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Bayesian QTL mapping using genome-wide SSR markers and segregating population derived from a cross of two commercial F_1 hybrids of tomato

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Abstract

Key message **Using newly developed euchromatin-derived genomic SSR markers and a flexible**

Bayesian mapping method, 13 significant agricultural QTLs were identified in a segregating population derived from a four-way cross of tomato.

Abstract So far, many QTL mapping studies in tomato have been performed for progeny obtained from crosses between two genetically distant parents, e.g. domesticated tomatoes and wild relatives. However, QTL information of quantitative traits related to yield (e.g., flower or fruit number, and total or average weight of fruits) in such intercross populations would be of limited use for breeding commercial tomato cultivars because individuals in the populations have specific genetic backgrounds underlying extremely different phenotypes between the parents such as large fruit in domesticated tomatoes and small fruit in wild relatives, which may not be reflective of the genetic variation in tomato breeding populations. In this study, we constructed F_2 population derived from a cross between two commercial F_1 cultivars in tomato to extract QTL information practical for tomato breeding. This cross corresponded to a four-way cross, because the four parental lines of the two F_1 cultivars were considered to be the founders. We developed 2,510 new expressed sequence tag (EST)-based (euchromatin-derived) genomic SSR markers and selected 262 markers from these new SSR markers and publicly available SSR markers to construct a linkage map. QTL analysis for ten agricultural traits of tomato was performed based on the phenotypes and marker genotypes of F_2 plants using a flexible Bayesian method. As results, 13 QTL regions were detected for 6 traits by the Bayesian method developed in this study.

Key Words: Tomato (*Solanum lycopersicum*), Four-way cross, SSR, Bayesian estimation, QTL mapping

Introduction

Tomato (*Solanum lycopersicum,* $2n = 2x = 24$) is an important horticultural crop, with the highest production quantity in the world (about 164 million tons in 2013, FAO 2013) . Tomato fruits are grown for fresh market or various processed products. The average fruit weight differs among cultivars, from about 10–20 g in cherry tomatoes to more than 180–250 g in beefsteak tomatoes (Costa and Heuvelink 2005). Tomatoes can be cultivated either in a greenhouse or in a field, and nutrient culture systems can be used. This flexibility in culturing systems enables worldwide production, even in the desert areas.

Because of the flexibility in cultivation and the diverse product usages, many tomato varieties have been bred to improve various agricultural traits related to quality, yield, growth habit, and pathogen resistances (Foolad 2007; Sabatini et al. 2013; Scott et al. 2013). Since the late 1980’s, important major genes contributing to such traits (especially pathogen resistances) in tomato have been identified due to their high heritability and ease of linkage analysis (Levin and Schaffer 2013; Pillen et al. 1996; Tanksley et al. 1992). The development of molecular or DNA markers using restriction fragment length polymorphisms (RFLPs) made it possible to isolate these major genes (Bernatzky and Tanksley 1986; Tanksley et al. 1992). Since the 1990's, the development of various types of genome-wide molecular markers, including random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) has accelerated genomic studies. More recently, QTL analysis for important agricultural traits has been facilitated by the development of various statistical methods (Ganal 2013; Ohyama and Hayashi 2016).

Important agricultural traits related to yield and quality are generally controlled by many QTLs that have small or medium effects on the phenotypes (Yamamoto et al., 2016). To detect the many QTLs associated with such traits, it is considered appropriate to conduct genome-wide association studies (GWAS) with multi-allelic populations consisting of various cultivars (Yamamoto et al. 2016), cultivars and landraces (Lin et al. 2014; Ranc et al. 2012; Ruggieri et al. 2014; Sauvage et al. 2014; Shirasawa et al. 2013), or multi-parental cross progeny (Pascual et al. 2015). However, linkage-based QTL mapping using segregating population is still widely applicable for populations from biparental crosses (Albert et al. 2016). This QTL mapping strategy could be extended to multi-parental crosses, where more than two alleles of QTLs might be segregated.

The founders of the experimental population are important for QTL mapping of agricultural traits. Many QTL mapping studies in tomato have been performed by using progeny obtained from a cross of two genetically distant parents (Ashrafi et al. 2012; Bernacchi et al. 1998; Chapman et al. 2012; Chen et al. 1999; Estan et al. 2009; Frary et al. 2004; Fulton et al. 1997; Fulton et al. 2002; Fulton et al. 2000; Gonzalo and van der Knaap 2008; Grandillo and Tanksley 1996; Paterson et al. 1991; Sun et al. 2012). However, quantitative traits, such as those related to yield (e.g., flower or fruit number, and total or average weight of fruits), are difficult to evaluate in intercross populations, because individuals in such populations have specific genetic backgrounds derived from their genetically distant parents (e.g., domesticated [large fruit] tomatoes and wild [small fruit] relatives). Evaluation of intracross populations avoids this problem of disparate genetic backgrounds, but reduces the number of polymorphisms available for study. Therefore, the use of versatile and highly polymorphic PCR-based molecular markers (e.g., SSR markers) is particularly important (Ohyama and Hayashi 2016) for the study of intracross populations. Because the number of SSR markers available for tomato is still very limited (Frary et al. 2005; Ohyama et al. 2009; Shirasawa et al. 2010a), there have been few examples of QTL mapping for agricultural traits in intracross populations (Causse et al. 2004; Causse et al. 2002; Stevens et al. 2007). Information available from the Sol Genomics Network (Mueller et al. 2005; current URL: https://solgenomics.net), including the reference genome sequence of tomato (Tomato-Genome-Consortium 2012) is facilitating the development of genome-wide SSR markers (Shirasawa et al. 2010a) and sequencing-based SNP markers (Hirakawa et al. 2013; Pascual et al. 2015; Shirasawa et al. 2013; Shirasawa et al. 2010b; Sim et al. 2011; Yamamoto et al. 2016) applicable to intracross populations.

Here, we developed genome-wide SSR markers and used them to perform QTL mapping for agricultural traits, including yield-related traits and soluble solid content, in an F_2 segregating population derived from a cross between two commercial F_1 hybrids of tomato. This cross corresponds to a four-way cross, since the four parental lines of the two F_1 cultivars, although unknown, were considered to be the founders. One of the F_1 commercial cultivars is a high-yield variety, and the other is a high-quality (sugar content) variety; hence, the segregating population derived from the cross of these varieties is suitable for simultaneous analysis of QTLs responsible for quantity and quality. We developed 2510 new EST-based SSR markers and selected 262 segregating SSR markers from these new SSR markers and publicly available SSR markers to construct a linkage map of this population. In QTL analysis, we adopted the method of Bayesian multiple QTL mapping proposed by Hayashi et al. (2012). The accuracy of the Bayesian mapping of multiple QTLs was evaluated in comparison with the results of analysis with a method of interval mapping which was also developed in this study for the segregating population derived from a four-way cross. The QTL mapping was performed under four different environmental conditions, i.e., combinations of cropping season and concentrations of nutrient culture medium (i.e., electrical conductivity).

Materials and methods

Construction of experimental populations

We grew the high-yield F_1 cultivar ‘Geronimo’ (De Ruiter Seeds, Bergschenhoek, the Netherlands) and the Japanese F_1 cultivar ‘Momotaro 8’ (Takii & Company, Kyoto, Japan), which has a high sugar content in the fruit, in pots filled with soil in a greenhouse of the Institute of Vegetable and Floriculture Science

(NIVFS) in Mie, Japan. Both cultivars were crossed to produce a “four-way” F_1 population of 240 plants; the cross corresponds to a four-way cross because the four parental lines of the two F_1 cultivars are considered to be the founders (Fig. 1). We then generated F_2 plants from the four-way F_1 plants by selfing with single-seed descent (SSD). Hereafter, following the notation of Broman (2012) in the study of mouse multi-parental lines, these four-way F_1 and F_2 populations are referred to as G_1F_1 and G_1F_2 populations, respectively, with parental generation being denoted as G_1 (Fig. 1).

Cultivation and phenotyping of parents and F_2 population

We sowed seeds of the G_1F_2 population and the parental F_1 cultivars in seed trays filled with a nursery soil on 27 August 2008 (autumn planting) or 24 February 2009 (spring planting). The trays were placed in a seedling growth chamber (Seedling Terrace, MKV Dream, Tokyo, Japan). After 3 weeks, all plants were planted directly on rockwool slabs (900 × 195 × 75 mm, Grotop Expert, Grodan B.V., Roermond, the Netherlands) at 22.5 cm intervals in beds; the width between beds was 193 cm. The temperature in the greenhouse was maintained at more than 16 °C. Cultivation was in hydroponic solution (revised-A nutrient prescription, Otsuka Chemicals, Osaka, Japan) with an electrical conductivity (EC) of 0.8 dS/m or 3.2 dS/m in a greenhouse at NIVFS, Mie, Japan. The maximum number of flowers per truss was limited to four, and plants were pinched above the fourth truss. Cultivation conditions were assigned to four experiments, 1, 2, 3, and 4 (n = 90 each, Supplementary Table S1) as follows: 1 and 2 are autumn plantings, 3 and 4 are spring plantings, 1 and 3 are low EC conditions (EC = 0.8 dS/m), and 2 and 4 are high EC conditions (EC = 3.2 dS/m). Cultivation continued until all fruits at the 4th truss of each plant were harvested.

Phenotypes related to growth habit (days to flowering [DF], height to the first truss [HFT], and number of leaves under the first truss [NLFT]), various measures of yield (total fruit weight [TFW], total marketable fruit weight [TMFW], average fruit weight [AFW], average marketable fruit weight [AMFW], number of fruit [NF], and number of marketable fruit [NMF]), and fruit quality (soluble solids content [SSC]) were measured in the parental F_1 cultivars in G_1 and each G_1F_2 individual. The criterion for “marketable fruit” is defined as fruit that does not show any physiological disorders such as blossom-end rot and fruit cracking, whereas non-marketable fruit show at least one type of disorder. If total weight, average weight and number of non-marketable fruit are abbreviated as TNMFW, ANMFW and NNMF, respectively, TFW is presented as TFW=TMFW+TNMFW. Further, TFW, TMFW and TNMFW can be expressed as TFW=AFW×NF, TMFW=AMFW×NMF and TNMFW=ANMFW×NNMF, respectively. Hence, TFW is also written as TFW=AMFW×NMF+ANMFW×NNMF.

Soluble solids content in fruit was measured with a refractometer (PAL-1, ATAGO Co., Ltd., Tokyo, Japan). Details of traits analyzed in this study are listed in Table 1.

Isolation of genomic DNA from tomato leaves

Genomic DNA from the leaves of the parental F_1 hybrids in G_1 and individuals from the G_1F_1 and G_1F_2 populations were isolated by using a DNeasy Plant Mini Kit and a DNeasy 96 Plant Kit (both from Qiagen, Tokyo, Japan), respectively.

Development of EST-anchored (euchromatin-derived) genomic SSR markers

To isolate euchromatin regions of tomato genome, a high-density genetic linkage map constructed using an intercross F_2 population of the Tomato-EXPEN2000 (Shirasawa et al. 2010a) was divided into segments with a bin size of 10 cM. Genomic sequences of the regions were extracted from the selected bacterial artificial chromosome (BAC) clone mixture (http://www.kazusa.or.jp/tomato_sbm/about.html) by identities with source sequences of EST-based markers located in each 10 cM bin. SSR loci were then isolated from these sequences by using the srchssr2.pl program (Fukuoka et al. 2005), which searches independently for repeated sequences of four dinucleotide motifs (GA, GT, AT, GC) and 10 trinucleotide motifs (AAC, AAG, ACC, ACG, ACT, AGC, AGG, ATC, TAT, CGC) and identifies the core motif with the highest repeat number. More than 4,000 SSR loci whose core motif numbers were 10 to 30 were newly isolated. PCR primers were designed from the flanking sequences of the isolated SSR loci by using the Primer3 program (Rozen and Skaletsky 2000), and the PCR primer pairs obtained were designated as tbm markers (2,510 in total, Supplementary Table S2).

Screening of SSR markers

EST-based genomic (see above) and publicly available SSR markers (Frary et al. 2005; Ohyama et al. 2009; Shirasawa et al. 2010a) were screened using the post-PCR fluorescence-labeling method (Ohyama et al. 2009) with genomic DNAs isolated from the leaves of the parental F_1 hybrids as templates. The characteristics of the SSR markers used for the map construction are listed in Supplementary Table S3.

Genotyping of SSR alleles

Forward primers were 5′-end-labeled with 6-FAM, NED, PET, or VIC (Applied Biosystems, Foster City, CA, USA). PCR using multiple fluorescent primers for SSR alleles and genomic DNA of the individuals from the G_1F_1 or G_1F_2 populations was performed in a 10-μl reaction mixture by using the Type-it Microsatellite PCR Kit (Qiagen, Tokyo, Japan) under the following conditions: an initial 5 min at 95 °C; 28 cycles of 30 s at 95 °C, 90 s at 60 °C and 30 s at 72 °C, and a final 30 min at 60 °C. PCR products were analyzed by using an automated sequencer (3730*x1* DNA Analyzer, Applied Biosystems) with a GeneScan-500 LIZ Size Standard (Applied Biosystems). Fragment length was determined by GeneMapper v3.7 software (Applied Biosystems). Following genotyping, SSR markers were classified into eight categories depending on the combination of genotypes inherited from the two parental F_1 cultivars as shown in Table 3.

Construction of linkage maps

Our experimental population was regarded as a three-generation family consisting of two parental cultivars, P1 and P2, in the first generation G_1, G_1F_1 plants derived from a cross between P1 and P2 in the second generation and G_1F_2 plants created by self-pollinating G_1F_1 plants in the third generation (Fig.1). To build a linkage map of such a three-generation family, we used CRI-MAP 2.503 (www.animalgenome.org) which can handle a three-generation family and estimate marker orders and genetic distances among markers with multipoint likelihood (Lander and Green 1987) from the information about transmission of marker alleles both between G_1 and G_1F_1 and between G_1F_1 and G_1F_2. Although this software was originally developed for outbred population, it could be applied to our experimental family including self-pollinated plants by modifying the input file as follows; each self-pollinated G_1F_1 plant was duplicated for its genotype information and regarded as a pair of crossed parents of G_1F_2 plants derived from the G_1F_1 plant.

Linkage groups were first inferred based on the information of chromosomes harboring SSR markers and subsequently confirmed with two-point function with an LOD cut-off point >5.0. Maps for each linkage group were then constructed using the build function, where we selected and located only markers with the difference of LOD scores between its most likely placement and other placements being more than 3.0. Orders were checked with the flips*n* function. The linkage map was drawn with MapChart v.2.1 software (Voorrips 2002).

Bayesian QTL mapping

A method of Bayesian multiple QTL mapping developed by Hayashi et al. (2012) to analyze a four-way RIL (recombinant inbred line) population was applied to the G_1F_2 population with some modifications. This method allows multiple QTLs to be simultaneously detected using a Bayesian mapping procedure, and enables the number of QTLs and the configuration of alleles at each QTL in P1 and P2 in G_1 to be estimated for a four-way segregating population. Here, we modified this method to enable the analysis of a G_1F_2 population instead of a four-way RIL population, as described below.

We assumed that the genotypes at the *l*th QTL of P1 and P2 are $Q_{l1}Q_{l2}$ and $Q_{l3}Q_{l4}$, respectively, with Q_{l1}, Q_{l2}, Q_{l3}, and Q_{l4} derived from the four founders (L1, L2, L3, and L4) of a four-way segregating population, respectively; L1 and L2 are assumed to be the parents of P1, and L3 and L4 are assumed to be the parents of P2 (Fig. 1). As the four founders were unknown in this study, Q_{l1} and Q_{l2} were arbitrarily assigned for the two alleles of the QTL in P1 and Q_{l3} and Q_{l4} were likewise assigned for the two alleles of the QTL in P2. The genotypes of putative QTLs located at any positions of a linkage map were inferred from the genotypes of the linked markers in G_1F_2 plants as described in Hayashi et al. (2012). In short, marker haplotypes of P1 and P2 were estimated from the marker genotypes of the G_1F_1 plants and the genotypes of the *l*th QTL for G_1F_1 plants were inferred from the genotypes of linked markers given marker haplotypes of P1 and P2, where there were four possible QTL genotypes $Q_{l1}Q_{l3}$, $Q_{l1}Q_{l4}$, $Q_{l2}Q_{l3}$ and $Q_{l2}Q_{l4}$ in G_1F_1 plants and the probabilities of QTL genotypes were calculated via hidden Markov model (HMM) with transition probabilities being determined by recombination frequencies among the QTL and linked markers. The QTL genotypes of G_1F_2 plants obtained by self-pollinating G_1F_1 plants were similarly inferred using HMM given the QTL genotypes of parental G_1F_1 plants. Consider G_1F_2 plants derived from self-pollination of G_1F_1 plants with QTL genotype $Q_{l1}Q_{l3}$, for example, then there are three possible genotypes $Q_{l1}Q_{l1}$, $Q_{l1}Q_{l3}$, and $Q_{l3}Q_{l3}$ in the G_1F_2 plants and the probabilities of the genotypes can be obtained with HMM using transition probabilities calculated with recombination frequencies among the QTL and linked markers (Broman 2012; Jiang and Zeng 1997) as in a usual biparental F_2 population. Combining the probabilities of QTL genotypes of G_1F_1 plants and those of G_1F_2 plants given the QTL genotypes of parental G_1F_1 plants, we calculated the probabilities of eight possible QTL genotypes, that is, $Q_{l1}Q_{l1}$, $Q_{l2}Q_{l2}$, $Q_{l3}Q_{l3}$, $Q_{l4}Q_{l4}$, $Q_{l1}Q_{l3}$, $Q_{l1}Q_{l4}$, $Q_{l2}Q_{l3}$ and $Q_{l2}Q_{l4}$, for G_1F_2 plants (Hayashi et al. 2012).

The phenotypic value of a trait for the *i*th G_1F_2 plant, y_i, is expressed using a linear model as

$$y_i = \mathbf{x}_i\mathbf{b} + \sum_{l=1}^{N}(u_{il1}a_{l1} + u_{il2}a_{l2} + u_{il3}a_{l3} + u_{il4}a_{l4}) + e_i ,$$

where **b** is a vector of fixed effects including an intercept of the model, cropping seasons and EC conditions with $\mathbf{x}_i$ being the *i*th row of the design matrix relating **b** with the *i*th G_1F_2 plant, N is the number of QTLs included in the model, u_{ilk} is a covariate indicating the genotype at the *l*th QTL for the *i*th plant showing the number of allele Q_{lk} (k = 1,2,3,4), i.e., taking values of $u_{ilk} = 2$ for genotype $Q_{lk}Q_{lk}$, $u_{ilk} = 1$ for genotype $Q_{lk}Q_{lh}$, ($h \neq k$) and $u_{ilk} = 0$ otherwise, a_{lk} (k = 1,2,3,4) is allelic effect of Q_{lk} and e_i is a residual error following a normal distribution with mean 0 and residual variance σ_e^2. The allelic effects are assumed to act additively at a QTL without interaction in this study. For identifiability of the model parameters, we confined $a_{l1} = 0$. We classified the configurations of QTL alleles, Q_{l1}, Q_{l2}, Q_{l3}, and Q_{l4}, into 14 types based on which of four alleles were equivalent and which were different to each other, as shown in Supplementary Table S4, referred to as configuration types hereafter. The configuration types included the case of the existence of four different alleles (Type 1) and the case of bi-allelic patterns (Type 10) indicating that Q_{l1} were identical with Q_{l2} and Q_{l3} were identical with Q_{l4}. In Type 10 configuration, accordingly, it was assumed that the genotypes of P1 and P2 were both homozygous with $Q_{l1}Q_{l1}$ and $Q_{l3}Q_{l3}$ and the equivalence relations $a_{l1} = a_{l2}$ and $a_{l3} = a_{l4}$ held true in the model. In the Bayesian procedure, the configuration types were also treated as variables moving over the 14 possible states. The number of QTLs (N) and the configuration type of each detected QTL were inferred with Reversible-Jump Markov Chain Monte Carlo (MCMC) (Green 1995). We adopted a Poisson distribution with mean 2 as a prior distribution of N and equal prior probabilities for the 14 configuration types of QTL alleles.

At each MCMC cycle, this Bayesian method proposed to add one new QTL, remove one existing QTL or maintain the number of QTL included in the model with equal probability. When adding one new QTL was proposed, the QTL position was randomly sampled from a whole genome which was assumed to consist of small bins of 1 cM interval. Thus, a bin was sampled as a new QTL position. One of the configuration types was assigned with the additional QTL as well as the allelic effects to accept or reject the proposal of adding a new QTL in the model based on the model fitting for data. When removing one existing QTL was proposed, a QTL to be removed was selected and two models with the QTL and without the QTL were compared by the model fitting to accept or reject the proposal of deleting an existing QTL. When maintaining the number of QTL was proposed, the positions, the configurations of alleles and the effects of alleles all existing QTLs were updated for increasing the model fitting.

The analyses were performed by modifying the original Fortran program developed by Hayashi et al. (2012). For sampling values of parameters including N, the location, allelic effects, and the configuration of alleles for each QTL as well as **b** and σ_e^2 from posterior distributions, we performed 120,000 repetitions of MCMC cycles; we discarded the initial 20,000 cycles and then sampled parameter values every 10 cycles of the last 100,000 cycles. The posterior probability of QTL position was calculated on each bin as the ratio of the number of cycles fitting the QTL on the bin into the model of the total sampled MCMC cycles, which was referred to as the posterior QTL intensity (QI) of the bin. We summed QI over all bins on each linkage group and adopted such a sum of QI (SQI) as a test statistic for QTL detection on the linkage group as in Hayashi et al. (2012). An empirical null distribution of maximum of SQIs in all linkage groups was obtained by a permutation test of 200 repetitions for each trait and P-values of SQI were calculated based on this empirical distribution. We regarded 95% quantile of this empirical distribution as the threshold for SQI corresponding to genome-wise 5% significance level. We determined the detection of QTL on a linkage group when the SQI on the linkage group exceeded the genome-wide threshold of 5% significance level. In this criterion of QTL detection, we assumed that at most one QTL was located on each linkage group. The Bayesian estimates of the positions, the configuration types and the effects of alleles for detected QTL were obtained following the manner of Hayashi et al. (2012). Specifically, the estimate of the position of detected QTL, L, was calculated as the position averaged over the linkage group using QI of each bin as a weight,

$$L = \sum_j q_j p_j \Big/ \sum_j q_j ,$$

where p_j was the position of the jth bin (j-1 cM) on the linkage group and q_j was QI of the jth bin with summation taken over all bins on the linkage group. The posterior probabilities of configuration type k for QTL, C_k (k=1,2,…,14), were likewise averaged over a linkage group as

$$C_k = \sum_j q_j r_{jk} \Big/ \sum_j q_j ,$$

where r_{ik} was the posterior probability of the configuration type k for a QTL on the jth bin fitted in the model. The estimates of effects of QTL alleles, a_i (i=2,3,4), were calculated as

$$a_i = \sum_j \sum_k q_j r_{jk} a_{ijk} / \sum_j \sum_k q_j r_{jk} ,$$

where a_{ijk} was the estimate of the effect of the ith allele when the configuration type k was assigned with the QTL located in the jth bin.

For the comparison with IM method described below, the Bayesian mapping was performed by simultaneously using the data of all experiments (see above section and Supplementary Table S1). For the detection of QTLs expressed differentially in certain experimental conditions, the Bayesian mapping was also performed using subsets of experiments extracted according to cropping season or EC condition.

QTL analysis with interval mapping method

Interval mapping (IM) method was also applied to QTL analysis in the G_1F_2 population to evaluate the reliability of QTLs detected in Bayesian analysis. We developed a new IM method based on least-square approach proposed by Haley and Knott (1992) for a four-way F_2 population. In the framework of IM, a QTL was scanned on a linkage map every small step, say, every 1cM, where the non-zero allelic effects were tested for a putative QTL located any positions on a linkage map one at a time. Assuming the additive QTL, the phenotypic value of the ith G_1F_2 plant was assumed to be written as

$$y_i = \mathbf{x}_i\mathbf{b} + u_{i1}a_1 + u_{i2}a_2 + u_{i3}a_3 + u_{i4}a_4 + e_i .$$

In this linear model, $\mathbf{b}$ is non-genetic effects with $\mathbf{x}_i$ being the ith row of the design matrix relating $\mathbf{b}$ with the ith G_1F_2 plant as described in Bayesian analysis, a_i (i=1,2,3,4) denotes the effect of the ith allele Qi of a putative QTL assuming that Q_1, Q_2, Q_3 and Q_4 are originated from four unknown founders, L1, L2, L3 and L4 (Fig.1), respectively, with the condition of a_1=0 for model identification and u_{ik} (k=1,2,3,4) is a covariate indicating the genotype of a putative QTL with $u_{i1}=2p_{i11}+p_{i13}+p_{i14}$, $u_{i2}=2p_{i22}+p_{i23}+p_{i24}$, $u_{i3}=2p_{i33}+p_{i13}+p_{i23}$, and $u_{i4}=2p_{i44}+p_{i14}+p_{i24}$, where p_{ikl} means the probability of the ith plant having genotype Q_kQ_l at a QTL which can be calculated in the manner as described in the section of Bayesian analysis. The model fitting was performed using the least-square approach proposed in Haley and Knott (1992).

Analysis with IM was performed for phenotypic data of all experiments incorporating two non-genetic factors, cropping season and EC condition, in the model. The genome was scanned at every 1cM. One thousand permutation tests were performed to establish empirical null distribution of maximum of LOD scores obtained on an entire linkage map (Churchill and Doerge 1994). The thresholds of LOD were obtained as the values with P-value of 5% of this empirical distribution. The statistical procedure of IM was carried out with Fortran program written by the authors.

Results

Characteristics of the parental F_1 hybrid cultivars

The characteristics of the parental F_1 cultivars, 'Geronimo' (P1) and 'Momotaro 8' (P2), under various experimental conditions (Experiments 1 to 4) are summarized in Table 2; the conditions in each experiment are described in Supplementary Table S1. The phenotypes related to growth habit were analyzed in all four experiments. DF tended to be longer in P2 than in P1 ($P < 0.05$ in 3 of 4 experiments, Student's t-test), HFT tended to be greater in P1 than in P2 ($P < 0.05$ in 2 of 4 experiments, Student's t-test), and NLFT was similar between P1 and P2 in all four experiments (Table 2). The differences in DF and HFT between P1 and P2 were confirmed as significant by two-way ANOVA with cultivar and experiment as the independent variables (Supplementary Table S5).

Yield-related traits and SSC were analyzed in experiments 1 to 3 only. Several yield-related traits, i.e., TFW, TMFW, AFW, and AMFW, were significantly higher in P1 than in P2 in all three experiments, whereas fruit numbers (NF and NMF) were similar between P1 and P2 in all three experiments, with the exception that NMF was significantly higher in P1 than in P2 in Experiment 3 (spring planting, low EC condition; $P < 0.05$, Student's t-test) (Table 2). In contrast, SSC of P2 fruit was significantly higher than that of P1 fruit in all three experiments. The results of two-way ANOVA confirmed that the differences in yield-related traits and SSC between P1 and P2 were significant, and showed that NMF but not NF was significantly different between P1 and P2 (Supplementary Table S5). Since the significant difference in NMF between P1 and P2 was observed in experiment 3 only, it is necessary to further evaluate this trait using more individuals to determine whether the difference is stably observed.

The effects of experimental conditions on traits, after taking account of the cultivar effect, were examined by two-way ANOVA followed by Tukey–Kramer multiple comparison tests (Supplementary Table S5). In the case of phenotypes related to growth habits, DF of spring planting was significantly longer than that of autumn planting when the EC condition was low, whereas HFT of autumn planting was significantly longer than that of spring planting regardless of the EC condition (Supplementary Table S5, Tukey-Kramer multiple comparison tests). By contrast, NLFT, AFW, AMFW and NF were not significantly different among the experiments. In the case of yield-related traits, although significant differences among experiments were observed for TFW, TMFW, and NMF by two-way ANOVA, the differences were not detected by Tukey–Kramer multiple comparison tests (Supplementary Table S5). It is necessary to further evaluate the traits using more individuals to determine whether the differences observed by two-way ANOVA are stably observed among the experimental conditions. In contrast, for SSC, significant differences among experiments were observed in both the two-way ANOVA and Tukey–Kramer multiple comparison tests (Supplementary Table S5), suggesting that SSC was affected by the cropping season and/or the EC condition.

Correlation analysis

Correlation analysis between traits was performed using phenotypes of the G_1F_2 population in each experiment (Supplementary Tables S6–S9). Highly significant correlations ($0.7 \leq r$) were observed between TFW and TMFW (Experiments 1 and 2, Supplementary Tables S6 and S7), TFW and AFW (Experiments 1 to 3, Supplementary Tables S6–S8), TFW and AMFW (Experiments 1 and 2, Supplementary Tables S6 and S7), TMFW and AMFW (Experiments 1 and 2, Supplementary Tables S6 and S7), AFW and AMFW (Experiments 1 to 3, Supplementary Tables S6–S8), NF and NMF (Experiment 1, Supplementary Table S6), TMFW and AFW (Experiment 2, Supplementary Table S7), TMFW and NMF (Experiment 3, Supplementary Table S8), DF and NLFT (Experiments 3 and 4, Supplementary Tables S8 and S9), DF and HFT (Experiment 4, Supplementary Table S9) and HFT and NLFT (Experiment 4, Supplementary Table S9). In the case of the yield–related traits such as TFW and AFW, relationships among the traits are presented as equations (see Materials and methods), hence, those correlations may reflect contributions of the traits as covariates in each experiment (Supplementary Tables S6–S8). While plant growth-related traits, DF, HFT and NLFT are physiologically distinct traits from each other: e.g., NLFT increases proportionally with a temperature in an optimum range, whereas DF and HFT necessarily do not (Heuvelink 2005). Hence, the highly significant correlations among those traits observed here (Supplementary Tables S8 and S9) may indicate apparently cooperative increase in the trait values depending on the cultivation time until the differentiation of the first truss in some experimental conditions.

Screening and classification of SSR markers available for G_1F_1 and G_1F_2 populations

Tomato SSR marker stocks developed mainly *in silico* (see Materials and methods) were screened for polymorphisms between the DNAs of P1 and P2. The markers were then classified into eight categories according to the combination patterns of alleles in the parents used for the construction of the two (G_1F_1 and G_1F_2) populations (Table 3). As shown in Figure 1, we assumed that four pure lines, L1, L2, L3 and L4, were parents of P1 and P2 and regarded as founders of the four-way cross family including G_1F_1 and G_1F_2 populations. Therefore, marker informativeness was evaluated based on the probability that a marker allele randomly sampled in G_1F_1 and G_1F_2 populations can definitely traced back to four haplotypes derived from founders. For example, considering a marker with “ab-cc” for allele combination pattern of P1 and P2 (category 4 in Table 3), two marker genotypes, “ac” and “bc”, occur with equal frequency in G_1F_1 population and, in G_1F_2 population, there occur five genotypes, “aa”, “bb”, “ac”, “bc” and “cc”, with frequencies 0.125, 0.125, 0.25, 0.25 and 0.25, respectively. At this marker, alleles “a” and “b” are available for discriminating two haplotypes of P1 while allele “c” cannot discriminate two haplotypes of P2. Accordingly, the probabilities that an allele randomly sampled can be definitely traced back to one of founder haplotypes are 0.5 both in G_1F_1 and G_1F_2 population. These probabilities were listed as well as the number of different alleles present in the marker (2 to 4) in Table 3. Markers tended to be genetically more informative as the category number increased, although some categories were equivalently informative (i.e., category 2 and 3, and category 4 and 5). Markers in category 7 could detect four different alleles whose parental origins could be definitely identified, indicating that they are fully informative and highly valuable. However, the frequency of such fully informative markers in the tomato genome was very low (data not shown). Although markers in categories 0 and 1 were not available for discriminating founder haplotypes when used as a single marker, they had information of linkage analysis and contributed to discrimination of haplotypes when combined with linked informative markers. Hence, for QTL analysis, such uninformative or partially informative markers closely located on a linkage map were combined and used as fully informative markers. A total of 262 SSR markers were selected (Table 3) and used for the construction of the linkage map.

Construction and evaluation of linkage maps

SSR markers listed in Table 3 were used for the construction of a linkage map by estimating the recombination frequency in gametes transmitted from the G_1 generation to G_1F_1 generation and from G_1F_1 generation to the G_1F_2 generation. The map, which was designated as the GMF2 map, consisted of 12 linkage groups including 222 SSRs as framework markers, covering a total genetic distance of 1,283 cM

(Fig. 2) and corresponded to the tomato genome (chromosomes) SL2.50 (Tomato-Genome-Consortium 2012, http://solgenomics.net/). The average distance between markers on the map was 6.1 cM, and the maximum gap was 35 cM. The GMF2 map covered 97.2% of the tomato genome version SL2.50. Comparison of the GMF2 map with the standard high-density linkage map of a tomato F_2 intercross population (Shirasawa et al. 2010a) also revealed that the GMF2 map covered nearly the entire tomato genome (Supplementary Fig. S1). Although large (more than 20 cM) gaps were still present, the coverage rate and the average interval between markers (less than 10 cM) (Lander and Botstein 1989) suggest that the GMF2 map is substantially sufficient for whole-genome scanning of the G_1F_2 population. Remaining 40 markers were unmapped with mapping criterion adopted here, but most of these markers could be located at most likely positions in the framework map (data not shown).

Comparison between IM and the Bayesian mapping using all experiments

We used the same data in all experiments to compare the QTLs detected by Bayesian method and those detected by IM method. Table 4 shows QTLs detected by the Bayesian method with EC condition and the cropping season as two non-genetic factors; for each trait, the experiments included in the analysis (Experiments 1 to 3, or Experiments 1 to 4), SQI, estimated position, most probable configuration type and effects of alleles for each QTL are listed as well as LOD scores for QTLs obtained by IM method with *P*-values for comparison. Positions of QTLs are also shown on the linkage map GMF2 (Fig. 2). By using the Bayesian method, we detected a total of ten QTLs for six of the ten traits listed in Table 4; no significant QTLs for TMFW, AMFW, NF and NMF were detected. On the other hand, the method of IM detected 16 significant QTLs in eight traits except for TMFW and NMF. The results of QTL analysis with IM method including position of QTL estimated as a tested position with highest LOD score and the LOD score were summarized in Table 5, where SQI values and their *P*-values with Bayesian method calculated for chromosomes including the detected QTLs were listed for comparison. Some of QTLs detected with IM method coincided with those detected by Bayesian method, but others did not. In IM method, the existence of one QTL was tested at a time and four different alleles were assumed for a putative QTL while multiple QTLs were fitted in a model with configuration types of QTL alleles varied and inferred for each of fitted QTLs in Bayesian method. The difference in the models and statistical procedures between two methods might lead to the inconsistency in the results of QTL analysis.

Detection of a QTL at a tested position in IM method was carried out without controlling the effects of

QTLs located in other region and the model of IM presumed the existence of four different alleles at QTL, which might cause overfitting of the model to data. Bayesian method simultaneously searched multiple QTLs with inferring the allele configuration of each QTL at the same time in prior setting of two QTLs expected for each trait, which was conservative setting. Therefore, we considered that the QTLs detected by Bayesian method were more reliable and were worth reporting, which were named following QTL nomenclature described in McCouch (2008) as *hft1.1*, *hft2.1*, and so on, as listed in Table 4 and in Supplementary Tables S10-S12. When the positions of a QTL detected with Bayesian method were included in the 1-LOD interval of a QTL detected with IM (Table 5) for the same trait, these two QTLs were regarded as an identical QTL. Of ten QTLs detected with Bayesian method, six QTLs were also detected as significant QTLs with IM method including *df2.1*, *df11.1*, *hft1.1*, *nlft1.1*, *afw1.1* and *ssc11.1* (Table 4). While other four QTLs, *hft2.1*, *nlft2.1*, *tfw1.1* and *afw4.1*, were not significant in IM method, the existence of *nlft2.1* and *tfw1.1* were also suggested by IM with P<0.066 and P<0.071. Most probable configuration types for QTLs detected with Bayesian method were inferred as type 7 for *df2.1* and *nlf2.1*, type 8 for *afw1.1*, type 10 for *hft1.1* and *ssc11.1*, type 12 for *hft2.1* and *afw4.1* and type 13 for *df11.1*, *nlft11.1* and *tfw1.1*, indicating that only two different alleles were segregated at detected QTLs (Supplementary Table S4). For example, at QTLs with type 10 configuration, *hft1.1* and *ssc11.1*, P1 and P2 were inferred to be homozygous with different alleles. For *df2.1* and *tfw1.1*, the posterior probabilities for most probable configuration types were relatively low with 0.469 and 0.350, respectively, accordingly, the possibility of other configuration types might not be ignored. The fraction of phenotypic variance explained (R^2) by these QTLs ranged 0.021 to 0.064 (Table 4). QTLs with considerable effects of $R^2 \geq 0.4$, *hft1.1*, *nlft11.1* for *afw1.1* were also detected as highly significant QTLs (P<0.009) with IM method.

Of 16 significant QTLs detected with IM, 6 QTLs were shared by Bayesian method (Table 5) but most of 10 remaining QTLs were not supported by Bayesian method except a QTL of HFT on LG 9 for which SQI was obtained as 0.365 with P<0.105 and its existence was suggested.

Bayesian mapping of QTLs expressed differentially under different experimental conditions (cropping season or EC condition)

As mentioned above, two-way ANOVA for DF, HFT, and NLFT in P1 and P2 in all four experimental conditions revealed that DF and HFT were significantly influenced by cropping season, whereas NLFT was not significantly influenced by the experimental conditions (Supplementary Table S5). These three traits were subjected to QTL mapping in subsets of experiments extracted based on environmental condition (i.e., EC condition [low, experiments 1 and 3; or high, experiments 2 and 4] or cropping season [autumn, experiments 1 and 2; or spring, experiments 3 and 4]) (Supplementary Tables S10–S12). These subset analyses detected additional QTLs which were not detected with all experiments for DF (Supplementary Table S10), HFT (Supplementary Table S11) and NLFT (Supplementary Table S12), where additional QTLs were mapped on linkage group 4 with spring planting for DF, on linkage group 9 with spring planting for HFT and on linkage group 5 under low EC condition for NLFT. These QTLs were considered to interact with cultivation conditions. For HFT, we detected QTL on linkage group 1 consistently in each combinations of experiments, but the estimated positions of linkage group 1 QTL were much varied as 34-91 cM and configuration types of the QTL alleles were inconsistent among four combinations of experiments, where type 10 was inferred in three combinations while type 11 was supported in a combination of experiments 3 and 4 (Supplementary Table S11). Although these estimated positions were deviated from the position obtained with the analysis using all experiments (60 cM, Table 4), these variations might be caused due to decreased sample size in subsets of experiments, thus, QTLs for HFT on linkage group 1 were considered as identical and referred to as the same name *hft1.1* considering configuration type 10 supported for the QTL in the analysis of data from all experiments.

Although NLFT trait in P1 and P2 did not differ significantly among experimental conditions (Supplementary Table S5), the additional QTL for the NLFT was detected under low EC condition (Supplementary Table S12). This result suggests that the changes of the expressions of the genes linked to QTLs depending on the EC condition might occur in the NLFT trait in G_1F_2 even though both P1 and P2 were unchanged phenotypically in the same condition.

Discussion

By crossing two commercial F_1 hybrids with different pedigrees, i.e., the high yield strain ‘Geronimo’ (P1) and the high sugar content strain ‘Momotaro 8’ (P2), we obtained experimental populations, G_1F_1 and G_1F_2; each locus in these populations has up to four different alleles derived from the four unknown founders of P1 and P2. As expected, P1 and P2 showed different characteristics, in particular, in terms of SSC (which mainly reflects sugar content) and fruit yield (TFW and TMFW) (Table 2). The segregating G_1F_2 population derived from the G_1F_1 population by selfing was grown under four different experimental conditions (two cropping seasons and two EC conditions) (Supplementary Table S1), and then agricultural traits related to plant growth habit, quality, and yield were measured. SSR-based genotyping of P1, P2 and the G_1F_1 and G_1F_2 populations was conducted to construct a genome-wide linkage map consisting of 12 linkage groups (Fig. 2), and subsequently QTL mapping was performed. The marker genotypes of the G_1F_1 population were used to infer the marker haplotypes of P1 and P2, each of which was assumed to be derived from four unknown founder lines (Fig.1). In QTL mapping with Bayesian method, there were assumed to be up to four different alleles at QTL each originated from each founder line and QTL genotype was inferred for G_1F_2 plants based on genotypes of linked markers and recombination frequencies among QTL and linked markers, but considering equivalence among the four possible QTL alleles, which were referred to as configuration type of QTL. Depending on the configuration type of QTL, the number of different QTL alleles ranged two to four and QTL genotypes of P1 and P2 and segregation patterns of QTL alleles in G_1F_2 populations were determined (Supplementary Table S4). A total of 13 QTLs were detected for 6 traits, DF, HFT, NLFT, TFW, AFW and SSC, with Bayesian method.

Several traits were influenced by both the experimental conditions and the differences in the genetic background of P1 and P2 (Supplementary Table S5): e.g., HFT differed significantly among the four experiments as well as between P1 and P2. Therefore, in QTL mapping for the integrated data from four experiments, experimental conditions were included in the model as covariates. In specific conditions such as planting season and EC condition, different QTLs from those detected in all data were detected for some traits, suggesting the interaction between some QTLs and specific cultivation conditions (QxE).

The reliability of QTLs detected with Bayesian method was evaluated by comparison with the result of QTL analysis with IM method developed for a segregating population derived from a four-way cross in this study, where it was assumed that there were four different alleles at a tested QTL. The reliability of some QTLs with Bayesian method were supported by IM method. Although more QTLs (16 QTLs) were regarded as significant with IM method, most of the QTLs not detected with Bayesian method might be considered to include false positives.

Reports of QTL mapping using intracross populations are limited (Causse et al. 2004; Causse et al. 2002; Stevens et al. 2007),whereas mapping using intercross populations is relatively common probably due to the high frequency of polymorphisms and large phenotypic differences between tomato and compatible smaller-fruited wild relatives including *Solanum pimpinellifolium*, *Solanum pennellii*, *Solanum chmielewskii* and *Solanum habrochaites*. Intercross populations have been studied worldwide

(Muller et al. 2005, https://solgenomics.net/), and many major genes and QTLs have been characterized (Grandillo et al. 2013; Ohyama and Hayashi 2016; Scott et al. 2013); these include genes or QTLs for important traits (e.g., resistance to pathogens) that have been used for breeding new tomato varieties (Foolad 2007; Sabatini et al. 2013; Scott et al. 2013). However, despite the lower frequency of polymorphisms, there is a great need to identify genetic variations in intracross populations, because these variations can be used for breeding with lower risk of linkage drag, and important agricultural traits such as yield and SSC can be accurately evaluated in populations derived from parents with similar-sized fruits. By using an intracross population, we were able to identify various QTLs (Table 4). To confirm the reproducibility of the QTLs detected in the G_1F_2 generation in this study, repetitive phenotyping using fixed populations such as RILs is necessary. Hence, the populations presented here are currently being subjected to repeated SSD to develop RILs. The results of mapping of QTLs in the RIL population with a similar analysis method to that used here will be presented in future. Once RILs are constructed, the capture of many QTLs that are expressed in different conditions is expected.

Populations derived from multiple parents such as those in this study and the MAGIC population (Pascual et al. 2015) are useful for the detection of more QTLs than biparental progeny, because QTLs derived from multiple parents are segregated in the populations. Genotyping by sequencing or sequencing of restriction-site-associated DNA tags is easily applicable to many crops today even if the target crop genome is not sequenced (Davey et al. 2011). The multi-parental populations would become suitable materials for QTL mapping of various crops, not just tomato, based on the effective genotyping system and flexible mapping methods such as Bayesian mapping as adopted here.

Conclusion

We constructed an experimental F_2 population of tomato derived from a cross between two commercial F_1 cultivars. For genetic analysis of this tomato intracross population, 2,510 EST–based genomic SSR markers were developed and these new markers were used to construct a linkage map as well as publicly available ones. The map consisted of 12 linkage groups which corresponded to the tomato chromosomes and covered nearly the entire genomic region. Considering the parents of the two F_1 cultivars used for cross as four founders, this F_2 population was regarded as a four–way segregating population although the founders were unknown. To derive more detailed information of QTLs affecting agricultural traits of tomato using such a multi–parental population, a flexible Bayesian method were proposed in this study, which allowed the effects of haplotypes of detected QTLs originated from founders to be inferred. The tools of genetic analysis obtained in this study would be useful for breeding practices of tomato, including new developed SSR markers and the flexible QTL mapping method which will also be applied to QTL analysis of the multi–parental populations of various crops as well as tomato.

Author contribution statement

AO, KS, HM, HI, HF, and TH conceived the project and designed the experiments. HM and AO supervised phenotypic analysis. KS and HF designed SSR markers. AO, KS, SN, KM, HY, and TN contributed plant materials, and performed DNA extraction and genotyping. TH and AO performed statistical analyses. AO and TH wrote the manuscript. All authors reviewed and approved the manuscript.

Compliance with Ethical Standards

Conflict of interest

The authors declare that they have no conflict of interest.

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Table 1 List of traits analyzed in this study

Traits	Abbreviation	Trait category	Details
Days to flowering	DF	Plant growth	Number of days from seeding to flowering
Height to the first truss (cm)	HFT	Plant growth	Height of the first truss from ground
Number of leaves under the first truss	NLFT	Plant growth	Number of true leaves under the first truss
Total fruit weight (g/plant)	TFW	Yield	Total fruit weight per plant
Total marketable fruit weight (g/plant)	TMFW	Yield	Total marketable fruit weight per plant
Average fruit weight (g)	AFW	Yield	Average weight of all fruits from a plant
Average marketable fruit weight (g)	AMFW	Yield	Average weight of marketable fruits from a plant
Number of fruit	NF	Yield	Number of all fruits from a plant
Number of marketable fruit	NMF	Yield	Number of marketable fruits from a plant
Soluble solids content (°Brix)	SSC	Fruit quality	Degree of Brix measured with a refractometer (average of marketable fruits at the first truss)

Table 2 Characteristics of parental F_1 cultivars in each experiment

Experiment	Cultivar	*n*	DF	HFT (cm)	NLFT	TFW (g/plant)	TMFW (g/plant)	AFW (g)	AMFW (g)	NF	NMF	SSC (°Brix)
1	Geronimo	6	46.0	65.5	8.2	4279.0*	4279.0*	308.5*	308.5*	14.0	14.0	4.2
	Momotaro 8	6	47.5	64.0	9.0	2989.2	2745.2	197.4	203.8	15.2	13.7	5.9*
2	Geronimo	6	46.2	65.2	8.3	4985.3*	4619.2*	347.9*	338.1*	14.5	13.8	4.6
	Momotaro 8	6	49.5*	61.2	9.8	3061.3	2845.0	215.1	205.5	14.3	13.8	6.3*
3	Geronimo	6	50.5	49.5*	8.7	4556.8*	4429.5*	321.9*	320.3*	14.2	13.8*	3.8
	Momotaro 8	6	51.7*	42.8	9.0	2642.2	1861.8	181.9	198.4	14.5	9.5	5.1*
4	Geronimo	6	48.0	49.5*	8.3	-	-	-	-	-	-	-
	Momotaro 8	6	50.0*	39.5	8.3	-	-	-	-	-	-	-

Data represent the means of individual values; the conditions of each experiment are shown in Supplementary Table S1.

‘Geronimo’ and ‘Momotaro’ are abbreviated as P1 and P2 respectively in the main text.

* Significant difference between the values for the two cultivars at $P < 0.05$ level (Student’s *t*-test).

Table 3 Classification of mapped SSR markers

Category	Marker allele combination patterns[a]	Expected number of alleles in progeny	Probability of marker allele in G_1F_1 traced back to founder haplotype[b]	Probability of marker allele in G_1F_2 traced back to founder haplotype[c]	Number of selected SSR markers	Number of mapped SSR markers	Frequency (%) of mapped SSR markers
0	aa-bb	2	0.00	0.00	47	40	18.0
1	ab-ab	2	0.50	0.00	6	6	2.7
2	ab-aa	2	0.50	0.25	49	41	18.5
3	aa-ab	2	0.50	0.25	28	23	6.3
4	ab-cc	3	0.50	0.50	36	32	14.4
5	aa-bc	3	0.50	0.50	15	14	10.4
6	ab-ac	3	1.00	0.75	45	34	15.3
7	ab-cd	4	1.00	1.00	36	32	14.4
					262	222	

[a] The first two characters indicate the genotype of the F_1 cultivar 'Geronimo' (P1), and the two characters after the hyphen indicate the genotype of the F_1 cultivar 'Momotaro 8' (P2).

[b] Probability that an allele randomly sampled in G_1F_1 plants can be definitely traced back to one of four founder haplotypes.

[c] Probability that an allele randomly sampled in G_1F_2 plants can be definitely traced back to one of four founder haplotypes.

Table 4 QTLs detected by the Bayesian method using three or four experiments with EC condition and cropping season as two non-genetic factors

Trait	Number of experiments used	LG	SQI of LG including QTL	QTL position (cM)	QTL ID	Configuration type[a] with highest posterior probability	Effects of QTL alleles				R^2	Genome-wise 5% threshold of SQI[c]	LOD score in IM for detected QTL[d]
							a_1[b]	a_2	a_3	a_4			
DF	4 (1, 2, 3 and 4)	2	0.993	23	*df2.1*	7 (0.469)	0.000	0.674	0.765	0.270	0.021	0.664	4.15 (P<0.035)
		11	0.864	11	*df11.1*	13 (0.864)	0.000	-0.001	0.876	-0.003	0.024		4.69 (P<0.008)
HFT	4 (1, 2, 3 and 4)	1	1.006	60	*hft1.1*	10 (0.851)	0.000	-0.024	3.995	4.058	0.065	0.587	10.86 (P<0.001)
		2	0.752	82	*hft2.1*	12 (0.927)	0.000	-2.464	0.012	-0.008	0.025		3.03 (P<0.296)
NLFT	4 (1, 2, 3 and 4)	2	0.998	22	*nlft2.1*	7 (0.822)	0.000	0.244	0.238	0.011	0.029	0.724	3.87 (P<0.066)
		11	0.990	14	*nlft11.1*	13 (0.911)	0.000	0.003	0.372	-0.001	0.045		5.23 (P<0.009)
TFW	3 (1, 2 and 3)	1	0.669	90	*tfw1.1*	13 (0.350)	0.000	59.514	-74.686	43.050	0.024	0.642	3.83 (P<0.071)
TMFW	3 (1, 2 and 3)	-	-	-	nd	-	-	-	-	-	-	0.694	
AFW	3 (1, 2 and 3)	1	1.004	100	*afw1.1*	8 (0.523)	0.000	9.952	-2.126	6.241	0.040	0.678	5.74 (P<0.002)
	3 (1, 2 and 3)	4	0.796	8	*afw4.1*	12 (0.798)	0.000	-11.802	0.148	0.390	0.035		2.87 (P<0.338)
AMFW	3 (1, 2 and 3)	-	-	-	nd	-	-	-	-	-	-	0.710	
NF	3 (1, 2 and 3)	-	-	-	nd	-	-	-	-	-	-	0.781	
NMF	3 (1, 2 and 3)	-	-	-	nd	-	-	-	-	-	-	0.684	
SSC	3 (1, 2 and 3)	11	0.784	73	*ssc11.1*	10 (0.578)	0.000	-0.002	0.141	0.104	0.035	0.710	4.71 (P<0.010)

Posterior distributions for QTL position, configuration type and effects of alleles were obtained by 10,000 MCMC sampling cycles for all bins of 1 cM length on a whole genome and summarized for each linkage group in the manner as described in 'Materials and methods'.

nd, Not detected; LG, linkage group (see Fig. 2); a_1 and a_2, the effects of QTL alleles from 'Geronimo' (P1) haplotypes; a_3 and a_4, the effects of QTL alleles from 'Momotaro 8' (P2) haplotypes; R^2, estimated proportion of phenotypic variance explained by the QTL.

[a] Configuration types are listed in Supplementary Table S4.

[b] We assume that $a_1 = 0$ for all configuration types.

[c] Significance levels were calculated by a permutation test with 200 iterations.

[d] LOD scores obtained with IM for the QTL regions detected with Bayesian analysis. Empirical P-values of LOD scores were indicated in parenthesis, which were obtained based on 1000 cycles of permutation test in IM.

Table 5 QTLs detected by interval mapping (IM) method using three or four experiments with EC condition and cropping season as two non-genetic factors

Trait	Number of experiments used	LG	QTL position (cM) and 1-LOD interval	LOD	Threshold value of LOD[a]	R^2	SQI of LG including QTL[b]
DF	4 (1, 2, 3 and 4)	1	47 (43-54)	7.90	3.99	0.061	0.076 (*P*<0.535)
		2	26 (20-32)	4.15		0.033	0.993 (*P*<0.005)
		11	0 (0-20)	4.69		0.037	0.864 (*P*<0.020)
HFT	4 (1, 2, 3 and 4)	1	62 (53-69)	10.86	4.0	0.101	1.006 (*P*=0.000)
		6	36 (30-43)	6.03		0.058	0.241 (*P*<0.195)
		9	66 (54-73)	4.62		0.045	0.365 (*P*<0.105)
NLFT	4 (1, 2, 3 and 4)	1	52 (44-63)	6.62	4.0	0.076	0.151 (*P*<0.430)
		3	87 (81-92)	4.93		0.058	0.175 (*P*<0.405)
		11	21 (11-25)	5.23		0.061	0.990 (*P*<0.005)
TFW	3 (1, 2 and 3)	3	57 (46-66)	4.55	3.99	0.073-	0.188 (*P*<0.565)
AFW	3 (1, 2 and 3)	1	108 (98-120)	5.74	3.93	0.093	1.004 (*P*=0.000)
		11	58 (50-67)	4.71		0.077	0.191 (*P*<0.465)
AMFW	3 (1, 2 and 3)	11	58 (39-68)	4.15	3.96	0.066	0.221 (*P*<0.410)
NF	3 (1, 2 and 3)	9	52 (43-61)	4.31	4.08	0.070	0.208 (*P*<0.430)
SSC	3 (1, 2 and 3)	1	38 (24-46)	4.12	4.06	0.055	0.231 (*P*<0.385)
		11	78 (59-87)	4.71		0.062	0.784 (*P*<0.04)

nd, Not detected; LG, linkage group (see Fig. 2); R^2, estimated rate of phenotypic variance explained by the QTL.

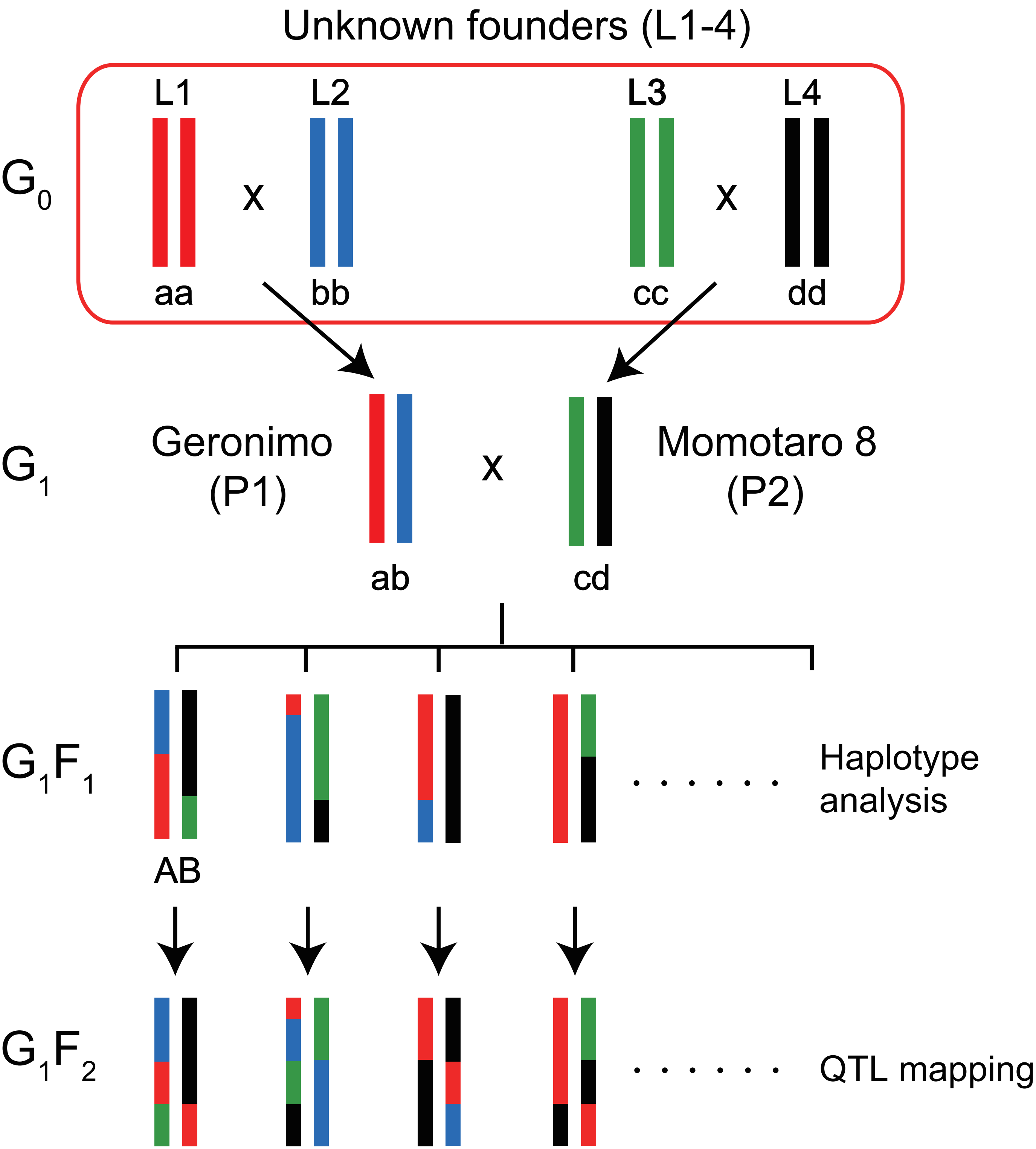
[a] Threshold values of LOD scores with genome-wise 5% significance level calculated by permutation tests with 1,000 iterations.

[b] SQI values obtained with Bayesian method for the chromosomes including QTL regions detected with IM analysis. Empirical *P*-values of SQI values were indicated in parenthesis, which were obtained based on 200 cycles of permutation test in Bayesian method.

Figure legends

Fig. 1 Outline of Bayesian QTL mapping using tomato experimental populations, G_1F_1 and G_1F_2, derived from a cross of two commercial F_1 hybrids. Genomes of four unknown founder lines at G_0 generation are shown as a, b, c, and d. A diplotype of one individual at G_1F_1 generation is shown as AB. The haplotypes A and B at G_1F_1 generation are converted to a or b and c or d, respectively by corresponding the haplotypes to the genomes at the G_1 generation. To handle multiple QTLs simultaneously, positions of multiple QTL candidates on the genome are determined in advance, and a linear model of the effects of the virtual QTLs at these positions is presumed.

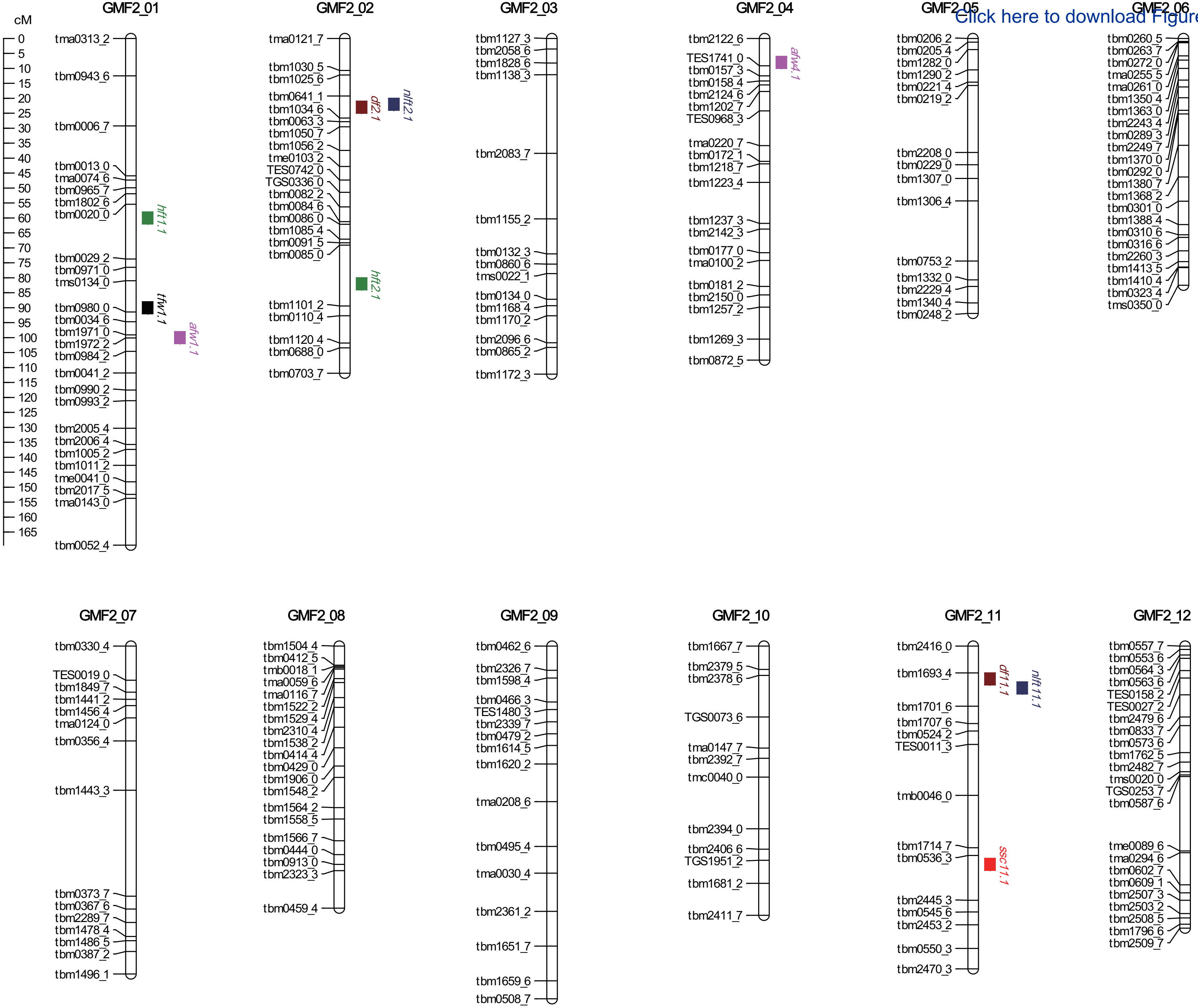
Fig. 2 GMF2 linkage map constructed using G_1F_2 (n = 360) and G_1F_1 (n = 240) lines derived from a cross of two F_1 hybrids, 'Geronimo' and 'Momotaro 8' and 222 SSR markers. The map consists of 12 linkage groups, the genetic distance covered by the map is 1,283 cM, the average distance between markers is 6.1 cM, and the maximum gap is 35 cM. Characteristics of SSR markers are listed in Supplementary Tables 2 and 3. Numbers 0–7 following marker names are the category number of the markers (see Table 3). Positions of QTLs detected by the Bayesian mapping (see Table 4) are also shown.



Unknown founders (L1-4)
L1
L2
L3
L4
G_0
x
x
aa
bb
cc
dd
G_1
Geronimo
(P1)
x
Momotaro 8
(P2)
ab
cd
G_1F_1
AB
Haplotype
analysis
G_1F_2
QTL mapping

Figure

Click here to download Figure Fig_2R.eps



Supplementary information for:

Bayesian QTL mapping using genome-wide SSR markers and segregating populations derived from a cross of two commercial F_1 hybrids of tomato

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Supplemental Tables S1-S12
Supplemental Figure S1

Supplementary Table S1 Number of G_1F_2 individuals in each experiment

	Autumn planting (2008)		Spring planting (2009)		
Experiment	EC 0.8 dS/m (low)	EC 3.2 dS/m (high)	EC 0.8 dS/m (low)	EC 3.2 dS/m (high)	Number of traits evaluated
1	90	-	-	-	10
2	-	90	-	-	10
3	-	-	90	-	10
4	-	-	-	90	3

Supplementary Table S2 EST-anchored genomic SSR (tbm) markers developed in this study

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al. 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0001	1	(AT)28	ACTTACTTACGTCCCACGGAGT	GTTTGGGAATCAAAGACTTCAAACA
tbm0002	1	(TA)18	ACTACCTTTTGCCTAATCTCTCT	GTTTCCCAACCCTATTGAAAATGAAA
tbm0003	1	(TA)15	ATTGAGACTTTAGGAGTCACCAT	GTTTGAGTGGTTGATTGCATGAAAAA
tbm0004	1	(AT)14	ATATTTGCCCCAAATGATAAGA	GTTTCCGTGGGACGTAAGTAAGA
tbm0005	1	(TG)5(TA)24	ATTTCAAGATAATTGGTGCGCT	GTTTCGATCTCAATATATTCGATGCAAA
tbm0006	1	(TA)24	AGGGTGACCAAAGAATAAAATG	GTTTCTGGTGATTGCTTGTTTT
tbm0007	1	(AT)23	ATTTGTCTTGAATCCAATTGCC	GTTTCTTTTTCGAATCTCTTCTGGTACG
tbm0008	1	(TA)21	ACGCTCTGTATCAGGTTTTCTT	GTTTGTATCAGTTTGAGGGATTTCTG
tbm0009	1	(AT)20	ATTATTGCATTGCATTTCATCC	GTTTCGACAACGAAGAAGTAGTGACG
tbm0010	1	(TA)19	ATAGGTTGATAGCAGGCCATGT	GTTTAGTTGCATGATTTTTCTCAAA
tbm0011	1	(AT)19	ACAAAAGGGCCCTAATTACATC	GTTTGAGCTAAACTTTAAGTCTCCCTTT
tbm0012	1	(GT)18(AT)9	ACTTCCTCAACAAATTTATTATTTCC	GTTTGTGCTCACTTTACCATTCAAA
tbm0013	1	(AT)18	ATAGACACCAAGGCCAATTTTT	GTTTGCAATAGTTTCAGTTGCTTCACC
tbm0014	1	(TA)16	ACTTCGAATTTTCAACTACCCA	GTTTCTCCGAGATTTCAGGCATAG
tbm0015	1	(AT)25	ACTGTCTACTTTTAATTTTCATGTTCA	GTTTCCCCTCCATTCACTTTATAAGAA
tbm0016	1	(TA)24	ACGTAAATGACAGTGGCCTAGC	GTTTGCCATGATTGGATAGTGATG
tbm0017	1	(TG)16(TA)21	ATGCATCCATTATTTCAGCTTG	GTTTGTACTATAGGGGAGGGAGAAAAA
tbm0018	1	(TC)8TTTC(TA)20	AGAGAAAAAGATAAATAACAATGATGG	GTTTACACCCGCAATCTTTCTC
tbm0019	1	(TA)19	AGACAAGACTTAGCCTTTTTCC	GTTTGTATTCGATCTCTTGGAGG
tbm0020	1	(AT)19	ATGGAATATTTGGTCGGAGGTT	GTTTCGACATTTTTGCACCTATAATTT
tbm0021	1	(AT)19	ACTTGTAATCCCCATTTTAAAGC	GTTTCAAAGAGAAGAAAAAGCAATAAAAGC
tbm0022	1	(TC)17	ATGCCCCAAATTTTAAGAAGCA	GTTTAGGTGAGAGGTGGAAGATGAAA
tbm0023	1	(TA)16	ATTCCCAAGGAATTCAAATCAC	GTTTCCCACATAGGTGCTCAATA
tbm0024	1	(AT)8AA(AT)16	ACGCTTGAAGAATCAGTACACA	GTTTGGGTTCATAAGAGGACCAAT
tbm0025	1	(AGA)15	ATGAAGATGATGAAGAGAGCGG	GTTTAACCAATTTTGGTGGGAAAG
tbm0026	1	(TA)15	AGACTCGTGTAGTTGGTAAGTGG	GTTTCTTTTCACCGTTTGAAACTAACA
tbm0027	1	(TA)15	ATTGGGTGCACCATTATAAAAA	GTTTGCATCTCTCCGCAAGATTAGAA
tbm0028	1	(TA)15	ATTACAACATCATCCACGCAGT	GTTTCATCCTTTTCACTTTTTGGC
tbm0029	1	(AT)22	AGATGGAATAATGTTTCGTAAAGG	GTTTAAAGTGAAATTAGATTCATTAATTCGT
tbm0030	1	(AT)21	AGACCATTGTTTGTAATTTCGG	GTTTAAAAAGGGTTTAACTTTCCAAAAA
tbm0031	1	(AT)14	ACAATGATGACCGGATACTTTT	GTTTCAACATTCATATCTTTTGGAAATAGG
tbm0032	1	(TA)13	ATGTGTCCGCTGATCTCAATTA	GTTTGCATCAATGACCCCTTAAAC
tbm0033	1	(TA)24	AGCAATATAACCAAATCAACCG	GTTTGACTTGGACCTTGGATTGTAGC
tbm0034	1	(AT)22	ATGCCTTAAAAATGGGGTAATG	GTTTCTTTTTAATCAGGTTGATTCG
tbm0035	1	(AT)15	ATGACCAATAGTTGATTTGAATTGG	GTTTAAGTGTTGGGCTTGAGAAAA
tbm0036	1	(TA)12	ATGGAGAAACTTCTTCTAGTTTAATGA	GTTTAAGCAATACAGAACAAGAAATAGAGGT
tbm0037	1	(AT)13	ACTTCACAAAATTTTAGAATGCAA	GTTTATAGTGCTTCTTTGGTGGCG
tbm0038	1	(TA)6C(AT)11(AC)7	AGGGCATATGTATACGTAATTATTTT	GTTTGGCTTACTTGTTCGTCTTC
tbm0039	1	(AT)10(AC)4	AGATAAATCTCTATCAGGATCATTTTT	GTTTCCGCTTATTACCTTTTATTTGTG
tbm0040	1	(AC)5(AT)9	ATTTAAACGAGGGCAACTTTCA	GTTTGCCTTTCTCGCTTTCTCATTT
tbm0041	1	(TAT)13	ATGGTTGGAAGTCTCAAGAACC	GTTTCTTTCTCTTGGTTTCGTCC
tbm0042	1	(AT)11	ACGCCAACTTTACTTAATACCC	GTTTCAACCTACATGTTGGAGATCA
tbm0043	1	(AT)11	ATAAATTTATCGTCATTGTTTCCA	GTTTGGACAAGATCCAGAAAAGGT
tbm0044	1	(TC)9	ATGCCTATTTCACCCCTACAGT	GTTTACCCATTCACAACTGATGAGC
tbm0045	1	(AT)19(TA)19	AGATTTGTTTACAAAAACATCACA	GTTTACGCCTGAATGAATTTTT
tbm0046	1	(TG)4(AT)10(GT)6	ACTCTCTGTGGCAGAGGTAAGT	GTTTCATTACAGCACCTATCATCGC
tbm0047	1	(AT)15	ATTTTGACCTTCCAAAAACAGC	GTTTGAGGTATTACGCCGACAAAT
tbm0048	1	(AT)11	ATTATGGTTCATGATTGGATCG	GTTTCCATCTAATATCTTTGGGACATCT
tbm0049	1	(AT)10	ACGACAAACTTTCATTTCTGGT	GTTTGTCGACGAAGTGCAAGATAA
tbm0050	1	(TA)9GTAT(ATA)4	ACTCTGTTTGGGACTCTTCTCC	GTTTGAAACAGTAGTGCAAGCTG
tbm0051	1	(TA)15	ATTCTCATTGGTTTGCTGACAC	GTTTGCCAAGTGAAAACTCACATC
tbm0052	1	(AT)9	ACTCGGATCATCACTTATTTCC	GTTTCGCGTACAATGTTTGATCCTAT
tbm0053	1	(TG)9	ATTTTGTGTGCTTGGAGAACTG	GTTTCTGCAACATCTTTCTGCTGT
tbm0054	2	(AT)24(GT)6	AGACCATGATAAGCCAATTCAA	GTTTAATACCCTGACTGCCCTGAA
tbm0055	2	(TA)23	ATTTAGCTTCGCATATCTTGGC	GTTTAGCCATGCATGTTACACCCTA
tbm0056	2	(AT)21	ATACTCATCTTCCTTCCGTTCG	GTTTAGAGAAACAAGCGAGAACATGA
tbm0057	2	(TA)19	ATTGGGAGTGGTTTCCTTTTT	GTTTCTTTTGACCGAATTTAATTTTAACAC
tbm0058	2	(TA)19	ATCTCTTCAACTATCAATTGTTCCC	GTTTAGGCCTTCAAGTATGTGGCT
tbm0059	2	(AT)17	ATCCCAACAGTTTTTCCAAATG	GTTTCAAGACCCAAATGATGATGA
tbm0060	2	(TA)6TC(TA)15	ATAACCAATTGTTTGGTGTAAGG	GTTTGAATTTACCCAAGTACACCAACG
tbm0061	2	(TA)17	ACAATTGACATTGGATAACACG	GTTTAGCTGGGCATAAAGCTATGGTA
tbm0062	2	(TTA)10T(TTA)16	ATAACCGAGTTTAGGGGTGTTT	GTTTGCATTTGGAAATTACTGAAAAGA
tbm0063	2	(TA)13	ACCTACCATATTCACTAATTCTTTTTG	GTTTCTCGTTCGTTTCTCTCCCTAC
tbm0064	2	(CA)12(TA)5	ACACAATAATCGGTTTTCACCT	GTTTAACCTGCCTTACTATGGCGTAA
tbm0065	2	(AT)24	ATAATGAATTTTGAGTTCCTTGG	GTTTGGACCTTTCATTCCTACTGCT
tbm0066	2	(AT)20	ATCACACATATTGTACGTTAATTTTGC	GTTTGCATTAATTCCCCCACC
tbm0067	2	(AT)20	ATTCTCTTATTGCATCTCCACG	GTTTGCCCGTAAGTATCACACAACAA
tbm0068	2	(TA)18	ATTTTCCAAGACACGAGAAAGG	GTTTAAAAATTAAGGTGCACCACTCAC
tbm0069	2	(AT)17	ATATAACCAAACGATTCCTAAATGA	GTTTACCAAAAATTCAGTGAGGGG
tbm0070	2	(AT)15	ATATAGCTGAGCAGATTGATCG	GTTTCAGACTGTGACAAGGCTGATTC
tbm0071	2	(AT)15	ATCGAAATTTTTGGATGCAGTA	GTTTCTGATCCCGACTTAATCATCA
tbm0072	2	(AT)37	ATAGCGTTCTTCACGCTCTAAG	GTTTGAAGAAAATAAATCATGCCGA
tbm0073	2	(AT)26	ACAAACCCTTTTTGCAATTTTA	GTTTACTTTGTCCCTCCCCAAACT
tbm0074	2	(AT)14TATA(ATT)5	AGATGACAAAAATTACGATGTCA	GTTTCACAATTTGACTTGGTACTCCA
tbm0075	2	(TA)7(AT)11	ATGTGGAAGAAACACACCCTCT	GTTTCGAAGTCAAAAGGAATTTACCA
tbm0076	2	(AT)23	ATTTATGCGCGATACAATTTGA	GTTTGGTCGACAGTTTCATCT
tbm0077	2	(TA)23	ATACCCCATTCGATGGATATTA	GTTTATTAGCTTCAAGCCGTCGAT
tbm0078	2	(TA)19	ATTGTCTGAGTTTCTTGCTTGC	GTTTCGAGCGAGATTCTATAGGGAGA
tbm0079	2	(AT)19	ACATGACAAATAATATCAAATGGAGA	GTTTCTTTTCTTCGTTTTTGCTTTTCC
tbm0080	2	(TA)17	ACACGTCAACACCAAAATTGAC	GTTTCGAACCTACTAACTCCCTGAGC
tbm0081	2	(TA)17	ACCTTGAATCCATGTTTAAGTTC	GTTTCTTGAGTTATTGTGAGATTTTTGT
tbm0082	2	(AT)16	ATTTTTAAATGCAGTGGGAGGA	GTTTAACAATAATTTGGTCAGAAAAA
tbm0083	2	(AT)25	ATTGTCGGTATTTGCCTTTATG	GTTTCAAAATTTATAAGCGTAGACAATCA
tbm0084	2	(AT)24	ATATTTTGCTAAGCATCTTCCG	GTTTAAGGCTTTCAATTTTGGGTTTT
tbm0085	2	(AT)23	AGGTTTTGTGTTCATATGTGTTAAA	GTTTCCCATCCATGATTTCATACCTT
tbm0086	2	(TA)23	ACAAACAAGTTTAGGGATCTGTTT	GTTTCGATAGCCATAATTTGTTCATGT
tbm0087	2	(TA)22	ATATCGTATTGCAGGTAAAATCA	GTTTGCACTTTTGATCCTTTCGT
tbm0088	2	(TA)20	ATCACTTGGAGAAATCGGAGAG	GTTTGATGAGGGTTTGAATGTCTG
tbm0089	2	(TA)20C(AT)11	ATCTAATCAAAATAGAATGATCCAACA	GTTTGCAACGACATATTGGAATACTGAA
tbm0090	2	(AAT)4AAC(AT)19	ATTTTGGGAAAGCAAATTCAGT	GTTTAACAACATTTTTGACCCATTCC
tbm0091	2	(TA)19	ATTGTCGGTATTTGCTTTTATG	GTTTAGTCCATATACAACGGTCAAAA
tbm0092	2	(AT)18	AGCTTGAAACACACAACCTTTA	GTTTCCCTTCGGCAGTAAACTACATT
tbm0093	2	(AT)18	ATACTTTTGTTTGTTGGAACGC	GTTTAATGTGGATCCTCGTGTCA
tbm0094	2	(TA)18	AGGTAACAAGCACTACGCGATT	GTTTCCGGGGACTCATTTATCTA
tbm0095	2	(TA)16T(TA)5	ATAGAGGGAAGAAAAGTGAAAAA	GTTTGGAAAAGTGTTAGGCAAAGA
tbm0096	2	(AT)15	ATACCTTTGGGTCGGTAACAAA	GTTTAGTTTCGGAGAACGTGCG
tbm0097	2	(TA)15	AGTGGGCATAAATTGCCTTAGA	GTTTCCAACAGTGTTACTTGGATGC
tbm0098	2	(AT)18	AGCCTTTCTCTCTCTCTCATCC	GTTTGAGAGAGGCGAGTGAGACTCTG
tbm0099	2	(TA)15	ACCGTAACTTAACCCTCATTCA	GTTTGAATGTCAATTTCTAGCGTCCC
tbm0100	2	(TA)15	ATTTTGAATAAAAATTAACCAAACG	GTTTCTTTTTCGGATGTCAAGAAAGAAA
tbm0101	2	(TA)15	AGGTGTCACAAGTGATTGTTTG	GTTTCTTTTATATTCTGGCGACCGAC
tbm0102	2	(AT)22	ATCCTATTATCATTGCATTCACC	GTTTGTCATTTTTATATTTTGAGGAAAGTG
tbm0103	2	(ATA)17(GTA)6(ATA)4	ACATCTACCGGACGTATTCACA	GTTTGCAAAGGTAGAGACAAACCCAT
tbm0104	2	(TG)4(TA)16	ATAATATTTCCCTGCCCAGGTC	GTTTCACATATAGCAAACACAAAATTCA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0105	2	(TA)16	ACCAGATTTGAACTCTTAGATGGTT	GTTTGAAATCGGTGTCGTTAACCT
tbm0106	2	(AT)24	ATGGGAGGAGTGAACAAAAAGT	GTTTAAGCTTATGTGACGGGACG
tbm0107	2	(TA)20	AGAGTGCATTCATGTTTTATTTT	GTTTGGAATATTTCGCTGATAAACA
tbm0108	2	(TA)16	ATCTGCTAGTCCAAGCACGTTA	GTTTCTTTTCTGGGTTGAAATATGGC
tbm0109	2	(TC)13	ATAACTGTCTGCATAAGCTGGT	GTTTAATTGGGAAAACTGGTATGGC
tbm0110	2	(TA)21	ATCCCTTTTCGTGTCATTTCTT	GTTTGTTTTGAAATGGAGGGAG
tbm0111	2	(GT)21(AT)10	ACAGCTAGTCCGAAATCCAAGT	GTTTGCATGGAGACCACGTATAG
tbm0112	2	(AT)20	ATATCATCATCTCGGTACATCG	GTTTGGAACAGGACTTCTTTCG
tbm0113	2	(AT)14	ACTGATACGTCAACAGGAATGG	GTTTAACAGAATTGGCCAAACCAA
tbm0114	2	(CT)15	AGGCCACAAAAAGATTACTTCA	GTTTGCCTTCTTTGGAAAGATTGATG
tbm0115	2	(AT)10	AGCAATTTATTAGGCCGAAAGT	GTTTAGGTGAATCCTGGCATTCTT
tbm0116	2	(AT)10	ACTAGGACAGGTGCTGAAAGTT	GTTTGAATCAAATCCTCCCTTT
tbm0117	2	(TA)8C(TA)7	ACTCCCAATCTCACTTGCACTA	GTTTGAGAGAGAGAGCAGAGAGG
tbm0118	2	(ATT)13	ATGATAGGGAAATGAGTCGAATG	GTTTAAGAGGATGCAAAATGACGAA
tbm0119	2	(AT)12	ATCCGAAGAAAACAGCACAGAT	GTTTGGACATGGTTGTATTAGGTTG
tbm0120	2	(AT)12	AGAGAAAAGGAGGAGAGAGGC	GTTTGCGAATTATACAAATCATTGCC
tbm0121	2	(TA)11	AGTTACTCCAAATGGTCAAATG	GTTTGAAATTTCTAGTCAAATTCTGG
tbm0122	2	(AT)19	ATCCCCGTCATGTAATTTGATT	GTTTAGGCCACTAAGTCAACCTC
tbm0123	2	(TA)18	ATGCGAGAGAGAAGGAAGAGAA	GTTTGGCATATGATTCGATGGAGATT
tbm0124	2	(TA)16	ACAAAATGGATGGAAGTTGTTT	GTTTGTGAGAGTGGCTCCATAGT
tbm0125	2	(GT)7(GA)12GTT(TG)4	ATCCCTTAACCTTCCCCTGTTA	GTTTACCAAACCTCTGAAAGGACAAA
tbm0126	3	(TA)24	ATAAGGAATGGAGGCCATAGAG	GTTTCAACAAGAGATCTTGGATAAATGC
tbm0127	3	(TA)19TC(CA)6T(AC)4	ATTCAAAAGCCTGATGAATTAAA	GTTTGAGGAGTACTTATGCATTTTTCC
tbm0128	3	(AT)25	ATTGGTGGAGAGTCTTGCAACT	GTTTCCATCGATCTAACCTAATTCAA
tbm0129	3	(TA)21	ATGTGCGTGAAAACAGAGAAAA	GTTTAGGAGGAAATGTTTCAATGGAG
tbm0130	3	(TA)17	ATTTCGCTTTTCATGCTTGTTC	GTTTGAAATATCGCTTGACACTGCT
tbm0131	3	(AT)16	ATAGTTCAGACCATCATCTCCA	GTTTCATATTTATTCGCTCCAACTGA
tbm0132	3	(AG)16	AGTTTTGCTGGTGAAGAAGAAG	GTTTATTCCAAAGGCCCTTCC
tbm0133	3	(AT)15	AGTCATGATGTGGCAGTGAC	GTTTCTAAACCCGTTTGCTACTCG
tbm0134	3	(TA)16	AGAAAGTGTTATTACGATATCAAAGG	GTTTACCAAACGTTCGAAATGACTTT
tbm0135	3	(TA)9	ATGTTAGCCGTTGGATATTTTGA	GTTTGTCAATCCAAAAGACCAGG
tbm0136	3	(TA)9	ACCTAAATGAGCTTGCAATACG	GTTTCAATTGTAGATGAGGGACC
tbm0137	3	(CT)4TT(TA)22	ATGAGGAGGTGTTTGCTACGAC	GTTTAACAAATACTTGATCCGAACATCA
tbm0138	3	(AAT)11	AGTTTTCTTGGTAACTCTCCGT	GTTTCAACATTTCGCAAGGATCAATA
tbm0139	3	(GA)9	ATGGGAGGATATAAGCGAGTGA	GTTTCAATTCACCTCTCTCCCAATCT
tbm0140	3	(AT)24AC(ACCT)4	ATAGTGATATATTTGGGGAGCTG	GTTTCATGACCAACAAATCAACAA
tbm0141	3	(TA)23	ATTAGGCAACGCAATTATCCAA	GTTTAAATCAAAATTTTTCACGCACC
tbm0142	3	(TA)21	AGATTCAGCCTTAAAAACCAAAA	GTTTCCAAGTTGTGACAAACTCCAAA
tbm0143	3	(TTA)5(TAT)13	ATATAAACAGAAAAAGTATTTGTCGAA	GTTTAAGAACCCGAAGAAGAAAGAGG
tbm0144	3	(AT)14	ATTTGGTCCCAGTTTGTGGTAT	GTTTACAACTTCCTCGATCATTGCTT
tbm0145	3	(CT)9	ATTAATGCGCCTCTCTCCACTA	GTTTGCATTTGGTGCTCTATGATTT
tbm0146	3	(AT)9	ATATGCGCCTCTCTCTCTCTCT	GTTTCCCTTAAACTAGTCCCCCACTC
tbm0147	3	(TA)22	ACGCTCCCTCTCGATTTTATAC	GTTTAGCGAGTGAGATTTTGAAGAGG
tbm0148	3	(AAAT)4(AT)11	ATCTTGGGAGTGTTGTTGTTCG	GTTTAAAGCGTTCCTCCAAAATCTTA
tbm0149	3	(TA)10	ACTGGGAGGAAAGAGAAAGATT	GTTTAAGCGCAAAGTGCAAATAAA
tbm0150	3	(AT)10	ATTGAGGTGTAATCGTTGGTCG	GTTTAAGGGAAATCTTGTTTGTGGTG
tbm0151	4	(AT)10	ACAGGAAGTTTTGACACCACAC	GTTTGCATTGCATGACTTTGTC
tbm0152	4	(TAT)9	AGGTTCATTGACTTGCAAGAAT	GTTTCCATATCGAACACCGAAAAT
tbm0153	4	(CT)15T(TC)17(TA)23	ACTAATATCATGACCCGTCGTT	GTTTAAAATAATAAAATTGCATGGTCTCC
tbm0154	4	(TC)14(TA)20	ACTTTTATCCAATGGGTGCTTA	GTTTAACTAAGCTATGTCACCAGGGG
tbm0155	4	(AT)19	ATGTCTCGTGAAAACGTGTGTG	GTTTCTCTTTTTATAAATCATCATCCTCA
tbm0156	4	(TA)19	ATATTATTCCCCAAGAGTGCTCA	GTTTGTGATTGGTCAAAAGTGTGG
tbm0157	4	(AT)15	AGACATTATTTTGTGGGTCCAA	GTTTATGGAGCGATCAATAGGAG
tbm0158	4	(TA)20	AGACCATTAACCTCGATCAGAA	GTTTGTCGAATTGAAAACTCTACCA
tbm0159	4	(AT)19	AGATCATGCAGAGTGCAATTTA	GTTTCTTTTTGGTGTCGAAACACTTTT
tbm0160	4	(AT)18	AGTAAAAATAAGACAACAATGCGA	GTTTATTAAATTTTCGCACGAGGC
tbm0161	4	(AC)4(TC)9(TA)13	AGAGGTGAGAGAAAAAGGTTTGA	GTTTGAATTCCCATGTGCAACTA
tbm0162	4	(TA)17	ATTCAAAAATTGCAACATGACA	GTTTCTCACTTTTCAACAATCAAACA
tbm0163	4	(AT)16	ACAATGACGTGAAAGTAACGAA	GTTTAGACGTGGAAATGGTGGAGTAG
tbm0164	4	(AT)4(GT)14T(TG)9	ATGTTCCTCTCTCTTCCCTCTC	GTTTAAGAGTGGCGAGTGATATCTGG
tbm0165	4	(TA)35	ATTGCTAAGGTGAAATAACTAGAGGA	GTTTGGCTAACGTTATTGAATTTTGA
tbm0166	4	(AT)31	ACACATAAAATGAGACGGAGAAAA	GTTTGCATGTGTTGTGGAAGTGTTA
tbm0167	4	(AT)8AC(AT)7	ATCCACATGGGATAGGGTACTG	GTTTCATCTCTCTGCGTATTTGA
tbm0168	4	(TA)25	ATTCAGTTGTTTTGTGTTTGGC	GTTTACACGAATAGTGACGCATTGAC
tbm0169	4	(AT)22	ATAATCAAATCAAAATGAAAAACA	GTTTAACAAAATATGCTCGGTTTCTTT
tbm0170	4	(AT)21	ATGGGTGGGTTTGTTAGGAAGA	GTTTCCCCACACTCCTACGTACTCTC
tbm0171	4	(TA)21	ACAGAAACATAAATAAGGTGCG	GTTTCTTTTTGAAGGAATGTAATCTTGAAC
tbm0172	4	(AT)18	AGGCTCACTTGTACCATTTCTT	GTTTGGCATGACATTGAAAAATGAAAG
tbm0173	4	(AT)31	ACAAGCAACATTTGAACACATAA	GTTTCAGCACAGCTGATATGATGTATGA
tbm0174	4	(TA)17	ACATTCAATTTGACCACCTGTA	GTTTGACCCTTTCTTTTTGTCTTGA
tbm0175	4	(TA)9	ATTAAATGCATTATTCGTGTTTCA	GTTTCCATCGAACATTCACATCAAAT
tbm0176	4	(AGG)7(AAG)5(ATG)5(AGG)7	ATGGTGGAGAAGGATGAGGTAG	GTTTCCAGCTCTGAACGAGAAG
tbm0177	4	(AT)25	AGGACAGAAACTTGGTCACTCC	GTTTCACTTCAAGGTCAATGAAT
tbm0178	4	(AT)22	ATGTCGTAGACTTGTGGTGCAA	GTTTACGCGTAAATTTTCAGTCAAAT
tbm0179	4	(TA)18	ATGCATCTGGTCTTCTGATGTG	GTTTCTTTTCAGTGTTGCTCGTCTC
tbm0180	4	(AG)11	ACTCCTCAGAAGATGGAACAAT	GTTTGGGAAGAACAATTGAGAAATCG
tbm0181	4	(AT)22	AGGTCAAGATAGATAATTGTCGG	GTTTAAATTTGAAATGTGAGTTGTATATCTG
tbm0182	4	(AT)10ACA(CG)14(CA)5	ACAATTCATCTATGCCATGAAA	GTTTACACCCATCATCCCACCTTAT
tbm0183	4	(TA)11	AGTGACTAATATGCAGGGGTGG	GTTTAACCAGCTCACCCACAACTACT
tbm0184	4	(TC)11	AGGTAAAACAGGAAACTGGAGG	GTTTGGTTTTAGAGTGCCCTTGTTT
tbm0185	4	(CT)11	ATAATGTTTTAAGGGCATGGCT	GTTTCCAAACGATGTTCCTTTAGACTG
tbm0186	4	(TA)11	ATAGGTTGCCATCAACTTTTGC	GTTTGGGAAGAACTCGAACCTTACAA
tbm0187	4	(TA)25	ACAGCTCAAGAGAGAATTGACA	GTTTCTCGTCTTCGACTCCTTTCTC
tbm0188	4	(TA)23	ATTTGATTAAACAATCTTTTCCG	GTTTCTTTTTATGGTATTTCTCATGGCA
tbm0189	4	(AT)21	ACCCTATTTGTCTCACTTCTTTTT	GTTTCTCGAAATGCGAAAAGTGT
tbm0190	4	(CT)19	ATGAATGGAAGATTCATCCCAA	GTTTCAGTGAAGAATCACCGAAGTTG
tbm0191	4	(TA)16	ACAAATTTTTATTCACACAAAAGATAG	GTTTCCGTTTTATGTATTTTAAAGCATGAC
tbm0192	4	(ATT)18	ACTCGATCTCTAAACATGGTCAA	GTTTGACACTTGACAGTTGTCCTCTC
tbm0193	4	(TAT)12	AGTTGATACTTGCAAAAGAATTGG	GTTTAGATATTGCAGAAGGTGTTCCC
tbm0194	4	(AT)11	AGTTAAGCCTTTGGATTGTGTG	GTTTACAAAATGAACGATAGAGGGGA
tbm0195	4	(TA)11	ATCATCTACTGGATCGGTGAAG	GTTTCCTTTTTGTGCCACTTTTG
tbm0196	4	(TA)22(GATA)4	ATTCCAGCCCTTAGAGGCAT	GTTTCATGATCATTAGCTACCGCAC
tbm0197	4	(AT)18	ATGTGAAGTCACGAGGATACGC	GTTTCGATATGAGCTTAATGGGTGCT
tbm0198	4	(AT)18(AC)5	ACATGTTAGGTAACCTTCGAGC	GTTTCAAGGATCGTTTTTGTTTTGTG
tbm0199	4	(AG)13	ATTCTCCCCTATGCACAGAATA	GTTTCCCTGATTCCTTCCTTTTAGGT
tbm0200	5	(TA)24	AGATCATATTCAGTCTTTGCCA	GTTTGGAGGTGTCTAAAATCATCCCA
tbm0201	5	(TA)22	ACTTATTGCAAGAATCAAGGAA	GTTTGTGAAAACATATGAGTCAAACTT
tbm0202	5	(TA)19	AGAAAATTTGTATTCATGACGGA	GTTTGATCACTAGATCGTCACACCC
tbm0203	5	(AT)16	AGTGAAGGGCCAAAATAGCATA	GTTTGACCGTTGCATGTAAATTGATG
tbm0204	5	(AT)24	ATCATCAGAACCACATCGAAAT	GTTTCAAAATTACCAACACCAGCA
tbm0205	5	(TA)22	AGAGTGATGAGCGAGATTAGGC	GTTTCGATCAATTATCAACATATTCAAAC
tbm0206	5	(AT)21	AGGCTATCGTTTAAGTATGCAC	GTTTGACATGCTTGACACACATTATTGA
tbm0207	5	(TA)6TG(TA)21	ATGAGTTTAATGATTTGCTTGTGA	GTTTCTCTTTTTGGTTTGGGTTTTT
tbm0208	5	(AT)20	ATCTGATTGAAGAGCCTATCTGG	GTTTAATTCGAGGGACAATATTCCG
tbm0209	5	(AT)20	AGTCTTTAGTCAAGGGGACCAT	GTTTCTTTTCGTTCGATTTTCCTTTTT

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0210	5	(AG)20	ATAACACAATTTCTCAAATCTCAAA	GTTTCTTTTATTCGGCAATTGTACGC
tbm0211	5	(AT)20	AGAAAAATGACACAAAAATAGAAAA	GTTTCCTTTGTAGAAAATGTCATGATT
tbm0212	5	(TA)19	ATTTTTCTTGGTCCTATTCGTTG	GTTTGCCTCAAAAACTAAGGAGTG
tbm0213	5	(AAT)4(AT)17(AC)4	ACATAGTATCACAAAGCTGACCA	GTTTGGAAGTTGTAGACATGGAAGCC
tbm0214	5	(TA)17	ATTGTCCAGTAACTCCATTATCTAAA	GTTTGAGCAATTTTTGATGTGATCT
tbm0215	5	(AT)15	ATACATGGAAACAAGTCCCAAC	GTTTCAAATTAAGCGATGAAATCAAAA
tbm0216	5	(AT)15	ATGCGTAAACCATGATGTTAAT	GTTTACATCAAAATCATATCGCTTATCTT
tbm0217	5	(TG)9(TA)23	AGAAATAGAAGGGGATATAGCAAAT	GTTTCCCCTCTCTCCTCCAAATAAC
tbm0218	5	(AT)21	ATAATGACAAACGCCTCACTTT	GTTTAGCCATGAGCGTTAGATGAG
tbm0219	5	(TA)21	ACACCAAATCGAACAACAAGTA	GTTTCCGCTAGCTGATAAGAGAACCT
tbm0220	5	(AT)18	ATATTGTGATCGTACAAGAATTTGA	GTTTCTTTTGGACTTTTGGTAGCTTTT
tbm0221	5	(AT)16	ATAATTTAGGGAAGGTGGGGTT	GTTTCTTCGAATCCTTTTATTTCG
tbm0222	5	(AT)16	ACAAAAATAATTGGCAACTTTCA	GTTTGCCCAAGTCTCTTTCTCTTTC
tbm0223	5	(TA)12TG(TA)16	ATCTCTCTAAATATTGTGCAAGCCT	GTTTCCTGTACACGTGTGTCTCGT
tbm0224	5	(TA)15	ATGTTGCTTTAAATATTTCTTTTTCG	GTTTGTCCATGCAAAACAAAACAC
tbm0225	5	(AT)11	AGCTTCCATCGTATATTGACAGA	GTTTCAAAATGCCTTTGTTGAATTT
tbm0226	5	(AT)9	ATCTCGTAAGGGCAGACGAATA	GTTTATGTGGCACCTTTTGCTT
tbm0227	5	(TA)9	AGACAACGAAGAAGTAGTGACG	GTTTATTGCATTGCATTTCATCC
tbm0228	5	(TA)9	ATTAACCTGCAGCCATTCAACT	GTTTGGAGTGCTTGGGATTGTGTTAT
tbm0229	5	(AT)24	ACAATGTTAGGACTTTAGGGGTTC	GTTTAGCAAAAGCAGAGCCAG
tbm0230	5	(AT)20	ATTAAATAAGACAAACAGAAAAGAAGG	GTTTGAGAGGTACAAAATAAGTGCAAAAG
tbm0231	5	(TA)19	ATCGTAATCATCATGAAAGGCA	GTTTAAGTGTAGAGGTGTGGGGTG
tbm0232	5	(AT)17	AGAAGTGTATCTGGTTGAGGGA	GTTTCCAAGGATCACTTGAAACTGC
tbm0233	5	(AT)11	AGGGGCAAAACAGTAATTCAAC	GTTTGACTCTCTAAATATTGTGCAAGCCT
tbm0234	5	(AT)20	ATGCTCAAAATACCCCTCAAAA	GTTTGTCATATGAACATACGAAGAAAACA
tbm0235	5	(AT)10	ATTAGATATGCTCAAAATACCCCC	GTTTCTCAAACATTGTGCGTTG
tbm0236	5	(TA)19	AGTAAATTTGAACAATTTTTGGTTT	GTTTGCAAATGGATGGAACACATA
tbm0237	5	(AT)4T(TA)14	ATTTACGATACTCGCGGACAAT	GTTTCTTTTCAAAGGAGAAGTTGAGGA
tbm0238	5	(TA)12	ATTGGACTTGGACCTTCTCAAA	GTTTGGTTCGTTTTATCCAAAAATCA
tbm0239	5	(TG)5(TA)11	ACTTCTAGGGGATACTTTCGGG	GTTTAAGTTGTCAGAAGCGGACCTAT
tbm0240	5	(AT)22AATCG(TA)4	ACGCAAATTGAGCTATGCTTTA	GTTTCGATTCCTTCTTCTCCCTT
tbm0241	5	(AT)20	AGCGTTGAAAAGTTCTCCTTAC	GTTTAAAATTCTCCCTGTATACTGGACTTC
tbm0242	5	(AT)19	AGAGCTCTTGACTCACTGCATC	GTTTACAAACAAATATGCCACATCCA
tbm0243	5	(AT)18	ATAGTGAATCATCAAATTCTGGC	GTTTCAACTTGCGTGAACTTA
tbm0244	5	(AT)18	ATGGAAACAACCTCTCTCCTTC	GTTTCAACACTTCCCATGATCCAATA
tbm0245	5	(AT)17	AGTAGAGTTGAATAACCGCCAA	GTTTACCCCACCTTACCTAACCCT
tbm0246	5	(AT)17	AGATTTCTTGTTCAAAAATTACTCAT	GTTTGAGAGGCGATCAAGAGAAGAGA
tbm0247	5	(AT)16	ACCCTTATCCGTGTGAGGTAGA	GTTTCAATCAGTTTATCGCTGTGAGC
tbm0248	5	(AT)15(TTAT)4	ATAAACCCGAAATTTAATGAACA	GTTTCGGCTACTTTCTGCGTCTATTT
tbm0249	5	(AT)28	ATCGTTAGCGTGTGTGTTTGAC	GTTTAAGTGATGGTTTGTACAGTGAAAAT
tbm0250	5	(AT)23	ATGTTTCACAAGTGACACGCC	GTTTAAAAAGGGGAAATTGAATGGAT
tbm0251	5	(AT)17	AGAAGAATTTGATATATACCGAAGGA	GTTTGGAAGAATTTCACCTCACAAG
tbm0252	5	(TC)12	AGTGAAACATGTCATGAGCGTA	GTTTAAAATCCATGAACAACAAGGG
tbm0253	6	(TA)25	ATATAACTTCGGATCTTTACACAAAA	GTTTCAAATTTAGGCTTGTAAAAATTG
tbm0254	6	(AT)24	ATAAAGTGTAATGAACACATCAAAAA	GTTTCCCAACGGACTCTAAGTAACAA
tbm0255	6	(TA)23	ATGAGGTACAAAATAAGTGCAAAAG	GTTTAAGACAAACAGAAAAGAAGACATGAA
tbm0256	6	(TA)23	ACTCATTTCCCATCTCACCC	GTTTCAAGGAACATTGAGCAGCTTTA
tbm0257	6	(TA)22	ACTTTTTCTTGCCAACGAGTGT	GTTTCAAAATGCAAATAATGTGTGGG
tbm0258	6	(AT)20	ATCATTTGTTCCTTTTAGTTGTCTT	GTTTCAACGCACGTTCCCTAAAACTA
tbm0259	6	(TA)20	AGAGAGAGGGCATAGAGTAGGA	GTTTGGAGCACAATTAAATCAAACCC
tbm0260	6	(AT)19	ACATATTGATTTCATTTGTTGGAA	GTTTGGCTTGACTATTTCGATTCATTTT
tbm0261	6	(TA)19	ATCAGCGGATCAAGATTCAGAT	GTTTAAAAACTCGAGACCAAACCAAC
tbm0262	6	(AT)18	AGAACTCACTCGTGCTTCTTCT	GTTTGAAACCACCCATTAGATTTTGC
tbm0263	6	(TA)16	ACAACTCTTACCGCTACGCTTC	GTTTACAAGGACGTTGGAATTCACTT
tbm0264	6	(AT)15	AGATCTCAGGACCTCTCTGACT	GTTTCCTAGAACCATTGGGTCAACT
tbm0265	6	(AT)24	ACCGACATCCAAAAATCGATAA	GTTTCACATAGGAGGGAAAGTGT
tbm0266	6	(TA)24	ACAACAAAAATAAAATACAATCGAA	GTTTAAAATCATACACACACAAAAGCAAA
tbm0267	6	(TA)23TG(TA)6	ATCATGATGATTCTCTTCACCG	GTTTGCATTGAATTTGGAAAAAGG
tbm0268	6	(AT)23	ATAATTGTATTTCGGTGATCAAA	GTTTCCACCAAGTATGCTATTTTCTCG
tbm0269	6	(AT)23	ATTTTTTCAAGCAACCAAACAA	GTTTACCCAATAGGTGATTGTGAAGG
tbm0270	6	(AT)22	ATGAGACGAGTCAAAGACCCAT	GTTTGGGAGCATTATGTTGAGTCAC
tbm0271	6	(AT)21AC(AT)4	ATGTGAAAAGGACTCCAACATC	GTTTGGTGCTAATGACTTGATATGC
tbm0272	6	(TA)20	ATGGTGGTAAAAACTCGACAGG	GTTTAAGCGGACGTAAGATTCTC
tbm0273	6	(TA)19	ATGCTTTTGTGTGTGTATGATTTTT	GTTTGATTGGTCCTCTCTTTGTC
tbm0274	6	(AT)18	ATGGTTGGGGCAGAGCTAAGTA	GTTTCGAAATTGATACTGTTGCATCG
tbm0275	6	(TA)18(CA)11	ATCAAGATTTGACTCTCATCACAT	GTTTGGAAGATAATTGTAGTCAAAGATAGCA
tbm0276	6	(TA)17	ATAAATCAAATCGAACCCAAAT	GTTTAAATTTTACAAGCCCAAATAAAAA
tbm0277	6	(TA)17	AGAGTACGAAACCACGTGTACC	GTTTCATCCCATCATTCATTCTTG
tbm0278	6	(TA)16	ACAGCATCATTTTCTGAATCAA	GTTTGGTGGATGGTAGTCATCTGAG
tbm0279	6	(AT)15	ATTAGTTTTGGCTCCCCTTTTC	GTTTGTGCGCTTCGATTAATTT
tbm0280	6	(TC)14(TA)15	AGGTATTTTAGACCCTTGTCCG	GTTTCAAACCAATATCTGTATGTCGCTT
tbm0281	6	(ATAC)4CG(AC)15(AT)9(AC)4	AGTCTCTCTCATCGTTCCCTCT	GTTTGGTATTAGACACGCAAGCAC
tbm0282	6	(AT)15(GTAT)4	ACAATGAAACAGACATGTTGAAA	GTTTCAGCTTATTTCATATACACACACACA
tbm0283	6	(TA)15	AGGATCATTTGTTGCTGGTTAG	GTTTCCGGTGAGAGGATAGAGGTAA
tbm0284	6	(TA)20	ATTTTTCAAGCCCTTAGAGGCA	GTTTAGCGAGATTTTTGGGAGAGAG
tbm0285	6	(AT)14	ATTTTCAGTTTCGTTATTCGCTT	GTTTCGGATATAAACTATCCCGTTCTT
tbm0286	6	(CT)14	ACGGAGTAGATTCGTGGATTTT	GTTTACCTTTGAAGGCTATCGTGGT
tbm0287	6	(AT)14	ATGTGAAATCCTATTGGCGTG	GTTTGTGGATCCAGATTCACCATT
tbm0288	6	(AT)25	AGGGATATAGTTTGACTGACGA	GTTTGCTATCTCCTACGTGTCA
tbm0289	6	(TA)24	AGGATTTCAGCTGCCTACTGAG	GTTTCTTTTCGGAGAACATAATAGGGG
tbm0290	6	(AT)16	ATCACCCACAGAAGAAAGTTCC	GTTTCTTTTAAATGGTTAAGAAAGAGAGTGGA
tbm0291	6	(TA)15	ACTTGACACCTAATTCAAAAACTCA	GTTTCCCATAACTTGAAAAATGATGAA
tbm0292	6	(TA)24	ACACGCTTCAACTTCGAGTGTA	GTTTAAAATCAGGGGTGAATTTAACG
tbm0293	6	(AT)23	ATCGTCTTGTGAAGTTCGTGTT	GTTTCACAACATATTTTTACATTTCTCA
tbm0294	6	(AT)20	ACATCAGAAATTAAGTTCCATTGTT	GTTTCATGACAGACAGAACCAAA
tbm0295	6	(AT)20	AGCTTGTTAAGCCCAACATTT	GTTTCGACTGAAAATCACAACAAAAA
tbm0296	6	(TA)18	ATGAATTCATAAGTTTATCATTCCATA	GTTTAATAATAAGCTGTACCCAAAAA
tbm0297	6	(AT)17	ATTGTTCATATTCAAAGTTAAAGGACA	GTTTGCTCATGAAATTGCAACTATTTT
tbm0298	6	(AT)16	AGTGAATAAAAACTTTTCCGGC	GTTTCAACTCATCAATCAAAACCG
tbm0299	6	(TA)16	ACATGGGATACTGTCAACCAAG	GTTTGTTATTGAGGGGGTTCAAA
tbm0300	6	(TA)15(AT)9	ACCTCAATATTCACATCAAACAAGA	GTTTGACCAAAACTTGAGGTTGA
tbm0301	6	(AT)25	ATATCCATGAATGAGAGCAACA	GTTTGATCTGCATTATTTGAGATAGATT
tbm0302	6	(TA)23	ACACTTGGTGGTCAGAAAATTG	GTTTGCCGAAAAACTACATTG
tbm0303	6	(AT)21	ATATCGAATGACAATTGAAACAA	GTTTGCGCAATTAGGTTATATTGATG
tbm0304	6	(AT)21AAAAT(TA)4	AGCAATTTCATAACATAGGGCA	GTTTGGGTCTCTGGCAACATTGTATC
tbm0305	6	(TA)21	ATTTCAAAGGAGGCAAAATGAA	GTTTACGTGATGCTCACAGAGCTAGT
tbm0306	6	(TA)17TTT(AG)10	ATTTATCCCTCCAACACCAACT	GTTTAGGTTTTGCGACAAACTCTAGC
tbm0307	6	(AT)17	ATATCTTTCACCCCAGGTTTTC	GTTTCAACAAACCATTGTTCAGCAAC
tbm0308	6	(AT)16	ATTGGGGTCAAATGTTTGGATA	GTTTCCTTTGCGTCTCATAAGAATG
tbm0309	6	(TA)16	AGTAAGGATGCATTTTGTGGTT	GTTTGAATATTTTTGCGGCTCTCATC
tbm0310	6	(AT)25	ACTTTTTATTGTGATTTTTCTTGTCA	GTTTGAGAGAAATTTGGTTTAAACATT
tbm0311	6	(TA)20	AGCAAGACAAAAGAAAATTGGG	GTTTCTCTCCCTCAAGCTCTCGT
tbm0312	6	(ATT)19	ATGGGCAGGTACTCCATCAATA	GTTTACATGCACAGCAACATTACCA
tbm0313	6	(AT)18	ATTGAGTCTTCTCAAAGCGAGG	GTTTGGGTCTTTAAGCACAAAAGCAC
tbm0314	6	(TA)17	ACCATGGATTCTGCTTGATATT	GTTTACCAAACTGAACCAACCGATAC

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0315	6	(AT)16	ATTAGGGGCTCATGTAAAGTGC	GTTTCGTTGCTTTGACAATTAGCAT
tbm0316	6	(AT)30	ACAAGCAATTGCAAAATAGAAA	GTTTACGACACAATTGAAGGAGGAAT
tbm0317	6	(TA)20	ATGTGAAAGTTGCCCAATTAAA	GTTTGTACTTCATGGAGGTTAGCCA
tbm0318	6	(TC)4TT(TA)16	ATCCCTTCATCCGTTGATTTAG	GTTTGAACGGAGAGGAACACAAT
tbm0319	6	(CA)11(TA)5(CA)4	AGGTAGCACCCCCTAGAAATAA	GTTTGATGTTGAGTCTAAGATGGCAA
tbm0320	6	(AG)4ATGA(AT)9	AGGAGGAGGTAGATTGATTGTG	GTTTAGGAACAACTCGAAATCCAATG
tbm0321	6	(AT)25	ATTTGTATGGGCAACTTTCAGA	GTTTGCCCAGATCTCTTTCTCTTTC
tbm0322	6	(TA)21	ATTCTGAAAAGGAGCCAACAAA	GTTTGGGAAAAATTTCTTTTCGCAAC
tbm0323	6	(AT)21	ATCACAACACTGATAATAGCCAAAT	GTTTGCACCTTTGGGATGATTTAAGTA
tbm0324	6	(AT)18	ATAAGCACACGATTGAAGCATT	GTTTCCGTTAATAACACATAATCAATACACA
tbm0325	6	(TA)15	ATCCCCCTCTTATTTGTCATCA	GTTTGACTCTCAAAATTGTGCAACCA
tbm0326	7	(AT)25	ATAAGGTGAAGTCAGAAACGAAA	GTTTAGCAAAAACAAATCAAGAATAAG
tbm0327	7	(GT)5(AT)22	ACGATTGATCCATAAATTCCAT	GTTTCCAGATGACAATTTAGACCTT
tbm0328	7	(AT)21	ACCATATTTCTATGGCTCTTGC	GTTTGAATCCCACAAAAATGTCATCA
tbm0329	7	(TA)20	ATCGTGGGTTGACTTTGTGTTT	GTTTGAGGGCAGAGAGTGAGAGAGAG
tbm0330	7	(TA)18(CA)6	AGAAATTAGGAGAGACAATCACATTT	GTTTAAATCAAAATAATTAACAACGTTAGGA
tbm0331	7	(AT)16	AGAGAATGTGAATGGAAAGGAG	GTTTCTTTAATCATGAACAAAACACAAA
tbm0332	7	(TA)16T(TA)8	AGGGTAAATATAGAAAAGGAATAAGGA	GTTTGCATATTTATGTAAAGTTCCCGTT
tbm0333	7	(AT)16	ACGGTTTGATTTGGTTTTCTCT	GTTTGGATTTATGTTTGGTTTTGGA
tbm0334	7	(TA)4T(TA)16	AGGGACATGAGTGTCTATTTGC	GTTTGTTGGCTTATTTCATTGGA
tbm0335	7	(ATT)16	ACAGGAACTGGATTTCGTATGC	GTTTACTAACGCTCCAAATGCC
tbm0336	7	(AT)28	ATCATCCATTTGCCTGGAGTAT	GTTTCCTTGTATTTCCCACTTTAAAACA
tbm0337	7	(CT)12	AGCTGGGTAGTACCTCCAATTT	GTTTAGCGAACAAGGGAAATACCTCT
tbm0338	7	(TG)9(TA)8(TG)8	AGCCAGAACTAGAACCCCTTTC	GTTTCAAACTGCAAATTGTATTCCG
tbm0339	7	(TC)8C(CT)8	ATTAAAACCCAAAAAGCAGGTG	GTTTGGGTTTGGAGTTTCTGATCCTA
tbm0340	7	(AT)24	ATAGCCGGTTGAGCTAAGAAAG	GTTTGCTCGTTGTTGTTTGTAGC
tbm0341	7	(TA)24	ACTAGGGTTAGGTTTAAAGCAGAG	GTTTAATCACGCGTCATGTAAACG
tbm0342	7	(TAA)24	AGACACACATGGATGGATGATA	GTTTCCAATTCCTCCTTCGTATTCAC
tbm0343	7	(AT)22	ATTTCATGCACTGGTGTAATGG	GTTTCGATAAGATCAAACTAAACAATCAAAA
tbm0344	7	(AC)21	ATCACACAAACACACACACACA	GTTTCACGTGCACTCAATTTCCTAAA
tbm0345	7	(AT)20(TAT)6	ACCTATTCTCTCACGTGCCCTA	GTTTGATAAGGAATAATTTAGGTACTCCGA
tbm0346	7	(TA)20	AGCTTTGGCATAATATCCGTGT	GTTTCTTTTGGATCAGGGAAAGAAG
tbm0347	7	(AT)19(AC)10	AGCATTAAATAAGAGTGTGGTTGC	GTTTGGTAAAGTTATAATGTTGGCATC
tbm0348	7	(TG)4(TA)4C(AT)18	ATCTCTATGCGACTTCAGGAGC	GTTTAGCTTTCGCAACATTTCC
tbm0349	7	(TA)17	ATAACAAAAGCAATTAATGATCCA	GTTTGGCAACTCTAAAAAGTTGAAAAC
tbm0350	7	(CA)17(TA)7	ATGATCCCATGCTGATAATTGA	GTTTCCCGAAATGCTAAGAGGTATCA
tbm0351	7	(AT)16	ATTTAAATGCAGCAAAATTATTGAA	GTTTGGTAGATTGGAAGATTGAAA
tbm0352	7	(TC)16	ACCCTTGTCATTTTTACTTTCCT	GTTTCGATATTCAAACAAACACGGAA
tbm0353	7	(TA)4TT(TG)16	ACATAGTCTCAATTACGCAAAGAA	GTTTGAGAGTATTTGGGAGAATGAAAAA
tbm0354	7	(AT)15	ACAACCATTCACAAAATTCCAA	GTTTAACAATTGAAACAGATCAGATACG
tbm0355	7	(TA)15	ATGCTAACACATTCCCTAGTGTGA	GTTTAATAAGAATCCCCGAACCCT
tbm0356	7	(TC)7TTATT(TA)23	AGGAGCACAATTAAATCAAACTC	GTTTAGGGAGAATGAAATTCGTGAGA
tbm0357	7	(AT)20	ATACAAACCTATTCGCTATGGTG	GTTTGCTTTATCACTTTCTCCTTCTTT
tbm0358	7	(AT)20	ATGACTAAGTTTGTTCTTGTGTCTAGC	GTTTGTGTAGTTAGCTCTGGCTGG
tbm0359	7	(AT)20	ATGAAGGCAAGTGATTAGAGCA	GTTTAGAACACCTTTAAATTGTTTTTCAA
tbm0360	7	(TA)20	AGTGTCAATGGTTATCGAGGAT	GTTTAAGCTTGTCCAGCAAGGTACA
tbm0361	7	(AT)18	ATTTCCATTACCATGGGACTAA	GTTTGTTGTCATGTTCACTATTTTCTCA
tbm0362	7	(AT)16(TAT)4	AGATAATGGAACTCCTACGCCT	GTTTAGAGGTACCACGTCACCTTGTT
tbm0363	7	(TC)5(TA)5T(TA)8C(AT)15	ATTCTCCAGTCCCAACTTCG	GTTTAAAAGAACACAACAGAATCATATTTCA
tbm0364	7	(AT)23	ACAGCCAAATAGAAATTGGAAG	GTTTCACATGTTAAAAGGTTGGTCACA
tbm0365	7	(AT)22	ACAAAATCGAATCACCATCTCA	GTTTAACAGTACATGCAGGAGACAAGA
tbm0366	7	(TA)21	AGACTCAGCCATATACAACGAAA	GTTTAAAAGCCAATGCTTATGGTGAG
tbm0367	7	(TA)20	ATGTCGTTCATCTTTGTCAACT	GTTTGGGGTTCTTTCGAACCTTATTT
tbm0368	7	(AT)18	ACTACCATTCATCCCACAAAAA	GTTTGCATCAATTTGTAACCTTGTGAA
tbm0369	7	(TA)17	AGTAGCTTTTGAAACTCAATGC	GTTTGTTATTTCCCCTTCCCTACC
tbm0370	7	(TA)17	ATTCTCATTCCTCGACTGGTGT	GTTTGCACCTCTTATTGCAGAGGTTT
tbm0371	7	(AT)17(AC)5	ATAATGGTAATAAACAAAAAGTATCGC	GTTTACGGCGATATAAACGTTACCTG
tbm0372	7	(AT)16	ATATGGCCAACAACCTAAAAA	GTTTGGATAAGATCAAAAGCTCCA
tbm0373	7	(AT)15	ACGAGCAGAAGTTCTCTTCCAC	GTTTCACCACCGTCCTTCTTT
tbm0374	7	(TA)15	ATTGACAAGCGAGATCAGGAGA	GTTTCCACCAGCGACTAACTTACTCAT
tbm0375	7	(AT)15	ATAATGTGCCACAAATCAGACA	GTTTCCACTAATAAGGATCAGGCAAA
tbm0376	7	(AT)15	ATTCCCAATTCCCCTACAAAGT	GTTTGAAATAGTGGGAGTATTCATTTTT
tbm0377	7	(AT)16	ATTTTAAAAGATTGAGCGTATAAGG	GTTTCCTCCATTTTATCTCCCTCA
tbm0378	7	(AT)15ACAG(AC)4	ATAATCGAAAAGATGGTAAACGATA	GTTTCGCGAGTTGTTTCACATTTACT
tbm0379	7	(AT)15	ACAAGAGGTACAAACTAAGGGCA	GTTTCTTTTGTTAGAAGCCGACTTACG
tbm0380	7	(TA)15	AGGTTATTGATAACACTTTTGACCTT	GTTTCCAAATTAACTTTTATTTATTCAA
tbm0381	7	(TA)29	ATTGTGGACCTCCTTCGACTAC	GTTTCACCTAACCCAGTACCACCTT
tbm0382	7	(AT)21	ATTCCTTTTTAAATGCCTAAAACA	GTTTCTCTGTCCTAATTTATGCG
tbm0383	7	(AT)16	AGGCATTTTTCATTTTAATCAGG	GTTTGGAAAAGTTCTTTTTACTTTCTTGG
tbm0384	7	(AT)14	AGAACTTCAATACATGTGTGCG	GTTTCGTGAGGAATAACTTTCA
tbm0385	7	(AT)20	ATTTTCAAGGCCTAAACACGAC	GTTTAAATGAGGGATTTGGATTTAGAA
tbm0386	7	(AAT)5(AT)16	AGTCCATTTTGTCATTTCTCAA	GTTTCGCCATTGAGGATATTTT
tbm0387	7	(TA)15	ATTGTCTTTTTAGTTTGTTCCGA	GTTTGGCCTAAAGTCAAAAATAAATTGC
tbm0388	7	(TA)14	ATCTCTCCTTTGGTGATGAATTT	GTTTCTTTTAAAAGGTGACTTGGCCTC
tbm0389	7	(AT)24	AGCCTTCTAAACTCATCGTGAC	GTTTATGGCCTACCTTGCTTTCTTC
tbm0390	7	(TA)16	ATAAATGTGCATGGAAACAAGG	GTTTGACATTACATGTTCGAGCC
tbm0391	7	(AT)15	ACATCTGCATAGGTGAAATTCATAA	GTTTGGGGAGCTGAACTTGGTAACTT
tbm0392	7	(AT)15	ATTTTTCAGTGTTGCTCGTCTC	GTTTAAACGCCGGTTCTAATCATCT
tbm0393	7	(TA)27	ATGTCACCTCTCCCACTCTTTG	GTTTAGGGAGTAGAGAGGCTAGCGAT
tbm0394	7	(TA)19	ATTCATCAACTCCTCATCAACG	GTTTGATCACCATGTTTCATCTGC
tbm0395	7	(AC)6(TA)16	ATAGTCACGGCTTAGGAAGAGG	GTTTCTGATCCCACGTAGGTAAA
tbm0396	7	(TA)14	ATAATCTTGCCTAGTGGCATTC	GTTTGTGGAATATCATCAAATGTGGA
tbm0397	8	(TA)36	AGACAATTCTGGGTTGGTAATG	GTTTGCATCAAATTGCGAACTAAA
tbm0398	8	(AT)10	AGCCGTTATTAGACTTTCCGAT	GTTTATGTTGCACCTTTATGGCCT
tbm0399	8	(GT)10(AT)23	ATCTATAATAAGTCGATACGTGAAAAA	GTTTCGCACTTTTATGTTGAATATGAGC
tbm0400	8	(AT)23	ATTTGACAGGCGATTTGACTAA	GTTTCCCCTCTAGTTACTTTCCCTT
tbm0401	8	(AT)23	ATCAAATCAGTTTCCTCGCAAT	GTTTAAATGAGACGCTTCTTTTGAGA
tbm0402	8	(TA)22	ATTGCCAAGTGTGTTAACTTGC	GTTTGCAATGTTCATTCTTTCACG
tbm0403	8	(AT)22	ACATCTCTCCTCCCTCTAACAA	GTTTGTTCCTTAGACTATGTGATTTGC
tbm0404	8	(AT)22	ATATAAAGCATGATTCGTCCAA	GTTTGCCACATAAGCTGATTGAAG
tbm0405	8	(AC)7(AT)22	ATCACCTAAATTTGGTAAGATTCG	GTTTAAGGGTCTAATTGGGCTACGA
tbm0406	8	(TA)21	ATTCGCCAGAAGAAGAAGAAAC	GTTTCGACTTTGATCAGCTACACC
tbm0407	8	(TA)21	ATTCATCCTACGCAGCATTCTT	GTTTAAACTTTGGGTAAGCACA
tbm0408	8	(CT)8GTG(TA)20	ATAAAGAAATATTGAGTGAAACATGC	GTTTGCCTCTTAAGTGATGGTTGTC
tbm0409	8	(TA)5AC(TA)20	ATCGTCAATTCTGTATGTACGCA	GTTTAAGGTATAGGACAACCTTGGCA
tbm0410	8	(TA)6C(AT)20	AGAGATTAGGAGAGAGAGGCAA	GTTTGCAAATATACGAACACAACCA
tbm0411	8	(AT)19	ATTTAGGAAAGGTAGACACAAAAGAAA	GTTTCGCCTCTCTCCTCCATATAA
tbm0412	8	(AG)19	ATAATGTCGCACTATCGGTCAC	GTTTCGAACAAAGTTTAAAAACCCCA
tbm0413	8	(AT)25	AGACTCACTCCTTGATTTTCGC	GTTTGCAAACTGCACGAATTTCAATA
tbm0414	8	(AT)24	ATAAATTTAGTGGCGGATCCAA	GTTTCAAGCCCACTTCATTGAAAAAT
tbm0415	8	(TA)22	ACATGTTACAAGATCGGAGGTG	GTTTCAAGAATAAGGGTCCACCACAC
tbm0416	8	(AAT)4AA(AT)8AA(AT)22	ACGTCGGCGTAAATGAATTATC	GTTTGAAAAATGACAAAAGCGTTCAA
tbm0417	8	(AT)21	AGAGTAATCGGGACAAGTTTGA	GTTTCTTTTGCCATGTCATCATTTTGT
tbm0418	8	(TA)20	AGGAGAAAGACAAGCGAGACTG	GTTTAAGTGGCCTGACTTCGAG
tbm0419	8	(AT)19	AGTCATCTGATTTATTTTTGAAAGAAG	GTTTCTTTTCCAGAATGCATAACCA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0420	8	(AT)18	ATTGCAAAGCGTTTACAATCAT	GTTTGAAAAGGAGGCCATAGAGAGGT
tbm0421	8	(TA)17	ATGCAATCTCATTGTATCTGCAT	GTTTCACACTCATTTCATTGTATAAGGT
tbm0422	8	(TA)17GAT(AC)4	ACACAAATCAAATTTATATGGAGGG	GTTTGATTTACTTTTATTATTGTTCCA
tbm0423	8	(ATA)17	AGGTAGTCCACCTAGGTATTTTCA	GTTTAAATTCAAAGGTCCCTTTTTCC
tbm0424	8	(ATA)17	AGCATAGTTAATTCTCTCTTTTGTTC	GTTTCGTCATCACTCAATCATCACA
tbm0425	8	(TA)16	AGCATCATTGCATGTGTAAGAA	GTTTAAAAATGCCAAGATTTGAGGTG
tbm0426	8	(AT)16	AGGAAATCAGGTCGCTATAGAT	GTTTCCAAACCTTTTCTTAAACGGTAA
tbm0427	8	(TAA)15	AGCGCATCTAGTTTTCCACAAT	GTTTGAGATGACATTTGTTGCCGTTA
tbm0428	8	(TA)15	ATCGAGCAGCTTCTTAAATGTG	GTTTCGCTTAAAAGGAAAGGAGAAA
tbm0429	8	(TA)20	ACAATTAAAATATTCTTTGTCACTTTC	GTTTCTTTTTGAAGACACTACAATGG
tbm0430	8	(TA)19	ATGTTTCACGGTAAGCATTCAA	GTTTACAGTGGCGTAGCCACATATAA
tbm0431	8	(TA)18	ATGTTTCACGGTAAGCATTCAA	GTTTAAAAATTGCTTTTCGATTTGCT
tbm0432	8	(AT)16	AGGTTCATGTGAATTTGAGCTT	GTTTCTTTTGCTTGCCAAAAATCAT
tbm0433	8	(TA)16	AGATGCAACACTTATTGAAATTGA	GTTTCTGCAATTAAGCAAATCCC
tbm0434	8	(TA)16	ATGAACCTACCCTCGAACCTAA	GTTTCGGAAAACTTCGACATTTTGAT
tbm0435	8	(TG)5(TA)15	ATACCCACATCCACCCTATATC	GTTTGATATTTCGGTAATTTGACCT
tbm0436	8	(AT)32	ATATTGGACACCGACTTTTCAA	GTTTCGACATTGAAATGGAAATCAAA
tbm0437	8	(TA)20	ATTACAACGTACGTGTTCGAGA	GTTTGAGACCCATTGATAATGCTTG
tbm0438	8	(ATAA)4ACAA(AT)14	AGTATCTATTTGGCTTGGCTTT	GTTTGGAATGTGCTATACGAGTGGTC
tbm0439	8	(AT)9(AC)7AT(AC)4(AT)4	ATAGAAGTGCAAAAGTCATTACCA	GTTTCTTTTTATTCTTGTTCATGTTATCCAA
tbm0440	8	(AT)25	ATCCTTTGGGTCGGTAACAAAT	GTTTGCGTTGCACGTTTATCCTAAAA
tbm0441	8	(TA)24	AGACACCACGGTTGAAAATAAG	GTTTCCAAATCACATGAGTAGTCGTT
tbm0442	8	(AT)22(TAT)5	ATAAAGGAACGGATAAGTAAGGTAT	GTTTCTTTTAAGTTTTGAGCTTCATGC
tbm0443	8	(AT)21AG(AC)14	AGTGAGGGATGGCTGATACTAC	GTTTGGTCCTTAGTCCCTAGGTCA
tbm0444	8	(TA)21	ATGTCTAATATCACTGCGCTGC	GTTTCCTATATACCTCCAATCAAATCAA
tbm0445	8	(TA)19	ACTTGCTAGCTAGTTGTGGAACC	GTTTCCATTAGTTTGCCCTCCATTAG
tbm0446	8	(TA)16	ATTTCTAATGCGAGAACCATCC	GTTTCTTTTTCGCTCGTATTTCTCACT
tbm0447	8	(TA)16	ACAAATGAATTCACAAAACCAA	GTTTCTTTTGCTGATGAGAAAAGCC
tbm0448	8	(AT)15AAA(TG)10	ATAAAGGGTAAAATCGTAATTCAA	GTTTCTTTTTGCCAAGGAAAACTCAA
tbm0449	8	(AT)15	ACACAGAAAACGAAGAACCCAT	GTTTCTATACACTCCCACCCCAC
tbm0450	8	(AT)22	ATGCATGGACCTTAAGTCAACTA	GTTTATGGGCTCAACCAATGAAA
tbm0451	8	(AT)21	ACAGGCCCAAATGTTCTTATCT	GTTTGTGTGTGTGTGTGTTTGTGTG
tbm0452	8	(TA)13	ACAGATTCCCAAAAACTGAAAAA	GTTTCCACTTCATGATGGAGCAATA
tbm0453	8	(AT)13	ATTCTGTCCCAGCACAATTAAA	GTTTGTCATGAATCTTCAATCCAAGT
tbm0454	8	(TA)22	ACTAAAGGGCCTGGTTAGCAAT	GTTTCCCTTCACTAAGGGTAGCTCG
tbm0455	8	(TA)20	AGTCTGCTCATCGGATTCATAA	GTTTACTTCGTGCTTGGAGATGAA
tbm0456	8	(AT)20	ATTGTATATCGAAAATGACTAGGTGT	GTTTAGCCCAAACATACTTCCCCTAT
tbm0457	8	(AT)18	ACTATTTGTTATTTTCCTTAGCGAGA	GTTTAACTTTTGCTTTTCGAAAGTTGA
tbm0458	8	(AT)17	AGGTTGATCCACACCAAAGATA	GTTTAGGTTAATTGGACATCAGGTGG
tbm0459	8	(AT)17	ATAGCGGGTTAGATTAAATGGG	GTTTCTTTTTGCACAGAAAGTCACTCAA
tbm0460	8	(TA)17	ATACAGTGGTGCAAGTCGATTC	GTTTAAGAACTTGAACCCCCTCAACT
tbm0461	8	(TA)17	ATCTTGAAAGATGTCAAGGGAA	GTTTGGGATCCCTTCTTAATCTGAGG
tbm0462	9	(AT)12G(TA)21	ATAAGGTTCACGAAGGGAAAAT	GTTTCAAAACACCTTCAACGACT
tbm0463	9	(TA)20	ACTCAGATATGGTAAAATTGGTGA	GTTTGCTTTTCTAGTCAAGTGCATTA
tbm0464	9	(AT)20	ATCGAATGACTATATGTGAAAGTTCC	GTTTCCCTGATCAAAGGGTACTTCTG
tbm0465	9	(TA)14	ACATAGAATACACGTGCGAAGC	GTTTAAATTGTGTTGCAAAAAGTGACA
tbm0466	9	(AT)17	ATTCCTTTTAAATTGGACCTCA	GTTTCCCCTTTAATTAGCACACACCT
tbm0467	9	(AT)12	ATTGGGATTTGTCCCATTTTT	GTTTCAAAACAGAAGCAGAAAAAGAAC
tbm0468	9	(AT)9(AC)6	ATACCTAAATAACCGCAGAGCC	GTTTACACACAAATAGCCGGTCG
tbm0469	9	(AC)7ATAA(AG)5GG(GA)4	AGTGCAGCGACAGACTGTTTTA	GTTTGATGAGTCTTCTTGGAGCAA
tbm0470	9	(AT)17	ATGGCTTTTGGGGTGTGAGTTA	GTTTCATTTGCAAACTTGAAATAATAACC
tbm0471	9	(TTA)15	AGGTTATAAGGTAGGAGGGCAA	GTTTAACTTTATTTCACGCATGTCA
tbm0472	9	(AT)15	ATATCATTTGCAGATGGTGTGC	GTTTACAAAATTTCCCAATTGTCGAT
tbm0473	9	(AT)13	ACGAGAGAATTAATGGTCTTAAAAA	GTTTGAAGGCAAAGACCAACATTCAG
tbm0474	9	(AT)22	ATAAGTTGTTCGCATGGTTGAG	GTTTCAATGCATACTTTCTATGATTTTTGA
tbm0475	9	(AT)19	ACCATCTCCACTATTCAAGGAA	GTTTCCATATTTGGAAAGCACAATTT
tbm0476	9	(TA)18	ACGTTGAATCGAGAATCTATCAAA	GTTTCGACTCAAAGAAAACGTGAAA
tbm0477	9	(TA)17	ATTAGGTAGACAATGGGTGGGG	GTTTATTGTCCTCTCTCGCTTGC
tbm0478	9	(TAT)17TGTTA(TTG)4	ATACTGTGAAATTTTACTCTCCTCAAA	GTTTATGACAAAGCACAATAATCCT
tbm0479	9	(TA)16	ACACAATGGAAGAAAAAGATCC	GTTTATGCCTCACTCCCAAACAAG
tbm0480	9	(AT)16	ACTCCATCCTAGCTACCCTTTT	GTTTCACGCAAGCTGTAGTCATATCC
tbm0481	9	(TA)22C(AT)22	ATCAGCCACACCCATATTGATT	GTTTAACAGGTTTGTCCGTTTGTTTT
tbm0482	9	(GA)22	AGTCCTCTTTGCCTTTCTCTCT	GTTTCGATGACAACCTTTCCATTC
tbm0483	9	(TA)20(TGTA)9	ATTTGAAATGGCGGTCATAGAG	GTTTCCCTCTCTACTCTCTTCCTCTC
tbm0484	9	(AT)19	AGCAATTTGCATACCTTTTCTT	GTTTAAACTCGAAATACGCCCAACT
tbm0485	9	(TA)19	ACAAGGAAAAACAAAAACAAGC	GTTTAACCCTCTATAGCACTGATCCAA
tbm0486	9	(AT)16	ATTAATCATGTTTGTAGAGGATGTTTT	GTTTCACTCACATTTCTCCCCTTTT
tbm0487	9	(AT)15	AGTCTCAATTATATCATGCTAACACA	GTTTATTGTTAGGTTGTGGAGCC
tbm0488	9	(AT)24	ATGCCCGTAATTTTGTTCTGGT	GTTTGAAGGCTATTATAAATATGCGAAAGC
tbm0489	9	(TA)21(CA)8	AGCAATATTTATTTTACGCAATTTT	GTTTCAACCTTGGGTATTTTTGAA
tbm0490	9	(TA)19	AGGTGACTTTTGGAGTGATTTC	GTTTAGACCTCATGCTTGGTTCAAAT
tbm0491	9	(TA)18CAC(GT)5GCGCC(CG)4	ATGAATGCATTGAGAGAATGGT	GTTTCACTTTCTCCCTACATGGG
tbm0492	9	(CT)8(AT)17	ACTTCAAGTGTTGAGGCTGATA	GTTTAAGCACAAAACTGCCACCT
tbm0493	9	(GA)17	ATCCCTAAATGAAATGTTTCGG	GTTTAAGACGAACGGTTGTTGAAAAT
tbm0494	9	(ATAC)5(AT)7GTATG(TA)15	ACACGCACACACACAAAATA	GTTTGAACTATATCTTTTTGGAATGTCAGA
tbm0495	9	(AT)8AC(AT)15	ACAAAGGTTAATATAAGGAAAGATGAA	GTTTCTTTTTGGAATGTCAGATAAACA
tbm0496	9	(AT)6T(TA)15	ACGGTCAGGTACATCTTCAACA	GTTTCTTATCCAAAACGGTTCA
tbm0497	9	(AT)16	ATACGTTTATTTCACTTTGAACCA	GTTTCGGTATACTGTACCCCACGTTT
tbm0498	9	(TA)15	AGGATCTAAATTCTAAAAGCACCA	GTTTGGACATCCAAGACACAAAG
tbm0499	9	(GA)9	ACAAGCACATTCCCAATGTAAG	GTTTCAAGCAAGCTTATGGCGATATT
tbm0500	9	(TA)10	ATTGGTTTGTGCTCTTTTCTCA	GTTTAGCGAATACCTCAAAACGGT
tbm0501	9	(TA)9	ATCGATGAAAGTCAAACACTCG	GTTTCCAATTTGATTCTTCCCACATT
tbm0502	9	(AT)21	ATGGGACAAAGTGTTTAACTCCA	GTTTGATTTATTTTGTTTGACTTTTTGG
tbm0503	9	(AT)21	ATTTGCATTTTCTCTATCGATTTG	GTTTGTCCAACAGGAAAATAACATCA
tbm0504	9	(GAT)19	ATTGGCTTACAATGTGGGACAA	GTTTGCCTTTAGTTCACCGAGAAAAA
tbm0505	9	(AAT)19	ACCGAGTTTTGTCATTTTAGTG	GTTTAGGAGTCATTTGGTAGGGG
tbm0506	9	(TA)19TTT(TG)4	ATTTTGGAGAAGAATGGTGGTC	GTTTGACACCTTAAATGGACAGAGGAA
tbm0507	9	(AT)16	ATTGACGACCATGATTACCAGC	GTTTAAGAGCTCGTGCAAGAAGA
tbm0508	9	(AT)23	ACAAACATAAATATGTACAATTCGC	GTTTCCGTTTGTGTTTGTATAAGCG
tbm0509	9	(AT)16	ATGGACTGTGCTTGTCATGAAG	GTTTGCTCCTGACCAGATTTT
tbm0510	9	(AG)14	ATCAGCTGGGCAACTACTCTTC	GTTTGAAGCCAACCTAGAGAGCTT
tbm0511	9	(AT)8(AC)9	ATCCTTGTGAAGCTGTAGTCCA	GTTTGCTTTTATGGGGGATGATA
tbm0512	11	(ATGT)4(AT)21	ATGTTGATTCGGACACTACCGT	GTTTAGGCATCAATTTAACCCATGAA
tbm0513	11	(TA)21	ACCTACCCACATTACTAGCTGC	GTTTGCCTTTTAATAGCGATACATCACA
tbm0514	11	(TA)15	ATGTTGGTTAATTTAGCCCCCA	GTTTGAACACCTCATGGTTCAAAAA
tbm0515	11	(AT)9AC(AT)4	ACAAGTTGGATCGGACATTACA	GTTTCTTTTAACCCCGTTATAGCCGTG
tbm0516	11	(AT)28	AGCACCTATCGCTACGTATCAC	GTTTCAATGTAGATACTGAGTAGGCGTG
tbm0517	11	(TA)19	ATCCAAGCATTAATTAAAAGGC	GTTTGAGTTCGTCTATCAAGGACTTCG
tbm0518	11	(AT)16	ATATTGCAATACCAAATGGACA	GTTTGCTTCTTGCGTCTCAAAATAA
tbm0519	11	(AT)13	ACCATCTCACTTGTCTCTTTCC	GTTTGATTTCAAGCTAGGGAGTGTT
tbm0520	11	(AT)27(GT)5	ATTTAAAAGTAATATGCATGCCG	GTTTGAATTGGTCAAAATAGGGAGCA
tbm0521	11	(TA)27	ATTTAAGCTAATGGAAGATACAATGA	GTTTGGAAGGAGCTAAAACCTCAAAT
tbm0522	11	(AAT)10G(ATA)4	AGTCAGCCATGACAATCTTCTA	GTTTGTGTCTCCAAAGGGTTAAAGG
tbm0523	11	(AT)25C(TG)10	ATTTTGATGATGAAGAATGGGA	GTTTACGCACACACACACACATAAAA
tbm0524	11	(TA)23	ATAAGTGCTTTTGTTTGTTTCC	GTTTCGACGATATATTTTAGCATTTTTG

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0525	11	(TA)21	ATAGGGTTCGGATAAAATTACG	GTTTCATTTCCGCTTAAGCTTCC
tbm0526	11	(TA)17	ATATGTGTCAAATTCTTACCAAAAA	GTTTACAACCCAATCCATCCATAAAG
tbm0527	11	(TA)17TC(TG)7	ACCTTCGTTACGAGCTAGGGTA	GTTTGGATCTCCTCTCCTTTTGTTGA
tbm0528	11	(AT)24	ACTGCCTTCATGTTATTATTTCG	GTTTCTAGGGTTCTCATTTTGTGGA
tbm0529	11	(AT)22	ATTTTGTCCAAGAAATAGGTGAGTC	GTTTAGGTGAAGGCCGTTTGTAA
tbm0530	11	(AT)22	ATGTTCAAGATGATTTGCGATG	GTTTGAAAATGACCCATTTATTGTGTT
tbm0531	11	(TA)22	ATGAGGTACAAAAATAAGTGCAAAA	GTTTAAGACAAACAGAAAAGAAGACATGA
tbm0532	11	(TA)18	ATTAGATCAGAATACCACCGGC	GTTTGGAAAGGATTCACAATAATGG
tbm0533	11	(TTC)18TA(CCT)5(CTT)4	ATCTGCTGCTTCTTCTCTTCCT	GTTTGAATGTTGGTTCGATTGATTG
tbm0534	11	(AT)16	ACACAAGACGATTATCGAATGA	GTTTAAGTGTGTCTCTGGGATTTCG
tbm0535	11	(AT)21	ATAAACGCAAAAGCAGAAGC	GTTTGGCTAAGGGAAAGAGATGAACA
tbm0536	11	(TA)17	ATTAATCAAATCGAACCGACAAA	GTTTCGGGTCCTAGTGTCATAAACAA
tbm0537	11	(TA)12(TTA)5	AGTGGGACTCACATTTTTGACA	GTTTCCAAATGAGGATGATTCAGG
tbm0538	11	(CT)11	ATCTCTTCTCCCTCCCTTTTTC	GTTTGGCTGTTGTTGCTTGTCTC
tbm0539	11	(TA)22	ATGATATTTTGGCTAGACTCTCCC	GTTTCGCTTTTCACGTAGTGATTTC
tbm0540	11	(AT)19	ATTTTTACTTTTTCCGGTGGAG	GTTTAATTATCATACGTTGGGTCGC
tbm0541	11	(AT)18(TA)10(CA)4	ATTCGCGATATTATTCCGTCTT	GTTTAAAAATTGGGTTTTTCTTCATCA
tbm0542	11	(TA)16	ACCAAAAACAAAAATTAAGGCA	GTTTCCATAGTCACCTTTGGAGACA
tbm0543	11	(AT)16	AGCGTGATAGCAACAACAATAA	GTTTGCCAATATGATTTAAGTCCAAAA
tbm0544	11	(AT)22AC(AT)6C(TG)16	AGTCTTTTCTGCAGTGACCAAG	GTTTCTTGGCTGGAATGTAGGATT
tbm0545	11	(TA)24	ATCGTAGGCTAAAAAGGGGTAG	GTTTGGAGAAAAATTATTGAAAACAAAATGA
tbm0546	11	(AT)23	ATTCGTTGCAATAAGCAATTTTT	GTTTGGGTCTACTATTGTCATGTGATCC
tbm0547	11	(AT)21	ATAGCTCCGGTAAGAAAAATCG	GTTTCCTCATGATTTCTCATCAA
tbm0548	11	(TA)19	ATTTTTTCACGTCAAGCGAGTT	GTTTAAATGGTTGTTTAATACGTCGAA
tbm0549	11	(AT)21	ACTTTTTAAATCCCAACTCCAAA	GTTTCCAAACACCTTAAATGAAAAGAA
tbm0550	11	(AT)16	AGTGTGTGTGTGAGTGCTCTTT	GTTTCTTTTTGATACATGGTATTTTCACGA
tbm0551	11	(AT)16	ATTGGTCAAAGAATATGCACCT	GTTTAAAAGACAATTTCCAGAAGGGA
tbm0552	11	(TG)4GTCTA(TG)8(TA)9	ATTCCTTGTGATAGGTGTGCTG	GTTTGGACTTGACTTGCACAGA
tbm0553	12	(AT)23	ATCCAGCTATATGTCATTAGTTTTCG	GTTTAACCCTTTAATTATGACTGTGACTC
tbm0554	12	(TA)23	ACATACTAGTTTCTGTGCACGC	GTTTCCACAACATATAGGAATCTTTCACTT
tbm0555	12	(TA)21	ATCTGGCATAAACTACCAAATCAA	GTTTGAAATTTTGTGTTCGAGCTTCA
tbm0556	12	(TA)20	ATGTTTTAGTTTAATTAAGTTCGATGA	GTTTGTGAATCCGAATGTCTCTA
tbm0557	12	(AT)19	ATTTGATTCTTAAAATTTCATCAGTG	GTTTGAATAATTAGCAGCGAAAATC
tbm0558	12	(AT)18	ATAGATAAGGCCCACACCATTT	GTTTAAGATGAGTCTCCTTCGC
tbm0559	12	(AT)18	AGAGATTTTCATTTTCAATCTCCT	GTTTAAAGTTAAAATGATGTCTTTCCTTCA
tbm0560	12	(TA)23	ATAACTAAGAGGGTAGCGAGGA	GTTTGACAACAAATGCAAAAA
tbm0561	12	(TA)22	ACAAAAGCTACCGTTTTGCTTA	GTTTCTTTTTGAGTAGCAGGAGTTTAGTTT
tbm0562	12	(AT)20	AGTTGATTTTGAACTTCAGGCA	GTTTGGCATACCACCTAGACAGTG
tbm0563	12	(AT)19	ATATCGTGTGAAAATATGAGGTGA	GTTTGCTAAGGATAATCATTCGAAGTC
tbm0564	12	(AT)18	ATGTTGCACAAGGGTAGACGTG	GTTTGCCAACATTCAAGTGATTC
tbm0565	12	(AT)16	ATTCGCTTATTACCTTTTATTTTTG	GTTTCTTTCATTCTCCTAAATTTCTTTCA
tbm0566	12	(TA)24	AGGTTTGGATATATATGTGATTTGG	GTTTACAATTTCATCACGCGAATATG
tbm0567	12	(AT)21	AGCCCTAGCCATAAAGACATT	GTTTGCGTCGAAAATAGTTGCAT
tbm0568	12	(AT)16	AGGGGTAGGGTTCATTAGAGTC	GTTTCATTGAGACAAATCTCACTTTCC
tbm0569	12	(AT)16	ATTATGATTTCAATGGGGGTGG	GTTTATTTTTGTTTCGAAGATTCA
tbm0570	12	(TA)20C(AT)7	ACTTCTTTGCGGTCTATCTCTC	GTTTCCCTTCTTTTTGTGGAATCTC
tbm0571	12	(AT)18	ACCAGAATTTTCACAACGAAGTT	GTTTCGGAGTAAAGTAGGGAAAAAGG
tbm0572	12	(TA)13	ACCCTACAACACAAACCAAACG	GTTTGACATTTTATTAACTTGATCTCTTGGC
tbm0573	12	(TA)11	ACGATAATCTCATTCAACGCAC	GTTTCAACGGTGGAAACTATTGAAA
tbm0574	12	(TA)24(TG)8	AGAGTGTGTGTGTGTGTGTGTG	GTTTCCACCTATATCCATCTTTATTTCTTC
tbm0575	12	(AT)64(GT)5(GA)23	ACAATCTCTCTTGCCATATCTACA	GTTTACACACACACTCTCACACTCA
tbm0576	12	(AT)23	ACGCAAAGGGTAAAAAGAATAC	GTTTCAGTGTCGTCTTGAAGGT
tbm0577	12	(AT)23	ACGCAAAGGGTAAAAAGAATAC	GTTTGTGTGCTTCAGTGTCGTCT
tbm0578	12	(TA)22	ATATTGCAGTGGGCTTGAATCT	GTTTGGCAGATCCAGGAATTTAAC
tbm0579	12	(TA)22	ACAACGCACGTATTCAAGAACT	GTTTAGGTCGTGTAGCTCCGATACAT
tbm0580	12	(AT)21	ATTTGGGGCCTATTTTTAGTCA	GTTTCAAGAGATTTTTGGGATGCT
tbm0581	12	(CA)10TAC(AT)20	ACTTGTCATATATTTTTCATCCATGTC	GTTTCGCAAAATAGTTTTAAGGTCCG
tbm0582	12	(AAT)19	AGCAAATAAATTGGCAAAAATAGA	GTTTAGAGTCCTCCCGTTCATC
tbm0583	12	(TA)19	ATTTTCTATCAACATGTGTTGTTTTT	GTTTGTATTTGCATAAATCAAAACGG
tbm0584	12	(AATA)4(TA)18	ATATGTGTCAATTTCTTACCAAACA	GTTTGGTTAATTTAAGATAGACGATCAAA
tbm0585	12	(AT)18	ATAAAAGCCATCGTTTCTAGGG	GTTTCTAAAGAAGTGGAAAAGTCATTAACA
tbm0586	12	(AT)13(GT)17(GC)6	AGTTCAATGAATATCAAATATCGAA	GTTTGGACTAAAAACAAGTGATTTTGAACA
tbm0587	12	(TAA)17TC(TA)4	AGTTTCCACGAAAACGATCAAC	GTTTGTGTTGATGACATGTGACCTT
tbm0588	12	(AT)17	ATATGCTAACGTAGGAGCTTGC	GTTTATTACCTGTGAAGGGCCAA
tbm0589	12	(TA)17	ATGGGGTACAACCGTAATTCAA	GTTTAGGCTGACTTGTCTTGGTGA
tbm0590	12	(TA)17	AGTGTTTTGTGGGTAGAAATCATC	GTTTCGCTGGATTTGCCTAATTAAA
tbm0591	12	(AT)8(GT)17(GC)5	AGGAATACAAAAGAGGTGGACA	GTTTACACACAGACACACACACACG
tbm0592	12	(TA)4ATT(TA)16	AGTGAATAGTGTTTTGGAATGGA	GTTTGATATGACTTTTAGTTTGGTGACAA
tbm0593	12	(AG)16	ACCTTACGTAAACGCGAGATAC	GTTTGGCTTTAGGTTTTGCTTCTTC
tbm0594	12	(AT)15	AGCGAATTCAGAGGAATTAGAG	GTTTGACATCAAAATATCATTCAAAATTAGG
tbm0595	12	(TA)7TG(TA)15	ACACATACACACACACACACAC	GTTTAAATAACTCACACACACACACACA
tbm0596	12	(GT)15ATA(TG)9(TA)6	ATAAAGAGTGGGAGAAAGGTGA	GTTTACACACACACACACACCACA
tbm0597	12	(AT)15	ATAGTCACACACGATGAATGAAA	GTTTCGCAAAAAGATAAACCAAAAGG
tbm0598	12	(AT)14(AG)15	ATAATACATTTGCATGATACCTCA	GTTTGTATTTTCTCGAATCTTCCTC
tbm0599	12	(AT)27	ATTGAGTTGGGTCAAAGTTTTT	GTTTCTGAAATTTGATTTGTTTTCAA
tbm0600	12	(TA)15C(AT)4	ATGGTGCACGCATATTTTATCT	GTTTCCAAATTTCAATTCTAAGGTTAAAGC
tbm0601	12	(AT)13	ATCTTGGCTCTGCTCAACTCAT	GTTTGATGGTTGTCGGTTAAAG
tbm0602	12	(AT)26	AGAGAATCCTTAAAGAACCGAAA	GTTTATAAATGCGGTGGGTTGTATG
tbm0603	12	(TA)22	ATTTTGAGTTTTTGGTTATGCC	GTTTCGTTTGGTATGTGGAATTAAA
tbm0604	12	(TG)10TTT(GA)14	ATGGATTTCTGTCATCCTTGTG	GTTTCTTTTCTGGGTTGCTATTCTG
tbm0605	12	(TA)13	ATGTCGCCTTAGGTCTAGGGTT	GTTTCCGTCAACATGCCTTATCTT
tbm0606	12	(AT)29	ATTGCATCATGGCTAATTTTCA	GTTTGTATCTTGAAACTTGACTTGTTTACC
tbm0607	12	(AT)15	ACGAAGAAATCAAAAAGACCGA	GTTTCTCATCAACCAAAGTTGCATT
tbm0608	12	(AT)13	ATGGTGGACAAGGTTTTGGTAT	GTTTGAACCAACAAAAAGTGGCAAAT
tbm0609	12	(TA)13	ACTGATAAGACCCGTGGAGTTT	GTTTACTTCTTCTGTTGCAGTCCCA
tbm0610	12	(AT)14	ACGCTTTGACATAATTTTCGAT	GTTTATCAATTAATTAACGAGCTTCT
tbm0611	12	(AT)14	ACGTAGGCTGAAAAGGGGTAA	GTTTAGGGCATAGCCTATTAAGATCG
tbm0612	12	(TA)13	ACTAAACAAAAGTACCGGGGGT	GTTTGCGAAAGAATTAGGATTTTCGT
tbm0613	12	(AT)11	ACGCTTTGACATAATTTTCGAT	GTTTGCCCAACCCCAAAATAAAAA
tbm0614	12	(TA)12	ACTTTGAAGGAGCTTGTAATGG	GTTTGGACAACATGGAAGGATTGT
tbm0615	12	(AC)10	ATAGTTCAATTCAGCAACCCAT	GTTTGCTGGGGTTTCTTTTATTGTT
tbm0616	1	(GA)5(TA)6TG(TA)4	ATGTGTGTGTGTGTGTGTGTGT	GTTTCCTCCACACCCACTTACTTCT
tbm0617	1	(AT)10	ACCAAAAGTCAAAACCAACCTT	GTTTCGCTTCTCTACTTTCTCTTTGA
tbm0618	1	(TA)10	ACATCATTTTGACTCCACCTCT	GTTTAGGACAAATAAAACAATGGATAATAGA
tbm0619	1	(AT)11	ATTGCAAGGGTTTTAGCAAGTT	GTTTAAATCTGAATTGCCTATCCGTC
tbm0620	1	(AT)35	ATAAATCTGCTGCTCAAAACGA	GTTTCAGTCGAACGTCTATCGAA
tbm0621	2	(TTA)9	AGCATGGTTTATACATGACAAGA	GTTTCAATTTGCTTGATGCTTTTG
tbm0622	2	(TTA)9	AGCATGGTTTCTACATGACAAG	GTTTCTTTTCAATTTGCTTGACGCT
tbm0623	2	(AG)9	ATAGGGAGAAGGGCGAATAAAG	GTTTCTTCAACACAAAAGACCC
tbm0624	2	(TC)10(TA)10	AGCTTAGGTTAAGGGAGGATTC	GTTTCCCTGGTTCTTACAAGGTCAT
tbm0625	2	(TC)11CT(TC)5	ATAGGCGAATCCCATTCTGTTA	GTTTGCAAAGCGAGAGTTCCTATC
tbm0626	2	(TA)12	AGATGCGAAAGAGAGACTGTCC	GTTTAATTTGTCCTTTGCCCAATTC
tbm0627	2	(AT)5TGTAC(AT)13	ATGAATGGAGCAATCTTCCTTG	GTTTCCAAACTTTAAGGGGGAGTT
tbm0628	2	(GT)14(AT)6(GT)15(AT)5	ATAGAAGTTTCAACGGGAGTTT	GTTTGCATTGAATTTCATCACATCAT
tbm0629	2	(TA)16	AGAGTTTGCAAGAATCGTGAGT	GTTTGCATTGAATTTCATCACATCAT

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0630	2	(AT)17	ATAAATCCCCCTCTCCTAGACG	GTTTCAAGTTGAAGATTAATTGAAGAAAGA
tbm0631	2	(AT)19	AGTAGCATGTAAATCCCCCTCC	GTTTGATTGCTTTGACAGGTTTC
tbm0632	2	(GT)19(AT)10	ATCTGAAGAAGTAGTGACGGGG	GTTTGCATTGAATTTCAGCACATCAT
tbm0633	2	(AT)19	AGCTTCACTATTGCCTTTGAAC	GTTTGCAACAAGGATAAGATGTCAAGG
tbm0634	2	(AT)23	AGTAGTACTCACTCAACCGTGG	GTTTGGCTGTCTCTTCAACTTCTGCT
tbm0635	2	(AT)9	AGCTGGTCATAACCTAAACCGA	GTTTAAAGCTCGAATTGAACTATCAGAAA
tbm0636	2	(AT)9	ATTTAAGAGAAAATCACACATGCAC	GTTTAAATTTCCATCCCAAATCTGC
tbm0637	2	(TTA)9	ATTTTGTTTTCTCTTTTCCCCTC	GTTTAAAAATCGAATAAAAGTGGAGGA
tbm0638	2	(AT)9	ATTGATCGACCCAAAAATTGAC	GTTTGAAAACCATTTCCACAATCC
tbm0639	2	(TA)10	ATCAACTTGCTTGGAATTGAAC	GTTTGTCTGATTGGGAATTGAAGG
tbm0640	2	(AT)11(AG)11	ATGGCTTGCATATTCCATTAGA	GTTTCACGGTCATATTTTCTCAATC
tbm0641	2	(AT)11	ATAAATCTTCGGCAGTAACCAA	GTTTATTTTGACTCCGCTTGA
tbm0642	2	(TA)13	ATAGGCCTTCAAGTATGTGGCT	GTTTAGGGTCAAAACATGCCTAATGT
tbm0643	2	(TA)13	AGTTAATGGTGTGTCAAACTTGT	GTTTAACGCATATGACTGGTCCAA
tbm0644	2	(AT)31	ACAAATTAAGATTGGAAAATGAAAA	GTTTGAAGAAAAGATAGTTCCAAATCTCA
tbm0645	2	(AT)33	ATACAGGGTAAAAACAATGTTGC	GTTTAAAAAGACTTCAAACAAAGTCATAAGC
tbm0646	2	(TTA)10	ACGTAACTATCAACGCAGATTTT	GTTTGGAACCGCTTCATTCTT
tbm0647	2	(AT)9	ATACAGTGTCTGATGCTGCCAA	GTTTGGCACATATAGCCAAAGAGGAC
tbm0648	2	(TA)9	ACTGCAAGACCATTTCAAGAGA	GTTTCCTCGCCCTCTATTGTTTTA
tbm0649	2	(TCT)9	ATCCTCCTCTGAAGAAACTTCG	GTTTGAATCTGAAAGCGATGATGACA
tbm0650	2	(AT)9	ACTATACAAAGGTGCCACATCA	GTTTGAAATTGAGTTGGATCACGTCC
tbm0651	2	(AT)9	AGTGTGCATCCAAAAAGGATAG	GTTTCAATTAAATGCCAGCCACT
tbm0652	2	(AT)9	ATTGAGATCGCATGTTAATTTTT	GTTTCAGGTCACATTTGGTTTTGAAC
tbm0653	2	(AT)10	AGTTCAAACTCTGATCTCGTCAA	GTTTGTATTTTCACCCCTTATTTTT
tbm0654	2	(TC)10	ATGCATCTTTTGGAAAGTGGAG	GTTTACACCTCTGGAATATCAATGGG
tbm0655	2	(TA)10	ATAGGTTCATACCATAATGGGGA	GTTTCGGCATAACTATTGTTCGTTCA
tbm0656	2	(TA)11	ACTCTCAGACCGTCCTCTAAGC	GTTTCATTGATGTGATCCTCACG
tbm0657	2	(CCA)12	ATTTGTGTTGCTGATGGAAAAA	GTTTCCAATATTTGCAATCTCC
tbm0658	2	(AT)12	ATCTCAAATTTCTCAAAGGATAAACA	GTTTGCAAAAACTCACATCATTTAGAGA
tbm0659	2	(AT)13	ATCTTGGCTTTAGAAGTGTTATGC	GTTTATCGTACTTTCTATCAATTTCTCAAA
tbm0660	2	(TA)13	ACAAATTGCTGACATAATCCAA	GTTTAAGGCCCATGAGATCACTTT
tbm0661	2	(TA)14	AGTTAATAGGTTGGGCTGGAAT	GTTTACAGTGATGGCACAAGAGAAAA
tbm0662	2	(TA)14	ATTTCCTCGTCTGCGATATCAT	GTTTGACGAGATCAGAGTTTGAACA
tbm0663	2	(TA)7(TG)4TT(TG)5	AGATTAATAAACCCTGATGGGG	GTTTGAGATAAAATTAATGGGTAGAACA
tbm0664	2	(AT)9	ACTCGTGCCTATCGGACTATTT	GTTTCATGAAAATGAAATAACTCTTCG
tbm0665	2	(TC)10(AC)7	ATCGATAGAAGATGTGGTGCAT	GTTTCTTTTCTTCGCATTTTCTTCCA
tbm0666	2	(TTA)10	ATCACCTCACAAACACCAAACT	GTTTAGGGAAGGACCAGAGTACAAGG
tbm0667	2	(AT)11	AGGAAGATCTTTTATTCATGGACC	GTTTATGATTTATTTGGGGAAAAA
tbm0668	2	(AT)27	ATATGCACTCATTCAGCCAAAA	GTTTAATTTATCCATTAGATCGCC
tbm0669	2	(TA)5GA(AT)6(AG)7	ATAGAAACGAAAAGGACCAAGTT	GTTTATGAGTCTGGAGAAAGGCG
tbm0670	2	(ATA)9	ATATTCTAACGTGCAAGATGGC	GTTTGTCACGTAGGCTAAAAAGGGT
tbm0671	2	(AT)9	ACCATTTTCCCTACTCTACCCT	GTTTGTGATAGCAGTCGAATGAGGT
tbm0672	2	(TA)9	ATAGATTATGACTAGGGGCGGA	GTTTAATCAGTGGCAAAACCATGA
tbm0673	2	(TA)9	ACTCACTCTTCCATGAAATTAAAAA	GTTTGAAAACTCCGACATATTCATCTATCA
tbm0674	2	(TA)9	AGAAATTCTGACCAAACGCTAA	GTTTAGGCGTATAAATTTCTAACACATAAAG
tbm0675	2	(GA)9	ATACTTCTCCCAATTCACCTGG	GTTTAGCTTTGAAAGTGGCAAGTAGC
tbm0676	2	(TA)10	AGAACTGTTGAAATGTCTCACG	GTTTACGCACCTACACAACAATC
tbm0677	2	(TA)10	ATAGAGGGAGACAAAGTCATCG	GTTTCGCTCTTTACGAAAATCAACA
tbm0678	2	(AT)10	ATGAACGTACGTGTTGTTGTGA	GTTTCTTTTGAGATTGGAAATGGAA
tbm0679	2	(AT)11	AGTGCATGAGGACATCAATGAG	GTTTCGAAATCTATGACTAAACGCTGC
tbm0680	2	(TA)11	ATAAACACAAGGACCCGTTAGG	GTTTGATTAGGGTTTCCGTTTGAAT
tbm0681	2	(AT)11	AGCCCTCACACCTAAAAAGATT	GTTTAGCATGTGAATAACAGCAGCTC
tbm0682	2	(TA)12	ATAGGAAATACGCGCAAAAAGT	GTTTCGCCACATAGACGAACCTAAAG
tbm0683	2	(TA)12	ATTAAAATCGCAAGATGGATCA	GTTTCTTTTGGTGGTTTTCCTGACT
tbm0684	2	(AT)13	ATACGGTGAATTCCTTCGGATA	GTTTATGTTTTTCACCTTGTTCCCC
tbm0685	2	(TA)10	AGCGGACTCTAGGAAAAAGTCT	GTTTGGCGAACGAGAAAATAGGTGTA
tbm0686	2	(AT)9	ATTGTATCCAACGCTTCATCTG	GTTTAGCAAACAATTCCCCTCATTT
tbm0687	2	(AT)9	ATGAATCAAGTTTGCTCGTCTTT	GTTTCGGCGGGAAATAGTCAAAATTA
tbm0688	2	(AT)9	ACTTCAGCTGCTCTGCTTCTCT	GTTTCCGGATGAGTATGAATGTGAAA
tbm0689	2	(AT)10	AGAATATGAAGCGCATGGATAC	GTTTGGAGTGAGGAAGAAACGAG
tbm0690	2	(TTA)10	AGGAAAGGGGTATTACATGTGC	GTTTCAATTGCCATTGACCTATGCTA
tbm0691	2	(TA)9	AGTTTGACTGCAAAACCATTCC	GTTTGCGACAAAACGCATACAAATTA
tbm0692	2	(TA)9	AGATTCACCCGAACATCATT	GTTTCACATGTATGTTTATTTTGTGGGA
tbm0693	2	(TA)9	AGCTTTGACAGAAAACTTTTACCA	GTTTCGCATATTGAGGAGACTGA
tbm0694	2	(AT)9	AGTTTCTCCTTTCTGAACGACA	GTTTGTGAAGCTGGAACATTCAAC
tbm0695	2	(TAT)5G(ATT)9	ATATCATATGCGTCTCAAACGG	GTTTGTTCATCCTTTAACTCGGT
tbm0696	2	(TA)9	ATAAAAGCATTCCAAACTCGAC	GTTTAGCTAAGGCCGGAATTAAACAT
tbm0697	2	(TA)9	ATGTGCTTGCACAAGCTAATTC	GTTTCCAAAATAGTTCATAGAACCTTGA
tbm0698	2	(AT)9(GT)5	ACCAGGATTAGTCCAAACAAAC	GTTTCAATTCTTGGGAGATCAACA
tbm0699	2	(TA)10	AGAGTTAAATTTTCGTGGCAGA	GTTTCAAAAGTTTGTTGCGTGAAATC
tbm0700	2	(TA)10	ATACCCACGTCATTTAAGACCA	GTTTACCGATTTCAAAAGGTTGTACC
tbm0701	2	(TA)11	ATGAGGGGACGTATTGAAGAGA	GTTTACATGGAGTATGAAAGGTTGGG
tbm0702	2	(AT)12	ATTTAAGTTCCTCCTTCCTCCC	GTTTCAATCATTCTTCCGAAAGTTCC
tbm0703	2	(AT)33	ACCCAATAAAATGGAGGTTTTG	GTTTGAAACTAAACGGAATCAGAATTT
tbm0704	3	(AT)9	ACAACTAGACAATGCCCTTGAG	GTTTGCCAATTGTCCATTTTCT
tbm0705	3	(AT)9	ACAGCTGCTGAAGCCTAACTAT	GTTTCCGGCAACACTTGATTATTTTT
tbm0706	4	(TA)9	AGAGGGTAAATATGTTAAATCCCAA	GTTTGAAAGATAAACAGACCAGAAAGCA
tbm0707	4	(AT)9	ACCATCACTGAACTGTTCCTTC	GTTTGAAGCAAGCAAAACCCAAATAC
tbm0708	4	(TG)9(TA)8	ATGGCTACTGCAAACCTCACAA	GTTTCACGGTGCAGATCTAATTCA
tbm0709	4	(ATT)10	AGGGGCTAGGAAAGCTAAAATC	GTTTGAAATAATTGAAAGGGGTTCG
tbm0710	4	(TA)32	AGATGTTGAGTCTAGGATGTCAAA	GTTTCTCAGAGGTCTTATACAAACCCA
tbm0711	4	(TA)34	ATATTCTCCAACATGGCACAAA	GTTTCAAATCTCATATTCCACTAAAAGG
tbm0712	4	(TA)9	ACTTTGTTAGGATCGAATCCAC	GTTTAGGCTGCAATTTTTATTCTCCA
tbm0713	4	(AT)36	ATGGATTTGGTAGGATGTTAGGG	GTTTGTTGTGCTTGTGCTGTGTAA
tbm0714	4	(GT)4(AT)8AA(AT)4	ATATTGGAAATTGTTCCGTTTT	GTTTCCGTATATTTTTATGAATTTCCACA
tbm0715	4	(AT)9	ATAAAGCTAAAGGGCACACAAA	GTTTGCGAATCAAATTGGATAATCAAG
tbm0716	4	(AT)9	ATTGGGTCCCTCTTAATACCCT	GTTTCAAGATACATGATGGAAATTAAAAGAA
tbm0717	4	(AT)9(AC)4	AGAATAGCCGAGCAGATTTAC	GTTTCTTTTGGCAAGGATAGATGGAG
tbm0718	4	(TA)9	ATCCACATGTTTTCTTCATTGC	GTTTCAAAAATACGACGGATG
tbm0719	4	(ATA)10(GTA)10(ATA)4	ATCACCGAGTCAAGCATAAGAA	GTTTAAGGAAGATGTGTGTTCTTTTCA
tbm0720	4	(TA)11T(GA)4	ACCGAAAAGGTTCTCAAAATAA	GTTTGAGCTTGAGGTCCTCTTTTCAA
tbm0721	4	(AT)27	ATTTCCACAGCTTCTCATCTCC	GTTTGATTCATATGCCCGATCTC
tbm0722	4	(TA)9	ATTTCAGCGACACATGTCATTC	GTTTGGAAAGAAACAAAAGAAACCAAA
tbm0723	4	(TAT)10	ATGCAAAAGAATTGGTATTGAATC	GTTTGGCCAACCATTCACTAAG
tbm0724	5	(TA)10ACAC(AT)4(GT)6	AGCTATTTAAATTTATGTGAATCGTCT	GTTTATTTTTCCAATTGACTCCAAA
tbm0725	5	(AC)10	ATGAGGTGTACAAAGGAAACGC	GTTTGCTGGGACTCTTTACCTTTTC
tbm0726	5	(TAT)10	ACAAAGGCAAAGTAGTTGCATA	GTTTGCATGCATTTCCTTAATTTTCC
tbm0727	5	(TA)11	ACCGGTATAGATAAGTTTTTACCA	GTTTGCCAATCCATGAGATTTAGTTTC
tbm0728	5	(AT)11	ATCTTTCATACTCAATTTATCCAATTT	GTTTCTTTTTGTTTTTGAAACAGTAGAACAA
tbm0729	5	(AT)11	AGAGAGGAGAATGAACAAGAAAGA	GTTTGTCTGAGTTCAATGGCAA
tbm0730	5	(TA)12	ACTATCCGATCCCAATTCCTAT	GTTTAACTCTGACCTTTCACACGAGA
tbm0731	5	(AT)13	ACTTAAAAGGTGCTTCTCGTGC	GTTTACTGCAATCCAAACGAAAAA
tbm0732	5	(TAC)4TAATA(AT)13	AGATTACATTCACATGAATTGGC	GTTTCGTGAAAAACATTTTCCTTCC
tbm0733	5	(AT)13	AGCGTGTTTCTTGACCTTCTTG	GTTTGACTTAGAGCTTGCTTGA
tbm0734	5	(TA)13	ACATTATTGTGCATTGGAAAAA	GTTTACACTTCTTTGGCATTGGAATC

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0735	5	(TG)7(TA)13	ACACAAGGTAGGGGTAAGGCTA	GTTTGCAGCTCTCCATTTTTACC
tbm0736	5	(AT)13	ACATTGTACGGCCTTAATTCAT	GTTTGCATAGAATTTCCCATTTGGAC
tbm0737	5	(AT)14	ATAAACAAAACAAGCATGAGCC	GTTTAATCGGAAAACAACATTTCA
tbm0738	5	(TAT)14	ATACATTTCGTCTGTTTTTGTAATG	GTTTGCGATGAGATCGACTCAAAAAT
tbm0739	5	(AT)14	AGGAAGGTGAGGTTTATTGTCA	GTTTGCAATAACATGTATATCCTCGTG
tbm0740	5	(ATG)7(ATA)4ACAT(TAA)8	ATTCCAATATAAGTTGTCCCAAAAA	GTTTGACCCAATCATCACATGTTTTA
tbm0741	5	(TA)9	ATTGAGCTATCAATATCATCTTCAGT	GTTTGCCCTTTTTGCTCACGTATATT
tbm0742	5	(AT)5(GT)10	AGTCGTAATCATGACTCTTCCA	GTTTCAGGAGGGTGATAGGACCTTA
tbm0743	5	(TA)11	ATGTCTGATAACGAAAGATCCTTAAA	GTTTGAGTTAATATCTCAAAAGCTCACACAA
tbm0744	5	(AT)11	ACGCTGGTTATTAGTCTCATGG	GTTTGGAATCTTAGAAACAAAAACACC
tbm0745	5	(AT)4AC(AT)6AC(AT)12	ATATTGGAGCATTCACATCTTG	GTTTCGCATCTAAAATAGCTCGAAA
tbm0746	5	(AT)13	ATCGATATTTTGCTTGTTCATCA	GTTTGACACATGTCCCTATTAAATAAATC
tbm0747	5	(TA)29	ATTGAAGAAAAATTCTCATTTATTTG	GTTTCACCTTTCAACAATGACCAAAA
tbm0748	5	(TA)5C(AT)6CG(AT)37	AGTATCCCTCACACGATGTTTT	GTTTCAGGTTGTGCAACAATTTAGG
tbm0749	5	(TA)6(GA)8CAGT(GA)6	ATTTGTACAAAAGAATTGAAAGTTTG	GTTTCAAGTTTCAAATCACCACCAC
tbm0750	5	(AT)9	ATAAGACTTTCGCTTAAAGGGG	GTTTGACAAAAGTCAAAAATTTCGC
tbm0751	5	(AT)9	ATCTTGAACTTGATTGGGAAAA	GTTTACCTAACAGCTTCCCATTGCT
tbm0752	5	(TA)9	ATGATTGTGCTTGTGTCAGTGAA	GTTTAAATAATCTTTGGGACACGACC
tbm0753	5	(AT)10	AGGAGTCTGGAGTCAAAATGGA	GTTTCAGAGCCTAACAAAAGGA
tbm0754	5	(TA)16A(AC)4(GC)6	ACTTCAAAGGTGGAGGAGTAAA	GTTTCTTCAATTGCAGGAGATGTG
tbm0755	5	(TG)9	AGTAAAGAAGCACATGCATACAGA	GTTTCACCTTACGTTGCTCCATA
tbm0756	5	(TA)9	ACAAGTGTCAAAAAGTCTTCCA	GTTTGCTATTCTTCGGAAATGTCAC
tbm0757	5	(TCT)9ACTA(CTT)5	AGCGTGAACTTGCTTAACTTGT	GTTTGTATCAGAGGCAAGAAATCCA
tbm0758	5	(TTA)11	ATAATCTGTTTGGCGATTGATG	GTTTCATACAAAACCCTTTCTGGGT
tbm0759	5	(TA)11	ATATGTGTTGCAAGTTAATCGG	GTTTGAACCCTTTTCGCATTAAG
tbm0760	5	(TA)12	ATATAGTCATTTAACTCACACAAATCG	GTTTAAAATATTAATAGTCAAGGAGCGACA
tbm0761	5	(TA)13	ATGGCGAGAGAGAGAGAGAGTG	GTTTAATTACGTGGGCTGACTTCAA
tbm0762	5	(TTA)14	AGAGGTGACATAAAACCAACCA	GTTTCAAGCCCACTTTATGAACCAAT
tbm0763	5	(AT)14	ATTCACAAGCCAACCACTTTTT	GTTTGGTTGAGCTTCTTTTTGAAT
tbm0764	5	(AT)28	AGTGATTGACACTTAAAAAGGCA	GTTTGGACCCAACTTCATTCATCT
tbm0765	5	(AT)30	ACGTCTCATATTGAAGATTTATTGA	GTTTCGATGGCGTTATGTATGGATAG
tbm0766	5	(TA)37	ATAACAGACACATGTATCCTACCC	GTTTAAATTCAAGTGTATCGCCGTCT
tbm0767	7	(AT)9	ATCAAGTACTCTCCCAGGACAA	GTTTCTTTTTGGTTTGAACAAGCTATTTTT
tbm0768	7	(AT)9	ATGAAGAAGACCCAAATAGTGGA	GTTTGCTTTGGTTTCGATTTAGA
tbm0769	7	(GAA)11	ATGAATTTTCATGGGGAAAGGT	GTTTCCCTTAGACACCTCAATTACGC
tbm0770	7	(AT)12	ATTGTCAAAACAAATTTTCCGC	GTTTGCAAACATTTAAGCATTTTCAGC
tbm0771	7	(TG)4TC(TA)35	ACAAGTCCAAATTTGAAATAAAAAG	GTTTACATCCAAAGCAAACTGACATT
tbm0772	7	(AT)5(AC)9	ATTTTTTGGAGTTTGCATGAGA	GTTTGCATTAGAGCGTTGACAAACT
tbm0773	7	(AT)10	ATTGACATATCACTTGTTCGCC	GTTTCATGCTGCATCAAACTTCTTT
tbm0774	7	(ATA)11	ACCCTTAATTATGCGAACAGAT	GTTTGGCAATCTCTAGTGAAAATGTC
tbm0775	7	(GA)11	ACGTCAGAACAGGTACAAGAGC	GTTTCCCAAATCCTTGGGTAAACT
tbm0776	7	(AT)13	ATTTAAGTCAATTCAAACGGACA	GTTTCCCAATTCGATTTTCTCACTTC
tbm0777	7	(AT)29	ATGGACTAATCTAAAAGGCATTGA	GTTTGGCAAATGTGAGACATTCA
tbm0778	8	(TA)11(AT)6	ACAGGATGATTTCGAGTTTGTA	GTTTATGTACATGGCAAGCGAGATT
tbm0779	8	(TG)10(AG)11	ATCTCTATCTTCCGTTTGCTCC	GTTTACAAGAATCGAAGCATGAAACA
tbm0780	8	(AT)12	ACGTAATTGATTCGATTGTTGG	GTTTAAGGAAGAAGCAAAGTGTTGGT
tbm0781	8	(AT)13	ATGGGGAATTTAGAGGGTTCAT	GTTTCACGCATATGTTGTTGAT
tbm0782	8	(AT)14	ATAAATGAAAACCGAAAAGCAA	GTTTGGACAAAAGTGGTTAACTCCAA
tbm0783	8	(AT)14	ATCACACTTTGCTAAACCCAAC	GTTTGTCAAATGGACGGGTAAAAT
tbm0784	8	(CT)14	ACTTGTTCTTGCTGCACAACTT	GTTTGCTTCACCGTTTCTACA
tbm0785	8	(AT)16(GTAT)10	ACTTAATCCCTAAGGGTGTCCA	GTTTGACAAAATCAAGAGTGATAATTTCT
tbm0786	8	(AT)16	ACATCATCATCACCATCAAAAT	GTTTCACGGAAGAGAGAAAAGGAGAA
tbm0787	8	(TA)16	ATTGTGTTTTTCCCATTATCCT	GTTTGGAAGGAAATTGTTTAGGATGT
tbm0788	8	(AT)17	AGTGCATTACGAAAGTTGAAGG	GTTTACCCCCACTTCAAACCATAC
tbm0789	8	(TA)18	AGCGAACTATCTCTTCATTCCA	GTTTCTCAAAAAGAGTGATTAGGGATTC
tbm0790	8	(AT)19	ATTCATTATTTGCGTTCTTACTTCA	GTTTGGACTTTATCCCCATTCAACAA
tbm0791	8	(AAT)20	AGAATGCAACCACACCTCTTTC	GTTTGAATTCAAGTAAAAGTTATTCCCA
tbm0792	8	(AT)21	ATTCTCTCCTCCCTCTTCCATT	GTTTGCAAGAGAGGGCAAAGAGTTAG
tbm0793	8	(AT)22	ATTTGTTGGTTTGGTTTTGGAT	GTTTGTACTTTGATGCTTCCCA
tbm0794	8	(AT)22	ATTTGTTAGGGGTCTCATCTTCA	GTTTCAGCGAACACATTTTACAAGAA
tbm0795	8	(AT)23	ATCCTTCGTACCAAACACATTC	GTTTAGCTACCGACACCACATCTTCT
tbm0796	8	(TA)24	AGAAATTCGTATTTTAACGCAA	GTTTGTCAATGAAGTGGGGCTAT
tbm0797	9	(AT)12	ACCGTTAATTTTTACTTGTCCGA	GTTTCGATGTTTTGATTTTCTCTCA
tbm0798	9	(AT)31	AGGTAGTGTTTTAAAATGATGACAAT	GTTTAAAACCAATAGAAGTAAAGGAAA
tbm0799	9	(AT)10	ACATCTTCATATGTTCGAGTGAA	GTTTGCGGATAACTTTAAGGGGTT
tbm0800	9	(TTA)10	ATCCAACTCCAAAGAGATAGGG	GTTTGGTGAAAATGATTGTGGTTG
tbm0801	9	(AT)6G(TA)10	ATGTCTCTCATGGTTTTGTCAAT	GTTTGGATACTTATGCATTATTCCTTGAA
tbm0802	9	(TA)10	ACTTCTACCTTGATAAGTCGATTACG	GTTTGGGCGTTTTGACAAATTAT
tbm0803	9	(AT)10AG(AT)8	ATTATGATCTAATCAATAGAATGTCCA	GTTTAATAGCTAAATCATCATCGTCATC
tbm0804	9	(TCT)11	ATACCCCTTAAAACTGACGTGG	GTTTATAGTGGGTTGGATGGAAA
tbm0805	9	(ATA)11	ATTTTAGGGGCATCAATATGTAA	GTTTCAACACATTAGAAAGCTCAGTT
tbm0806	9	(TAA)6(TA)12	ATACACTAACATTTTACATGATTCACA	GTTTAGGCATCTTGGTAGGGTGATAC
tbm0807	9	(AT)12(GT)10	ATTCCAAAACTTTTTGCATTGT	GTTTCTTTTGTTATCTGGGCACTAGCA
tbm0808	9	(AT)12	ATGCATAACACATAGCACCACA	GTTTCCCATACATCTGGTTAAGGGTG
tbm0809	9	(AT)13	AGACGGAATTAAATTATACGGTG	GTTTCATTAATATGTACGTGTGTGTGTG
tbm0810	9	(TA)4TG(TA)13	ATCCGGGGTGAGTATCTAAAAA	GTTTCGGAAAAATCAAAACTCATTG
tbm0811	9	(AT)14	ATTCTTCTCTGCGCTAGAATCC	GTTTAATGGCATGTCAATCACCAA
tbm0812	9	(GT)4GAG(TA)26	ACAAAATCTCAAGAAATGCAACA	GTTTCCTTGTAATATTTCCCTCTTT
tbm0813	9	(AT)27(TTAT)4	ATCAAGAAAGAATGGCTTTTAGC	GTTTAAGAAAAACCACCTCATCATGC
tbm0814	9	(AT)32	AGTACATGGCTAGACTTCTTACAACA	GTTTGCATTATGAAAGTTGAAGG
tbm0815	11	(AT)4ACAC(AT)6(AC)6	ACGAAAGTTCATCGAAAACAAC	GTTTCTGAAGAGGAGCCAATGAA
tbm0816	11	(TG)8(TA)8	ATTCCATCAACAAAAACCATCA	GTTTGAATTCTGAGGAGTACCGGA
tbm0817	11	(TTA)9	ATCTTCATTTGAACAGATCGACTT	GTTTCAAAAGTGTCTCAACAACCCTT
tbm0818	11	(AG)9	ACACCCACATGGAAAAATAAGC	GTTTGCCAAATATACTTCCAGCAACC
tbm0819	11	(TG)9	ATGGACATCTCCTAGTGCAAAA	GTTTAGCTTCAAATTCTCATTGGCAT
tbm0820	11	(GA)9	ATTCAACCAATTCTTGATCTTCC	GTTTCATAGTTTGTTAGTCCCTTTCAA
tbm0821	11	(TG)7CGTGC(GT)10	ACTGTGTGTGTGTGTGTGTGTG	GTTTCTATCACCATCACTGTCGGA
tbm0822	11	(TA)10	ACAAACACAAATTGTTACGATTCA	GTTTGGTAGGTCCATAAACTTTTCCC
tbm0823	11	(TA)12	AGTCCTTGAAGTTCTTCTCCCC	GTTTCCATCATCACATACGTCAAACA
tbm0824	11	(AT)13	ACTTTCATGCAAGTGCTTTGTT	GTTTGATAGATCGGTGACTCGAA
tbm0825	12	(AAT)6(AT)5G(TA)8	ATGCAGAGAGGAGATTCAAAGG	GTTTAACCACACGTACCAATGTCA
tbm0826	12	(AT)9	ATTGCGAGATTCAAACAGGTAA	GTTTAGGACTCCCTTTGAGTTGAGC
tbm0827	12	(TA)9	ATTGCGATGTACTTATTTCGTG	GTTTATGGACTAAGCCATCCTCACC
tbm0828	12	(GA)9	ATACGAGGATCATTTTCCTTTC	GTTTGTCGAAGCTCTGATAATTTGG
tbm0829	12	(ATT)10G(TTA)4	ACTTTTCCAAATTTTGCTTTTG	GTTTGGGATATTATTTTAAAGCTTTTTCCA
tbm0830	12	(TA)10	AGCGATATATAAAGAGCGAACA	GTTTCTCATCCCAAGGCAACTA
tbm0831	12	(TA)11	ATACCAGCTACTAACAACCCCA	GTTTAGATTGTCCATTTGACCGC
tbm0832	12	(TA)14	AGATGTGGAGATGAAAATAAACTG	GTTTGGGGGATGATAATGTTATGTTAGA
tbm0833	12	(TTA)26	ACTCATTAAAAAGGAATTGCCA	GTTTGCAAGCTGTTCTTTTCAGACT
tbm0834	12	(AAT)4(AT)34	ATAGCTTCCTCGACATGACAAA	GTTTCAGAAATAGTGGAATGGGATCA
tbm0835	12	(AT)10	ATCTCCAATTTAATGCCCACAC	GTTTACATCCAATTGGTGCTTTTT
tbm0836	12	(TA)10	AGGCCTTTTTCATCTTTCCTAC	GTTTGGTGGTTATCGTATTCGTCA
tbm0837	12	(AT)11	ATTTCCCTTGCAATCAAATCAT	GTTTGTGCGTCAAACTCTATTCAGA
tbm0838	12	(TA)11	ATGACAGACGGAGTACAAAACCT	GTTTGATATTTCTTGGTTTTGGGG
tbm0839	12	(TA)12	AGCTGCTAATTTTCTTAATTGGA	GTTTGGGATCCTATTTATCCTCACG

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0840	12	(AT)37	ACAAACAATTATAGTGGTAATAATCAA	GTTTAAGTTTCATCCATGTGCAATTTT
tbm0841	12	(AT)9	ATGTGGGACTCAATGAATCAAG	GTTTGGCAATTTGATGAAAATATGA
tbm0842	12	(TA)5C(AT)9GTATG(TA)4	ATGTTGACACCCAATTTTGACC	GTTTCAAAGCGTATTCGAAGTAACA
tbm0843	12	(TA)6C(AT)10GTATG(TA)4	ATATCGAGCTTCGAGAATTTTT	GTTTCAAAGCGTATTCGAAGTAACA
tbm0844	2	(AT)9	ATTTCAATACCTATGCGACGAG	GTTTAAAATCTGCTGCTCAAAACGA
tbm0845	2	(AT)9	ATTTTGACACCATCTTCGACAC	GTTTAGGACCACATGTTCTCAAACTAA
tbm0846	2	(AC)7(AT)9	ATCGAATATGTCATTTTTGCCT	GTTTGTATCAACAAGTTTGGCAATG
tbm0847	2	(AC)10	ACCTTCTAAACCTTGACGCATT	GTTTAGGTTCTTTTTCTGTTTTCCCC
tbm0848	2	(TA)10	ATTGTATTCGTTGTATTTCATGTTTTT	GTTTAGGTCCAGAGCTAATATTTTT
tbm0849	2	(AC)8(AT)5(GT)8TT(TA)6	ATGCATGAAACATGACCATCAG	GTTTGACCAGTCCTGTGTTCTTTG
tbm0850	2	(AG)8GGG(GA)8	ACCAACACGAGTTCCAAGCTAT	GTTTCAAGGTCGAGCAACAAAACATA
tbm0851	2	(TA)11	ATTCAATCAATCCACATGCAC	GTTTGGATTTGATTTCATTTGATCG
tbm0852	2	(TA)12	ACACATGGTATATTTATTCCCCC	GTTTCTTTTTCTGGTGTTATATAAATGGCTT
tbm0853	2	(TA)14	AGGCCAAAGTTTTAGTTTGGGT	GTTTGATACCATCTAGACGGACTTG
tbm0854	2	(AT)26	ATGCTTTTGACCGATTTGACTT	GTTTAACAGATATAAAACGCGCATCC
tbm0855	2	(AAAT)5(AT)14	AGATGTAGAGTTGAATAACCACCA	GTTTCCCCAAAACACATTCTTTCT
tbm0856	3	(AT)10	ATGGGGATGAACAAGAACATCT	GTTTGCAAAAATTGCAAGTAATGGTA
tbm0857	3	(GA)10	ATGCCAAAGCAATATTAGCGAG	GTTTGAAGTCGTTGTAGGAACCC
tbm0858	3	(AT)12	ATTCATTTCTTGATTCTTTTGTCG	GTTTAAATTCTTCGGGTGATGAGAGA
tbm0859	3	(AT)12	ATGCACCTTTAATTTTGTTTGC	GTTTGAGTTTGGGAAAAGGAAAAA
tbm0860	3	(AT)13	ACAATCTCACTAAGTAAAGTCATCCG	GTTTCCTCAAAAATAGGCCTTGCTA
tbm0861	3	(AAT)14	AGGAAAGTCAACATTCCACGTT	GTTTAGGGATTGGTGGAGTACATTTG
tbm0862	3	(TTA)8T(TTA)8	ATAATTCATTTCATGTTGACCAAG	GTTTCACATAGTTCTTTCTCATCACA
tbm0863	3	(AG)9	ATTCTCCAAATGGCAGAGAATC	GTTTGCAACAAATTCCAAGGCTATTC
tbm0864	3	(TA)9	ACAAGTCAGTGTCTATGGGCAG	GTTTAGAAAGTGGCGAAATCAGA
tbm0865	3	(AT)11(AG)8	ATTTCTCGCCCTATGGAAGGTA	GTTTCTTGAGGAAGCTTTGCATT
tbm0866	3	(TA)12	ATTATACGAAATACCGGCGGAG	GTTTCGGAAAGGCTAAATCTAATCTGA
tbm0867	4	(AT)11	ACAATTTGACTCATCTTCGAGAAA	GTTTAACCATGATAATTAAAATGACAAGAA
tbm0868	4	(AT)11	ATGCAGCAAAATAGGTGTTGGT	GTTTCGACTTCGAGATTGACAAAGA
tbm0869	4	(TA)11	AGCCACATCTATTAAATGCACA	GTTTGCGTAATTAGTTTTTCTACATCGAGAG
tbm0870	4	(TA)12	ATTGCATCATTACCCTCAAGTG	GTTTCGAACCCCTCCTTTTTCTTATT
tbm0871	4	(AT)13	AGAAATGGTCCTCATGTGAAAG	GTTTGAATGTTGAAAAGAGGGAGG
tbm0872	4	(TA)29	ATCTGAAAGAAAGAGGTGGACG	GTTTCAATCACAGATTGCCATTTCAC
tbm0873	5	(AT)9(AC)7	ACTTTTCCTCTTTCTCCCAATC	GTTTGTATAAATGGCAAGCGAGA
tbm0874	5	(TA)9(CA)7	ACCAAGGAAATGATGTCTGATT	GTTTATAAGCCTGCATCTGCAAGAA
tbm0875	5	(TA)10	ATATCAAATTGCCATTATGGTGTA	GTTTAAGTTGGAACATGTGGAGG
tbm0876	5	(AT)10	ATTCCAACATTACGTTCACCTC	GTTTCTTTTGGCATGCATCAAGTACA
tbm0877	5	(TA)14	AGCAAAATTACCTCGTTTCTGA	GTTTGTCACCGAAAAAGTTGAGGT
tbm0878	5	(AT)26	ACACTAATTGGAAGGAAAGGGA	GTTTCAAAAGCAGAAAGTGCAAAAA
tbm0879	5	(AC)5TAGGT(TA)7(TG)8	ATTCAATGTGCAAATCTTGGAG	GTTTGGAATTAGTCGAAATGCACAC
tbm0880	5	(TC)8(TA)6TT(AG)5	AGTGTGTGCCTCTCTCTCTTTC	GTTTCACGAAATTTTAATAATACCACAACAA
tbm0881	5	(AT)13	ATATCAATAACGAAACGTCCCC	GTTTAGCCCAAGCATACACCACTTAT
tbm0882	5	(GA)4AA(AT)13	ATAAAGCCACCTCCTAGCTTTC	GTTTCTGAATTCCTCTTCTGCTC
tbm0883	5	(TA)14	ATTCTCTCTTAAATCCTCCTCTCA	GTTTCGAAAACATACTCTTCCAAACTT
tbm0884	5	(AT)26	ATCTTCAAATTCACAACCACCC	GTTTATCCCAAGTTCGTCTTTTTCG
tbm0885	6	(TA)9	ACTGATCACTTATGAGATTTCAATTTT	GTTTGAACACGCATTCTTCTTT
tbm0886	6	(TC)9	AGGTGTTACCACGAAATATTGG	GTTTCAAATGACGTCTAAAGGCT
tbm0887	6	(TC)10	AGTTTACTCACGGGGTGTTACC	GTTTCAAACTTCTCGATTCCAAGC
tbm0888	6	(AT)11	ATAAATAGTGGCATTTGACGCA	GTTTCATTTTGAAGCTTTCCATGTT
tbm0889	6	(AT)13	AGTTTGTTTGGATGGAAAGTGC	GTTTGAAGATGTTAAGCAACAATTCACA
tbm0890	6	(AT)31	ATACCATTACATATGCTCACGC	GTTTCACAAGAATATTTGCCGT
tbm0891	7	(TTA)9	ATTCACACACTTTGGTGAATGC	GTTTGCCTTTAAGACTAGCATGTGGG
tbm0892	7	(AG)10	ACAAACAAAATTTTTCCAGTTCA	GTTTCCTGACAAATGCAAACAAATC
tbm0893	7	(AT)10	AGGTCACACTTGTGTTAGTGGA	GTTTCATGAGCTAGCTTTTGGTTGA
tbm0894	7	(TA)12	ATGGGATAGGATGGTCTAAGGA	GTTTCTGGATTCAGACGAACATAATAA
tbm0895	7	(AT)12	ATTGGGAGTAGTTTAATAACTAGAGGA	GTTTAGCAAAACCCCATAGCTCA
tbm0896	7	(TA)11	ATATTTTTGTCTTCGCTTTATTTTT	GTTTGAACTTAACTCCCAAAGCGT
tbm0897	7	(TC)11	ATCGTGTCATTTGACAATTCCT	GTTTGATCAAGAAGGTGCATGTG
tbm0898	7	(AT)12	ATCCAATTGCTGAGAAGAATCC	GTTTCATATGTTTGCGTTCGATTTC
tbm0899	7	(TA)12	ACAATATTTAAATCCTCGACCG	GTTTAACGTAAGTTTACCTTTGCATCA
tbm0900	7	(TA)12	ATTTGGAAATTGAGAAGGCAAA	GTTTAGTTTGTGACAGTTGACCCG
tbm0901	7	(AT)13	AGGAGTTAATATCTCAAAAGATCACA	GTTTCTTACCGGAGTCCATTAAAC
tbm0902	7	(TTA)10	ACCAAAACGGATATGAGACAAT	GTTTGAGGAAAAGGTTTGAGGA
tbm0903	7	(TTC)10	AGCAGAAAACATAAGATGACCA	GTTTAGAAGGGAATCCCGTTAAGTTC
tbm0904	7	(AT)11	ATATTTAAAAAGATGACATGACATGAA	GTTTCTTTTACTTGAAAATTAACGAGGATGA
tbm0905	7	(TA)12	ATCTTTTTCCATGTGGTGCTTA	GTTTGAATCTAGAATTGGAACCTTCAGA
tbm0906	7	(AT)13	AGCAATGAGCTTTCCTTCTTTC	GTTTCCCCTTGAGAACCTAAGGATAC
tbm0907	7	(TA)13	AGTCTTTCTTTTAGGTTGTTTCG	GTTTGGAGGCCTAACTTCTACTTCTT
tbm0908	8	(TA)9	ATTGACTTTGCCACAATCTTTG	GTTTCTTTTGTGGAAAGGTATTTGCC
tbm0909	8	(TA)9	ATATTTTCTTCGCACATCACAT	GTTTCTCAAACACATGCAAAATCAA
tbm0910	8	(AT)45	ATAATCGAATCCAAACCAAACT	GTTTAACTTCGGATGTTAATACAAAATAAAA
tbm0911	8	(AT)9	ACGCTTTTACACAACGAATCAC	GTTTGACCTCCAAAGCCACCATATAA
tbm0912	8	(AT)10	ATCCCCCTTTTAAGTCAATTTTT	GTTTCATTGGTTCCAAAATAGCAAA
tbm0913	8	(TA)12	ATATTTTGTGAGACGGACTTCA	GTTTGCCTAAGTATCCTGCAACTCA
tbm0914	9	(TTA)11	AGCACGTGAAAAATTAAAATCC	GTTTCTTTTTCTCTGTCTGATCCATGTG
tbm0915	9	(TA)11	ATAAGAAACAGCTATGCACACG	GTTTCACCCATCTTTTGCCATTTATT
tbm0916	9	(TA)11	ACCCTCCTTCATAAAACACTTACA	GTTTAACAACTTTAGGGACCTGCGTA
tbm0917	9	(AAT)12(AT)9	ACGCTCGATTGATAAGTTGGTT	GTTTCAATTTTCCTTTGGCTTTGT
tbm0918	9	(TA)12	ATTTTCAAACTTCTTTCAAAACATAGA	GTTTCATCTCCATTGGGCATATT
tbm0919	9	(TA)12	ATGCAACAACCTGTAATTTGCT	GTTTGGCCGATGTAGAAGTAAAGAA
tbm0920	9	(AAT)11A(TAT)6	ATCGAAAAGAGAGAGGGGTTAAA	GTTTCCAAATCTCTAACGGTTTTCCA
tbm0921	9	(AT)13	ACCTCTTTACATCTATACCTTACCAAA	GTTTCGGAAAACTGTTATTAGTCAATG
tbm0922	9	(GT)14	ATGTGGTGATAAATGAGCCATC	GTTTGGAAAAACGCTCAACAATTT
tbm0923	9	(ATT)27	ATGCTTCCCACCCCTTAGTTAC	GTTTGACAGAATGTTTTCTTTTTGCT
tbm0924	9	(AC)4AAGA(TC)5(CT)4CGCTT(TC)4(CT)5	ACCTTTCAACGTCAGATCCAAT	GTTTACCCTAGCAAAGAAGAAAGCG
tbm0925	9	(AT)11	ACCCGGTAAAGTTCTCATTAAA	GTTTAAGGGGTGATTTAAGCCAAA
tbm0926	9	(AT)12	ATGCTTCACCCACAAATAAATG	GTTTACAACTCCGTCAGTCTTTTCGT
tbm0927	9	(ATT)13	AGCCCTCCATCAATGTATGTTC	GTTTGAGTATTTTCATCACCTGTATTTCA
tbm0928	9	(AT)31	ACTTCAATCATGTTGGAAAACTAGA	GTTTGTTTTAAATGGATACCCCC
tbm0929	11	(AT)11	ATCTCAAAACAATGAAGCAAGC	GTTTAGAACCAATGTTGCTAAAGGCT
tbm0930	11	(AT)11	ATCGATTCATATGCTTGTGATAA	GTTTCCATATCCAGGAATCGAACTT
tbm0931	11	(TAT)12	AGTCTGATTCTTGGCTCCTCTA	GTTTCACAATTCACATGATCCACT
tbm0932	11	(AT)13	AGGCAATTAACAATCAAATTCAA	GTTTGAATCCTGTTGAACTCGTAAA
tbm0933	11	(AT)29(TTAT)5	ACCAACTTTATCACATTATTCAAGA	GTTTCTTGCTTTTTCAAGGATGG
tbm0934	11	(GA)9	ACACAAAATTAGGAAAAGGTAAAAA	GTTTCCTTTTCGATTTGTTCCAGT
tbm0935	11	(TA)9	ACCAACTTTTTATTTACGCTCG	GTTTAATTTCGAGCCTCTCAAGTGC
tbm0936	11	(AT)9	ACCTTGCTATAAGTGGTGTCGT	GTTTAACGTAGAAAAGGTACATTCATTG
tbm0937	11	(ATA)10	ACTTCTTTAGTATCCCCACCCC	GTTTCGCAAGACATGACCAATTATCT
tbm0938	11	(AT)10	ATTTCTCGCGATCCCTACTCTA	GTTTCAATATGTCACCGTAAATCCCC
tbm0939	11	(AT)13	AGGATTGATATTGACATGTGGG	GTTTAGAGTTTGTTCATGCAATGTGG
tbm0940	12	(AT)12	ATACATCTTGCTCAAAAGCGAA	GTTTGGGTTATTGGTTTAGCGATTT
tbm0941	12	(AT)29	ATGTTTAAATTCGGGGACGAAA	GTTTAGTTCGAGGATGAAGCTCGT
tbm0942	1	(AT)20	ATTTGTGTTTGTAAGTCGTTTTGAA	GTTTCAGAAGTCGTAAGACATCCCTTTT
tbm0943	1	(TA)11C(AT)4	ACGCTAGAAAAATAATAAGTGAATCAA	GTTTGTACACAATGTCCACCACAA
tbm0944	1	(AT)10G(TA)4TG(TA)6	ACAAAGTTAGGGAGGCTGTTTC	GTTTCCACAGGACATTACATGATGGT

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm0945	1	(TA)25	ATATGCTTGATTTGGCCTCACT	GTTTCTGCAAGAGACTGTTTCCA
tbm0946	1	(TA)23	ATTTTCGAATCTCTTCTGGTACG	GTTTGTCTTGAATCCAATTGCC
tbm0947	1	(AT)33	ACTCCTGTGGAATCAATCAATG	GTTTCTCTTCTTCCTTCAACTTGCC
tbm0948	1	(AT)32	ATCTTATAAAGTGAATGGAGGGG	GTTTAACTTTGACCAAATGAAATCAAAT
tbm0949	1	(AT)29(TA)7	ATTGCCATGTTCTGACAAGCTA	GTTTAGGATCACAAGGCTATTCCACT
tbm0950	1	(AT)29	AGAGAACATGACTGACCAACAA	GTTTGGGAGGTGGTGGTGTAGATAAT
tbm0951	1	(AT)27	ACTTGGAGGTCTTATTCAAGCC	GTTTGATGTTGAGTCTAGGATGACAAAA
tbm0952	1	(TA)26CACAC(AT)4	ATGGCGGAGTCAGGATTTATGT	GTTTGCAACCTGAGTTCGAATAAAA
tbm0953	1	(TA)24	ACAGATGAATATCAAGCAACATT	GTTTACAAGATGGATTTTTGTTTTGAA
tbm0954	1	(AT)17	ATAAGATGAAGTCTTTGGCCCT	GTTTAAGCCACCTATTGAGTTCCGTA
tbm0955	1	(TG)13(TA)16	ATAGAGGGTCTTGTTAATCCCA	GTTTGCAACTAGTGAGCAAGCATTT
tbm0956	1	(AT)16	ATTGATTGCTCGAGTAAAATAAAAA	GTTTGTAATCAGAGGCCCAAAATG
tbm0957	1	(AT)37	ATCTACTTCTCACCACACAGCC	GTTTATTGATGCATTCTGCTGGA
tbm0958	1	(AT)30	ACAATGGGTTAACAGTACGCAA	GTTTGGAACCCAATTCTTGAATCACT
tbm0959	1	(AT)25	AGCACAAACAGACACTTTACCTG	GTTTAAAATCAAGTGGCGACTCTGTC
tbm0960	1	(TA)22	AGTTGTTAGGACTTATGGGCCT	GTTTAATTCTTCTCCCATTGCTGC
tbm0961	1	(TA)21	AGAAAAGCTAACTGGAGTGTCA	GTTTGGAATCCTTATTTGTGGTGGAA
tbm0962	1	(TA)17(CA)6	ACTCGTCAAAAATCACAACCCT	GTTTGCAATTAATATTTGTGACCGC
tbm0963	1	(AT)16	AGCCGCATAAATTCTTTCATAA	GTTTCTACACCTTCTCCCATAACCAA
tbm0964	1	(TC)11(TA)12TG(TA)15TCA(AT)6	AGTCTATTCTGAAATTGCTGTGA	GTTTATTGAGTATACCTAGACCCTTCG
tbm0965	1	(AT)15	AGCTAAATCACTCAAGAAAATTCA	GTTTGGACTATTGGAGGTGTGTGTC
tbm0966	1	(GAG)6(AAG)7AT(GAA)14	ATGAATGGGGAGTAGGAGAAGG	GTTTCAAAGGGTTTCATCTCCA
tbm0967	1	(AT)38	AGTTTAAGAAACCTTAATGATACAACA	GTTTCGAATAATGGATAAACCGCAAT
tbm0968	1	(AT)34	ACAAAAGTCATAGGAGGTCATTCTC	GTTTCAAAGGTCGACACATCAAT
tbm0969	1	(AT)26	ACTAGCTAAATTTGTGTGTCACGAT	GTTTCAAATTCTTACCAAACAAACA
tbm0970	1	(TA)21	AGAAATGATGCAATGAAGAAAAA	GTTTCTCCGAGCGTTCATATAAAAAT
tbm0971	1	(TA)21	ATTGTGCTACTTCACCATGGAA	GTTTGCGGATAGAAGGAGAAAAACAA
tbm0972	1	(ATT)20	ATTCCTCAGCAAAGTTCCACAT	GTTTAAGGGGGCCAAGATAAAATAAA
tbm0973	1	(TTC)15	ACTTTTGTCTTTAATTGCCAGG	GTTTGGTCTCCCACGATCAATAC
tbm0974	1	(TA)15	ACGTGTATACGTACACTTCTCCG	GTTTAAATAAAAATAGGCTTGCCGCT
tbm0975	1	(AT)14	AGATCTCCACATAACTAAGCCC	GTTTCCAACAAGCAATCCCTTACATT
tbm0976	1	(TA)14	ATCTTACTTGTGATGACGCTACC	GTTTCCCTTTATTGATGCAAGTTTCC
tbm0977	1	(AT)35	ACCACTTGCTTGATATGAGTACAA	GTTTCTTTTGCAATTGAATTATGGGAA
tbm0978	1	(AT)15	AGCAAATAAAAATGGAGGGAGG	GTTTAAGACCATGTTTTCATCATCTCTTC
tbm0979	1	(TC)11	ACAGGCTGGTTCTAAGGTACAC	GTTTAGGATCATGGATGGACATTTTT
tbm0980	1	(AT)10	ATGTTGATCAAGGATAAATTACATGA	GTTTCAATGTATCAAATTTTTACCAAACTTA
tbm0981	1	(AT)10	ATTAATTTGGGAAATCAGGGAA	GTTTCACAGAATTGCCTCAAGACTCA
tbm0982	1	(AT)24	ACCCTTTTCATTAAATACCCCA	GTTTCCTCCAGAAATAATTAGCCGA
tbm0983	1	(AT)21	ATCGATAAGCTAACAAGGCCAG	GTTTCGGAAGAAAAGCTCAAAGA
tbm0984	1	(TA)20	ACATTCAACCCAATGTGAGTTAT	GTTTGGGAGTGACTTAGCATCAA
tbm0985	1	(GA)12	ATACGCTTCCTCTCTCTGAGTT	GTTTGTTTTTCTCTCCCTCTGA
tbm0986	1	(TTA)11	ATTTTAAGAGATGTGTAAAACAAAACA	GTTTAAGCCTAAGCGTGTAAAATAGAAA
tbm0987	1	(TA)10	AGCAATCTTATTCGTCGATTTG	GTTTATGCAAATATCCTCCGTCA
tbm0988	1	(TC)13	ACACTGAGAAAGAAGGCCTCAG	GTTTAGCAGAATCTAATCGTGCATCA
tbm0989	1	(TA)23	ATGGAAAACTAAGGAGCCGTTT	GTTTGCCATGATTAGTTATTCATCTTTT
tbm0990	1	(TA)20	ACTGAAATATGAGGCACATGAA	GTTTACTCAACATTCGACCAAGTGC
tbm0991	1	(TA)13	ATCGCGCTTAAGCAAACTTACA	GTTTGGAGAATGGGATAAAGGTGAAA
tbm0992	1	(TTA)6(TCA)6TCG(TTA)12(TAT)12	ATCGATTATTATTTGTTGATTTTGTCA	GTTTGCAAAATTCCAATCTTGTTGAG
tbm0993	1	(TA)12	AGATTTGTTTACAAAAACATCACA	GTTTACGCCTGAATGAATTTTT
tbm0994	1	(TA)11	ATTCTAAGGCATACTTCTCCGC	GTTTCAAAAGCATAAAACGCAAAAA
tbm0995	1	(AT)14	ATAATGTAATCCAATCCAAGCC	GTTTGATTTCGTTTTCAATTTGG
tbm0996	1	(AT)10	ATTCCATAAGTAACCCGATCCA	GTTTCTCCGTCTCCTCAACATTT
tbm0997	1	(AT)10	ATTGCGAAAAGTTTGACCTGAT	GTTTGTGACAATTTTTGTGGGAC
tbm0998	1	(CT)14	ATACACTAAAGCGTGATGGTGG	GTTTGACATTGACGGAAGTTTTCACA
tbm0999	1	(TA)14	ATATAACACCCACATGGCAAAA	GTTTCGAACCTATTCCCCTCCTATTC
tbm1000	1	(TA)12	ATAATTCTTATTTGTGGGAGCG	GTTTGTGTCAAGTCAAATAGTGTCAAGA
tbm1001	1	(TG)11	ACAGGGCAACTTTCACACATAG	GTTTCCAAGTCTCTTTTTCTTTCTCG
tbm1002	1	(CT)11	ATGGCTTTTTCAATCAAGGCTA	GTTTCAGCTATACCAACTCCATCCC
tbm1003	1	(AT)38	ATGTGCATCCAGCCTAGTTTTT	GTTTGGATTCTGAGCAACTGAACAT
tbm1004	1	(TA)21	ATTTTACTTTGGAGCTTCCCAC	GTTTGATGTTTAAAATTCTTCACAAG
tbm1005	1	(AT)20	ATTTCAGTTCGCCTCTAGCCTT	GTTTAGATTCTCTATAAAGGAACCAGTACAA
tbm1006	1	(AT)20	ATACCCACTTCACCCTTTGTAG	GTTTCTGATGCTTCTTGTCCCACTA
tbm1007	1	(TG)5(AC)5ATTAT(AG)16	ATAATGAATGGGCAAAAGAAGA	GTTTGCTCGCTGACTCAAGTGATA
tbm1008	1	(AT)16	AGTTCCCAATTGCATCAGTAAT	GTTTAGCCTTGGTTGGGTATTTGT
tbm1009	1	(TA)10	ACCTGCTTATTTCTGGTCCTAA	GTTTGGAAGGGGGTTAGACCATTTT
tbm1010	1	(TA)20	ATATCGATGAGGCAACCTCTAA	GTTTCGCCTCTCTTACCCATTCATAC
tbm1011	1	(TA)17	ATAGATTGGTGAGAGGAGGATG	GTTTACGAGACATGAACGACCCTTAT
tbm1012	1	(TA)16(TTTA)4	ATGGACCACAGGACGTAGCTTA	GTTTAGGAAGTCACCGATGGAGAT
tbm1013	1	(ATA)13	ATCACCGAGTCAAGCATAAGAA	GTTTGGATGTTGGACAAAAGTTCAAA
tbm1014	1	(AT)12	ATCTTTTTCATGACTAACTTCAGACG	GTTTGGACCTTTTCACCTTCAACT
tbm1015	1	(AT)11	ACAATACCCCTCATAATATTCGGT	GTTTGGTTTAACTTGCATTCACAAA
tbm1016	1	(AT)10	ATTCTCAGGTGAAACGACGAGT	GTTTCCGTCCCAAAATTTAGTT
tbm1017	1	(AT)10	ATCCGTGTTTCGTCAATTCTAA	GTTTCGCTTTTTACATTTCCATCATT
tbm1018	1	(AG)10	ATCCGTCAAATCCAAATACCTT	GTTTAACATTGCACAGCCTTTCTTTT
tbm1019	1	(TA)38	ATCAATCCGATTTTCATTAATCTT	GTTTAATTCGCATTGACTCGTGA
tbm1020	1	(TA)16	ACGGGAGAAGTCATCTTTTAGG	GTTTCAAACAAAATGCTCCCTATCTG
tbm1021	1	(AT)12	ATCGATTGAAGGTAAGTTAGCCC	GTTTAAAATGTAATTGATGTGCGTGTC
tbm1022	2	(TA)23	AGCTGATAGTGGTGGTTTTCTC	GTTTGGATGAACTTAGCTTGGCTCT
tbm1023	2	(TA)20(GA)20	AGAAATGAGAAGAATAGATGAAGAAGA	GTTTGCTGATTCTTTTTAGTGGGTG
tbm1024	2	(TA)42	ATAATTCTGATTTGTGATGGCA	GTTTAGCCCTACTTGTTGGTTTTTCA
tbm1025	2	(AT)41	ACTTCAATCGTATCACATAAATCA	GTTTGGTGATGAGCTTTCTCAAAGA
tbm1026	2	(TA)25	ACATCAGCATGCCTAACATCC	GTTTCAAATTTATTTTAATTCACACCTCAA
tbm1027	2	(AT)22	AGTCATTAAAAGATTTATGAGTTTCTG	GTTTGGAAAAACCCCAACAAATTTAGA
tbm1028	2	(TA)19	ATATGGGTAACAATGATCCAAA	GTTTAAAATGACACACCATGTACTCTCTG
tbm1029	2	(ATT)15	ACGCTCACATAGGAGGGTAAGT	GTTTGGACACCCCAACACGTTATACT
tbm1030	2	(AT)10(AG)12	AGAGCTACTTGTGCATTTTTCC	GTTTGTTTTAGAGTATGACGCACAT
tbm1031	2	(TA)12	ATCAATTTTACGGTAATTAATATCTCC	GTTTGAAAATTGAGCGAAATTCAAA
tbm1032	2	(TA)11(CA)7	AGTTGGTTTGACTATGTTTAGATGG	GTTTGCGGAAATTTAAAACTTTTCATC
tbm1033	2	(TA)11	ATTGGCCCACTAAATATTGGAA	GTTTGCACCGACTATTCGTTTTATG
tbm1034	2	(TA)35	ACAGATTAGAAAAGAACAGAAAGAAAA	GTTTAAATCGTTGACATTTATTGCC
tbm1035	2	(TA)24	ATTGTGGGTTCTCAAACAAAAC	GTTTCACAAAGTTAGGTTACACACTCG
tbm1036	2	(AT)21	ATATGGCAATAAATGTCAACGA	GTTTCGCACCATATTTGGTTTTAAT
tbm1037	2	(TA)18	AGGAGGACATTCTTGTTCCTTT	GTTTCCCTCCTTTTCTGGGTATC
tbm1038	2	(AT)15	ACACCGAAAAGCATGTACTCTA	GTTTACAAAATCAATTCGTCCACCTC
tbm1039	2	(AT)15	ATGCACGATATGTGTTTGTGTT	GTTTGGAAGTCTTAAACGCGCATTAC
tbm1040	2	(TA)15	ATATGCCCTTAATCTTGTGGTC	GTTTAGCAGTATGAAAATACCTGCCA
tbm1041	2	(TAT)12	ATGGGATAGAAACGACCACGTC	GTTTGGTTGTTGCTAAAACGATATTT
tbm1042	2	(TA)12	ATCTTATCCCCTTCGCCTACTT	GTTTAGCTAGGACCAATGTCCCCTA
tbm1043	2	(AT)11	ATATTGCTATTCACACACTCCTCA	GTTTAGAAGAATGTGTGTTGCGTGC
tbm1044	2	(TA)35	ATCTTTCATGTAATTTTGTTAGACAGC	GTTTGAAAGGAATTATAAAGATGGA
tbm1045	2	(TA)34	ATATATATTCTACCATTCTCTCCGAA	GTTTGCATCCTGAGTTGGAATTT
tbm1046	2	(AT)30	AGAAAATTGGGAGAGTGGATAG	GTTTCCGCGTCTCTCTCTCTTTTATC
tbm1047	2	(AT)30	AGAACTTGGACCTTTCATTCCT	GTTTAAAATGAATTTTGAGTTCCTTGG
tbm1048	2	(AT)25(GTAT)4(AT)7G(TA)8TG(TA)12TG(TA)9TG(TA)7TG(TA)6	ATAATTGGTAACAATGCTTGGC	GTTTCGAATGAGATCAAAGTTGAGG
tbm1049	2	(AT)22	AGAATTTTTCTTCCTTCAAATAGAGA	GTTTCAAGAAATACGATTTTTATCC

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1050	2	(AT)20	ACTTGCCTCTCTCCTTCAAATA	GTTTGGGTTATTTTGATATTTCAACTTTTT
tbm1051	2	(TA)19A(AG)5	AGAGATTTCAAATATTTTGAGAGGTAT	GTTTGCAGTCCTCTTATGTTGTGA
tbm1052	2	(TAT)19	ACACGTGTTATAAATGGTTTTGC	GTTTGATCACTCTCTATTCCTCCA
tbm1053	2	(TA)18(GA)15	ATAGGTCAAAATTTTACGGGGT	GTTTACAAACTCGAAGTCAGCCCA
tbm1054	2	(AT)24	ACCTAACCATACATGTCCTCCG	GTTTAACGAGAATTTTCAGGTGCAT
tbm1055	2	(AT)22	ATAATTGCGGCTAAAAATAGGG	GTTTAAAGAATCTTAAGCACCCACCC
tbm1056	2	(AT)19	ATCGAGGCTGCATAAAGAGAAA	GTTTCAATCCTTCTTAGCCCTTT
tbm1057	2	(AT)14	ACTTTTCGATGGGCTCTATGAT	GTTTGTGTCAATTCAAAAGTGGACAA
tbm1058	2	(AT)14	AGATGTAACATGGTTGACTTTAATGA	GTTTGCATGCCAAAGTTATCAAT
tbm1059	2	(AT)13	ATGTGTTGTTGCATGTCCATTA	GTTTCAATCAAATAGAAAGCCCCAAG
tbm1060	2	(AT)12	ATGAACATAAATATGAAGTCATCCACA	GTTTGAGAAAACCCCCAAAACATACA
tbm1061	2	(TA)12	ACTTAAACCGTTGTTTGAGGCT	GTTTGGATGAATACTGGATGGTGTTG
tbm1062	2	(AT)10	ATTTTTCGGATAAGCTCTCAGC	GTTTCGTTGGAAGGTTATGGATGT
tbm1063	2	(GA)10	ACCAGTGTTCTCAAAGGGAACT	GTTTCATGCTCCACATTTCAATCTC
tbm1064	2	(AT)17	ATGGTTAGGAGGTGTAATGCTCA	GTTTGCCTCAATGTTGAGAAAAA
tbm1065	2	(AT)13	ATGTATCACTTTTGGCCCACCT	GTTTGTGGAAGATGGGTATTTTTGA
tbm1066	2	(AT)10	ATCTCTCTCTCTGATGGGAACG	GTTTCGATATGAGAGAGTGGCAAGTG
tbm1067	2	(AT)41(AC)6	ATGGAAAACTTACGAAGAACCG	GTTTGCTTGTAGGTTTTATTCTTCTTCA
tbm1068	2	(TA)41	ATCATCTTTAGCTTCCAACCGT	GTTTGCCTAACCAACCAAAAATTATCT
tbm1069	2	(AT)39	ACCAAAACATAACTAACATCAAAAA	GTTTGACTTTCACCCTGTACGATT
tbm1070	2	(TA)35	ATGCTATATACCATGTTAAAGCATTTT	GTTTGGCTGCCAGATAGACATATCG
tbm1071	2	(TA)35	ATTCCATCAAATTCCATTTCTTC	GTTTGCTTCACCGCTCACTACTC
tbm1072	2	(AT)34	ATACATCCAAAATTTAGGGGAA	GTTTCCATTTTGATAACTGGTCCG
tbm1073	2	(TA)32	AGTTTGAGTTGTTATATTGGTTGATTG	GTTTGAACTTAAACATGGATTCAAGGC
tbm1074	2	(TA)30	ACCACCCAATAGGACTGGAATA	GTTTAACTGCGATTCAATAGGTGGA
tbm1075	2	(TA)30	ATTTTCCACTCACAAAGACTTCTA	GTTTCGCTGTAATCACTTTCAGAATCC
tbm1076	2	(AT)20	AGTTTGATATTGTATCGGAGCA	GTTTGTCATGCCTGAGTAAGGA
tbm1077	2	(AT)42	AGAGCAAAAACTGGAAAAACAG	GTTTACGATATAAGCGTCCACTTTGC
tbm1078	2	(AT)38	ATCATATGTGTCACCGTCGTCT	GTTTCTTTTTCCATGTGTCAGTCAA
tbm1079	2	(AT)10GTGTG(TA)29	ATTTTTTCTTAGTTTCATCAGCC	GTTTATACATAAGTGCAACGCACG
tbm1080	2	(TA)27	ATTTGTACCTTTTTCACAATCTTCA	GTTTAAGGAATTCAAAGGTCGAATGA
tbm1081	2	(TA)27	AGATGAACTTACCTTGGCTTTG	GTTTGAATTAAGAGTTTACACTGTTTGACCA
tbm1082	2	(AAT)4AAAA(AT)26	ATCAACTTTAGGGACCTGCGTA	GTTTAGCAAATGAAAGGGAATCAGAA
tbm1083	2	(AT)26	AGTGCTCACTTTACCATTCAAA	GTTTCACCAAGTATGCTATTTTTCCCA
tbm1084	2	(TA)24	ATCGTGAAAACATGCATATCG	GTTTCACTCAAGTCAACAGGGGT
tbm1085	2	(AT)23	ATACCCTGAGTTGCTGTTGTAG	GTTTGATTTGATCGACAATACGTGA
tbm1086	2	(TA)23	ACCATGCAAATAATTAGGGTCC	GTTTGAATGTGTCCACAAAACCTTCA
tbm1087	2	(TA)34	ACGGGATACTATAATTTGTTTTCCA	GTTTCGATATTCTACGGAATTGTCTCA
tbm1088	2	(AT)31	ATGTTAAAATCATCGCATTGCT	GTTTCCAGCTTTCCGACATTATTTT
tbm1089	2	(TG)5(TA)21	ATGTGGTCTGTATGTTCTTGCC	GTTTGCATAAAAGCACAACTTGCCAT
tbm1090	2	(TA)19	AGTTGATGTAAAACCTGGAAGC	GTTTGCTATATGTGAAAGTTGCCA
tbm1091	2	(AT)18	ATCGGAAAAAATTTACCCACCTT	GTTTACTGCATTTTGGCATTTT
tbm1092	2	(TA)17(CA)8	ATAACGAAAAGACGGTAAACAA	GTTTGGAACTGAAGTGCCGATACACT
tbm1093	2	(AT)16	ATCACACCCATTTGAATATTTTACTA	GTTTCTTGAATGAAAAATTGTGTTTT
tbm1094	2	(AT)4AC(AT)14	ATGACTCTCACCTTAAATATCATACAA	GTTTGTCATGTAATTGAGACGAAGGA
tbm1095	2	(AT)13(TTAT)5	ACAATCATTGTGTGATACGTGTT	GTTTGAAAGTAGGAGCGAAAGA
tbm1096	2	(TA)11	AGTGATGATGCTACGTAGACGG	GTTTGTGATCTGATGGACTTCAACAA
tbm1097	2	(AT)18	AGTGTGGCCGAAATAGTACTTG	GTTTAATCAGATGATGCCTTTGGC
tbm1098	2	(AT)17	ACGATGTATGTGTATGATTCATTGTA	GTTTCCTCATGTTCCAACTTGGTTA
tbm1099	2	(AAAAT)4AATAA(AT)16	AGAGAACAGGTGCAGGAGAGAC	GTTTGCCACCATACCATACACAAATC
tbm1100	2	(TA)16	AGAATCTCAAAATTCGAAAAATGT	GTTTGAATTGGGTTGACGTTATTTGTT
tbm1101	2	(AT)15	ATCTCATTTGGTATGCGTGAGG	GTTTCTTTTGCACAAATCAAGTTGG
tbm1102	2	(TA)10	ACCTCACTGCGATATATGAACA	GTTTGGGGCACAATATTGACTTGTCT
tbm1103	2	(ATA)10	ACCATGAAGGGACAGAGAGTTT	GTTTCTTTTTACCAGCTGAGAATCTATCAAA
tbm1104	2	(AT)10	ATTTCCAGAATGAAGAGGCACA	GTTTGGGTAGGGATAATTGGACC
tbm1105	2	(TA)32	AGAGAGGAAGAGAGTAAAAGTCAAC	GTTTGCAGTTTGAGCAAATTTAGACG
tbm1106	2	(AT)25	ATGAAGATTCGAAGGGTGCTAC	GTTTCGCTCTCCATACTCCTCCTTTA
tbm1107	2	(TA)21	ACCTCTCTTCATTTGAACCATC	GTTTACACACATTCATTCCTGCTGAC
tbm1108	2	(AT)20	ATGGGCCATATCAATGGAATTT	GTTTGACAAACAATTCCAGACGAAG
tbm1109	2	(AT)18	AGGTACTCCCTTTGTTTAATTTCA	GTTTGCATCAACTAATTGTCCATCTC
tbm1110	2	(AT)17	ATGGCTGTGGAAAGGCTAGTTA	GTTTAGCAAGAAAAACAAGGTCCAAG
tbm1111	2	(TA)14	ATGTTTGAGCGTAAATAATTGTCA	GTTTCACAAATAGCCTAAACAAGAGCA
tbm1112	2	(AT)5(GT)13	ACACTTGTGGTCCTAGGTTTCA	GTTTAAAAGTTGCAACCCTTCAAAAA
tbm1113	2	(AG)13	ATGATGAAAGGGGTTTTCCAAT	GTTTGTAGACGCGTGAAAGGGTAT
tbm1114	2	(TA)12	AGTCTTTGAAGCAGGTTTGCTA	GTTTGACATGCCAGGTTACTTCAT
tbm1115	2	(TA)22	ATTCATTGGAGGAAGAAAATGC	GTTTATGTGAAATGGAGCTCAGA
tbm1116	2	(AT)20	ACATTGTTGTTGTTGTTGAAGATG	GTTTAAAAAGTGTACCATAGATAATATCCCC
tbm1117	2	(TA)19	ACCAAAGCCTTGTGAGATCAAT	GTTTCGACAAAGACGTATCTGCACTC
tbm1118	2	(ATA)18	ATAACTCGTTTGTTCAATTGCG	GTTTAATTGTGGAGTGATCTCATTT
tbm1119	2	(TA)15	AGGTCTGAGGGTCAACTAATGA	GTTTGCCGAAATTTTCAAATAAGGAA
tbm1120	2	(AT)12(AG)10ATAG(AT)4	ATTGTGGTCATACCCAAGGACT	GTTTCAATTAGCTTTGTTAGGGG
tbm1121	2	(AT)12	ATACGGCGAGTTAGATTGAATG	GTTTCCAGTTTTTGATCCCTCTTTTG
tbm1122	2	(AT)19	ATATCAGAAAAGAAGGCATGAA	GTTTGAGAGGTACAAAATAAGTGCAAAAA
tbm1123	2	(AT)15	ACGAATTATACAAATCATTGCC	GTTTGAGAAAAGGAGGAGAGAGGC
tbm1124	2	(AT)11	ACACTTTGTCCAATTTTTCATCT	GTTTCCGAATTTGGTGACATTTA
tbm1125	2	(TA)31T(TG)7TATAT(AC)5	ATTCGCACACACATTTTCTCTC	GTTTCTTTTCTTTCCAGATCTCGCTTG
tbm1126	2	(TA)12(GA)11	ATCATGCATCAACCGTTTTACT	GTTTGGCCATGAAGTTTTGAGT
tbm1127	3	(TA)28	ATAAATGTTTCCAAAAGAGAGAAAA	GTTTAAACTTGCAGTAGGGGTCCTC
tbm1128	3	(AT)27	ACAATAATAGTGTTTTCGATCCC	GTTTGAAGTGTTAATCATCCAATTCCA
tbm1129	3	(AT)23	AGAACGTTGCAACTTAAAAGGG	GTTTGAAGACGGAGAAGAGAGGAG
tbm1130	3	(AT)20	AGTTCAATCCTAATTCATTTCAGC	GTTTCACTCAAAAGTAGCTTGGGC
tbm1131	3	(TA)12	ATACTCGCAGCCGTTACTACTC	GTTTATCTTTGGACAGCCCATTCTT
tbm1132	3	(TC)11	ATAGATGGCAATTTCAAAGCAT	GTTTCTTTTGTGTGCGTGCATTTTT
tbm1133	3	(AT)10	AGCTACGTGGAACGAATCATCT	GTTTGCAGTTGTGATGCAATAACCAT
tbm1134	3	(TA)12	ATAATTTGATCGAACAGACGTG	GTTTGCATAATCATCCCGTAAAGAA
tbm1135	3	(AT)12	ATACTACGAGTCTTCTTATGCTATGTC	GTTTGCATGAGTACACAATATCCAAA
tbm1136	3	(AT)17(AC)5	ACAACATTAAAAGGAAAACAAAGAA	GTTTCTTTTCATGTTCAGTCGTGATTTC
tbm1137	3	(AT)11	ACAAGTTCAGGCAGGAGAAATC	GTTTGAGTTCAACATTTCAAATAGCA
tbm1138	3	(AT)25	ACAAACATAAGGGGCAATCTCT	GTTTGCAATGATGGAAACAATTTA
tbm1139	3	(TA)28	ATAGGGCGGATCCATCTTTAGT	GTTTCTTTTTCGTCACACCTTCACC
tbm1140	3	(TA)27	AGGAAATAAACCAAAATGAGAAGA	GTTTAGCAGCAATCAGAAAATGGG
tbm1141	3	(AT)26	ACGGTCAGTAGAAACCAACCAT	GTTTCCACCTATGGACCGTAGAA
tbm1142	3	(AT)25	ACAATTCAATAAAGCTCCAAGTG	GTTTGCCTCTTGAATTCCAAATGAGT
tbm1143	3	(TC)11(TA)24	ACTCCTTTCTTTAGGTGACCCC	GTTTCTTCTTGCAGGTTTTGAAC
tbm1144	3	(AT)23	ACATCTAAACCTAGAAACCACAACA	GTTTCATGGAAGAAATGAGTGAAAAA
tbm1145	3	(AT)23	AGCACTTGAGTATGGTGTACTGG	GTTTCACTAGATCACTTTGTCACATGC
tbm1146	3	(TA)16	ATACCTAGTGATGTTTTGGTTGA	GTTTGGAAGGAAACAATGTATCTATGG
tbm1147	3	(TA)14	ACCATTGTAATTAACTAATGCGTG	GTTTGCCAGAAATCTCTCCTCAAC
tbm1148	3	(TA)13	AGTTGACACCCAATTTTGACTC	GTTTCAGCGAAATCTTTTTGAGATGA
tbm1149	3	(AC)7AAAAA(AC)11(AT)5	AGATATCAAGTATACATAGACCCTTCG	GTTTGATGTGTGGGTTATGTCCAAT
tbm1150	3	(TA)27	ATTTACTTGACGGAGCTCGATT	GTTTGCCACATCACCTTGTCTATG
tbm1151	3	(AT)21	ACGTGACGTAGTGTATTCGACC	GTTTGAGGCCCTACCATATTGACTT
tbm1152	3	(AT)36	ATTATCCCCTCCTTGTATGCAC	GTTTGAAAGAAAAGATGCCCAAACAC
tbm1153	3	(AT)14	ATAATATCTCGATTCTTGCGCT	GTTTGAGTGAACTCTTTTTATGATTTGG
tbm1154	3	(TA)12	ATGTTAATCTGTGACGATGCCA	GTTTGTACAAAATTCATGCGAGTCC

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1155	3	(TA)11	ATAATATTGTCATCTTTTTCGAATG	GTTTAAATCCTACCGACAAAGGCTG
tbm1156	3	(AT)10	AGCTGCTGCAACTACCTAACTC	GTTTGCAAGTGGTACTCTTCCTTGTTG
tbm1157	3	(AT)34	ATACTAGGCAAGGAAAGATTGG	GTTTCCCTCTATGAGATCTCGCTCAC
tbm1158	3	(AT)32	ACCAAAAACACTTACGAAAGTTAGAA	GTTTGATTAGAGTTGTTGGTGGAA
tbm1159	3	(ATAC)5(AT)30	ATTGTTTTATTTAGTTGGCATTGAA	GTTTGGTTGCGAAAAATAAGGAGA
tbm1160	3	(TA)26	ACAGAGAGTTGGGAGAAATGAA	GTTTGTGTAAAGCAAGAGAGAGATTCAA
tbm1161	3	(AT)25	AGATTTATGGTTTGGTTCGATT	GTTTGGGTAACCACATTTGTTCCACT
tbm1162	3	(TA)23	ATTTAAGTGGCTACACGTGAAAGT	GTTTAACTTTTGAAGTAGAGGCTTTCCA
tbm1163	3	(TA)17	ATAATCAAAGCATGAGTTCACC	GTTTCAAAGCTCAGAAGTTTTGCC
tbm1164	3	(TA)16	ATGAATGTGATAGCAAAGCCAA	GTTTGGTGGGGACTTGTAAAGGATA
tbm1165	3	(AT)6(GT)15	AGGTTCAACCGATCTCAATAAA	GTTTCAGAGGCCTATCCTGAATTTTG
tbm1166	3	(AT)15	AGTTTGTATGTGTATAATTCGCC	GTTTAGGTGAATTGTGTGTGTGTGTG
tbm1167	3	(AT)27	ACTTCTAGACTCTCCTCTGTTTTCAA	GTTTGAGGTGAGACGTTCTGTAA
tbm1168	3	(TA)11	ACAATTCATAGAGTAAATTGAAGCTC	GTTTCTTTTCAAATTTTCTAAGTTTTTCGG
tbm1169	3	(TA)10	AGTGGAGTCGGTTAAGGAGATT	GTTTCCAACTCATTGTTAAGAGCTCAAG
tbm1170	3	(TA)18	ACCATTCCTACACTTCGCTTAG	GTTTCATGTTGAAAGCATCACCTTC
tbm1171	3	(TA)15	AGCTCTGTTTTTCTTTTGTCTTTC	GTTTCTAAGTTGGTGGAGTCATTGC
tbm1172	3	(AT)28	AGTAAGCGAACAAAGTCACTCA	GTTTAAAAACCTAGAGATGGGTTCAAT
tbm1173	3	(AT)24	AGGAGTGTGTTATACGTCAGCA	GTTTCGGGGTGTGGTTAAAGAAGAT
tbm1174	3	(AG)14	ATGTCTGATTCAATGCTGGGTT	GTTTGCATGCTCATTTTCAAGCATAG
tbm1175	3	(TA)10	AGGTTTATTTCAATGCTCACAA	GTTTGCCACACTCAAAACACACAAAT
tbm1176	3	(CT)10	ATGAGTGAAGTGGGTGAAAACC	GTTTAACTAGGCGATTAGACGAGGTG
tbm1177	3	(AT)21G(TA)11	ATCCAACTTCTTGTACTGGTGC	GTTTCCAACTTACTGGGCATATTGA
tbm1178	3	(TA)18	AGGTAAAACTTACTCACGGGCG	GTTTGGAGAGGAAAATCAATGAGTAACAA
tbm1179	3	(AT)17(TTAT)6TTT(TA)8	ATCTAACCTCACGTCCTCTGCT	GTTTGTGATTGAAACTGCTATATTTGTCA
tbm1180	3	(AT)15	ATCGTATCCTCATTCATTCGTG	GTTTCCCAATTAATTTCGCTTAGCTG
tbm1181	3	(TA)16	ATCTTAGATGGACAATTTTACTAACCA	GTTTAACGGATTATACAATTAGTTTCTTTGT
tbm1182	3	(AT)11	ACACCCGTACATGCAAATATAA	GTTTGAGTTGGTGAGGCACATGTAAA
tbm1183	3	(AG)15	ATGGCTTGACCAAGCTAAACAC	GTTTCTCTTTTGTCAATCCCAGGT
tbm1184	3	(AT)13	ATTAGTGGGTGTCGACGTGTAG	GTTTCGAATTCGAACTTGGAACTTAGTAAC
tbm1185	3	(TC)10	ATGCAAGTGGTTCTTGTGGTTT	GTTTAATGATGGCCATTGAGAGG
tbm1186	3	(GT)7(AT)7G(TA)10	AGCCAAAAGCTAGTCTATTCCA	GTTTAACCCTTTACTCTGAACCACCA
tbm1187	4	(AT)22	ACCCTTAAATTGAACTTCCTGA	GTTTGCGAATCCGACACATACCTATT
tbm1188	4	(AT)16	ATCTAATGAAACCAGGGCGAAT	GTTTCTAGAGTCGGTTCCGATAA
tbm1189	4	(TA)13	ATAAAAAGTAGGATGGGCTTGC	GTTTGAGATTTGCATACACTTGAATAAGA
tbm1190	4	(AT)32	ACATCAAAACGAAGTGAAAGGG	GTTTATCCTATCTTGCCAAACCA
tbm1191	4	(AT)22	ATATGAGCCAATTTCACAACGA	GTTTGCCAAACCACTTACCAATATG
tbm1192	4	(AT)18	ATGAAAGAATATAGGGGCGGTT	GTTTAAATTGGTGCTTGACTTGGATT
tbm1193	4	(ATT)6(AT)17	ATGAGAAATGTGACAACACAAAAA	GTTTGCAAAACTGTGACAGAGTGA
tbm1194	4	(AT)16	ACAAAGGCAAATTAAAGGATCA	GTTTGCATTTTCTCGTTCTTTGCTA
tbm1195	4	(AT)15	ATGAAAATGCATCAAATGCAAA	GTTTCGTTATAAGGGTCAGGATTGG
tbm1196	4	(TAA)13	AGCAAAAGGAATACTCATAAATGC	GTTTGCAGTGTGTCTAGTGTGGAGGA
tbm1197	4	(TC)11	AGGTTGGATATGCACTGTTTTC	GTTTCCCTGTCCATTTCTTCTTCA
tbm1198	4	(CG)4(CA)10(TA)4	ATATGGCTTCCTTCACTTTAGG	GTTTCCGATGAAAATTACTGATATTGG
tbm1199	4	(GA)10	ACCAGCTCAGCTTCAAGTTTAT	GTTTGGTGTCGTAACTTGCATTGT
tbm1200	4	(AT)35	ATATGTGATCGATGATATGTGTACT	GTTTGTCACCAAAAATCAAACGAAG
tbm1201	4	(TC)11(TA)23(CA)6C(GT)7	ATGCTCATTCAATACTCTTTTTGC	GTTTACAAAACATCAAAAACAACCCC
tbm1202	4	(TA)4TGTA(AT)23	AGAGAGCAATCTCTTCCAAATTC	GTTTAAAAATAAGGGGTGTCAATGGTT
tbm1203	4	(AT)21	AGATGTTCTTTGGGATTCCTTT	GTTTCAATTAGTAATGTCTTTCCAACTTC
tbm1204	4	(AT)15	ATGGGGCTATTTAATTGATGAGA	GTTTGAGGTGTAGAATTGGAAACTTTTGA
tbm1205	4	(AT)14	ATGTTATGTTACGCTCATCGAA	GTTTGAATAACCCATTCCACTTGTTT
tbm1206	4	(AT)12	AGCCACATTAATCTAGAAAAAGCA	GTTTAAATGTGGACAACGAAGAGTCA
tbm1207	4	(AT)11	ATGTCCAAACGGTCTCCATAAT	GTTTGAAACTCAATAGTGCTTCACCA
tbm1208	4	(CA)10	ATGGTTGGTATTCATGGTTCCT	GTTTCAAGGGGAAAGAAAACACAGTT
tbm1209	4	(AT)10	ACTGTTCGAAACATGAATCACT	GTTTCTATTGTCTAAGCGTCGTGGA
tbm1210	4	(AT)28	ATAGGTTGTAACCGCTTTGATG	GTTTACGTCACATTCAATGCCTTC
tbm1211	4	(AT)27	ATTAGTATGCAACATTTGGGGG	GTTTCTTTTGCACCTACAAAATTCC
tbm1212	4	(AT)21	ATTATGGTCCCTACTATGCATGAC	GTTTCTCTTCTACGACCAGCAACT
tbm1213	4	(TA)19TG(TA)9	AGAGTTTGTCGTGGTTCCTAAC	GTTTCTTTTGATTTGGGTGTTTGAA
tbm1214	4	(AC)18(AT)6	ATCACAAAATGAGACCTCGCAC	GTTTCAATACCATGCCTTCACTCTCA
tbm1215	4	(TCT)8(TAT)4TAATT(TTA)15	ACGCAAGATTGATCTTCAACCA	GTTTAGAACGAGAAGGAGAACGAGTG
tbm1216	4	(TA)10TG(TA)7(TGTA)4(TA)4	AGTGATTCCCAAAGGATTTAGA	GTTTGTTATTTAAACCACACTATTGGTC
tbm1217	4	(TA)30	ATTTAACCTGCATCCATTCAAC	GTTTATATTGTCGGAGTGGTTGGC
tbm1218	4	(AT)25	ACGCTCGCCAAATATACAAATA	GTTTAGAGGCGAGAGAGAGAAGACAA
tbm1219	4	(TA)22	ACATGTCACCCAATGTAAACAC	GTTTGGCACATAGTTTATGGGA
tbm1220	4	(AT)22	ATTACATGTTTTTCCCAATGAAA	GTTTGGACCCTTTGAAGAGTTTGTTG
tbm1221	4	(TC)14	ACATAAGCCCTTGTTGCTTTAC	GTTTGGACGGGGTTTAGAGTTTTA
tbm1222	4	(TA)35	ACTCCCTAAATCTAAATCTGTATGGT	GTTTGGCATGCCGTACATTAACATAA
tbm1223	4	(AAT)19	ATGCAATGCCATTAATGAAACG	GTTTCGACACGTATTTCAATCTTTCAA
tbm1224	4	(AT)18	AGTTGGGAAACATCAAACCATA	GTTTCGACCCTTTATTGTCCTCATTC
tbm1225	4	(TA)16	ATAGTTCAGCCACATCCCAGTT	GTTTGGATTACCCCACTGGTATCTCA
tbm1226	4	(TA)15	AGGGCTGAGAGTGAGAGAAGTG	GTTTGGTTAGTCGTCTCGCTGTTTA
tbm1227	4	(TC)5C(CT)12	ATAGGACAAGTGGAAAAATGGG	GTTTGGGGTTTGGAGTTTTCTAATC
tbm1228	4	(TC)10	ATTACAGGATCGCTTTGGCTCT	GTTTCAAAAGGCAACCTCGAGTAA
tbm1229	4	(GTT)33	ATAAAGATCAAAATTTTACGGTGG	GTTTCACATGTATTTCACGGATCCAA
tbm1230	4	(AT)29	AGAAGAAAAATTCCCTTTCCAA	GTTTGAATTCATAGTTGAGTGACATTTTGA
tbm1231	4	(AT)24	AGAGGAATATATCGGCTTCAAA	GTTTACGGGACTTGAAAGGAGTA
tbm1232	4	(AT)20	ACATCTTTTCCCTCTTTCTTTTACA	GTTTCAAAACTTCAATTAATACATGATGAG
tbm1233	4	(TA)17	AGTCAAGGAAGATGAAATGCTG	GTTTGTACCACTCATCAAAGGACC
tbm1234	4	(TA)10	ATTCCTCTCTCTCCAAGTTTCG	GTTTAGAATTCCCAAATGAATCCTCA
tbm1235	4	(TAT)10	ATGTTCGTGTTTATTGTTGCAT	GTTTCCCATGTATTCCCTTATTAGGTT
tbm1236	4	(AT)43	ATCAGAAACTTGGTCACTGCTG	GTTTCGGAGGGTGTTAGATGACAATA
tbm1237	4	(AT)38	ATTGAAATGATTTAAGTTTGGGAA	GTTTGGTGAAGTAGCATTTGTACGC
tbm1238	4	(AT)31	ATTTTCAACTATTGAGTGGCGA	GTTTGTGATTTCTGTCATTTGTCCA
tbm1239	4	(AT)30	ATAATAAATATAATTGACCAGAGGCAT	GTTTCATGTCTATATGATGGATTTGATACA
tbm1240	4	(AT)27	ACAAATAGGCCATATACATCACTTC	GTTTAGCCTTGTGCATGTTGTG
tbm1241	4	(AT)26	ATTCTCCATTGGTCAATTATTTCAT	GTTTCAGTGCTCTAGCTCAAAATCTC
tbm1242	4	(TA)25	ACCAAGTCTCGCTTATGGTTTA	GTTTACCATCTTTTGCCTCTGGTT
tbm1243	4	(AT)19	AGCTTCGTTCGTCTCAATTTAT	GTTTAGCTGAATGGTAGCCTGA
tbm1244	4	(AT)18	ACAAATCCATCATATAGACATGAAA	GTTTGAATGAGAACCAAACAATTCG
tbm1245	4	(AT)17	ATTTGAGTGCATCTCCTCTACG	GTTTCTTTTTAGGGCTGAAAATCGTTA
tbm1246	4	(TA)39	ATATGAGCTCCGAACACTGGAT	GTTTCTGTCGTGATCCAAAGCTAA
tbm1247	4	(TA)11	AGGGGTGGACATAATCTTGAAT	GTTTCAGCTGTAAGGGCTGTTTCTTT
tbm1248	4	(AG)11	ACACACACTCACTCACACACAC	GTTTGGGCTGTTTGTACTGCTTTCTT
tbm1249	4	(TA)11	ATTCTAGCACCTCGGACTCTTG	GTTTCAAACTAATGTGAAGAAAAATGCC
tbm1250	4	(AT)9	ATCGGATATCAGGGAAGTTTGT	GTTTGTCACAACCTACTGGCTTT
tbm1251	4	(CT)9	ATTCCTGCTCCCTTCTCCTATC	GTTTGCTTGTTGCTTTTGCAT
tbm1252	4	(AT)9	AGTCAATTAGACACAGACAACTAAACA	GTTTGGCAACCAATGGAAAATTATGT
tbm1253	4	(TA)17	ATGATTCATCAAAACTCAACTCC	GTTTCAATCAACTTCATAGTTGCCCC
tbm1254	4	(AT)14	ATGGTAGAGATTTACATCCATCG	GTTTGTAATATACTCTCCACTCCCAAA
tbm1255	4	(AC)14	AGGGACGTGGTCTTTACTCTTT	GTTTGTACACCGTATGTTTCCCCT
tbm1256	4	(AT)10	ATTTAAGCTTCTAAACGACTCAAGTG	GTTTCAACTGATCTGATCCCCAC
tbm1257	4	(AT)10	ATGTGCATGTGAATTGACACAA	GTTTGTCTATGCAGCGATTTCCTT
tbm1258	4	(TG)9(CG)4(TG)4(TA)9	AGAAAAGCAGGAAAAGAGGACC	GTTTCATTTAGGGCATTCCAAGAGT
tbm1259	4	(TA)10	ATTGTGTGTGTGCGTGTTTTAG	GTTTAAACATGGGTTTTCTTGCT

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1260	4	(TA)9	ATTAGCTACTGAATAGCGGGGA	GTTTACCAAAATGCCCTTCAATCTT
tbm1261	4	(AT)23AA(AT)4	ATCATACGATATTCTAAGGAATTGTG	GTTTGTTCGGGACACTATCATTG
tbm1262	4	(AT)19	AGGTCCATATATGACACAGACAAA	GTTTGCGTTATTGTGGAGAAATTCA
tbm1263	4	(AT)17	AGATGAAAATTGTTCACTTTCAAAT	GTTTAAAGTTGTTTCATGATCCC
tbm1264	4	(AT)4(TAT)6A(ATT)15GTTAA(TAT)4	ATAGTAAGATCGATCCCCCACA	GTTTACGACAAGGAAGACTCCAACTT
tbm1265	4	(AT)15	AGAACGGGCCTTCAATTATCTA	GTTTGTGTGATTACACTTGCCAT
tbm1266	4	(AT)13	AGATATCTTCTTTGGACATGATAGG	GTTTGCAATTTTAATGTGTCTGTGCAA
tbm1267	4	(TA)11	ATTGACACTCGATTTTGACCCT	GTTTCGATATTTATTATTCAACGAGCTTCA
tbm1268	4	(AT)11	ACATTCAGCCTTCTCTTGGAAC	GTTTGCCCCTCCAAAATACTTATGCT
tbm1269	4	(TA)10(GATA)7	AGAGATTTGACCTCGAACGTAA	GTTTGAAAGTGAGATGCTTTGTG
tbm1270	5	(AT)26	ACATACCGAGATCATGAGTCTTTT	GTTTCTTTTGCATATTTAGCCTCCA
tbm1271	5	(AT)25	AGGAGAGAAAATTTCGTGAAAAA	GTTTGACTTTTAAAATCCAGAATGTGA
tbm1272	5	(TA)22	ATATTTGCTCAATCTTTTGCCAT	GTTTGCAGCCAAATTAGTTTGAAAAA
tbm1273	5	(TA)21	ACCACAGAAACAACCTACAAAA	GTTTGAAAATCCTATAAACTGGTATGG
tbm1274	5	(AT)17	ACCAATTCAAGCAAATTTCAGA	GTTTAAATAACAACCATGCAAACAAGT
tbm1275	5	(TC)14	ACTTCTACGGAGAACGATTGAT	GTTTGCCTAGAGTTGTGCCCATTAAA
tbm1276	5	(AT)13	ATACTGCAATCCAAACGAAAAA	GTTTAAAAGGTGCTTCTCGTGC
tbm1277	5	(AT)12	ATTTAGTCTTCCCAGAATGCCA	GTTTGAAGAACGTGAACTTTGCAG
tbm1278	5	(TA)11(CA)5	ATGCGGATAACAATTTCACACA	GTTTGCCTGCAGGTCATTAAATATG
tbm1279	5	(AT)11	ACTCAAACCAGTTGAACTCACA	GTTTACACGCACGTCCTACTTCTACA
tbm1280	5	(AT)38	ATGCCACAAACAGAGAAGAAGC	GTTTGCGGATGGTCTATCAGAAAC
tbm1281	5	(AT)29	ATGAAAGCTAATTTATGTGGGG	GTTTACAGTAATATAACGGACACGATG
tbm1282	5	(AT)27	ATTGTTTACCACAAGAAGGGGT	GTTTGCAGCAAATATAAAACGAA
tbm1283	5	(TA)27	ACGGTCACCTTACAAAAGGTTC	GTTTCATCAAGTACAATGGATGACACA
tbm1284	5	(TAA)13	ATAATCCAAAATGGTTGTTGCC	GTTTGACATCTTTAAGAAGGTTCTGCG
tbm1285	5	(AT)13	ATACTGCACGAATAATAAATGTGAT	GTTTAAGCGAAATTCTTGTCCTTT
tbm1286	5	(AT)11CTCC(AT)12	ACTCACTTAGTGGGGCTTTAAT	GTTTCTTTTACTATCTGCGTTGTCAATTTTT
tbm1287	5	(TA)12	ATCCCATCTCGCAATATTCTTC	GTTTAGACACACATCCATGCCG
tbm1288	5	(AAT)12	AGTTATAATCCACCGGCATGAT	GTTTACGGTGAAAATGTAGAGACCAA
tbm1289	5	(AT)11	AGCCAATGACTAATATTTCAACTTC	GTTTACATATGAAGATGGTCTCAAAAATAA
tbm1290	5	(AT)38(AC)12	AGAGTAGGGAAGGGACTATGGC	GTTTCGAAACACGTCCTCAGAAACTA
tbm1291	5	(TA)36	ATTCAATCAATACGATGAGCCC	GTTTCACAAATTTCACTTGCAAAA
tbm1292	5	(AT)30	AGTGGGTTGAGGAAATGAATTA	GTTTGAAAGAGTTTTCCCGTTG
tbm1293	5	(TA)24	ATCGAAAAGGTAGGGTGAGGTG	GTTTCGAGTCATGCAAATTAAAACGA
tbm1294	5	(AT)15	ACCTCATCTCCATCGCTTATAC	GTTTCGAGAAAGAGATAAAAGCAAAAA
tbm1295	5	(AT)13	AGATAAAACCGTAATTCAACTTTCA	GTTTGCCGAATTCTGTTTCAGACAAG
tbm1296	5	(TA)12	ATATGAATAAGGTTTGTGCATTTT	GTTTCAACATTATTTGAGTGCTCTAGTTTGA
tbm1297	5	(TA)10	ACTCAACACATTTTGGAACAAAT	GTTTGCCAAGAAGAGTTGAAGAACCA
tbm1298	5	(AT)33	ATACGCCACATTCCACTGTTAC	GTTTGGGAATTTCTTCATGCCTTTTA
tbm1299	5	(TAA)26	AGTTTTGGAATTTTTCACCTCC	GTTTGGAAAACTTGATGGGATGATA
tbm1300	5	(ATT)22	ACAAAACTTTCCAGAAGCTGAA	GTTTAAAAGAATTCATTAGCCCACCA
tbm1301	5	(GT)7(AT)11	AGCACTGTTCATCTCTAACCAA	GTTTCGAAGAGCCAATCAAACAT
tbm1302	5	(GA)10	ATCTAGCTTCGCAATGGATTTT	GTTTGCACACCTTTCAGATGGTTT
tbm1303	5	(AT)29	ATACATGTTCTTTGAAATGGGTC	GTTTCTTTTGTTGCTTCGTCATTTCA
tbm1304	5	(TA)4TG(TA)24	ATAAATTGGGGTCTTGAAGATG	GTTTCACCTTTTTGGCTCACTTATATC
tbm1305	5	(TA)19	ATCCATGTTGTGTGTGTGTTGT	GTTTGCACAATATCCACCTCATTTT
tbm1306	5	(AT)41	ACATGGTGTGAATTCAATATTTTT	GTTTGCACAAATTAGCCTTTCTT
tbm1307	5	(AT)20	ATTTACAAGTTGGCCAGTCTCA	GTTTGGACATATGTTCCATCAGAAAGG
tbm1308	5	(TG)5(TA)18	ATTTCGATTTGTGTCCATTCAA	GTTTCTTTTCCCTACACAAATTCTAATTCC
tbm1309	5	(GA)15	ATGGGAAGAGAGAGAAAGGGAA	GTTTGACGTTAAACTCGGACACCTTC
tbm1310	5	(TA)15	ATTCATCCTTTTCACATTCTCA	GTTTGTTCTCAAAGACCATAAATACCTT
tbm1311	5	(AT)15	AGTACGTGTACGCTTTGCCTAT	GTTTCACCTCTTTGAACATAGAAGGTAAGA
tbm1312	5	(TA)13	ACTTTTTCTCAAGAAGCAGAAAGTA	GTTTCGTCGACCAAGACAGTTT
tbm1313	5	(TA)13	AGTGCATCCTCGTACGTTCTTT	GTTTCTTTTTGATATGTTCGATAATTTTCAC
tbm1314	5	(AT)12	ACAAATTACATGGTCAAACACC	GTTTGCAACTACTGCAACTTTTT
tbm1315	5	(TG)4(TA)7(CA)11(TA)8	ATGTGTGATGAACGAACGAGAT	GTTTCGCTCAGGTGTCATTTCTTTAC
tbm1316	5	(TA)37	ATTGCACAATATCAAATATGACCA	GTTTGATGTTCAGTAAAATTTGAAGGG
tbm1317	5	(AT)35	ATGCACATAGAGGCAGAGCTAA	GTTTCTCAGGTTCGAAAATCTGGT
tbm1318	5	(AT)28GT(AC)6	AGACGGACTTACCAATGTTGTC	GTTTCACCATTTTCCACACTGTCACT
tbm1319	5	(TA)26	ATGAACCCATGCATTACAAGAA	GTTTCAATCAAATCAATGATCCA
tbm1320	5	(AT)22(AG)19	AGAAAGGATTATTTAGCCGTTTTT	GTTTCCCTTCACACTTCAAAATCAA
tbm1321	5	(TA)21	ACAACAGCCATGTAGTGACCTG	GTTTAGGTGTGTAGTAGCTGGGGAAG
tbm1322	5	(TA)17	AGGATAAATATTTGACGTGGCA	GTTTGGCCTCTTTAGACTTGAGGA
tbm1323	5	(TA)15	ATCATGGTCAAACTGACCTTAAA	GTTTACCATGTTACCATGTTTGGC
tbm1324	5	(AT)15	ATTTTAATTTGTACCCCGGAGC	GTTTGAGCGGATAACAATTTCACACA
tbm1325	5	(CT)4CACT(CA)4(CT)14(AT)14	AGTGAATAAATATTTCTGGCAAATG	GTTTGGAATGTATTGACGTTTGA
tbm1326	5	(AT)34	ATGGCTCGTCTTAGTCCTCAAA	GTTTCAGACTGAAAAGCAAAAGAGG
tbm1327	5	(AT)31	ATCCCCACACTTACGCTAGAGA	GTTTGCAGAATCTTCGTTGATGACAA
tbm1328	5	(TA)14	AGTGACGTCCATTTGAGACTATG	GTTTGAGGACTAAGACGAGCC
tbm1329	5	(TA)12	ATTGGACTTGGACCTTCTCAAA	GTTTGGTTCGTTTTATCCAAAAATCA
tbm1330	5	(AAT)14	ATTCTTGTAAGTTGGGACCACA	GTTTGAGACCGACCATTACAAACAA
tbm1331	5	(AT)8AAAA(AT)11	AGAACAGGGAAATAAAAGGAAAA	GTTTCCCTACTCTATATTTGCAATGGG
tbm1332	5	(AT)10	ATGAGGAAGATGCAACCAAGAG	GTTTGCTCACTCGCTTTTTACCT
tbm1333	5	(TA)10	AGTTTTAGTGGTGGATATATTCCTTT	GTTTAGGCTTTTGCACACTCTTGTTT
tbm1334	5	(TA)35	ATCCCAAAAACTTGGGATTAGTT	GTTTGCTCAAGGTTGGAGAATATGA
tbm1335	5	(AT)33	ACCGAACTTTACCATAAATCGC	GTTTCGCTTCTATTTAATTTTATTTGTCCA
tbm1336	5	(TA)27	AGAAAAACCCAAACAGGATTCA	GTTTCGTTTTGATTGAACACAGAGG
tbm1337	5	(AT)26CTTTT(TGGG)5	ACTTTCCTCCTCCTTTTGAAT	GTTTATCACCACACTCCCTCTCC
tbm1338	5	(AAT)26	AGGACAAGCTTTAGGTGGACAT	GTTTCATTTTCCAATGGTGTCAA
tbm1339	5	(TA)25	ACTGTCCCAACTAATAAACCAACA	GTTTCAAAAATGGATAACCTTATTGAGATG
tbm1340	5	(AC)4AGA(AT)21	ATATCTCGAAATTCAAAATATGTCAA	GTTTAAATCCATGTCATGCACAAGTC
tbm1341	5	(AT)21	AGCCGAAGTTTTCTAATCCACA	GTTTAACAACATTGTATACCGTCGGG
tbm1342	5	(AT)21	ATAAGCATTATGATGAAATTAAATGAC	GTTTCTAAATACAAATCGCAACTCTTCA
tbm1343	5	(AT)19	ATCCTAGGGTTGACATTGATGG	GTTTAGCCTTTGCACATATTGTCCTT
tbm1344	6	(AT)30	ATATGCACGCAAAGGTTATTCC	GTTTCATTAGGTTTACGGCCTTGAT
tbm1345	6	(TA)25TCG(AT)4	ACACTCTTCTGTCAGCATGGTA	GTTTGGAATGTAACACCATGAGAGG
tbm1346	6	(AT)38	ACTTTTTATGGTATTTCTTATGGCAA	GTTTCTTTTGAGTAAATAATCTTTTCCGTGA
tbm1347	6	(AT)31	ATTTGCGTTTCTCAAACAAATG	GTTTGACACTTGCTGGTGTTTGTGTT
tbm1348	6	(TA)27	ACTTTGAAGTTCATGGCTGAGA	GTTTGGTCCAAATGCAGTCATGTAT
tbm1349	6	(TA)27	ATTTGCAATTCCCTTTTACACG	GTTTCTTTTCGGATTGTTCAGGTTTTT
tbm1350	6	(AT)24	ATAGAATAATGAAAATAAGCACCA	GTTTCCTACTTCGACTTTAAAACAAAAA
tbm1351	6	(AT)9(GT)22(AT)6	ATATTTGGCTTGTTTAATATGGTTT	GTTTATATGGGACAAACGTGCAAC
tbm1352	6	(AT)17	ACGGATACGTTTCGAGTCTATG	GTTTAATGATACAACCATTCACAAAAA
tbm1353	6	(TTA)17	AGAAATTCTGATTTGAGATGGC	GTTTACGTATGGGCCTACATCACA
tbm1354	6	(TA)17	ATTGCAAAATGGTGATCAAAAG	GTTTCTGATGAAGAGGAACTATTCAAG
tbm1355	6	(TTA)17	AGAAATTCTGATTTGAGATGGC	GTTTCAAAAGCAGGAACTGACCAAAT
tbm1356	6	(TA)34	AGAGTCCTCTTCAAGGCATAAT	GTTTAACCCCGAGGGTTATTACAACT
tbm1357	6	(TA)34	ATAGTGAATTGAACGAATTTGG	GTTTCACTACAGGGGCCAATCATACT
tbm1358	6	(AT)31	ATCATGTAAGCAACCACCATGT	GTTTCGCCTATGAGAGAAGACAGAA
tbm1359	6	(AT)28	ACTTTGGAATGATTTCTCACTCT	GTTTGCGCACTTGTTGTAAAATC
tbm1360	6	(TA)27	ATAACCAAACCGAATCGAGAAA	GTTTGGAGTTGGACTTAGGATTGC
tbm1361	6	(AT)22	ACTTAACAAGAATAGCAAAGCAAA	GTTTCTGTTAAAAACAGGAAAAATGTCA
tbm1362	6	(TA)21	ACGGTGTCTCTCTCTCTCTTTC	GTTTAGACTTAAGCAATCCAAGGGTG
tbm1363	6	(AT)20	ATGAATAAGCCCTTAGAGCGAA	GTTTGATTTATGTTATTTAGAAATTTGGG
tbm1364	6	(TTA)6C(ATT)10(GTT)19(ATT)6A(TAT)6	ACAAGTATATTGTCTTTTTGCCC	GTTTGAATTTTCGAAGTGTTACAATAA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1365	6	(AAT)19	ATTGAAGAGAGGATTGCGAGTT	GTTTCTGGTTTGCTTCACTTACC
tbm1366	6	(AT)24	ATTTCGGAGAACATAATAGGGG	GTTTAGGATTTCAGCTGCCTACTGAG
tbm1367	6	(AT)22	ACAAAGGCCACTAGCTCTTTCT	GTTTCTTGCCTTTTGCTTTTGAAT
tbm1368	6	(AT)20	ATGTGGGAGACAGGTAAACTGC	GTTTACAATTCGTCTTTCTCTGCCC
tbm1369	6	(AT)16	ATCACCCACAGAAGAAAGTTCC	GTTTCTTTTAAATGGTTAAGAAAGAGAGTGGA
tbm1370	6	(TA)12	ATTGCTAAGTCGCTTTCAATCA	GTTTAAACAAGCAAACGAGCA
tbm1371	6	(TC)12	ATCTGCATAAAGTTTGAATTCGT	GTTTGCCCTTTATCTTTCTCTCTCG
tbm1372	6	(TA)11	ATCATTTTGAAGCTTTCCATGTT	GTTTAAATAGTGGCATTTGACGCA
tbm1373	6	(AT)11	ATTGCTTCACCTCGATTCATAA	GTTTCAGCATGTTGGCTATTTTTGTC
tbm1374	6	(AC)10(AT)8	AGTTTTTAAACTCATTTTTCACTTTTG	GTTTGGAGTATGCAAGCTGATCTGAA
tbm1375	6	(AT)10	ACCCTGGTCTTAAGGGTGGTAT	GTTTATTTGTTGCTAGAGGCGGAC
tbm1376	6	(TA)43	ATTCTTCGACACTCACAGGTGC	GTTTGTAAGGAGTTTTTGCAACCC
tbm1377	6	(TA)38	ATAAATTTAAATGGACAAGTAATAGCC	GTTTCACGATAGGTTGGTATTTTCTGG
tbm1378	6	(AT)35(GAT)5	ATCAACTTTGAGTTTTGAATTTTTC	GTTTAACCTTGAGTACTTGAGGAGAATA
tbm1379	6	(AT)33	AGTTGGTTCCAATCGCTTATTA	GTTTCAATGTGTGTGTATGCGTG
tbm1380	6	(TA)31	ACAAAGGTGACAAGCCATGATA	GTTTACGGTTCATACCATGCAAGA
tbm1381	6	(AT)30	ATCCGGAAGGTCCATGATTAAA	GTTTGGATCAAGTGGACAGCAACAA
tbm1382	6	(TA)24	ACACGCTTCAACTTCGAGTGTA	GTTTAAAATCAGGGGTGAATTTAACG
tbm1383	6	(AT)23	AGGAAGTACCAAGTTATTGTGAAA	GTTTAAATTCTGAATCGCGAGC
tbm1384	6	(TA)22	ACGCCTAAGCAAGCTATAAAAC	GTTTGCGGAGAAAACAAAGCAAAGTA
tbm1385	6	(AT)20	AGATCAATTTTTAGATTTAACTTTCAC	GTTTGCATAGGCAGTGACAACTC
tbm1386	6	(AT)23	ACACATTAGCGGATCAAGATT	GTTTACCTCCCCTTCATTAATTCCAT
tbm1387	6	(TAA)8(TA)22	ATTTTATGTACGTTTTGTGTCATTTTT	GTTTAAATCGAAAAGGATGGATTCAA
tbm1388	6	(AT)22	ATCTCTACGTCAATAATCTCAGGG	GTTTGGGTTGATTTTGGTATTGGAGA
tbm1389	6	(AT)20	ATCCATTTCTCAAATTGGGATG	GTTTGATGTAAATAATGGGTGCGA
tbm1390	6	(AT)17G(TA)5	ATTCAAGTGGAAAATCACTGGG	GTTTCTTTCATGCATAAGTTAAAACC
tbm1391	6	(TA)17	AGAAGTTAATCAATTTTGTCCCTTT	GTTTCGATTTGGTTAATTGGTTATGTCA
tbm1392	6	(AT)17	ATTCAAAGGTTTTTATGGTCCC	GTTTAAGCATTCTTGTTTTCAACTTTTT
tbm1393	6	(AT)16	ACCTTCTGTTATAACTGCAACAA	GTTTCGAAAAGGTTTAGAAGAACCTCC
tbm1394	6	(AT)15	ATAATGTGTTGAAATTGGGTTG	GTTTCTTTTCACTTTGGAGCTTCCC
tbm1395	6	(AT)14	ATAATGAATGGAGAGGCAAGTT	GTTTGGCTAAGTGAGTGCTTTT
tbm1396	6	(TA)21	AGTGAAAATCTTCGAAACATGC	GTTTAGGCCTGCGTCGTATAGTAAAG
tbm1397	6	(AT)28	AGAAGGTGATTTTTCTTGACCA	GTTTGAAGTTTCATTGTTTGCCCT
tbm1398	6	(AT)26	ATATTGAAATCAAGCTTATCGCC	GTTTGAATGATTGGACATTTGGAC
tbm1399	6	(AT)23	AGAAGAAAAGGGATCTGAAGGG	GTTTCCAAAAACAAGTCCTTCCA
tbm1400	6	(TA)22	ATCGTGGTTTCACATTCCTCTT	GTTTCACAATATACATTTTCTTCG
tbm1401	6	(AT)22	ATGGAATGGGAATTGAAAATGA	GTTTATCAACAACTTTTGCTGTGAA
tbm1402	6	(TA)20	ATGTGAAAGTTGCCCAATTAAA	GTTTGTACTTCATGGAGGTTAGCCA
tbm1403	6	(TA)20	AGGGGACTTAACTTGCCTAACT	GTTTCTTTTCCTCACCATTCAACACAC
tbm1404	6	(TA)20	ATGCAAAGCAAGTTCCCTATCT	GTTTAAATAGCTTCTCGGTCGAATCA
tbm1405	6	(AT)18	ATTGAGTCTTCTCAAAGCGAGG	GTTTGGGTCTTTAAGCACAAAAGCAC
tbm1406	6	(AT)18	AGATGTCAAATAGCAGCGAAGT	GTTTAGCCACATGTAGTGCAGGA
tbm1407	6	(TA)22(GA)16GT(GA)7	ATGAATTTCAAACAGCCTCCTT	GTTTCCCAATGATGTTAATTTGGC
tbm1408	6	(AAAT)5(AT)30	ATGATTTTGTTGAGGCCTCTCT	GTTTAATACGCGAAAGGACCAT
tbm1409	6	(TA)29	ATTGAGAGGCGGAGTCAGTATT	GTTTGAAGTGGTAATCCTTTGGGA
tbm1410	6	(AT)27	ATCAATTTAACGAATTAATACATGTCC	GTTTCCCCTAAAATCAAGCCTAT
tbm1411	6	(AT)27	ATCAAATTATGCCCAATCGAAC	GTTTCTAGCAAAATGTGATCGTGA
tbm1412	6	(AT)20	AGTGCACGAGCTAAAATCCTTA	GTTTGTCGTAAACACCCTTGTCATC
tbm1413	6	(TA)15	ATCTAGCAAAATGTGATCGTGA	GTTTAACAAATTATGCCCAATCGAAC
tbm1414	6	(TA)15	AGCATTAAAATCAATTATAGGTCACA	GTTTGACAAAAATGTCCACAGAGC
tbm1415	6	(TA)14	ATTAGGATAAACGTGCAACGC	GTTTAAACAAAATATAACGCCGCAAG
tbm1416	6	(TA)13TG(TA)10(CA)8(TA)4	ATGAGGGAGGAGAGAGGTGAAT	GTTTACGTGGTCTGAATGTGAATTT
tbm1417	6	(AT)12	AGCCTACATGGTCAACAAACTA	GTTTGAACGTCATGTTTGCTTTTC
tbm1418	6	(TA)36	AGTAGATTATACGCACGACGAAA	GTTTGTAGGGATAAAACACGGAACA
tbm1419	6	(AT)27	AGTGCCATAACAAAGAAAATCC	GTTTCACATTATCCCTTTCCTGCAAT
tbm1420	6	(AT)26	ATTACACGCCCAAACTTTACGA	GTTTCCAATAACAATTTTTGTGTGTGA
tbm1421	6	(TA)25	ACCAAAATTGCACCATTACCAT	GTTTAGATGCAAGTCGCAAATCA
tbm1422	6	(TA)19T(TA)6	AGGATAACAATGATTCAAACAAAA	GTTTACACCAACATGCAATGGTTT
tbm1423	6	(TA)19	ATGAATGTATTAACGGGGTCCA	GTTTAGCTGGTCTTGACAATCGTG
tbm1424	6	(TA)15	AGAAGAAAAGTGAAAGAGGGGT	GTTTAACACACGCTTGACCTACAAGA
tbm1425	6	(AAT)15	ACTGAGTGCACACTATGTTTTTGA	GTTTGGAGGGATACGATTATTTGG
tbm1426	6	(TA)14	ATGCACCTTCCATCTCCTTTTA	GTTTGGTCCATGCTGCTATTAGTG
tbm1427	6	(TA)13	ATATGTTTTCCCACCAACTAGC	GTTTACAAGTATGCCATTGTCTTCA
tbm1428	7	(AT)31	ATTTGACCACTAGGCACACACT	GTTTGGAATGTGATTTAAGCCATATCAA
tbm1429	7	(AT)24	ATGTGGACCCCATTTCTATGC	GTTTGCGTTCAATATTAAGAACCTGC
tbm1430	7	(TA)21	ATTCAAATCCCAATAGAAAGTAAAAA	GTTTGCATCTCTCTTTGTTCTGACTCC
tbm1431	7	(TA)17	ATCTATTACCGATCTTTTAAGCACA	GTTTGGACAAAATGCCCTTTAATGAATA
tbm1432	7	(TA)14	ATAAGGCTTTAAATCCACAACAA	GTTTCTTTTGTTATATGGTATGGAATCTCCT
tbm1433	7	(TA)13	ATCTTGGTTTGGTTTTGGATTT	GTTTCGGTTTGGTTAATCGGTTATGT
tbm1434	7	(AT)13	ACCAATTTTGCTTTGTGTGAAC	GTTTGTGCTAACTATGGACTCGAA
tbm1435	7	(TA)13	ATCTGATCCACCGTCACTGTTA	GTTTCAAAATATTCAAATTAATGAAAGGC
tbm1436	7	(AG)11AA(AG)12	ATCTGATTTTGTTGCACACCAG	GTTTGCACTTCACCTCTCCTCTTT
tbm1437	7	(AT)12	ACCTTCACTTGGCTATCTATGG	GTTTCAACTAATTGATCCCACCA
tbm1438	7	(TA)16	ATGCAATATTCATCTAAATGTTCGG	GTTTATCCACCGTATTGCATCAT
tbm1439	7	(AT)11	ATAACTTGGATAAATCTTTGTTTCC	GTTTCGTCACTCTCCCTAATTTCG
tbm1440	7	(AT)30	ATAAGCAATAATAAGAGAAAATGGG	GTTTCATAGTCATGGTTTTCGG
tbm1441	7	(AT)28	ATAACCAAAAATGGAGCAAAGA	GTTTAAAATGTTCAGAACTTGATGGTTG
tbm1442	7	(AT)24	AGGATTGAGGTGTTGAGATTCC	GTTTCTTTTCACAAATGATCCACGA
tbm1443	7	(TA)22	ACTATCAAACGACCCCTAAGTG	GTTTCCCCAAAAGACTAAAATAACCC
tbm1444	7	(AT)19	ATGTTGATGGAATTGTTGAAAA	GTTTCCATGTAAATTTCTTCCTCCAA
tbm1445	7	(TA)17	ATTGAGTTGCATTTTGATGTGC	GTTTGGACTTAACCTACACGTGCAAT
tbm1446	7	(CT)9T(TA)12(TTA)13	AGCATATTGAGGCGACTGTTTT	GTTTGTCTCATGCTCGAGTGAC
tbm1447	7	(TA)4C(AT)5G(TA)4TG(TA)13(TGTA)6	ATGGTTTTTGAAAATCTTTAATGGA	GTTTCCAATAAGGAGTGTTTCTCTTTGA
tbm1448	7	(AT)4(AC)13	AGGCAGCAGTTAGATCAACAAT	GTTTCACTTCTTTTTGAATAATTTCTAAGCG
tbm1449	7	(AT)6TTG(AT)12	ATACCCCAACAAATTTACGAAT	GTTTCACGCTAAGGTTTTCATCCA
tbm1450	7	(TA)44	ATATCCTCCTTTCGAACTATGG	GTTTCGTAATTCCGTTGACTTTCC
tbm1451	7	(TA)37	ACATTAGGCACCAACGTCATAG	GTTTGAGGCAAGTTTTGCTTCTTCTC
tbm1452	7	(TA)36	ATGATGGAAGGTTGAAGAAGGA	GTTTGATTTCTTTGTTAAGCCGC
tbm1453	7	(AT)6(GT)33	AGCTTTGCTCAACTCAAAAGAT	GTTTGGCTAGAGAAACTCCCACAAAA
tbm1454	7	(TA)32	ATTATCCAACCTTTTCCCCCTT	GTTTGAAACGATTAGGTGGTAGC
tbm1455	7	(TA)31	ATCAAGAACAAAGGAAAACTTTGA	GTTTCCACGCTTGAATCTTCTTT
tbm1456	7	(TA)30T(TA)7	ATACGATAATTTCTCACTAAATCCC	GTTTGGCACAATCGTGAAGAGTA
tbm1457	7	(AT)29	ATTAAACTCTATGTTAGCGAGAATGA	GTTTCATGAGATGAATTATATTCTTGGAA
tbm1458	7	(AT)29	AGGATGCTATAATTTGAAGGGG	GTTTAGCTTTCAATGGTTGTCAG
tbm1459	7	(AT)25	AGATAATGGCGTGTGGAAAAAC	GTTTGCGGAGCTATAACCACTTCAAT
tbm1460	7	(AT)30	ATTTTGCCCTTCTTCTTTTGGA	GTTTCGAGTTTGAAGTAAAGTAGTCATCTG
tbm1461	7	(AT)29	ATTCAATCAGAATTTTGTGGCA	GTTTGGAAAGAACAAAAGATGAAACGA
tbm1462	7	(AT)26	AGAGGCCAAATGGTTTCAATC	GTTTCCATGTAACTATCGCCCT
tbm1463	7	(AT)24	ATCAATGTTCAATTTCTTTTACTTCA	GTTTCTTTTTCTTTTTGCTTGGTAACTCTT
tbm1464	7	(AT)23	ATCCATCCTTGATTTCCGACTT	GTTTAAATCGAAATAAATCCGCAAAA
tbm1465	7	(AT)22(AG)14(ATAG)7(AG)12	ATTTTTCCGCCAAGTTTAGAGA	GTTTCCAAATTGAATAAGTATTGTTGGAA
tbm1466	7	(AT)20	AGTCCACTACTTGACTGATTTGC	GTTTGGGTTCTTTTGGTTTTTCAACTT
tbm1467	7	(AAT)18	ACGGACATACTTATCAGGCCAT	GTTTGGAAAAGGTAGTTGGCACGTAA
tbm1468	7	(TA)18	ACCATAACCAAACCAACCATGT	GTTTGCACACTCTTTAATTTGCCAC
tbm1469	7	(AT)15AA(AT)4(AC)6	ATGAACAAAACATTAATAGTGCTACAA	GTTTATTTCTCCTCGTCTGCGAT

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1470	7	(TA)6C(AT)26	AGTGTGAAAAATTTGAAAGGTCA	GTTTGTTCGTTTACCGGGTTC
tbm1471	7	(AT)22	ACTCATCTTCTCCAGCATTGGT	GTTTCTCAGGTGCTTTTCATGTTGT
tbm1472	7	(AT)10	ACATCGTTAGCCATTTTTGTTG	GTTTCGCGTTTTAAAATGTGTTGTT
tbm1473	7	(AT)13	ATGCTAGTTTTATCTCCGGCTG	GTTTACCAATCACCATCAATTCGTTT
tbm1474	7	(TA)13	AGGCCTTCATTCGTAATTCTTC	GTTTGACTAACGCAACTACACAA
tbm1475	7	(AC)6(AT)12	ATGAATTGAAATGAGCTAAAATATGAA	GTTTGAAATTTTACAGTTTATTGAGGC
tbm1476	7	(AT)11	ATTTTAAAGTCGCTTTTGGGAA	GTTTAACTTCCCCACACCCTTAAAGT
tbm1477	7	(AT)11	ATACCTTTGGGTCGGTAACAAA	GTTTGGTTGACATTTCTTTCGACAT
tbm1478	7	(AT)32	AGAGACATTTCAATTTCGATTCA	GTTTAACCTCTAATCATGCATCAGGC
tbm1479	7	(AT)22	AGCTAGACGGAAAACCAAAATA	GTTTGGGTGCATATTCTACGTGAC
tbm1480	7	(AT)18	ATTTGAATTTCACCCCAATCAT	GTTTGATCGAAAGGAAAGACCA
tbm1481	7	(TA)18	ATATAGGTGCATGCAGATTGAA	GTTTCATCATCAATCAAATCCATCA
tbm1482	7	(AT)15	AGTGAAAGTTGGATTATTCAATAGAGA	GTTTGCAATATAAATCGCGATAAAGGA
tbm1483	7	(GT)4(AT)14	AGAATGTAGCATGTCAAAAGGA	GTTTCACTCACTCCCTGCACTAACTG
tbm1484	7	(TA)14	ATGTCTGCTCAGCATGGTTTGT	GTTTCAATCGAGTGATTGGCTAAAA
tbm1485	7	(AT)14	ACGATATCGAAAATCAACGGTC	GTTTCACAATATGACAAATAAAAATGAAACA
tbm1486	7	(AT)13	ATCCACATACATGAAATCACCTG	GTTTGAGTTTTTGGATATAGGGTGCG
tbm1487	7	(TA)11	ACATGTTTGGTGAAGCTCATGT	GTTTGACTTCAGCCTTTTGAACACT
tbm1488	7	(TA)28	ATAAGAGGGGTATTCATGTTGG	GTTTAAGGTGAAGGTCATATGCGTG
tbm1489	7	(AT)24	AGTGAAAGTTTTCTCCATGTAAGG	GTTTAACATTGACATCTCCAATGCAC
tbm1490	7	(TA)19	ATAGGTGAAGGTCATATGCGTG	GTTTCTTTTCTTGATGTTTTAAATTGAC
tbm1491	7	(AT)11	ATAGAGCTTAAGTTTTATGCATCG	GTTTCGAGCTAACTGGTTTAAGTTCA
tbm1492	7	(AT)10	ATATTTCATAAGTCAAAACATTGTCA	GTTTGAATTTCGAACACGAGTGAA
tbm1493	7	(AT)10	ATAGTGTTGGAGATTTAGCATTTT	GTTTCACCCGACAAGAGTTTTGATA
tbm1494	7	(TA)14	AGATCAAATATTTTCTAAGTTGTTCC	GTTTATGAAGCGCAATTATGCAA
tbm1495	7	(AT)31	AGTTTTGAATAACGTTAAGCTCG	GTTTGGCAAATGTGAGACATTCA
tbm1496	7	(AT)19	ATTCAATCGATTCCTTTGTGTG	GTTTGGGGGTTTGCTACTCACCTAGT
tbm1497	7	(AT)19	ATGACAATATGAATTTGACCAACA	GTTTACATTCCCTCCATTCCT
tbm1498	7	(TA)11	ATCCACAAAATTCAAATCATCG	GTTTGTTTGCTTGTGTGTTGATG
tbm1499	7	(TA)11	ATTTTTTGGTAACAATTAATTAACGAC	GTTTCGTCCATATATTGGGGTTGA
tbm1500	7	(AT)10	ATAGGGAAGCATCCAACCTAGA	GTTTCTGCATCAAAAGTCAAACCT
tbm1501	7	(AT)10	ATCCCCACAAACCTCTTTACCT	GTTTAGGGGCAATGTAGAAAAA
tbm1502	8	(AT)35	ACCGCGTTACACTAGGAACACT	GTTTGGTGAAACTAAACGAACATCG
tbm1503	8	(AT)31	ACCCTCTCTCAATCTAGCTCGT	GTTTGGGCAATTATCACAAATAGC
tbm1504	8	(TA)27	ACCTCTCCTTCCCTCTATTTCC	GTTTAAAGTGTGACCAATTCAAATCTCA
tbm1505	8	(TA)26	ATATCCGAGCAACTCTCTCATC	GTTTAAAAAGCATGTTCAAAGCAAAG
tbm1506	8	(AT)25	ACGAATAAATCTGTTTACCCTGAA	GTTTCCAACCAACATATAAACCCC
tbm1507	8	(TA)25	AGAAGTATAGAGTACAGTACCAAAGTG	GTTTCAGACACGGAGAAGTTCAAGAG
tbm1508	8	(TA)21	ATCCAAAGTTAAAATGAAACAAAAA	GTTTGAGAAAAACTTCTTGGAAGCCA
tbm1509	8	(AAAT)5(AT)18	ATTATTTACGAATTTGCCCTGA	GTTTGACAATGCAATACACAACAATCAA
tbm1510	8	(ATA)12	ATAAAGAGGGAAGGAGTATTCTTG	GTTTGGTGGAGTTGTTCATTTTT
tbm1511	8	(TA)12	ACGACCGAAAAATGGAATAGTT	GTTTCAAAATGGAGGTCAATCATCAA
tbm1512	8	(AT)35	ACTGGGAGGATTAGAAATGGGT	GTTTCGATCGATTTCGATTTTG
tbm1513	8	(AT)16	ACCCTGAGTTTAAAAAGAACGA	GTTTGGAAGCAAGTTTTGATTGTG
tbm1514	8	(AT)35	AGCACATGTGTGGTAGTGAGTA	GTTTAGACCCAAACGATGATGACTCT
tbm1515	8	(TA)21C(AT)6AC(AT)7	ATAACTCGCAGATTGTTCCTTT	GTTTGGCTATGTCAGCTCCAAAT
tbm1516	8	(AT)32	ATTTGACGAAATCAGAGTTTGAA	GTTTCTTCTCGTTGTCTGCAATAGA
tbm1517	8	(TA)27	ATAATGTTTGGGTGGTGTTCAT	GTTTCTTTTGTACATCGTAAGTCGAGTTCT
tbm1518	8	(AT)26(ACAT)6(AT)12	ACCACATCGATGCTCAATACTA	GTTTCTCAAATCACAGAATCAGTATGTTTT
tbm1519	8	(AT)26	AGAGAAGAAGGCTTTGATTTGA	GTTTGAAGTTTGATAAATAAGAAAAAGGA
tbm1520	8	(AT)26	ATACTCGACTTACGATGTACAAAA	GTTTCCAAGAGGTACAAACTAAGTGCAA
tbm1521	8	(AT)26	ATTCTATTTTACGCTCTCCATTTT	GTTTGTAGGGCCAATTCTTTCAT
tbm1522	8	(TA)25G(AC)9ATAA(AT)8(TTAT)5	AGCGTTTGTATAAAGCGAGAGA	GTTTGACGGAGAGAGATTGAGAGG
tbm1523	8	(AT)25	ATAATCTTGACCCGTTTTAGTGA	GTTTCTAATTTGAAAAAGAACTTATTGCT
tbm1524	8	(AT)24	ATTTAAAAATAGTCGGCCCGTT	GTTTCACTCCCTACGCTCACTAAA
tbm1525	8	(AT)24	ACACGTGTTTTGCACGTTAGTC	GTTTATGCCAAATATGTTTTTGTTT
tbm1526	8	(AT)45	AGGAGGGGAATATCAGAGCTAA	GTTTGTGTTGGATATCGTGTTTG
tbm1527	8	(AT)40	ATAAAATTGTCTTTGTTGCCTTC	GTTTGCTATATGTGAAAGTTGCCC
tbm1528	8	(TA)29	ATTGAGCCTGAATCCCAAATAA	GTTTGTAAGATGCCATTAGGAGGTT
tbm1529	8	(TA)28	ATAAGCCACACTAACGCAATTT	GTTTGACAAAACATAACTAATTCAAAAGGA
tbm1530	8	(TA)19	ACCTTGAACTTTCAAAAACGGT	GTTTGTCATAAGTTGGACACATGTCATT
tbm1531	8	(TA)16	ATATGGAAAGTCCGTGCTAAAC	GTTTAAGGCAAATAGGGAAGGGATTA
tbm1532	8	(TA)15	ATGAGATGTACAATCAGTGGCG	GTTTAAAATCGCGTAGAAGCCAA
tbm1533	8	(TA)14(GATA)11A(AG)5	ATACTTTTCACTTTGAAGTTCCC	GTTTGTCTGCAGTGATGAAAAATG
tbm1534	8	(TA)14	ACAAAAACAAATCTTCCGATGC	GTTTAAGTGGGAACTTCAAAGTGAAAA
tbm1535	8	(TA)14	ATGGTGTGCACAAAGACTTTCA	GTTTGAATTCCTGTTGTCAAGCATCA
tbm1536	8	(TA)14	ATGTTGAGTTGTATACATCCTTTTTCA	GTTTCGTCGAGTTCCTTATGGTTTT
tbm1537	8	(TA)30	ATGATGTGTGAAGCAAGAATTGA	GTTTAACTTTGAGCTAAGGGGTTTCC
tbm1538	8	(AT)26	ATGGAAACATACTAAATCTTCAAACA	GTTTCACTTTCCTCTAAGTGGATGGG
tbm1539	8	(AT)21	ATTCCGGGTGGAGGAAGTATTA	GTTTAAGTTGCAATTCAACCAAAA
tbm1540	8	(AT)14	ATTCCTGAAAAGCAAAATGGAG	GTTTAAAATAAACGTGCAACGCA
tbm1541	8	(TA)13	ATTCAGCTGAGTACGTCTCCCA	GTTTCTCTGAAACGAGACAGAGGAA
tbm1542	8	(AT)12	ACCAACACTAAAGTTAGGGTATGAAT	GTTTCAAGAAGGTGACAGCATCA
tbm1543	8	(TA)12	ATCTTCTATTTCCAGGGCTCAA	GTTTGGAGAAAGAGATATTGGTAA
tbm1544	8	(TAT)11TAC(TAT)6C(ATT)7	ATTTGCCTAATATTGCTTTCACTG	GTTTAGAGGTAAAACATGCAAGGCAC
tbm1545	8	(TAA)4TG(ATA)11(AGA)8	ATTTTAGAGGCATCAATATGCAA	GTTTCTTCATTTTACTTTGCTCTTTT
tbm1546	8	(AT)11	ATCCCAAAAGCTTTCCTTTCTA	GTTTGAGACTGCAGATCACTCAA
tbm1547	8	(TA)37	ATACCTTTTGTTAGGAATTTGGA	GTTTCGAGTCATAAAGTCAAACTCGAA
tbm1548	8	(TA)29	ATTCCTTCCCCTCTCAGATACA	GTTTCAATTTCAATAAGTGTTGCATCAAA
tbm1549	8	(TA)27	ATTCGAAAGCCTCTTAACTCAAA	GTTTAAGCATGTGACACGCAAT
tbm1550	8	(AT)21	ACACATGGAGTAACTGACCTCG	GTTTGAAGGGTTGGAGTCAAAATCAC
tbm1551	8	(TA)20	ACACGTGAAGTAACTGACCTGG	GTTTGAAGGGTTGGAGTCAAAATCAC
tbm1552	8	(AT)15	ATCTCTTCCAAAGCCTTCTCAA	GTTTGCTCTTCCTCTACTTCTCCG
tbm1553	8	(TA)15	ACTTGACGTAATTGTGAGACCA	GTTTGCGGTGACAACATACATTCATT
tbm1554	8	(TA)15	ACTTTGAACCATCTCAGCCATT	GTTTACCTAACGTCGGTTAAGCAATC
tbm1555	8	(AT)14	ACCCTTAATAAGATTGGAGGGT	GTTTAAGCTCAAACATGGTTGGTAGA
tbm1556	8	(CT)14	ATCGAGGACATGACATCATCAG	GTTTAAGGGGAAAGCTTCATATCCA
tbm1557	8	(AT)21	ATAACGTAGTGAGTTGTACGTTCTTG	GTTTGAGACGACGGAGAAATAAGAGA
tbm1558	8	(TA)20	ACGAAGAGGAAGAAGTAGTGCTTTA	GTTTGCGCTCCTTAATTTATTCGTT
tbm1559	8	(AT)19	ACAGTTTGGTCACTTGCAGTCT	GTTTCAGGTCCCAAGCTTAAAAA
tbm1560	8	(TC)10(TA)14	ATGTGAAATTAGTTCAGGTGCG	GTTTGGGATTATGAGGTTGGATTGAA
tbm1561	8	(GT)4(AT)13	ACTTCCTAATTTGTAATTTTGGCT	GTTTGATTGAGGTACATGCTTCCA
tbm1562	8	(AC)12(AT)5(AG)5	ATGGACAAAAGTGGTTAACTCCA	GTTTGTAGGGGTGTGCACTATTCG
tbm1563	8	(TA)12	ATAGTATTGCACCACGATTGTT	GTTTAGGCTGCAGAAGCATGAATA
tbm1564	8	(ATA)11	AGGCAAGGTGTGATATTTTTAG	GTTTGGGGTTCCAAAATGTCTAACT
tbm1565	8	(TA)10	ATAACCAACTCACCCACAACTG	GTTTAGGGTCCTTGCTAAGGTTTTCT
tbm1566	8	(TA)44	ATGGAGTTCCAAATTCAAAGGA	GTTTCTCCACTCACAATGTCGAA
tbm1567	8	(AT)32	AGTGCTATACGTACCCCCACTC	GTTTGCCGGAATTTCTTTCTTA
tbm1568	8	(AT)21	ATGCTATACGTACCCCCACTCT	GTTTCGCAAAATATGAAGCTTTG
tbm1569	8	(AT)19	ATATCGAGCCTTAGGGTGTGTT	GTTTCGGATGGATGAAAATGAGAC
tbm1570	8	(AT)15	ATTGGAATTTGTCCATCAAAGA	GTTTCCAGCTTTTAAGTTGAGTCAAACA
tbm1571	8	(AT)14(AC)6	ACATCAAGTACAGTGGATGAAACA	GTTTCTTCTTGTTCTTGGAGGCAA
tbm1572	8	(AT)14	ATGGGTTCTGAAATATGGAGGA	GTTTCAGCAAATTAGTCTGGGGAAAT
tbm1573	8	(TA)14	ATGTATAAGGCAAACGTGCAAC	GTTTGGGAGAGAGGCAAGTGATA
tbm1574	8	(AT)14	ATGAATTATGGGTTTGGTGGTG	GTTTGGCATTTTGACCCCAATTATTA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1575	8	(AT)8AC(AT)13	ATCCTCTCAGTTCGAATCAAGC	GTTTAAACTTTTCCTTTTTGCCTTTTT
tbm1576	8	(AT)12	ATTTTGGATTGACTATTGCACG	GTTTCAATCAAAACATGAATTTGCC
tbm1577	8	(AT)25	ACTTTTCGGGAACATTAAGCTA	GTTTCTTTTTCTTGTTTGATGACGG
tbm1578	8	(AT)18	ATCTTCTGATATGTATACGCCACT	GTTTGAAGAGAGGGGAAGAAACTGTG
tbm1579	8	(ATT)17	ACCATCTCTCTCTCTTTTTCCC	GTTTAGGGACCAGGTAGGTCTCCTTA
tbm1580	8	(TA)17	ACCTTCACTAAGGGTAGCTCG	GTTTAAAGGGCCTGGTTAGCAAT
tbm1581	8	(TA)15	ATCACGATTGAATGTGGTCTCT	GTTTGTACCATATGATGCCCAACTC
tbm1582	8	(AT)13(AC)5	ATCTGTTGCCTTCTTTTTGCTT	GTTTGGCAGAAAAGGAGATTCAAAGA
tbm1583	8	(TAT)13	ATATCTGGATTCACGTCGATTG	GTTTCACTCTCTTCATTTGCCA
tbm1584	8	(TTA)12	AGTTTGGTGCAAACAAAATCAT	GTTTGACACCTAAATTAGTTCATTGCTG
tbm1585	8	(AT)12	ATGCAGATCCAAAGTTTTACCC	GTTTCGTCTGGTGCATGATACTT
tbm1586	8	(CT)11(AT)7	AGTTACCAGAAACAGGTCCGTA	GTTTGGGGGTTGTCTGTCTAATCAAG
tbm1587	9	(AT)37	ACATTCAATTTTGAAATTTTCTTTC	GTTTCTTTTAAGTTTTGTGCTTCATGCTT
tbm1588	9	(AT)25	ATCCACTGAGATGTGTTTCTCAA	GTTTCTTTTGATTTTCCCTTTGTTCG
tbm1589	9	(TA)25	AGTCCTAAATATCAAATCACACAATAA	GTTTGTCATCATTATAGGTTCAATAAAAA
tbm1590	9	(TA)20	ACTCATGTAGAGTTTTGCGGAG	GTTTGGGGTTCATGTAAATTATGG
tbm1591	9	(AT)17	AGATGTTACATTAGCCATCAAAAA	GTTTGACCAAACAATGATCGTCTC
tbm1592	9	(AT)13	ACCCGTTCTCAAAATAACAATG	GTTTCCAATCCGCCATAGCTTAGTAG
tbm1593	9	(AT)13	ATCGGTTAGTGACCAAATGACA	GTTTGTGACTAGAATGGATTAGTTTTCA
tbm1594	9	(TA)10	ATGGATGTTGGAGATTTGGAGT	GTTTATGGTCCATTTTTGGATGCT
tbm1595	9	(AT)43	ATAGTTGTGGTGTAGTAGAAAGTACGA	GTTTAAAGCCGTGATCGAGAATTAGT
tbm1596	9	(AT)33	AGCGTTATAGTGTTACATTTTCAAGA	GTTTGAATCGAGAGTCTTTCGCGTAG
tbm1597	9	(AT)25	ATTCGAGTGAAAAATACAGGCA	GTTTCGCAACAATATAAAGACATGGTG
tbm1598	9	(AT)24	AGAAAGGAATCTATGCAACGGA	GTTTAAAAATCCAGAGAATTCAAGATCG
tbm1599	9	(AT)24	ATCTTCAAATGCGTTTCACACT	GTTTACCGAACGGAGGAAGTACA
tbm1600	9	(TA)22	ACACATTATCACATTGTCAACACA	GTTTGAGAAGTTGGTCTCCAAGCAAT
tbm1601	9	(AT)19A(AT)8	ACCATGGAACCTTCCGTATTAT	GTTTAGAGAGGGAGCTAAGTGGGAGT
tbm1602	9	(AC)5(TA)18	ACCTTAAGGGAAGTAGTGTCGC	GTTTAGAGATTTCGCGTGGTTAAAAA
tbm1603	9	(AT)14	ATGGCGAGCAAATTAGTCATGT	GTTTAGCTTGACCCATCATGTCA
tbm1604	9	(TA)14	AGTTCAATGTGAGATAGGATTTGA	GTTTCCTTGTCATCCTTCCTTTG
tbm1605	9	(TTA)11	AGCACGTGAAAAATTAAAATCC	GTTTCTTTTTCTCTGTCTGATCCATGTG
tbm1606	9	(AAT)10	ATTCCGTTCACTTTTACTTGTCA	GTTTAAGTTTGTGGGGAATGGAC
tbm1607	9	(TA)20	ACCCTAATATCTATTGGAGTCAGAA	GTTTGGGCCTAATAAAATTGGTTG
tbm1608	9	(TA)9TG(TA)18	ATTAATTTACAATCACACGCACG	GTTTCCTACGACTTTTTGACTATTTTT
tbm1609	9	(AT)13	ACCTCTTTACATCTATACCTTACCAAA	GTTTCGGAAAACTGTTATTAGTCAATG
tbm1610	9	(CT)11	ATTCTCTACCGTCCGATCAAAT	GTTTGTGCGAGCTACTGTGTGT
tbm1611	9	(AT)10	AGAGAAGCACATTGGGATTAGC	GTTTCCCTTACCAAATTCTTTGTTGC
tbm1612	9	(AT)10	ATTTTACGATGTGCTTCCCAAT	GTTTCAGACACTGAATTTGATGGTT
tbm1613	9	(AT)40	ATCTGATTAGCAACAATTTGGG	GTTTCTTTTTCACCGTTTCAATGTCAC
tbm1614	9	(TA)37	ATCATGCTTTATCCTCCAAATG	GTTTGTTATCAAAGTGGGACCCT
tbm1615	9	(AT)36	ATGTGTCCAACGAATTCTCACA	GTTTGTGTCAATGACTGCAGTTGAG
tbm1616	9	(TA)33	ATGATTTGAAACTTCACATTGC	GTTTGGATGTACAAATGCAACCAT
tbm1617	9	(TA)32	AGTGCACCCGATAACTATAGAAAA	GTTTAGGTTTGATGGATGGATTCTGT
tbm1618	9	(TA)31	ACATTCAACTATTCCTCCCACA	GTTTAGAGACCAGCTTGCGGCTAT
tbm1619	9	(TA)28	AGAAAAGTTTGTTTTCTTTACGG	GTTTAGAGATCGTGTGGAGGTCAAAT
tbm1620	9	(AT)27	AGTCCGAGATGGCAATAATAAA	GTTTACCGAACAAGTGAAAACCCTT
tbm1621	9	(AT)26	ATAATACAAATGTTAAACTTGATGC	GTTTGACATGATGTAAGTAGCGCGT
tbm1622	9	(AT)25	ATTGAGGGGGTACTTGGGTATT	GTTTGATATGTTGGTGTTGCTTTG
tbm1623	9	(TA)36	ATACTTTTCCCTTGATTTTCATC	GTTTCAATGTTATTGTAGGTTTCCGT
tbm1624	9	(AT)30(AGAT)10	ACGGAAAAATCAAAACTCATTG	GTTTCAAAGAAAAGAAAAAGAAGATGCC
tbm1625	9	(TA)24(CA)8	ACATGCTAAATTGTTTGGAGGT	GTTTCTCTTCAATTTTTGTGCAGC
tbm1626	9	(TC)12TT(TA)23G(AT)19	ATTTATCTTTTTGTCACATTGTATGA	GTTTCTTTTGATGTACAAATGCAACCA
tbm1627	9	(TA)23	ACATACTAATCTCGGGCACCTG	GTTTACGATGACAAAAGAGGAGCG
tbm1628	9	(AT)23	ATAGGAACCTGCTGTTTTCTCC	GTTTCAGTCCCTGATATGCAATCGTA
tbm1629	9	(AAT)16ATTG(ATA)6	ATCTTTGCGATTCTCTTCCAGT	GTTTCAATAGATGATACCCATGCAAA
tbm1630	9	(TA)13	AGACAACGAAGAAGTAGTGACG	GTTTATTGCATTGCATTTCATCC
tbm1631	9	(ATA)13	ATTTTGGCATTATTATGGAATGT	GTTTCTAAAAATCCGGGACAA
tbm1632	9	(CA)12G(AT)10	ATTGGTGAAGTCACGTAGGCAA	GTTTCACGCCATCAGATAAATAGCAA
tbm1633	9	(AT)37	ATTAAACACATTGTCAGCCCCA	GTTTAACCCGATATCAAGCCCATA
tbm1634	9	(TA)36	ATCAATGTTGATTGAAAGGATGA	GTTTAACATTGAAAGCTTCTAGGGAAA
tbm1635	9	(AT)35	AGAAACTCCCACAAATGCAATA	GTTTGGCTCTACTCAACTCGAGAAT
tbm1636	9	(TA)5T(TA)33	ATAATTTGTCTGCATGGGTTTG	GTTTAAAAATGGAAGTGGTCCAACTA
tbm1637	9	(TA)32	ACTCAGGGGAGGATCTATGTGT	GTTTGCACCAGGCGTTTACTTGTTAT
tbm1638	9	(AT)30(AG)11	ATTCGAAAAATCACAACCCTTT	GTTTCCAATCTTACTCTCTCCCCC
tbm1639	9	(AT)30	ACACACATTCATTCCTGCTGAC	GTTTGCCTCTCTTCATTTGAACCATC
tbm1640	9	(TA)28TC(TG)10	ACAGGTCGATGACAAAAATAACA	GTTTCAATTGAGGACAAAATCTCTACTACG
tbm1641	9	(TA)28	ATTTTTGGACATAGGTTGAGGG	GTTTGAACTACTTTTCAAACGGGGGT
tbm1642	9	(TA)28	ATTGGTGGGGTTTGGTATTTAT	GTTTACAACCACAATTCAACAACCAA
tbm1643	9	(AT)10	ACAGCCCAAAAACATTCTACAT	GTTTGAATTGACGAATACAATAAAGAACA
tbm1644	9	(TA)29	ACGACAAGTCAATAGTGGACAA	GTTTCCCTTCTTATGAAAAATATTGAAAAAC
tbm1645	9	(AT)25	ATACAACCATCTCATCAATGCC	GTTTCACCTTTCTAGAGACATTTGCTTTT
tbm1646	9	(TA)16	ATATAACATACATATCATGCTCCTCTT	GTTTACCAAAGAAGGAAAAATGTCA
tbm1647	9	(AT)14	ACATTGGAAACAAATTTCTGC	GTTTGGTGAAAGAAGAAGAGGTGG
tbm1648	9	(TA)13	AGACCTTGGGGTTGAAATATGA	GTTTCAACCCAACTCTTCAATCCTCT
tbm1649	9	(AT)13	ACGTCTTGCCAGATTTTTGTTT	GTTTCAAAATTAGCAGCCCTTCTTC
tbm1650	9	(AT)11	ATGAAAAGCATTCATTGCAGC	GTTTGATGTTGCTTTTTGAGTCCA
tbm1651	9	(AT)34	ACCTTCCTACCCTTTTTGGATA	GTTTCTTTTTAGAGATGGTCAAAGACACC
tbm1652	9	(TA)29	AGATTTAAAAACCTCATTAAAAGAAAA	GTTTAGATTATTTCTGTCATTTGTTGC
tbm1653	9	(AT)28	ATGGGGTAAACAAACCCAATTA	GTTTCGGTTCTTTTAGGGATTTAGGG
tbm1654	9	(AT)22G(TA)5	ACTCCAAATTTATTTCTCAATGC	GTTTGTTGAACGTTCCAAGTAAAT
tbm1655	9	(TA)19	AGTCCAAACAAACATTGTATTTATTAT	GTTTGGTGTATTTGCTCTATTTAAATTTGT
tbm1656	9	(AT)19	ACAGCTTCACGTGGTAATGATA	GTTTGGAAATAAGAAAAACATTGACG
tbm1657	9	(TA)14	AGGGCTAGTTTTTAATGTATTCG	GTTTCTTTTGTCGCAACTAAGGGAG
tbm1658	9	(AT)12	ATTTGTTGTCTTTTCATCCGTT	GTTTCAGCTCGGACCTTAATCAT
tbm1659	9	(TA)27	ATAAAATAACATCCTTCTCCGC	GTTTATGCCTTGCCAATTACCTCA
tbm1660	9	(AT)22	AGAGCTAAGTGAAAACTGTGGG	GTTTACATGAATCGCAGCAATCAA
tbm1661	9	(AT)20	ATAAGAAAGCACAATTATGGGC	GTTTGAATTAAAAGTGGTCAAGTAAAAA
tbm1662	9	(TA)18	AGTTATTCTCACACACACTCGCA	GTTTACGAAAGCTGAATGTGGAA
tbm1663	9	(GAT)16	AGAATGCATTTTATGGCTTACA	GTTTGCCTTTAGTTCACCGAGAAAAA
tbm1664	9	(AT)13	AGAATTTCGATTCAGATCTTCTAA	GTTTGGGGCTACAAATTTTTGTGTTT
tbm1665	9	(TA)10	ACCCGTGTTTTTCCTAATTTAC	GTTTCACTTGAGGGGTATATTCGTCG
tbm1666	10	(CA)9(TA)21	ATTTGCAATTCAAACATTCGAT	GTTTCCACCAAATTACCTTGACTTTGA
tbm1667	10	(AT)21	ACGATCCACGAACTTGAAAATA	GTTTCAACGCTTTAGGAAATCGTACC
tbm1668	10	(TA)16	ACATTTTGCCTGAAAAATTGGT	GTTTGGAATAATTTCTACATTATCGAATCA
tbm1669	10	(TA)14	ATTCCGTGAATTTCGTGTGTAA	GTTTCCATAAGCTATAAGCCCATCCA
tbm1670	10	(TA)11	ATGTCACCTATCATGGACAACA	GTTTAAGTCCCTTAATGGTTCGCATA
tbm1671	10	(TA)11	ATATCGTGATTTAGAATCATGTCG	GTTTCTTTTTGTATCTTTCATGCCAAA
tbm1672	10	(GA)10	ATGAAGAAAAGCCATGAATGAA	GTTTAAATCACAAAACGCGAAAA
tbm1673	10	(TA)10	ACCTTTGACCTACGTGGATTCT	GTTTCAGGAGTTTGATCCTAGGTTGG
tbm1674	10	(AT)30	ATTCCACATGAAAGTGAAAGCA	GTTTGCCGTTAGTTATGTCAAATG
tbm1675	10	(AT)20A(AT)6	ACACAATTTTCTCCCATTTGCT	GTTTCCCGCGAAACTCTTCATATTTA
tbm1676	10	(AT)29	ACCTAGAAGTTAGGGCATCCTT	GTTTGGGTTGTGACCCTAAGATTG
tbm1677	10	(AT)25	ATAGGATGTGGTTTTGGGATGT	GTTTCGTAGAATTCGTCCCCTAA
tbm1678	10	(AT)12GTATG(TA)5	AGATTTTTGTCACTTTCCTCATGT	GTTTCTTTGAGAGAGCAAAGACAA
tbm1679	10	(AT)35	ATGGTGGTCAAGTAATTGGAAA	GTTTGCATGTTTTGAAAAGAAAA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1680	10	(AT)31	ATCGAATTTCAAATCAAAGTGTAT	GTTTGCCCTACATATGAGGAGGCTAA
tbm1681	10	(TA)14TTCGT(TA)9	ATCTGCAGCTGCTGTGATACTG	GTTTGAGACTCAAACTGGGAAGGA
tbm1682	10	(AT)4TC(AT)10	AGCTAAGCACTGGATTAATGGT	GTTTGAATGAAAGAAGAAGAAAAAGACAA
tbm1683	11	(AT)29	AGAGAGGTGGCACATTACCTTC	GTTTCAAGGCGATTAAGTTGGGTAAC
tbm1684	11	(AT)28	ATGCGGATAACAATTTCACACA	GTTTAAGGCCAAATTTGAACTCTTAGG
tbm1685	11	(AT)24	ACATATGAGAGGAGAGGAAAGAAA	GTTTCAAGGCGATTAAGTTGGGTAAC
tbm1686	11	(AT)22	AGGCCAATTTTCCTTCAAGTTT	GTTTCAGTATAGGGCAAAAACTACCCA
tbm1687	11	(TA)20	ACCAAAACTTAACCCATAATGTGA	GTTTGCATGCTGTAATGTGAAGA
tbm1688	11	(AT)18	AGCATGCATAGGATTCTCTCTT	GTTTGCAAACTATGTTTTCGTCTGAA
tbm1689	11	(AT)5A(AT)4GTAC(AT)14(AC)7	ACCGCATATGACCTACACCTAT	GTTTACTCGCTCTTTTCTCTCCAA
tbm1690	11	(GT)4(AT)13	ATGCCTGCAGGTCAACTTTAAT	GTTTCAGTAAAATTTGAAGGGAAAA
tbm1691	11	(TA)13	ATACCGACCTCTTTGTGTCGAT	GTTTCGATGATCAATTTAAGGAGATTT
tbm1692	11	(AT)12	AGCAATGTCAAACATGTTCCTA	GTTTGACAAAGTCTTTAAAATAAACTTGC
tbm1693	11	(AT)37	ACAAGACCAATAATGAAAAAGGA	GTTTGAATGATTTTTAAGAAGAGGCAA
tbm1694	11	(AT)25	ATTGTTTCAAACTCCGTATGGT	GTTTCGACAATTGGTTGTTCACATCT
tbm1695	11	(TA)18	ATTGCTATTGTGTCTGTGGCAG	GTTTGCAAAAGCAAGAAAATAACACCA
tbm1696	11	(TA)11	ATGGTTCTTTGCATTTTGTTTG	GTTTATGGTTGAGCACTCTCAAAA
tbm1697	11	(TA)11	ACATATTCAATTATTCCTTTTCCCTC	GTTTGATCACATCTAGTTCGGCA
tbm1698	11	(CA)13	ATTTTATTTTCCCTTAACGCCA	GTTTGGAGTTTGACTGTATGCGGAGT
tbm1699	11	(AAT)13	AGGCTAAGGCAATCAAATCAAA	GTTTCCAATTTGAGGCAAAACAAAAT
tbm1700	11	(AC)10	AGCCGAAACCAACTATCTTAGG	GTTTCCACCTAGCGGAAGAAATACAC
tbm1701	11	(AT)33	ACTGCGATTTATACAAACAAGACAA	GTTTCCAAAAGACCTATCAACCA
tbm1702	11	(AT)17	AGAAGGTTCGATTTTTCATATTG	GTTTGCTTGATTTTTGTCGACTACG
tbm1703	11	(AT)8(TA)15	AGGAAGAAAATTGATGAAATCG	GTTTAAGACATAACGATGTGACACGA
tbm1704	11	(TA)15	AGGGGTAGGGTTCATTAAAGTC	GTTTGGAGACAAATCTCCCTTTC
tbm1705	11	(AC)7AGAG(AT)11	AGCTTCACTTGAAACATTCTCC	GTTTCTCTGAGATTTCGGGCATAG
tbm1706	11	(CT)11	ATGATTCAGATAGCAATGCGAG	GTTTAAATTCATGTCAGGCCAA
tbm1707	11	(AT)33	ACATAATGAAGTGGCATGTGTT	GTTTCCACTGCAATTCTTGTTGTTCA
tbm1708	11	(CA)12(TA)6	ACGTGACAAGTTTAATCGATGG	GTTTGCCCTATCATTCAAAAACTGGA
tbm1709	11	(AT)41	ACAAACTAAAAATTATATGATGGCAG	GTTTCAAATTTTGTTTTATTGAGTGCAG
tbm1710	11	(AT)39	ACGAAAGAACACGGAATAATTT	GTTTGCCCACAATAGAAGAATTAAGC
tbm1711	11	(AT)36	ATCTCATTTTCTCAACCATAAACC	GTTTGCGAATTAAAATATTGAGGAAA
tbm1712	11	(AT)4AG(AT)33	AGAATCATGAGTTTATCTCACTCTCA	GTTTCGAGGACATGTGTGTATCATCTT
tbm1713	11	(TA)31	ATAAAATGGAAAAGGCACAAAT	GTTTCCCTTTAATAAATGTCCGAACG
tbm1714	11	(AT)27	ATATTATTCCGTGTTCTTTCGC	GTTTGGGACAAAATTAAAATGTTTATTCAA
tbm1715	11	(TA)26	ATGTTACAATCAGTGGCCTCAA	GTTTGGAGGATGATGTTTCAAAGAA
tbm1716	11	(TA)23	AGGAATGAATCCCACAATGTAT	GTTTAGGGGAGGACCTACTTGTTTTT
tbm1717	11	(TA)23	ATGAACAAATGGGTCGTTACAG	GTTTATTTGAGATCCTGCATTGCC
tbm1718	11	(CA)22(TA)7	ATGGGTCAAAATTAGCGGAAA	GTTTGGTGATGAGATGAGACATCCT
tbm1719	11	(AT)36	ATAATCAACTAGCACGCCAAAT	GTTTGCAATGGAGTTGATCCATAA
tbm1720	11	(AT)32T(TA)4	ATGCCTAGACAGCGATTTTCTT	GTTTAAGTTGACATGTGATTATCTTCAAAAA
tbm1721	11	(TA)30	AGCTTGTTTTCAAACACTTCAA	GTTTGGAAACACTGATTATCGAACA
tbm1722	11	(TA)28	ATGTGTTCTGCACTGCTAATGA	GTTTGAAGAAAAATGTGAAAACCTCA
tbm1723	11	(TC)15(TA)27	ATGTCATTGGTCGTCCTTCTCT	GTTTGTTTCATCATTTCCATCGTC
tbm1724	11	(TA)26	ATTTGCCTATCAGTTGAATCCG	GTTTCGCTTTTCATGTAGCGATTT
tbm1725	11	(TC)5TTTC(TA)22	ATATGAAGGCCACAGAGAGGT	GTTTAAAAAGGATAAATGATCACATTTCAA
tbm1726	11	(TTATA)4(TA)22	ATTTAATATGCCAGCTTTCTTGA	GTTTCTTCTGTTGTTCGAAATCC
tbm1727	11	(TA)6(AATA)6(TA)20	ATATACGTGCAATTCCCTCGAT	GTTTGCACCTTTCAATAAGCCATAGG
tbm1728	11	(TC)16(TATC)6(TA)5(AT)10	ATGATTCAGACAAAATGAATGAACA	GTTTGGCTTTTAGCAAAGACTTTTTCTC
tbm1729	11	(TA)11	ATTTTCTGCCACGAAATATGAA	GTTTAGTTGGTGATGAGCTGAC
tbm1730	11	(TA)13	ATAATCAATCTTTGTATGTCGCTT	GTTTCTCCCTCTCTCTCCCTCTCTT
tbm1731	11	(ATA)5ATC(ATA)11	AGGGGTGATCTCATTTTTGTCT	GTTTGGTGAATAAAAATAACCAGGCA
tbm1732	11	(AT)11	ATCTTTGATGCTCTTTGGGATT	GTTTGAAACAATGAAGAAGTTGGAAA
tbm1733	11	(TG)4(TA)10	ATGACTACAAAAGCAAGGGGAA	GTTTGACTCTCTCCAACCATGTTC
tbm1734	11	(TA)36	ACAAAATCCATAACTTCAATATTTGT	GTTTACAAGCCACTGAAATGTACCCT
tbm1735	11	(AT)25	ATAACGAATCGGGACAGAACTT	GTTTAAAATCGTTTGAAATCATCATAAAT
tbm1736	11	(AT)20	ATCGTGTAAATAACTCTTCAGACAA	GTTTGAAATGAGAATCTAACCGCTTTT
tbm1737	11	(TA)17	ATTACACCCCAACCCCTAACTT	GTTTGATTTATCAATTCAGCTTTGACC
tbm1738	11	(TA)14	AGCATCAAATTTATGTGTCCCC	GTTTCCTTTGATGAAACCTTTACAGTG
tbm1739	11	(ATT)10	ATGACCATCCACATTTCTGATGT	GTTTATCCAAGCAATTCCAATCC
tbm1740	11	(ATT)14	ACGAATCTTAACGTGGAAACAA	GTTTGAACTTCGTGCCTGACTA
tbm1741	11	(AAT)11	ACGAGGAATGAAAGAAACCCTA	GTTTGGGTCCCACTTCTTACATGTTC
tbm1742	11	(TA)23	AGAAATCACGGGTGTTACAATA	GTTTGTCAATTGTCGTGAATGATGA
tbm1743	12	(AT)24	ATCACCGTTGCGGTAAATAAAT	GTTTGCTAGTATAAAAATATGAATGGTGTG
tbm1744	12	(AT)22	ATTGTGGTCCTCTGCTGAATTT	GTTTCCAAGTTCAAATCCCAAATGAT
tbm1745	12	(TA)17	ACCTGTGGAATGATTGTTAGACC	GTTTCAATCTCGTTCTTCGCTTGT
tbm1746	12	(TCT)11	ATAAATAAAAGTTTTTCCCCCG	GTTTAAATGAAATTTGGTCCACCAGT
tbm1747	12	(AT)10	ATCATTTGGGATTTGAACTTGG	GTTTGGCGTATCTAGGGTTGAGAGTG
tbm1748	12	(TA)29	ATGTACGCACAGGATAAAACCC	GTTTGGTTCTTCACAATAAAAAGATG
tbm1749	12	(TA)17	ACTCCGCTCTTTTCTCTTTGTC	GTTTGGAGGGAGAAGAGAGGT
tbm1750	12	(TA)37	AGTCTTCACTCAACGAGGTACG	GTTTCGACTTTGTCGCATTTTATTG
tbm1751	12	(AT)13(AG)11	ACCAGAATCCAGATAACCAAAC	GTTTGGTAATTCAGCTTTGCCTTCT
tbm1752	12	(AT)13	ACGATGGATTCTCCCTTTTTAG	GTTTCTTTGCATGAAATTTTGTTGA
tbm1753	12	(AT)10	AGGGTCAAATTAAGAGGGTAGC	GTTTAAAATGGCTCCACAAATGTACC
tbm1754	12	(AT)25	ATTGGTTGGATATTAGAACAAAGG	GTTTATCATTGTTGCAAAACACTCTT
tbm1755	12	(TA)4(AT)4G(TA)6TT(TA)13	ATCCTGGAAATTCTGCTGGAAC	GTTTAGAACTTGGGGAAAATGGAGA
tbm1756	12	(TA)12	ATGGATTCGAACTTGCATTGTG	GTTTCTATGTAGAAGGGTTGGGGG
tbm1757	12	(TA)27T(TA)7	ATTAATAAGCCAACACTTCGCC	GTTTGCACCGTAACACATAACACAAA
tbm1758	12	(TA)4G(AT)16	ACATGATGAGAAGGATGAATGC	GTTTCCAATTGCAAGTTAGCAAGCTC
tbm1759	12	(AT)42	ATAGGCGCAAAGAGTAAAAAGA	GTTTCACTTTATGTGCGCTTCAGTGT
tbm1760	12	(TA)42	AGGAAGAGATTGTGATTTGTGG	GTTTGAAGAAACTAAGGGAGTACCGGA
tbm1761	12	(AT)35	ATGAGAGAGAGAGAGAGAGAGAGAGAG	GTTTGCCGTGTTCTCCAACTCTA
tbm1762	12	(AT)32	ACAGTGTCGTCTTGATGGTTCT	GTTTAAAGACGCAAAGGGTAAAAAGA
tbm1763	12	(AT)31	ATATCGCGCTCAATCACATAAG	GTTTAAATGCAAATCCTTCGGTTG
tbm1764	12	(AT)28	ATTTGTTTCTTCTAATTCTTGCCA	GTTTATTGCTTTCGTCAAACGGT
tbm1765	12	(TG)8(TA)27TG(TA)9(GA)9T(AG)7	ATCATACATTTGCATGATACCTCA	GTTTCTTTTGATTACCTCTCCATCAATC
tbm1766	12	(AT)26(CT)9CA(CT)4	ACTCTCTCTCTGCGAGCACT	GTTTGGAATGTCAATGTTTGTAGTAACAAG
tbm1767	12	(TA)24	ATTGGACACAGTTTGCATGTGA	GTTTATGGACACAGTTTGCATGTGA
tbm1768	12	(AT)23(AAT)9	ATCATGCAAGGCAACAATGTAT	GTTTGTGGTCTCATCCACCTTT
tbm1769	12	(TA)28	ATACTTTCCCTCTCACCACTGA	GTTTGTCACAACACCAAACTTCG
tbm1770	12	(AT)28	AGAGCATTATTTGATGAGGCTG	GTTTAAACTTCATTACTGGCATTGGG
tbm1771	12	(TA)27	ATCGTAGCTTCTTTCACGTTGT	GTTTGAGTGGAAAAAGACGAAGCAGT
tbm1772	12	(CA)24(TA)9	AGGCGTGTTTAAGACCACAAAT	GTTTCATACATCTTTCCGTTCCC
tbm1773	12	(AT)29	AGTTGATGGTTGTCGGTTAAAG	GTTTCTTGGCTCTGCTCAACTCAT
tbm1774	12	(AT)28	ACAAATTTCAATTCTAAGGTTAAAGC	GTTTGGGTGCACGCATATTTTTATCT
tbm1775	12	(AT)24	ATATTTCGGGCATAGGTTGAGA	GTTTACTGACAAGTGACAACTAGGAATTA
tbm1776	12	(AT)20	ATTTGAGACAATTTTCCAATATTCA	GTTTGGACTTGTCTTGGTGGGATAAG
tbm1777	12	(TA)15	ATGAGCCCACGTGGTAAGTAAA	GTTTGAGCAGAGAAAGATTTGACGA
tbm1778	12	(GT)5ATT(TA)14	AGCTTGGTATATCCAATGGAAC	GTTTCCACTTCTACATTTCTTTCAACTTCA
tbm1779	12	(AC)12(AT)11	ACATTAGGCCAATTTCATCATT	GTTTCAAGATGTTACAGTCGGTGCTC
tbm1780	12	(ATA)11	AGAGATTTCGGACATAGGTTGA	GTTTGCAAGTATAAATTATGCAATTTCG
tbm1781	12	(TA)25	AGCAAGTTTGAGAAGAAAACGA	GTTTGATCAAGGTCATGTGTGC
tbm1782	12	(AT)12	ATTGCGCATTATAAGATCCGTT	GTTTCCAAATGATTGTGAAAAAGTC
tbm1783	12	(TA)37	ATGCCCACCTTTGAAGAAAATA	GTTTATACGCGTAGGAAAAGGTCC
tbm1784	12	(TA)33	ATAGATCCATTACACAGGTTAACAA	GTTTAAGGTAAAATGAAGGTAATGTGGA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1785	12	(AAT)12	ATGCAATCCTTCGCATTAATCT	GTTTGGTTAGGCACATGGTTTTC
tbm1786	12	(AT)12	ACAAAAGCATAACGAAAGGTGT	GTTTCGGGCCGTTATTTATGTGATTA
tbm1787	12	(TA)11TG(AT)4	ATAAGGCAAGTGACCGATACAT	GTTTCCTTATCATGACTTGCCACA
tbm1788	12	(TA)11	AGAGTGTACACAAACTATGCCC	GTTTCCTACATATCTCTTTACCAATTT
tbm1789	12	(TC)10(TA)9	ATGGAATCCAATCAAATGAACG	GTTTGACATTTTTGACATTATTGCTA
tbm1790	12	(TA)10(GA)9	ACCATTACCAGGGGTAGGAGTT	GTTTGGTCTTCTACATACATCAACTGAA
tbm1791	12	(TA)10	ATGTGTAAGCCTGGAAAAAGGC	GTTTGGTGGACAAGGTTTTGGTAT
tbm1792	12	(TA)10	ATCTCTATCAAACCAAACGCAA	GTTTGCTTACCAAATCATTCAAG
tbm1793	12	(AT)11	ACATTTCCCCTTGAACTCGTAA	GTTTGGGGCATATATCATTTTCCCTT
tbm1794	12	(AT)36	ATCTTCAAGCAAGATAGCTGGG	GTTTGACTCTCTCTCACACACGC
tbm1795	12	(AT)21	ATTTCGTTAGCAAATCATCTCG	GTTTACAGCTGAAACTTTGACCA
tbm1796	12	(ATA)19(AGA)10	ACAACTGTGAGGAAAATTGAAA	GTTTCTACTAATCAACACAAAGAAATCTCA
tbm1797	12	(TA)15	ACATAGGGTGAGATTTGCATGT	GTTTACCTCTTTTGGCCTTTCATGT
tbm1798	12	(AT)15	ACAACACACGTATTCGAGAACT	GTTTATGCGGCTGTAGTAAATTC
tbm1799	12	(AT)11	ATATTGAGCATTTTTAGTACCGC	GTTTCAAAAGATATTCATCGTTCACTTG
tbm1800	12	(GA)11	ATGAGAGAAGGAAAGGGAAAGG	GTTTCAGAGCTAGTTCGCCAGAAAAT
tbm1801	12	(AT)10	AGCACAGACAAAACTTACACCA	GTTTCCATTCATGATGACCTGATTTG
tbm1802	1	(TA)14(CATA)5	AGGTGTTGCATCTCTCTTGGAT	GTTTCAATCCCTTACCACTTTCAACC
tbm1803	1	(TA)13	ATCGGAATATGGCGTACTTGA	GTTTTAAAGACAATTAGAATGTTGTGA
tbm1804	1	(AT)13	ATCCACTTTTTAACTGTTGGGG	GTTTAGATGAGGATTCCAGGCAGA
tbm1805	1	(AT)11	ATTTCAATTTTCATGACTTTTTACC	GTTTCCAACAAAATAAAGTGCGTAATGA
tbm1806	1	(GAA)11	ATGATGCAGAACAATTGATAGTGA	GTTTGTTAGCCAGCTGTCCTTT
tbm1807	1	(AG)11	ATTCATGCATGTGTTTGTGTGT	GTTTACAAGCATTTTGATTGACAGAA
tbm1808	1	(TG)10	ATACATGATCATCCCAAAGGG	GTTTCACACACACACATGCACACAC
tbm1809	1	(TG)7(AG)7ATA(GT)9	AGCAACAGATGAACTCACCTCA	GTTTACACACACACACGTATGCAC
tbm1810	1	(TA)9C(AT)7	AGGCTCACAATTATGGTTATCA	GTTTAAAATCATTGTAAAACGGCAAAA
tbm1811	1	(TG)6(AG)8(TG)5(CGTG)5	AGCAAAAGATGAACTCACCTCA	GTTTCATACACACACAAACACATGC
tbm1812	1	(CAT)7(TAT)8	ATCACAATTAAGTGGATTTGCG	GTTTCACCTCATGCCTCACCTTTTA
tbm1813	1	(GT)7A(TG)4(CG)4	AGGACAACATCTTGCATAAATACC	GTTTCTCACACTCACACACATACGC
tbm1814	2	(TA)11	ATCGCAGATCAATGAGGATTTT	GTTTAGGTGTGTTTCGAGGAAAGAA
tbm1815	2	(TA)11	ATTGGCGTGCTTATAATCTCAT	GTTTAAACCCCTTGTCGAGTCAAAT
tbm1816	2	(AT)10(AG)9	ATCTCATTGTGGATGAAACACG	GTTTCCCTATGTACTGAAATTGCCA
tbm1817	2	(AT)10	ATTCGAAATTGCTGTAGTGACG	GTTTGAGAAGCTTTTACACCTGCAT
tbm1818	2	(AT)10	ATCAAGATCAAGTCAGCCACTC	GTTTAGCGATTTGGCCATTTTAGTTA
tbm1819	2	(CT)10(AC)5	ATATAGTTGGGACACGTTGCAC	GTTTGATGGTGCAAGCAAAAATAA
tbm1820	2	(AT)10	AGGAGGTTTACATAGACTCTGCAT	GTTTAGATGGTTATGAGATGGGATGA
tbm1821	2	(AT)10	ATATTCAAATTGCTTCAGCGTG	GTTTCCCATCGATAGTAAAAGGAAATCA
tbm1822	2	(GA)10	ATCAGAGGAAAGGAACAAACCA	GTTTGCATCTTTAATCTCAACCGTCC
tbm1823	2	(CT)9(AT)9G(TA)5(TGTA)4	ATGTAGTTATATACAAATTGTGCGAGG	GTTTGGTTAGAAAAATCAAATGACACA
tbm1824	3	(TA)15	ATGTCGAGAGGTGGTGAGTAGG	GTTTAAACTTGCCACTTTTCCAGC
tbm1825	3	(AT)12	AGACGATGTTCCTCTCCTCTTT	GTTTGGGTCTGTACAAGTTGGTCCTC
tbm1826	3	(AT)34	AGAACATTTTGAAGTTCTTGTGG	GTTTGCCTTATTTTTCTTTTTCGAG
tbm1827	3	(AT)25	ACAAACATAAGGGGCAATCTCT	GTTTGCAATGATGGAAACAATTTA
tbm1828	3	(AT)25	ATCAAAATTATCCAAAAGCCCA	GTTTGAATCAAAATGTGGTGATCGAA
tbm1829	3	(TA)22	ACCAAATTGAAAAATCAAATCAA	GTTTGTCTCCAACTTTATAGTGCAAAA
tbm1830	3	(TAA)19	ATCAAATGGAGGAAAAAGGGAG	GTTTCAGTTTTAACCATTGTCTGCCA
tbm1831	3	(TG)5(TA)17	ATTTCATGTTCAGTCGTGATTTC	GTTTCAACATTAAAAGGAAAACAAAGAA
tbm1832	3	(AT)17	ACCAATTCAAGCAAATTTCAGA	GTTTAAATAACAACCATGCAAACAAGT
tbm1833	3	(AT)11	ATTGAGTTCAACATTTCAAATAGCA	GTTTACAAGTTCAGGCAGGAGAAATC
tbm1834	3	(AT)10	ACAAACATAAGGGGCAATCTCT	GTTTGCAATGATGGAAACAATTTA
tbm1835	3	(TG)10(TA)7	ATTTTTTGCACTCTGGTGACAT	GTTTAACTCATTTTCGACCAACCC
tbm1836	3	(ATAC)10(AT)8	ATTGGTTTTGGGACATTGTTTC	GTTTACACACACACACACAAACGC
tbm1837	3	(TA)10	ATCTGTATACGTTATCCTCCTCAGA	GTTTACGTAACCAATCATGCAAACAG
tbm1838	3	(AT)5GTA(TG)4TA(TG)5(TA)6	AGACGACTGCCCAAAAAGAATA	GTTTAAGCTCGACCTTTCAAAATCAA
tbm1839	3	(AT)23	ATGCGTTTAAACATGAAATCGT	GTTTCAACTTTCATTTCCTTTGGA
tbm1840	3	(TA)6TGTG(TA)9	ATGCTTTTGACTCTTTACTTCCCA	GTTTCAACCAAACTCTCGAACACATC
tbm1841	3	(TA)27	ATAAACCTAGAGATGGGTTCAAT	GTTTGTAAGCGAACAAAGTCACTCA
tbm1842	3	(AT)10	AGATGATCACTTGCCTAAATGC	GTTTCTTTTTGCTATTTGCACTCCATAA
tbm1843	3	(TC)15	ATCTCTTTTGTCAATCCCAGGT	GTTTAAGGCTTGACCAAGCTAAACAC
tbm1844	4	(TC)5TT(TC)9C(CT)5	ATAAATGGATCAAAACCCAAAA	GTTTCGATAAAGTAAAAGCGTTCGGT
tbm1845	4	(TA)5(GA)5A(AG)6	ATTTCTAGTTTGTGGAGGTGCC	GTTTGCCACGAGTAAGTAAGTTTGGG
tbm1846	4	(AT)47	AGACAGGAGGGATATATTTGGC	GTTTCACACACATACCTTCCACCAAC
tbm1847	4	(ATA)6(ATT)9	AGACATGAAATCTCTTTAACTCGC	GTTTGCAAAGGTAATCCAAGTGAAGAA
tbm1848	5	(AAT)4(GAT)4(GAA)9	ACAAAATGGCACAATAACAACAG	GTTTAGAGCTTATTTGCGCGTTT
tbm1849	7	(AT)46	ATATAATAAAACGACCCACGGA	GTTTCATGTAAACTCCCTTCCACAA
tbm1850	7	(TA)12	ACCTGATTGTTGTTTGCTTCCT	GTTTATTTGTGGTTTCTTCGTCCG
tbm1851	7	(AT)11	ATTTTCGAGTTTCCGCTTATGT	GTTTGATAGAAATTTTGTGTGGCTG
tbm1852	7	(GAA)11	ATGAATTTTCATGGGGAAAGGT	GTTTCCCTTAGACACCTCAATTACGC
tbm1853	7	(AG)11	ATGAGAGAGAGGGAGAGAGGGG	GTTTCGAGATTCATGCACTTTCAGAC
tbm1854	7	(AT)5(AC)10	ACCATCATGAACTTGGATCTTT	GTTTGGTTTCATTGGTACTGGT
tbm1855	7	(TG)9(TA)8(TG)8	AGCCAGAACTAGAACCCCTTTC	GTTTCAAACTGCAAATTGTATTCCG
tbm1856	7	(AT)9A(AT)8	ATAACGTGTCATTCCACTTTGC	GTTTCAACGAGAATAATACACGTCGC
tbm1857	7	(AT)9(AC)7	ATATGAACTTCCAACAAAAGCAA	GTTTGGATTCAATGTAAAGATTTGGTCA
tbm1858	7	(CA)8TAC(AT)7	ATTGATAGTCTTGCTAGCGTGC	GTTTACCTCATTGCTTTCCAAGCTAC
tbm1859	7	(CAC)6(ACC)5(AAC)4	AGTTAACACGTTAGAACACTGAAAA	GTTTAGCTTCTGTTGTCTCCTTCCTG
tbm1860	8	(TA)24	ATAATCTGTGGCCTTCTTTTCT	GTTTACACTTGCTGATGATGTGTCG
tbm1861	8	(AT)21	ATAAGCAAAGCATTTCCCTCAT	GTTTGTGTTTGTTTGGAGTGGAA
tbm1862	8	(AT)18	AGCATGGTCAAACACCTATTTA	GTTTGTTCGATTTCAAATGATGACA
tbm1863	8	(TAA)18	ATAGCTTAGATTCGCCCTTTTT	GTTTGTTATGGAGCGCAATTATG
tbm1864	8	(AT)17	AGAACAAAAATGGTTAAACTCCA	GTTTCGAAAAACCAAACCAAATCA
tbm1865	8	(AT)17	AGATGATTAAATTAGCAAAAGCA	GTTTAACGAAAGGTTAAGATTGAACG
tbm1866	8	(TA)16	ACATGTCATTGTTTCAGTTTGA	GTTTAATTGGTTGAAGATCACGA
tbm1867	8	(TA)16	AGCAAAACATAGGTGCGATAAC	GTTTGAAAGGTCAAGATTATGAAATGA
tbm1868	8	(AT)15(AC)7	AGCATTCTTATCTCTGCCACTG	GTTTCAGAATATCCAGGGATGGTG
tbm1869	8	(AT)15	ATTTGAAATATGTAACAGAAACAAATG	GTTTCCGTCAAGTTGGACACAATAGA
tbm1870	8	(AT)14(GTAT)6	ACTCAGCGGATAATAATGGTAA	GTTTATTTCGCTTGCCTCTTTC
tbm1871	8	(AT)14TA(AT)4	AGGACAGGAGAATCCATAGAAA	GTTTCGATACATAGAAACATGAGATGGAA
tbm1872	8	(TAA)14	ATTTGCCCCATCACACTAACTT	GTTTAGAAACTCTTAGGGGATGGACC
tbm1873	8	(AC)13(AT)6(AG)7	ATCAAATCAAAGGGTATGCACC	GTTTCCCCACTCAGATATACCGAGAA
tbm1874	8	(CT)13(ATCT)4	ATACGCAAGGTCTTTTGGTTCT	GTTTAAGGACAAGTCAATTCAAACAACA
tbm1875	8	(AT)13	ATAATAATTGAAAAATTGCACAAA	GTTTCCATATTTGGTGGAAAATTATGTC
tbm1876	8	(TC)13	ATACTTCTCTCTTCTCTCTGCCG	GTTTGCTTGGAACCACATCAAATAA
tbm1877	8	(AT)12	ACCAAAACCTGTATGGATTGAC	GTTTGTGGCTAAAACATGACCAAA
tbm1878	8	(AT)12	ATAAACCCGAACACTCTTGGTA	GTTTAAGCTAGAGGCAAACAAAATGC
tbm1879	8	(AT)12	ATCCGATTTAACCTTTGAAACT	GTTTCACCGGTTATCCATTTTTCAAT
tbm1880	8	(AT)12	ACCAATTTTGCGATTTTATATTG	GTTTCCCCGCAACTGTGATTATTTAT
tbm1881	8	(TG)8(TA)11	ATCTCCTCCCTCTCCCAATATC	GTTTGAGAGGAAAGAGGGCAAAGAGT
tbm1882	8	(TA)11(CA)7	ATGAAAAATCAAAGGGTCCTCG	GTTTGGCACATGTAGCAACACATGAT
tbm1883	8	(AT)11	AGAATTTGTGACTTTGAAAGCG	GTTTGAAAGCGAAGATGAAAAAGGAA
tbm1884	8	(AT)11	ACTCCCCCTCTTATCTTTCAAT	GTTTCTTTTCCAGTTTGCTTAATCGGT
tbm1885	8	(AT)11	ATATCGAAGCCATAAAAAGGTG	GTTTGCGATCGGTTTTTGTATATGTTT
tbm1886	8	(TAA)11	ATGTACCCCTAAACTTGACGAAAA	GTTTCACCTCGTAATCCACTTCATCA
tbm1887	8	(TAT)11	ACCTTCGAACTCAATTATCTCCA	GTTTGAAGTCAATTTGTAGCCGC
tbm1888	8	(AT)11	ATGCAAAAACGGAGCTAAAATG	GTTTCCGGTTTGTTCTACCTTGTTC
tbm1889	8	(AT)10	ATTTTCTGAACCGTATGCAACA	GTTTAAAGGGATTAACCTGACACGAA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1890	8	(ATA)10	ACATAATCAAGATTTGCCAACG	GTTTAGAATTATCTGCATGTGCCCC
tbm1891	8	(TA)10	AGAGTTGATTTTGACCCTTTTC	GTTTCATGTGCGTCGTCCTATTA
tbm1892	8	(TA)10	AGAGCGAATAAATAAATTTAGCA	GTTTCCTTCAACTTTGAATGTGAATAAA
tbm1893	8	(AT)10	ACGTGATACCACTTTTGTTTGC	GTTTCTTTTTCGTGTTGGCTTGAATA
tbm1894	8	(TAA)10	AGAGCACAATTAAATCAAACCC	GTTTCCCCGTAATTAAGGAAAATCA
tbm1895	8	(AT)10	ATCCGTAAGTCCTACACAAACAA	GTTTCAAAAGCGATTTTAACCTAGCAA
tbm1896	8	(AT)8(GT)7	ACCATGATTTAAGCAAAACATTC	GTTTGAGACAAAATCAGTTACACACAAA
tbm1897	8	(CT)7CGC(CT)4(TC)4	ATCTTCTTCTCTCCCAGTCTCG	GTTTATAGGGAGGAGATAGGCG
tbm1898	8	(AC)4ATA(CT)7CGATA(TC)4	ACTTAAACTTCGTGCCAAGTCA	GTTTACCAAATCACCCAAGATTTCAT
tbm1899	8	(AT)14	ACCCCTTTGATTAACTTTCTCAC	GTTTCCCTCTTTCATGCAATATTCAAC
tbm1900	8	(AAT)14	ATCGCAGCTGTAACTCAACAAA	GTTTACATCCTTTGAATAGGCCTCAC
tbm1901	8	(TA)14	ATTTGCCTTAGTATTTTCGGGG	GTTTGCAAAATTTGGTTTAGCAT
tbm1902	8	(TA)8(GATA)13	AGATGATTAAATTTATTTACGCTTATG	GTTTGGGTAAGTTGTTGTTGATGCAG
tbm1903	8	(TA)13	ATTCGTGTATTTTCGAAGAGAAAGT	GTTTGAGGCGAAGGATGATAAGAGAA
tbm1904	8	(TA)13	ATTGATGTTCAAATGCTTGCTT	GTTTCCTCACTTTTCATGTTGCTCT
tbm1905	8	(AT)13	AGTAGAAATGGCAAGGTGTAATTTT	GTTTGAAAAAGCAAATATATCACCACA
tbm1906	8	(TA)12	ATCGAGGTGTTCAGCGTAAAAT	GTTTGCCACAACAGCAAACTAAAG
tbm1907	8	(AT)12	AGTTTCTCAGAGGCTCGGTTA	GTTTGTGTGAGAAATTTGAAAGGTCA
tbm1908	8	(TA)6(TG)11	ATCCTGAAGAGTATGCCAGACA	GTTTCTTTTGGTTTGGTCGGTTTATTC
tbm1909	8	(AT)11	AGAAACCTTAATGATGTCAATACAAA	GTTTGGGAAAACTGAGCAAATAATCC
tbm1910	8	(AT)11	ATGAAATTGCGTGTGAACTCAT	GTTTATTTGAGTTAAGAGGCTTTCG
tbm1911	8	(CA)10(TA)8	AGGTTTAGATGAACCCCCTCAT	GTTTGAAAATTCTGGTTCCGTCAT
tbm1912	8	(TA)10	ACATCAGGTGGACAAGGAAAAT	GTTTCCACTTCCGACTATGTCATCAA
tbm1913	8	(AT)9(AC)7	ATAATAATATCGGACGGAGGAA	GTTTGGGACATCAATGTTCCAAAAAT
tbm1914	10	(TA)33	ATAGCAAACAAATTAGGACAAAA	GTTTCCCAGAACACAAACAATCTACAA
tbm1915	10	(AT)6(TA)19	ATGGACCCTTTTGAGCTATTTTT	GTTTCTTTTCTCCCATTTGCTCAAC
tbm1916	10	(TA)16(TGTA)4(TA)4	ATTGGCATTCATGTTATTGGGA	GTTTCCATGTTTCTTGCCATGTGTAT
tbm1917	10	(AT)16	AGCAAAGAATAAGCTGTCTACG	GTTTAAATCATTTAGAGAGAGTTGCTTGTT
tbm1918	10	(ATT)15	ACGCACTAGGATTAGACTACCTATGTT	GTTTGGAGAGGATTGTAGAGTCCTAAGTT
tbm1919	10	(AT)11	ACGTGCTGAAGCTATTAATCCA	GTTTCCATTTCTCTTTGTTGTTGACAT
tbm1920	10	(AG)10AAAT(AG)4AA(AG)5	ACAGACTCGAAAATTCCAAAAG	GTTTAGGATGTGATGCCATTTTAACC
tbm1921	10	(AT)7C(TA)9	ACCATGTGAGGCATTTTTACAT	GTTTGGACCTCTACACACACACACA
tbm1922	11	(TA)7(GA)9	ATTTCAAGAAAAATGAGGCCAT	GTTTCATTTGAATTCTTTTCGC
tbm1923	11	(CA)7(TA)4C(AT)6	ACAAAAGGACAAGTTTTGAAGC	GTTTGGCACTTAACTAATGCCGATA
tbm1924	11	(CT)6(AT)6AC(AT)4	ACCAACCCTGTCTCTCTCTCTA	GTTTGGAACAATATGCTGATCG
tbm1925	12	(TA)7A(AAT)8	ATGTGGCGAAGAGACTACGTTA	GTTTGAGTTGCCACATTCAAAATTCA
tbm1926	12	(AT)20	AGTAAGACTTTTGAAACTTCAATCTG	GTTTGCTGACATCCTATCATCCC
tbm1927	12	(TA)11	AGTAGCTGAACAGGAGGGACAG	GTTTAGCATGCATCACCAAAAA
tbm1928	12	(AAT)11	ATTGCATGACCAAAAACATTCT	GTTTCCCTTTACCTGATGAAACCAAA
tbm1929	12	(AT)6AC(AT)9	ATTGGACCCAGCGGACTTAT	GTTTGGATATTTTGAGTTGGTGAGGG
tbm1930	12	(AT)15	ATTCAGCGATTTTGTCATTTTG	GTTTGGACTTCTGTTTTAAGCTTGC
tbm1931	12	(AAT)12	ATGCAATCCTTCGCATTAATCT	GTTTGGTTAGGCACATGGTTTTC
tbm1932	12	(AT)11	AGTGCGTCAAACTCTATTCAGA	GTTTCCCTTGCAATCAAATCAT
tbm1933	12	(TA)10	ATCTTGGGTTGTAATGGTTTCG	GTTTGAACCCTCTTGTTATGAAATTGA
tbm1934	12	(TA)10	AGTGTTCACCAGCATACAAAGA	GTTTGCACATTCAATCGAAAAAG
tbm1935	12	(TA)10	ATCTTGGGTTGTAATGGTTTCG	GTTTGAACCCTCTTGTTATGAAATTGA
tbm1936	1	(TA)24	ACGAAAGGATGAGAGAAAACCA	GTTTCCCCTCCTAATTTCTCTTGGAT
tbm1937	1	(TA)16	AGTAGAGTCTATTGTTAGGGGCAA	GTTTGCAACTCCTAAAAGGCTAAAA
tbm1938	1	(TA)18	ATCTGAGATTTCGGACATAGGC	GTTTGCATGTGATCTAACTTTTATTTGAA
tbm1939	1	(AT)18	AGTTTATTGAATCGAAACACGG	GTTTGCTATGGAGCGCAATTAT
tbm1940	1	(AT)16	AGTCTTTAACTCGCTGATTGTG	GTTTGAAGAAACACCAAAAGAGACCTG
tbm1941	1	(ATT)4(AT)19	ATGTTTGTTCATAAAGTTAGTTTCCC	GTTTGAAACTTATTTGGTTACACTACGA
tbm1942	1	(AT)18	ACGTAACTAATTTGATGTGACATTTT	GTTTGATCATGAGATGTTGAGGA
tbm1943	1	(AT)19	AGGAGGTGCTAAGTTCAAGTTT	GTTTGACACTAACACATGAGTACGAGAA
tbm1944	1	(AT)31	AGTTCTGATGGTATCAAGGAGG	GTTTCATATCCCCTATGACGAA
tbm1945	1	(AT)22	ATGGCATCCAAAGTAAGTTCCA	GTTTCAGTTAAGGGCACAATTGCATA
tbm1946	1	(AT)25	ATTGTTTCAACCCTCAATTTGG	GTTTGTTGAAATAAATAATTGGCAGA
tbm1947	1	(TG)25	AGGAATCAGTTGCCACATTTTA	GTTTGCGACAATCCCACTATATGAAA
tbm1948	1	(AT)24	ACATCAGCAATTGCCTAATTTTT	GTTTCAGCACCATGATCCAAAATAAA
tbm1949	1	(AT)24	ATTTGTTAGGTAAGTCTTGTTTTCAA	GTTTACACCCTAACCCCTTAACCTTT
tbm1950	1	(TA)24	AGGCTACATGATTTTTGTGGAG	GTTTGAAATGAAGCAAGCAAAGAAA
tbm1951	1	(TA)24	ATAACAAAGCAAAGAAAGAAGCA	GTTTGCGATTTTGGTCCTTAAAGTT
tbm1952	1	(TA)24	AGATCCACTGACCAACTCAGGT	GTTTATTTCCACATCGAAGCGTT
tbm1953	1	(AT)24	ACTATCGGGCTTGATTGATTAG	GTTTCCACTTGTCTATGGGAACCT
tbm1954	1	(TG)5(TA)6(TG)23	ATGTTTAGTGAACCCAAGTTGC	GTTTGCACATACGAACACGCACAC
tbm1955	1	(TC)17(TA)23	ACTTCGAACTCACGTAACGACA	GTTTGGGCATAGATTGAGGGGATAAT
tbm1956	1	(AT)24	AGTGGTCGTAGGTAGAATTGACA	GTTTCGACATTCAATATTAACCGACCT
tbm1957	1	(TA)24	ATATGGAACCTTTGCTCTTTGA	GTTTACCATGGTTACATAGTGCCTTT
tbm1958	1	(AT)24	ATCTCAAGTCAAGGGCAACAGA	GTTTACATACTCGTGCTTGGTGTGAC
tbm1959	1	(AT)24	ATAGTTTGCGCTCTTCCTCTCT	GTTTGTAACTTCCCCTTCTCCTTGA
tbm1960	1	(AT)26	ACTTTGCCACAACTTTTGTGTA	GTTTCGCTCCATTGTCATCTCTA
tbm1961	1	(TA)21	AGAAAACACTCTGAAACTTGGC	GTTTGGCATATATGAAATTTTCCC
tbm1962	1	(TA)21	ATTTTGTGGTGCTATTGGAGTG	GTTTGACTTTATGGTGTGAACCTACAA
tbm1963	1	(AT)24	ATACGTAATTGAGGGGCTAAAA	GTTTAAGGATGTTTTTCAATTTTGAGTTG
tbm1964	1	(AT)20	ACTTAATAAATCAAATAAGTGAAGGAA	GTTTGAACACTCTATTATCGTGTCCCT
tbm1965	1	(AT)16	ATTCTATGAATGTTTTGTTGCCA	GTTTACTAGTTTCGGATGAGCACG
tbm1966	1	(AT)18	AGATCATAATATCACATGGGGG	GTTTACCACTCCTCCCCTAAAAGAAA
tbm1967	1	(TA)16	ATGCTTTTGGGCTCATTAGTTT	GTTTCACATAAAAGGATGTTGCCAGA
tbm1968	1	(AT)18	ATTTGGGTCCATGTTAGTACGG	GTTTCATTTTCGATTTTGCGGT
tbm1969	1	(AT)23	ACACATATAGTGTAGGGTGGTTAGTCA	GTTTGCAATTTAATTCAAGCTTTCG
tbm1970	1	(AT)16	ATAGAGGGTTCTGTTGGATTTC	GTTTAGGATGTTGGAAAAGTGCTGAT
tbm1971	1	(AT)20	ACACAGCCCAAAAATTATGTGA	GTTTGGCAGTTGCGTATTAAGAAAA
tbm1972	1	(TA)23	ATTTGTTCAGGTTCGATGTTTC	GTTTCTCTCCCCAGACAAAGAAAA
tbm1973	1	(AT)14	ATCACTTCTTAAAGTCGCAGAAA	GTTTCATGCACAGCCACTACTTCTT
tbm1974	1	(TA)14	AGAAAACTTGTCATTTCTCCCA	GTTTAAACGTCAAGAACCCTAAACCA
tbm1975	1	(TA)25	ATGTTGGTGTGGAATTGAATG	GTTTCAAACACACAACTAAAATTAACGAA
tbm1976	1	(AT)24	ATTCGTATCCAGTCCAAACTCC	GTTTCCAATGGCCAATACAGAAAAAT
tbm1977	1	(AC)22	ATCTTTGAAATTGGCAGAGAGC	GTTTGAATAGATCTTCACGCACG
tbm1978	1	(TC)10(TA)15	ACTACTCTCTCTCCTTTCCCCC	GTTTCGCAATATTGGAGACACACA
tbm1979	1	(AT)14	ATTTCACTTATAAGGGGATGCAG	GTTTGCAACCACCATAATTGCTACT
tbm1980	1	(TA)23	ACTGTGACAACCGTAGTGATCG	GTTTGTGCAGAGGTACATGCAG
tbm1981	1	(GA)16	AGTTTAAACCCCAAAGGGTCAT	GTTTCCATTTCATCATCTTCTCCA
tbm1982	1	(TA)18	ATAGCCTGTCATTCCAAACATA	GTTTGTTGGCCATAAAGAAGTGTG
tbm1983	1	(GA)14	ATGCTCCAACATCATTAGTCCC	GTTTCCCCAAAGTTGTTCCTTATGT
tbm1984	1	(AAT)17	ATGAAATTCCTGCAACAACGGT	GTTTACACGTTAGGAAAGTCGCA
tbm1985	1	(TA)18	ACACACGTTTTACAAAATGACA	GTTTAAGCAATGAAAATGAAAGAGTTG
tbm1986	1	(AT)15	ATGCCCAAATAATCAAAATCCA	GTTTAAACTCAAAGATTTGGCCG
tbm1987	1	(AT)17	AGATTAGTGGTGCCATCAATTT	GTTTATACGCTGAGATAGGTGCG
tbm1988	1	(AT)17	ATGGATAGCTGCACCAGAAGAT	GTTTCAATATAGAAGCAACGCCAAGA
tbm1989	1	(AT)14	ACGGATTTAGGAGAGGAAGACC	GTTTCTAATGGATTGCTCATGG
tbm1990	1	(AT)14	ATAGTCTCGTTCTCTCCTTCGC	GTTTAGAGAGACAAGTGAGCAAGCG
tbm1991	1	(AT)22	ATCATAGTGAAGAACATATAATGCAA	GTTTAACTTGAGTGACTATTTGAGAA
tbm1992	1	(TA)20	ATACTCAAGCTCCATCACTCCA	GTTTCCAACTTCTAAGCCATCCAAAC
tbm1993	1	(AT)20	AGCATCATGCAGAAGCTAATAAT	GTTTCACATATTTCATGCATGTTCCA
tbm1994	1	(TA)19	AGTTTTTAGGCCCAAACTGACT	GTTTCATACAATATTTATATATGGGGAAA

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm1995	1	(AT)16	ACTAGCTAGGAACGTGTAGATGA	GTTTAAAAAGTATGGATTCTGCCGAC
tbm1996	1	(AT)17	ACTCTCGATCTCATTCACCAGA	GTTTGATAGATGGTGGAGAGAGGC
tbm1997	1	(TA)16	ATAGATGAGACTACACCAAATTTCC	GTTTCCGGTTAGAAGAGACTTGCGTA
tbm1998	1	(AT)17	AGTGTTCAGCGGTGAGTAGAAT	GTTTGAATCATTTTAAACTATACTCCGTCC
tbm1999	1	(AT)15	ATTTGATCCAACTCCCAAACAC	GTTTGCTCATCGAACATTCTTG
tbm2000	1	(AT)19	AGAGGTCTGCAAGTTTCACATT	GTTTCCAGAGGTCAAAGGGTGATAAA
tbm2001	1	(GA)16	AGGGAGACTTTGCTATCTCGTA	GTTTACCCAGAAGATGACATGAAGGT
tbm2002	1	(AT)16	ACCGAATTTTCTTGAACCATCT	GTTTGGAAATCAATGAAGACCTTTGG
tbm2003	1	(TA)25	ATGATTCTTACATTTTTCGCGG	GTTTAAAATCAGTCCAGCACTTGAAA
tbm2004	1	(AT)14	ACGATGTGCATTTGGTTAAATA	GTTTCCATGAAAAATTAGGACTCTGATG
tbm2005	1	(AT)20	ACGCGGCCAAAATATACTGTAA	GTTTATTGCTGCACAATCACGAC
tbm2006	1	(GT)5(AT)27	ATCTATTTGGTCAACCATTGCC	GTTTGAGTATTGGTCACGACAAGCAG
tbm2007	1	(AT)21	ACTCCACATAAACGGACCTAAG	GTTTCCCAAAACCCTAGTTTGATG
tbm2008	1	(AT)20	ATACTGGCAGAAAACAAGACTC	GTTTCCCTTTGGTAATATAATCTCAATC
tbm2009	1	(TG)17(TA)6	ATATCCGACTAATATGTTAATGTTGA	GTTTCTTTTTATACGCGAGATGTGTATG
tbm2010	1	(AT)16	ACGTTCTACAACAAACATCAGTG	GTTTGGAAATGTATCTTGAGACGAGAGG
tbm2011	1	(AT)19	ATTTGACTCGATTCGCTGACTA	GTTTAGGCCATATTAGGTCGCATTT
tbm2012	1	(TA)26	ATACTTCTACCAGCGATCTCGT	GTTTAATTTTGAGGGGATTTTCAGA
tbm2013	1	(AT)26	ATCAGAAATTTTGTAACCGCAAA	GTTTGATATTTAATGATTTGAGTGTGTCT
tbm2014	1	(TA)23	ATTGAAATGGAGGCCATAGAGA	GTTTGCTCTCAAAGTTCGTGAAG
tbm2015	1	(TA)23	AGAATGCTATATCCCCAAATGA	GTTTAAAGGAGACATGATTCTATGTGAAA
tbm2016	1	(TA)24	ACCACGTGAAATATGTGAAAAA	GTTTCCCATGTTCACTTTTGTTG
tbm2017	1	(AT)23	ACACAGAGCAATTTAAGGGATT	GTTTCTTTTGTGCTGCTAAATACCCAA
tbm2018	1	(TA)18	ATCACCTAAAGGCTAAAGTTGTAAA	GTTTAAGCAATAAAAAGATCAACTGGA
tbm2019	1	(AT)16	AGTTTGGGTAAAAATCTATAATCCTCA	GTTTCAAAATTTTAAGTTAGCGCTTT
tbm2020	1	(AT)21	ATGAATAATCATGTGCCCAGGT	GTTTGAATTCAATAAAGATGCAATGG
tbm2021	1	(AT)22	ATCTTTTCAAAAATACAACGCAAA	GTTTACCAAACGGGTCCTAAGTGTT
tbm2022	1	(TA)22	AGCATACGCATATAACATAATTTGG	GTTTAATTGACCACGTGCACTACC
tbm2023	1	(TA)21	ATTGATGCATGGTAGAATCTCA	GTTTGGGGCTAAACCCATAAAC
tbm2024	2	(TG)8(TA)16	ACTTACCTGGCTCAACCCAATA	GTTTCTTAGGTGATGGTTGTCGGT
tbm2025	2	(AT)15	ATAATGTTGAGTGGCGTATTCA	GTTTACAAAATCCGGAGGCCTAGT
tbm2026	2	(TC)12(TA)15	ATGCGAAGCAGCTACTGAAACA	GTTTGGCCTCTTTCCCTGTTTGTATT
tbm2027	2	(TA)16	AGAACAAACTATAAGCATATGGGG	GTTTAAATCGAAAAAGAAAATTCAAAACA
tbm2028	2	(AT)21	ATGGAGGATCAAAATGTACCCA	GTTTCAGAATTGATAGTTCTCGTTAGAAAA
tbm2029	2	(TA)15	AGAAGAAATAATCGAATTGGAGC	GTTTCCTAGAAGGAAGAAATCACACAA
tbm2030	2	(AT)19	ACGAAACACGAAAATTACTTTGA	GTTTCAAAATGCACCTGCTTATGAGA
tbm2031	2	(TA)25	ACCAACACACTACTGATCCACC	GTTTGAGCAACTGTTGAGAACCCTCT
tbm2032	2	(AT)14	ATTTTGTGCCAAGAAACATTTG	GTTTGTGCCACGCTTGTAAATAG
tbm2033	2	(AT)27	AGTGGCCATACTTCTTCCTTTT	GTTTGAGAGATTTGACTTTCATGACCA
tbm2034	2	(AT)17	ATATATCGCCTCCGCTTCTTTA	GTTTGTTGTGCATTGTAAAAATTGA
tbm2035	2	(TA)16	ATTTTACAAGTGATGAAGGCCA	GTTTCTGCGTTTGAGTTGTCTG
tbm2036	2	(TA)15(GTTAG)6	ATCATTTCTAACATGGGTGCAG	GTTTAAACTAAACCGTAAACCTAAACCG
tbm2037	2	(AT)14	ACTAAAACGCGCACTTCAACTA	GTTTAGGCATTTTCCAGTGTCAAAGT
tbm2038	2	(AT)14	ATAGGACCTCCATTTCAGGAGA	GTTTGAACAGGTCCTCAGACTT
tbm2039	2	(AT)17	ATTTGACAGACATTTCTTGAGGA	GTTTGGAACAGAAATTGAAAAGGA
tbm2040	2	(AT)14	ATTGAAACGCACAAGACAAGAG	GTTTGACTAAACGAATTGCGAAGAAAA
tbm2041	2	(TA)14	AGACAACTTTAAGTAATTGTGGATGA	GTTTCGTTGCCTAACACTTTTCC
tbm2042	2	(AT)21	ATTGCTAGAGCCTTACATGTGC	GTTTAAAGACACGTGATCTGGC
tbm2043	2	(TA)19(TGTA)5	ATGAGAAAGGCGACCTACAGTT	GTTTGGCATTTAAGGCAAAGAAA
tbm2044	2	(TA)28	AGTGTTTTTCTTATCACCTTCTTTC	GTTTGAGCGTGATCCTTGAGTTTT
tbm2045	2	(AT)22	ATGACTACTGCTTTTTGGGCTT	GTTTGATATGTTGTGAGGGTGAA
tbm2046	2	(AT)14	AGCTAATATGGCGAAGTGAGTG	GTTTACAAAGGTGGAAGCGATTT
tbm2047	2	(AT)14	AGAGAGGAACTTTTGGAATTAGAT	GTTTCCAATTGTAATCCTTCGGTC
tbm2048	2	(AT)15	AGAGGGGAATAAAAACAGAGGA	GTTTCTAATTTCTTCCCGTTTCG
tbm2049	2	(AT)20	AGAATTGAAATGAAAGGGAACA	GTTTGCGAGATTGAAAAAGAAAGGAG
tbm2050	2	(AT)16	ATGACCAAATTATTTCATTTATCGAC	GTTTGAAAATTGTTCTATCTTTCAATATCA
tbm2051	2	(AT)14	ACGCTAGACGCTCTATCTAGTGG	GTTTCCGATGATCAATTCCATTTTCT
tbm2052	2	(AT)23	AGCCTCCGGTATCTTATTTTTC	GTTTATGTTACTTCGGTGTCCCAAT
tbm2053	2	(TA)15	ATCATACGTAAGCGAATTGCAC	GTTTAAAGTTTGCTCCACCTCAGC
tbm2054	2	(TA)11	ACACTGTACCTCTTCTCCCAAT	GTTTCATGCGTGACACCAGAATA
tbm2055	2	(TA)21	ATGATATGCAAAGGGTGGTTTT	GTTTCTTTTCAAATTTCATTTGTGTCA
tbm2056	3	(TA)13	ATTCACAATCCTCGACTACGGA	GTTTAAAACACGACACCACTACCCA
tbm2057	3	(AT)13	AGAAAAAGTTGTTGCTTTTGGC	GTTTGGCCAACCAATTAGGTACA
tbm2058	3	(AT)23	AGGTTCTACATCAACCAACAGTG	GTTTAAATTGTTTATTTAAAACCGGACT
tbm2059	3	(AT)17	ATTCGTTCACTTTCGACCTAGC	GTTTAAGGAAGAAAACCACTCCATTTT
tbm2060	3	(AATA)7(TA)13	ATTCTTATAGCAGCAATCATTGACA	GTTTGCTTGTTAATGGCATAATGA
tbm2061	3	(TG)7(TA)12	ATTGACAAACTTTCGATGCACA	GTTTAAAAGGGAGAAAATCAAGGGAG
tbm2062	3	(AT)13	ATTGCTCGCCTTGTTAATTTTT	GTTTGAAGGCGAAGAAAAAGATG
tbm2063	3	(TA)11	ATCAAGTGGCAATACAAAGTGG	GTTTAGGAATGACCCCCTATCT
tbm2064	3	(AAT)14	ACCAAGTTTAGAGAGGTGCCAT	GTTTGGAATTTTGCCCTTAGCTTTTT
tbm2065	3	(TG)4(TA)11	ACCAATTGAACTTTCCTAATGC	GTTTAAAGAAAATGGTGCCATAAACG
tbm2066	3	(AT)14	ATAAGCAAACAATTACCCTACCC	GTTTCTTGCTCACTTCACCGA
tbm2067	3	(AT)11	ACTGTTTCATGTTGGTTCATTG	GTTTAGAAATTAGGGCTTGTTTGGC
tbm2068	3	(TA)11(CA)6	AGACAATTGATCGGGAATAACA	GTTTGAAATTGGGTTACCAAG
tbm2069	3	(AC)18(AT)11	ATTTTTGCAGGAGAGGGATGTA	GTTTAATACCAACGTGGGTCAAAAT
tbm2070	3	(TA)17	ATTTCGTTTGTTGTTTGGAAAA	GTTTCCAAGCTTGAGTGCTTGACATA
tbm2071	3	(TA)15	ATTCAACAGGAAACAGGACAAA	GTTTCAATTGACTTCGCCTCAT
tbm2072	3	(TA)14	ATTACAGCGTTTTGTTAGGCAC	GTTTAGATGAATTGCTCGTTGTTGTG
tbm2073	3	(GT)6(AT)19	ATAATCGATTCGAACGGACTAA	GTTTGACTAGCAAGTAAGCCTGTTTTG
tbm2074	3	(TA)25	ATGAAACAACGGTCAAACCTCT	GTTTGTTTTATTTGTGACTTTGTCCA
tbm2075	3	(TA)17	ATAACCAAGTCAAAACAAACCA	GTTTCCCAATTTTAGGGGGCTAATTT
tbm2076	3	(ATA)16	ATCAACCAAGTTTTCAAAAAGG	GTTTCACCCATAAAGCAGACAATG
tbm2077	3	(TA)21	ATAGCACATCCATATGTGTCAA	GTTTCAACCATCGTTATATGCTCCT
tbm2078	3	(TA)16	ATCTCACTCGCAAGATTTGACA	GTTTCTTTTTATCGAATTAAAATAACTTGAGG
tbm2079	3	(AT)22	ATATGTTTGGAGTTTTGGCATT	GTTTCGAAAACTTTGAAGGTGGTTT
tbm2080	3	(TAT)16	ATATTTTGTAACATTGGGTTGAAA	GTTTAACCGGCGATTTAAATGACTT
tbm2081	3	(TA)20	ATAACCCAAATACCGGAGATAA	GTTTAAGGTCCTATTACCCTCTTGGC
tbm2082	3	(AT)23	ATCAGGCTCGCATTAGAAAATC	GTTTGTGGAGTGTGATGTGACAA
tbm2083	3	(TG)7(TA)18	AGTATTCACATTGGTAGGCTGG	GTTTGCATCGTGACAAAGGCATAATA
tbm2084	3	(AT)22	ACATTTTAATTGTCTAAACCAATGTG	GTTTAACAAACAACAGTGGAGCA
tbm2085	3	(AT)23	ATGTCAAAGTCTTGATGAAATAATGG	GTTTAAAACTTAGGGACAAAAGTGCAA
tbm2086	3	(AT)14	ACTCAAGTGCAGCAAACTCAAA	GTTTGGTGTTTGTCGTTGCACTAAT
tbm2087	3	(AT)20	ATTGGCTAAGCGCATTTTGAC	GTTTAGAAGAGATTTGAGTTGGCCG
tbm2088	3	(AT)15	AGCTCGAAGTCTTGGAAGAAAA	GTTTATGTTCCAACTTTGACAAGCG
tbm2089	3	(TA)27	ATGTAAGAACGACAATTTTCTTAAGTG	GTTTCCATCCCGTTTAATCTTATTTG
tbm2090	3	(TA)24	ATTGAGGTAGGAATTGCAAAGG	GTTTCCATGCAAATTATGTGGTG
tbm2091	3	(CT)19(AT)27	ACCGCAGGATATGAAGAGTTGT	GTTTGTAATGCCGACGAATTTATG
tbm2092	3	(AT)25	ACATCACATTTCGCGTACTAAC	GTTTAAATGGCTCTAGGCTCACACA
tbm2093	3	(TA)20	AGCTAAAAGACGTGATACACTCA	GTTTGATTTCTATGCACGGTAAG
tbm2094	3	(AT)16	ATTTTTTGACCTCTTTGCTCCT	GTTTGAAAATCTTCAACTAACCCACCA
tbm2095	3	(AT)15	AGTAACGTGCACTTCTCAATTCT	GTTTCTCTTTTTGGGATGTGGAG
tbm2096	3	(TA)26	ACTATCACTCAGATCGGTCAGC	GTTTGGTCAGTGGAAAAATCAGAAA
tbm2097	3	(TA)18	ACTTTTGTGTCTCATTATGGCA	GTTTCACGAAGCTATGCGTAGGTAA
tbm2098	3	(AT)22	ATTTGTGTTGCTCATTATTTTGG	GTTTGGATAACTCCCTCGCGTACATA
tbm2099	3	(TA)21	ATCTTTGAGAAAGTGCAAACCA	GTTTGTGTCAATATGCAGTAGCGTG

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm2100	3	(AG)15	ACTCCTTCTCCCTCTGGATATT	GTTTAACCATGTTCCTTCTCCTGCT
tbm2101	3	(AT)22	AGTTTCTCTTTTCGACTTCAACA	GTTTAACCTGAATCGTTGTTTGGAGA
tbm2102	3	(AT)14(TA)11	ATGAGGAAGTAAAAGATGAGTTTTGA	GTTTACCTTTTTGAAAGCATGCAC
tbm2103	3	(TA)22	ACTGAAGAGGGTTCGACACTAC	GTTTGGGATGTTAGTCCATGTGTTAATG
tbm2104	3	(AT)19	AGTTCAATTGATCAAACAAAATCA	GTTTACCCTTCGCGTTGTTTTA
tbm2105	3	(TG)10(TA)14	ACACAAGTGAGCAGAAATTTGA	GTTTCGATGTTAGAAGCTTGGTCA
tbm2106	3	(AT)19	ATCGTTAAAGTAACACTTCCAATCA	GTTTAATTTTGGACTTTGATGCG
tbm2107	3	(AT)14	AGGATACTTGTGCATTATCCCG	GTTTGTTAGAAACGCTCGACTCAA
tbm2108	3	(TA)28	AGTGATGCCTTAGGATATTTCG	GTTTGGACTTGTAATTTGAATTTCTTT
tbm2109	3	(AT)22	AGATAACCAATGCTAATGGATGA	GTTTGGCCAATCAAAGCCTTATCTCT
tbm2110	3	(TA)14	ACGTGTTACCCTTCTCATGGAT	GTTTAGTCCACCTTTAGGCGATG
tbm2111	3	(AT)20	ACTTGGGTAATTTGCCAAACAT	GTTTAACGATGACGGACTGAAGAGA
tbm2112	3	(AT)17	ACCACAAGGCATTGCATATACT	GTTTGCAGCTCAGTAAAATGTTG
tbm2113	3	(AT)12	ACTCAATTTACCATGGTGTGCT	GTTTCTTTTCCTTTCAATCTGTGGGAC
tbm2114	3	(TA)19	AGGAAACTTATTCACCCTTTAGC	GTTTCGGTAGTGACGGAAAGAAAT
tbm2115	3	(AT)12	ATGGGATTTGATGAGGCAATCT	GTTTCATTGTTGTTATTGCATCGG
tbm2116	3	(AT)16(AC)4	ATATCAGTTGAGCTAATCGAACG	GTTTGCCTAACGATTCAAACACATGA
tbm2117	3	(AT)11	ATGCCACTAAAAGATGAAAACTCC	GTTTCCAAAATAAGAAAAATGTGCAAC
tbm2118	4	(AT)21	AGTCAAATGATTAAATAATCGAGAAAG	GTTTGCAATGCATTTGTCTTAGTG
tbm2119	4	(AT)17	AGCACATCTACAGCCATCATTA	GTTTGTGTTTGGGTTTGGATAGATG
tbm2120	4	(AT)16	ATCAAATTAATCAAATTCCAAACA	GTTTAATAGCAGACTAAGGAATCGAAA
tbm2121	4	(AT)29	ATAATTAATCAAATTCCAAACATGA	GTTTAATAGCAGACTAAGGAATCGAAA
tbm2122	4	(GT)6(AT)16	ACCACTTGCTTTAAAATGACCG	GTTTGACCAACAATCCAATACAAAAA
tbm2123	4	(TA)16	ACCAATCCAACATGGTTATTTT	GTTTCTCATCATGGAGAGTGATGG
tbm2124	4	(AT)22	AGCGCATAGTTCAAGAAAAAGT	GTTTGGTCTAACAACCTATTTGGGA
tbm2125	4	(AT)16	ACGATAACCGAAGGACTAACAA	GTTTGGACATGGTAGGATGTGAGTT
tbm2126	4	(AT)16(AGAT)4(AG)11	ATGGCAAACAAGGAGAAGAAAA	GTTTAACTCTATTGTGAACAGCGCCT
tbm2127	4	(TA)20	ATACAAGTTTGGGGATCTGTTT	GTTTACCCATATTGACATCCCTTGAC
tbm2128	4	(TA)23	AGCTTGAATCTAGCAAGCCAAG	GTTTGGGCTTAAAACATTCTATCACAA
tbm2129	4	(TA)19	ATACCAGACATCGACATAATCC	GTTTCCAAAGCTGGAGGACATAG
tbm2130	4	(TA)24	ACATGTCTATTTCTTTGCCCCC	GTTTGAGCCCGTACTAACATGGA
tbm2131	4	(AT)22	ATGACACCTGTCCTTGTGAAAC	GTTTCAATAGTTCTGAAACGAAACCAA
tbm2132	4	(AT)24	ATTCTTGTTTCTCCGATTCCAT	GTTTCTCGAAAGAGTCAAGGCTAGAA
tbm2133	4	(ATAA)5(AT)24	AGGTTGTATCCTCTCGAAAACA	GTTTGGCTCATAGTGATGGTTGTCAG
tbm2134	4	(TG)6(TA)19	ATTCTGAAAATTTTGTTGAGTGAT	GTTTGGACCAACTAGACTCGATCCAA
tbm2135	4	(TA)22	AGGAACTACAAACACTCTTTTGTTTT	GTTTACTGATTTCCCCAAACACGA
tbm2136	4	(TA)21	AGTGGATCGAACGTGTTTTTAC	GTTTAGCCATAACTTTGGTCTTCGAG
tbm2137	4	(TA)20	ACGACATCAAAGATCTCTCCTT	GTTTGGAATAAATGTGCAACCCAT
tbm2138	4	(TA)17	ATCCGTTCGGTCGAGTCTCT	GTTTATCGATCGGCATCAAAG
tbm2139	4	(CT)13(AT)24	AGTAGGATAAGTGTGGGTGCCA	GTTTGCCCTTGATCATTATTCAC
tbm2140	4	(TA)18	AGCTTTTAAATTGTTTGCATCA	GTTTCACGAAAAGACCCATTAGAA
tbm2141	4	(AT)24	ATAACCAAATTATTTCACCACGA	GTTTAGATGGTATTTGACTTGACGCA
tbm2142	4	(AC)17	AGCATGGCAGAATGATGTATTT	GTTTAGAAAATGTCATGCAAGGTGG
tbm2143	4	(AT)20	ACCTTAAATTAATCCTCGATGTG	GTTTGGTTGACTCTAGCCAAAGC
tbm2144	4	(AT)14	ATTCCTAATTCCAACTCTGCCA	GTTTCTCTCTCGTGACAATGGTGTT
tbm2145	4	(AT)15(AG)14	ATCTTTCCTAGTCGATCACCACA	GTTTGATGTGTCGATGTTGTTGAA
tbm2146	4	(TA)15	ATGTGATATTTGACCAAGCTGTAGA	GTTTATGCACAGTCTCTCGGT
tbm2147	4	(AAT)22	ATTTTATCCGTCCCAATCAAAG	GTTTCGTCATTTTGATTCTTGGGT
tbm2148	4	(ATA)10(TA)18	AGCATGAGCAAGTTGTATGTAATG	GTTTCGTCTTATTGACATTTTGCAT
tbm2149	4	(AT)16	ATCCAGAAGTGGTCCACATACA	GTTTAGTCTCACGAATGGTTCC
tbm2150	4	(TA)28	ATTGTAGGCTTCACCGATTTTT	GTTTCCACTTAACTTGTTTGGTTTGAA
tbm2151	4	(TA)14	AGCTAGCAACCACCTCAAACTT	GTTTGAGAAATAAAAGCCCCATACCC
tbm2152	4	(TA)15	AGAATACTCATTTTGGAGCTATGA	GTTTAAAAAGACGAGTAGCTTTCATCA
tbm2153	4	(AT)14	AGTTCACACGGTTCTCAAAATA	GTTTACGAATGCCTATTAAAGACGGA
tbm2154	4	(TAA)8	ATAGATCCAGATGAACGTTTTACA	GTTTAAATGCTGACAAGGAAGGG
tbm2155	4	(AT)12	ACAGAGGGATGTTGATGTTGTA	GTTTAAGTGGACCAACACACACAAAG
tbm2156	4	(AAT)6(ATA)7	ATATTATTTATGGACGAAGGGA	GTTTGCACTCTTCTAACCATTTTTCTC
tbm2157	4	(TA)11	ATTGGGCTGAGATAAGCTGAAG	GTTTGATATCCATTGGTTCACG
tbm2158	4	(TA)10	ATTATCCATGATATGGGGGTGA	GTTTCCCTTGCAAATAAGAAGCAAAG
tbm2159	4	(TA)17	AGAGGAATTTCAAAGTGGTTCA	GTTTAAACCAAGAAACACATGACAAGAA
tbm2160	4	(AT)10	ATGCGATAAGGTTACTCCATCA	GTTTGCTTTAGTGGAGACAGTTTGA
tbm2161	4	(TA)16(TGA)5	ATAACAAATTAAAATGGAGGCA	GTTTCAAATGTACTCTTGATTTAATTTAGCA
tbm2162	4	(AT)10	ACTAGGTCGTGGGACTTTTTCA	GTTTAAATCCAACCACCAACTTATGG
tbm2163	4	(AT)15	ATGCCTCCCCCTAAAAAGTGTA	GTTTCAAATCGAAGTTATTTCAGCCC
tbm2164	4	(TTA)10(TA)9	ACGCCAAAATCTTTAAAGCAAA	GTTTAACAAGTTAGTCGTCGAGGTGC
tbm2165	4	(ATT)10	AGTTGGTTGTTAATTGCACCAT	GTTTGCGCTGCAAAAGTAGAGAGACT
tbm2166	4	(TA)12	AGACCTAATATCAAACCAAGTGGA	GTTTAACAAGCAAGGTAGAAATGTT
tbm2167	4	(TA)19	AGGAATTTCTCGTCTCCTTTTT	GTTTACTCGCTTTCTCTCAGCCAT
tbm2168	4	(GA)7(AG)4	ATAAAAAGTGGTGTTGTTGGGG	GTTTGTCGGTTGTTTTCTTATGCAC
tbm2169	4	(AT)6(GT)7	ACTTGCCAAGGGTCATACTTGT	GTTTGACTTTGAAAAATGCAGTGGA
tbm2170	4	(TA)11(ATA)5	ACTTGACAGATGACAATGTGCT	GTTTGGAGTAGCCATCACAACG
tbm2171	4	(AT)12	ATAGTGTCTTTTGCACACTCCC	GTTTGGAAGGATTCTGCATACAATG
tbm2172	4	(TA)17	ATCATGAATTATGCCACCTCCT	GTTTGAACAAGCTCCTCAAAGG
tbm2173	4	(AT)16	ATGTGACCTCAACTCGAAAATG	GTTTGAGCCGGAGTCGTTATACATCT
tbm2174	4	(TA)13	ATGCCTCTGTAGTAGCAACACG	GTTTCAGCACCAGCCCTATCTAA
tbm2175	4	(TA)12	ATCATAAAATTCGAGACGGTCC	GTTTAAATCTTTCAAATTTTACCAGC
tbm2176	4	(AT)16	ACAATATGTTAAGCATTCGAGG	GTTTCTACAGAGCCCACTTGGA
tbm2177	4	(AT)20	ATGAGGATAGTGGGGCTAAGTC	GTTTCGTAACTCTTTTTCGATGCAA
tbm2178	4	(AT)15	AGTACGTATTCACATTGACATGCT	GTTTCTCCACCGAAATACTAGGG
tbm2179	4	(AT)17	ATCTTTTTCATAACTGCCCCAC	GTTTAAAAATGAACGGACGAAACACT
tbm2180	4	(AT)14	ATCCGACTGTGTAAGCAACAAC	GTTTAGAAGAGTGCTCGAAATCAACC
tbm2181	5	(TA)24	ACATAAAAGCTTAGCAGTGATCC	GTTTCGATTTTCAATCTCTTCTCAATTT
tbm2182	5	(AT)18	AGAAGCGAAAGATGTTGTCAAT	GTTTCAAACAAACTTTTAAAGCGGG
tbm2183	5	(AT)22	ACAAACCTTTGAATGAACAACA	GTTTCCCTTGAGAGTTATTAGTGTTGAGAA
tbm2184	5	(AT)28	ATTTTAAGGTGCATCTTTGATATG	GTTTCAAATTTTTAAACTTCAGTTTCATGT
tbm2185	5	(AT)15	ATGATGTAAACAACCATTACCGA	GTTTGGGTTATTTGGCTTGAATATAAGAAA
tbm2186	5	(TA)12	ACTCAAATCATTTTTCAGGACG	GTTTCAAAACCGTAGAGCAAGG
tbm2187	5	(TA)12	AGAATCCCACCATAAATTCACA	GTTTAAAAGAACAGAAGGCCAACATC
tbm2188	5	(TA)12	ATTATAAGGAAACAACTCTTCAAGAAA	GTTTCGAGATGAAGCTCAAAAGTCCT
tbm2189	5	(AT)13	ACGAAAGAGTAGGGATGCAAAC	GTTTATCCGCATAATTTTCCC
tbm2190	5	(AAT)12	ATCCGCTTTTAGACGTCCTTGT	GTTTCGTGCGAAAGCTACTATCAAA
tbm2191	5	(AT)12	ACACAAGGCTTTAGCACTGGA	GTTTGCAACGGATTCAATTAAAGA
tbm2192	5	(AAT)14	AGTTTGGGATAAATGGGTCAAG	GTTTCGTCGACTTTTCCTTCTTC
tbm2193	5	(TA)12	ACCAAGTCCAACTTAGAGGCAG	GTTTCAGTGACGGAATCAAGGTT
tbm2194	5	(TA)12	ATAAGTAGTAGAAGACGAACGATGG	GTTTGGATCGAAATAATCAAAGCGTC
tbm2195	5	(AT)26	AGGTCCCTTAAGAGCCAAAAAG	GTTTCATCATATTTTTGGGTGGG
tbm2196	5	(TA)21	ATCGGGATGGAAGTGAAACA	GTTTGAAACAAAATGTACCCATTC
tbm2197	5	(TTA)21	AGAAAATAAAAAGTATGGGGCG	GTTTCATTCGTCTCATCGTTCTC
tbm2198	5	(ATT)14	ATGACAATAAAAGTATGGGGCG	GTTTCTCTAACATGTTTTCTTCTGCCA
tbm2199	5	(TA)24	ACATTTTCCTTTCTAAATTTGCTA	GTTTGCATCATTAACGCACAATTA
tbm2200	5	(TA)17	ATGATATAAATACTGCGATGAAATGA	GTTTAAACCGTCCTAGCTACTTTCTAACA
tbm2201	5	(AT)25	ATAAGAAATTGATGTTGAGGGG	GTTTGTAAGTTTTAAAGGGAAATGTCG
tbm2202	5	(AT)16	ATCACATCACAAACACTCCACA	GTTTGAATCCATGAAATAAGGTG
tbm2203	5	(AT)16(AC)7	ATCATATCATGATGCAACCAAC	GTTTGACTTGCAACAATAAATAAGTAAAA
tbm2204	5	(AT)23	ATCAGTGAACCTTTTGTTTCTGA	GTTTGCATGGTGTGTGAGAGAGAG

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm2205	5	(TTA)16	ATGAATTTGAGTCCGTTAAGCC	GTTTGATTAGTCGTTATTGGCAAGC
tbm2206	5	(TA)19	ATGCTCAAAATTTTCCGTTGAA	GTTTGGGGCATTATTTACCTTGT
tbm2207	5	(TA)19	ACAAATCTGAAGAAGAGCCAGC	GTTTCTTTAACCATACCCCGGAT
tbm2208	5	(AT)27	ATATCAATTTGACAATAAATTTGGA	GTTTGAAGTTGAGAAGGTGGCTGAA
tbm2209	5	(GT)8(AT)19	ATATAACAAATATTGGGCCCGT	GTTTCCTTTCAATCCAAGTCGAAGT
tbm2210	5	(TA)21	ATGACCAATACTTGACGTGTGA	GTTTCATTATGAAATTTACGTCCCA
tbm2211	5	(TA)26	ATATCGCTTCCCTTAGCACAAT	GTTTATCGGTCTTTGGGTGCTTACT
tbm2212	5	(TA)21	ATTTCAAACACCATAAAATGCTT	GTTTGCGAGTTTTCTGGTAAAAA
tbm2213	5	(AT)21	ATCAACATGAAAATAGTACTCTTGGG	GTTTGCACACACTATTGTCTACATTTTTC
tbm2214	5	(AT)25	ATACTCCCCGGATGTGACATTA	GTTTGTGATAATCTAAACAAGGAAAGAACA
tbm2215	5	(AT)25	AGTTTCGCTCAAACAAGTAGGA	GTTTGAATTGTCTTGATTGGCAT
tbm2216	5	(TA)24	AGTTTTTGGTAATCAAGTTAGGG	GTTTCGCTCCAGAATATTGAGT
tbm2217	5	(TA)25	ATTAAAACGGGGAGATCTCAAA	GTTTCAGAAAGGGATTCAGAGTGA
tbm2218	5	(TA)15	ATTATGTCATTTGGGGTTCACA	GTTTAGCTACACGCATTTTAGGGTGT
tbm2219	5	(TA)19	ATTGAGATTGAGGTGTCTCCCT	GTTTACAACCCATGTCGGTAAACTTC
tbm2220	5	(TAT)16	ATAGGAATGGCAAGTGATGATA	GTTTGCACATAATTTGGCACTAA
tbm2221	5	(TG)19(TA)7	ATCCGTCGACACAGTCAATTAT	GTTTCTTTTTCCTACACAAATTCTAATTCC
tbm2222	5	(AT)10	AGCTCAACTCTCCTTTTCTTTCA	GTTTGTAATCTCACACGTCGAAT
tbm2223	5	(TA)11	AGTTGGTTTGCTTTATAGGCATT	GTTTGACATTTAGCTCTTTTTGTGTGGA
tbm2224	5	(AT)11	ATACCAATCGCATTGACACTTT	GTTTCAAAAGAAAGAGGGAGAGAGGA
tbm2225	5	(TA)11	ATTTTTAATTGATTGCGGTTGG	GTTTACATCAACTTACGTTTAAAATGATTC
tbm2226	5	(TA)10	AGATGAAAGTCATTAGGTGCTTG	GTTTAAGATACAATCGCATCTCCGTT
tbm2227	5	(TA)17	ACCACTTGTGGAAACTTACCTT	GTTTGGATAGATTTGTTTCCTTATCAAT
tbm2228	5	(AT)17	AGCTTGCATAGCTAGGGAGAAA	GTTTCAATAACAATGAACATGCCA
tbm2229	5	(AT)17	AGGCGCTGCTGTATTTAATAGT	GTTTGAGATGATGTGTTTTAATCCAA
tbm2230	5	(AT)21	AGTCCAATGAGATATTTTCCACTT	GTTTCAATAACCAACAAAAATGGACTCA
tbm2231	5	(AT)28	ACAAAATTGAAGTGTGAACTGAGA	GTTTGAGACCAAGTTAAATGACACGA
tbm2232	5	(TA)15	ATAGGCCACAAAAAGAAACAAG	GTTTGGACAAATTACTTAAGGCCAGA
tbm2233	5	(TA)18	ATTTCAAAGTAAAAACAATCAATATCA	GTTTGGGGGTGCACGTATAGCTTAAT
tbm2234	5	(AT)24	AGAAATGTTTGTTGCGAATTACA	GTTTAAAAAGCTGGCTCTATTGGTCA
tbm2235	5	(AT)16	AGAGCTAAGAGGTGTCAAGCAA	GTTTAAAAAATACGTCAACCCACAAAAA
tbm2236	5	(AT)16	ATGCCTAATGTTCTCATTTAACTTTG	GTTTAAATAATGGTCCAAAAGGGAAAA
tbm2237	5	(ATA)14	ATACAAGAAACCAAATAAAAGGAAA	GTTTCTTTTTGTTTGGGGAGAAGGG
tbm2238	6	(AT)23	ACGATCCGTCTAGGCTCTATGT	GTTTCCCTTATTTCCACATCAATGGT
tbm2239	6	(GT)9(AT)24	ATACTAACATACATTGCCTGCG	GTTTGGTTGATTTGATGGTTT
tbm2240	6	(TA)23	ACCTTCTTTCATTTTGGTATCG	GTTTCATCTCAAAACAAAGCCCTC
tbm2241	6	(AT)23	ATAGCTTGGAGAGGGTGTATGG	GTTTGAGCACATAGCTGGAAGTCAAA
tbm2242	6	(AT)22	ACACCATGACACCTAATCTTGA	GTTTAGAAAATCAAGGAAATTTGCGA
tbm2243	6	(AT)26	ACATCACATCAAGCAACTCCTA	GTTTACTTCGTCCTGCGAGACAT
tbm2244	6	(AT)21	ACATTACACCAATAACAATAAAACA	GTTTCTTGAACAAATGAATGATACACAA
tbm2245	6	(AT)23	AGAAGTGCAACAAAATAATAAGTTACG	GTTTGCCAACAGGTTCAAAATACAC
tbm2246	6	(TA)21	ACATTGATCATTATTCGCTTCA	GTTTGAGTTTTACAACGATTGCG
tbm2247	6	(TA)23	ATCATTGGGCTTATGCTCTTCT	GTTTGCATTTAGTCACTGAACGGGTA
tbm2248	6	(AT)21	ATTAAAATTCGAAAAACATCCAAA	GTTTCTTTTCAAAATTGGGTTGAAGTT
tbm2249	6	(AT)25(AC)8	AGTACTCGGCATTCTAAAAGCA	GTTTCGAATCCACTGGCTTTTCTAT
tbm2250	6	(AT)19	ATTTTAGAAACGCGCTAAGGTC	GTTTGCAAATACGTTGCTCGATGATA
tbm2251	6	(TA)21(AT)9	AGCATGAAAAGGTAAAACATACG	GTTTCTATACATGTAGTTTCTTGGTTG
tbm2252	6	(TA)20	AGAGCCTAGGAAACTCACTTGT	GTTTATTGGTATGTCAAGGGGTG
tbm2253	6	(TA)19	ATTTCACCTATATCACATTAATCACAA	GTTTCGGACATTGAGGGATTTATTC
tbm2254	6	(TA)15	AGGTCATCATTAATCAAAGGGA	GTTTAAACGCCCACCTTATCTGA
tbm2255	6	(AT)17	ATATCAAAACAATGAAATCGGG	GTTTCAAGAATAAGACCAATACAAACAACA
tbm2256	6	(AT)20	ATTTGCGATTCATAGCAAACAT	GTTTCTCCTAGATCTCGCTCGCT
tbm2257	6	(TA)18	ACAAGGTTGATGTGGTTGGTTA	GTTTCCTTGATCAAATTAAAATCCT
tbm2258	6	(AT)18	ATGCAAGTGATTTGAAGCCTTT	GTTTCCAAAGCAGTGTGAGTGAG
tbm2259	6	(TA)24	ATCTATCATTATTCCTATTTTTATCGC	GTTTCTCACACTTTGTGCCATC
tbm2260	6	(GT)4(AT)24	AGTTGACGCAAATTCAAACACA	GTTTGGCGTGACAATATGGTGTAT
tbm2261	6	(AT)14	ATCTGGGATTTCCTCCATTCTT	GTTTGGGTTCAAATTTCCCTCT
tbm2262	6	(AT)14	AGAGGGGGAAAAAGGAACATTA	GTTTGCAGCAACTCAGAGATGAACAG
tbm2263	6	(AT)19	ATCCGGTCAACACGTAAATTAGA	GTTTGGTCAACGCGTAAATTAGA
tbm2264	6	(TA)26	ATTCATTGTTTGAAAAGAAAGTCAC	GTTTAAGACCATGGACCCAAGTAATC
tbm2265	6	(TA)14	ATATCTCTAGAGCTACAAGTTTTGCTT	GTTTCAAATTTCAATTGTTGGCT
tbm2266	6	(TA)14	ATGATGACGTTACATAGACGGG	GTTTAAGGACGCGACCAAATATAAGA
tbm2267	7	(AT)23	ATCGCAAATTTGGCATAACTGT	GTTTCACCTAGATTCCTTCCCACTTG
tbm2268	7	(AT)23	ATGAAGGAGTAATAATATGTGTGCG	GTTTAAATTGGAGATTTGGGTTTGG
tbm2269	7	(TA)25	ATCCAAGCCCTGTAAATAACCA	GTTTCTGTATAATTTCACTGGCAAGC
tbm2270	7	(TA)21	ATCACCACAATAATAAAGTACGATACA	GTTTGAAAGTTTATTTGGATGATTGT
tbm2271	7	(AAT)16	ATTGTCCACATCCTAACAAGACA	GTTTCCATTTGTAAAGGCCCAC
tbm2272	7	(AT)29	ATGCCCCCTAACAAAAATCTTC	GTTTGAGACTTTAGGGTGTCTGTGGG
tbm2273	7	(AT)20	AGTCCTGTTGATTTCTAGTGGAAG	GTTTGGATTATTATTTTAGGCACACACAA
tbm2274	7	(TA)20	ATCATTGAACTTTGAGAAAGCG	GTTTAGATGTGGAGAGACAAGAAGCA
tbm2275	7	(TA)15	ATTTTCTTTAAAGGGGAAGGCT	GTTTGAATGCATTTCGATTACCATC
tbm2276	7	(TAA)15	ATAGCAAATGTTCCCATCTACA	GTTTAATTGACCTTTGACGGA
tbm2277	7	(AT)22	ACACTACATGTACCGAATGGTG	GTTTCTTTGGACAATTTTTGCGTT
tbm2278	7	(TA)18	ACTTTGTGGATTTTGTGACTAGG	GTTTATCATGTCAATGTTGAGCCGT
tbm2279	7	(GT)11(AT)19	ACACGATTTGCCAGAACTAAGA	GTTTCTGACATCGTTCGACTCATCT
tbm2280	7	(AT)17	ATCATTATCCAAGTCTCCGTGC	GTTTAGATTTGGGGTTCCAAAAATTA
tbm2281	7	(TC)16	ACTTGATGATCACCATGCACTC	GTTTGAATAACCTCGTTTGTTGGAGC
tbm2282	7	(AT)23	AGACATTCATAGGAATAGAGGCAA	GTTTCCGAGAGCTATAAGACCGAGAA
tbm2283	7	(AT)23	AGAGGTACCACAATTTTGATGAAT	GTTTAATCTGCTTCACATGACAAA
tbm2284	7	(TA)24	ATCCTTTTACCCACTAGGTCCC	GTTTCGTAACTGGAGCATGTAATTTG
tbm2285	7	(AT)24	ACTCACCAAAGCCAACTTTATT	GTTTCCGAAACATGTCATTTCAAAG
tbm2286	7	(TA)24	AGTCCTGGTCTATAGGGGACTC	GTTTCACATGCAAATTAAGTATAGAACA
tbm2287	7	(TG)5(TA)23	ATTCCATAGCCGATTGAATACAT	GTTTCACAATTTCAAGTCCACAC
tbm2288	7	(TA)25	ATTGAAGTGTGACACCTGGAAT	GTTTCAAACAGAAAAGAAGGCATGAA
tbm2289	7	(AT)22	ATGTTGATCCTATTTAGCAGTGTG	GTTTAAAAGTTAAAAGGGCCAAAATG
tbm2290	7	(TA)26	AGAGTTCAGTTGAACCCCCTTT	GTTTGCAAATTTAGGCTTCCAACT
tbm2291	7	(AT)14	AGAAATAAAAAGGGGAGGAGGG	GTTTGAGTTTAGGTGGCATTCAAACC
tbm2292	7	(AT)14	ATTGGATCTATGTCGCAGGACT	GTTTGCATAAGCATTTACTAGAGGTC
tbm2293	7	(AT)7(AG)18	AGTTTTATGAGGGCATACGTGC	GTTTCAAAATTTTCTATTTGGATCTTCC
tbm2294	7	(TA)25	ACATTGATTTATCACATCAAAGTTTTT	GTTTAAACTTATCAATGGTGTAATTTGC
tbm2295	7	(ATAC)8(AT)10	ATCAATCAAACATTGAAACATGC	GTTTAAAGTAGGTCGGAAGAAACTAAAAA
tbm2296	7	(AT)10(AC)5	ACCAAAATGAACAATTAGGAAA	GTTTCCCAGAGAAGATCAGTTAGGG
tbm2297	7	(GA)10	AGAGAGAGAGAGAGAGAGAGAGAGC	GTTTAAAAATAACCAGCATAATTGAAAACC
tbm2298	7	(AT)10	AGCAACTTAAGAGGAGCTCAAA	GTTTAACAATGACAATCCATCCCC
tbm2299	7	(AT)13	ATTCTTGGACTTCTTGCTACGC	GTTTCAACATTAGATTCGCGTCCA
tbm2300	7	(TC)8(TA)8(TG)10	ATAAAGAAAGGTTGTGTGAGCA	GTTTAGAATGTAATCTGGCTTCAGGC
tbm2301	7	(AT)10	ATACTGAGACACCAAAATCCAA	GTTTGATGATCGATGTTAGCGAG
tbm2302	7	(AC)6(AT)6	ATCGTAGCACAGTGAGAGTATCG	GTTTAGAACCATATGAGATCCGCA
tbm2303	7	(AT)12	ACCGGATTTTGCTCTTCAAGTA	GTTTACCCAGGCAGTATCGTATGAAG
tbm2304	8	(ATA)19	ACCTCCTACCAACACATCCTAA	GTTTATTTCATTGGCCCCATCTA
tbm2305	8	(ATT)18	ATGTGATAAGCGTGGCTGAGTT	GTTTCTTTTATGTTTGCTATGGAGCGT
tbm2306	8	(AT)26(AC)7	ATAATCCAGTGCTTTCAGTTCA	GTTTAAGCTATTAGGGCAGCATTCAA
tbm2307	8	(AAT)18	AGTGCAGTGTGATCTGACGAAT	GTTTGTCCCTTCTCATTTCCAA
tbm2308	8	(TA)16	ATTTCAAACAACAACGTACGACA	GTTTGTGATTTTTAGCCTTTGCT
tbm2309	8	(AT)16	ATATTGCATTTCTCCCCATGTT	GTTTATGAGATTGCGGAATTG

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm2310	8	(AT)16	ATTTTGCCTTTTCTACCACAAT	GTTTAAAATCTGCTGCTCAAAACGA
tbm2311	8	(TA)16	ATGATTCTTCGGACTGATCGAC	GTTTGAATGCGGAAGATAAGGTTTTG
tbm2312	8	(TA)26	ATTCACTAATCCAATGGGAAATG	GTTTCCATTAACACATAGAAACTCCA
tbm2313	8	(GA)28	ATGAGCCTGGAGTTTTTCATTT	GTTTCGCTAATCCCTTTCCTTTGT
tbm2314	8	(TA)22	ATTGGCCTCTACACCACATTTA	GTTTCGCTATTTACTTTTAAAATGAGGGA
tbm2315	8	(AT)17	ATTTGTACTTTGCCCATTAGCC	GTTTGTCATATGAACAAAATTAAATCATCA
tbm2316	8	(TA)18	ACATTGATACAAGCCAGAAGAA	GTTTACTAGACATAGGACATGGAGC
tbm2317	8	(ATA)16	ATCCAAAAACCGATAAACCAAA	GTTTCACCTCTCGTCCTGAAAAAT
tbm2318	8	(TA)20	ACTCTGAGTCACATCTTTAAATGC	GTTTGGTCTGCCATCTACCAAAAG
tbm2319	8	(AT)24	ATGGAAAGCCAAATGATTGAGG	GTTTAACCCCTGAAACTTGGAGAA
tbm2320	8	(AT)19	ATGATTTGAAATAAGGGAGAAAAAT	GTTTCCAGAACTAGGCCATCTCAAAC
tbm2321	8	(TA)21	ATTTTCATAAACGGGACCAATG	GTTTCAAGGGAAAAGACGAAAAAGAA
tbm2322	8	(AT)22	ATGTAGTCCAACCAACTCGGCT	GTTTGCAAAAATTAACCTACGTTCGC
tbm2323	8	(AT)21	ATAGGGTGGTCAGTTGAATCTT	GTTTCGCCCTATAGTTTCTACTCCTCC
tbm2324	8	(TA)18	ACGCTGAACTTTTAAAATGTAATGTC	GTTTGTGTTAATCCTTTTTGTTTTTGA
tbm2325	8	(AT)20	ATCAAGCTCGACTCAAAAGACA	GTTTCTGGTCCAAGCTATGACGTA
tbm2326	9	(AT)25	AGCTTTTTCAATCTACTCCACG	GTTTCTTTTCACTTTGATGGTCAAGAAAA
tbm2327	9	(TA)20	ACCGGTTAAAATTACACTTGCC	GTTTAAAGCTATCAATAGTTTAGAAACGAAA
tbm2328	9	(AT)18	ATCATGCTCTAGTGCTTGGAGA	GTTTCTTTTGTGTCAGATCAAATTACGAGA
tbm2329	9	(AT)19	ACTAGGAGCGAATGGATTTTTA	GTTTCTTAGTGTAATTTTCGGGATTT
tbm2330	9	(AT)17	ACCATTCGATAACCCTACTTTG	GTTTCGCGAATACTTGATTTTGAGA
tbm2331	9	(AT)5(TA)17	ATAAAGGAAAGGGGTGAAAGAG	GTTTAGCACACTCAAATACACATGCC
tbm2332	9	(AT)28	ATGGAGTGTGACGAGCAACTTA	GTTTCCTACATCGATGCTCAAGATTT
tbm2333	9	(AT)14	ACCATTTGTCTTTCTAGCACCT	GTTTAATTCTCCAAACTCGTGCG
tbm2334	9	(TA)20	ATTTTCGTCCCTTTATTATCGG	GTTTGAGGCCTAATGTCTCTTCAAA
tbm2335	9	(AT)16	ATCAACAAGCACTTGAAGAGACA	GTTTGAAATCTATGGGCTGTTTGACC
tbm2336	9	(AT)21	AGTGGGAAGTGAAAAGATTCAA	GTTTGAAGTTCACCATTGGAAGA
tbm2337	9	(AT)16	ATTCGCATGTATCTTGAACACA	GTTTAAATTTCTTAATTAGTTACGACGATGA
tbm2338	9	(TA)25	ACAAAGTTCAAATAGACCAAACAA	GTTTCCATGACCAGTGTTGGTAAAAA
tbm2339	9	(TA)26(CA)8	ACTTTTACACTCTGCAGTATTTAATGT	GTTTATGGAAGACATTTCCCCCT
tbm2340	9	(AT)20	ACATGCACTTGCAAAATTAAAG	GTTTGGCAAAAAGCCAAACAGTAT
tbm2341	9	(AT)16	AGAGGAGAATCAAGGGAGGAAC	GTTTAACACGAACTATTTTGATGAGCA
tbm2342	9	(TA)25	ATAAGTCAGTTACGGGCATATTG	GTTTACCTTCAGCTTCAGCCTCAT
tbm2343	9	(CT)20(AT)17	ACTGTGCAAAGAAATCATAGTTGA	GTTTCTGCAATAAGTCATTCCCA
tbm2344	9	(TA)18	AGACCATGTACGCTCATTTCAT	GTTTCACCTGTGTACCCAAAAT
tbm2345	9	(TAT)18	ATCAGCTTTCATACTCCCAAGG	GTTTCCCCAGTTCCACTTTTTATTG
tbm2346	9	(GT)5(AT)21	ACTGAAAAGTTAATGGTCCTTTT	GTTTGTTGTAAATCATCCCCACA
tbm2347	9	(AT)23	ATATACGAGGGGTACATTTCGG	GTTTGTACTTTGATGCTTTCCA
tbm2348	9	(AT)26	ACAAATACATGCATTCAAAAGG	GTTTGACCCAAAATGTGGCTTAAAT
tbm2349	9	(AT)21	ATTGTGTTTCCCAAGGAGAAGG	GTTTACGTCGTATGGTAGAAACGTCA
tbm2350	9	(TA)23(GA)14	ATTAAAATACCATAATTCACTTGATGA	GTTTCTTTTGATTTTTCCAAAGTTAAGC
tbm2351	9	(AT)20	ATCATAACTCCTTAAAATTATCTGCAT	GTTTAGCCATGGTCAGGTGTCATAA
tbm2352	9	(AT)20	AGCGACCTATGAATAATATGTTGTAAA	GTTTAGACGAATAATGTCGGCACA
tbm2353	9	(CA)9(GA)18	ATCACCCTTTAGTGAGTCGTGA	GTTTATGGAATCACGATTATGCG
tbm2354	9	(TA)24	ATGCTTTTAGCACATCGAAAAA	GTTTGGTAAAAGATTGACAACAAACAA
tbm2355	9	(TA)24	AGGTAAAACATATTTGGTCGGG	GTTTCGCGTGTCAACATGAAAATAAC
tbm2356	9	(AT)24	ATTTTGCACAAAACCCCTTATT	GTTTGACAAGGTTGGTTGAAATGAA
tbm2357	9	(TA)24	ATACAAAGTGCCCAAAAAGAAG	GTTTGGGAATTTCCAATTCATTGTCT
tbm2358	9	(TA)18	ATAATATAGGTGGGACCATGAAA	GTTTCATCAAATCTCATTTTATTCTTT
tbm2359	9	(AT)21	ATATGTGTCGCCAATTCATGTT	GTTTCACTATGTTAGGCATAATGCGA
tbm2360	9	(TA)20	ACATGGATTTCTAAGCATTAACA	GTTTGCATTGCATTAAGAAAATTATTTACAA
tbm2361	9	(AT)18	ATTTGTTGTCTTCCACATGTTG	GTTTCTTTTCTAACCAAGAAAGACCAATTA
tbm2362	9	(AT)16	ATTTATTAGCAGCACATTGCCC	GTTTCTCAAGCCGTAAAGCATTTT
tbm2363	9	(TA)21	ATTGGAAATCAAGTAAAACGAAG	GTTTCAATTTTGATCCTTCATGGT
tbm2364	9	(AT)25	ATGTCACGAGACCACTCGTATG	GTTTATCTTTTTGCCGTCTTTGG
tbm2365	9	(AT)14	ATTGGTGAAAAATGGAAGCTGT	GTTTGAGAATGAGCTGAAAAACGAA
tbm2366	9	(TA)17	ATGGCACAACTTTCATGTACAAA	GTTTGTCATCTAAAACACAAACAGGAA
tbm2367	9	(AT)26	AGTGTATGTTATGCCAACAAGC	GTTTGGATTTAAACAACGCCATACA
tbm2368	9	(AT)15	AGCCCCTCAAAATAAAAATTGG	GTTTCTCCTCATCATTTGTTCCCT
tbm2369	9	(TTA)19	ATGGCCCAAGGAGTAATTAAAA	GTTTGAAAGATACAATTAGCCCCAAA
tbm2370	9	(TAA)16	ATAACGCTCAAAATTAAGCTGG	GTTTGAAAAGGTGCTAAAAATAGGAGG
tbm2371	9	(ACT)4(CT)15(AT)18	ATTCAATCACATCTCTCTCTCTCTC	GTTTAACAAGTAATATTGGAAGTTACAAAGC
tbm2372	9	(AT)15	ACGTACAAGACTCGTAAGAATCAA	GTTTGAATTTCAATTCCTTTTAGCACA
tbm2373	9	(AT)14	AGCAATCTTGTTCAACCTTTTG	GTTTGGCGTTAAGGTATCAGACA
tbm2374	9	(TA)15	ATGTTTATATCAGTGCGTCCAA	GTTTGGGACACATTTGTCTCTTCAAA
tbm2375	9	(AT)18	AGGCAAGATTGAAGTAAAAGAAAA	GTTTCGGAATATTTATTGGCCATCAC
tbm2376	10	(TA)14	ACTGGTCTACGAAACCAGAGAT	GTTTCTTTTATGCAACAACCAACCAAC
tbm2377	10	(TAT)16	ACATTCCAAACTTAGTGGAACC	GTTTCCAAACATTAGAATGCTGAAGA
tbm2378	10	(AT)20	ACCCAACATGTGGTAAACTAAA	GTTTCCAATCAAATATCATGGTCAAA
tbm2379	10	(TA)14	ATTTTGTAATTGGTATTTCTTTACACG	GTTTCGTTAGATAGCAATGAACTCAA
tbm2380	10	(AT)14	ATTGTGAGGATAGAATGGAGGG	GTTTCACCACCCACCCATTAGACTAT
tbm2381	10	(TA)22	AGATTATCGAATGAGAAATAAAAGAA	GTTTCGTAATTATTCGATGATGTGAAGA
tbm2382	10	(AT)20	ACGTCGAGTAGAAGAATCAGGTC	GTTTCGCTGGAGATATTTGGTTTCTC
tbm2383	10	(AT)24	AGCAAAGGCCATAACACTTTT	GTTTCCGTCTCAAAATTGTAAAGCAA
tbm2384	10	(AT)22	ATAAATAATGTGTATTTATCCTTTTCG	GTTTGTGAGGTGGATTACACGAG
tbm2385	10	(ATAC)7(AT)23	AGACGATGTTAAGTTTCTTCGTTT	GTTTCTTTTTGTTTAAATTCATTAGGCACA
tbm2386	10	(TA)20	ACTGCATTACTAATCGTGGTAAA	GTTTCCAACCTTGTTGGCTTATAACA
tbm2387	10	(ATAC)4(AT)20	ATTGTTGTATGAAGAGGGGCTG	GTTTCGATGCAGCTTAAAACTCAGA
tbm2388	10	(TA)17	AGAAATTTCGTCATGCAAACTG	GTTTCCATGGTTGAGAATTTGG
tbm2389	10	(AT)16	ATCTCACATATACCCTTTTCCTCAA	GTTTGAAACATAAATAAATTTGACCATCA
tbm2390	10	(TA)17	ATAGGTACATTTTCTGTATTTGGTG	GTTTCCTTGTAATCGAAGGGGTT
tbm2391	10	(TAT)18	ACTTCACTAATTCGTCATTAAATAAAA	GTTTGCTAAACTTCCAACCACTATTGA
tbm2392	10	(TA)21	ACCGTTAAAATTACTTCGGACA	GTTTGACAGACGAATAGCGGACAACT
tbm2393	10	(AT)23	AGAATCTTAAAGAAAATAGGCTTATCC	GTTTATCAGCCACATGCATTTTT
tbm2394	10	(AT)20	AGGCTTACATTGGTCTTCTTCA	GTTTCAATTGCCTTGTGCAAATC
tbm2395	10	(TA)21	ACAAACAATTCCTTATCCTTCA	GTTTGCGTTTATCATGTATCTGGTCA
tbm2396	10	(TA)25	ATCCAGACTTTTTGTGAAAGCC	GTTTAACCTGAGGTCACCGATTC
tbm2397	10	(AT)18	ACGTAGGATATGAAAGGTGGTC	GTTTGATTCATTTGTTCATTCATTCA
tbm2398	10	(TA)26	ACGCTTCTAATCTGTCGATCTG	GTTTCAAACATTTTCATGCATCAGC
tbm2399	10	(AT)19	ATATGGGAATGATTTCTTTGGA	GTTTGAATTTCGGTCATAGGTTGAGC
tbm2400	10	(TA)23	ATAGAAGGGACGTATCCACGAT	GTTTGAGACTTGCACACAATCATCATC
tbm2401	10	(AT)26	ACTTCTGTTATAAGCAAGCTTTGG	GTTTAGGTCGATTTGGAAAAACA
tbm2402	10	(TA)24	ATGGGGAAAATATTTCATGGGA	GTTTCACACATTCCCCTCTTCTTTCT
tbm2403	10	(AT)16(AC)5	ATTGACTCCGATTCTGAAACAGT	GTTTCCTCCACATTCATTATGGT
tbm2404	10	(TA)16	AGTAAATTAATCGAACGAAGCG	GTTTCTTTTTCTGCTTGCTAGTTGGC
tbm2405	10	(CT)17(AT)9	ATCAAAATTAAAAGGTGAGATGTG	GTTTGTCAATTGTCGTGCTAGCTTT
tbm2406	10	(AT)14	ATTGACCTTTCGTATTCGTTCA	GTTTGCATTCACTTGATGTGACCAAC
tbm2407	10	(TA)24	ACACCCTTTAATGTAACTTAACTTTTT	GTTTGAATTAAGAACACATTCCCATCG
tbm2408	10	(TA)14	AGGGATTTTAAATTTCCAAGAA	GTTTCACTGGTTTGAGCCGTAAAAT
tbm2409	10	(TA)24	ATCCGAAACCTTTGATCTTCAT	GTTTGCAGCAAGAAAACGGATATAA
tbm2410	10	(AT)16	ATACTGGATTCGTCATACTGGA	GTTTGCCACTTTCATAACAAGGGGTA
tbm2411	10	(AT)20	ATTTTGCTATTTTGTTGCCGAT	GTTTAAAAGATTGTGATTGGGCGT
tbm2412	10	(AT)16	AGAAATATGCTTTAATTTGTGAAGAA	GTTTACAATTTTCCACCGCTAACAAT
tbm2413	10	(TG)4(TA)17	AGAGATGAGTGTCGACCGAGAT	GTTTCCCTGGACGTGTTTAAAGAAAG
tbm2414	10	(AT)21	ACAAATCTTGTCTGCATCCCTT	GTTTCGAGCAAGAATAGGAGAGAGGT

Marker name	Corresponding linkage group of EXPEN2000 map (Shirasawa et al., 2010a)	SSR motif	Forward primer sequence	Reverse primer sequence
tbm2415	11	(AAT)18	ATTGCTGTCTGGCTCATTGTAA	GTTTGAACATAAGGCAAATTCTTGGC
tbm2416	11	(AT)22	AGATGCTATGCTTCTCCAATTC	GTTTAACATTTATAATCCTTGGTGGA
tbm2417	11	(AT)17	ACGAGGCCACTAATTTCCAATA	GTTTGCGGTGGTTTTCATTTAT
tbm2418	11	(AT)21	ATTTAAGGACCAGCAATTCCAT	GTTTGTGTCAAAGGATGAGAAGGAC
tbm2419	11	(AT)14	AGCATGATTGAGGTATCTCGTA	GTTTGCTTTGCATGAAGCCTA
tbm2420	11	(AT)15	AGGTTGCAACTAGGGAAGATTT	GTTTGGTTTGGTATTCTTTCCATT
tbm2421	11	(AT)10	ACATCCAAATTAATATGATCTCCAA	GTTTGGGCATGTTTATCCATC
tbm2422	11	(TA)20	ACGAATACGTTATTCTCGATTCA	GTTTCATAGGACAAATAGAGGGTTCA
tbm2423	11	(TTA)15	ACAAAACCAAGAAGCTAAGGTG	GTTTAAATCTCCCCCATAACA
tbm2424	11	(TTA)15	ACCTTCCTCCGTTTATGTTTTT	GTTTCTTTGACCAAATATTGGAA
tbm2425	11	(AT)22	ATAGTTTTTGCCACTTTTACAGC	GTTTAAAAAGGAGCATCCAAAGTTTTT
tbm2426	11	(AT)16	AGGAAAGGGAAAATCAAAACAC	GTTTATACCTTTTCGGCCTTGAAA
tbm2427	11	(AT)16	ACCACCTTCAACTCTCTTTCAC	GTTTGGTTTCATGCATGGATTTTTA
tbm2428	11	(AT)28	ATCTCGCATTCTCAAATCAATG	GTTTCACATTTGATGTACTCCTGATGA
tbm2429	11	(TA)17	ATGGAATTCTTTCTTCAAGGCA	GTTTAACCTGAGGCACACGTACAAC
tbm2430	11	(AT)28	ATCAAAATTGTTCATGTGGTCA	GTTTGAATTTATGTGTTTTATTTCCCC
tbm2431	11	(AT)24	ATACATGGTGCATTTGAAGGTT	GTTTCTCCCTTTTCAAAACCCTTT
tbm2432	11	(TA)24	ATGAGTGCATGCATAGGTGAAG	GTTTCGTCTTCAATGACATGTTTG
tbm2433	11	(AAT)15	ATTTAAGACCAAAATAGCCGCC	GTTTAGGAAGGATTTCCATACATCCC
tbm2434	11	(TA)16	AGAATCCTTGCTTGTGATAGGC	GTTTGGAGGCATAAGGATATTGTGGA
tbm2435	11	(TTC)17	AGTTTCTCTCTGATTCCTCTCA	GTTTGCAGTGGACTTTGGATGTCAC
tbm2436	11	(AT)17	ACTTAACGCTTGTCTTTACTTACGTG	GTTTCCGAGGCGAATCTTGAATAC
tbm2437	11	(TA)26	AGAAATATTACCTAAGCCACAGGA	GTTTAACGGAAGTTCTAGGCTGT
tbm2438	11	(AT)20	ATGCATGTATTTTTGGAGGGTC	GTTTCTTTTCCAGTAACTAGGCTGTGA
tbm2439	11	(TA)25	ACAAAATCCATTAAAGGAAATGAT	GTTTAGGGGATTGCATGTGTGTTA
tbm2440	11	(TA)24	ATGTCCATGATAAAGACTCGGG	GTTTCGAGATTGGGAGAGAGAAGAGA
tbm2441	11	(TA)24	ATTTATGCGGACAACTTTGAGG	GTTTAGGTGGGCTGATTAAGACAAAA
tbm2442	11	(AT)24(TAT)8	AGAAAGGTTAATGACTTTTGCACT	GTTTCTCATCAAGTAGAAGGCAATTAAG
tbm2443	11	(AT)22	ATAGTCTCTAACTCCTCCCGAA	GTTTACCAAATCATCACATTTCCTCC
tbm2444	11	(TA)14	ATCATGCCCCCGTAGTATATCA	GTTTCATGAATAGGGGAAAATAACCA
tbm2445	11	(TA)28	ATTCAACCCTTAAGAAATGGGA	GTTTCTTTTGGCCAGTGCAAAGTTATT
tbm2446	11	(TAA)18	ATTGGATTCCTACAACAACTTAAA	GTTTCAGTGTTCGATATTTGCTTTGG
tbm2447	11	(TA)27	ATTTATTGAGGTGCGTGCAAAT	GTTTCATCACCAAACGAGAAATCA
tbm2448	11	(AT)14	ATCTAAAAATCGCTGCCTTTTG	GTTTAAGTTGCTACCTTGACAGCGAT
tbm2449	11	(AT)22	ATCACGTGTCACAGATCACAAT	GTTTGAAAATCATTGCACTGTTTGATG
tbm2450	11	(TA)18	AGAAAGTTCCCGCTCTAAAAAG	GTTTGAATTTCCTCATATCATTCCTC
tbm2451	11	(AT)15	ATGAAACGGAGGGAGTACTGTT	GTTTAAATGCAACAAGGTGCAAG
tbm2452	11	(AT)20	ACACATTTTCAAATTTCAAGTCA	GTTTCCTATCTTGTTTGAATCCC
tbm2453	11	(AT)20	ATTCATCGCATTATGGAATCAG	GTTTCGACGAATTCAACATCCTAA
tbm2454	11	(TA)15	ATAGGAAAGAGATATACGTGAACCA	GTTTCCTAAATCGTATATCCAAACGAA
tbm2455	11	(AT)18	AGTTTGCTAGATGATAGTAGGTAGGG	GTTTCGATTCCGATGAACTTAGAGA
tbm2456	11	(TA)17	AGTTGTGTTGCTATGGCCTAAT	GTTTACATTCTTAGCTGTTACAATTTGA
tbm2457	11	(TA)16	AGATTTTAAATTTGGTTGATTTTGA	GTTTAAGCGAATCAACAATTTGTCAC
tbm2458	11	(TA)20	ATGAGTTGCAATTAAGTGGATGC	GTTTCTCCCTAAATCTAAATCTGTATGGT
tbm2459	11	(TA)14	AGAAGTTGTGTGAGACCAAGAG	GTTTGGGTTCAATTTGAGAAACG
tbm2460	11	(AT)16	ATACAAATCAATGTTATGTGTACCAA	GTTTACGAGCGCAAAAATTATGTC
tbm2461	11	(ATA)14	AGTATCGATGGACTTGTTGACC	GTTTCTTTTCACTATGGATGCAAAACG
tbm2462	11	(AT)20	ACACACACCTTACGTTATCTCG	GTTTCAGGGTAATCAATCGAACATTT
tbm2463	11	(AT)5(GT)14	ACTAAAAGTTGGCCCCTAAATG	GTTTATTGGTGTCTTATGGCGCT
tbm2464	11	(AT)15	ATCAATTTTGTGTTGTAATTGTAGAAA	GTTTGAAATCGATGGTCAATGAG
tbm2465	11	(GT)4(AT)21	ATTCTTTGTCCAATTTCTAGCAT	GTTTCACAAAAGGACAAACATCGAAA
tbm2466	11	(ATT)15	ATGATGGTGTGTGTTTCCACTT	GTTTGGTCCAATAAATAGATGCACG
tbm2467	11	(AT)14	ATTCATATACGTCCAATAGCAAATA	GTTTCTCCCCATTTTCTGACTTCAC
tbm2468	11	(AT)14	AGGGGCTAACTATAGGTTGAAA	GTTTCTGATTGATGTGGATGG
tbm2469	11	(AT)14	AGGTCTTTCATGTTAGTGGCTTT	GTTTCAAGGAAATTTCATAGGCTTTT
tbm2470	11	(TA)20	ACTTGAGGACAAGAAATTAAAGTGTG	GTTTCACATAAGGATTGTAGGAGTAGCA
tbm2471	12	(ATT)17	ATCAACTGACTTAGGAGAAATTGATG	GTTTCGATAATATTCAGGTGCAGG
tbm2472	12	(AT)21	ATTCTGTCATTGTGATTCCAGC	GTTTAAATAACGATGTTGTTTGTTTGAA
tbm2473	12	(AT)18	ATATTCATGCAATTTTGCCTTT	GTTTCGATTTTAATATTCAATGGTAGGGA
tbm2474	12	(TA)24	ATCGCATCACTAAGGTCGATTT	GTTTGCATTTTGTTAAACTTCCCCT
tbm2475	12	(AT)21	ACACTCTTCTACATATGTGGTATCTC	GTTTCGAAATATGGACTCAGGGACAT
tbm2476	12	(TA)21	ACACTCTTCTACATATGTGGTATCTC	GTTTCGAAATATGGACTCAGGGACA
tbm2477	12	(TAT)19	ACTTGTCTAACTAGGCATTTGACAT	GTTTAGGGTTGATATGGATGGTT
tbm2478	12	(AT)14	ATCAAAAATTGAGATCCGCATA	GTTTGATGATCAAGGCAAGAAAATG
tbm2479	12	(AT)20	ACCATTAGGCCAAGAGTCACAT	GTTTGCAAAAGTCAAGTGGGTTCATA
tbm2480	12	(TA)21	ATATCAATAGCGGTGTGGAAGG	GTTTCCAGAAATAAGAGGATGGAGGA
tbm2481	12	(AT)22(TAT)7	ATAAATGGCTCAGGAATTTGAA	GTTTAGAAAGTAGACTTTTAGCTTCCCA
tbm2482	12	(TA)23	ATAAATCATATTGCATTTTTACGA	GTTTGAATGTGCATATCAAATTAAACG
tbm2483	12	(AT)23	AGCAATTTCGTAGTGATGTCTTG	GTTTGATTATTCTTTGTCTCTCTCTCTCTC
tbm2484	12	(AT)16	ACGGATTATAATTCAATAGAGTATCG	GTTTAAGGTTGATGATTGGACTAAA
tbm2485	12	(TA)17	AGGGTAAAATGGTATTTTGACTTTC	GTTTGGGGGTGAGGGTACTTAT
tbm2486	12	(AT)18	ATGCTTTTCCGCACATACATTT	GTTTGTCGTCTCGATGAGAGTGTG
tbm2487	12	(TA)16	AGTGGTTACAAGACGATTGAACA	GTTTCTTCCTGGTTTTGATGGA
tbm2488	12	(AAT)19	ACCCAATCAAAAATATCCCTTG	GTTTCGCGTGTATTTTACTTGAAGG
tbm2489	12	(TA)17	ATGGGTTGGTGGATTTAGTAGC	GTTTGCCTTCATGACACTTTGATTT
tbm2490	12	(TAT)19	AGTGTGTTGGAATGAAGTTTGT	GTTTCGAAAAAGGTACACGTTGAA
tbm2491	12	(TA)23	ATAACATTGATTGGAAGTTGGA	GTTTGAATTTAACCCGTTATGCTT
tbm2492	12	(AT)17	ATTAATTTAGGTGCACACGGCT	GTTTCCTAGCTTAAAGGGGGTTAAA
tbm2493	12	(AT)14(TTAT)6	ATCACACCTCAAAATGAACCAA	GTTTCTTTTCCCCCACATTTTACTGTT
tbm2494	12	(TA)16	ATGTGAGGGGTCAGTTCACATT	GTTTGGATAATGAGCATGAAGCACAA
tbm2495	12	(TA)14	ATATTACTCACTCTCTGCAGGC	GTTTCCCATAAAACTTTGCCAGAAAT
tbm2496	12	(AT)15	ATCGCTCGTAACTCTTCCTCAT	GTTTAAAGAGAATTGCTGGGAAAACA
tbm2497	12	(TA)14	ATGGCAGAAAAATCACATCCAT	GTTTGCCTTTTTCACCATCTTTT
tbm2498	12	(TA)29	ATGTTGTCATTAAGGCAGATGA	GTTTGAGTGATTTCCGAACAAAAA
tbm2499	12	(AT)14	ACAAGTGACGGAGAAGTCGTTT	GTTTGAAAAAGGAAAGACGAGTGGAA
tbm2500	12	(AT)24	AGATCCTAACACTTATGCCATC	GTTTAGACGATTCATGTGTGAACATT
tbm2501	12	(AT)15	ATAGCATCTTTCACAGTTTCCA	GTTTGAATTCAGATGAACTCGATCTTT
tbm2502	12	(AT)18	ATGGAGTACCAGACTTGCAGTG	GTTTGAAACACCCATTTTAGATAAACGA
tbm2503	12	(ATA)16	ATTAAAGAGTGGAAAGGGACAGG	GTTTATTTTGGGGGATCAAAGGT
tbm2504	12	(TA)31	ATCTCGACTCAAACACAAATTCA	GTTTGGTGATTTTGAAGATGGAAGA
tbm2505	12	(TA)14	AGTTGAGGAAATACTTGTGCATT	GTTTGCCAAATCTGTTTGAAATTA
tbm2506	12	(AT)29	ATGTGCCGTGGACTACTACTCA	GTTTAAAATTTTGATTCCGCGACT
tbm2507	12	(AT)17	AGGATTTTCACTTGTTCCCTAA	GTTTCAAGGATTCAATATGATCACGA
tbm2508	12	(TA)15	ATCAAAGGGTGTCCATTTTTGT	GTTTGGATCTATGACAAATTGCACTAA
tbm2509	12	(AT)15	AGACAAACATGTTCTCATTGTCC	GTTTCTTTTTATCCTTGGTCGTCCT
tbm2510	12	(TC)8(TA)16	AGAAGAATTAAGTGTGGAGTTTGA	GTTTCAACCACGAAAAAGATTAGATGG

Supplementary Table S3 Characteristics of SSR markers used for the construction of GMF2 map

Marker name beginning with	Number of mapped markers	Origin	Developer	Core motif of SSR[a]
tma	15	Genomic (BAC end)	Ohyama et al. (2009)	AT
tmb	2	Genomic (BAC end)	Ohyama et al. (2009)	2-base motif other than AT
tmc	1	Genomic (BAC end)	Ohyama et al. (2009)	3-base motif
tme	3	cDNA	Ohyama et al. (2009)	various
tms	4	cDNA	Frary et al. (2005)	various
TES	8	cDNA	Shirasawa et al. (2010a)	various
TGS	4	Genomic (BAC end)	Shirasawa et al. (2010a)	various
tbm	185	EST-anchored genomic	This study	various

[a] The core motif was defined as the longest continuous repeat sequence in each SSR region.

Supplementary Table S4 Types of configuration of QTL alleles (Hayashi et al. 2012)

Configuration type	Estimated configuration of QTL alleles[a]
1	$\{Q_{l1}\},\{Q_{l2}\},\{Q_{l3}\},\{Q_{l4}\}$
2	$\{Q_{l1}\},\{Q_{l2},Q_{l3}\},\{Q_{l4}\}$
3	$\{Q_{l1}\},\{Q_{l2}\},\{Q_{l3},Q_{l4}\}$
4	$\{Q_{l1}\},\{Q_{l2},Q_{l4}\},\{Q_{l3}\}$
5	$\{Q_{l1}\},\{Q_{l2},Q_{l3},Q_{l4}\}$
6	$\{Q_{l1},Q_{l4}\},\{Q_{l2}\},\{Q_{l3}\}$
7	$\{Q_{l1},Q_{l4}\},\{Q_{l2},Q_{l3}\}$
8	$\{Q_{l1},Q_{l3}\},\{Q_{l2},Q_{l4}\}$
9	$\{Q_{l1},Q_{l3}\},\{Q_{l2}\},\{Q_{l4}\}$
10	$\{Q_{l1},Q_{l2}\},\{Q_{l3},Q_{l4}\}$
11	$\{Q_{l1},Q_{l2}\},\{Q_{l3}\},\{Q_{l4}\}$
12	$\{Q_{l1},Q_{l3},Q_{l4}\},\{Q_{l2}\}$
13	$\{Q_{l1},Q_{l2},Q_{l4}\},\{Q_{l3}\}$
14	$\{Q_{l1},Q_{l2},Q_{l3}\},\{Q_{l4}\}$

For definitions of the QTL alleles (Q_{l1}, Q_{l2}, Q_{l3}, and Q_{l4}), see Bayesian QTL mapping subsection of the Materials and Methods section in the main text.

[a] Alleles listed in the same brace are regarded as identical in state and alleles in different braces are regarded as different alleles.

Supplementary Table S5 Comparison of phenotypes of parental F_1 cultivars among experiments

		Experiment				Significance by two-way ANOVA		
Trait	Cultivar	1	2	3	4	Among cultivars	Among experiments	Interaction
DF	Geronimo	46.0^{d}	46.2^{d}	50.5^{ab}	48.0^{bcd}	**	**	ns
	Momotaro 8	47.5^{cd}	49.5^{abc}	51.7^{a}	50.0^{abc}			
HFT (cm)	Geronimo	65.5^{a}	65.2^{a}	49.5^{b}	49.5^{b}	**	**	ns
	Momotaro 8	64.0^{a}	61.2^{a}	42.8^{bc}	39.5^{c}			
NLFT	Geronimo	8.2^{b}	8.3^{ab}	8.7^{ab}	8.3^{ab}	*	ns	ns
	Momotaro 8	9.0^{ab}	9.8^{a}	9.0^{ab}	8.3^{ab}			
TFW (g/plant)	Geronimo	4279.0^{a}	4985.3^{a}	4556.8^{a}	-	**	*	ns
	Momotaro 8	2989.2^{b}	3061.3^{b}	2642.2^{b}	-			
TMFW (g/plant)	Geronimo	4279.0^{a}	4619.2^{a}	4429.5^{a}	-	**	*	*
	Momotaro 8	2745.2^{b}	2845.0^{b}	1861.8^{c}	-			
AFW (g)	Geronimo	308.5^{a}	347.9^{a}	321.9^{a}	-	**	ns	ns
	Momotaro 8	197.4^{b}	215.1^{b}	181.9^{b}	-			
AMFW (g)	Geronimo	308.5^{a}	338.1^{a}	320.3^{a}	-	**	ns	ns
	Momotaro 8	203.8^{b}	205.5^{b}	198.4^{b}	-			
NF	Geronimo	14.0^{a}	14.5^{a}	14.2^{a}	-	ns	ns	ns
	Momotaro 8	15.2^{a}	14.3^{a}	14.5^{a}	-			
NMF	Geronimo	14.0^{a}	13.8^{a}	13.8^{a}	-	*	*	*
	Momotaro 8	13.7^{a}	13.8^{a}	9.5^{b}	-			
SSC (°Brix)	Geronimo	4.2^{cd}	4.6^{bc}	3.8^{d}	-	**	**	ns
	Momotaro 8	5.9^{a}	6.3^{a}	5.1^{b}	-			

Data represent the means of individual values for 'Geronimo' (n = 6) or 'Momotaro 8' (n = 6) cultivar. Conditions of each experiment are listed in Supplementary Table S1.

For each trait, means sharing the same superscript letter (a, b, c or d) are not significantly different between experiments according to the Tukey–Kramer multi-comparison test.

* and **, Significant at $P < 0.05$ and $P < 0.01$ levels, respectively; ns, not significant.

Supplementary Table S6 Correlations between traits in experiment 1 (n =90)

	DF	HFT	NLFT	TFW	TMFW	AFW	AMFW	NF	NMF
HFT	0.517 **								
NLFT	0.670 **	0.591 **							
TFW	0.174	0.183	0.197						
TMFW	0.185	0.270 **	0.195	0.930 **					
AFW	0.124	0.210 *	0.129	0.722 **	0.638 **				
AMFW	0.152	0.213 *	0.139	0.838 **	0.776 **	0.925 **			
NF	0.063	-0.062	0.101	0.443 **	0.444 **	-0.284 **	-0.036		
NMF	0.065	0.065	0.098	0.207	0.395 **	-0.348 **	-0.249 *	0.746 **	
SSC	0.167	0.249 *	0.252 *	0.101	0.023	0.223 *	0.214 *	-0.168	-0.299 **

* and **, Significant at P < 0.05 and P < 0.01 levels, respectively.

Supplementary Table S7 Correlations between traits in experiment 2 (n =90)

	DF	HFT	NLFT	TFW	TMFW	AFW	AMFW	NF	NMF
HFT	0.373 **								
NLFT	0.452 **	0.396 **							
TFW	0.041	0.393 **	0.267 *						
TMFW	0.017	0.379 **	0.293 **	0.923 **					
AFW	0.069	0.315 **	0.246 *	0.855 **	0.770 **				
AMFW	0.050	0.382 **	0.278 **	0.911 **	0.884 **	0.930 **			
NF	-0.022	0.237 *	0.111	0.498 **	0.479 **	-0.015	0.211 *		
NMF	-0.086	0.066	0.078	0.178	0.394 **	-0.187	-0.064	0.643 **	
SSC	0.171	0.378 **	0.242 *	0.448 **	0.436 **	0.342 **	0.346 **	0.264 *	0.221 *

* and **, Significant at $P < 0.05$ and $P < 0.01$ levels, respectively.

Supplementary Table S8 Correlations between traits in experiment 3 (*n* =90)

	DF	HFT	NLFT	TFW	TMFW	AFW	AMFW	NF	NMF
HFT	0.550 **								
NLFT	0.777 **	0.556 **							
TFW	-0.020	0.179	0.077						
TMFW	-0.025	0.153	-0.036	0.280 **					
AFW	0.009	0.067	0.073	0.756 **	-0.016				
AMFW	0.116	0.150	0.160	0.678 **	0.162	0.832 **			
NF	-0.038	0.138	0.000	0.342 **	0.407 **	-0.348 **	-0.220 *		
NMF	-0.088	0.062	-0.124	-0.083	0.866 **	-0.454 **	-0.320 **	0.525 **	
SSC	0.045	0.061	0.088	-0.216 *	-0.182	-0.205	-0.238 *	-0.003	-0.060

* and **, Significant at $P < 0.05$ and $P < 0.01$ levels, respectively.

Supplementary Table S9 Correlations between traits in experiment 4 (n =90)

	DF	HFT
HFT	0.755 **	
NLFT	0.822 **	0.731 **

* and **, Significant at $P < 0.05$ and $P < 0.01$ levels, respectively.

Supplementary Table S10 QTLs for DF detected by the Bayesian method using combinations of experiments with EC condition or cropping season as a non-genetic factor

Combination of experiments[a] used for mapping	Environmental condition of each combination	Non-genetic factor included in analysis	SQI of QTL fitted in the model	LG	QTL position (cM)	QTL_ID	Common with QTLs shown in Table 4[b]	Configuration type[c]	Effects of QTL alleles				R^2	5% threshold of SQI[e]
									a_1[d]	a_2	a_3	a_4		
1 and 2	Autumn planting	EC condition	-	nd	-	-	-	-	-	-	-	-	-	0.959
3 and 4	Spring planting	EC condition	0.891	4	17	*df4.1*	no	12 (0.576)	0.000	-1.068	-0.094	-0.187	0.051	0.863
			0.936	11	9	*df11.1*	yes	13 (0.862)	0.000	-0.008	1.338	-0.003	0.076	
1 and 3	Low EC	Cropping season	-	nd	-	-	-	-	-	-	-	-	-	0.869
2 and 4	High EC	Cropping season	0.920	2	20	*df2.1*	yes	7 (0.819)	0.000	0.748	0.771	0.002	0.030	0.870

Posterior distributions for QTL position, configuration type and effects of alleles were obtained by 10,000 MCMC sampling cycles for all bins of 1cM length on a whole genome and summarized for each linkage group in the manner as described in ‘Materials and methods’.

nd, Not detected; LG, linkage group (see Fig. 2); a_1 and a_2, the effects of QTL alleles from 'Geronimo' (P1) haplotypes; a_3 and a_4, the effects of QTL alleles from 'Momotaro 8' (P2) haplotypes; R^2, estimated proportion of phenotypic variance explained by the QTL.

[a] Conditions of each experiment are shown in Supplementary Table S1.

[b] QTLs listed in Table 4 were detected by the Bayesian method using three or four experiments with EC condition and cropping season as two non-genetic factors.

[c] Types are listed in Supplementary Table S4. The posterior probability of most probable configuration type was indicated in the parenthesis.

[d] We assume that the allele effect of $a_1 = 0$ for all configuration types.

[e] Significance levels for SQI were calculated by a permutation test with 200 iterations.

Supplementary Table S11 QTLs for HFT detected by the Bayesian method using combinations of experiments with EC condition or cropping season as a non-genetic factor

Combination of experiments[a] used for mapping	Environmental condition of each combination	Non-genetic factor included in analysis	SQI of QTL fitted in the model	LG	QTL position (cM)	QTL_ID	Common with QTLs shown in Table 4[b]	Configuration type[c]	Effects of QTL alleles				R^2	5% threshold of SQI[e]
									a_1[d]	a_2	a_3	a_4		
1 and 2	Autumn planting	EC condition	1.090	1	91	*hft1.1*	yes	10 (0.779)	0.000	1.135	1.922	1.957	0.063	0.833
3 and 4	Spring planting	EC condition	1.008	1	34	*hft1.1*	yes	11 (0.616)	0.000	-0.038	2.106	5.070	0.104	0.827
			0.828	9	72	*hft9.1*	no	8 (0.673)	0.000	-2.445	-0.049	-2.085	0.044	
1 and 3	Low EC	Cropping season	0.937	1	42	*hft1.1*	yes	10 (0.614)	0.000	0.041	2.950	3.009	0.045	0.788
2 and 4	High EC	Cropping season	0.983	1	62	*hft1.1*	yes	10 (0.778)	0.000	-0.042	4.118	4.240	0.078	0.745

Posterior distributions for QTL position, configuration type and effects of alleles were obtained by 10,000 MCMC sampling cycles for all bins of 1cM length on a whole genome and summarized for each linkage group in the manner as described in ‘Materials and methods’.

nd, Not detected; LG, linkage group (see Fig. 2); a_1 and a_2, the effects of QTL alleles from 'Geronimo' (P1) haplotypes; a_3 and a_4, the effects of QTL alleles from 'Momotaro 8' (P2) haplotypes; R^2, estimated proportion of phenotypic variance explained by the QTL.

[a] Conditions of each experiment are shown in Supplementary Table S1.

[b] QTLs listed in Table 4 were detected by the Bayesian method using three or four experiments with EC condition and cropping season as two non-genetic factors.

[c] Types are listed in Supplementary Table S4. The posterior probability of most probable configuration type was indicated in the parenthesis.

[d] We assume that the allele effect of $a_1 = 0$ for all configuration types.

[e] Significance levels for SQI were calculated by a permutation test with 200 iterations.

Supplementary Table S12 QTLs for NLFT detected by the Bayesian method using combinations of experiments with EC condition or cropping season as a non-genetic factor

Combination of experiments[a] used for mapping	Environmental condition of each combination	Non-genetic factor included in analysis	SQI of QTL fitted in the model	LG	QTL position (cM)	QTL_ID	Common with QTLs shown in Table 4[b]	Configuration type[c]	Effects of QTL alleles				R^2	5% threshold of SQI[e]
									a_1[d]	a_2	a_3	a_4		
1 and 2	Autumn planting	EC condition	-	nd	-	-	-	-	-	-	-	-	-	0.894
3 and 4	Spring planting	EC condition	1.006	11	15	*nlft11.1*	yes	13 (0.872)	0.000	0.000	0.549	0.000	0.098	0.797
1 and 3	Low EC	Cropping season	0.903	5	63	*nlft5.1*	no	5 (0.423)	0.000	0.324	0.256	0.259	0.043	0.865
			0.986	11	15	*nlft11.1*	yes	13 (0.818)	0.000	0.000	0.412	-0.008	0.059	
2 and 4	High EC	Cropping season	-	nd	-	-	-	-	-	-	-	-	-	0.866

Posterior distributions for QTL position, configuration type and effects of alleles were obtained by 10,000 MCMC sampling cycles for all bins of 1cM length on a whole genome and summarized for each linkage group in the manner as described in 'Materials and methods'.

nd, Not detected; LG, linkage group (see Fig. 2); a_1 and a_2, the effects of QTL alleles from 'Geronimo' (P1) haplotypes; a_3 and a_4, the effects of QTL alleles from 'Momotaro 8' (P2) haplotypes; R^2, estimated proportion of phenotypic variance explained by the QTL.

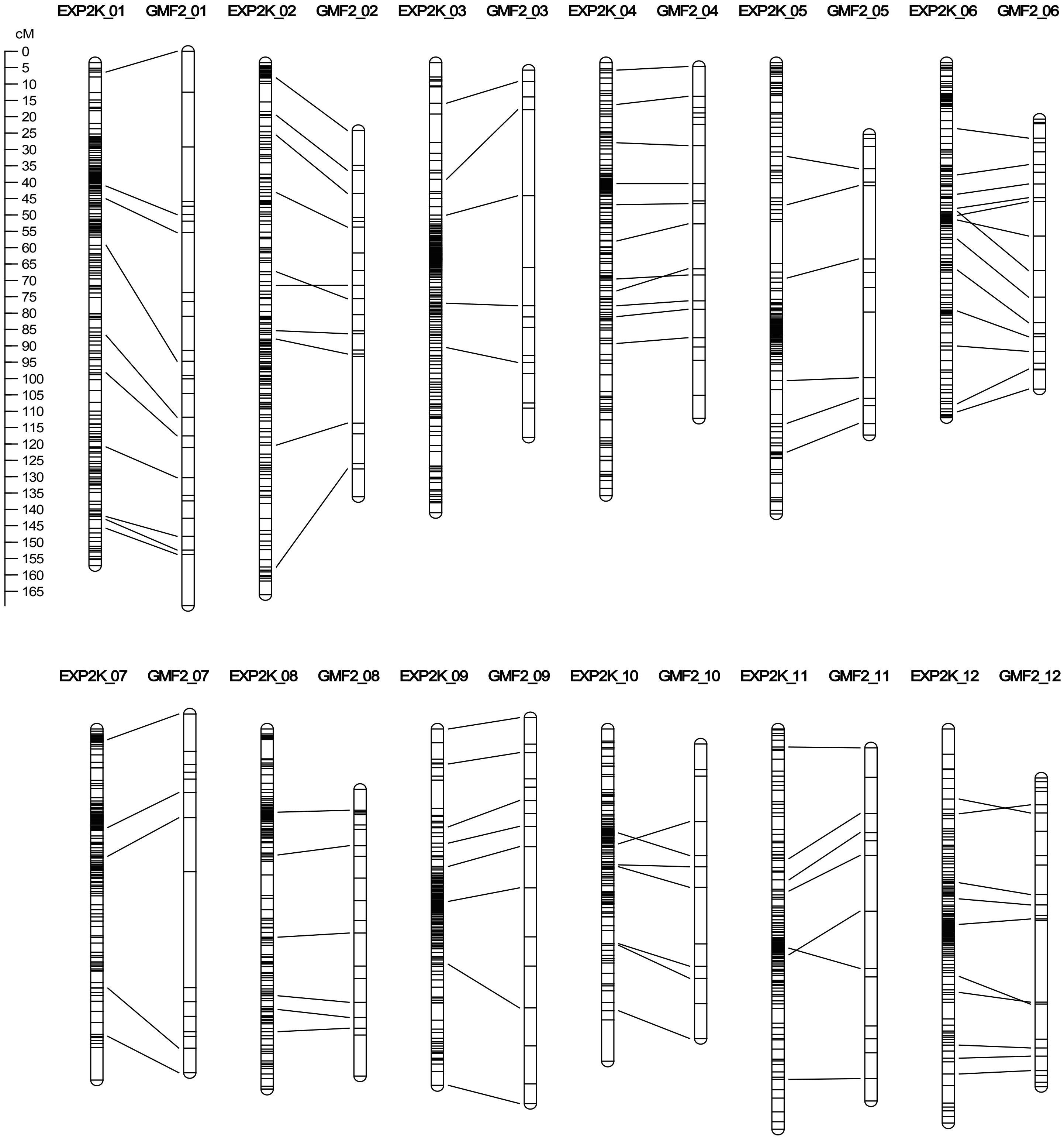
[a] Conditions of each experiment are shown in Supplementary Table S1.

[b] QTLs listed in Table 4 were detected by the Bayesian method using three or four experiments with EC condition and cropping season as two non-genetic factors.

[c] Types are listed in Supplementary Table S4. The posterior probability of most probable configuration type was indicated in the parenthesis.

[d] We assume that the allele effect of $a_1 = 0$ for all configuration types.

[e] Significance levels for SQI were calculated by a permutation test with 200 iterations.



Supplementary Fig. S1

Comparison between standard EXPEN2000 map from intercrossed F2 (left, Shirasawa et al. 2010a) and GMF2 map (right) developed in this study.

Anchor markers located on both maps are connected by lines.