAACAG	054B1F01
AUBES3311	700	545	13	20.6	CCTGTGGCTAGATAAACAGAGGT	GGGTTTCAGCAAGAACAACAG	054B1F01
AUBES4517	416	320	13	32.3	ATCCAGCGCATCCCATTAT	GATTTTACGCCTGCGTCCT	091A2D06
AUBES4516	416	320	13	34.2	CGATATCATCGTCGCAAATTC	AAATGCCGAATGACAGTTCC	010A2H04
AUBES1567	992	318	13	36.0	GAGGAATGTCGTGATCTTTGC	GGCATTTCATTTCAGGACTCA	022A1F04
AUBES5174	1906	291	13	39.1	CCCGTGACTTCCTTTAATGC	TGCTCGAGTCTGCAGTCAGTA	014A2H07
AUBES2071	2822	306	13	41.4	TTTCCCCTGCTTTCATCATT	TTGCAGCATCTGGAAAATGT	039B1G06
AUBES2775	631	524	13	43.4	GCCATTGGTTCTGCTAATGC	TAAAGGCAGCGAGCGTTAAG	053B1E12
AUBES2795	980	374	13	44.2	GCAGCGAGCGTTAAGAGAAT	CAGTACGCCATTGTTCTGCT	002B1E07
AUBES2908	929	538	13	46.0	ATAAGGTGGCAGTGCTGGTC	GCGAGGAAATAGCAGAGGAA	045B2F11
AUBES3089	199	683	13	46.7	CCCAAAAAGGCTCTCTGTAGAA	AGTAGGAAAGCAACGCTGGA	051B1F04
AUBES1794	singleton		13	46.8	CTGCATCAAACCAGCAAAGA	AGACACCCTTATCCACAGCAA	033B1H10
AUBES3555	401	318	13	47.8	CATGGGTTCATAATTATTGGTTCA	TGTGCTTTCACACACACTCG	022A1C03
AUBES3702	199	683	13	47.9	GCACATGACCAGAGCACATT	GAAGGTTTTTGCCAAACTGC	004B1D10
AUBES2609	199	683	13	47.9	GCACATGACCAGAGCACATT	AGGTTTTTGCCAAACTGCAC	014A1A07
AUBES3110	59	1071	13	48.2	GTTTCTTTCTCCCCGAGCTT	GGCTTTCAGAGTCGGAAGTG	058A2H03
AUBES1887	929	538	13	48.3	CATGGAAGGAGTCTCCAGTG	CAGCACAATGCAGTTTTGAA	029A2C07
AUBES3734	59	1071	13	48.5	GTTTCTTTCTCCCCGAGCTT	GGCTTTCAGAGTCGGAAGTG	074A1G06
AUBES3486	401	318	13	48.7	AGGCTTCGTGCAGACACAC	TGGTGCCGGAGAACTTTAAC	082A2E03
AUBES4007	1131	252	13	48.9	GAGGATGAGGACTGGCAGAG	GAGGTTGCACACACACACATC	075B2E04

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4082	773	311	13	49.0	GGACACACTGGGCTGAAAAA	CATGGCTGACAAGCAAATGT	021A2B03
AUBES5281	2575	328	13	49.3	TAGGCATCCATCCATCCATT	TGGAAACTGTGGCCAAAAA	072B2E08
AUBES3060	32	555	13	49.6	CATCCAATCAGAGAGCAGCA	GCGGTCACAGTTGTGCTTAT	102A2A03
AUBES3733	9	2006	13	49.6	TAGCTGCTGGCACTTCACAG	GTGGCCAAGGTTGTCTCATC	073B1D11
AUBES3393	79	281	13	49.6	GTCCCCACAGCACAGAGTTT	TGGATGTGTCGAATACTTCCTG	105B2F05
AUBES3149	199	683	13	49.6	TGTGAACCTCTAGGATAAGAGTCA	CTTCAGGGGTTTCCTCCAGT	054A2G09
AUBES3557	738	304	13	49.6	CAGTGGCATCACGCATTACT	TTGTGGTGGAATAGGGCTAGA	068B2H03
AUBES4907	257	502	13	49.7	ACAGCTTTCATGGGCTGAAT	TGTGTTCACACCCATTTCTGA	068B2F08
AUBES3439	652	404	13	49.7	GCTGAAATGCGTCACATGAT	GGGTTAGGGCTGCTTGATTA	053A2C06
AUBES2761	344	570	13	49.7	GTGGCCAAGGTTGTCTCATC	TTTAGCTGCTGGCACTTCAC	052A2F09
AUBES3392	79	281	13	49.7	GCCAAAGCCTTGAGCTACTG	TGCTACTGTTTACTGCTCTTTTGG	105A2B07
AUBES4622	2163	245	13	49.7	CCGTCCTGGTATGAATCTCC	CACACAAAATCTCGGCACAC	072B1B12
AUBES3678	59	1071	13	49.8	TGAATTTGCACTGATGGTTCA	TCCCCTCATTGTATAACCTCAA	035B1F04
AUBES2637	59	1071	13	49.8	TGCACAGAGGCAAAATTACG	GACCAAAGGTTCCCACAAAG	005A1C12
AUBES3476	251	257	13	49.8	CCAGTGCCAGTGCTTTGTAA	TCCTTCACCAGCCTTTCTTG	062A2E09
AUBES2422	929	538	13	49.8	TGCTGGTCTGCAGTGGAATA	GGGAAGGCCTTATAGAGTTGC	045B2F11
AUBES5087	1493	304	13	49.8	TTTCTTGCCACTGTCACCAC	CCTGACCATCACACCCTTATG	050A1H07
AUBES2045	2462	191	13	49.9	CGGCTGATGCAGACATAGTG	ATGTGCCAGGCCATGTTTAT	038B2H09
AUBES5411	3536	193	13	50.3	CTTCCTGTCCACCAGAGAGC	ATTCTCCTGGTGCTCCCAAT	002B2C02
AUBES3440	652	404	13	50.4	GGAATGAAAACGCTCAAACG	GATGCTCGGCTTGGATAGAG	104B1G10
AUBES2704	92	369	13	51.1	TTATGCTGTGTGTTTGCGTGT	CCCAGCATGAAATAAAAGACC	027B1G06
AUBES4464	932	184	13	51.3	CGTGCTTGTGTTTGTCTGCT	ACCCAATTTGTCAGCGCTAT	051B1F10
AUBES2864	92	369	13	51.5	TTCAATCCCCAGGAAGAAGA	GGACACAACAACTCGGATGA	074A2H07
AUBES4918	417	316	13	54.0	TCAATCACTCTCTTGATCCTTTCA	GCCAATGTAAAGTTGGCATGT	051B1F11
AUBES4362	738	304	13	54.6	TTGCACCACAGTGCTATTGA	TCCCTTGGTATCTTCATTTTCTG	056A1F09
AUBES4006	1131	252	13	55.1	CACGGGCACAGAAAGGTATT	TGGTGTTTGCTTGATTTTGC	084B1F03
AUBES1594	3393	303	13	56.8	AAATTAGGCCACGTGTAGGG	CCCTCAGTGTTGTGAACCTGT	020B1E04
AUBES2425	3455	213	13	56.8	CAGGTGGATGGATTGTGTTG	GCTCAGTATCTCTGCGCATTT	040A1B02
AUBES3030	1303	446	13	61.1	ATCCCAGTCCCGATACACAC	TGGCATGAAACAGCTTATGG	054B2A08

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5058	1358	365	13	61.3	GCCCAATATGTTTCGACCAA	CGAGCTCTCTTCTGAGTCGTC	053A2F12
AUBES2924	1116	497	13	61.9	TCCTTCACTTGACAGCCTCT	TTCCCTACCGCAAATTCTTG	045A2D05
AUBES4761	2683	240	13	64.4	TCACTCAGGCTTGACTGTCCT	TCCGGTCATGTGTTTTATCG	086B1A01
AUBES5329	3010	381	13	68.0	GCACCAGACAGATGTCCTCA	GAAATGTCACTGGTGCTGCT	051B2H03
AUBES1331	2881	171	13	71.1	AGCATCAGCATGGACCTCAG	TGCACAGTTAAATCATCACCAGC	004A2H08
AUBES1856	2410	683	13	74.7	GCTGGTTAAGGCACAAATTGA	CCCATCCCACTTTTAAATCC	036B2E03
AUBES1896	634	353	13	75.9	TTCATTCAGCTTTGCGTCAT	TGGTTTACTTGGGACCATCTT	032B1H04
AUBES2158	634	353	13	77.9	CCCCACTGAAACTATAGGAACG	AAACCCACATCTTCATTCTGC	023B2H06
AUBES4264	1354	602	13	81.2	TGTCACACTGGTGTCAAGAGC	ACGGTCTTTGGATGTTGGAC	104B2G03
AUBES2538	36	526	13	83.1	CCTCAGACTCGTGCTCCTCT	TCAAATTTCAAACGTTGACCA	049A2E08
AUBES5015	1171	296	13	84.6	CGATAGGAGCTTGCTGTTGA	CTCCACCTCCCGAAAACAT	075A2F08
AUBES2678	36	526	13	84.8	ATAAAGTTTCCGACCGCATC	TCTTCACGCTCTTCTCTTTGC	004A1H08
AUBES2977	36	526	13	84.8	CTGTTCTTTTGCAGCAGCTC	AAGCACCATTAAGGCAGGTG	083A1F10
AUBES4150	1246	572	13	88.7	ACAAGGAAAAGCTCAATCGAA	GCAAACATCAGGAAATGAAGG	021A2F08
AUBES4149	1246	572	13	90.3	CGCCTACCAAATTCACCTTC	CCTACCCAAAACATAGCCACA	067B1C03
AUBES5381	3383	304	13	90.8	TCATGCCACTGCTTCGAATA	CAGCCCATAAAGAGGTGCAT	072A1C04
AUBES5240	2391	431	13	92.1	GCCATTTCCTCCTCATCGT	TTGGTGTGTTTTTGGCTTCA	107B1A03
AUBES4118	1534	435	13	94.7	CCGTGGAGACTCCTTTCAGA	GAAGTCCACTTCAGCCATGT	067B1D09
AUBES4397	1891	331	13	100.7	CCATTAATGAGCCGCTATCC	TGGTTATCCAACTCTGCTTGTG	107A2B05
AUBES4820	3124	216	13	101.5	TCAAACGAACACAAGGATGC	TATGGCTCCTGATGTGTGGA	046A2H09
AUBES2510	singleton		13	105.1	ACGCATGACACACCAGTACA	CATTGCCGGTTTATCGATCT	048A2C11
AUBES2526	singleton		13	109.7	TGACATCCGTTTTGCTTTTG	TGTGTACATGCCCATGTGAGT	048B2F10
AUBES4604	1989	193	14	7.1	CTCACGGATGGAGCTGAGAT	CCACAAGCTGGAGGTCAGAT	074B1H06
AUBES4605	1989	193	14	8.7	CGGAGGTCATGCACAGTCT	TTATCCTTTCAGCGCCTTTC	111B1B04
AUBES2398	3189	315	14	9.6	CGCGGGTAACGATGTTTAGT	CTTCTAGAACTTTCCGCACCA	045A1E10
AUBES4467	1115	309	14	15.6	AGGACGTTCTGATCGACTGC	TGTTCTTGTTAACCCGAAAAGAG	053A2B05
AUBES5401	3475	249	14	18.0	AAGGTCACGGCTAGGTCAAA	TATCCGCTGGGCAATTCTAT	053A2B06
AUBES2433	2327	186	14	19.2	ATATCCGCTGGGCAATTCTA	TGTCTCTTCCTGTGGGGAAA	040A1G12
AUBES4783	2883	252	14	27.1	GTGAGCGTTATTCCAGACAGC	ACTTCCGGGAGGTAGAGTCC	063B2E07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3987	1955	247	14	30.4	GGAGATGGCCGAATATAAAGC	ACGTCTGCTGCTTTGCTTCT	049A1F02
AUBES3932	1344	315	14	48.0	TACTGGCAGCTTCGGGTAAT	TGCTGACATTGGAGACTCCTT	072A2F10
AUBES5037	1266	419	14	48.9	CACACAATTTTGCCCTGTGT	CTGGGAGTGGACAGAACTGG	079A1H01
AUBES4322	2043	205	14	49.7	TGCTTGTCCGAATGTGTGTT	GTGGGGTGAACCTCAAAATG	087B1H01
AUBES2235	156	294	14	50.4	GGCTTACCGAGACTAGGTGCT	TGAGGAATAGTCACTACATGGAGAA	042A2B10
AUBES4872	2508	375	14	51.8	GCCCAGATTAATTCACATCACA	TTGGAACTCCGCAAATTAGG	096A2B05
AUBES4871	2508	375	14	52.3	AGAATGCATGTCCACACACC	TCGTTGCCATTGTATTCACAG	052A2E04
AUBES2352	1324	335	14	52.8	CTCGTGTGGTCCCCAGTAGT	CCAAAAAGTAAAACTGGTTTCAGA	047A2B01
AUBES4155	1324	335	14	52.9	TTCCCCTTCCATTTCTCTGTT	AACAGATGCTGAAACCAAAGC	093A2E09
AUBES4473	1294	230	14	53.3	AGAAGTTGGGTTTGCACTCG	AGCTCCTCACTGGACCAAAG	074A2C09
AUBES4447	3090	230	14	53.6	GGATTCAACAATGAGCAGCA	CTGTCTGAAGGGATGCTGTG	033B2A05
AUBES3584	1046	502	14	53.9	ACACCAGTCTGCTCCTCCAG	CACTGCAGGCATTCTTCTCA	101A1H04
AUBES4431	3090	230	14	54.1	GGATTCAACAATGAGCAGCA	CTGTCTGAAGGGATGCTGTG	033B2A05
AUBES5278	2561	245	14	54.4	TCACAACCCAGCATTACCAA	GCTCGTGTCAACAAATTGGA	083B2G06
AUBES3585	1046	502	14	54.8	TGGGGAGAAACACCAAGAAT	CACTCCCGGTCAAAAGTTTA	106A1H10
AUBES1340	184	396	14	54.9	TGCTGGTAGGCCCAGTG	GTAGGCAGCGTTCCAGC	028B1B06
AUBES2566	1363	940	14	54.9	TCCCATGTAATTGCACCATC	CAAAGCCAATGGAAAAGGAA	010A2G07
AUBES2753	197	418	14	54.9	TCAGCCTCCCTCATAACCAC	GCACACAGGGTTGAACTGAC	046A2B03
AUBES5034	1241	222	14	54.9	CTGCCACATGGTCTGTCTTC	CTCAGTGAGTCCCTCGCTTT	102A2C10
AUBES4811	3086	193	14	55.1	GTTGGATGAGGGTCAGCTTC	GGATCAAGCTGTGGAGCACT	001B1B11
AUBES1166	345	589	14	55.1	ATACAGGGCTCGCTTCACAG	CTGGGATTACTTGCTCACTGG	008A2E03
AUBES4430	3090	230	14	55.4	ACATCCGAGATGAGTCAAACTT	GAGGGAATGACAGAGGCAAC	006B1D03
AUBES5325	2885	362	14	55.5	CATGTGTGGCACTGCATCTT	AACATTCTCCTCGGCTGTGT	101A1H11
AUBES4154	1324	335	14	56.0	CGATCGAATTGTCTGTCACG	CCTATGAAGGGAGCCAGGAT	053A2G09
AUBES5324	2871	316	14	56.4	CCTGCACCGGTACCTTCTTA	CGGCTTGTAGTTTGTTTGATG	104A1D08
AUBES5399	3472	151	14	57.7	CAGAATACGGCCCAGACATT	CAGCCTTTCTGGAGCTTTGT	087B2C09
AUBES3618	175	274	14	57.7	CCACTGTTGTGCCAAAGAGA	TTGAGACCATCCAAGAATGC	034B2B06
AUBES3617	175	274	14	57.9	CCACTGTTGTGCCAAAGAGA	CCATCCTGGGTGATTCTTACA	082A2D10
AUBES5150	1709	254	14	58.4	AGTCCAGTAGGTGGCGGTAA	GGAAAGCTGCGTCATTCCTA	040A2D03

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3435	595	394	14	58.6	ACATCCCCCTGGCTCTTAAT	TGGGAATTGGAGTAGAACAGG	095B2G04
AUBES2079	442	915	14	58.8	TCCACAACCCTAAATGTGGAA	CAGCCTGAAGAGACAAAACG	039B2G10
AUBES3214	55	614	14	58.9	CCGCACCAAACTAACAGACA	TGAGTGGGCGCTATGATAAG	105B2C09
AUBES3616	156	294	14	58.9	GGTGGCAGCTGGTTAATATTGT	AGCCTTGCTCTTTAGCATCG	054B1B09
AUBES3615	156	294	14	58.9	TGGTGATGAACATGAAACAGAAG	TTTTGGCCATAATCATGCAG	031B2A07
AUBES3254	336	291	14	58.9	AACGCATCCTCATGCAGTAA	TGACCTTGAAAATGCTGAAAAG	084B1D06
AUBES2456	526	386	14	59.8	CCAATCAGAGCAAGAAGCAA	GTGCCGAGTTGCTGACTACA	040B1F10
AUBES1112	singleton		14	59.9	ACCTGGAGCTGCTCAGCGTG	CTTGGCACTTCACCCGCCAG	
AUBES1855	1424	487	14	60.5	CTTGCCATTTCCCTGCATAC	GGGAGCAGACCAGGTAGACA	036B2C08
AUBES3436	595	394	14	61.6	GCGAGGGCAAGGAGTATCT	TGATGCACCAGAGAACCAGA	067B1F10
AUBES3426	526	386	14	61.6	TCACCCTGACATTACCTGGTT	CATCATGCTTCTGCAACTTCA	069A1D11
AUBES3549	526	386	14	62.9	TATGTGCAAGCAGCCTTCAG	CCATGAACCCATGAACTTCC	005A2C12
AUBES1922	526	386	14	63.3	GGGAAAATGCACGAGAGAGA	CCATGAACCCATGAACTTCC	036A2C11
AUBES3329	191	695	14	64.5	GACTGGGTGTAAACAGAATGACC	GCCATCAGCCATTCATGTAG	104A1E06
AUBES5339	3211	272	14	65.9	AAGCCTTTTGTTCTGTTCCA	GAATGCTATTGCCAGCAGGT	065A2G12
AUBES4982	944	438	14	70.2	CGCATCAACTTTCAGGACAA	GCACACTTCTGGTTGCATTT	073A1D11
AUBES3640	710	340	14	71.0	GTGCCACACATTGAGGAAAG	AATGCATGCAATGTCCAAGA	073B2C12
AUBES2767	446	536	14	71.5	AGGAGTAGGCGTCTCCAGTG	TTGACCATTGTTTCCAGCAA	002B1B05
AUBES4455	1700	255	14	73.2	CCATGTGCTGAGTATGGCATT	GGAGCCTCGAAGTTGATGTT	103A2G11
AUBES1965	704	524	14	74.3	TATGGCCAAGGCCGATGTAT	CCCAACAAATGGCAGGTACT	028B1B01
AUBES4361	710	340	14	75.3	GCTCAAAAGGTGAGGACTGC	AGATCGGGTTTCTGTCTGGA	034B2B05
AUBES3957	704	524	14	76.0	ACCTGATTGGCCCTGAGAC	ACCCTCGGACATATCCATCG	083A1C12
AUBES1529	1671	279	14	77.0	TGCATGCATATCCTCGTAAA	CCTTGGCAGAAGTCTGTGTG	030B2C04
AUBES1575	1240	276	14	80.1	GCCTTCACACGATGTCAAAA	TGCATGGGGAATCTTTTCAT	028A1C07
AUBES3581	1033	245	15	0.0	CTGGACAGTTGAAGCATGGA	GTCGATGAAGGAGGGAAACA	060B2D05
AUBES2891	514	502	15	2.8	GTGACCGCAGTGAGTACAGC	CCCCGAGACCCAGTAAGAAT	077B1E08
AUBES3541	140	726	15	4.6	TGCAGACAGGGAGGAGAAAT	CCTCGTCCTGCAAAGTATCC	096A1H10
AUBES1775	697	220	15	5.2	TGAGGCAATGTTTGAGCAAT	CAACCCAAAAACAAACAAAACA	034B2A09
AUBES3304	584	347	15	6.5	CAGTGGAAGCCCCATAATGT	CTTGCCAGAACAGCTGGATA	069B2A03

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3873	869	502	15	6.5	ATGGCCAGCGGTTCATATAC	CGTTCATTTTGCTGAACGAG	032B2C11
AUBES3875	869	502	15	6.5	GGCCAGCGGTTTCTTATACA	CGTTCATTTTGCTGAACGAG	075A2D06
AUBES2999	514	502	15	6.5	GTGACCGCAGTGAGTACAGC	CCCCGAGACCCAGTAAGAAT	077B1E08
AUBES1906	363	328	15	8.3	GCACCATAACCCTCCTGCTA	AGCGATGAGCTGGTGTTTTT	036B1A04
AUBES3407	363	328	15	8.4	GCCTCAAAGCCTTCTGTTTG	GATTGTGCTCCAGTCATCCA	069B2F02
AUBES3132	890	863	15	9.0	CCCATGCACGTGATATTGAT	TGGTCATGACTCACTGGACTG	108B2F02
AUBES2357	1492	228	15	9.9	CGTTGAGACGTCTTTGTTACG	TCGTTCAGCATAGTGTCTGC	047A2F10
AUBES5403	3483	240	15	11.4	CGAACGTCTTTGAGTTGTTGT	TGGAAATCTCCTTTTCCAGGT	052B1G11
AUBES2479	1097	220	15	11.4	TGTGGAAATGCCTGTTTCCT	CCATTGTCTCAAACGCTCCT	046A1F05
AUBES2404	179	340	15	15.2	CACAGCAAACTGCCTACGAT	GATCAGCTCTCAGTAAGCGACA	045A2B10
AUBES3620	208	348	15	17.5	GGAGGGGAAATGACATCATACT	CCACAAAGTTTTGGCACAGA	006A1G05
AUBES1737	958	553	15	20.7	TGCTCAGCACTGAAATCACA	AAAGCAAGCAGTCATCACGA	031A1F10
AUBES3040	958	553	15	22.0	CCCAACCTTGCCTTATGCT	AGGGGGTAGGGTTAGTGTGG	062B2B11
AUBES3031	86	288	15	25.7	TTCCGATCAGTAAACCAGCA	CACCCTGTCCAGGATGTACC	055A1E05
AUBES3937	76	463	15	28.0	GGCCGATGTCACTCTGAATA	ATCAGAGTTTGCGGAGATGG	095A1A04
AUBES5310	2728	173	15	29.4	CACGCCAGCTCTCACTACAG	GTGGACCTGGGAATAACAGC	105A2C07
AUBES2861	76	463	15	30.1	TGGGGAAGGTCTGTAGCATT	AGTGAGTATGCCCCAAGAGG	053B2B07
AUBES2522	1152	264	15	30.8	TGAGGATGTGATGGATTTGC	CCCAGCCTTAAAGCCTCAAT	048B2A06
AUBES3131	214	580	15	31.0	GCCTGAGGTTGCTTCAAAAG	GCTCTGTGCAATTTGTGTGC	102B1A02
AUBES3728	34	490	15	31.3	ACGGGGTCAGTCAGATCAGT	GGATGCAGGTGGTTACGAGT	064A1B10
AUBES3431	588	276	15	31.5	GGCCGTTGACGTTACCTTTA	GTCCCAACCTGTGAGCTGTT	045A1B01
AUBES5038	1268	230	15	31.9	TAACCAGGGTCAGAGCAAGG	TCGTCTCAGCTGCAAAAACT	080A1H12
AUBES3619	208	348	15	32.1	GGACGACGTCTCCTTCAGAT	CTGTCAACCAGTGGAGTCAGA	110A2C07
AUBES4931	567	315	15	32.1	CCACTGCCCTCACTAGCAG	TGAGGTTCACGTGCTGATTC	095A2E09
AUBES2570	2	403	15	32.2	CCATGCTGCAACATATCCAG	GCTCATGTTGGAGACGTGAA	035A2C05
AUBES3072	34	490	15	32.4	CGGGGTCAGTCAGATCAGTT	AGAGGATGCAGGTGGTTACG	030A1A03
AUBES2725	118	440	15	32.4	GACTTGCCCGAGTGTCAGTA	AAAGCGCAAATTGCTAAGGA	013B1F03
AUBES3938	76	463	15	32.8	GTGGTGGGGAAGGTCTGTAG	AGTGAGTATGCCCCAAGAGG	061A1D11
AUBES3965	1602	289	15	33.0	AGCCTGGCTCTACACTGGAC	GAACCTTTCACCGCAATGTC	086A2B10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2903	671	541	15	33.2	TGTGCCCTATGATGGGTTG	ACCTTCTGCCCATTGTTCAC	043B2D09
AUBES3506	28	474	15	33.5	TCTTCCCTGTTTGAGGCACT	CCAGGAAACAAAAACGATGG	054A2E04
AUBES3071	214	580	15	33.6	TTGTTGGGAAACACTTCAACAG	AGCCTATCCCAGGGGACTC	020B1A09
AUBES4240	924	294	15	33.6	GCAAAGACCCCACTTCTGAG	ATCGGCAATTAACGGCACTA	110B2H01
AUBES2943	256	511	15	33.9	AGCTCCAGGGCTTCTGATG	TATGAGCCAAGCACTGCAAG	006A1D11
AUBES1912	323	585	15	33.9	GAGCAGTGGCCATTTTGTTT	GAAATAGATTGGGGGAAGGA	036B1D01
AUBES3265	671	541	15	33.9	TGTGCCCTATGATGGGTTG	ACCTTCTGCCCATTGTTCAC	079A1F03
AUBES4124	818	338	15	33.9	AGCAACAAATGGGGTGACTC	TGTCTGGACAAAGGATGTTCA	095A1F07
AUBES2752	187	529	15	33.9	GCCAGCACCCTTACAGACAT	CCTCTTTAGGCTCCAGCAGA	047B1C07
AUBES2391	588	276	15	33.9	CGACTGACAGCGGAGATTT	GTCCCAACCTGTGAGCTGTT	045A1B01
AUBES3354	116	621	15	34.0	ATCGCCCCAACTTTCGTTTA	CTCACTCTCGCCACGTGATA	063B1C11
AUBES2599	116	621	15	34.0	AAGGGCCTTTGTCACATGAT	CACTCCAGTTTCTGGCCAAC	022A2D11
AUBES3100	104	852	15	34.1	CCTGAAATCTTTCCTGTTTTTG	GCGGTCATGTTACCTTTGGT	098B1D06
AUBES4621	2156	237	15	34.1	TGTTATGTGCCTTCCAGCAG	GAATGTGCAAATGCAAGCAC	014B2H03
AUBES3191	116	621	15	34.4	CCCCATACAAGGTAAAGTGCT	CAGAGGCAGTCAGCTTTTCA	031B1B09
AUBES2622	104	852	15	34.4	TGGTCGAGGTCATTTCTCATC	CAGTAGTTTTAGGCAGCACGTT	014B1B09
AUBES2581	214	580	15	34.6	TGTGTAATGGGATTCTCATGC	CCTCGTGTGGCTAAATGTGA	066A2G10
AUBES2469	116	621	15	34.8	GACTTGTGCCATGGTTGTTG	TTGATGAGCCTGTTCCCACT	040B2F06
AUBES3432	588	276	15	35.0	TCTGTCTCAAATGCTCGGTCT	GTGCCAAATGTTCAAAGCAA	068A2H05
AUBES3736	818	338	15	35.1	TTTCACAGCTTTCTCTGCTCA	ACCCCACTGTGAAATCCTGT	076B2B08
AUBES3158	104	852	15	35.4	CGGTGATGGAAATGTACACG	CAGTACGGGGAAGTGTTTTGA	082A2C10
AUBES1728	657	424	15	35.7	TTGGCCTCTAAATTTGTGCTC	GCATGAATGAGCTCACAAGC	023B1C08
AUBES1733	104	852	15	35.8	CGCATCCCAGCGTACAATTA	AACTGACCGGAACTACCTGTG	027A2E05
AUBES2881	323	585	15	36.4	TGTTTGCCTTTTGAACCAGA	AAGGCAAATTGATGGATGGA	058B1E12
AUBES1936	1471	215	15	36.7	CAGTGGGGCTCTGTCAAACT	GTGCACTATGGGGATTTCGT	036A1D09
AUBES3507	28	474	15	37.4	TGGCTTGAAAAAGCCAACAT	CAGCCCGAAGGACTGTTTAG	061A1B09
AUBES5265	2515	370	15	40.0	GCATTATTTGTGCGAACGTG	CGGTAAAAATGCCAGGTGAT	102B1A01
AUBES4848	1719	419	15	40.9	GTTGGCATTGTACACGTTCG	CTTCGACGGTGAGGACTTTC	009A2E07
AUBES4208	648	338	15	41.8	GCATGGAGACACTGATGGAC	TGCAAATTACAAGGTGATTCCA	069A2D05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5379	3374	215	15	42.7	TGTCCGCATCTCATGTCATC	ATTGTGCTTCATGTCGCTTG	087A1C06
AUBES3314	717	472	15	42.9	TTTGGCCCAATAATTTTGCT	CGTTTCCACTTCCGCACTAT	112A2A07
AUBES1571	singleton		15	44.1	CACACACACATTCCTTTCCAA	GAGGGGTTCAGAGCATGTTT	024B1C02
AUBES3835	1919	311	15	44.7	GTTGGCATTGTACACGTTCG	CTTTTCACGGAGCCAGATGT	111B2D10
AUBES5363	3293	250	15	46.0	CGTAGTTTGGTTTTCGTTATAGG	CGATATGAACGCGAACATTAAA	013B1A01
AUBES2783	950	666	15	48.6	GCCATACTGCCCACCCTATC	ACATGGTGACGGTGATCTGA	076B2G02
AUBES2831	717	472	15	49.2	CCCTCATTGCTTGTTCTTCG	CCAGTTCCTCCTGGTGCTAC	009B2C01
AUBES5215	2263	218	15	49.4	ATGGGACATGATTGTTTGTTTG	GATGGAAGGAGACCTGGACA	038B2H05
AUBES4030	1349	345	15	51.6	CAGTTGCCTCACACTTGAGC	CTCTGTACCGCTGCATCTGA	104A2F05
AUBES4739	2350	225	15	57.6	AAACGTTTCCTGTTCAACGTC	GGACTAGTTATGGGGCAGCA	079B1A10
AUBES5223	2316	178	15	64.1	CGATCCTCCAGGGAACTACA	GCTGTTTCCAGTTGGTACATGA	108B2B03
AUBES2344	singleton		15	69.5	CCTGCAGAAACACAAGCAGA	CTCTTGCTGATGGTTCCTTTC	047A1D12
AUBES4329	2146	298	15	83.2	TGGCTCAGCATGTTTTTCAG	GCTTCAGCACTGTGAGATCATT	011A2F06
AUBES5358	3282	225	15	93.4	TCGCCAATATATTACAGCATGAA	TGCTGGATCAAGTGCTATTCT	032A1B05
AUBES1869	singleton		15	93.7	TTGCTACAGCTGAGGCATGT	GAGCCGGGTTACACCTAACA	025A1E08
AUBES2910	1100	397	16	0.0	AAAAGAAGCGCCAGACTCAC	TCAAAGGAAGGTCTCACAAGG	054B1E02
AUBES2679	1100	397	16	11.4	CACGTCCCACATCTTTCACA	TGAATCAGTGGGCATTCAGA	004B2B07
AUBES5243	2400	291	16	12.9	AGTTTTCGGTGTATCGCTTG	AGGCATGTGGCTCCAATTA	057A2D04
AUBES3586	1062	480	16	14.3	TGCGCTCAAGAGTTGCACTA	TGGAGATGCATTGAGGAGAA	096A2G09
AUBES4305	1914	387	16	15.8	TTCTGTGGAAGCCCTGAACT	AGGTTCCACTGTGACCCTGA	054B1F03
AUBES3587	1062	480	16	18.0	CGCCAATCATTCTGGAGTTT	CACTTGGCAGCATCAAGAAA	075A1E10
AUBES4629	1956	489	16	18.1	AGGGGGAAGCGACATGATTA	ATGTTTGCCGATTACAAATGG	096A1G08
AUBES4799	3014	196	16	18.1	CAGTACTCGTCGTTGGCATC	CGGGTGGAGAGAGATTGTGT	104A1B10
AUBES4628	1956	489	16	19.8	CCTGGAAAAGTTTGGGAACC	TCTGCGTGCTTTTGTTTTGT	058A2E09
AUBES4445	2920	269	16	24.4	CACAGCGAGATTCCAGATCA	GACTTGGGACACGCCTTTAAT	055A2B08
AUBES4429	2920	269	16	24.4	GCCATCCCAAACGTGTACTT	GCCAAAGATCGAAGGTGAAA	055A2B08
AUBES4428	2920	269	16	24.4	CGACAAAAACAAATCCGATG	GGAAACGTGCTAACCGCTAA	038A2D02
AUBES2072	singleton		16	30.5	CCGAATTTGCATCTTTCACC	GCGCACACACAAAGAGGTAG	039B1H02
AUBES4835	3193	132	16	37.1	ACTGCAAATTGCTGCGGTAT	ATTTGGGTGGTGCTTCATTC	004A2G05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2431	singleton		16	45.1	GTCACAAAGTGTCGGTCCAG	GGGCGAGTGTGAAAAAGTGT	040A1E02
AUBES2488	singleton		16	46.0	TCCTGAAGGGAAATATTCCTGA	CCGAATGTAAATCGCATCAT	046B1B06
AUBES4314	1947	198	16	50.4	AGACGGAGCAGAAACAGCAG	GCTTGCAATTCTCTCACACC	102B1C11
AUBES1374	1051	306	16	50.6	GAGCTGAGCTGAGCTGC	CTCCCGCACAACAGACG	022A1F10
AUBES5375	3354	250	16	50.9	GCCTCCTGACCAATCACAAT	TCACGGTGCTCAAGTACTGC	052B2B09
AUBES3014	435	465	16	54.6	CCCAAAAATCAGAAGGCAGA	GATGAGACCGTGGCTGAACT	040B1A03
AUBES4818	3116	100	16	60.9	GTCCAGGGCTCGATTATGTC	AGGAGAAAACGTATCTGCCAAT	092B1B11
AUBES3366	442	915	16	63.4	GTTTCGGCAGACCAATAGGA	CCACCATTGCCGTCTAAAAC	095A2C07
AUBES2749	132	675	16	64.0	CGTTCAGCAATAAAACGGAAT	CCAAACTCTGACTGAGAGGACA	023B1A06
AUBES1950	singleton		16	64.2	CTACACCATGAAGGGCCAGT	CTGGCCACAGAGCAGAGAG	003B1H09
AUBES2758	332	480	16	64.3	AAGGCATCAGGATGGATCAG	TCCCTGCTTGATTTAGCACA	041A1G04
AUBES3562	761	348	16	64.8	AGCTTGTGGTGGCCTAACAG	ATCATCCCAGACCCAAAGGT	105B2B07
AUBES5115	1537	161	16	65.7	CTGAGTTTGCTGGATTTTGG	TGTGAATGGACCTTCTTGGA	078A2D07
AUBES3915	1079	330	16	66.3	TGACCCTCTACTTCCCTCCTC	TGAAGACGGACACTGGAACA	106B1C04
AUBES2620	101	927	16	69.5	TTCACCCTGCCATGTGATTA	GGGTGGAGTCTTCCTTTAACC	032A2D10
AUBES3723	435	465	16	70.8	TGCATTCATTGTTGTATCATTCTG	AATGTTTTGGGGAAGCACCT	049A1H06
AUBES2611	241	913	16	71.2	GATGGGTGATGAGGGTATGC	GGGTTCCTAAAAATGAAGTGGA	070A1A08
AUBES2274	241	913	16	71.6	GGTTGCATTCGATTTTTCCA	TGCTCCAAACTGGAGGAGAT	043B1E12
AUBES3783	1813	331	16	71.9	CTCAGTCTTGCAGCATCAGG	TTTCTCTTCCTCCTACCCCTCT	077B1D03
AUBES3919	1145	279	16	72.3	GTACACCCTGAAGGGCTTTG	CAGAATTCAGAAAGGCTGTGC	008A2A10
AUBES4808	3079	245	16	72.4	CTGTGTGCCTGATTGTCTGC	TGTGGCATAGAGTGCTGCAT	021B1E12
AUBES3224	101	927	16	73.1	TTGGTTTATCTGTGGGTAGGAAA	TTTCGCAAACTTTCAAGCAC	035A1A12
AUBES2387	153	416	16	73.1	CTGCTACTTTCACCCCGAAA	CACCTGCACCAGAATCACAT	044B2A11
AUBES3023	621	441	16	73.2	AAACGGATTTCAAGCAAGAGA	GGGGAGGTGTAGTAGGAGGA	051B1C07
AUBES3196	101	927	16	73.2	GCCTCTGGGTGAGCAAAATA	ATGGCCAAACAGAGACAGGT	006A2C06
AUBES3362	241	913	16	73.3	CAACCTCATGTGGGGTCAC	GAGAGCGTGTTGGACTTGGT	084A2F05
AUBES2069	singleton		16	73.3	AGCTGTGATCGTCCTGAGGT	AAGGGGCTTGTGAAGAAAGG	039B1D03
AUBES3861	342	272	16	73.3	CAGATTCAGTGTGATGGTGGA	GTACGGGGACAAATGCAATG	034A1G04
AUBES2632	45	1120	16	73.3	GGAGCTCTGTGAAAAGCTGTG	GACTTGAATCGCTGGGTGAC	074A1C04

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2786	1185	509	16	73.3	CCAAGCACTGAAGGTGCATA	ACTGCCCTCTATCACTGTGC	051A1G04
AUBES3368	101	927	16	73.3	CACATGGGTGTTGGATCACT	GCTGCTACTGAAAGTGCACAA	074A2D05
AUBES4910	299	228	16	73.3	CATGGACAGTGCACAAAACC	AGCCACAACTCGTTCCAAAT	069A1G11
AUBES5360	3285	184	16	73.3	AGCCACCGCTTCCTCTTAAT	GACAGGGATAGGCTGGTGTG	057B1F09
AUBES3151	241	913	16	73.4	GAGGATGCAGTGAGGACACC	TGTGCACCGAGTGTGTTGTA	111B2G05
AUBES2397	4	348	16	73.4	CTGATTCACCCGAGGAAAAA	ATAAAACCACGCAGGAGGAG	045A1D11
AUBES4883	685	215	16	73.5	GCAGGGTGATCACAGATGAA	TTGAAAATCTGTGTAGGCATGG	064B2C11
AUBES3348	38	702	16	73.7	ACATGCCTTAACCTCCCACA	CGACCTGTCCTTTAGGCAAC	068B2A02
AUBES2594	38	702	16	73.7	GCATAAATGTATGTGCCCTGTC	ACCATGGTGAGCAGAAAAGC	018A2A12
AUBES3249	153	416	16	73.7	CGTGTCCAATCCAGTAACCA	TGCCCTGATTTGTGTGTGA	040B1D07
AUBES1876	38	702	16	73.7	CCAGCTGAAGTGAGATGGTG	GGTGCTGAAGTGCCAAGACT	026A2A04
AUBES3353	6	633	16	74.2	GCCAGGATATCTCGCTTACA	GTGCTTCAGCTGCTTCAAGA	070A2A05
AUBES4234	833	411	16	74.2	TGAGCTTGGATCAATGTATTCC	TGACCCCTAAATCATCCCCTA	011B1E06
AUBES3219	6	633	16	74.2	CACGGCAGACCTTAGCAATA	CAGAGCTGCTGCAACGTAGA	045A1A06
AUBES3190	6	633	16	75.1	CCCTTCCCTATGACCTCCTC	GGTTAAGAGGATTTGCATCCAT	059B2A04
AUBES4948	662	277	16	75.3	CATATCCCAGCCCTCAGTGT	CACTCCACTTCTGCAGCCTA	053A2B07
AUBES4905	235	240	16	76.2	GACAAACACTTCCTGCTATCAGTT	TAAAATTCGGCCTTGGGTCT	109B1A08
AUBES2588	169	715	16	76.5	TGGTTAGTGTGAGGGGTTGC	AAACAACGTTGGTCCTGTCC	012A1C10
AUBES3788	430	328	16	77.3	CAACAGAATAAACGGAATCATAAAGA	CACATGTTTGGACATGCAGA	021B2C05
AUBES4806	3074	271	16	77.3	GTGTCCCCTGTTACCTGTGC	GGGTAGTGGCAGGATCAATG	092B1G12
AUBES3637	644	335	16	77.4	CACCTGAGAGATCATGAAAACA	ACACCGGAACTGTCACTGGT	105B2F04
AUBES1886	644	335	16	77.5	GGCTCTTGACCTGAATTGTG	GTTGCACTTGATGCAAAGGA	029A1A12
AUBES3112	9	2006	16	78.1	CGCCGCAAATTTGGTTTAAT	TTACATCCAGCACGCACAAT	109A1B07
AUBES5022	1199	200	16	79.5	GAGTGCATTACTTTGAACCTTGC	CACAAACTGCCAGCAATACAG	051B2E09
AUBES5145	1689	233	16	80.2	TCATGGATGCAAAGGCAATA	GCAGCGTCACTTAAGCTCGT	106B2H02
AUBES2978	38	702	16	81.5	GATGCCAAACCCTGTAGAGC	GCGTTTGAGCATGTGTTTGT	100B1E07
AUBES2940	160	375	16	82.5	GTTCCTGCCAAATTTCCAAC	CTGGGCTATGAGGAACAAGG	012B2H06
AUBES2877	245	426	16	83.2	TGAGATGGGTTGACATGTGG	GGAAACAAATGGGGTTATCTCA	033B1A05
AUBES1852	46	335	16	83.5	GTGTTTTGGGGGCAGAACT	TCTTTCTTGGGTCATCAATCC	036B1G09

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES1096	singleton		16	84.4	GTCAAGCACATGGCATGACC	AATCTGCCACTGCTGTTGAG	010A2C11
AUBES4954	694	225	16	87.3	CCCTGCTATTCCGCAGTCTA	ATGTTTCGATTAATGAGATGAGG	102A1A11
AUBES5210	2209	240	16	92.4	CCATGGGGTGTACTTATTTTTCA	CCTGCAGGACCTTCATGACTA	013B1A07
AUBES4534	1977	233	16	97.5	CATTGCACATCAACAAACCA	CACGGAATTCGTGACAAGTG	004B2A08
AUBES4433	900	218	16	102.8	TGACTTTGCATTCTGTCTTTTC	TCGACTCGTCCTCTTTTTGG	108B1H01
AUBES4432	900	218	16	103.8	CGAGTCCTCTGGGAAATGAC	GCAGGAGCAAACAGACTTGG	033A2F03
AUBES4965	824	252	16	105.9	GTGTTCAAACCCCTGCTCAT	ATTGTGTCCTGCTGCTCAAT	004B2H03
AUBES5383	3398	90	16	109.5	CCCTTTGGGACCACTATCAA	CGACGGCAGATAAATCCAGT	047A1B11
AUBES4063	445	342	16	111.6	TAACGGTTGTGGGAGGAGAC	GGAGTTGGGGAGGTCAGAGT	006A2C12
AUBES4415	2476	279	17	4.1	CGGCTGGATCGTTAAAATGT	CGCGTAATGATCCGGAAA	030B1H05
AUBES3213	58	631	17	4.2	GTCTACTGCCAATCCTTAAGAGC	GCTCCTGCATCGGTAAAGTC	030B1E04
AUBES3742	790	651	17	4.6	TGGTTTGTACCCATGCTTCA	GTGCTCCTGTCACTCACCTG	087B1D01
AUBES1536	1027	448	17	4.6	TCCATGGGGTGTACTTGTCC	TGCTGGCTGTAATTTGAACA	029A2A02
AUBES4853	1761	266	17	4.6	CCCACAAAAACACACACACAC	AATCTGTCCGTCTGTGATCG	011B2E06
AUBES4969	856	348	17	4.6	AATGGGGCTGTTATTCCAGA	TGCTCTTTGGGAATCCTCAC	062A2C09
AUBES2616	885	1133	17	4.7	ACAAGCCTCGTGGTATGCTC	GCATTGGAACCTTTGTTTCAG	057B2F02
AUBES3222	885	1133	17	4.7	CCGTTGAATTATTTCACTCACAA	TGACCGGAGCTTTATTTATGC	031B1C07
AUBES2974	1650	421	17	4.7	GGTGGGAATACACCCTGGA	TGCACATTCTCCTCTTGTGC	002B2F08
AUBES3300	499	455	17	4.9	TCAAGCACCTATTAGTCTGCAA	TGGGTAATCTCATCGGACAT	064B2G07
AUBES1550	1938	201	17	5.2	GCGTGGCAATAATATAGATGTCG	AAGGAGCTGAGATCTGCTTGG	027A1F04
AUBES4664	386	277	17	5.3	AGAGGGCTCAGTGTTGTTGC	CCTCACTCACCTCCACACCT	073A1F06
AUBES4185	231	582	17	5.3	GCCACAGATTCCTCCTGAGA	GGACCAGACGTGCTCTTGTT	084A2F12
AUBES5035	1247	242	17	5.3	CACGGCAGACACTCAAAGAG	GCGGTTTACCTCGGCTTTA	062A1H05
AUBES3085	13	585	17	5.3	CAGCTTGGCAATTTATGAGG	ACTGCGGTGACACAAATGAA	020B1D09
AUBES2604	13	585	17	5.3	TCATTGTCTTTAGACTTGCTTGTAATG	ATACCCCAGGGAAATTGGAC	014A1C04
AUBES3168	139	1167	17	5.3	GACGCAGCGGAATAACTGA	CATTACGCTCCAGCCAGAGT	107B2D09
AUBES2636	139	1167	17	5.3	CAACGCGTGTATGCATTGTT	TGATAAATCCCACACGTTGC	035B2G10
AUBES4663	386	277	17	5.3	TGGAATCCAAGACTTTGTGG	TCTGAATCTGGCAAAAGTGC	011A2G06
AUBES2659	393	286	17	5.3	GTGTCAGTGCTTTGCAGCAG	GGAATGTGTGCAAAACAAGC	005B1F07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3551	604	323	17	5.3	GCACATGTGACTCTGATCGT	GCTGGTTTCCTGAAGGTTTG	109B1C07
AUBES2730	750	445	17	5.3	GAACAGCAGCGCATCAAATA	GGTGGACACCAGACACTGAC	021B1B07
AUBES3221	885	1133	17	5.3	CAGCTAACCTGCACAGACCA	CACAGCCAACAATGAGTGCT	104A2D04
AUBES2466	1034	309	17	5.3	AGTGGTGTTGGGGGAACAAT	TCCCCATCCACCACATAACT	040B2D11
AUBES5083	1453	282	17	5.3	CACTGTTCACCCACAGCAAC	GCAAACTGGATGTCTTTGAGAA	032B1B01
AUBES3609	1575	313	17	5.3	GCCTAGACGCCGAAGAATTT	AAGTCCAACCTAGATACAATAGGC	013A1F04
AUBES4375	1575	313	17	5.3	ATCCACAAATGATCCGAAGTG	CCGAAGCACTAACAACAGCA	008A1B11
AUBES4320	2017	191	17	5.3	GAGAACACGTGCTGAAAAGC	TGGCTGTAATTATCCGCTCTC	072B2C03
AUBES4416	2476	279	17	5.3	ATTCCAGCCACAATTCCTGA	GCCTTGGACTTGCAGCTACT	112B1F04
AUBES5135	1644	276	17	5.3	GAGTGCCTTCAGGTTGCCTA	AACATTTCCCACTGGAGCAC	071B1F09
AUBES3379	9	2006	17	5.3	ACCCTTGTTCTGTGCAGGTC	CCTTGTGCAAACACAACAGC	081B2D08
AUBES4896	24	304	17	5.3	CGGTTGCAACACACTCAAAG	CCAGCCCACTAGACAAGCAT	096A1C04
AUBES2750	151	585	17	5.3	TTGACAAGGGAAATTCACACA	CTCATTTCCACAGTCTCACAGA	062B1B09
AUBES1704	361	196	17	5.3	CAACATTCAGCCAAAAGCAA	GGAAAGAATCCCACACCTGA	033B1H02
AUBES4512	394	416	17	5.3	TGCAGTCCATCTCTGGAACA	GCAGCTGGAGTTTCATCACA	078B1F09
AUBES2121	726	746	17	5.3	GAGCAGTATTGGGGTCCAGA	TCTGTTTGCTGTTAAGTCATTGC	018B1A11
AUBES2605	726	746	17	5.3	CACATCTCATAGCCTCATACATGG	TGCATCTGCTTCAGGTGTTC	062A1F10
AUBES4242	1012	306	17	5.3	CGGCCTCTATAGGCGAAATA	AGGAGATTTCCTCCCCTCAT	072B1E11
AUBES4009	1150	161	17	5.3	TCATCCCATCAACTCTGCTG	GATCCTGGTGGTGTCAGAGG	063A1C02
AUBES3924	1165	208	17	5.3	GCCAAGGACCACTCAGAAAG	TCCATTGGTTGAGTTCCAGA	096B1D10
AUBES3779	1449	396	17	5.3	GAGTGTTGCTGGGGTAGCAC	GGTGGGCTGTGAAATTCAGT	042A2B12
AUBES5082	1452	338	17	5.3	CTGGCTAAAATGCATGGTGA	AGCAGGTCTGATTCGCAACT	031B2C01
AUBES3466	1509	375	17	5.3	GCTCTGTTAATGACCCGTGAA	ATGACTGCCGCTCACTGTAA	060B1H03
AUBES2054	1917	167	17	5.3	CAGCCGTGAGGTTCAGTCTA	TGACAGCCATGGAATCAGAG	039A2C09
AUBES4402	1988	203	17	5.3	CAGCTCTGAGCAGACACACA	CTGTTTCCCTCCTTTCATGC	020B1D12
AUBES4323	2065	201	17	5.3	TTTTCATTTCTCAGGGTCCAG	CCCTTTCACTGTCAAGCACA	044A2A06
AUBES2108	2205	188	17	5.3	TCATCGACCAGGACAAACAA	GTGGATTGCTCAGGTGTGTG	041B2A11
AUBES5233	2367	281	17	5.3	GGGTCGGTTAAAACACAGGTT	AAACAGCCTATAGCATCCTCCA	070A2E10
AUBES4750	2592	235	17	5.3	GAAAGCAAACAAAGGAAAAGG	GAGCCTCTCGTCTGAGCACT	049B1F10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2417	singleton		17	5.3	TGCTGTATGCTTCAAAATGAGC	CAGTGTTTTCTTGTGATGCTGA	045B2B04
AUBES3347	454	550	17	5.3	CCATGGGATTGTGAAGTTGA	CTGCAAGGCCCTTAACACTC	110B2F02
AUBES2955	756	399	17	5.3	ATCATTTCCAGAAGGCCAGA	TCGCCGTGTACAGTACCTGA	030A1F09
AUBES3583	1034	309	17	5.3	CATGCTCAAGCAATTTTTGG	TCATTTCAATCTTCTGCTTTCTG	061B1A01
AUBES3374	50	1049	17	5.3	CCCCTTTTCCTTGCATTACC	TGAAGTGCTGCTTGAATGGT	098A1F11
AUBES2392	2065	201	17	5.3	AACATCCTCAACTCCACAGAA	TTGAGCATAACTGTAGGGAAAATG	045A1B05
AUBES3579	987	326	17	5.8	GGGCAGGCCTAATTTCTGTC	AGGAGACTTCGTCCGGAAAT	004A1B07
AUBES3947	180	890	17	5.9	GCACACAAGCCTAAACATGC	CCCAAACACCATAACAAGGAG	008A1C09
AUBES2567	790	651	17	5.9	TGGCTGATCGGTGTAGAGC	TACTGGCAGTGATTGGCTGA	038B2F10
AUBES3454	997	338	17	5.9	GAACAGCTTTCGCTCATTCA	CGTGAAAAATTGCCGGTATC	006B1D09
AUBES4403	1988	203	17	5.9	TCAGAAAGCTGGGGAGAAAA	GCATCGACCGAATGTAAGTG	075A1B04
AUBES2873	180	890	17	5.9	ACACAAGCCGTAACATGCAG	TCCCAAACACCATAACAAGGA	051A1A12
AUBES4279	1668	250	17	6.0	TTTCAGATGACACCAATTTCAA	ACAAAATCAGCAGGGGATCA	005B2F10
AUBES3437	604	323	17	6.1	TCACCCATTAACCAGCACAA	CTTCCAGAGTCGGTTCCACA	108A1E08
AUBES4884	688	266	17	6.3	CCCATGCACATCAGAACAAC	GACCGAGCATGAGTGCTTGT	039A1C05
AUBES4909	289	386	17	6.7	CCCCAAAGCCATAGGACTAC	GGCAATTGATTTGCTGCATT	083A1B10
AUBES1982	singleton		17	6.9	AATGACGACCGTGATGACAA	TTTCAAGCTTGGTAAGCACCT	022B2G10
AUBES3346	454	550	17	7.1	GACCATGGGATTGTGAAGTTG	GCCCTTCTGCAAGGTTCTTA	045A1G03
AUBES1916	219	423	17	7.2	CAGGGCACTGCATAGCATC	GGCCCATTTGTATTTCTTCTCA	036B2H10
AUBES2267	1034	309	17	7.8	GTGCAGTGGAGCAGCAATAA	CAATGACCAGGAGGGTTTGT	043A2F03
AUBES4369	987	326	17	8.5	CCAGGCCAGAAGTCTTCATT	TGCAGCTGGGAGCTCTTATT	007B2A05
AUBES3465	1509	375	17	8.7	AAGCTGAAGAGTGCAAATGAGA	TCCTTGAGCTTGTGGAAAGG	011A2B06
AUBES2002	579	479	17	10.3	CGATAACGGGCTTAATCTGC	CCTGTTAACCTTTGCGGTTC	028B1F05
AUBES3580	987	326	17	12.1	GCACTGGGCTTCTAGTGGAC	GTGGCTTGAAAGTGGGAACT	007A1A04
AUBES2930	1444	531	18	0.0	TGGGGCATTTGTTCCTAAAG	GGTGTCACAAGGAGGGAGAA	053A2E12
AUBES5251	2435	205	18	0.6	GTGAGGGTTTGTGTGCGTTA	GCGCGCTACATTTACTTCCT	063A2C09
AUBES2067	901	485	18	3.3	GGAGGCCCTAAGCTTCATTT	TTTTGATGGGGGACATTGTT	039B1B08
AUBES3449	918	533	18	8.7	GCGAATAAAGCACTGTTTCCA	CCATAAGACGACACGCACAT	102A1C09
AUBES3552	918	533	18	8.7	CCCTGCTGATAGGGATTTTG	TGAGATTGGATGCAGGTGTG	013B2F08

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4933	573	355	18	9.6	TGTAAATGAGCAACGCTGGTA	AGCCCAATATGCTGCTTTGT	063B2A09
AUBES5314	2739	271	18	9.7	CGGAAGTCGGTTTTCCAAAT	AAACTCAGCAAGTTGCATCG	053B1D12
AUBES5390	3417	225	18	9.7	TCATCCCAAGACAACCTGAAC	GACCCCTTTCCCAGATCAAG	088A1D10
AUBES2968	1267	543	18	11.8	GCATCGTGCTGTAATGTTCG	AAGTCGTGCCGGCTAGTTC	022A1H06
AUBES4183	168	381	18	12.6	GACTGCAGGACACCCCTTC	GCACTTATTGCTCATGCTTCC	109A1B04
AUBES1325	168	381	18	13.5	GTTTAGTCGCATACTGTTGCTCAC	AAGAATCACAGCCCAGATGC	027A2B01
AUBES2650	168	381	18	15.3	CGTGTAAGTTGCGGGCTAGT	GGCAAGCAGAAATCTCCAAA	022A1G08
AUBES5345	3231	184	18	18.7	GCAGTGAGCTGATGAGGATTC	TGCGCATTAAAATTTGCAG	074A1F10
AUBES5333	3122	216	18	19.2	CCAGACAGTTCTATGGGCTACC	TGATTTGGGGTGGTAGCTTG	108A2D02
AUBES1619	3375	260	18	20.6	CACCGGAGACAATGTACTGG	GCGAGATACTGCCGTTTGAT	020A1A11
AUBES4260	1253	374	18	25.2	GCTAAAACTGCGCTCACACC	AGCGGCACATAGATCAGTCC	049A1D06
AUBES4182	168	381	18	25.7	ACCGACTCATGACCTCACAG	CCGAAGAAATCGGTGGTAAC	082A2E10
AUBES2900	632	474	18	27.6	GGACTGGGTGTGTTGAAGGA	CCCCCAGTCTTCCTGATACC	030B1B01
AUBES2696	893	666	18	30.3	TGGTTTGCATCTTGTGGTATG	GAAAGTGCTTTCACATATCATGC	019A1H02
AUBES3785	18	306	18	30.4	AACAGCTGTGAACTCTCTCTGTGT	AGAGCACGAGCGTGAGCA	072A1C06
AUBES3361	222	688	18	30.9	TGATCCGGGGTTGTGTATATC	ACCCTTTCCATGCAAGTGAC	104B2F03
AUBES2826	564	345	18	31.7	TGTGCAGGTCACGCTCTATC	TACTGCTCAGAGCGGAGTGA	052B2F12
AUBES3303	564	345	18	32.7	TGTGCAGGTCACGCTCTATC	CTGCTCAGAGCGGAGTGAAT	052B2F12
AUBES3391	200	654	18	32.8	TGTTTAAAGCCGGATGTCCT	CCTGTCCTGATGACAAACTGG	088A2D01
AUBES4051	133	289	18	32.9	TTGTGTGCAATTCAGGAAGG	TGGATATTTGGGACAAAAAGA	087A1G07
AUBES5374	3352	196	18	33.4	AATGCAATATGCTTGACAACCT	TGCATATATCCACCTTTGCTT	022B2D10
AUBES2608	222	688	18	33.4	AAGGTGACTGGATCTTCCACA	AGGTTTTGCACTGTGCTTTG	047B1C06
AUBES4912	309	311	18	33.4	GGGGTTGTACTTTGTTTTGACC	CCCTTGTTTCTCTTGATTGGA	012B1G05
AUBES4682	2844	147	18	33.5	AGCCGGCTAGAATGTTGCT	TTGCATTCAGCTTTCCACAG	051B2B05
AUBES2932	63	189	18	33.5	CAGTGGATTTTGTGGCAAGA	TGTCATGCTTTGTGGGTCTG	010A1C06
AUBES2812	218	252	18	33.5	CGTGGGGGCACTATACAAAT	GCTAGACGAGCTCCGAGAGA	054A2F10
AUBES1539	632	474	18	33.5	CTCAAGACACGGTGACCAAA	GAGGCTCACTCCTCCATCTG	030B1B01
AUBES3310	673	318	18	33.5	TGGGTGATTGAGTGGAGTGT	TTCCGAAGAGCTAAAAGGTTGT	100B1A07
AUBES5242	2398	151	18	33.5	ACATGCCAGGTTGGTTTGTC	TGGGAAGTTTTCCTGCATTC	043A1G05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5271	2536	222	18	33.5	CAATGTCGTGAAGACCATGC	CACAGTTATGGCGTGAATACAGA	080B2E10
AUBES3415	406	298	18	33.6	ACGTGGGCCTCTGTAATCAG	GTCTTGCATGCTCAGCTGTC	075A1A08
AUBES3414	406	298	18	33.6	TTGACCCAGGACCTCAGTG	CTGCTTAAGAGCGAGGAAGC	104B1E10
AUBES5389	3412	198	18	33.6	GTGCAGTGCGTGTTCAGTTT	CAGCGTCTAACAGCACACAAG	087B2B05
AUBES3689	603	443	18	33.6	ACCTTCTACCACAGGGAGCA	CAATGCGTATGAGGAATGGA	058A2E08
AUBES3263	603	443	18	33.6	ACCTTCTACCACAGGGAGCA	ATGCGTATGAGGAATGGAATG	058A2E08
AUBES2501	274	612	18	33.6	GCCATGCGTTCACATGTATT	TGGTTCATGGCCTGTGTATG	048A1C01
AUBES1772	singleton		18	33.6	GCATTTTCTAAATGTGGCGTAA	CAACCCTGGTGGGGTTAATA	033A1H10
AUBES1768	1050	359	18	33.7	TCTCAGTTGAGCTGCTGCAT	TATCCCACCCCTTCACAAGT	034A1D04
AUBES3208	274	612	18	33.9	TCATGTCAACAAGCGGTCTG	TCAGACGCTGCATTTTTCTG	077A2D04
AUBES3161	200	654	18	33.9	CCTTCATGGCTGAACAGGAC	GCAAAACATGTCCCACCATT	112B1A02
AUBES1980	641	477	18	34.2	TCGAGTAAATGATGTTAGCTGAGG	TGGCTATAGTCAGGGGTAAGAGA	022A2G07
AUBES2549	2481	296	18	34.4	AATCCCGCATCTAACCGTAA	TTTACACATTTCTGATGGAAGGAA	049B2D01
AUBES3088	222	688	18	34.9	ACGGAGTTCGCATGTTCTCT	TGCTCACGATGGCAAGTTAG	073A1D03
AUBES4285	1662	320	18	37.0	GGTCTTTTCTAGATCGGTGTGG	TGCTACGTGGTTTGACCTTG	064A1H11
AUBES5018	1181	325	18	39.5	TTCGGCATATCTTTTCACCA	GCAAAGTTGTAAACTGAACAAACC	087A2A04
AUBES4615	2115	225	18	39.6	TGCAATTTCAGGACAAACCA	ACATTCATGGACACATATCATGG	011A2F02
AUBES4856	1841	245	18	39.9	CGTGTTAGGCTTTCTGAATGG	TGGATCTCATGACAGTTGGAG	018B1C04
AUBES2686	639	604	18	40.1	TCAGTGTTTATTTGTTCCAGAAAATC	CAACATCTGAAGGGTTTTCCA	009A1H01
AUBES2341	639	604	18	41.3	TGCTGCTTCGAGATTGTAAAG	GGTGGTGATCCCATACACAA	047A1B07
AUBES3991	2126	328	18	43.3	GTTGAACGTTGCTGAAATGG	TGCAGTTTTCTCCCCAAATG	106A1C05
AUBES2102	singleton		18	44.2	GCCGTGATGCTTTAAGCTGT	GCGTGTGCTCGTGTGTTTTA	041B1A12
AUBES2856	1179	622	18	44.9	CACTGGTATAGAAAAATAGGCAGGT	CCAAGTGTTGCTCAACCTCA	048A2C07
AUBES5136	1649	409	18	45.9	GGTACTGGGTTCACTGGCTTT	TTACGCAGCCAATACTTACCC	107B1C02
AUBES5334	3178	178	18	69.2	CCTTTCCTGCACTCCAGACT	TGCAGGCTGAAAGAAACACA	042B1A05
AUBES4738	2323	211	18	73.6	TTCCCCCATTTGTCCTTTCT	AGCACACGGCAGGAAAATAC	083B2A06
AUBES4224	528	386	19	19.0	CTTTTTCCCAAATGCCACTG	TTCATGCCATGTTTCCTGTG	108A1A12
AUBES4754	2635	215	19	21.1	TAAACGGTTCGCCAATGACT	CTGGGAGTGAGGTTCGAAAG	006A2C10
AUBES5338	3202	266	19	22.6	GCCGACACGAGAATTAATGA	ACCCACCCGAGTTTGATTCT	080B1F04

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES1090	2044	216	19	22.6	ACAGACGCATGACAGCTTCC	GTGATGAGTCAATGCAACTCAGG	018B2C07
AUBES2101	1859	271	19	26.3	AGGGGTTGCGAAATCTGAC	GGAAAGAAGTGCGTCAAAAG	041B1A07
AUBES3979	1788	348	19	27.4	AGCCTCTGACTTTTCACAAACA	AAATGGCTCTCCTCCAACAG	001A2F12
AUBES1971	1299	298	19	27.6	CCACCATGTGCCCAGTCTAT	CCAGTCCGACATAGTGAGGA	032B1D02
AUBES2909	948	519	19	31.1	TGCTGTCAGATTTCCCGTTA	GACCAGGAGAAGTGGGCTTA	061B2H11
AUBES4241	1053	294	19	31.6	CCAAGCCCAAGCATAATGAA	GCCATGTGGAACCTGAGAGT	087B1B11
AUBES1892	181	695	19	33.5	GCATCACCATTCGTGGTCTA	TGCCATCAAGCGTTAGCATA	031A1D03
AUBES2348	1376	272	19	34.1	GCAGTGGGTTTTTAGGGTTTT	TCTCCAGTGTCGGTGCATTA	047A1G08
AUBES2612	181	695	19	34.5	GTGTGAGATGTTGTTTCGTTGAG	GGGACAGCAGTCACACACAC	025A2C11
AUBES3516	173	558	19	35.7	TCAGGGATTGTAACAGCCAGT	TTATGGAACGCCCACTAAGC	083B1F11
AUBES2245	1727	455	19	39.2	GCCCAAGTGTGTGTGTGAGA	GGCCATTACATTCCGACACT	042B1C11
AUBES2509	singleton		19	39.7	CAACTTTTTCGAATCGTTGTG	CGAGGTGTGAAGCAGAATCA	048A2C09
AUBES3755	141	320	19	40.4	ACCTGGCAACATGTGAGCAT	ATCACCAAAACGCAAAAAGC	083A2B11
AUBES5366	3307	186	19	40.9	GGATCCACCATACAGAATCCA	ACAGCCAGCTCAATGTTGC	048B1E11
AUBES5326	2901	238	19	41.0	CGTTGGTCCGTATTGTGGTA	GCTCACCCAACGTCATTAAA	006A1B10
AUBES1699	141	320	19	41.2	GCACGTTTTATTTCGGGATT	ACGCAAAAAGCGACATTTCT	034A1H04
AUBES3296	431	316	19	41.3	TTGCTTTTGTGAGCTCTGGA	AAGAGGCAACACGGAGTGAT	048B1D09
AUBES1880	1456	309	19	41.7	TTCAGGGTGGTTGTAGAATGC	ATGGGAACCTTTGAAGCTGA	027A1F03
AUBES2919	956	352	19	41.7	CCAGTGAACACGTGGCAATA	AATGGAGGTTTCAGCCAGTG	038B1E09
AUBES4005	1113	282	19	41.9	TTGTGATGTGGTGTAAGGTTCC	TATCATGGGCAATGCACCTA	075B1D12
AUBES4863	1984	419	19	42.4	TATTGAAACACGGTGCAGGA	GATTCAGACTCCGGACCAAG	049B2A05
AUBES1946	759	455	19	43.4	TCTGGAAGTGGCAATTAGCTT	AACCCTGCTCTTTCCTGTCA	036B2G11
AUBES2354	1984	419	19	43.4	AAACTTTCCAGTCCTTGTTTGTG	GAACGCCTTGCCTCTCTTCT	047A2C04
AUBES4034	1360	288	19	43.9	GCAGTTGGGTGTGGTTTCTC	ACTGCTGCCAGTGTGAAATG	083A1C05
AUBES2746	114	384	19	44.0	GGGAGATTGTTGAAAGGGAAT	AGCACATTACTGCCCACCTC	005B1A11
AUBES5369	3320	213	19	44.3	AACTCGTACCGAGACGAAGC	GATGAAGCGTGTTTCACAGC	075A1D06
AUBES4947	659	238	19	44.7	TTCACTGCAGACATCGCTCT	ATGATCTGTCAGCCGTCCTC	109A1D02
AUBES3933	1359	271	19	47.6	AAGCCTGCAGCTGTTAGGAG	TCGGAAAGGAACAGAAAACG	029A1A11
AUBES2641	26	413	19	48.2	TTGGTGGCTGTTTGTTTGAG	GGGATCGTGTCTCTTCTACTGC	009B2E10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2463	1300	463	19	51.1	ACTTTTCACCGTGTGGGAAT	GAGCACCATCCACTGACAAA	040B2A02
AUBES5159	1796	340	19	55.0	ATGCATGCGTGTTTGTATGC	GATCTCTTCACGAGGCATGAG	052A1B01
AUBES3763	529	240	19	57.5	TGTGAGCGAGTTTGGAAATG	TGGTGTCGTGTGCTTCTGAT	031A2H01
AUBES5365	3303	260	19	60.7	TGCACTTGGTTGATATTGGAA	GGACGCCACAATTTTCTGTAA	111A2B10
AUBES4942	613	260	19	62.5	CGGATTGCACAATTCATCAG	GCGCTTGTAATCCAGACGA	043A1C05
AUBES2163	876	573	19	63.2	TCAGGGGTTCCCAAACTTTA	TCAACAATTGGTGTGGAAAA	024B2H04
AUBES4259	1249	228	19	64.0	TCTCAGATTCCCCAGCTCAG	TCATTCCCTCCAACTGCTTC	018B1E06
AUBES3770	876	573	19	64.7	TCCACTTTCTCTCCTCCCTTC	TGTAAACCAGCCATGTGAGC	085A2G11
AUBES1332	3218	140	19	68.0	GTAAAGTGTCCCTGAGCTGTG	CAGATACAAATAGGAGGCACACG	022A1D08
AUBES4585	1948	244	19	70.0	GCAAAGACTCCTGGGTAACG	TTGCAACTTGAAGCCTCCTT	104B1A02
AUBES1544	843	333	19	71.9	TTGCCTATAGTTTACGATCACAAT	AATGCAAGTGGTACAGCCCTA	019A2C08
AUBES5021	1198	223	19	76.1	CATGTCGGATGAGCTTCCTT	GCAACCTAGCCTTGAGATGA	004A1C04
AUBES1284	917	387	19	80.0	TCAGAACCAAACAGATGCAGC	CTGAGGTCTTCAACTGCCAG	011A1D09
AUBES4479	1497	282	19	90.9	GCCAGGGAGAACTGAAGACA	AACACTGAGCCAAGGAGCAT	038A2G08
AUBES1434	2661	130	20	0.0	CTGGGTCTCCTTCAGCATCT	GAACATCACATCAAGTGGAGGA	020A1F12
AUBES4526	874	293	20	1.1	AAATTGATCACTGAACTCATTCG	CCATCCACGTCCTTGTAGTG	008A1B10
AUBES4021	1273	267	20	4.1	ATTGGGTGCGTGCTATTTTC	GGTAGGTGGATTGGCACTTG	045A2C02
AUBES3801	1029	360	20	5.6	CATCGCTCAAAAGCAGACAC	AACAGTATGAAACATGCTCCAATTA	023A2D08
AUBES3009	1502	545	20	5.6	AATAAGTGCTCCCGGAGTGA	CAATCAAAAGCTCTGTAACTGAGAG	050A2B09
AUBES3320	1067	514	20	5.6	AGACTGAGATACTAGCGGTGGA	TTCAGGATACCATGCCCAGT	047A1A07
AUBES4020	1273	267	20	5.6	TGAACCCATTTTGCACAGAG	ACCATTTACATGGGGGAACA	030B1C07
AUBES2798	1067	514	20	5.6	AGACTGAGATACTAGCGGTGGA	TTCAGGATACCATGCCCAGT	047A1A07
AUBES2996	1502	545	20	5.6	AAGCCGAGTTAAACCTGCAC	TTCGTGAGATTGCGTGTCAT	110A1B06
AUBES5288	2610	194	20	5.6	GGCGGTGAAAAAGTATTTGC	ATGCTGGAGCGTAAACAGGT	030B1D01
AUBES3802	1029	360	20	5.9	TCTGCTACTTGCTACTGCTGCT	GCGTGACCGGTATGTGAAG	077B2D08
AUBES2415	singleton		20	6.0	GCCATTGTGCATTGTGTTTC	TGGATGTTTCACTCCAGCAG	045B1G08
AUBES4379	1563	220	20	6.5	GATGGGGTCCTGAAACACTG	CACTCCCCATCACCAAGAAC	024A2H03
AUBES2019	2691	232	20	7.3	CCTGGCTCAAAACACAATCA	TGGGGGTTACAATGAACAGC	032A2A05
AUBES3909	1029	360	20	8.9	TCTGCTACTTGCTACTGCTGCT	TTCCCTGAGAAGGAAACGAG	038A2A05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2618	193	868	20	11.1	ATGCTTTGACAGATCGCTTG	AGATCTGGCAGTCCACAAGAA	073B2H12
AUBES1161	535	331	20	12.5	TCTGATAAGAGCAGGGGTGAC	CAGGTCAGCAAGGGGGTTCG	008A1G06
AUBES3741	744	516	20	16.6	TTTCAGCTCTTTGCTTGGGTA	GTGATAGTCGGGTGTCCACAT	085B1F07
AUBES3270	744	516	20	17.2	GGGCATCAAATGCAAAAAGT	TTAAAACAGTTATTTGACATGAGTCAC	080A2B07
AUBES2694	463	448	20	18.7	TTGCTGGAGCCTATTTGACA	AGTCATCCCCATGCTTTGAC	012B1H07
AUBES5382	3395	306	20	19.9	TTGGCACCATTCTGTTTCAC	AATGCCTAGGTCACGGTTTC	056B2B02
AUBES2724	283	470	20	21.5	TTAGACTCCGCAGCTTTGTG	ATGCAACATTCCCTGGATTC	012B2D01
AUBES1338	580	372	20	29.0	TTTCCAAGCCCGCTGAG	GACCACATGACGGCTTCC	025A1E11
AUBES3494	580	372	20	29.8	GGGCACTGTATGTGCATGTT	AGTGAAGGGTGTGGGACACT	034A1F05
AUBES2059	959	353	20	33.0	CCGCATAACTGGGATCATTT	CGTTTATGTTGGTGCCGAAT	039A2F04
AUBES5010	1134	228	20	34.2	CACCATGGAGTTTCTTGGAGA	TTGGAGTGTGTTGCTCAAGG	095B2E10
AUBES1759	1396	186	20	37.2	GCCCTCTGGCAATAACAAGT	TGGAAGATGGTACGGGAGAC	027B2B05
AUBES5353	3260	213	20	37.4	CAGATATCCATCTCTGTCCATCA	ACAGACAGACCGGCAGATG	022A2F11
AUBES4525	715	409	20	38.3	ACACACCACAGCAAGCAGAG	GTTTGCTGGTGTGTTGCACT	085A2E10
AUBES5004	1096	211	20	39.5	CAGTCCATGCACGTTACGAA	ACCAGGTGGCAACAAATACA	024A1E01
AUBES2367	singleton		20	39.7	GCCATTAGACAAACCAGATGAA	TGTCCTACCCCACCCATATT	047B2H05
AUBES5178	1966	266	20	40.7	GTGTGATTGAGTGCCAGGAA	GCCCAAAGAGAAATGGCATA	095B2A08
AUBES4019	1262	485	20	41.8	GGTGTGTGAACAGCACAAGC	AAACCTTTTCACTGCCATCG	004B2A11
AUBES4749	2577	233	20	42.1	AGCAAACAGTCCATCGCATA	GGTGTCCCCATACCTCTGAC	086B1D10
AUBES2889	481	355	20	43.1	ACAGTTTGTTCATGCGTCCA	GAAACCAAAGCGCAACAGAT	033B1B12
AUBES1271	1898	282	20	43.8	TGCCCTGTGGAGGTTGTTGG	GTTTCGCCTTTGACTGCGTC	034A1D08
AUBES4787	2902	189	20	45.0	AATGCTGGGATGATTGGATG	GCATTCACAAACGCCTAACA	054A2D09
AUBES5320	2772	259	20	45.5	CTCAACCCCACTGAACACCT	GCCAGAATGAAAGGAGGAAC	081B2D02
AUBES1277	1167	208	20	47.0	ACGGAGACTCCATGCTGAGC	GAATTTACGGGAGGCCGCTG	014A1E03
AUBES2990	481	355	20	47.4	TTGCGGTTGTGAGTCAGTCT	TCTCTCGTCCTCATCCACCT	100A2A04
AUBES4746	2548	169	20	47.5	AGAAACCGTTGAAGCTGGAG	TCAACTGTCACCTGGTCCTG	111A2C05
AUBES3746	481	355	20	47.6	TTGCGGTTGTGAGTCAGTCT	TCTCTCGTCCTCATCCACCT	100A2A04
AUBES1750	481	355	20	47.6	TCACCATATGACGGAATGGA	CTGCAGCCAGCTCTTTCTTT	032A1F10
AUBES3560	752	337	20	47.6	TAACGCACAGCTAGGCACAC	GCTGTGGGCTCGTAATTAAA	002B2D09

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2701	643	629	20	48.2	TGTTGGGTAAGGAGCCAGTT	TTGAAAACGCTGTTCCTGTG	023A1E04
AUBES4776	2827	316	20	49.3	TTGGCTCACAAAGCCAAAAT	GTGCCTACGCACCTTTGGT	052A2F03
AUBES2928	1284	313	20	50.4	TCATTTGTGAACAACCATACTCC	CACACATTCAACCCCTCCTC	054B2A06
AUBES3535	1142	587	20	50.5	CTTGAAGTCAGACAGTACTCATGG	CGGCCATGTTTCTGAAGATT	038A1B06
AUBES4660	263	260	20	50.9	CCTGAAGATCATGGGGAGAC	CGAGCGCTTTCTAACAGTCA	026A1B09
AUBES3390	281	1157	20	50.9	CTGCCCCCATCATTAGACAT	GACAATTGAAATCATATGGTGGA	070A2G04
AUBES3839	2257	316	20	50.9	CGGTTCTGTGGCTTCATTTT	CAACGAACGGCTCCATATCT	035B2D06
AUBES4661	263	260	20	51.0	TGAATCTGTCCTTTGCACCA	TTCAGACCCAGAAGATGAGGA	095A1D09
AUBES4662	385	468	20	51.0	TCTTCTTCCAGAGGTCTTCCAG	TGAGAAGAATCTGCTGCATCC	052A2B02
AUBES1351	singleton		20	51.1	ACTGATCTCGTCCACGGTG	GCATTCCACATGCTCACCTC	028B2A03
AUBES3228	281	1157	20	51.1	CCATTGTCCCTACATGAAAGC	ATGTGCTCTGAACAGACATGC	039A2G11
AUBES3227	281	1157	20	51.1	AGGGGATTACACCTCCAAGC	TTGTTGGCAAGACCATACACA	058B2A05
AUBES3905	942	213	20	51.2	CATCTTGTCCGGTTTTGAAGA	ACATCGGGAAGTGACAGTCC	040A2B04
AUBES1591	957	457	20	53.5	TGCAGTTGAGCTCTCGGTAA	GCCAAAATGCCGGACTATCT	029A1C01
AUBES3313	714	343	20	54.0	CCTTTACTGCATGGTGTTGC	CCTCCAAGCATGACCTTCAC	103B1G09
AUBES3133	130	511	20	54.4	GAATGCTTTTGACTAGGAGCTTG	TGGGCTTCTCATTGTGACTTT	041B2C02
AUBES2716	315	426	20	54.6	TGGTCATCTGTGGTGTCTGC	TTTTGCAGGTCCTCCTCATC	010B2D02
AUBES4497	2406	164	20	54.9	TTGGTTTATCAGCGGGACAT	CGCTCCTACTGTGGTGATTG	013B1F04
AUBES3539	276	739	20	55.0	GCAGTCAGCATAAAGTGCCATA	CCAAACTTCAGCAGGTTTTGT	074B1D03
AUBES2933	85	374	20	55.1	TGGCATGCAGATGCTTCTAT	TTGCATGCCTCTTGTTTACAT	040B1D02
AUBES2822	482	301	20	55.4	CAAAGTCCAGGTCACTGTCAT	GGAACAGGCGAAAGATGTGT	036A1G04
AUBES1710	857	208	20	55.4	TGCCTCAAGATGGAGGAATA	AAAGTGCTGGAGTCCTGAAAA	034B1A04
AUBES3382	130	511	20	55.4	ATGTGGACACCTGACCATGA	GTAGTAGCAGGGCAGTTGCTG	112B1E07
AUBES3621	228	279	20	55.4	AGCATGTCACACCCTGCATA	GATGGCTACCGGATTCAACA	078A1B06
AUBES2127	1559	242	20	55.4	ATCGTGAACAGGGGACAATC	CACGTCTGCTCTCTAGCAACA	019A2E09
AUBES4311	1943	225	20	55.4	GCTGGTCCAGGATCTGTGAT	AGCACGTTCCTCTCCTTCAG	047B1G05
AUBES5294	2637	188	20	55.4	CTGTGGACGGGAATTTGTTT	CAATGCAAATTAATGCCTTGC	021B1E01
AUBES5316	2743	161	20	55.4	TCCCTCACAGCAAAAAGACA	CAAGTGTGCAATGCTTTCCT	030B2D10
AUBES3520	355	463	20	55.4	AAGCATGAGAAAGGCTTAGGG	TGCATTTCTTCCTCCATGTT	090A1D10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4695	2950	144	20	55.4	TCGCTCTGTCTTTTGGGAAT	TTTCAAACCGACCGACAATA	002B1E03
AUBES4236	873	222	20	55.5	AATCGCATGCAATCATAAAGTG	ACACTCCCTGAATGGGACAC	060A2B01
AUBES2596	306	589	20	55.6	TTTCACCAGCCACTGTTCTG	AATTTCCTGTCACTCTTCTCTCTC	054A2D08
AUBES4237	873	222	20	55.6	CACCTGTTTGGTTTGACTGG	TTCAGACTTCCTGCTTCCAA	006B2D09
AUBES5250	2428	169	20	55.6	GGACACATTTGTGCAATGCT	CAGGGAAATGTGGCACTCTTA	036A2C04
AUBES5253	2445	140	20	55.6	AACTGCGCTACAGGACTCGT	TCGCGAGGAGACAGAAGTG	086B1F04
AUBES4064	459	250	20	55.6	AGAATTTCTCCGGCCTTCAC	CTCACGTGGATGAAGTGTGC	065A2D12
AUBES3464	1490	387	20	56.0	GCGCCTAATGTTGATATTCGT	CAGTAGGCGAAATGCATGTAA	005B2H01
AUBES3463	1490	387	20	56.0	CGTAGATTGCTGTTGCGACT	GGTCGCGTGCACACTATTT	112A1C10
AUBES4045	1512	242	20	56.0	TGCCTACTCTTCCTCCATGTG	AGGTGTGCGGTGTGGATAAT	039A2G10
AUBES5030	1226	210	20	56.3	TCCATACAGCTGGCATGTTC	CGGATGTAAACAGCAGTGGA	075B1D11
AUBES2778	747	704	20	56.5	TGTGAGAGCGTAAGGCTGAA	TGAAAACTTTGCCTCATGGA	075A2A11
AUBES3079	306	589	20	57.0	CATCATGTTTGAAGGCAGGA	CATGCAAAAATGTGCAAAGA	021B1B09
AUBES4283	1824	222	20	57.6	TTGTGTTCATGCAGCATAAGATT	TGACAAACACAGATGCCACA	109A1A12
AUBES2467	singleton		20	58.1	GCAGATTCAAAACCCCAAAA	CAAGCTGTGCTGAAAGCAAC	040B2D12
AUBES2147	2009	249	20	58.5	CAGCAAGGATATGGGGACAA	GGGAATGACACCAAAGTGTG	022B1C12
AUBES2882	329	605	20	59.6	GATGGAGGAAATGGTTGGTG	TGGTGTCACTGTTCTGTCAGG	073B1D05
AUBES1245	singleton		20	60.9	ACGAGCGAAGAGCGCGTTAG	GCCATTGTCACCGCAAGATG	
AUBES4711	3175	122	20	61.8	GCGCCACATGATGAGAATTA	ATTACGGGCCTTGCTTATCA	105B1B03
AUBES4857	1873	382	20	63.8	TCTCCCGCTATATGGTAGGC	GCATCAGCCCTGAGAACACT	109B2H08
AUBES4536	2020	174	20	64.7	TGCTTTGGATAAAAGTGTCTGC	CTTCCATGCTGGACAGAGGT	024A1G01
AUBES3234	130	511	20	68.3	GCGAGGAGCAGCTCATAAAA	CAAGGTCTCTCCTCAGTGGTG	066A1F04
AUBES5047	1313	330	20	83.5	AACGTGCACTTTTGGTGTATTT	GGTCACGAGTAGCAGGGTTG	045A2H11
AUBES2564	209	590	21	0.0	CCTGATTCAGAAGTGCTGACC	AGAGACGATGGTGCCACTTT	035B1G08
AUBES3001	242	496	21	0.8	CAGGACCTAAACAGCCCTGA	AGCACAGCCTTGGTTTGAAG	053B1H12
AUBES2876	242	496	21	1.4	CATCAAGAATCCGCGACATA	TGGCTTTAAGACCTTTTGCAC	057B1D06
AUBES5013	1151	441	21	1.7	TCTTGCATGTGTTTGGGTTT	GCAGGACAGTGCAAAACAAC	090B2E04
AUBES3336	209	590	21	2.4	GGTTCCAGTTGTTCCACGTT	ACATGTTTGTGAAGTGCTGGA	075B2G07
AUBES3087	183	825	21	5.1	TTAATGGGACGGAGTGTGGT	GCCAAAACTGTCAGCCTTTC	109A1D11

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2607	183	825	21	6.6	AATGCCAAGGGTGTCAGAAT	TCGATTCCTCTCTGCTCACAT	044A2D06
AUBES3360	183	825	21	6.9	GCAGACGTATTGCGTCATTT	GGCAGTAGATTGGCAGGAAA	072A1H03
AUBES3147	183	825	21	7.4	CAAATCCAGAGAGGGGACAA	CCTTTCGTCTGAGGGTCACT	058A1F12
AUBES1569	43	556	21	7.5	TGCATGATTGCCTCATACG	CCTCTTGAAAATGAGCAAACG	023A1C10
AUBES2874	212	519	21	8.3	ATCACAATTTGGCCCTTGTC	AGCGATTCTGCTGAAACTGG	045A1H12
AUBES1629	1214	512	21	8.8	CACGCCTACAAAACTCCGTA	CAGAGCACTTGCATCAGGAG	031A2A05
AUBES4803	3036	252	21	8.9	CAAAGAGCAAACCCCAGTGT	ACGCACATGTAGCTCCCATC	050A1D01
AUBES2808	174	352	21	9.5	TGAAGGGGTTTTGTGGTTTC	CCCGCTCTTTTACCATAGCA	054B2H05
AUBES2603	455	727	21	9.6	ACCCACTGCTGGGTTAAAGG	CAATGCATGTGCCGTTTTAT	013A2F02
AUBES3169	59	1071	21	9.6	AACAGGTTAAATGCTGCTTATGA	TCGAATAAGACATGGCAGCTAA	062B2H04
AUBES3948	212	519	21	9.9	TTGACCCCCGTTCTTTTAAC	CCATTCGCTCAGATAGGAAAA	038B2A03
AUBES1973	462	357	21	10.3	CCAGTCTGGCTATTTTCCTCTG	CTCCTTGTGACTGTGCAGGA	020A2B10
AUBES5307	2700	313	21	10.4	GAAGAAAAATCCAAATGGGAAA	CATTTTGTGGCAAAAGTTTCA	074A2H04
AUBES3757	354	335	21	10.5	AGAAGCCATTAGACAGAGAAGCA	ACCTGTTTAACGGTGGAGGA	004B2E03
AUBES2936	98	301	21	10.6	TGTCCCTGATGTGAGAACCA	GTTTTGCCATGTCGCTGTC	018B2F09
AUBES5221	2284	147	21	10.6	GCATCATGCAGAGATTCCAC	AGGCCAGTTATTCATCAGGTT	048B2G12
AUBES2511	1692	173	21	10.6	TGTTGTCTTGTTGAAAGGGAGA	TGCGCACTTTTCTTACCATT	048A2D06
AUBES3218	182	768	21	10.6	TTCCCTAATGTGCCTGACATC	ACCCAACCCTGAAAGTGTGA	096A2E04
AUBES1879	singleton		21	10.6	TGAAGGTTGACAGCATCAGG	GGTGCATTAACCGTTTCTCTG	026B1F12
AUBES2735	1	321	21	10.7	TGCATTCATGCAAAAAGCAC	CCATGGTTGGTTCTTGGTTC	027A1E06
AUBES1502	1214	512	21	10.8	TTTAAGGGGTTAAAGTGAAACAA	GGCAGAAACGACAGAAAGGA	013A1A08
AUBES3084	455	727	21	11.3	CTGGATGATGGTTGGCTGTA	AAGTGCGACCCAACTGTTTC	062A1B09
AUBES3927	1243	293	21	12.0	TTGTCCCACTTCTCCCACAC	TGGAGCTTCAGGAGAAGGAG	002A1G12
AUBES3142	182	768	21	12.2	GTTTGGGTAGCTCCATGGTC	CCGGCCTAGATAAGATGTGC	047B2B10
AUBES3352	182	768	21	13.1	GGGCTTTGATTGAATGCTGT	CAGGTGTGAAAATGCCTGAA	062A2F02
AUBES1700	418	272	21	13.8	ATCGCTGGAAAATGAGATGC	CGACTCTTTGCTGAGTTGGA	033B2B02
AUBES2619	39	751	21	14.6	AATGCCCATTTGTCTTCACC	GCTTGTAAACCAAGCCATCC	006A1A05
AUBES1168	singleton		21	14.9	TTTCTTTTGAGAGTCCAGTGTGC	CAGAGCCAAAGTTCCCTCTG	008A2F08
AUBES3295	418	272	21	15.2	CGGGATCAATTCAACACCTT	TTACTCTTTGGGCTGTGTGC	093A1G05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5086	1488	201	21	15.4	TAACAGCAGCTTTGACAGCA	CCAACAAAAGTCGACCAAAGT	028A1H09
AUBES2212	122	362	21	16.6	AGGGGGTAAGTAAGCCCTCA	CAATCCTCGGGAGCAATAAA	031B1G06
AUBES2099	1007	879	21	17.1	CGGCTTCGAGGAAAGTTTTT	CCACGCTTAAAATCGATACTGC	041A2F10
AUBES3643	742	284	21	18.9	CCTTGAGCTCAGGAAAAGCA	TTGGGATAGATTGACTGCTTGA	031B2A02
AUBES3642	742	284	21	18.9	CATTGATGAAGTCAAGATAGCTAGAGA	AAGGGACAATTGATGCTGGA	054B1F05
AUBES3534	1118	626	21	19.1	CAAGAGGCAGGGCTGAACTA	TTCAATGTTTCGGGTGTGTG	095A1A12
AUBES2755	239	565	21	20.1	TTAGGCCATAAGCATGCAGT	GGCTTGCACCTTCCAATAAG	035A2F09
AUBES3523	402	570	21	21.7	GAGAGAAATAAGGCAGTCAAAAGC	TGATTGTTTACACACTGTTGGTG	054B2H06
AUBES5069	1404	233	21	22.8	AAAGGCATTAGAGCCTGGAT	GCCGAAAAGCGACTAGTTTG	106A1D07
AUBES5012	1149	291	21	23.1	TCTGCAAAAATTGCTTGTGA	GTGAGTGGAGCGAAGGTCTC	061A1A05
AUBES3232	9	2006	21	24.9	TGACTAGGCTAAAGGCTCAACA	TGACTGTTTCGCATCCTCAG	006A2G05
AUBES1418	2706	171	21	31.0	TGATGGGGAAGCTGAGAGTT	TGTCAACATGTTAAGCACACTAGC	032A2G10
AUBES4997	1060	215	21	34.9	GGTTGAGGGCTGTTTCCTG	ACCGCTGAGAGGAGTGAGAG	035A2C09
AUBES4095	1001	281	21	36.8	CACACGCTGCACACAATAGAT	TCATTGCTTTTGTTCGATGC	006B2C06
AUBES4096	1001	281	21	41.1	TGATTGATGGGCATATTGTAGG	CATTAAATGCACGCAGTTGG	046B2E04
AUBES5283	2586	276	21	43.6	CAACTTGGAACACGCAATACA	CCAGTAATCGGAAGCGTTTG	052A1C04
AUBES3242	41	502	21	45.2	GTTCTCCCCGGCGATATTAG	AGTTGCACAACAGGACATGC	105A2C08
AUBES5405	3496	220	21	45.6	ACCAGAGAACAGCCGGTAGA	GGACCTCGGGATCGTTATTC	048B2A10
AUBES4419	2530	428	21	50.2	GCTTGTTGTCACAGCGTTCA	CGAACACACAACTCCCACAT	092B1F04
AUBES1945	103	445	21	50.2	TATGGTTTGGGGTTTTGTGG	CTACCGGCTGACACCTTCAT	036B2G10
AUBES1624	103	445	21	59.1	AGCACTAAGCACAGGTGCAA	CCTCTTTTAGGTCGGCTGAA	023A2H12
AUBES3972	1695	304	21	61.9	ACCTCGGATAAAGCAAATGG	TCATGTTTTCCCTCAGAGGAC	105B2E05
AUBES3971	1695	304	21	62.9	GACCCATGATGCACTGAAGA	CAGCTGTGTAGCACGTTTACC	090A1H02
AUBES3556	586	413	21	63.9	GTGGGTCATTTAGGCAAAACA	TGCTAAATACGGGCTCTGCT	007A2D02
AUBES4405	2092	335	21	65.3	TCCTTCTCCGCCGTATTATC	TGATTGCAGCTCGTTAGTGG	094B1F03
AUBES4404	2092	335	21	69.8	CATGAGCGTTAGTGCTTTGC	CTGCCAACCATTACGAGGTT	046B2G06
AUBES1299	singleton		21	72.0	AGCAGTTTAGACATGGCTGC	TCCAAAACCATCCGCGACAG	021B2E09
AUBES1298	singleton		21	72.3	AATTCACTCACACAGCTCACAC	ACTCCAGCAAAACATGCAGC	021A2F07
AUBES1405	singleton		21	72.4	TCACACAGCTGCTGATCAAA	CAAAACATGCAGCCTGAGAG	021A2F07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4026	1341	274	22	0.0	TTTACTGGCCTCCAACTGGT	GATGGAACCCCATCAGACTC	052A2E09
AUBES4025	1341	274	22	0.1	CGGTCCTCAACCACTACCAG	GTATGGTGTCCTGGCGAAAT	108A2F04
AUBES4775	2825	205	22	3.9	GTTGCGCTGATACTCGTTTG	TCGGTGGTTAAAAAGAGAACG	110A1C06
AUBES5239	2390	215	22	6.2	ACCAAACAACGATGCTGAAT	TCGGGCAAATATGAAATTGA	051B2A09
AUBES5368	3316	134	22	12.9	GTGTGTCAAAGAAGGTCACGA	CGAAGCCGGTCTGAAAGTTA	052B2A07
AUBES4459	785	220	22	14.7	TTTGTATTCCGTCTCCTCTGC	AAGTGCTCCGAGTGCTGTGT	035A1H01
AUBES4094	975	259	22	20.3	GCCGCTTACTTCAGAGAGCA	CAGGTCCAGCATTCAATCAG	003B1D03
AUBES1448	973	583	22	26.0	ATGCAAGCAAATCGAAATGG	GGTCAGTGTCCCCTCAGAGT	027B2C11
AUBES4779	2856	233	22	27.1	CAGCCTGTTTGCCAGTAGAA	CACGACCCAAAAACAGGAAC	109A2E09
AUBES1941	973	583	22	28.7	TCTCTCTCTCTCTCTCTCTCTCTCTC	TCCTGTCATTTGCATGCTTC	036B2D11
AUBES4723	3317	183	22	30.3	TGCTTAGGCAACTGCTTTCA	ACCATGCACACACACAGAGG	025B1C02
AUBES3925	1166	345	22	40.4	CCTCTCATGCTCCCATGAAT	CGTGATCGGCTCTATGACAA	104B1E08
AUBES3167	166	890	22	59.8	AACGTTTCAATGGGTGCTGT	GGTTGTGTGACAAAAACGACA	108A2E02
AUBES2635	166	890	22	59.8	TAACGTTTCAATGGGTGCTG	GGTTGTGTGACAAAAACGACAC	009B2F10
AUBES2232	166	890	22	60.6	TGTATCGTAGGACGCCATTT	TGCATTCACAAGGCGATAAA	042A1H02
AUBES3378	166	890	22	60.9	AACGTTTCAATGGGTGCTGT	GGTTGTGTGACAAAAACGACA	072A1C05
AUBES3163	252	835	22	61.9	GCACTACCCTCCAGTGCTTT	AGTACCTTGGGCAGCATCAG	053B1E09
AUBES1863	singleton		22	62.1	AGTTGTTGTCAGGGGCTTCA	GGGTGCAGTCTATGCAGGTC	021B2H11
AUBES1593	1912	262	22	62.9	AATGGCATTTGGCTGAAGAG	CATTGCCTCGTCCAGAGAATA	029B2E02
AUBES4854	1761	266	22	63.2	CACACACACACACCCAAACA	CCTGCAGGTCTCTGTCACTC	048B2A07
AUBES3814	1496	249	22	63.8	TATTCAGCTCCCGAATCACC	TCAGTCTTCTGGCCTTCACA	048A2C03
AUBES2593	135	619	22	63.8	AGGCTAAAATGGCTGGGTTT	CCTGGAAATGAGCTTCATCC	045B2H12
AUBES3553	1017	309	22	63.8	TGCCTCTATTTGCCTGTTTC	TGTATAAAGTGCCTTGAGAAGCTG	092B2D03
AUBES4930	558	286	22	64.5	ATGGCGTAACACTCTGAACTCAT	CTTGCATCCTTTGCAGTCAA	053A1F01
AUBES1323	1451	216	22	64.7	ATGACCCTCTGCGGAACCAG	CCAGTGTTTTCAGCCATGTGAG	023B2F01
AUBES1968	39	751	22	64.8	GCCTGGTTTTACGCTGACAT	CGCATTGAGCAACTGTGTCT	030A1F10
AUBES4670	2760	162	22	64.9	TCCAGCTAGCGATGTTAGGTT	GGGTGACGTGTTTTTGTTTG	077B1G08
AUBES3156	39	751	22	65.1	GCTCGATAAAAGGTTGACAAAG	CCCACTATGAAAACACACAATTT	029A2D07
AUBES3815	1496	249	22	65.6	AGTTGTGGGTGGTGGTGAGT	TTGTGTCCCACCATTGTTTG	094B2A03

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3059	107	496	22	66.0	TGGCAGATCTCAGGTAGCAA	AGCCACAGGTTTAGTCTCAAAT	060B1F12
AUBES4488	1578	218	22	66.1	CTTTGGGAGAGCTCACTTGC	CTGAATGCATGGTGGTTGAG	112A2G02
AUBES2830	635	462	22	66.1	TGTGTATGCCTAGACAACATGG	TGCACTGTGAACAGGAGCTT	046B2A10
AUBES3729	475	313	22	66.1	GGAACCCCAAATTTCTCTCC	AGAGGGGAGCTGGTGTAGTG	065B1F08
AUBES4844	1642	316	22	66.1	GACTCATTGTGGCCCAACTC	AGTAATGCAGGCCAATCAGC	059B1C06
AUBES4845	1642	316	22	66.1	GAGAGACCGAGAGACCGAGA	AGTTCTGCATGCACACATTTC	106B1E07
AUBES2565	107	496	22	66.2	GCCAAAGAGCCACTTCAACT	GCTCCTTGTGCTCTCCAGAC	054A2C12
AUBES3406	358	269	22	66.2	GCTCTGGATAATGAGGGTGTG	GGTCGAGCAGAACAACGTCT	038A2C08
AUBES2817	395	413	22	66.2	TGACTTTGATCATCGCATGG	CTCACAATTTTATTTTGCACCA	034A2F02
AUBES1996	2848	203	22	66.2	CATCACAGAACCTCCAACCA	TTTGGGGGAAATTCACAAAG	027A2B06
AUBES3187	135	619	22	66.2	TACCTTGTTGGCACAGCAGA	TTTGAATCGACTGTTGCTCAG	051B2C10
AUBES2591	404	868	22	66.2	GACGCAGCTAAGTGCCAGAT	TGTGCTGGTTAGCCAAGGAT	075B1A10
AUBES2369	1045	232	22	66.2	TACGGAAGGCTTTGGGTAGA	CGGATTTGGGATAACTCTCG	044A1A08
AUBES2737	19	431	22	66.3	AACAAACATCCGACCTCTGC	TGGTACACTGAACTGATGGATGA	063A1D02
AUBES3198	252	835	22	66.3	GATGTGGTTCCAACCTCGTTA	GGACTTGGCAGATGTGCTTT	108B1D11
AUBES3719	453	468	22	66.3	ATGATCAAATCGGACCAACC	CTCAACTAATGCCTCTGTGTGTG	039A1C09
AUBES3297	474	318	22	66.3	TTTGATGTTTGTCCCGATCC	CAATTTCCCTTGTGGAATCA	039B2B04
AUBES3456	1017	309	22	66.3	GGATTCCTCTGCATTTCTGC	GTGAAGTATCAACCTAATCATTGACA	014A1A01
AUBES4470	1242	189	22	66.3	CGCTTCAGCGGACATAAAGT	GGGACTTCCACTGCATTTTC	096B1B07
AUBES1227	1548	286	22	66.3	AGGGCACAGGCAAGCCACAC	GCTCCCAATAGTAAGCCTAACTGG	028B1F11
AUBES4558	1740	193	22	66.3	TGATCAACGCACACAAGTCC	CACACAACAAGCTTCTGGACA	086B1D04
AUBES5393	3429	174	22	66.3	ATGCCACAGTGATGGAATGA	ATCGCACCGAGAGAAGAGAA	112B2A02
AUBES3192	29	847	22	66.3	GTACATCACCTGAGGGCACA	GGGAGCCAAGTGCATAAGAC	008A1G04
AUBES3038	66	298	22	66.3	GGAGCCTTCAACTGAAGAAAAC	TGTTGAGCTGTTTCAAGAAATG	062B1G08
AUBES3292	389	362	22	66.3	ACAGGCAGCTGGAAATAAGC	GTTGTCATGTCTTGGCCAGT	076A2F08
AUBES1717	820	605	22	66.3	CTACCGGAGTCACATTTCCA	GTTGCGCAAACGAAATACAG	033B2D12
AUBES3813	1496	249	22	66.3	AGTTGTGGGTGGTGGTGAGT	TTGTGTCCCACCATTGTTTG	003B2D06
AUBES1702	887	333	22	66.3	TCCCGGGATAGTCTCCAGAT	CAACACAATGCCATCATTCC	033B2G04
AUBES2645	120	445	22	66.3	CGAGACATTTTGTCCCAACA	TGCAAAGTGACACTGAATGCT	023B2H08

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3405	358	269	22	66.6	CACCCTAATGGCATCGATTT	TGTGCAGACAGGTGGGAATA	084B2E02
AUBES5031	1230	320	22	66.6	CAGCTACTGGAGGGTTGCAC	GGCTTGGTGTACTTCAGTGGA	007B2H11
AUBES3916	1111	259	22	67.4	TCATCATGTGCTTGCTTCCT	CACACCGGTTCTTTCAGGAT	079B2H08
AUBES3518	240	551	22	67.6	GCAAATCCTGAGGAGGATCA	AAAGGAGGGCTGTGAGTGAC	072B2E06
AUBES3807	1148	203	22	67.8	GCAAATGGGTTTTTATCAGCA	CCCAACCACAACAAGATCAA	107A2B10
AUBES2271	358	269	22	68.3	CCCACAAACAGGACAAGTAGAA	CATTCAGATGCTTTGCAGATG	043B1B07
AUBES5209	2206	179	22	68.9	CAAATTGCTGCTCATGCTGT	AATGTCCGAGACATCTGTGG	009A1E04
AUBES2237	453	468	22	69.5	CACATGGAGCCAATAAACACA	CTTCCCTGAAACTGCTTGCT	042A2E04
AUBES2888	453	468	22	69.7	GGGGAGAATTTGGAGAATCTG	CAGGTAACGGGATGGCAATA	048B1G07
AUBES2389	166	890	22	69.9	ATGGTCAGATTACCCCAAGC	TTCAACGATCAGCGTTTAGG	044B2B11
AUBES2047	487	272	22	69.9	TGCCCTCTCTTTGCTCTCTC	GCCTCTGCCATTTTTATGGA	039A1C08
AUBES3519	240	551	22	70.8	GAGTGAATGTCCTCAGGGACT	TCAACAGGGGTCATTTAGCC	102B2E03
AUBES3109	166	890	22	71.2	TCACCTGCATCCAATTCAGA	TGGCACCCTTGGTAAATCA	011B1E05
AUBES4636	293	222	23	0.0	GCAGTGGTTGCTGGTCTTTT	TGTCCATCTTGGTGATCTGC	087A1E07
AUBES2875	237	389	23	0.6	CAGGATATAAACGGCCCTGA	TTTCCGAAGAGGGTATTCACA	078B1B07
AUBES4200	449	468	23	0.6	TCAGGCATTAGGATCGCTTT	ACTGCTGTTCTGGAGCCAAG	087B2A04
AUBES4266	1370	348	23	0.6	AGCTGCCACTTTCACTTTCTG	CAGCTATCGGATCCCCATTA	050A2C07
AUBES4804	3052	194	23	0.7	GCGGACATGGACACTGATG	GTGCGCGTGTATACGTGTGT	022B1A09
AUBES5091	1517	546	23	3.7	GAACTCACGCTGCTCCACTT	CGTCCGTTCACGTAAAGCTC	073A1E04
AUBES3033	421	266	23	5.0	TTGGTGCAGTGTGTTTCTTTG	CGAAAATCAGTGTCGCATTC	058A1F07
AUBES3847	2697	203	23	5.6	TACCTTGCATGCTGGCTTTC	ACTCCGCCTTCTGAGGATTT	073A1E09
AUBES4735	2288	252	23	7.3	CCCGAAACTGAAGCTGATTG	TGTCTTTTCCTGCTGCTCAA	035A2D03
AUBES4392	1857	360	23	7.4	TGTGGAACTGTGCCTTTTCA	CTGTGTTCCAGCATACTGAAGG	079B1F02
AUBES2255	382	555	23	9.8	CGGAGTGATTTTCCGTCATT	GTACACTTCCCGCACACACC	042B2B08
AUBES3046	382	555	23	14.1	TTCAGGTGTTAGTGCATGACTGT	TAGGAGCCAGCATCCTTTTG	074A2E03
AUBES2736	12	457	23	17.3	CCTCGCTTTCTCTCGTTCTG	TTGACGGGGATTTTAGTTGC	004B2G06
AUBES3102	74	900	23	18.6	GGAAGTAACATGGACCCAGAGA	AGGAATCAAATCCCCAAACC	110A1H06
AUBES4900	90	274	23	18.9	TAGCGTTCGTTTATGCGATG	TGATCGAGACATAAGGGGTGA	051B1G04
AUBES2025	371	409	23	20.0	GTCCTCTCGGGTCTCCTCTT	CAGACCCACACACACAGACC	038A1D10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3188	211	954	23	22.0	CAACAAATCTCGTGGGAACA	GTGTGAAAGCGCTCATCTGT	005B2B08
AUBES1606	301	379	23	22.6	GGTTAAACAGCTAGGTGCACTG	ACAGCCAGATGATTTCCAGTT	031A2G03
AUBES5129	1622	215	23	23.5	ACATGCGGATGTGCAAGTAA	GGCATCTCTGCTGGATACCT	042A1C01
AUBES3159	74	900	23	23.8	GTTGGAGAAAGACCGCACAT	ATGTGGGAGAGCCCACTAAA	087B1A01
AUBES4137	1040	364	23	23.8	ATACACATCCTGCCCTCGAT	CACTGTTCCTGCCTTCACAT	068B2C07
AUBES5394	3443	145	23	23.8	ACGGAGACGAGGGAGAAAAT	ATCTTGTTTCCCGGTGAATG	084A2G11
AUBES3217	211	954	23	24.6	CAGATCCTTCCCAGTCTCCA	CCAAAATGGGGAAATCACAA	011B2C08
AUBES1361	650	433	23	24.6	TATTCTGGCTGGAGGCTACG	GTTTGAGTCGGCAGCACTAC	024A2D06
AUBES2251	727	200	23	25.1	CATATGCACAGACACACATGC	TGTTGAAATACTGGCCCACA	042B2A07
AUBES2484	982	284	23	25.1	GATGTTTTCGATTCCAACAGG	CATAAAGGCCGTATGGGAAA	046A2D03
AUBES3691	809	443	23	25.1	GGTGGCGTAACCAGATTTGA	TGACCTGATTTCTTCGGTGTT	019A2G04
AUBES4412	2434	272	23	25.1	CTGGGATAGGCTCCAGGTTC	GGGGATGCAGTTAAACTCAGG	077A2F09
AUBES2937	105	276	23	25.1	AGAAAAAGTCGCGTCTGTGC	TCTTCCCTGTGTTCCTGCTC	054A2H08
AUBES2625	74	900	23	25.2	CCAAAGCCGGTACCATAAAA	ACAGCTGTGACGTTGGACAC	008A1A03
AUBES4132	982	284	23	25.2	CACTGGGGTGGTATCCTCAT	CCACCTCGGCAGTACTTTTC	062B1C09
AUBES4010	1169	260	23	25.2	GCAGGAGCCTGTATTCTTCC	TTGCCTCCAGATGCTAAACA	032A1D12
AUBES4113	1419	318	23	25.2	CATCCTGGCGAAGCTCTTTA	CCATGCGAGGCCAGTAACTA	110B1G04
AUBES5084	1470	196	23	25.2	CAGCTCTGACAACAGCATGAG	TCAGGTGTATTTGCCCTTGAT	002B2F12
AUBES1330	2434	272	23	25.2	AGCCTATCCCAGGGGACTTG	CTTACCCATGTATCATTGGGACC	033A2G04
AUBES5354	3268	205	23	25.2	CTGAAGCCAGTTCTCCTGTG	CAGCATGTGAAGTTGTGTTGG	073A1D07
AUBES5359	3283	399	23	25.2	CACTGTCAAGCTGCAAAAGC	TGATTCAGTCTGCTGCTTGG	078A1G06
AUBES4136	1040	364	23	25.6	TCAGGGGAAATTATGGCAAG	TGGCAGTGCTTTATCCACAC	068B2A07
AUBES5065	1382	193	23	25.6	CGGAAATCCATTGTTTTCTTTC	GGAGCTCCAGATTGAATGATG	073B1D02
AUBES1801	1227	232	23	25.7	GCAACTGGATTATGCAGCAA	GAAACAAAGGCAACCTGAGC	033B2C01
AUBES3657	211	954	23	26.4	CTCCACAGGAAAGCCTTTGT	ATGCCGTGTAACTCCCACA	083A1B07
AUBES5009	1130	360	23	26.4	TGCTTGAGTGGGCACTATGA	CCGCACCAAACTAACAAACC	104B2C05
AUBES4148	1229	255	23	26.5	GAGAGCATGGCCAACAACAT	TTGTCAGCAGACAGGTAGGC	095B2D06
AUBES4147	1229	255	23	26.5	TGTGTATTTACAGCCAAAAGCA	GGGAAACATGTTAAAATTCTTGTCT	086A2C08
AUBES5301	2671	294	23	26.5	TAGCGGTTAAAGGGGCAAC	TGTCATTTTTCGCAATTTTCA	027A1A10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5285	2601	264	23	27.3	GCTTTAGGGGTTTCCTCCAA	GGGGACTCAAGGCTCAAAGT	048B2F01
AUBES5302	2672	259	23	27.8	TGGAAGTGGCTGAATTTTACA	CCTGGACTGGTATTGGGTTC	074A2D07
AUBES4313	1947	198	23	29.7	GGTGCTCGCTGTTAACCTCT	TCTCCGAGCCGCTGTTATAG	077A1A06
AUBES1506	200	654	23	30.8	AAGCGATGATGACAGCTCAC	AACCCCATGCACATATCACAC	013A1E05
AUBES5386	3401	269	23	32.3	TGTTCCTGCTGTCTGAGCTTT	CCTCAGTCCTTCCTTCTTGCT	005A2C05
AUBES5211	2215	299	23	34.7	TCGACAGTTCGAGTGTCCAG	TTGGCTTGTGAGATGCTGTT	048B1G11
AUBES2962	1038	276	23	35.5	GATTATTTCGAGCGCGTAGC	GCTCAGGGGATCATAAAGGA	074A2C01
AUBES5238	2389	154	23	37.4	TTGTGATGAGTTGCATGACG	GCAGGTTTTCCCCTTTACCT	108A2H12
AUBES4683	2855	179	23	38.4	CAGGATAGCATCAGGACGTTG	GGTACAAGCGCGCTAAATTC	060B2D09
AUBES4327	2114	198	23	43.3	TGTTCCTGCCACTGTGTTTC	ATCTGACCGTCTGTTTGCAG	046B2C05
AUBES1900	2114	198	23	45.8	GCACAGGCAAATAAATGCAA	AAGCGCTGACACTGGAGACT	036A2A08
AUBES1411	2855	179	23	46.2	GTGATGAGGAAAGGGACAGC	ACGCTGTTAGGGGGTTGAT	024B1H05
AUBES4116	1465	484	23	47.8	GGGCACATGTGGTAAAGAGG	AGGGAGAGGGATGGAGAGAG	011B2F08
AUBES4115	1465	484	23	48.0	GGGAGGGTTAAAGAGGGTGT	GATCCTGCATGAGTGTCGTC	081B2H09
AUBES1877	singleton		23	49.4	CGGCCGTTTATAGCTTCTGT	TGAAGGCAGGATAAGCGGTA	026A2E12
AUBES4032	1351	245	23	53.4	GACTCCTGAGCTGGTCTTGG	ACGGTGGAAGCAACTGAGAG	105B2C03
AUBES4580	1904	206	23	53.6	GCTGAAACGCTTTAGGTCCA	CGATTTGAGACGCATCTGTT	086B1G08
AUBES4676	2803	201	23	53.6	TCCACATGAGCGCATTTAAG	AAGCAACAGAAAGCCATTAAGAG	092B1A11
AUBES1328	1351	245	23	53.7	ACACAGAACGAGACAGGTGAG	AGGTACTCCGACCTCCACAG	022A1H01
AUBES4031	1351	245	23	60.7	CTGCGGCATAAAACAAAATG	GTGGTATAATCCGCAAGAACG	062A1G09
AUBES5291	2619	208	23	71.9	GACGCCTATTTTCAGGCATT	ACCGTCGTAATCGTCAGGAG	066A2E08
AUBES4290	1697	269	23	84.5	TTCTTCACAGCAGGTCGTTG	ATGGCTATTTGGAGCGTGTC	039B2D09
AUBES4289	1697	269	23	86.2	TCTTCACGTAGGGATGACACC	CTGGAGCCATATTCGCAGTT	031A1G02
AUBES3062	790	651	24	4.8	GCAGTGTCTTGACAAATGGACT	TTGCACAAATTCTCACTTGGA	004A2F01
AUBES2490	295	359	24	5.2	AGTGCGCAGTCTGTGCTG	AAGACACACAGGAGGCCTTG	046B1C02
AUBES1978	3272	140	24	7.2	TGCAACATTTCCCCAAGTTT	GGGGACCTTATGGCACTGTA	022A1H11
AUBES2563	246	494	24	11.2	TGGCAAACTTTTGTTTGAACC	CATCACGTGAACCAGCTCAT	022B1F03
AUBES2583	890	863	24	11.2	ACCAGCTTAAGACAGCAGCA	AAGACCTTCTACACTACAGTGATCTTT	032A1H04
AUBES3281	188	296	24	12.5	ACGCTTCCTCCAAGTCATGT	CTTGGTGCGAGGGTTGTAAT	112B2E07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3931	1338	490	24	12.9	TTCGTGTACGAGTGCCAAGA	CACTGCTCGGGGATGTAACT	074A2C10
AUBES4630	1997	240	24	13.7	CTACCAGGTTGGGCAGACTC	TGTTTCAGTTCGCTGCACTT	061B2A05
AUBES3711	398	761	24	14.1	GAAATCTTTGTATGCCTGGGTA	AGAGCAGGCCTCTCCTCTG	023A2F11
AUBES2513	838	260	24	14.4	TCCCTGATTAATGCCATTCG	GAGAATGCTTGCACATTCCA	048A2F03
AUBES3902	915	218	24	14.4	ATGGCATGAGAACATCAACG	GGAATCACGGGAAGACGTTA	036A1A07
AUBES2788	589	303	24	14.4	ACTCCAGGTGAGGGGATGT	TCATTCATCGCCAGATGGTA	055B1A06
AUBES3335	246	494	24	14.4	CAGAGCCTCCGAATGTTACC	GCTTTCTGTGAGGATGCATTT	083A2D09
AUBES2658	372	438	24	14.4	AACAGGAGCAATTCTGCAATC	GCACAGCCTTCACTATGCTG	057A2H10
AUBES2848	444	296	24	14.4	GGAAGGTTCTGTGCCGAGTA	GCCCCATCCTGATTTCTTCT	030B2E03
AUBES3305	589	303	24	14.4	CACTCCAGGTGAGGGGATGT	TCATTCATCGCCAGATGGTA	055B1A06
AUBES3073	890	863	24	14.4	GCAGCGTGACACGGTTTAT	CCCCTGCTACTTCACCATTC	011B2H02
AUBES4742	2436	223	24	14.6	CATTGCTCCAAAACCACAGA	GGGCATCAATCACTTCAACA	048A2B03
AUBES4995	1048	272	24	14.9	CCCTGATGGAAGGATCTGTT	TGTGAGCATTGTGACCCATT	034B1G06
AUBES3481	295	359	24	14.9	AGACACCGTCGTATCGCATT	GACTCTCCACAGGCATCACC	111A2G04
AUBES3375	50	1049	24	15.0	CGTGTGCTTTATTTGGCAGA	GGACCGAGTACCTGTTCCAG	106A1B04
AUBES3206	246	494	24	15.0	CAACAGACTGTGCCGGAGT	ACGTGGTCGATAAGGCATTC	035B1H08
AUBES4917	415	282	24	15.0	CACTACGAGGGCAGGGACT	GACGAACAGCATTGTGGGTA	014B1B07
AUBES5008	1129	401	24	15.0	GGAAAATCCTCCGCTTATTCA	CAAATCCGACCATGACACTG	107B2A03
AUBES3041	823	411	24	15.0	CAGGGTCAAGTGGATGGAAA	TCACATGGCTGAATTTGGTG	062B2C02
AUBES1551	878	338	24	15.1	GCTCAAAGGACAGCAGAACC	AGGGTTGGAAGCAGAGTTGA	025B1A12
AUBES2720	823	411	24	15.1	TGTGAAAAGGATAACTGCATTG	CATAATGAGGAACTGGTCTGGA	012A1A04
AUBES3693	838	260	24	15.5	TGCTTTGGTACTTCCCTTCAA	AGCCTGCAAGCAGAATTATTTA	010A1E04
AUBES4826	3157	127	24	15.7	ACACAGAGCAGGGACGTTTC	TTCTCTACCGCCCAGCTTAC	082A2B06
AUBES3910	1043	166	24	16.1	CCCTCTCTGAAACCCAGCTA	GAGCACAGCCTGAGAAAAGG	030A1F04
AUBES5179	1985	282	24	16.4	CGGGACTAAAGGATTGGAAA	AGAGGGAGCTGCAAGAACAC	006B1D10
AUBES5063	1375	240	24	18.0	GTCAAGCCAGGCCACATTAC	GCAAACTGTCAGCCAGTCAT	073A2A06
AUBES4865	2094	374	24	18.8	ATCCTTCTGCAGCTCGACTC	GAGTACCGGCTTCTGAGTGC	052A1A02
AUBES2681	398	761	24	19.7	GTTGACGGTGATCGAAGACA	GGGGTGTAGACAGCCCTTTT	006A1D04
AUBES4360	695	565	24	21.0	ACCAGGAGCTTGTTGACTGG	TTCGTTCAGGAATCCAAACA	080A2D12

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4864	2094	374	24	22.3	TCAGCGTCAAGAGACCAACA	CATAGTGGCGCAATCAACAC	013B2F04
AUBES3503	695	565	24	22.7	ACCAGGAGCTTGTTGACTGG	TTCGTTCAGGAATCCAAACA	110B2C06
AUBES3502	695	565	24	24.2	CTTGACCCTGATTGGGTTACA	CCCCTCTTTATGGGAAGCTC	054B2B10
AUBES4728	3543	101	24	29.1	GCCTTGGTCCTTTCATCTCA	CACCTCTTCTGCAACCACAG	063B1E09
AUBES4616	2117	222	24	30.8	GAAATTGCCGGGAAAGTGTA	TGTCTATTATGGCATTTTCTCCAA	028B2A09
AUBES2732	550	524	24	31.5	GAACGCTACTGTGGAGCTCAT	AGTGACCAGGTGAAGGATGG	022B2F01
AUBES3926	1225	399	24	36.6	GCTTCACTAAGACGCCCTCA	TCTTTCCAAGCCTCATTTCG	047A2H06
AUBES1334	1480	215	24	40.3	CCCAAGTGCCTGAGGCGAGC	GTTCACGAGGACGTGGGTCG	002B2G03
AUBES1956	1107	568	24	42.2	CAACCGATTGCAGGGTACA	CCCAGTCCAAAGGCATACAC	021B2D08
AUBES2068	2882	223	24	49.0	TGTGCGTTAACTCAAATCCTTG	GCAGACCTGTCGTCTTAGCC	039B1B10
AUBES5003	1095	255	24	50.6	CGAGCGAGGGATGTACTTGT	CAGCACGTCCCGAAGTTTAT	006A2C03
AUBES4807	3078	145	24	66.3	CCCATTTTGCTGTAGCAGGT	AGTTCCAGTTTGTGAAAATGTGT	071B1D07
AUBES4381	1626	259	24	68.2	GAAGTCAAGCGCACTCTTCAG	GAAGATGTATCATATGGATAGCTAGGA	001B1C10
AUBES3944	146	274	24	69.1	CCAGATCACTCAAAGGTCCAG	TGAATGATGGGAATGTCTGA	031B2F11
AUBES4674	2779	222	25	0.0	CATCATATATTGGTTTGTTTAAATTGG	TGGTGCTAATACGATGATACAAGG	109A1E11
AUBES2383	singleton		25	3.5	GGCGTGAAGGAACAAGAGAA	AAAGGAGGACGCGTCTACAA	044B1A05
AUBES4141	1123	568	25	12.1	AGATCAACCGCTTCCAATCA	TCCATGAGTTCTTCCGCTAAG	012A1B08
AUBES1179	singleton		25	16.8	ACTCCATTGGTTTGAGGCAC	ACGTGCATTAGTGGCCCCTG	011A2C01
AUBES1857	1123	568	25	17.4	TCACTCTCCTCTCTGGCACA	CGTTAGGCGTCGGTCATAA	036A1G11
AUBES2418	singleton		25	18.0	AAAAAGGTATTAATTTTCACTTCAACA	AAGTCACTTTCTCATGTAAATTTTTG	045B2B05
AUBES1858	1123	568	25	18.9	GCCTCCATGTCCTCCATTTA	CCTGAACGGAGCAGAGGTTA	036A1G11
AUBES4142	1123	568	25	19.8	GAATTCTGCCCATTTCTGGA	ACTGGATGTGCCGGATTACT	086B2A08
AUBES2530	277	702	25	21.5	CAGAAACTCATGTGGCCTGA	GCCTTGCATAAGCTCCTGTC	049A1E03
AUBES5295	2641	274	25	27.8	GCTGCTTGTGATGAGCTCTG	ACGTTGAGCGAAATCGTCTT	103B2B12
AUBES4180	81	585	25	38.6	GCTTCTGTATGCATGGACTTCT	AGGGATTGAGATTACACGGAGA	108A1A05
AUBES5188	2062	382	25	42.4	CACTCGACAAAACCGTGTGT	GTTAGCCTGCGTTTCTTTGG	095A2C10
AUBES5184	2015	211	25	43.5	CTGTCCTGTGCACTCGTAGG	GATGGGCCATGACTCCTTAC	104B2D05
AUBES3489	469	311	25	44.9	TGCTCTGTGTTACGTGTTTTCA	GACTTCAGGCTCTGGAATGG	038A2E02
AUBES4926	507	279	25	45.0	CCTGCTGCCTTAACCAATGT	ACAGGCGGAGAACGTACAAC	102B1E10

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4632	2029	260	25	46.0	GGTTTTAACGCACACCTTCC	AAGCTGGCTGCACGGTATTA	004A1E03
AUBES4179	81	585	25	47.3	GCAGCTCTGAGAGTCCTTCC	TGACAACGGCAAAATAGACAA	103B2A11
AUBES4295	1768	198	25	47.7	CTTGCGTGCACAGATACAGC	CACTGAGCTGCCTTCCAAAT	112B1C08
AUBES4087	1886	474	25	53.9	CTGGCCCTTTAATTCAGCAC	CTGTTGTGTGGAACGGTGAC	084A2H02
AUBES4990	1000	193	25	55.2	GGACCGTTTCTCTTGAGTTGA	GAATCGGCTTTACCATTCCA	004A2G06
AUBES3101	177	881	25	56.0	GGGGGAAATTTCATTTGACTT	GCTTCAGTGCTGTGCAGTTT	046A1B09
AUBES2450	572	271	25	57.0	GGGTTTTCTTTCCATGCTCTC	ATCATCTTTGCCTGGCTTGT	040B1C08
AUBES3042	572	271	25	57.2	ATTTGGGGGTATTGATGCAC	CTTTGTAGAATGCACAATGAAGG	062B2G04
AUBES5024	1204	284	25	57.8	CATGCAAGACCTGTGGTGAG	GGCACGTGATGCATTTTTCT	020A1B02
AUBES3920	1147	260	25	58.1	TCACGTTCCCCTACATCTCA	GATGGTGGACAACAACAACAA	112B2G09
AUBES5166	1846	281	25	58.9	ACCTCCATCCCAAAACACCT	GCTTTATATGGCCATGTGATCTT	006A2C11
AUBES3243	70	413	25	59.0	CAGAAAGCTGCTGCATCTCA	TTTGTCATGACCACTAAGGTGTG	110A2B02
AUBES3047	884	490	25	59.0	GAGAAGATGGAGCCTGTTGC	GATTATCCTGAGCGCCACTG	074A2G10
AUBES3505	16	545	25	59.2	CAGACATGAATGTGGACTGACA	CACATGGATGAAGGAAGCTG	109A2D11
AUBES3985	1897	326	25	59.2	CTTCCCCAGTCCAAAGACAC	GGTGGAATCGACACAAGGAG	096A1H08
AUBES5118	1550	266	25	59.9	TGGACTTTGGAAATGAAGAGAAA	CACCGATTTTGAAGGTTTGAG	096A2E12
AUBES4451	1507	189	25	59.9	GACCCCAATCCACCTACTGA	TTCCTACCTGCCATTCCTCA	029A1D02
AUBES2475	144	430	25	59.9	CACAGTCTTGGAGGGGAAAA	CCGTTAAGAGCCCTTTCAGA	046A1A12
AUBES3099	392	1013	25	59.9	ACCTCGATGCACAAGGAAAT	TCACCAGGAGGGGATAGAAA	004B1C05
AUBES3687	483	257	25	59.9	GCTGCCTGCCCAGTAAAGAT	GGTCAGAGGGTGTGACCTGT	013A2B01
AUBES4029	1348	286	25	59.9	CACGTAGGCGTAGATCGTCA	TACGTGGACCATAGCCTTCC	104B2G08
AUBES1873	177	881	25	60.0	CTGCCCTCTGATACCTGCAT	TTGCCTGCTGAACATGATTG	025B1H07
AUBES2869	144	430	25	60.0	GGAACTCTCTGTTCCCACTCA	TTAAGCCTTGGTGGTTCGTT	060B1H06
AUBES2656	357	320	25	60.0	GCCCTCTGGGAGTTTAAGGA	TGCATGCCAGGATAACAAGA	001B2A05
AUBES2553	411	719	25	60.0	GGTTAGTGCTGAACGAAATGC	CGTCCAGAGAGAGGAATGGA	012B1G02
AUBES2847	434	347	25	60.0	TGGCAGATTTGTTTCCATCA	GGCATGGTCATATGGTGTTG	012B2C10
AUBES2770	505	384	25	60.0	CCAGAATTCACACACCATGC	CCAGCTTGAGCTGCTAGGAC	023A2C10
AUBES4284	1851	404	25	60.0	ATTTCAGCACCTTGGAGAGG	GGGATGTGCCACTAGAGACC	030A1E12
AUBES1798	1992	167	25	60.0	AGAGGCTTCAGTGTGACTTGG	TGGATGCAAGTGTGTGTGTG	034B2H02

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4028	1348	286	25	60.0	TCTCTGCATCACTGCGAAAT	TTGACTTGGCCTCCAAATTC	007B1B04
AUBES3157	392	1013	25	60.0	TGAGGACTTCTGCATGGTTTC	AGGAAAACAGGGTGCTGTGA	010A1F03
AUBES4646	554	298	25	60.0	AGGGTGTGTTGGCTTTCTTG	CAAACAACTGTTGCCTCGAC	065A2F06
AUBES4450	1507	189	25	60.1	TGCCTTAAGGGAGCTCACAA	ACATGCAAACTCCGCACAC	004A1G05
AUBES2624	177	881	25	60.4	TTGGGGTTTTTACCAAATGAAG	TGTCTGTCCAGCTATCTATCTACCTA	003A2D09
AUBES5254	2455	210	25	60.6	AGCCACCCTCCTGTATAGCC	GCGAGAGTGAGAACGAGTGA	108A1C07
AUBES2677	678	526	25	60.6	CCCAAATTCAGAGAGCCTGT	TGTGGTCTTTCTGTAAGGTGTCC	003A2H10
AUBES3547	451	311	25	60.6	CGGACATGGTACTGGTGATG	GCAGTGAGAGGGAGACCATT	108A2B12
AUBES4548	2830	338	25	60.7	GAGAGGACGTCGGTGTAGGA	AACACCCCCTCATTTTCCAC	011A1H01
AUBES3419	451	311	25	60.7	GATGGCTTGGTTTCAGTGCT	CTGTGGGACAAGTGAGCAAG	040A1G09
AUBES3032	599	494	25	61.2	TGGATCCAGAGCCTATTCCA	CTTGCCCATAAGGGTGAAGA	056A2B01
AUBES1749	1851	404	25	61.5	ACCTTGGAGAGGGAACGTCT	CTGTCTCGAAGCTGTGCTTG	030A1E12
AUBES3901	842	232	25	61.6	CAGATTGTGCCTGCTGTGTC	TGAGCTGAAGATATTCACAGGA	058B2H01
AUBES2904	678	526	25	62.2	CACTGCTTATTGAAATCCATGC	TGGGAGTTAAGGCAACTGAGA	058A1B09
AUBES1570	599	494	25	62.8	ATGGCACACAAAAGCATGAC	GCAGACTCAAAACACAGCAAA	023A1E06
AUBES5248	2425	183	25	63.6	AAGCCACAGACTGGAAAGCA	TGAGCTCAGGATGGGAGAAT	034A2B01
AUBES2621	392	1013	25	64.1	TGTGGGTTTGAGGGGATTAC	TGAGATAGGCTCCAGGTTCC	053B1B08
AUBES3467	1598	433	25	64.9	TACACAGTTGGGTGTAAGTAAGGTA	GCCCAAAGTTCAGGGTTTCT	085A2D10
AUBES4951	687	355	25	65.2	CGTCCATCTTTCCAGTGTTC	CGTCAGTCACGAAGATCGAC	024B2F06
AUBES1960	1494	242	25	65.6	TGAATTAGCCACGACAGACAA	AGCCACCAGAAGGCTAAAGG	023A1D10
AUBES4619	2132	411	25	66.2	TCTGGTGCAGTAAGCTGTGG	CCTCGCTCATTCAGAAATCC	105A1A03
AUBES4921	432	325	25	66.9	ACGTGGCTAGCAACTCGTTT	TGCCGTTTATTTGTGTACGG	042A2C03
AUBES4679	2811	200	25	69.7	AAATCACAGGCTACCGCAAC	CTCAGCATCCACCTGCAAT	011B1D09
AUBES4474	1298	274	25	70.4	TCCAGTGGAAAAGAGCCTGT	AGAAGCCAGAAGTGGGTTGA	075A2E11
AUBES4791	2929	262	25	70.4	TGCCATGTTTTCTCTGCTTG	TGTATGCAAACTGCATTCGTC	102B1C07
AUBES4736	2295	238	25	70.8	CCGGCGATTAATTTGAACAT	ACCGGTGTTTAAAAGCCTCA	030A1G02
AUBES4793	2942	201	25	71.0	TCCCACCACCATAGAGCAAT	CATCAGCACGAACGCATTA	023B2E03
AUBES4530	1797	316	25	71.7	AAGAAGCGTTTGCAAAAAGG	GGGCACTGCAGGAAGATAGA	052B2E04
AUBES5230	2354	230	25	74.1	GGGTGTGGAACCAAATCAGT	ACACACGCAAACGAAACATT	102B1H02

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4452	1596	279	25	75.2	CGCTTAATAGGACGGCTGTT	ATGAAAGGCACAGACGCATT	032B2D06
AUBES2491	782	304	25	77.1	CCGATCATCCTGATCTCCAG	GCGTTTAACCCTCAAACGAG	046B1F03
AUBES2074	2953	242	25	84.5	CCTCTGCTCGGATAAGACGA	GCATCAAATGACAGCTCGAA	039B2B06
AUBES4291	1704	303	26	0.0	CGACGGACGAACTCCTATGT	TCCAGTCGCTTACACTGAGC	063A2C02
AUBES5414	3541	110	26	1.6	AACCACTGTCCTGAGGGATG	GATATCCTCGGGGAATAGGG	108B1G01
AUBES4753	2634	145	26	10.1	GGATTTTGCCTTGCCCTTAT	ATTAGTGATGCCTGCGAAGC	051A1F05
AUBES1808	singleton		26	12.0	CTGACGTCCTGCTCTGTTCA	TATGTGGAGACGGGGTCAAT	034A1D12
AUBES4603	1982	223	26	15.3	CAATCGCAGGTGGTCAGACT	TCGACTCATCTGTGAGCTGAA	049B2C03
AUBES1964	1536	440	26	18.3	TCCTGTTTTCCCTTCACAGC	GCTCCCCATCTCTCTGTTTG	027B1G12
AUBES4984	979	348	26	18.4	GCCTGGCCTTCTTAATTTCG	GGGAACTTTCCCTCACTGCT	054A1B12
AUBES4836	1536	440	26	18.4	ACCTGGGTATGAACCACGAC	ATATTTGACGGCTGCTTGAG	112A1C11
AUBES4837	1536	440	26	19.2	CACATGCAAACACACACTGG	CCCTGCTCTCAGGAATTCAG	003B1H01
AUBES1891	2357	266	26	19.2	CGCACGACTCGGACAGTAAT	GCAGAGAGTCATGTAGGGTGTG	030B1F12
AUBES4618	2122	233	26	25.2	CGTCGCTTCAGTGGATTCTG	TTATTTTTCATTTTGTATGTATTCTGC	053B2B05
AUBES5406	3512	157	26	25.7	GAGCTAGCTAGGCAGCATGAG	CAGGTTACCCCGCTAGCTAGTAT	014B2D09
AUBES4411	2357	266	26	25.9	CCACCCCGTCATTGATTTAT	TCGGCATGTCCACAGTGTAT	074A1D06
AUBES4794	2955	178	26	26.4	TTCGAGAGAAAGGTTTGCTGA	CAGGGACCGTAACTGGTTTG	084B1A03
AUBES4805	3059	161	26	26.4	GGTCAGTCCCTCATCGACAC	TACCCTCACACCACAAACCA	111B1A08
AUBES4410	2357	266	26	29.5	CGCACGACTCGGACAGTAAT	TCTGAGTCACGCCATGAAAG	030B1F12
AUBES4634	255	227	26	31.4	GCACTCTAACTAACCAACCCACA	ACCACCTGCACAATGTCATC	001B1D04
AUBES1865	1314	570	26	31.5	TGAAACTGGATCAGAGGCTTT	CGTGTGGAGCAATTTGAGTG	022B2C01
AUBES4239	923	210	26	31.7	CAGGGGATTTGTCCCATCTA	TTGCCCATAACACAGGGTCT	021A1D08
AUBES1301	singleton		26	31.9	TCCTTCACTGCTGTCTGAGC	GCAGTCATCCAGAGTCCCAG	
AUBES1300	singleton		26	31.9	CTATGTTCAGATGACCCATGAAGG	CTATGTCAAGACTATGGCGATGTTG	021B2H07
AUBES1333	399	249	26	32.6	TTGTGAGGGTCCTCATGCTC	GGATTGTACGTTCTGCTTGACG	014B1H11
AUBES4877	399	249	26	32.7	GTTTGTGAGGGTCCTCATGC	AAAATCCCACACGTCAGGAG	052A1C01
AUBES4230	760	277	26	34.2	TGCATGGAGGAGTGAAGTTG	AGGGTGATGAGAAGCAGCAG	075B1G11
AUBES4741	2403	210	26	34.6	TTCCCTGGAGGAATGAAGAG	TCACCAACCACCTTCTGTTG	072A1H10
AUBES5052	1334	357	26	35.0	GCCCCAGGGTGATACAGTAA	GCACGGACAGCACCATCTA	085A2C02

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3034	1232	633	26	35.2	AACACAGCGCCTCAGATAGC	TAGCTGGGCATGGTGAAAAT	058A2E03
AUBES4439	1427	238	26	36.3	GAGGAAGCAGGCTGAACTTG	CCAGGAGCTCTGTCTCGACT	108B1F03
AUBES2789	658	328	26	40.6	CCAACTGACATGTTTTCAGGA	TGTTAGAGGTCAAAGATGGATGA	007A1D10
AUBES4292	1732	250	26	40.8	GCCATGAAAATAAAGCCACAT	TGCCATTAATCTCTGTGAAAAAG	023A1E05
AUBES1595	singleton		26	41.6	GGGTGCAATTTTTCACATGG	CATGGGCATGATCACAGACT	021A1F09
AUBES4825	3155	220	26	42.2	TGACTTAAATCAACATCATGTGC	GTGGCCACCAAATTATCAGG	059B2A08
AUBES1872	658	328	26	43.0	CTGGAATACACCCTGCATGA	TCCTGAAAACATGTCAGTTGG	007A1D10
AUBES2372	142	418	26	45.0	CCGGTTATTCCGTGGGTATT	GTCGGCGTTCAAAGTTCAAT	044A1C03
AUBES2698	142	418	26	45.7	ACGGAAGCTGATTCGCTTAG	GTCGGCGTTCAAAGTTCAAT	019B2G07
AUBES4312	1944	242	26	47.2	GGACTGGAAGCCAGATGTGT	ACCCGAGAACACAAACTTGA	029B1D08
AUBES2923	1106	446	26	47.5	ATCACGTTTGCTTGTCCAAA	CCACTGTTGCTGTGAGCTTG	008A1F03
AUBES2824	532	272	26	47.8	GAGCAGGTCGTTTGTGTCAA	TGCTCTTTCCAAGCCTTTGT	020A2F04
AUBES4520	663	227	26	47.8	CTTCAACCAGGCCACAAATC	AGTGTTCCACTTGCATTGAGC	004B1B11
AUBES3091	40	671	26	48.2	ACTCTGAGCCTGAGGGGAAA	TGGAAGAAATATGAGGATTCTGAC	106B2C01
AUBES3095	403	966	26	48.4	ACTGCTGCATGTTCTGGATG	TGACGCCTTCTGTTTTCTGA	084A1F12
AUBES5413	3538	123	26	48.4	GCGTGGTCTTTGTACTGTGG	AACTGTCGTTACTAAAAGGCTCA	043B2H10
AUBES3764	541	386	26	48.6	AGCACTCTCAGTCACGCTTTC	GGGATGAACTTCAGGACAGG	043A1F08
AUBES3153	403	966	26	48.7	CCCTGGCCATCTCAAAGTAA	CTGCTGTAATGTCGCAAAATG	052B2H05
AUBES2477	1398	526	26	48.7	TCATATGTGCATGGGATTTGTT	CCCATCACTCACACTCTCCA	046A1C04
AUBES4194	360	416	26	48.7	GCTGAGAATTAGCCGCACAT	ATGACAGCTGGCGTAACACA	110B2F05
AUBES2547	403	966	26	48.8	AGCCAGCAGAACAGCTTGAC	GCCTCTCCCTCTCCTCTCTC	049B2A11
AUBES4934	575	470	26	48.8	CCCGTTTGCAAGATGTCTTTA	GCCCTAACAATTTGGTCTGC	073A1E05
AUBES4218	1621	487	26	48.8	ACAGGCAGTTTAAAACCATTCC	CCTTCCACCTTCCATTTTTG	013B1E02
AUBES1847	40	671	26	48.8	GCTATTAAAGGCTCGGAAGG	GCCTTCAGCAGGGAAATCTA	036A2B09
AUBES4333	2201	293	26	49.5	TCCCACACTTTGTGGTTTCC	GCTGTGGAACGTCCACTAAAC	095A1G08
AUBES4220	1621	487	26	49.8	GTAAGGCATGCACAAACACG	TGCACACAGTCTGTCCAAGT	047B2C09
AUBES4130	972	220	26	50.3	CTTCATTGATTTGGCAGATTGA	CCAGTTCCTATGTCTGGACTCTG	002B2A06
AUBES3911	1049	267	26	50.6	CACAACTCAGCAAGCACACT	GCTGTGTTGCACAGGCTTAT	068B2H04
AUBES1754	51	233	26	51.0	AGAGAGGCCTTTTCACAGCA	TGTAAAGTGCCTTGAGAAGCTG	024A1G05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3593	1093	462	26	51.8	TGACGTGTGGTTGCTTAAAGA	GACCGATGTTCCTTCACCAT	090A1E09
AUBES3592	1093	462	26	52.1	CACGCCCTTTCACAGTACAA	CTGCCACCCATCCTTCTATC	087A2G05
AUBES2615	403	966	26	55.0	TCATGATGTTCAGTAAGTTCAAAGG	CATTTGTTGTGTGAGCAACATT	072A2F09
AUBES2655	333	279	26	57.5	GCTTGCTTGGTTATCATGTGC	AACAGGACGCAGCAAAATGT	023A1A09
AUBES5060	1366	362	27	1.6	CACGTTGGCCTTATGACCTT	GCTGCGATATTTAAAGGTGTTTCT	073B2C01
AUBES4058	359	309	27	13.7	GCACAACAGTGAGCGATTCC	GGTTTCGATACGGAGCGTTA	035B1C05
AUBES1727	singleton		27	20.4	CAAAACAGTCCTGGCTGACA	TCGATCCGTGGCCTAAATAC	023A2C12
AUBES4914	353	308	27	25.5	CCATGTTGAATATCCACCAAGTTA	ATGCAGTGCTCGCTATGCTA	048B2C04
AUBES4944	638	271	27	29.6	GCATGCTTCTGTCATCTAGCA	GGTGTTGGATAACCTTTCTTGC	064B2H05
AUBES2117	9	2006	27	30.4	CGATATTTCTTACGCTCCACA	TGCTTTGAGACAGCGTCCAT	041B2H10
AUBES3260	463	448	27	32.1	ACCATCGCACCTAGCAGAAC	AGTTGGAGCCAGGTAAGTGC	046A1B03
AUBES4107	1281	250	27	34.4	GCATATGCCTGCACAAAGAG	GTGGTGACATGCTGTGAATG	109B1D02
AUBES3571	844	271	27	35.8	GCCTCACTGGGTAACTTGCT	CAGTTGACATTTTGCTGACG	033B2G03
AUBES3572	844	271	27	35.8	GCCTCACTGGGTAACTTGCT	CAGTTGACATTTTGCTGACG	084B1F08
AUBES1533	2578	183	27	36.6	CAGCAAACAATCTGATGTGGA	AAGCCTTCCTGTCTGTCAAAG	023B2F11
AUBES1281	2724	179	27	38.6	TGGAGAGAGTCAACACGCAG	ACCATAATCTTGCCACAAGCAG	019A2C04
AUBES4654	758	277	27	39.3	GGGGCTAAACTCGGCTTATT	TGAACTCTTATGATGGGAAAACTT	061B1D09
AUBES4334	2227	254	27	39.3	TTCGACATAGAACACCAGAAGG	TTTGTTTTCAGGCTTGTTTTG	083B2H09
AUBES1395	1858	299	27	39.7	GTTCTGGGGTCGCCATTAC	CTTCCTAATCTCTTGTGGACAGC	018A1D06
AUBES2629	154	1130	27	40.1	GATTAAACTAATGGATGGAGAATCG	GCGAAGTCATTCAGCGTTAG	012A1D01
AUBES1714	990	286	27	40.1	CCCACCTCATGTCTGTGAGT	TTGCATCCTCTTCCTGCATA	033B2D03
AUBES2412	1791	352	27	40.1	TGAATAGCCCAGGAAGCAAT	GCAATGAATCCGAGAAACAAA	045A2F08
AUBES3231	9	2006	27	40.2	CTTGAGCAAGGCCTTTAACC	TGGCTGTGATTGATGAGTGC	064B1A10
AUBES3959	728	766	27	40.2	CACTGGTCACAGGGGGATAC	CACAGTGCTGGAGATGTTGG	102A1B03
AUBES3462	1196	266	27	40.2	TAGCAGGAAATTAGCGGTCA	CACTTGCACAAATGCTTCCT	022B1H11
AUBES5207	2195	293	27	40.2	CCACATCGATTGGTGGTACA	CACTCCAGCTATGGCAAAGG	069B2E11
AUBES2124	990	286	27	40.2	TTGACTCAATGGGCTTTCTG	AGAGGGTTACACACGGCATC	018B2C02
AUBES3732	1139	266	27	40.3	TCTCAAGCATGTGAGAAATCTG	AAGTAATCAATGCGGCCAGT	073A1D08
AUBES4966	832	340	27	40.3	CAAACAGGAGCAATGGAAGG	TACTCATGGCCACACAGCAC	109A2A07

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES5053	1335	196	27	40.6	TGGCACGCTTGATGCTATAA	AAGGACGGGCTGAGATGAAT	098B1E11
AUBES3372	154	1130	27	40.7	GATTAAACTAATGGATGGAGAATCG	GCGAAGTCATTCAGCGTTAG	084A1H10
AUBES1773	990	286	27	40.7	TCAGCTTCCCTGCTTGATTT	CCCAGTGTCCCAAAAAGAAA	033B2D03
AUBES3918	1010	386	27	40.7	CAGAGCAGAACACAAGGGTTT	AGGAGTAGTGGGGCTTTCCT	062B1C04
AUBES1721	463	448	27	41.5	ACCATCGCACCTAGCAAAAC	AGTTGGAGCCAGGTAAGTGC	019A2F09
AUBES2693	744	516	27	41.6	AAGGCCTTGAATCATGTTGG	TCGATTTGACACCTCACCTG	012A2D07
AUBES1747	1335	196	27	42.0	TTCTGCTCAGAACCCTTTGC	GCAACATGACAACTCGGCTA	074B2G08
AUBES3021	1387	648	27	43.0	TGCAAGTGAGAAAACACCACA	CGCACATACACAGCGTTTCT	047B1G04
AUBES3737	1387	648	27	43.1	AGCTGCATGGGCTTTCATAA	CTTTTGGCTTCCACTCAAGC	077A2E06
AUBES4109	1377	264	27	44.4	ATTGGGGTAGAGGCAGTTGT	CCTGGAACCATATTGGCATT	010A2F12
AUBES1878	2270	272	27	45.8	TGAGGATCAGGCAACATCAG	GAGTCCCTGCTTGCACTCTT	026A2G10
AUBES4378	1551	201	27	46.4	TTGTGCCTAAGCAACAACTCA	CATGGCCCAGTGAAATCTG	072B2G03
AUBES4672	2775	198	27	48.5	ATTGCCGAAGCCTAATTTCC	TGTATTTGTCCGCCCTTAAA	006B1G03
AUBES1547	1551	201	27	50.6	CTGGAAGCAATGTGTTGTGC	TGGCCCAGTGAAATCTGTTT	008A2G06
AUBES1951	1377	264	27	51.0	CTGCTGAGATATGGAGGAGGA	CCACCCCTCCCTTTGTTTAT	020B2D10
AUBES5225	2324	210	27	63.4	CAGGGAACTCCCAGCAGTAA	AAAGGTTTGTCCTTCGCTTG	073B2A03
AUBES2273	singleton		27	66.7	CTCGCTGGTGAACTCTAGCA	CAAAAGAAGGTTCGATGAGG	043B1D05
AUBES5025	1212	282	27	73.2	CCAGCAGATTCTGGGAGATT	TGCCACTGGAAATTATGGAA	053B1G08
AUBES1279	3339	288	27	80.5	CATGCAGCACATGGCCGTGG	TCGTGAGCAGAACCCTGGAC	022B1G11
AUBES5000	1078	387	27	86.5	GATCAGCTGGTGGAACGAAC	GCGAAGAGGTCCTGAGTTTG	056A1E11
AUBES4623	2165	320	27	93.8	TTTTACCCTGGGAACGAATTT	CATTCTGTGCAGCGTTCACT	047A2A01
AUBES4317	1964	228	27	98.2	GAACTCATGATGGAGCAGCA	TCAGACCACCCAGTGTTTAGG	021A2D07
AUBES4946	656	286	28	0.0	CGGTGGTTAAAGGTGACGAT	AAGGGAGCAGTTTTGTGGATT	071A2A11
AUBES2721	230	357	28	0.7	TGTTCCCTGTCACTGGACTG	TTTCCCAAATATTCCCAGTTG	012A1B09
AUBES3430	581	353	28	0.8	GAGGACGCTGATGGAGTCAT	CCGGAAATTGGATTCTGGAT	054B2C08
AUBES4355	581	353	28	0.8	CTGCATGAGATTTAAAGGGGTTA	GGGGTCATGACGTGAGAAAT	093A2G05
AUBES3288	318	453	28	5.0	GCGTGCATAAATGAACACAA	TACGCCTCAGTATGGCACAG	103B1E07
AUBES5205	2184	196	28	5.0	TTCCCTTTTCCAGGTAGTGC	CTCTCAATCAAATCTGCTTCCA	078A2G04
AUBES1789	318	453	28	6.1	CGGGGCACATCTTACAATTT	CGTGCCATGAAAGATGACAA	034B2C05

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES1979	460	690	28	11.5	GCGTAAGTGAGAACAGGAACG	TAAACTGCGGAAAACACCTC	022A2D02
AUBES5033	1239	282	28	15.4	CGACGTGTTTCCTGTTTAATGA	GGAGGACGTTAGCGTGAAAA	110A2A09
AUBES4747	2550	223	28	19.2	CATGTGGAGCACCCATAGTG	ACCACTGTCACACCGTCAGT	007B1F07
AUBES4748	2554	277	28	19.2	CGGAAGGAGTCTCCAGTTACG	CAATCGACTTCAGGATGGTG	084B1H05
AUBES3028	21	291	28	28.0	GGGAAATTCCTCAAGAAATCG	GTGGTGTGAGGGCTACATGA	053A2D05
AUBES3888	1288	242	28	28.4	ACGCAGACAGAGCTTCCAGT	CCAGCCCTTAGCACATGTTT	046A1E05
AUBES5290	2616	238	28	30.6	ACCGATTAATGCCCTTGGAT	GGATATGGCTAACATGGCTGA	106A1C11
AUBES1736	1902	516	28	31.0	CCCACCCTATGTCCTTAGCA	GGTGAACAATGGCTGGAGTT	030B1C05
AUBES5213	2230	244	28	34.3	GCTCTCTGGGTGTCTTCGAG	GGCTTTAGTAAGGAGGTGATGAA	014A2D07
AUBES4890	951	210	28	35.8	GTACCCCAGGTGTGTTTGCT	CTCAGGAGTTTTCCTCCACTG	020A2E12
AUBES4891	951	210	28	36.0	ACCCTGCACTGCTCTCTGTC	TGCAGGCGGATTGTCTTAG	108A2A11
AUBES3956	582	758	28	36.2	TTGCGATATCCGTAAGTCATGT	GCCGTACAAAGCAGCTCATC	075A2E04
AUBES3078	335	744	28	37.3	TTACACGCCATACAGCCTGA	GACTCTGAGCCACGGAAGTT	055A1H05
AUBES2895	582	758	28	38.8	AACCGATTGGTCAAGGTTCA	TGGGAGTTCATCCAAATGGT	064A1A04
AUBES3563	762	379	28	43.0	CGTTCCGTTATCATCGTGTG	CATGCAATGCAGGTTTGAGT	029B1D01
AUBES4726	3467	186	28	46.5	TTGTAGGTGCACGGATGAAG	TTGTGCTTTCGCGATAAAAG	032A1H05
AUBES4608	2038	291	28	47.9	CATCGCGTTCTGATCTCTCA	CCATCCGGTAATGCAATTTA	042A2D12
AUBES3564	762	379	28	48.0	CTTCACGTCCAGCAGAGACA	GCTGGGTATTGGATCTGAGC	005B1B09
AUBES3176	1363	940	28	48.6	TCACAGGGTTGCACTACAGC	ATTTTTGACCGGGGGTGTAT	034B1E03
AUBES2651	192	303	28	55.4	CAACCAGAGCAACGAGGTTT	TGGGTAAGCGTAGTGAGCTG	054A1C08
AUBES2375	9	2006	28	56.5	GCAGTCCAGAAAAGGACAAGA	CCACCCACTCAAGTTGCATA	044A2A07
AUBES4027	1343	326	28	57.7	GCATTGCCGATCAGATTACA	CCATGCAAAAATGCTTTCCT	077B2A01
AUBES2578	5	418	28	60.0	TGGTATTCTCACAAGGCAGATG	CATACCAATTGCAGGTTCCA	055A1B10
AUBES4061	437	257	28	62.0	CTGGCCAGGATGAATCAATTA	CAATGTTCTGAAATGACCCAAA	078B1B08
AUBES3550	581	353	28	62.8	CTGCATGAGATTTAAAGGGGTTA	CTGGAACGCTTCATTTCCTC	044A1C12
AUBES4062	437	257	28	63.2	TGGCCAGGATGAATCAATTAC	CAATGTTCTGAAATGACCCAAA	086B2F11
AUBES4823	3148	194	28	64.1	TGTATTGCTCCAACCTGGAA	TCCACCCATGTTTATGAATGA	049A1A08
AUBES3686	437	257	28	64.6	TGGCCAGGATGAATCAATTAC	CAATGTTCTGAAATGACCCAAA	086B2F11
AUBES3068	5	418	28	65.9	TTAAGTGCATGAGCCCACAC	TGTCCATCATGATTCCCAAA	104A1A03

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES4894	22	291	28	66.0	CTGGATAAGTTGTGTCCCTTGA	CACTTTTTCCGAAATCACAGC	008A1F11
AUBES4370	1076	484	28	66.6	ACACGAAGCTCCATGTAGGG	GAAAGCGCAACACATTGAGA	094B1B12
AUBES2077	2913	171	28	66.9	AGGAACTGTGGCATGAGAAA	GAGAGAAGGCCAGAGGTGAG	039B2E11
AUBES4788	2913	171	28	67.1	CGGCGTCGCTTCATATTCTA	GAGAGAAGGCCAGAGGTGAG	039B2E11
AUBES3589	1076	484	28	67.7	TGCTTCCCATACCAGTGTGA	ATGCCAATGAAAGGTCCTCA	028B1F04
AUBES3022	781	438	28	69.8	CCTGGAGGTGTGAGGTGAAT	CCAATAGTGGAGGGCACTGT	049B2E04
AUBES4255	1202	293	28	70.0	AAGAGATGGGTGCTCAGCTT	GCCAGCTCATGAAGTGTTTG	029A1B01
AUBES4655	138	453	28	70.0	AAGCCTCCATGGGCTAGTAGT	TGGGAATGAAAGAAATTGCAC	080B1A07
AUBES4275	1589	406	28	70.6	GGTTTGTGCAGGCATAGAGA	CCTCACAGGAACACATGCAG	036B1D07
AUBES2546	495	866	28	71.1	TTCATTGCAGGGTGCCTTAT	GTGGGTTTCCTCCAGGTTCT	049B2A02
AUBES2684	147	416	28	71.2	CGAAACAGCCAGCTACCCTA	CGTACTGTGTGTGCAGTGGA	007B1E07
AUBES3094	155	884	28	71.4	CAGGCGGACCTATTGTTTGT	TGGAAAAGGACATGCATCAG	013B2C01
AUBES4657	138	453	28	71.6	CATGCTGGCACAAGAGAGAG	TGGGAATGAAAGAAATTGCAC	112B1D03
AUBES3364	276	739	28	71.6	AGGGTATCCCAAAGGTCTCC	CTGGGATAGGCTCCAGGTTC	078A2C02
AUBES2613	276	739	28	71.6	ATTTCCCCACAAAGGCAAA	TAAAGGAAGCAGGGGGAAAT	004B2B09
AUBES3756	285	288	28	71.7	TGGTGCAAGAGATCGAAGAC	GCCCTAACCACTGAGCTACC	064B2A08
AUBES3193	276	739	28	71.7	TTCATTGCAGACAGCTGAAAG	TGGGGAATATCACAAAGTTCCT	001A1A10
AUBES4656	138	453	28	71.9	GGATGGCAGAGAAGGAATGA	TTTCAGAATTGGGGTTGTACG	109A1E05
AUBES3152	155	884	28	72.5	CAATGTGAGGAAGCCTGGTC	GTGTTTTTGGTTGCCCAGA	048A2G04
AUBES1748	155	884	28	73.6	TGACTGTGAGTAGTTTCCCTGCT	CACCTGCAACTGCACTATGA	028A2F04
AUBES4901	115	244	28	74.6	GGGGAGGAAACTGGAGTACC	TCTGTAGTGGGTTTTCAGCAA	001A2A05
AUBES2870	147	416	28	76.2	CAAGGTAACGTAGCCCTGTTTC	TAGGGCTTCTTGGGTGGACT	060A1B08
AUBES4582	1918	249	28	78.4	GGCTCAACTCTCCCACAAGA	CTCCATACCGTGTCCTGCTT	105B2A11
AUBES4581	1918	249	28	79.0	TGGTTAGTGGTGGTGAAGCA	CAATTGGTGGACAAGATCAGG	014A1D06
AUBES3340	262	795	28	80.0	CATGATTGAGGGGAACACTG	GGCTCTCGCTTGATCCTATG	074B1B10
AUBES3179	262	795	28	80.3	CACTAGATGCAGCACTGGTAAG	GGATGCCTGTTGCACTTCTA	063B2F02
AUBES3341	262	795	28	80.4	TGGAAGACCGATCTCCAGTT	GGCAACCTGAACAAACACAA	094A2B03
AUBES4277	1632	386	28	80.6	TTGCTGGCTTTGCATCTGTA	ATTGTGCATGGTTGCTCTGA	096A2H08
AUBES3493	537	321	28	81.4	TGGGTTTATGGCTGAAGACAC	CTGCTCATGGTGCCGTTAAT	043A2D04

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES3007	622	541	28	82.5	TTAGCTGCTTCACCCTGGTC	ATGGGTTTCCCCTAGTGCTC	080A2B05
AUBES1957	131	257	28	85.0	TTTGCATGGTACCTTCATGG	CCCCTCGATCTATGCTCACT	022A2H04
AUBES1146	262	795	28	86.9	TCAAAACCAAAAGCAGGTCAGAC	AGTGGCTGCTCTGAGGCGTG	007B1F03
AUBES1874	247	472	28	88.5	GGATGGGACGTCAATCCAT	CCCACTGTTCAACAACATGC	026A1E04
AUBES2899	622	541	28	93.4	CATGTGCATACACACACTTTCTG	TGACACAGCAGCACAAGTAGG	040A2E07
AUBES4767	2733	139	29	4.3	TGGAAGACCTGATTATTCTGTACG	AACGGAAAGGAGCGATTTTAG	096A1H09
AUBES5244	2411	220	29	7.2	TGCGGTAGCACTGTAGATCG	GCAGGTACCGCTGTAACGAG	079A1E04
AUBES4866	2174	262	29	7.6	CATCGCTGCCTATGGTGTC	TGCATTACGTTTCCAAACCA	109A1A04
AUBES4797	2997	249	29	11.3	TCTTGCCTGCCCTTGTTTAC	CGTACGTTGTTTTCTCCAAGG	051B1D06
AUBES3854	3420	260	29	29.6	TACAACTCGCTCACGCACTC	AGTAAACGTGTCCCGGTTTG	050A2H04
AUBES4119	1558	424	29	34.6	TTCACAGGTGGGTGAAAACA	TTTCTATCCGCCAGTTCCTC	059B1B10
AUBES4221	513	276	29	36.2	CAACCTACCGGGATTTCTGA	CTCTTGGCCATCTTGGTGTT	077B2H05
AUBES3977	1769	161	29	36.2	TGATGGAGTTCACCAAGTTCC	CCAGCCAATCAGATTCCACT	019A1A07
AUBES4691	2909	171	29	36.3	TGGGGGAATAAATGTGTTTTG	GGCTTCGTGCATCATTAACC	076A1F05
AUBES5395	3457	276	29	39.2	GAACCCATCACTTTGTCACG	TCTTATTTCCCCAAAATCAATCA	079A2A05
AUBES4696	2954	232	29	40.5	TCTCGACTTTCTCTGCCTGTC	TTCCATCATCCTGCACTCTG	003B2A01
AUBES1955	singleton		29	42.2	CCACACATGCTTCCAATGAG	GGAACTCGCTGAGCCTTTTT	021B1A04
AUBES4705	3088	365	29	45.7	CGTTTGCCAACAAACATCAC	TCTCCAAAATTTGCAATCCA	052A1D09
AUBES4103	1099	406	29	52.8	GCAGAAGGAAACACCACCTC	CCCCACGACCCTGTGTACTA	109A2A08
AUBES2189	1371	271	29	54.4	TGGCTGAATTGTCTGCCTAGT	GGAATATTGTACGCTGCTTGC	027B1H08
AUBES3623	294	220	29	54.9	CCGATACCAGTCACAGAACCA	CCTCACTCTTTCTCGGTGCT	009B1F10
AUBES3624	294	220	29	55.0	CCGATACCAGTCACAGAACCA	CCTCACTCTTTCTCGGTGCT	026B1E01
AUBES4762	2704	173	29	55.9	ACAGCATCCGAATGTTCACC	TGTGAATCCAGGGAGACTGA	057B1H03
AUBES3200	50	1049	29	56.6	AGGGTCCATCATGCTTTCTC	GGGTAAAGTGCTATGCCTGTG	092B2B01
AUBES3289	324	320	29	56.6	TTTTGCATTGCTGGTCAGAG	CGTCCAGTGTGAACAAGGTG	102B2G06
AUBES4484	1553	183	29	56.6	CTGGTTCAGCATGGATCAGT	TTCACAGCCTTCTTTGCTCA	071B2B02
AUBES4337	2240	249	29	56.6	GACGGGCCGTTGAATTATTA	ACTTATCGCACATGCTCTCG	077A1B07
AUBES1305	259	512	29	56.7	GTAGGCGGTCTGCCTCTCAG	AACACAGCCTGCCTCTCATC	003A1D11
AUBES2699	259	512	29	57.5	TGCACCACTGGACTATGGAG	CTGTAAGCTCACTGCCACCA	019B2H06

Marker	Contig	Contig length (Kbp)	Linkage group	Map position	Forward primer	Reverse primer	BAC_ID
AUBES2819	420	309	29	57.5	CCCTCTTCACTGCTGGTGTA	TGTCATGCATATACTACTGCTACAAGA	031A1A08
AUBES3731	675	377	29	57.5	ACGTGTGCTGAGGGAGAGAC	TTCTCACCAAATGCACCTACA	072B2D04
AUBES3554	261	174	29	57.6	GGTCTGTTTTTACTCTCGCTGAA	TCTTCCTAAACCTCCTTCCTG	031B2F06
AUBES3478	261	174	29	58.0	GGTCTGTTTTTACTCTCGCTGA	TGTCACCCAAGTCCATTAACA	078B1E09
AUBES5088	1503	166	29	58.1	GGCATTTCATTGAGGCAAA	CAGTGGTGCTTTTGGAGTGA	106B1E04
AUBES3035	203	404	29	58.8	GACACGGGGAGTTCTGAAAC	GTGCATTGTCTCATTCACAACA	058B1D07
AUBES2939	157	296	29	59.4	GCTGCCTGTTTGACCCTTAC	TCGGTCATTACCTTGGCTGT	039A2F02
AUBES2740	60	688	29	59.7	GGAGTGTGGGCAGTAGATCG	GAAAAGTGCACCGTCCTGTAA	057B2B03
AUBES3726	60	688	29	59.8	GCAGTAGATCGACAGGGAAAG	AAAAGTGCACCGTCCTGTAA	053A1F05
AUBES3645	770	249	29	63.5	CCAACATGAAAACCTGTACCA	GGCATAAAGGCTGGATTTACC	034B1D03
AUBES3644	770	249	29	63.6	CAGCTACTGCTTTGCTGCTG	TTCGGCACGCTATACGAAG	056B2G04
AUBES2355	1920	281	29	77.8	AGGGTTCAAAAGTCCACTGC	GCAATTCTCAAATGGGTAAATGA	047A2D10
AUBES2109	2022	208	29	80.1	GTGGCTCAGCTGGGTTTTT	ACCACCAGCAACGTTAGACA	041B2B03
AUBES4583	1925	272	29	97.2	CAGCGTTAATGACGCAAGAA	TCCAGTCCTCCGAGTCAAAC	080B1B10
AUBES5206	2194	316	29	97.2	GAACCGTCCTCTGCGTATGT	CTGTTTGTGGGAATGCAGATT	054B1C04

Supplemental Table 2: Ratios of physical to genetic distance across all 29 LGs. Ratios were estimated based on the difference of the physical distances (Kb) and genetic distances (cM) between multiple BES markers mapped from the same contigs.

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
1	1702	2148-2400	171	2.9	59
1	767	3565-3566	157	2.2	71
1	2142	3992-3993	259	2	130
1	2276	4540-4541	215	1.6	134
1	42	1924-2634-3108	961	6	160
1	597	1803-2358-2772	502	2.3	218
1	772	3567-3568	189	0.6	315
1	2439	1075-4414	347	1	347
1	316	3178-3209	573	1.3	441
1	949	3451-3452	162	0.2	810
1	468	3420-3421	179	0.1	1790
1	370	2627-3160	592	0.3	1973
1	2239	3745-3752	249	0.1	2490
1	1940	4860-4861	154	0	NA
1	1272	4436-4437	162	0	NA
1	351	3403-3404	216	0	NA
2	3007	1881-4698	176	8.4	21
2	343	2884-3952	166	7.4	22
2	145	2258-3394-3395	266	7.9	34
2	337	3625-3626	249	3.9	64
2	407	3627-3628	166	1.3	128
2	1706	4456-4457	232	1.7	136
2	1513	4162-4163	396	2.9	137
2	121	3184-3215	649	3.2	203
2	1693	1947-4170	247	1	247
2	1930	4848-4859	279	1	279
2	14	2676-3238	266	0.8	333
2	998	4434-4435	157	0.1	1570
2	570	1615-2085	178	0.1	1780
3	919	3771-3879-3880	223	6.8	33
3	377	3544-4350	228	5.3	43
3	477	1846-3491	259	4.4	59
3	335	2347-2595-3139	338	4.3	79

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
3	97	3074-4343	193	2.4	80
3	227	3065-3536	289	2.3	126
3	2932	4875-4876	164	0.7	234
3	480	2555-3327	201	0.7	287
3	789	3646-3647	216	0.7	309
3	702	3443-3444	203	0.4	508
3	1893	4578-4593	159	0	NA
4	703	2792-3312	161	2.7	60
4	442	2617-3154	440	2.2	200
4	623	2829-3306	242	0.7	346
4	676	3638-3639	303	0.8	379
4	94	2427-3012	127	0.2	635
4	787	1926-4083-4084	142	0.2	710
4	1487	3607-3608	159	0.2	795
4	3120	4708-4709	179	0.1	1790
4	1431	2505-4270	210	0.1	2100
4	2233	1555-4869	157	0	NA
4	557	4070-4071	200	0	NA
5	95	2982-3940	242	6.2	39
5	961	2182-4127	206	3.6	57
5	1110	1952-2993	284	4.1	69
5	2861	4685-4686	164	2	82
5	1002	4528-4529	205	1.8	114
5	341	2883-3002	490	2	245
5	2839	4425-4440-4441	183	0.7	261
5	1209	3594-3595	375	1.3	288
5	427	3629-3630	169	0.4	423
5	534	2478-2638-3170-3237	720	1.5	480
5	1044	3695-4244	151	0.2	755
5	853	3445-3446	369	0.4	923
5	190	2557-4346	173	0.1	1730
5	3037	2005-4700	304	0	NA
5	339	3402-4349	178	0	NA
5	1234	3596-4374	169	0	NA
6	1894	3701-3784	191	13.4	14
6	530	3004-3954-3955	174	4	44
6	974	3798-3799	220	4.8	46
6	93	2805-3280	142	2.7	53
6	346	2987-3255	296	4.7	63
6	786	3792-3793-3794	208	3	69

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
6	766	1306-2689	173	2.1	82
6	590	3433-3434-3664	223	2.7	83
6	1090	3591-4371	233	2.3	101
6	278	2602-3355-3384	208	1.8	116
6	776	2779-3690	184	1.5	123
6	1182	2195-4143-4144	301	2.1	143
6	229	3397-3398	230	1.6	144
6	2533	3844-3845	140	0.7	200
6	1098	2062-4003	228	0.9	253
6	193	3097-3155	247	0.8	309
6	37	1185-2623	225	0.7	321
6	1369	3777-4108	238	0.7	340
6	1058	3804-3805-3806	360	0.8	450
6	645	3789-3791	391	0.7	559
6	171	3514-3681	306	0.5	612
6	3026	4802-3852	191	0.3	637
6	196	2227-2811-3282	193	0.3	643
6	466	1935-2734-3016	445	0.5	890
6	29	2606-3359	595	0.3	1983
6	1031	3457-3458	159	0	NA
6	1455	3698-3892	151	0	NA
6	2630	3899-3900	203	0	NA
6	1635	3613-3614	377	0	NA
7	369	3408-3409	264	7.4	36
7	690	2318-2905	161	4.3	37
7	275	2562-3056	386	9.6	40
7	963	1809-4667-4668	191	3.5	55
7	9	2639-3703-3744	254	3.2	79
7	986	4134-4135	174	1.8	97
7	267	3399-3400-4348	208	1.9	109
7	608	2897-2898	337	2	169
7	1016	4097-4098	359	0.2	1795
7	328	1805-3718	318	0.1	3180
7	429	3487-3488	294	0	NA
7	216	2592-3136	196	0	NA
8	376	1786-2886-3256-3257	240	8.2	29
8	780	1283-1287-3569-4366	220	4.8	46
8	1907	4400-4401	257	5.5	47
8	159	3115-4345	213	4.2	51
8	314	1610-1635	352	5.9	60

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
8	2866	4426-4427-4442-4443	174	2.5	70
8	375	3747-3750	189	2.5	76
8	1208	2801-3321	127	1	127
8	189	3203-3326-3380	485	3.4	143
8	885	3194-3365	403	1.4	288
8	236	1763-2597-3717-3749	178	0.6	297
8	2128	1353-1990	149	0.5	298
8	455	3144-3357	127	0.2	635
8	388	3484-3485	201	0.3	670
8	1353	2802-3322	145	0.2	725
8	1909	1730-2057	201	0.1	2010
8	895	3573-3574-4367-4368	331	0.1	3310
8	443	3051-3324	394	0.1	3940
9	176	1843-2809-4659	161	14.3	11
9	72	2379-3199-3229-3230-3653-3713-3716	1049	29.4	36
9	1684	3781-3818-3819-4280	233	2.4	97
9	154	3105-3162	397	1.9	209
9	1401	2103-2709-3720	401	1.3	308
9	490	2561-3055-3118	524	1.4	374
9	981	1761-3533	612	1.6	383
9	409	1410-4060	198	0.3	660
9	985	2051-3048	257	0.1	2570
10	89	2863-3939	252	4	63
10	111	3942-3943	166	2.5	66
10	559	2437-3302	167	2.4	70
10	1315	3600-3601	216	2.3	94
10	904	3317-3739	189	1.8	105
10	381	3412-3545	156	0.6	260
10	37	1867-3225	271	0.7	387
10	625	3500-3501	191	0.4	478
10	458	3631-3632	244	0.5	488
10	436	2580-3070	663	0.6	1105
11	793	3648-3649	228	20	11
11	360	2217-2844-4192	298	9.3	32
11	941	1765-3577	266	7	38
11	41	2859-2979	255	1.6	159
11	1178	4372-4373	139	0.8	174
11	20	1859-2601	413	2.3	180
11	225	3473-3474	184	0.8	230

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
11	161	2610-3090	435	1.6	272
11	646	2123-3527-3665	271	0.7	387
11	801	3867-3871-3872	205	0.5	410
11	1743	4293-4294	222	0.5	444
11	471	3424-3425	250	0.3	833
12	169	2050-3345	220	16.3	13
12	1552	4838-4839	245	7.3	34
12	609	1726-2579-3233	95	2.8	34
12	1800	3469-3470	235	4.8	49
12	441	3416-3546	281	4.5	62
12	596	3496-3497	232	3.6	64
12	828	4232-4233	137	1.8	76
12	1646	4383-4384	211	1.7	124
12	271	1888-3049	142	0.8	178
12	217	1725-3542	220	1.1	200
12	194	2075-3342	337	0.9	374
12	3196	4713-4714	299	0.2	1495
12	518	2420-2571-3124	331	0.2	1655
12	601	2773-3708	257	0.1	2570
12	897	4887-4888	203	0	NA
12	1073	4101-4138	137	0	NA
13	1131	4006-4007	223	6.2	36
13	738	3557-4362	216	5	43
13	929	1887-2422-2908	369	3.8	97
13	416	4516-4517	228	1.9	120
13	634	1896-2158	277	1.9	146
13	199	2609-3089-3702-3149	446	3	149
13	1246	4149-4150	318	1.5	212
13	401	3486-3555	222	0.9	247
13	59	2637-3110-3678-3734	448	1.6	280
13	36	2538-2678-2977	501	1.6	313
13	1221	2039-4017	225	0.7	321
13	652	3439-3440	323	0.8	404
13	92	2704-2864	218	0.5	436
13	700	2791-3311	211	0.1	2110
13	79	3392-3393	228	0	NA
14	156	2235-3615-3616	225	8.6	26
14	710	3640-4361	282	4.3	66
14	3090	4430-4431-4447	156	1.8	87
14	1324	2352-4154-4155	284	3.2	89

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
14	526	1922-2456-3426-3549	326	3.6	91
14	595	3435-3436	279	3	93
14	1989	4604-4605	174	1.7	102
14	704	1965-3957	166	1.6	104
14	1046	3584-3585	453	0.8	566
14	2508	4871-4872	291	0.5	582
14	175	3617-3618	222	0.2	1110
15	208	3619-3620	194	14.7	13
15	76	2861-3937-3938	117	4.8	24
15	717	2831-3314	225	6.3	36
15	588	2391-3431-3432	186	3.5	53
15	514	2891-2999	218	3.8	57
15	28	3506-3507	337	3.9	86
15	214	2581-3071-3131	399	3.6	111
15	323	1912-2881	299	2.5	120
15	818	3736-4124	157	1.2	131
15	34	3072-3728	144	1.1	131
15	671	2903-3265	139	0.7	199
15	958	1737-3040	296	1.3	228
15	104	1733-2622-3100-3158	624	1.7	367
15	116	2469-2599-3191-3354	413	0.8	516
15	363	1906-3407	286	0.1	2860
15	869	3873-3875	157	0	NA
16	435	3014-3723	181	16.2	11
16	1100	2679-2910	360	11.4	32
16	1062	3586-3587	303	3.7	82
16	38	1876-2594-2978-3348	700	7.8	90
16	101	2620-3196-3224-3368	518	3.8	136
16	1956	4628-4629	255	1.7	150
16	900	4432-4433	216	1.1	196
16	153	2387-3249	151	0.6	252
16	6	3190-3219-3353	291	1	291
16	241	2274-2611-3151-3362	649	2.1	309
16	644	1886-3637	215	0.1	2150
16	2920	4428-4429-4445	267	0	NA
17	987	3579-3580-4369	250	6.3	40
17	1509	3465-3466	374	3.5	107
17	1034	2267-2466-3583	269	2.5	108
17	454	3346-3347	200	1.8	111
17	604	3437-3551	181	0.8	226

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
17	2476	4415-4416	277	1.2	231
17	1988	4402-4403	189	0.6	315
17	790	2121-2605	435	1.3	335
17	885	2616-3221-3222	521	0.6	868
17	2065	2392-4323	161	0	NA
17	180	2873-3947	216	0	NA
17	386	4663-4664	152	0	NA
17	13	2604-3085	157	0	NA
17	139	2636-3168	494	0	NA
17	726	2121-2605	438	0	NA
17	1575	3609-4375	222	0	NA
18	632	1539-2900	129	5.9	22
18	168	1325-2650-4182-4183	367	13.1	28
18	222	2608-3088-3361	616	4	154
18	564	2826-3303	211	1.1	192
18	200	3161-3391	392	1.2	327
18	639	2341-2686	534	1.2	445
18	274	2501-3208	242	0.3	807
18	406	3414-3415	161	0	NA
18	918	3449-3552	267	0	NA
18	603	3263-3689	140	0	NA
19	876	2163-3770	331	1.5	221
19	181	1892-2612	240	1	240
19	141	1699-3755	198	0.7	283
19	1984	2354-4863	418	1.1	380
20	130	3133-3234-3382	242	13.8	18
20	481	1750-2889-2990-3746	266	4.5	59
20	1029	3801-3802-3909	286	3.4	84
20	1273	4020-4021	137	1.5	91
20	306	2596-3079	391	1.4	279
20	744	3270-3741	215	0.7	307
20	580	1338-3494	227	0.7	324
20	873	4236-4237	166	0.1	1660
20	263	4660-4661	186	0.1	1860
20	281	3227-3228-3390	966	0.2	4830
20	1067	2798-3320	198	0	NA
20	1502	2996-3009	232	0	NA
20	1490	3463-3464	164	0	NA
21	1001	4095-4096	179	4.3	42
21	103	1624-1945	428	8.9	48

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
21	2092	4404-4405	286	4.5	64
21	1214	1502-1629	176	2.1	84
21	455	2603-3084	173	1.7	102
21	212	2874-3948	225	1.7	132
21	418	1700-3295	194	1.4	139
21	209	2564-3336	396	2.4	165
21	182	3142-3218-3352	594	2.5	238
21	1695	3971-3972	240	1	240
21	183	2607-3087-3147-3360	622	2.3	270
21	242	2876-3001	389	0.6	648
21	742	3642-3643	184	0	NA
22	166	2231-2389-2635-3109-3167-3378	822	11.4	72
22	1017	3456-3553	193	2.4	80
22	973	1448-1941	233	2.7	86
22	1496	3814-3815	225	2.5	90
22	453	2237-2888-3719	330	3.5	94
22	358	2271-3405-3406	216	2.2	98
22	240	3518-3519	328	3.3	99
22	252	3163-3198	467	4.4	106
22	135	2593-3187	387	2.4	161
22	39	1968-3156	132	0.3	440
22	1341	4025-4026	240	0.1	2400
22	107	2565-3059	364	0.1	3640
22	1642	4844-4845	269	0	NA
23	2855	1411-4683	178	7.8	23
23	1351	1328-4031-4032	240	7.3	33
23	2114	1900-4327	120	2.5	48
23	382	2255-3046	313	4.3	73
23	74	2625-3102-3159	558	6.6	85
23	211	3188-3217-3657	539	4.3	125
23	1697	4289-4290	220	1.7	129
23	1040	4136-4137	362	1.8	201
23	1465	4115-4116	350	0.2	1750
23	982	2484-4132	218	0.1	2180
23	2434	1330-4412	156	0	NA
23	1229	4147-4148	232	0	NA
24	295	2490-3481	216	9.7	22
24	246	2563-3206-3335	279	3.7	75
24	2094	4864-4865	311	3.5	89
24	398	2681-3711	521	5.6	93

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
24	695	3502-3503-4360	426	3.2	133
24	838	2513-3693	169	1.1	154
24	890	2583-3073	502	3.2	157
24	823	2720-3041	252	0.1	2520
24	589	2788-3305	181	0	NA
25	81	4179-4180	223	8.7	26
25	1123	1857-1858-4141-4142	370	7.8	47
25	1851	1749-4284	134	1.5	89
25	678	2677-2904	186	1.6	116
25	599	1570-3032	250	1.6	156
25	177	1873-2624-3101	805	4.4	183
25	392	2621-3099-3157	839	4.2	200
25	1507	4450-4451	167	0.2	835
25	572	2450-3042	198	0.2	990
25	451	3419-3547	129	0.1	1290
25	1348	4028-4029	244	0.1	2440
25	144	2475-2869	247	0.1	2470
26	2357	1891-4410-4411	257	10.3	25
26	658	1872-2789	206	2.3	90
26	403	2547-2615-3095-3153	830	6.7	124
26	1621	4218-4220	254	1	254
26	142	2372-2698	184	0.7	263
26	40	1847-3091	232	0.6	387
26	1536	1964-4836-4837	387	0.9	430
26	1093	3592-3593	186	0.3	620
26	399	1333-4877	205	0.1	2050
27	463	1721-3260	208	9.4	22
27	1377	1951-4109	247	6.6	37
27	1551	1547-4378	176	4.2	42
27	9	2117-3231	419	9.9	42
27	1335	1747-5053	173	1.4	124
27	154	2629-3372	183	0.6	305
27	990	1714-1773-2124	284	0.6	473
27	1387	3021-3737	369	0	NA
27	844	3571-3572	161	0	NA
28	581	3430-3550-4355	220	62	4
28	762	3563-3564	200	5	40
28	622	2899-3007	482	10.9	44
28	5	2578-3068	308	5.8	53
28	147	2684-2870	335	5	67

LG	Ctg	Markers (AUBES)	Kbp	cM	Kb/cM
28	262	1146-3179-3340-3341	521	6.8	77
28	138	4655-4656-4657	238	1.9	125
28	437	3686-4061-4062	164	1.2	137
28	318	1789-3288	169	1	169
28	582	2895-3956	692	2.7	256
28	155	1748-3094-3152	720	2.2	327
28	1076	3589-4370	360	1.1	327
28	1918	4581-4582	247	0.6	412
28	2913	2077-4788	162	0.2	810
28	951	4890-4891	159	0.1	1590
28	276	2613-3193-3364	416	0.1	4160
29	261	3478-3554	100	0.4	250
29	259	1305-2699	364	0.8	455
29	770	3644-3645	167	0.1	1670
29	60	2740-3726	222	0.1	2220
29	294	3623-3624	166	0	NA

Literature Cited

Agresti J.J., Seki S., Cnaani A., Poompuang S., Hallerman E.M., Umiel N., Hulata G., Gall G.A.E. & May B. (2000) Breeding new strains of tilapia: development of an artificial center of origin and linkage map based on AFLP and microsatellite loci. *Aquaculture* **185**, 43-56.

Baird N.A., Etter P.D., Atwood T.S., Currey M.C., Shiver A.L., Lewis Z.A., Selker E.U., Cresko W.A. & Johnson E.A. (2008) Rapid SNP discovery and genetic mapping using sequenced RAD markers. *PLoS One* **3**, e3376.

Beaumont A., Boudry P. & Hoare K. (2010) *Biotechnology and genetics in fisheries and aquaculture*. Wiley Online Library.

Booth N.J. & Bilodeau-Bourgeois A.L. (2009) Proteomic analysis of head kidney tissue from high and low susceptibility families of channel catfish following challenge with Edwardsiella ictaluri. *Fish & Shellfish Immunology* **26**, 193-6.

Cairney M., Taggart J. & Høyheim B. (2000) Characterization of microsatellite and minisatellite loci in Atlantic salmon (Salmo salar L.) and cross-species amplification in other salmonids. *Molecular Ecology* **9**, 2175-8.

Chen X. & Sullivan P. (2003) Single nucleotide polymorphism genotyping: biochemistry, protocol, cost and throughput. *The pharmacogenomics journal* **3**, 77-96.

Chistiakov D.A., Hellemans B., Haley C.S., Law A.S., Tsigenopoulos C.S., Kotoulas G., Bertotto D., Libertini A. & Volckaert F.A.M. (2005) A microsatellite linkage map of the European sea bass Dicentrarchus labrax L. *Genetics* **170**, 1821-6.

Coimbra M.R.M., Kobayashi K., Koretsugu S., Hasegawa O., Ohara E., Ozaki A., Sakamoto T., Naruse K. & Okamoto N. (2003) A genetic linkage map of the Japanese flounder,< i> Paralichthys olivaceus</i>. *Aquaculture* **220**, 203-18.

Córdoba J.M., Chavarro C., Schlueter J.A., Jackson S.A. & Blair M.W. (2010) Integration of physical and genetic maps of common bean through BAC-derived microsatellite markers. *BMC genomics* **11**, 436.

Davey J.W., Hohenlohe P.A., Etter P.D., Boone J.Q., Catchen J.M. & Blaxter M.L. (2011) Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nature Reviews Genetics* **12**, 499-510.

Eschmeyer W.N. & Fong J.D. (2012) Species by Family/Subfamily in the Catalog of Fishes. URL:http://research.calacademy.org/redirect?url=http://researcharchive.calacademy.org/research/Ichthyology/catalog/fishcatmain.asp.

Espeso E.A., Cobeño L. & Arst H.N. (2005) Discrepancies between recombination frequencies and physical distances in Aspergillus nidulans: implications for gene identification. *Genetics* **171**, 835.

Fishman L., Kelly A.J., Morgan E. & Willis J.H. (2001) A genetic map in the Mimulus guttatus species complex reveals transmission ratio distortion due to heterospecific interactions. *Genetics* **159**, 1701-16.

FitzSimmons N.N., Moritz C. & Moore S.S. (1995) Conservation and dynamics of microsatellite loci over 300 million years of marine turtle evolution. *Molecular Biology and Evolution* **12**, 432-40.

Fuji K., Hasegawa O., Honda K., Kumasaka K., Sakamoto T. & Okamoto N. (2007) Marker-assisted breeding of a lymphocystis disease-resistant Japanese flounder (Paralichthys olivaceus). *Aquaculture* **272**, 291-5.

Gilbey J., Verspoor E., McLay A. & Houlihan D. (2004) A microsatellite linkage map for Atlantic salmon (Salmo salar). *Animal genetics* **35**, 98-105.

Groenen M.A.M., Wahlberg P., Foglio M., Cheng H.H., Megens H.J., Crooijmans R.P.M.A., Besnier F., Lathrop M., Muir W.M. & Wong G.K.S. (2009) A high-density SNP-based linkage map of the chicken genome reveals sequence features correlated with recombination rate. *Genome research* **19**, 510-9.

Gustafson J., Butler E. & McIntyre C. (1990) Physical mapping of a low-copy DNA sequence in rye (Secale cereale L.). *Proceedings of the National Academy of Sciences* **87**, 1899.

Gustafson J. & Dille J. (1992) Chromosome location of Oryza sativa recombination linkage groups. *Proceedings of the National Academy of Sciences* **89**, 8646-50.

Hansen A., Rolen S.H., Anderson K., Morita Y., Caprio J. & Finger T.E. (2003) Correlation between olfactory receptor cell type and function in the channel catfish. *The Journal of neuroscience* **23**, 9328-39.

Hubert S. & Hedgecock D. (2004) Linkage maps of microsatellite DNA markers for the Pacific oyster Crassostrea gigas. *Genetics* **168**, 351-62.

Jemal A., Barker S.A. & Means J.C. (2010) Dose–response relationship, kinetics of formation, and persistence of S-[2-(N7-guanyl)-ethyl] glutathione–DNA adduct in livers of channel catfish (Ictalurus punctatus) exposed in vivo to ethylene dichloride. *Environmental Toxicology and Chemistry* **29**, 1537-44.

Jiang Y., Lu J., Peatman E., Kucuktas H., Liu S., Wang S., Sun F. & Liu Z. (2011) A pilot study for channel catfish whole genome sequencing and de novo assembly. *BMC genomics* **12**, 629.

Karsi A., Cao D., Li P., Patterson A., Kocabas A., Feng J., Ju Z., Mickett K.D. & Liu Z. (2002) Transcriptome analysis of channel catfish (Ictalurus punctatus): initial analysis of gene expression and microsatellite-containing cDNAs in the skin. *Gene* **285**, 157-68.

Knapik E.W., Goodman A., Atkinson O.S., Roberts C.T., Shiozawa M., Sim C.U., Weksler-Zangen S., Trolliet M.R., Futrell C. & Innes B.A. (1996) A reference cross DNA panel for zebrafish (Danio rerio) anchored with simple sequence length polymorphisms. *Development* **123**, 451-60.

Knapik E.W., Goodman A., Ekker M., Chevrette M., Delgado J., Neuhauss S., Shimoda N., Driever W., Fishman M.C. & Jacob H.J. (1998) A microsatellite genetic linkage map for zebrafish (Danio rerio). *Nature genetics* **18**, 338-43.

Kocher T.D., Lee W.J., Sobolewska H., Penman D. & McAndrew B. (1998) A genetic linkage map of a cichlid fish, the tilapia (Oreochromis niloticus). *Genetics* **148**, 1225-32.

Kreike C. & Stiekema W. (1997) Reduced recombination and distorted segregation in a Solanum tuberosum (2x)× S. spegazzinii (2x) hybrid. *Genome* **40**, 180-7.

Kucuktas H., Wang S., Li P., He C., Xu P., Sha Z., Liu H., Jiang Y., Baoprasertkul P. & Somridhivej B. (2009) Construction of genetic linkage maps and comparative genome analysis of catfish using gene-associated markers. *Genetics* **181**, 1649-60.

Lee B.Y., Lee W.J., Streelman J.T., Carleton K.L., Howe A.E., Hulata G., Slettan A., Stern J.E., Terai Y. & Kocher T.D. (2005) A second-generation genetic linkage map of tilapia (Oreochromis spp.). *Genetics* **170**, 237-44.

Li Y., Byrne K., Miggiano E., Whan V., Moore S., Keys S., Crocos P., Preston N. & Lehnert S. (2003) Genetic mapping of the kuruma prawn (Penaeus japonicus) using AFLP markers. *Aquaculture* **219**, 143-56.

Liu B.H. (1998) *Statistical genomics: linkage, mapping, and QTL analysis*. CRC.

Liu H., Jiang Y., Wang S., Ninwichian P., Somridhivej B., Xu P., Abernathy J., Kucuktas H. & Liu Z. (2009) Comparative analysis of catfish BAC end sequences with the zebrafish genome. *BMC genomics* **10**, 592.

Liu S., Zhou Z., Lu J., Sun F., Wang S., Liu H., Jiang Y., Kucuktas H., Kaltenboeck L. & Peatman E. (2011) Generation of genome-scale gene-associated SNPs in catfish for the construction of a high-density SNP array. *BMC genomics* **12**, 53.

Liu Z. (2007) *Aquaculture genome technologies*. Wiley-Blackwell.

Liu Z. (2011) Development of genomic resources in support of sequencing, assembly, and annotation of the catfish genome. *Comparative Biochemistry and Physiology Part D: Genomics and Proteomics* **6**, 11-7.

Liu Z. & Cordes J. (2004) DNA marker technologies and their applications in aquaculture genetics. *Aquaculture* **238**, 1-37.

Liu Z., Karsi A., Li P., Cao D. & Dunham R. (2003) An AFLP-based genetic linkage map of channel catfish (Ictalurus punctatus) constructed by using an interspecific hybrid resource family. *Genetics* **165**, 687-94.

Liu Z., Li P. & Dunham R.A. (1998) Characterization of an A/T-rich family of sequences from channel catfish (Ictalurus punctatus). *Molecular marine biology and biotechnology* **7**, 232-9.

Lorenz S., Brenna Hansen S., Moen T., Roseth A., Davidson W., Omholt S. & Lien S. (2010) BAC-based upgrading and physical integration of a genetic SNP map in Atlantic salmon. *Animal genetics* **41**, 48-54.

Lu J., Peatman E., Yang Q., Wang S., Hu Z., Reecy J., Kucuktas H. & Liu Z. (2011) The catfish genome database cBARBEL: an informatic platform for genome biology of ictalurid catfish. *Nucleic acids research* **39**, D815.

Maillard J.C., Berthier D., Chantal I., Thevenon S., Sidibé I., Stachurski F., Belemsaga D., Razafindraïbé H. & Elsen J.M. (2003) Selection assisted by a BoLA-DR/DQ haplotype against susceptibility to bovine dermatophilosis. *Genetics Selection Evolution* **35**, 193-200.

Malek M. & Lamont S. (2003) Association of INOS, TRAIL, TGF-beta2, TGF-beta3 and IgL genes with response to Salmonella enteritidis in poultry. *Genetics Selection Evolution* **35**, 99-112.

Matsuda M., Nagahama Y., Shinomiya A., Sato T., Matsuda C., Kobayashi T., Morrey C.E., Shibata N., Asakawa S. & Shimizu N. (2002) DMY is a Y-specific DM-domain gene required for male development in the medaka fish. *Nature* **417**, 559-63.

McConnell S., Beynon G., Leamon J. & Skibinski D. (2000) Mocrosatellite marker based genetic linkage maps of Oreochromis aureus and O. niloticus (Cichlidae): extensive linkage group segment homologies revealed. *Animal genetics* **31**, 214-8.

Moen T., Hoyheim B., Munck H. & Gomez Raya L. (2004) A linkage map of Atlantic salmon (Salmo salar) reveals an uncommonly large difference in recombination rate between the sexes. *Animal genetics* **35**, 81-92.

Morin P.A., Luikart G. & Wayne R.K. (2004) SNPs in ecology, evolution and conservation. *Trends in Ecology & Evolution* **19**, 208-16.

Nachman M.W. (2002) Variation in recombination rate across the genome: evidence and implications. *Current opinion in genetics & development* **12**, 657-63.

Nandi S., Peatman E., Xu P., Wang S., Li P. & Liu Z. (2007) Repeat structure of the catfish genome: a genomic and transcriptomic assessment of Tc1-like transposon elements in channel catfish (Ictalurus punctatus). *Genetica* **131**, 81-90.

Naruse K., Fukamachi S., Mitani H., Kondo M., Matsuoka T., Kondo S., Hanamura N., Morita Y., Hasegawa K. & Nishigaki R. (2000) A detailed linkage map of medaka, Oryzias latipes: comparative genomics and genome evolution. *Genetics* **154**, 1773-84.

National Marine Fisheries (2010) Top 10 Consumed Seafoods. URL http://www.aboutseafood.com/about/about-seafood/top-10-consumed-seafoods.

Nichols K., Young W., Danzmann R., Robison B., Rexroad C., Noakes M., Phillips R., Bentzen P., Spies I. & Knudsen K. (2003) A consolidated linkage map for rainbow trout (Oncorhynchus mykiss). *Animal genetics* **34**, 102-15.

Nielsen R. (2000) Estimation of population parameters and recombination rates from single nucleotide polymorphisms. *Genetics* **154**, 931-42.

Nievergelt C.M., Smith D.W., Kohlenberg J.B. & Schork N.J. (2004) Large-scale integration of human genetic and physical maps. *Genome research* **14**, 1199-205.

Ninwichian P., Peatman E., Perera D., Liu S., Kucuktas H., Dunham R. & Liu Z. (2012) Identification of a sex-linked marker for channel catfish. *Animal genetics*.

Notter D.R. & Cockett N.E. (2005) Opportunities for detection and use of QTL influencing seasonal reproduction in sheep: a review. *Genetics Selection Evolution* **37**, S39.

Oetting W., Lee H., Flanders D., Wiesner G., Sellers T. & King R. (1995) Linkage analysis with multiplexed short tandem repeat polymorphisms using infrared fluorescence and M13 tailed primers. *Genomics* **30**, 450-8.

Ohara E., Nishimura T., Nagakura Y., Sakamoto T., Mushiake K. & Okamoto N. (2005) Genetic linkage maps of two yellowtails (Seriola quinqueradiata and Seriola lalandi). *Aquaculture* **244**, 41-8.

Palti Y., Genet C., Gao G., Hu Y., You F.M., Boussaha M., Rexroad C.E. & Luo M.C. (2012) A Second Generation Integrated Map of the Rainbow Trout (Oncorhynchus mykiss) Genome: Analysis of Conserved Synteny with Model Fish Genomes. *Marine Biotechnology*.

Palti Y., Luo M.C., Charlet A., Gao G., Hu Y., Castaño-Sánchez C., Tabet-Canale K., Krieg F., Yao J. & Vallejo R.L. (2011) A first generation integrated map of the rainbow trout genome. *BMC genomics* **12**, 180.

Peichel C.L., Nereng K.S., Ohgi K.A., Cole B., Colosimo P.F., Buerkle C.A., Schluter D. & Kingsley D.M. (2001) The genetic architecture of divergence between threespine stickleback species. *Nature* **414**, 901-5.

Phillips R.B., Keatley K.A., Morasch M.R., Ventura A.B., Lubieniecki K.P., Koop B.F., Danzmann R.G. & Davidson W.S. (2009) Assignment of Atlantic salmon (Salmo salar) linkage groups to specific chromosomes: Conservation of large syntenic blocks corresponding to whole chromosome arms in rainbow trout (Oncorhynchus mykiss). *Bmc Genetics* **10**, 46.

Quiniou S., Waldbieser G. & Duke M. (2007) A first generation BAC-based physical map of the channel catfish genome. *BMC genomics* **8**, 40.

Rhyne C.L. (1962) Enhancing linkage-block breakup following interspecific hybridization and backcross transference of genes in Gossypium hirsutum L. *Genetics* **47**, 61.

Rico C., Rico I. & Hewitt G. (1996) 470 million years of conservation of microsatellite loci among fish species. *Proceedings of the Royal Society of London. Series B: Biological Sciences* **263**, 549-57.

Robison B., Wheeler P., Sundin K., Sikka P. & Thorgaard G. (2001) Composite interval mapping reveals a major locus influencing embryonic development rate in rainbow trout (Oncorhynchus mykiss). *Journal of Heredity* **92**, 16-22.

Romanov M., Price J. & Dodgson J. (2003) Integration of animal linkage and BAC contig maps using overgo hybridization. *Cytogenetic and genome research* **102**, 277-81.

Rothschild M. (2003) From a sow's ear to a silk purse: real progress in porcine genomics. *Cytogenetic and genome research* **102**, 95-9.

Ryynänen H.J., Tonteri A., Vasemägi A. & Primmer C.R. (2007) A comparison of biallelic markers and microsatellites for the estimation of population and conservation genetic parameters in Atlantic salmon (Salmo salar). *Journal of Heredity* **98**, 692-704.

Sakamoto T., Danzmann R.G., Gharbi K., Howard P., Ozaki A., Khoo S.K., Woram R.A., Okamoto N., Ferguson M.M. & Holm L.E. (2000) A microsatellite linkage map of rainbow trout (Oncorhynchus mykiss) characterized by large sex-specific differences in recombination rates. *Genetics* **155**, 1331-45.

Sanetra M., Henning F., Fukamachi S. & Meyer A. (2009) A microsatellite-based genetic linkage map of the cichlid fish, Astatotilapia burtoni (Teleostei): a comparison of genomic architectures among rapidly speciating cichlids. *Genetics* **182**, 387-97.

Scaglione D., Acquadro A., Portis E., Tirone M., Knapp S.J. & Lanteri S. (2012) RAD tag sequencing as a source of SNP markers in Cynara cardunculus L. *BMC genomics* **13**, 3.

Schlötterer C. (2004) The evolution of molecular markers—just a matter of fashion? *Nature Reviews Genetics* **5**, 63-9.

Schultz K. (2004) *Ken Schultz's field guide to saltwater fish*. Wiley.

Shimoda N., Knapik E.W., Ziniti J., Sim C., Yamada E., Kaplan S., Jackson D., de Sauvage F., Jacob H. & Fishman M.C. (1999) Zebrafish genetic map with 2000 microsatellite markers. *Genomics* **58**, 219-32.

Singer A., Perlman H., Yan Y.L., Walker C., Corley-Smith G., Brandhorst B. & Postlethwait J. (2002) Sex-specific recombination rates in zebrafish (Danio rerio). *Genetics* **160**, 649-57.

Somridhivej B., Wang S., Sha Z., Liu H., Quilang J., Xu P., Li P., Hu Z. & Liu Z. (2008) Characterization, polymorphism assessment, and database construction for microsatellites from BAC end sequences of channel catfish (Ictalurus punctatus): A resource for integration of linkage and physical maps. *Aquaculture* **275**, 76-80.

Sonesson A.K., Guimarães E., Ruane J., Scherf B., Sonnino A. & Dargie J. (2007) Possibilities for marker–assisted selection in aquaculture breeding schemes. *Chapter in book*, 309-28.

Stam P. (1993) Construction of integrated genetic linkage maps by means of a new computer package: Join Map. *The Plant Journal* **3**, 739-44.

Sun X. & Liang L. (2004) A genetic linkage map of common carp (Cyprinus carpio L.) And mapping of a locus associated with cold tolerance. *Aquaculture* **238**, 165-72.

Tautz D. (1989) Hypervariabflity of simple sequences as a general source for polymorphic DNA markers. *Nucleic acids research* **17**, 6463-71.

Tiersch T. & Goudie C. (1993) Inheritance and variation of genome size in half-sib families of hybrid catfishes. *Journal of Heredity* **84**, 122-5.

Tiersch T.R., Simco B.A., Davis K.B., Chandler R.W., Wachtel S.S. & Carmichael G.J. (1990) Stability of genome size among stocks of the channel catfish. *Aquaculture* **87**, 15-22.

Van Oeveren J., De Ruiter M., Jesse T., Van Der Poel H., Tang J., Yalcin F., Janssen A., Volpin H., Stormo K.E. & Bogden R. (2011) Sequence-based physical mapping of complex genomes by whole genome profiling. *Genome research* **21**, 618-25.

Van Ooijen J. (2006) JoinMap 4. *Software for the calculation of genetic linkage maps in experimental populations*.

Waldbieser G.C., Bosworth B.G., Nonneman D.J. & Wolters W.R. (2001) A microsatellite-based genetic linkage map for channel catfish, Ictalurus punctatus. *Genetics* **158**, 727-34.

Wang C., Loong Lo F.F., Gong P., Li J., Zhu Z., Lin G. & Yue G. (2008) Construction of a BAC library and mapping BAC clones to the linkage map of Barramundi, Lates calcarifer. *BMC genomics* **9**, 139.

Wang S., Xu P., Thorsen J., Zhu B., de Jong P.J., Waldbieser G., Kucuktas H. & Liu Z. (2007) Characterization of a BAC library from channel catfish Ictalurus punctatus: indications of high levels of chromosomal reshuffling among teleost genomes. *Marine Biotechnology* **9**, 701-11.

Watanabe T., Fujita H., Yamasaki K., Seki S. & Taniguchi N. (2004) Preliminary study on linkage mapping based on microsatellite DNA and AFLP markers using homozygous clonal fish in ayu (Plecoglossus altivelis). *Marine Biotechnology* **6**, 327-34.

Watanabe T., Yoshida M., Nakajima M. & Taniguchi N. (2005) Linkage mapping of AFLP and microsatellite DNA markers with the body color-and sex-determining loci in the guppy (Poecilia reticulata). *Zoological science* **22**, 883-9.

Wellborn T.L. (1988) Channel Catfish: life history and biology. *SRAC publication*.

Wilson K., Li Y., Whan V., Lehnert S., Byrne K., Moore S., Pongsomboon S., Tassanakajon A., Rosenberg G. & Ballment E. (2002) Genetic mapping of the black tiger shrimp Penaeus monodon with amplified fragment length polymorphism. *Aquaculture* **204**, 297-309.

Woods I.G., Kelly P.D., Chu F., Ngo-Hazelett P., Yan Y.L., Huang H., Postlethwait J.H. & Talbot W.S. (2000) A comparative map of the zebrafish genome. *Genome research* **10**, 1903-14.

Woram R., McGowan C., Stout J., Gharbi K., Ferguson M., Hoyheim B., Davidson E., Davidson W., Rexroad C. & Danzmann R. (2004) A genetic linkage map for Arctic char (Salvelinus alpinus): evidence for higher recombination rates and segregation distortion in hybrid versus pure strain mapping parents. *Genome* **47**, 304-15.

Xu P., Wang S., Liu L., Peatman E., Somridhivej B., Thimmapuram J., Gong G. & Liu Z. (2006) Channel catfish BAC-end sequences for marker development and assessment of syntenic conservation with other fish species. *Animal genetics* **37**, 321-6.

Xu P., Wang S., Liu L., Thorsen J., Kucuktas H. & Liu Z. (2007) A BAC-based physical map of the channel catfish genome. *Genomics* **90**, 380-8.

Yim Y.S., Moak P., Sanchez-Villeda H., Musket T., Close P., Klein P., Mullet J., McMullen M., Fang Z. & Schaeffer M. (2007) A BAC pooling strategy combined with PCR-based screenings in a large, highly repetitive genome enables integration of the maize genetic and physical maps. *BMC genomics* **8**, 47.

Young N. & Tanksley S. (1989) RFLP analysis of the size of chromosomal segments retained around the Tm-2 locus of tomato during backcross breeding. *TAG Theoretical and Applied Genetics* **77**, 353-9.

Young W.P., Wheeler P.A., Coryell V.H., Keim P. & Thorgaard G.H. (1998) A detailed linkage map of rainbow trout produced using doubled haploids. *Genetics* **148**, 839-50.

Yu Q., Tong E., Skelton R., Bowers J., Jones M., Murray J., Hou S., Guan P., Acob R. & Luo M.C. (2009) A physical map of the papaya genome with integrated genetic map and genome sequence. *BMC genomics* **10**, 371.

Yu Z. & Guo X. (2003) Genetic linkage map of the eastern oyster Crassostrea virginica Gmelin. *The Biological Bulletin* **204**, 327-38.

Yuan Q., Liang F., Hsiao J., Zismann V., Benito M.I., Quackenbush J., Wing R. & Buell R. (2000) Anchoring of rice BAC clones to the rice genetic map in silico. *Nucleic acids research* **28**, 3636.