DEMONSTRATION FOR INTEGRATION OF GENETIC LINKAGE AND

PHYSICAL MAPS OF CATFISH USING BAC-ANCHORED

MICROSATELLITES

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DEMONSTRATION FOR INTEGRATION OF GENETIC LINKAGE AND PHYSICAL MAPS OF CATFISH USING BAC-ANCHORED MICROSATELLITES

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DEMONSTRATION FOR INTEGRATION OF GENETIC LINKAGE AND PHYSICAL MAPS OF CATFISH USING BAC-ANCHORED MICROSATELLITES

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Parichart Ninwichian, daughter of Prajin and Banchuen Ninwichian, was born on November 3, 1981 in Phuket, Thailand. She graduated from high school at Stree Phuket, Thailand in February 2000. She earned her Bachelor of Science in Fisheries Technology from Prince of Songkla University, Pattani, Thailand in April 2004. In January 2007, she enrolled into the Graduate School to pursue a Master of Science in Fish Genetics and Biotechnology at Auburn University.

THESIS ABSTRACT

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Catfish is the major aquaculture species in the United States. The development of genetic linkage maps with high marker densities and the development of physical maps are important steps toward genome-enable genetic improvements. The integration of genetic linkage map and physical map should further enhance genomic research. In this work, sex-specific linkage maps and a sex-averaged genetic linkage map of catfish was constructed using the BAC-anchored microsatellite markers. For female map, a total of 413 markers were used. Of these, 398 were assigned into 29 linkage groups. The total female map size spanned 964.4 cM. For male map, a total of 158 markers were used. Of these, 142 markers were assigned to 19 linkage groups. The total male

map size spanned 276.1 cM. The sex-averaged map was constructed by using 435 microsatellite markers, of which 416 were assigned to 29 linkage groups. The estimated total length of sex-averaged map was 974.1 cM.

It appeared that a greater recombination rate existed in the female than in the male. The female:male recombination ratio was 1.7:1. Mapping of the 416 BAC-anchored microsatellites allowed mapping of 191 contigs to the genetic linkage map, thereby placing these contigs on the genetic linkage map. Of these, 138 contigs were mapped with at least 2 microsatellite markers, thus allowing orientation of the contigs on the linkage map. Some of the microsatellites from the same contigs were actually mapped to different linkage groups, raising the question of the correctness of the physical map. Considering the duplicated genomes of teleost fish, mapping of BAC-anchored microsatellites will provide a great tool to verify the quality of the physical map, and allow the correction of any mistakes on the physical map. This work, therefore, serves as a pilot study for integration of genetic linkage map and physical map, contributes to the marker density of the linkage map, and provide guidance to genetic linkage and physical mapping.

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Style manual used Aquaculture

Computer software used Microsoft Word 2007, Microsoft Excel 2007, Adobe Photoshop 7.0, Msatfinder 2.0, Joinmap 4.0, Microsoft Access 2007

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1. INTRODUCTION

Catfish is the leading aquaculture species in the United States accounting for over 60% of the US aquaculture production. Most of the catfish production is located southeastern United States including Mississippi, Alabama, Louisiana, and with some production in Arkansas, Texas, Georgia, Florida, Missouri, Oklahoma, Idaho, and part of California. In 2003, production of catfish hit a record level of 300,000 metric tons, but the total production has since been declining, and in 2007, the estimated catfish production was approximately 200,000 tons. This decline is mainly caused by the increased prices of fish feed. In addition, keen international competition accounted in part for this decline. The total catfish imports into the USA reached 32,000 tons in the first ten months of 2007, which is 32% more than in the same period of 2006 (Josupeit, 2007). However, the prices of catfish in the US market have gone up recently, and are predicted to increase further in the coming year due to lower domestic production and strong demand (Josupeit, 2007).

Several problems could have diverse impact on the production of catfish industry; for instance, severe disease outbreaks, poor water quality, off-flavor problems etc. All these problems must be dealt with in order to make the catfish industry profitable, increase the current export figures, decrease the trade deficit, reduce pressure from wild-caught fish, and make the industry grow substantially enough to meet demand.

Genetic improvement is one of the methods that can be used to reduce the production problems in aquaculture. As many production and performance traits are inherited traits, genetic improvement programs can be developed to enhance performance and production traits

such as growth rate, feed conversion efficiency, disease resistance, carcass yield, harvestability, resistance to poor water quality, tolerance to stress, body conformation and reproduction. Traditional selective breeding programs are effective for some of these traits such as growth rates, and genetically enhanced broodstocks have been generated using traditional selective breeding. However, traditional selective breeding programs have their limitations. For instance, the limited information on the availability of genetic variation and the lack of genetic markers to sort inferior and superior genotypes early in the life cycle make traditional selective breeding efforts inefficient, especially if genotype-by-environment interactions unwittingly select different genotypes in different locations or if unrecognized negative genetic correlations among desirable characteristics force trade-offs among traits (Camara and Banowetz, 2005). All these limitations require novel approaches. Genome-based approaches provide promising alternatives such as marker assisted selection (MAS) that can improve the production traits efficiently through the use of traits linked DNA markers for the purpose of selection of broodstocks.

Marker assisted selection is the use of genetic markers for selection of a linked characteristic, such as disease resistance. It has a great potential to improve agricultural products and help to increase accuracy of selection in desired traits. It was successfully implemented in farmed animals, such as cattle (Maillard et al., 2003), swine (Rothschild, 2003), poultry (Malek and Lamont, 2003) and sheep (David and Noelle, 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). For aquaculture species, MAS would be especially valuable for traits that are impossible to record on the candidates for selection such as disease resistance, fillet quality, feed efficiency and sexual maturation. Marker-assisted selection requires the availability of dense genetic maps. Genetic maps have been constructed for a number of aquaculture species, such as tilapia (*Oreochromis* spp.) (Lee

et al., 2005; McConnell et al., 2000; Agresti et al., 2000; Kocher et al., 1998), channel catfish (*Ictalurus punctatus*) (Waldbieser et al., 2001 and Liu et al., 2003), 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*) (Nichols et al., 2003; Sakamoto et al., 2000 and Young et al., 1998) and Salmonid fish (May and Johnson, 1990). However, the marker densities on these genetic maps are still too low to implement MAS. Due to limited funding and low numbers of available molecular markers in many aquaculture species, MAS has not been extensively used in fish breeding schemes today (Sonesson, 2007). The only successful example is the MAS program in Japanese flounder for the selection resistance against lymphocystis disease (Fuji et al., 2007). The major reason for the successful application of MAS in this species is because 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.

In order to apply MAS as a tool for genetic improvement, molecular markers are needed to construct genetic maps. Molecular markers are polymorphic pieces of DNA that can be mapped genetically on a genetic linkage map. Upon use of molecular markers in proper reference populations, molecular markers can be mapped 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. In addition, molecular markers can be used for selecting plants or animals that have desired characteristics in the early stage of life without waiting for them to grow to maturity.

Currently, several types of molecular markers are available including isozymes, restriction fragment length polymorphism (RFLP), mitochondrial DNA (mtDNA), randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP),

expressed sequence tags (EST), single nucleotide polymorphisms (SNP) and microsatellites (Dunham, 2004).

Isozymes are allelic forms of individual enzymes. Analysis of isozymes is easy but the available number of loci and polymorphism are limited. However, the major advantage of isozymes analysis is its technical simplicity. In some cases, correlations of isozyme isoforms with performance traits have been reported. For example, isozyme variation is correlated with growth rate (Hallerman et al., 1986), associated with disease resistance, temperature tolerance, developmental speed and salinity tolerance in channel catfish (Dunham, 1995). Other advantages for isozymes are their mode of inheritance; they are inherited in a co-dominant fashion. This makes hecterozygotes and homozygotes easily distinguishable. Thus, this marker type is useful for tracking inbreeding, stock identification, gene mapping, population-genetics studies and determining parentage. The major drawbacks for the isozymes are the requirement of a large amount of fresh or frozen samples. Thus, this method requires lethal sampling. Moreover, isozymes can measure only small portion of the genomic variation because of limited number of loci. Mutation that causes from similar amino acid replacement may not be detected by isozyme electrophoresis. Furthermore, the number of isozyme and the polymorphism is low.

Restriction fragment length polymorphism (RFLP) is widely used to construct the genetic map in many species. This method uses restriction endonuclease enzymes that cut DNA at restriction specific sites to generate fragment size polymorphism. The product is separated on the agarose gel and then transferred to a membrane and hybridized with labeled probes to produce DNA fingerprints. Most RFLP markers are co-dominant (both alleles in a heterozygous sample will be detected), size difference is often large, easy to interpret and score. However, the disadvantages of this technique are that it is time consuming, the level of polymorphism is low, it requires sequence information (for PCR analysis), and probes need to

be developed (for Southern blot analysis), it is time consuming to develop marker for species that lack of known molecular information (Dunham, 2004; Liu and Cordes, 2004 and Liu, 2007). Restriction fragment length polymorphisms of mitochondrial DNA (mtDNA) is also widely used for tracking ancestry through maternal lineage and has been used to track the ancestry of many species back hundreds of generations. Mitochondrial DNA has been used to analyze genetic variation in many aquaculture species such as striped bass (Wirgin et al., 1991; Garber and Sullivan 2006), bluegill (*Lepomis macrochirus*) (Chapman, 1989), red snapper (*Lutjanus campechanus*) (Pruett et al., 2005), Salmonids (Nielsen et al., 1998; Crespi and Fulton, 2004), walleye (*Stizostedion vitreum*) (Merker and Woodruff, 1996) and many others. Mitochondrial DNA (mtDNA) is different from nuclear DNA, which is inherited maternally. There is usually no change in mtDNA to offspring. Although mtDNA also recombines, it does so with copies of itself within the same mitochondrion. Because of the maternal inheritance and the high mutation rate of animal mtDNA (Brown et al., 1979), mtDNA is a powerful tool for tracing the species or populations.

Random Amplified Polymorphic DNA (RAPD) markers are DNA fragments from PCR amplification of random segments of genomic DNA with a single primer of arbitrary nucleotide sequence. Unlike traditional PCR analysis, RAPD does not require any specific knowledge of the DNA sequence of the target organism: the identical 10-mer primers will or will not amplify a segment of DNA, depending on positions that are complementary to the primers' sequence. For example, no fragment is produced if primers annealed too far apart, or 3' ends of the primers are not facing each other. Therefore, if a mutation has occurred in the template DNA at the site that was previously complementary to the primer, a PCR product will not be produced, resulting in a different pattern of amplified DNA fragments on the gel. The great advantage of RAPD is that it can be applied to any species without prior knowledge. However, RAPD also has its major limitations, nearly all RAPD markers are dominant, i.e. it

is not possible to distinguish whether a DNA segment is amplified from a locus that is heterozygous (1 copy) or homozygous (2 copies); co-dominant RAPD markers, observed as different-sized DNA segments amplified from the same locus, are detected only rarely, PCR is an enzymatic reaction, therefore the quality and concentration of template DNA, concentrations of PCR components, and the PCR cycling conditions may greatly influence the outcome. Thus, the RAPD technique is notoriously laboratory dependent and needs carefully developed laboratory protocols to be reproducible. Mismatches between the primer and the template may result in the total absence of PCR product as well as in a merely decreased amount of the product. Thus, the RAPD results can be difficult to interpret (Williams, 1990; Liu, 1998 and Mbwana, 2006).

AFLP uses restriction enzymes to cut genomic DNA, followed by ligation of complementary double stranded adaptors to the ends of the restriction fragments. A subset of the restriction fragments are then amplified using two primers complementary to the adaptor and restriction site fragments. The fragments are visualized on denaturing polyacrylamide gels either through autoradiography or fluorescence methodologies (Zabeau, 1993 and Vos et al., 1995). AFLP technology has the capability to detect various polymorphisms in different genomic regions simultaneously. It is also highly sensitive and reproducible. As a result, AFLP has become widely used for the identification of genetic variation in strains or closely related species of plants, fungi, animals, and bacteria (Ulrich, 1999). The AFLP technology has been used in criminal and paternity tests, in population genetics to determine differences within populations, and in linkage studies to generate maps for QTL analysis. There are many advantages to AFLP when compared to other marker technologies including randomly amplified polymorphic DNA (RAPD), restriction fragment length polymorphism (RFLP), and microsatellites. AFLP not only has higher reproducibility, resolution, and sensitivity at the

whole genome level than other techniques, but it also has the capability to amplify between 50 and 100 fragments at a time. In addition, no prior sequence information is needed for amplification. As a result, AFLP has become extremely beneficial in the study of taxonomy including bacteria, fungi, and plants, where much is still unknown about the genomic makeup of various organisms (Ulrich, 1999). AFLP was used to analyze the genetic diversity in channel catfish (Mickett et al., 2003 and Simmons et al., 2006) and AFLP was also used for genetic linkage map construction in channel catfish (Liu et al., 2003). On the other hand, the disadvantages of AFLP are dominant nature of inheritance, difficulties in transferred information across laboratories, technical demand, special equipment requirements (Liu et al., 1998; Liu et al., 1999; Liu et al., 2005 and Liu, 2007).

Single nucleotide polymorphisms (SNP) are the most common type of genetic variation. A SNP is a single base pair mutation at a specific locus, usually consisting of two alleles (where the rare allele frequency is $\geq 1\%$). SNPs are often found to be the etiology of many human diseases and are becoming of particular interest in pharmacogenetics. Because SNPs are the most abundant polymorphism in genomes of any species, they have been proposed as markers for use in quantitative trait loci (QTL) analysis and in association studies in place of microsatellites. Significant numbers of SNPs in the aquaculture species have been reported by He et al. (2003) for interspecific hybrid catfish, for salmonid fish, (Ryynänen and Primmer, 2006) for Atlantic salmon (Hayes et al., 2007; Moen et al., 2008) and for Japanese flounder (He et al., 2008). However, large-scale genotyping of SNP markers is still expensive.

Expressed sequence tags or ESTs are single pass sequences of cDNAs. They may be used to identify gene transcripts, and are instrumental in gene discovery and gene sequence determination (Adam et al., 1991). The development of EST resources has proceeded rapidly, with approximately 54 million ESTs now available in public databases for all species and approximately 302,000 sequences for channel catfish and 139,000 sequences for blue catfish

(*Ictalurus furcatus*) (e.g. GenBank 6/2008). An EST is produced by one-shot sequencing of a cloned cDNA (i.e. sequencing several hundred base pairs from an end of a cDNA clone taken from a cDNA library). The resulting sequence is a relatively short fragment whose length is limited by current technology to approximately 500 to 800 nucleotides. Because these clones consist of DNA that is complementary to mRNA, the ESTs represent expressed genes. They may be present in public databases as either cDNA/mRNA sequence or as the reverse complement of the mRNA, the template strand. ESTs can be mapped to specific chromosome locations using physical mapping techniques, such as radiation hybrid mapping or fluorescent in situ hybridizations (FISH). Alternatively, if the genome of the organism that originated the EST has been sequenced one can align the EST sequence to that genome. The current understanding of the human set of genes (2006) includes the existence of thousands of genes based solely on EST evidence. In this respect, ESTs become a tool to refine the predicted transcripts for those genes, which leads to prediction of their protein products, and eventually of their function. Moreover, the situation in which those ESTs are obtained (tissue, organ, or disease state - e.g. cancer) gives information on the conditions in which the corresponding gene is expressed. ESTs contain enough information to permit the design of precise probes for DNA microarrays that then can be used to determine genome expression files. For aquaculture species, ESTs have been developed from cDNA libraries in a variety of fish and shellfish species (Matinez, 2007). These include Japanese flounder (Nam et al., 2000; Kono and Sakai, 2001 and Nam et al., 2003), winter flounder (*Pleuronectes americanus*) (Douglas et al., 1999), channel catfish (Liu et al., 1999; Ju et al., 2000; Liu and Feng, 2001; Serapion et al., 2004; Karsi et al., 2002; Kocabas et al., 2002; Cao et al., 2001 and Li et al., 2007), Japanese eel (*Anguilla japonica*) (Miyahara et al., 2000), rainbow trout (Kono et al., 2000; Rexroad et al., 2005; ; Coulibaly et al., 2005), Atlantic salmon (*Salmo salar*) (Davey et al., 2001; Martin et al., 2002; Tsoi et al., 2003), Atlantic halibut (*Hippoglossus hippoglossus*) (Park, 2005),

common carp (*Cyprinus carpio*) (Savan et al., 2002; Yue et al., 2004) and yellowtail (*Seriola quinqueradiata*) (Kono et al., 2002). Several of these studies were specifically designed to identify genes involved in innate and acquired immunity.

Microsatellites consists of multiple copies of tandemly arranged simple sequence repeats (SSR) that range in size from 1-6 base pairs (bp) (e.g., AC, CCA, or GATA) (Tautz, 1989). The advantages of microsatellites are their abundance in genomes, relatively even distribution, small locus size facilitating polymerase chain reaction (PCR)-based genotyping, codominant nature of Mendelian inheritance, and high levels of polymorphism. Although they are the top choice markers in genetic studies in economically important crop species, the disadvantages of microsatellites include the requirement for existing molecular genetic information, the large amount of work for their development, and the tedious and labor-intensive PCR primer design and selection. Microsatellites were found in various eukaryotic genomes and have been used in field of fisheries research such as genome mapping, parentage identification, kinship analysis, and stock structure analysis (O'Connell and Wright 1997). In channel catfish, microsatellites represent 2.58% of the catfish genome (Xu et al., 2006). Microsatellites can be identified and sequenced directly from genome sequence surveys such as EST analysis and bacterial artificial chromosome (BAC) end sequencing.

Microsatellites are one of the most useful types of molecular markers for constructing genetic linkage maps and QTL maps because microsatellites have high polymorphic rate. 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).

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), channel catfish (Waldbieser et al.,2001), Yellowtail (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; Woods et al., 2000; Shimoda et al., 1999; Singer et al., 2002), Japanese flounder (Coimbra et al., 2003), ayu (*Plecoglossus altivelis*) (Watanabe et al., 2004), Pacific oyster (*Crassostrea gigas*) (Hubert and Hedgecock, 2004), Eastern oyster (*Crassostrea virginica*) (Yu and Guo, 2003) and common carp (Sun and Liang, 2004).

In order to understand the physical organization of the genome, most studies often study 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 (Xu et al., 2007). In 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 into genetic linkage map, they allow integration of linkage map and the BAC-based physical maps. In addition, BAC-end sequencing can be used to study about evolutionarily conserved syntenies (Xu et al., 2007).

The objectives of this project are to identify microsatellites from BAC end sequences in order to generate polymorphic microsatellite markers in our resource family for genetic linkage map construction and integration of genetic linkage map with physical map by using

BAC contig-based physical map of the channel catfish. The mapping of microsatellites to linkage maps should enhance the density of markers and therefore 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, laying ground for whole genome sequencing in catfish. The results from this project will be one step further toward developing a marker-assisted selection program in catfish. The application of genome-based technologies in catfish should enhance the genetic enhancement programs.

2. MATERIALS AND METHODS

2.1. Resource Family

The resource family used in this study was developed as previously published (Liu et al., 2003). Briefly, channel catfish females with blue catfish males were mated to make F_1 interspecific hybrid catfish. F_1 (channel catfish x blue catfish) hybrid catfish, channel catfish and blue catfish were screened prior to the 1997 spawning season to determine which mating of these parents were most informative. Backcross families were made in spawning season of 1997 by mating the F_1 fish with channel catfish (channel catfish backcross). A specific family, F_1-2 x Channel catfish-6, was used for this project. The resource family was reared in 1,000- liter tanks until collection of blood samples for genotyping. Individuals sampled for genotyping were heat branded for future identification.

2.2. Genomic DNA Isolation: DNA Isolation

DNA was extracted from 64 samples plus their 2 parents from resource family F_1-2 x Channel catfish-6. Blood samples (0.5 to 1 ml) were collected in 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 instruction manual from manufacturer.

2.3. Identification of Microsatellites, Primers and PCR Amplification

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 were used for microsatellite mining. 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 *Msatfinder* program. Clones containing microsatellites that fit the criteria described below were selected from both ends of the contig to test polymorphism. Since the contigs that contain polymorphic microsatellite(s) on both ends are useful for map integration, if a clone positioned at either end of a contig did not have microsatellite, the next microsatellite containing clones were selected. Clones located at the center of the contigs, and contigs containing clones without microsatellites were ignored.

A Perl-based script *Msatfinder* (http://www.genomics.ceh.ac.uk/msatfinder/; Thurston and Field, 2005), was used for microsatellite mining. Program parameters were set to design a maximum of 5 forward and reverse primers flanking the microsatellite region from these BES. The primer mining and design methods were conducted according to procedures provided in *Msatfinder* manual.

The BES containing microsatellites were examined to determine whether they had sufficient flanking sequences for primer design by harboring at least 50 bp of flanking sequences on either side of microsatellites. They were excluded if the flanking sequences are less than 50 bp (flanking sequences were calculated from the total lengths of BES minus the sequence lengths before/after finding microsatellites sequences). Thus, the remaining BES containing microsatellites were regarded as microsatellites with enough flanking sequences for primer designs. Tab-delimited outputs containing microsatellite information from *Msatfinder* were then imported into excel spreadsheets. One of the primer pairs with closer Tm values

was selected and all primer sequences were subjected to the following criteria: primers containing simple sequences and primers with low G/C content were removed because they are not useful. Although G/C content was considered suitable when it was between 40%-60%, primers with low G/C content (minimum 33%) were also considered acceptable. Primers were designed to amplify product sizes between 100-250 bp. However, in some instances, if the sequences were very rich in microsatellites and *Msatfinder* parameters did not allow primer design, longer PCR product sizes 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 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: a final volume of 5 µl reaction mixture contained 1 µl of 50 ng/µl Genomic DNA, 0.5 µl of 10X PCR buffer, 0.3 µl of 25mM $MgCl_2$, 0.4 µl of 2.5 mM dNTP's, 0.2 µl of 100 ng/µl upper primer (with tail), 0.3 µl of 100 ng/µl lower primer, 0.1 µl of 100 pmol/µl labeled tail primer, and 0.25 units of JumpStart Taq polymerase (Sigma, Saint Louis, MO). PCR amplifications were conducted using 384 well plates to reduce the variation as much as possible. Two step PCR profile were used for amplification. An initial denaturation step at 94°C for 3.5 minutes is followed by a first denaturation at 94°C for 30 seconds, first annealing step at 57°C for 30 seconds, and a first extension at 72°C for 30 seconds. This first step was repeated 20 cycles and 15 cycles of second step had the following parameters: denaturation step at 94°C for 30 seconds, an annealing step at 53°C for 30 seconds, an extension step at 72°C for 30 seconds followed by a final extension step at 72°C for 15 minutes. The samples were

held at 4°C for 15 minutes. In this two-step PCR profile, the annealing temperature window can be accommodated to determine the best Tm for the primer pairs. PCR products were analyzed on 7% polyacrylamide gel by using LICOR 4300 DNA Analyzer (LICOR Biosciences, Lincoln, NE). After gel electrophoresis, the polymorphic microsatellite bands were scored and genotyped based on the allele segregation within the resource family.

2.4. Genotyping

After running through the LI-COR automated sequencers, genotypes were called by recording the amplified fragment sizes (in base-pairs) in an excel spreadsheet. The fragment sizes were determined by using labeled size markers (LICOR Biosciences, Lincoln, NE). Loci that did not show any polymorphism is recorded as "non-polymorphic". The complex loci and parental type microsatellites were also recorded. Chi-square goodness-of-fit test used to assess the departures from the expected Mendelian allele segregation patterns. Genotype configurations of markers were categorized into three expected segregation types 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). Segregation data from expected 1:1:1:1-type markers into 1:1 ♀- and 1:1 ♂-type were partitioned by creating maternal and paternal datasets using JoinMap 4.0 (Kyazma, Wageningen, Netherlands) to perform linkage analysis for each sex (Jacobs et al., 1995; Viruel et al., 1995). This option in JoinMap 4.0 creates maternal and paternal genotypes by converting genotypes from 1:1:1:1-ratio type (♀ x ♂: AB x CD or AB x AC) to 1:1 ♀ type (AB x AA or CC), and 1:1 ♂ type (AA or CC x AB). All the statistical analyses were made using JoinMap version 4.0 software (Van Ooijen, 2006) with the cross-pollinating (CP) coding scheme, which handles the data containing various genotype configurations with unknown phase (Sekino et al., 2006).

2.5. Linkage Analysis

Linkage between markers was examined by estimating LOD scores for recombination rate (Θ) and map distances were calculated using Kosambi mapping function. JoinMap first calculates the G^2-statistic for independence of segregation; then obtained G^2 is multiplied by a constant of 0.5 x $\log_{10}{}^{e}$ to convert the G^2-value into the normal LOD scale. Significance of marker linkage was determined at a LOD threshold of 3.0, a threshold Θ of 0.6 was set to detect suspect linkage possibly resulting from allele-coding errors. Six individuals of fish were omitted from analyses because of many missing data points from them.

Markers were linearly aligned in each linkage group, converting the recombination rates into the 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'' 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.

3. RESULTS

3.1 Resource Family and BAC Anchored Microsatellite Markers

The microsatellite markers used for mapping and integration of genetic linkage and physical maps were BAC-anchored microsatellite markers. In order to identify BAC-anchored microsatellite markers, BAC end sequences were first generated. While all identified microsatellites are useful for genomic and genetic work, only the informative polymorphic BAC-anchored microsatellites were useful for genetic linkage mapping and integration of the linkage map with the physical map constructed with BAC contigs (Xu et al., 2007). Therefore, the usefulness of the BAC-derived microsatellites was evaluated by PCR analysis using the resource family.

Each BAC contig contains a variable number of BAC clones, and only some BAC end sequences contain microsatellites (Xu et al., 2006). In this study, 207 BAC contigs were used. BAC clones harboring microsatellites were selected on both ends of each contig (to increase the possibility of recombination between the microsatellites within the same contig) for the design of PCR primers. Successful PCR amplification of the selected microsatellites, along with their polymorphism in the resource family would allow them to be mapped on the genetic linkage map. As their location on the physical map was known, their mapping to genetic linkage map would allow alignment (integration) of the BAC contigs with the genetic linkage map. For orientation of the contigs on the genetic linkage map, at least two polymorphic microsatellites are needed in order to detect any possible recombination between them. A total of 555 primer pairs was designed from the 207 contigs and tested for PCR amplifiability. Of

the 555 unique loci, 539 pairs of primers produced PCR products, and 16 pairs of primers did not generate any PCR products. Of the 539 amplified PCR loci, 431 were polymorphic in the resource family (77.66%) (Table 1).

3.2 Characterized Repeat Types of Informative BAC Anchored Microsatellites

Variable polymorphic rates were observed with various types of microsatellites. Of 431 selected polymorphic microsatellites, 216 were di-nucleotide repeats (e.g., AC, TA); 119 were tri- nucleotide repeats (e.g., ACC, TAA); 88 were tetra- nucleotide repeats (e.g., AGAT, TATT) and 8 were penta-nucleotide repeats (e.g., TATAT, AATTG) (Table 2). It appeared that di-nucleotide repeats had a slightly higher polymorphic rate at 50.12%, followed by tri-nucleotide repeats (27.61% success rates) while the penta-nucleotide repeats had the lowest polymorphic rate at 1.86%.

3.3 Linkage Maps and Marker Distribution

The genetic linkage map of catfish was constructed by using an interspecific hybrid, F_1-2 x Channel-6, resource family and the polymorphic BAC-anchored microsatellite markers. From 431 polymorphic primer pairs, of which 462 microsatellite markers were generated, 435 of them can be used to analyze in this program. The remaining 27 microsatellite loci cannot be analyzed by JoinMap 4.0 because of the characteristics of their genotypes that were difficult to determine their mode of inheritance. Sex-specific linkage maps and sex-averaged genetic linkage maps were constructed based on the segregation data.

For the female map, the LOD score was initially set at 8.0 in order to generate the linkage groups based on the segregation data. A total of 413 markers were used for the female map, of which 398 were assigned into 29 linkage groups. The remaining 15 were unlinked markers. The total female map size was 964.4 cM. The average inter-marker distance was 2.4

cM. The size of individual linkage groups ranged from 3.4 to 97.9 cM. The number of markers on 29 linkage groups varied from 2 to 23 markers. The largest linkage group spans 97.9 cM with 21 markers (Figure 1).

For the male map, there were only 158 markers that could be used to construct the map because a large number of markers were not polymorphic with the male parent. Of the 158 polymorphic markers used for the male map, 142 markers were assigned to 19 linkage groups at a LOD of 5.0. The remaining 16 were unlinked markers. The total male map size was 276.1 cM. The average inter-marker distance was 1.9 cM. The size of individual linkage group ranged from 3.1 to 45.3 cM. The number of markers on 19 linkage groups varied from 2 to 14, and the largest linkage group spans 45.3 cM with 7 microsatellite markers (Figure 2). Because a relatively small number of polymorphic markers were used for the construction of the male map, it is expected that the male map should be incomplete.

The sex-averaged genetic linkage map was constructed by using all polymorphic markers segregating in both the female and the male parents. The sex-averaged map was constructed by using 435 microsatellite markers, of which 416 were assigned to 29 linkage groups, while the remaining 19 were unlinked. The estimated total length of sex-averaged map was 974.1 cM. The average size of the inter-marker distance was 2.3 cM. The length of the individual linkage groups ranged from 3.4 to 93.5 cM. The number of the markers per group ranged from 2 to 23 (Figure 3). It is apparent that many of the linkage groups contained only markers from the female map, once again a reflection of the incompleteness of the male map due to small numbers of polymorphic markers.

3.4 Difference in Recombination Rate between Male and Female

The recombination rate appeared to be higher in the female than in the male. As presented above, the female map has 29 linkage groups whereas the male map has 19 linkage groups. The linkage groups with which a common set of markers were mapped should allow a comparison of recombination rates among markers in different sexes (Figure 4). The shared markers that were present in both female and male map were calculated for the recombinant rates between adjacent microsatellite markers. Apparently, the recombination rates were greater in the female than in the male. On average, the ratio of recombination rate of the female over that of the male was 1.70:1, i.e., on average, recombination occurred 70% more frequent in the female than in the male.

3.5 Integration of Genetic Linkage and Physical Map

Integration of genetic linkage map and physical map is an important step to enhance genomic research and genetic improvement using marker assisted selection. Genetic linkage mapping using polymorphic markers derived from BAC clones whose location is already known on physical map should allow integration of the linkage and physical maps. The 416 mapped microsatellites on the genetic linkage map allowed placement of 191 contigs to the linkage map. Clearly, each linkage group in genetic linkage map contained more than one contigs (Figure 3). Mapping of these contigs would allow the inter-relationship of these contigs to be revealed for the establishment of super scaffolds. In addition, of the 191 mapped contigs, two or more microsatellites were from 138 contigs of the 191 contigs, allowing positioning of the contigs with correct orientations (Figure 5). However, some of the markers that belong to a given contig were mapped into several linkage groups, i.e., contig 9, 193, 442 etc. (Figure 3). This suggested that the contigs were erroneously constructed, and mapping of all the BAC-associated microsatellites, therefore, not only integrate the linkage and physical

maps, but also provide a critical examination of the BAC contig-based physical map. Apparently, mistakes in the physical map can then be corrected.

4. DISCUSSION

Previous studies were conducted for the construction of genetic linkage maps in channel catfish by using microsatellite (Waldbieser et al, 2001) and AFLP (Liu et al, 2003). Unfortunately, those studies did not bring the number of linkage groups to equal to the number of chromosome pairs in channel catfish. The most likely explanation for this discrepancy is the insufficient numbers of markers used. In the case of AFLP, the dominant nature of AFLP may have further reduced the genetic information. The low markers density could also cause an inflated map distance (Yu and Guo, 2003). For instance, in medaka (*Oryzias latipes*), a map distance of 2,480 cM in 29 linkage groups was generated using 170 markers (Wada et al., 1995) whereas a map distance of 1,354.5 cM in 24 linkage groups was generated using 663 markers (Naruse et al., 2000). Similarly, in channel catfish 293 microsatellite markers produced a map size of 1,958 cM (Waldbieser et al., 2001) while 418 AFLP markers covered 1,593 cM (Liu et al., 2003). In this study, 416 microsatellite markers were used for the production of the sex-averaged map. This map had a map size of 974.1 cM. For female map, 398 microsatellite markers were used, producing a female map with 964.4 cM. In both sex-averaged map and the female map, the microsatellite markers were assigned into 29 linkage groups that equal to the number of haploid chromosome number in channel catfish (Wolters et al., 1981) and blue catfish (Legrande et al., 1984). The total map distance was reduced in this case by using a larger number of microsatellites markers than previously reported. However, in this study, an interspecific reference family was used while in the previous study, an intraspecific resource family was used (Waldbieser et al., 2001). A direct comparison may

prove to be difficult unless the same set of microsatellites is used in both interspecific and intraspecific resource families.

The linkage map of the male was relatively incomplete because of the small number of polymorphic markers. The male linkage map had only 19 groups. In order to cover all 29 chromosome pairs, additional markers are needed.

The mapping of a common set of markers on both the female and male maps should allow a direct comparison of recombinant frequencies in the male and female. In most vertebrates, significant differences in recombination rates have been reported, with greater recombination frequencies in the female (Barendse et al., 1994; Ellegren et al., 1994; Dib et al., 1996; Dietrich et al., 1996). In aquatic species, such as zebrafish (Knapik et al., 1998), sea horse (Jones et al., 1998), rainbow trout (Sakamoto et al., 2000), Atlantic salmon (Gilbey et al., 2004; Moen et al., 2004; McClelland and Naish, 2008), Arctic charr (Woram et al., 2004), eastern oyster (Yu and Guo, 2003), Pacific oyster (Li and Guo, 2004; Hubert and Hedgecock, 2004), Ezo Awabi abalone (Liu et al., 2006) etc., the recombination ratio is higher in females than in males. However, the opposite with greater recombination frequency in the male have also been reported such as in the case of Japanese flounder (Coimbra et al., 2003). In this study, the recombination frequency was greater in the female than in the male; the recombination ratio (Female:Male) was 1.70:1, which is similar to the cases reported from most aquatic species. The lower recombination in the male may have been caused by heterogametic sex (Haldane, 1922), and the recombination is prevented by maleness itself (Matsuda et al., 1999).

The determination of sex differences in recombination has very important implications for implementation of marker assisted selection using QTL-marker associations, since the sex with lower recombination rates is expected to transmit marker QTL associations in tighter linkage (Coimbra et al., 2003).

The mapping of BAC-anchored markers allows integration of genetic linkage and physical maps. In this study, microsatellites from 191 contigs were genetically mapped, allowing these contigs to be placed into linkage groups. For complete integration of genetic linkage and physical maps, markers need to be developed from all and each of the contigs. Clearly, this would be a very major project that requires mapping of at least one microsatellite per contig. This would translate into mapping of 3,307 microsatellites. In addition, for many larger contigs, more than one marker per contig would be required to provide orientation of the contigs on the linkage map. Therefore, many more than 3,307 markers are needed.

In addition to integration of genetic linkage and physical maps, mapping of BAC-anchored microsatellites also allow detection of mistakes on the physical map. In this study, 43 contigs were assigned into more than one linkage groups, suggesting mistakes on the physical map. Work is needed to evaluate the correctness of these contigs. Perhaps a greater level of stringency is needed for the assembly of the "problematic" contigs (Xu, 2007).

5. CONCLUSION

This work allowed mapping of 416 BAC-anchored microsatellites to the genetic linkage map. That represented a significant increase in marker density. The use of BAC-anchored microsatellites allowed integration of 191 contigs to the linkage map. However, full integration of the genetic linkage and physical maps require thousands of BAC-anchored microsatellites, but this work demonstrated that it is possible to integrate a large proportion of contigs with genetic linkage maps without too much trouble. However, in approximately one third of contigs, 1,099 out of 3,307, contain no microsatellites. Other approaches will have to be considered. One way is to develop BAC end-anchored SNPs followed by mapping of such BAC-anchored SNPs to genetic linkage maps. Integration of genetic linkage map with physical map will greatly enhance the capacity of genome analysis, paving the way for genetic improvement programs and marker-assisted selection.

TABLES

Table 1. Summary of the number of microsatellite loci derived from BAC contig-based physical map.

Total tested primer pairs	555
Total primer pairs that produced PCR product	539
- Polymorphic microsatellite loci	431
Number of polymorphic markers	462
- Not polymorphic microsatellite loci	72
- No segregation	14
- Duplication	22
No product	16
Percentage of polymorphism in resource family	77.7

Table 2. Repeat compositions of the polymorphic loci in the $F_1$2 x Channel-6 resource family.

Repeat type	Amount	Percent (%)
Dinucleotide microsatellites	216	50.12
Trinucleotide microsatellites	119	27.61
Tetranucleotide microsatellites	88	20.42
Pentanucleotide microsatellites	8	1.86
Total	431	

FIGURES

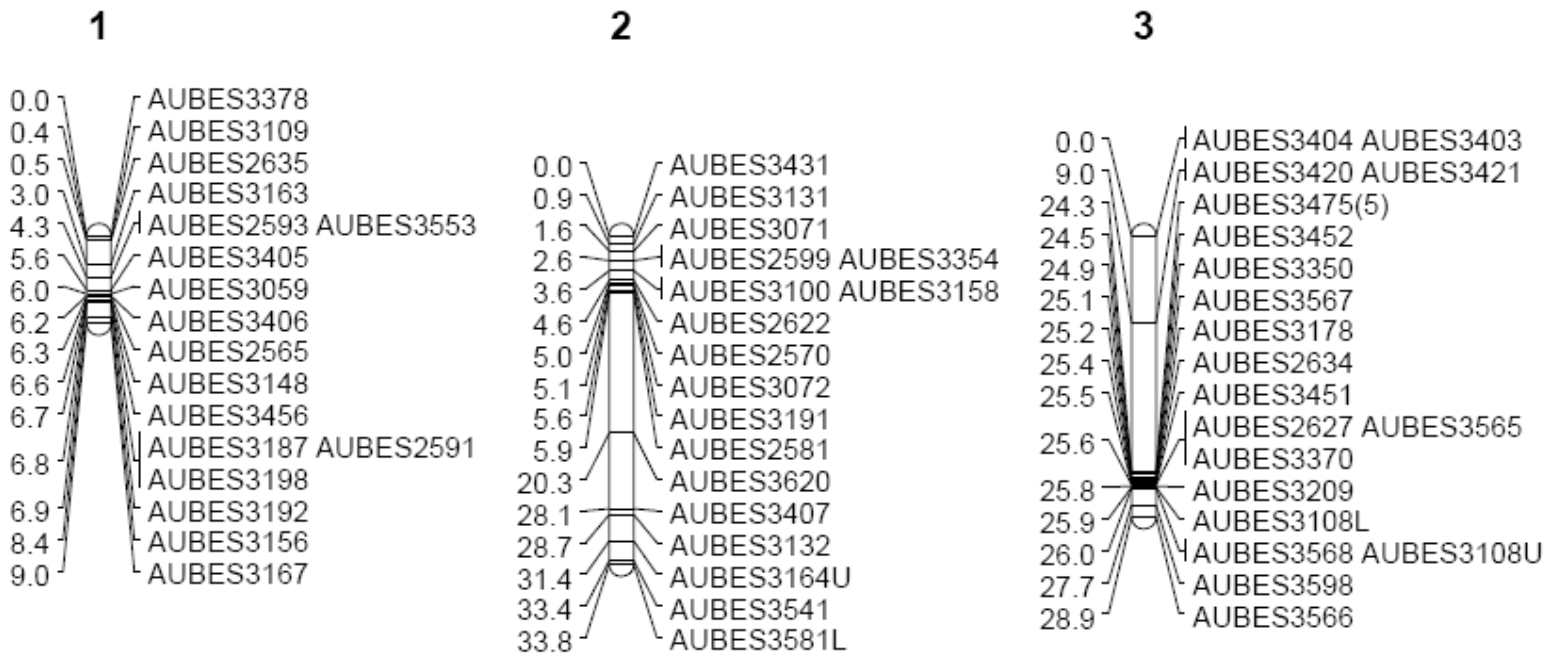
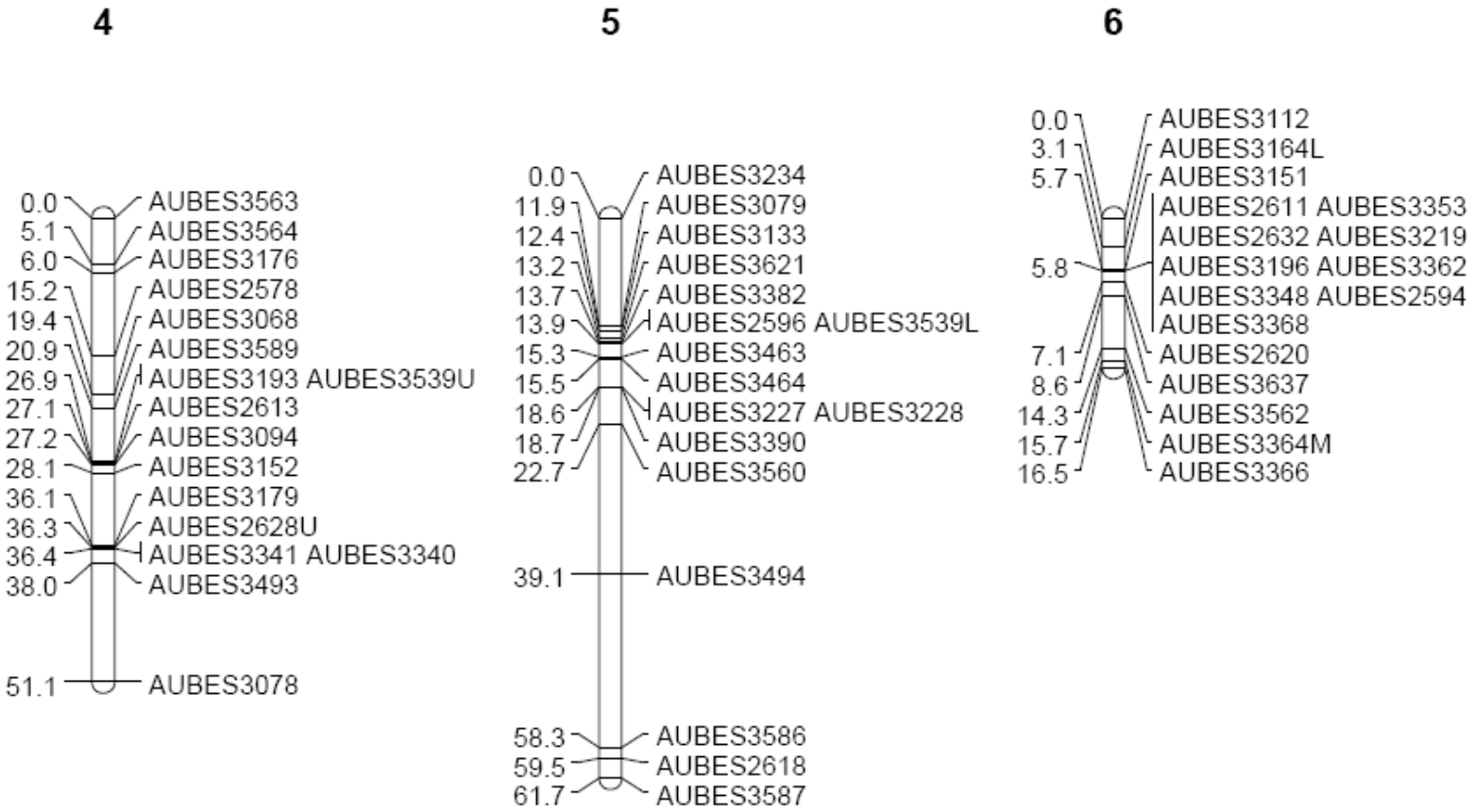


Figure 1. Female linkage map of channel catfish based on microsatellite markers. Genetic map distance was given in centimorgans to the left side of the marker positions.



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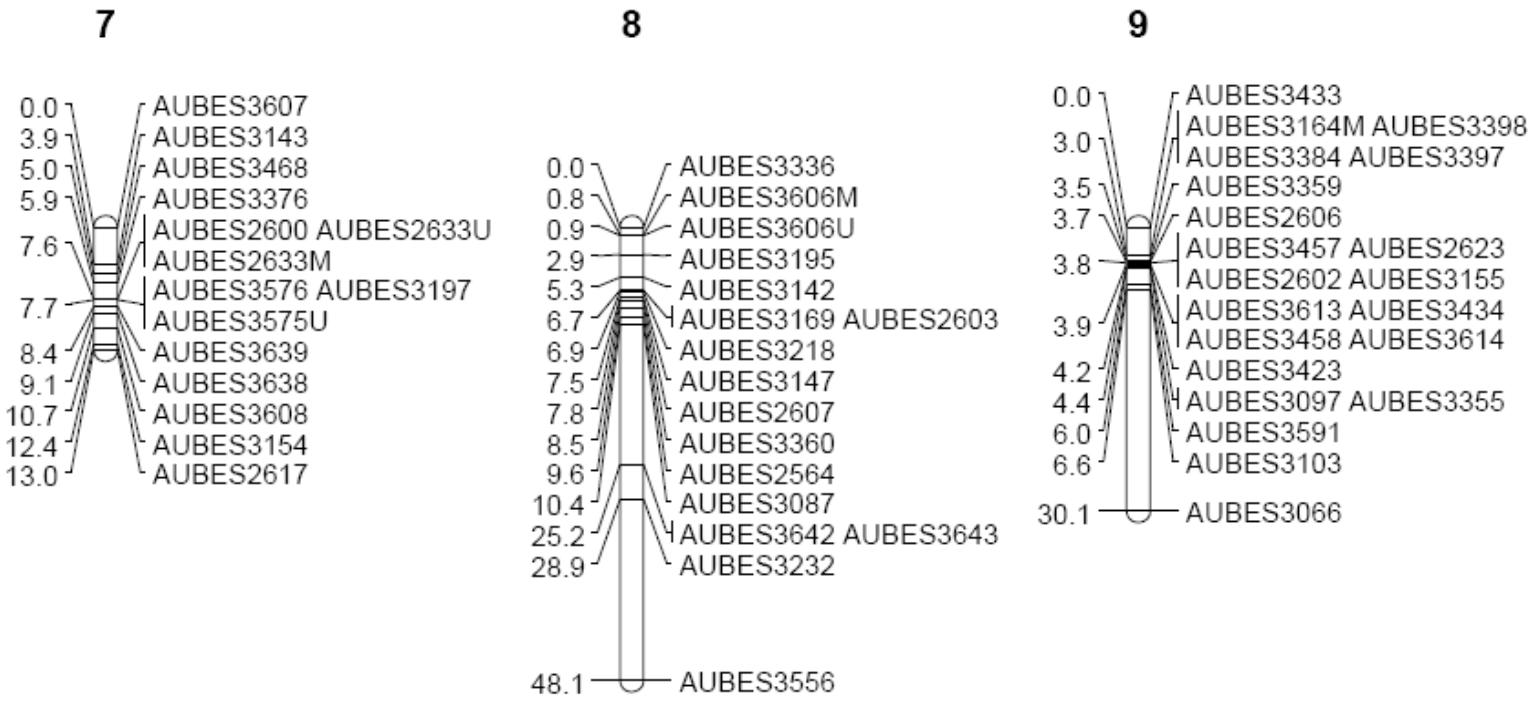

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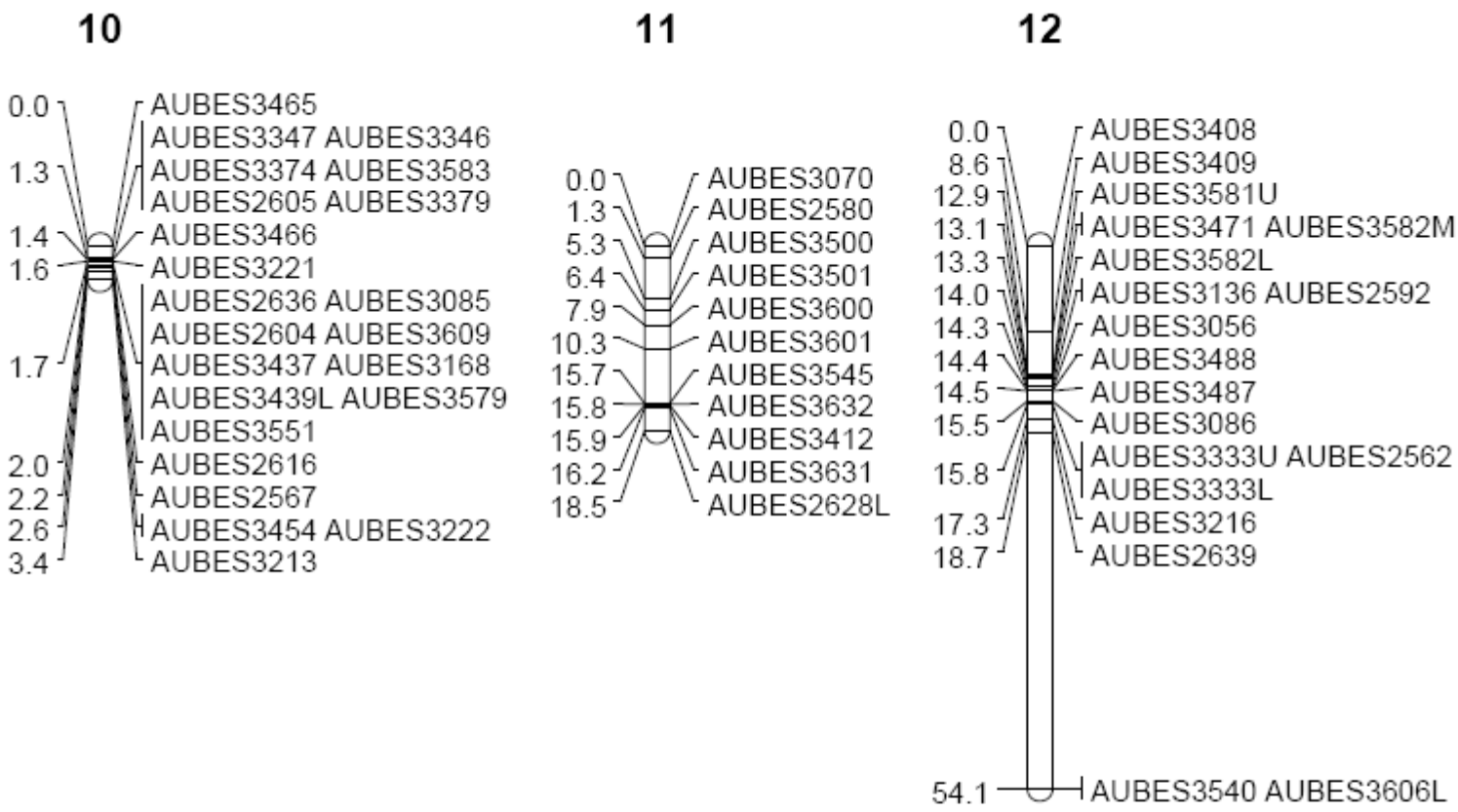

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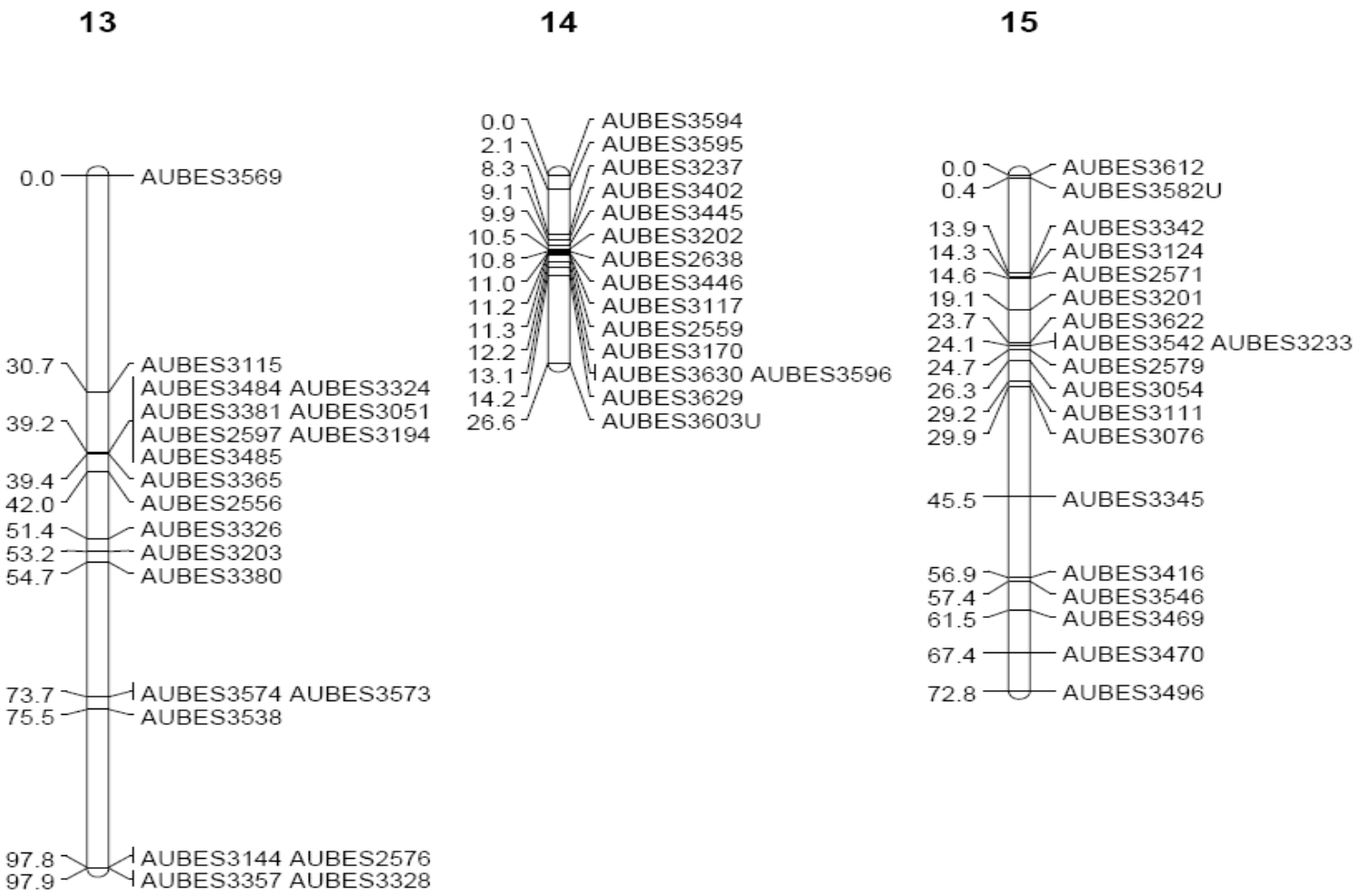

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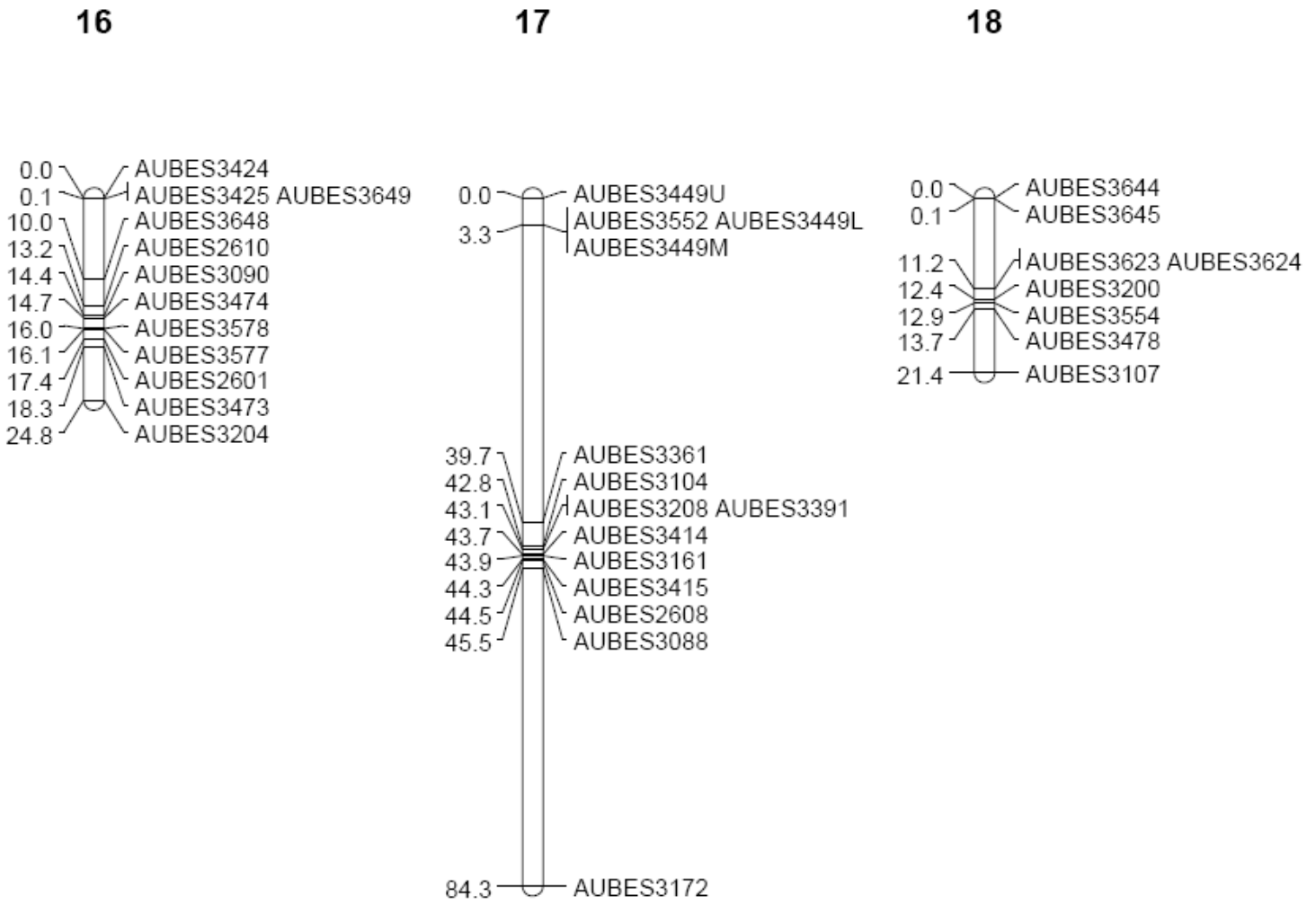

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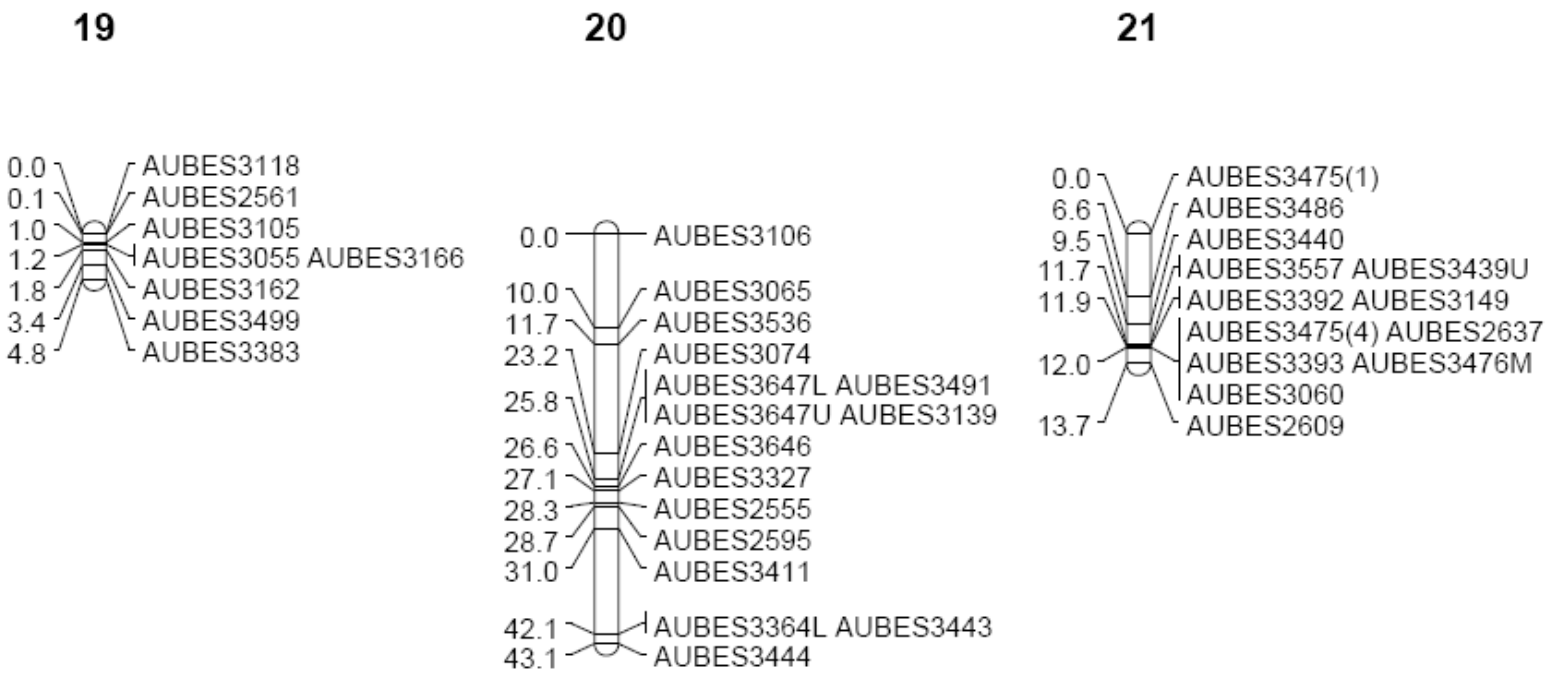

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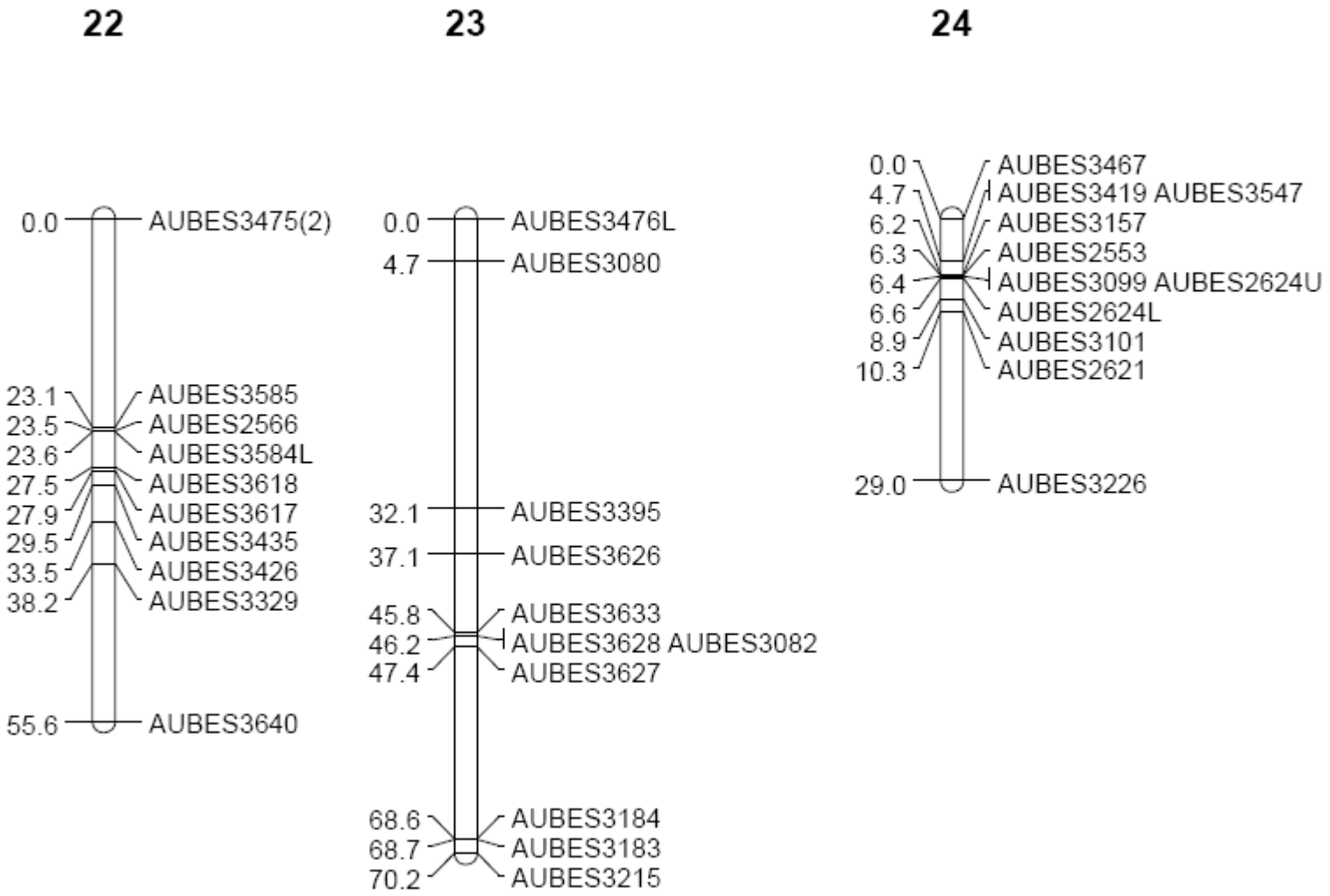

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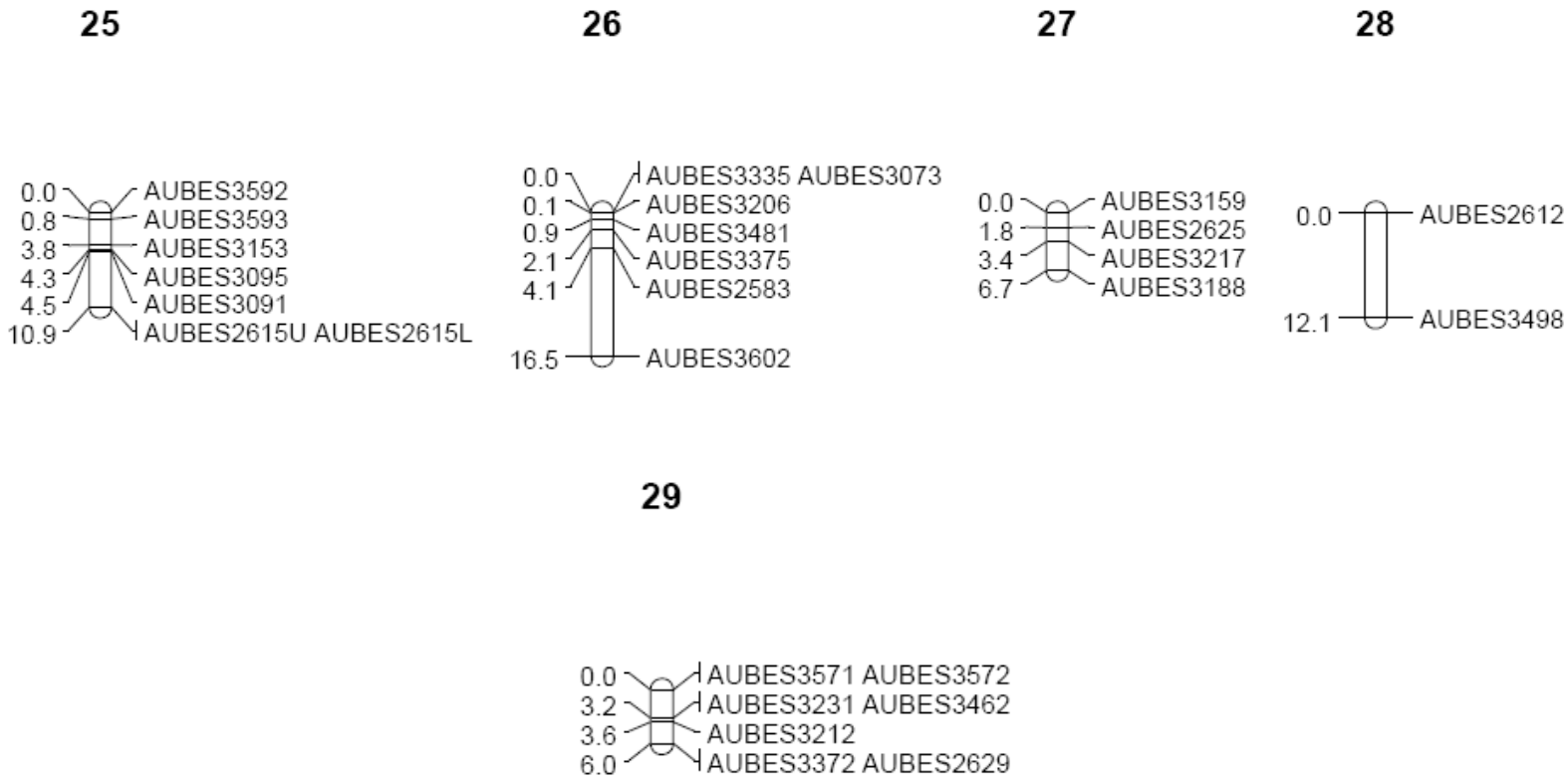

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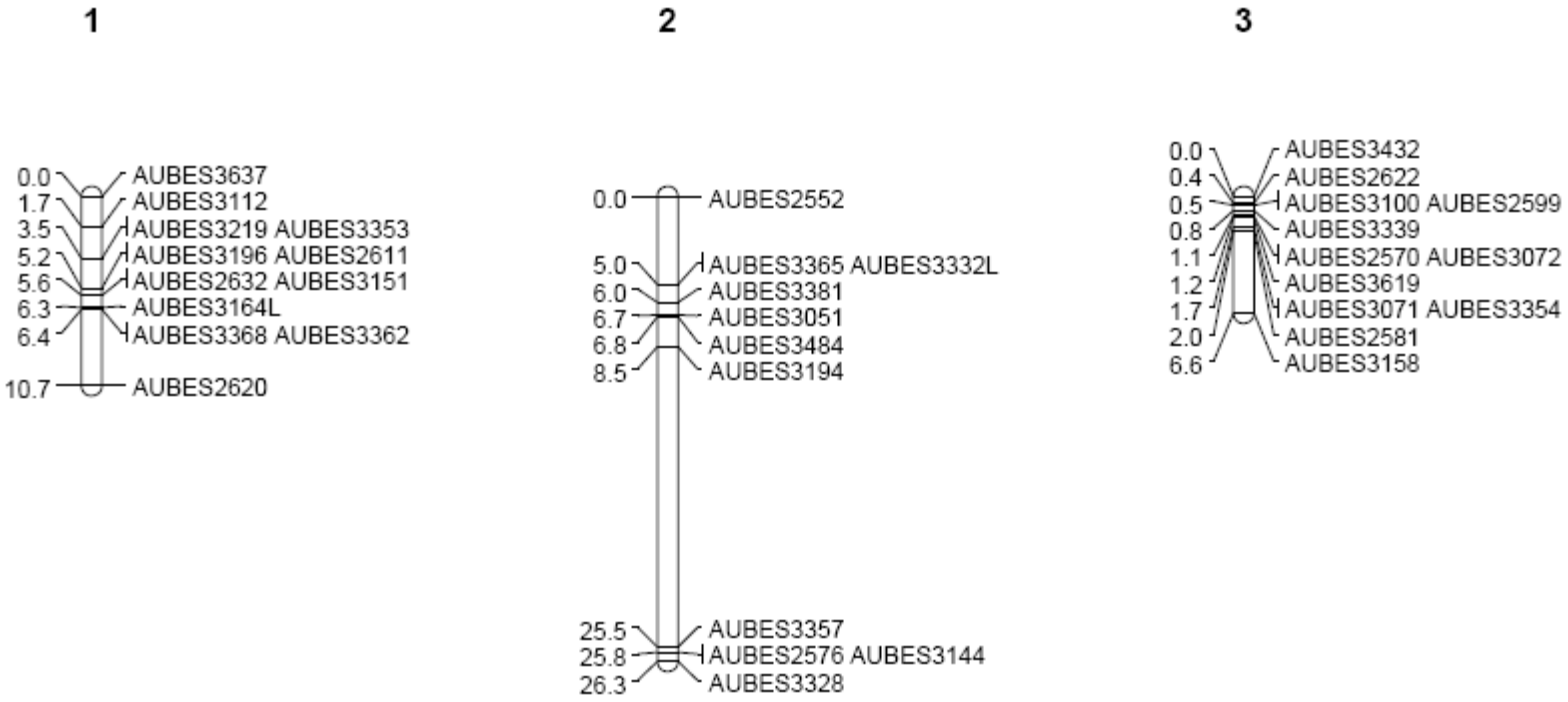
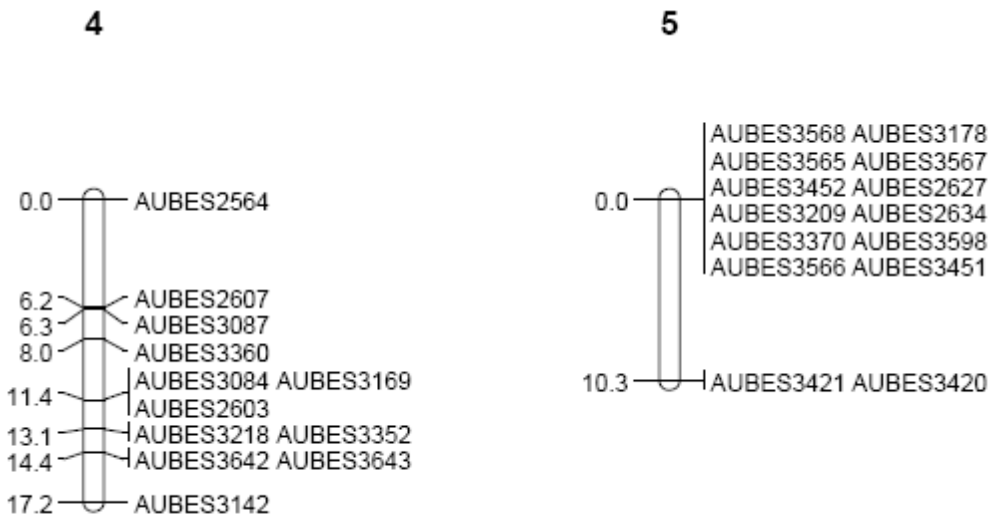


Figure 2. Male linkage map of channel catfish based on microsatellite markers. Genetic map distance was given in centimorgans to the left side of the marker positions.



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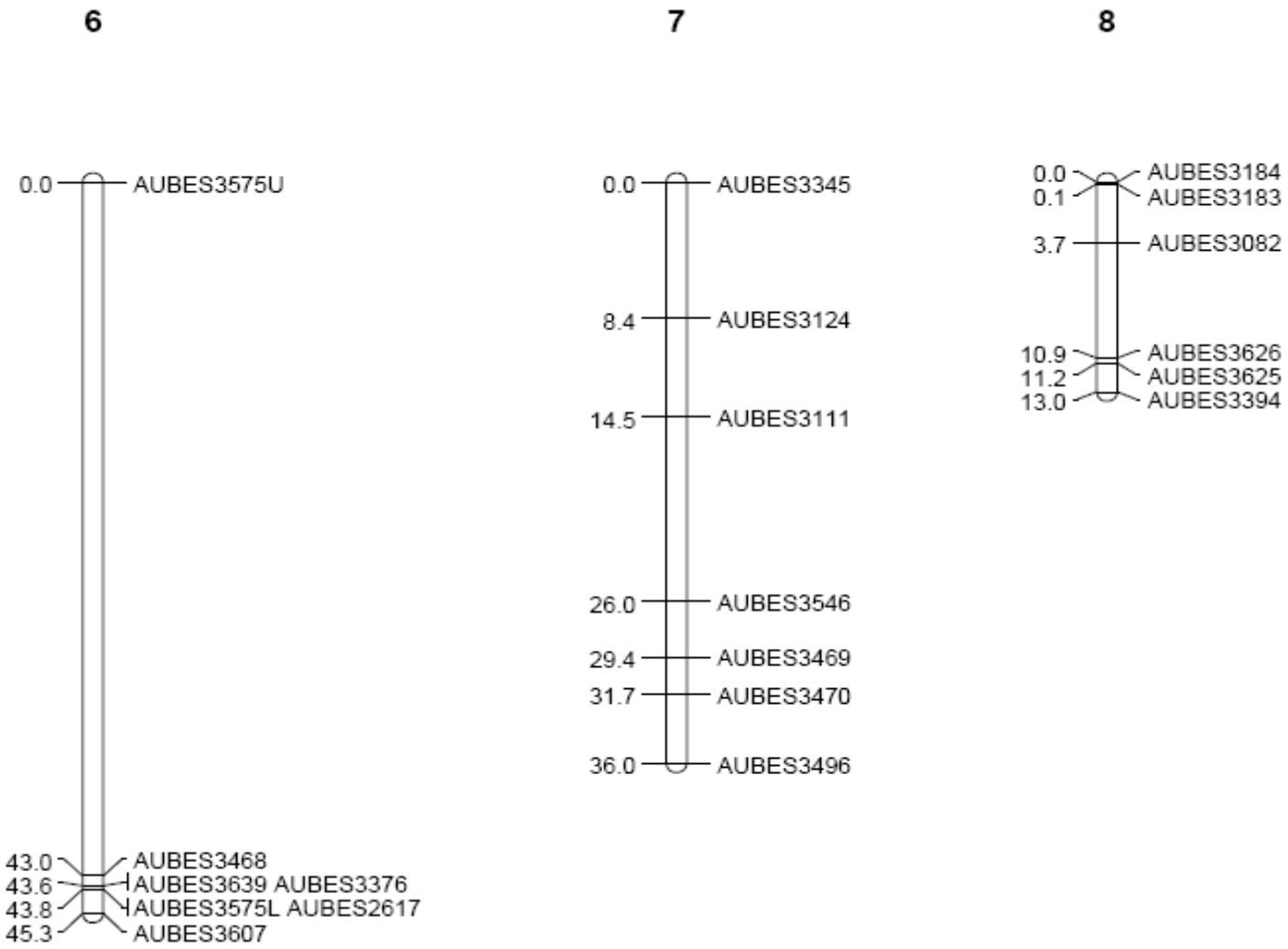

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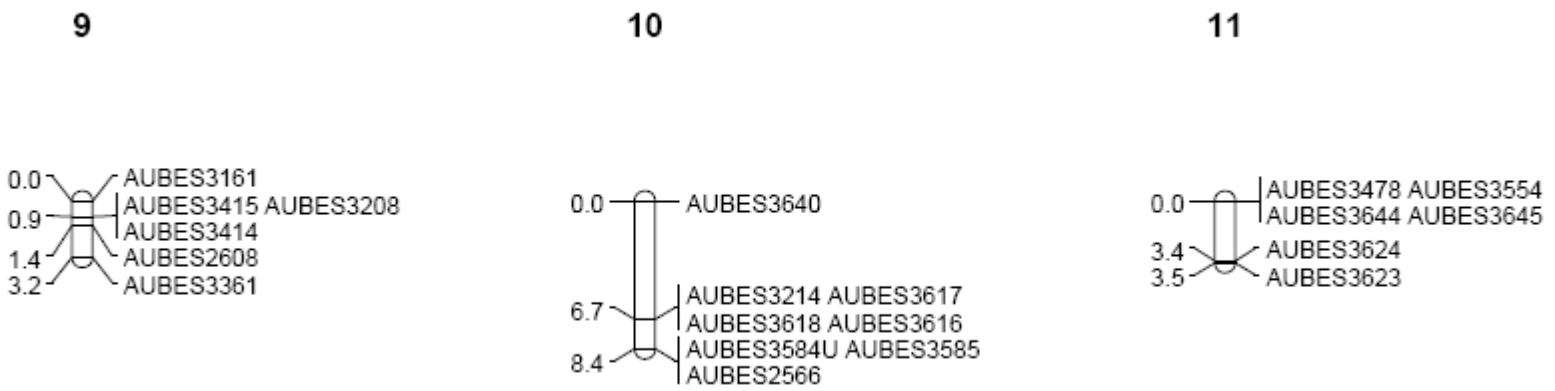

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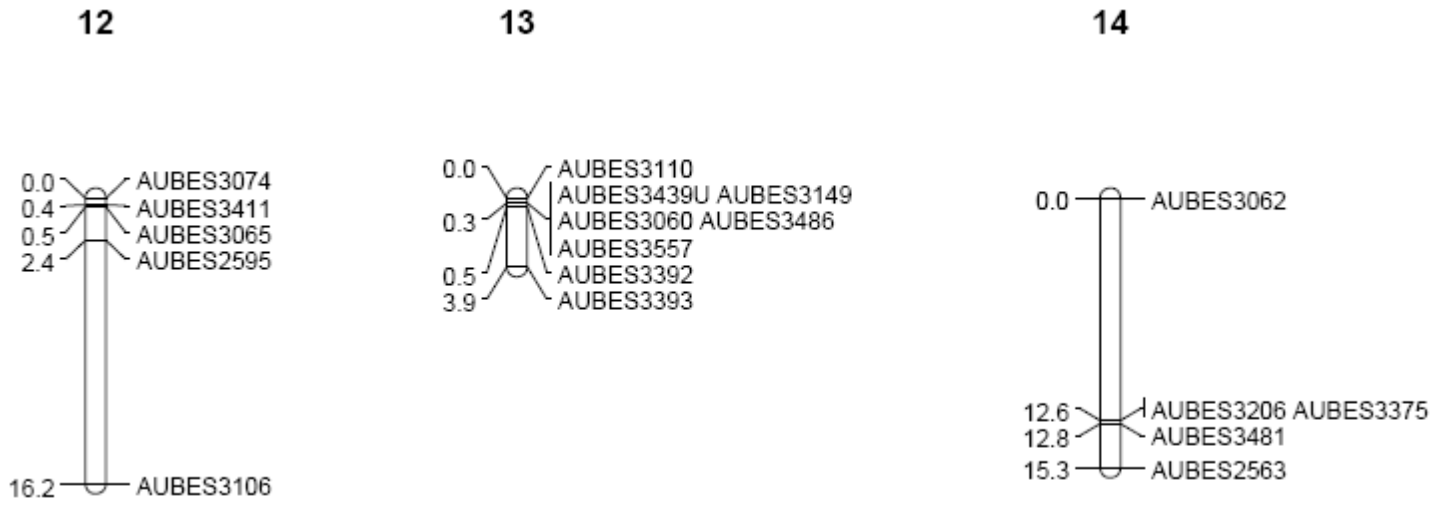

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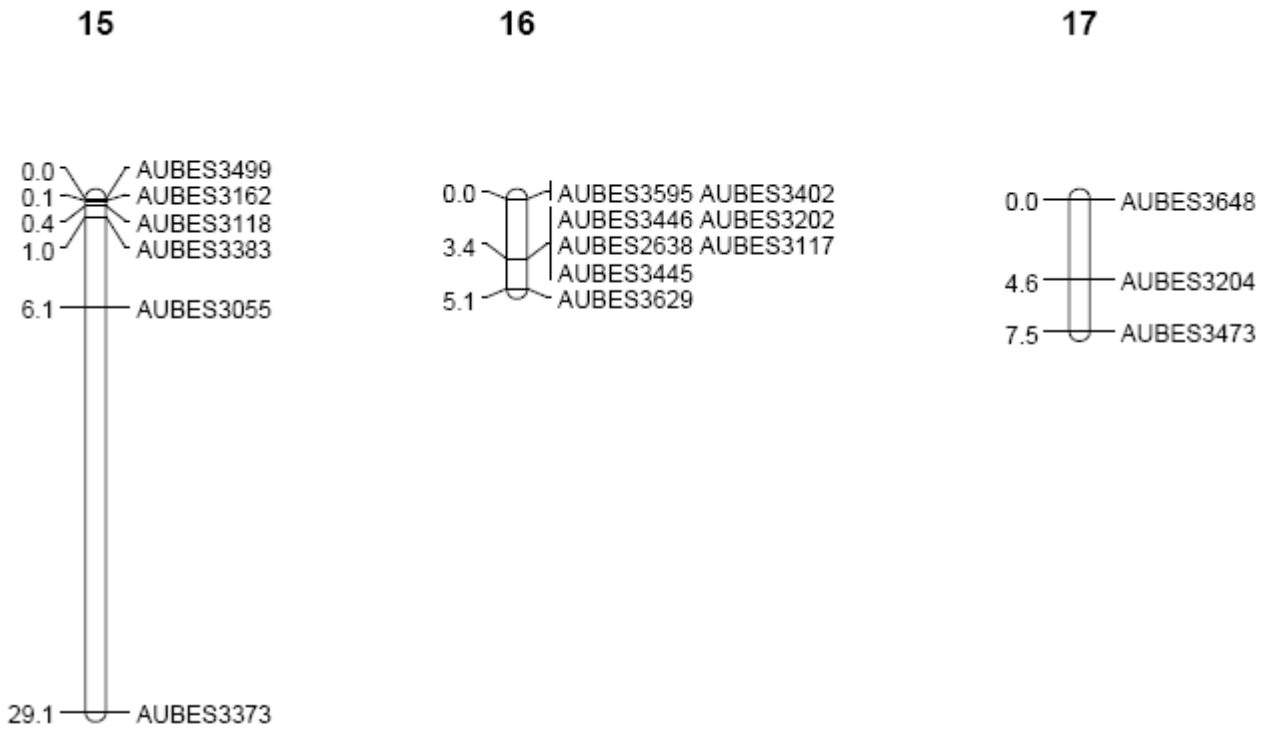

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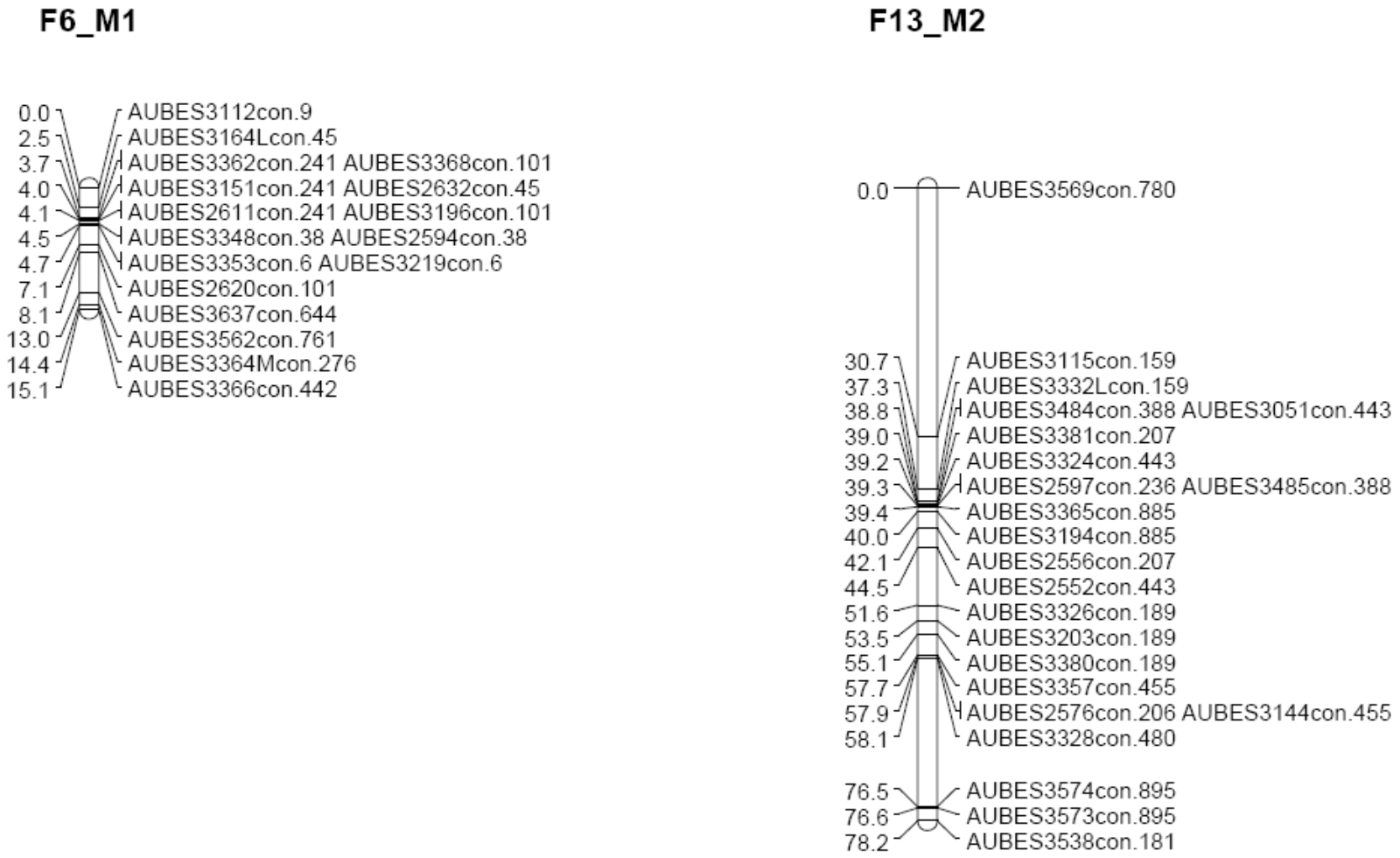
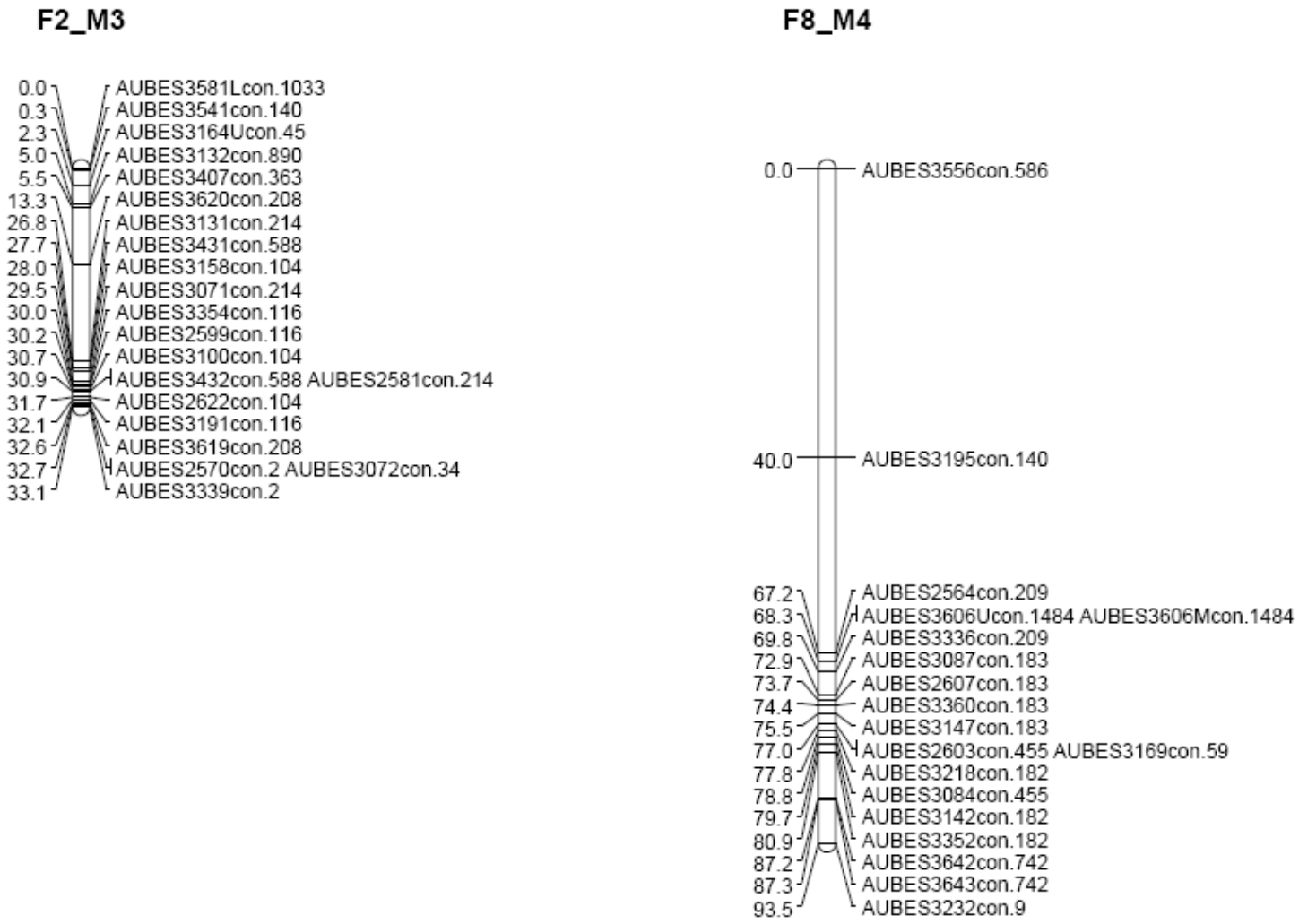


Figure 3. Integration of sex average map and physical map in channel catfish based on microsatellite markers. Genetic map distance was given in centimorgans to the left side of the marker positions. Con. represented contig.



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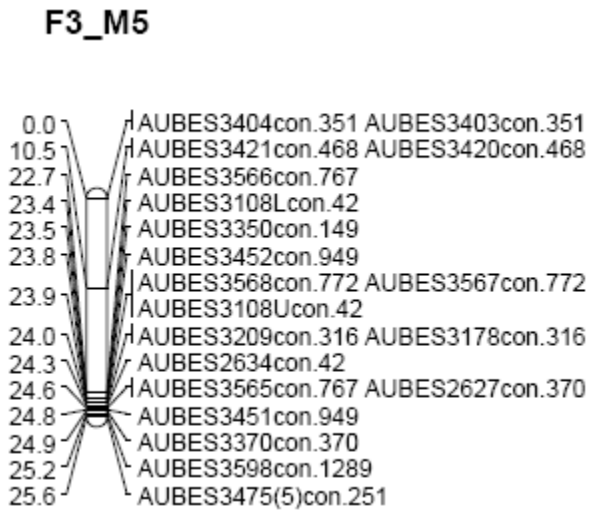

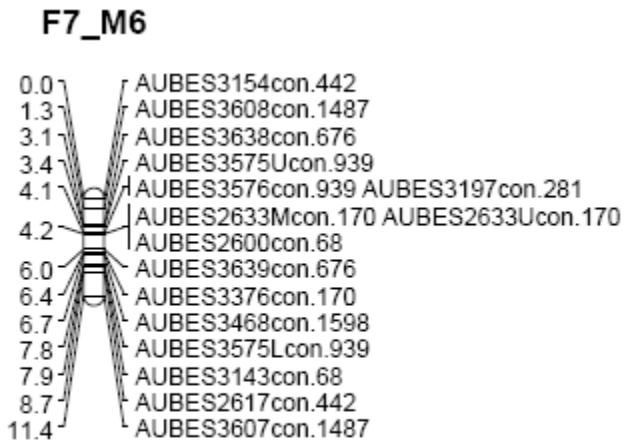

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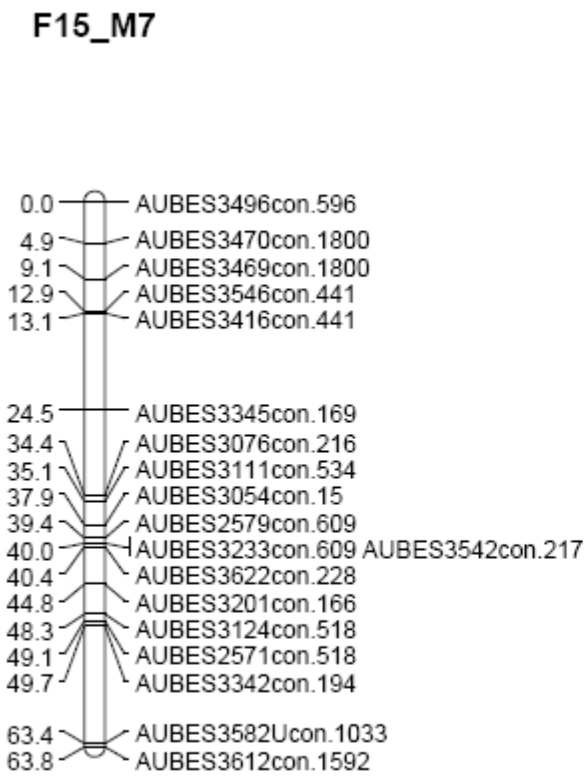

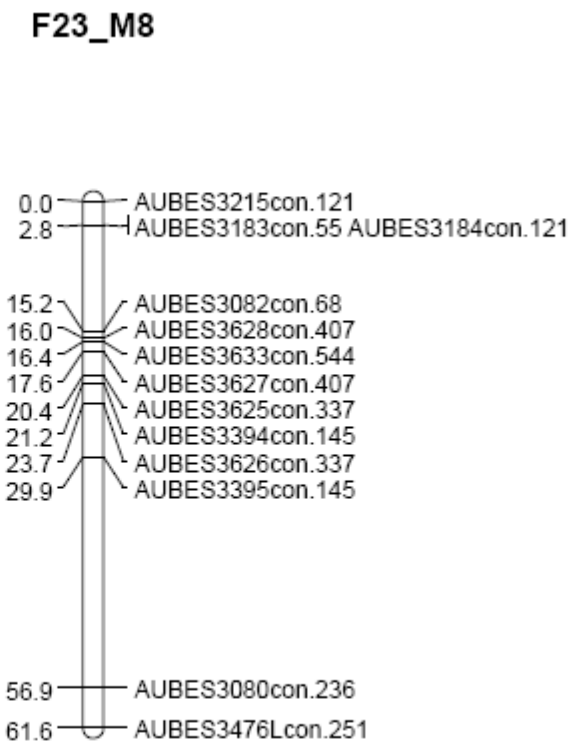

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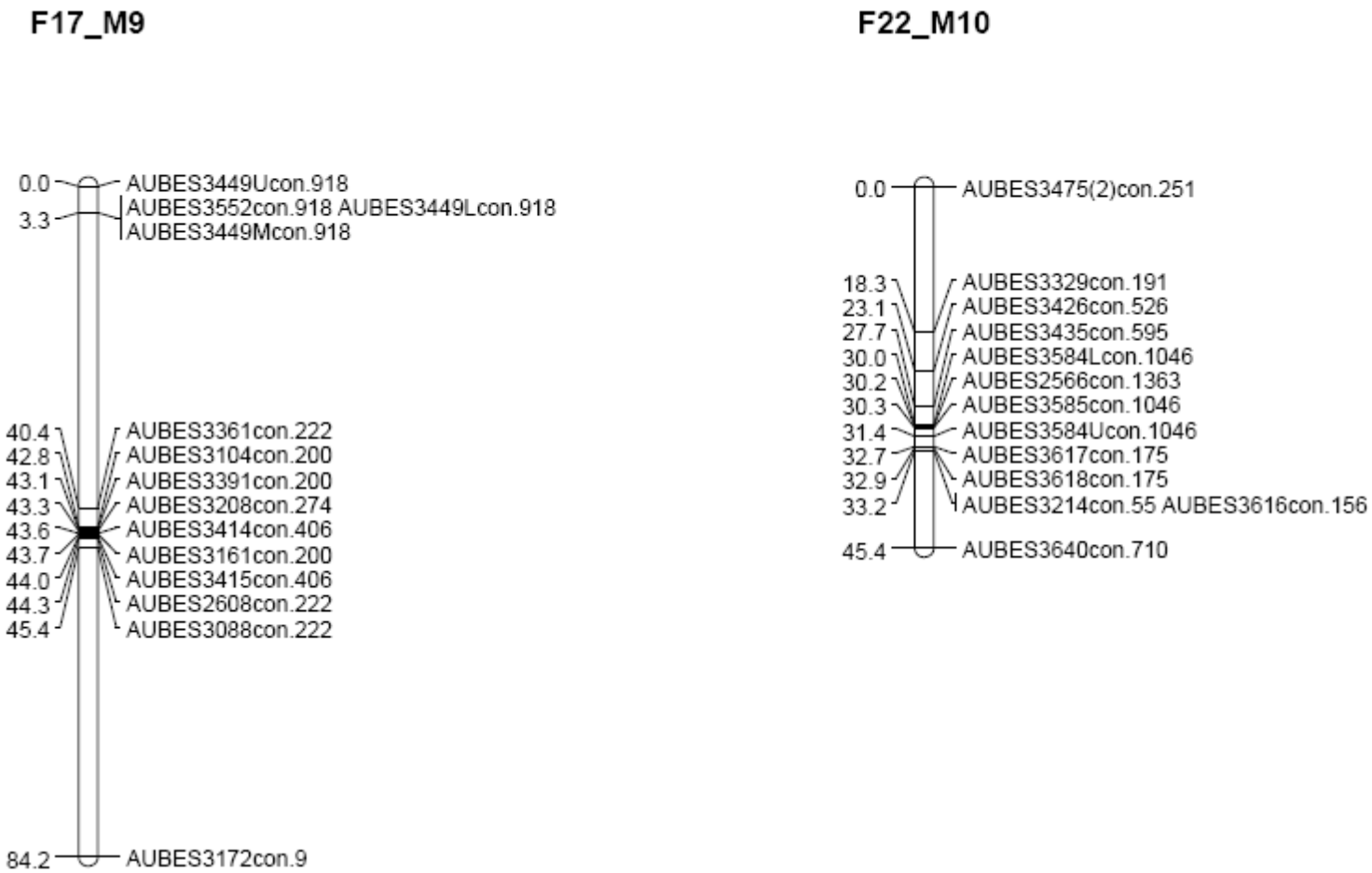

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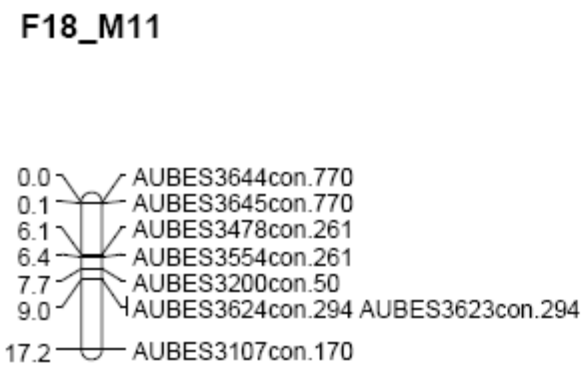

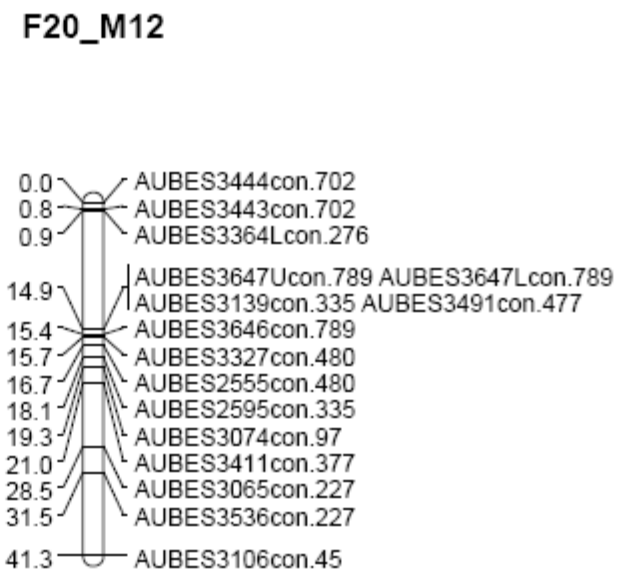

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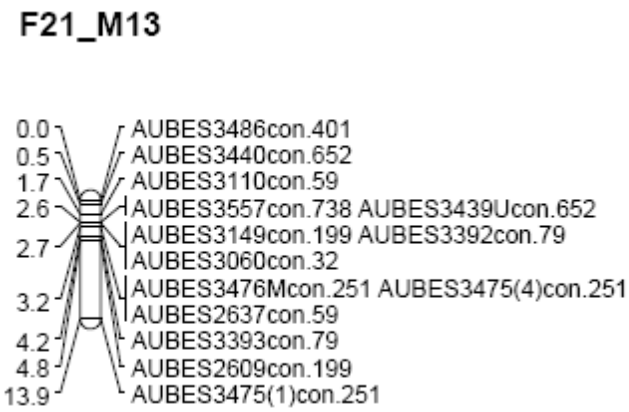

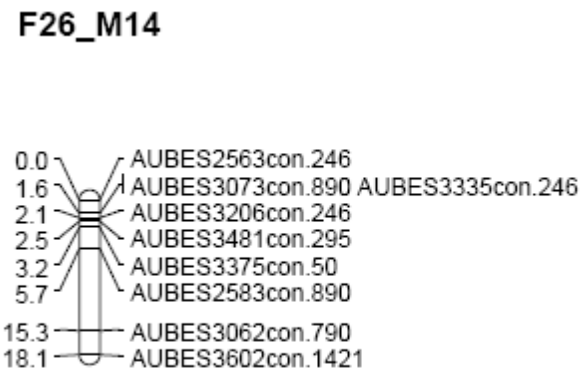

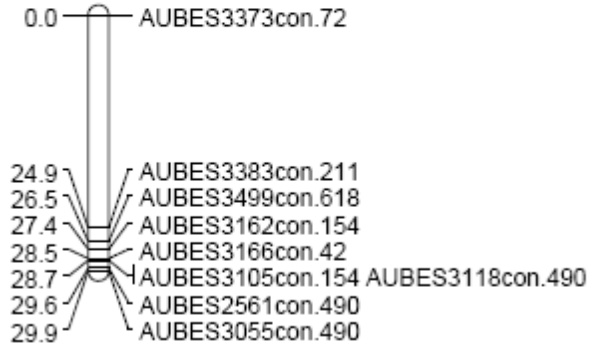

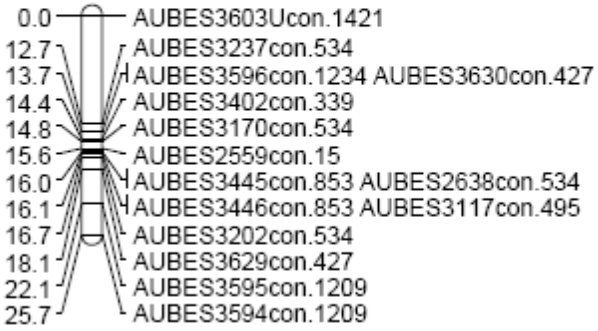

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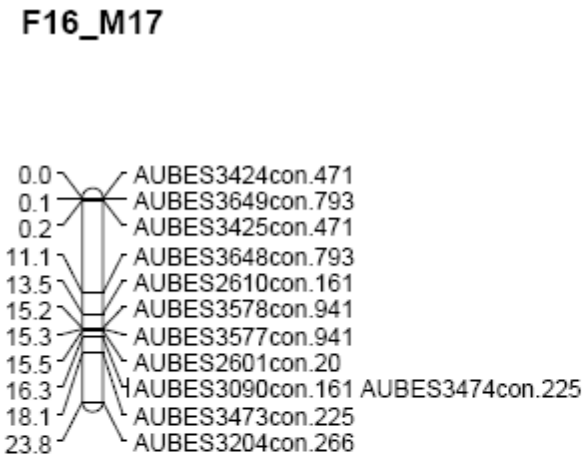

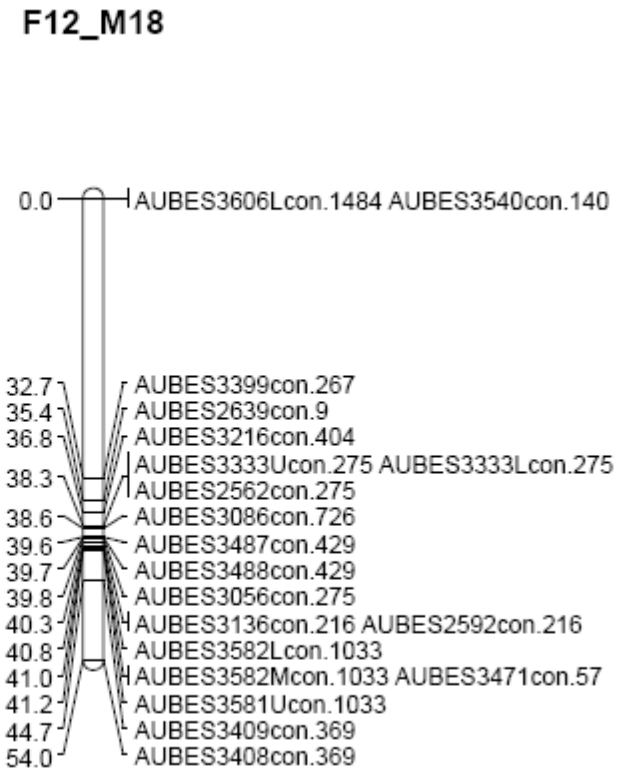

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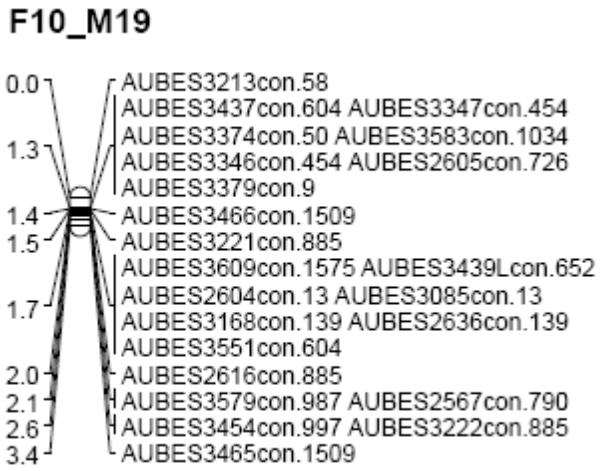

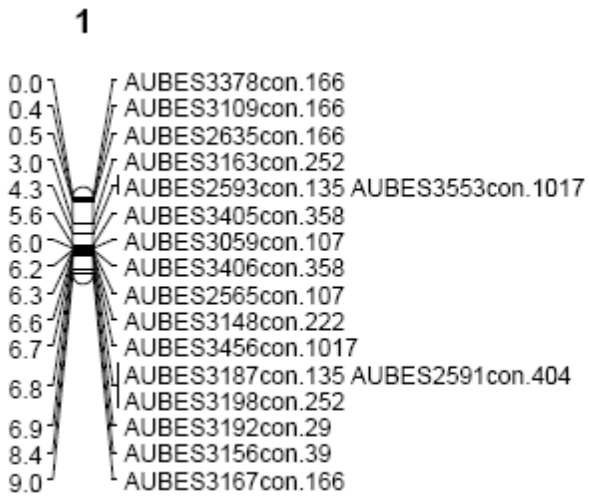

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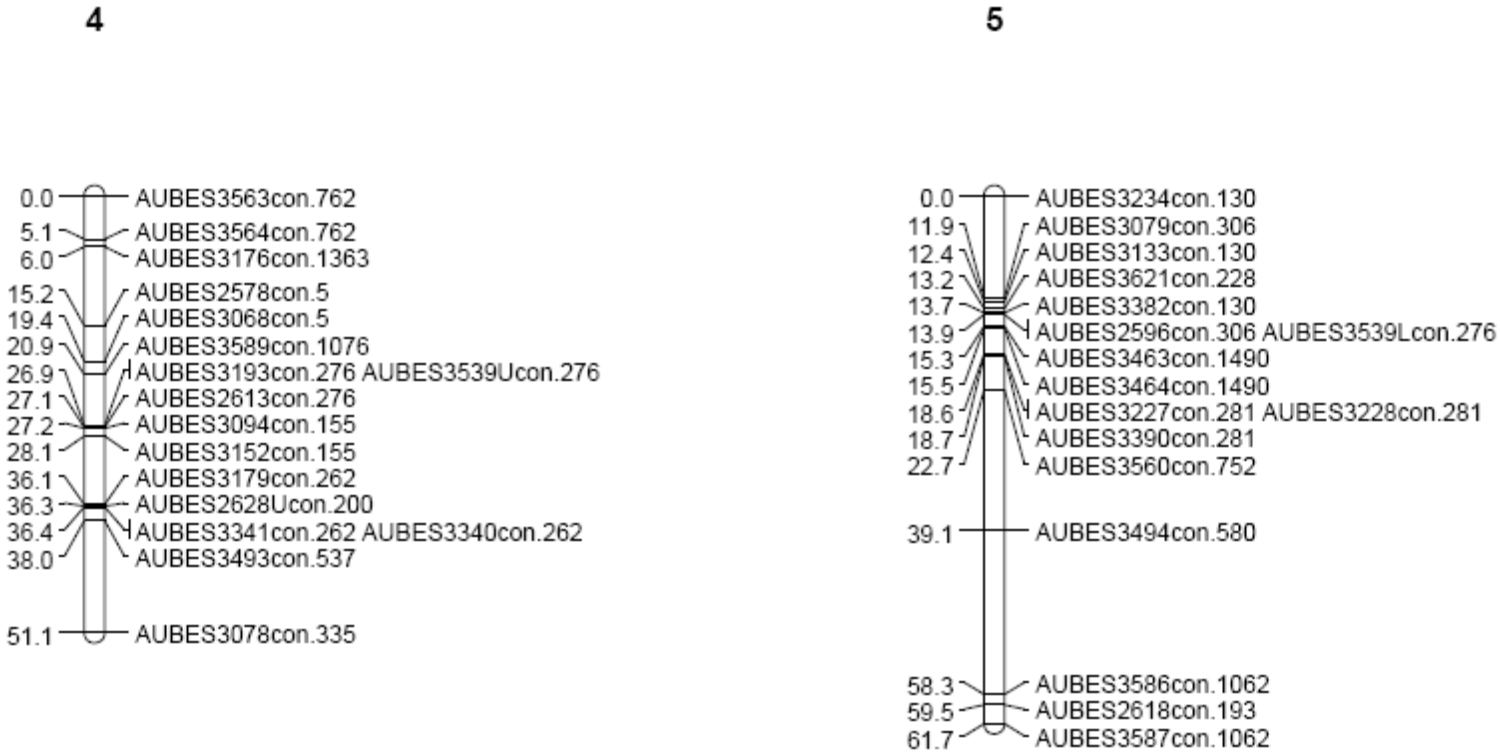

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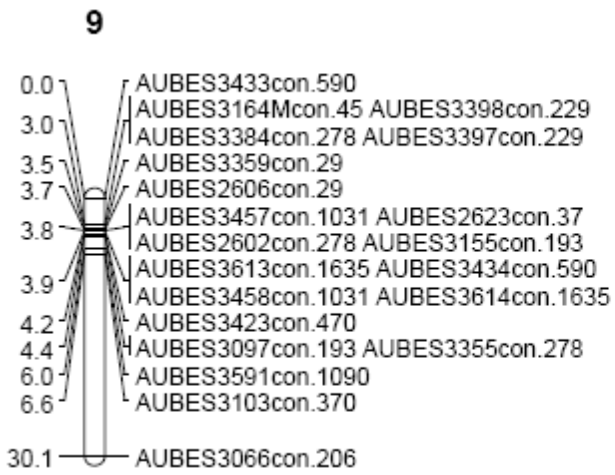

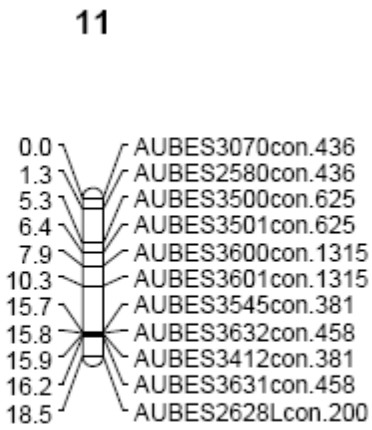

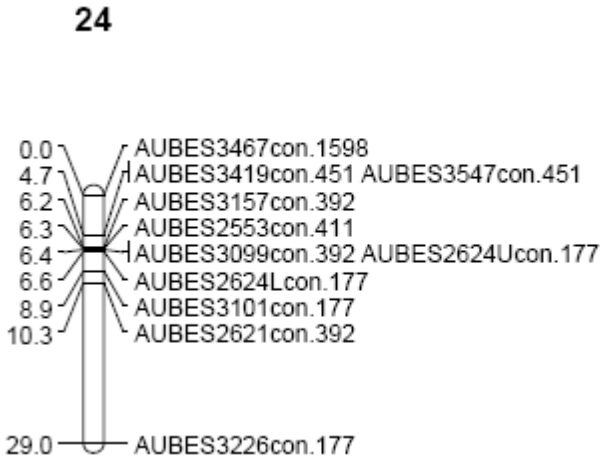

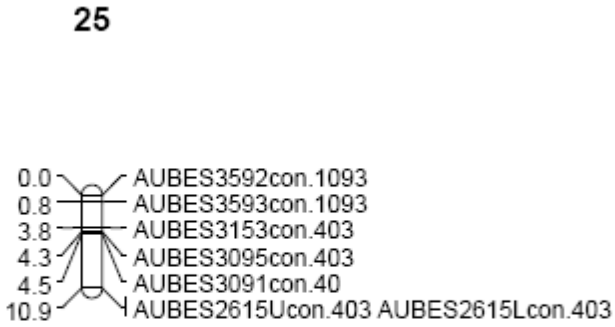

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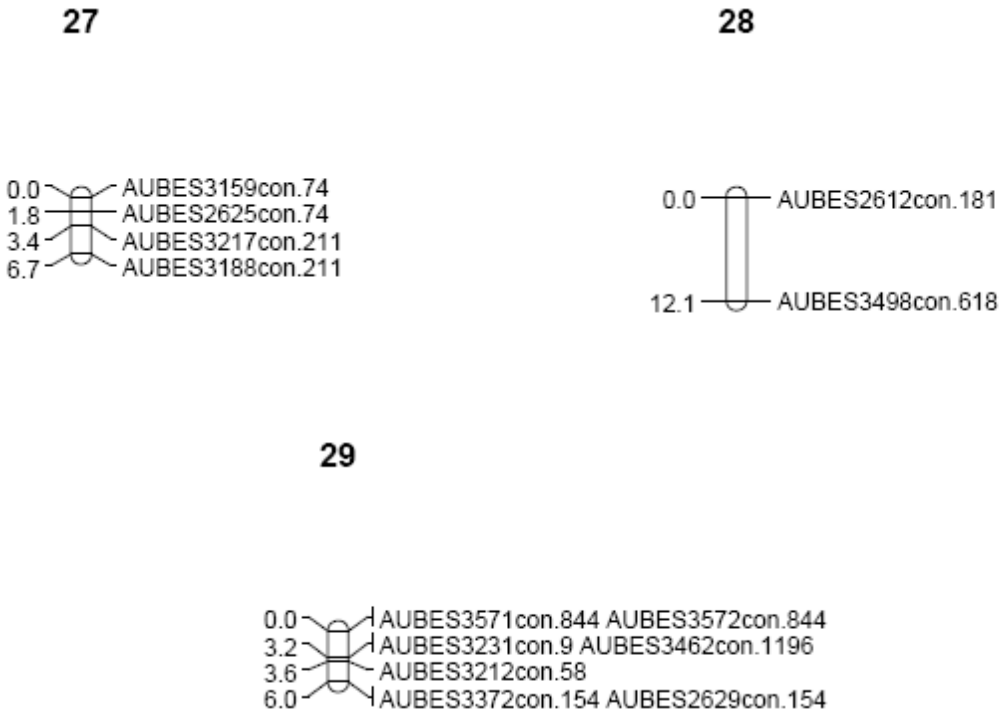

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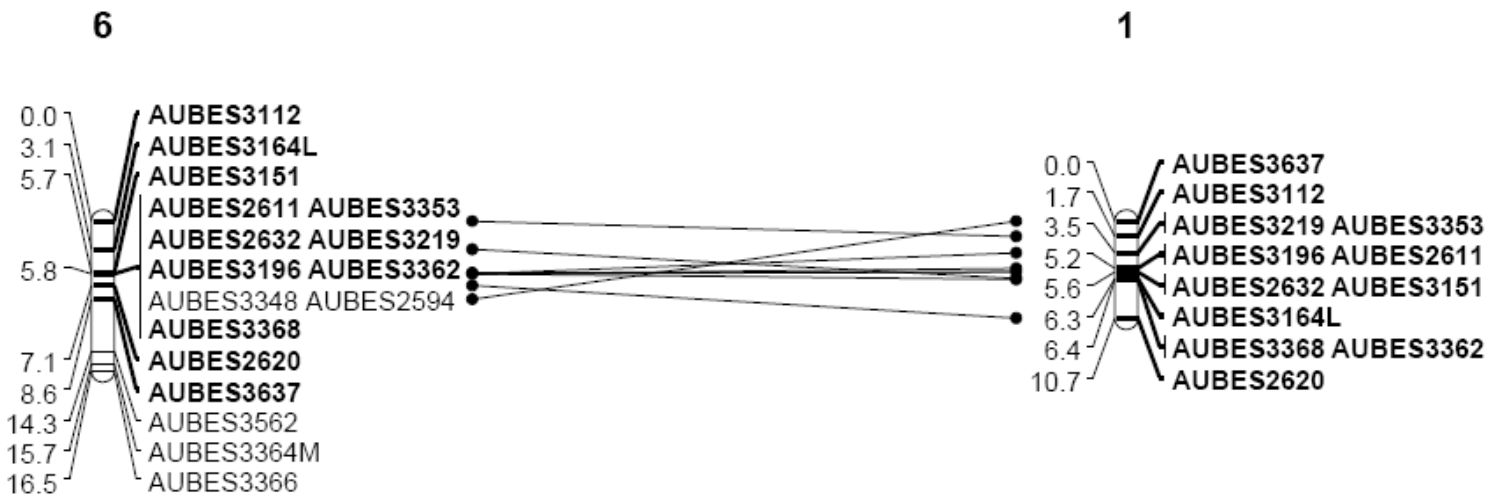
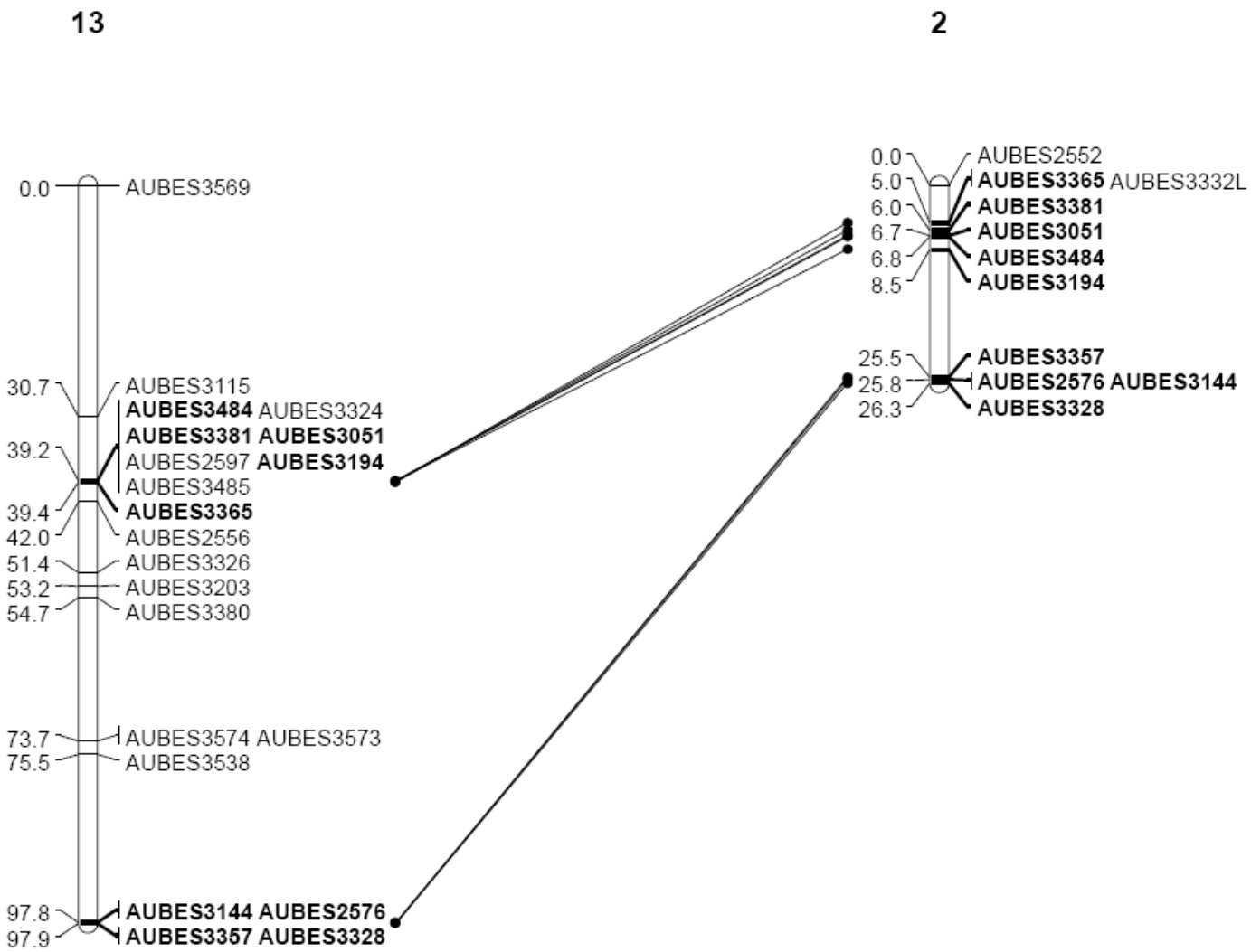


Figure 4. Female (left) and male (right) linkage map of channel catfish based on microsatellite markers. Genetic map distance was given in centimorgans to the left side of the marker positions. Lines between the markers and the boldfaced markers indicate the common markers between female and male maps.



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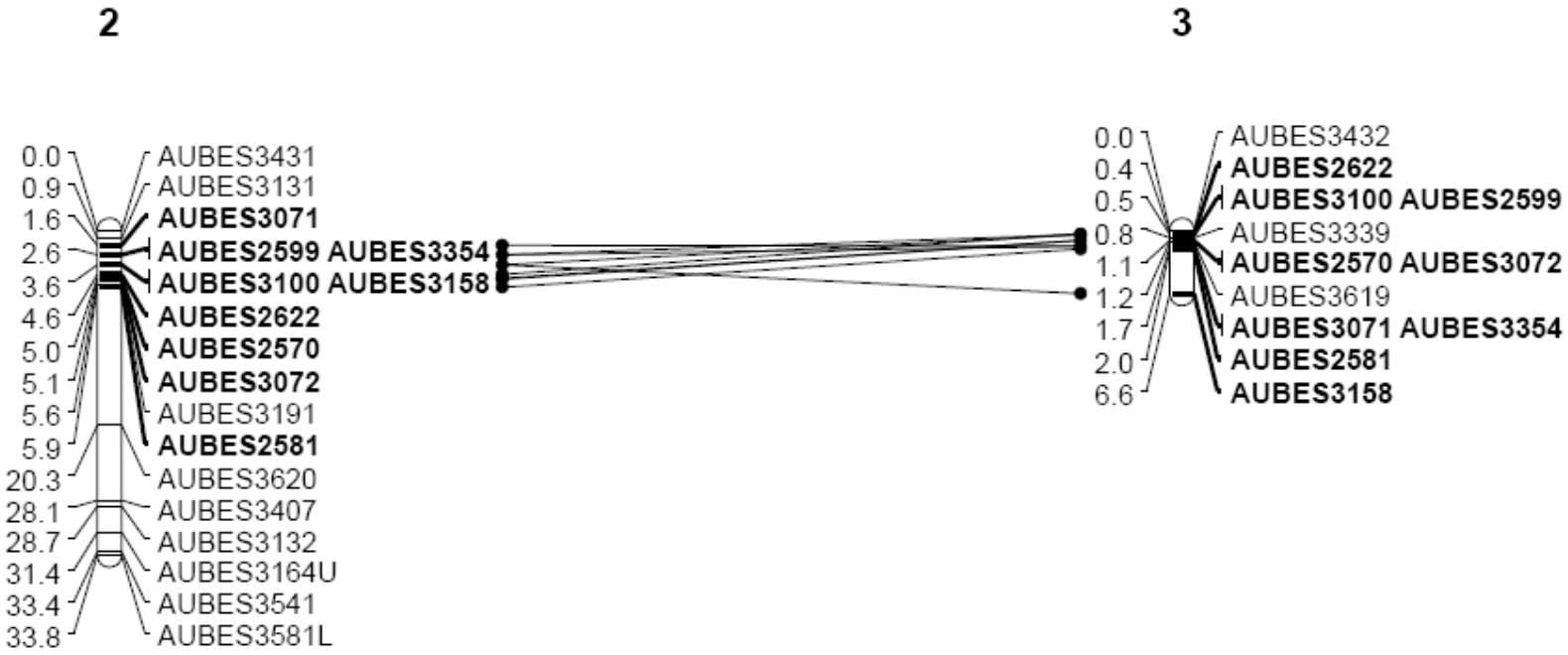

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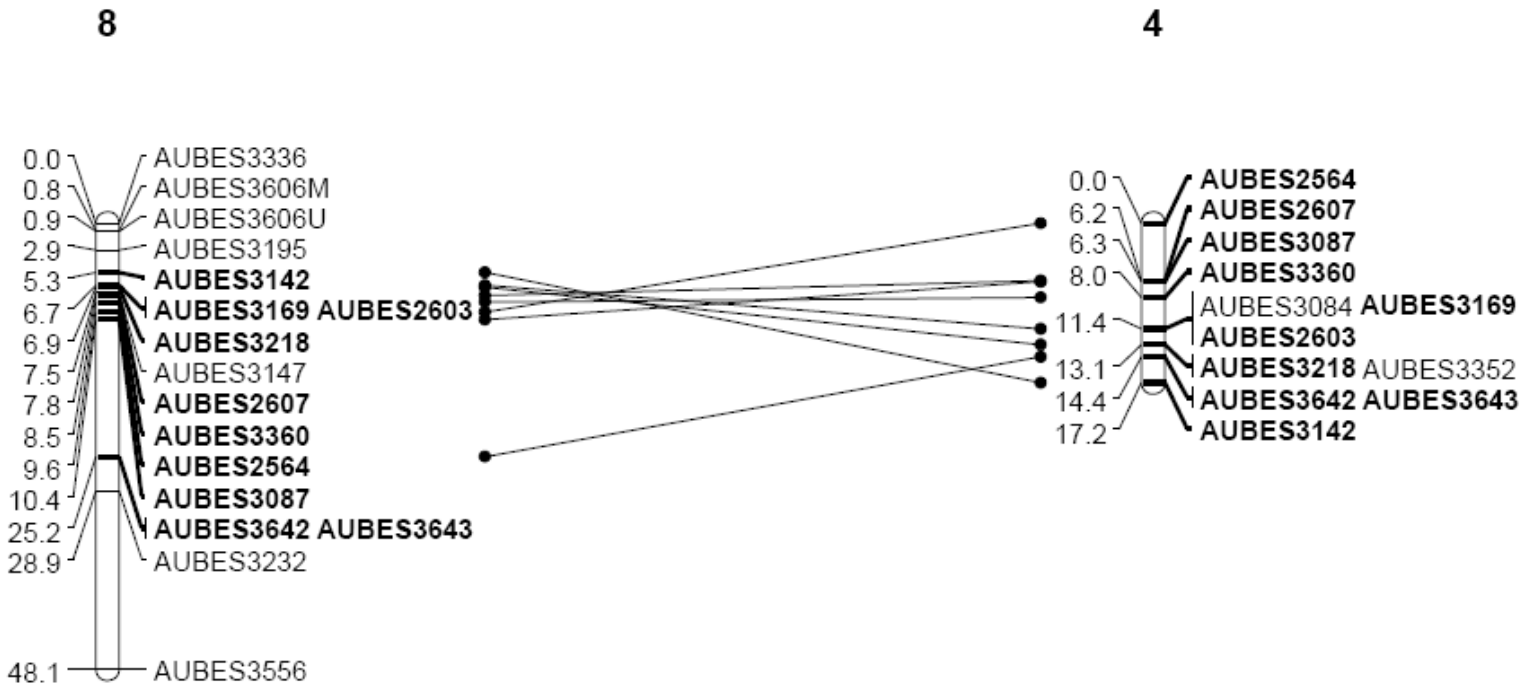

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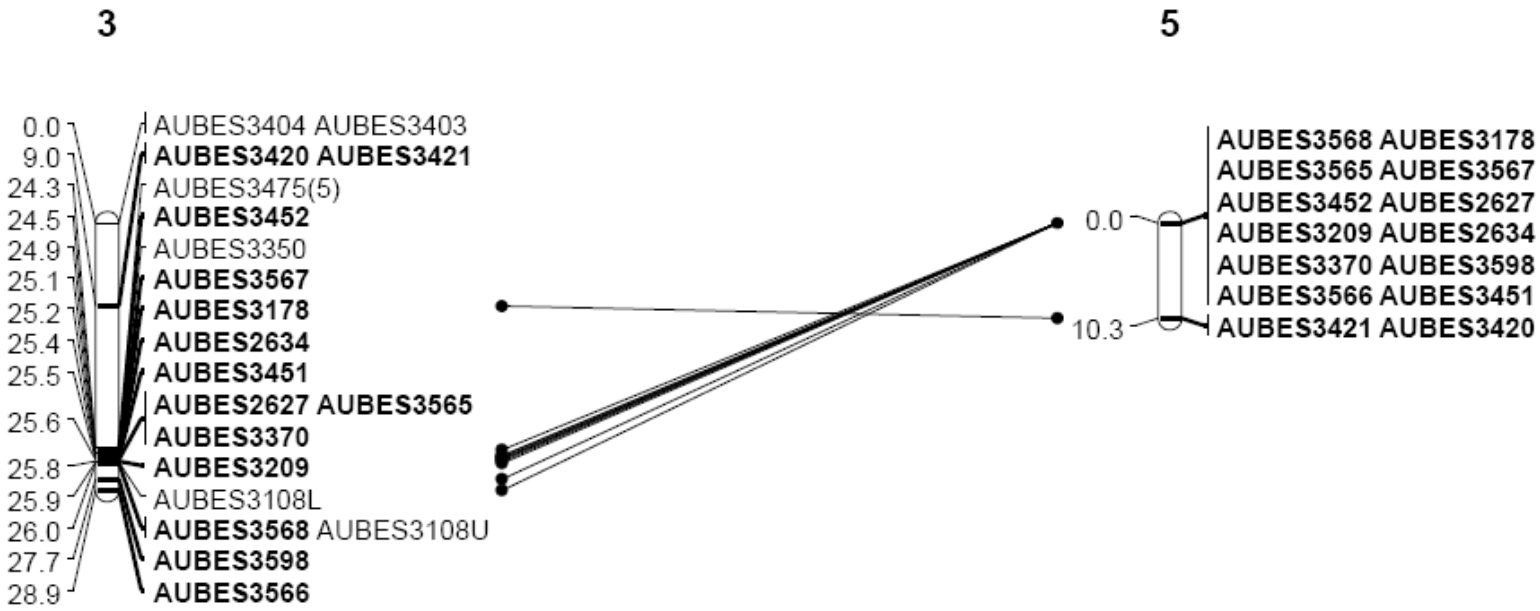

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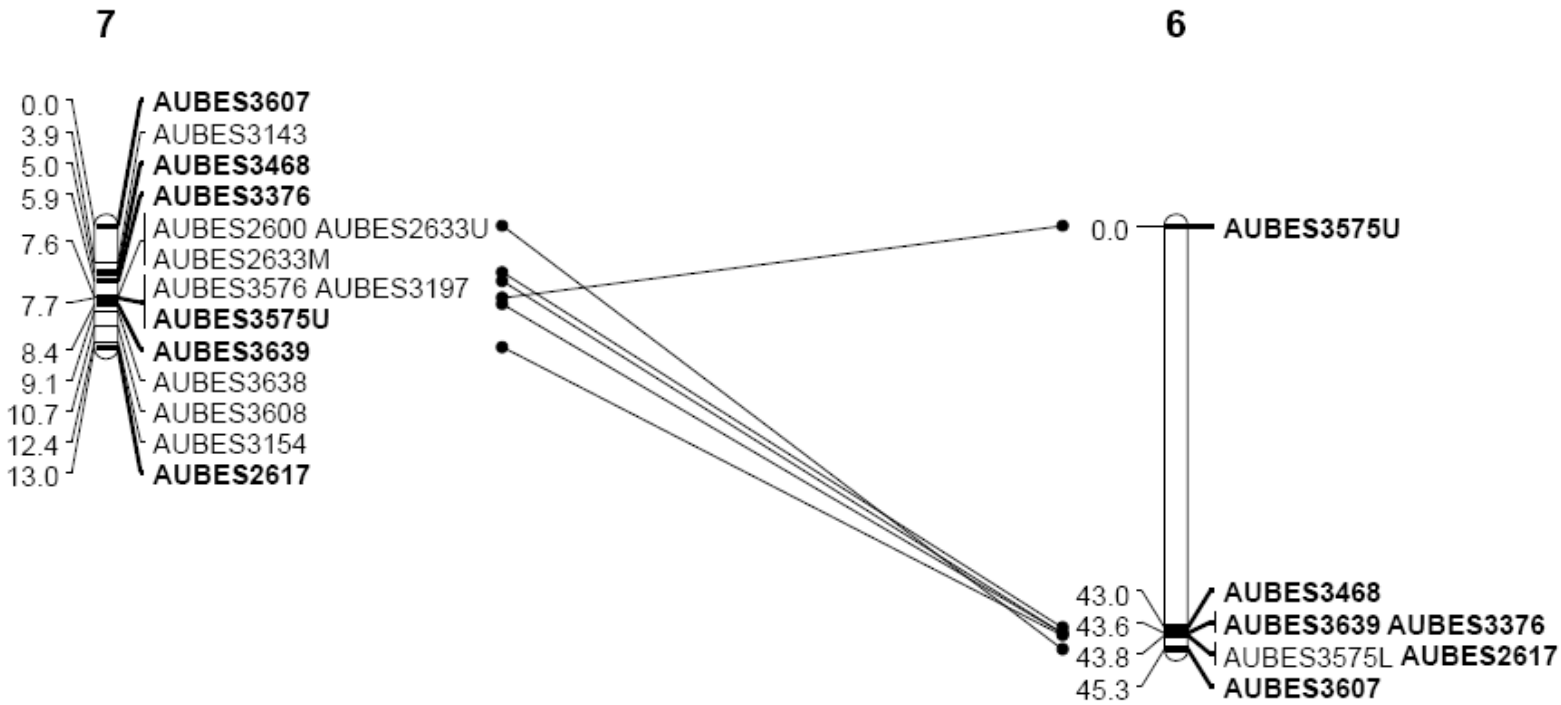

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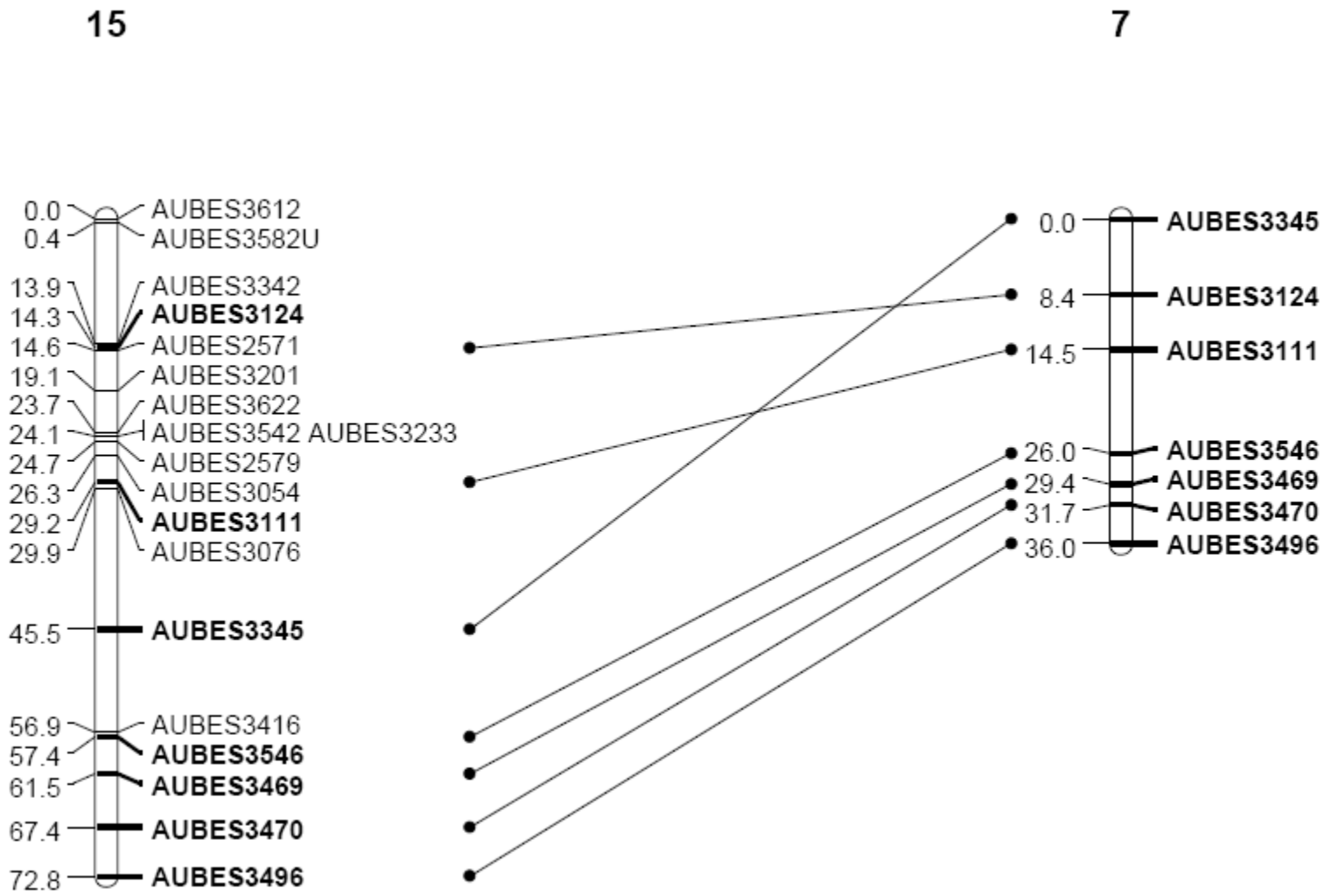

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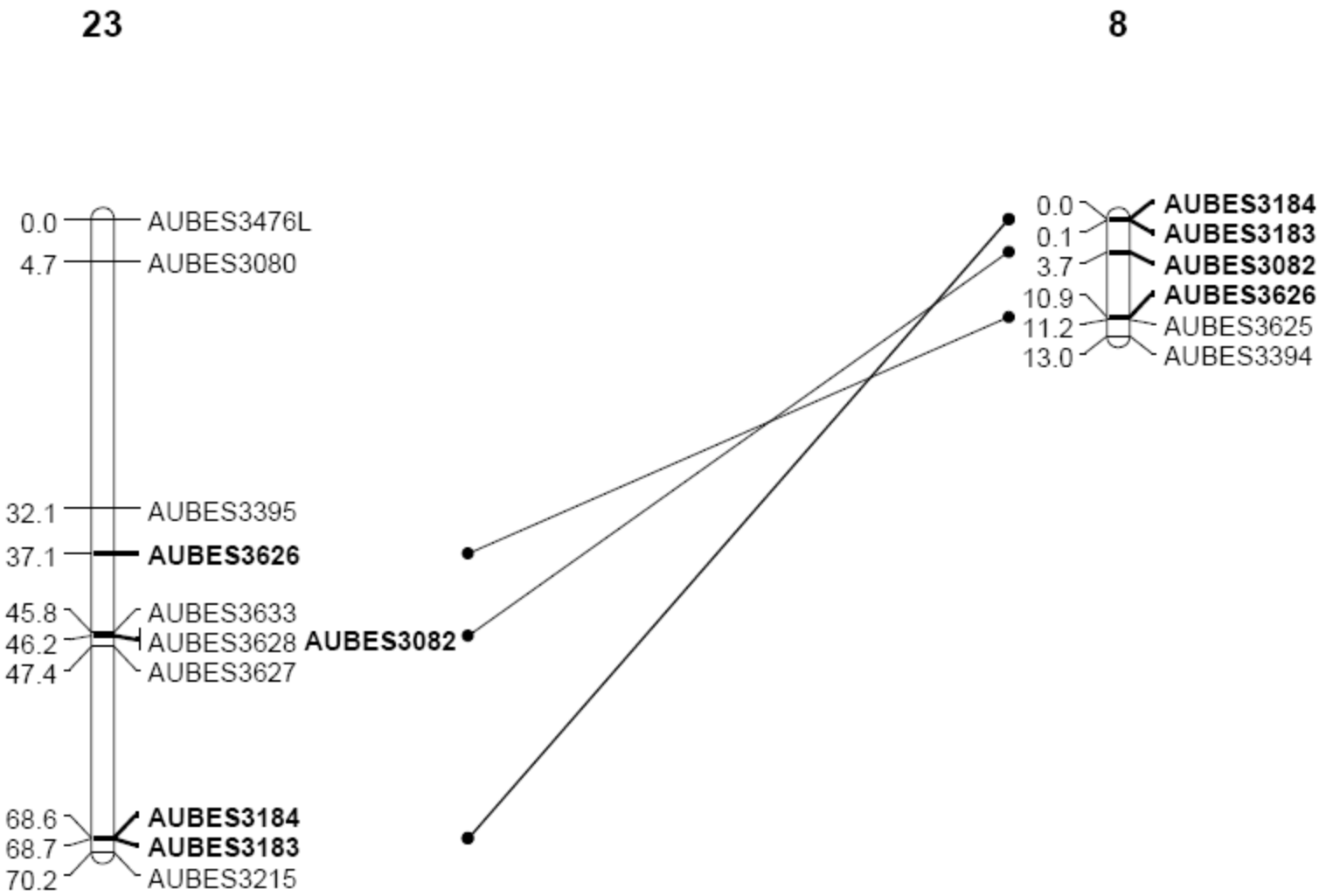

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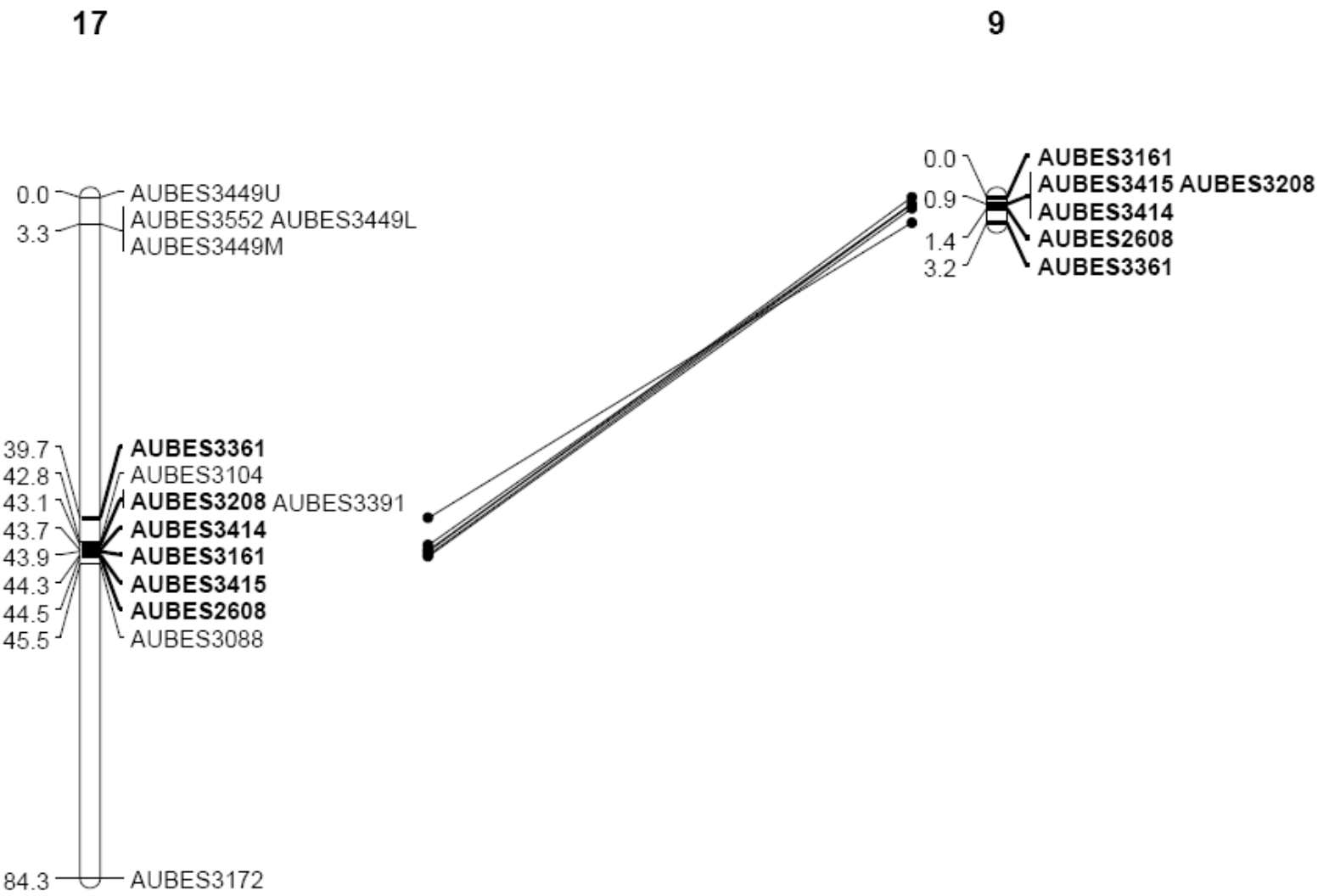

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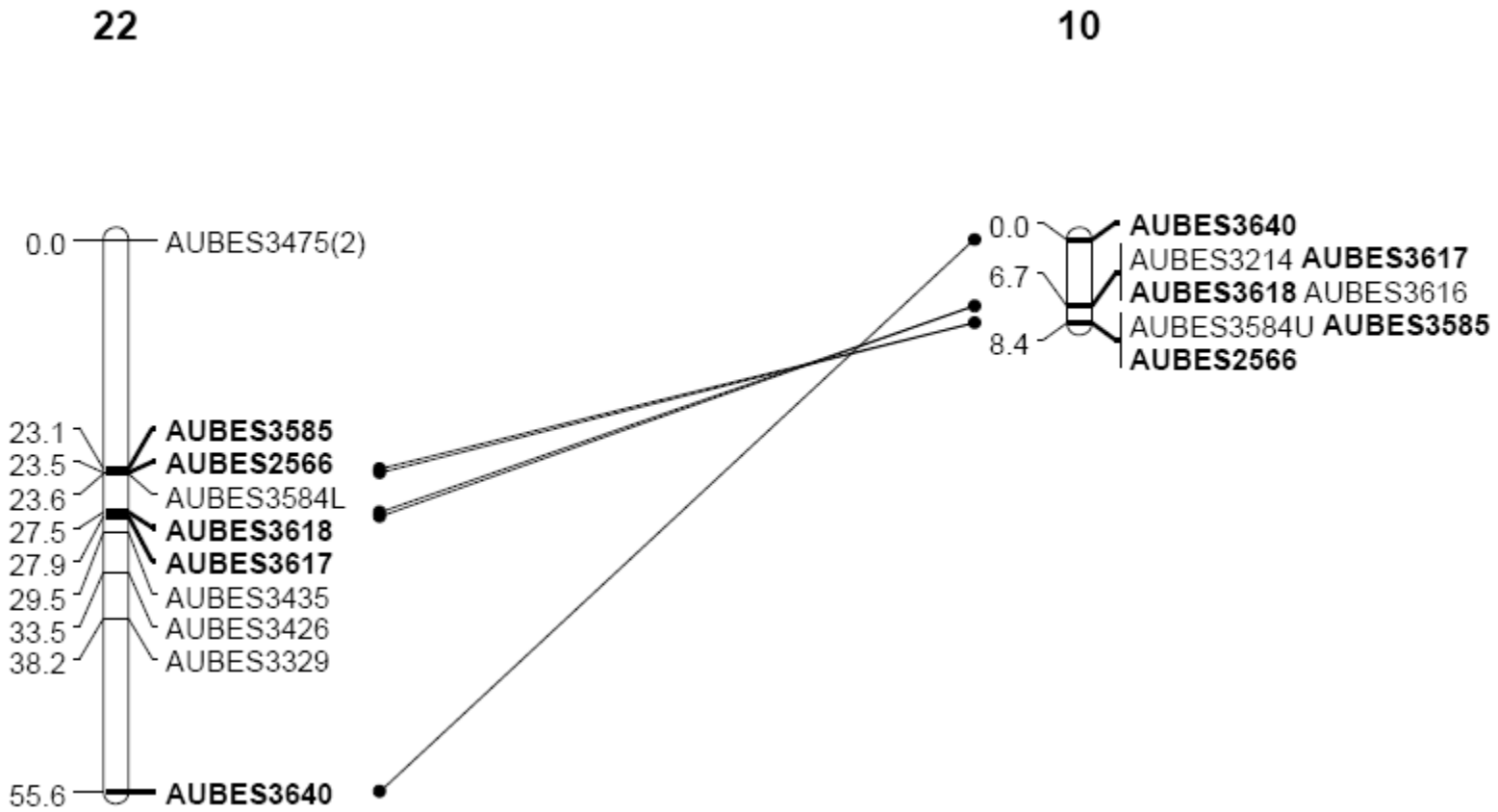

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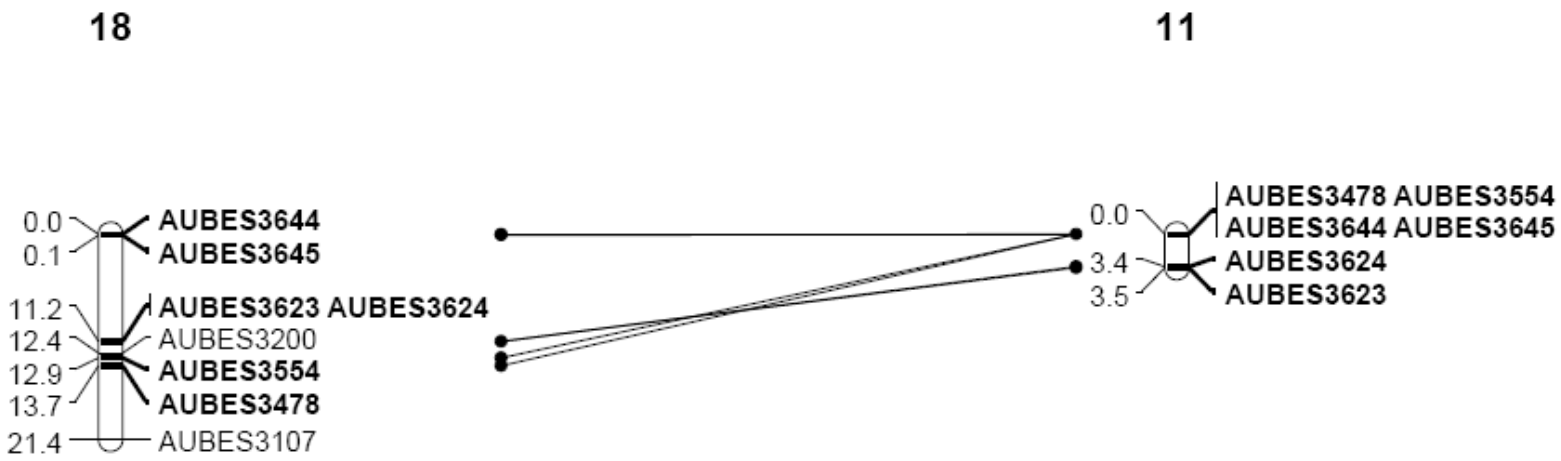

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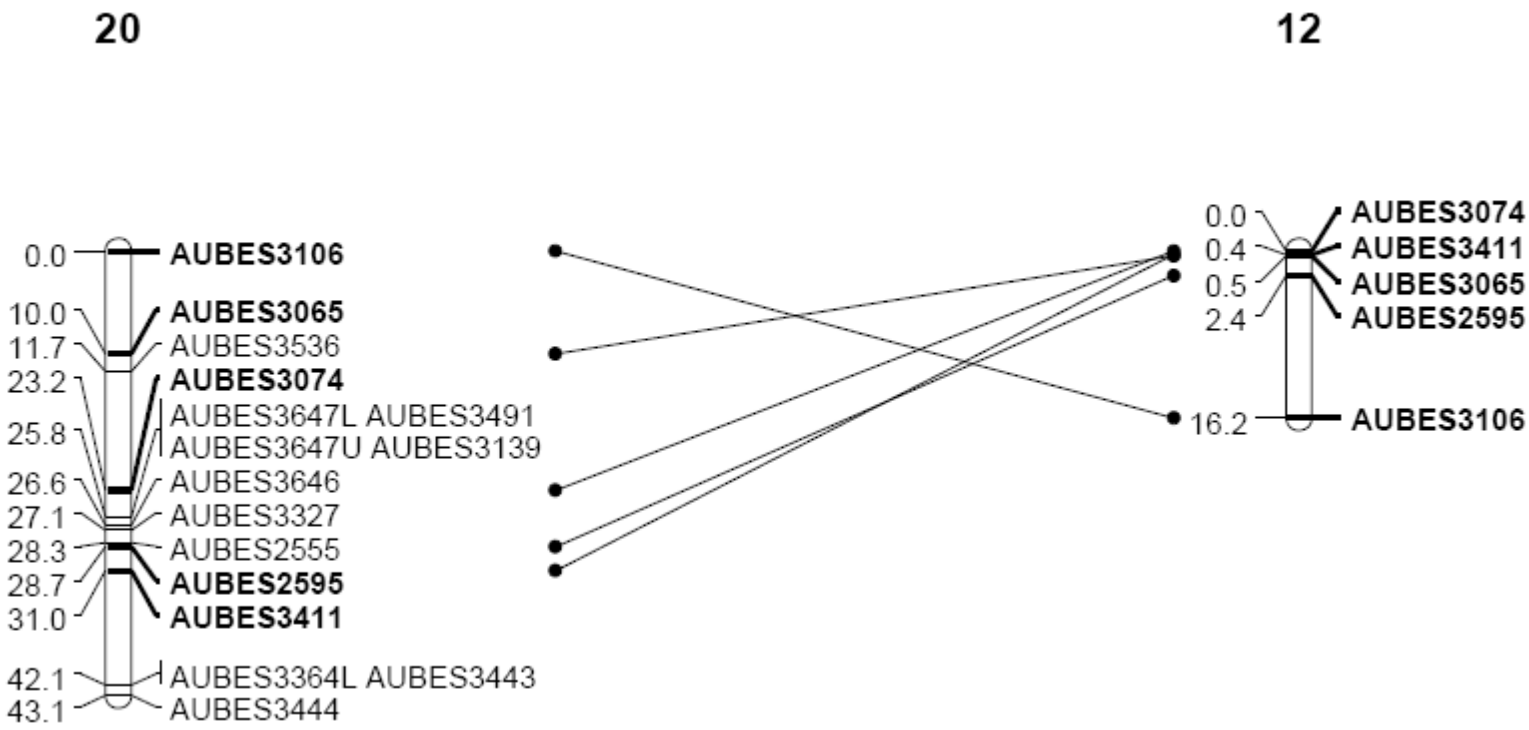

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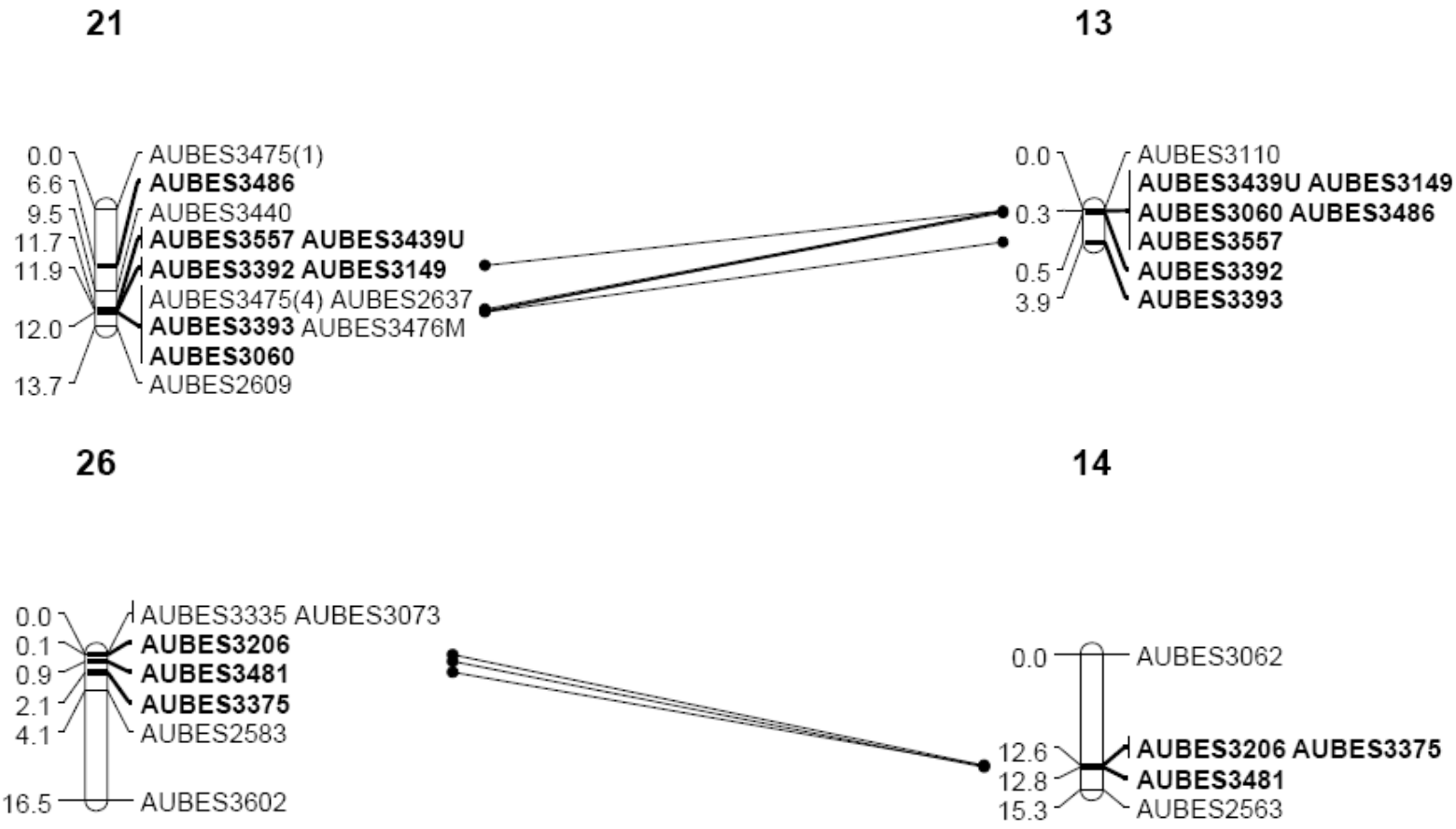

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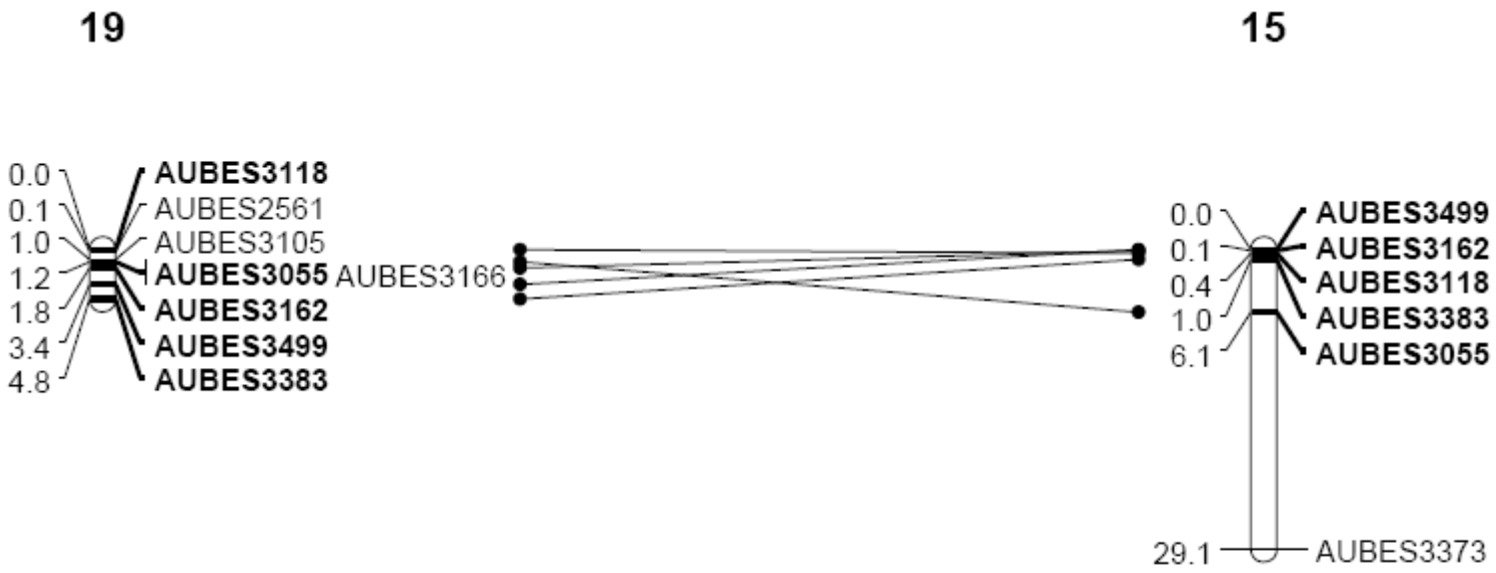

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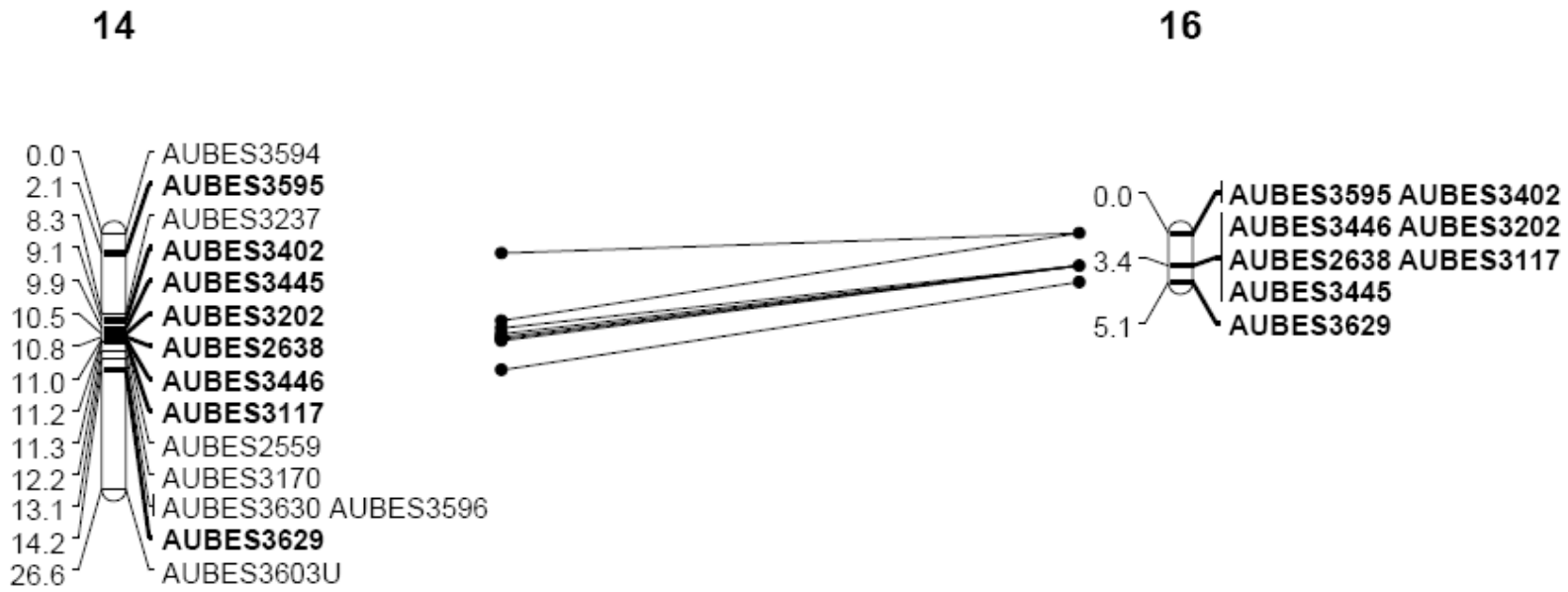

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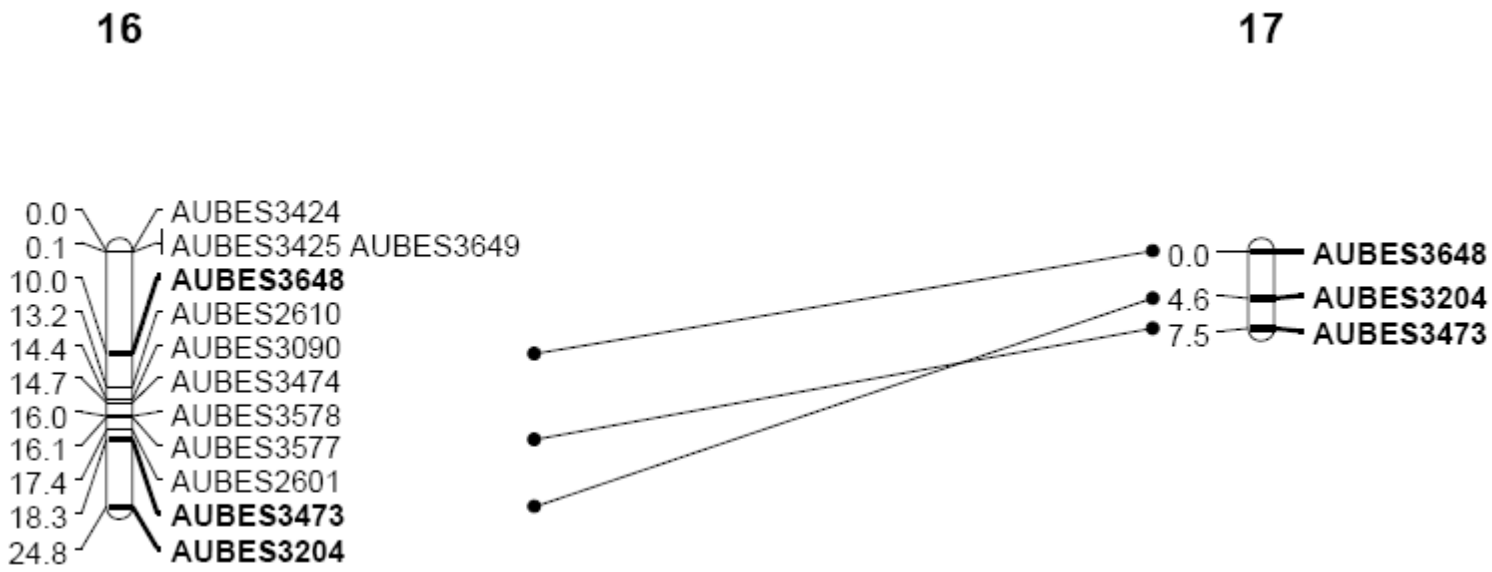

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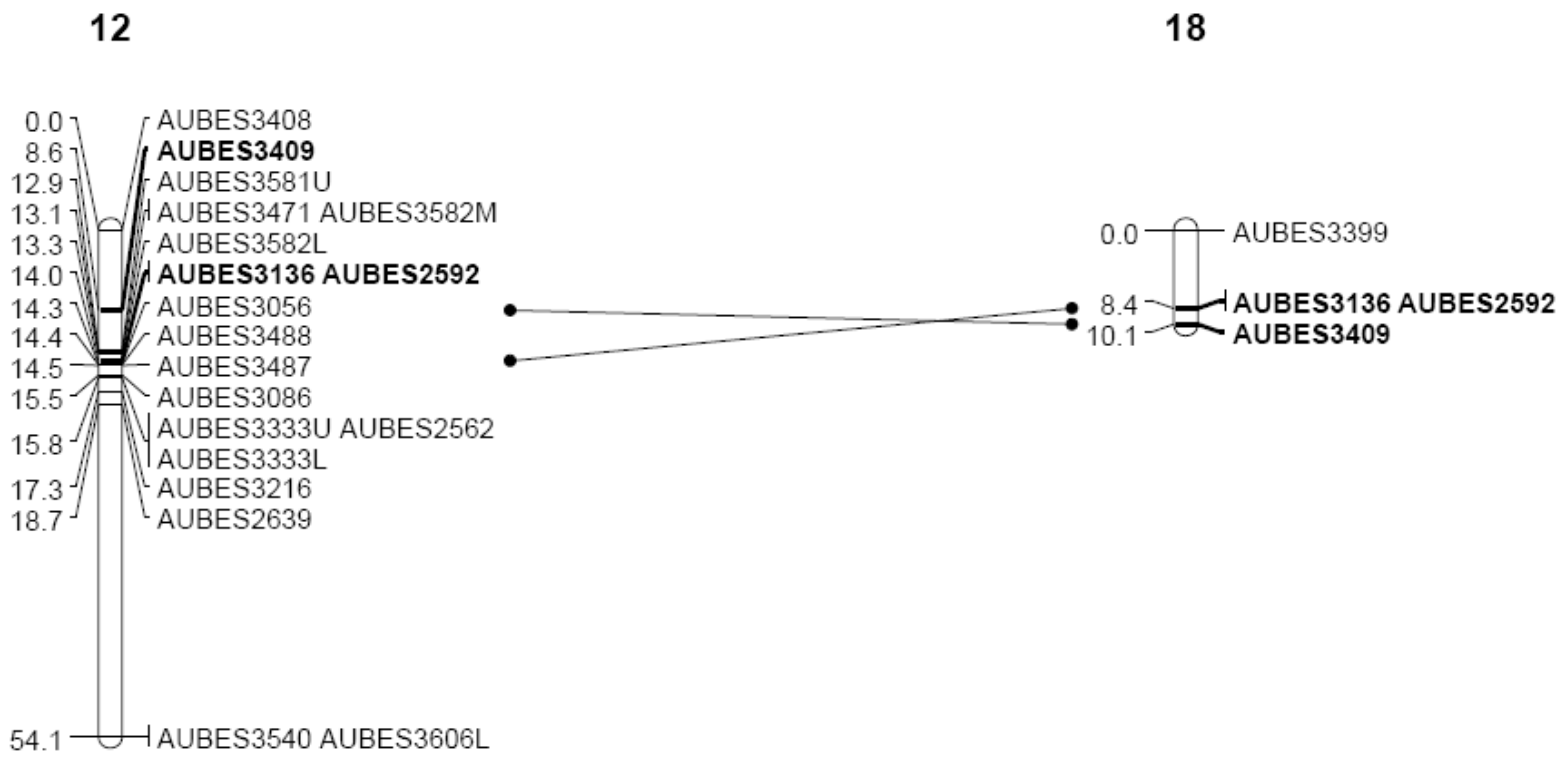

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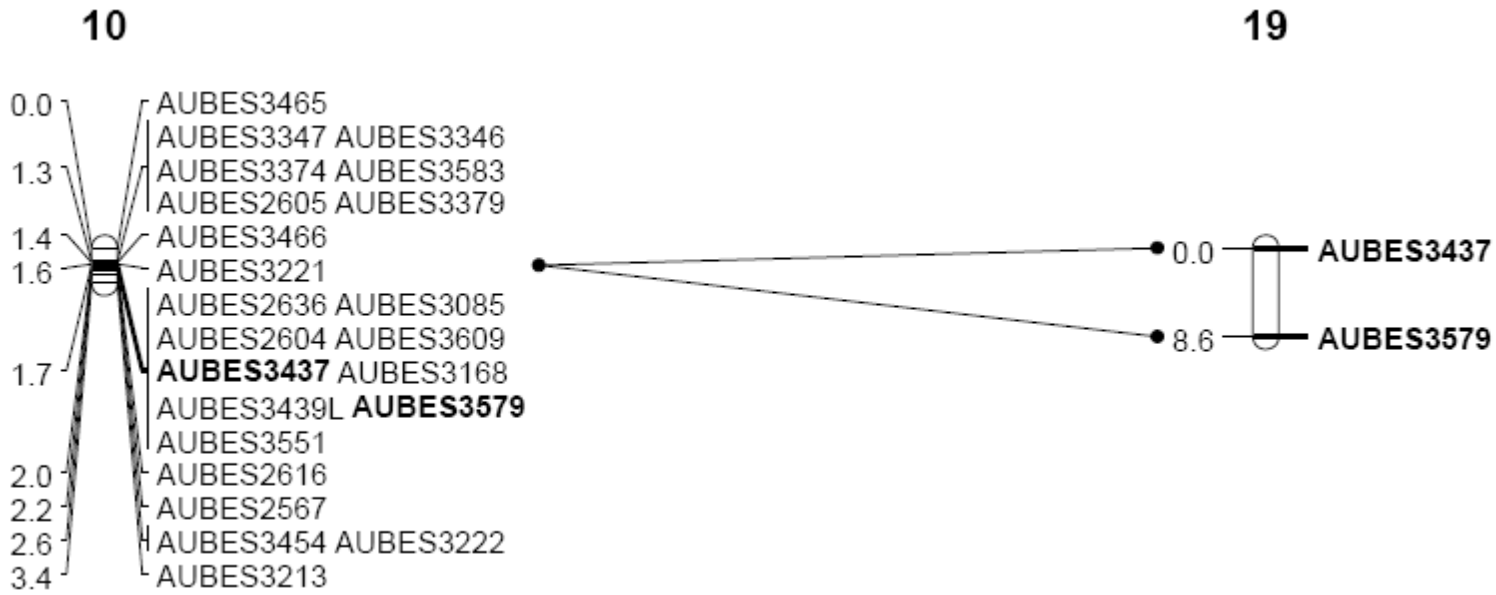

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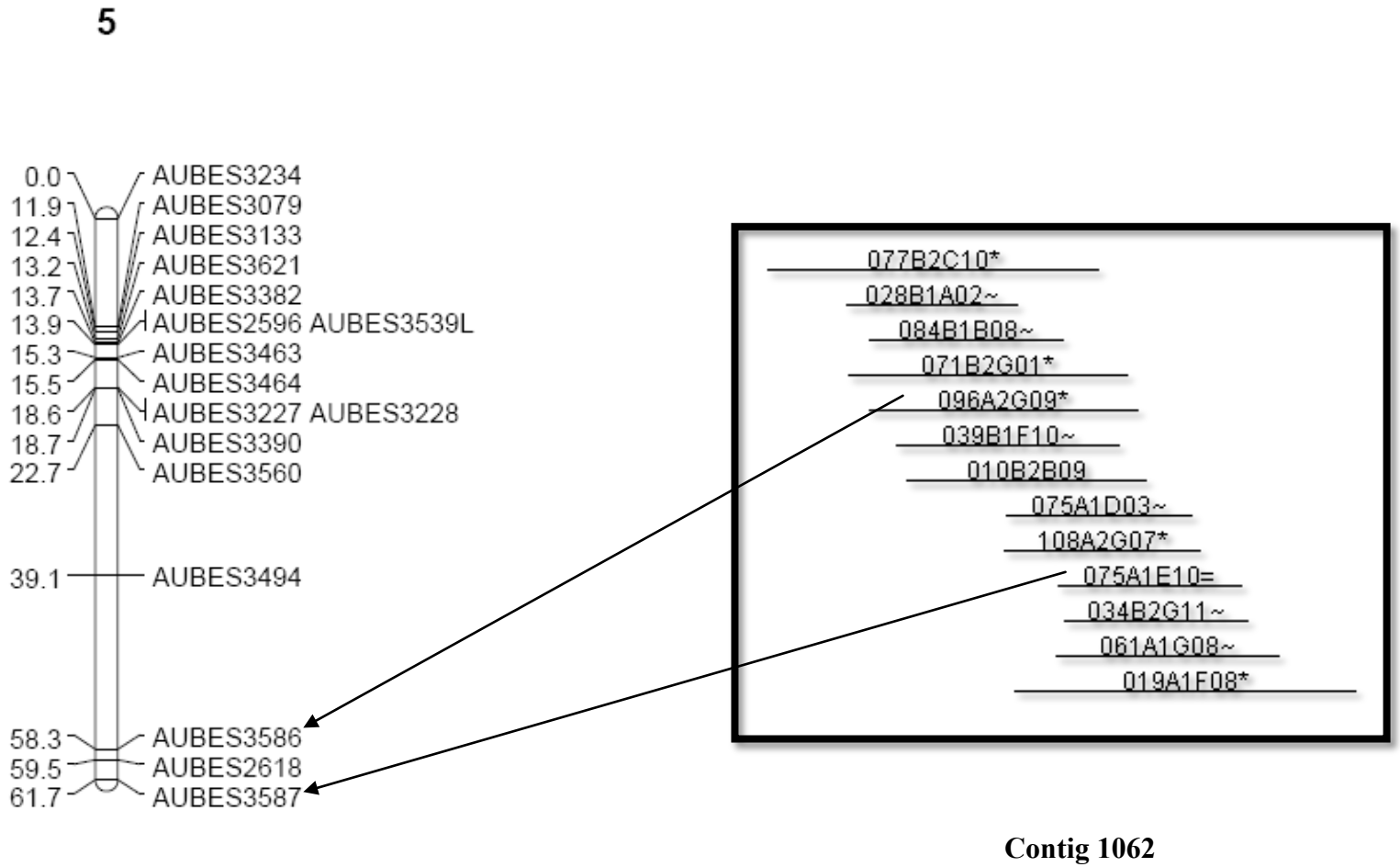

Figure 5. The orientations of the contig in the physical map identified from the order of the correlated markers in the genetic linkage map.

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APPENDIX

Appendix. Identification of microsatellite loci from BAC end sequences in resource family by using PCR.

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
443	ta.17	AU2552	211	57oC/15cycles,53oC/20cycles	TCAACTCAGTCAGCATTTTAAGG	TCAACTCAGTCAGCATTTTAAGG	Polymorphic
411	gt.10	AU2553	240	57oC/15cycles,53oC/20cycles	GGTTAGTGCTGAACGAAATGC	CGTCCAGAGAGAGGAATGGA	Polymorphic
189	taa.7	AU2554	230	57oC/15cycles,53oC/20cycles	GGCCCTTTAAGGAATGATGA	TTGGCACCCCTATGAATTAAG	No product
480	tct.16	AU2555	197	57oC/15cycles,53oC/20cycles	ACTGTTGTTGCTGTTGTTGTTG	GCACAAACTGACAAACAGATTCA	Polymorphic
207	ata.18	AU2556	213	57oC/15cycles,53oC/20cycles	GCCGTTTCATTATGTTGTCC	CACCCTAACCAGGGTGTCC	Polymorphic
190	taa.6	AU2557	255	57oC/15cycles,53oC/20cycles	CGTGTTTGTGTAAATGCGTGT	ATTGCAACTGGGTGAATGTG	Polymorphic
159	ag.24	AU2558	215	57oC/15cycles,53oC/20cycles	TCCAGAAGGTGTGCACTGAC	TTTCAGGCAGGTTCTGAGGT	No product
15	at.32	AU2559	163	57oC/15cycles,53oC/20cycles	ACATTTCATGCAGGAGCAGTT	TAATTGCAGGGAATGGAAGG	Polymorphic
495	ac.8	AU2560	223	57oC/15cycles,53oC/20cycles	CCATGCTGTTGCACCTAATG	CCCTAACCGCTAATCACCAG	No product
490	ca.13	AU2561	203	57oC/15cycles,53oC/20cycles	TCGAGGTGTCCAACAGTGAG	ACAAGAAGTGATGCGCTCTG	Polymorphic
275	ttg.5	AU2562	210	57oC/15cycles,53oC/20cycles	ATTAGTGGTCTGGGCGCTTT	GAACAGCAAAATGTCACCAAA	Polymorphic
246	aac.12	AU2563	200	57oC/15cycles,53oC/20cycles	TGGCAAACTTTTGTTTGAACC	CATCACGTGAACCAGCTCAT	Polymorphic
209	att.13	AU2564	210	57oC/15cycles,53oC/20cycles	CCTGATTCAGAAGTGCTGACC	AGAGACGATGGTGCCACTTT	Polymorphic
107	ct.9	AU2565	202	57oC/15cycles,53oC/20cycles	GCCAAAGAGCCACTTCAACT	GCTCCTTGTGCTCTCCAGAC	Polymorphic
1363	ac.12	AU2566	175	57oC/15cycles,53oC/20cycles	TCCCATGTAATTGCACCATC	CAAAGCCAATGGAAAAGGAA	Polymorphic
790	ttta.10	AU2567	181	57oC/15cycles,53oC/20cycles	TGGCTGATCGGTGTAGAGC	TACTGGCAGTGATTGGCTGA	Polymorphic
408	tatt.9	AU2568	190	57oC/15cycles,53oC/20cycles	AAAAGCAACCTCTGGCAAAA	AAACCCAAAGGGGAATTCAA	Not polymorphic
274	tca.16	AU2569	204	57oC/15cycles,53oC/20cycles	TTGGACTCATGGTAGCACAGA	TCCACAACTTCACAGCATCTTT	Not polymorphic
2	tat.9	AU2570	231	57oC/15cycles,53oC/20cycles	CCATGCTGCAACATATCCAG	GCTCATGTTGGAGACGTGAA	Polymorphic
518	aata.5	AU2571	200	57oC/15cycles,53oC/20cycles	GACTGGTGATGGAAAAGCTG	GTGGAGATTCACCCCTTCTT	Polymorphic
316	tg.8	AU2572	112	57oC/15cycles,53oC/20cycles	GTGTGTGTGAGAGAGAGAGAGACAG	AGCTGAGGAGTGCAAACACA	Not polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
262	ttgtt.5	AU2573	200	57oC/15cycles,53oC/20cycles	CTTTGCATCAGCACTGGACT	TTCAGAACCTTCACCCTGATG	Not polymorphic
258	taaa.8	AU2574	200	57oC/15cycles,53oC/20cycles	GCTGCTAAAGGTGGCACAA	CAGAATCCCGGACCTTTTCT	No product
227	ga.17	AU2575	190	57oC/15cycles,53oC/20cycles	TGCAGGGTACAAACACTTGG	TGCAAGTTTTAAGAGGAATCTGC	No segregation
206	ac.8	AU2576	232	57oC/15cycles,53oC/20cycles	CATGGTCTGAGCCTGAAGGT	ATATTGCCCAGCCCTAATCC	Polymorphic
194	ag.9	AU2577	191	57oC/15cycles,53oC/20cycles	AAAGTGCATCGCATCCTTCT	GATTTGGGGATTTCATGTGC	No segregation
5	tc.19	AU2578	257	57oC/15cycles,53oC/20cycles	TGGTATTCTCACAAGGCAGATG	CATACCAATTGCAGGTTCCA	Polymorphic
609	gca.5	AU2579	191	57oC/15cycles,53oC/20cycles	CAGGTCCTGGGTGGAATGTA	CAAACAAGCCCAGAACCAGT	Polymorphic
436	tc.15	AU2580	213	57oC/15cycles,53oC/20cycles	TGACATCAAAGATGCCCTCA	CAAGGCGTCAAAGAGGATTC	Polymorphic
214	attc.9	AU2581	209	57oC/15cycles,53oC/20cycles	TGTGTAATGGGATTCTCATGC	CCTCGTGTGGCTAAATGTGA	Polymorphic
34	gag.5	AU2582	198	57oC/15cycles,53oC/20cycles	GCATGGGAGGCATATCTCAG	CTGACCTTCCTGGCTGTTCT	Polymorphic
890	aaat.5	AU2583	166	57oC/15cycles,53oC/20cycles	ACCAGCTTAAGACAGCAGCA	AAGACCTTCTACACTACAGTGATCTTT	Polymorphic
130	ag.27	AU2584	197	57oC/15cycles,53oC/20cycles	GAACAGGCCCCTTTTGAA	AGAATCCATGCTGAGCTGTG	No product
97	tcat.5	AU2585	186	57oC/15cycles,53oC/20cycles	TAGATGTGGTGGGTTGCTCA	CCGGTATGTGGATTGGTCAC	Polymorphic
58	att.6	AU2586	212	57oC/15cycles,53oC/20cycles	CCCCAATTTTGCAAGTTGTC	CAGACAACCACACACCCAAT	Not polymorphic
55	ag.9	AU2587	215	57oC/15cycles,53oC/20cycles	TGCTTCTGATGATGGGATGA	TCACCACGGTTGTAAAGAATGA	Not polymorphic
169	tttg.5	AU2588	126	57oC/15cycles,53oC/20cycles	TGGTTAGTGTGAGGGGTTGC	AAACAACGTTGGTCCTGTCC	Polymorphic
121	aat.5	AU2589	217	57oC/15cycles,53oC/20cycles	CACGGTATATAGGACCGCAAA	AGAGCCGGGCAATATGATG	Not polymorphic
454	aga.5	AU2590	209	57oC/15cycles,53oC/20cycles	GGGATTGTGAAGTTGAACAGC	GCCCTTCTGCAAGGTTCTTA	Not polymorphic
404	ag.9	AU2591	199	57oC/15cycles,53oC/20cycles	GACGCAGCTAAGTGCCAGAT	TGTGCTGGTTAGCCAAGGAT	Polymorphic
216	ag.30	AU2592	188	57oC/15cycles,53oC/20cycles	GGAGCATAATCCCAGAGCAC	TGTTCACCTTTATACTTCCATCTTATT	Polymorphic
135	taa.12	AU2593	257	57oC/15cycles,53oC/20cycles	AGGCTAAAATGGCTGGGTTT	CCTGGAAATGAGCTTCATCC	Polymorphic
38	aaat.5	AU2594	201	57oC/15cycles,53oC/20cycles	GCATAAATGTATGTGCCCTGTC	ACCATGGTGAGCAGAAAAGC	Polymorphic
335	ct.16	AU2595	199	57oC/15cycles,53oC/20cycles	CCGGGTCTCTCAGTCTCTCA	GTGCAGACATCTCCAACACC	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
306	ag.9	AU2596	228	57oC/15cycles,53oC/20cycles	TTTCACCAGCCACTGTTCTG	AATTTCCTGTCACTCTTCTCTCTC	Polymorphic
236	ga.12	AU2597	212	57oC/15cycles,53oC/20cycles	CAGCAGCTCCAGAAAGAGGT	TCGGCATGCTGCTAAAAAC	Polymorphic
6	aaac.5	AU2598	213	57oC/15cycles,53oC/20cycles	ACATGGGTGATAGGTGTTGGA	TCTTTGCTCCATCCTGATTTC	Not polymorphic
116	ga.26	AU2599	208	57oC/15cycles,53oC/20cycles	AAGGGCCTTTGTCACATGAT	CACTCCAGTTTCTGGCCAAC	Polymorphic
68	ggat.7	AU2600	204	57oC/15cycles,53oC/20cycles	CATAAGTCAAACACCCTGTCCA	GGGCAATGAATTTCCACAAA	Polymorphic
20	tttg.5	AU2601	210	57oC/15cycles,53oC/20cycles	TTCCGAAGGAGTCTCCAGTG	GGTTGCAACAGCTACGAACA	Polymorphic
278	tta.14	AU2602	180	57oC/15cycles,53oC/20cycles	GCGCAATGACAGCTTAAACA	TTACACCTGGCGGCATATTT	Polymorphic
455	ta.9	AU2603	208	57oC/15cycles,53oC/20cycles	ACCCACTGCTGGGTTAAAGG	CAATGCATGTGCCGTTTTAT	Polymorphic
13	at.38	AU2604	252	57oC/15cycles,53oC/20cycles	TCATTGTCTTTAGACTTGCTTGTAATG	ATACCCCAGGGAAATTGGAC	Polymorphic
726	ac.57	AU2605	172	57oC/15cycles,53oC/20cycles	CACATCTCATAGCCTCATACATGG	TGCATCTGCTTCAGGTGTTC	Polymorphic
29	gaa.13	AU2606	181	57oC/15cycles,53oC/20cycles	GATCTTTTTCGGTCTCCCATC	GTCTGCCAACAGGAGTGTCA	Polymorphic
183	tc.10	AU2607	187	57oC/15cycles,53oC/20cycles	AATGCCAAGGGTGTCAGAAT	TCGATTCCTCTCTGCTCACAT	Polymorphic
222	taaa.5	AU2608	198	57oC/15cycles,53oC/20cycles	AAGGTGACTGGATCTTCCACA	AGGTTTTGCACTGTGCTTTG	Polymorphic
199	gt.8	AU2609	183	57oC/15cycles,53oC/20cycles	GCACATGACCAGAGCACATT	AGGTTTTTGCCAAACTGCAC	Polymorphic
161	ttta.5	AU2610	215	57oC/15cycles,53oC/20cycles	AACCAATAGACCAAACAAATCAG	GGCACCAATGCCAGTCTATC	Polymorphic
241	att.5	AU2611	268	57oC/15cycles,53oC/20cycles	GATGGGTGATGAGGGTATGC	GGGTTCCTAAAAATGAAGTGGA	Polymorphic
181	ct.12	AU2612	143	57oC/15cycles,53oC/20cycles	GTGTGAGATGTTGTTTCGTTGAG	GGGACAGCAGTCACACACAC	Polymorphic
276	ac.24	AU2613	202	57oC/15cycles,53oC/20cycles	ATTTCCCCACAAAGGCAAA	TAAAGGAAGCAGGGGGAAAT	Polymorphic
155	ga.24	AU2614	207	57oC/15cycles,53oC/20cycles	TGGAAAAGCTTCCAGTGACC	AGCGGGACTGTTTTTGCTTA	Can't score
403	taaa.8	AU2615	181	57oC/15cycles,53oC/20cycles	TCATGATGTTCAGTAAGTTCAAAGG	CATTTGTTGTGTGAGCAACATT	Polymorphic
885	taa.15	AU2616	198	57oC/15cycles,53oC/20cycles	ACAAGCCTCGTGGTATGCTC	GCATTGGAACCTTTGTTTCAG	Polymorphic
442	ag.33	AU2617	190	57oC/15cycles,53oC/20cycles	GGGTCACTAACTCAGGTGTGG	AGGTACAAAATGCCTTGACG	Polymorphic
193	gt.15	AU2618	203	57oC/15cycles,53oC/20cycles	ATGCTTTGACAGATCGCTTG	AGATCTGGCAGTCCACAAGAA	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
39	tct.5	AU2619	204	57oC/15cycles,53oC/20cycles	AATGCCCATTTGTCTTCACC	GCTTGTAAACCAAGCCATCC	Polymorphic
101	at.26	AU2620	210	57oC/15cycles,53oC/20cycles	TTCACCCTGCCATGTGATTA	GGGTGGAGTCTTCCTTTAACC	Polymorphic
392	atcc.5	AU2621	205	57oC/15cycles,53oC/20cycles	TGTGGGTTTGAGGGGATTAC	TGAGATAGGCTCCAGGTTCC	Polymorphic
104	at.11	AU2622	198	57oC/15cycles,53oC/20cycles	TGGTCGAGGTCATTTCTCATC	CAGTAGTTTTAGGCAGCACGTT	Polymorphic
37	tc.18	AU2623	197	57oC/15cycles,53oC/20cycles	ACCTAGCGTGGATTCAGCAC	CTGCTTCCGTCCACTCCTT	Polymorphic
177	gaca.5	AU2624	160	57oC/15cycles,53oC/20cycles	TTGGGGTTTTTACCAAATGAAG	TGTCTGTCCAGCTATCTATCTACCTA	Polymorphic
74	att.9	AU2625	195	57oC/15cycles,53oC/20cycles	CCAAAGCCGGTACCATAAAA	ACAGCTGTGACGTTGGACAC	Polymorphic
281	aag.5	AU2626	219	57oC/15cycles,53oC/20cycles	GAGGCTTTCAAAGGTGGTCA	CGATGTGTTCGTCACTCCTG	Not polymorphic
370	ac.30	AU2627	223	57oC/15cycles,53oC/20cycles	CCATACCCAGATGTCTGCAA	ATTGGCCCTGGTTATGAATG	Polymorphic
200	aaat.5	AU2628	202	57oC/15cycles,53oC/20cycles	AGAGCCTAGGTGGTGGAATG	CCCGATAGGTCACGGACTAA	Polymorphic
154	tga.9	AU2629	193	57oC/15cycles,53oC/20cycles	GATTAAACTAATGGATGGAGAATCG	GCGAAGTCATTCAGCGTTAG	Polymorphic
252	tg.14	AU2630	227	57oC/15cycles,53oC/20cycles	GGCATGAATCAGGCACTTG	TGACGGGAACGTCTAAATGG	No product
50	tc.19	AU2631	202	57oC/15cycles,53oC/20cycles	ACTGAAACGCACGACTCCTC	CTGGCCGACAGTTTGTAGGT	Not polymorphic
45	tta.11	AU2632	225	57oC/15cycles,53oC/20cycles	GGAGCTCTGTGAAAAGCTGTG	GACTTGAATCGCTGGGTGAC	Polymorphic
170	ca.11	AU2633	167	57oC/15cycles,53oC/20cycles	TTATGCTTTGGGGGAAAAAG	ATTGGAAGGTCCGCACAAG	Polymorphic
42	ta.17	AU2634	126	57oC/15cycles,53oC/20cycles	TCCTGAGCTGCTGTGAGTTG	TGGTGTCCAGGAAGTGTTCA	Polymorphic
166	tta.15	AU2635	194	57oC/15cycles,53oC/20cycles	TAACGTTTCAATGGGTGCTG	GGTTGTGTGACAAAAACGACAC	Polymorphic
139	tta.12	AU2636	182	57oC/15cycles,53oC/20cycles	CAACGCGTGTATGCATTGTT	TGATAAATCCCACACGTTGC	Polymorphic
59	ac.9	AU2637	205	57oC/15cycles,53oC/20cycles	TGCACAGAGGCAAAATTACG	GACCAAAGGTTCCCACAAAG	Polymorphic
534	ca.45	AU2638	214	57oC/15cycles,53oC/20cycles	CTGCTTGGACTGTGTTGCAT	GCACTCCAGCCAGCTTAGTC	Polymorphic
9	cta.5	AU2639	206	57oC/15cycles,53oC/20cycles	AACCCTCACTAATGGCTAATGC	TAGCAGCAGTGGTTGAATGG	Polymorphic
443	ca.23	AU3051	203	57oC/15cycles,53oC/20cycles	TTCACTGCTTTCCTCCAACC	GCCACATAACAGGACCAGTG	Polymorphic
480	ac.9	AU3052	221	57oC/15cycles,53oC/20cycles	GCACAGCTGCTCAGTTTGAC	TGAACATGCTTCAGGGAAAA	Not polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
207	gt.9	AU3053	188	57oC/15cycles,53oC/20cycles	TGGAGCTGAATGCCCTACTT	CACAGCCTAGTGTGACCGTACT	Not polymorphic
15	aac.5	AU3054	209	57oC/15cycles,53oC/20cycles	AAATGGGAATTCGGTACGTG	GTGGTGTCGAATCAACATGG	Polymorphic
490	aga.6	AU3055	199	57oC/15cycles,53oC/20cycles	ACTGAACACCAGTCCGTTCC	CACACTTCCATCTGAAAGACACA	Polymorphic
275	ac.21	AU3056	205	57oC/15cycles,53oC/20cycles	CATGAAAGCAGGAAAGTCAGG	CAAGCAAACATCAGGCTCTTC	Polymorphic
266	ttca.5	AU3057	227	57oC/15cycles,53oC/20cycles	CTGGCCAGTCAATTTTCAGC	TAGCTTGATGGTGGTCATGC	Not polymorphic
246	ag.8	AU3058	201	57oC/15cycles,53oC/20cycles	TGTCCACAAGCAGGACTCAG	GGACCGTCATCCTCCTACAG	Not polymorphic
107	ac.34	AU3059	203	57oC/15cycles,53oC/20cycles	TGGCAGATCTCAGGTAGCAA	AGCCACAGGTTTAGTCTCAAAT	Polymorphic
32	aat.6	AU3060	205	57oC/15cycles,53oC/20cycles	CATCCAATCAGAGAGCAGCA	GCGGTCACAGTTGTGCTTAT	Polymorphic
1363	tg.8	AU3061	203	57oC/15cycles,53oC/20cycles	AAGTAGCGCGTGTTGCTGTA	GTGCCTGGACCAGCTAGAGA	Not polymorphic
790	ta.13	AU3062	205	57oC/15cycles,53oC/20cycles	GCAGTGTCTTGACAAATGGACT	TTGCACAAATTCTCACTTGGA	Polymorphic
2	ttga.7	AU3063	173	57oC/15cycles,53oC/20cycles	TGTCACATGCCTATGTTGAGG	TGGTCCCACAAGGGAAATTA	Polymorphic
518	ac.11	AU3064	200	57oC/15cycles,53oC/20cycles	TCTGGTCACTGGTTGTGCAT	GGATGGTGTCAGTGAAAGCTG	No product
227	ttta.7	AU3065	180	57oC/15cycles,53oC/20cycles	TGTTGAGGTGTCTAGGATGCTG	AAAAGGGCCTGGCTAATTGT	Polymorphic
206	aaag.9	AU3066	230	57oC/15cycles,53oC/20cycles	CATCAACTGCCTCGGTTTTT	CGGAAGGAGTCTCCAGTGTT	Polymorphic
194	ta.12	AU3067	192	57oC/15cycles,53oC/20cycles	TCTGAGAAACGGGATTCCAC	GCTGGGACACTGAGGAGAAA	No product
5	ac.11	AU3068	210	57oC/15cycles,53oC/20cycles	TTAAGTGCATGAGCCCACAC	TGTCCATCATGATTCCCAAA	Polymorphic
609	ca.19	AU3069	204	57oC/15cycles,53oC/20cycles	CAGTTTTATTCCGGGTCACG	CCTCCCAGAAACATTCCAGT	No segregation
436	att.5	AU3070	209	57oC/15cycles,53oC/20cycles	GCACATCCCAGAACAACCT	ACTGTGCCCTGTAGTTTTGGA	Polymorphic
214	gt.12	AU3071	198	57oC/15cycles,53oC/20cycles	TTGTTGGGAAACACTTCAACAG	AGCCTATCCCAGGGGACTC	Polymorphic
34	ac.13	AU3072	208	57oC/15cycles,53oC/20cycles	CGGGGTCAGTCAGATCAGTT	AGAGGATGCAGGTGGTTACG	Polymorphic
890	ta.34	AU3073	237	57oC/15cycles,53oC/20cycles	GCAGCGTGACACGGTTTAT	CCCCTGCTACTTCACCATTC	Polymorphic
97	tcat.5	AU3074	193	57oC/15cycles,53oC/20cycles	GGAAGTTACCTGCAAAACACC	TGCTTTCAACAGTGTTTCCAAC	Polymorphic
404	aat.5	AU3075	152	57oC/15cycles,53oC/20cycles	CGAGTAACTGCGTGAATTGC	CTGCCCTTCAGACGCTAAAT	Not polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
216	tg.11	AU3076	224	57oC/15cycles,53oC/20cycles	GGAGCAATGCAAACGAAATC	CAGGCTGGGCTAAGTCTGTT	Polymorphic
135	agat.5	AU3077	259	57oC/15cycles,53oC/20cycles	GCCACTAAAAGGGCTGAGAG	AGCCACTAAAAGGGCTGAGAG	No product
335	ca.24	AU3078	189	57oC/15cycles,53oC/20cycles	TTACACGCCATACAGCCTGA	GACTCTGAGCCACGGAAGTT	Polymorphic
306	ta.39	AU3079	250	57oC/15cycles,53oC/20cycles	CATCATGTTTGAAGGCAGGA	CATGCAAAAATGTGCAAAGA	Polymorphic
236	ca.11	AU3080	197	57oC/15cycles,53oC/20cycles	TCCTCTGGAAGGCTCTCAAC	TTCTGCTTGCACCAAATCAG	Polymorphic
116	ttta.5	AU3081	227	57oC/15cycles,53oC/20cycles	GCAGAATTTTTCCTTTATTATCCA	GGCAATGACCATAATTCCAAA	Not polymorphic
68	ata.10	AU3082	192	57oC/15cycles,53oC/20cycles	TACACACAGCCTTCCCATCA	TGAACATCCAGCCCAGTTATC	Polymorphic
278	at.9	AU3083	238	57oC/15cycles,53oC/20cycles	CATGTGGTCCCTGCATTTTA	TGTGTGTGTGCGTGCATCTA	Not polymorphic
455	aaac.7	AU3084	226	57oC/15cycles,53oC/20cycles	CTGGATGATGGTTGGCTGTA	AAGTGCGACCCAACTGTTTC	Polymorphic
13	at.38	AU3085	241	57oC/15cycles,53oC/20cycles	CAGCTTGGCAATTTATGAGG	ACTGCGGTGACACAAATGAA	Polymorphic
726	ac.8	AU3086	232	57oC/15cycles,53oC/20cycles	ACCCTGTGCAGGATAAGCAG	GCCAGCTTGTCTCACATCAA	Polymorphic
183	gtt.5	AU3087	194	57oC/15cycles,53oC/20cycles	TTAATGGGACGGAGTGTGGT	GCCAAAACTGTCAGCCTTTC	Polymorphic
222	ca.9	AU3088	195	57oC/15cycles,53oC/20cycles	ACGGAGTTCGCATGTTCTCT	TGCTCACGATGGCAAGTTAG	Polymorphic
199	atga.7	AU3089	207	57oC/15cycles,53oC/20cycles	CCCAAAAAGGCTCTCTGTAGAA	AGTAGGAAAGCAACGCTGGA	Polymorphic
161	atg.6	AU3090	200	57oC/15cycles,53oC/20cycles	GAAATTGAAACGGCTCTTGC	GATGCTTTGCCATGCTTTAAC	Polymorphic
40	tc.8	AU3091	196	57oC/15cycles,53oC/20cycles	ACTCTGAGCCTGAGGGGAAA	TGGAAGAAATATGAGGATTCTGAC	Polymorphic
181	ta.30	AU3092	171	57oC/15cycles,53oC/20cycles	TGCAAGCAACCTTTTAAATCTG	CAGCATTAATGGCGCACTAC	Polymorphic
276	tcg.5	AU3093	219	57oC/15cycles,53oC/20cycles	AGGCCGTCTCATTGACAGAC	AGAATCCAAGCGTGCAGTG	Not polymorphic
155	aat.10	AU3094	218	57oC/15cycles,53oC/20cycles	CAGGCGGACCTATTGTTTGT	TGGAAAAGGACATGCATCAG	Polymorphic
403	att.7	AU3095	197	57oC/15cycles,53oC/20cycles	ACTGCTGCATGTTCTGGATG	TGACGCCTTCTGTTTTCTGA	Polymorphic
885	tttg.5	AU3096	234	57oC/15cycles,53oC/20cycles	ACTTCCAAACCCATCAGCAG	TGCCATTCCTTAGCTTTGCT	Not polymorphic
193	at.13	AU3097	235	57oC/15cycles,53oC/20cycles	AAGCATTGTGAGTCCCTAGCTC	TGCATTGCTCAACTCTAATACAC	Polymorphic
101	ac.10	AU3098	182	57oC/15cycles,53oC/20cycles	GCACGCTCTCGTACAGTCAA	CCCTTCTACTGTCCTACATATCCT	Not polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
392	ac.10	AU3099	201	57oC/15cycles,53oC/20cycles	ACCTCGATGCACAAGGAAAT	TCACCAGGAGGGGATAGAAA	Polymorphic
104	ac.27	AU3100	189	57oC/15cycles,53oC/20cycles	CCTGAAATCTTTCCTGTTTTTG	GCGGTCATGTTACCTTTGGT	Polymorphic
177	aaag.6	AU3101	213	57oC/15cycles,53oC/20cycles	GGGGGAAATTTCATTTGACTT	GCTTCAGTGCTGTGCAGTTT	Polymorphic
74	tta.15	AU3102	201	57oC/15cycles,53oC/20cycles	GGAAGTAACATGGACCCAGAGA	AGGAATCAAATCCCCAAACC	Polymorphic
370	ata.5	AU3103	215	57oC/15cycles,53oC/20cycles	GTGTTCAGATGGTGGTCCAA	GTTTGAAGGCAACTGCACCT	Polymorphic
200	ta.15	AU3104	177	57oC/15cycles,53oC/20cycles	CAATATCCGACTGTGTCAGCA	TAAAGAACGTTTGGGCACCT	Polymorphic
154	tat.13	AU3105	190	57oC/15cycles,53oC/20cycles	GAGCTCTGGAAAGGCCCTA	AAAACGCTTGCAGACCAATC	Polymorphic
45	tc.13	AU3106	181	57oC/15cycles,53oC/20cycles	TTTCAAACGGATGCAAACTG	CAACTGGAGTGGAGGAGCAT	Polymorphic
170	ctat.13	AU3107	173	57oC/15cycles,53oC/20cycles	TTGACGCGTTCAACCCTTAT	TCATGAAAATCCCATACATTCAG	Polymorphic
42	at.8	AU3108	204	57oC/15cycles,53oC/20cycles	GCATGGGCTGCGTAGTTTA	ACCCGTGTTTTCCGATACAG	Polymorphic
166	at.43	AU3109	244	57oC/15cycles,53oC/20cycles	TCACCTGCATCCAATTCAGA	TGGCACCCTTGGTAAATCA	Polymorphic
59	ag.9	AU3110	199	57oC/15cycles,53oC/20cycles	GTTTCTTTCTCCCCGAGCTT	GGCTTTCAGAGTCGGAAGTG	Polymorphic
534	ac.29	AU3111	205	57oC/15cycles,53oC/20cycles	CAGAAATACACCCTGGAGCTG	CCCATGGCTCAGCTTGTAA	Polymorphic
9	ctt.5	AU3112	214	57oC/15cycles,53oC/20cycles	CGCCGCAAATTTGGTTTAAT	TTACATCCAGCACGCACAAT	Polymorphic
189	ttta.7	AU3114	161	57oC/15cycles,53oC/20cycles	CCACCAATAGGAGGACGGTA	CAAAGCCGTCTGACAGGAAT	No segregation
159	at.32	AU3115	199	57oC/15cycles,53oC/20cycles	TAACCCAGCACTGCCTTTG	GCAAGATCTTCACATGAGAAACATAA	Polymorphic
495	ac.8	AU3117	164	57oC/15cycles,53oC/20cycles	TACACTGGCAGATGCCTTCA	TGTGTTTCTTGCATGACGTGT	Polymorphic
490	aaat.12	AU3118	220	57oC/15cycles,53oC/20cycles	CGGGGCAATTAGTTTTCACA	TTTGGATAAACCCGTGTTCTG	Polymorphic
790	at.12	AU3121	194	57oC/15cycles,53oC/20cycles	CACATTGGTCATTCAGGCTCT	TGGATATTCCAGTCCGCATT	Polymorphic
518	gt.15	AU3124	197	57oC/15cycles,53oC/20cycles	TTGAATGCCGTGAAAATGTC	GCAACTGGCCCATTATCCT	Polymorphic
258	caa.6	AU3125	186	57oC/15cycles,53oC/20cycles	ATGTGTCACCTGTTCCCTGAG	GAGGAACTGCTGGATGATGC	Can't score
194	taa.12	AU3127	190	57oC/15cycles,53oC/20cycles	TCAGAAGCATTTGGTTGCAG	CAAAGGCAACCTGTGTAAGC	Not polymorphic
609	ac.13	AU3129	262	57oC/15cycles,53oC/20cycles	GGGCTGGTGGACTGTATGAA	TCGAGAACGGACACTTTCAA	Not polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
214	ga.8	AU3131	228	57oC/15cycles,53oC/20cycles	GCCTGAGGTTGCTTCAAAAG	GCTCTGTGCAATTTGTGTGC	Polymorphic
890	ac.16	AU3132	190	57oC/15cycles,53oC/20cycles	CCCATGCACGTGATATTGAT	TGGTCATGACTCACTGGACTG	Polymorphic
130	aac.5	AU3133	227	57oC/15cycles,53oC/20cycles	GAATGCTTTTGACTAGGAGCTTG	TGGGCTTCTCATTGTGACTTT	Polymorphic
216	ag.30	AU3136	198	57oC/15cycles,53oC/20cycles	GCCCATGCCTAAGAGGATTA	CCACAGCCCTGTGTAGGATA	Polymorphic
135	aat.8	AU3137	164	57oC/15cycles,53oC/20cycles	CGTCGCCACTGGATTAAGAG	CTCACATGACCATGCCAATC	Not polymorphic
335	ta.34	AU3139	198	57oC/15cycles,53oC/20cycles	TCATGATCAGGGTTCATCACA	GTGTCCGCTTAGTGGGTTTC	Polymorphic
182	act.7	AU3142	238	57oC/15cycles,53oC/20cycles	GTTTGGGTAGCTCCATGGTC	CCGGCCTAGATAAGATGTGC	Polymorphic
68	ac.19	AU3143	230	57oC/15cycles,53oC/20cycles	TCCAATGTAGCAATTTGACAGA	CCATGAGCTATAAGCCGTTATCA	Polymorphic
455	ag.25	AU3144	173	57oC/15cycles,53oC/20cycles	TGGCTGAGGAGCTAGAGCAT	GAAGTCCCATCACCAGCAAT	Polymorphic
183	ac.10	AU3147	197	57oC/15cycles,53oC/20cycles	CAAATCCAGAGAGGGGACAA	CCTTTCGTCTGAGGGTCACT	Polymorphic
222	ct.14	AU3148	171	57oC/15cycles,53oC/20cycles	ACCCCTGTGAACAAGTAGGC	CAGAGGCTTGAGCCAATGA	Polymorphic
199	ca.22	AU3149	200	57oC/15cycles,53oC/20cycles	TGTGAACCTCTAGGATAAGAGTCA	CTTCAGGGGTTTCCTCCAGT	Polymorphic
161	at.13	AU3150	217	57oC/15cycles,53oC/20cycles	GGGGCAAGGTACATGAGAGT	GATGACCTCCCGAGCTGTAG	Can't score
241	aac.11	AU3151	280	57oC/15cycles,53oC/20cycles	GAGGATGCAGTGAGGACACC	TGTGCACCGAGTGTGTTGTA	Polymorphic
155	ttta.12	AU3152	192	57oC/15cycles,53oC/20cycles	CAATGTGAGGAAGCCTGGTC	GTGTTTTTGGTTGCCCAGA	Polymorphic
403	ag.10	AU3153	204	57oC/15cycles,53oC/20cycles	CCCTGGCCATCTCAAAGTAA	CTGCTGTAATGTCGCAAAATG	Polymorphic
442	ct.8	AU3154	196	57oC/15cycles,53oC/20cycles	CGGACGTCACAGAACTCAAG	GCTTAGACGCGCAGAGTGAT	Polymorphic
193	ac.24	AU3155	196	57oC/15cycles,53oC/20cycles	AAGGCTGGCTCAGAAAAGTG	CTACCAGCTTGCTCCTCTGC	Polymorphic
39	attct.5	AU3156	278	57oC/15cycles,53oC/20cycles	GCTCGATAAAAGGTTGACAAAG	CCCACTATGAAAACACACAATTT	Polymorphic
392	ta.9	AU3157	201	57oC/15cycles,53oC/20cycles	TGAGGACTTCTGCATGGTTTC	AGGAAAACAGGGTGCTGTGA	Polymorphic
104	tc.13	AU3158	197	57oC/15cycles,53oC/20cycles	CGGTGATGGAAATGTACACG	CAGTACGGGGAAGTGTTTTGA	Polymorphic
74	ca.21	AU3159	197	57oC/15cycles,53oC/20cycles	GTTGGAGAAAGACCGCACAT	ATGTGGGAGAGCCCACTAAA	Polymorphic
370	tta.17	AU3160	188	57oC/15cycles,53oC/20cycles	TCATGTCATGGAGGGTTTTT	CTCCACTCAGACATGGGACA	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
200	ttg.6	AU3161	228	57oC/15cycles,53oC/20cycles	CCTTCATGGCTGAACAGGAC	GCAAAACATGTCCCACCATT	Polymorphic
154	ca.14	AU3162	169	57oC/15cycles,53oC/20cycles	ACACTGCGTGCTGAACAGAG	TTGCCCACGTGACATTTAGT	Polymorphic
252	tg.14	AU3163	169	57oC/15cycles,53oC/20cycles	GCACTACCCTCCAGTGCTTT	AGTACCTTGGGCAGCATCAG	Polymorphic
45	ag.18	AU3164	191	57oC/15cycles,53oC/20cycles	GGTAACGCGTGACGATTCTC	GAGGCAGGCTTGAAACAACT	Polymorphic
170	ac.19	AU3165	249	57oC/15cycles,53oC/20cycles	GCTCTCCCAGTCCATCATGT	GCTTTGGGCGTCTTCTTACA	No segregation
42	tg.8	AU3166	181	57oC/15cycles,53oC/20cycles	GTCTCGAGCAGGTGATAGCC	AGACGTCCTGTCTCGGAAAA	Polymorphic
166	tta.15	AU3167	192	57oC/15cycles,53oC/20cycles	AACGTTTCAATGGGTGCTGT	GGTTGTGTGACAAAAACGACA	Polymorphic
139	atcc.5	AU3168	204	57oC/15cycles,53oC/20cycles	GACGCAGCGGAATAACTGA	CATTACGCTCCAGCCAGAGT	Polymorphic
59	ttaa.13	AU3169	246	57oC/15cycles,53oC/20cycles	AACAGGTTAAATGCTGCTTATGA	TCGAATAAGACATGGCAGCTAA	Polymorphic
534	atcc.5	AU3170	203	57oC/15cycles,53oC/20cycles	CCCATTGCCAGTATTGGTATC	CGGTGACCCTGTGTAGGATAA	Polymorphic
9	taga.6	AU3171	195	57oC/15cycles,53oC/20cycles	GGAAAAAGTGAAGCACTGTGAA	CCAGCTGTCTTCGGTCAAAT	Polymorphic
9	at.26	AU3172	182	57oC/15cycles,53oC/20cycles	CGAGATATCTGGGGGAACATT	TCTGACTGTCTCTGCGCATC	Polymorphic
189	acaa.6	AU3173	240	57oC/15cycles,53oC/20cycles	ATGCTTTGCCATGTCTGTCA	CCTTTGGGCATGCTTTCTAC	Not polymorphic
207	ata.18	AU3174	214	57oC/15cycles,53oC/20cycles	GTGCCGTTTCATTATGTTGC	CACCCTAACCAGGGTGTCC	Can't score
246	gt.17	AU3175	198	57oC/15cycles,53oC/20cycles	AAAGGGCCGAGAGAAGCTC	TGCTGTCCTAAAGCAAATTCC	Can't score
1363	aaat.5	AU3176	201	57oC/15cycles,53oC/20cycles	TCACAGGGTTGCACTACAGC	ATTTTTGACCGGGGGTGTAT	Polymorphic
274	aaat.13	AU3177	259	57oC/15cycles,53oC/20cycles	TGCAATGAAGACAGTGCAAA	GAGATGCAGAGCCTGGAAGT	Not polymorphic
316	tc.14	AU3178	195	57oC/15cycles,53oC/20cycles	GTGACAGGAAATGCAGCAGA	CACTACTGTTTGTCGCCAGAAT	Polymorphic
262	ttg.7	AU3179	222	57oC/15cycles,53oC/20cycles	CACTAGATGCAGCACTGGTAAG	GGATGCCTGTTGCACTTCTA	Polymorphic
258	caa.6	AU3180	170	57oC/15cycles,53oC/20cycles	TGTGTCACCTGTTCCCTGAG	GATGCATGTCAACAGCGACT	Can't score
130	atcc.6	AU3181	199	57oC/15cycles,53oC/20cycles	ATGGAAAGAAGCCAGGAATG	ATTGTGCCCTGTGATGGACT	Not polymorphic
58	at.36	AU3182	160	57oC/15cycles,53oC/20cycles	TGCAGTTTAGCGTGTGCCTA	GCACATATTCACTGTCCATAGCC	Can't score
55	attt.8	AU3183	213	57oC/15cycles,53oC/20cycles	GAAGCATTGTGGTGCATTGT	CCAGTGTTTTCCAGGGTCAT	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
121	ttgt.6	AU3184	267	57oC/15cycles,53oC/20cycles	TGGGAGTTAACCAGGGAAAG	GAGGTTTTTCTCCCCAGTTG	Polymorphic
454	aga.5	AU3185	205	57oC/15cycles,53oC/20cycles	CCATGGGATTGTGAAGTTGA	CTGCAAGGCCCTTAACACTC	Not polymorphic
404	aat.5	AU3186	152	57oC/15cycles,53oC/20cycles	CGAGTAACTGCGTGAATTGC	CTGCCCTTCAGACGCTAAAT	Not polymorphic
135	aaac.8	AU3187	203	57oC/15cycles,53oC/20cycles	TACCTTGTTGGCACAGCAGA	TTTGAATCGACTGTTGCTCAG	Polymorphic
211	acag.5	AU3188	191	57oC/15cycles,53oC/20cycles	CAACAAATCTCGTGGGAACA	GTGTGAAAGCGCTCATCTGT	Polymorphic
182	ata.12	AU3189	222	57oC/15cycles,53oC/20cycles	GGGCTTTGATTGAATGCTGT	GGGCGAGTCAGGAGAAAAA	No product
6	tca.5	AU3190	201	57oC/15cycles,53oC/20cycles	CCCTTCCCTATGACCTCCTC	GGTTAAGAGGATTTGCATCCAT	Polymorphic
116	att.13	AU3191	214	57oC/15cycles,53oC/20cycles	CCCCATACAAGGTAAAGTGCT	CAGAGGCAGTCAGCTTTTCA	Polymorphic
29	gt.17	AU3192	208	57oC/15cycles,53oC/20cycles	GTACATCACCTGAGGGCACA	GGGAGCCAAGTGCATAAGAC	Polymorphic
276	ata.10	AU3193	231	57oC/15cycles,53oC/20cycles	TTCATTGCAGACAGCTGAAAG	TGGGGAATATCACAAAGTTCCT	Polymorphic
885	taga.10	AU3194	197	57oC/15cycles,53oC/20cycles	TCCTAACATGATTTCCACTGAGG	GTAACCAAGGGCTGGATGTG	Polymorphic
140	gt.12	AU3195	216	57oC/15cycles,53oC/20cycles	ACTTCACGCAGGGTGTCTGT	GCCGTGTACCGGTTTAATCT	Polymorphic
101	ag.18	AU3196	198	57oC/15cycles,53oC/20cycles	GCCTCTGGGTGAGCAAAATA	ATGGCCAAACAGAGACAGGT	Polymorphic
281	ga.8	AU3197	246	57oC/15cycles,53oC/20cycles	TGGTGGACATCCTCCTCTG	CGTGTCCCAAATGTAGCCTAA	Polymorphic
252	tg.8	AU3198	185	57oC/15cycles,53oC/20cycles	GATGTGGTTCCAACCTCGTTA	GGACTTGGCAGATGTGCTTT	Polymorphic
72	gt.9	AU3199	200	57oC/15cycles,53oC/20cycles	CGCTGTATCTGAGCGATGAC	AGTTGGGGGACACCCTAGAC	Polymorphic
50	ct.9	AU3200	200	57oC/15cycles,53oC/20cycles	AGGGTCCATCATGCTTTCTC	GGGTAAAGTGCTATGCCTGTG	Polymorphic
166	ca.10	AU3201	196	57oC/15cycles,53oC/20cycles	CCTCCAGGAGCTTGAGATTG	GGCCATAGCGATAAGAGCAC	Polymorphic
534	ac.12	AU3202	204	57oC/15cycles,53oC/20cycles	CCTGAGGCCTGAAACTGAGA	GAAAAGCAGCCCAGTTCATT	Polymorphic
189	ata.10	AU3203	198	57oC/15cycles,53oC/20cycles	GCTGGGTACTCTGGTTACACAA	AACAGCTTTAACCCCGATGA	Polymorphic
266	tg.10	AU3204	209	57oC/15cycles,53oC/20cycles	GTTTCCTCCCACAGTCCAAA	GTGAAATCCTGGAGGGACTG	Polymorphic
246	ca.22	AU3205	262	57oC/15cycles,53oC/20cycles	TCACACGGCCACATTAGGTA	CAGAAGGGGCAGAAGGTACA	Polymorphic
246	agtg.5	AU3206	195	57oC/15cycles,53oC/20cycles	CAACAGACTGTGCCGGAGT	ACGTGGTCGATAAGGCATTC	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
274	act.6	AU3207	168	57oC/15cycles,53oC/20cycles	GAAGCGTGCCAATAATTCTGA	GTCTTTTGACCAAATATGAGAACA	Not polymorphic
274	tg.19	AU3208	199	57oC/15cycles,53oC/20cycles	TCATGTCAACAAGCGGTCTG	TCAGACGCTGCATTTTTCTG	Polymorphic
316	tg.27	AU3209	187	57oC/15cycles,53oC/20cycles	CATGAATGAGAGGGCATCAG	GATGCCAATCAAAGCAGGAT	Polymorphic
609	aat.5	AU3210	252	57oC/15cycles,53oC/20cycles	CGGTCGTAGTGAACCATGC	CTTGCTGAGCTTACGGGTGT	Can't score
130	tta.6	AU3211	153	57oC/15cycles,53oC/20cycles	TGGTGTTCACTTTATCCACAGC	GTGCTTTTCAGTTTCTCTGCAA	Not polymorphic
58	at.34	AU3212	188	57oC/15cycles,53oC/20cycles	TGCAGTTTAGCGTGTGCCTA	CCACCCATACTGTTATCTGCTC	Polymorphic
58	tatc.6	AU3213	201	57oC/15cycles,53oC/20cycles	GTCTACTGCCAATCCTTAAGAGC	GCTCCTGCATCGGTAAAGTC	Polymorphic
55	tta.15	AU3214	209	57oC/15cycles,53oC/20cycles	CCGCACCAAACTAACAGACA	TGAGTGGGCGCTATGATAAG	Polymorphic
121	at.8	AU3215	202	57oC/15cycles,53oC/20cycles	TGTGTAGCCAGAAATACAGATGC	GACAGCCAGGCACAGAGATA	Polymorphic
404	ttta.5	AU3216	201	57oC/15cycles,53oC/20cycles	GTGAGGCGGAAATGCTACTT	AATGCCTTGACAGCATGTTC	Polymorphic
211	ataa.11	AU3217	213	57oC/15cycles,53oC/20cycles	CAGATCCTTCCCAGTCTCCA	CCAAAATGGGGAAATCACAA	Polymorphic
182	ta.39	AU3218	206	57oC/15cycles,53oC/20cycles	TTCCCTAATGTGCCTGACATC	ACCCAACCCTGAAAGTGTGA	Polymorphic
6	ac.9	AU3219	202	57oC/15cycles,53oC/20cycles	CACGGCAGACCTTAGCAATA	CAGAGCTGCTGCAACGTAGA	Polymorphic
181	aaat.5	AU3220	199	57oC/15cycles,53oC/20cycles	TCATATTGGTGAAAGGTGTTGC	TAGTTCACGTGCGCTGAAAG	Not polymorphic
885	tg.13	AU3221	198	57oC/15cycles,53oC/20cycles	CAGCTAACCTGCACAGACCA	CACAGCCAACAATGAGTGCT	Polymorphic
885	aac.8	AU3222	180	57oC/15cycles,53oC/20cycles	CCGTTGAATTATTTCACTCACAA	TGACCGGAGCTTTATTTATGC	Polymorphic
140	gt.9	AU3223	211	57oC/15cycles,53oC/20cycles	AAAGCGGTTTACTGTACTTCCAA	GTGTACGAGCTGAGGAGTGCT	Not polymorphic
101	tcta.5	AU3224	202	57oC/15cycles,53oC/20cycles	TTGGTTTATCTGTGGGTAGGAAA	TTTCGCAAACTTTCAAGCAC	Polymorphic
37	aaat.6	AU3225	223	57oC/15cycles,53oC/20cycles	TGAACCTTGCTAACAAAACGAA	CTTAAGCTGTATTGCAAAAATAGGA	Polymorphic
177	ttta.5	AU3226	208	57oC/15cycles,53oC/20cycles	CAAAGGGTCGTCACACCAA	CCAAACGCATCCTACACACA	Polymorphic
281	ac.10	AU3227	210	57oC/15cycles,53oC/20cycles	AGGGGATTACACCTCCAAGC	TTGTTGGCAAGACCATACACA	Polymorphic
281	ac.36	AU3228	209	57oC/15cycles,53oC/20cycles	CCATTGTCCCTACATGAAAGC	ATGTGCTCTGAACAGACATGC	Polymorphic
72	ata.6	AU3229	214	57oC/15cycles,53oC/20cycles	ACCGCTCCTCCACAGACTAA	CCCAGTTCCTGTAGGTTTGC	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
72	ac.10	AU3230	192	57oC/15cycles,53oC/20cycles	GTGTCTGAAGGGCCAAAGAG	CGCTAATCAGTCTAAATGCTTTC	Polymorphic
9	ctt.5	AU3231	195	57oC/15cycles,53oC/20cycles	CTTGAGCAAGGCCTTTAACC	TGGCTGTGATTGATGAGTGC	Polymorphic
9	ta.32	AU3232	181	57oC/15cycles,53oC/20cycles	TGACTAGGCTAAAGGCTCAACA	TGACTGTTTCGCATCCTCAG	Polymorphic
609	tc.16	AU3233	164	57oC/15cycles,53oC/20cycles	CTGCTTGAAAAGCAAGATGAAA	GACACCCATGATTGCGTCTA	Polymorphic
130	gt.12	AU3234	204	57oC/15cycles,53oC/20cycles	GCGAGGAGCAGCTCATAAAA	CAAGGTCTCTCCTCAGTGGTG	Polymorphic
140	att.19	AU3235	233	57oC/15cycles,53oC/20cycles	CCACCACTGAAATCACCATT	CGCATGTTCCATGTTTTGTT	Can't score
281	aaat.5	AU3236	181	57oC/15cycles,53oC/20cycles	GGGTGATAGATGTTGGGTCAC	AAGTATTTGCCCCATCCTGA	Polymorphic
534	at.8	AU3237	194	57oC/15cycles,53oC/20cycles	GTGCAGATCCACATAAGTCCA	GGATAAACCCGTGTTGTGGT	Polymorphic
443	catc.7	AU3324	169	57oC/15cycles,53oC/20cycles	TGCAAATTGCCCCAAGTAGT	CCCTGGGATAGGTTCCAGTT	Polymorphic
189	ca.17	AU3325	279	57oC/15cycles,53oC/20cycles	CATGTGCTTACTCTTTCTCTCTCG	TGTGGGTTCCCATGGATATT	Not polymorphic
189	ttta.5	AU3326	206	57oC/15cycles,53oC/20cycles	GTTAGAGGCCAAGGCGAAAT	GGATTTGCATGTCCAAAATG	Polymorphic
480	gat.5	AU3327	206	57oC/15cycles,53oC/20cycles	GCCCGTAAAGGATTTGTTCA	ACGATCCCATCCACACTGAG	Polymorphic
480	ga.20	AU3328	188	57oC/15cycles,53oC/20cycles	AAGGAGTCTCCAGTGTCAGCA	TGAGGAACATCCAAGAGTTTCA	Polymorphic
191	taaa.10	AU3329	198	57oC/15cycles,53oC/20cycles	GACTGGGTGTAAACAGAATGACC	GCCATCAGCCATTCATGTAG	Polymorphic
191	tta.5	AU3330	195	57oC/15cycles,53oC/20cycles	GCCGTGAGAAAAAGCACACT	TGTTGATGTACACGCAGCATT	No segregation
190	ga.8	AU3331	201	57oC/15cycles,53oC/20cycles	GCTCTTCCAATCAGCTGGAC	CCAGAGTGTTTCAGCCTCCT	Not polymorphic
159	ga.20	AU3332	182	57oC/15cycles,53oC/20cycles	GCCTATCCATCATGCTTTGC	AGGCGCTGGAAATGGATATT	Polymorphic
275	ca.17	AU3333	205	57oC/15cycles,53oC/20cycles	GCAAACCCAAGGAAGTGTTG	CCTTGCTGCTACGTCTTTGA	Polymorphic
266	ca.9	AU3334	204	57oC/15cycles,53oC/20cycles	CTCAGTAGATCCCCCAATGC	TGAATGGGAACGCCATACAT	Polymorphic
246	tta.7	AU3335	246	57oC/15cycles,53oC/20cycles	CAGAGCCTCCGAATGTTACC	GCTTTCTGTGAGGATGCATTT	Polymorphic
209	ttta.7	AU3336	179	57oC/15cycles,53oC/20cycles	GGTTCCAGTTGTTCCACGTT	ACATGTTTGTGAAGTGCTGGA	Polymorphic
1363	ac.13	AU3337	210	57oC/15cycles,53oC/20cycles	AGGAGTCTCGGTGCACTAGC	CTCCATGTGACACGTATGGTG	Not polymorphic
274	tta.9	AU3338	221	57oC/15cycles,53oC/20cycles	CCTCCAGCTCTACCCCTTTT	CTCGGCAGCACCTGTACATA	No product

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
2	gt.11	AU3339	196	57oC/15cycles,53oC/20cycles	AGGAGTGCCAATGGTAGTGG	CCACCAGCACATGCAAATAC	Polymorphic
262	tatat.11	AU3340	225	57oC/15cycles,53oC/20cycles	CATGATTGAGGGGAACACTG	GGCTCTCGCTTGATCCTATG	Polymorphic
262	aaat.8	AU3341	206	57oC/15cycles,53oC/20cycles	TGGAAGACCGATCTCCAGTT	GGCAACCTGAACAAACACAA	Polymorphic
194	ag.9	AU3342	207	57oC/15cycles,53oC/20cycles	GCCATTTACCGAGAGTGGAG	ATTCCCGTACAGCAGAGCAC	Polymorphic
194	ag.8	AU3343	215	57oC/15cycles,53oC/20cycles	CGTATCGGACTTCCTTCTGC	CTCTTATTGCCAGCACAGCA	Polymorphic
130	ag.32	AU3344	204	57oC/15cycles,53oC/20cycles	CAGCAATGTGAACAGGCTCT	AATCCATGCTGAGCTGTGTG	Not polymorphic
169	acc.5	AU3345	219	57oC/15cycles,53oC/20cycles	CCGCACCTTAGTAGCAGTGT	TGGGCATTTTGATGAAACCT	Polymorphic
454	aga.5	AU3346	215	57oC/15cycles,53oC/20cycles	GACCATGGGATTGTGAAGTTG	GCCCTTCTGCAAGGTTCTTA	Polymorphic
454	aga.5	AU3347	205	57oC/15cycles,53oC/20cycles	CCATGGGATTGTGAAGTTGA	CTGCAAGGCCCTTAACACTC	Polymorphic
38	ag.10	AU3348	207	57oC/15cycles,53oC/20cycles	ACATGCCTTAACCTCCCACA	CGACCTGTCCTTTAGGCAAC	Polymorphic
211	ga.18	AU3349	204	57oC/15cycles,53oC/20cycles	GCAGCAAACAAAATAAAACCTG	CGTTTCTACGGCTCTTCACA	No segregation
149	ga.16	AU3350	177	57oC/15cycles,53oC/20cycles	GTACCGATGCCACCAAAAGT	GTGTGCGTTTAGGAATGCAG	Polymorphic
149	tg.8	AU3351	193	57oC/15cycles,53oC/20cycles	GACCGGCATCTCAATCTTGT	GATCAGGTGACGATGCAAAT	No product
182	ata.20	AU3352	214	57oC/15cycles,53oC/20cycles	GGGCTTTGATTGAATGCTGT	CAGGTGTGAAAATGCCTGAA	Polymorphic
6	tttg.7	AU3353	231	57oC/15cycles,53oC/20cycles	GCCAGGATATCTCGCTTACA	GTGCTTCAGCTGCTTCAAGA	Polymorphic
116	tca.7	AU3354	197	57oC/15cycles,53oC/20cycles	ATCGCCCCAACTTTCGTTTA	CTCACTCTCGCCACGTGATA	Polymorphic
278	tcta.9	AU3355	197	57oC/15cycles,53oC/20cycles	GGATGTGTAAAGCCCCAGTG	ACTGGTGCTCCCAACTTCAA	Polymorphic
278	ac.11	AU3356	187	57oC/15cycles,53oC/20cycles	CTCACCGGGAGAAGAATGAG	CATCCCGGAAATGAATGACT	Not polymorphic
455	ag.23	AU3357	169	57oC/15cycles,53oC/20cycles	TGGCTGAGGAGCTAGAGCAT	GAAGTCCCATCACCAGCAAT	Polymorphic
13	aaat.5	AU3358	224	57oC/15cycles,53oC/20cycles	TGTGCAAAAGTCTGAGACACG	CTTGCAGCTCATTTCCTTGA	Not polymorphic
29	tca.5	AU3359	200	57oC/15cycles,53oC/20cycles	AGAAGGGCAATTTGTGCAAT	CAGCAGACCTGTTTGGAGGT	Polymorphic
183	ctt.7	AU3360	245	57oC/15cycles,53oC/20cycles	GCAGACGTATTGCGTCATTT	GGCAGTAGATTGGCAGGAAA	Polymorphic
222	ta.36	AU3361	218	57oC/15cycles,53oC/20cycles	TGATCCGGGGTTGTGTATATC	ACCCTTTCCATGCAAGTGAC	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
241	tta.12	AU3362	205	57oC/15cycles,53oC/20cycles	CAACCTCATGTGGGGTCAC	GAGAGCGTGTTGGACTTGGT	Polymorphic
181	tg.8	AU3363	211	57oC/15cycles,53oC/20cycles	AAGAGGGAAAATTCGGAGGA	CTGGGTTTCAGAGAGGGAGA	No product
276	atcc.5	AU3364	205	57oC/15cycles,53oC/20cycles	AGGGTATCCCAAAGGTCTCC	CTGGGATAGGCTCCAGGTTC	Polymorphic
885	aat.10	AU3365	217	57oC/15cycles,53oC/20cycles	TCAAATGATGCCCAGGAAAT	GGCCTGCCAGAATCTACTGA	Polymorphic
442	tcccg.5	AU3366	199	57oC/15cycles,53oC/20cycles	GTTTCGGCAGACCAATAGGA	CCACCATTGCCGTCTAAAAC	Polymorphic
193	ta.17	AU3367	191	57oC/15cycles,53oC/20cycles	CAGGAGGAGCTGGACTCTGT	TCATTACCCAGGGTTGCATT	No product
101	aaat.7	AU3368	194	57oC/15cycles,53oC/20cycles	CACATGGGTGTTGGATCACT	GCTGCTACTGAAAGTGCACAA	Polymorphic
281	tatt.5	AU3369	209	57oC/15cycles,53oC/20cycles	GGGACAAAGGCAATTTGAGT	CAGCGCTGTGAAAGACTGAT	No segregation
370	ta.18	AU3370	196	57oC/15cycles,53oC/20cycles	GGTGTCAGGTGACTTTAATGTGATT	CTCCCATTCAATTGCAACAA	Polymorphic
200	attc.5	AU3371	174	57oC/15cycles,53oC/20cycles	TTGGATCTGTCAGCTTCGTCT	TGACCCCGACCAGAATAAAG	Not polymorphic
154	tga.8	AU3372	192	57oC/15cycles,53oC/20cycles	GATTAAACTAATGGATGGAGAATCG	GCGAAGTCATTCAGCGTTAG	Polymorphic
72	ag.8	AU3373	174	57oC/15cycles,53oC/20cycles	TCGTTCCTCTCCTCCATCTG	CAGATCAGATTCCCCGTCTC	Polymorphic
50	ttat.9	AU3374	224	57oC/15cycles,53oC/20cycles	CCCCTTTTCCTTGCATTACC	TGAAGTGCTGCTTGAATGGT	Polymorphic
50	tg.11	AU3375	191	57oC/15cycles,53oC/20cycles	CGTGTGCTTTATTTGGCAGA	GGACCGAGTACCTGTTCCAG	Polymorphic
170	acag.5	AU3376	197	57oC/15cycles,53oC/20cycles	CATGAGCTGCACACACTCG	TGTCAAACCCCAATACTGAGAG	Polymorphic
170	gt.10	AU3377	181	57oC/15cycles,53oC/20cycles	CTCCGAGTTGTTTTCACATTG	TTGGTCCCCTGGAGTTTGTA	No product
166	tta.15	AU3378	192	57oC/15cycles,53oC/20cycles	AACGTTTCAATGGGTGCTGT	GGTTGTGTGACAAAAACGACA	Polymorphic
9	tcc.9	AU3379	176	57oC/15cycles,53oC/20cycles	ACCCTTGTTCTGTGCAGGTC	CCTTGTGCAAACACAACAGC	Polymorphic
189	agat.13	AU3380	300	57oC/15cycles,53oC/20cycles	CTGACATGTTTCTGATGGATACAA	CGCATCTGCATTACACAAAC	Polymorphic
207	ac.12	AU3381	194	57oC/15cycles,53oC/20cycles	GACCCTGAGGACTTGGATTG	TCCCCAGTAATCCACACTCTG	Polymorphic
130	ca.25	AU3382	196	57oC/15cycles,53oC/20cycles	ATGTGGACACCTGACCATGA	GTAGTAGCAGGGCAGTTGCTG	Polymorphic
211	aagtc.27	AU3383	216	57oC/15cycles,53oC/20cycles	CAGGTCAGGTCAGGTCAGGT	CAACCTGGCACCATTATTCA	Polymorphic
278	atct.20	AU3384	195	57oC/15cycles,53oC/20cycles	CGAATTGCACCTACAGAGATGA	CGTGCACCTGAAACGTAATTT	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
40	ca.14	AU3385	221	57oC/15cycles,53oC/20cycles	CACAGAATGCCATGGAGAAA	CTACCAGGAGCCTTGACTGC	Not polymorphic
181	aaat.8	AU3386	292	57oC/15cycles,53oC/20cycles	CATCAGCATTTCCTGAAGATCA	ATCCGTGCTAATGCCAGAAG	Can't score
276	taga.5	AU3387	207	57oC/15cycles,53oC/20cycles	CCCATATTGGAGGAGACCAG	CATTCATGTCCATACCTGTCC	Not polymorphic
140	ac.8	AU3388	200	57oC/15cycles,53oC/20cycles	AAGAGTGTAGGTGGACGGTCA	CCCCTTTTCTGTACCCCATAC	Can't score
140	caa.6	AU3389	227	57oC/15cycles,53oC/20cycles	GCCGCAAGATTTTTCCAAT	ATACCTGCAACCTGGAATGG	Can't score
281	tta.15	AU3390	207	57oC/15cycles,53oC/20cycles	CTGCCCCCATCATTAGACAT	GACAATTGAAATCATATGGTGGA	Polymorphic
200	taaa.5	AU3391	196	57oC/15cycles,53oC/20cycles	TGTTTAAAGCCGGATGTCCT	CCTGTCCTGATGACAAACTGG	Polymorphic
79	aata.5	AU3392	250	57oC/15cycles,53oC/20cycles	GCCAAAGCCTTGAGCTACTG	TGCTACTGTTTACTGCTCTTTTGG	Polymorphic
79	ag.25	AU3393	200	57oC/15cycles,53oC/20cycles	GTCCCCACAGCACAGAGTTT	TGGATGTGTCGAATACTTCCTG	Polymorphic
145	ca.22	AU3394	197	57oC/15cycles,53oC/20cycles	GTGTTGACGCTGTAACACACA	AGCGAATTTATCTGGGGCTA	Polymorphic
145	gt.14	AU3395	231	57oC/15cycles,53oC/20cycles	GCCAAAATGTCTTTGGAGGA	CTACGGTGACATTTGGGTCA	Polymorphic
217	tta.11	AU3396	226	57oC/15cycles,53oC/20cycles	TTGGATTCTCTGGGAAGGTG	CCATGTGTACACTGCAGAAAAA	Not polymorphic
229	aat.5	AU3397	189	57oC/15cycles,53oC/20cycles	GAGGCCACTGCTTAGTGACG	CACGGAATTCCAGCATTCTT	Polymorphic
229	tta.5	AU3398	194	57oC/15cycles,53oC/20cycles	CACGGAATTCCAGCATTCTT	TGTAGTTTGAGGCCACAGCTT	Polymorphic
267	tc.22	AU3399	215	57oC/15cycles,53oC/20cycles	TTGTCCCGACCTTACCATTC	ATGAGCAAGCGGTAATGGAG	Polymorphic
267	tcca.5	AU3400	219	57oC/15cycles,53oC/20cycles	CTAGCAGCACAATTGGCATT	TTCCCTGTGACCCTGAAAAG	Polymorphic
339	aatg.5	AU3401	167	57oC/15cycles,53oC/20cycles	AATTGCATGTTCCCAGTGTTC	CATGGTCGTGTTATGTGCTG	Not polymorphic
339	cac.9	AU3402	221	57oC/15cycles,53oC/20cycles	CTCGGTCAGCTGATGGGTAG	TTCTCCCAATCTGACGTGCT	Polymorphic
351	ga.9	AU3403	245	57oC/15cycles,53oC/20cycles	GCCGTTGGAGTCTTTGACAT	CCCTTTGCTTTCTCTCTCCA	Polymorphic
351	att.7	AU3404	219	57oC/15cycles,53oC/20cycles	AACGCTGCAATGTGGATTTT	CGGTGTTCTTTATGTCCACCA	Polymorphic
358	gt.13	AU3405	234	57oC/15cycles,53oC/20cycles	CACCCTAATGGCATCGATTT	TGTGCAGACAGGTGGGAATA	Polymorphic
358	tc.11	AU3406	194	57oC/15cycles,53oC/20cycles	GCTCTGGATAATGAGGGTGTG	GGTCGAGCAGAACAACGTCT	Polymorphic
363	ag.8	AU3407	180	57oC/15cycles,53oC/20cycles	GCCTCAAAGCCTTCTGTTTG	GATTGTGCTCCAGTCATCCA	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
369	at.8	AU3408	190	57oC/15cycles,53oC/20cycles	CAGAAATATGCGTGCAAACC	GCGCCCTAAATATGGGAGAT	Polymorphic
369	ttg.7	AU3409	234	57oC/15cycles,53oC/20cycles	CACCTGAGGTCAAATCACCA	GTGCGTTTGGGCTATAAAGTG	Polymorphic
377	tgga.5	AU3410	206	57oC/15cycles,53oC/20cycles	GATGAGTTGGCACCTTGTCC	GCCTTACATCAGCGTTTTTCA	Not polymorphic
377	tcta.7	AU3411	200	57oC/15cycles,53oC/20cycles	TTCTTGCCCAAACACAGTTTC	GATCCCAAAGGAAATTCTTGC	Polymorphic
381	taa.13	AU3412	228	57oC/15cycles,53oC/20cycles	TTATTCCAAAAGGCCTGGTC	CAGTTGATTGCTGATGCCTTC	Polymorphic
381	ttta.7	AU3413	206	57oC/15cycles,53oC/20cycles	GCATTTTGGATCAGTTGCAG	GGCACATTAACGTTACCATCG	Not polymorphic
406	ct.15	AU3414	200	57oC/15cycles,53oC/20cycles	TTGACCCAGGACCTCAGTG	CTGCTTAAGAGCGAGGAAGC	Polymorphic
406	ga.21	AU3415	198	57oC/15cycles,53oC/20cycles	ACGTGGGCCTCTGTAATCAG	GTCTTGCATGCTCAGCTGTC	Polymorphic
441	gaa.5	AU3416	200	57oC/15cycles,53oC/20cycles	CTGCAGGTTGCTGAGACTGT	AGGTGCGCATAGACACACTG	Polymorphic
441	attt.6	AU3417	208	57oC/15cycles,53oC/20cycles	CTGCGTTCTAAAGAATTCAGCA	CTCCGTGGACTTTCGGAATA	No segregation
451	ac.10	AU3418	214	57oC/15cycles,53oC/20cycles	GATGGCTTGGTTTCAGTGCT	CTGTGGGACAAGTGAGCAAG	No segregation
451	ac.10	AU3419	214	57oC/15cycles,53oC/20cycles	GATGGCTTGGTTTCAGTGCT	CTGTGGGACAAGTGAGCAAG	Polymorphic
468	ag.37	AU3420	193	57oC/15cycles,53oC/20cycles	GCGCTTAAAAGCAAATAGATTG	GGGCATGCCTTGGTTATATG	Polymorphic
468	ca.11	AU3421	195	57oC/15cycles,53oC/20cycles	TTCTTCATGCCTTGCTCTAAG	GGGCATGCCTTGGTTATATG	Polymorphic
470	ggt.5	AU3422	207	57oC/15cycles,53oC/20cycles	AGTGTCTGGAGGAGGACGTG	TTGTATGGGGCAGCACAGTA	Not polymorphic
470	ggt.5	AU3423	235	57oC/15cycles,53oC/20cycles	TCGCACTCTCATAAGGACCA	CACTCAGCCCCAGTCCTAAC	Polymorphic
471	ttta.10	AU3424	243	57oC/15cycles,53oC/20cycles	TACAAAATGGTGCCCACAGA	CGAGCTACAAATTGGGGTGA	Polymorphic
471	gtga.5	AU3425	193	57oC/15cycles,53oC/20cycles	CAGCTTTCCCGAAACGTAAA	GTGCATTGAGAAAGGCACAG	Polymorphic
526	ata.12	AU3426	209	57oC/15cycles,53oC/20cycles	TCACCCTGACATTACCTGGTT	CATCATGCTTCTGCAACTTCA	Polymorphic
526	tatt.5	AU3427	205	57oC/15cycles,53oC/20cycles	CAGCTTGGAACGCTATCAGA	GAGGGGAATCCATGACACC	Not polymorphic
538	ttg.8	AU3428	179	57oC/15cycles,53oC/20cycles	GTGCAGCGAAACTGAATCAA	AAACTGCTGCGGGTCTACTG	Can't score
581	aat.22	AU3429	221	57oC/15cycles,53oC/20cycles	GGTTTCTTGATGAAGCACCTG	TCGTGTTTCTGCTTGGAGTTT	Can't score
581	aat.5	AU3430	200	57oC/15cycles,53oC/20cycles	GAGGACGCTGATGGAGTCAT	CCGGAAATTGGATTCTGGAT	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
588	aat.7	AU3431	187	57oC/15cycles,53oC/20cycles	GGCCGTTGACGTTACCTTTA	GTCCCAACCTGTGAGCTGTT	Polymorphic
588	aaat.6	AU3432	204	57oC/15cycles,53oC/20cycles	TCTGTCTCAAATGCTCGGTCT	GTGCCAAATGTTCAAAGCAA	Polymorphic
590	tg.13	AU3433	174	57oC/15cycles,53oC/20cycles	GTGGGGGAGAAAATCCATTC	ACAAGCACACATTCCCTCGT	Polymorphic
590	ga.20	AU3434	201	57oC/15cycles,53oC/20cycles	AGCCGCAGTGTATCCAGACT	CTGCTTCATCGCTCTGTCAA	Polymorphic
595	att.5	AU3435	228	57oC/15cycles,53oC/20cycles	ACATCCCCCTGGCTCTTAAT	TGGGAATTGGAGTAGAACAGG	Polymorphic
595	tg.10	AU3436	209	57oC/15cycles,53oC/20cycles	GCGAGGGCAAGGAGTATCT	TGATGCACCAGAGAACCAGA	Polymorphic
604	tta.19	AU3437	201	57oC/15cycles,53oC/20cycles	TCACCCATTAACCAGCACAA	CTTCCAGAGTCGGTTCCACA	Polymorphic
604	atga.5	AU3438	200	57oC/15cycles,53oC/20cycles	CAAGGCCACAGAGGACATTT	GTGCACAATTGTTTTCACCTG	Not polymorphic
652	attt.11	AU3439	256	57oC/15cycles,53oC/20cycles	GCTGAAATGCGTCACATGAT	GGGTTAGGGCTGCTTGATTA	Polymorphic
652	tat.8	AU3440	194	57oC/15cycles,53oC/20cycles	GGAATGAAAACGCTCAAACG	GATGCTCGGCTTGGATAGAG	Polymorphic
653	attt.5	AU3441	215	57oC/15cycles,53oC/20cycles	CAGAGTGATTTCAATCAATGTAGC	GGTGCTGCTTGAGTGTGGATA	No segregation
653	attt.5	AU3442	242	57oC/15cycles,53oC/20cycles	GCCCAACTCTAACCATAAATCC	CTGATTTCATCTTTGGAGCAA	No segregation
702	ca.16	AU3443	212	57oC/15cycles,53oC/20cycles	CAACCTGCAGCACAAACATT	AACAGGCAGCTGCATTCAT	Polymorphic
702	tc.10	AU3444	214	57oC/15cycles,53oC/20cycles	TGGAAGCGGTAACGAAACTT	CGTGAACTGAGGAGTGGCTA	Polymorphic
853	ata.8	AU3445	205	57oC/15cycles,53oC/20cycles	CCTGGAATACTGGGCTCAAA	CGATAAGCAAATGACAGTACAACA	Polymorphic
853	tta.6	AU3446	235	57oC/15cycles,53oC/20cycles	GCACACTCCTACCAGCCCTA	GTAATGCAACGCAATGTTCG	Polymorphic
875	atgg.5	AU3447	200	57oC/15cycles,53oC/20cycles	CCAGGTTGTCACCTCCTTGT	CCACTGTTGTAGGTGGGTCCT	Not polymorphic
875	ta.27	AU3448	191	57oC/15cycles,53oC/20cycles	GCTGCTGAGAGTGGTGGTAA	AAAAATGTGAGGGGTGTACTCA	Polymorphic
918	tat.11	AU3449	200	57oC/15cycles,53oC/20cycles	GCGAATAAAGCACTGTTTCCA	CCATAAGACGACACGCACAT	Polymorphic
918	tg.17	AU3450	248	57oC/15cycles,53oC/20cycles	CATATGGCGGGTTTGTTTCT	TTGGGACACTATGGAAAATGC	No product
949	ta.19	AU3451	195	57oC/15cycles,53oC/20cycles	GCATAAAGGAACAGAAAATTACCC	TCTGTTGAATACAGCACCAGAA	Polymorphic
949	tg.18	AU3452	193	57oC/15cycles,53oC/20cycles	TGGTAAGCCTCTGTTGAGTGA	GGTGTAGGCAGTTCCAGCTT	Polymorphic
997	ag.37	AU3453	173	57oC/15cycles,53oC/20cycles	TTGTCCATTGCTGTTCCAAT	CAGTCATAACATCGCTCTCG	Not polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
997	at.33	AU3454	237	57oC/15cycles,53oC/20cycles	GAACAGCTTTCGCTCATTCA	CGTGAAAAATTGCCGGTATC	Polymorphic
1017	ttcc.6	AU3455	224	57oC/15cycles,53oC/20cycles	TGTGGAGACTGCAGAGTTTGTT	GCGTCTGACAAATGCCATAA	Not polymorphic
1017	ttta.9	AU3456	186	57oC/15cycles,53oC/20cycles	GGATTCCTCTGCATTTCTGC	GTGAAGTATCAACCTAATCATTGACA	Polymorphic
1031	taa.12	AU3457	186	57oC/15cycles,53oC/20cycles	TGAACACCAGGACAACATGAA	GGTAACCACTACGCCACCAT	Polymorphic
1031	atga.5	AU3458	179	57oC/15cycles,53oC/20cycles	TGGTGTCCCAGATAGGGTGT	CTTAAACCCCTGGACCCACT	Polymorphic
1178	aaat.5	AU3459	238	57oC/15cycles,53oC/20cycles	GCTCCATGGATGGAATTTGT	CGTCAGTTGCTGGGATTTTT	Can't score
1178	aaat.5	AU3460	238	57oC/15cycles,53oC/20cycles	GCTCCATGGATGGAATTTGT	CGTCAGTTGCTGGGATTTTT	Can't score
1196	tta.5	AU3461	219	57oC/15cycles,53oC/20cycles	TGTGAATGACCTTGAGTTGGA	GCATTCAGTAGCCTGCATCA	Not polymorphic
1196	ga.16	AU3462	235	57oC/15cycles,53oC/20cycles	TAGCAGGAAATTAGCGGTCA	CACTTGCACAAATGCTTCCT	Polymorphic
1490	tta.9	AU3463	203	57oC/15cycles,53oC/20cycles	CGTAGATTGCTGTTGCGACT	GGTCGCGTGCACACTATTT	Polymorphic
1490	tta.16	AU3464	186	57oC/15cycles,53oC/20cycles	GCGCCTAATGTTGATATTCGT	CAGTAGGCGAAATGCATGTAA	Polymorphic
1509	ata.19	AU3465	202	57oC/15cycles,53oC/20cycles	AAGCTGAAGAGTGCAAATGAGA	TCCTTGAGCTTGTGGAAAGG	Polymorphic
1509	gt.9	AU3466	196	57oC/15cycles,53oC/20cycles	GCTCTGTTAATGACCCGTGAA	ATGACTGCCGCTCACTGTAA	Polymorphic
1598	acaa.6	AU3467	191	57oC/15cycles,53oC/20cycles	TACACAGTTGGGTGTAAGTAAGGTA	GCCCAAAGTTCAGGGTTTCT	Polymorphic
1598	ga.18	AU3468	211	57oC/15cycles,53oC/20cycles	TCCCAACATTCCGTAGTAGACC	CAAATTGTGTGAGGGAGAACAA	Polymorphic
1800	taaa.9	AU3469	213	57oC/15cycles,53oC/20cycles	TGGTCGGAAGGTGTTCCTAT	CGACGCAGCATTCTGTAAAA	Polymorphic
1800	ca.10	AU3470	206	57oC/15cycles,53oC/20cycles	GCACGCTCATGTGAAAACAC	TCACACTGTCCGACGTGACT	Polymorphic
57	ata.16	AU3471	229	57oC/15cycles,53oC/20cycles	TCCCCGTGAAGTCTGTGATA	GCAAGCTTGGCTTGTTGATT	Polymorphic
220	tc.17	AU3472	180	57oC/15cycles,53oC/20cycles	GATCTGACAGCCCGACATTC	CATTAAAACGGGGGAACCTT	Can't score
225	ta.24	AU3473	230	57oC/15cycles,53oC/20cycles	GGCCCTGTTTCAAAGATGAT	GGGGGTGAGCAATACGACTA	Polymorphic
225	ga.11	AU3474	180	57oC/15cycles,53oC/20cycles	GCGCTGAACAGAACTGGATT	CCCAAGAACCACTGAGGAAA	Polymorphic
251	ttgtt.5	AU3475	201	57oC/15cycles,53oC/20cycles	AGTCTCCAGTGCCAGTGCTT	CCTTCACCAGCCTTTCTTGT	Polymorphic
251	ttgtt.5	AU3476	197	57oC/15cycles,53oC/20cycles	CCAGTGCCAGTGCTTTGTAA	TCCTTCACCAGCCTTTCTTG	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
261	ta.30	AU3477	266	57oC/15cycles,53oC/20cycles	GGAAAAAGTGAAGCGCTGTG	GCTCCATGTATATGCCCAAA	Not polymorphic
261	ata.20	AU3478	274	57oC/15cycles,53oC/20cycles	GGTCTGTTTTTACTCTCGCTGA	TGTCACCCAAGTCCATTAACA	Polymorphic
282	tc.20	AU3479	190	57oC/15cycles,53oC/20cycles	TGTACGTCTGCGAGGCTATG	TACACCGTAACGCTGGGAGT	Polymorphic
282	gaaa.10	AU3480	207	57oC/15cycles,53oC/20cycles	TCCACTCCAGCATGTTTCAT	GCCGTGTATTGGTGGAATGT	Polymorphic
295	ttat.8	AU3481	188	57oC/15cycles,53oC/20cycles	AGACACCGTCGTATCGCATT	GACTCTCCACAGGCATCACC	Polymorphic
326	aaac.5	AU3482	169	57oC/15cycles,53oC/20cycles	CCAACTTTGAACCACATTGC	TACCGGATGCTTTCCAACAG	Not polymorphic
326	aaac.5	AU3483	170	57oC/15cycles,53oC/20cycles	CCAACTTTGAACCACATTGC	ATACCGGATGCTTTCCAACA	Not polymorphic
388	ac.12	AU3484	224	57oC/15cycles,53oC/20cycles	AACAGCATGGGTGATCATAGG	GCACAGGTGCCTGTCAGTAA	Polymorphic
388	gaat.5	AU3485	201	57oC/15cycles,53oC/20cycles	GCACCTGGAGTGAACTGAATG	TTTCCATTGCATCTGTTCGT	Polymorphic
401	ac.9	AU3486	184	57oC/15cycles,53oC/20cycles	AGGCTTCGTGCAGACACAC	TGGTGCCGGAGAACTTTAAC	Polymorphic
429	ca.13	AU3487	196	57oC/15cycles,53oC/20cycles	TCTCCCTCTTGGACATCTGC	GCAGTCCAAGGACAAACCAT	Polymorphic
429	ga.14	AU3488	200	57oC/15cycles,53oC/20cycles	CTGAGGATGGTGGTTTTTGC	AAGTGGCGGTGGATATGGT	Polymorphic
469	tg.16	AU3489	165	57oC/15cycles,53oC/20cycles	TGCTCTGTGTTACGTGTTTTCA	GACTTCAGGCTCTGGAATGG	Polymorphic
469	ca.36	AU3490	243	57oC/15cycles,53oC/20cycles	GCTAGTGCCCCTGAAGTTTG	GGTGACAGACCCTTCAGAGC	No segregation
477	gga.5	AU3491	200	57oC/15cycles,53oC/20cycles	CACCTGAAGGATGAGCGAAC	TGTCACAGTAAGCCTCCGGTA	Polymorphic
537	tag.5	AU3492	215	57oC/15cycles,53oC/20cycles	GCTTGTTCGACGCGTATTCT	GATGGATGGATAGAGCCTGTG	No segregation
537	taa.19	AU3493	198	57oC/15cycles,53oC/20cycles	TGGGTTTATGGCTGAAGACAC	CTGCTCATGGTGCCGTTAAT	Polymorphic
580	ta.31	AU3494	188	57oC/15cycles,53oC/20cycles	GGGCACTGTATGTGCATGTT	AGTGAAGGGTGTGGGACACT	Polymorphic
586	gt.14	AU3495	202	57oC/15cycles,53oC/20cycles	TCCTCCAACAGTCCGAAGAC	CGCTTATCCTACACAGGGTCA	Not polymorphic
596	tct.5	AU3496	206	57oC/15cycles,53oC/20cycles	CGTCTCCGAGAAACACCGTA	CCATTAGGTGGCGGTAACAC	Polymorphic
596	aaac.5	AU3497	201	57oC/15cycles,53oC/20cycles	AGGGTGTGAACGACTGTGTTT	GAATTCATCGAGGTGCCAAT	Polymorphic
618	ac.18	AU3498	215	57oC/15cycles,53oC/20cycles	GCAGGTCTCAGAGCGTAGGT	CGGACACTTTCAAACACACC	Polymorphic
618	ac.16	AU3499	185	57oC/15cycles,53oC/20cycles	ACACACAGCCCACCTCTTTC	GTTATGCAAATTGGCCCTGA	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
625	tc.10	AU3500	201	57oC/15cycles,53oC/20cycles	GCACGCACACATACAAACCT	TGGGATTCTGGGAGCATTTA	Polymorphic
625	ca.11	AU3501	191	57oC/15cycles,53oC/20cycles	CATTCATCAATGCAGCCAGT	TGTCATTGTTGCTGCCATTT	Polymorphic
695	tta.10	AU3502	202	57oC/15cycles,53oC/20cycles	CTTGACCCTGATTGGGTTACA	CCCCTCTTTATGGGAAGCTC	Polymorphic
695	tg.8	AU3503	195	57oC/15cycles,53oC/20cycles	ACCAGGAGCTTGTTGACTGG	TTCGTTCAGGAATCCAAACA	Polymorphic
227	ac.8	AU3536	184	57oC/15cycles,53oC/20cycles	CATTCCCTTGCTCCTTCATC	TTGAAATGGATTTCCCATAGC	Polymorphic
161	at.10	AU3537	188	57oC/15cycles,53oC/20cycles	GCCTTCTTGTGCACTCCATA	CTTCAGCGTTGTCACATGAA	Can't score
181	tg.12	AU3538	209	57oC/15cycles,53oC/20cycles	CAATTGGGCGTTTTATTTGG	ATGAAGCGTTGGATGGATTC	Polymorphic
276	ttg.8	AU3539	217	57oC/15cycles,53oC/20cycles	GCAGTCAGCATAAAGTGCCATA	CCAAACTTCAGCAGGTTTTGT	Polymorphic
140	ac.8	AU3540	197	57oC/15cycles,53oC/20cycles	GTGTAGGTGGACGGTCAACTAAG	CCCCTTTTCTGTACCCCATA	Polymorphic
140	tg.20	AU3541	200	57oC/15cycles,53oC/20cycles	TGCAGACAGGGAGGAGAAAT	CCTCGTCCTGCAAAGTATCC	Polymorphic
217	aaat.9	AU3542	230	57oC/15cycles,53oC/20cycles	CTTCTGAGCCCATGTCACCT	GCCTGTCTCTCTTCAAAAGCA	Polymorphic
339	aatg.5	AU3543	157	57oC/15cycles,53oC/20cycles	TCCCAGTGTTCCCTGGATAA	CATGGTCGTGTTATGTGCTG	Not polymorphic
377	ga.25	AU3544	193	57oC/15cycles,53oC/20cycles	GGGAAATATCACAGCCAGGA	AACGTTCATCCCATGTCTCC	Polymorphic
381	tg.21	AU3545	219	57oC/15cycles,53oC/20cycles	CTGCGTCACATTTTCAGCAC	CTGACACCTGCCATCAAAAA	Polymorphic
441	at.8	AU3546	196	57oC/15cycles,53oC/20cycles	CCACTGCATGGTCAAGTTTT	CATGGACAGCTCATTGCCTA	Polymorphic
451	ac.10	AU3547	213	57oC/15cycles,53oC/20cycles	CGGACATGGTACTGGTGATG	GCAGTGAGAGGGAGACCATT	Polymorphic
470	ggt.5	AU3548	204	57oC/15cycles,53oC/20cycles	GTCTGGAGGAGGACGTGAAG	TTGTATGGGGCAGCACAGTA	Not polymorphic
526	ga.13	AU3549	182	57oC/15cycles,53oC/20cycles	TATGTGCAAGCAGCCTTCAG	CCATGAACCCATGAACTTCC	Polymorphic
581	aat.5	AU3550	229	57oC/15cycles,53oC/20cycles	CTGCATGAGATTTAAAGGGGTTA	CTGGAACGCTTCATTTCCTC	Polymorphic
604	ta.17	AU3551	158	57oC/15cycles,53oC/20cycles	GCACATGTGACTCTGATCGT	GCTGGTTTCCTGAAGGTTTG	Polymorphic
918	ca.8	AU3552	236	57oC/15cycles,53oC/20cycles	CCCTGCTGATAGGGATTTTG	TGAGATTGGATGCAGGTGTG	Polymorphic
1017	aac.11	AU3553	188	57oC/15cycles,53oC/20cycles	TGCCTCTATTTGCCTGTTTC	TGTATAAAGTGCCTTGAGAAGCTG	Polymorphic
261	ata.20	AU3554	252	57oC/15cycles,53oC/20cycles	GGTCTGTTTTTACTCTCGCTGAA	TCTTCCTAAACCTCCTTCCTG	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
401	cg.8	AU3555	160	57oC/15cycles,53oC/20cycles	CATGGGTTCATAATTATTGGTTCA	TGTGCTTTCACACACACTCG	Polymorphic
586	gat.5	AU3556	196	57oC/15cycles,53oC/20cycles	GTGGGTCATTTAGGCAAAACA	TGCTAAATACGGGCTCTGCT	Polymorphic
738	tat.5	AU3557	191	57oC/15cycles,53oC/20cycles	CAGTGGCATCACGCATTACT	TTGTGGTGGAATAGGGCTAGA	Polymorphic
738	taa.6	AU3558	296	57oC/15cycles,53oC/20cycles	GGTCAACTGGCAACTCTGGA	GCTCTCTGTGGCACCGTTA	Not polymorphic
752	ata.5	AU3559	178	57oC/15cycles,53oC/20cycles	ATGGGTGCATATGGGAGTTG	GGCTAGAATGATGATGCACAG	Not polymorphic
752	gt.15	AU3560	184	57oC/15cycles,53oC/20cycles	TAACGCACAGCTAGGCACAC	GCTGTGGGCTCGTAATTAAA	Polymorphic
761	tatt.5	AU3561	171	57oC/15cycles,53oC/20cycles	CTGAAGTCGTGGCTTCACAT	TCCACAGGCTAAACCGCTAT	Not polymorphic
761	agat.11	AU3562	193	57oC/15cycles,53oC/20cycles	AGCTTGTGGTGGCCTAACAG	ATCATCCCAGACCCAAAGGT	Polymorphic
762	taaa.8	AU3563	225	57oC/15cycles,53oC/20cycles	CGTTCCGTTATCATCGTGTG	CATGCAATGCAGGTTTGAGT	Polymorphic
762	gt.11	AU3564	196	57oC/15cycles,53oC/20cycles	CTTCACGTCCAGCAGAGACA	GCTGGGTATTGGATCTGAGC	Polymorphic
767	ga.22	AU3565	197	57oC/15cycles,53oC/20cycles	CCCATGATTGGCTAATGTCTCT	CGGGACTCCATGAGCACTA	Polymorphic
767	tatat.11	AU3566	183	57oC/15cycles,53oC/20cycles	CCGAAAGTGGACCTTTCAAC	CAAATATGGAAAGGAGGCTGT	Polymorphic
772	tg.22	AU3567	164	57oC/15cycles,53oC/20cycles	ACTTCAGCCATTGAGGAGGA	CCATCTCACATGTTGCTTCC	Polymorphic
772	tg.22	AU3568	164	57oC/15cycles,53oC/20cycles	ACTTCAGCCATTGAGGAGGA	CCATCTCACATGTTGCTTCC	Polymorphic
780	aaat.6	AU3569	201	57oC/15cycles,53oC/20cycles	GATCATTTTCCGGAAGGACA	GGGAGCATGTCACCAATCAT	Polymorphic
780	ta.8	AU3570	239	57oC/15cycles,53oC/20cycles	TGTTGAAGTATGCCACCCATC	AGAAATGGAGCTGCAACGAT	Can't score
844	aaat.6	AU3571	234	57oC/15cycles,53oC/20cycles	GCCTCACTGGGTAACTTGCT	CAGTTGACATTTTGCTGACG	Polymorphic
844	aaat.6	AU3572	234	57oC/15cycles,53oC/20cycles	GCCTCACTGGGTAACTTGCT	CAGTTGACATTTTGCTGACG	Polymorphic
895	ttta.6	AU3573	201	57oC/15cycles,53oC/20cycles	GACACCCAGTCAGTTGTGGA	CAGTGTTTGGTAGGGTTGCAT	Polymorphic
895	ta.29	AU3574	280	57oC/15cycles,53oC/20cycles	TGTTTGTCCCGGTACTATGTTG	CCTTCATGAACCATGATCTGC	Polymorphic
939	ac.27	AU3575	216	57oC/15cycles,53oC/20cycles	CCTTCCTCGCCGTCTAAACT	GGGCCTGTGAGATCCGTAA	Polymorphic
939	ctg.5	AU3576	199	57oC/15cycles,53oC/20cycles	CCACCATCCCGTACAGTTTC	TGTCGCATTTGGATAAGACG	Polymorphic
941	attc.9	AU3577	206	57oC/15cycles,53oC/20cycles	TTGTCTCAGCCAAGAACAGG	GGGACCAGGGTAAAGCAGTT	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
941	tg.36	AU3578	241	57oC/15cycles,53oC/20cycles	CATTTGACAGGAAACAGCCTCT	GGACTAGCAGCAGTGAGACAAA	Polymorphic
987	gag.8	AU3579	193	57oC/15cycles,53oC/20cycles	GGGCAGGCCTAATTTCTGTC	AGGAGACTTCGTCCGGAAAT	Polymorphic
987	taa.14	AU3580	201	57oC/15cycles,53oC/20cycles	GCACTGGGCTTCTAGTGGAC	GTGGCTTGAAAGTGGGAACT	Polymorphic
1033	gt.9	AU3581	219	57oC/15cycles,53oC/20cycles	CTGGACAGTTGAAGCATGGA	GTCGATGAAGGAGGGAAACA	Polymorphic
1033	tc.8	AU3582	217	57oC/15cycles,53oC/20cycles	GCACTGCTTTTCACCTGCTA	GCTGATGAGTGTTTGGCTGT	Polymorphic
1034	atg.5	AU3583	178	57oC/15cycles,53oC/20cycles	CATGCTCAAGCAATTTTTGG	TCATTTCAATCTTCTGCTTTCTG	Polymorphic
1046	gt.11	AU3584	197	57oC/15cycles,53oC/20cycles	ACACCAGTCTGCTCCTCCAG	CACTGCAGGCATTCTTCTCA	Polymorphic
1046	tta.11	AU3585	261	57oC/15cycles,53oC/20cycles	TGGGGAGAAACACCAAGAAT	CACTCCCGGTCAAAAGTTTA	Polymorphic
1062	at.11	AU3586	214	57oC/15cycles,53oC/20cycles	TGCGCTCAAGAGTTGCACTA	TGGAGATGCATTGAGGAGAA	Polymorphic
1062	gt.16	AU3587	172	57oC/15cycles,53oC/20cycles	CGCCAATCATTCTGGAGTTT	CACTTGGCAGCATCAAGAAA	Polymorphic
1076	ttat.5	AU3588	208	57oC/15cycles,53oC/20cycles	GTGTTGCGCTTTCTGAGATG	CCCACAACAGTCTCTAGCGTTT	Can't score
1076	ac.22	AU3589	180	57oC/15cycles,53oC/20cycles	TGCTTCCCATACCAGTGTGA	ATGCCAATGAAAGGTCCTCA	Polymorphic
1090	gt.11	AU3590	207	57oC/15cycles,53oC/20cycles	CGCTTTGTACATGCAGTGTTG	CATCCTGATTAGGGCTGTGG	Polymorphic
1090	ag.28	AU3591	208	57oC/15cycles,53oC/20cycles	CAAATCTGGGCCAAATGAAG	GAGGAGTTGCCTCAGGAAGA	Polymorphic
1093	ttta.6	AU3592	200	57oC/15cycles,53oC/20cycles	CACGCCCTTTCACAGTACAA	CTGCCACCCATCCTTCTATC	Polymorphic
1093	ta.16	AU3593	198	57oC/15cycles,53oC/20cycles	TGACGTGTGGTTGCTTAAAGA	GACCGATGTTCCTTCACCAT	Polymorphic
1209	att.6	AU3594	205	57oC/15cycles,53oC/20cycles	CCACCAATAGGGCAAGTCTG	CTCCGAATCTGGTGACGATT	Polymorphic
1209	tg.8	AU3595	218	57oC/15cycles,53oC/20cycles	AACACCCGACTCTCCATCAG	GCACTGGGCTACCTACTTGC	Polymorphic
1234	ca.13	AU3596	185	57oC/15cycles,53oC/20cycles	CTTGCAGTTTTGCAGCAATC	GCTACAGCCTGCACCATTCT	Polymorphic
1234	ta.17	AU3597	206	57oC/15cycles,53oC/20cycles	TGAAGCATGAAGCAGCAAAG	GCAAACCTTTTGGGAGAATG	Not polymorphic
1289	ac.11	AU3598	218	57oC/15cycles,53oC/20cycles	AGCACAAAACTGTGCAGGTG	TCGGATTCTCCAGTAACTCCA	Polymorphic
1289	tg.8	AU3599	177	57oC/15cycles,53oC/20cycles	GTCCTCTTTGCCAAGGTTTG	CTAGGTCTTGCTGGGCACTC	Not polymorphic
1315	aat.10	AU3600	219	57oC/15cycles,53oC/20cycles	GGTCTCGCTCCCAAATGTAA	TGGAAGATTTTAAGGCAGTGG	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
1315	aat.5	AU3601	195	57oC/15cycles,53oC/20cycles	GGTTGGATTCTCTGCTGGAC	TTGCAAGGACCTGATTTATCG	Polymorphic
1421	ttg.5	AU3602	205	57oC/15cycles,53oC/20cycles	GGCACCACCAGTGAAAAGAT	GGGTTGTTGGAGGAAACAGA	Polymorphic
1421	gt.19	AU3603	204	57oC/15cycles,53oC/20cycles	CCCTTTTGCAAGGTGTCTTT	CACTCTCAGACAACCACACG	Polymorphic
1481	aac.7	AU3604	213	57oC/15cycles,53oC/20cycles	CCACTTGATGAAGACAACTAGTCAG	GACTATCTCCATCCCCCATGT	Not polymorphic
1484	att.8	AU3605	217	57oC/15cycles,53oC/20cycles	AGCACTTGCATTGGAAACAT	CGTTTGTGCTGCTTCAGTTC	Not polymorphic
1484	aat.15	AU3606	188	57oC/15cycles,53oC/20cycles	GACCTCACCTGTCGATCTCC	GAGGAGGTGGCTGTCTATCG	Polymorphic
1487	tta.5	AU3607	236	57oC/15cycles,53oC/20cycles	CATGCGACCCTTTGTAGGAT	TCAGCCAAAGGAAAATGTCA	Polymorphic
1487	att.5	AU3608	189	57oC/15cycles,53oC/20cycles	TCTGCAAATCCAGTTCACCA	AACCTTTTCTGGCTCTGGAA	Polymorphic
1575	cta.14	AU3609	174	57oC/15cycles,53oC/20cycles	GCCTAGACGCCGAAGAATTT	AAGTCCAACCTAGATACAATAGGC	Polymorphic
1575	tttg.5	AU3610	206	57oC/15cycles,53oC/20cycles	GTACCGAACGGTCGACAATC	CACTAATGGAAACACGCATTG	Not polymorphic
1592	att.7	AU3611	273	57oC/15cycles,53oC/20cycles	CTCTGCCCTTTATGGGCTTT	CCCACTAAGCAACCCTGAAA	Can't score
1592	gttt.5	AU3612	197	57oC/15cycles,53oC/20cycles	GAGGATGCCTTGTCCTAACAT	TGGCATTTTGCTGCTGAATA	Polymorphic
1635	agat.10	AU3613	192	57oC/15cycles,53oC/20cycles	ACGGCAAAAGGAAACTGATG	GCCAGCTAACGCATTCTCAC	Polymorphic
1635	cat.5	AU3614	188	57oC/15cycles,53oC/20cycles	GGTCGCTAATACCCTCATCG	CTGGAAAATCACGAATTGGA	Polymorphic
156	at.35	AU3615	197	57oC/15cycles,53oC/20cycles	TGGTGATGAACATGAAACAGAAG	TTTTGGCCATAATCATGCAG	Polymorphic
156	aat.13	AU3616	208	57oC/15cycles,53oC/20cycles	GGTGGCAGCTGGTTAATATTGT	AGCCTTGCTCTTTAGCATCG	Polymorphic
175	ac.21	AU3617	252	57oC/15cycles,53oC/20cycles	CCACTGTTGTGCCAAAGAGA	CCATCCTGGGTGATTCTTACA	Polymorphic
175	ac.21	AU3618	164	57oC/15cycles,53oC/20cycles	CCACTGTTGTGCCAAAGAGA	TTGAGACCATCCAAGAATGC	Polymorphic
208	ac.9	AU3619	198	57oC/15cycles,53oC/20cycles	GGACGACGTCTCCTTCAGAT	CTGTCAACCAGTGGAGTCAGA	Polymorphic
208	att.5	AU3620	264	57oC/15cycles,53oC/20cycles	GGAGGGGAAATGACATCATACT	CCACAAAGTTTTGGCACAGA	Polymorphic
228	tttc.14	AU3621	287	57oC/15cycles,53oC/20cycles	AGCATGTCACACCCTGCATA	GATGGCTACCGGATTCAACA	Polymorphic
228	ta.12	AU3622	231	57oC/15cycles,53oC/20cycles	GGTGCTTTTTGTGCATCCAT	TCAGGCACCATCAGACAAAG	Polymorphic
294	at.11	AU3623	212	57oC/15cycles,53oC/20cycles	CCGATACCAGTCACAGAACCA	CCTCACTCTTTCTCGGTGCT	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
294	at.11	AU3624	212	57oC/15cycles,53oC/20cycles	CCGATACCAGTCACAGAACCA	CCTCACTCTTTCTCGGTGCT	Polymorphic
337	ac.11	AU3625	199	57oC/15cycles,53oC/20cycles	CAGAGCTACGAGCAGAGCAT	CCGTACTGGAGCGGAGTAAG	Polymorphic
337	aat.8	AU3626	195	57oC/15cycles,53oC/20cycles	ATGCATGCAATTTACCCACA	CCCTAAGGCTCCAATAAGTGC	Polymorphic
407	taa.10	AU3627	207	57oC/15cycles,53oC/20cycles	AGTCTGGTGAACGGGTTTGA	CAACACCTACCATTAGCCACCT	Polymorphic
407	taa.12	AU3628	191	57oC/15cycles,53oC/20cycles	AGCCAATGTTTCTGGACTCG	CTGGAAACAGACTCCACACTGA	Polymorphic
427	aata.7	AU3629	175	57oC/15cycles,53oC/20cycles	CCAGGCCACCTCAATATGAT	AAGGAACTTACACAAACAACTTTGC	Polymorphic
427	ca.8	AU3630	202	57oC/15cycles,53oC/20cycles	CCTGAGTTTTGGGTGCAAAG	AACAAAAGCCCCTCACACAC	Polymorphic
458	gt.16	AU3631	188	57oC/15cycles,53oC/20cycles	CCATTGGGATAACGTGGTCT	GAGATAGCCGGTGGCACTT	Polymorphic
458	tta.12	AU3632	189	57oC/15cycles,53oC/20cycles	CGTGGTGGTTGAGCAGATTT	ATCGAGACGATCTTGCCACT	Polymorphic
544	aattg.5	AU3633	231	57oC/15cycles,53oC/20cycles	GTCGGGTTCCTCTCAAGGTT	TTGCAAACACAACACAGTGC	Polymorphic
544	gt.9	AU3634	222	57oC/15cycles,53oC/20cycles	CTCGGACTAACCGCTGTGTT	TCCATGAAATGTCCGCATAA	Not polymorphic
562	ac.15	AU3635	234	57oC/15cycles,53oC/20cycles	TGCCTGGTTTTGTTGACCTT	AGGCAATCTCTGCCTGTCAT	Not polymorphic
562	ac.12	AU3636	227	57oC/15cycles,53oC/20cycles	GCCTGGTTTTGTTGACCTTT	AGGCAATCTCTGCCTGTCAT	Not polymorphic
644	taga.9	AU3637	233	57oC/15cycles,53oC/20cycles	CACCTGAGAGATCATGAAAACA	ACACCGGAACTGTCACTGGT	Polymorphic
676	tgg.5	AU3638	231	57oC/15cycles,53oC/20cycles	CAGCTTGTTGCTTTCCCTTC	GCGGCTGTATCATTTCAGAG	Polymorphic
676	ca.12	AU3639	205	57oC/15cycles,53oC/20cycles	CAGCTCAAGGGTTGTCATCA	ACGGTGACAGGAAAGAGGTG	Polymorphic
710	ag.25	AU3640	201	57oC/15cycles,53oC/20cycles	GTGCCACACATTGAGGAAAG	AATGCATGCAATGTCCAAGA	Polymorphic
710	tga.6	AU3641	192	57oC/15cycles,53oC/20cycles	CCAGCACGGCTCTGTTTTAT	GAAACATGCAGTGGAACAGC	Can't score
742	taga.8	AU3642	238	57oC/15cycles,53oC/20cycles	CATTGATGAAGTCAAGATAGCTAGAGA	AAGGGACAATTGATGCTGGA	Polymorphic
742	tat.7	AU3643	149	57oC/15cycles,53oC/20cycles	CCTTGAGCTCAGGAAAAGCA	TTGGGATAGATTGACTGCTTGA	Polymorphic
770	gt.10	AU3644	214	57oC/15cycles,53oC/20cycles	CAGCTACTGCTTTGCTGCTG	TTCGGCACGCTATACGAAG	Polymorphic
770	at.35	AU3645	269	57oC/15cycles,53oC/20cycles	CCAACATGAAAACCTGTACCA	GGCATAAAGGCTGGATTTACC	Polymorphic
789	ttat.7	AU3646	236	57oC/15cycles,53oC/20cycles	TGTAACGGCAACGGTTTGTA	GCTATGGTTAACGAGCTGGA	Polymorphic

ctg_ID	Repeat Type	Primer Name	Size	Temperature	Upper Primer Sequence	Lower Primer Sequence	Polymorphic
789	tg.18	AU3647	191	57oC/15cycles,53oC/20cycles	TCTTGAGCATTTCCCAGGAT	CGACACACATGGCATACACA	Polymorphic
793	tg.9	AU3648	204	57oC/15cycles,53oC/20cycles	ATCAGATTGGCGAGGTGAAC	CAATTCGACCCCTGTAAAGC	Polymorphic
793	ta.28	AU3649	205	57oC/15cycles,53oC/20cycles	CCAGCAAATGTCAGGGGTTA	CTGTGAATGGGCTGTTGCTA	Polymorphic
813	ca.15	AU3650	212	57oC/15cycles,53oC/20cycles	TGTTTTATTGGCACACCACA	ATCTGAGCCACAAGCAGGTC	Polymorphic
813	ttcaa.5	AU3651	209	57oC/15cycles,53oC/20cycles	TGGGCAGGTCAAATACAGAA	GTTGGGATAAATTCGCACCT	Not polymorphic