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Comprehensive Structural Analysis of the Genome of Red Clover (*Trifolium pratense* L.)

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Abstract

With the aim of establishing the basic knowledge and resources needed for applied genetics, we investigated the genome structure of red clover *Trifolium pratense* L. by a combination of cytological, genomic and genetic approaches. The deduced genome size was ∼440 Mb, as estimated by measuring the nuclear DNA content by flow cytometry. Seven chromosomes could be distinguished by microscopic observation of DAPI stained prometaphase chromosomes and fluorescence *in situ* hybridization using 28S and 5S rDNA probes and bacterial artificial chromosome probes containing microsatellite markers with known positions on a genetic linkage map. The average GC content of the genomes of chloroplast, mitochondrion and nucleus were shown to be 33.8, 42.9 and 34.2%, respectively, by the analysis of 1.4 Mb of random genomic sequences. A total of 26 356 expressed sequence tags (ESTs) that were grouped into 9339 non-redundant sequences were collected, and 78% of the ESTs showed sequence similarity to registered genes, mainly of *Arabidopsis thaliana* and rice. To facilitate basic and applied genetics in red clover, we generated a high-density genetic linkage map with gene-associated microsatellite markers. A total of 7159 primer pairs were designed to amplify simple sequence repeats (SSRs) identified in four different types of libraries. Based on sequence similarity, 82% of the SSRs were likely to be associated with genes. Polymorphism was examined using two parent plants, HR and R130, and 10 F_1 progeny by agarose gel electrophoresis, followed by genotyping for the primer pairs showing polymorphisms using 188 F_1 plants from the mapping population. The selected 1305 microsatellite markers as well as the previously developed 167 restriction fragment length polymorphism markers were subjected to linkage analysis. A total of 1434 loci detected by 1399 markers were successfully mapped onto seven linkage groups totaling 868.7 cM in length; 405 loci (28%) were bi-parental, 611 (43%) were specific to HR and 418 (29%) were specific to R130. Each genetic linkage group was linked to a corresponding chromosome by FISH analysis using seven microsatellite markers specific to each of the linkage groups as probes. Transferability of the developed microsatellite markers to other germplasms was confirmed by testing 268 selected markers on 88 red clover germplasms. Macrosynteny at the segmental level was observed between the genomes of red clover and two model legumes, *Lotus japonicus* and *Medicago truncatula*, strongly suggesting that the genome information for the model legumes is transferable to red clover for genetic investigations and experimental breeding.

Key words: red clover; EST; microsatellite marker; genetic linkage map

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1. Introduction

Plant genetics has experienced a drastic change in the last decade with the emergence of genomics. A large quantity of genomic and cDNA sequences have been accumulated and systematic analyses of gene function have been conducted at a genome-wide scale based on the available sequence information. Identification and isolation of causative genes for a variety of mutants have been accelerated by the use of genomic libraries and DNA markers that are generated in association with sequence analysis. Fusion of conventional genetics and genomics is typical in two well-known model plants, *Arabidopsis thaliana* and *Oryza sativa* L. (rice), and in several major crop plants to a lesser extent but has not been very widespread in other plant species including a variety of agronomically important plants. To understand the genetic systems in the plant kingdom and be of benefit to plant breeding processes, collection of genome-wide information and subsequent adoption of genomic approaches in a diversity of plants is urgently needed.

In the legume family, genomics and molecular genetics have rapidly advanced for the last several years with a central focus on two model legume species, *Lotus japonicus* and *Medicago truncatula*.[1] These species are closely related to two forage legume crops, birdsfoot trefoil (*Lotus corniculatus* L.) and alfalfa (*Medicago sativa*), respectively, and it is anticipated that their genomic and genetic information can be applied to crop legumes, including forage crops. Several comparative analyses among legumes have been reported [2–6] and have demonstrated that genomic and genetic information of model plants may be beneficial for crop breeding. To facilitate such comparison and subsequent transfer of information among model legumes, the availability of genomic information and genomic resources for each species is a prerequisite. These resources would also be useful to investigate genetic systems specific to individual crop legumes.

Red clover (*Trifolium pratense* L.) is an important forage legume widely cultivated in most temperate regions because of its characteristics of high seedling vigor, rapid growth, and tolerance to acidic and humid conditions. It is also used as a green manure crop because of its high nutrient content resulting partly from symbiosis with nitrogen fixing bacteria of the genus *Rhizobium*. Red clover has a diploid genome ($2n = 2x = 14$), with a DNA content of 0.97 pg/2C,[7] which is slightly larger than that of rice.[7] Several studies have shown that the genome of red clover is extremely polymorphic due to its strongly self-incompatibile fertilization. In fact, intra-population genomic heterozygosity was higher than inter-population heterozygosity.[8–10] The genetic diversity of red clover has been intensively studied using amplified fragment length polymorphism (AFLP) markers.[11,12] The high level of heterozygosity has hampered intensive genetic and genomic analyses of red clover. Recently, the first genetic linkage map with 256 restriction fragment length polymorphism (RFLP) markers was constructed,[13] while in another *Trifolium* species, the white clover *Trifolium repens*, a genetic map with 566 microsatellite markers was reported.[14]

In this study, we investigated the genome structure of red clover using a variety of genomic technologies including fluorescence *in situ* hybridization (FISH) and genomic and cDNA library construction and sequencing. In parallel, we constructed a high-density genetic linkage map of the entire genome with a large number of DNA markers, which is invaluable for genome comparison, map-based gene identification and isolation, and marker-assisted breeding. We specifically focused on microsatellite markers associated with protein-coding genes, which are more informative and useful than those randomly distributed in the genome, in combination with a user-friendly and cost-effective detection system. Furthermore, transferability of these markers to other germplasms was examined to assess the feasibility of using these markers in selective breeding of red clover. In addition, macrosynteny with the genomes of two model legumes, *L. japonicus* and *M. truncatula*, was investigated using the developed microsatellite markers to explore the possibility of sharing knowledge among red clover, models and related crop plants.

2. Materials and Methods

2.1. Plant materials

A cDNA library was constructed from the Japanese red clover variety 'Hokuseki'.[15] A genetic linkage map was constructed using a mapping population of 188 F_1 individuals derived from a double-pseudo test cross between HR as the female parent and R130 as the male parent. HR is an elite plant selected from early progenies between 'Hokuseki' and a Swiss variety 'Renova' with characteristics of early flowering, erect shape, red flower color and middle-sized leaves. R130 is a progeny of a mapping population used in the development of the previously reported RFLP map,[13] originating from a Russian variety and a wild variety from the Archangelsk region (approximately N 65°, E 40°), which exhibits late flowering, semi-prostrate shape, white flower color and small leaves.

2.2. Flow cytometry

Nuclear DNA content was measured by flow cytometry according to the method described by Galbraith *et al.*[16] and Ito *et al.*[17], with minor modifications. The nuclei were isolated from fully expanded leaves of red clover and young leaves of *A. thaliana*, to provide a reference sample, by chopping the leaf tissues and filtering the minced tissue through double-layered nylon meshes (20 and 50 μm pore size). Nuclear samples were stained with 41.7 μg/ml of propidium iodide for 60 min, and then analyzed using a flow cytometer (FACScan, Becton Dickinson) according to Ito *et al.*[17]. More than 800 nuclei were measured with a minimum of triplicate analyses performed for each plant.

2.3. Generation of BAC libraries

Genomic DNA of HR was partially digested with *Mbo*I and cloned into CopyControl pCC1BAC (Epicentre, WI, USA.) according to the previously described method.[18] Two independent libraries containing genomic segments of different size ranges, 108 and 80 kb on average, were generated. Three-dimensional (3-D) DNA pools for PCR screening were generated as described previously.[18]

2.4. Chromosome analysis of condensation pattern and FISH

Chromosome samples for microscopic observation were prepared as previously reported.[19] Briefly, root tips of red clover were treated in 2 mM quinolin at room temperature for 4 h, followed by fixation in ethanol : acetic acid (3 : 1). On the next day, the tips were washed thoroughly and subjected to enzymatic maceration in a cocktail of 2.5% Pectolyase Y-23 (Seishin Pharmaceutical Co., Ltd, Japan) and 1% Cellulase Onozuka RS (Yakult Honsha Co., Ltd, Japan), and incubated in a thermal bath at 37°C for 40 min. The tips were then macerated in a few drops of methanol : acetic acid (1 : 1) fixative using the tips of a fine forceps and air dried on glass slides.

The 28S rDNA, the 5S rDNA and bacterial artificial chromosome (BAC) clones representing each linkage group were used as probes for FISH analysis. The 28S and the 5S rDNA probes were produced by PCR using primer pairs designed based on the rRNA and 5S RNA gene sequences in the red clover genome. The BAC probes were selected from the 3-D DNA pools of the BAC libraries by PCR using the primer pairs to amplify simple sequence repeats (SSRs).

The FISH analysis using rRNA genes and the BAC clones were performed on well-prepared chromosome spreads according to the method described previously by Ohmido *et al.*[20], with modifications. The chromosome spread on glass slides, prepared as described above, were incubated in 100% ethanol at 90°C for 2 min and air dried. They were denatured in 70% formamide/2 × SSC at 70°C for 4 min, and then dehydrated in a series of 70 and 100% cooled ethanol for 5 min each and air dried. After hybridization with digoxigenin- or biotin-labeled probes at 37°C for 8–48 h, slides were incubated with Sheep-Anti-Dig FITC (Roche, Switzerland) and StreptAvidin-cy3 (Jackson Immuno. Res. Lab, USA) in 4 × SSC at 37°C for 30 min in a humid dark box, followed by incubation in 4 × SSC at 37°C for 30 min in the dark with Anti-sheep FITC (Vector Labs, USA) and StreptAvidin-cy3 to amplify the signal. After washing in 2 × SSC and air drying, the chromosome sample was stained with 1 μg/ml DAPI in Vectashield.

The preparations were observed under a fluorescence microscope (OLYMPUS BX50) equipped with a sensitive cooled CCD camera (PXL1400), and the prometaphase chromosome spreads with clear patterns were photographed by blue or green light excitation and emission filters. Captured images were digitally stored in a computer and analyzed using the CHIAS3 imaging software.[21]

2.5. Random sequencing of the genome

The total cellular DNA was extracted from leaves of HR using a DNeasy Plant kit (Qiagen, The Netherlands). The obtained DNA was segmented by sonication and size-fractionated by agarose gel electrophoresis, and DNA fragments of ∼2 kb long were cloned into the *Hinc*II site of M13mp18 followed by introduction into *Escherichia coli* ElectroTen-Blue (Stratagene, USA) by electroporation. Single-stranded DNA was prepared from each colony according to the standard protocol, and was subjected to sequence analysis with DNA sequencers type 3700 and 3730 (Applied Biosystems, USA) using the Dye-terminator Cycle Sequencing kit according to the protocol recommended by the manufacturer. The sequence data can be retrieved from the DDBJ/EMBL/GenBank public DNA Database under the accession numbers DE244757–DE246660.

2.6. EST collection

Expressed sequence tags (ESTs) were collected from a variety 'Hokuseki' and a plant R130. cDNA libraries were constructed from 3-week-old plantlets of 'Hokuseki' and leaves of R130. Total RNA was extracted from 5 g of tissue by the guanidium thiocyanate/CsCl ultracentrifugation method, as described previously.[22] Purification of polyadenylated RNA and conversion to cDNA was performed as described previously.[22] Synthesized cDNA was resolved by 1% agarose gel electrophoresis, and a fraction ranging from 1 to 3 kb was recovered. The recovered fragments were cloned into the *Eco*RI–*Xho*I sites of a pBluescript II SK- plasmid vector (Stratagene, USA) and introduced into an *E. coli* ElectroTen-Blue strain (Stratagene, USA) by electroporation. Normalization of the libraries was performed by self-hybridization, as previously described.[22] For generation of ESTs, plasmid DNAs were prepared from the colonies and sequenced using the BigDye Terminator cycle sequencing ready reaction kit (Applied Biosystems, USA). The reaction mixtures were run on the automated DNA sequencer ABI PRISM 3730 (Applied Biosystems), and the collected data were processed as described below.

2.7. Sequence data analysis

Raw sequence data were quality-evaluated by the Phred program[23,24] prior to data analyses. BLAST programs were used to search public DNA databases, a proteome database of *A. thaliana* and datasets of the TIGR gene indices of three legumes, *M. truncatula*, *Glycine max* and *L. japonicus*. For DNA regions adjacent to SSRs, a cut-off value of $E \leq 10^{-5}$ or bit scores ≥ 30 against the predicted genes of *A. thaliana* and *L. japonicus* or bit scores ≥ 30 against sequences in the TIGR gene indices were considered significant.

EST data were analyzed as follows. Chromatograms were evaluated with Phred[23,24] and vector-derived sequences were trimmed with Crossmatch (P. Green, http://bozeman.mbt.washington.edu/phrap.docs/phrap.html).[24] The EST reads were quality-trimmed by the Phred quality score at a position where 5 ambiguous bases (Phred score under16) were found within 15 contiguous bases. Reads that comprised >50 bp of contiguous satisfying quality were submitted to the DDBJ/EMBL/GenBank databases with the accession numbers BB902456–BB928811. A similarity search against the UniProt Non-redundant Reference 100 (UniRef100) Databases (http://www.ebi.ac.uk/uniref/) was performed for each EST using the BLASTX program after translation into their respective amino acid sequences in six frames. EST sequences were clustered into non-overlapping groups by BLASTN using a criterion of 95% identity for >50 bases.

2.8. *Identification of SSRs*

Four types of genomic and cDNA libraries were constructed for identification of SSRs in the red clover genome.

An SSR-enriched genomic library was constructed from HR and R130. The total cellular DNA was extracted from leaves of each plant using the DNeasy Plant kit (Qiagen, The Netherlands). The isolated DNA was mixed and fragmented by sonication followed by size fractionation by agarose gel electrophoresis. DNA fragments of length ranging from 800 to 1000 bp were cloned into an *Eco*RV site of the pBluescriptII SK-plasmid vector (Stratagene, USA) and introduced into *E. coli* ElectroTen-Blue (Stratagene, USA) by electroporation. Enrichment of SSR sequences in the genomic library was performed by a method modified from a previous report.[25] Biotinylated oligos, 100 pmol each of $(AAC)_8$, $(AAG)_8$, $(ATC)_8$, $(GGA)_8$ and $(GGT)_8$, were bound to Dynabeads (Dynal Biotech, Norway). Plasmid DNAs were prepared from the genomic library and the inserts were PCR-amplified using the vector-derived primers 5′-CGCTCTAGAACTAGTGGATCCC-3′ (A) and 5′-TCGAGGTCGACGGTATCGATAAGC-3′ (B). Predominantly single-stranded copies of the inserts were obtained by asymmetric PCR using a 1 : 10 ratio (0.5 and 5 pmol) of the A and B primers. Hybridization of biotinylated oligos and insert fragments was performed twice. After the second round of hybridization, the eluted supernatant was PCR-amplified using a equal amounts of vector-derived primers (5 pmol each). The PCR product was TA-cloned into pT7 Blue T-Vector (Novagen, Germany) according to the manufacturer's instructions.

A cDNA library was made from seedlings of 'Hokuseki' for generation of an SSR-enriched cDNA library. Extraction of total RNA and polyadenylated RNA and conversion to cDNA were carried out as described in Section 2.6. cDNA fragments ranging from 0.5 to 1 kb were cloned into pBluescript II SK-. Biotinylated oligos, 100 pmol each of $(AAC)_8$, $(AAG)_8$, $(ATC)_8$, $(GGA)_8$, $(GGT)_8$, $(CT)_{12}$, and $(AAAG)_6$, were used as the driver. Hybridization of the biotinylated driver and PCR-amplified cDNA inserts and subsequent washing and cloning were performed as described above.

Construction of a methyl-filtration genomic library was performed by cloning the sonicated genomic DNA segments of ∼1 kb length into the *Eco*RV site of pBluescript SK-, followed by introduction into three *mcrBC*+ *E. coli* hosts, JM109, DH5α and XLI-Blue.[26]

A normalized cDNA library was prepared from leaves and leafstalks of HR and leaves of R130 plants, as described above. The plasmid DNA was amplified directly from each colony for sequencing using the TempliPhi DNA amplification kit (Amersham, UK). Sequence analysis was performed from one end of each insert and the SSR motifs used for the enrichment process described above were searched. Only repeats equal to or longer than 15 bp were used for the subsequent steps.

2.9. *Amplification of SSR-containing regions and detection of polymorphisms*

Primer pairs for amplification of SSR-containing regions were designed based on the flanking sequences of each SSR with the assistance of the Primer 3 program[27] so that amplified fragment sizes were between 90 and 300 bp in length. PCR was performed in a total volume of 5 μl containing 0.5 ng of red clover genomic DNA, 1 × PCR buffer (TaKaRa Bio Inc., Japan), 0.2 U TaKaRa Taq (Takara Bio Inc., Japan), 0.2 mM dNTPs and 0.8 μM each of the primers. Reactions were run using a modified 'touchdown PCR' program:[28] 3 min at 94°C for the initial denaturation, 3 cycles of 30 s at 94°C and 30 s at 68°C, followed by 2 rounds of the same program in which the annealing and extension temperatures were decreased by 2° every 3 cycles, then 4 rounds of a 3-step program of 30 s at 94°C, 30 s at 62°C, 30 s at 72°C, followed by 3 rounds of the same program in which the annealing temperature was decreased by 2° every 3 cycles, with a final extension for 10 min at 72°C. PCR products were resolved either on 3% MetaPhor agarose gels (BMA, USA) or on 10% acrylamide gels. The primer pairs giving a polymorphism among the parents of the mapping population, HR and R130, and 10 F_1 progenies were selected and used for scoring a mapping population of 188 F_1 plants.

2.10. *RFLP assays*

Total DNA was isolated from young leaves of red clover using the CTAB extraction method described by Doyle and Doyle.[29] Approximately 3 μg of DNA were digested with each of the six restriction enzymes, *Bam*HI, *Dra*I, *Eco*RI, *Hin*dIII, *Kpn*I and *Pst*I. The restriction fragments were separated on 0.6% agarose gels and blotted onto nylon membranes according to standard procedures. Red clover cDNA probes which had been mapped on the previously generated RFLP map[13] were labeled using the ECL direct-labeling system (Amersham, UK) and used as probes for Southern hybridization. The signals were detected by chemi-luminescence using an X-ray film.

2.11. Linkage analysis

Segregation data obtained from a mapping population of 188 F_1 plants using microsatellite and RFLP markers were analyzed by a combination of a color map method[30] and a JoinMap program version 3.0 (http://www.kyazma.nl). To increase the efficiency and accuracy of the map calculation, the scored markers were roughly classified into seven linkage groups using the color map method prior to the JoinMap calculation. Segregation data were scored by 'cp' population type codes for the JoinMap analysis, which was followed by conversion into color codes showing marker types according to the color map procedure. The color-coded genotypes were displayed in a matrix for each parent and classified into seven groups representing individual chromosomes. Two data subsets of individual linkage groups from each single parent were recalculated independently by the grouping module of JoinMap with LOD = 5. Two parental data subsets were merged to one data subset using a join module of JoinMap. The marker order was calculated by a mapping module of JoinMap with the following parameters: Kosambi's mapping function, LOD $\geq$ 2.0, REC $\leq$ 0.35.

2.12. Allele frequency of the markers of other red clover germplasms

A total of 11 red clover varieties bred in different countries were used for polymorphism analysis: 'Natshyu' (Japan), 'Hokuseki' (Japan), 'Sapporo' (Japan), 'Hokuiku-20' (Japan), 'Rannij2' (Russia), 'Start' (Czechoslovakia), 'Krano' (Denmark), 'Renova' (Switzerland), 'Merviot' (Belgium), 'Kenland' (USA) and 'Altaswede' (Canada). Genomic DNA was extracted from eight individuals of each variety and subjected to PCR examination with the 268 primer pairs for the selected microsatellite markers distributed throughout the entire genome. The presence or the absence of amplification and the number of different sized fragments, which was regarded as the number of alleles, were recorded. Loci where no amplification was observed were regarded as null. The heterozygous/homozygous ratio of single amplified fragments was estimated based on the ratio of individuals with no amplification to the total 88 individuals. The number of alleles and polymorphism information content (PIC) were estimated based on the SSR marker data obtained. PIC was calculated using the following equation:

$$\mathrm{PICi} = 1 - \sum_i P_{ij}^2,$$

where P_{ij} is the frequency of the jth allele for the ith marker.

3. Results

3.1. Cytological analysis of the red clover genome

The nuclear DNA contents of two red clover plants, HR and R130, were calculated to be 0.91 pg/2C ($n = 7$) and 0.89 pg/2C ($n = 7$), respectively, by comparison with an *A. thaliana* standard (0.32 pg/2C)[31] (data not shown). These figures differ somewhat from a previous report (0.97 pg/2C) by Arumuganathan and Earle [7], in which chicken red blood cells (2.33 pg/2C) were used as a standard. Given that 1 pg of DNA is equivalent to 980 Mb,[32,33] the genome sizes of HR and R130 are estimated to be 446 and 436 Mb, respectively.

A karyotype of the red clover genome was analyzed by microscopic observation of prometaphase chromosomes stained by DAPI (Fig. 1a). The lengths of the prometaphase chromosomes ranged from 5.1 to 7.4 μm, and uneven condensation patterns that have proven useful in chromosome identification were observed. The resolution of individual chromosomes was better than a previous report[34], in which the length of condensed metaphase chromosomes ranged from 1.9 to 2.9 μm, but seven chromosomes could not be definitively distinguished.

To further characterize individual chromosomes, FISH analysis was performed using 28S and 5S rDNA fragments as probes. As shown in Fig. 1b, the 28S rDNA (green signals) loci could be detected most intensely in the nucleolar organizer regions (NORs) on the short arm of Chromosome 1 (arrows) and as a less intense signal in the internal regions on the short arm of Chromosome 6 (arrowheads). An additional signal was observed on one Chromosome 5 homologue in HR, but not in R130 (Fig. 1b). The 5S rDNA loci (red signals) could be detected proximal to the NOR signals on Chromosome 1 (open arrows), and in an additional two loci on the short arm of Chromosome 2 (open arrows). The results are summarized in Fig. 1d.

3.2. Sequence features of the genome

To explore the general sequence features of the red clover genome, 960 plasmid clones from a random genomic library of HR were sequenced from both ends of the inserts, and 1920 sequence files with an average length of 732 bp and a Phred score of $\geq$20 totaling 1.4 Mb in length were generated. A total of 244 (12.7%) and 14 (0.7%) sequences showed a high degree of similarity ($E \leq 10^{-50}$) to the

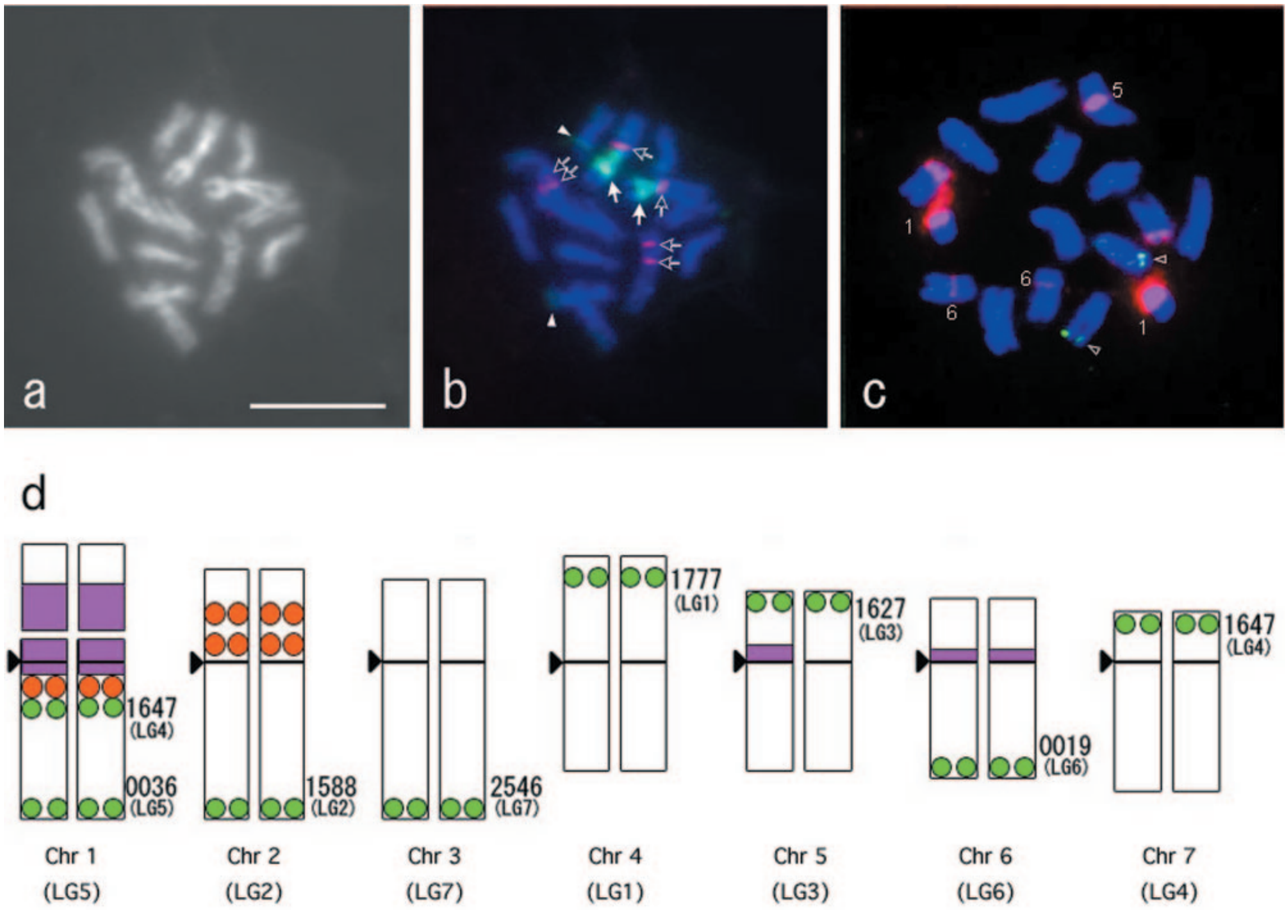

Figure 1. Cytological analysis of the red clover genome. (a) Red clover chromosomes stained by DAPI. (b) FISH analysis using 28S rDNA (green signals) and 5S rDNA (red signals) in R130. Arrows and arrowheads indicate 28S rDNA loci on Chromosome 1 and 6, respectively. Open arrows indicate 5S rDNA loci on Chromosomes 1 and 2. (c) FISH analysis using RCS2546 (green signals indicated by open arrowheads) and 28S rDNA (red signals indicated by chromosome number) in HR. (d) Chromosome map of the red clover genome. Green circles, loci of seven BACs corresponding to LG-specific markers; red boxes, 28S rDNA loci; orange circles, 5S rDNA loci.

genomes of chloroplast and mitochondria of *A. thaliana*, respectively, indicating that these sequences are derived from these organelles. Ninety-three files (4.8%) matched higher plant rDNA sequences. The average GC content of the putative chloroplast and mitochondrial genome sequences were 33.8 and 42.9%, respectively, while that of the remaining sequence files, which are likely to originate from the nuclear genome, was 34.2%.

Di-, tri- and tetra-nucleotide motifs were extracted from the genomic sequences to assess the composition of SSRs in the red clover genome. A pattern search for SSRs of 15 nt or longer identified 126 such SSRs in the 1.2 Mb nuclear genomic sequences (one SSR in every 9.7 kb). The poly$(AT)_n$ (37 loci, 29% of the identified SSRs) was the most abundant motif, followed by poly$(AAT)_n$ (35 loci, 28%) and poly$(GA)_n$ (12 loci, 10%).

The proportion of gene spaces in the entire genome was roughly estimated by determining the protein-coding regions in the genomic sequences. The sequence files (1662) that were likely to have originated from the nuclear genome were used as a query to search the proteome of *A. thaliana* and the sequences of *M. truncatula*, *G. max* and *L. japonicus* available in the TIGR gene indices (http://www.tigr.org/tdb/tgi/plant.shtml), with a minimum cut-off value of $E = 10^{-5}$. As a result, 1018 out of 1662 files showed significant similarity to sequences of protein-coding genes in the dataset examined, and of these 177 files (10.6%) showed sequence similarity to genes related to transposons. The total length of the sequence files containing putative protein-coding regions but not transposons was 518 kb and their proportion in the files of the entire nuclear sequences was 50.6%.

3.3. *Gene features*

A total of 33 024 clones from cDNA libraries were single-pass sequenced from their 5′ ends and 26 356 ESTs which met the criteria described in Section 2 were obtained (Table 1). The quality of the libraries with respect to 5′-termini coverage was assessed by comparison of 5′-end sequences to known protein sequences. Among the randomly selected 100 clones, 50 contained a translation initiation codon. To determine the number of

Table 1. List of cDNA libraries constructed for EST analysis.

Library	Source	Material	Number of sequenced clones	Number of ESTs	Number of non-redundant group
RCE001-144	Hokuseki	3-Week-old plantlet	13 824	12 427	
RCE201-400	R130	Leaf	19 200	13 929	
Total			33 024	26 356	9339

Table 2. List of libraries for identification of SSRs.

	Number of clones sequenced	Number of clones containing SSR	Number of primer pairs designed	Number of clones with similarity to genes
SSR-enriched genomic library	37 248	15 427	3094	1889
Methyl-filtration genomic library	3264	533	175	156
SSR-enriched cDNA library	13 440	6568	919	896
Normalized cDNA library	29 184	6801	3056	3029
Total	83 172		7244	5970

non-redundant ESTs, EST clustering was performed as described in Section 2, and the 26 356 sequences were classified into 9339 non-redundant groups comprising 3508 contig sequences and 5831 singletons.

The 9339 non-redundant sequences were searched against the UniRef100 database to assign putative functions. At the time of writing, 7264 (78%) showed significant similarity ($E < 10^{-10}$) to registered sequences. Most of the clones (4279) showed the highest similarity to *A. thaliana* genes; 670 were most similar to rice genes. Genes conserved between red clover and *A. thaliana* were classified into functional categories according to the Arabidopsis Gene Ontology (GO), provided by The Arabidopsis Information Resource (http://www.arabidopsis.org/). The 7941 red clover genes showing similarity to *A. thaliana* genes ($E < 10^{-5}$) were subjected to this analysis. The distribution of genes in the molecular function, biological process and cellular component categories are shown in Appendix Fig. 1. As for legume species, 251, 224, 100, 61 and 52 red clover genes were similar to genes in *Pisum sativum*, *G. max*, *M. sativa*, *M. truncatula* and *L. japonicus*, respectively. The EST sequence of each clone and similarity search results are provided at www.dnaresearch.oxfordjournals.org.

3.4. Development of microsatellite markers

To identify SSRs in the red clover genome, we generated four different types of libraries, SSR-enriched genomic and cDNA libraries, a methyl-filtration genomic library and a normalized cDNA library, as shown in Table 2. The preliminary analysis of the cDNA sequences of *M. truncatula* and *G. max* in the TIGR gene indices, genomic and cDNA sequences of *L. japonicus* and cDNA sequences of red clover revealed that specific SSR motifs frequently occur in the protein-coding sequences of the legume genomes (data not shown). These motifs were used for selective enrichment in the construction of the SSR-enriched genomic and cDNA libraries, as described in Section 2. It has been reported that low-copy number gene-containing regions of the genome can be enriched by methyl filtration.[26] We adopted this methodology to concentrate SSRs occurring in gene spaces in the red clover genome. A standard normalized cDNA library was also used as a source to isolate SSRs directly associated with expressed gene sequences.

A total of 83 172 clones were isolated from the four libraries and subjected to sequence analysis. As summarized in Table 3, 15 427 (53%) and 6568 (57%) clones from the SSR-enriched genomic and cDNA libraries, respectively, contained SSRs of 15 nt or longer, while 533 (28%) and 6801 (25%) clones in the methyl-filtration genomic and the normalized cDNA libraries, respectively, contained such SSRs. Based on the nucleotide sequences obtained, we designed a total of 7244 primer pairs to amplify SSRs by PCR, with putative amplified products ranging from 90 to 300 bp in length. We performed similarity searches of unique sequences adjacent to each SSR against the sequences of the predicted genes of *A. thaliana* and *L. japonicus* as well as cDNA sequences in the TIGR gene indices. Cut-off values of $E \leq 10^{-5}$ or bit scores ≥ 30 were adopted according to the preliminary alignments examined by eye. As shown in Table 2, 5970 (82%) out of 7244 query sequences showed similarity to the protein-coding genes described above, indicating that a significant fraction of the SSRs identified in this study are associated with genespaces.

Polymorphism was examined for the 7159 primer pairs using the mapping parent plants, HR and R130, and 10 F_1 progeny as templates. Some of the SSRs found in the random genomic sequences and cDNA sequences used in the RFLP map construction were also tested. As a result, a total of 1488 primer pairs identified

Table 3. Description of the integrated linkage map.

	Length (cM)	Number of locus[a]				Marker loci density[b]	Distortion ratio(%)[c]
		Bi-parental	HR specific	R130-specific	Total		
LG1	136.7	29 (17.2)	108 (63.9)	32 (18.9)	169	0.81	40.8
LG2	149.7	83 (29.5)	121 (43.1)	77 (27.4)	281	0.53	52.3
LG3	113.6	71 (28.6)	106 (42.7)	71 (28.6)	248	0.46	19.8
LG4	126.6	74 (33.9)	83 (38.1)	61 (30.0)	218	0.58	19.3
LG5	113.5	41 (28.9)	60 (42.2)	41 (28.9)	142	0.80	7.7
LG6	108.2	46 (30.1)	56 (36.6)	51 (33.3)	153	0.71	25.5
LG7	120.4	61 (27.4)	77 (34.5)	85 (38.1)	223	0.54	13.9
Total	868.7	405 (28.2)	611 (42.6)	418 (29.1)	1434	0.61	27.1

[a] The number in the parentheses shows the ratio (%) to total number of locus.
[b] Average distance between two loci.
[c] A Significant at $P > 0.05$.

polymorphisms among the 12 plants on 3% agarose gels. The primer pairs producing multiple bands likely to have originated from multiple loci of the genome were excluded as much as possible to avoid confusion in map construction. The selected primer pairs were then used to score polymorphisms in 188 F_1 plants of the mapping population. Ultimately, from a total of 1305 primer pairs, 1024 gave clear polymorphisms on 3% agarose gels and 281 on 10% acrylamide gels and these were used for construction of a linkage map.

3.5. Screening of RFLP markers

To integrate the previous genetic linkage map generated with RFLP markers[13] into the new map, 121 cDNA probes were examined for detection of RFLP among the HR and R130 mapping parent plants and 14 F_1 progeny. Using 188 F_1 plants from the mapping population, 95 probes that showed polymorphisms were used for further RFLP analysis. Of the 95 probes 37 produced 2–6 polymorphic bands. In these cases, each band was separately scored. In total, 167 RFLP markers were successfully scored for subsequent construction of the linkage map in combination with the microsatellite markers.

3.6. Construction of a genetic linkage map

Linkage analysis using 1472 informative markers (1305 microsatellite and 167 RFLP markers) resulted in the assignment of 1463 loci to seven linkage groups by the color map procedure. Next, 1434 loci derived from 1399 markers (1286 detected by microsatellite markers and 148 by RFLP markers) were mapped onto the seven linkage groups by JoinMap. The results are summarized in Table 3, Appendix Fig. 2, Appendix Tables 1 and 2, and Supplemental Data at www.dnaresearch.oxfordjournals.org. The total map length was 868.7 cM with the shortest linkage group being 108.2 cM (LG6) and the longest being 149.7 cM (LG2). The average locus distance was 0.61 cM ranging from 0.46 cM in LG3 to 0.81 cM in LG5. Marker locus density seemed to be slightly higher in the proximal regions and lower in the distal regions of each linkage group (Appendix Fig. 2). A total of 34 markers (33 microsatellite and 1 RFLP) detected duplicate loci, of which 24 were bi-parental, 6 were HR-specific and 4 were R130-specific, and 17 of the duplicate loci mapped between linkage groups, 17 were within linkage groups.

Table 4. Number of locus and distortion ratio at each segregation type.

	Number of markers[a]	Distortion ratio (%)
Bi-parental		
<abxcd>	167 (11.6)	28.1
<efxeg>	160 (11.2)	31.9
<hkxhk>	78 (5.4)	67.9
HR specific		
<lmxll>	611 (42.6)	22.7
R130-specific		
<nnxnp>	418 (29.1)	23.4

[a] The number in the parentheses shows the ratio (%) to total number of locus.

Bi-parental or parent-specific marker loci segregating from HR and R130 were distributed among the seven linkage groups. Out of 1434 loci 405 (28%) were bi-parental, while 611 (43%) and 418 (29%) were specific to HR and R130, respectively (Table 3). LG1 harbored HR-specific markers at the highest frequency (64% of all loci on LG1). Of 405 bi-parental loci, 167, 160 and 78 were <abxcd>, <efxeg>, and <hkxhk> segregation types, respectively (Table 4). Distorted segregation was observed for 27.1% of all the marker loci on the map ($P < 0.05$). The loci showing distortion were distributed among all the linkage groups (Table 3), but the proportion of distorted loci was different for each linkage group. Only 7.7% of the marker loci on LG5 exhibited segregation distortion, while 52.3% showed distortion in LG2. The distortion ratio was fairly similar among segregation types (22.7–31.9%), except for the <hkxhk> type (67.9%), as shown in Table 4.

3.7. *Linkage between genetic and cytological maps*

To confirm the authenticity of the genetic linkage map constructed above, each linkage group was assigned to a chromosome by FISH analysis. Seven microsatellite markers located close to the end of each linkage group were selected as representatives: RCS1777 (LG1), RCS1588 (LG2), RCS1627 (LG3), RCS1647 (LG4), RCS0036 (LG5), RCS0019 (LG6), RCS2546 (LG7) and the 3-D DNA pools of the BAC genomic libraries were screened by PCR using the corresponding primer pairs. The selected BAC clones were used as probes in FISH analysis for chromosome mapping. As shown in Fig. 1c and d, the BAC clones harboring the markers RCS1777, RCS1588, RCS1627, RCS0036, RCS0019 and RCS2546 exclusively hybridized to the distal regions of Chromosome 4, 2, 5, 1, 6 and 3, respectively. RCS1647 was detected in the distal portion of Chromosome 7 and the central portion of Chromosome 1 adjacent to the NOR.

3.8. *Evaluation of allele frequency in germplasms by polymorphism analysis*

To analyze transferability of the generated markers to other red clover germplasms, 268 randomly selected microsatellite markers were examined by PCR in 88 red clover individuals. The list of markers and the results are summarized in Appendix Table 3. All the tested markers produced amplification products (data not shown). Homozygous null alleles, where no bands were produced, were observed in at least 1 individual in 78 of the 268 markers tested. The number of alleles per locus ranged from 2 to 19 with a mean value of 6.5 (Fig. 2a). Markers detecting four alleles were most frequent. PIC values ranged from 0.05 to 0.89 with a mean value of 0.60 (Fig. 2b). Markers with PIC values between 0.7 and 0.8 were most common.

3.9 *Comparison with the genomes of L. japonicus and M. truncatula*

We performed BLASTN searches of the red clover sequences adjacent to mapped microsatellite markers against the genome databases of two model legumes, *L. japonicus and M. truncatula*. Sequences with $E \leq 10^{-5}$ were considered similar. Of the 1286 sequences that corresponded to mapped microsatellite markers, 434 and 566 showed sequence similarities to the genomes of *L. japonicus* and *M. truncatula*, respectively, 257 of which were common to both genomes (Appendix Table 1). For 133 and 161 red clover sequences a single match was found to the genomes of *L. japonicus* and *M. truncatula*, respectively, but the remaining 301 and 405 sequences had multiple matches to the respective genomes (Appendix Table 1 and Supplemental Data at www.dnaresearch.oxfordjournals.org). Two or more neighboring marker sequences of 52 loci on the red clover genetic linkage map had hits to either a single clone or clones closely located in the genomes of *L. japonicus* and *M. truncatula* (data not shown), suggesting the presence of microsynteny between red clover and the two model legumes.

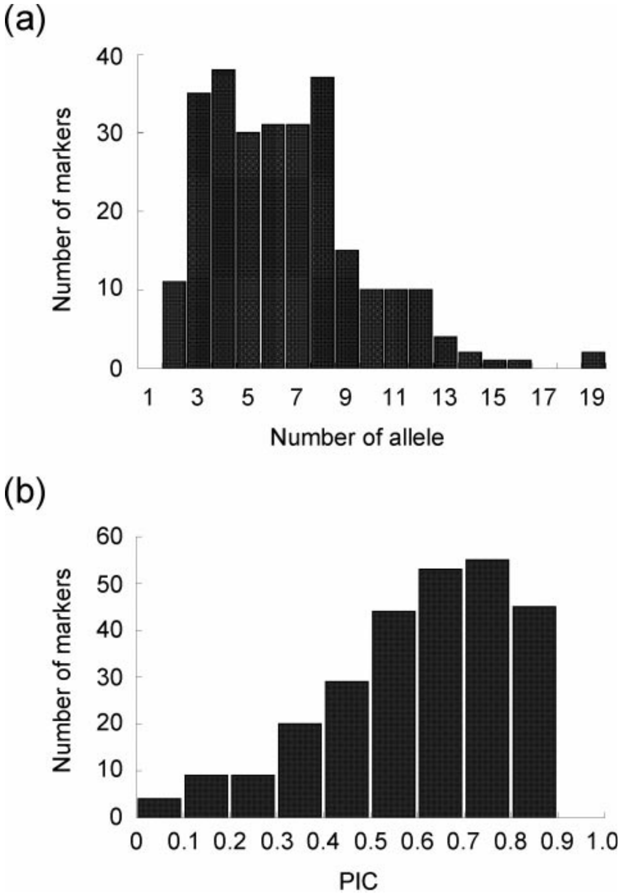

Figure 2. Allele frequency in germplasms. (a) The number of alleles per locus; (b) distribution of the PIC values.

Because significant portions of the genomic sequences of *L. japonicus* and *M. truncatula* have been anchored on their respective genetic linkage maps, the syntenic relationship between the red clover and model legume genomes could be explored by simply comparing the map locations of the red clover DNA markers and the corresponding best-hit genomic sequences of the model legumes. As shown in Fig. 3, alignment of homologous sequence pairs along each linkage group revealed an obvious syntenic relationship. The alignment appears relatively simple in the case of the red clover (rc) LG1, *L. japonicus* (Lj) chr5 and *M. truncatula* (Mt) chr1. Lj chr1, on the other hand, appeared to correspond to two alignments, rc LG6–Mt chr7 and rc LG7–Mt chr3. In contrast, the relationship of other linkage groups of red clover with those of the two model legumes seemed to be more complex at the macro level. At the segmental level, however, syntenic relationships could be detected in all the linkage groups. Some of the linkages, such as rc LG 2–Lj chr2–Mt chr6 and rc LG 3–Lj chr4–Mt chr4, have

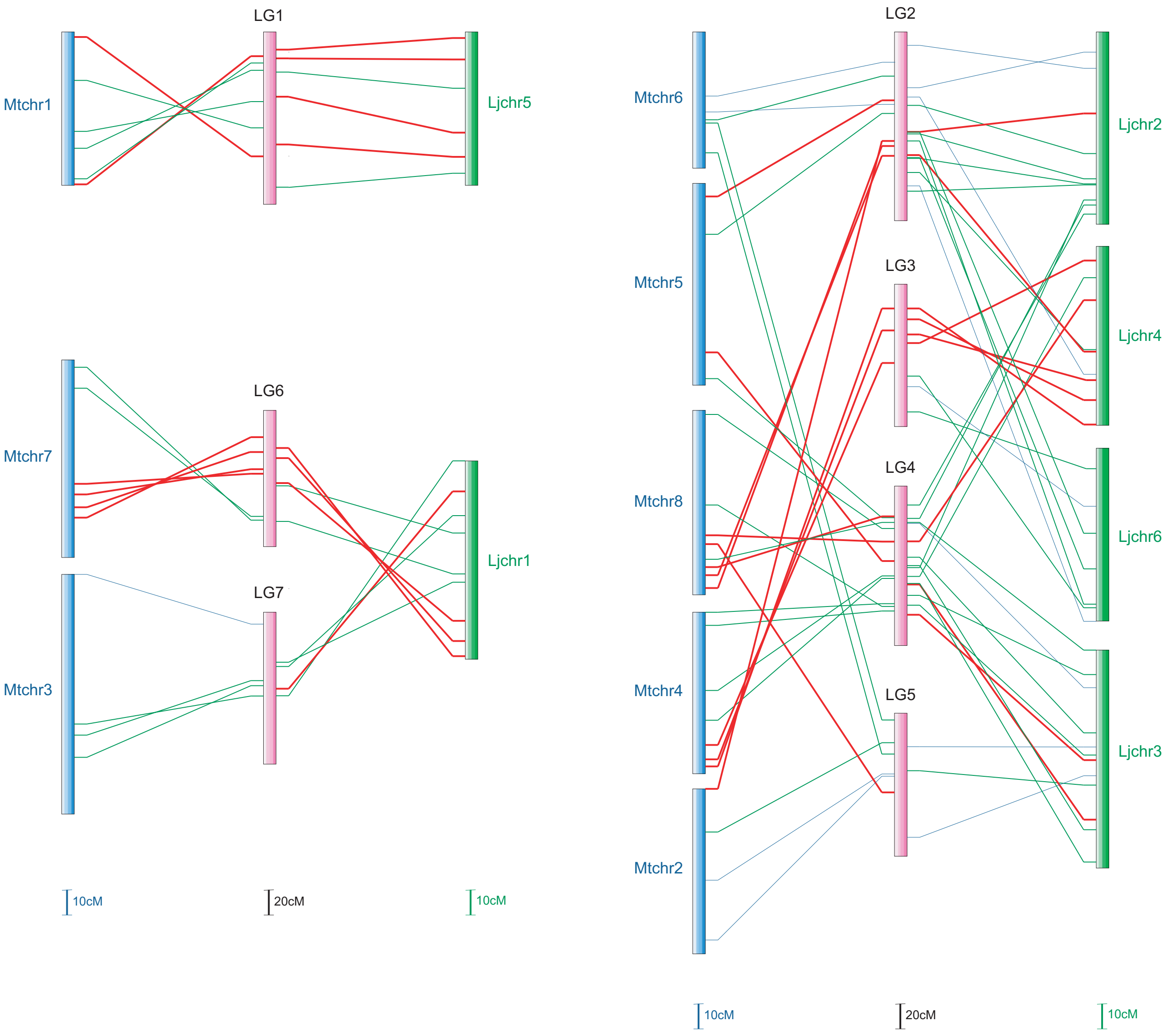

Figure 3. Macrosynteny between the genomes of red clover and two model legumes. Putative syntenic relations were estimated by ordering the red clover DNA markers along with the linkage map positions of the corresponding best-hit genomic clones of *L. japonicus and M. truncatula*. In cases where multiple red clover LGs were assigned in a region of the *L. japonicus* and *M. truncatula* linkage maps, a representative red clover LG was selected for every 10 cM interval. For each represented syntenic region one or two representative pairs were drawn with the color code indicating the number of assigned homologous sequence pairs represented by colored lines, blue: one; green: two to four; red: five or more.

been supported by the synteny analysis based on the genomic sequences of *L. japonicus* and *M. truncatula*.[1]

4. Discussion

The nuclear DNA contents of two red clover plants, HR and R130, were estimated to be 0.91 and 0.89 pg/2C, respectively, by flow cytometory using *A. thaliana* (0.32 pg/2C) as a standard. This result is not in close agreement with a previous report by Arumuganathan and Earle, which estimated the red clover DNA content to be 0.97 pg/2C and which used chicken red blood cells as a standard.[7] The discrepancy between these studies may be due to the use of different standards and/or the heterogeneous genome structure of red clover due to its cross-pollination breeding system. Using the conversion factor of 1 pg DNA/980 Mb,[32,33] the genome sizes of HR and R130 were estimated to be 446 and 436 Mb, respectively. In comparison, the nuclear DNA content and the corresponding genome size of rice were estimated to be 0.88–0.89 pg/2C and 435 Mb, respectively, under the same conditions (data not shown). However, this is an overestimation because the genome size of rice was shown to be 389 Mb by genome sequencing.[35] Therefore, it is likely that the genome size of red clover is smaller than our present estimation, possibly as small as that of rice. The genome size of HR was slightly but consistently larger than that of R130. Whether this reflects a difference in genome structure or variability within the error range of our measurements remains to be clarified.

We could not uniquely identify the seven chromosomes by DAPI staining because the banding patterns of the smaller chromosomes were not clear and some of the chromosomes were similar in size.[34] However, FISH analysis using 28S and 5S rDNA as landmarks discriminated four of the chromosomes. Moreover, the presence of minor loci for 28S rDNA in addition to the NOR is a novel finding. One of the Chromosome 5 homologues in HR hybridized with 28S rDNA, but no Chromosome 5 staining was detected in R130. This may reflect a difference in genome structure between the two haplotypes in the HR genome.

By random sequencing of the total cellular DNA, the GC content of three genomes in red clover was deduced as follows: chloroplast, 33.8%, mitochondrion, 42.9% and nucleus, 34.2%. The GC content of the nuclear genome was similar to those of two model legumes, *L japonicus* (37.0%) and *M. truncatula* (33.3%), as well as that of *A. thaliana* (34.8%). SSRs seemed to be distributed rather evenly throughout the genome. AT and AAT were the major motifs and comprised over 57% of all the di-, tri- and tetra-nucleotide motifs, whereas AT, AG and AAG were dominant in *L. japonicus* and *M. truncatula* (data not shown). With respect to each repeat motif, 35% of the AT and 37% of the AAT motifs were linked to protein-coding sequences (data not shown). In contrast, 100% of ATC and 71% of AC motifs were associated with coding sequences, although these represent only 3.2 and 5.6%, respectively, of all the SSR motifs examined (data not shown).

A similarity search against the registered sequences of plant genes indicated that approximately half of the red clover genomic sequences contained protein-coding genes. Considering that 78% of the red clover ESTs showed significant similarity to registered sequences, the genespace of red clover could be as much as 65% of the entire genome, while the remaining regions are likely to be occupied by known and unknown transposon-related and other repeat sequences. No highly repetitive sequences were detected in this analysis.

We generated 26 223 red clover ESTs that were grouped into 9339 non-redundant species. At the time of writing, the EST database in GenBank (dbEST) contained only 53 ESTs from a clover, *Trifolium purpureum.* Undoubtedly, the EST information as well as the cDNA clones generated in this study will facilitate gene isolation and large-scale analysis of gene function in *Trifolium* species. A similarity search against the UniRef100 protein database found that ~80% of the ESTs showed significant similarity to the registered genes, indicating that the functions of the majority of genes obtained in this EST project can be deduced by similarity to known genes. The result of GO classification of the red clover ESTs indicated that the cDNA clones were rather evenly distributed among a variety of functional classes, suggesting that we obtained a representative selection of gene species, probably by normalization of the cDNA library. To encourage the use of these data by the research community, we have created a database to provide EST sequence information for each clone and primary annotations deduced by similarity to known protein sequences (www.dnaresearch.oxfordjournals.org).

In this study, we aimed to develop a genetic linkage map of the red clover genome with a sufficient number of gene-associated microsatellite markers to facilitate map-based gene cloning and precise mapping of quantitative trait loci genes. We intended to adopt a cost-effective system to make use of the generated markers for a wide variety of purposes including breeding. For identification of SSRs, we constructed four different libraries: SSR-enriched genomic and cDNA libraries, a methyl-filtrated genomic library and a normalized cDNA library. SSRs were found in 53 and 57% of the clones from the SSR-enriched genomic and cDNA libraries, respectively, indicating that enrichment of SSRs by hybridization was successful. It should be noted that even the methyl-filtrated genomic library and the normalized cDNA library that were generated without any SSR enrichment process contained substantial amounts of SSRs.

DNA markers associated with genes are more informative and useful than those randomly generated from genomes such as genomic microsatellite, RAPD and AFLP markers. A similarity search against the predicted gene sequences of *A. thaliana* and *L. japonicus* and the cDNA sequences in the TIGR gene indices was performed to evaluate the libraries derived from red clover genomic DNA. Methyl filtration proved to be effective in enrichment of gene sequences because >90% of the clones from the methyl-filtrated genomic library showed similarity to presumptive genes. Of the SSRs identified in the SSR-enriched genomic library 60% were likely to originate from genespaces partly because hybridization was performed for SSRs preferentially located in the protein-coding sequences. Together with the SSRs from the two types of cDNA libraries, >80% of the SSRs identified in this study were likely to be originated from the genespace regions, demonstrating that the SSRs isolated in this study are an excellent source for the generation of gene-associated microsatellite markers.

Out of 7159 primer pairs we selected 1488 (21%) to amplify SSRs based on detection of polymorphisms in a mapping population on 3% agarose gels. In fact, ~70% of the microsatellite markers corresponding to the selected 1488 primer pairs could be genotyped fairly clearly on agarose gels with the 188 F1 mapping population. This screening ratio (21%) is much lower than that in white clover (63%), where polymorphisms were detected by capillary electrophoresis arrays.[14] We adopted the agarose gel system instead of more cost-intensive but sensitive systems, such as a fluorescent capillary gel system, to meet the requirements of a wide variety of users including breeders. This decision affected the success rate of selection of polymorphic markers. However, the primer pairs were screened under stringent conditions, thus allowing stable amplification and polymorphism detection in other detection systems. Sequence analysis of the amplified products showed that SSRs were indicative of polymorphism for most of the bands ranging from 200 to 500 bp in length, while polymorphisms observed in bands longer than 500 bp were often allocated to non-SSR regions (data not shown).

We constructed a genetic linkage map of 868.7 cM composed of 1434 marker loci, most of which were detected by microsatellite markers. Recently, high-density genetic linkage maps have been reported in several plant species: a rice map with 2740 microsatellite loci (157 kb/locus) by electronic-PCR,[36] a sorghum map of 1713 cM with 2926 loci mostly detected by AFLP markers[37] and a integrated soybean map of 2524 cM with 1849 loci mostly detected by microsatellite markers.[38] The red clover linkage map in the present study is comparable to these maps in terms of locus density and marker quality (co-dominant and gene association). Furthermore, only 2.3% of the markers detected duplicate loci, a phenomenon which often leads to confusion in map construction. These data also demonstrate high level of transferability of our markers and the map to other red clover germplasms and other plant species.

The total length of the genetic linkage map generated in this study was 868.7 cM, which is substantially longer than that of the previous RFLP map (535.3 cM),[13] indicating that a larger number of marker loci extended coverage of the genome. An alternative explanation is that the lengths of linkage maps are variable depending on inherent differences in mapping populations.[2] The parents of the present map originated in Switzerland and Japan (HR) and Russia (R130), while those of the previous map were derived only from Russia. The proportion of HR-specific loci (43%) was significantly larger than R130-specific (29%) and bi-parental (28%) loci, indicating that genetic diversity between two the haplotypes in HR was wider than that in R130.

We observed large spaces between marker loci at many of the distal portions of the linkage groups. The causes of this uneven distribution of loci remain to be studied. Since the majority of markers generated in this study are likely to be gene-associated, it is possible that the lower density reflects a lower gene density due to the presence of repetitive sequences in the distal regions of the chromosomes. Another possibility would be that the markers were mapped on these regions simply by type I error in the linkage analysis. Nevertheless, the FISH analysis for the markers in the distal regions of each linkage group, especially RCS0019, mapped at the terminus of LG6, which demonstrates the authenticity of the genetic linkage map generated in this study.

The relative ratio of the physical length to the genetic distance can be roughly estimated to be 507 kb/cM by simply dividing the genome size (440.1 Mb) by the length of the linkage map. The relative physical/genetic distance is shorter in red clover than in other legumes: 970 kb/cM in *M. truncatula*,[2] 907 kb/cM in *L. japonicus* [39] and 835 kb/cM in white clover[14]. The genome size of red clover is comparable to those of *M. truncatula* and *L. japonicus*. Generally, genome diversity is wider in allogamous plants than in autogamous plants, and this might influence genetic segregation, resulting in different relative ratios of the physical to genetic distance. Alternatively, the difference in physical/genetic distance between two allogamous plants, red clover and white clover, may simply reflect the difference in genome size, 440.1 Mb in red clover versus 956 Mb in white clover[14].

The density of the marker loci varies among the seven linkage groups. LG5 is a relatively short linkage group with a low density of loci. LG5 corresponds to Chromosome 1 harboring a large satellite which hybridizes with 28S rDNA. The long stretch of 28S rDNA, where genetic recombination is restricted, might result in the short genetic distance. The small number of marker loci, on the other hand, may reflect a lower gene density in this chromosome. Sequence conservation of rDNA and of other regions of Chromosome 1 may also contribute to the low degree of polymorphism and the short length of this linkage group. LG1 is an intermediate sized linkage group with the lowest density of loci. The distinctive feature of this linkage group is the highest proportion of HR-specific marker loci (64%). As described above, HR originated from varieties that were bred in two countries, Japan and Switzerland. These data suggest that LG1 was much more conserved within the red clover germplasms before they spread worldwide. Interestingly, a high degree of macrosynteny is observed between red clover LG1 and the genomes of two model legumes, *M. truncatula* and *L. japonicus*. Further analysis of LG1 with respect to synteny and gene function may provide clues to the evolution of red clover, as well as of other legume species.

Approximately 27% of the marker loci exhibited segregation distortion in the present map, while 37% showed distortion in the previous RFLP map. A high degree of genomic diversity in the mapping population used in this study may have contributed to reduced levels of distortion. The distortion ratio was especially high (68%) in the <hkxhk> type, possibly because some mechanism to avoid inbreeding weakness affected segregation. Distortion ratios varied among the seven linkage groups, ranging from 8 to 52% (Table 3). LG2, the longest linkage group, showed the highest distortion ratio.

The linkage between the genetic map and the cytological map was investigated by FISH analysis. The marker RCS1647 for LG4 hybridized to two different loci, the distal portion of Chromosome 7 and the central portion of Chromosome 1. The signal on Chromosome 1 might be due to duplication of a gene or a chromosomal segment during genome evolution. All the signals except that of RCS1647 on Chromosome 1 were detected at the distal portions of each chromosome, which agrees well with the positions of the respective markers on the corresponding linkage groups. This, together with the clear one-to-one relationship between each linkage group and each chromosome, strongly demonstrates the authenticity of the genetic linkage map.

Breeding involves thousands of individuals with a wide variety of genetic variations, whereas genetic linkage maps generated using F_1 mapping populations reflect only four haplotypes. Thus, in order to utilize DNA markers and linkage maps for breeding processes such as development of screening markers and diversity analysis, transferability of the markers is crucial. In this study, we confirmed transferability of 268 selected markers on the genetic linkage map to 88 red clover germplasms derived from 11 varieties. The number of alleles per locus ranged from 2 to 19 with a mean value of 6.5, which is greater than the number identified in the previous RFLP map (average 3.1 alleles per locus ranging from 1 to 10). This result strongly indicates that the microsatellite markers developed in this study are suitable tools for analyzing numerous red clover germplasms.

PIC estimates the number of polymorphic pairs among all possible pairs in a population. In this study, the average PIC of 268 microsatellite markers was 0.6, which means that 60% of the germplasms (or two haplotypes) have heterozygous loci. For construction of a map using F_1 progeny at least one of four haplotypes needs to show polymorphisms. To estimate the polymorphism ratio in four alleles PICi/4 allele $= 1-\sum_{\mathrm{i}} P_{ij}^4$, where P_{ij} is the frequency of the jth allele for the ith marker, was calculated. The mean value of PICi/4 allele for the 268 microsatellite markers was 0.85 (data not shown), which means that the probability of detecting a polymorphism between a pair of mapping parents per marker is 85%. In this study, we observed distortions from the normal distribution of allele number per locus and PIC. The allele number per locus observed most frequently was 4, which is smaller than the mean value of 6.2. However, the PIC distribution peaked at 0.7–0.8, which is larger than the mean value of 0.6. Because PIC is determined by the number and deviation of alleles in each locus, these data suggest that the higher PIC value could be largely attributed to an even distribution of polymorphic alleles rather than the total number of alleles.

Utilizing the sequence and map information obtained in this study, we compared the genome structures of red clover and two model legumes, *L. japonicus* and *M. truncatula*. A similarity search indicated that a substantial proportion of the red clover marker sequences showed sequence similarities to the model legumes, even though the sequences of only half of the entire genomes of each model species are currently publicly available. This demonstrates that genomes of red clover and the model legumes can be linked by the use of the DNA markers and the corresponding sequences. It is implicative that approximately two-thirds of the red clover markers examined have two or more matching sequences in the genomes of *L. japonicus* and *M. truncatula*. This may be due to gene and/or segmental genome duplications, which have diversified the genome structures during evolution. Nevertheless, a moderate degree of macrosynteny was observed between the genomes of red clover and the two model legumes as shown in Fig. 3, and the presence of microsynteny was also suggested.

The genome information and resources that we generated for red clover in this study are not as abundant as those accumulated for *A. thaliana* and some major crop plants. However, even these resources are sufficient for multiple applications. For example, combination of the microsatellite markers with known gene sequences and the genomic BAC libraries, which provide a 7.9-fold coverage of the genome, would allow isolation of most of the genes homologous to those of agronomic importance. A combination of information and material resources of the genomes not only in red clover but also in other plant species would provide further possibilities, including identification and isolation of genes utilizing synteny information from the model plants, development of DNA markers for candidate genes based on sequences from other plants, generation of consensus genetic maps among intra- and inter-specific groups, evaluation of variation among genetic resources and an efficient association analysis.

One of our major intentions in this study was to connect genomics to breeding. There is a large gap between plant genomics and breeding, even though breeding has been considered one of the most important and expected outcomes of genomics. Although various reasons for this discord could be hypothesized, financial and technical difficulties are among the leading issues. As one of the attempts to fill this gap, we insisted on a cost-effective and simple marker system which is user-friendly to breeders. We believe that PCR-based microsatellite markers, together with the detection system adopting agarose gels rather than acrylamide or capillary gels, would facilitate interchange of information and technologies between the two contrastive research fields. Breeding is often compared to an art because it pursues the creation of 'ideal genotypes' which have never existed. It is said that a great artistic work is born from a mixture of essential knowledge and sensibility. In this study, basic knowledge on the genome structure of red clover as well as material resources has been provided. We hope that these, mixed with the sensibility of the breeders, will contribute to the birth to fabulous new varieties in the near future.

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Supplementary Material: Supplementary material with additional information is available online at http://www.kazusa.or.jp/en/plant/redclover/marker/ or http://dnaresearch.oxfordjournals.org

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Appendix

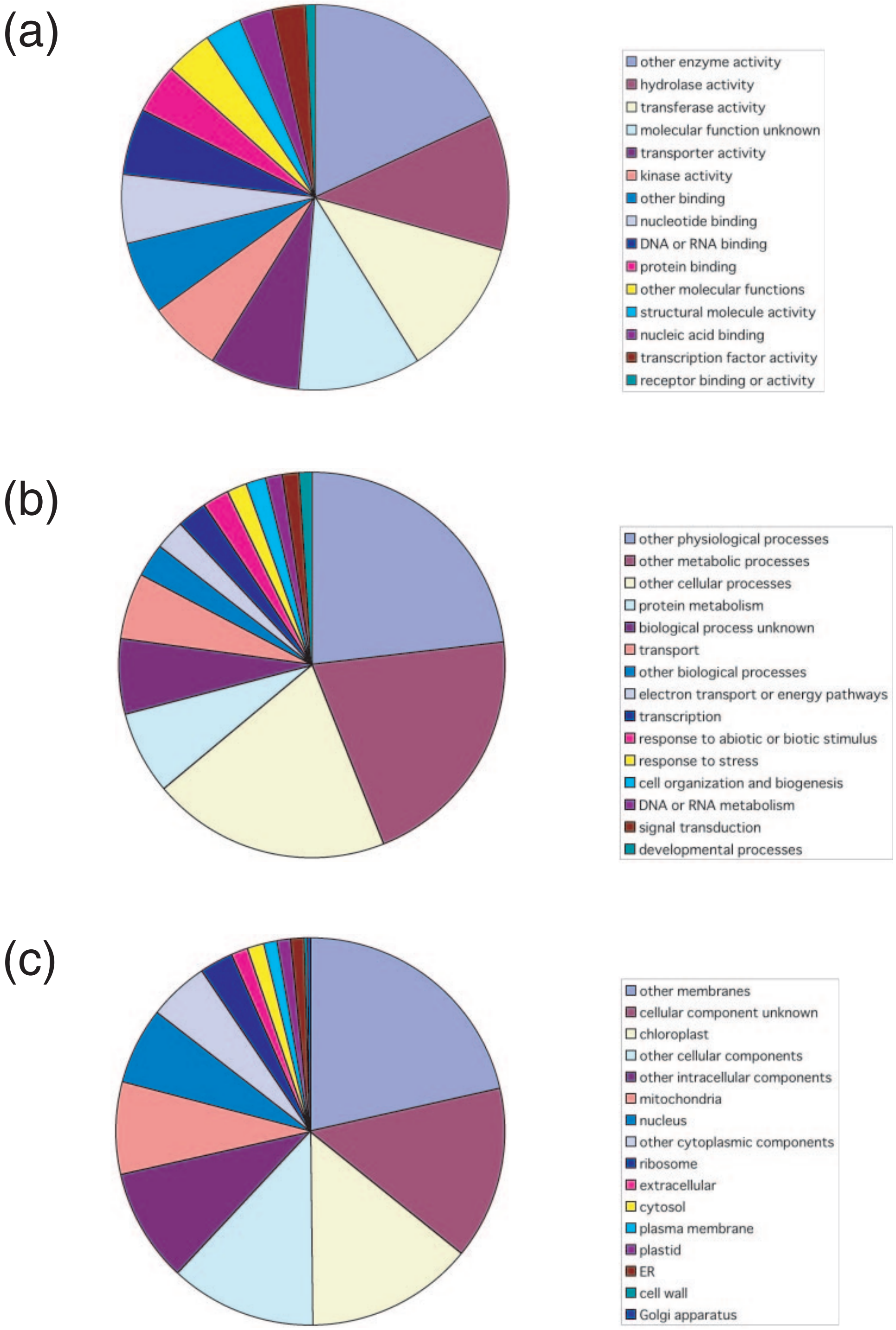
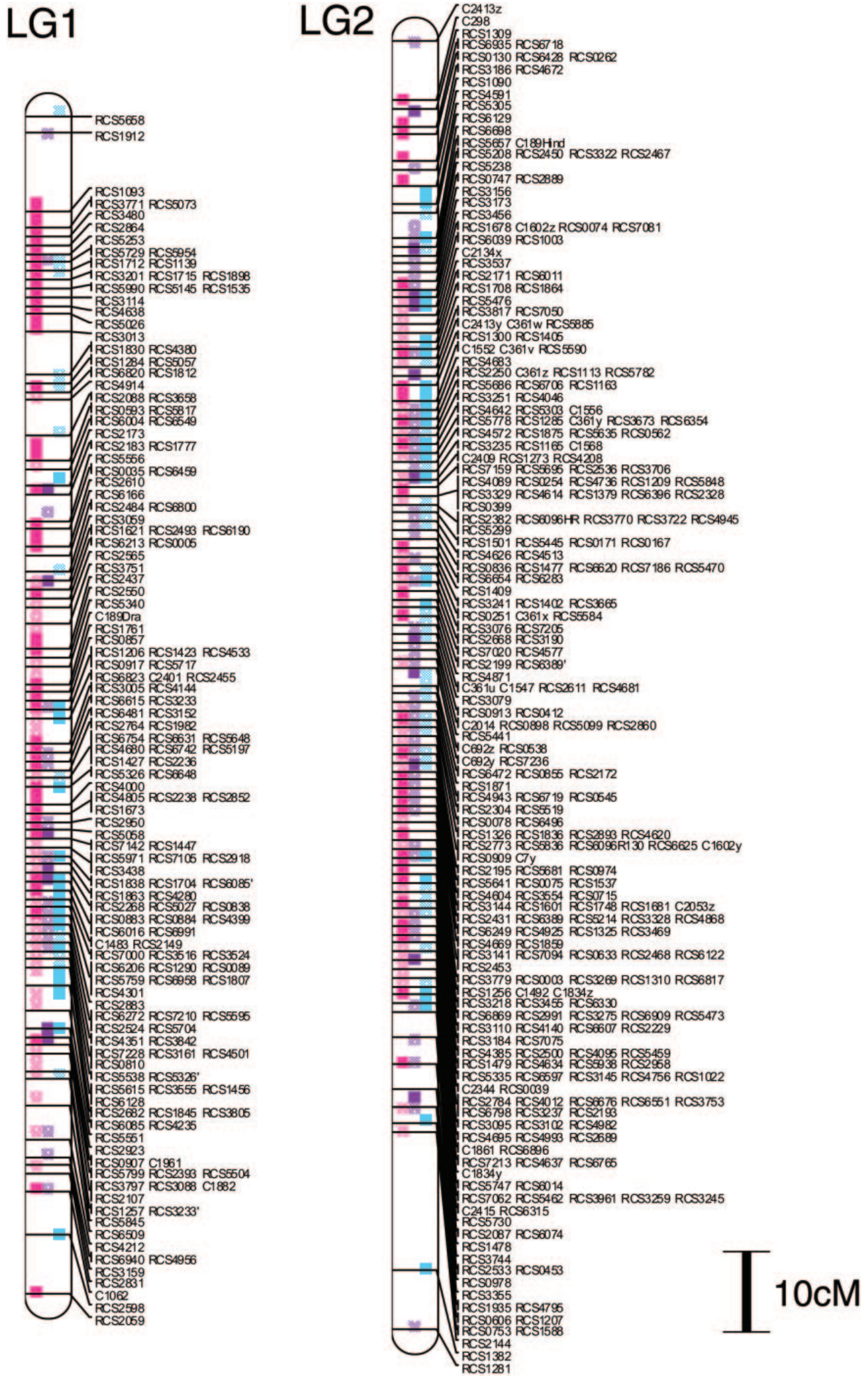


Figure A1. Classification of ESTs into functional categories according to Arabidopsis Gene Ontology. (**a**) Molecular function category; (**b**) biological process category; (**c**) cellular component category.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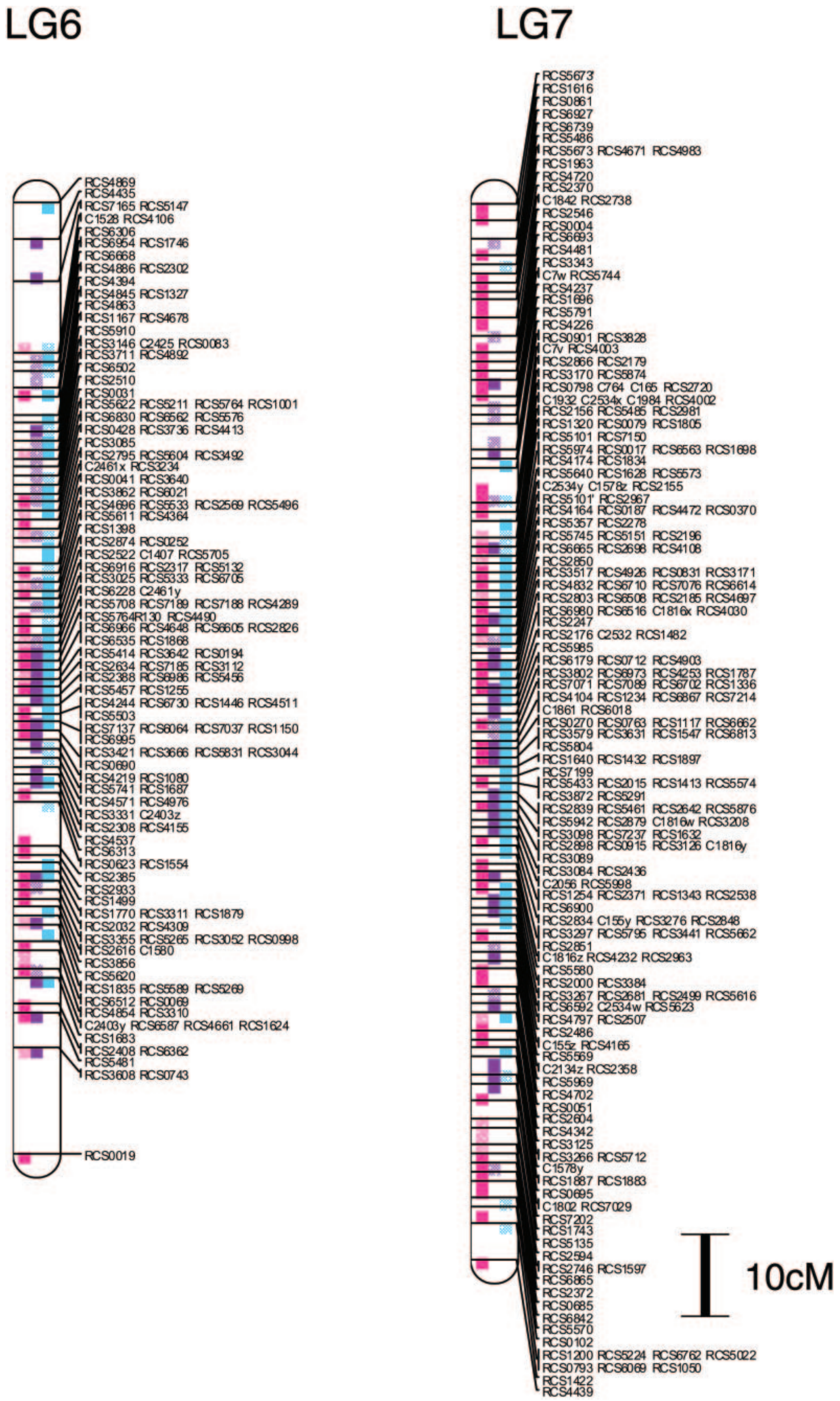

Figure A2. Genetic linkage map of the red clover genome. Each linkage group corresponds to that in the previously reported linkage map.[13] LG2, LG1, LG3, LG4 and LG5 are inversely shown to match the chromosome map in Fig. 1. Positions of bi-parental, HR-specific and R130-specific marker loci are indicated by purple, pink and blue boxes, respectively. Distorted loci are preferentially represented when multiple markers including the distorted loci are closely located.

Table A1. List of microsatellite marker loci.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS5658	LG1	0.00	BB914538	B	ATC	18	TCCTGAATCATCCCTCCTGT	CCCCTTTAGACAATTGGGGT	197						
RCS1912	LG1	2.09	BB933232	A	AAG	21	GCACGAGGCTCATCTCTTCT	GATCCGATGGGAAACTACGA	191				mth2-122l24	1	49.4
RCS1093	LG1	11.30	DE217772	D	AAC	15	TGTTCCAGCTGTGGTTATCCT	GGCCACAAAAAGAAAACAGC	150						
RCS3771	LG1	13.01	BB903241	B	GGA	15	TTCCAGACAAAACCAAACCC	TTCTCCAAGGCTGCTTCATT	192				mth2-14b10	1	62.8
RCS5073	LG1	13.03	BB911410	B	ATC	44	AGTCGAAACGCCTCTAGCAA	TTTGGGCAATTTCCTTTGAG	225						
RCS3480	LG1	14.09	DE236207	D	AAAT	23	ACCTCTTCCAGCTTCGTCAA	GCGGGAAGTTGAAAATGAAA	184	TM0698	5	2.4			
RCS2864	LG1	14.58	DE229977	D	AAAT	21	GAGTTACATGCACAAGCAATAGA	TCCTTTTCCTCTTTCTGCCA	290						
RCS5253	LG1	15.78	BB912740	B	AGC	15	CGGATAGAATCAGTAGAAGAGAGACA	AAAGGAGAAGCGAGAGAGGG	90						
RCS5729	LG1	16.92	DE239368	D	AAAT	21	CCTCCTTTTGTTGAGCAAGC	TTTGATATGGTGCAAGCAGG	178	BM1380	5	4.8			
RCS5954	LG1	17.09	BB914939	B	ACT	15	GCCAAACGTTGAAAACACAA	ATGAGGTCCACGTGAGTTCC	266	BM1451	5	5.2			
RCS1712	LG1	17.71	BB931141	A	GGA	15	CGATTCTCTCCGTATCCGTC	2GCACGAGGTCTATCTACAGGTAATC	234						
RCS1139	LG1	18.31	DE217968	D	AAG	15	AACCAAACAACAACTCATTTCG	GTGGTGAATGCCAACAAAAA	183						
RCS3201	LG1	18.72	DE233075	D	AAAT	18	AGAGGTCCCGAGTTCGATTT	TCACATGCAGTCCCTAATGC	280	TM0218	5	7.2	mth2-29h7	3	72.5
RCS1715	LG1	19.11	BB931231	A	AAC	15	ATTCTCCCCGTTTTTCTTGC	TGGGATTAGATCGAAGGTCG	186	BM1271	ND		mth2-34l12	1	60.4
RCS1898	LG1	19.27	BB933120	A	AAG	15	ATCCGGCATCTCAGCTCTTA	AGTCCACTCTCGACGATGCT	254	TM1692	5	7.6			
RCS5990	LG1	19.57	BB915208	B	ATC	15	TCTTCCATTAAACATAAAAACAATCAA	TTGAGGACCAATGTCCTGGT	282	BM0925	2	67.8	mth2-14g13	8	49.5
RCS5145	LG1	19.59	BB911988	B	ATC	15	AGTCCACTCTCGACGATGCT	ATCCGGCATCTCAGCTCTTA	251	TM1692	5	7.6			
RCS1535	LG1	20.24	BB930236	A	AG	18	CCAGCATAAAATCCCAAACC	TTTCCAAATCCCAAATCTCAA	231	TM1692	5	7.6			
RCS3114	LG1	21.08	DE230868	D	AAAT	19	TCATATCAATATCAATGTGTTCAATTC	TTTACCGGCCTATCATTTGG	143	TM1062	5	10.9	mth2-33j22	1	58.9
RCS4638	LG1	22.23	DE237012	D	AAAT	24	ACTTGGTGACTCCACAAGCC	TGTGAGGGAACATTTCAGGA	150				mth2-105p11	3	25.6
RCS5026	LG1	23.14	BB911045	B	GGT	27	GCCATTATTGCCTTTCTCCA	GATGGAGAAGCAACACCACA	191				mth2-13c11	1	58.9
RCS3013	LG1	24.54	BB938533	A	GGT	21	CGATGGCATTTGTGATTCAT	TTCCGGCAAATACTTCAACC	224	TM0537	5	10.9	mth2-66m17	1	58.2
RCS1830	LG1	30.26	DE221038	D	AAG	16	GGATGAATCAAGAGGCCAAA	TGATGATGAAGATGATGATGAGG	164						
RCS4380	LG1	30.40	BB907250	B	GGA	15	TCCCCTCCTCTCTTCTCCTC	AAAGTGGGGCCATATCAGTG	204	TM1766	2	22.1	mth2-15e9	1	46.1
RCS1284	LG1	30.93	DE218969	D	AAG	21	CTTCCACAAGTTCGCACAAA	TGCTTTTGTTGGTTCCATTG	208						
RCS5057	LG1	30.98	BB911229	B	AAG	15	TTCTTCAACCCACCAACCAT	AGCATTCAAGTGAATTCGAGC	289						
RCS6820	LG1	31.84	BB923242	B	ACT	15	ACGAACCAAACCGAACTCTG	CCTTCGTGCATCCTCCTAAC	295	TM1493	5	22.3			
RCS1812	LG1	32.16	BB930975	A	GGAT	15	TGCCATCATCTGAATCTCTCTC	CCTCTGTAAAATCTTTGCATCA	90	TM0506	3	73.6	mth2-50l17	1	58.9
RCS4914	LG1	33.04	BB910121	B	ACT	17	TCCATCCATCCTAATGCAAA	TGGACAATCTATGCCACCAA	206	TM0773	5	23.9	mth2-18n7	1	52.4
RCS2088	LG1	37.02	DE224655	D	AAC	20	TCAACATGCTTCCACATTGC	TCACTTGCAATGTAATTTCCG	163						
RCS3658	LG1	37.42	DE243789	E	AAT	15	GGTTCCTTCGAATTGTTCCA	TGCAGGTCTGGACCATGTTA	174						
RCS0593	LG1	39.53	DE214805	D	AAG	15	AAAAAGACACCAACGCCATC	TTGAGTGTTAAACGGTGGTTTG	222				mth2-10p9	ND	
RCS5817	LG1	39.81	DE240285	D	AAAT	22	AAGGGTCAAAACTTGCCAAA	CGTTTCAAGGGTCTTCCGTA	136	TM1709	ND		mth2-15k17	5	16.5
RCS6004	LG1	40.53	BB915282	B	AAG	30	CACTGCCAATTCCAAATCCT	AAACCATTGCCAAAGAAACG	255	TM0211	5	32.7			
RCS6549	LG1	41.22	BB920167	B	GGT	15	TTTGGCACATCCAAGACGTA	ACGACACCGTAGCTGCTTTT	257				mte1-58h9	2	0
RCS2173	LG1	43.28	DE225249	D	AGC	23	AACTAAGAACAGAGTTTTGGAGTCA	GGATGCTTCCTCCATTGAAA	160						
RCS2183	LG1	43.72	DE225382	D	AGC	18	AAAAGACAGACGCCAGGAAA	TGTGTGCATTGGTTTGGTCT	164						

RCS1777	LG1	44.19	DE221001	D	AAG	22	AGGCCTCTTCTCATCGCTTT	TTGCTTGGAATTTGCCTCTT	205	TM0980	1	71.4			
RCS5556	LG1	46.63	DE238342	D	AAG	20	TTCCTTGCTAATCACGTCCC	TGGTGTTGAGACAGACGGAG	141						
RCS0035	LG1	48.00	DE244807	F	AC	18	CATTGTAGGTTATGTTTATCAGG	CCCAAAGCCTACAAGGAAAG	162	TM0062	5	33.5	mth2-14a16	ND	
RCS6459	LG1	48.17	BB919172	B	GGT	18	AATGAACCGGTTTCGAAGTG	TCGTCGGAGCTATTAGCGTT	236				mth2-71g17	ND	
RCS2610	LG1	49.84	DE222971	D	AAAT	16	GGCCCAACAATCATCTGAAA	CCGACACACATCAACACACA	104						
RCS6166	LG1	51.34	BB916556	B	GGC	15	GAGCTTTGTCTTGGTTTGCC	AGCTGGTGGCTTAGAAGGGT	201	TM0071	5	39.9	mth2-151m4	4	60.4
RCS2484	LG1	52.65	DE227549	D	AAC	15	ACCGTATTCCGAGCACATTC	TCAAGAATGGTTGCCAATGA	190						
RCS6800	LG1	52.67	BB923099	B	ATC	16	GTACTGGATGTGGCTTCCGT	GGCCTTAAAACCTGGGAAAG	161				mth2-146o17	3	25.6
RCS3059	LG1	54.20	BB939241	A	AG	17	CTCAATAGGGGGAAGTGCAA	TGCTCCTCTCTTTGTTGGCT	255				mte1-28e19	ND	
RCS1621	LG1	55.07	BB932440	A	ACT	17	AAAGTTGTGGATATTGGCGG	CACTCCTCAAAAACCCTTCC	225	TM1454	4	40.9	mth2-29b13	2	17.8
RCS2493	LG1	55.13	DE227731	D	AAC	15	AAATCAAAACGAGCCACTGC	CTGGCTGTCTTAAAGCTGGC	140	TM1221	ND		mth2-11a6	1	39.4
RCS6190	LG1	55.41	BB916724	B	AC	17	TTCACTCATCTAACAAACTCACTCTTC	TGTTGGTCTTAGGATTGCCC	193				mth2-11l13	ND	
RCS6213	LG1	55.87	BB916850	B	AAT	18	CCGATTTCTTCCATCGGATA	TCCAAAGAGAACAAGGAACCA	192	TM0640	ND				
RCS0005	LG1	56.01	AB234880	C	AAT	15	TCCAAAGAGAACAAGGAACC	GAAACCGGCGATGAAATTAG	169	TM1391	1	71.4	mth2-152f22	1	4.4
RCS2565	LG1	56.94	DE228732	D	AAG	15	GCAACTTCTTGGGTCGTTGT	ATCCTCTCCCACGACCTCTT	248				mth2-168f23	4	58.3
RCS3751	LG1	59.38	BB903036	B	AAAT	16	CCTTCCAAAATCCAACTCCA	TGCTCTGAAATGGTCTCAAGAA	152	BM1529	ND				
RCS2437	LG1	62.35	BB935489	A	GGT	27	AACACCATTTCCTCCACCAC	CGGATCCGGATATGGTTATG	193						
RCS2550	LG1	63.19	DE228558	D	AG	29	AATAATACTCCCTCCGTCCCA	CCCTCCGTCCCAAAATAGAT	272						
RCS5340	LG1	64.37	BB913355	B	AAG	15	GTTCTTTACCTGGGTTGGCA	TGAAGCTATTTCCTGGTGGG	154						
RCS1761	LG1	67.08	DE220687	D	AAC	19	CGTAATCGGTGCAAGGAGAT	TTCCATTGTTAGGGTTTCCG	101	TM1303	5	17	mth2-31g22	1	19.2
RCS0857	LG1	67.52	DE216274	D	AG	41	ATCGTGATCGTTTGCAGTCA	TTGCATTGGATTCTTTGCTG	222						
RCS1206	LG1	68.69	BB928887	A	GGA	24	ATGCCATCATAGGAGGAGGA	TTTAGGAAGCCAGCTGGAGA	214	TM1493	5	22.3	mth2-65l2	1	61.9
RCS1423	LG1	68.70	BB929374	A	GGA	24	GATGCTGCTGCTGTTGTTGT	GACTTGCCAGGTACGATTCC	174	TM1493	5	22.3	mth2-65l2	1	61.9
RCS4533	LG1	69.15	BB908326	B	AATG	20	TCACATTCACATTCACCTACCA	GCCGAGGAAGAAGTTGTGAG	214	TM0260	5	0			
RCS0917	LG1	69.45	DE216928	D	GGA	15	TCCTCTTCGTCCTCCTCATC	CAACTGGAGTCTTTGATTTTCTTC	151						
RCS5717	LG1	69.47	DE239198	D	AAC	17	CGCTCTTTTCAAGCACCTTC	TCAAGGGAAGAATTTGGAGC	249				mth2-22c4	1	22.2
RCS6823	LG1	69.53	BB923304	B	ATC	20	TGGCCCTACTCGTACCATTT	TAGGAAGAACAACGGCTGCT	182	TM1733	5	2.4	mth2-57h18	1	60.4
RCS2455	LG1	70.01	DE227300	D	AAAG	16	TCCTGATCCTCTTCCTCCAA	CAAGGGGGAAGATGTGAAAA	140						
RCS3005	LG1	72.68	BB938356	A	AAC	15	CTCCTGGCCGTACGATTAAA	ACCCTCCTCCTGAAACAACC	147						
RCS4144	LG1	72.93	BB905730	B	GGT	15	TCCAATCCAAACAAACAAAACA	CTCCTGGCCGTACGATTAAA	254	BM1380	5	4.8			
RCS6615	LG1	73.55	BB920170	B	ATC	20	TCCAATTTCTCCACTCTCACA	GATATCAGGGTGGCATCGTT	171						
RCS3233	LG1	73.78	BB940034	A	AAT	21	AGGTGGTGGAAGTGGAAGTG	GTTGGAGGGAGAGAGGGAAT	239	TM1534	2	39.6			
RCS6481	LG1	74.73	BB919405	B	AAAT	16	TTGTCTGACATGATAGGGTATTTGA	CAAGCCAATTATCAGCACCA	269	TM1466	5	7.6	mth2-24d19	5	0
RCS3152	LG1	75.05	DE231458	D	AAT	15	CCTGGCATCTGTCATTTTCC	AAATGGTCGCCGTTGTAAAG	295						
RCS2764	LG1	75.92	DE223696	D	GGT	17	TTCCATTGTTAGGGTTTCCG	CGTAATCGGTGCAAGGAGAT	101				mth2-31g22	1	19.2
RCS1982	LG1	76.01	DE221166	D	AAC	22	TTTTGTTCATCATGGATGGC	TGAAGGAGTTGTTGGTGCAG	128				mth2-25c14	7	22.6
RCS6754	LG1	76.75	BB922447	B	AAC	21	TCTTGTTTGCTGTGTGCCTT	ATACGATTGCGACAACACCA	166	TM1382	5	10.5			
RCS6631	LG1	76.78	BB921085	B	AAC	21	AAGCTCGTGTTTGCTGTGTG	CCAAGAACGTGAGCAACGTA	153	TM1382	5	10.5			
RCS5648	LG1	76.83	BB914512	B	AAAC	16	GGATGGAACCAAAACTTTGAA	CCGGCAACGTATCATCTCTT	204	TM0847	2	0.4			
RCS4680	LG1	76.94	BB908995	B	ATC	23	TGACGGAGAAAGATATATCATCAA	AGCAGTGAGGGCAGTAGCAT	140				mth2-70c24	7	60

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS6742	LG1	77.08	BB922328	B	AAAC	16	GGATGGAACCAAAACTTTGAA	GTAAAGCCAGGGTGTCCTCA	295	TM0847	2	0.4			
RCS5197	LG1	77.28	BB912323	B	AT	16	TTCTCTTCTCTTCTCTATCAAGGTAGG	ATTTCCTCCACCACCATTCA	192				mth2-13c11	1	58.9
RCS1427	LG1	77.32	BB929306	A	ATC	17	TTTTCATCGCCACCTTTAGC	GATTGATGATGGGGATGAGG	198				mth2-48b19	1	58.2
RCS2236	LG1	77.37	BB934145	A	ATC	17	GTAAGGATGAAAAGGCGGAG	ATCCTCATCCGGAATAGCTG	134				mth1-51o19	ND	
RCS5326	LG1	78.13	BB913317	B	ATC	15	CAACTGGGACACCAACTCCT	TTGTACAGGGTTGGAATGGG	193				mth2-57e16	1	55.2
RCS6648	LG1	78.47	BB921380	B	AAAT	23	CACACACTCACACAATACACCC	TCGTGCTGTCTATGATGGGA	194						
RCS4000	LG1	80.11	BB904779	B	AAG	18	AACTGCAGACTACGCAGCAA	ACCTCAAAACTGCCTCATGC	300						
RCS4805	LG1	80.82	BB909872	B	AAG	15	CGCAGCAATACAAACAAGCA	CCACCTCAAAACTGCCTCAT	299	TM0344	5	12.1			
RCS2238	LG1	81.14	BB934168	A	AGC	21	TTTTTGAAAGTAGCCGGTGC	ATATGGCGCTACGTCAGCTT	189						
RCS2852	LG1	81.44	DE229941	D	GGA	15	CTTAACGCCACCCATCATCT	GTTGTGAGGAACCGGTAGGA	142						
RCS1673	LG1	81.45	BB932799	A	GGT	30	CCACCTGAATTGCCATAACC	GATCAGCACCAGGAAGTGGT	280				mth2-30o16	1	55.2
RCS2950	LG1	82.28	BB938064	A	GGA	17	AAAACAACCCAAAGCTGACG	GCCTGCTTCTCAACTTGGTC	285	TM0344	5	12.1			
RCS5058	LG1	82.94	BB911232	B	AAC	22	ATACTGCATCATTCCAGGGC	TCTGGTCCACCATCTCAACA	237						
RCS7142	LG1	84.09	BB927224	B	AAG	15	CGCTACTATGCTGCCCTAGC	CTGCTATTGTTTCCGCCTTC	233						
RCS1447	LG1	84.22	BB929660	A	GGT	15	ATTTCAATCTTGGGCACCAC	GTGGACACAAACGTCGTCAC	229	TM0096a	5	53.1	mth2-12n15	1	
RCS5971	LG1	84.99	BB915048	B	AAAT	22	TAAATCGTATTGGCCAGCCT	AGTTCGACGATTATGCGACC	202						
RCS7105	LG1	84.99	BB926762	B	ATC	24	ATCAGAGTTACCGGACACCG	CGATCGAATTGCAGAGAGGT	264						
RCS2918	LG1	85.08	BB937452	A	AAG	25	CGCCAATTTCATTGTTGGAT	GAGGTTTGGAGTGTTGCCAT	136						
RCS3438	LG1	85.30	DE235726	D	AAG	18	CTAACAGGGTGCGAAGAAGG	CCATGCGGTAATCCCATAAC	257				mth2-53p19	ND	
RCS1838	LG1	85.88	BB931708	A	ATC	21	TCAAGACGATGAACAAACCAA	GGATCGAAGGTGGAAGTGAA	108	TM1159	1	1.2	mth2-15j20	1	0
RCS1704	LG1	86.06	BB931175	A	ATC	15	GAGCCAACATCTTTTGGAGG	TCCAACACAATTGGTTCTGC	282	TM0909	5	21.9	mth2-109d3	8	50.9
RCS6085′	LG1	86.34	BB915857	B	ACT	18	ATTGGGTGCAGAAAATCAGG	TCATTGCCGGTGTATTTTGA	140	TM0456	5	10.9	mth2-21b7	1	50.9
RCS1863	LG1	86.67	BB932101	A	AAC	21	CTGAAAGCACAAGGCACAAA	TCAAGTTGAAGCGTTGGATG	201	TM0852	5	53.9	mte1-29a5	ND	
RCS4280	LG1	87.01	BB906599	B	GGA	18	AGCTTGGCCATTCAAAACTG	AGGTTGGTGAGGTCCACAAG	110						
RCS2268	LG1	87.57	BB934648	A	GGT	15	CAATCATCCAAGTGACCACG	CTTTGATTGCTTGGTGGGTT	195						
RCS5027	LG1	87.75	BB911046	B	ATC	28	AAACTCATCAACAATGGCGA	CTTTCTTTACCTTGGCAGCG	272	TM1159	1	1.2	mth2-15j20	1	0
RCS0838	LG1	88.23	DE216027	D	AG	17	ATGAGTAGTGCCTGGCTGCT	AGAAGAGGGTGTGGTTGTGG	243						
RCS0883	LG1	89.03	DE216510	D	AAG	21	CACGTTACTCAATTTGGATCTTTG	GAAGAGATAGCTTGCCTTGGA	157						
RCS0884	LG1	89.19	DE216538	D	ATC	15	ACTCCGAACCCAAACATCAT	TTGGATTTTGACGCATTTCA	203				mth2-6a23	1	1.9
RCS4399	LG1	89.26	BB907355	B	GGT	15	CGAACAAAACAATGGCAACA	CTTTGCAAGTGCTGCTTCTG	200	TM0963	5	49.5			
RCS6016	LG1	89.27	BB915377	B	GGA	18	CCTCCACCACCTTCACCTAA	AAGCAATGCACAACACTTGC	192				mth2-161i17	8	50.9
RCS6991	LG1	89.43	BB924955	B	AAT	21	GGGGAAAGAAACAACAAGAGG	ATGGCTATTCTTGCACCTGG	192	BM0976	ND		mth2-5e21	3	13.8
RCS2149	LG1	90.46	BB935107	A	GGT	15	GTGGACACAAACGTCGTCAC	ATTTCAATCTTGGGCACCAC	238	TM0096a	5	53.1	mth2-12n15	1	
RCS7000	LG1	90.74	BB925300	B	AAT	15	TGATGGAGAGGTTGATTACATGA	GGCCTAAAAGAAACTTGGGG	243	TM0096b	5	53.1	mth2-70b22	ND	
RCS3516	LG1	91.01	DE242945	E	AAAT	16	CCGATGAAAACTTCTAACATTGA	TCAAATTCAGTCAGCGGAAA	252				mth2-7m9	1	1.5
RCS3524	LG1	91.35	DE242955	E	AAT	15	TTCCAAGAGCAGCTTGCATA	TGAGGCTTTGAGCCGTTACT	215						
RCS6206	LG1	91.62	BB916771	B	AATG	16	GCCAATTGCCCACTTACACT	TAATTTCAAGGGATGGTGGC	147						

RCS1290	LG1	91.99	BB928984	A	AAC	16	CCAGCTTTCGCTTTCTTCAC	GGAGATCCGAATCAGACCAA	241	TM1598	5	30.3	mth2-17j9	8	65.3
RCS0089	LG1	92.01	DE244883	F	ATC	15	CAAACCAATGCCAACAACAG	AATGATGATTCCCGTGATGG	158						
RCS5759	LG1	92.04	DE239779	D	ATC	15	TGGAACAAATCATCATCTGGA	CCAAAGTGGAGTTTTAGCCC	297	BM1618	ND		mth2-24p23	1	2.2
RCS6958	LG1	92.13	BB925101	B	AG	37	TCAACAAAACACAAACCACTCTC	AGGGAGAAATGCCATGTGAG	115	TM0043b	5	51.1			
RCS1807	LG1	92.24	DE224368	D	AG	20	GAACCACCCTATTTCTTCATCC	CCATGAAGATGGTGGCTTTT	270						
RCS4301	LG1	92.37	BB906762	B	AAT	15	TCTTCCGAAACCAAAGGAGA	TTTTTCTTCCGTGACAAGGG	228	BM1617	ND		mth2-109d3	8	50.9
RCS2883	LG1	93.30	DE223579	D	AG	16	CGTAGCTTCTTTGCCGGTAG	GATGCTGTCAGCTCAAGGCT	114						
RCS6272	LG1	93.78	BB917418	B	AAG	15	TCATAAGCCAAATGAGCACG	GGATGGTTGTTCCTGATGCT	157	TM1165	2	41.6	mth2-155o19	1	4.4
RCS7210	LG1	94.03	BB928188	B	AAG	15	CACAAGACAAAGCGTGGAGA	TCATAAGCCAAATGAGCACG	239	TM1165	2	41.6	mth2-155o19	1	4.4
RCS5595	LG1	94.16	DE238732	D	ATC	15	TGAGGTTGGAAGAGGGAATG	CCAAATAGTTCCAAAGCCCA	218						
RCS2524	LG1	94.35	DE228280	D	GGA	15	GTAATCCACCACCAACACCC	CATCCAAATCAGCCAAACCT	249				mth2-37m7	3	72.5
RCS5704	LG1	94.45	DE239027	D	AG	15	TGAGTGCTGATGAGAATGCC	GCGCAACAACATCACCATAG	175						
RCS4351	LG1	94.53	BB907030	B	AAT	15	ATTACATGGACGGACACGGT	AATTGAAAACGGCTGGTGTG	242	BM1400	6	14.8	mth2-84j21	1	49.4
RCS3842	LG1	95.26	BB903661	B	AAT	17	AAGCACACGCTGGCAATAG	GCTCGAGTAAATGTCGAGGG	246				mth2-151m4	4	60.4
RCS7228	LG1	95.57	BB928474	B	AT	18	TCAACAATGTGGCTTCTCCT	AAGGTTCCCAACCCAATTTC	185	TM1096	4	66.6	mth2-19b12	ND	
RCS3161	LG1	95.90	DE230790	D	AATG	15	CCAATGCAAAAATCATCACG	GGTCTGGTTCTAACAAAGGTGAA	285						
RCS4501	LG1	96.06	BB908062	B	AAT	17	TTGTCCCTAATGAATTTCCACC	TGTGTTCCGACAAAAATCCA	222				mth2-151m4	4	60.4
RCS0810	LG1	96.15	DE215917	D	AATG	15	CCAACGTCGATACCCTCTTC	TCGAATGCAATCGTAAGAGAGA	188						
RCS5538	LG1	96.63	DE238137	D	ACT	15	TGGATTGTTGATTTGTTGGTG	TAGAAATTACCAATGGGGCG	146						
RCS5326′	LG1	96.83	BB913317	B	ATC	15	CAACTGGGACACCAACTCCT	TTGTACAGGGTTGGAATGGG	193				mth2-57e16	1	55.2
RCS5615	LG1	97.53	DE238880	D	AAG	17	TGATGGTGGTGAGTGGAGAG	ACGGCATGGTGGTTAGAGTC	164						
RCS3555	LG1	97.57	DE243162	E	AAAT	20	GCAAAAGATCCCGTCACAGT	CTCAGTAGCAGCACCACCAA	227						
RCS1456	LG1	97.63	BB929728	A	GGT	15	CGAATTCATGACGAGTGCTG	ATTAATTCCCTTCCCCCACA	194	TM0744	5	37.9			
RCS6128	LG1	98.16	BB916106	B	AG	16	TGTGGGGCACAATAGACTGA	GGATCTTTGCCATGTCAGGT	239						
RCS2682	LG1	98.59	DE229418	D	AAAG	16	ACGGTGTCAAATGAATGGGT	CGTACCCACCGTACAATTCC	153	TM1423	5	53.1	mth2-15h11	1	2.2
RCS1845	LG1	98.84	BB931756	A	AAG	18	GAGCCACCACTTCCATCTTC	TCCATTTCCAAGTCAATTGTTG	101				mth2-162b23	1	4.4
RCS3805	LG1	98.98	BB903332	B	GGT	15	AAGAGAGCCAAAACCACACG	TTGAATGATGGGTGATGATGA	273						
RCS6085	LG1	101.31	BB915857	B	ACT	18	ATTGGGTGCAGAAAATCAGG	TCATTGCCGGTGTATTTTGA	140	TM0456	5	10.9	mth2-21b7	1	50.9
RCS4235	LG1	101.41	BB906272	B	GGA	15	TAGAACTAGAACGGGTGGCG	AGGCAATCAATACCTGACCG	178	TM1667	5	13.4			
RCS5551	LG1	104.10	DE238340	D	AAC	20	ACAACTCTGCACCCTCTGCT	GGAAACTTCGAGGGAAAAGG	151						
RCS2923	LG1	106.20	BB937581	A	ATC	17	CCTTTCTGCTACGAACCTGC	ACACAACAAATCCCCAGCAT	200						
RCS0907	LG1	106.61	DE216761	D	AAC	15	ATTTGAGCACAAGGCCTCAC	TGGGGAAGTGAAGGATGTTC	206						
RCS5799	LG1	107.63	DE240096	D	AAG	73	CAAACAATTAGGGCGTGTGA	TCGATCCGTTCAGCTATTCC	289				mth2-34l12	1	60.4
RCS2393	LG1	108.27	DE226083	D	AAC	19	TTGTCCGAACGTAGTGTCCA	TCAAAGCGCTACACATTTGG	124				mth2-187h4	8	67.5
RCS5504	LG1	108.34	DE238028	D	AAG	15	CACCGGTGAAGTGCTGTTAAT	TTGATTCACGTGGTGTCCAT	173	TM0428	5	48.7			
RCS3797	LG1	108.50	BB903380	B	AAAT	16	CACGTGATATTTGCACCCAA	AATGCATGGGAGAGTGGAAC	285	TM1322	1	69	mth2-32m9	1	39.4
RCS3088	LG1	108.90	DE231932	D	AATT	15	AATAATGGGCCTTGTCGGTT	AAATGGCCCCTTTCTCAAAC	175						
RCS2107	LG1	109.20	DE224791	D	AGC	18	ACACATCAGGCATGGCTACA	TAAACCCAGTACGAGGCTGC	154						
RCS1257	LG1	110.74	DE218650	D	GGT	23	TCTCTTTTCACCATCCTGGTC	TTTCACCCACAAACCCATTT	153				mth2-15m12	3	69.6
RCS3233′	LG1	110.81	BB940034	A	AAT	21	AGGTGGTGGAAGTGGAAGTG	GTTGGAGGGAGAGAGGGAAT	239	TM1534	2	39.6			

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS5845	LG1	112.41	DE240701	D	AAAT	15	CCTCAAGGGTACTCGTTCACA	AGCAGTGATTTTCCCCACAG	298	TM1146	4	71			
RCS6509	LG1	114.68	BB919692	B	AAT	15	TTGGAACCCAAATAAGTCGC	TGAATTGCGCAAACTAGGAA	216	TM0221	1	67	mth2-65l2	1	61.9
RCS4212	LG1	118.98	BB906161	B	AAT	27	CAGAGCAAAGAGAGTGAGTGAGA	AGTTCCCCAACCTGAAAAGG	134				mth2-145p10	8	26.1
RCS6940	LG1	121.13	BB924425	B	AAG	15	GCCGTCAAAGCTCTATCACA	GAAACTGAAAAATACCAGATTGGC	150						
RCS4956	LG1	121.49	BB910490	B	AAAC	15	AAAATCAGACAAAACCTATGAAAAA	CTTTTTCTCCCCTTCCCAAC	272						
RCS3159	LG1	121.90	DE231678	D	AAAT	20	TGAGCAAACAGGATGTTGGA	TGGTTATTCGGCCTTTCTTG	291						
RCS2831	LG1	123.16	BB936420	A	AG	15	CGGAGTTGAGCTTGACAACA	GAGACTCCAAGTTACGCCGA	259	TM0852	5	53.9	mth2-20m5	1	46.1
RCS2598	LG1	129.51	DE222824	D	AAC	18	AAACTATCACGGGGAGGGAG	GCCGATGGATGTGACATTAAG	141						
RCS2059	LG1	136.70	DE222224	D	AAC	15	ATACAGTGCGTTGTTGCTGC	TGGCCAGAATCAATTTTACAGA	116				mth2-155o19	1	4.4
RCS1309	LG2	8.25	BB929069	A	GGT	15	TACGGTGGAGAATTGTGCTG	TCAATCCAATCCAATGAGCA	195						
RCS6935	LG2	10.05	BB924423	B	AAG	16	TTAACTAAGCAGTGTGGCGG	TTGTCGGGAACAACAACTGA	246						
RCS6718	LG2	10.20	BB922130	B	AAT	15	TAAAAATTCCTGGCTGTGGG	GAGGAGCATTGTGCAGTTCA	262						
RCS0130	LG2	10.55	DE246914	D	ATC	24	TTCTGGAGGAGAGCTCAAAAA	GTTGCAGCATTCACCGAGTA	190	TM0373	2	14.4			
RCS6428	LG2	10.56	BB918705	B	AAT	15	AAAAAGCTCTAACAATTCATTCAAG	GAGGAGCATTGTGCAGTTCA	239	TM0672	3	35.2			
RCS0262	LG2	10.56	DE213651	D	AAC	15	CCACAATGACGTCCACATTC	CCGAAGTCTGCAGTTCAAAA	225						
RCS3186	LG2	13.69	DE232636	D	AAAT	15	GCATATTTTATTCAGCTGAGGTTTC	GCAACCAGTGCATGTGGATA	289						
RCS4672	LG2	14.00	BB908896	B	AAG	16	GGTACTACAACTGCTGCCCC	TTTTTGCCCATTGAGGGTAG	294						
RCS1090	LG2	15.42	DE217787	D	AAT	16	ACCACCACCACATCCATCTC	AGTGTTTGTGTTTGGGCTTG	181						
RCS4591	LG2	17.00	DE236625	D	GGA	20	CATTCCTCCTGATCCCTTCA	CGGCTGATGTTATTTTGCTG	143						
RCS5305	LG2	18.53	BB913160	B	AC	16	CATTATGCCAATAAATTCATCCA	TGTGGTGTGTCAATGTCGTG	105				mth2-93e11	7	2.2
RCS6129	LG2	20.08	BB916135	B	ATC	18	ATGATCTTGACCGGTTTTGC	GCACCATTGCACCAATAGAA	229				mth2-48b19	1	58.2
RCS6698	LG2	23.29	BB921178	B	AT	22	TGGAATACAACAGAAAGGCCA	TGGTTGCAGATGGAAGAAGTT	170	TM1711	ND		mth2-66m17	1	58.2
RCS5657	LG2	23.54	BB914598	B	GGA	15	TGGAATGGAGATTCCTCGTC	ATCAATCCAATTCCAGCCAG	111	TM0522	2	58.2	mth2-8e1	ND	
RCS5208	LG2	24.61	BB912394	B	AG	27	TCCATCGTTTAAATCTCACGC	ACGCGCTTTTTCAAAACACT	190	TM0537	5	10.9	mth2-66m17	1	58.2
RCS2450	LG2	24.70	DE227281	D	AAG	16	GGAATGAAGATTGAGTTTTGGTC	CGGCACCCTCTCTTTGTTT	262						
RCS3322	LG2	25.01	BB939876	A	AG	26	TTCACAACTTGATCTGCATTCC	TGCAATCCAGCAAAGAATCA	197						
RCS2467	LG2	25.13	DE227368	D	GGA	15	CAAGCAGCAGAGTTTCATCA	AAGGCTAGGAGTGCTGACCA	96						
RCS5238	LG2	25.98	BB912642	B	AAG	21	GAAAGTGTAAAAGCAGGCCG	TTCTGAACCTTCTCCTCCGA	174				mth2-175h23	6	25.4
RCS0747	LG2	26.58	DE215600	D	AAG	15	GTACCGAATGCGGGAGTAGA	AACTTTCAATCAGCCAATTTTCA	151	TM1061	1	50.9			
RCS2889	LG2	27.47	BB936792	A	AAG	19	TGGCACCTATCTAACCCCAA	CGGTTTCCATGACGTGAAAT	159						
RCS3156	LG2	27.80	DE231554	D	AAT	32	CCTGCCACATCACCCTTTTA	GAAATTGAGCTAGTTGGCGG	168						
RCS3173	LG2	29.43	DE232238	D	AAAT	22	CGATGCTGCTGGTAAGACAA	CGCAAGGTAAAAGGCCTAGA	243	TM1504	2	43.5	mth2-24h22	7	71.4
RCS3456	LG2	30.37	DE235849	D	AAAG	23	GCTCACTGGTCCATTGCTTT	TTGCGATGAATGAATGAATGA	279						
RCS1678	LG2	30.94	BB932866	A	AG	28	GCTTCCCTTCCTTCCTCCT	GGCTTTGAGTTCAAGATCGG	216						
RCS0074	LG2	31.20	DE246023	F	AG	30	TGAAACCCTTCCCTCTTCTTTC	AGGGGGTCGTCTCGTTTTATG	173						
RCS7081	LG2	31.32	BB926508	B	AAT	15	CGGACTTTGCCCAAATACAC	TGAAGAAGCATATTTGTCGGC	241						
RCS6039	LG2	32.06	BB915586	B	AAAC	16	TGTGAAAGTAGTACAAGATGTACACAA	GGGTGATGCTTCTTTTGCAT	184				mth2-12k22	ND	

RCS1003	LG2	32.29	DE217390	D	GGA	17	AACAACACCTCCTCCAGCAC	GGAAAGAAGCAAAAGAAGCAGA	227	TM1713	4	9.6	mth2-22g24	8	59
RCS3537	LG2	34.10	DE243042	E	AAT	30	CATTTCCATCCACATCCACA	CCCAAATCACATCCAAACAA	157						
RCS2171	LG2	34.71	DE225240	D	AAC	15	TAACGAGCGCTGTTGAAGGT	CAAGCCCCAGTTCACTTCAT	236						
RCS6011	LG2	34.97	BB915287	B	AAAT	18	TCATTTATTTTGAAACGGATGAAG	ATGGGATGATGGATTCGAGA	118				mth2-156d20	6	31.7
RCS1708	LG2	35.66	BB931187	A	ATC	19	TGCCACTGAAATTAGCGATG	TCTTCAATGGCTTCCATTCC	202				mth2-9p17	6	34.8
RCS1864	LG2	36.08	BB932103	A	ATC	28	AACCCAACAACACCAACACA	CGTTTCAGAAGTGGCACTGA	173				mth2-9p17	6	34.8
RCS5476	LG2	37.37	DE237855	D	AAC	29	CGCAGTAGCTTTGGAACCAT	ATCACCGGACAAGAAACAGC	110						
RCS3817	LG2	37.70	BB903419	B	AATG	16	AAATCCCTAAATCCCCATCG	GACTGCGAGAGGTGAGGAAC	194						
RCS7050	LG2	38.30	BB925969	B	AAG	16	TTCTTCGCTCTCATTCCTTCA	ATGGCGAGCAGTTCTGTCTT	148				mth2-4g10	2	24.5
RCS5885	LG2	38.86	DE244122	E	AAT	15	TCACACTTCCATCATCCAACA	TGGGTTCGGTAGAAAGGTTG	127				mth2-10p9	ND	
RCS1300	LG2	39.85	BB929038	A	AAC	15	TATCTCCGTGGTCCTTCTGC	TGATGGTGAAGAGTGGCTTG	167				mth2-22l4	3	71.8
RCS1405	LG2	39.93	DE219972	D	ATC	15	ATGATCGCTGGAAGCTCAAT	TTCATGTTTCGGGTGTGGTA	202				mth2-52b4	3	63
RCS5590	LG2	42.11	DE238678	D	AAC	15	CATTGCATTTTTATGAAACCCT	TGTTGGGTTTGGTGGTTTCT	245						
RCS4683	LG2	42.76	BB909023	B	AAC	15	CACCAACATGTCTCTGGCAC	TCTTGAACCCTCACCAAAGC	240						
RCS2250	LG2	43.61	BB934298	A	ACT	15	GGACATCATGTTTCCTCTTTCT	ATGATGGAACAATATCCCCG	212						
RCS1113	LG2	44.20	DE217912	D	GGT	21	CATCCTCCAAAACCCTCCTT	TCATCATCATCACCGGAAAG	158	TM0490	2	8			
RCS5782	LG2	44.38	DE239918	D	AAAT	23	CGATCCTTTTAAGCTCGGAA	AAAGTGCCTGAACAATTGGG	127				mth2-12b2	3	63.7
RCS5686	LG2	45.14	BB914791	B	AGC	18	GCGATCCTTGTCTGCTCTTC	CTCCTCGTCTCCTCCTCCTT	104						
RCS6706	LG2	45.30	BB921192	B	AAG	19	CCACTCATCATCATCAATTTCC	ACGTTTTCCAAGCAGCATCT	169						
RCS1163	LG2	45.38	DE218148	D	AAG	15	TCATTCCAACAAATGGAACTGT	CAGGTCCCACACATACCACA	192	TM1305	1	0.8	mth2-134j11	3	65.9
RCS3251	LG2	45.81	DE234170	D	GGC	18	CTACCCTCGCAACAAACCAT	GCTCACGTCGTCAAGAATCA	113						
RCS4046	LG2	46.27	BB905099	B	AATG	36	ACATAAGCACGCTGCAAACA	TCCCGTGGTTTCTGGTTTAG	275	TM1492	2	48.2			
RCS4642	LG2	46.59	DE237070	D	AAAT	20	AAGGTTGCCAAACAAATTGC	ATCACCTGGGGATGTGTAGC	161						
RCS5303	LG2	46.66	BB913065	B	AG	16	ACCAAACCGAACCCTAGCTT	CGAGCTGAGAGAGCTTCGAT	250						
RCS5778	LG2	47.59	DE239204	D	AAAG	20	ATCTTCTATTTGCCCCACCC	GGTTTTGGTGAGGGTCATTG	210						
RCS1285	LG2	47.71	DE218981	D	AG	39	GATCCCCAACATCACCAATC	CAGACAAGGGTTGAGTTCAGTG	164						
RCS3673	LG2	47.91	DE243893	E	AAG	49	TGCTGCCACTCCTCTATTTG	GCCACCAAGTTTGAAGACCT	300				mth2-36g15	ND	
RCS6354	LG2	48.20	BB918142	B	AAT	21	GGGAGGAGCAAATGAAACAA	TGAGAAGCATGGTAAGCGTG	237						
RCS4572	LG2	48.67	BB908621	B	AAG	15	CAAAACGTACAAGTTTTTGTTGAA	GCTGCTTTGAATCCTGGAAC	113	TM0685	ND				
RCS1875	LG2	49.18	BB932160	A	AG	15	CCGGTATGAATATCGTCGGT	CGTTTATCTATCTTCCGGCG	91						
RCS5635	LG2	49.47	DE238654	D	AAG	15	TCCTCCCCATAATGATCAGC	ACTTGAGGCGCTTCTGTTGT	261						
RCS0562	LG2	49.48	DE214732	D	GGA	15	AATCACCGGTCACCACAAC	GGAGGACGAAGCAAAAATTG	150						
RCS3235	LG2	49.68	BB940106	A	AAAT	20	TTTAAACCGGTCATTCTCCG	TCCTGATACGCACCAAAACA	91						
RCS1165	LG2	49.99	DE218156	D	AAC	17	TTTGACGATTTTACATCGGTTG	GCCATGAAGGTCTCAAAGGA	92	TM0551	5	10.9	mth2-142i4	5	4.4
RCS1273	LG2	50.72	DE218890	D	AAC	15	CTGAGTTACCGGCAAACGAC	CCACCTCAGATTCTTCAAATCC	183						
RCS4208	LG2	51.06	BB906142	B	GGT	15	CGCGGTGGTTTTAAGTTTGT	AACCTTCACATTGCCATCAA	248				mth2-34i10	3	72.5
RCS7159	LG2	51.69	BB927469	B	AAG	24	TTCTCTCCTACCTATTATCCATCCC	CTCCCAAAATAGCGGTGAAG	262	TM0044a	4	50.7	mth2-14l3	ND	
RCS5695	LG2	51.70	BB914856	B	GGAT	26	CCCTTCTTCACCGACACAAT	CGTTACGGATCTCGGAGAAA	212						
RCS2536	LG2	51.81	DE228360	D	AATG	15	TTCCAAATATTTTAGATCATCGTCTC	CGTGCTTATGTACAATGGCG	290						
RCS3706	LG2	52.19	BB902761	B	AGC	15	AGGGTCACTTGTCCTTGGTG	GGGACAATCTTCGTGGAAAA	177				mth2-20m5	4	55.4

Table A1. Continued.

Marker name	LG	cM	Accession no^a	Library^b	SSR motif	Length^c	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size^d	Lj clone	chr	cM	Mt clone	chr	cM
RCS4089	LG2	52.55	BB905338	B	AC	22	TTTCAATCCAATTGCTGTTCTC	AGGACCACCGTACTCACCAG	249	TM0209	3	34.4	mth2-28m10	4	55.4
RCS0254	LG2	52.62	DE213712	D	GGT	21	TTCAACAAACTGGGTCAACG	GCCAAAGAGGGTAAGAGAGGA	155						
RCS4736	LG2	52.64	BB909402	B	AAG	16	TCAATTCGCAATTTGCTTCA	GATCCAACGCTTACTCGCTC	194	TM0521	2	60.6	mth2-104c10	5	8.4
RCS1209	LG2	52.64	BB928895	A	AAC	15	AAAATCCAGAAGCACGAGTGA	TGAACTTTGAAGCCACATTGA	247						
RCS5848	LG2	52.65	DE240757	D	AAC	15	CTCTTTCTTGCTTGCTGGCT	CAAGACGACCTGACGAAACA	272						
RCS3329	LG2	52.66	DE235117	D	AC	17	CTGAACCGTCATCGCCTAAT	TTCATCAAAACAAGAGCAGCA	208						
RCS4614	LG2	52.88	DE236795	D	ATC	15	TCCTTCAATGACATCGTCTCC	GCTCAGTCACTCACCGTCAA	96						
RCS1379	LG2	53.06	DE219527	D	AAC	16	TGGGGTTGAGATCCAAACAT	CCTGTTGTCAACGGATCCTAA	233						
RCS6396	LG2	53.12	BB918923	B	AAG	15	CCTTCTCTGTCTTTTCCCTTCA	ACGCAAAATCCTTGAACACC	164	TM0556	ND				
RCS2328	LG2	53.21	DE227924	D	ATC	22	CCAATGCACCAACAAACAAG	AGAGGGAAAGCAAAAACCGT	152				mth2-129l3	8	49.5
RCS0399	LG2	53.22	DE214175	D	AAG	15	GATTCTGGGAGAAGGTGAAGG	TCCACTATCCACCAACACCA	185	TM0161	4	24.4	mth2-49f2	8	38.3
RCS2382	LG2	53.51	DE225981	D	GGT	15	AGAGAGGATCGTGGCTTTCA	TATGGTCCACCGGCTACTTC	245						
RCS6096HR	LG2	53.51	BB915913	B	ACT	15	GTTGCAACGAAGTTCACGTT	GGAGTTGAAGACCGATTGGA	146	TM0559	2	58.2			
RCS3770	LG2	53.62	BB903174	B	ATC	15	TGGAACCGAAGTCATCTTCA	CCCCTCGAGAATTGTGAGAA	228						
RCS3722	LG2	53.95	BB902858	B	GGT	21	TAAGTGCCGGAAGTGAGGTT	AGTTGCCTTGGAGACGAGAA	156	BM1233	2	55.4	mth2-27m3	5	4.7
RCS4945	LG2	54.24	BB910380	B	AAC	15	CGTTGAAACAGCGTTGAAAA	TGGGTTTGTTTGAGGGAGAC	210	BM1206	2	54.5	mth2-17d19	5	5.2
RCS5299	LG2	54.35	BB913119	B	AG	18	CAAGATCTCTCTCTCTCTTTCTCTCTC	CCACTCCAGTGGTGCTGTAA	180	BM1362	2	59.8	mth2-16l23	5	3.8
RCS1501	LG2	54.64	BB930059	A	AAG	35	AGAAGGAAGCGTCGGTACAA	CAAGACGTCCACGAGCAATA	180	TM0123	1	0			
RCS5445	LG2	54.79	BB914304	B	GGT	15	AAAGGAGGAGGCTGTGTTCC	CCTTGCTTCAACCTCTTTGC	221	TM1134	3	76			
RCS0171	LG2	55.09	DE213376	D	AAC	15	TCGGCAAAGTTTTGTTGATG	ATCTGGGCCTTCTGATTCAA	234						
RCS0167	LG2	55.43	DE213379	D	ATC	15	TCTCCATTCCCATTCTTCCA	GACAAGACAATCTCCGATGACA	156						
RCS4626	LG2	55.58	DE236866	D	AATG	15	TGAAACGAGAAGACTGCGAG	AAGTCGAAATCGATGCGG	152						
RCS4513	LG2	56.20	BB908099	B	AC	16	TGGAGAACAAACAAATCCCAG	ATTTCGCCGTAAGATTGGG	186						
RCS0836	LG2	56.57	DE216051	D	AAC	31	TGTTTCCCAGTTGTTGTTGC	CACTCACTCACTCACTCCCATT	157						
RCS1477	LG2	56.75	BB929804	A	ATC	34	AGCTTCTTCTGCCTCCATCA	CCGTACATAGCCACTGCTGA	194	TM0309	1	49.3			
RCS6620	LG2	56.90	BB920870	B	ATC	31	CCAAATTCCTCTCAAACCCA	AAAGCCGGGTACTGATCCTT	246				mth2-31b1	5	7.4
RCS7186	LG2	57.45	BB927814	B	AAG	27	GCAACCTTAAAGGGTCCAAA	AATGGGAAAAACAAAAGCCC	266				mth2-31k24	6	31.7
RCS5470	LG2	57.48	DE237791	D	AAAG	19	TGGGGATTACCCCTAGCTTT	CCCCCTCGAGCTAAAACTTA	179						
RCS6654	LG2	57.75	BB921391	B	AT	25	AAATCCAAAATTGCACAATCG	AAGTTGGGGAAGAAAGGGAA	144						
RCS6283	LG2	58.12	BB917542	B	AAAT	16	AGCCCTGCTTTTTCTCCTCT	GCAGGGCTGAGACTCCAGTA	240	TM1492	2	48.2			
RCS1409	LG2	58.80	DE219930	D	ATC	17	TGCCCCTTTCTCTCTTCCTC	GGATTTGAGGTTGACACTTTGA	163						
RCS3241	LG2	59.74	DE234021	D	AAAT	20	CCCTAAACCCTTGCTTCTCC	CTCTTTCGGGCCAGTTTTTA	91				mtab-8d15	5	
RCS1402	LG2	60.02	DE219833	D	ATC	19	AAAAAGCAGAAAGCAATTAGATGAA	CGAGGAAGAGGGATCTGACA	95						
RCS3665	LG2	60.08	DE243861	E	GGT	15	CAGTCAAGCAGAGACGCAAG	CAACTTCAGAACCACCACCA	164						
RCS0251	LG2	60.74	DE213641	D	AAC	15	TCAAATCAAGTCACAATACAAAAGC	CATGCCAGAATCCTGATGTTT	91						
RCS5584	LG2	61.39	DE238607	D	AAC	18	GATCGAACCGGATGAAAGAA	AGCCAATCACTTCTTGACGC	248						
RCS3076	LG2	61.98	DE231719	D	AAAT	19	CGTCAACGAAACAACCAATG	ATCCACTAGTTGACGAGGCG	131				mth2-6c9	5	20.9

RCS7205	LG2	62.12	BB927980	B	GGA	15	TATCACACCCCATTTGGCTT	ATGATGGCAACGGTGGTAA	299				mte1-58k20	ND	
RCS2668	LG2	62.55	DE229259	D	AAC	15	AATCTTCCCCCTTTCTCACC	CCACCACCATCGAGAGTTTT	190						
RCS3190	LG2	62.68	DE232712	D	AAG	15	ATTTTGGTTTCCCCTGCTCT	TCTTCCGAAAGCACTTCGAT	121						
RCS7020	LG2	63.87	BB925519	B	AAAT	16	TCCTCCCTGCTGTCCTTTTA	AGGGACTTGGATTGGATCAG	140						
RCS4577	LG2	64.29	BB908020	B	AAG	18	ACTTTCTTCCCCCAAACACC	GGAACATTTGCAGGGAGGTA	164	BM1057	3	42.4			
RCS2199	LG2	64.65	DE225657	D	AG	15	AAAAAGAAAGCGTTAAAGGGG	GCATTGCCTTTTGCTTCTTC	190				mth2-9i24	5	20.2
RCS6389′	LG2	64.77	BB918488	B	AGC	15	GCTCGATTGGTAAGCTGAGG	CAGCTCATCCAGCTGTGAAA	221	TM0836	6	28.4			
RCS4871	LG2	65.78	DE237525	D	GGT	15	CACACATGGCTTGCAGTTCT	GAGGTTGGGTTTGGTGAAGA	122						
RCS2611	LG2	67.04	DE222975	D	ATC	15	TTCGATGAAGGAAGGGAATG	TGCTCCATGCTTTGAATTTG	159						
RCS4681	LG2	67.32	BB909020	B	AAAT	16	TGGTGAACCTTTGTGTGAAATC	CATGTCCGGTTATGTTGCAG	268	TM1505	2	41.2			
RCS3079	LG2	67.99	DE231842	D	AAAT	21	TTGACTGCTCCTAACACTTGGA	GCAATGGAACACCAAGACCT	183	TM1523	2	48.6	mth2-17i21	2	0
RCS0913	LG2	68.88	DE216767	D	GGT	15	CATCACCATACCCACCATCA	GCGGCTATGGGAACAATAAT	180						
RCS0412	LG2	68.98	DE214168	D	GGT	18	AAGATCGTGACACAATAGAATGAGA	TTCATTGCAACCATCACCAC	179						
RCS0898	LG2	69.99	DE216649	D	AAC	21	TCCAGATTTTAATGATGCAGTTTC	GAGGGTGGTGATATGCCTGT	154						
RCS5099	LG2	70.12	BB911585	B	AG	18	TGTTCCAGAAATTTCATTCTCC	CTCCAGCACCACAAGCATAA	277	TM0120	2	35.7	mth2-99p24	4	56.1
RCS2860	LG2	70.32	DE229922	D	AAT	21	GAAGCAAAGCTGTGAAAGGG	GAGAATCTTGAGTGTGTGAAGGTT	93						
RCS5441	LG2	71.18	BB914291	B	AGC	18	CCACAAGTGGAAGTGCTTGA	CTCCTTTGTGGATTTGGGAA	94	TM0120	2	35.7			
RCS0538	LG2	72.05	DE214624	D	GGT	21	TGATAGAGGCGGAACTTCTGT	GGGTTTTGAGATGGTGTTGG	186						
RCS7236	LG2	73.18	BB928635	B	AAT	21	TGCCACCCTACAATGTCAAA	TGAAGGAGAGGGTTGGAGAA	129						
RCS6472	LG2	74.57	BB919318	B	AAT	15	CTCCCTTTCCTATTGCCTCA	CCAGCTGATGCTGATTCAAA	202	TM0467	2	32.7			
RCS0855	LG2	75.29	DE216260	D	AAC	15	AAAAACTTCGCACCTGCAAC	CCACCTCAGATTCTTCAAATCC	160						
RCS2172	LG2	75.38	DE225246	D	AAG	16	CACATTCCTTTCCGATGCTT	GGCCAGTTTAGAATTGTGGC	298	TM0654	4	1.6			
RCS1871	LG2	75.94	BB932153	A	AAC	15	CTCGGAAGGAGCATGAACTC	AGTTGGAAGCATAAGCACGG	157						
RCS4943	LG2	76.65	BB910359	B	GGA	15	GGCATGTCCTCCAACTGTTT	GTTTGGTGATTTTGCGAGGT	212	TM0749	2	32.3			
RCS6719	LG2	76.67	BB922057	B	GGA	15	GGCATGTCCTCCAACTGTTT	TGCGCTTGATAATGCTTCAC	281	TM0749	2	32.3			
RCS0545	LG2	77.41	DE214661	D	AAG	18	TGTTCTTCCTCTTCTTGATCCTC	AATTCGGCAACCCTCTTTTT	165						
RCS2304	LG2	77.84	DE227019	D	AG	16	GGTAGTCATTGTTGTTGCTGC	AATCCGAAATCCATTTTCCC	161						
RCS5519	LG2	78.26	BB913593	B	AAC	15	CAGTGACTGGAGCTATGGCA	GATTTTGAGGCCAAAGGTGA	91	TM1368	4	31.9			
RCS0078	LG2	79.15	DE245157	F	AG	32	ATTCCCCCAATTTCCATCTC	TGCCCTGAAACCAAAAATGT	178						
RCS6496	LG2	79.42	BB919567	B	AAG	17	CCCAATTCCAAACCCTTTCT	ATCAGCTATGGATTCCGCAC	210	TM0041	6	33.7			
RCS1326	LG2	79.53	BB929118	A	GGA	16	TCCATTGCCCCTCTTGTTAG	TCCTAAACCCTCTGGTGGTG	183	TM0749	2	32.3	mth2-103j7	1	54.5
RCS1836	LG2	79.79	BB931675	A	GGA	15	TCCTAAACCCTCTGGTGGTG	TCCATTGCCCCTCTTGTTAG	183	TM0749	2	32.3	mth2-103j7	1	54.5
RCS2893	LG2	79.99	BB936924	A	AAC	15	CATCACCACGTTCGAGAGAA	CGCCAGGGAGTTGGTATTTA	291	TM0939	6	61.8	mth2-17k4	2	0
RCS4620	LG2	80.44	DE236824	D	AAAT	19	GTTCCAAATGGGAAGGGAAT	TGTCAATCCATTGCATACAACA	298				mth2-79e23	ND	
RCS2773	LG2	80.56	DE223806	D	AAG	30	AATAACAATATGCGGCTTTGC	GATTTCGATCCTCCTCCTCC	162						
RCS5836	LG2	80.86	DE240490	D	AAAT	24	ACGGATCTCAAAACGTGACC	GTTTTTGCAGCGGTTTTCAT	289						
RCS6096R130	LG2	80.86	BB915913	B	ACT	15	GTTGCAACGAAGTTCACGTT	GGAGTTGAAGACCGATTGGA	146	TM0559	2	58.2			
RCS6625	LG2	81.18	BB920939	B	AAAG	16	TCATCTTTGATGTGGACGGA	TACAGACGGCGAATCCTCTT	158						
RCS0909	LG2	81.41	DE216765	D	ACG	21	TTCTAAAATCGAAGCCTGGAAC	CAATAGCACGGTTCTGTTTCC	164						
RCS2195	LG2	81.96	DE225654	D	GGT	16	TCACCACATCCACCATCAAC	CTGAGCCCATGGCTAGAGAC	109				mth2-78b21	2	1.5

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS5681	LG2	82.04	BB914743	B	AAG	15	CATGTTCATCTTGCCCTTGA	TTGTATGTGGTTTTGTGGGG	225	TM1240	6	67.8	mth2-31j12	2	0
RCS0974	LG2	82.05	DE217215	D	AAC	16	TGGGAATGTGTTTATTATGTTTCTTT	TCCCTGAAAATTCACAATCG	241						
RCS5641	LG2	82.74	BB914436	B	ATC	18	TGAGAACCAACTTTCAAGTCCA	CCCATGATCCACTTGAGACC	194	BM1588	4	40.1			
RCS0075	LG2	82.97	DE245049	F	AG	20	AGAGGGTGTGGGAATGACAG	GTTGAGTGGCGTGGTTCAAT	193						
RCS1537	LG2	83.05	DE220097	D	ATC	22	CAAGAACCCCAACTCCTCAT	CCCATTCAACACACCCTTTT	239						
RCS4604	LG2	83.75	DE236757	D	AAC	34	AACAAGTCCTGGCTCGTATCA	GATGACCTGCACAGAAGCAA	122						
RCS3554	LG2	83.91	DE243120	E	AT	32	ATAAAAGAAAACGGCGGTGA	GAATCGGACCGGTCATTAAA	222						
RCS0715	LG2	84.43	DE215416	D	AC	15	CGATGTGGGACTTAAACACTCA	GCAGGTTGTGGTGGTCTCAT	150				mth2-14g3	8	46.6
RCS3144	LG2	84.51	DE231299	D	AC	15	GATTGATTGCCCAATTCCAG	TTGTGTTGCTGTGTGTGTGG	184				mth2-80i8	2	0
RCS1601	LG2	84.53	BB930692	A	AAC	26	TATTCAATCACCACCGCAAA	GCGTGCGAAAATGAAGAAAT	119						
RCS1748	LG2	84.93	BB931523	A	ATC	24	TTCTTCCGATCACGGATCAT	GAAGCTCACCCAACAAAGGA	266						
RCS1681	LG2	85.05	BB932902	A	AAC	15	GGACTCGGAAGGAACATGAA	GAAGCATAAGCACGGCACTT	152						
RCS2431	LG2	85.60	DE226426	D	AAC	15	CCAATCGAGGATGAAAGGAA	ACCAAAAACGCTAAACACGG	92						
RCS6389	LG2	85.67	BB918488	B	AGC	15	GCTCGATTGGTAAGCTGAGG	CAGCTCATCCAGCTGTGAAA	221	TM0836	6	28.4			
RCS5214	LG2	85.79	BB912428	B	AAT	15	ATTCTTCCATCCACACGCTC	TGGAATTTGTGCAGAAGCTG	275	TM1331	4	2			
RCS3328	LG2	86.32	DE235136	D	AAAG	16	CACACACACGTGAGTAGCCA	GATCTCCGCTCAGTTTCACC	229						
RCS4868	LG2	86.32	DE237530	D	AGC	24	GGTAAGCATCAGACGGCATT	TCCTGCCGGAGATTATTACG	290	TM0939	6	61.8	mth2-17k4	2	0
RCS6249	LG2	86.69	BB917085	B	AAG	15	AACTAGAGAAATTAGTAAAGGGTGTGA	TCAGAAGCATCAGGCACAAC	112				mth2-24f21	ND	
RCS4925	LG2	87.22	BB910198	B	AAG	15	AATCAGATTTAATCACACCTCTGTAA	AGTGAAGAACGGGAACATGG	202				mth2-11f14	2	0
RCS1325	LG2	87.30	BB929117	A	GGC	15	GCCATCAAAAGCATCGAAAT	GGCTTTTCCTTTGGCTTCTC	245	TM0841	4	1.6			
RCS3469	LG2	87.48	DE235975	D	AAG	15	GCTCTACAGAATTCGTCCGC	CCCACACACACACAAACACA	169	TM1055	4	41.7	mth2-18j19	4	35.4
RCS4669	LG2	87.96	BB908839	B	AAG	28	TCATCCCATGGCCTTATCTT	TGTGGTGGATTAAGGGTGGT	167				mth2-11f14	2	0
RCS1859	LG2	88.45	BB931941	A	GGT	15	GGTTTCAAAACAAACCACCAA	ATTGTGTTTCCACTCCCTGC	188				mth2-17i21	2	0
RCS3141	LG2	88.69	DE231267	D	AAAT	20	TCTCTCTCGAGGAATTAAACCAA	GTTGCGCAAGTTGAAGATGA	108						
RCS7094	LG2	88.87	BB926705	B	AAT	15	TGTGTTACCACACGCCAGTT	ATTACTGAGGGACGGGCTTT	108						
RCS0633	LG2	88.90	DE215058	D	GGT	15	AAACTGGCGACACAAAAACC	TGTTGGAGTTCGCAATAGGG	159						
RCS2468	LG2	89.06	DE227387	D	AAG	19	TCCAAAATGAATACAGAATCAGC	TGACTCCAACAAGGCAAGTG	101						
RCS6122	LG2	89.12	BB916073	B	ACT	15	CTTGTGTTCCCCAAAACCAC	AATCACCAAGACCGTGAAGC	136	TM0353a	4	2			
RCS2453	LG2	89.32	DE227330	D	ATC	16	ACACGTCAGCCAAACTACCC	TTGTCCAATGTTTAGGGACAGA	102				mth2-28o14	2	0
RCS3779	LG2	89.56	BB903293	B	AAG	21	CCGTTCCCGTTAAACTCAAA	GGACGGAAGCTATGACCGTA	169				mth2-5f21	8	33.9
RCS0003	LG2	89.73	AB234881	C	AAC	22	ACACACAATCCCCCAACAAT	GAGGAGGAGGTTGAGCGTTA	119	TM1536	4	3.2	mth2-21l2	8	70.4
RCS3269	LG2	89.81	DE234336	D	AAAG	15	CGCCGTGCTTCATAGGTAAT	GATTTTCTTGGGATGGCTCA	153						
RCS1310	LG2	90.29	BB929079	A	ATC	15	ACCCAACAAAGGATTGCAGA	TTCTTCCGATCACGGATCAT	250						
RCS6817	LG2	90.33	BB923249	B	GGT	18	ATGATACAACAAGCCCAGCC	TGTATCAAGGTGGTGCTGGA	274	TM0452	3	41.6	mth2-101n14	8	70.4
RCS1256	LG2	90.81	DE218713	D	AAG	15	AACCTCACCTCCTCCCTCTC	ACAGAAGAGCGTGGCTAGGA	201	TM1353	ND		mth2-23d6	8	70.4
RCS3218	LG2	92.00	DE234606	D	AAAC	16	GCCACTCCTGCAAAAACAAT	CATTGGCAGAAATGAAGCAA	290						
RCS3455	LG2	92.16	DE235802	D	AC	20	CGGCATATGACAATGGTTTG	TGCTAGACTCGGCACTTTCA	150						

RCS6330	LG2	92.18	BB917925	B	AGC	15	ACTCTGCAAATCCACTCGCT	ACCGTAACCGTCATCGGTAG	149	TM0043a	5	51.1	mth2-36n3	8	67.5
RCS6869	LG2	92.56	BB923769	B	ATC	15	TGCATTGGAGTGACTTTGCT	TTTTCGGATCAAGAAATGGC	272				mth2-5j2	8	68.2
RCS2991	LG2	92.69	BB938218	A	AC	34	TTGAGGGCAGCAAAAGAGTT	TTCTCTGGCTGAAGGATTGG	243						
RCS3275	LG2	92.82	DE234425	D	AC	18	TGATTCTTGGTGGTGGATCA	CCAAAACTTTAAAATATCATGGTCA	168						
RCS6909	LG2	92.92	BB924162	B	ATC	23	ATTCCAATTCCCCTTTCCAC	AATGCTGCTTCCTTCCTTGA	275	TM1055	4	41.7	mth2-12f13	8	65.3
RCS5473	LG2	92.92	DE237820	D	ACT	20	TGCAGATGGTTAAGCATGGA	ACCATGTCTGCCACAAACAA	275						
RCS3110	LG2	93.79	DE230738	D	AAAT	22	TCCCAAATTGGATGGCTTTA	TACTGCACACGTACCCCTCA	191				mth2-52p13	1	51.6
RCS4140	LG2	93.80	BB905688	B	ATC	35	GAATGGGGAAAGAGATCCGT	TGGAACATGGAACATGGAAG	272				mth2-36n3	8	67.5
RCS6607	LG2	93.99	BB920738	B	ATC	16	TTGTTCTACATTGCATCATAACAG	TTCGATTGCTTCACTTGCTG	259	TM1144	3	68.4			
RCS2229	LG2	94.39	DE226751	D	AATT	20	TGACAACCCCAATCAACTCA	ACGCCGCACATTGTTAGATA	273						
RCS3184	LG2	94.65	DE232532	D	AAT	21	TTTTTGGTGCATTTTTGTGG	GGCGCAACTTATTGTCCATT	272				mth2-2k12	8	33.9
RCS7075	LG2	95.38	BB926303	B	AAT	15	CAATTCAAAATAATCAACTTCCTCAA	AGGTGAAGGAAGTGCCAATG	134						
RCS4385	LG2	95.67	BB907275	B	GGT	16	GCAAAAGCAATTGAAGCACA	CGCCACCATTCTCCTTAACA	250				mth2-17n16	5	67
RCS2500	LG2	95.70	BB934981	A	AAC	22	ATGGATATCGGCTCCATCAG	GGTGTCGGTTGTTGTGATTG	275	TM0297a	4	40.9			
RCS4095	LG2	96.06	BB905394	B	ATC	15	TGCTTCACTTTCAATCCATCA	GGGAGTTTGAGGAGGAGGAC	185				mth2-11b3	4	56.9
RCS5459	LG2	96.06	DE237768	D	AAAC	16	CGCGCGAATGGAACTTATAC	TTCGTCGTCGATTACAGGAA	233				mth2-11k13	4	56.9
RCS1479	LG2	96.60	BB929808	A	AG	22	TTTTCTGGCGACGAATTAGG	ATCAACTCGATGGGAACACC	199				mth2-34h6	4	61.1
RCS4634	LG2	97.08	DE236930	D	AAT	24	CTTGTTTGGCCGTAACAGGT	GGAGACTGATCCCCACTGAA	154						
RCS5938	LG2	97.14	DE241677	D	AG	16	GAAGGTTCGAAAAGGCAGAA	AAAGGAACGGAAATCGAGGT	187	TM0227	4	14.4			
RCS2958	LG2	97.29	BB938059	A	AAG	21	GGATGCAAGAACAGATGGCT	GAAGAAAAATTCGACGGTGC	253	TM0303	4	40.1			
RCS5335	LG2	97.53	BB913398	B	AAC	16	CCCTCATCTTCCTCCTACCTG	AATTGTGGTGGAGTTAGCGG	104						
RCS6597	LG2	97.68	BB920605	B	GGT	18	ACCGATCAAGACCAATCCAA	GAAATAATGGTTCCGGCTCA	279	TM1055	4	41.7	mth2-12f13	8	65.3
RCS3145	LG2	97.89	DE231308	D	AACG	15	TGTTTTGGGTTTGGATCTTTG	CGCAATGAGTTAGCAGAGCA	125				mth2-12f13	8	65.3
RCS4756	LG2	98.18	BB909547	B	AAG	15	CAGAAACAGAGATCCATTGTTATTGTA	GGCCATTGATGGAGAAAAGA	174	BM1316	4	41.7	mth2-12f13	8	65.3
RCS1022	LG2	98.28	DE217438	D	GGT	15	CCATCCGCACCACTTTAGTC	GATTTGGAAAGCGGTCAGAG	180						
RCS0039	LG2	98.98	DE245310	F	ATC	15	AGTAAAGAGAATCATCTAAGTTGG	TCCAAGTGTGCTTGTAGCTG	166	TM1570	3	57.5	mth2-7g24	4	55.4
RCS2784	LG2	99.53	DE224052	D	AAG	31	TCTTCTTCAACCGAACAATTCA	TGCGCGAAAATTTTGATTTA	91						
RCS4012	LG2	99.54	BB904870	B	AATC	16	CATCTCCCACACACAACCAG	CGATTGATTTTGAAATGGGG	204	TM1067	3	32.8	mth2-5p10	4	55.4
RCS6676	LG2	99.57	BB921687	B	ATC	24	CTCTTTCACCGCCTTGAGAC	TGGTGGAGTTGTTTTGGTGA	161				mth2-36b12	8	69
RCS6551	LG2	99.64	BB920134	B	AAC	15	TCAGTGCAAGCTAAATGTCCTC	TGCTTCCTCGTCATCAAAGA	298				mte1-17c12	ND	
RCS3753	LG2	99.64	BB903081	B	ATC	15	ACATTTCCGTTGAAGGCAAG	ATCAGGTGGATGGCATGATT	226	TM0944	6	47.8	mth2-8m3	2	6.4
RCS6798	LG2	100.02	BB923075	B	AGC	17	TCTCCACCTAGTCCACCACC	CAATCAGGTTTCGGGAAAGA	260						
RCS3237	LG2	100.19	DE233912	D	AAAT	19	CGCCGTATCACAGATTCCTT	TTCAGTTCCACACGAAGCAG	247				mth2-99p24	4	56.1
RCS2193	LG2	100.30	DE225637	D	GGGA	20	CCATCAACACCAATTTCCCT	TTTGCGGTTTATGATGGTCA	173	TM0635	2	60.2			
RCS3095	LG2	100.51	DE230393	D	AAAT	28	GTGTTCCATTAGAGGCGGAA	AGCGGCTCGTTTTAATGCTA	208				mth2-26c3	7	60.3
RCS3102	LG2	100.80	DE230579	D	AAAT	28	AGCGGCTCGTTTTAATGCTA	CTTTTAGTGACAGGTTTGTATGTCA	163				mth2-26c3	7	60.3
RCS4982	LG2	101.34	BB910710	B	AAT	15	CTCAACTCTCGTTCCTTCCA	ACCAATTGAACTTGAACGCC	160	TM1744a	5	41.9	mth2-28o14	2	0
RCS4695	LG2	101.53	BB909079	B	AG	16	AAACAAATCCAGCACCGAAC	TTGGAGTAACCACCGTAGCC	197				mth2-15j7	2	1.5
RCS4993	LG2	101.81	BB910765	B	ATC	22	CACACTCACTCACTCTTTTCAGG	TGTTAAGACGAAGGGAACGG	155				mth2-36b7	2	0
RCS2689	LG2	102.25	DE229483	D	ATC	16	GATGTCGTTGTTGACGGTTG	CCACCATTCATAAGCCGGTA	220						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS6896	LG2	103.10	BB924032	B	ATC	17	TCAACCAAAAAGTCCCATAAAA	CATGGAACATGGAACATGGA	133				mth2-36n3	8	67.5
RCS7213	LG2	103.66	BB928238	B	AC	20	GAACAAATTCTGATTTACAGGGC	AGATGGATCAGGCATTGGAG	145	TM0018	2	60.6			
RCS4637	LG2	104.09	DE236984	D	AAAT	25	TGAGAGAAATACTTAAAATGAAAAGGA	TTGAGTGGCTGCGTGATTAG	208	BM1137	1	0	mth2-28n22	4	48.1
RCS6765	LG2	104.20	BB922567	B	AT	20	TGAAGGTGCCAATGTGAAAA	TCGGAGGAGTCACTTTTTGC	296						
RCS5747	LG2	105.60	DE239510	D	AAAT	40	AGCGGCTCGTTTTAATGCTA	GTGTTCCATTAGAGGCGGAA	220				mth2-28h7	ND	
RCS6014	LG2	105.62	BB915311	B	ATC	23	GACTGGGGAAAGAGATCCGT	AACATGGAACATGGAAGATGC	257				mth2-36n3	8	67.5
RCS7062	LG2	106.62	BB926171	B	AT	22	CACTCCCTCACTCTCACTCTCA	TGTTGGAAACCCCATTTTGT	171	BM1174	4	62.9	mth2-77n20	ND	
RCS5462	LG2	106.68	DE237778	D	AAAC	16	TGCTTCTTTGGTTTGATTTGG	TTAGCAGGGAGAAGCAATCA	202						
RCS3961	LG2	106.73	BB904511	B	AT	33	ACTTCGGCCAAAGCCTTATT	GGAGCTTGGTGTGCAAACTT	234	TM1331	4	2			
RCS3259	LG2	107.00	DE233676	D	AAAT	19	TCACTAAACCCTTTCCTGCG	CTTCCTTCTGTTTGGTTGGC	100						
RCS3245	LG2	107.25	DE234017	D	AAAT	26	TGAGCACTCGGGTAAAAAGG	GCCTTCCCATTGCTTCAATA	154						
RCS6315	LG2	108.40	BB917771	B	AT	48	GCAAAGGGACAGGTGTGTTT	TCCATACTTAAACTTGGCAAAGTAAC	275	TM0387	4	47.9	mth2-56f20	8	70.4
RCS5730	LG2	108.64	DE239362	D	AAAT	28	CCTAAGGCAAAGGCAAACTG	CTTGTTTGGCCGTAACAGGT	268						
RCS2087	LG2	109.70	DE224633	D	ATC	15	CATTGCGACCGAACTATGAA	CCGTAAAATTCTTATCCATCATCG	136						
RCS6074	LG2	110.42	BB915775	B	ATC	18	GATCAAAACCATGAGGACCAA	CCCATGATCCACTTGAGACC	205						
RCS1478	LG2	111.16	BB929805	A	AAC	22	CGTTCACACAAACAAAAAGCA	TGCAGAAGTGTCGTTGAAGC	250	TM0297a	4	40.9			
RCS3744	LG2	111.95	BB903014	B	AAG	18	ATTCATTCATGGCTCCCAAT	TGCAAGCTGAGAGAACGAAA	298	TM1643	1	67.8	mth2-34h22	ND	
RCS2533	LG2	112.59	DE228389	D	GGT	16	TGGGAGTACGTCCCTTATGC	TTAGGTCGGTGTTTCTTCCG	117						
RCS0453	LG2	113.32	DE214280	D	AAG	15	TCGCCACAAGGTCTCTTTTT	CGCTCTCTCTCTCTGCTTCA	189				mth2-28e9	5	0
RCS0978	LG2	116.49	DE217226	D	GGT	15	GAGCAACTTGCACAACAGGA	ATGAGAGGTTTGGGGATGTG	162						
RCS3355	LG2	118.59	DE235375	D	AC	15	TTCACTTTGTTTATTTGAGAGAGTTT	TAATCACACACACACCCCGT	107						
RCS1935	LG2	121.59	BB933439	A	ATC	23	TCTGCCACCACAAAAGTCAG	TCTGATGAGGAAGACGCAGA	298				mth2-23e14	ND	
RCS4795	LG2	121.97	BB909825	B	AAG	16	CTCCAGAAAGAAAGCGATGC	AGAGTGCGGTGAATGAAACC	196	BM1560	6	68.6	mth2-63e12	ND	
RCS0606	LG2	123.94	DE214981	D	GGA	30	TCGGTATTGCAAACATCCAG	GGGACCATCCAAGTGCTAAA	190						
RCS1207	LG2	124.34	BB928891	A	AAG	17	AGAAGGTTGGGGGACTTGAC	GGGACAGGATCGCATTTCTA	235				mth2-28o14	2	0
RCS0753	LG2	125.93	DE215587	D	GGA	35	CCTCTTCATCCTCTATCTCCTCCT	TTGTTTGGTTTCTTCAACTGTGA	92						
RCS1588	LG2	126.13	BB930572	A	GGA	30	TAGCTTTATCCCCAGCCTGA	GGGACCATCCAAGTGCTAAA	276	TM0018	2	60.6			
RCS2144	LG2	127.33	BB934976	A	AAAC	15	TGCAGCTCCCAATTGTTAAA	CCCTGAGCTCAATGGAGAAG	146						
RCS1382	LG2	142.99	DE219555	D	AGC	15	CCCAAGTCTCTCTCTCTCAACC	GATCGTTGAAGAGGTCACGA	161						
RCS1281	LG2	149.69	DE218987	D	GGT	15	CTCTTCTCTCTTCTCACCACGA	CTGCAGAAGCCAAACTGAAA	155						
RCS3554	LG3	0.00	DE243120	E	AT	32	ATAAAAGAAAACGGCGGTGA	GAATCGGACCGGTCATTAAA	222						
RCS5760HR	LG3	2.15	DE239744	D	AAG	15	GGTGTCCAACACTAGCACGA	TCCGGGTGAAGGTGTCTAAC	291	TM1291	4	60.9			
RCS6761	LG3	6.80	BB922544	B	AAT	27	GCTAACTGCAAACTGCAACG	ATGGCAGTGAGGGCTAAGAA	104	TM0042	4	71	mth2-9b23	4	61.1
RCS6001	LG3	8.64	BB915261	B	AAC	43	TCATTGTATAAATAGGAACCAGCAA	AATGGTGCAGCAACTGAACA	239				mth2-14d10	4	52.6
RCS5144	LG3	11.36	BB911980	B	ACT	15	CATTTTGCCCACCACATAGA	AGCCCATATTGGATGCAAAG	286	TM1286	4	69.4	mth2-20m14	8	49.5
RCS1627	LG3	14.93	BB932420	A	AAC	15	ATTCCCTTTCTTCTCCGCAT	GCTGTTAACGCTCAAGCTCC	246	TM0922	4	65.4			
RCS4864	LG3	16.86	DE237445	D	GGA	15	CTAAATCACCGTCGGAATCG	GAAACTCCGAAGAAACTCCG	98	TM1317	4	60.4			

RCS5154	LG3	17.13	BB912034	B	GGT	17	CAAAATTCTTCAGCTTCATCCA	ACATTGTGGCGTGTACCAGA	131	TM1216	4	69	mth2-20m15	4	60.4
RCS6427	LG3	17.37	BB918704	B	AGC	15	GTCTTGAAAGGAATGGCTCG	GGGTTTGCTGTGTTCTTGGT	206				mth2-49l23	7	
RCS0294	LG3	17.48	DE213818	D	GGT	23	TCGTCTCTCTAACTTCCACCA	CCATGAGTTCCCAAGAGTTGA	153				mth2-9b23	4	61.1
RCS2629	LG3	19.10	DE228794	D	AAC	18	TAGGCCACATTCTCGTGACA	CTGCAACAGCCATTTTCCAT	218	TM0658	4	70.6	mth2-9n11	4	61.1
RCS5245	LG3	19.93	BB912687	B	AAT	33	CATGTCACAAGTTTCCACCG	TGGAAGAAAGAAGCACATGG	212	TM1749	4	70.6	mth2-69d7	4	61.1
RCS6527	LG3	20.12	BB919910	B	AAG	15	CAAATTCAGCTTCATTGCCA	GTGGGGTTGAGGAAAGTTCA	165	TM1146	4	71			
RCS3015	LG3	20.30	BB938601	A	AAC	19	GAGGTCGTCCCCCTAAGC	TGTGGGAGGAGGAGGTACAG	110	TM0107	1	59.4	mtab-58m19	7	51.8
RCS3587	LG3	20.85	DE243387	E	AAAT	19	TTTTGTGTAGGTGGGGGTGT	GGTTGCTGCAAATTTGGTTT	245						
RCS1332	LG3	21.38	BB929131	A	AAC	16	CTCAATTCACCAGCCTCCTC	TGTTGTTGTTGTGGTGGAAGA	172				mth2-9b23	4	61.1
RCS1667	LG3	21.91	BB932824	A	AAC	15	AAACCAAAATGCCACGAAAC	TTTCTGAGTTCTTGCAGCGA	238				mth1-7g13	ND	
RCS4622	LG3	22.15	DE236881	D	AAT	20	AATCAACGTGCATGGAACAA	GCATCCAGTGTTGAAGAGCA	185	TM0617	4	68.2	mth2-24g3	4	60.4
RCS5926	LG3	22.28	DE242039	D	AAC	23	TCTCGACACTACTACTACTGCTACTGC	AGCCAGCATTGGAGACAGAT	176				mth2-9b23	4	61.1
RCS3381	LG3	22.61	BB940319	A	GGT	16	AAGAGATGGGTCATCGGTTG	ACTCCTCCTCCTCCTCCTCA	247						
RCS6204	LG3	23.83	BB916799	B	ATC	15	CCAATGAAAGCATCGGTCTAA	CAGCAACTTTTTCAGCCACA	270				mth2-9b23	4	61.1
RCS2857	LG3	24.20	DE229884	D	ATC	15	AACTATCATCATCGTCGGCA	TGAAGATCGGGAGATTACGG	191						
RCS4110	LG3	24.20	BB905511	B	AAC	15	ACAATGAGAACCCAACGCTC	AGTTGGCCTGGATTTTGTTG	236	TM1286	4	69.4	mth2-16a10	8	63.7
RCS4470	LG3	24.65	BB907799	B	GGC	18	GAAGCAAACGAAGCTTCACC	GACCCACCAATCATTCCAAC	197	TM0844	4	58.8			
RCS2741	LG3	24.66	DE223321	D	AAC	16	CTGTCCAATCACCAACCAAT	CCGTTCCACATGTGAATATTTTT	133						
RCS6010	LG3	25.71	BB915286	B	GGT	15	CTTGTGAACAAAGCTGCCAA	TTAGCGGTGTGCACATGATT	238	TM0922	4	65.4			
RCS5033′	LG3	25.96	BB911101	B	AAG	15	ACAGCAAAATCCCAAACTGG	GTGAGGAGAACAACGCCATT	269	TM0844	4	58.8	mth2-15m12	3	69.6
RCS6098	LG3	26.57	BB915932	B	AAAT	16	CATAGAAACAAACTTTGATACATCTGA	GCCAAATGATGAATGGCTTT	196	TM0552	4	52.7	mth2-35e5	4	58.3
RCS3657	LG3	26.74	DE243780	E	AATG	16	CGAATGTCCAGAAGAAAATGC	ACAATGGCGTTTCCAGCTAC	171				mth2-7g7	ND	
RCS2449	LG3	27.35	DE227275	D	ACT	21	GAAATTGAAAGGGCACGAAA	TGACAATTGGCCACCATAGA	108						
RCS6848	LG3	27.64	BB923568	B	AAT	15	GAAGATTGGAAATGACCCCA	GGCCACTTGCCAACAATTAC	233	TM1317	4	60.4	mth2-14h5	ND	
RCS5760R130	LG3	27.85	DE239744	D	AAG	15	GGTGTCCAACACTAGCACGA	TCCGGGTGAAGGTGTCTAAC	291	TM1291	4	60.9			
RCS3048	LG3	28.02	BB939096	A	AAG	19	CACGAGGCTCCTTCATTCTT	TCAGAACCCAATCCACCTTC	271	M1120					
RCS7110	LG3	28.64	BB926781	B	GGA	15	TTTGACGACAAAGACACCCA	GCAGTGGCGTTACAGTTGAA	120				mth2-24n16	ND	
RCS5230	LG3	29.07	BB912603	B	AAG	15	CCTTTACCTGCTGCTGCTCT	GAGAGGCCATGGTGTGATCT	172	TM0558	4	60.9	mth2-20g20	1	2.2
RCS3057	LG3	29.65	BB939290	A	GGT	16	GGCACGAGGCTCCTTTCTA	CTTTGCTCACTCTTAGCGGC	167				mth2-31d18	6	1.4
RCS1924	LG3	29.72	BB933342	A	ATC	17	GCTTCCAGAAGAAGACGACG	TTCTGCCTCTTCCTTTTCCA	203	TM1246	2	60.2	mth2-78c9	4	59.7
RCS1007	LG3	29.95	DE217381	D	ATC	15	TTGTCCCAATCCAAATCTCA	AAGGAAAAGCAAAAAGGACCA	230						
RCS6548	LG3	29.98	BB920157	B	GGA	21	CCTCCTCTTCCTCCACCTCT	GAAAATTGTGGGAGAGGCAA	125	TM1498	6	68.6	mth2-24n16	ND	
RCS4479	LG3	30.02	BB907868	B	AAG	15	CTGCTGCTGCTCTTCCTCTT	GAGAGGCCATGGTGTGATCT	168	TM0558	4	60.9	mth2-20g20	1	2.2
RCS2343	LG3	30.25	DE227954	D	AC	35	CGATTGCTACAAACACAGCC	TTCAATCGGGAGTGTCAGTG	139						
RCS5033	LG3	30.39	BB911101	B	AAG	15	ACAGCAAAATCCCAAACTGG	GTGAGGAGAACAACGCCATT	269	TM0844	4	58.8	mth2-15m12	3	69.6
RCS6683	LG3	30.94	BB921740	B	AT	26	GGAGCTTCTTTGTGTTATTGTCTT	TGCATCTGCTGAAACTGGTC	282	TM0032	1	1.6	mth2-7h7	4	58
RCS1999	LG3	31.00	DE221402	D	AAC	19	CCCACCCAAATAAAAACCCT	AAAATCCCCCTCTTCTCTCG	184						
RCS4988	LG3	31.36	BB910743	B	AAAG	16	AACAATTCACAATTCCTCGC	AGTGAGGGACAAGTTGACGG	186				mth2-78c9	4	59.7
RCS3858	LG3	31.61	BB903773	B	AAAT	16	TGGAAATTTCATGCTTGATAAAAG	AACTTTTCCAATCCCCCAAC	110	TM0322	1	67.4			
RCS6455	LG3	31.92	BB919157	B	AAG	15	TCAACCTTTCATCTCCGACC	GAATCGTCTTCGCCATCTTC	292				mth2-4j24	3	62.9

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS5781	LG3	32.25	DE239513	D	AG	16	GATCGATCCGAAAACCAAAA	TGCCATCGAGAGAGAAGGTT	199				mth2-80k8	4	58
RCS5765	LG3	32.39	DE239877	D	AAT	23	AGTGGCACACCAAGAGAAGAA	TTTTGTTGCTAGGCACTCCC	287						
RCS4596	LG3	32.60	DE236705	D	AAG	25	AATTTGAAGCTTCCACGTCAA	AACCGAGTCAAAGTGATCCG	193						
RCS2010	LG3	33.26	DE221654	D	ATC	15	GCTTCCACAGTTTTTGCTCC	GAACCTGCACAACCAAAGGT	137				mth2-47l12	4	59
RCS1735	LG3	33.43	BB931448	A	AAC	15	CCTGCTCCGTACCATTGTTT	GGTGCTAGCTCCAACCTCAG	189						
RCS7219	LG3	34.24	BB928256	B	ATC	21	GGGGTCACATTCATGAGGTT	TGGCTAACTCCGTCCTCCTA	262						
RCS6455′	LG3	34.29	BB919157	B	AAG	15	TCAACCTTTCATCTCCGACC	GAATCGTCTTCGCCATCTTC	292				mth2-4j24	3	62.9
RCS6318	LG3	35.26	BB917801	B	AAAT	16	TCACTCCACAACCCAAACAA	GCATCTTTATTGGGCCAGAA	218				mth2-28o14	2	0
RCS4358	LG3	35.43	BB907057	B	AAT	18	GAACATTTCCCACCCAAATG	TGAAATGCATCCCAGTTGAA	292				mth2-16l23	5	3.8
RCS3947	LG3	35.86	BB904358	B	AAG	15	GGAACCATCCCAAACCAGTA	CTCGCATGTACTTTCGCAGT	294						
RCS6026	LG3	36.31	BB915499	B	AAC	21	AGAAGGGCCAGAATCAGACA	TTGCAGCCTGCTCTTAATCA	191				mth2-2b2	3	62.9
RCS5159	LG3	36.52	BB912089	B	GGA	15	TCAATCAACCTTCCACCTCC	CTCATCACCAACAAACACCG	152				mth2-36p23	4	58.3
RCS3987	LG3	36.60	BB904662	B	AAG	15	CAACCGTGTTTCTTTCAAGG	AAGTACCATCGCATTTTGGG	243	BM1083	1	0			
RCS4825	LG3	36.82	BB909970	B	AAAG	15	TGCAATTTCAACGTTTGAGG	TTTCAGACCAACCAGGAAGG	280						
RCS1710	LG3	37.00	BB931200	A	AGC	15	AGCGCCCAGTATAAGGACAA	GTTCTGCTGCTGATGTTCCA	267				mth2-64b23	4	60.4
RCS4659	LG3	37.05	BB908668	B	GGA	15	TCAACGAAGAAGAGAGGGTTG	CAAGCGATTCAGACAACGAA	220				mth2-123c24	4	58.3
RCS6455‘	LG3	37.12	BB919157	B	AAG	15	TCAACCTTTCATCTCCGACC	GAATCGTCTTCGCCATCTTC	292				mth2-4j24	3	62.9
RCS2897	LG3	37.34	BB936998	A	AAG	26	AGCAGTCGAAACTCTTCACAA	GAAGGTGCGGTGAGAGAAAG	178				mth2-23d2	4	57.9
RCS0033	LG3	38.30	DE246375	F	AAT	39	AAATTATCATTTTGCAAATTTTA	GCAGATTATGAGGAATAACATTG	182	TM0265	4	7.6	mth2-113d3	4	
RCS7019	LG3	38.85	BB925488	B	ATC	17	AATCCACCAAACACACAGCA	AGATGAGCATCGTCGTCCTT	197	BM1751a	4	70.6	mth2-20m15	4	60.4
RCS4791	LG3	38.89	BB909786	B	AT	18	GGCTGAATATCCTCCGGTAA	TCCGTCTTGAGCTGAATGTG	282	TM1120	4	65.4			
RCS3353	LG3	39.47	DE235389	D	AAAG	20	ATAGACTGCCCCAACACAGG	TTGAATTTGGTGCATTTCTCTTT	251						
RCS2026	LG3	39.49	BB932363	A	GGA	15	CCCTTATCATCAGCCTCGAC	GGAGGAGGAGGAAGATTTGC	111						
RCS5821	LG3	39.74	DE240303	D	AAAT	23	CACGTAGCACCGATGATTGT	CCTCATGAACCCTTTTGCTC	234						
RCS6165	LG3	39.80	BB916551	B	AAC	15	ACATCGTTCCACACCCATTT	GTCGACCTCATCATCGTCCT	179				mth2-23a16	4	58.3
RCS0126	LG3	39.84	DE246778	D	GGA	17	CTCTAGTTCCCCACCCAACA	ATGCAATTCGGCAACAAAAT	216	TM0552	4	52.7	mth2-4c9	4	58.3
RCS3901	LG3	39.85	BB904050	B	AAC	21	AGAAGGGCCAGAATCAGACA	TGTGGTAGCCCCAGCTATTC	233				mth2-2b2	3	62.9
RCS0465	LG3	39.86	DE214359	D	GGA	17	ATGCAATTCGGCAACAAAAT	CTCTAGTTCCCCACCCAACA	216	TM0552	4	52.7	mth2-4c9	4	58.3
RCS2600	LG3	40.44	DE222918	D	GGT	34	TCTAGTGGGGGTGCAATAGG	TCACCTTCTCCTGCTCCTGT	94						
RCS3279	LG3	40.84	DE234533	D	AAT	17	TTTCTCTTGTTCCATTGGGG	CATTGTTGTCGCGGTTATTG	288	TM0162a	4	53.9	mth2-30e7	4	58.3
RCS2910	LG3	41.64	BB937235	A	AAC	16	AATCTGAAGGGGAAGTGGCT	GCACGAGGAAACACAACACA	262				mth2-10n2	3	70.3
RCS4887	LG3	41.80	DE236815	D	AAAT	24	GGCTTTACAGAAATCAGTAAGCAAA	TTTGAACTTTGAAGCCTTGTGA	97						
RCS3690	LG3	42.35	DE244035	E	AAG	15	ACACAACGCATGCAGACAAA	TGAAGCTCAGCTGCTTTCTG	153						
RCS1776	LG3	42.41	DE220982	D	ATC	16	TACCGCCAAAGACTTTCCAC	CGGATCCAAAACCCTGATAG	145	TM1576	ND		mth1-51o19	ND	
RCS2707	LG3	43.94	DE222436	D	AATG	16	AGTCGTGGATTGGAATTTCG	GATCCCCGTTGTTGAGTTTG	233						
RCS1952	LG3	44.57	BB933659	A	AAC	32	CATGGGCTGTGTTGATTGAG	CTGCAGCAACAGCAACAACT	210	TM0555	4	49.1	mth2-20b20	3	
RCS1068	LG3	44.58	DE217715	D	AAC	23	CTGCTGTTGTTGCTGTTGCT	TCAGTCTCAGGCTCAAACACA	175						

RCS4532	LG3	44.80	BB908316	B	AT	18	TGGTGCTGGAGCTAACATTG	CCTGATGCTTTCATCGTCAA	237	TM1865	ND		mth2-8d22	ND	
RCS3070	LG3	45.54	BB939414	A	AG	15	ATGCTTGTGCCCTAACCATC	TGGTGCTGGAGCTAACATTG	254	TM1865	ND		mth2-32k10	8	62.1
RCS1850	LG3	45.66	BB931870	A	AG	15	AAATGGATTTGGAGCTGGTG	TCGATCCTACTGGATGGGAG	179	TM0045	6	40.1			
RCS4600	LG3	46.45	DE236690	D	ATC	15	ACTTCCTCTCTCTCCGCCTC	TAAGGAAGGACGGGATGTTG	99						
RCS6448	LG3	46.65	BB919087	B	AAC	15	CTCACTTCATTGCACCTCCA	CCGGTGCCAACAACTTTATC	275	TM0577	4	5.6			
RCS6724	LG3	46.69	BB922184	B	AAG	15	CCTTCACATAAAACAAATGAGCC	TGTGGTGTTCAGAGATGGGA	147	TM1170	4	6.8			
RCS3821	LG3	47.43	BB903507	B	ATC	15	AACGTGTGGATCACAAATTCA	CCTGACAAACAAGGGGCTTA	259	BM1140	4	8.4	mth2-12n2	ND	
RCS4061	LG3	47.67	BB905165	B	GGT	23	ATCTTGTTGGACCTATGCCG	CTATCACCGTTGGCCATTCT	214	TM0172	4	26.6	mth2-85c24	ND	
RCS5901	LG3	47.88	DE244733	E	AAG	15	GAACCGTTGAAAATCGAGGA	GAAGAACCACAACGACGACA	146	TM0265	4	7.6	mth2-113d3	4	
RCS5810	LG3	47.90	DE240174	D	AAAT	20	ATTCATGTGGTTGGTGGTGA	TGCTTGCTGTTGCTCATTTT	216						
RCS4593	LG3	48.93	DE236672	D	GGA	15	CAACTCCATCCCCTTCAAAA	GAGGAGGAGGAGGAGGAAGA	136	TM0173a	4	26.2	mth2-27m3	5	4.7
RCS4520	LG3	49.06	BB908207	B	AAAC	20	AAGCTTCTTTAAATCAAGGGAACA	CGGATTACGAAATTGTGGCT	263				mth2-89c9	4	58.3
RCS6002	LG3	49.30	BB915275	B	GGT	20	TCCCAAATCCTCCTCACAAC	ATTCAAGGAGGAGGAAAGGG	155	TM1600	4	8.4			
RCS6248	LG3	49.95	BB917155	B	GGT	17	TAACCATGCTCCTCCTCCAG	ACCCATAACGGCAGAAACAG	130	TM1228	4	8.8			
RCS5593	LG3	50.12	DE238750	D	AAG	21	CCTCTCGCTCAGTTTCCATC	GCAGAAGAAGAGAGTGGGGA	190	TM0100a	4	8.8			
RCS6582	LG3	50.22	BB920461	B	AAC	15	CGGACTCGTGTCCATATCCT	AAGGCCAAAACTCATGGAGA	235	TM0577	4	5.6			
RCS1587	LG3	50.66	BB930560	A	ATC	15	TTCACACCAATTCCTCCTCC	TTCCAACCAAAAACTCCGAC	191	TM0480	4	8.8	mtab-58m19	7	51.8
RCS1839	LG3	53.02	BB931711	A	ATC	15	CGTGGCAGTTGAGATTGAGA	CCTGCTCCGTACCATTGTTT	235						
RCS4269	LG3	54.21	BB906530	B	GGA	15	ATCCTTCCCGTCTTTGGAGT	GGCAAAAAGGATCAGGACAA	216				mth2-15j7	2	1.5
RCS2645	LG3	54.75	DE228976	D	GGT	15	CGCCGCAGAATCTTTTTATC	AAAACCCTCCCACGAAAATC	289	BM0938	1	8.8			
RCS3914	LG3	54.76	BB904124	B	GGA	15	TTCAGGTGCACTTTCTGGTG	GGCAAAAAGGATCAGGACAA	270				mth2-15j7	2	1.5
RCS5866	LG3	55.54	DE241148	D	AC	20	GCTTGTGTATCCCTAAGTTCACG	GCATTGGTCGTAGGGTGACT	168	TM0365	3	10.5			
RCS3570	LG3	56.10	DE243256	E	AAAT	18	TTGACCATTCATTTTTCTGGG	TCCAACATCCAACCAAACAA	277						
RCS3348	LG3	56.38	DE235300	D	AC	16	CCAATTGTTGGTTCCAAATG	TGTTGTGGTTAGGCTCATGG	231						
RCS4484	LG3	57.17	BB907943	B	AAAC	16	ACCGAAACATCACACAGCAC	ATGGCCGGAGAGAAGAAAGT	115	TM0320a	1	1.2			
RCS6174	LG3	57.97	BB916633	B	AAAT	20	GCCATCCAGCAAAAGAAATC	GGGGCCATTCTTTACCAAGT	208	TM1443	ND		mth2-49e16	4	54.6
RCS6431	LG3	58.50	BB918757	B	AAAT	16	GGTCATGGCATGCAACAAT	GTCGAACCGTTGAGGAATGT	233	TM0666	3	5.3	mth2-9m5	7	55.5
RCS7187	LG3	58.56	BB927826	B	AAG	16	CTCATTTTGGGGCATTTTTG	CCGTCTCAGAACGAACATGA	295	TM0083	3	38.4			
RCS3811	LG3	58.76	BB903471	B	AAT	15	CGCAGGACCCATTTAGTTCA	TCCACTTGATGAAGCCATGA	294				mth2-31b9	4	52.6
RCS3586	LG3	60.07	DE243376	E	AAC	15	TGAAATTGGGAGTTGCATGT	TGAGGTCCTGAGTTCGATCA	218						
RCS1517	LG3	60.27	BB930045	A	ATC	15	CCGGAACTAACGGATCTCAG	GAAAATGCCAAAAGAGTCAACA	220	TM1266	1	48.7	mth2-14p3	4	56.9
RCS2481	LG3	60.53	DE227596	D	AG	15	TAAATTCGTCACCACCCTCC	ACTGAGGTGGAACAGGTTGG	226				mth2-168f23	4	58.3
RCS7241	LG3	61.08	BB928722	B	AAG	15	TTCAACATGGTTCTGTCGGA	TCAGCCGGAACTGATAATCC	196						
RCS4166	LG3	61.28	BB905860	B	AG	17	AAATTTCGAATCTACCCCCG	TCAACAAGGTTGGGTGTGAA	297				mth2-9b23	4	61.1
RCS2161	LG3	61.41	DE225123	D	GGAT	15	GTGGTGCCATTAGAGAGGGA	GAAAGAAATACAGAAATGTCACATGG	204	TM0032	1	1.6	mth2-20g23	3	69.6
RCS5755	LG3	61.85	DE239568	D	AAT	18	ATTCATTCACCCACCCAAAA	AGTCCAAGGGTGTGCATGTT	288				mth2-135i19	6	36.1
RCS6939	LG3	62.18	BB924492	B	AGC	15	GCTCTGAATGAGGCGCTTAC	GGCGTTACCATTTTGCTGTT	237	TM1217	3	77.2	mth2-16c13	4	49.5
RCS6239	LG3	62.34	BB917107	B	ACT	15	GCACTTGCTATAACCTAAACTTCTTC	ATGAGCACTTTCCCATCCAC	162	TM0641	2	37.9	mth2-7g24	4	55.4
RCS5254	LG3	62.40	BB912773	B	AAG	16	CTCTTCCCGCTCTTTTTCCT	TGTCTAACCAATGGCGATGA	192	TM0267a	3	77.2	mth2-36n9	4	52.6
RCS0967	LG3	62.40	DE217172	D	AAG	15	TCGGATATTACGGGTCCAAA	TCCCGGAGAGCTTCATATTC	150						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS5982	LG3	62.58	BB915146	B	AC	15	CAAGCAGACGCAAACTCTGA	GATTGTTGTGGGAGTGGCTT	196	TM1359	1	49.3	mth2-161d9	4	51.8
RCS6633	LG3	62.74	BB921164	B	ATC	20	TAGCTGCATCTGCAACAACT	TGTTCTTGTTGTCTTGGTGGA	226	TM0874	ND		mth2-21k24	4	49.5
RCS2960	LG3	62.99	BB938013	A	AAC	18	AGAGGAAGTGCAACGCTGAT	CACAACAGGAACCAGCAAAA	205						
RCS0894	LG3	63.26	DE216616	D	AAG	70	CCTCATCATCAAATTCATTCTCA	AGCCAGAACCAGAACCTGAA	156						
RCS6484	LG3	63.82	BB919427	B	ATC	20	TCACAAGTAACATGCAAAAGATGA	CCCAGTGTTGATAGTGGGCT	157	TM0460	3	81.6			
RCS0397	LG3	63.94	DE214144	D	AAG	21	TGCGTAGGTTGGAGTCCATT	TTCTTCATCCAGATCGTCCA	173	TM1574	5	42.3	mth2-13k5	ND	
RCS3336	LG3	63.97	DE235188	D	AAC	15	TGGGGATTTCGTGGTTTAAG	TCTTCTCAATTCCAGCCACC	125				mth2-14h5	ND	
RCS5236	LG3	64.21	BB912634	B	GGC	15	TTCCTCCTTCCTCCCATTCT	CCGTGTCCGTCATTACCTTT	262						
RCS7044	LG3	64.28	BB925860	B	ATC	18	TGCACTCAATCTGTTGATCCTT	TGGAAAAAGGTAGAGGCCAG	248				mth2-65k8	3	69.3
RCS5826	LG3	64.53	DE240394	D	AAAT	23	ATTCCCCAACTCCAAGGTTC	CGAAAGAGAACCGGAATCAC	291				mth2-165n2	ND	
RCS6415	LG3	64.95	BB918581	B	AAT	18	TCATCAATCATCAAACAAAATCG	TCACAGCTTGGTGAATTGGA	291						
RCS6919	LG3	64.98	BB924259	B	AAAT	16	CCGCACCCAAAATAAATGTC	CTACATGCAGCCAGTGTCGT	191	TM1395	1	1.2			
RCS0047	LG3	65.17	DE244840	F	AAAT	17	CTAGCCCATTTTGACAGCTC	GAATTTTCTCAAAGGTATATTGAC	130						
RCS6804	LG3	65.18	BB923133	B	AAG	16	AATTCCTGAGTGACCTTGCG	CAGTGGTTGCCATTGTTACG	221	TM0955	1	3.6			
RCS6126	LG3	65.36	BB916095	B	GGA	15	TTGATTCATGCAGGTCAAGC	GGGAAGAGTCTTAGGGGCAG	135						
RCS6722	LG3	65.44	BB922140	B	GGA	15	ATGTCCGTTGTTCTTTCCCA	GGGTGCCCAACAGAAAGATA	256						
RCS6771	LG3	65.51	BB922648	B	AGC	15	ATGATCCAAAACCAATCGGA	AGCTTAACGGTGGTTGATGC	238						
RCS1630	LG3	65.86	BB932488	A	AAC	15	CAATCTCTTCCCATCATCCG	TTGTTTTGAGTGCGTTTTCG	299	TM0460	3	81.6			
RCS3998	LG3	66.88	BB904777	B	AAAC	16	TCACTTACCGGTTTCGGTTT	ATGGCCGGAGAGAAGAAAGT	91	TM0320a	1	1.2			
RCS2377	LG3	66.99	DE225953	D	AC	16	CGTGCTCTCTGTTTCTCATCA	TTCATTTTGAAGTGTGTGAATGTG	123						
RCS4664	LG3	67.26	BB908719	B	AAAG	16	CACACCCAAGCATGAAAGAA	CGGATGAAATTGCCGAGTAT	138				mth2-64d17	3	69.3
RCS4623	LG3	67.73	DE236826	D	AAAT	20	GAAAAAGGGCGACAAACAC	GAGCAGAGTCCGGCTATGAG	215						
RCS4416	LG3	67.90	BB907476	B	AAAC	16	TCAGCTTTGAATCCTGACCC	ATGGCCGGAGAGAAGAAAGT	240	TM0320a	1	1.2			
RCS1067	LG3	68.01	DE217722	D	AAC	15	CACCAGGAATAGGCCACATAA	ATGGATTGAGTGGTGGTGGT	226						
RCS7203	LG3	68.07	BB928036	B	AAAT	16	TTGATTAGCACCGAGTAGAAACC	TGTGGCACCACATGTCTTTT	186						
RCS1008	LG3	68.36	DE217391	D	AAG	15	TCTCGTTCTCGTTCCCATTC	TGATTCACGCCAGATTCAGA	156						
RCS0193	LG3	68.79	DE213408	D	AAC	17	TACAACGTGCGCCTAAGACA	AAGCGAGACGTTTACGGAGA	212				mth2-9f16	3	69.6
RCS5823	LG3	69.00	DE240320	D	AAAT	36	ATGTATTGGTGTGCGTGCAG	TGGGAACAAAAAGGCAAAAG	205				mth2-7f22	ND	
RCS4897	LG3	69.44	DE237513	D	ACT	15	TGAGAGAGAAAGAGAAAAGGAAAG	GGTGCTAAGACCGAATACCG	209						
RCS1679	LG3	69.54	BB932890	A	AAG	19	GAGAAAGAAAAAGTAGCAGAGGAAAA	GGAGCTAGCTTCCGTTTGTG	107	TM0939	6	61.8	mth2-12b2	3	63.7
RCS2004	LG3	69.94	DE221532	D	AAAT	16	GCGGGGATGACAAAGAAGTA	CTGCCAAGGTTTGTCCATTT	143						
RCS4873	LG3	69.95	DE237563	D	ACT	15	CGGCGAAATTAATCCTCTCA	TGAGAGAGAAAGAGAAAAGGAAAG	237						
RCS3452	LG3	70.29	DE235770	D	AAAT	15	AGTGGAACCGACTTGATGGT	GTGTGTTGCTAGCACTCCTCT	147	TM1230	1	72.2			
RCS4657	LG3	70.47	BB907919	B	AAC	15	CAACAACAATGCTGCGAACT	CACCGCTACTACTTCCTGGC	119						
RCS2875	LG3	70.72	DE229988	D	AAAT	23	TGAATGTGTTTGACCACACG	CTTGAAGCACCATTTCAAAAA	244						
RCS1866	LG3	71.02	BB932055	A	AAG	21	GCAGCTTCCAGTAAAATCGC	GAGAGGAATCGGAGTGGTGA	294						
RCS6419	LG3	71.39	BB918614	B	AGC	18	TCATTTCTCTCACTTCCACTATGT	AATTGGTGCAGCCAAAGAAG	186	TM0359	5	45.1			

RCS3002	LG3	71.65	BB938392	A	ACG	15	CTACGGCGCGTCTTAATTTC	AGAGCATCAACTCTAGCACCG	139				mth2-22l4	3	71.8
RCS6538	LG3	72.17	BB920035	B	ATC	18	AAGCTAGCGGAGCAATACCA	TCCTCAGCAGCTGTCTCAAA	131	TM0258c	3	77.2	mth2-181h2	4	52.6
RCS3047	LG3	72.17	BB939089	A	GGT	26	TCAAGAATGGGTTCCGAAAG	ATGAGAAGGTGGTGGAGGTG	125						
RCS1865	LG3	72.28	BB932098	A	AAG	18	CCCAAACATGATTGATGCAC	TCGAGGGTTTCGTTTTTCC	91	TM1038	ND				
RCS7156	LG3	73.33	BB927391	B	AATG	16	TCCGCGTTTCCTTTCATTAC	TGAATCCACTTTTGCGTGTC	282						
RCS2574	LG3	74.13	DE222445	D	ATC	33	CAATGGTTTCCACAAAATTCC	GGTGTAGGAGGAGGAGGAGG	262						
RCS3175	LG3	74.88	DE232267	D	AAAT	22	ACATGGGAGCCTCATGGTAA	CGTATCAAAGGAGCCAGAGG	234				mth2-14m10	1	61.9
RCS5549	LG3	75.31	DE238283	D	AAC	19	TCTTCTCTTCAAAAACCACAACA	TCCTTCTTCATCGCCTTTTC	136						
RCS7144	LG3	75.47	BB927233	B	GGT	18	TGGCGAATGTAGCAGCTATG	TTGGTTCTGGAAATTCGGAG	184						
RCS2544	LG3	77.99	DE228415	D	AAAG	15	GGTGTGGTATCTTTGGTGTGC	GGTGTCGATGACTCCCTCTG	101						
RCS3659	LG3	78.68	DE243757	E	AAT	15	CTTGACACTCGAACAATTCACTC	GCATGCATGAGTAGAGCCAA	292						
RCS4753	LG3	79.33	BB909528	B	AAT	15	TGTTCCTTAAACTCTCTCTGTTTCA	TTGTGAAACCAAAGCAACCA	91	TM0014	6	8.1	mth2-25n18	4	61.1
RCS0404	LG3	79.57	DE214140	D	AAG	18	TGTCCCATCTTCATCTCAAACA	TTGTTGCAAAGATCGAGACC	151						
RCS6976	LG3	79.59	BB924768	B	AAC	15	CGCACACAGAAAAGAAAAGTG	TCTTCATGGGGTCCAATAGC	259	TM0321	5	53.1			
RCS3064	LG3	81.11	BB939322	A	AAC	17	TTGTTTGCAGAATCAAACCCT	AACAACAGGGACAGAGTGGG	291	TM1514	6	22.8			
RCS5081	LG3	81.15	BB911407	B	GGA	21	AAATCCACCAGACCAGTTGC	CGAGAGGCTCCGACAATTAC	141				mth2-60a22	3	38.5
RCS4240	LG3	81.95	BB906350	B	GGT	20	CACGACCATGTCATTTTCCA	ATTGGAAATTGCGGCATAAG	107				mth2-10n2	3	70.3
RCS5421	LG3	82.11	BB914129	B	AG	15	TTGGAGCAGATTTCCAATCC	TCAAAGAAGCAGCAAACCCT	187						
RCS2486	LG3	82.76	DE227645	D	AAG	15	CGACCAATTCAGGTTTGTGA	CCATTTCTTTGCTTTTTCTCCA	240						
RCS5069	LG3	82.97	BB911389	B	GGA	15	CATGTCATCTCCACCGACAC	ACGGTCGATGAGTTCGTACC	196	TM0935	1	67.4	mth2-12b2	3	63.7
RCS5913	LG3	83.11	DE241522	D	AGC	15	TAAGGGCTTCTCTGCGTGAT	TCCAGCCAATATTCAAGCAA	138						
RCS5972	LG3	83.94	BB915052	B	AAG	16	GGATACTCGAACACATCAACGA	TCAAAGGCTTCGACATCTTG	274				mth2-55b12	ND	
RCS6375	LG3	84.35	BB918359	B	AT	15	AAGAGGCTAGTTGAAGGGGC	GACGCGATTCTTTACAGGGA	294	TM0774	6	61.8			
RCS5732	LG3	86.34	DE239375	D	AAAT	27	AATGGACCGCCGTAAATATG	TTACACCAATCCGGATCCTC	287						
RCS6394	LG3	86.81	BB918538	B	AAT	15	AACCAAATGCCACTCTCACC	TTGTGATTTTACTGCATGTCAATG	182						
RCS6524	LG3	88.76	BB919845	B	ATC	19	AATTTCATGTGGTGGAAGCC	TGAAGGTGATGATGAAGTTGTTG	118				mth2-19c18	3	32.3
RCS5092	LG3	92.10	BB911564	B	AAG	15	TGGTGATGTGCACCATTAGG	TCCACGAAACCTGTTCCTTC	92				mth2-36n23	3	68.9
RCS5846	LG3	92.16	DE240744	D	AAT	25	TTGCCACCCATACCCTTCTA	TTGTTGCTACCACTTGCTGC	296	TM1051	ND		mth2-7h18	8	1.6
RCS1655	LG3	92.17	BB932652	A	AG	15	CACCGCTTCACCTCTCTCTC	CTGATTTGAATCGAGGAGCC	166						
RCS0899	LG3	96.15	DE216665	D	GGT	32	CAAACAGGGTTTGTTGCTGA	TGTTGTCAGGTCAAAGACTCAAA	227	TM0351	3	77.2	mth2-180a12	4	52.6
RCS0796	LG3	96.21	DE215870	D	GGT	15	CGATGTCTCTTTCGAGAAGATTG	TCCGATTACCACCACAATGA	104						
RCS5035	LG3	97.27	BB911105	B	ACT	24	TTCTTCCTCTGAATGCTTTCTC	TCTGAATGAACCCCAGAAGC	228						
RCS1526	LG3	97.71	BB930193	A	AAG	29	ATGGCTGTGTCCATTGGTTT	CCTGCTCCTTTCTTGTGAGC	209						
RCS0199	LG3	99.47	DE213437	D	AAC	17	AAATCGCCACAACACTTTACA	GTTTACCCATGTGGCTCTTCA	150				mth2-7h21	1	3.7
RCS5722	LG3	100.14	DE239235	D	GGT	15	TCAAAATCGAAAGAAACCGC	TCTGACAAGGTGGTGCAGAG	154						
RCS6832	LG3	101.04	BB923374	B	AT	16	CACAATGTGCATGCTAAAATCA	GGATTTGGGAAATGTTGGTG	194				mth2-5d16	3	0
RCS6623	LG3	101.13	BB920894	B	AG	15	TGTTCAAATCAATTGGGCCT	AGAAGTTTGAAATTCCCCAAA	111	TM0014	6	8.1	mth2-32f21	3	53.2
RCS7182	LG3	101.45	BB927751	B	AT	33	TATCCGAAATCGCCTATCCA	ATTTGCGCAGAGCATTTCTT	157				mth2-145c3	8	44.3
RCS4633	LG3	101.78	DE236917	D	AAT	22	CATCCCAAGGATGAGCTTGT	AGATGCTTAAAGTGTGCCCC	105				mth2-17p13	3	11.9
RCS6139	LG3	103.10	BB916266	B	ACT	24	TGATCAGCTTCAGCTATTCAAA	GGACATGCATTCCCTTTCTT	299						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS6258	LG3	104.61	BB917187	B	AAT	15	TGCTTTCTCTATGATCAGCTTCA	TGAACCACAGAAGCTTAAAAACA	208						
RCS3847	LG3	106.42	BB903706	B	AT	15	TCAATTGAAAAGAAATCTCTCACA	ATCCATTGCAGACCCAAAAA	223						
RCS3832	LG3	107.08	BB903594	B	AAG	24	AGTCTGGGAGGAAAATCGGT	AACCATCGACGAGGAACATC	160						
RCS3051	LG3	112.88	BB939218	A	AG	20	CACTCTCTCTCCCAAAGCCA	CAGTTGAAGCAGGTGAACGA	150	TM0083	3	38.4	mth2-7h1	3	1.5
RCS1303	LG4	0.00	BB929060	A	AAC	15	CAGCAATCCAACGTTTCTGA	ATCATCACCAGCTTCAGCAC	234	TM0453	2	72.2	mth2-123m17	8	50.9
RCS0992	LG4	8.20	DE217304	D	ATC	22	CAATTTCAACCATAGACATAAACCT	GAGGGTTTAGAAGAGCGAAGG	168						
RCS5727	LG4	10.26	DE239334	D	AAAT	18	ACCTTTCAACTGAGGCGAGA	ACCATGACCAAGACTCACCC	286						
RCS5460	LG4	12.67	DE237788	D	ATC	22	CAATTTCAACCATAGACATAAACCTT	GGGTTTAGAAGAGCGAAGGG	163	TM0453	2	72.2			
RCS3620	LG4	12.80	DE236558	D	AG	32	TTTTGAAGGAGATTTCTTTCTTATTTT	TCTCCTTTTCCAAACAACCG	192				mth2-14p23	1	2.2
RCS4189	LG4	15.05	BB906003	B	GGT	17	TGGGGATTTGCTGGAGTTAT	GCTGCTTCCATTTCCAGAAG	194	BM1341	2	72.2	mth2-28b24	ND	
RCS0923a	LG4	15.12	DE216962	D	ATC	16	TCACGGGCTACCTCAATCTT	TTGTTGCAGCTTCAAGATCAC	150				mth2-7g10	8	38.3
RCS4899	LG4	15.85	DE237601	D	AAAC	16	TTTGGTTCTTCCCTTTGTCG	TGACAGGAGAGGGTCAATCA	203						
RCS4625	LG4	17.56	DE236842	D	AAT	23	GTTGGCAAGAGATAATCCCC	GGGAGCTATTGTATGAGATTTGTTT	201				mth2-32m22	ND	
RCS2270	LG4	17.57	BB934694	A	AAG	15	CCTTTGCAGCCTCTTCAGAC	GAGGGGAATACGAGGAGGAG	177	TM0380	2	72.2			
RCS4310	LG4	18.31	BB906825	B	AGC	15	GCCATTGCTGGAATCGTAAT	GCCATTTGCTTCAACCTTGT	249				mth2-53o24	4	63.4
RCS6347	LG4	18.80	BB918087	B	AAC	15	GGTGCTTCTTCTTTTTCTTGTTG	CGAGGAGCATCTCCAACTTC	165						
RCS0440	LG4	19.59	DE214238	D	GGA	21	TTGAAGAGAACATCAAATCCTAAAA	GTTCATTTATTCATTTTATTTGTACCC	91						
RCS2598	LG4	20.15	DE222824	D	AAC	18	AAACTATCACGGGGAGGGAG	GCCGATGGATGTGACATTAAG	141						
RCS3477	LG4	20.52	DE236140	D	AAG	21	GCTAGCATCAGGATCAAGGC	CAGGTGTTGTCAAAGTACCACG	236	TM0932b	2	71.8			
RCS1647	LG4	20.84	BB932627	A	AAG	26	CCGGAACCGGTCACATATTA	ATCCTGCTGAGATGAAGCGT	273	BM1047	2	71.4			
RCS5015	LG4	21.47	BB910915	B	AAG	16	CTTCTCTTCCTTGCTGGTGG	GAGCATCATTTTCACAAACCAA	245						
RCS4268	LG4	21.93	BB906528	B	GGT	24	AAGAACTCGAAGAAGCTCGC	GCGAGACGGAGTTTCACTTC	212	TM1218	4	32.8	mth2-6k4	8	61.9
RCS3123	LG4	21.95	DE230918	D	AAAT	18	TCTCGTGGGCAGCTATTTCT	AAGACGCCCCTGGAGATAGT	181						
RCS5051	LG4	22.90	BB911276	B	AC	16	TCATGGCTACACATGCCAAT	CACTTTCTCCACCGGATGTT	113	TM1401	4	47.9			
RCS3160	LG4	22.97	DE230588	D	AC	16	TAATGTGTCTACCTACCTATCAACATC	TCATGCATTTTCTAAAGTCCTTTTT	140						
RCS1669	LG4	23.20	BB932835	A	AAC	15	TTTCCGATCGTTGTGATTGA	CTTCCAAACGACGCTTTCTC	156						
RCS1586	LG4	23.51	BB930558	A	AAC	19	CTTCCAAACGACGCTTTCTC	TTTCCGATCGTTGTGATTGA	162						
RCS1307	LG4	24.07	BB929066	A	GGGA	22	CCCTTCTAGCCTAGCAACCA	GCGGAAAAGATTCAGCCTAA	155				mth2-32k10	8	62.1
RCS3892	LG4	24.98	BB904024	B	AGC	24	GGCAAAGACCAATTTTCCAA	GCCTATTCACCGGAATCTCA	131	TM1285	2	67	mth2-135i19	6	36.1
RCS5521	LG4	25.04	BB913612	B	ATC	16	GCTGGAATTGGATACGGAGA	GTTGACCACAGTACCGCCTT	93	TM1248	2	68.6	mth2-133o10	5	77.4
RCS7023	LG4	25.20	BB925603	B	AAT	15	GAGCAGAAATTTCATCCAATATTTA	TCCAGGAGGAAGGATAACCC	244						
RCS5330	LG4	25.67	BB913363	B	AT	16	TGGAAAATGTTGCACAAACAA	AGTTAAGCGAGCGAAATCCA	212	TM1248	2	68.6	mth2-133o10	5	77.4
RCS4682	LG4	26.37	BB908950	B	GGT	18	AGGGATCATGTTACCACCCA	TGCCAGAGGCTAAAAATGGT	287						
RCS4874	LG4	26.87	DE237584	D	AG	18	AATCAGCAGGGAGAAGCAAA	CATCCCCTCTTTGTTGTTGG	211						
RCS5800	LG4	27.43	DE240054	D	AAT	24	AAACACAGCAACACCCAACA	CGCAAAACTTTCGTCCCTTA	221						
RCS6567	LG4	28.81	BB920350	B	AAG	15	GCTAAACCCAGAAACCACCA	TGCATCTCGTGCTGAGACTT	227	TM0793	3	0	mth2-62c22	8	59
RCS0869	LG4	29.68	DE216454	D	AAC	62	CATCTGGAGCATCCCTTTGT	GCATAAAGCCCAGACTCGTT	245	BM0532	3	14.9	mth2-26m10	8	1.6

RCS3709	LG4	30.16	BB902774	B	AAC	27	TTCATCTTTCTCAACTTCATAATCA	CTGGGCTTGAATGAATTGGT	278	TM0521	2	60.6			
RCS2558	LG4	30.17	DE228584	D	AC	16	AAGGAGAGCAGAGGAAACCC	CGTTTCATTCGCCGTTACTT	291						
RCS4453	LG4	31.99	BB907732	B	ATC	18	TGATTAAGGGCTTGCTCGAC	TGATCTCCGGAAACAACCTC	121						
RCS3730	LG4	32.54	BB902943	B	AGC	21	GGCAAAGACCAATTTTCCAA	AGAACCAACAACAACAGCCC	196	TM1285	2	67	mth2-135i19	6	36.1
RCS1809	LG4	32.62	BB929681	A	GGT	15	TTGTCCCTCTTTCTCTTGCG	CTGCATGAGGTTGAAAACGA	126				mth2-5i18	8	50.2
RCS5623	LG4	33.38	DE238952	D	AAG	19	GTTTCGTTTTCGTTTTTCGC	AATCCCAGCCATCAGATTCA	151						
RCS1629	LG4	33.95	BB932470	A	GGT	23	TTGAGGTGGTTGATCCATGA	GTTTTGGGGACTCTGCTCTG	213						
RCS3157	LG4	34.84	DE231622	D	ACT	17	TCAGAATGCTGCTGAGTTTCA	CGCAACATGCTTGAAAGAAA	147						
RCS1931	LG4	36.65	BB933450	A	AAG	17	TCCATCCAAGACGAGTCAAA	ACGTAGACGTGTTGCCAGTG	146						
RCS0812	LG4	37.38	DE215946	D	AAC	36	TGGTGGTTTAACGACGATGA	AGGTTCTCCTCCCCTGTTGT	243				mth2-31m6	2	0
RCS4978	LG4	37.45	BB910679	B	GGT	18	TGCACCATTGGCTAAAACAA	AATGTCAGGTGACGGAGGAG	235						
RCS6981	LG4	38.65	BB924826	B	AAT	15	TGAGGGGACGAGAATACCTC	AGCTGGTTCCTAACACCCCT	286	TM0091b	3	75.6	mte1-25p15	ND	
RCS0121	LG4	39.07	DE246735	D	AAG	33	GGAAAGAATATGCAATTTCTCGAT	CTGCTTTGGTTTGGAAGAAA	179						
RCS0867	LG4	39.81	DE216385	D	AAG	77	CGATTTCGATGGGTGATTTC	TTTAACCATAGCCGTAAGTTACCA	164				mth2-28n22	4	48.1
RCS3383	LG4	39.86	BB940357	A	AAC	17	AACAGCGACGACGAAGAAAT	TGGGAGTTGACGAATGATGA	171				mth2-48d4	8	50.2
RCS5659	LG4	39.93	BB914529	B	AAG	15	TCGACGATGAGTGACAGAGG	TCAGCAATTGTCCAAAGCCT	247						
RCS6511	LG4	40.09	BB919718	B	AAG	15	TGGTCAAGGGTCCGTCTAAG	CGGCTCTGGAAGTGAAGAAG	225	TM1427	4	19.3	mth2-14m21	8	50.2
RCS5235	LG4	40.70	BB912630	B	AC	15	GATGTCTCAGCTCTTGCTAAAAA	GGCATTGTCTTTTACGCGAT	253				mth2-4l6	8	49.5
RCS4986	LG4	40.74	BB910730	B	AAC	17	GTTCGTTTGTGGAAACCCAT	GATGGGTCATTTTCATTGGC	284	BM0787	2	58.2	mth2-14m21	8	50.2
RCS1475	LG4	41.24	BB929751	A	ATC	15	TCTTTCTCTTGCGGTGTGAA	GACAGGCTGAGGCTCTCAAT	153				mth2-5i18	8	50.2
RCS5903	LG4	42.15	DE244614	E	AAC	18	TTCCACAAATCATTCCCACC	GGATGAAGTTGCGTTGTAGTTG	93				mth2-36j24	3	72.5
RCS4747	LG4	42.98	BB909479	B	AAC	15	TGAAATTGCAAGAAGCAACG	AGCAGCGTACGATGAGGAAT	106	TM0737	2	53	mth2-70o13	8	49.5
RCS5565	LG4	43.32	DE238450	D	AAC	32	ACAACCATGATGTGGGAATG	AGATAGGAATTTGGGTCGGG	119						
RCS5462	LG4	43.40	DE237778	D	AAAC	16	TGCTTCTTTGGTTTGATTTGG	TTAGCAGGGAGAAGCAATCA	202						
RCS6634	LG4	43.84	BB921166	B	AGC	27	CAAACTCCCCTCACTTTCCA	GAGCACCTTTCTCTCCCACA	283	TM1014	4	21.3	mth2-20m14	8	49.5
RCS4304	LG4	43.91	BB906783	B	AAT	15	GCGTCCAAGCAACCTAACAT	CAAATGAAGAAGGCAATGGA	234	BM1378	4	21.3	mth2-75a15	8	49.5
RCS3445	LG4	44.07	DE235797	D	AGC	17	GTTTGTGTTGGTGCTGCTGT	GCCAAGAACAGAGAGATGGG	198	TM1014	4	21.3	mth2-20m14	8	49.5
RCS6581	LG4	44.97	BB920393	B	AAAT	15	CTATGAGACCAACTGCACCG	CCCCTTTTTGGAAAAATATGA	199				mth2-11n13	2	39.4
RCS3285	LG4	46.03	DE233587	D	AAAT	23	GCTCACTTTCTTTCCTTCCG	CAACGTTGTTGCTTCCTCTG	192						
RCS5493	LG4	46.34	DE237927	D	AAAC	15	TCAGTGTTGTGTCCGGTGTT	GTTATAGCGCCGTGATTCGT	293						
RCS4100	LG4	46.70	BB905439	B	AT	19	CCACAGTGCATAAAGCAAGC	AGACACTGACCCTGACCTTGA	292				mth2-24i13	8	38.3
RCS3377	LG4	47.01	BB940181	A	AAT	23	TGTAGCCCATACAGCAATTACAA	CACACCACACCTTATTCCCC	213						
RCS2977	LG4	47.54	DE230176	D	AAAT	18	TGAAAGGGTTTTGGGTTTTG	CGGAGAGAGTGAGAAGGGAA	273						
RCS5061	LG4	47.86	BB911311	B	AAAT	17	AACTTTGGATTACCGGGACC	TTGTTTGTAGGTTCCCCTGC	252	TM0797	3	85.6	mth2-123c10	4	17.5
RCS0040	LG4	48.95	DE245543	F	AAAC	17	GGGACATTTTCTATCTTAGATTC	TTAATTTGTCCATATAGTTCAGG	172						
RCS1475′	LG4	49.40	BB929751	A	ATC	15	TCTTTCTCTTGCGGTGTGAA	GACAGGCTGAGGCTCTCAAT	153				mth2-5i18	8	50.2
RCS3346	LG4	49.98	DE235268	D	ATC	33	CAGAAATAGCAGCAGCACCA	CCCCCTTAACTTGTAGGAGCA	122						
RCS0969	LG4	50.05	DE217178	D	ATC	21	CAACTCATGGAAAACGAGAGAA	CCCTTTTTCCTTACCCATTTT	167						
RCS5331	LG4	50.78	BB913370	B	GGT	21	TCAACCATGTTCTCACCTGC	AGGAGACTTTTGGGTTTGGG	140				mth2-139m18	7	50.4
RCS1333	LG4	51.18	BB929137	A	AAG	15	TTCCCATCCACTTCCTCATC	ACATTTCTTCACCGCAAAGG	217						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS2711	LG4	51.23	DE222875	D	AG	15	CCTTTCACGCCATTCAAACT	CTTTGGTGAAGGTTTTCGCT	118						
RCS2331	LG4	52.02	DE227861	D	AAAT	21	CTCAATGCCCTCCCTACAAA	GGATTAAAATTGCATATCTTGAGTG	101						
RCS5186	LG4	52.08	BB912206	B	AAG	15	AGCATCTCCTTCCCCAAAAT	GGTGTTTCAAGCTTCAGTTGC	268				mth2-7f19	5	61.3
RCS2962	LG4	52.39	BB939765	A	AAT	20	ACCCAACAAAACCCATCTCA	GTGTTGCTGCTGTTGCTGTT	283				mth1-51o19	ND	
RCS6603	LG4	53.46	BB920701	B	AAC	15	GGAACCGGGAGGTATGAGAG	CTTGCAAATTCAGGCCTAGC	266	TM0212	4	20.9	mth2-27m3	5	4.7
RCS5390	LG4	53.51	BB913830	B	AC	16	CCACACCCTCTCTTCAATCA	ATTTGATCCAATCCAGCGAC	171				mth2-11c8	5	64.7
RCS1668	LG4	53.62	BB932828	A	GGA	15	AAGAGGCGAAGAAGCACAAC	TCTTTCTCCACGCTGTTCCT	229				mth2-151j16	8	63.5
RCS7061	LG4	55.60	BB926167	B	ATC	17	TTCTTTCCATTTCCGAAGGA	CACGGTTATTGCTCGAACCT	205	TM0116	3	33.2	mth2-9l7	ND	
RCS5418	LG4	55.69	BB914044	B	AAG	15	TTCGTTCTCTTCCAAACAAAAA	AAATCAGCAAGATCCAAAAAGC	152				mth2-13b8	5	58.8
RCS5805	LG4	56.31	DE240136	D	AAAT	24	ATAAAGGGCAGAACCAAGCC	CCCCAGTACACCCACACTCT	242	TM1110	3	32.8	mth2-6b10	6	47.2
RCS5743	LG4	57.04	DE239503	D	AAAT	20	AAGTGATAGCGAGGCCATTG	GATGAGAATGAAAAGGCGGA	213	BM0921	2	60.6	mth2-23c14	7	3.6
RCS6690	LG4	58.02	BB921913	B	AGC	15	ATGTGCCTGCATACTTGGAT	CCTGCCAGGCATGGTATAGT	275				mth2-39k21	8	9.5
RCS5353	LG4	58.38	BB912799	B	AATT	24	ACTAACCCAAACCCCAAAGG	CCGTTTAAGAATGGGTCGAA	253	TM0157a	4	16	mte1-41j24	ND	
RCS6008	LG4	58.96	BB915315	B	ATC	16	CGCAAACCTCTTCCTCTCTC	TCGGTGGATCCTTCAACTTC	110						
RCS6684	LG4	59.45	BB921757	B	GGT	17	TTCCGAATTTGTCGGCTAAC	CCACCTGATTTGGGCTTAGA	206				mth2-17n16	5	67
RCS2359	LG4	60.03	DE228071	D	AAG	20	ACCGCGAAACCTATCCTTCT	CGTGGGATTTGCGATTCA	128						
RCS3448	LG4	60.54	DE235773	D	AAAG	19	AAAAATAAGAGAGTGTTCTACAAGGAC	GATTTGGGATGACGAGATGG	138						
RCS3325	LG4	60.90	DE235028	D	AC	15	TTCTGTATGCAACTTTCTATCATACC	TGACTGCAATTTTGTCACGA	97						
RCS7149	LG4	61.17	BB927294	B	AAT	32	AAGGCAAGGCTAAGGGTGAT	TCAAAATGTGAAATCGACAACA	208				mth2-16a10	8	63.7
RCS6690′	LG4	61.22	BB921913	B	AGC	15	ATGTGCCTGCATACTTGGAT	CCTGCCAGGCATGGTATAGT	275				mth2-39k21	8	9.5
RCS5547	LG4	62.32	DE238311	D	AAC	32	CTCGCTTTCATTTTGGCTTC	ATTGATGGTCCTAGCATGGC	288						
RCS5408	LG4	62.61	BB914049	B	AAG	15	CGCAATTTGAGCCAATACAG	GCTGAAGACGAGGGAGCTTA	223				mth2-28b4	4	56.9
RCS2514	LG4	62.70	BB935606	A	AAG	19	ACCGCGAAACCTATCCTTCT	AAACCTTCGTGGGATTTGC	135						
RCS5440	LG4	62.93	BB914277	B	AAAT	20	GATTCATGCACCCTAAACGG	ATGAAGCGAAAAGGATGGTG	255	TM0616	3	71.2	mth2-7m1	4	56.9
RCS6929	LG4	63.96	BB924341	B	AAAT	20	TGCGGTACTGCAAGACAGTT	ATGAAGCGAAAAGGATGGTG	230	TM0616	3	71.2	mth2-7m1	4	56.9
RCS6686	LG4	64.61	BB921826	B	AT	18	CCTTAAACCAACAAAATGCCA	CTGTGAAACAAGCAGTGGGA	153	TM1032	2	66.6			
RCS4621	LG4	65.23	DE236837	D	AAAT	29	CACAAGGGACATAATTGCGA	TTTTGCATTTCCACCTCTCC	108	TM0299	5	32.3	mth2-143d17	7	66.2
RCS4880	LG4	65.57	DE237684	D	ACT	18	TGCATTACAAAAGTTAAAGCTCAA	TCTTATTCCATGACCCGACC	152	TM1567	2	66.6	mth2-77f21	4	33.2
RCS1928	LG4	66.30	BB933403	A	AGC	21	TACCCTCTTGAGCACCCATT	CCTTTCAGAACAGATGGCGT	243	TM0170	4	28.2	mth2-33l22	5	75.1
RCS2383	LG4	66.67	DE225960	D	GGA	15	TCCACTTCTCTCCGTCGTCT	ATGAATCTTCTCCCGGAGGT	94						
RCS1904	LG4	66.74	BB933140	A	ATC	15	TCAGCCCATCCACTAGTTCC	CCTAACGCTCCAATGTTCGT	281				mth2-34c3	3	5.2
RCS3989	LG4	66.92	BB904681	B	AGC	15	ACGGGTTCACTTTTTCATCG	TGCGAATATCGGCAATCTTA	230				mth2-13m6	8	49.5
RCS6108	LG4	67.77	BB916020	B	AC	19	TTGAATACACACTTGAAAGGAAACA	CTCGGACGAAAACATGGAGT	241						
RCS5600	LG4	68.45	DE238774	D	AC	64	CACCGGGACACACCTAATCT	TCCACATGGTTAAGCAAGCA	238				mth2-15m13	4	56.9
RCS3906	LG4	68.98	BB904089	B	AAG	36	TGGCTCAAACCATCTAATTCC	GCAGAAGTTGGTATCCAAAACC	293	TM1144	3	68.4	mth2-5j8	4	38.8
RCS6242	LG4	69.09	BB917122	B	GGT	15	TAAGAGTGTGCTGCATTGGC	AGCCAATACTTTCGCCTGAA	245				mth2-7m1	4	56.9
RCS5452	LG4	69.20	DE237760	D	AAG	25	ATTCGATAAGGATGGCGATG	GGGCAAAACAGGAAATGAAA	263				mth2-10g3	5	75.8

RCS3962	LG4	69.50	BB904515	B	AAG	15	GATTCCGACTCCGATTACGA	GGAGATGATCCATTTTGCGT	276				mth2-28b4	4	56.9
RCS6514	LG4	69.84	BB919724	B	AAT	15	CCACGATTTCGTCTCCAGAT	GCTGAACAGAACTCATCCAATTC	278				mth2-158e24	8	59
RCS1180	LG4	70.36	BB928814	A	GGT	15	CAATGGCGATGGACTCTTTT	CCTCCTCCTTCTCCTTCCAC	235						
RCS1083	LG4	71.04	DE217776	D	AAG	18	CCACAACGGAACTAAAACCA	TCCTCCGTTATTCCACATCC	226						
RCS2728	LG4	71.21	DE227408	D	AAC	24	GTCCATGAAGGCCGAAAATA	CAGAGGACCAGGAGGTGAAG	202				mth2-11o9	4	31
RCS1411	LG4	71.54	DE220076	D	AG	22	GGGTGTTTCATCGGAACAAT	CAACGAAACTAAACCCTAACCAA	187	TM0709	4	12.4			
RCS1358	LG4	72.54	DE219232	D	GGT	26	TGTAAATACATGCAAGAGCTTAAAA	TACTCCCTCCTCACGCAAAC	211						
RCS3568	LG4	72.68	DE243242	E	GGA	17	CCTTTCATTCATCGCTCCAT	TGGATGATCAATTCGAACCA	238	TM0764	3	66			
RCS0179	LG4	72.88	DE213318	D	AAG	16	TGTTTCCGCCATTATTGTCA	GCTGCTATGTGGCTGCTATG	194						
RCS2970	LG4	73.16	DE230149	D	AAAT	26	GGAGCACCATGTGTCAACTG	TTCATGCCATTTCCTTCAAA	257	TM1002	3	68.8	mth2-11o4	4	42.8
RCS0325	LG4	73.17	DE213904	D	AAG	20	TTAGATCTGTTAGAAATGGAAAAA	AAGCAAGACAAGGCCACATT	154						
RCS3140	LG4	73.62	DE231268	D	AAAT	22	TGGTGACGTGTTAATTGCTCA	CCGGGATAACACCAAGATCA	125						
RCS5069	LG4	74.08	BB911389	B	GGA	15	CATGTCATCTCCACCGACAC	ACGGTCGATGAGTTCGTACC	196	TM0935	1	67.4	mth2-12b2	3	63.7
RCS3264	LG4	74.16	DE233735	D	AAAT	26	CCGGGATAACACCAAGATCA	TGCCTTATTTTCCCTCTCCA	209						
RCS0880	LG4	75.08	DE216466	D	ATC	15	TGGATCCTCTCATTCTCCAAA	GATGGAGGTTGATTTGGGTTA	224						
RCS5177	LG4	75.67	BB912194	B	ATC	15	TCCATTCTCTCCACCTCTTCA	TTGTTGCTGCTTCAAGATCAC	227				mth2-151m16	3	46.8
RCS4710	LG4	75.92	BB909124	B	AAAT	16	CAACCAAAGTTCTAGACGGATTTT	TCTAATTTGGTGGGGCAAAG	231				mth2-65c4	4	11.4
RCS5915	LG4	76.38	DE241626	D	ACT	30	TGGGAATCATGAATAAGGGC	TGGATGCCTTCTTCCCTAAA	90						
RCS3976	LG4	77.19	BB904593	B	ATC	23	TGGAACCAAAAGTGTCCCAT	AGGAGACAGGATTCCCTCGT	283				mth2-10d6	4	27.2
RCS5381	LG4	77.23	BB913769	B	AAG	15	TTCCCACAGCAAAAGAAACC	GCTCTTTGAGCGTCCATAGC	129	BM1023	3	84			
RCS2597	LG4	77.59	DE222791	D	AAAT	15	AAGGGAAATGAAGCTGCTGA	GCTGGGAACTCGTAAAAACAA	194						
RCS5556	LG4	77.80	DE238342	D	AAG	20	TTCCTTGCTAATCACGTCCC	TGGTGTTGAGACAGACGGAG	141						
RCS1672	LG4	78.02	BB932820	A	AAG	15	CGGCTTCAATTTTAGCTTCG	GCTGAAGTAGCCGAGGAGAA	214						
RCS6791	LG4	78.18	BB922933	B	ATC	15	ACAGCTGTGAACCCTCCATC	ACCGTATGGTATTCGGGTGA	234	TM0164	3	67.2	mte1-84h13	ND	
RCS2296	LG4	78.20	DE227011	D	AAG	18	ATGAGCCCATATTTCGCAAC	TGAAGATTGCAGTGAAAGCG	127	TM1144	3	68.4	mth2-5j8	4	38.8
RCS7109	LG4	78.23	BB926779	B	AT	24	TCTTTCCAAACACTCCCCAC	TTTGGCAGCCTCTTTAGTTGA	227				mth2-10d6	4	27.2
RCS2829	LG4	79.80	BB936377	A	GGT	15	TGGTAGCGGACAAAAACCTC	TAGGTCTTGGAGAAGGGGGT	134	TM1419	3	83.2			
RCS0824	LG4	79.85	DE215947	D	AAC	15	AACGAACCAGATACAAGTAATCCA	CAGGGAACAACGAAGAGAGG	176						
RCS1672′	LG4	80.10	BB932820	A	AAG	15	CGGCTTCAATTTTAGCTTCG	GCTGAAGTAGCCGAGGAGAA	214						
RCS6646	LG4	80.15	BB921359	B	ATC	15	AAAACAGAACGCATTTTGGG	AAGGTCCCCTTTCTTTCCAA	233				mth2-11o4	4	42.8
RCS4486	LG4	81.75	BB907146	B	AG	16	CAAAATCGGAAGCCGAATAA	CGGCTCATTGTGTGAGAGAA	183	TM0468	3	64.4			
RCS2043	LG4	82.29	DE221872	D	AAG	18	TTCTTCCTCAGATTCAGCTTCA	CAACAATTCAACCAATATCTCGAA	96	TM0227	4	14.4			
RCS5798	LG4	82.40	DE240072	D	AGC	15	AGGAGTGCCACAAGGTGAAA	AAACCCTCATTTTGTTTGCG	270	TM1519.1	ND				
RCS5006	LG4	83.50	BB910789	B	AATG	16	TCTGAAACACTATATTTTCCAACACA	GGCATTTTGTCTGGACTCGT	273						
RCS2567	LG4	84.78	DE228709	D	AAAC	21	ATAAGGGCACTTGTGGCATC	GCATGCATCATGGCTAACAC	153				mth2-77f21	4	33.2
RCS4350	LG4	84.89	BB907029	B	AAAT	16	AACAATCTTGGAAAATTCATGTC	TATGATGCTGGCTTCACCAA	226	TM0326	ND		mth2-15l24	5	62.5
RCS5709	LG4	86.14	DE239134	D	AAC	15	AACGGACCCTTTCCAAGAAT	GGTGAAGGATTTGACGTGGT	140						
RCS5736	LG4	86.55	DE239464	D	AAAT	20	AAAATGTCGATAACTCGCGG	CAATCGAACTCAAAGTTACGAGA	107	TM0877	3	9.7	mth2-116a3	4	17.5
RCS6050	LG4	86.67	BB915615	B	AAC	15	CCACCACCCTCTCACAATCT	GCGTTCGTTTCTTAAGCGTC	112				mth2-15l5	6	47.9
RCS6425	LG4	87.32	BB918683	B	AAG	15	CTCACATCACTCCACAACCC	TGATGGGTTGTGTTCCAAAA	110						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS5137	LG4	87.58	BB911931	B	AAAT	20	TCCACGATAACTCAATGGTGA	GCCACCATCCTTCCAAGTTA	233						
RCS3315	LG4	87.59	DE235031	D	AC	16	GCTGCTTCTGTGAGATCCCT	CTCAACTTCCACACCTGCAA	117				mth2-16c16	3	72.5
RCS2359′	LG4	87.89	DE228071	D	AAG	20	ACCGCGAAACCTATCCTTCT	CGTGGGATTTGCGATTCA	128						
RCS1729′	LG4	88.49	BB931403	A	AAG	19	ATGGCTTCCTTCTTCACCCT	TCGACTGGGAAATCGATAGG	224	TM0820	3	43.6	mth2-18h17	4	2.3
RCS5724	LG4	88.57	DE239232	D	AAAT	15	ACAAGTGCATGGACAAGTGC	GAGGCCAATGACATCCAAGT	203						
RCS3272	LG4	88.82	DE234353	D	AAAT	23	AACAAAGACGAGGGGGAAAT	AATTGCAGGTTCAGGTTGCT	187						
RCS6794	LG4	89.14	BB922967	B	AATC	16	TGCTAAATAATGCGCAGACG	CCGGTCAGGCTTGAATAAGA	209	TM0208c	3	53.5			
RCS1920	LG4	90.44	BB933307	A	AAG	15	GAGAAAAGAAAGAAGTCTCTGAAGGA	CCCCCAAAATACAAAACCCT	220	TM1058	3	42.4	mth2-62c22	8	59
RCS2667	LG4	90.54	DE229260	D	AAG	23	CCTCAGCAGAATCTTCACCC	GGTGGTGTTGCTGATTACGA	208	BM1187	3	2.4			
RCS3763	LG4	91.73	BB903172	B	AAG	18	TCATGGCCAAGAAATCTCAA	ATCGACCAGTCCAACGATGT	162	TM0452	3	41.6	mth2-36b12	8	69
RCS6852	LG4	91.78	BB923608	B	GGA	16	CTTTTTCCAACAACGGAGGA	TCCATTTAAACATTGGGGGA	124	TM0445	ND		mth2-53o24	4	63.4
RCS1401	LG4	92.68	DE219880	D	AAG	22	CAGCAGCAATGGAAAAACAA	ACCGCTTCACCTTCATCATC	196						
RCS3165	LG4	93.00	DE232054	D	AAAT	18	TTTATACACAAGCCGAGCCC	GATGGAGTTGAGACGGTGGT	190						
RCS2011	LG4	93.13	DE221778	D	AG	15	CCCTTTCCTTCTCACACACC	TCAAGGCCATCATTGAGAAA	143				mth2-70o13	8	49.5
RCS1598	LG4	93.23	BB930651	A	AAC	39	GTCTAACAGCCCAAACCCAA	ATGGTGAAACTGGTGAAGCC	252	BM1057	3	42.4	mth2-8n20	4	0
RCS3518	LG4	93.67	DE242902	E	AAAT	18	TTCAAACAGATTTCGGGAGG	GAACCTTGCTCGTCTTCCTG	268						
RCS6373	LG4	94.47	BB918329	B	AAC	15	CCAAAAGGAAGGAAGGAAGG	TCTTATCCCCGGAGTGAGTG	214	TM0452	3	41.6			
RCS0916	LG4	95.02	DE216826	D	GGT	16	GCAGTAGCATGAGCATGAGC	CCTCCCAAGTGGTGAAGAAA	233	TM0180a	5	0.4			
RCS6410	LG4	95.34	BB917875	B	AG	22	CAACCAGTGGTGTGAGTAGGAG	ACGTTGGTGGAGAGGTTGAG	108	TM1078	1	22.5	mth2-7k4	8	37.5
RCS2345	LG4	96.00	DE228004	D	AAG	15	AAACCTTCGTGGGATTTGC	GGGGAAACTCATTCGTCAGA	111						
RCS2988	LG4	96.80	BB938261	A	GGA	15	TCGGAGGAAGGAGAAGGAAT	AGGGCGTGTTCTTCTAGGGT	147				mth2-13f22	4	3.5
RCS6333	LG4	97.09	BB917870	B	GGA	15	GGGAATGGACTTGGTTTTCA	AGTCCCCTCTGTGTGTCTCG	249	TM1250	3	40.8			
RCS6163	LG4	97.76	BB916516	B	AAG	22	CTTCTCCTCCACGACCTCTG	GAGCTCAGAATATGCCTGCC	275						
RCS2997	LG4	97.78	BB938346	A	GGA	16	AGTCCCCTCTGTGTGTCTCG	CAGCAGCAGCAATGTTGTTA	150	TM1250	3	40.8			
RCS6840	LG4	98.14	BB923434	B	AAAT	16	TAATGGCTCTGCGTGTCATC	GAGCCGGTAATAATTGCAGC	187				mth2-16c16	3	72.5
RCS3416	LG4	99.01	BB902610	B	AGC	15	TGCTCCAATTCACGTTAGGA	GCATTCCTTGGTTTTGCTGT	253				mth2-34f15	4	5.2
RCS5188	LG4	99.06	BB912262	B	AGC	21	GGCAAAGACCAATTTTCCAA	GCCTATTCACCGGAATCTCA	128	TM1285	2	67	mth2-135i19	6	36.1
RCS5036	LG4	100.12	BB911144	B	AT	18	TGGAGTCCTAAAATGATTCTCCA	GCTCCATGCCCTGTGACTAT	239	TM0240	1	49.3	mth2-97e5	2	12.7
RCS0859	LG4	100.14	DE216261	D	ATC	28	TTTATCCACGGTAGTCGTCGT	CAAGAGCAAGACAACGGATG	104						
RCS6942	LG4	100.31	BB924500	B	GGA	15	TGTTGTCGAGCACAAGGGTA	TAATCGACTTCCGGGTCTTG	288				mth2-5j8	4	38.8
RCS6070	LG4	102.03	BB915724	B	AATT	16	TCTTCATGCAAGGAATTGACC	TTTTTGTTGACTGACTTGTCTCTTG	220	TM0246c	3	43.6	mth2-94j16	4	47.4
RCS1729	LG4	102.50	BB931403	A	AAG	19	ATGGCTTCCTTCTTCACCCT	TCGACTGGGAAATCGATAGG	224	TM0820	3	43.6	mth2-18h17	4	2.3
RCS0441	LG4	104.33	DE214239	D	AAC	18	TGAATTTTGCCTTAAGGTTTG	TCTTGGAACAAAGATGGGGTA	192						
RCS1747	LG4	104.74	BB931543	A	AAC	15	CTTGGCTTCAAAGACCGAAC	TGTTTTGGGTTTGGTTCCAT	93				mth2-21b19	4	0.8
RCS1454	LG4	107.89	BB929713	A	AAAG	21	GCACGAGGCAGAGAGATATAACA	TCATCCCAAACAAGACCAGA	162				mth2-22d10	2	60.7
RCS5056	LG4	111.51	BB911300	B	AAAG	20	CGCTAGATTCTGCTCTCGCT	TGAAAACGCCGAAGAGAAGT	226						
RCS1940	LG4	116.09	BB933563	A	AAG	19	TAGAATCCTCACCCAAACGC	CCTGCAAAAACAAACCACAA	265						

RCS1170	LG4	124.26	DE218168	D	AAC	21	TGCATCAACATCGACAACAA	GCTTGAAGCATGACAATGAGG	104						
RCS2166	LG4	126.56	DE225228	D	AAC	18	AAGTAGCAAACAACCCGCAC	GCCACCCTTCTTTGAATCAG	279				mth2-102h2	1	51.6
RCS2467	LG5	4.13	DE227368	D	GGA	15	CAAGCAGCAGAGTTTCATCA	AAGGCTAGGAGTGCTGACCA	96						
RCS3892	LG5	5.44	BB904024	B	AGC	24	GGCAAAGACCAATTTTCCAA	GCCTATTCACCGGAATCTCA	131	TM1285	2	67	mth2-135i19	6	36.1
RCS2836	LG5	7.65	BB936522	A	ATC	15	TCCAGGTCGAGATTTTGGAT	TGGAAACTGCCCTTGAAAAC	201						
RCS6244	LG5	9.33	BB917136	B	AAC	15	AACAAAGACACACAAAGAGGCA	CATGGCTTGAAGGTTGAGGT	190	TM0498	1	12.1	mth2-21e10	4	58.3
RCS4421	LG5	12.32	BB907518	B	AAC	18	CGCAATGGATTTCACATCAG	TGACGCTCTTCGGTTTCTTT	138				mth2-15c17	ND	
RCS2580	LG5	13.64	DE222537	D	GGA	19	TATTGAGATGTTTGGCAGCG	GAGAAAGCTGTGGAGGCTGT	98						
RCS3376	LG5	15.01	BB940212	A	ATC	18	CACACCGTATCCGTCAACAG	GATGATGCGATAGGCAGGAT	166						
RCS1762	LG5	15.27	DE220683	D	AAG	27	AAATGGCGCAAGAGAACAAT	ACCAACCCAAGCAGATGAAG	98						
RCS6215	LG5	16.41	BB916881	B	AG	16	CGCTCAACTACCACCCTCTC	AAATTCCGCGGAGAATGATA	176	TM0343	4	41.7			
RCS5023	LG5	17.82	BB911021	B	ATC	15	CATGAAGCAAATTACACAAACCA	GGACATGGAACAGGAACAGG	295	BM1338	5	32.3			
RCS3470	LG5	19.54	DE235978	D	AC	16	GATTGGCAAAGAATGCAGGT	GGTGTTGCTCTCTCTTTAATTCC	205				mth2-62i21	ND	
RCS6066	LG5	20.37	BB915603	B	ACT	15	CCGCAAACAATCAATCAAAA	GTTTGAATCTCGCAGAAGGC	176						
RCS5958	LG5	21.08	BB914941	B	ACT	15	GTTTGAATCTCGCAGAAGGC	CCGCAAACAATCAATCAAAA	176	TM1368	4	31.9			
RCS6591	LG5	22.33	BB920570	B	AGC	15	TGAAGTAACAGCCCCTGCTT	TACCCCCACCATCAGACATT	173	TM0928	4	50.7			
RCS5104	LG5	23.49	BB911616	B	AG	17	CACCGTAATCCAATCCACAG	GTTTGGTGGTGGGAGAGAAA	133	TM0045	6	40.1	mth2-26n6	2	17.1
RCS5448	LG5	25.25	BB914300	B	AAT	29	TTGATATGGTGCTTTGGCAG	TTTTAAGAGTCTGTTTGGTTTGTTTTT	140						
RCS1594	LG5	25.33	BB930588	A	AAG	19	AAACAGCAACCATACCACCA	TAGAATCCTCACCCAATCGC	134						
RCS5643	LG5	25.95	BB914459	B	ATC	15	TGGGAATCGCTTAGTATCGG	TGTGTTTGGACTTCTTCAGGC	171				mth2-19h23	2	17.8
RCS2217	LG5	26.65	DE226526	D	AG	21	CCACCTGCCAATCTTGATCT	GGATGCATGTTCGATTCCTT	210	BM1211	3	38.4			
RCS1148	LG5	27.72	DE218109	D	GGT	19	ACAAGCCCAACTGTGACTCC	TCAGCACCATATCCACAAGC	167						
RCS2202	LG5	28.40	DE225689	D	AC	25	GCCGATATTGCTAGGTTGGA	CGGCAGACGAAGTGACAAAT	110						
RCS1771	LG5	28.60	DE220846	D	ACT	15	GGGAAGAAATTCAAGAAAGGG	CCATCTGATGCAACCTTTTG	138						
RCS2632	LG5	28.91	DE228788	D	AATG	15	AAGTGGTGGGTATGTCTCCG	TATGTATTGGTGGGCTTGGC	203						
RCS0843	LG5	29.79	DE216050	D	GGAT	15	GCCAAGCCCACCAATACATA	TTGGCATCTCAAAGCTGAAA	231						
RCS1044	LG5	30.15	DE217518	D	GGA	15	TGCCTCATATGCTCATCACC	TCGATCTGTTGAAGGCAGTG	153						
RCS3086	LG5	30.43	DE231890	D	AAAT	18	CAACCTCCGATTTCACCCTA	CCTAAAGCCTCAGCCAAAGA	174						
RCS2881	LG5	30.86	DE223315	D	AAG	15	CCAATCCTCATCTTCATCTTCA	CCTCCTCCACCTCAGATTCA	258						
RCS3510	LG5	31.16	DE242919	E	AT	21	TTCACAAGTTTTTCGGGTGA	GCCAAAGGGAAGGTTCAATC	271	TM1635	1	30.6	mth2-194a22	ND	
RCS0315	LG5	31.76	DE213925	D	ATC	15	ATGACGCAGCTGCACTAACA	CGAAGATGAAGATGAAGATGAAG	194				mth2-24g3	4	60.4
RCS3827	LG5	31.99	BB903560	B	AAT	15	ACCAAAAGGAGAATCCACCC	TGTGTTTGTGTTGTGTCCGA	208						
RCS4430	LG5	32.46	BB907582	B	AATG	16	CACTTTTCATTTTCCTTTGCATC	GACGGAGAAAGTGAAGTCGC	155	TM0180a	5	0.4	mth2-28o14	2	0
RCS5393	LG5	32.49	BB913853	B	AAC	31	GGTCGGCGTAGAAACAAGAA	GATTGGTCGAGGTTGGATGT	167				mth2-27i5	6	47.9
RCS6829	LG5	32.56	BB923396	B	ATC	16	GTTTCTGGCTGTTTCCTTGG	GCAGCAGCAACGTGTGTTAT	141	TM0385	ND		mth2-46o19	ND	
RCS4602	LG5	33.04	DE236754	D	AG	52	GCACTGATTTCCCTTGCATT	GACTTGAATTTTCCCGAGCA	254				mth2-97e5	2	12.7
RCS1232	LG5	33.93	DE218252	D	GGT	18	CCTCTACCACCACTTCTACTCTATTCA	TTTACACGATGCGTAACATAACC	151						
RCS1618	LG5	35.39	BB932386	A	AAC	17	CCTCCAAAACGAACTCGAAA	CGACGTTGGCAATAAATGTG	164	TM0627	2	55	mth2-101o15	1	2.2
RCS0131	LG5	35.78	DE246916	D	AAC	16	ACGTGACGGAGAGAGCTACG	AACCCTTCAAACCCAAAACC	211						
RCS2125	LG5	36.18	DE224968	D	GGT	15	AGATCCCAACCACCACCATA	CGGACCTGTTTTTCCAGTGT	159						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS1724	LG5	36.79	BB931291	A	ATC	15	TGGCCACCAAAAGTAGGAAG	CAGAAGCCATTGTCACCAAA	282	TM1635	1	30.6	mth2-75b23	7	49.1
RCS1345	LG5	37.21	DE219086	D	AG	24	AAATCAGGAAAGAGAGAAAGAAGA	CCTGACATCACCATGTCCAC	160						
RCS0036	LG5	37.43	DE244851	F	AC	27	ATTCCCCATAACAAATAGGC	TGTGGATTAAAAGACTAGCG	111						
RCS3625	LG5	37.60	DE236571	D	AAAC	18	TCAACCAAACAAATAAATCCTGAA	CCTTCTGTGAGGGTTGGGT	132						
RCS2845	LG5	38.02	BB936663	A	AAG	18	CGGTGAGTTGATGTCCTGTG	AAAACACAAACAAAGGAAGAAGA	131				mth1-5j15	5	38.4
RCS3151	LG5	38.91	DE231512	D	AGC	15	AGGTGAGGTGGACCTGATGA	GCAACTCTTGCTGGAGAAGG	292						
RCS3211	LG5	39.70	DE233450	D	AAAT	23	GATGTTGTTCATGTTGCTGGA	AAAGAATCCTTCTTGATACGAGG	238				mth2-70e16	6	47.9
RCS1248	LG5	39.83	DE218529	D	GGT	22	GTGCACAGCTGCAAAGCTAC	GGACTGGGTGATTTTCTTGG	178				mth2-2o12	7	61
RCS0937	LG5	40.05	DE217026	D	AAC	15	CCGTTGAGAGTCCTTTTGCT	AGAACAACGGCGAACAACA	196						
RCS5957	LG5	40.71	BB914888	B	AAAT	16	CACATCATCCACAAAATCCAA	CAACGCACCAGAGAGGAACT	135						
RCS5936	LG5	41.43	DE242254	D	AAAC	22	CACACACAGCACAAAATCAAAA	TGTTCGGTATTGTTCAGGTACG	279						
RCS1228	LG5	42.05	DE218234	D	AAC	18	AATGTTCGGTGCTCTGTGTG	GTTCAATTCATCCCCACGAC	183						
RCS3122	LG5	42.11	DE230897	D	AAAT	22	AAAAAGGGAACTTAGGGCTCA	CGGTGTTGGTTTTTATTGGG	118				mth2-49f2	8	38.3
RCS2802	LG5	42.21	BB935846	A	ATC	26	TAGCCACCACTGCTACATGC	TGTTGTTGTTGGTGGTTGGT	206	BM1338	5	32.3			
RCS2320	LG5	42.72	DE227847	D	AC	15	TCAGCATGAATGAAAACGAAA	CTTGGGGTTAAGCTTAGGGG	220				mth2-17b23	ND	
RCS6640	LG5	43.59	BB921312	B	AAT	15	CCTTACCCTTTTCCTCCCTC	CAGCATTTCAGCTGTTGCAT	277	TM0968	4	69.4			
RCS2955	LG5	43.98	BB937744	A	AAG	18	AATCGAATGAGAACGATCCG	GTGGTGGTCGGAATCCTAGA	287	TM0406	3	50.2			
RCS5010	LG5	44.73	BB910879	B	ATC	15	AAAGCACCGTTATAATCTCTGG	CCATGTTTTGTTGCCAACTG	155						
RCS1932	LG5	45.38	BB933462	A	ATC	17	TGGGTTCCAGTCACACAAGA	AACAGCACCACCACCATTTT	205	TM1471	ND		mth2-144f20	ND	
RCS5345	LG5	45.61	BB913436	B	AATC	16	TTCCTGCTTATTCACGGTCG	ACAGGCAAAGGAAAATGTGG	259	TM0493	3	53.5			
RCS5376	LG5	46.32	BB913717	B	AAC	29	TCCAAAACCACAAACCACCT	TGCTTGAAAATGAATGCGAT	300						
RCS0007	LG5	46.46	AB234882	C	GGA	26	GCTCCGAAGGAGATGAAGAA	CTGGCAATCGTTTGACTTTG	144						
RCS1360	LG5	46.93	DE219279	D	GGA	15	CGGTGGTGGGTCAAGGTT	TTGGTTACAAAGTAGTAATTCAATTCG	162						
RCS4608	LG5	47.97	DE236746	D	AAG	17	CGATCTTCAAAATGCAGGCT	GGAAGAGAAAGAAGGGTTGAAAA	122						
RCS2807	LG5	48.21	BB935942	A	AAC	15	TCCTCCCTTCATTCCTTCCT	GGATTCACAGCGAGGACATT	175				mth2-34d6	2	36.2
RCS1155	LG5	48.41	DE218089	D	AAG	17	TCAGCATCTTGTGGTTTCTTG	AACAAACATTCTTCACAACAACA	160						
RCS2892	LG5	48.86	BB936864	A	AAG	15	TGCTTTGCAAACACTCTCTCTT	TGGATGATGAAGGTTTGTGG	106						
RCS2213	LG5	49.27	DE226486	D	ATC	19	CAACCATCACATCCGTCAAC	GTCATCGTCGTCGTCATCAT	177						
RCS1518	LG5	49.73	BB930133	A	ATC	40	GCACGAGGCACACACTACTT	CGAAGCAGGTTGGAAAACAT	188	TM1762	ND				
RCS4503	LG5	49.90	BB908083	B	AG	16	AACAAGCGAAGAAGAGCGAG	TCGACATCAGTGGTGAGAGC	273	TM0724	3	55.5	mth2-17j18	2	59.9
RCS5966	LG5	49.90	BB914994	B	AG	16	GCGCTCTTTCACCATCTTCT	CATCGCCATCCTTATCGAAT	166	TM1640	1	62.6	mth2-10g3	5	75.8
RCS2052	LG5	50.25	DE222068	D	ATC	20	TCACCCTCCTCGTCTTCATC	GTTGCAAAGAAGGTGGAAGC	215				mth1-51o19	ND	
RCS4797	LG5	50.52	BB909791	B	AT	33	GCCCGTCTACCTTTTGTTCA	GCGCCATAAGCAACTGTGTA	190				mth2-14p11	5	16.5
RCS3681	LG5	51.45	DE243942	E	ATC	15	AAAGCACGTGAAGAAAATGGA	CCCTTCATCAATGGCTTTCT	141						
RCS5800	LG5	51.75	DE240054	D	AAT	24	AAACACAGCAACACCCAACA	CGCAAAACTTTCGTCCCTTA	221						
RCS5949	LG5	52.56	BB914911	B	ATC	15	TCACAATGGCAGAATCATGG	TTTCATTTGGATCCTCCTCG	255	BM1082	4	25.8			
RCS4863	LG5	52.64	DE237470	D	AAC	21	CGGAAGAAGCATATACAGGGA	GCTGGTTTTTGGTGCCTTAC	256						

RCS0060	LG5	53.24	DE245206	F	AAT	15	AGGATGAAGAAGCCATGGAA	GCCGTGTAAATGACGGAGAT	145						
RCS5204	LG5	53.58	BB912355	B	AT	80	CCCCATTTATTTTGTTCCCTT	GGAAAATGGAAGGGTGGATT	288						
RCS1737	LG5	55.14	BB931457	A	ATC	37	GGCACGAGGCACACTACTTC	AGCTCAAGCTCAACGGACAT	107	TM1762	ND				
RCS6109′	LG5	55.36	BB916021	B	AAG	15	GGTTAAGTAACTTGCAAACTGCC	GGTGATTTCTTCGACGGTGT	242						
RCS5047	LG5	55.61	BB911243	B	AG	16	TCTCATCCCACAGAAAACCC	TGAGCACGACAGAGTGTTCC	226	TM1438	1	63.8			
RCS1523	LG5	56.82	BB930157	A	GGT	18	TTCCAAATGGCTTCCAATCT	GGTGTCTTTGGTGGCTTACC	239	TM1257	ND		mth2-161i17	8	50.9
RCS3101	LG5	57.03	DE230552	D	AAT	23	CAAATCTGCGAAGGGAAGAG	CCGTGATAATAACTACCTCCGTTT	216						
RCS0889	LG5	57.37	DE216559	D	ATC	15	GGAAGGGTCGTTGGTTAGAA	AATGCCGATCATCAAAATCA	121						
RCS5337	LG5	57.58	BB913352	B	ATC	18	ATCGCAAAGACAACCTCCAC	CGCGTCAAGTTCATCTTCAA	109				mth2-75i8	8	50.9
RCS5859	LG5	58.37	DE240920	D	AG	22	GATTCCATCCCATGATCACC	AGTGTTGGAGGAAGTGGTGG	131	TM1321	4	24.6	mth2-22p8	8	50.9
RCS2095	LG5	58.38	DE224699	D	AATG	15	GGCCCAAGAATGTTCAGAAA	CCCACTAACCATAATCCAGGAA	179				mth2-75i8	8	50.9
RCS6937	LG5	59.26	BB924474	B	AAT	15	GCAATTGCATTCTGTTTGGA	CGCTCTTGCTTGAGCTCTTT	198				mth2-11o23	4	11.4
RCS0764	LG5	59.47	DE215618	D	GGA	15	TCACAAAAATTATCTTCATCTTCTCTC	ACGACCCTTTGCAAGTCTGA	153						
RCS2987	LG5	60.01	BB938238	A	AAG	17	CTCTCCTAAAATGTTCGCCG	TCGCAGTAACAGAAGGAAGGA	256	TM1006	ND		mth1-3f12	6	
RCS1541	LG5	60.32	DE220209	D	AC	15	TCACTCCAACTAACTCCAAACG	TGATGAGGCAACATTCATGG	150						
RCS1225	LG5	60.74	BB928947	A	ATC	15	TGCAAACTCCGCTTTATGC	CTCGCTGAAGGAGGAAACAG	200						
RCS4972	LG5	61.12	BB910645	B	ATC	15	GGCACCGTTTGTCAAATCTT	CCCTGGAATCCCACAAAATA	198	TM0561	ND		mth2-38m20	8	50.9
RCS3094	LG5	61.51	DE232004	D	AAAT	30	CCTGTTAGTCAGGGTGGGAA	CATCCATGTGGTTGCATAGC	225				mth2-30n15	4	60.4
RCS5088	LG5	61.65	BB911538	B	ACT	15	GACACCGAAACACGCCTAAT	TGGTTGGGGAAAATGAGAAG	253						
RCS6109	LG5	61.82	BB916021	B	AAG	15	GGTTAAGTAACTTGCAAACTGCC	GGTGATTTCTTCGACGGTGT	242						
RCS2697	LG5	62.57	DE221857	D	AAG	25	CAGCAGTAGTCGAAATGGGAG	ATCCTCCTCCAGAGCAGACA	111						
RCS3236	LG5	62.63	BB940156	A	AAAT	22	ACCACCATGATGATTCCGTT	CCAATTTGCCAACTTCCAAT	300						
RCS4473	LG5	62.76	BB907826	B	AAG	18	AGCCAAGACATATGCAGCAA	ACAAATGGTGATGTGGAGCA	237				mth2-24j8	8	53.3
RCS4783	LG5	63.10	BB909672	B	AATT	17	CCACATCCAACGTTATCAGC	ACTCCTGTCATTTTGGTGGG	276						
RCS3931	LG5	63.15	BB904298	B	AAC	15	GGGTGGTGCTAAGAAGGTCA	TGGTCATCAAACCCTCAACA	191				mth2-24j8	8	53.3
RCS4288	LG5	63.23	BB906634	B	AATT	17	CATCAACTACAAACATAAACCACCA	TTGAAGGAAAGAGGGATGGA	189						
RCS5827	LG5	63.37	DE240334	D	AAAT	27	GTTTTCGAAATCGGTGATCG	CATGGTGGTTGTCCCATCTT	234						
RCS1157	LG5	63.50	DE218170	D	GGA	55	CCACATAGACCGAAGATTCCA	ATCGCAACCGGTAATTGAAC	193						
RCS4115	LG5	63.86	BB905544	B	AAC	15	AAATGCCAATGCAATTTGGT	CGTTATTTATCCCTCCGGGT	138				mth2-151m10	8	49.5
RCS5562	LG5	64.65	DE238387	D	GGT	15	TGGAAACCTTGGTTTTCGTC	TGGAGGAGAAGGAGAAGTGC	178						
RCS2448	LG5	64.97	DE227216	D	AG	72	AAAACCCACTTGATTGCTGC	GTGTGGGGTGAAGAAGAGGA	219	TM0172	4	26.6			
RCS2945	LG5	66.27	BB937977	A	AAC	18	CCTAAGCACCACCACCAACT	CGGATAGTTTTGGCGTAGGA	150						
RCS6826	LG5	66.95	BB923297	B	AAT	21	CCGGCCAATAAAAACAAAAA	ACCTTAAATTTGTAACACACCAACT	206						
RCS2186	LG5	67.27	DE225395	D	AGGT	16	TGATAGCCCATACATGATATTGAT	GAGAGTGTGGCGGTGGAG	95						
RCS2325	LG5	67.50	DE227871	D	ATC	30	TGACGGTGAAAGAATGTGGA	CAGATGGCACAAGAATTGGA	201	TM0735	3	75.6			
RCS7143	LG5	68.38	BB927227	B	ATC	19	TACCGCGTAAGCAAGCTACA	GCGGGAGTTTTTCTCTTTCC	172	TM1624	ND				
RCS6145	LG5	69.37	BB916346	B	AAT	18	TCCTTTTTCATGGTTGTACGG	GTTCGATCCCAAAACTGCAT	237				mth2-58m16	8	15.5
RCS5004	LG5	70.05	BB910847	B	AAC	17	TTAATCAATCAAACTTCGCGG	CTAGTTTGGCGGCTTTTGAG	208						
RCS5288	LG5	70.12	BB913012	B	AAT	17	TTCTTCAATTGTTTGTGGCAG	TGAGTGGAAGAGGATTTGGG	240	TM0170	4	28.2			
RCS2068	LG5	70.34	DE222421	D	AAC	20	TTAATCAATCAAACTTCGCGG	TCAGTTTCAGATGCTGCTCG	110						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS3825	LG5	70.77	BB903542	B	ATC	15	TTAGCACCAACCCATCATTG	CCCTTTTGTGAATTCCCTTG	230	TM0105	1	77.4	mth2-23m13	ND	
RCS5808	LG5	72.81	DE240123	D	AAT	29	TGATTACCGGGAATGTGTCA	TGGTGAGGAATGGAGAAAGC	284						
RCS0714	LG5	74.00	DE215397	D	GGT	15	AGGGTTTGGAATGTGTTGGT	TGGTTCAAGCTGTACAAAAGGA	167						
RCS3192	LG5	74.42	DE232800	D	AAAT	19	ACGGGGGACCTGAGAGTAAT	TCATACTCTTGCTAGGGCGG	288	TM0075	4	14.8	mth2-154g23	ND	
RCS3060	LG5	76.75	BB939303	A	AAG	18	GGTCGGATGATGAAGAGCAT	GTGCACTCCCTTTATTCCCA	210						
RCS6195	LG5	77.00	BB916748	B	AGC	21	TGGCTGAAGAGACTGCTCAA	CGATCTCACTGAACGCATGT	274	TM0697	ND				
RCS6346	LG5	77.22	BB918076	B	AAG	15	TGGGACATCCTCTTCCTTTG	AAGACTACAATGCCGTTGCC	285	TM0206b	1	72.2			
RCS1000	LG5	79.73	DE217330	D	AAG	15	ACGGATCGAAAACGAAGATG	ACGAACCTAGGTAAAAGAAAGTTG	160						
RCS0914	LG5	80.67	DE216772	D	GGT	19	GTGCTCACCCCTCAAGACTG	AGATGGAGGTGGTGTGGAAG	221						
RCS1557	LG5	81.08	DE220347	D	AG	48	TGTCATATGTTTGCAGAGAACG	GGCCAGGAAAATGTTCACAA	204						
RCS4948	LG5	84.60	BB910418	B	AAG	27	GTTGCGCTCCTCCTCTTTCT	AACCGAAGAGATTGAGTGCG	132	BM1451	5	5.2	mth2-24j8	8	53.3
RCS0907	LG5	86.15	DE216761	D	AAC	15	ATTTGAGCACAAGGCCTCAC	TGGGGAAGTGAAGGATGTTC	206						
RCS2936	LG5	92.96	BB937857	A	AAC	16	CGTTATTTATCCCTCCGGGT	CCAATGCAATTCGGTAATCC	130						
RCS0874	LG5	94.35	DE216408	D	AAC	27	TCAGTCTTACTCAATCGACCACA	CAGACACATCACAGACCGAGT	151						
RCS6854	LG5	98.42	BB923614	B	AAG	15	ACATGATTGAAATCGCGACA	TGAAGGTATTGGTGGTGGTCT	296	TM1648	3	49.8			
RCS5007	LG5	99.93	BB910798	B	AATT	17	TTGATATTATCCCCACCCCA	GAGGGATGGATTCAACGAAA	291						
RCS1281	LG5	113.51	DE218987	D	GGT	15	CTCTTCTCTCTTCTCACCACGA	CTGCAGAAGCCAAACTGAAA	155						
RCS4869	LG6	0.00	DE237536	D	AG	20	GAGGAGCAATCCAACAAAAGA	TTGCATCTCCCTCCCTATTG	195						
RCS4435	LG6	4.17	BB907603	B	AAG	15	ACTACCATTGACCGACCGAC	CTTGTCAAGAGAGGCCGAAC	95	TM0035	3	30	mth2-77l23	4	58.3
RCS7165	LG6	8.51	BB927495	B	AAAC	15	ACACACGAACGCAGAGTGTC	AACACTTGAATGCACCACCA	157						
RCS5147	LG6	9.43	BB912002	B	AAAT	16	TATGGTCTGCTCTGCCCAAT	AGTTCCCGTCATAGGTGCTG	276	TM0236	1	60.6	mth2-31e20	7	
RCS4106	LG6	17.37	BB905492	B	GGA	15	CCCAGTCATTTCGTCGTCTT	CGACTTGACTAGGGACTGGC	236	TM1462	1	77.8			
RCS6306	LG6	18.46	BB917711	B	GGT	18	CAACCTCTGTTTCAACCCTCA	ATTGGAGAAGATGGTTTGCG	226	BM1487	3	9.7	mth2-25e14	7	65.5
RCS6954	LG6	18.63	BB925043	B	GGT	16	GCTTCCATTCAACCACCACT	TAGCATCTGAAGCAGCGAAA	252				mth2-12i20	2	5.2
RCS1746	LG6	19.41	BB931532	A	AAG	16	TTCAATGGCTTCCAACAACA	CGTGGTGGGAGAATTCAGAT	143	TM0206a	1	72.2	mth2-49j14	1	51.6
RCS6668	LG6	20.99	BB921533	B	AAT	17	TTGAACCTGAAAATCGAGCA	CAAGAGATGTGAAGGCACGA	268	BM1177	5	29.1	mth2-34o21	7	62.5
RCS4886	LG6	21.59	DE236771	D	GGA	23	TTGGAATTTTGATCTTGGGG	CACATCCACCATGCAAAGAG	188				mth2-8i21	ND	
RCS2302	LG6	22.26	DE226989	D	AAAC	15	GCCTTGGTTGTTGCCTATTC	GCATTAACACCTTGGGATGAA	131						
RCS4394	LG6	23.88	BB907301	B	ATC	15	GCAGACGGAAGAATAGAGCAA	TGGGGGTAACAGGAAAAAGA	203						
RCS4845	LG6	24.85	DE237258	D	AC	23	TCTACGGGAAGCTGCATGAT	ACTTTGAAGGGCATGAGGCT	127				mth2-15d23	7	63.2
RCS1327	LG6	25.04	BB929119	A	ATC	24	ACGGTGGAATTATGGGATGA	AAACAAACCAAGCAGCACCT	244				mth2-70d8	ND	
RCS4863	LG6	26.22	DE237470	D	AAC	21	CGGAAGAAGCATATACAGGGA	GCTGGTTTTTGGTGCCTTAC	256						
RCS1167	LG6	27.02	DE218187	D	AAC	15	TCCGGTGCATTTCTTTTCTC	TATCACGGTGGTGGCAATAA	220	TM1479	1	71.4			
RCS4678	LG6	27.35	BB908940	B	GGA	18	TGTCAATTTTGACTCCAGCG	AGGCAGCATTGAAAAGGAGA	300	TM0820	3	43.6	mth2-18n7	1	52.4
RCS5910	LG6	28.40	DE241552	D	AAAC	17	ATGTCATCGACGGAACATCA	GGAAATTTAGGCCGGTGTTT	162						
RCS3146	LG6	28.71	DE231283	D	AAAT	20	ACTGTGTTGACGCAGCAATC	GGTAATAGGGTGTTGGACGG	188						
RCS0083	LG6	29.50	DE246606	F	AT	22	AAACTCACGTTTAACAAGCTCTCA	TGGTATGTTCAATTGCACTCCTT	145						

RCS3711	LG6	29.73	BB902782	B	AAG	18	TCAAGGACCAAACCCTCATC	AACCTTTGAGCATGTGGGAC	148	TM0918a	1	77.4	mth2-6m16	1	19.2
RCS4892	LG6	30.45	DE237309	D	AC	15	TCAAATTCAGTTTTGCACGC	TGTCAATGCCAATAACACCTG	131						
RCS6502	LG6	30.97	BB919638	B	AAT	15	TCACAATGTCACCAACAAAACA	TTGCACTTTTTCTCAGTGGCT	164	BM1702	ND				
RCS2510	LG6	32.35	BB934798	A	AAG	18	CACGAGGGAACACTTCATCA	GCCCTAAAAGTTGAAAGAGCA	252	TM0426	3	30.8			
RCS0031	LG6	32.71	DE246109	F	AAAG	19	CCTCCTTGCATCATCTTTTC	AAAACTCGTTCGAGAGAGTG	135	BM1282	1	73	mth2-6g4	7	64
RCS5622	LG6	33.81	DE238948	D	AAAG	16	TTAACGGGATTGGAGGTGAG	TGTTGTTGGAAGCCATTGAA	258						
RCS5211	LG6	34.30	BB912407	B	AAG	15	CCAAAACACAACAACCTCAA	CGATTTTTGTGGTGAAAGGG	110				mth2-104a2	7	64
RCS5764HR	LG6	34.31	DE239808	D	AAAT	16	TCATGCATAACGGGTCGTAA	ATGCATACATGGTCGGCATA	188						
RCS1001	LG6	34.44	DE217348	D	GGT	24	TGCACAATGTGTGCTGAGTG	GAGTTGGAGGTGGTGCTGAT	217				mth2-8i21	ND	
RCS6830	LG6	34.57	BB923405	B	AAGC	16	CAACAGCATAAACCGAAGCA	CCAGCTTGATCCACACATTG	263				mth2-14n9	8	1.6
RCS6562	LG6	35.05	BB920280	B	ATC	15	GGCTGCTTTTTCCAACCATA	CCTCTGCCGTGTACACCTTT	269						
RCS5576	LG6	35.48	DE238555	D	AAAG	15	CCAATCAACCAACACAACACA	AATGGAAGTGAAATCCGTGG	107				mte1-84h13	ND	
RCS0428	LG6	35.64	DE214240	D	ATC	19	GAATGCCAAGACACCTGTGA	TCTCATCAAGGGAGGTGGTC	175						
RCS3736	LG6	35.65	BB902916	B	AAAC	16	CCAGCCCAAAAGAAAAATGA	GTTGGAGGCAGGTGTTTGTT	143	TM0144	1	72.2	mth2-17d15	7	62.5
RCS4413	LG6	36.42	BB907465	B	AT	20	TGAAATTTGAAACAAACTTTATGATGA	AACCTGATTCAAAACCGCAG	274	TM0122	1	72.2	mte1-84h13	ND	
RCS3085	LG6	36.63	DE231848	D	AAAT	34	ATAAGGGTGCATCTGTTGGC	TCCCATCAGGAATCGAACTC	192	TM1198	1	72.2	mth2-24h22	7	71.4
RCS2795	LG6	37.81	DE224251	D	AACG	16	GGGAAGAAGGAGCCACTAGAA	GTTCAGCGTCAATCACCACT	300						
RCS5604	LG6	37.89	DE238837	D	GGT	15	CCGACCTCCACCTGATTAGA	GGTGATGGTGGAGCTTTGAT	300	TM1141	1	71.4	mth2-26c3	7	60.3
RCS3492	LG6	38.21	DE236362	D	AC	22	ACTGTCTGGGATGTTGGAGG	TATCCCTATCATGCGGAACC	175	TM0122	1	72.2	mth2-24h22	7	71.4
RCS3234	LG6	39.35	BB940038	A	AAT	21	CAACACTTCAAATGCAATACCA	TCAAGCTTGGTCTTGAGAGAAAC	132						
RCS0041	LG6	40.54	DE245531	F	AAT	54	GCTACGATTTTGAACGAATG	AAACTCCCTTATCCCCTTTA	119						
RCS3640	LG6	40.62	DE243659	E	AT	46	GGTCTGGATTTGATCCCTGA	TGAAAAAGTTTACCAAGGGCA	157				mth2-145p5	ND	
RCS3862	LG6	41.88	BB903830	B	AG	18	TGTTCCAACCAACTATTCTCATTT	TGGGGTTCCAGTTTGAACAT	237	TM0397	1	71.8			
RCS6021	LG6	42.42	BB915212	B	AG	16	TCCACAAACACCTTCAGCTC	GGGTTTTGGTTTTGGGAGAT	138	TM1275	1	71.4	mth1-3f12	6	
RCS4696	LG6	42.62	BB909090	B	AAAT	16	ACCCCAATTAAAAGCATCCA	CTTTGGGACTGCAAAGAAGC	252				mth2-24f5	7	58.4
RCS5533	LG6	42.67	DE238091	D	AGC	15	GCGGCCATTATACATCGAAT	TTTTCTCATGGTGGCTTTGA	279				mth2-24j7	4	
RCS2569	LG6	42.93	DE228701	D	ATC	18	AGAGAGACGGGACCATTTCC	TGTTGTTGTTCATGGTGGTG	283						
RCS5496	LG6	43.33	DE237991	D	AAAC	17	GGAAATTTAGGCCGGTGTTT	ATGTCATCGACGGAACATCA	162				mth2-28a1	7	64.2
RCS5611	LG6	43.56	DE238848	D	AAC	18	CCGTTCTTCAAAAATAGGGTTT	TCTTGAAGCCATTGCAAAACT	160						
RCS4364	LG6	44.24	BB907068	B	AATT	16	ACCAAAACGCGGTTTCATAC	CCAGCATGATGAATCAACGA	243				mth2-43g15	ND	
RCS1398	LG6	45.27	DE219890	D	ATC	16	TCCAAATACAGATTCATCACCAT	GGTCGGAGGTGGTGTTGTTA	250						
RCS2874	LG6	46.03	DE229980	D	AAT	20	CCTTTTACGTCAGGGACCAA	TCCAAGATCCAACCAAGTCC	221				mth2-77o10	7	60
RCS0252	LG6	46.31	DE213664	D	ATC	15	GGTAGTTTCTGACTTTCCCGTGT	TACAAAAGGGACCTGCTGCT	153						
RCS2522	LG6	46.73	DE228223	D	GGT	17	ACTTCCCAACATTCTCACGC	GTGGAGGTGTCAGAGTGGGT	245						
RCS5705	LG6	47.29	DE239049	D	ATC	15	CAAGGGTGTTTGGAAGAGGA	GGGTCACCATCTAGAACCACA	197						
RCS6916	LG6	47.90	BB924246	B	GGT	16	GCTTCCATTCAACCACCACT	AAAGGGTTTGCATGTTCCAC	218				mth2-136k22	1	43.9
RCS2317	LG6	48.19	DE227812	D	GGT	26	ACTTCCCAACATTCTCACGC	GCCGGTAACCTGTTTGACAT	240	TM1518	ND				
RCS5132	LG6	48.47	BB911894	B	AAAC	16	CCGAACATGTCTCATCGTGT	AAGAGACAGCGACGAATGCT	198						
RCS3025	LG6	48.70	BB938547	A	ATC	54	CACTTCCACAACCAGCTTCA	GGTCTGTGGAGGGTGTTAGC	174						
RCS5333	LG6	49.43	BB913377	B	ATC	15	TCTTAGGACCAGCACCACCT	ATTGGAAGGTGTCTGCAACC	119				mte1-45n16	7	60

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS6705	LG6	49.47	BB921247	B	AATT	16	GCGGTTTCATACAAAATCGAA	GCCAACATGATGAATCAACG	240				mth2-43g15	ND	
RCS6228	LG6	49.64	BB917035	B	AAC	15	AGACCTCGTCAACATCCGAG	TCCTACTGGTTCAATAACATTGG	282				mth2-77o10	7	60
RCS5708	LG6	50.92	DE239036	D	AC	20	TCCATGAAGAAGGTGCACAG	CGCCTTGCTTGAAATCTCTC	130						
RCS7189	LG6	51.21	BB927833	B	GGT	16	TTTCAATTCTGGTGGCTTCC	TAGCATCTGAAGCAGCGAAA	266				mth2-135j6	1	43.9
RCS7188	LG6	51.23	BB927832	B	AAAT	20	TCCAAGGCAATGCTATGACA	ACCAGATGGTCATCCAGGTC	261	TM0940	2	41.6	mth2-9i24	5	20.2
RCS4289	LG6	51.30	BB906583	B	AG	21	TGGGGACCAAACCATAAAAA	TGGAAATGCCGGTAGAGAAC	284						
RCS5764R130	LG6	51.79	DE239808	D	AAAT	16	TCATGCATAACGGGTCGTAA	ATGCATACATGGTCGGCATA	188						
RCS4490	LG6	52.15	BB907986	B	GGC	15	TGAGTCTGACGAACCTGCTG	TCGCAATCGCATACTGACTC	197	TM0605	1	67.4			
RCS6966	LG6	52.56	BB925190	B	AGC	15	GCTTTGCCCATAAAATCCAA	AACCATGCCTCAAGTCAACC	244				mth2-17l1	ND	
RCS4648	LG6	52.66	DE237044	D	AG	42	CCTTAACCATCACTACCGCC	TCCATGAAGAAGGTGCACAG	147						
RCS6605	LG6	53.02	BB920655	B	AAT	17	TAAATGTCATGCCATGCTCG	TCCTGAGCATCATCAATCCA	167						
RCS2826	LG6	53.07	BB936332	A	GGT	19	GATTCTGAACTTCACGCGCT	CAGCGATGGAGAAAGTGGAT	265						
RCS6535	LG6	53.31	BB920015	B	AAAT	20	TATTGGTGCTGATTGGGACA	CCAAAGGGAAAAAGAAACACTG	239				mth2-75b23	7	49.1
RCS1868	LG6	53.41	BB932137	A	ATC	17	CCACCTTAGACCACAGCCAT	GCTCACCTTCAGAATCCTCG	162				mth2-27f3	7	50.4
RCS5414	LG6	53.93	BB914099	B	AAC	15	TAAGGATGACCCAACCAAGC	TTCTTCTTGGACTTGCACCA	285	TM0537	5	10.9	mth2-66m17	1	58.2
RCS3642	LG6	54.19	DE243608	E	AAAT	16	GCGGAGGTTTGGTTACATTG	TGACTTTTTAAAATAATTTGGGTTTTG	264						
RCS0194	LG6	54.44	DE213444	D	AAC	21	CGAAATCGGTTGAAGAAGGA	TGACATCAGAAACAACATCAACA	155	TM0650	1	63.8	mth2-28p22	5	0
RCS2634	LG6	54.80	DE228842	D	AAC	18	CCCCATTAACGTGTTCTGCT	TTTTTACTCCGTGCCGAATC	286				mth2-28g10	7	55.5
RCS7185	LG6	54.92	BB927448	B	AAAC	20	TCAAACAATCTCTCTCCCACAA	GACTCAGGGACGAGATCGAG	107				mth2-27f3	7	50.4
RCS3112	LG6	55.41	DE230753	D	AAAT	27	TTTTCGGGTGCAGAGAGAAT	CCCTTCCAAATCACCTCATC	289						
RCS2388	LG6	55.88	DE225998	D	AAC	15	TTGGATCTAAAATGACAATAAAATTCA	TTTGAAGGTCAATCATTGTTCG	143						
RCS6986	LG6	55.95	BB924887	B	AAT	15	CGCAACAGTTCTTCATTCCA	CGGAGACTAAACGGAACTCG	258						
RCS5456	LG6	56.43	DE237727	D	ACT	15	CGGCGAAAACCCTAATTACTC	GGTCCAATTTGAAGTCAACACA	186						
RCS5457	LG6	56.83	DE237748	D	AAAC	19	GAGAAAACAAAAAGCGGTGG	GCCAAAGGATATCTCTCTCTTTCT	170						
RCS1255	LG6	57.34	DE218632	D	AAG	24	TCAGTGATGAATCGATTTTGTTT	CGTCAACGGTGACTGCATAG	221				mth2-34a12	7	53.3
RCS4244	LG6	57.70	BB906376	B	AAC	21	ATTATGGCAGCAGAAATGGC	CCTTGGTGTCAAAAGGGTCT	195	TM0098e	1	63.4	mth2-34a12	7	53.3
RCS6730	LG6	57.78	BB922209	B	AAAT	16	GCATCATTCACGTACAACGG	CCGGTAAATCTGCTGGTGTT	266						
RCS1446	LG6	58.00	BB929656	A	GGT	15	GGACACGTGGCTACCTGATT	CGGAAAGACTCGAGACGGTA	182				mth2-6j14	7	53.3
RCS4511	LG6	58.06	BB908126	B	ATC	18	CAACCTGGCCCACACTTAAT	TGAGATGCAAAATGATGAAGC	270						
RCS5503	LG6	58.34	DE238008	D	ACT	15	CTTCCCCAACTTTGAAGATCA	CCACGGGATTGATTCCTTTA	204	TM1213	1	63.4	mth2-19l15	7	53.3
RCS7137	LG6	58.63	BB927097	B	AG	22	CACAGCTAAACCACCAGAGTGA	TGACAACAAAGGAACCCACA	267				mth2-11o9	4	31
RCS6064	LG6	58.65	BB915607	B	GGA	15	TTCCTTCACACTCACCCCTT	TTGTTCCTCCCTCTCCTTCA	286	TM1326	1	63.4	mth2-34a12	7	53.3
RCS7037	LG6	58.90	BB925757	B	AG	26	GAAAAGAAGCCAAAATCACCA	TGACAACAAAGGAACCCACA	300				mth2-2k12	8	33.9
RCS1150	LG6	58.99	DE218048	D	AAG	16	CTTCCCAAACACGCCTTAAA	AGCAGGGGTAACACAGCAAT	237						
RCS6995	LG6	59.49	BB924986	B	AT	18	CATGACACATGCCAACAACA	TTCTGGTGGTTTTCCCTACC	269	TM1715	3	9.7			
RCS3421	LG6	59.76	BB940278	A	ACT	16	TCAGTTTGGTCTTCCATCACC	CAGGTTCAATTGCAGGAGAGA	98	TM0386	1	23.3			
RCS3666	LG6	59.88	DE243864	E	AC	20	CATGGCTGCCTGAGGTTAAT	TCTGTTTCTTGTCTCGGCCT	212	TM0284	1	28.6	mth2-33n6	7	47.7

RCS5831	LG6	60.14	DE240429	D	AAAT	24	CGTGAGATGGGGACTTTTGT	TGGGAGGGAAAAAGTGAGTG	130				mte1-60d3	ND	
RCS3044	LG6	60.26	BB939111	A	GGT	15	GGACACGTGGCTACCTGATT	CGTTTCGAGATCTTTCCTGC	237				mth2-6j14	7	53.3
RCS0690	LG6	60.41	DE215297	D	AAC	15	CACCCACACACACACACTCTC	TTGTTGCAATGAGCATTATGG	103						
RCS4219	LG6	60.68	BB906171	B	AG	37	CCCTTTTTCATTTTTATAATAACCC	CACATCACCAATTCCACCTG	215				mth2-27l9	7	47.7
RCS1080	LG6	61.07	DE217789	D	AAC	15	CCAACGCCACTGTCTAGCTC	CGTGGGTTGTTTTTCGAGAT	207						
RCS5741	LG6	61.86	DE239440	D	AAAT	29	GGTGCCCAAAGCATAAGAAA	AGTGTGTGGGGTGGGTATGT	240						
RCS1687	LG6	62.12	BB933008	A	AG	21	CCTTGTTAAGTTCAGGAGAACCA	AGGATCGGAAGGACGAATCT	157						
RCS4571	LG6	62.76	BB908612	B	AG	23	AAATCATAACCAGATCCCGC	GAGACGAAGAGCGATAACGG	254	TM1602	1	31	mth2-36p20	7	49.1
RCS4976	LG6	63.07	BB910693	B	AAT	21	AACCGGACAAGCCTTCAATA	TCATGAATCCAAAAGGACGTT	296				mth2-72m3	ND	
RCS3331	LG6	63.60	DE235106	D	AC	116	AAAGGACGACGAAGACGAGA	GCCGTGTGGGTAGAGAGAGA	189						
RCS2308	LG6	65.25	DE227039	D	AAAC	18	CCCCATAGAACCATACCCAG	CATTTCCAACTCAACTTCATCG	285				mth2-9m5	7	55.5
RCS4155	LG6	65.47	BB905838	B	AAT	57	CGGAAGTTATCGATGCAAAG	GAAAAGGGGAGGAATATGGC	249	TM0386	1	23.3			
RCS4537	LG6	65.78	BB908324	B	GGA	15	AATCTCACCCGAGTCACCAC	GGGGCCTAACACGATCAGTA	245				mth2-192a14	7	
RCS6313	LG6	66.56	BB917753	B	AAG	15	TCGTATTCCACACACACAAACTC	GGCAAGGGAAAGAGAGAAGG	290				mth2-75b23	7	49.1
RCS0623	LG6	67.79	DE214993	D	GGT	16	CTCCTGGTTACGGATCTCCA	GGAGGAGGGTAGGTTGTTCC	154				mth2-27f3	7	50.4
RCS1554	LG6	68.06	DE220387	D	AAC	21	TCGAGTGTTGTTTTGCGAGA	TGAACCAACACCAATGGAGA	150				mth2-81g19	7	56.1
RCS2385	LG6	72.85	DE225976	D	AAAG	16	TGCTAGGGACACACTCTCACA	GGTTTGGGTTATGCCTCTCA	286				mth2-28h7	ND	
RCS2933	LG6	73.92	BB937827	A	AG	17	TTCAATTTCGCAAAAGGGTC	CGAGGGTCTCATTCTTGCTC	270	TM0502	1	70.2			
RCS1499	LG6	75.36	BB930055	A	ATC	15	TCATCGATCCAAATTCCACA	CCCATTATTATGGCGTGGAT	158				mth2-15l17	2	35.9
RCS1770	LG6	75.99	DE220892	D	GGGA	16	TCACGTGAAACGGAAAGAAA	GTAACCGTTGCTAATCCCGA	263				mth2-8g20	7	57.7
RCS3311	LG6	76.16	DE234966	D	AAAG	30	AGCAGAAAGGGACTATGAGCA	TAGTTGGGACTTGGGAATGG	155						
RCS1879	LG6	76.35	BB932269	A	AAC	15	AGGTGCGTTTGAGTAACGCT	CATGCACCACAACAACAACA	113	TM0881	ND		mth2-6e22	4	3.2
RCS2032	LG6	76.85	BB933343	A	GGT	17	AGTGGCTTTCGGGGTTACTT	CAAACTCATTTCCACCACCG	184	TM0326	ND				
RCS4309	LG6	77.42	BB906823	B	AAC	23	CACTAATTCAGACCACCAGCA	TCGGTGAGCTGTGACTAACG	223						
RCS3355	LG6	77.59	DE235375	D	AC	15	TTCACTTTGTTTATTTGAGAGAGTTT	TAATCACACACACACCCCGT	107						
RCS5265	LG6	77.68	BB910889	B	ACT	15	GCCAAGGCAAATTCAAGAAA	CACTTGCTTGCACCTTTGAA	129				mth2-34p9	4	11.8
RCS3052	LG6	78.13	BB939151	A	AAC	17	TCGGTGAGCTGTGACTAACG	CACTAATTCAGACCACCAGCA	217						
RCS0998	LG6	78.48	DE217366	D	ATC	19	TGAGGAAAATGAGACCAGTGA	TTCTTGCCACAACTTTTCCA	157						
RCS2616	LG6	78.67	DE223153	D	AAAT	15	ATCAATGGCGCCAAACTAAG	CCAATTTGCAACCAATTTTCA	168	TM0749	2	32.3	mth2-71h24	7	
RCS3856	LG6	80.06	BB903742	B	GGT	15	TTCACCACCAGCAGCATAAG	AAGGTCACGTCCTGGTTTTG	232						
RCS5620	LG6	81.25	DE238928	D	AAC	18	TGTTCCCTTAAACGCGTAGG	TGTTGGTGTTGCAAATGGAT	183						
RCS1835	LG6	81.78	BB931673	A	AG	25	TCTTGTTGAGTTCAGGAGAACC	AGGATCGGAAGGACGAATCT	161						
RCS5589	LG6	82.07	DE238653	D	AAC	24	TTGAAACGCCAACCATCATA	TTTGGCGTCATTGATTCTCA	257						
RCS5269	LG6	82.49	BB911699	B	AT	15	GCTCAAAGGGGCATTTAACA	CCTGCACGGAGTTTCTTCTC	263				mte1-61j12	ND	
RCS6512	LG6	83.96	BB919719	B	AAAC	16	TTGGCCAATAAAATTGTTTCC	CAGGTGGTGCTGGTCCTAAG	277				mth2-16n21	7	11.2
RCS0069	LG6	84.42	DE245983	F	AAT	31	ATTGCAAACCGAACCTGAAC	TACAATCCCTCGGTGCATTT	152						
RCS4854	LG6	84.84	DE237288	D	GGT	15	GAGTTAATGGCGATGATCCG	GTGGTGTAGAGTGTGGGGGT	101	TM1508	1	51.7	mte1-49d11	7	21.9
RCS3310	LG6	85.41	DE234978	D	AAAG	15	GATGTGGTGTTGTTGCCTTG	TTATTGTGGTTGTCAATAAGCCT	203				mth2-17l1	ND	
RCS6587	LG6	86.94	BB920534	B	AATC	16	CCCAAAAGGGGTTACCATCT	TGCCCTTGCTACAACAACTG	193	TM1542	1	0	mth2-7f11	7	2.9
RCS4661	LG6	87.08	BB908694	B	AAC	18	CACGAACAACAACTCCACCA	TGAGATTGGTGTTGATCGAAG	278				mth2-15p5	7	2.2

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS1624	LG6	87.08	BB932450	A	AAC	18	AAAACCAACACCTTTGAACTTGA	TCGTCTCACTCCCTCCAACT	219	TM0676	1	44.8	mth2-128d9	ND	
RCS1683	LG6	88.06	BB932926	A	AAC	15	ATCCCAAGTCTGTTGTTGGG	TGGTGAGATTGAGGAGGAGG	168	TM0676	1	44.8	mth2-128d9	ND	
RCS2408	LG6	91.32	DE226255	D	AAG	18	GCGGAATCCCAAGATGAATA	CATCAGCAACACCAATGACC	274				mth2-10e12	4	63.4
RCS6362	LG6	91.39	BB918217	B	AAAG	16	CATAGTGGTCAGCTCCAGCA	TGCCATGGTTGATGAAGAAA	128				mth2-75l24	7	10.6
RCS5481	LG6	92.34	DE237890	D	AAAC	18	CCCCATAGAACCATACCCAG	TCTCATCCTCATTTCCAACTCA	294				mth2-9m5	7	55.5
RCS3608	LG6	95.57	DE236474	D	AAAG	21	CGACGCACTCCACATAGTTG	AGCGGATATTGAACACTGGA	300				mth2-14c17	7	5.1
RCS0743	LG6	96.05	DE215565	D	AAG	18	GCTTCGACCATGCTCTTCTC	TGGGTCATTGCAAGCTTATG	109						
RCS0019	LG6	108.20	DE245223	F	AAT	30	TTTTTCTCTCATTAAATTCATTCACAA	CATTCATTGCATTGTTTCTTCAA	163						
RCS5673′	LG7	0.00	BB914656	B	AGC	15	GCTCCCTCAGCAACAGAATC	TTTTGTTCGTGCTGGTCTTG	225						
RCS1616	LG7	1.89	BB930941	A	ATC	15	CGCTGTGTCTCCTTTTGACA	TGTTGTTGTTGCGATCCATT	238						
RCS0861	LG7	3.76	DE216321	D	GGA	15	TCCCAAACCACAATCATCAA	CGGCATTCCGCTTCAGTC	250	TM0155a	3	32.8			
RCS6927	LG7	6.30	BB924294	B	AGC	18	TAAAGCGAGGGCAACTCCTA	GAGCAGGAGTAGTAGCCGGA	128						
RCS6739	LG7	7.37	BB922306	B	AAAC	22	ATTGGATTCAAGTTGGACGG	AGAAAGCACCCTCCGGTTAT	238				mth2-25m19	4	49.5
RCS5486	LG7	8.38	DE237948	D	AAAC	24	TTACGAATCCCGGTTCTGAC	ATTTGGGTTGGGATCACATT	240	TM0845	ND				
RCS5673	LG7	9.28	BB914656	B	AGC	15	GCTCCCTCAGCAACAGAATC	TTTTGTTCGTGCTGGTCTTG	225						
RCS4671	LG7	9.33	BB908887	B	AAAT	16	TGGGGACCGATTCTTGTTTA	TCTTCATTGCTGATTTTGCG	231				mth2-15n13	3	0
RCS4983	LG7	9.34	BB910712	B	AAT	15	TGGAAGTGCAAGCAAGAACA	GGCCTTCAACTGAGGAATCA	252	TM0845	ND				
RCS1963	LG7	9.89	BB933934	A	AG	16	AAATCCAATGAGGCGACAAG	AGCCTTCTTCCACAAGCAAA	293	BM1488	ND				
RCS4720	LG7	11.20	BB909260	B	AT	16	TCTTCTTGAATATACCTGCTGATTTTT	TGTTTCTGACGGTGGTGGTA	284				mth2-22p22	4	10.3
RCS2370	LG7	13.50	DE225939	D	AG	34	TGGGAGGGAACGTATTTGAG	CTTATCCGGGAGAAAGGGAG	194						
RCS2738	LG7	15.27	DE223305	D	AAAC	16	TGGAGATGGAGGAGAAGGAG	AAGGTAGCTGCTGTTGCTGA	291	TM0334a	1	17.7	mth2-34i10	3	72.5
RCS2546	LG7	17.27	DE228477	D	AAC	20	ATATTCCCCCACCACCTCAG	CGGAATTTCCAACGGTAAGA	104						
RCS0004	LG7	17.66	AB234883	C	AAG	22	GCATCTCCACCGTTCTTCTC	TGCGACGGTGTTTTCTAGTG	188	TM1565	1	71.4	mth2-47j13	2	57.8
RCS6693	LG7	18.61	BB921956	B	AAT	15	CATTGATGAAGACATGACATGAAA	ATTGGATGGAATGGGAACAA	137	TM1283	3	14.5	mth2-15j7	2	1.5
RCS4481	LG7	19.77	BB907795	B	AAG	18	GAGTTGGAGTTGGAGTCGGA	CAGGGATAGCATCAAAGGGA	295				mth2-2b2	3	62.9
RCS3343	LG7	21.52	DE235230	D	AGC	15	CCCTTTGCTAACCCTAGCTG	GAGACGAATGAAGGAAACGG	133						
RCS5744	LG7	22.77	DE239505	D	AAAC	19	GGAGATATGCTCATTCCCCA	TGTCGTCGTATCATTTCCGA	251	TM1437	3	84.8			
RCS4237	LG7	24.43	BB906301	B	ATC	18	TGCAGAAACAACTTGAGATACAAA	CGCAAAGTGTGTTGCTCTGT	173						
RCS1696	LG7	25.19	BB931064	A	AAG	27	GGCACGAGGTCAACTTCACT	ACGGTGACAGGAACAACCTC	215				mth2-49j14	1	51.6
RCS5791	LG7	28.39	DE240031	D	AAAT	20	ATGGATCGATTGTCTCCGAA	GGGCACTGGTTAAGGAGCTA	269				mth2-25k8	3	69.2
RCS4226	LG7	29.35	BB906233	B	ACG	18	CATCCTTTGTCATTGTGTTGCT	ATGGCGACATTAAAGCCAAG	289						
RCS0901	LG7	30.06	DE216635	D	GGA	15	CGTTGTTGTTGTTTTTGAGGAA	CCCGCTAAGGCATTCTATCA	151						
RCS3828	LG7	30.34	BB903573	B	AAT	36	CCACACATTTTCATGATCACC	GGCTTCTGTAATCGACTCGG	270				mth2-10o11	ND	
RCS4003	LG7	34.12	BB904794	B	ACT	15	TCACAATGGGCACCTAATCA	CAATTTTCGCTGACTGACCA	222	TM0217	3	76	mth2-9o20	8	67.5
RCS2866	LG7	34.70	DE230005	D	ATC	15	CGGTTTGAATTTGAACATGG	TATGAAGGTTTAGGCGTGGC	251						
RCS2179	LG7	34.73	DE225266	D	AAG	20	CTGCATTCGCTTGTTGATGT	CGCCACATGTTCAATTCTTC	234						
RCS3170	LG7	35.68	DE232151	D	AAAT	15	GAAGGAGGCAGTTGCAGAAC	ATCCGATCCGATGTGAGACT	275						

RCS5874	LG7	35.84	DE241262	D	AAAG	16	GCGGTCCAAACTGTTGATTT	AATTAATTTATCGTTGATTCTCACTTC	279						
RCS0798	LG7	37.54	DE215827	D	AAG	17	AGGCATCGATGAGGTAGTGG	CAGATTCAACTGGTGGTGAAAA	123						
RCS2720	LG7	38.35	DE225706	D	AG	42	TGTGACAGTGGCAGACTGG	TGTCTCCTCGCTGTTTCCTT	186						
RCS4002	LG7	39.42	BB904784	B	AAAT	15	GCACATGCACACCTCATCTC	CAGAAGCAATCCCACCAACT	229	TM0017	1	48.1	mth2-49l23	7	
RCS2156	LG7	39.58	BB935217	A	AAG	29	GGAAGATGGAGCCACCATAA	AGAACCACTTCTTCTGGCGA	255	TM0017	1	48.1	mth2-18n7	1	52.4
RCS5485	LG7	39.64	DE237938	D	AAG	15	CCATGAAACCACCACTTCAA	AGGCTGTGATTTGTTTTGGG	180	TM0580	4	53.9			
RCS2981	LG7	39.87	DE230300	D	AAAT	22	CCCTAGCAACACAGTGCAGA	GCAACATGTTCAATCCCAGA	217						
RCS1320	LG7	41.05	BB929104	A	GGA	15	AAGCCGCTTTTTCTCTAGGC	CGGAATGCGATACCTCTTCT	162						
RCS0079	LG7	41.11	DE245646	F	AGC	15	TGTGTGTGGTGGAAGTGTCC	GGTCCATGTTATGCCACACC	120						
RCS1805	LG7	41.30	DE224360	D	GGT	15	ACTCTTCCTCCACCTCCTCC	TGCTAACCCAACCCATATCC	142						
RCS5101	LG7	41.60	BB911602	B	GGT	15	CCGTGACCCAGGTAAAAAGA	AACATAACCGGACGAGCAAC	294	TM1012	6	57.6	mth2-53f22	2	1.5
RCS7150	LG7	41.69	BB927327	B	AAT	15	AGAACCCTCTGCAGATTCAA	AACTGCACCGTCGAGTTCTT	299						
RCS5974	LG7	42.54	BB915065	B	ACT	18	AACAGTAAATCAAACCCCCTCA	ATTTTGGCAAGAATGTGGGA	135	TM0026	4	2.8			
RCS0017	LG7	42.56	DE245306	F	AT	16	TAGTGCTGCTGCACAAATCC	GGACTTCTCTGATATTGAACTGAATG	164				mth2-22c4	1	22.2
RCS6563	LG7	42.67	BB920246	B	AAG	39	TGCAGTCACCAACCAATGTT	TAACCCGGTCATTCCTCAAG	250				mth2-29f16	2	3
RCS1698	LG7	42.89	BB931078	A	AAG	18	TGGTAGCCATGACTCCAACA	GCAGCGTTCTCTTCCATTTC	199				mte1-59b16	ND	
RCS4174	LG7	43.04	BB905901	B	AG	25	TCAGTTAATATCTTCCATTCAATTTCC	TCACTTCCACCAACATCCAA	243	TM1754	3	8.1	mth2-81g19	7	56.1
RCS1834	LG7	43.08	BB931665	A	GGA	18	TATTTCCCCATCCACCGTTA	TTTGGAGGGAAAGAATGTCG	139	BM1086	1	21.7			
RCS5640	LG7	44.00	BB914432	B	ACT	15	GCATGATGGCTTGAGGATCT	GGAGGGATAATTGGAGCAGG	164	BM1109	1	19.3			
RCS1628	LG7	44.18	BB932469	A	ATC	17	ATCTCAAAAACGACGATGGC	CGTCCAGTTTTCAAGGCTCT	259	TM0442	1	12.5	mth2-171n13	ND	
RCS5573	LG7	44.35	DE238567	D	AATT	16	CTGTCAAAGCACGTGGAAGA	TGCTCAAGAATGGAGACACG	299				mth2-94j16	4	47.4
RCS2155	LG7	45.32	BB935174	A	GGA	15	GGACACATCAGTGCCAGTTG	TGTTGGAACAGGAGCAACAA	166	BM1010	1	49.3			
RCS5101′	LG7	45.77	BB911602	B	GGT	15	CCGTGACCCAGGTAAAAAGA	AACATAACCGGACGAGCAAC	294	TM1012	6	57.6	mth2-53f22	2	1.5
RCS2967	LG7	46.14	DE230069	D	AAG	16	GGTCCCTTAAAGACCTTGCC	CGCCATTATTGTCGTTACCC	272				mth2-10f9	ND	
RCS4164	LG7	46.59	BB905847	B	AAC	16	TTGCCACGTATGCAGGTTTA	AAGGCTTCGTGAAAGCAAAG	116						
RCS0187	LG7	47.22	DE213346	D	GGA	17	GCCTCTGGCAATGATTGAGT	CCACAGAACCAAGCAAAACA	150						
RCS4472	LG7	47.29	BB907823	B	AAG	26	TCTCACCCTCCTCAACTGCT	ATGAGTTTGTCGGTCTTGGG	126	TM0017	1	48.1			
RCS0370	LG7	47.30	DE213977	D	AAC	15	GCTATCTGTTTGACGGAGGTG	CAAAACAAATATCACTTCATCTTCTT	159						
RCS5357	LG7	47.86	BB912838	B	ATC	15	ATCCGCTGAAAACAACCAAC	TTCGAAGAGCCAGAGGAAAA	198	TM0358	1	0	mth2-8i21	ND	
RCS2278	LG7	47.96	BB934757	A	AAG	26	ACCACCATCACCATCCACTT	AAGCTCCTCTGGTGGGAGAT	281						
RCS5745	LG7	48.55	DE239515	D	AAAT	21	TCGGTGTATGCGATTCTTTG	GGTCGTTGTGAATGTGTTGG	275				mth2-78b21	2	1.5
RCS5151	LG7	48.82	BB912029	B	AAT	15	TGGCACTCATAGCATTCCTG	AATCAATTTTGGCAGCAAGT	265	BM1085	4	60	mth2-10b9	2	15.6
RCS2196	LG7	49.28	DE225651	D	AAG	16	CAACGCGTTTTCTTCTCCTC	TACCCTGCAAAACAAAAGGG	198						
RCS6665	LG7	49.79	BB921500	B	ACT	15	TTCAAGATTTTTGGAAGTGATTTT	AGGTGGGGACACAGTAGTGG	270						
RCS2698	LG7	50.01	DE221921	D	GGA	26	TTGTGCAAAGCAGCAAGTTC	ACTCCAGATGCAGATGTCCC	290	TM0246c	3	43.6	mth2-22g24	8	59
RCS4108	LG7	50.39	BB905460	B	AAT	18	TTGAAGCAAACTTGGAAGCA	CACGGAAAGGGCAAGAAATA	250				mth2-16j22	3	72.5
RCS2850	LG7	51.25	DE229867	D	AATG	16	AAGAATTCCTTGGTTTCGCA	TGTTTCTGGAGCAGTGTTGTG	297				mth2-29h7	3	72.5
RCS3517	LG7	51.51	DE242893	E	ATC	15	TGGCATGAAATCAAGCACAC	AGGAAGTGGTGGAGAAAGCC	291						
RCS4926	LG7	51.56	BB910199	B	GGT	17	TCAGCAAACAGCTGGTGAAG	CTACTCGGTGGGATCGGTTA	130	TM0017	1	48.1	mth2-18n7	1	52.4
RCS0831	LG7	52.33	DE215996	D	AAG	15	TTTTCACCCCGATCTTTTGT	TTCAATCCAACCAACACAGC	152	TM0431	5	37.5			

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS3171	LG7	52.39	DE232180	D	AAT	21	CATAAACAGTTGGCGCCTTA	TTTGTTGCCTTAATCAATGTCC	194						
RCS4832	LG7	52.54	BB910083	B	GGA	18	TTGTAACACCCACTCGCTTG	GAATCACACGTGAAGGGAGG	114	TM1402	3	68.4			
RCS6710	LG7	52.66	BB921976	B	AAAT	15	AGCATAAACCAAATCACCAGG	TGGGTTTTAGGAGTGATGGTG	209	TM0412	1	12.1	mth2-33g10	3	72.5
RCS7076	LG7	52.85	BB926309	B	GGA	15	TCTTCCTCCACCACCACAAC	TGCTGTTGCTGTTCCTCCTA	123						
RCS6614	LG7	53.37	BB920024	B	AAT	18	CTCCATTGCAGTAGCCACAA	GGATCTTCACCACTTTCGGA	284						
RCS2803	LG7	53.57	BB935863	A	AAC	18	CAACGCTCTTCTTCGAAACC	CCGCTTTCCGTTGTCTTTAG	213	TM0498	1	12.1			
RCS6508	LG7	54.09	BB919666	B	AGC	21	CACTTCCCTGTCCCTTTGAA	ATCCAACCAGAAAACCCCA	203				mth2-10h12	3	71.8
RCS2185	LG7	54.14	DE225399	D	AAG	18	AAACAATCAAAAACCGACAACA	TGCTGTTCCATCACCAATTT	151				mth2-6m1	3	59.3
RCS4697	LG7	54.23	BB909095	B	AAAT	16	GGTCATCCACTGAATAAAAACCA	AAGTTGCTTCTGGGTGTGCT	290	TM0988	1	0	mth2-12a18	3	63.7
RCS6980	LG7	54.55	BB924822	B	AAAT	16	AAGATGGTCCATAGCATAAGCA	AGTCGTACCAGGACGTGACC	277	TM0988	1	0	mth2-12a18	3	63.7
RCS6516	LG7	54.63	BB919228	B	AT	36	ACATTGGATCAGCAAGGACC	GCTGGGATGGTTATTGGCTA	277						
RCS4030	LG7	54.97	BB904998	B	AC	19	TTGCAATAACATGGACTAGAGGA	TCAAGTTTATTGCGGAACCC	228	TM0487	1	16.1			
RCS2247	LG7	55.41	BB934280	A	GGA	15	GTTCACCAGGACTTTTGCGT	GCCTCCGGATCTTCTTCTCT	157				mth2-7g7	ND	
RCS2176	LG7	55.79	DE225267	D	GGT	15	AGCTTCACTCAGTGGCGTTT	CACGTGGAAGAGTTCTTGGAG	159						
RCS1482	LG7	56.13	BB929864	A	GGT	15	GAATCAACGGTCTCGGAAAA	TTCCATCCATCCATCATTCA	156						
RCS5985	LG7	57.31	BB915094	B	AAAG	16	TCAGCAATTCAAGTGGTTTACAA	CCCCTCCTGCGGTAGTAAC	209						
RCS6179	LG7	57.82	BB916459	B	AAG	30	CAATGTCAGAACCCAACAACA	TTGGAGTAGCTGAAGGACGG	205				mth2-6m1	3	59.3
RCS0712	LG7	57.87	DE215381	D	AAC	15	AAGTCACAACATTTCCTCACCA	TTGGTGGTGGAGTTGAAAAA	150				mth2-164l15	ND	
RCS4903	LG7	58.13	BB908801	B	AATT	22	TTGACGAATCAAGTGGCATC	GGATGAGGATTCCGTGAGAA	112	TM0099a	2	68.8	mth2-36j24	3	72.5
RCS3802	LG7	58.57	BB903405	B	ATC	22	ACACATCACACATGGGTTGG	CCAAACCAAGCCAACAACTT	231	TM0843	ND		mth2-49l23	7	
RCS6973	LG7	58.66	BB924700	B	AAG	15	ACAGAGCCTCATCGAGCAAT	CTGTGAAAGGTGCAGAAGCA	281						
RCS4253	LG7	59.03	BB906418	B	ACT	15	CAATTTTCGCTGACTGACCA	TCACAATGGGCACCTAATCA	222	TM0217	3	76	mth2-23j1	4	51.8
RCS1787	LG7	59.41	DE224302	D	AAG	21	ACCGGGTAGCTGATCTTCCT	ATTGGTGGTGTTTTTGAGGC	145						
RCS7071	LG7	59.54	BB926297	B	ATC	15	ATAGCTCCCTTCTGTTGCCA	TAAGCTGGCATGGATTTTCC	241	TM1166	2	60.2			
RCS7089	LG7	59.54	BB926684	B	AAC	15	CACCGTTGCCTACTTAGAATCA	TGTCAGCTGAAGCAAGCAGT	242	BM1289	2	67.4	mte1-58k20	ND	
RCS6702	LG7	60.07	BB921201	B	GGA	18	TCATCCAAATCATGGACCAA	GCACCTGGGTACAAAAGACC	200	TM0442	1	12.5	mth2-3j15	ND	
RCS1336	LG7	60.27	BB929154	A	AAG	22	ACCCATTTGATTCTCCACCA	CCGAATTTGGCTTTTGAGAG	169	TM1633	1	12.1			
RCS4104	LG7	60.63	BB905480	B	AAG	22	CCAGGGAATTTCACGAAGAA	GAATCGGAATGGATCGAAGA	105	TM1176	1	12.1	mth2-10h12	3	71.8
RCS1234	LG7	60.76	DE218364	D	GGT	15	CAACCACCTTTCATTCCTCAA	TGTGTCACTCAACTCATTTCCA	219				mth2-53f22	2	1.5
RCS6867	LG7	60.78	BB923767	B	AAAG	15	TAATTTCGCATTGGGAACAA	TGCATTCAATCAAATCACGA	233	TM1674	3	34.8			
RCS7214	LG7	61.05	BB928245	B	AT	22	TGCTACCTTGGATGTATTTGAA	AGCATTGGAATTGGGAACAC	188						
RCS6018	LG7	61.47	BB915418	B	AAAG	16	CACCCCAAAAACCATTCAAA	GGATTAAAGGGAGGTTTGCG	225	TM0043a	5	51.1	mth2-36n3	8	67.5
RCS0270	LG7	61.83	DE213717	D	AAC	16	TTGTCCTTGATTCCTTTGTCG	GTTGTTGTTCTGGGGACGAT	161						
RCS0763	LG7	61.85	DE215596	D	ATC	15	GTGCCAGTGTCCTCCATCTT	GGGGGATAGAGGGCTGATAG	108						
RCS1117	LG7	61.95	DE217915	D	AAC	15	CCCTTTCTCCTTGGATCCTC	GAGGTGGTGGTGAATGACG	201	TM1633	1	12.1			
RCS6662	LG7	62.22	BB921521	B	AT	16	TGATTCAATTCCTGTGGCAA	ATCAAAGTGGTGCCCCATAA	298	TM1570	3	57.5			
RCS3579	LG7	62.53	DE243292	E	AAAT	19	CTCTACGTTCACACCACCGA	TGCGCCAAATAATAATGTGAA	253						

RCS3631	LG7	62.73	DE243562	E	AAGC	16	GTATGCAAACCAAAACGCCT	GGCGTAGGGCAACCATATTA	294						
RCS1547	LG7	63.06	DE220360	D	AAAC	15	CCCATGTGCAATGAGAAAGA	TGGCCAATCCAAATTACACA	166				mth2-135p20	4	3.2
RCS6813	LG7	63.32	BB923201	B	AGC	21	CCACCTGGTGCTGATAAGGT	TTCAAGGACCAAAACTTGCC	236				mth2-77f21	4	33.2
RCS5804	LG7	63.41	DE240183	D	AAAT	19	GTGATGCAGGCATTTCCTTT	GGCCTGGAGTCTTCCAATCT	196						
RCS1640	LG7	63.58	BB932540	A	AG	53	TTGGAGGCTTGCTTTCTGAT	TGAAATCATCAAAACTGTGCG	164				mth2-78c5	1	39.4
RCS1432	LG7	64.23	BB929371	A	AAC	15	CCTTTCGAGGAACCAAATCA	ACTGAGTTTAGCGGGTGCTG	237	TM0671	1	8.8	mth2-12n15	1	
RCS1897	LG7	64.44	BB933110	A	AAAG	57	CATGTCAGCATATCCATTTTCC	ATGAGCACCTTCACCAATCC	280	TM0892	1	53.7	mth2-32i15	2	1.5
RCS7199	LG7	65.27	BB927969	B	AAAG	15	ACCAAAGAATCTGCACACCC	CATTGAAGGCTGGGTGATCT	111				mth2-66c24	ND	
RCS5433	LG7	65.64	BB914242	B	AAG	17	CATCCTCTCATCTTCCTCACA	AGAAATGGTGGATCGGTGAA	91				mth2-33n6	7	47.7
RCS2015	LG7	65.82	BB931717	A	GGA	17	GGTCGTCCCCAAGGTAAAAT	GGTGAAGGTGGTGGAGAAGA	212						
RCS1413	LG7	65.85	DE220015	D	GGT	24	CTGGAGCCAATTCCTTCAAA	GGGTTAATGATGAGGTTGCTG	162						
RCS5574	LG7	66.04	DE238505	D	ATC	15	TGGAGAATTAATTTTGGCGG	GGACGATACGGTGAGTGTGA	255				mth2-145a1	8	37.7
RCS3872	LG7	66.24	BB903885	B	AATG	16	CTCGCACAACCCAAAGTGTA	CTTAGAGGCAAGGCTGGTTG	182	TM1265	1	0			
RCS5291	LG7	66.38	BB913044	B	AAAT	20	CCCTTAGGAAAGGGGGAAAT	AGCCGCAGAGCAGATTGTAG	288	TM0204	2	66.6	mth2-24a18	3	59.3
RCS2839	LG7	66.78	BB936594	A	AAG	20	TCACTCCCAAATTCCCACTC	GGATGGGTTGAGGAATGATG	220				mth2-189o22	ND	
RCS5461	LG7	66.80	DE237772	D	AAG	15	TTGATCTTCATGACAAGGCG	AAGAATCGTCGGGAAATTCA	178				mth2-49f2	8	38.3
RCS2642	LG7	66.81	DE228959	D	AAG	15	AAGAATCGTCGGGAAATTCA	TTGATCTTCATGACAAGGCG	174				mth2-7g10	8	38.3
RCS5876	LG7	66.81	DE244141	E	GGT	15	GTCCTACAAGACCACCACCG	GTTGTTGTTGGTTCGGCTTT	181						
RCS5942	LG7	66.87	DE242541	D	GGT	15	TGACGATAGAACCACCCTCC	ACCGCTTGTGCTTTTTCTGT	156				mth2-11a20	3	59.2
RCS2879	LG7	66.92	DE229948	D	AAAT	20	TAACTGGCCACATTTTGCAC	TTGGATTCATGCTATTCCACA	128	TM0672	3	35.2	mth2-88g17	ND	
RCS3208	LG7	67.38	DE233209	D	AAT	25	TCCACTTATGTCCATAGACAACTACA	GTTGGAAGCATAGAGGGGGT	162						
RCS3098	LG7	67.55	DE230379	D	AAAG	15	ACGATGCTTCCTGCAAGTTT	GAGGTTGGCATAATGAGGGA	265						
RCS7237	LG7	68.14	BB928672	B	AAG	15	TTCTGAGTGGCAGCAACAAC	TGCGTCTTTTCTCTGCTTGA	215	TM0002	2	66.6	mth2-24a18	3	59.3
RCS1632	LG7	68.38	BB932503	A	AAG	25	GGACTTGGTCTTTGGTTGGA	GATTAATAAGAACACCCCGCC	224	BM1245	1	19.3			
RCS2898	LG7	68.54	BB937023	A	GGT	24	TGCCATCGTCATCATCATCT	TTGACTAATGGGTCCACGGT	254				mth2-15p5	7	2.2
RCS0915	LG7	68.64	DE216789	D	AATT	15	TGCAGTGTTTCATCAAAAGAAAA	GCCCAGTCAAAAATGGCTAA	171						
RCS3126	LG7	68.69	DE230994	D	AAT	15	TTTTCAAATTTAATAACTTCTTGCAC	CGAAACCATTCCATTCCATT	294						
RCS3089	LG7	69.37	DE232001	D	AAAT	20	TTGGATTCATGCTATTCCACA	TAACTGGCCACATTTTGCAC	128	TM0672	3	35.2	mth2-88g17	ND	
RCS3084	LG7	69.57	DE231801	D	AAT	23	TCCACAACTTTTGCGATCAG	GGAACAAAGTCCTGTTTGGC	213						
RCS2436	LG7	70.23	BB935407	A	AG	71	CTCTCCCCCATAGAAACCGT	ACGGGGTTGTGATTGTGTGT	150						
RCS5998	LG7	71.47	BB915248	B	AAT	17	TTGACTCAAACACACCCCAA	GTGGCGTTTCAAATCCTTGT	261				mth2-30o12	ND	
RCS1254	LG7	71.51	DE218572	D	AG	45	TCCTGATACATGTCACTGCTGA	TCCATGGCATAGAGAGAATGG	187						
RCS2371	LG7	71.89	DE225927	D	AAG	18	TTCCATTTCATGGCTCCTTC	CAATACGGAAAGGGAAACCA	268						
RCS1343	LG7	72.09	DE219058	D	GGT	15	CACACTTCACAAACAATGAATCG	TTGGATCGGGTGGTGGAC	166						
RCS2538	LG7	72.32	DE228372	D	AC	18	AAAGGAACCCTGCAATGAAA	TTTGCGCATGGAAAAAGAAT	102	TM0990	ND				
RCS6900	LG7	72.33	BB924057	B	AAT	19	AAGATTGCTTGATCGAACGG	GCCACCGTAACACGTTTTCT	211	TM0539	6	47.8	mth2-9e24	2	3
RCS2834	LG7	72.57	BB936475	A	AAAG	17	TCCTCTCCCTTGGTGTCATC	CGTGCTTCAGTTGTTCCTGA	274				mth2-9j13	1	43.9
RCS3276	LG7	72.62	DE234464	D	AAAT	24	TTGATCTAAAGTTGACACATCAACAA	ACTTAATGCATGGGAGCCAA	156						
RCS2848	LG7	73.46	DE229877	D	AAT	18	TGCTCTTCCTGTTCGGAGTT	GCTTTGCTTTGGCTTCATTC	296				mth2-158c2	8	28.8
RCS3297	LG7	73.67	DE234831	D	AG	51	CTAGTGCAACATCCGGGACT	TCGTTGGTTAAGACCAAAGGT	104						

Table A1. Continued.

Marker name	LG	cM	Accession no[a]	Library[b]	SSR motif	Length[c]	Fw_primer (5′ to 3′)	Rv_primer (5′ to 3′)	Size[d]	Lj clone	chr	cM	Mt clone	chr	cM
RCS5795	LG7	73.75	DE241072	D	AC	18	TGGGAGAGACAGGTTAGAACG	CTGCGATTGACAACACTGCT	292						
RCS3441	LG7	73.96	DE235724	D	AC	15	TTGTGCAGGTAAAAGTAAATTGTAGG	AATCAGGAAGAAGGGAGGGA	120						
RCS5662	LG7	74.02	BB914623	B	AATT	20	TTAGCCATAGCCACAAGGGT	AAAAATCCATCATAGCTGCCA	221						
RCS2851	LG7	74.49	DE229885	D	AAT	17	TCAACTCCACTTGTGTCAAAAA	CTGGATGGAACTGGAGGAAA	202						
RCS4232	LG7	75.02	BB906285	B	AAT	15	TCAAGTCACAACAAAACCAAAA	CTTCAGAAAATGGCATGGCT	187				mth2-8c24	8	50.2
RCS2963	LG7	75.40	DE230035	D	AAAT	25	GCTATATGCGAGATGGAGCC	GGTCCATAACGAAAGTGGGA	290				mth2-24n22	1	50.9
RCS5580	LG7	76.38	DE238599	D	AAC	27	AAATTTTGTTCCGGAGCCTT	TTACCCTCCAGTATTCATCCG	262						
RCS2000	LG7	77.21	DE221444	D	AAG	43	AAGTACCGATGTGGGACTTCA	GGCTTCCTGCAGATGGAATA	287	BM1377	6	48.6	mth2-9c15	2	6.4
RCS3384	LG7	77.49	BB940510	A	GGC	15	ACCGTAACAAAATCAACGGC	ACCGGTTCACTCCGAAATTA	192						
RCS3267	LG7	78.03	DE234255	D	AAAT	22	GCAACATGTTCAATCCCAGA	CCCTAGCAACACAGTGCAGA	217						
RCS2681	LG7	78.19	DE229400	D	AG	57	CCATTCCTGGTTGTCAGTCC	TTCTTAGCTTGAAGGGCACG	154				mth2-10d10	2	37.9
RCS2499	LG7	78.28	BB934899	A	ATC	33	ACCCATCAACCCAAACTCAA	AATTTGCACCGTTTCCATTC	297	TM1331	4	2	mth2-19l4	2	49.5
RCS5616	LG7	78.31	DE238886	D	AG	40	TGTTTGAGCGAAGTTGTTTGA	CCCGTTTAGTTCATCTCCTCTC	218						
RCS6592	LG7	78.65	BB920572	B	AG	16	CCCCAAATTTTCTTCCGTTT	CACGTGGACCTTACCGTCTT	161	TM0539	6	47.8	mth2-9e24	2	3
RCS5623	LG7	79.32	DE238952	D	AAG	19	GTTTCGTTTTCGTTTTTCGC	AATCCCAGCCATCAGATTCA	151						
RCS4797	LG7	79.58	BB909791	B	AT	33	GCCCGTCTACCTTTTGTTCA	GCGCCATAAGCAACTGTGTA	190				mth2-14p11	5	16.5
RCS2507	LG7	79.67	BB934371	A	ATC	33	AATTTGCACCGTTTCCATTC	ACCCATCAACCCAAACTCAA	297	TM1331	4	2	mth2-19l4	2	49.5
RCS2486	LG7	80.68	DE227645	D	AAG	15	CGACCAATTCAGGTTTGTGA	CCATTTCTTTGCTTTTTCTCCA	240						
RCS4165	LG7	81.75	BB905858	B	ATC	15	GCTTTACGTGATAGAGCGCC	TCCACAAGCCCCTTTAAGC	207	TM0139	6	47.8	mth2-15j7	2	1.5
RCS5569	LG7	83.14	DE238510	D	AAG	15	ATCATCTCACCGGATTCTCG	TCGGGTCGAATAAAATTTGG	264				mth2-17l10	8	50.9
RCS2358	LG7	84.26	DE228061	D	ATC	17	TCATCTCAATCTTCATCCCCTT	GGAGTAACCCGCAATGTGTT	123						
RCS5969	LG7	85.40	BB915030	B	AAG	18	TGCCAAATGTAATCAATGCAA	CGGTCATCCCACTTATCCAC	166	TM0674	ND		mth2-19g23	ND	
RCS4702	LG7	85.67	BB909166	B	GGA	17	AAAAATTTCCCCTTCCTCCC	AAGCCCTGGGCAGTAGAAAT	179	TM1181	6	52.3			
RCS0051	LG7	86.89	DE245353	F	AAG	26	CCATCGTAGGTTTCCCTGTC	GTCAGAGAAGTTGACAACGC	133						
RCS2604	LG7	88.93	DE222895	D	GGAT	16	AATTTGTGTGAACCTTCTTCTTTT	TGTAGCCATTTCTGTGTAGACTGT	91						
RCS4342	LG7	89.70	BB906975	B	AAC	20	AGAGAACGATGAAGAGGCACA	CCCGACAGCGGTTTAACTT	174				mth2-8c19	2	42.6
RCS3125	LG7	91.07	DE231021	D	AAAT	23	GCGGCCTAGTATGTCGGATA	GGCCATGGCTAATGAGAAGT	246				mth2-7k13	8	44.9
RCS3266	LG7	91.61	DE233881	D	AAT	15	CAAATTTTGGGTTTGTTATTGTTTT	CGGATTTACGGTTTAAGCAGA	107						
RCS5712	LG7	92.48	DE239111	D	AAG	18	GGGGTTGCTGCAAAATAAAA	TGCATGAGAGCAAGTGAAGG	202						
RCS1887	LG7	94.53	BB932316	A	AG	18	GCACGAGGCAACACTTTCTC	AATTTGGATTCATGGGGCTT	101				mth2-6e22	4	3.2
RCS1883	LG7	95.00	BB932305	A	ATC	15	CATCGGAGATAGCATCGACA	CATCTCACCACCCTCTCCAT	260	BM1001	3	27.6	mte1-49g8	2	
RCS0695	LG7	95.88	DE215250	D	AAC	15	ACTGCTCCATCACCAGAAGC	GATGTCATGGGGTGGTTTTC	168						
RCS7029	LG7	97.15	BB925657	B	ATC	21	GGGGAATATCTGCACCTGAA	TCGGTCTGTTCGAAACTTGA	268				mth2-28d22	8	28.8
RCS7202	LG7	98.70	BB928033	B	AAG	15	TGCATTATCCAAAACATCGG	AATTGCAGGACATTGAAGGG	128						
RCS1743	LG7	99.68	BB931489	A	AG	16	CCAAACAACCCCTAACCCTT	GAGGTGGTGTTGGAATTTGG	254	TM1754	3	8.1	mth2-32i15	2	1.5
RCS5135	LG7	101.78	BB911877	B	GGA	18	CGAGTGCTCCAACAGAACAA	TAGAGGGTTCATCTCCACCG	204				mth2-10p14	5	50.4
RCS2594	LG7	104.06	DE222805	D	AAC	15	ACGCACCGTTGTCTCTCTCT	AGGGTTGAATTTGTTGACACG	224						

RCS2746	LG7	104.95	DE223390	D	AAG	21	TTCGTCTACCATTTGTTCATGTG	TTTGTGAAAATTTCTTTGTAGGAAAA	98						
RCS1597	LG7	105.38	BB930638	A	AAG	17	TCCTGTTATTCCCCATGGAC	TTGAGTTGAGTTGGGAACGA	99						
RCS6865	LG7	107.35	BB923703	B	AAAT	16	ACTTGCGGTCTGGTTGTCTT	TAGGAAGGTTATGGAGGGGC	248				mth2-30d7	2	57.8
RCS2372	LG7	108.13	DE225913	D	AAAG	20	TTGGAATTGCCTTGAACCAT	TCTTAATTGTGCCATGCTCAG	106						
RCS0685	LG7	108.58	DE215324	D	GGT	21	TGTTGCTACAAGGCCAAAGA	AGCACTTTCGAACACAGCAA	178	TM1622	ND		mth2-5j8	4	38.8
RCS6842	LG7	110.35	BB923490	B	AG	18	CTTGAAAACACACGGAAACG	TTGGTGAAAGAGAGGCAGAAA	293						
RCS5570	LG7	111.10	DE238544	D	GGA	21	AATCCCCAAAAGCCATATCC	GGAAGATTGAGGTGGTCCAA	262						
RCS0102	LG7	112.80	DE246674	D	AAC	15	AAGGGTGTTGTTTCTGTTGTTG	TTTTTGGGTTCGGACAGCTA	150						
RCS1200	LG7	113.89	BB928863	A	AC	15	TCATTCTTCCACCGACAACA	CGTAGCGTTGAGCTTTTGTG	170				mth2-85c24	ND	
RCS5224	LG7	113.93	BB912518	B	AAT	18	TGACTGGTTCTCTTTTATCCTGT	TCTGGATGAAAAGCCGGTAG	267				mth2-85c24	ND	
RCS6762	LG7	114.20	BB922563	B	AAC	17	CTCCGACAGCGGTTTAACTT	CCTCATCGCTTGTCTCTTCC	298				mth2-8c19	2	42.6
RCS5022	LG7	114.34	BB911020	B	AGC	15	CATGGTTTCAAGTCGGGTTT	GCATTGTATGATGGACGACG	190				mth2-188k3	8	70.4
RCS0793	LG7	114.40	DE215825	D	AAG	20	CGCAATCTTTCTTCTCATTTCA	TTCAACATGCAGGCTAAGAAAA	199						
RCS6069	LG7	114.42	BB915713	B	AAT	15	TCCAACTTTGGGGTTTAACAA	GGCCTTCAACTGAGGAATCA	161	TM0845	ND				
RCS1050	LG7	114.46	DE217576	D	AC	31	AATGACGAGGGACGACAAAC	GCAGTAAAACACAGATAAAGGCAGT	163						
RCS1422	LG7	115.57	BB929355	A	AAC	17	AACTGAACCCAACCATGCTC	GTGGAAACCCTGGTGGTATG	215	TM0987	ND				
RCS4439	LG7	120.37	BB907581	B	AAC	15	CCGGAACCCGAATTTTTAGT	TCTTGTACTCTTCGCCGTTG	295	TM0702	3	60.7			

[a] Accession numbers in the DDBJ, EMBL and GenBank databases.

[b] The libraries where the SSRs originated are indicated. A, SSR-enriched cDNA library; B, normalized cDNA library; C, selected cDNA clones; D, SSR-enriched genomic library; E, methyl-filtrated genomic library; F, random genome sequences.

[c] Total lengths of the SSR motifs are indicated (bp).

[d] The product sizes estimated from the sequences are indicated (bp).

Table A2. List of RFLP marker loci.

Marker name	LG	cM	Seg.type[a]	Accession no[b]	Length (bp)	Hit CDS	Annotation
C189Dra	LG1	66.18	<lmxll>	AB236796	1459	At3g09630	Putative 60S ribosomal protein L1
C2401	LG1	69.54	<nnxnp>	AB236827	1917	At3g55760	Unknown protein
C1483	LG1	90.21	<lmxll>	AB236753	1952	At2g45550	Cytochrome P450
C1961	LG1	107.19	<lmxll>	AB236800	2522	At2g37040	Phenylalanine ammonia lyase (PAL1)
C1882	LG1	109.15	<hkxhk>	AB236795	1841	At5g42620	Major surface like glycoprotein
C1062	LG1	125.50	<lmxll>	AB236740	1922	At2g37550	Asp1
C2413z	LG2	0.00	<hkxhk>	ND			
C298	LG2	6.61	<lmxll>	ND			
C189Hind	LG2	24.32	<efxeg>	AB236796	1459	At3g09630	Putative 60S ribosomal protein L1
C1602z	LG2	31.02	<nnxnp>	AB236778	3282	TC233119	Weakly similar to GB|AAO39919.1|28372874|BT003691 At2g04235 {*Arabidopsis thaliana*}
C2134x	LG2	33.39	<nnxnp>	AB236815	1687	At3g56860	Unknown protein
C2413y	LG2	38.71	<hkxhk>	ND			
C361w	LG2	38.78	<nnxnp>	AB236843	2226	At5g52560	Unknown protein
C1552	LG2	41.61	<efxeg>	AB236763	1364	At3g09630	Putative 60S ribosomal protein L1
C361v	LG2	41.64	<nnxnp>	AB236843	2226	At5g52560	Unknown protein
C361z	LG2	44.15	<lmxll>	AB236843	2226	At5g52560	Unknown protein
C1556	LG2	46.93	<hkxhk>	AB236764	2068	At3g23820	NAD dependent epimerase, putative
C361y	LG2	47.80	<lmxll>	AB236843	2226	At5g52560	Unknown protein
C1568	LG2	50.13	<lmxll>	AB236768	2570	At1g77590	Long chain acyl-CoA synthetase 9 (LACS9)
C2409	LG2	50.71	<hkxhk>	AB236831	1797	At5g10170	Myo-inositol-1-phosphate synthase-like protein
C361x	LG2	60.95	<lmxll>	AB236843	2226	At5g52560	Unknown protein
C361u	LG2	66.74	<lmxll>	AB236843	2226	At5g52560	Unknown protein
C1547	LG2	66.93	<nnxnp>	AB236760	1455	At5g65470	Unknown protein
C2014	LG2	69.88	<abxcd>	ND			
C692z	LG2	72.00	<hkxhk>	AB236855	2531	At2g40360	Putative WD-40 repeat protein
C692y	LG2	72.83	<hkxhk>	AB236855	2531	At2g40360	Putative WD-40 repeat protein
C1602y	LG2	81.28	<lmxll>	AB236778	3282	TC233119	Weakly similar to GB|AAO39919.1|28372874|BT003691 At2g04235 {*Arabidopsis thaliana*}
C7y	LG2	81.48	<lmxll>	AB236856	1917	At5g53770	Unknown protein
C2053z	LG2	85.33	<hkxhk>	AB236807	1794	At3g48360	Unknown protein
C1492	LG2	91.07	<lmxll>	ND			
C1834z	LG2	91.31	<hkxhk>	AB236787	2215	At4g04720	Putative calcium dependent protein kinase
C2344	LG2	98.72	<lmxll>	ND			
C1861	LG2	102.92	<hkxhk>	AB236792	1438	At4g27000	Putative DNA binding protein

C1834y	LG2	105.08	<lmxll>	AB236787	2215	At4g04720	Putative calcium dependent protein kinase
C2415	LG2	107.52	<lmxll>	ND			
C461	LG3	10.03	<nnxnp>	AB236845	1552	At5g47210	Unknown protein
C1421	LG3	15.13	<hkxhk>	AB236748	2147	At5g41460	Unknown protein
C1770	LG3	21.70	<efxeg>	AB236782	1649	At5g61820	Unknown protein
C1867y	LG3	21.90	<nnxnp>	AB236793	2414	At2g30950	Zinc dependent protease (VAR2)
C2404W	LG3	23.54	<nnxnp>	AB236829	1797	At5g10170	myo-inositol-1-phosphate synthase-like protein
C2404v	LG3	25.04	<lmxll>	AB236829	1797	At5g10170	Myo-inositol-1-phosphate synthase-like protein
C2404x	LG3	28.48	<lmxll>	AB236829	1797	At5g10170	Myo-inositol-1-phosphate synthase-like protein
C2404z	LG3	33.37	<nnxnp>	AB236829	1797	At5g10170	Myo-inositol-1-phosphate synthase-like protein
C1873z	LG3	34.52	<hkxhk>	AB236794	2146	At5g46420	Unknown protein
C2404y	LG3	39.01	<lmxll>	AB236829	1797	At5g10170	Myo-inositol-1-phosphate synthase-like protein
C2047	LG3	40.97	<hkxhk>	AB236805	1847	At4g13940	Adenosylhomocysteinase
C1873y	LG3	42.17	<lmxll>	AB236794	2146	At5g46420	Unknown protein
C2407	LG3	47.97	<hkxhk>	AB236830	1391	At2g17120	Receptor-like GPI-anchored protein (lysM) 2
C2147	LG3	50.96	<lmxll>	AB236821	1526	At4g00620	Putative tetrahydrofolate synthase
CA1769	LG3	51.25	<nnxnp>	ND			
C1942x	LG3	51.86	<lmxll>	AB236799	2864	At2g16500	Arginine decarboxylase
C1867z	LG3	52.87	<nnxnp>	AB236793	2414	At2g30950	Zinc dependent protease (VAR2)
C1942z	LG3	54.89	<lmxll>	AB236799	2864	At2g16500	Arginine decarboxylase
C16	LG3	55.71	<lmxll>	AB236776	1448	At4g38970	Fructose-bisphosphate aldolase like protein
C559	LG3	56.13	<abxcd>	AB236849	2851	At2g16500	Arginine decarboxylase
C2428y	LG3	59.39	<lmxll>	ND			
C1942y	LG3	59.74	<nnxnp>	AB236799	2864	At2g16500	Arginine decarboxylase
C1410	LG3	61.74	<nnxnp>	AB236747	1899	At1g66130	Unknown protein
C2428z	LG3	63.48	<nnxnp>	ND			
C2134w	LG3	63.65	<nnxnp>	AB236815	1687	At3g56860	Unknown protein
C1525x	LG3	64.54	<hkxhk>	AB236756	1564	At1g09750	Unknown protein
C1602x	LG3	64.70	<nnxnp>	AB236778	3282	TC233119	Weakly similar to GB|AAO39919.1|28372874|BT003691 At2g04235 {*Arabidopsis thaliana*}
C1942w	LG3	65.81	<nnxnp>	AB236799	2864	At2g16500	Arginine decarboxylase
C1867x	LG3	69.54	<efxeg>	AB236793	2414	At2g30950	Zinc dependent protease (VAR2)
C1525y	LG3	70.63	<nnxnp>	AB236756	1564	At1g09750	Unknown protein
C2133z	LG3	71.71	<lmxll>	AB236814	1660	At5g63810	Beta-galactosidase (emb|CAB64746.1)
C1525z	LG3	72.88	<lmxll>	AB236756	1564	At1g09750	Unknown protein
C2133y	LG3	73.72	<lmxll>	AB236814	1660	At5g63810	Beta-galactosidase (emb|CAB64746.1)
C1860y	LG3	73.92	<nnxnp>	ND			

Table A2. Continued.

Marker name	LG	cM	Seg.type^{a}	Accession no^{b}	Length (bp)	Hit CDS	Annotation
C7z	LG3	74.64	<lmxll>	AB236856	1917	At5g53770	Unknown protein
C1860x	LG3	77.19	<nnxnp>	ND			
C1602w	LG3	78.62	<lmxll>	AB236778	3282	TC233119	Weakly similar to GB|AAO39919.1|28372874|BT003691 At2g04235 {*Arabidopsis thaliana*}
C2133x	LG3	86.68	<hkxhk>	AB236814	1660	At5g63810	Beta-galactosidase (emb|CAB64746.1)
CA61z	LG3	87.04	<lmxll>	ND			
C214z	LG3	87.39	<lmxll>	AB236819	915	At1g06680	PSII-P protein (PsbP1, OE23)
C214y	LG3	93.82	<lmxll>	AB236819	915	At1g06680	PSII-P protein (PsbP1, OE23)
C738y	LG3	110.10	<hkxhk>	AB236857	1618	At3g16520	Glucosyltransferase like protein
C738z	LG3	112.79	<lmxll>	AB236857	1618	At3g16520	Glucosyltransferase like protein
C1601x	LG4	6.19	<lmxll>	AB236777	1498	At5g56030	HEAT SHOCK PROTEIN 81-2 (HSP81-2) (sp|P55737)
C1601z	LG4	8.69	<hkxhk>	AB236777	1498	At5g56030	HEAT SHOCK PROTEIN 81-2 (HSP81-2) (sp|P55737)
C2391	LG4	16.92	<nnxnp>	AB236826	1731	At4g12730	Fasciclin-like arabinogalactan protein FLA2
C1601y	LG4	24.96	<nnxnp>	AB236777	1498	At5g56030	HEAT SHOCK PROTEIN 81-2 (HSP81-2) (sp|P55737)
C2454y	LG4	27.89	<nnxnp>	ND			
C471z	LG4	32.64	<lmxll>	AB236848	2018	At3g50670	U1 snRNP 70K protein
C471y	LG4	36.55	<hkxhk>	AB236848	2018	At3g50670	U1 snRNP 70K protein
C1860z	LG4	53.90	<nnxnp>	ND			
C669	LG4	55.16	<hkxhk>	AB236853	3563	At3g04880	DNA-damage-repair/toleration protein DRT102
C33	LG4	55.31	<abxcd>	ND			
C108	LG4	57.93	<abxcd>	ND			
C1535	LG4	60.08	<nnxnp>	AB236758	1564	At1g09750	Unknown protein
C618Dra	LG4	64.49	<abxcd>	AB236852	1443	At2g28000	Putative rubisco subunit binding-protein alpha subunit
C447	LG4	68.13	<abxcd>	AB236844	1999	At2g28000	Putative rubisco subunit binding-protein alpha subunit
C2559	LG4	68.90	<hkxhk>	ND			
C2140y	LG4	72.92	<hkxhk>	AB236820	1987	At5g25110	Serine/threonine protein kinase-like protein
C1254	LG4	73.64	<nnxnp>	AB236741	1405	UP|Q8LJS2	Nucleolar histone deacetylase
C1858y	LG4	73.95	<nnxnp>	AB236791	1963	At3g06580	Galactose kinase
C1858z	LG4	75.17	<hkxhk>	AB236791	1963	At3g06580	Galactose kinase
C143	LG4	81.75	<lmxll>	AB236749	2280	At1g72160	Cytosolic factor
C2132x	LG4	83.18	<nnxnp>	AB236813	1987	At5g25110	Serine/threonine protein kinase-like protein
C2132v	LG4	94.25	<nnxnp>	AB236813	1987	At5g25110	Serine/threonine protein kinase-like protein
C2132w	LG4	99.93	<hkxhk>	AB236813	1987	At5g25110	Serine/threonine protein kinase-like protein
C2000	LG4	102.49	<nnxnp>	AB236804	1568	At3g53780	Unknown protein
C2132y	LG4	105.73	<lmxll>	AB236813	1987	At5g25110	Serine/threonine protein kinase-like protein

C2140V	LG4	111.12	<lmxll>	AB236820	1987	At5g25110	Serine/threonine protein kinase-like protein
C2140z	LG4	113.83	<nnxnp>	AB236820	1987	At5g25110	Serine/threonine protein kinase-like protein
C2140x	LG4	116.82	<lmxll>	AB236820	1987	At5g25110	Serine/threonine protein kinase-like protein
C2132z	LG4	117.00	<nnxnp>	AB236813	1987	At5g25110	Serine/threonine protein kinase-like protein
C465	LG5	0.00	<nnxnp>	AB236847	1876	At5g43960	Unknown protein
C247	LG5	2.38	<hkxhk>	AB236834	1922	At2g37550	Asp1 (asp1)
C1430y	LG5	18.48	<nnxnp>	AB236750	916		
C2134y	LG5	37.80	<lmxll>	AB236815	1687	At3g56860	Unknown protein
C1787	LG5	54.44	<abxcd>	ND			
C7x	LG5	66.42	<nnxnp>	AB236856	1917	At5g53770	Unknown protein
C2138	LG5	77.29	<nnxnp>	AB236817	1627	At3g55010	Phosphoribosylformylglycinamidine cyclo-ligase precursor
C2052z	LG5	82.39	<lmxll>	ND			
C2534z	LG5	87.48	<lmxll>	AB236835	1205	At4g27520	Early nodulin-like 2 predicted GPI-anchored protein
C1528	LG6	17.01	<nnxnp>	AB236757	1848	At3g06720	Importin alpha
C2425	LG6	29.46	<hkxhk>	ND			
C2461x	LG6	38.98	<nnxnp>	AB236832	1125	At5g03740	Histone deacetylase-like protein
C1407	LG6	47.12	<nnxnp>	AB236745	2489	At5g43930	Unknown protein
C2461y	LG6	49.83	<lmxll>	AB236832	1125	At5g03740	Histone deacetylase-like protein
C2403z	LG6	64.20	<nnxnp>	AB236828	1546	At4g16830	Nuclear antigen homolog
C1580	LG6	78.91	<lmxll>	AB236772	1579	At5g60990	Replication protein A1-like protein
C2403y	LG6	86.59	<efxeg>	AB236828	1546	At4g16830	Nuclear antigen homolog
C1842	LG7	14.83	<lmxll>	AB236788	1248	At2g05710	Cytoplasmic aconitate hydratase
C7w	LG7	22.72	<lmxll>	AB236856	1917	At5g53770	Unknown protein
C7v	LG7	33.93	<nnxnp>	AB236856	1917	At5g53770	Unknown protein
C764	LG7	38.04	<lmxll>	AB236858	1664	At5g60980	Ras-GTPase-activating protein SH3-domain binding protein-like
C165	LG7	38.23	<nnxnp>	ND			
C1932	LG7	38.67	<nnxnp>	AB236798	2288	At3g03250	UDP-glucose pyrophosphorylase like protein
C2534x	LG7	38.95	<lmxll>	AB236835	1205	At4g27520	Early nodulin-like 2 predicted GPI-anchored protein
C1984	LG7	39.32	<hkxhk>	AB236803	2129	At5g52560	Unknown protein
C2534y	LG7	44.51	<nnxnp>	AB236835	1205	At4g27520	Early nodulin-like 2 predicted GPI-anchored protein
C1578z	LG7	44.53	<lmxll>	AB236770	1659	At5g60980	Ras-GTPase-activating protein SH3-domain binding protein-like
C1816x	LG7	54.93	<lmxll>	AB236785	2289	At3g08510	Phosphoinositide specific phospholipase C (AtPLC2)
C2532	LG7	56.08	<nnxnp>	ND			
C1861	LG7	61.14	<hkxhk>	AB236792	1438	At4g27000	Putative DNA binding protein
C1816w	LG7	67.25	<nnxnp>	AB236785	2289	At3g08510	Phosphoinositide specific phospholipase C (AtPLC2)
C1816y	LG7	68.84	<nnxnp>	AB236785	2289	At3g08510	Phosphoinositide specific phospholipase C (AtPLC2)

Table A2. Continued.

Marker name	LG	cM	Seg.type[a]	Accession no[b]	Length (bp)	Hit CDS	Annotation
C2056	LG7	70.65	<nnxnp>	AB236808	2102	At3g18380	Unknown protein
C155y	LG7	72.61	<lmxll>	AB236761	1839	At3g15180	Unknown protein
C1816z	LG7	74.97	<nnxnp>	AB236785	2289	At3g08510	Phosphoinositide specific phospholipase C (AtPLC2)
C2534w	LG7	79.10	<efxeg>	AB236835	1205	At4g27520	Early nodulin-like 2 predicted GPI-anchored protein
C155z	LG7	81.56	<nnxnp>	AB236761	1839	At3g15180	Unknown protein
C2134z	LG7	83.63	<hkxhk>	AB236815	1687	At3g56860	Unknown protein
C1578y	LG7	93.61	<nnxnp>	AB236770	1659	At5g60980	Ras-GTPase-activating protein SH3-domain binding protein-like
C1802	LG7	97.12	<efxeg>	AB236784	1367	At4g28390	ADP,ATP carrier-like protein

[a] Segregation type of each locus is indicated by the following codes: <abxcd>, locus heterozygous in both HR and R130, four alleles; <efxeg>, locus heterozygous in both HR and R130, three alleles; <hkxhk>, locus heterozygous in both HR and R130, two alleles; <lmxll>, locus heterozygous in HR; <nnxnp>, locus heterozygous in R130.

[b] Accession numbers in the DDBJ, EMBL and GenBank databases. ND; the corresponding cDNA sequence was not determined.

Table A3. List of the marker loci for evaluation of allele frequency.

Marker name	LG	cM	SSR Motif	Length	Seg.type[a]	Alelle frequency	PIC value
RCS2183	LG1	43.72	AGC	18	<nnxnp>	3	0.50
RCS0035	LG1	48.00	AC	18	<lmxll>	8	0.72
RCS0005	LG1	56.01	AAT	15	<lmxll>	3	0.52
RCS0883	LG1	89.03	AAG	21	<lmxll>	12	0.69
RCS0089	LG1	92.01	ATC	15	<lmxll>	6	0.69
RCS0907	LG1	106.61	AAC	15	<abxcd>	9	0.72
RCS0130	LG2	10.55	ATC	24	<lmxll>	4	0.69
RCS0262	LG2	10.56	AAC	15	<lmxll>	6	0.73
RCS3186	LG2	13.69	AAAT	15	<lmxll>	8	0.81
RCS2450	LG2	24.70	AAG	16	<abxcd>	7	0.63
RCS0747	LG2	26.58	AAG	15	<nnxnp>	5	0.56
RCS3456	LG2	30.37	AAAG	23	<lmxll>	8	0.56
RCS0074	LG2	31.20	AG	30	<abxcd>	8	0.81
RCS2171	LG2	34.71	AAC	15	<lmxll>	13	0.74
RCS1708	LG2	35.66	ATC	19	<lmxll>	5	0.70
RCS1864	LG2	36.08	ATC	28	<lmxll>	6	0.79
RCS1300	LG2	39.85	AAC	15	<lmxll>	3	0.31
RCS1405	LG2	39.93	ATC	15	<nnxnp>	8	0.56
RCS2250	LG2	43.61	ACT	15	<lmxll>	12	0.69
RCS1113	LG2	44.20	GGT	21	<lmxll>	4	0.56
RCS1285	LG2	47.71	AG	39	<abxcd>	8	0.82
RCS3235	LG2	49.68	AAAT	20	<nnxnp>	5	0.56
RCS1273	LG2	50.72	AAC	15	<nnxnp>	5	0.66
RCS2536	LG2	51.81	AATG	15	<nnxnp>	9	0.71
RCS3706	LG2	52.19	AGC	15	<nnxnp>	4	0.17
RCS0254	LG2	52.62	GGT	21	<nnxnp>	9	0.59
RCS1209	LG2	52.64	AAC	15	<nnxnp>	4	0.53
RCS3329	LG2	52.66	AC	17	<nnxnp>	8	0.64
RCS1379	LG2	53.06	AAC	16	<nnxnp>	9	0.85
RCS0399	LG2	53.22	AAG	15	<lmxll>	3	0.16
RCS2382	LG2	53.51	GGT	15	<nnxnp>	6	0.57
RCS1501	LG2	54.64	AAG	35	<abxcd>	7	0.85
RCS0836	LG2	56.57	AAC	31	<nnxnp>	12	0.82
RCS1477	LG2	56.75	ATC	34	<nnxnp>	5	0.58
RCS1409	LG2	58.80	ATC	17	<efxeg>	8	0.76
RCS1402	LG2	60.02	ATC	19	<efxeg>	6	0.71
RCS3665	LG2	60.08	GGT	15	<nnxnp>	2	0.20
RCS0251	LG2	60.74	AAC	15	<hkxhk>	4	0.55
RCS2199	LG2	64.65	AG	15	<lmxll>	8	0.78
RCS0913	LG2	68.88	GGT	15	<nnxnp>	4	0.26
RCS0412	LG2	68.98	GGT	18	<nnxnp>	4	0.20
RCS0898	LG2	69.99	AAC	21	<nnxnp>	5	0.50
RCS2860	LG2	70.32	AAT	21	<abxcd>	12	0.83
RCS0855	LG2	75.29	AAC	15	<nnxnp>	5	0.37
RCS1871	LG2	75.94	AAC	15	<hkxhk>	5	0.50
RCS0078	LG2	79.15	AG	32	<efxeg>	7	0.81
RCS1326	LG2	79.53	GGA	16	<lmxll>	3	0.05

Table A3. Continued.

Marker name	LG	cM	SSR Motif	Length	Seg.type[a]	Alelle frequency	PIC value
RCS1836	LG2	79.79	GGA	15	<lmxll>	4	0.08
RCS2773	LG2	80.56	AAG	30	<abxcd>	14	0.89
RCS2195	LG2	81.96	GGT	16	<efxeg>	6	0.63
RCS0075	LG2	82.97	AG	20	<lmxll>	6	0.62
RCS0715	LG2	84.43	AC	15	<lmxll>	8	0.82
RCS1601	LG2	84.53	AAC	26	<efxeg>	9	0.85
RCS1748	LG2	84.93	ATC	24	<abxcd>	3	0.63
RCS1325	LG2	87.30	GGC	15	<hkxhk>	5	0.61
RCS3469	LG2	87.48	AAG	15	<hkxhk>	12	0.81
RCS0633	LG2	88.90	GGT	15	<efxeg>	2	0.40
RCS2453	LG2	89.32	ATC	16	<lmxll>	8	0.81
RCS0003	LG2	89.73	AAC	22	<lmxll>	4	0.49
RCS3269	LG2	89.81	AAAG	15	<lmxll>	8	0.41
RCS1310	LG2	90.29	ATC	15	<abxcd>	4	0.61
RCS1256	LG2	90.81	AAG	15	<lmxll>	2	0.39
RCS3455	LG2	92.16	AC	20	<lmxll>	5	0.68
RCS3275	LG2	92.82	AC	18	<lmxll>	11	0.82
RCS1479	LG2	96.60	AG	22	<lmxll>	6	0.75
RCS2958	LG2	97.29	AAG	21	<nnxnp>	4	0.47
RCS3145	LG2	97.89	AACG	15	<nnxnp>	5	0.49
RCS1022	LG2	98.28	GGT	15	<lmxll>	3	0.27
RCS0039	LG2	98.98	ATC	15	<lmxll>	3	0.62
RCS3237	LG2	100.19	AAAT	19	<nnxnp>	6	0.69
RCS2193	LG2	100.30	GGGA	20	<lmxll>	3	0.58
RCS3095	LG2	100.51	AAAT	28	<hkxhk>	6	0.72
RCS3102	LG2	100.80	AAAT	28	<hkxhk>	7	0.70
RCS2689	LG2	102.25	ATC	16	<lmxll>	3	0.30
RCS1478	LG2	111.16	AAC	22	<nnxnp>	6	0.72
RCS2533	LG2	112.59	GGT	16	<lmxll>	5	0.76
RCS0453	LG2	113.32	AAG	15	<abxcd>	9	0.78
RCS1935	LG2	121.59	ATC	23	<lmxll>	11	0.71
RCS0606	LG2	123.94	GGA	30	<hkxhk>	3	0.21
RCS0753	LG2	125.93	GGA	35	<lmxll>	7	0.48
RCS1588	LG2	126.13	GGA	30	<nnxnp>	2	0.19
RCS1382	LG2	142.99	AGC	15	<nnxnp>	3	0.37
RCS1627	LG3	14.93	AAC	15	<nnxnp>	7	0.35
RCS0294	LG3	17.48	GGT	23	<efxeg>	10	0.65
RCS2629	LG3	19.10	AAC	18	<nnxnp>	9	0.64
RCS3015	LG3	20.30	AAC	19	<nnxnp>	9	0.80
RCS3587	LG3	20.85	AAAT	19	<lmxll>	4	0.61
RCS1332	LG3	21.38	AAC	16	<lmxll>	7	0.68
RCS1667	LG3	21.91	AAC	15	<lmxll>	7	0.78
RCS2741	LG3	24.66	AAC	16	<abxcd>	4	0.46
RCS3657	LG3	26.74	AATG	16	<lmxll>	6	0.48
RCS1007	LG3	29.95	ATC	15	<lmxll>	6	0.57
RCS2343	LG3	30.25	AC	35	<hkxhk>	12	0.87
RCS1999	LG3	31.00	AAC	19	<lmxll>	12	0.84

Table A3. Continued.

Marker name	LG	cM	SSR Motif	Length	Seg.type[a]	Alelle frequency	PIC value
RCS2010	LG3	33.26	ATC	15	<lmxll>	13	0.71
RCS1735	LG3	33.43	AAC	15	<nnxnp>	4	0.72
RCS1710	LG3	37.00	AGC	15	<nnxnp>	3	0.26
RCS0033	LG3	38.30	AAT	39	<abxcd>	13	0.86
RCS0126	LG3	39.84	GGA	17	<nnxnp>	3	0.44
RCS0465	LG3	39.86	GGA	17	<nnxnp>	3	0.43
RCS3690	LG3	42.35	AAG	15	<nnxnp>	6	0.71
RCS1776	LG3	42.41	ATC	16	<lmxll>	5	0.44
RCS1952	LG3	44.57	AAC	32	<efxeg>	12	0.82
RCS1068	LG3	44.58	AAC	23	<lmxll>	9	0.81
RCS1587	LG3	50.66	ATC	15	<lmxll>	5	0.66
RCS2645	LG3	54.75	GGT	15	<abxcd>	5	0.55
RCS3586	LG3	60.07	AAC	15	<abxcd>	14	0.46
RCS2481	LG3	60.53	AG	15	<abxcd>	2	0.53
RCS0967	LG3	62.40	AAG	15	<lmxll>	4	0.59
RCS0894	LG3	63.26	AAG	70	<abxcd>	12	0.80
RCS0397	LG3	63.94	AAG	21	<abxcd>	6	0.77
RCS3336	LG3	63.97	AAC	15	<efxeg>	8	0.83
RCS0047	LG3	65.17	AAAT	17	<nnxnp>	10	0.79
RCS2377	LG3	66.99	AC	16	<nnxnp>	4	0.61
RCS1008	LG3	68.36	AAG	15	<hkxhk>	8	0.68
RCS0193	LG3	68.79	AAC	17	<nnxnp>	3	0.37
RCS1679	LG3	69.54	AAG	19	<abxcd>	8	0.82
RCS2004	LG3	69.94	AAAT	16	<lmxll>	3	0.55
RCS2875	LG3	70.72	AAAT	23	<lmxll>	3	0.34
RCS1866	LG3	71.02	AAG	21	<nnxnp>	6	0.76
RCS3002	LG3	71.65	ACG	15	<nnxnp>	5	0.66
RCS2544	LG3	77.99	AAAG	15	<abxcd>	10	0.58
RCS3659	LG3	78.68	AAT	15	<lmxll>	4	0.44
RCS0404	LG3	79.57	AAG	18	<lmxll>	4	0.58
RCS3064	LG3	81.11	AAC	17	<lmxll>	9	0.84
RCS1655	LG3	92.17	AG	15	<nnxnp>	3	0.27
RCS0796	LG3	96.21	GGT	15	<lmxll>	2	0.50
RCS1526	LG3	97.71	AAG	29	<lmxll>	8	0.80
RCS0199	LG3	99.47	AAC	17	<lmxll>	7	0.79
RCS3051	LG3	112.88	AG	20	<lmxll>	8	0.59
RCS0992	LG4	8.20	ATC	22	<abxcd>	7	0.74
RCS2270	LG4	17.57	AAG	15	<nnxnp>	7	0.57
RCS1647	LG4	20.84	AAG	26	<nnxnp>	7	0.73
RCS1307	LG4	24.07	GGGA	22	<lmxll>	10	0.84
RCS3709	LG4	30.16	AAC	27	<lmxll>	8	0.80
RCS2558	LG4	30.17	AC	16	<lmxll>	7	0.60
RCS1809	LG4	32.62	GGT	15	<lmxll>	4	0.51
RCS1629	LG4	33.95	GGT	23	<nnxnp>	4	0.38
RCS1931	LG4	36.65	AAG	17	<hkxhk>	6	0.66
RCS0121	LG4	39.07	AAG	33	<lmxll>	8	0.81
RCS0867	LG4	39.81	AAG	77	<lmxll>	10	0.85

Table A3. Continued.

Marker name	LG	cM	SSR Motif	Length	Seg.type[a]	Alelle frequency	PIC value
RCS3383	LG4	39.86	AAC	17	<lmxll>	4	0.52
RCS0040	LG4	48.95	AAAC	17	<nnxnp>	6	0.75
RCS1333	LG4	51.18	AAG	15	<efxeg>	2	0.41
RCS2331	LG4	52.02	AAAT	21	<nnxnp>	7	0.65
RCS2359	LG4	60.03	AAG	20	<lmxll>	10	0.67
RCS1928	LG4	66.30	AGC	21	<nnxnp>	6	0.77
RCS1180	LG4	70.36	GGT	15	<nnxnp>	4	0.12
RCS2728	LG4	71.21	AAC	24	<abxcd>	9	0.77
RCS1411	LG4	71.54	AG	22	<abxcd>	7	0.78
RCS0179	LG4	72.88	AAG	16	<lmxll>	4	0.45
RCS2970	LG4	73.16	AAAT	26	<lmxll>	11	0.45
RCS3140	LG4	73.62	AAAT	22	<lmxll>	7	0.78
RCS3264	LG4	74.16	AAAT	26	<lmxll>	7	0.74
RCS2296	LG4	78.20	AAG	18	<lmxll>	3	0.63
RCS0824	LG4	79.85	AAC	15	<nnxnp>	6	0.31
RCS2043	LG4	82.29	AAG	18	<lmxll>	12	0.55
RCS3315	LG4	87.59	AC	16	<lmxll>	3	0.52
RCS1920	LG4	90.44	AAG	15	<lmxll>	9	0.85
RCS2667	LG4	90.54	AAG	23	<lmxll>	8	0.85
RCS2011	LG4	93.13	AG	15	<nnxnp>	9	0.69
RCS0916	LG4	95.02	GGT	16	<abxcd>	8	0.70
RCS3416	LG4	99.01	AGC	15	<nnxnp>	7	0.65
RCS1729	LG4	102.50	AAG	19	<abxcd>	8	0.76
RCS0441	LG4	104.33	AAC	18	<nnxnp>	4	0.53
RCS1940	LG4	116.09	AAG	19	<efxeg>	9	0.79
RCS2836	LG5	7.65	ATC	15	<lmxll>	7	0.45
RCS3376	LG5	15.01	ATC	18	<nnxnp>	5	0.44
RCS1762	LG5	15.27	AAG	27	<hkxhk>	3	0.64
RCS1594	LG5	25.33	AAG	19	<nnxnp>	7	0.67
RCS2217	LG5	26.65	AG	21	<efxeg>	5	0.69
RCS2202	LG5	28.40	AC	25	<nnxnp>	11	0.81
RCS1771	LG5	28.60	ACT	15	<lmxll>	4	0.54
RCS2632	LG5	28.91	AATG	15	<nnxnp>	13	0.61
RCS0843	LG5	29.79	GGAT	15	<nnxnp>	7	0.79
RCS1044	LG5	30.15	GGA	15	<lmxll>	5	0.51
RCS2881	LG5	30.86	AAG	15	<lmxll>	19	0.76
RCS0315	LG5	31.76	ATC	15	<lmxll>	3	0.43
RCS1618	LG5	35.39	AAC	17	<lmxll>	7	0.78
RCS0131	LG5	35.78	AAC	16	<lmxll>	10	0.56
RCS2125	LG5	36.18	GGT	15	<efxeg>	4	0.62
RCS1724	LG5	36.79	ATC	15	<lmxll>	5	0.32
RCS0036	LG5	37.43	AC	27	<abxcd>	11	0.86
RCS1248	LG5	39.83	GGT	22	<lmxll>	3	0.63
RCS0937	LG5	40.05	AAC	15	<nnxnp>	4	0.48
RCS1228	LG5	42.05	AAC	18	<nnxnp>	5	0.67
RCS2802	LG5	42.21	ATC	26	<lmxll>	6	0.76
RCS2955	LG5	43.98	AAG	18	<nnxnp>	10	0.67

Table A3. Continued.

Marker name	LG	cM	SSR Motif	Length	Seg.type[a]	Alelle frequency	PIC value
RCS1932	LG5	45.38	ATC	17	<nnxnp>	7	0.39
RCS0007	LG5	46.46	GGA	26	<lmxll>	4	0.58
RCS1518	LG5	49.73	ATC	40	<lmxll>	6	0.81
RCS3681	LG5	51.45	ATC	15	<abxcd>	10	0.54
RCS1737	LG5	55.14	ATC	37	<efxeg>	10	0.88
RCS1523	LG5	56.82	GGT	18	<lmxll>	5	0.38
RCS2095	LG5	58.38	AATG	15	<lmxll>	7	0.63
RCS0764	LG5	59.47	GGA	15	<nnxnp>	3	0.33
RCS1541	LG5	60.32	AC	15	<nnxnp>	4	0.13
RCS1225	LG5	60.74	ATC	15	<lmxll>	8	0.81
RCS3236	LG5	62.63	AAAT	22	<lmxll>	19	0.77
RCS1157	LG5	63.50	GGA	55	<nnxnp>	2	0.48
RCS2448	LG5	64.97	AG	72	<lmxll>	6	0.81
RCS0714	LG5	74.00	GGT	15	<lmxll>	4	0.50
RCS0914	LG5	80.67	GGT	19	<nnxnp>	5	0.64
RCS1327	LG6	25.04	ATC	24	<nnxnp>	8	0.79
RCS1167	LG6	27.02	AAC	15	<nnxnp>	5	0.70
RCS0083	LG6	29.50	AT	22	<nnxnp>	7	0.31
RCS3711	LG6	29.73	AAG	18	<lmxll>	4	0.66
RCS2510	LG6	32.35	AAG	18	<nnxnp>	11	0.64
RCS0031	LG6	32.71	AAAG	19	<hkxhk>	8	0.83
RCS1001	LG6	34.44	GGT	24	<nnxnp>	6	0.39
RCS0428	LG6	35.64	ATC	19	<abxcd>	11	0.84
RCS3492	LG6	38.21	AC	22	<hkxhk>	4	0.66
RCS2569	LG6	42.93	ATC	18	<nnxnp>	8	0.59
RCS1398	LG6	45.27	ATC	16	<nnxnp>	6	0.72
RCS0252	LG6	46.31	ATC	15	<abxcd>	5	0.64
RCS2522	LG6	46.73	GGT	17	<nnxnp>	7	0.74
RCS2317	LG6	48.19	GGT	26	<nnxnp>	8	0.76
RCS2826	LG6	53.07	GGT	19	<nnxnp>	7	0.74
RCS1868	LG6	53.41	ATC	17	<efxeg>	6	0.67
RCS3642	LG6	54.19	AAAT	16	<lmxll>	2	0.50
RCS0194	LG6	54.44	AAC	21	<lmxll>	5	0.40
RCS2634	LG6	54.80	AAC	18	<lmxll>	3	0.51
RCS2388	LG6	55.88	AAC	15	<nnxnp>	2	0.06
RCS1255	LG6	57.34	AAG	24	<abxcd>	7	0.82
RCS1150	LG6	58.99	AAG	16	<lmxll>	8	0.77
RCS3421	LG6	59.76	ACT	16	<nnxnp>	5	0.26
RCS3666	LG6	59.88	AC	20	<lmxll>	15	0.89
RCS3044	LG6	60.26	GGT	15	<efxeg>	4	0.23
RCS0690	LG6	60.41	AAC	15	<abxcd>	5	0.63
RCS1080	LG6	61.07	AAC	15	<hkxhk>	4	0.32
RCS3331	LG6	63.60	AC	116	<nnxnp>	8	0.74
RCS2308	LG6	65.25	AAAC	18	<abxcd>	8	0.31
RCS0623	LG6	67.79	GGT	16	<nnxnp>	6	0.72
RCS2385	LG6	72.85	AAAG	16	<lmxll>	4	0.46
RCS1499	LG6	75.36	ATC	15	<nnxnp>	6	0.64

Table A3. Continued.

Marker name	LG	cM	SSR Motif	Length	Seg.type[a]	Alelle frequency	PIC value
RCS1879	LG6	76.35	AAC	15	<nnxnp>	3	0.50
RCS3052	LG6	78.13	AAC	17	<lmxll>	11	0.85
RCS0998	LG6	78.48	ATC	19	<lmxll>	6	0.56
RCS2616	LG6	78.67	AAAT	15	<lmxll>	4	0.52
RCS1835	LG6	81.78	AG	25	<lmxll>	8	0.71
RCS0069	LG6	84.42	AAT	31	<lmxll>	7	0.71
RCS1624	LG6	87.08	AAC	18	<nnxnp>	8	0.74
RCS1683	LG6	88.06	AAC	15	<lmxll>	4	0.69
RCS2408	LG6	91.32	AAG	18	<lmxll>	5	0.73
RCS3608	LG6	95.57	AAAG	21	<hkxhk>	11	0.55
RCS0743	LG6	96.05	AAG	18	<lmxll>	3	0.43
RCS0019	LG6	108.20	AAT	30	<lmxll>	7	0.78
RCS0004	LG7	17.66	AAG	22	<lmxll>	8	0.83
RCS0079	LG7	41.11	AGC	15	<nnxnp>	3	0.15
RCS2185	LG7	54.14	AAG	18	<efxeg>	8	0.64
RCS0712	LG7	57.87	AAC	15	<nnxnp>	3	0.53
RCS0763	LG7	61.85	ATC	15	<nnxnp>	2	0.15
RCS1897	LG7	64.44	AAAG	57	<abxcd>	8	0.84
RCS0051	LG7	86.89	AAG	26	<lmxll>	9	0.81
RCS0695	LG7	95.88	AAC	15	<nnxnp>	6	0.42
RCS0685	LG7	108.58	GGT	21	<lmxll>	8	0.72
RCS0102	LG7	112.80	AAC	15	<nnxnp>	3	0.41
RCS0793	LG7	114.40	AAG	20	<lmxll>	11	0.83
RCS0094	ND		AAG	13	<abxcd>	4	0.70
RCS0235	ND		AAC	22	<hkxhk>	5	0.63
RCS0668	ND		AAC	15	-	8	0.26
RCS0721	ND		AAC	15	-	3	0.11
RCS0731	ND		ATC	15	-	16	0.57
RCS0739	ND		AT	16	-	7	0.31
RCS0757	ND		GGT	18	<nnxnp>	6	0.73
RCS0759	ND		GGT	15	<hkxhk>	3	0.10
RCS0774	ND		AAC	15	<nnxnp>	3	0.40
RCS3719	ND		AGC	15	<hkxhk>	3	0.50

[a] Segregation type of each locus is indicated by the following codes: <abxcd>, locus heterozygous in both HR and R130, four alleles; <efxeg>, locus heterozygous in both HR and R130, three alleles; <hkxhk>, locus heterozygous in both HR and R130, two alleles; <lmxll>, locus heterozygous in HR; <nnxnp>, locus heterozygous in R130; -, segregation type was not clear.