

## Diversity Analysis of Rapeseed (*Brassica napus* L.) Genetic Resources in Japan

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**Diversity Analysis of Rapeseed (*Brassica napus* L.) Genetic Resources in Japan**

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# **Chapter 1: General Introduction**

## **1.1 Introduction of rapeseed**

Rapeseed (*Brassica napus* L.; genome AACC,  $2n=38$ ) also known as rape, oilseed rape (and, in the case of one particular group of cultivars, canola), is one of the most economically important oilseed crops over the world, which is thought to have multiple origins resulting from independent natural hybridization events between *B. rapa* (AA,  $2n=18$ ) and *B. oleracea* (CC,  $2n=18$ ) (U, 1935).

## **1.2 Origin and diffusion**

The natural hybridization of *B. rapa* and *B. oleracea* was considered to occur at the Mediterranean region in the southern Europe (Röbbelen *et al.* 1989). The original wild rapeseeds were presumed to be grown on the steep cliffs along the coast of this region (Shiga 1971). From where it was introduced into Asia in the early 18<sup>th</sup> century (Röbbelen *et al.* 1989).

## **1.3 World Production**

The cultivation of *Brassica* crops was believed to begin in the Middle Ages in Europe (Kimber and McGregor 1995), and some researcher conjectured that in Holland in the 17<sup>th</sup> century the rapeseed has been grown as a source of oil (Appelqvist and Ohlson 1972) but other thought it should be earlier than that time (Schröder-Lembke 1989).

Since the beginning of cultivation, with the improving of agronomic and processing technology, the utilization of both oil and meal of rapeseed is increasing gradually. As an important part of progress, the status of rapeseed oil has improved in recent decades. The new rapeseed cultivars with double low (low erucic acid and low glucosinolate)

traits were widely cultivated.

Nowadays, over 450 million tons of rapeseed seeds are harvested worldwide every year and accounts for about 20% of the world grain production (Carré and Pouzet 2014). In the year 2012, the EU leded world's rapeseed production with approximately 20 Mt, followed by Canada (15 Mt), China (12 Mt), and India (6 Mt) (ISTA Mielke Gmb 2012).

In recent years, genetic modified (GM) rapeseed have been grown widely and occupied at least 21% of the total rapeseed cultivation area (Nishizawa *et al.* 2010). Different type of GM rapeseed such as herbicide-tolerant (HT), insect-resistance (IR) and HT/IR have been constantly created and introduced into the farmland. In some developed countries such as Canada, 98% of the total rapeseed production was made up of GM rapeseed (Katsuta *et al.* 2015).

## **1.4 Rapeseed cultivation and breeding in Japan**

### **1.4.1 Cultivation history**

The history of rapeseed in Japan was relatively clearer because of the late introduction to this country. Rapeseed was introduced into two areas of Japan during the Meiji period (19<sup>th</sup> century). The first one, a cultivar adapted to warm climates was introduced into Fukuoka Prefecture in the early Meiji period (Shiga 1971). This cultivar was called “Chosensyu” (Korean type), but some important traits of it were very consistent with European varieties such as late maturation, high plant height and large plant size. Plus, there is no record of the introduction via Korean, this cultivar was considered to be introduced from Europe (Shiga 1971). In 1886, three cold-resistant cultivars “Hamburg”, “Essex Rapeseeds”, “German Rape” were introduced from Germany to Hokkaido (Shiga 1971). These cultivars had the traits of very late maturation, fall sowing, strong cold-tolerance and tall but slim plants. Among them, “Hamburg” which most adapted to the local environment, was cultivated in some northern Japan areas such as Aomori, Iwate and Niigata Prefectures (Shiga 1971).

Until 1961, cultivation area and yield of rapeseed in Japan were increased only except being affected by the Second World War. But the liberalization of soybean trade in 1961 and the liberalization of rapeseed trade after a few years caused the comprehensive declining of Japanese rapeseed cultivation (Shiga 1971, Honda 2009). In 2015, the cultivation area of rapeseed in Japan was 1620 ha, the total yield was 3100t (MAFF 2015). That was equivalent to only 0.1% of annual imports (2441480 t) (MOF 2016).

#### **1.4.2 Breeding history**

Since being introduced to Japan, the breeding of rapeseed has been carry out continuously. 1930 is an important time point in this process, before this year, the breeding work was mainly performed by agricultural research institute belongs to each prefecture government and the pure-line selection was the predominantly used method (Shiga 1971). Into the 1930s, the Japanese government started a formal breeding program to improve rapeseed which was expected to be used as a means of developing the rural economy. The initial purpose of the program was to breed out new cultivars which could maintain the good traits of Korean type and the maturation should be earlier. From the late 1950s, new cultivar with adverse environmental adaptability, lodging-resistance, disease-resistance, high yield and high quality became the breeding purpose (Shiga 1971, Yamamori 2006).

The breeding method that began in the 1930s were mainly crossbreeding, which including intraspecific hybridization of *B.napus* and the interspecific hybridization between *B. napus* and *B. rapa*. Heterosis breeding for F<sub>1</sub> lines was also used by the breeders (Shiga 1971). In recent years, the improvement of fatty acid composition has become the target of breeding, new cultivars such as “Nanashikibu”, “Kirariboshi” have the double-low quality same as canola (Yamamori 2006).

Until now, more than 200 rapeseed varieties were breed out in Japan.

### **1.4.3 Challenges in rapeseed breeding in Japan**

Although large-scale cultivation has ceased, the Japanese breeders are still working on the improvement of rapeseed varieties. In 2014, NARO (National Agriculture and Food Research Organization) disclosed new rapeseed cultivar “nanaharuka”, which is suitable for growing in the warm southern region of Japan (NARO 2014). In 2015, another new cultivar “kirakiraginga” was disclosed, which is a double-low variety with higher yields (Honda *et al.* 2017). Besides these, other studies on vegetable rapeseed are ongoing too (Tsuge *et al.* 2015).

The aim of these studies is to provide new varieties and new cultivation methods for both actual and potential rapeseed requirements, which including the demand for vegetable rapeseed, demand for rapeseed meal for feed, demand for biofuels, green manure, landscape plant and the demand for high-quality varieties to meet future large-scale cultivation due to decline in cultivation inputs or the price increases of import rapeseed (Nonaka 2013, Fujii 2011, Honda *et al.* 2017).

## **1.5 Rapeseed genetic resources situation in Japan**

### **1.5.1 Definition of genetic resources**

According to the OECD definition, Genetic resources are genetic material of plants, animals or micro-organisms of value as a resource for future generations of humanity (OECD 1997). FAO also give a similar definition about plant genetic resources for food and agriculture: It means any genetic material of plant origin of actual or potential value for food and agriculture (FAO 2009).

In this study, I would like to use “Genebank resources” to refer to the rapeseed cultivars and landraces which were preserved in the genebank. And a phrase “Feral resources” would be used to refer to the rapeseed which are growing in the area with out of the human’s management.

### 1.5.2 Genebank resources

The gene bank belongs to the Genetic Resources Center, NARO (National Agriculture and Food Research Organization) is the largest one in Japan which collected more than 600 germplasms, including more than 300 Japanese germplasms and other overseas germplasms.

### 1.5.3 Feral resources

Although rapeseed is not a native species in Japan, many feral rapeseed populations were found around the country (Ministry of Agriculture, Forestry and Fisheries 2014). The observation and monitoring of some feral populations showed that there were no expansion or contraction of them (Katsuta *et al.* 2015). It is generally thought that most feral rapeseeds are derived from the escape of the domesticated plants (Nishizawa *et al.* 2010). Some studies also assumed that feral populations of rapeseed have formed after the 19<sup>th</sup> century (Kameda *et al.* 2010). But because rapeseed grows throughout Japan, the precise distribution records have not been created (Nishizawa *et al.* 2010).

In recent years, seeds spilled during transportation process of the large quantity of import rapeseed were assumed to be a new origin of feral populations. But it needs to be pointed out that GM rapeseed occupied more than 80% of the imported rapeseeds, and most of the rapeseed plants in the port and roadside were proved to be non-GM ones (Saji *et al.* 2005).

Based on the above information, I can draw a conclusion that Japan's feral rapeseed is very likely to come from the escape of more ancient cultivars. Which may include cultivars that have been cultivated in Japan, and may also include varieties imported as raw material for oil extraction. These rapeseeds are affected by the natural environment after being introduced into Japan, resulting in some variations which adapt to the Japanese environment. If such variations are present, some of the feral rapeseeds will exhibit genetic characteristics different from NARO rapeseed accessions in the diversity analysis (Fig. 1.1). In this case, they may have the potential as breeding

materials and become genetic resource that can be utilized. Here, I use "feral resources" this new name to refer to them, intended to emphasize their possibility.

## **1.6 Genetic diversity research of genetic resources**

### **1.6.1 Importance of genetic diversity research**

Definition of biological diversity could be written as the variation present in all species of plants and animals, their genetic material and the ecosystems in which they occur (Rao and Hodgkin 2002). The biological diversity can occur at three levels: genetic diversity (variation in genes and genotypes), species diversity (species richness) and ecosystem diversity (communities of species and their environment) (Rao and Hodgkin 2002). Diversity in plant genetic resources provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics (Govindaraj *et al.* 2015). But the cultivation, domestication and breeding will select elite individuals, this will lead to a decline in genetic diversity (Feuillet *et al.* 2008, Tester and Langridge 2010).

The availability of a gene bank with a high genetic diversity could provide a better range of parental selection for breeding, meanwhile, assessment of the genetic diversity of existing gene banks is also a means to improve the efficiency of utilization and construction of it (Govindaraj *et al.* 2015). It is also important to study the genetic diversity of feral resources. The remarkable diversity of regional landraces, local cultivars and related species offers a reservoir of genetic variation that has the potential to impact positively on crop improvement and sustainable agricultural production (Feuillet *et al.* 2008). Some agricultural traits such as male sterility, disease resistance, insect resistance were successfully introduced into cultivars from feral species (Duvick 1984, Feuillet *et al.* 2008, Yao *et al.* 1997).

### **1.6.2 Assessment methods of Genetic Diversity**

Morphological, and biochemical measure can be used to analysis genetic diversity, but the assessment based on molecular markers has gained more importance due to the speedy, quality of data generated and the widespread presence. Unlike other markers, molecular markers have an almost unlimited number and unaffected by environmental factors and/or the developmental stage of the plant (Govindaraj *et al.* 2015, Mondini *et al.* 2009).

Nowadays, new methods like Next Generation Sequencing (NGS) has become a useful way of genetic diversity assessment. Whole genome sequencing data could give comprehensive genetic information of the individuals (Pop and Salzberg 2008). However, although compared to traditional sequencing, the cost of NGS is much cheaper, it is still not very realistic in genetic diversity study of Japanese rapeseed resource.

### **1.6.3 Current Status of crop genetic diversity research in Japan**

Japanese researchers have made a lot of achievements in the research of genetic diversity of several crop species partially included their wild relatives. Some major crops such as rice, maize, soybean, wheat, sorghum have been analyzed for genetic diversity in recent years (Kojima *et al.* 2005, Ebana *et al.* 2008, Kaga *et al.* 2012, Shehzad *et al.* 2009). Several core collections, which can overcome the restriction of the utilization of large size of germplasm in breeding by using subsets of the entire collection of the species have been constructed too (Kojima *et al.* 2005, Ebana *et al.* 2008, Kaga *et al.* 2012, Shehzad *et al.* 2009).

However, there is no comprehensive study on the genetic diversity of rapeseed in Japan, both of genebank resources and feral resources. And a core collection of the NARO Genebank which will be very useful for breeding work is still waiting to be constructed.

## 1.7 Objectives

The purposes of this thesis were to assess the genetic diversity of the rapeseed genetic resources in Japan, to explore their situation and potential for further exploitation for breeding efforts. The three main components of this study were compiled in each chapter. In Chapter 2, the NARO genebank rapeseed resources were analyzed by SSR marker to obtain the information of its genetic diversity and genetic structure. Japanese germplasms from different regions were analyzed separately to explore the effects of breeding on germplasm resources. A core collection was constructed based on the polymorphic allele information to facilitate the future breeding work. In Chapter 3, the feral rapeseed resources collected from 13 locations of Japan were analyzed by SSR marker to reveal their genetic diversity and structure to reveal the possible formation way of them. Then, a comparison of the genebank resources and feral resources was preformed to understand whether there is similarity between them. Such comparisons will also help to determine whether the feral resources are valuable as breeding materials. Finally, in Chapter 4, the comprehensive discuss of the results of the above studies described in Chapter 2 and Chapter 3, and summarize the main conclusions of this study.



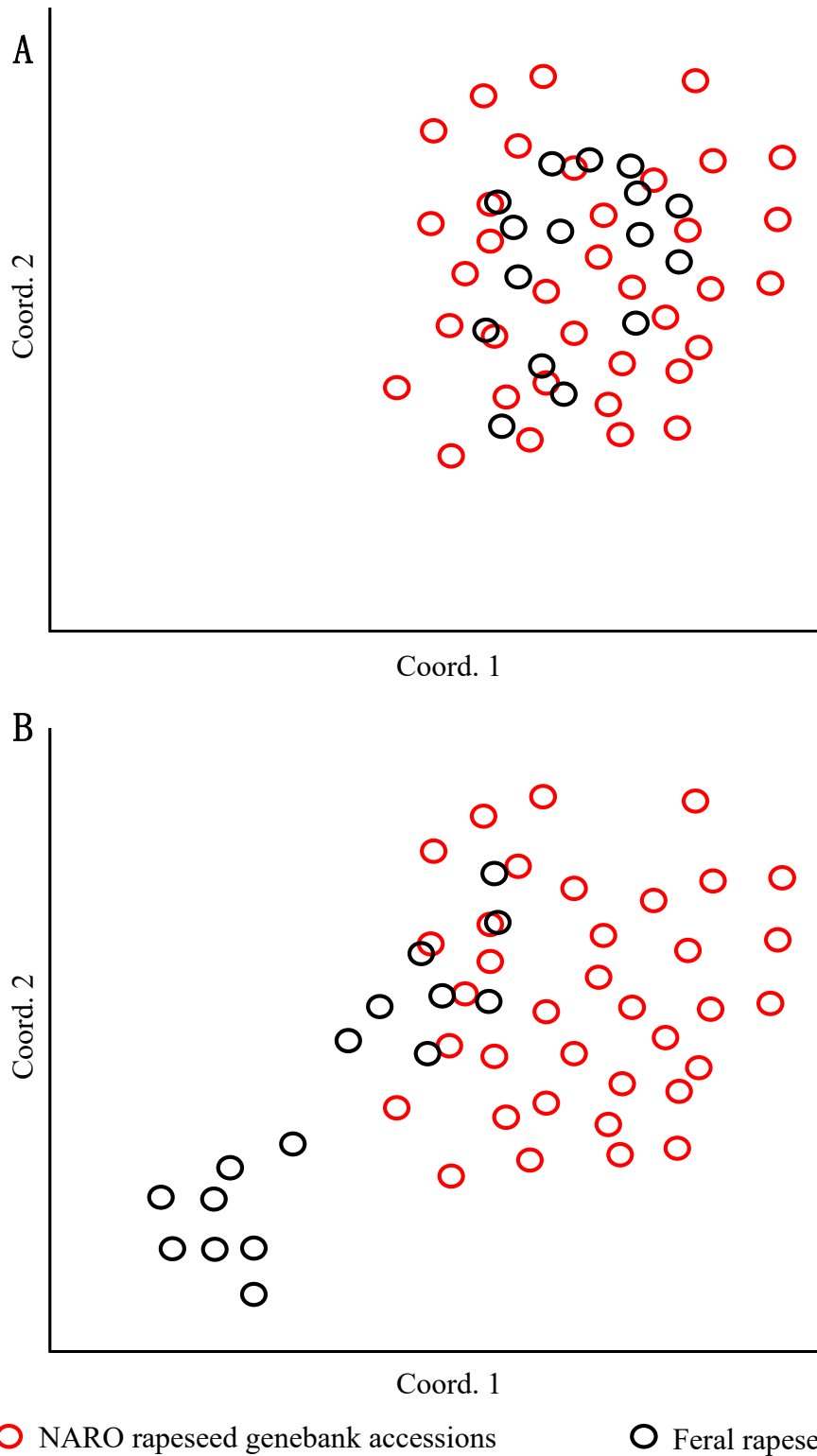


Fig. 1.1 The simulation PCoA of the relationship between NARO rapeseed genebank and feral rapeseed. A, assume that feral rapeseed comes entirely from the resources contained in the NARO rapeseed genebank; B, assume that feral rapeseed comes partly from the resources contained in the NARO rapeseed genebank. If the real situation is similar to B, then it can be considered feral rapeseed as genetic resources.

## **Chapter 2: Genetic diversity analysis and core collection construction in rapeseed genetic resources in Japan**

### **2.1 Introduction**

Genetic resources are key to progress in breeding, contributing to sustainable agriculture and associated industries. More than 600 accessions, including >300 Japanese landraces and cultivars, are maintained at the Genetic Resources Center of the National Agriculture and Food Research Organization (NARO Genebank). A collection of this size is expected to contain a wide range of genetic variation and offer opportunities for trait improvement. However, screening for target traits in the whole collection is often time-consuming, laborious, and costly. To efficiently use germplasm collections in breeding, knowledge of the genetic diversity and phylogenetic relationship among the germplasms is vital. In addition, establishing a representative subset of the whole collection, called a core collection, will be a feasible way for management, evaluation, and utilization of genetic resources.

A core collection should represent most of the diversity in the whole collection and should cover at least 70% of the alleles present in the whole collection (Brown 1989). Phenotypic traits have been used for constructing core collections, but they are easily affected by environmental conditions and are sometimes difficult to measure accurately. Recently, many core collections have been established by using DNA marker data, because DNA markers can be easily obtained and are highly stable and polymorphic (Taniguchi *et al.* 2014, Xu *et al.* 2016, Zhao *et al.* 2016). In rapeseed, several studies revealed genetic diversity of different collections using molecular markers such as RFLP (Song and Osborn 1992), RAPD (Ma *et al.* 2000), SRAP (Riaz *et al.* 2001), AFLP (Seyis *et al.* 2003), and SSR (Hasan *et al.* 2006). SSR markers are superior because they are able to detect multiple alleles per locus, are codominant at a single locus, and are relatively evenly distributed across genomes (Zalapa *et al.* 2012); they have been

widely used in recent diversity analyses of Brassica species (El-Esawi *et al.* 2016, Guo *et al.* 2016, Yao *et al.* 2012).

Over the last five decades, effort devoted in Japan to rapeseed breeding has resulted in considerable progress. Despite a large number of germplasms in NARO Genebank, only a few studies analyzed the small number of either Japanese or overseas accessions in this collection (Diers and Osborn 1994, Gyawali *et al.* 2013, Hasan *et al.* 2006, Ma *et al.* 2000). The number of rapeseed germplasms in the NARO Genebank has increased owing to both past studies and exploration of genetic resources.

The aims of this chapter are to examine the genetic diversity and population structure of NARO rapeseed collection using SSR markers, and to establish a core collection with good representation of the genetic diversity present in the whole collection.

## **2.2 Materials and methods**

### **2.2.1 Plant Material**

The rapeseed collection in NARO Genebank hold 639 germplasms, the seeds are preserved in cool dry storage. I excluded accessions from our analysis if both parental lines were in the collection. The total number of accessions analyzed was 582 (Appendix 1), including 305 Japanese accessions (landraces, breeding lines, and cultivars) and 277 overseas accessions from all inhabited continents except Africa.

### **2.2.2 Genotyping**

Seeds were germinated on moistened filter paper in 9-cm Petri dishes and then transplanted into a 72-cell tray filled with granular culture soil (Nippi-Engei-Baido-1gou soil, Nihon Hiryo Co., Ltd., Tokyo, Japan). Seedlings were grown in a climate chamber (25/22 °C 12 h/12 h) until the first true leaves had fully expanded. Genomic DNA was extracted from the first true leaf of each seedling by using the DNeasy Plant

Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol with some minor modifications.

A total of 504 Brassica SSR markers (Appendix 2) were prescreened against 8 representative accessions that were chosen on the basis of their origins and breeding histories: OOMINATANE (Japan), MICHINOKUNATANE (Japan), ASAHINATANE (Japan), CASCADE (USA), HAMBURG 1 (Germany), WESTAR (Canada), PROTA (Germany), RAPORA(Korea) (Wang *et al.* 2012, Cheng *et al.* 2009, Li *et al.* 2013, Li *et al.* 2011, Piquemal *et al.* 2005, Xu *et al.* 2010, Suwabe *et al.* 2002, Kim *et al.* 2009, Iniguez-Luy *et al.* 2009, Nagaoka *et al.* 2010, Lowe *et al.* 2002, AAFC Consortium 2016). SSR markers with clear reproducible polymorphic amplification products were then applied to all other accessions. PCR mixtures (10  $\mu$ l) contained template DNA (10 ng), 1 $\times$  KAPA 2G buffer A, 200 nM dNTP, 0.5 mM MgCl<sub>2</sub>, 0.1 U KAPA 2G Fast DNA polymerase (KAPA Biosystems Inc., Woburn, MA, USA), 2 pmol reverse primer, and 0.5 pmol forward primer. The forward primers were 5'-labeled with the fluorescent dyes 6-FAM, VIC, NED, or PET (Shimizu and Yano 2011). PCR was performed in a C1000 Thermal Cycler (Bio-Rad Laboratories, Inc., Hercules, CA, USA) as follows: initial denaturation at 94 °C for 3 min; 30 cycles of 94 °C for 20 s, 54 °C for 30 s, and 62 °C for 30 s; 3 cycles of 94 °C for 20 s, 49 °C for 10 s, and 72 °C for 5 s; and a final extension at 72 °C for 10 min. The size of the amplified fragments was estimated by using an automated DNA analyzer (model 3130xl) with a GeneScan-600LIZ size standard and GeneMapper v. 4.0 software (all Thermo Fisher Scientific, Inc., Waltham, MA, USA).

### **2.2.3 Genetic diversity and population structure analysis**

The number of alleles, major allele frequency, number of rare alleles (frequency <5%), and polymorphism information content (PIC) were calculated for the whole collection and for each geographic group in PowerMarker v. 3.25 software (Liu and Muse 2005). Observed heterozygosity (H<sub>o</sub>), expected heterozygosity (H<sub>e</sub>), Shannon's information index (I), pairwise F statistics (F<sub>ST</sub>), and Nei's genetic distance (Nei *et al.*

1983) were calculated in GenAlEx v. 6.502 software (Peakall and Smouse 2012). The components of variance between Japanese and overseas accessions, between different groups and among individuals within groups were estimated from the genetic distance matrix, as specified in the analysis of molecular variance (AMOVA) procedure using Arlequin 3.5.2.2 software (Excoffier and Lischer 2010). A nonparametric permutation procedure with 1000 permutations was used to test the significance of variance components associated with the different possible levels of genetic structure in this study.

Genotyping data for the SSR markers were analyzed by using the model-based STRUCTURE v. 2.3.4 software (Pritchard *et al.* 2000) to determine the most probable number of clusters (K value) and to assign rapeseed accessions to different clusters. The K value was determined by running an admixture and related frequency model with K = 1 to 20 (10 replications per K value); the burn-in period of each run and the Monte Carlo Markov Chain (MCMC) lengths were both set to 100,000. The website program STRUCTURE HARVESTER was used to estimate the optimal number of K value (Earl 2012). This program follows the  $\Delta K$  method of Evanno *et al.* (2005). The same set of genotyping data was used to perform principal coordinates analysis (PCoA) in GenAlEx 6.502, and to construct the phylogenetic tree based on neighbor-joining (NJ) method implemented in MEGA7 software (<http://www.megasoftware.net/>).

#### **2.2.4 Construction of core collection**

Core collections were constructed using four different methods: two maximization (M) strategy methods with different algorithms, the Core Hunter method, and the random sampling method. Both M strategy methods select a core collection to maximize the number of alleles of the SSR markers. CoreFinder v. 1.1 (Cipriani *et al.* 2010) is based on the NP-complete set-covering problem and uses a Las Vegas-style randomized algorithm. PowerCore v. 1.0 (Kim *et al.* 2007) uses an advanced M strategy with a modified heuristic algorithm (A\*) that can find the optimum path for sample selection. Core Hunter v. 2.0 (De Beukelaer *et al.* 2012) is a fast core-subset-selection

program based on multiple genetic diversity measures and using a Mixed Replica search algorithm. The software allows choosing sampling intensity and the genetic measures to be used as selection criteria. The Core Hunter software was run in R (<http://www.r-project.org/>); the modified Roger's distance (weight 0.7) and Shannon's information index (weight 0.3) were chosen to define a core collection comprising about 20% of the entry collection. In the random sampling method, before sampling, a neighbor joining (NJ) tree based on Nei's genetic distance is constructed in MEGA7 software. Sampling was performed according to Hu *et al.* (2000): initially, an accession is selected at random from each lower-order level subgroup, if there is just one accession in the subgroup, it is sampled; if there are two accessions, one is randomly selected. A new dendrogram was then generated, and the process was repeated until the number of selected accessions was reduced to 20% of the initial collection. To evaluate the representativeness of the different core collections, genetic diversity indices (allele number, allele retention ratio, number of effective alleles,  $H_o$ ,  $H_e$ ,  $I$ , and PIC) were calculated in PowerMarker v. 3.25 and GenAlEx 6.502 software. The differences between the whole collection and each core collection were tested by t-test.

### **2.2.5 Verify the core collection based on the phenotypic data**

To validate the representativeness of the core collection based on phenotypic data is a common method. In this study, although no large-scale cultivation experiments were conducted to verify the representativeness of the core collection, the NARO rapeseed genebank's existing characterization data could still be used for a rough validation. In the NARO genebank database, rapeseed phenotype data recorded in different years and locations were preserved. These data do not contain all accessions, and a accession may be investigated several times. Therefore, it is not feasible to accurately evaluate the representativeness of the core collection base on these data. However, if the accessions contained in the core collection only cover a fraction of the total range of data, then the core collection could be considered to be unsuccessful. On the contrary, if the core collection can basically cover the range of the total data, it could

be think that the core collection is basically successful. Therefore, I selected the characterization data of several important traits from the NARO rapeseed genebank to analyze the representativeness of the core collection. These traits include: plant type, plant height, panicle length, seed color, cold tolerance, snow resistance, disease resistance, lodging resistance, oil content, erucic acid content, oleic acid content, linoleic acid content, linolenic acid content, glucosinolate content, 1000 grain weight.

## **2.3 Results**

### **2.3.1 Genetic Diversity of the NARO rapeseed collection**

Prescreening selected 30 of the 504 SSR markers. The selected markers amplified a total of 311 alleles in the 582 accessions, ranging from 3 (BoGMS0660 and BoEMS0049) to 39 (BrGMS0070) per marker, with a mean allelic richness of 10.37 (Table 2.1); 214 alleles (68.8%) with low frequency ( $<0.05$ ) were regarded as rare alleles. In addition, the selected 30 SSR markers amplified only one or two alleles in each accession. Average genetic diversity indices were 0.56 for major allele frequency, 0.57 for  $H_e$ , and 0.52 for PIC. The average  $H_o$  value was 0.05 (range, 0.01–0.34), indicating that almost all accessions in the whole collection were highly homozygous.

The genetic diversity indices for geographical groups are summarized in Table 2.2. The average number of alleles per maker was 8.50 in Japanese germplasms and 9.37 in overseas germplasms. Among Japanese geographical groups, the average number of alleles per marker ranged from 2.90 (Chugoku-Shikoku area) to 5.43 (Chubu area), whereas overseas geographical groups had a wider variation, from 3.13 (Oceania) to 8.07 (Europe). The values of all other genetic diversity indices ( $H_o$ ,  $H_e$ ,  $I$ , PIC) were lower in Japanese than in overseas geographical groups. Hierarchical analysis of molecular variance revealed significant differences at all hierarchical levels (Table 2.3); the percentage of variation was highest among individuals within geographical groups (67.18%), followed by that between Japanese and overseas accessions (17.71%).

There was significant genetic differentiation between geographic groups in Japan, except between Kanto and Tohoku and between Kanto and Chubu. Pairwise  $F_{ST}$  ranged from 0.017 (Kanto and Chubu) to 0.192 (Hokkaido and Chugoku-Shikoku) (Table 2.4). The  $F_{ST}$  values between Hokkaido and western Japanese geographic groups (Kinki, Chugoku-Shikoku, and Kyushu) showed relatively high differentiation. Nei's genetic distance among Japanese geographic groups ranged from 0.044 (Kinki and Kyushu) to 0.173 (Hokkaido and Chugoku-Shikoku). Similar to pairwise  $F_{ST}$ , the genetic distances tended to be higher between the Hokkaido group and western Japanese geographic groups.

### **2.3.2 Population structure of the NARO rapeseed collection**

The STRUCTURE analysis suggested  $K = 2$  as the real value of  $K$  even though a secondary peak of  $\Delta K$  exists at  $K = 4$  (Fig. 2.1), indicating there are two genetic clusters in the NARO rapeseed collection (Fig. 2.2). With the membership probabilities ( $Q$ ) threshold of 0.80, 227 accessions, mostly originating from overseas, were assigned to subgroup 1, and 276 accessions, mostly originating from Japan were assigned to subgroup 2 (Table 2.5). The remaining 79 accessions are assigned to admixed group, i.e.,  $Q < 0.8$ . The result of PCoA was similar to that of STRUCTURE analysis (Fig. 2.3). The first and second factors of the PCoA explained approximately 19.1% and 7.3% of the variation in the genetic distance matrix, respectively. A bi-dimensional PCoA scatter plot indicated differentiation between Japanese and overseas accessions (Fig. 2.3). The neighbor-joining (NJ) tree further confirmed the differentiation between Japanese and overseas accessions (Fig. 2.4).

### **2.3.3 Construction of core collection**

Four different core collections were developed by different methods. Sample size and genetic diversity indices of each core collection are shown in Table 2.6. The random sampling strategy and CoreHunter selected the largest number of accessions (116; 19.93% of the whole collection), whereas the CoreFinder method selected the smallest number (96; 16.49%). The core collections constructed by the two M strategy methods



(PowerCore and CoreFinder) had the highest allele retention ratio (100%), indicating that they had all alleles observed in the whole collection, whereas approximately 30% of alleles were lost in the two other core collections. Other indices (except  $H_o$ ) were higher in the core collections constructed by the two M strategy methods than by the other two methods, although there were no significant differences among the core collections or between each core collection and the whole collection. Comparison of genetic diversity indices indicated that the core collections developed by PowerCore and CoreFinder were highly representative of the whole collection. Since the core collection by CoreFinder contains fewer accessions (96) than that by PowerCore (103), the former should be used as the core collection of the NARO rapeseed collection (Table 6). This core collection includes 39 Japanese accessions from seven geographic areas (Hokkaido, 2; Tohoku, 7; Kanto, 7; Chubu, 7; Kinki, 8; Chugoku-Shikoku, 1; Kyushu, 5; unknown, 2) and 57 overseas accessions (America, 6; Asia, 6; Europe, 41; Oceania, 2; unknown, 2) (Appendix 1). A bi-dimensional PCoA scatter plot also demonstrated that this core collection maintains genetic diversity, although it included fewer than 20% of accessions present in the whole collection (Fig. 2.5).

#### **2.3.4 Verification of the core collection**

Fig. 2.6-2.20 shows the representation of the core collection for the NARO rapeseed collection. Among them, for the data recorded in the form of grading (classification), I calculated the different levels (categories) as a percentage of the total number of samples, drawn into a histogram. For linear change data, it is performed by boxplot showing. From the figures, we can see that in the traits recorded in grading (classification), the core collection basically contains each level (category) (except for the extreme strong of lodging resistance. But at this level of this trait, NARO rapeseed genebank has only one accession) (Fig. 2.6, 2.9-2.13, 2.19). For linear change data, the core collection may cover most of the range of NARO rapeseed genebank (Fig. 2.7, 2.8, 2.14-2.18, 2.20).

Table 2.1. Summary statistics of the 30 SSR markers used for genotyping of 582 rapeseed accessions.

Marker name	Linkage group	Number of alleles	Number of rare alleles	Major allele frequency	Ho	He	PIC
BrGMS4028 <sup>a</sup>	A1	9	5	0.46	0.34	0.71	0.67
BrGMS4031 <sup>a</sup>	A1	5	3	0.86	0.04	0.24	0.22
BRAS084 <sup>b</sup>	A1	22	17	0.30	0.10	0.83	0.81
BrGMS1411 <sup>a</sup>	A2	7	4	0.58	0.05	0.59	0.55
BrGMS0667 <sup>a</sup>	A2	15	8	0.51	0.06	0.71	0.69
BrGMS2498 <sup>a</sup>	A3	4	2	0.52	0.04	0.52	0.40
sN2025 <sup>c</sup>	A4	10	5	0.44	0.04	0.70	0.65
BrGMS2252 <sup>a</sup>	A5	4	2	0.82	0.03	0.32	0.29
BrGMS0070 <sup>a</sup>	A5	39	36	0.28	0.06	0.87	0.86
BnEMS0753 <sup>d</sup>	A6	7	4	0.63	0.02	0.52	0.46
BrGMS3750 <sup>a</sup>	A6	6	2	0.60	0.02	0.57	0.53
BrGMS3837 <sup>a</sup>	A7	8	6	0.60	0.01	0.51	0.41
BnEMS0620 <sup>d</sup>	A7	17	14	0.54	0.08	0.64	0.60
BrGMS0742 <sup>a</sup>	A8	11	8	0.61	0.03	0.55	0.50
BnGMS0281 <sup>e</sup>	A9	8	4	0.43	0.06	0.71	0.66
BrGMS3857 <sup>a</sup>	A10	5	2	0.61	0.06	0.55	0.49
BrGMS3688 <sup>a</sup>	A10	6	2	0.41	0.06	0.71	0.66
BrGMS0086 <sup>a</sup>	A10	12	7	0.41	0.06	0.76	0.73
BnGMS271 <sup>e</sup>	C1	9	6	0.48	0.02	0.59	0.50
BoGMS2016 <sup>f</sup>	C2	15	9	0.30	0.03	0.84	0.82
BoEMS0016 <sup>g</sup>	C2	9	6	0.50	0.05	0.65	0.60
BoGMS0660 <sup>f</sup>	C2	3	1	0.61	0.01	0.48	0.37
BnGMS0289 <sup>e</sup>	C3	21	18	0.44	0.03	0.62	0.55
BnGMS347 <sup>e</sup>	C4	10	8	0.44	0.04	0.62	0.55
BoGMS0037 <sup>f</sup>	C5	9	7	0.85	0.01	0.26	0.23
BoGMS1909 <sup>f</sup>	C6	13	10	0.78	0.03	0.37	0.36
BnGMS0353 <sup>e</sup>	C6	8	5	0.54	0.04	0.62	0.57
BoEMS0049 <sup>g</sup>	C7	3	1	0.53	0.01	0.50	0.38
BnGMS0336 <sup>e</sup>	C8	4	1	0.81	0.17	0.33	0.31
BoGMS0525 <sup>f</sup>	C9	12	11	0.89	0.07	0.21	0.21
Average		10.37	7.13	0.56	0.05	0.57	0.52

Ho: observed heterozygosity, He: expected heterozygosity, PIC: polymorphism information content.

<sup>a</sup>Detailed maker information is available in Xu *et al.* (2010), <sup>b</sup>Piquemal *et al.* (2005), <sup>c</sup>AAFC Consortium (2016), <sup>d</sup>Wang *et al.* (2012), <sup>e</sup>Cheng *et al.* (2009), <sup>f</sup>Li *et al.* (2011), <sup>g</sup>Li *et al.* (2013).

Table 2.2. Genetic diversity indexes for the NARO rapeseed collection and variations among geographic groups.

Geographical group	Number of accessions	Average number of alleles	Major allele frequency	Ho	He	I	PIC
Whole Collection	582	10.37	0.56	0.05	0.57	1.18	0.52
Japan	305	8.50	0.67	0.04	0.44	0.90	0.41
Hokkaido	9	3.30	0.58	0.03	0.52	0.91	0.47
Tohoku	69	5.27	0.65	0.06	0.46	0.88	0.44
Kanto	33	4.77	0.68	0.06	0.42	0.82	0.41
Chubu	40	5.43	0.65	0.04	0.46	0.90	0.44
Kinki	72	5.17	0.73	0.03	0.37	0.73	0.37
Chugoku-Shikoku	11	2.90	0.70	0.07	0.37	0.65	0.36
Kyushu	65	4.63	0.72	0.03	0.37	0.71	0.36
Unknown	6	–	–	–	–	–	–
Overseas	277	9.37	0.50	0.06	0.59	1.22	0.58
Europe	202	8.07	0.53	0.06	0.56	1.14	0.54
Asia	30	5.37	0.60	0.07	0.49	0.97	0.49
Oceania	8	3.13	0.61	0.05	0.48	0.84	0.45
America	27	4.40	0.63	0.05	0.47	0.88	0.45
Unknown	10	–	–	–	–	–	–

Ho: observed heterozygosity, He: expected heterozygosity, I: Shannon's information index, PIC: polymorphism information content.

Table 2.3. Result of the hierarchical analysis of molecular variance (AMOVA) for geographic groups in the NARO rapeseed collection.

Source of variation	d.f.	Percentage of variation (%)	
Between Japanese and overseas accessions	1	17.71	***
Among geographical groups	9	7.01	***
Among individuals	555	67.18	***
Within individuals	566	8.10	**

\*\*\*, \*\*: significant at the 0.1% and 1% levels for 1,000 permutations, respectively.

Table 2.4. Estimates of pairwise  $F_{ST}$  (below diagonal) and Nei's genetic distance (above diagonal) among geographic groups in Japan.

	Hokkaido	Tohoku	Kanto	Chubu	Kinki	Chugoku -Shikoku	Kyushu
Hokkaido		0.105	0.125	0.110	0.148	0.173	0.143
Tohoku	0.059*		0.055	0.056	0.063	0.091	0.068
Kanto	0.102**	0.019		0.053	0.048	0.099	0.058
Chubu	0.122**	0.031**	0.017		0.056	0.091	0.049
Kinki	0.101**	0.039**	0.047**	0.058**		0.114	0.044
Chugoku- Shikoku	0.192**	0.084**	0.067*	0.076*	0.088**		0.075
Kyushu	0.138**	0.034**	0.063**	0.092**	0.055**	0.100**	

\*\* : significant at the 1% level, \* : significant at the 5% level.

Table 2.5. Geographic origin of rapeseed accessions assigned by STRUCTURE to two subgroups

Geographical group	Number of accessions	Subgroup 1 <sup>a</sup>	Subgroup 2 <sup>a</sup>	Admixed
Whole Collection	582	227	276	79
Japan	305	19	240	46
Hokkaido	9	4	3	2
Tohoku	69	5	46	18
Kanto	33	2	27	4
Chubu	40	4	27	9
Kinki	72	0	66	6
Chugoku-Shikoku	11	1	9	1
Kyushu	65	1	60	4
Unknow	6	2	2	2
Overseas	277	208	36	33
Europe	202	171	9	22
Asia	30	3	22	5
Oceania	8	5	0	3
America	27	25	1	1
Unknow	10	4	4	2

<sup>a</sup>Accessions are considered belonging to either of two subgroup when membership probabilities of  $\geq 0.8$ .

Table 2.6. Comparison of genetic diversity indexes for four core collections constructed by different methods.

	Number of accessions	Number of alleles	Allele retention ratio	Number of effective alleles	Ho	He	I	PIC
PowerCore <sup>a</sup>	103	10.37	100.0	3.77	0.05	0.64	1.41	0.59
CoreFinder <sup>a</sup>	96	10.37	100.0	3.57	0.06	0.62	1.39	0.58
CoreHunter	116	7.50	72.3	3.17	0.06	0.60	1.23	0.55
Random								
Strategy	116	7.20*	69.5	2.89	0.07	0.57	1.17	0.52

\*: significant at the 5% level between core collection and whole collection.

Ho, observed heterozygosity; He, expected heterozygosity; I, Shannon's information index; PIC, polymorphism information content.

<sup>a</sup> Maximization strategy methods.

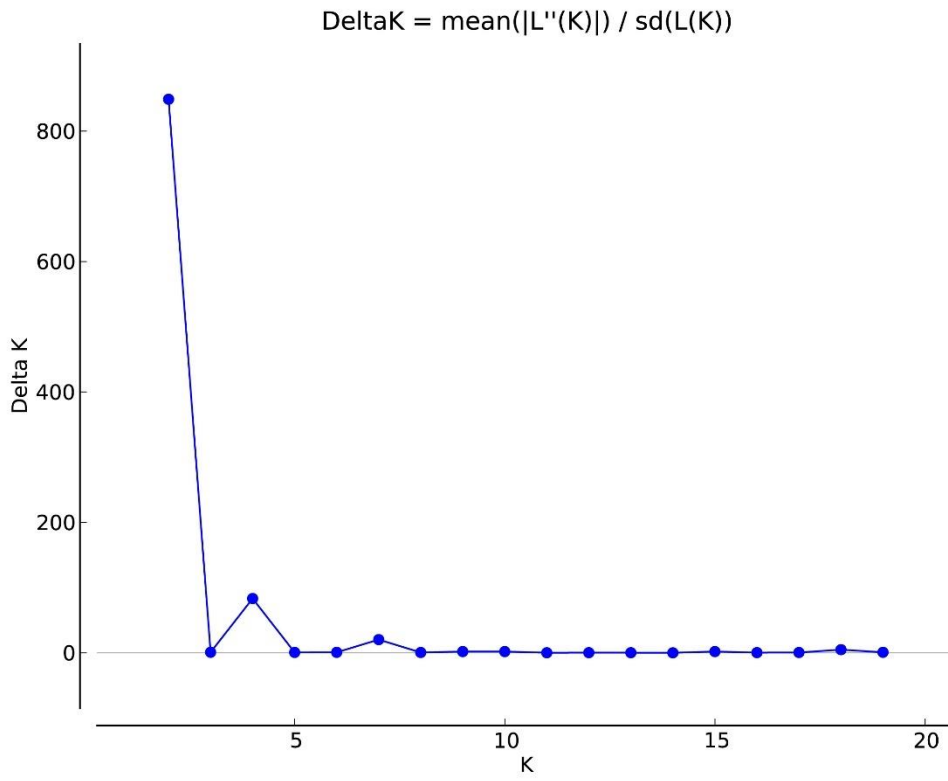


Fig. 2.1.  $\Delta K$ , from the structure analysis of the 582 rapeseed accessions.



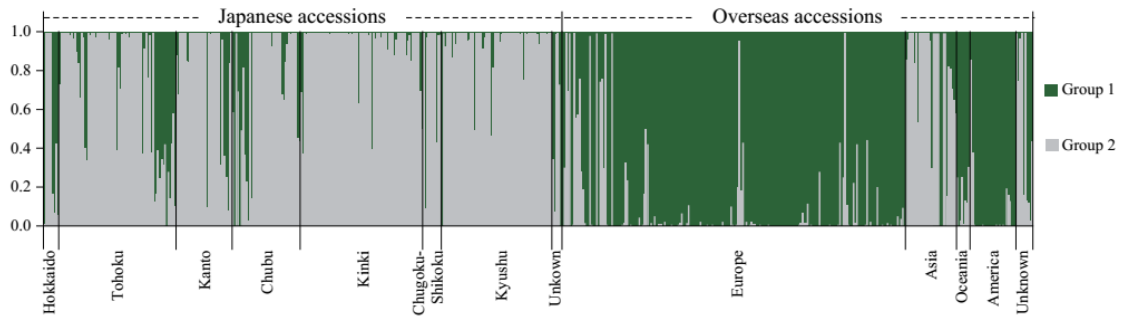


Fig. 2.2. Population structure of 582 rapeseed accessions based on 30 SSR markers. When  $K=2$ , the 582 germplasms were classified into two groups.

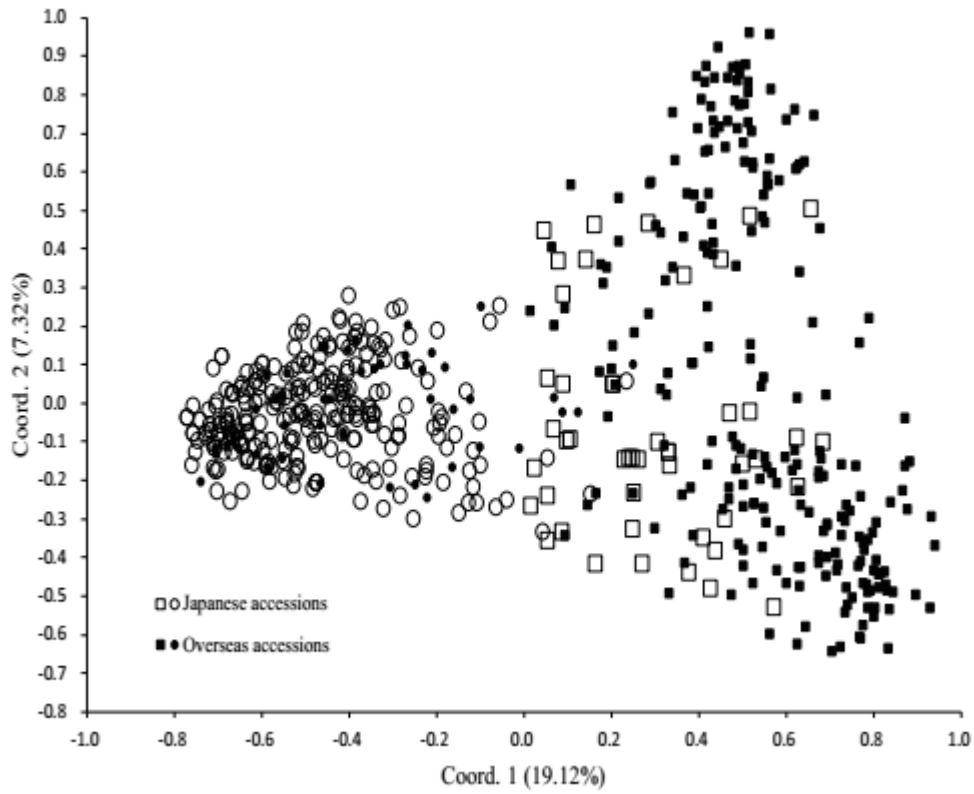


Fig. 2.3. Principal coordinates analysis (PCoA) of the 596 rapeseed accessions. Open symbols indicate Japanese accessions, and solid Symbols indicates overseas accessions. Square symbol indicates the rapeseed accessions assigned to group 1, and circle symbol indicates the accessions assigned to group 2 by the STRUCTURE analysis.

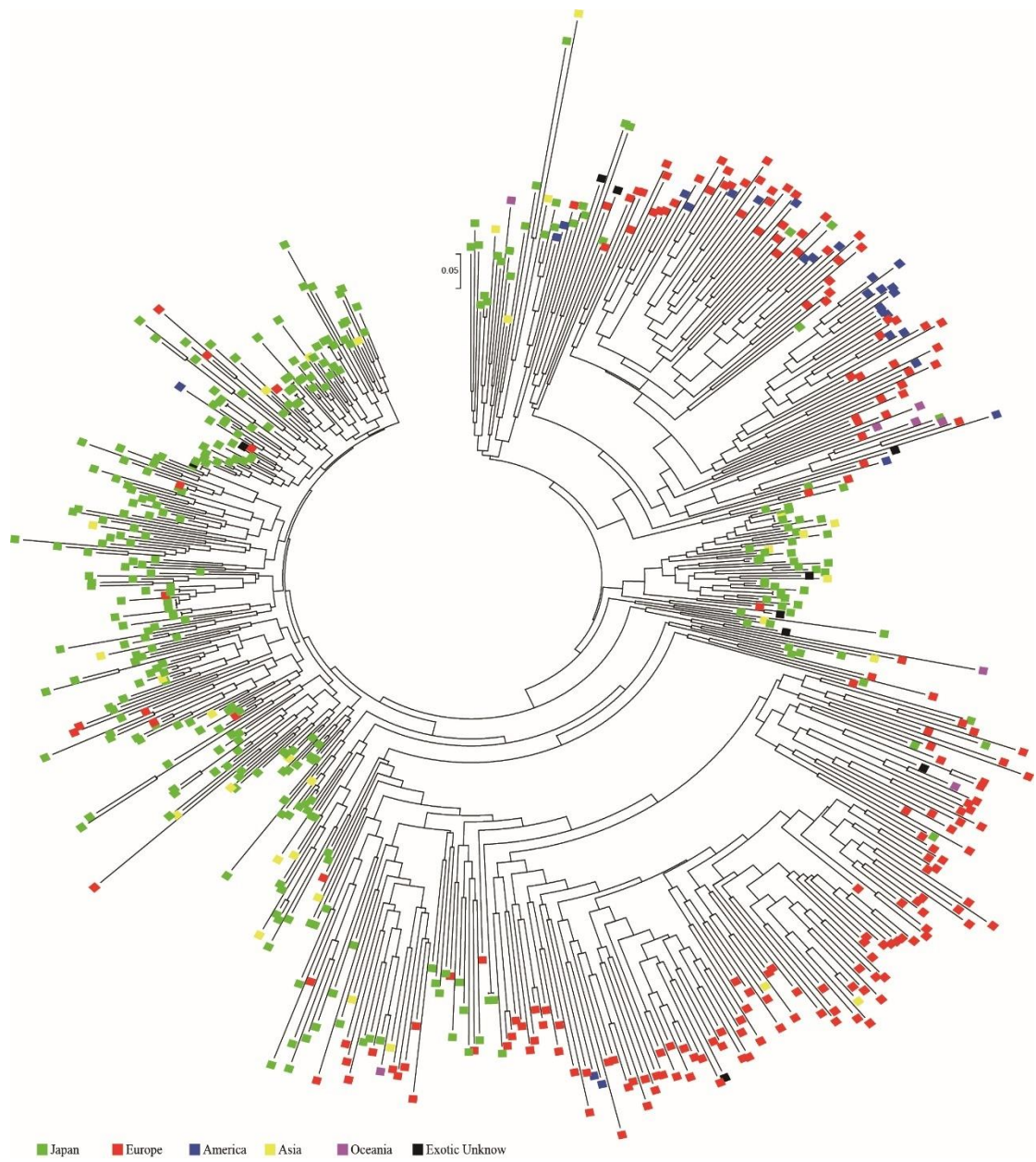


Fig. 2.4. The neighbor-joining (NJ) tree of the 582 rapeseed accessions constructed based on SSR analysis data.

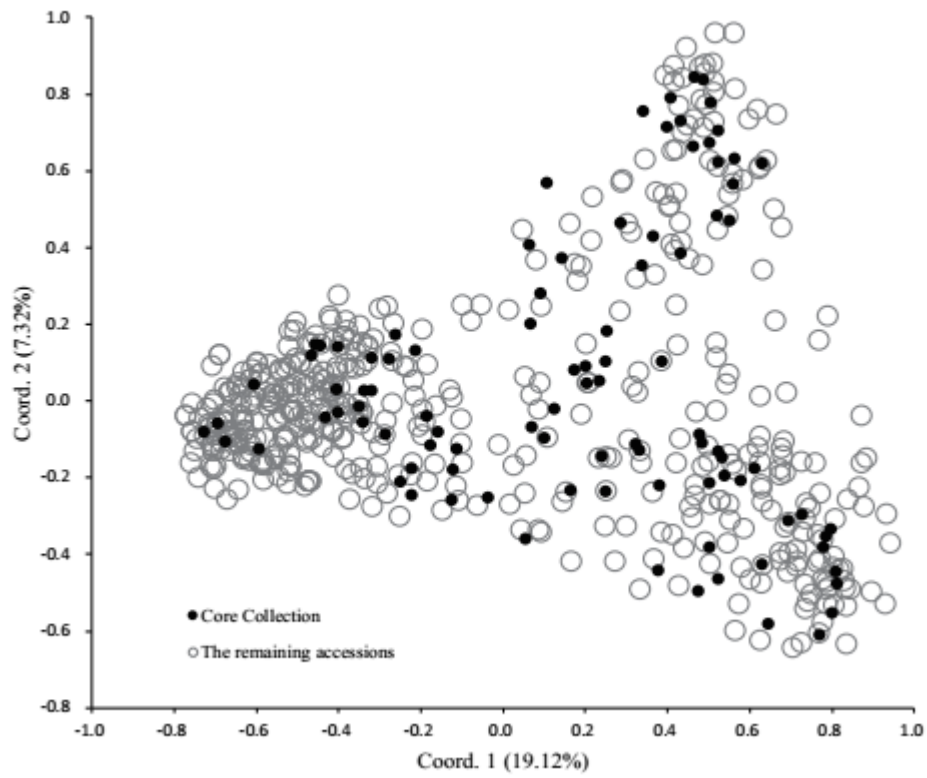


Fig. 2.5. Principal coordinate plot of the core collection constructed using the PowerCore and the whole collection. Solid and open symbols indicate the accessions included and not included in the core collection, respectively.

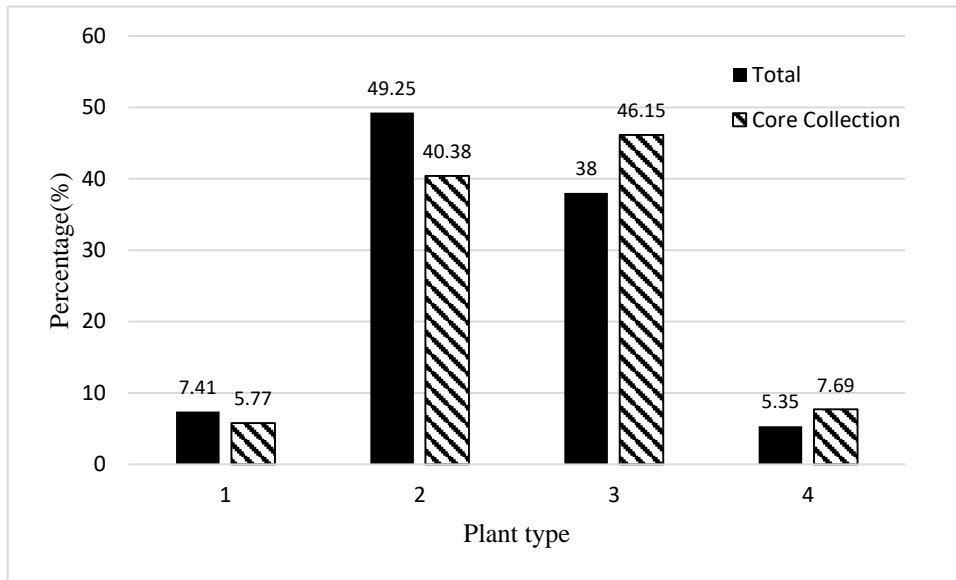


Fig. 2.6. The proportion of different plant types in NARO rapeseed genebank and core collection accessions.

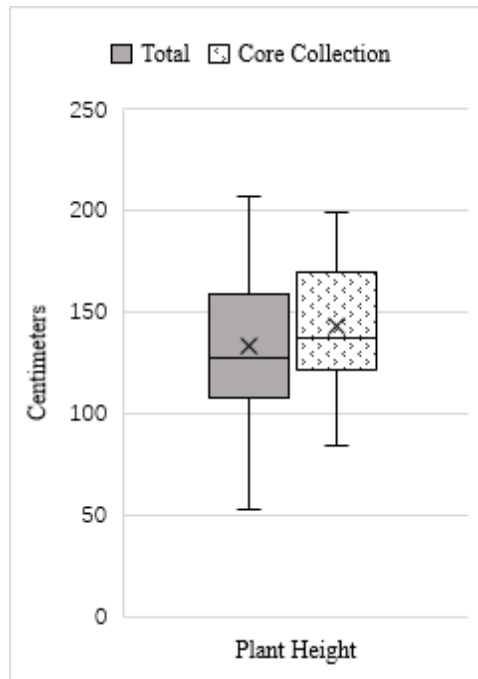


Fig. 2.7. Range of plant height in NARO rapeseed genebank and core collection accessions.

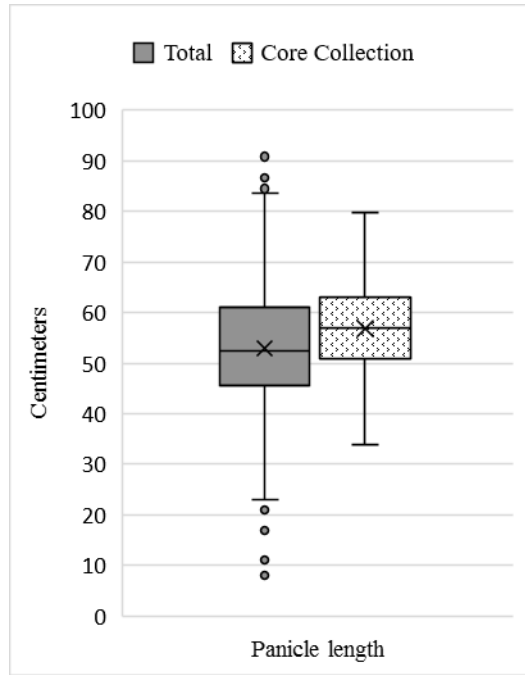


Fig. 2.8. Range of panicle length in NARO rapeseed genebank and core collection accessions.

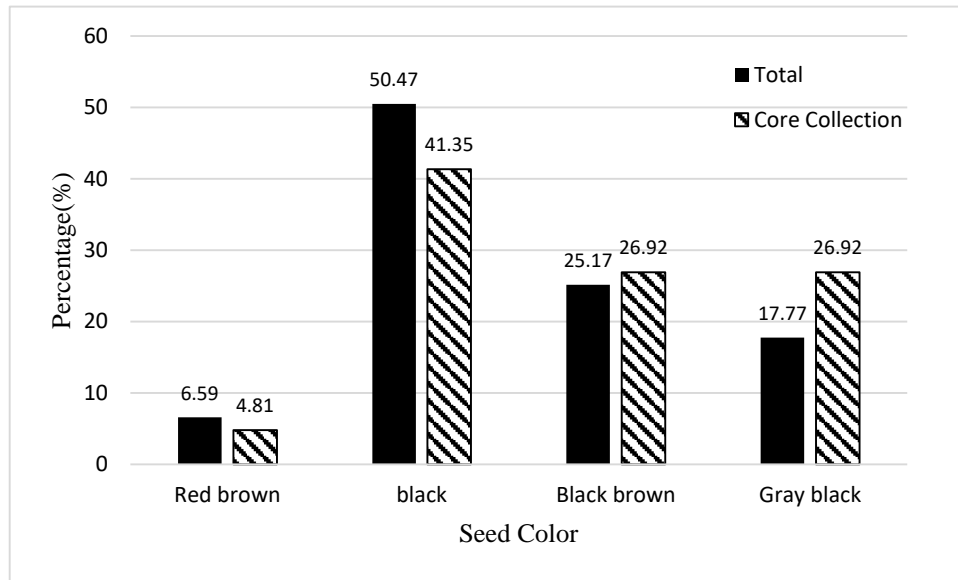


Fig. 2.9. The proportion of different seed colors in NARO rapeseed genebank and core collection accessions.



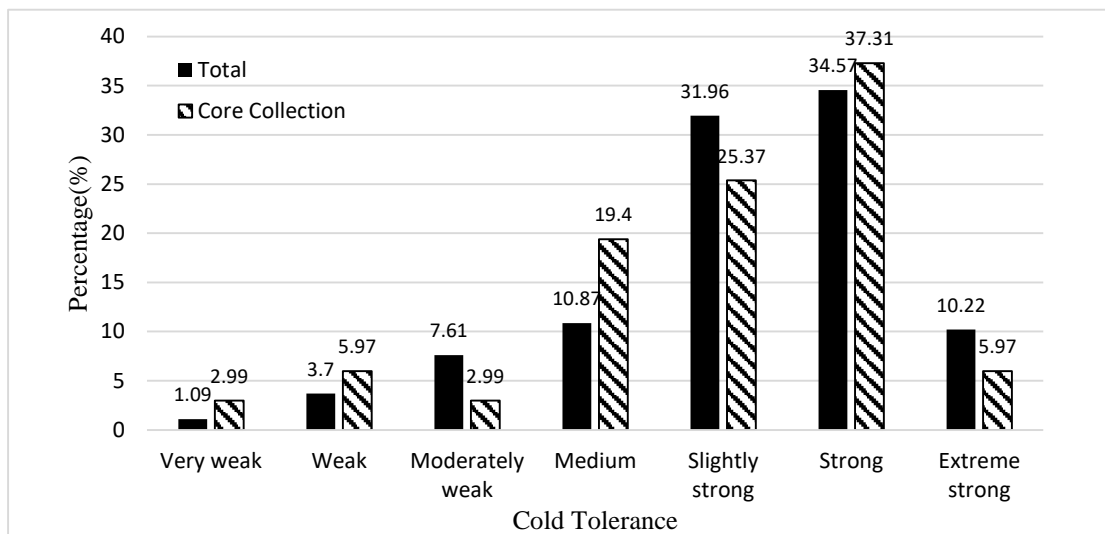


Fig. 2.10. The proportion of different cold tolerance abilities in NARO rapeseed genebank and core collection accessions.

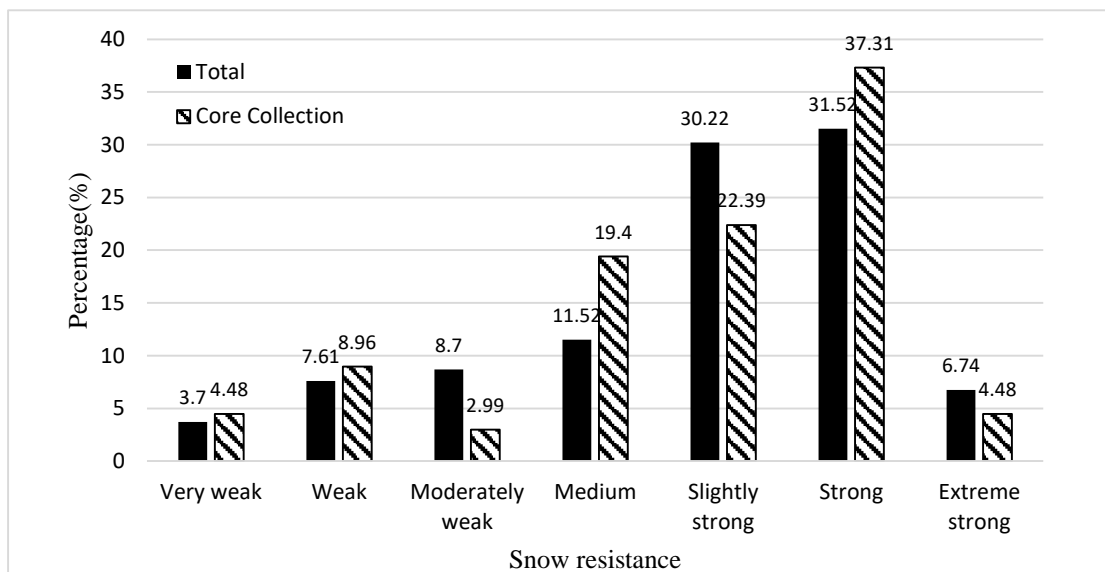


Fig. 2.11. The proportion of different snow resistance abilities in NARO rapeseed genebank and core collection accessions.

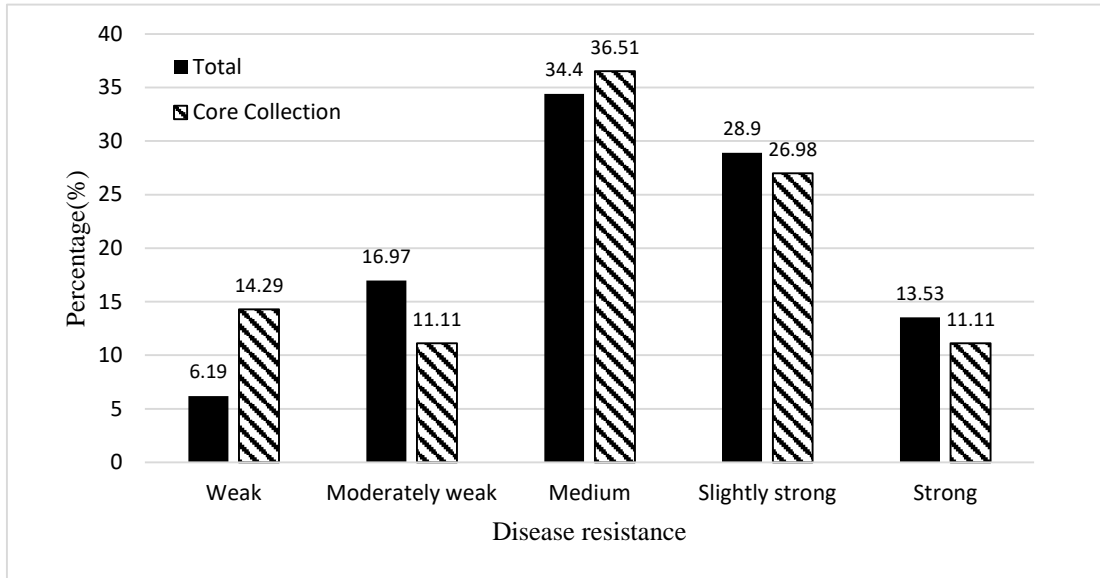


Fig. 2.12. The proportion of different disease resistance abilities in NARO rapeseed genebank and core collection accessions.

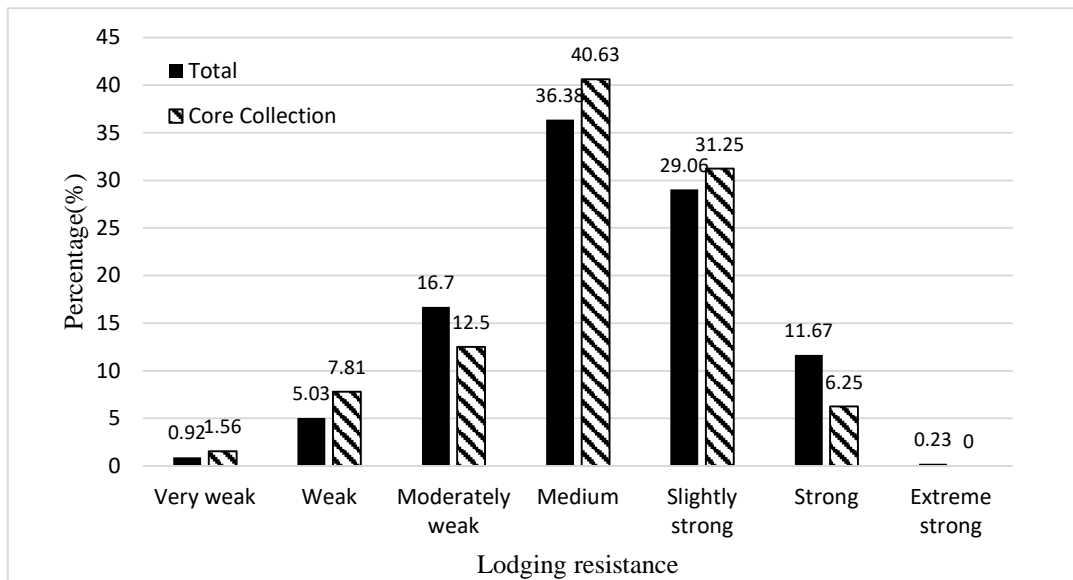


Fig. 2.13. The proportion of different lodging resistance abilities in NARO rapeseed genebank and core collection accessions.

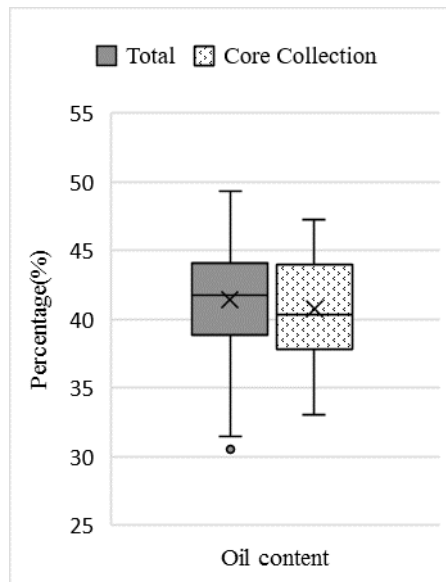


Fig. 2.14. Range of oil content in NARO rapeseed genebank and core collection accessions.

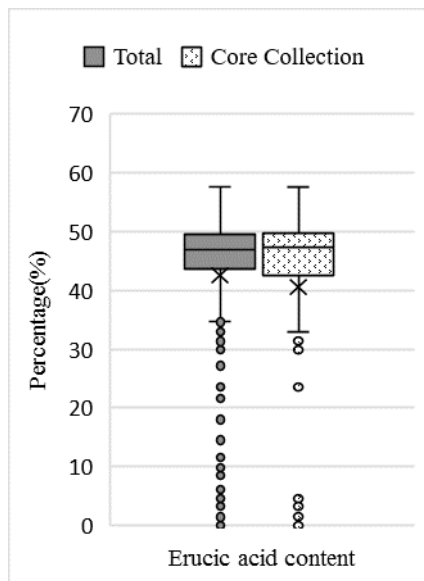


Fig. 2.15. Range of erucic acid content in NARO rapeseed genebank and core collection accessions.

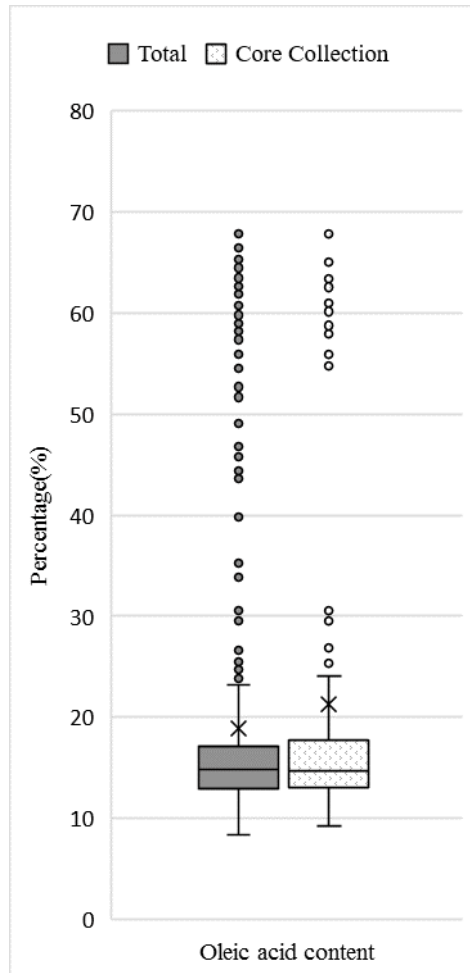


Fig. 2.16. Range of oleic acid content in NARO rapeseed genebank and core collection accessions.

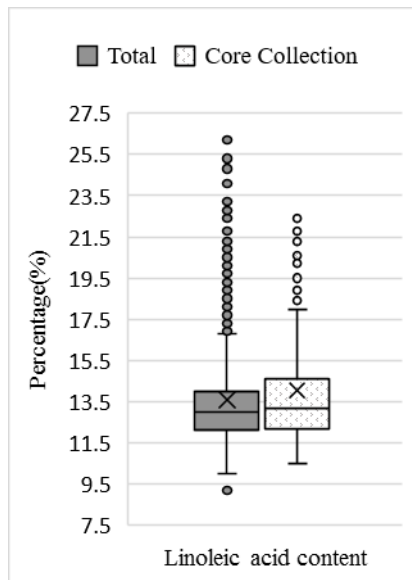


Fig. 2.17. Range of linoleic acid content in NARO rapeseed genebank and core collection accessions.



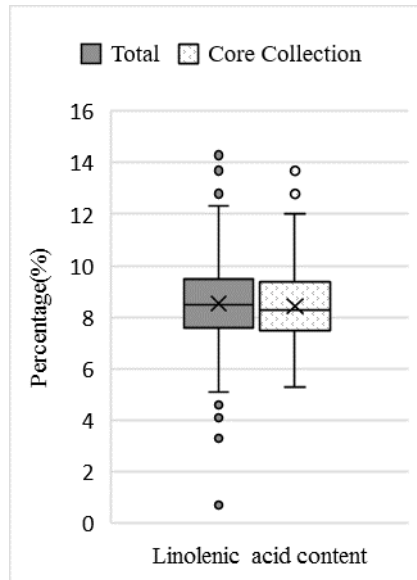


Fig. 2.18. Range of linolenic acid content in NARO rapeseed genebank and core collection accessions.

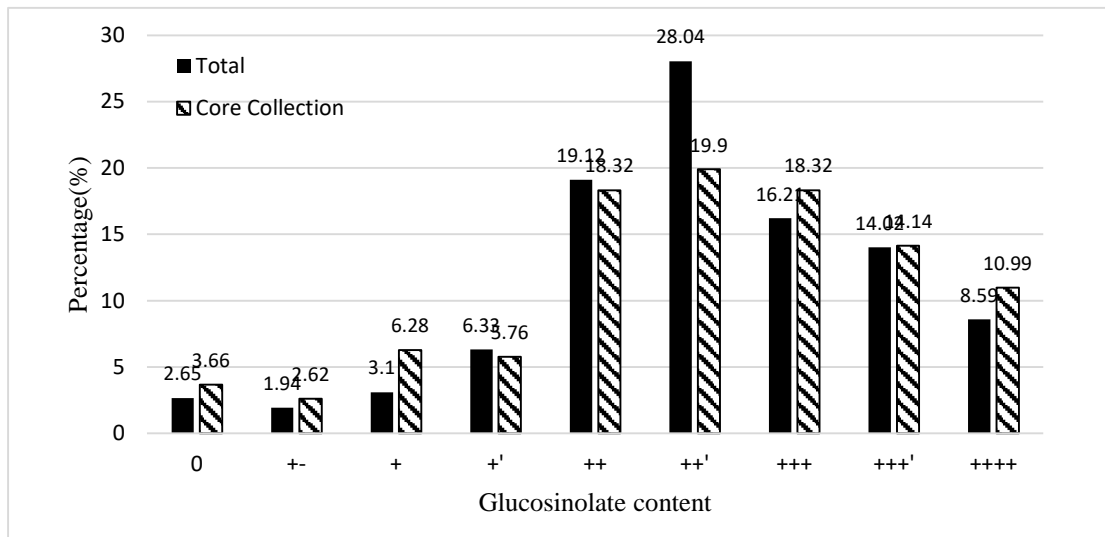


Fig. 2.19. The proportion of glucosinolate contents in NARO rapeseed genebank and core collection accessions.

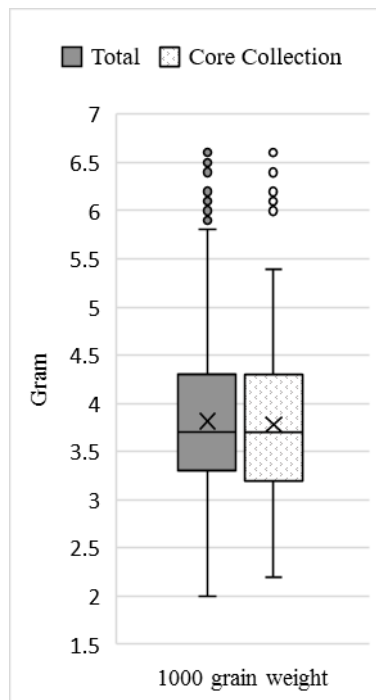


Fig. 2.20. Range of 1000 grain weight in NARO rapeseed genebank and core collection accessions.

## 2.4 Discussion

I evaluated the genetic diversity of the NARO rapeseed collection by using single-locus SSR markers. In allopolyploid plants, such as rapeseed, SSR primers usually amplify several alleles from multiple loci, which makes it difficult to assign these alleles to individual loci. Li *et al.* (2013) found a set of 230 single-locus rapeseed SSR markers. However, they used only 6 inbred lines and noted that not all of the markers might be true single-locus markers. In this study, I applied a total of 504 SSR markers, including the 230 markers of Li *et al.* (2013), to 582 rapeseed accessions, and found that 30 SSR markers (Table 2.1), distributed across all linkage groups, always amplified single alleles with high polymorphism. This finding indicates that these 30 SSR markers used in this study are useful for research on rapeseed genetic resources.

I identified 311 alleles in the whole collection, with an average of 10.37 alleles per locus and a PIC value of 0.52. Several studies calculated genetic diversity indices of diverse rapeseed collections on the basis of SSR markers. The average numbers of alleles per locus were 4.31 in 96 European rapeseed genotypes (Hasan *et al.* 2006), 3.4 in 192 inbred lines of various origins (Xiao *et al.* 2012), and 7.3 in 169 worldwide rapeseed lines (Gyawali *et al.* 2013). The PIC value in the 192 lines analyzed by Xiao *et al.* (2012) was 0.37. The differences in allelic richness between the NARO collection and other rapeseed collections are due partly to the differences in the SSR markers and the number of accessions used in this study. Nevertheless, the higher values of the genetic diversity indices in this study indicate that the NARO rapeseed collection has moderately high genetic diversity. In contrast, the PIC value of the NARO rapeseed collection was lower than those reported in other *Brassica* species: 0.57 or 0.64 in *B. oleracea* (El-Esawi *et al.* 2016; Louarn *et al.* 2007) and 0.90 in *B. juncea* (Yao *et al.* 2012); this would reflect a narrower genetic base in rapeseed than in other *Brassica* species.

Rapeseed originated and was first domesticated in Europe, and then spread

throughout the world. In Japan, rapeseed cultivation is considered to have spread after the Meiji period (from 1868 to 1912) (Matsuo 1954); since then, many landraces have been developed throughout the country. Modern rapeseed breeding in Japan began in the 1930s; government-led large-scale breeding projects initially used a limited number of accessions (Matsuo 1954), which may have restricted the genetic diversity of Japanese accessions. As expected, I found a significant genetic differentiation between Japanese and overseas accessions (Fig. 2.3; Tables 2.3, 2.4), and comparison of the genetic indices indicated that genetic diversity was lower in Japanese accessions than in overseas accessions (Table 2.2). However, the values of genetic diversity indices were not very different between Japanese and overseas accessions. Over the last five decades, repeated introduction of overseas germplasms and subsequent breeding may have increased genetic diversity.

In general, differences in breeding materials and targets among different breeders and regions may lead to genetic differentiation. In Japan, I found small but significant differences among geographical groups (Table 2.4). Genetic differentiation tended to increase with increasing geographic distance. For example, I found the highest  $F_{ST}$  values and Nei's genetic distances between the Hokkaido group (northern Japan) and three groups in western Japan. The genetic differentiation might be caused not only by the diversity of germplasms used as breeding materials, but also by their adaptation to local environments. The genetic diversity indices PIC and I were higher in eastern than in western Japan. The genetic diversity of eastern Japanese accessions may have been further increased by recent active rapeseed breeding there.

The STRUCTURE analysis indicated the presence of two main genetic clusters in the NARO rapeseed collection and demonstrated differentiation between Japanese and overseas accessions: with a membership probability threshold of 0.80, most of the overseas accessions were assigned to the subgroup 1, and the Japanese accessions were assigned to the subgroup 2 (Table 2.5). Yet the presence of several accessions in each subgroup is not consistent with their geographical origins (Table 2.5), as similarly

observed in previous studies (Chen *et al.* 2007, Hu *et al.* 2007, Li *et al.* 2012, Xiao *et al.* 2012). All of the Canadian cultivars, known by the trade name ‘Canola’ and bred in the 1970s or later, were classified into the subgroup 1. Many accessions from Asian countries other than Japan belonged to the subgroup 2. The neighbor-joining (NJ) tree and principal coordinate analysis (PCoA) further confirmed the STRUCTURE results (Fig. 2.3, 2.4). These results indicate that Asian rapeseed may have genetically differentiated from that in other regions of the world, and that Japanese, Chinese, and Korean landraces and cultivars may be closely genetically related (Fig. 2.2). Some studies have revealed a wide diversity of Chinese and Australian rapeseed accessions (Chen *et al.* 2007, Guo *et al.* 2016, Wang *et al.* 2009). The NARO collection holds only 7 accessions from China and none from Australia. Obtaining accessions from these countries would further expand the diversity of the collection.

The most important factor in core collection construction is sample selection strategy, and many strategies based on stratified sampling and clustering methods are available (Zhang *et al.* 2011). Because different strategies result in different core collections (Thachuk *et al.* 2009, Wang *et al.* 2007), I used four different methods. As the M strategy is based on maximizing the number of alleles, it can automatically generate a sampling ratio on the basis of the genetic diversity of the species; this strategy has been widely used in recent years (Belaj *et al.* 2012, Liu *et al.* 2015, Zhang *et al.* 2011). In this study, both PowerCore and CoreFinder, which are based on the M strategy, constructed core collections that retained 100% of alleles, and in this respect were superior to the other two methods used. The genetic diversity indices tended to be nearly same in both the PowerCore collection and the CoreFinder collection (Table 2.6). The number of accessions are fewer in the CoreFinder collection (Table 2.6), so I finally recommend it as the core collection of the NARO rapeseed collection. The core collection comprised 57 overseas accessions (20.6% of total) and 39 Japanese accessions (12.8%). The higher percentage of overseas accessions reflects their high allelic richness. However, the fact that approximately 40% of accessions in the core collection originated in Japan indicates their relatively high genetic diversity.

In conclusion, my study revealed the genetic structure of the NARO rapeseed collection and genetic relationships among accessions on the basis of single-locus SSR markers. Some accessions were genetically identical or closely related to each other. This information is important for decreasing redundancy in the collection, thereby reducing the management cost and avoiding unnecessary distribution of such accessions to breeders. Further integration of the data from other collections maintained in different countries will make it possible to exploit and preserve the whole rapeseed gene pool and to retain the largest number of allelic variants for genes controlling the most important agronomic traits in the NARO collection. My candidate core collection can be used in further research such as genome-wide association studies to identify genomic regions controlling important agronomic traits.

I did not analyze the phenotypic data recorded in the NARO rapeseed collection because they have been obtained by different investigators and methods under various environmental conditions. However, based on these data, it can still be a qualitative analysis. So, I compared sixteen important traits in rapeseed production between NARO rapeseed collection and the core collection constructed by this study. Through the results we can see that the core collection based on genotypic data also has a considerable degree of representation of phenotype. This suggests that it is possible to establish a core collection by genotypic data. With the increase of the number of accession, the difficulty and cost of comprehensively assessing the polymorphism of accessions by cultivating test method is increasing. The results of this study tell us that the establishment of core collection only by genotypic data is a cost-effective and highly accurate method. However, just as mentioned before, phenotypic data used in this study was obtained at different times in different locations, therefore, it will be necessary to evaluate the phenotypes of all the accessions under the same environmental conditions, and integrate the data on genotypic and phenotypic diversity. This will make the core collection, which comprises accessions that are genetically diverse at both genotypic and phenotypic levels, available to breeders for enhancing the genetic potential of this crop.

## **Chapter 3: Genetic diversity analysis and origin presumption of feral rapeseed genetic resources in Japan**

### **3.1 Introduction**

Content omitted

### **3.2 Genetic diversity analysis of feral rapeseed resources in Japan**

Content omitted

### **3.3 Determination of the agronomic traits of environmental adaptability of the feral rapeseed resources.**

Content omitted

### **3.4 Comparison of genebank resources and feral resources**

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### **3.5 Discussion**

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## **Chapter 4: General Discussion**

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## Summary

*Brassica napus* L., or commonly known as rapeseed, oilseed rape (and, in the case of one particular group of cultivars, canola), is one of the most economically important oilseed crops over the world. Over 450 million tons of rapeseed seeds are harvested worldwide every year and accounts for about 20% of the world grain production. Japan is not the original home of rapeseed, the existing rapeseed in Japan was introduced into two areas during the Meiji period (19<sup>th</sup> century). Rapeseed showed far more than Japanese traditional oil crop “Aburana” (*B. rapa*) production capacity and was promoted quickly. Japanese government started a formal breeding program in 1930s to improve rapeseed which was expected to be used as a means of developing the rural economy. Until now, more than 200 rapeseed varieties were bred out in Japan. In order to better promote breeding work, NARO (National Agriculture and Food Research Organization) collected a large number of Japanese rapeseed varieties and many foreign varieties. In addition, there are stable feral rapeseed populations in various locations of Japan, which constitute another important component of Japanese rapeseed resources. Their source is unknown, and lack of genetic background information, so it cannot determine whether they have utility value.

Knowledge of the genetic diversity and phylogenetic relationship among the germplasms is vital to efficiently use germplasm collections in breeding. In addition, establishing a representative subset of the whole collection, called a core collection, will be a feasible way for management, evaluation, and utilization of genetic resources. But until now, there is no genetic diversity study of Japanese rapeseed (genebank and feral resource). Therefore, the objective of this study is to assess the genetic diversity of the rapeseed genetic resources in Japan, to explore their situation and potential for further exploitation for breeding efforts via: 1) analysis the genetic diversity and genetic structure of NARO genebank rapeseed resources by SSR markers, and construct a core collection based on the polymorphic allele information to facilitate the future breeding

work; 2) analysis the feral rapeseed resources collected from 13 locations of Japan by SSR marker to reveal their genetic diversity and structure to reveal the possible formation way of them, and perform a comparison of the genebank resources and feral resources to understand whether there is similarity between them.

In the study of NARO rapeseed genebank, 582 accessions were genotyped with 30 SSR markers covering all 19 rapeseed chromosomes. These markers amplified 311 alleles (10.37 alleles per marker; range, 3–39). Analysis of molecular variance indicated significant genetic differentiation between Japanese and overseas accessions, which is similar with the result of STRUCTURE analysis. The genetic diversity of Japanese accessions was lower than that of overseas accessions. Small but significant differences were found among geographical groups, and genetic differentiation tended to increase with geographical distance. The core collection constructed comprises 96 accessions of diverse origin. It represents the whole collection well and thus it may be useful for rapeseed genetic research and breeding programs. The core collection improves the efficiency of management, evaluation, and utilization of genetic resources.

The genetic diversity study of the feral rapeseed sampled in 13 locations in Japan was performed with the same 30 SSR markers. These markers amplified 311 alleles (10.37 alleles per marker; range, 2–36). Genetic diversity indices showed that these feral populations have relatively high genetic diversity. Mantel test showed that there was no correlation between genetic distance and geographic distance between populations. Similar results can be seen from the STRUCTURE, PCoA and cluster analysis. These analyzes also showed that the genetic structure of a population is usually complex, indicated the multiple source of the feral rapeseed. Low heterozygosity and the Hardy-Weinberg equilibrium analysis showed that these populations reproduce mainly by selfing. The cultivation experiment results revealed that feral rapeseed had different phenotypes. These finding suggest that Japanese feral rapeseed has the potential to be used as breeding material.

A comprehensive comparison is carried out by combing the SSR genotype data.

Some unique alleles of the feral population were found to occupy 18.32% of the total number of alleles. Based on the PCoA and cluster analysis, some feral rapeseeds that was genetically far away from NARO rapeseed genebank cultivars was found. They may come from early cultivars that have not been collected and/or cultivars that have changed in the course of adapting to the natural environment of Japan. These results further confirmed the potential value of feral rapeseed.

I have successfully accessed the genetic diversity of rapeseed in Japan, mainly focus on NARO rapeseed genebank and representative feral accessions. A core collection of the NARO rapeseed genebank also be constructed. Based on these work, the basic panorama of genetic diversity of Japan rapeseed resources has just been drawn. This valuable information could provide a great help for future rapeseed breeding.

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# Appendix

Appendix 1. The list of 582 accessions used in this study.

Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR001	芯切菜	SHIN KIRINA	25942	Japan	Kantō	Landrace	Included
NR002	芯切菜	SHIN KIRINA	25951	Japan	Kantō	Landrace	Included
NR003	高系 10-1 号	KOUKEI 10-1	26139	Japan	Chūbu	Cultivar	
NR004	高系 11 号	KOUKEI 11	26140	Japan	Chūbu	Cultivar	Included
NR005	つみ菜	TSUMINA	26141	Japan	Japan Unknow	Landrace	
NR006	樺太	KARAFUTO	26142	Overseas	Europe		
NR007	岩内種	IWANAISHU	26143	Japan	Hokkaido	Landrace	
NR008	ハンブルグ 1 号	HAMBURG 1	26144	Overseas	Europe		Included
NR009		MR 1	26145	Japan	Hokkaido	Landrace	
NR010	タイセツナタネ	TAISETSUNATANE	26146	Japan	Hokkaido	Cultivar	
NR011	なたね農林 2 号	NATANE NOURIN 2	26147	Japan	Tōhoku	Cultivar	
NR012	なたね農林 5 号	NATANE NOURIN 5	26148	Japan	Tōhoku	Cultivar	
NR013	なたね農林 10 号	NATANE NOURIN 10	26149	Japan	Tōhoku	Cultivar	
NR014	東北 3 号	TOUHOKU 3	26150	Japan	Tōhoku	Cultivar	
NR015	東北 4 号	TOUHOKU 4	26151	Japan	Tōhoku	Cultivar	
NR016	東北 5 号	TOUHOKU 5	26152	Japan	Tōhoku	Cultivar	
NR017	東北 7 号	TOUHOKU 7	26153	Japan	Tōhoku	Cultivar	
NR018	東北 8 号	TOUHOKU 8	26154	Japan	Tōhoku	Cultivar	
NR019	東北 9 号	TOUHOKU 9	26155	Japan	Tōhoku	Cultivar	
NR020	東北 10 号	TOUHOKU 10	26156	Japan	Tōhoku	Cultivar	
NR021	東北 12 号	TOUHOKU 12	26157	Japan	Tōhoku	Cultivar	Included
NR022	東北 14 号	TOUHOKU 14	26158	Japan	Tōhoku	Cultivar	
NR023	東北 16 号	TOUHOKU 16	26159	Japan	Tōhoku	Cultivar	
NR024	東北 19 号	TOUHOKU 19	26160	Japan	Tōhoku	Cultivar	
NR025	東北 22 号	TOUHOKU 22	26161	Japan	Tōhoku	Cultivar	
NR026	東北 23 号	TOUHOKU 23	26162	Japan	Tōhoku	Cultivar	
NR027	東北 24 号	TOUHOKU 24	26163	Japan	Tōhoku	Cultivar	Included
NR028	東北 28 号	TOUHOKU 28	26165	Japan	Tōhoku	Cultivar	
NR029	東北 36 号	TOUHOKU 36	26169	Japan	Tōhoku	Cultivar	
NR030	東北 42 号	TOUHOKU 42	26173	Japan	Tōhoku	Cultivar	
NR031	東北 46 号	TOUHOKU 46	26177	Japan	Tōhoku	Cultivar	
NR032	東北 48 号	TOUHOKU 48	26178	Japan	Tōhoku	Cultivar	

Appendix1 continue

Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR033	東北 49 号	TOUHOKU 49	26179	Japan	Tōhoku	Cultivar	
NR034	東北 50 号	TOUHOKU 50	26180	Japan	Tōhoku	Cultivar	
NR035	東北 56 号	TOUHOKU 56	26181	Japan	Tōhoku	Cultivar	
NR036	東北 58 号	TOUHOKU 58	26183	Japan	Tōhoku	Cultivar	
NR037	東北 61 号	TOUHOKU 61	26184	Japan	Tōhoku	Cultivar	
NR038	ミホナタネ	MIHONATANE	26185	Japan	Tōhoku	Cultivar	
NR039	東北 6 号	TOUHOKU 6	26186	Japan	Tōhoku	Cultivar	
NR040	東北 11 号	TOUHOKU 11	26187	Japan	Tōhoku	Cultivar	
NR041	東北 15 号	TOUHOKU 15	26188	Japan	Tōhoku	Cultivar	
NR042	東北 18 号	TOUHOKU 18	26189	Japan	Tōhoku	Cultivar	
NR043	東北 20 号	TOUHOKU 20	26190	Japan	Tōhoku	Cultivar	
NR044	東北 30 号	TOUHOKU 30	26193	Japan	Tōhoku	Cultivar	
NR045	札幌	SAPPORO	26194	Japan	Tōhoku	Landrace	
NR046	北海道種	HOKKAIDOSHU	26195	Japan	Hokkaido	Landrace	
NR047	遠州黒種	ENSHUU KURODANE	26196	Japan	Tōhoku	Landrace	Included
NR048	東山種	TOUSANSHU	26197	Japan	Chūbu	Landrace	
NR049	宮城晩生	MIYAGI BANSEI	26198	Japan	Tōhoku	Landrace	
NR050	蟹	KANI	26199	Japan	Tōhoku	Landrace	
NR051	蕪菜	KABURANA	26200	Japan	Tōhoku	Landrace	
NR052	ムツナタネ	MUTSUNATANE	26203	Japan	Tōhoku	Cultivar	Included
NR053	東北 64 号	TOUHOKU 64	26204	Japan	Tōhoku	Cultivar	
NR054	バンドイナタネ	BANDAINATANE	26205	Japan	Kinki	Cultivar	Included
NR055	なたね農林 4 号	NATANE NOURIN 4	26206	Japan	Chūbu	Cultivar	
NR056	なたね農林 7 号	NATANE NOURIN 7	26207	Japan	Chūbu	Cultivar	
NR057	なたね農林 8 号	NATANE NOURIN 8	26208	Japan	Chūbu	Cultivar	
NR058	北陸 7 号	HOKURIKU 7	26209	Japan	Chūbu	Cultivar	
NR059	北陸 13 号	HOKURIKU 13	26210	Japan	Chūbu	Cultivar	
NR060	北陸 19 号	HOKURIKU 19	26211	Japan	Chūbu	Cultivar	Included
NR061	北陸 23 号	HOKURIKU 23	26212	Japan	Chūbu	Cultivar	
NR062	スエヒロナタネ	SUEHIRONATANE	26214	Japan	Kinki	Cultivar	Included
NR063		HANBAAKU(HAMBURG)	26215	Overseas	Europe		
NR064	なたね農林 13 号	NATANE NOURIN 13	26216	Japan	Chūbu	Cultivar	
NR065	北陸 25 号	HOKURIKU 25	26217	Japan	Chūbu	Cultivar	
NR066	Landrace 朝鮮	ZAIRAI CHOUSEN	26218	Overseas	Asia		
NR067	鴻分 2 号	KOUBUN 2	26219	Japan	Kantō	Cultivar	
NR068	鴻分 3 号	KOUBUN 3	26220	Japan	Kantō	Cultivar	
NR069	鴻分 7 号	KOUBUN 7	26221	Japan	Kantō	Cultivar	
NR070	鴻分 17 号	KOUBUN 17	26222	Japan	Kantō	Cultivar	
NR071	遠州	ENSHUU	26223	Japan	Kantō	Landrace	

Appendix1 continue

Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR072	晩生菜	BANSEINA	26224	Japan	Kantō	Landrace	
NR073	四石晩	YONKOKU OKU	26225	Japan	Kantō	Landrace	
NR074	ドワフエセックス	DWARF ESSEX	26226	Overseas	Exotic Unknow		
NR075	Cultivar ナプス	IKUSEI NAPUS	26227	Japan	Kantō	Landrace	
NR076	遠州3号	ENSHUU 3	26228	Japan	Kantō	Landrace	
NR077	吾妻種	AZUMASHU	26229	Japan	Japan Unknow	Landrace	
NR078	苔	UNDAI	26230	Japan	Kantō	Landrace	
NR079	晩生菜種	OKUTE NATANE	26231	Japan	Kantō	Landrace	
NR080	晩菜	OKUNA	26232	Japan	Chūbu	Landrace	
NR081	野中1号	NONAKA 1	26233	Japan	Kantō	Landrace	
NR082	中野種(矮性)	NAKANOSHU(DWARF TYPE)	26234	Japan	Kantō	Landrace	
NR083	水原種	MIZUHARASHU	26235	Japan	Kantō	Landrace	
NR084	吾妻(淡黄色)	AZUMA(LIGHT YELLOW)	26236	Japan	Kantō	Landrace	
NR085	吾妻(黄色)	AZUMA(YELLOW)	26237	Japan	Kantō	Landrace	
NR086	吾妻(肉色)	AZUMA(SALMON PINK)	26238	Japan	Kantō	Landrace	Included
NR087		INTEGRIFORIA	26239	Overseas	Exotic Unknow		
NR088		WAX-LESS MUTANT	26240	Japan	Kyushu	Cultivar	
NR089	普通朝鮮	FUTSUU CHOUSEN	26241	Overseas	Asia		
NR090		B.NAPUS,RAPIFERA	26242	Overseas	Exotic Unknow		
NR091	なたね農林1号	NATANE NOURIN 1	26243	Japan	Kyushu	Cultivar	
NR092	なたね農林3号	NATANE NOURIN 3	26244	Japan	Kyushu	Cultivar	
NR093	なたね農林6号	NATANE NOURIN 6	26245	Japan	Kinki	Cultivar	
NR094	なたね農林9号	NATANE NOURIN 9	26246	Japan	Kinki	Cultivar	
NR095	なたね農林11号	NATANE NOURIN 11	26247	Japan	Kyushu	Cultivar	
NR096	なたね農林12号	NATANE NOURIN 12	26248	Japan	Kinki	Cultivar	
NR097	なたね農林14号	NATANE NOURIN 14	26249	Japan	Kyushu	Cultivar	
NR098	なたね農林15号	NATANE NOURIN 15	26250	Japan	Kyushu	Cultivar	
NR099	なたね農林16号	NATANE NOURIN 16	26251	Japan	Tōhoku	Cultivar	
NR100	なたね農林18号	NATANE NOURIN 18	26253	Japan	Tōhoku	Cultivar	
NR101	ムラサキナタネ	MURASAKINATANE	26254	Japan	Chūbu	Cultivar	
NR102	ミチノクナタネ	MICHINOKUNATANE	26255	Japan	Tōhoku	Cultivar	
NR103	イズズナタネ	ISUZUNATANE	26257	Japan	Kinki	Cultivar	
NR104	チサヤナタネ	CHISAYANATANE	26258	Japan	Tōhoku	Cultivar	
NR105	アブラマサリ	ABURAMASARI	26259	Japan	Kyushu	Cultivar	Included
NR106	ハウマンナタネ	HOUMANNATANE	26260	Japan	Kyushu	Cultivar	
NR107	ミユキナタネ	MIYUKINATANE	26261	Japan	Tōhoku	Cultivar	
NR108	アサヒナタネ	ASAHINATANE	26263	Japan	Tōhoku	Cultivar	
NR109	コンゴウナタネ	KONGOUNATANE	26266	Japan	Kinki	Cultivar	
NR110	ハヤナタネ	HAYANATANE	26267	Japan	Kyushu	Cultivar	

Appendix1 continue

Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR111	オオミナタネ	OOMINATANE	26268	Japan	Kinki	Cultivar	
NR112	ゲンカイナタネ	GENKAINATANE	26269	Japan	Kyushu	Cultivar	
NR113	近畿 9 号	KINKI 9	26270	Japan	Kinki	Cultivar	
NR114	近畿 17 号	KINKI 17	26271	Japan	Kinki	Cultivar	
NR115	近畿 19 号	KINKI 19	26273	Japan	Kinki	Cultivar	
NR116	近畿 20 号	KINKI 20	26274	Japan	Kinki	Cultivar	
NR117	近畿 29 号	KINKI 29	26278	Japan	Kinki	Cultivar	
NR118	近畿 30 号	KINKI 30	26279	Japan	Kinki	Cultivar	
NR119	近畿 31 号	KINKI 31	26280	Japan	Kinki	Cultivar	
NR120	近畿 32 号	KINKI 32	26281	Japan	Kinki	Cultivar	
NR121	北陸 3 号	HOKURIKU 3	26282	Japan	Chūbu	Cultivar	
NR122	北陸 4 号	HOKURIKU 4	26283	Japan	Chūbu	Cultivar	
NR123	北陸 9 号	HOKURIKU 9	26284	Japan	Chūbu	Cultivar	
NR124	北陸 12 号	HOKURIKU 12	26285	Japan	Chūbu	Cultivar	
NR125	北陸 14 号	HOKURIKU 14	26286	Japan	Chūbu	Cultivar	
NR126	北陸 15 号	HOKURIKU 15	26287	Japan	Chūbu	Cultivar	
NR127	北陸 16 号	HOKURIKU 16	26288	Japan	Chūbu	Cultivar	Included
NR128	北陸 17 号	HOKURIKU 17	26289	Japan	Chūbu	Cultivar	
NR129	北陸 18 号	HOKURIKU 18	26290	Japan	Chūbu	Cultivar	
NR130	北陸 20 号	HOKURIKU 20	26291	Japan	Chūbu	Cultivar	
NR131	東海 1 号	TOUKAI 1	26295	Japan	Kinki	Cultivar	
NR132	東海 3 号	TOUKAI 3	26296	Japan	Kinki	Cultivar	
NR133	東海 4 号	TOUKAI 4	26297	Japan	Kinki	Cultivar	
NR134	東海 9 号	TOUKAI 9	26300	Japan	Kinki	Cultivar	
NR135	東海 11 号	TOUKAI 11	26302	Japan	Kinki	Cultivar	
NR136	東海 12 号	TOUKAI 12	26303	Japan	Kinki	Cultivar	
NR137	東海 14 号	TOUKAI 14	26304	Japan	Kinki	Cultivar	
NR138	東海 16 号	TOUKAI 16	26306	Japan	Kinki	Cultivar	
NR139	東分 3 号 (W)	TOUBUN 3(W)	26311	Japan	Kinki	Cultivar	
NR140	東分 3 号 (R)	TOUBUN 3(R)	26312	Japan	Kinki	Cultivar	
NR141	東分 4 号	TOUBUN 4	26313	Japan	Kinki	Cultivar	
NR142	東分 5 号	TOUBUN 5	26314	Japan	Kinki	Cultivar	
NR143	東分 6 号	TOUBUN 6	26315	Japan	Kinki	Cultivar	
NR144	東分 7 号	TOUBUN 7	26316	Japan	Kinki	Cultivar	
NR145		GANMAA M(40)2-3-1-1	26320	Japan	Kinki	Cultivar	Included
NR146		GANMAA M(80)4-1-2-1	26321	Japan	Kinki	Cultivar	
NR147		4X 8-1-1	26322	Japan	Kinki	Cultivar	
NR148		4X 20-1-1	26323	Japan	Kinki	Cultivar	
NR149	合成 5 号	GOUSEI 5	26324	Japan	Kinki	Cultivar	

Apendix1 continue

Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR150	早生朝鮮	WASE CHOUSEN	26325	Overseas	Asia		
NR151	早生朝鮮 2 号	WASE CHOUSEN 2	26326	Overseas	Asia		
NR152	中生朝鮮	NAKATE CHOUSEN	26327	Overseas	Asia		
NR153	早生村松	WASE MURAMATSU	26328	Japan	Kantō	Landrace	
NR154	四日市黒種	YOKKAICHI KURODANE	26329	Japan	Kinki	Landrace	
NR155	三重黒種	MIE KURODANE	26330	Japan	Kinki	Landrace	
NR156	伊勢黒種	ISE KURODANE	26331	Japan	Kinki	Landrace	
NR157	伊勢黒種 1 号	ISE KURODANE 1	26332	Japan	Kinki	Landrace	
NR158	伊勢黒	ISEGURO	26333	Japan	Kinki	Landrace	
NR159	水原種	SUIGENSHU	26334	Overseas	Asia		Included
NR160	吾妻	AZUMA	26335	Japan	Japan Unknow	Landrace	
NR161	京都吾妻	KYOUTO AZUMA	26336	Japan	Kinki	Landrace	
NR162	小型吾妻	KOGATA AZUMA	26337	Japan	Kinki	Landrace	
NR163	吾妻種	AZUMASHU	26338	Japan	Kinki	Landrace	
NR164	吾妻種	AZUMASHU	26339	Japan	Kinki	Landrace	Included
NR165	吾妻種	AZUMASHU	26340	Japan	Kinki	Landrace	
NR166	吾妻中生	AZUMA NAKATE	26341	Japan	Chūgoku-Shikoku	Landrace	
NR167	早生不二種	WASE FUJISHU	26342	Japan	Chūbu	Landrace	
NR168	不二種	FUJISHU	26343	Japan	Chūbu	Landrace	Included
NR169	不二	FUJI	26344	Japan	Chūbu	Landrace	
NR170	早生不二	WASE FUJI	26345	Japan	Chūbu	Landrace	
NR171	Landrace 朝鮮種	ZAIRAI CHOUSENSHU	26346	Overseas	Asia		
NR172	朝鮮種	CHOUSENSHU	26347	Overseas	Asia		
NR173	大朝鮮	DAICHOUSEN	26348	Overseas	Asia		
NR174	大朝鮮 33 号	DAICHOUSEN 33	26349	Overseas	Asia		Included
NR175	糟屋種	KASUYASHU	26350	Japan	Kyushu	Landrace	
NR176	唐種	TOUDANE	26351	Japan	Kyushu	Landrace	
NR177	村山種	MURAYAMASHU	26353	Japan	Kyushu	Landrace	Included
NR178	筑紫種	CHIKUSHISHU	26354	Japan	Kyushu	Landrace	
NR179	筑紫	CHIKUSHI	26355	Japan	Kyushu	Landrace	
NR180	晩生	OKUTE	26356	Japan	Japan Unknow	Landrace	Included
NR181	晩生菜	OKUTENA	26357	Japan	Chūbu	Landrace	
NR182	青森 1 号	AOMORI 1	26358	Japan	Tōhoku	Landrace	
NR183	宮城晩生	MIYAGI OKUTE	26359	Japan	Tōhoku	Landrace	
NR184	六ッ美早生	MUTSUMI WASE	26360	Japan	Chūbu	Landrace	
NR185	六ッ美晩生	MUTSUMI OKUTE	26361	Japan	Chūbu	Landrace	Included
NR186	六ッ美中生	MUTSUMI NAKATE	26362	Japan	Chūbu	Landrace	
NR187	中生六ッ美	NAKATE MUTSUMI	26363	Japan	Chūbu	Landrace	
NR188	六ッ美	MUTSUMI	26364	Japan	Chūbu	Landrace	

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR189	糸島種	ITOSHIMASHU	26365	Japan	Kantō	Landrace	Included
NR190	岩内	IWANAI	26366	Japan	Hokkaido	Landrace	
NR191	ハンブルグ	HAMBURG	26367	Overseas	Europe		
NR192	露 5 号	RO(USSR)5	26368	Overseas	Europe		
NR193	露 6 号	RO(USSR)6	26369	Overseas	Europe		
NR194	塊 3 号	OUAUSTRIA)3	26370	Overseas	Europe		
NR195	波 3 号	PO(POLAND)3	26371	Overseas	Europe		
NR196	独 1 号	DOKU 1(GERMANY 1)	26372	Overseas	Europe		
NR197	羅 1 号	RU 1(ROUMANIA 1)	26373	Overseas	Europe		Included
NR198	仏 1 号	FUTSU 1(FRANCE 1)	26374	Overseas	Europe		
NR199	仏 2 号	FUTSU 2(FRANCE 2)	26375	Overseas	Europe		
NR200	仏 3 号	FUTSU 3(FRANCE 3)	26376	Overseas	Europe		
NR201	仏 5 号	FUTSU 5(FRANCE 5)	26377	Overseas	Europe		
NR202	仏 7 号	FUTSU 7(FRANCE 7)	26379	Overseas	Europe		Included
NR203	仏 9 号	FUTSU 9(FRANCE 9)	26380	Overseas	Europe		
NR204	仏 10 号	FUTSU 10(FRANCE 10)	26381	Overseas	Europe		
NR205	仏 11 号	FUTSU 11(FRANCE 11)	26382	Overseas	Europe		
NR206		COLZA	26383	Overseas	Europe		Included
NR207		SVALOFSORIG	26384	Overseas	Exotic Unknow		
NR208		B.NAPUS,RAPIFERA	26385	Overseas	Exotic Unknow		Included
NR209		B.NAPUS,OLEIFERA	26386	Overseas	Europe		
NR210		NABO	26387	Overseas	America		
NR211	長州黒種	CHOSHUU KURODANE	26388	Japan	Chūgoku-Shikoku	Landrace	
NR212	四石晩	YONKOKUBAN	26389	Japan	Japan Unknow	Landrace	Included
NR213	早生黒 8 号	WASEGURO 8	26390	Japan	Kinki	Landrace	
NR214	伊勢黒種 125 号	ISE KURODANE 125	26391	Japan	Kinki	Landrace	Included
NR215	晩菜	BANSAI	26392	Japan	Chūbu	Landrace	
NR216	吾妻種	AZUMASHU	26393	Japan	Kinki	Landrace	
NR217	吾妻種	AZUMASHU	26394	Japan	Kinki	Landrace	
NR218	吾妻 1 号	AZUMA 1	26395	Japan	Kinki	Landrace	
NR219	新不二	SHIN FUJI	26396	Japan	Kinki	Landrace	
NR220	中生不二	NAKATE FUJI	26397	Japan	Kantō	Landrace	
NR221	糟屋選種	KASUYA SENSU	26398	Japan	Chūgoku-Shikoku	Landrace	
NR222	糟屋	KASUYA	26399	Japan	Chūgoku-Shikoku	Landrace	
NR223	小朝鮮	KOCHOUSEN	26400	Overseas	Asia		
NR224	大朝鮮 (福)	DAICHOUSEN(FUKU)	26401	Overseas	Asia		
NR225	大朝鮮 1 号	DAICHOUSEN 1	26402	Overseas	Asia		
NR226	大朝鮮 2 号	DAICHOUSEN 2	26403	Overseas	Asia		Included
NR227	雑種	ZASSHU	26404	Japan	Tōhoku	Landrace	Included
NR228	青柳 1 号	AOYAGI 1	26405	Japan	Kyushu	Cultivar	



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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR229	九大新 2 号	KYUUDAI SHIN 2	26406	Japan	Kyushu	Landrace	
NR230	福岡朝鮮 1 号	FUKUOKA CHOUSEN 1	26407	Japan	Kyushu	Landrace	
NR231	波 4 号	PO(POLAND)4	26408	Overseas	Europe		
NR232	波 5 号	PO(POLAND)5	26409	Overseas	Europe		
NR233	佛 4 号	FUTSU 4(FRANCE 4)	26410	Overseas	Europe		
NR234	佛 8 号	FUTSU 8(FRANCE 8)	26411	Overseas	Europe		
NR235	仏 12 号	FUTSU 12(FRANCE 12)	26412	Overseas	Europe		
NR236	西洋種	SEIYOSHU	26413	Overseas	Exotic Unknow		
NR237	波 1 号	PO(POLAND)1	26414	Overseas	Europe		
NR238	中野種 (矮性)	NAKANOSHU(DWARF)	26415	Japan	Kantō	Landrace	
NR239	水原種 (帯化性)	SUIGENSHU(FASCIATION)	26416	Overseas	Asia		Included
NR240	吾妻種	AZUMASHU	26417	Japan	Kinki	Landrace	Included
NR241	一色 2 号	ISSHIKI 2	26418	Japan	Chūbu	Landrace	Included
NR242	吉田種	YOSHIDASHU	26419	Japan	Chūbu	Landrace	
NR243		C.O.	26420	Japan	Kantō	Landrace	Included
NR244	鴻種系 1409	KOUSHUKEI 1409	26421	Japan	Kantō	Landrace	
NR245	近畿早生	KINKI WASE	26422	Japan	Kinki	Landrace	
NR246	福本一	FUKUMOTO 1	26423	Japan	Japan Unknow	Landrace	
NR247		SPRING RAPE REGINA	26424	Overseas	Europe		
NR248		SPRING RAPE GOLDEN ARGENTINE	26425	Overseas	Europe		
NR249		WINTER RAPE MATADOR	26426	Overseas	Europe		Included
NR250	東海 23 号	TOUKAI 23	26427	Japan	Kinki	Cultivar	
NR251	東海 27 号	TOUKAI 27	26428	Japan	Kinki	Cultivar	
NR252	水原	SUWEON	26429	Overseas	Asia		
NR253	吾妻種	AZUMASHU	26430	Japan	Kinki	Landrace	
NR254	近畿 26 号	KINKI 26	26431	Japan	Kinki	Cultivar	Included
NR255	近畿 27 号	KINKI 27	26432	Japan	Kinki	Landrace	
NR256	吾妻種	AZUMASHU	26433	Japan	Kinki	Landrace	
NR257	吾妻種	AZUMASHU	26434	Japan	Kinki	Landrace	
NR258	東海 21 号	TOUKAI 21	26436	Japan	Kinki	Cultivar	
NR259	東海 24 号	TOUKAI 24	26437	Japan	Kinki	Cultivar	
NR260	唐種	KARADANE	26438	Japan	Kyushu	Landrace	
NR261	九州 4 号	KYUUSHUU 4	26439	Japan	Kyushu	Cultivar	
NR262	九州 6 号	KYUUSHUU 6	26440	Japan	Kyushu	Cultivar	
NR263	九州 7 号	KYUUSHUU 7	26441	Japan	Kyushu	Cultivar	
NR264	九州 8 号	KYUUSHUU 8	26442	Japan	Kyushu	Cultivar	
NR265	九州 9 号	KYUUSHUU 9	26443	Japan	Kyushu	Cultivar	
NR266	九州 11 号	KYUUSHUU 11	26444	Japan	Kyushu	Cultivar	
NR267	九州 17 号	KYUUSHUU 17	26448	Japan	Kyushu	Cultivar	

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR268	九州 18 号	KYUUSHUU 18	26449	Japan	Kyushu	Cultivar	Included
NR269	九州 19 号	KYUUSHUU 19	26450	Japan	Kyushu	Cultivar	
NR270	九州 22 号	KYUUSHUU 22	26451	Japan	Kyushu	Cultivar	
NR271	九州 24 号	KYUUSHUU 24	26452	Japan	Kyushu	Cultivar	
NR272	九州 25 号	KYUUSHUU 25	26453	Japan	Kyushu	Cultivar	Included
NR273	九州 26 号	KYUUSHUU 26	26454	Japan	Kyushu	Cultivar	
NR274	九州 27 号	KYUUSHUU 27	26455	Japan	Kyushu	Cultivar	
NR275	九州 29 号	KYUUSHUU 29	26456	Japan	Kyushu	Cultivar	
NR276	九州 32 号	KYUUSHUU 32	26457	Japan	Kyushu	Cultivar	Included
NR277	九州 33 号	KYUUSHUU 33	26458	Japan	Kyushu	Cultivar	
NR278	九州 34 号	KYUUSHUU 34	26459	Japan	Kyushu	Cultivar	
NR279	九州 36 号	KYUUSHUU 36	26461	Japan	Kyushu	Cultivar	
NR280	九州 39 号	KYUUSHUU 39	26463	Japan	Kyushu	Cultivar	
NR281	九州 40 号	KYUUSHUU 40	26464	Japan	Kyushu	Cultivar	
NR282	九州 41 号	KYUUSHUU 41	26465	Japan	Kyushu	Cultivar	
NR283	九州 42 号	KYUUSHUU 42	26466	Japan	Kyushu	Cultivar	
NR284	九州 47 号	KYUUSHUU 47	26468	Japan	Kyushu	Cultivar	
NR285	九州 49 号	KYUUSHUU 49	26470	Japan	Kyushu	Cultivar	
NR286	九州 50 号	KYUUSHUU 50	26471	Japan	Kyushu	Cultivar	
NR287	九州 51 号	KYUUSHUU 51	26472	Japan	Kyushu	Cultivar	
NR288	九州 52 号	KYUUSHUU 52	26473	Japan	Kyushu	Cultivar	
NR289	九州 54 号	KYUUSHUU 54	26475	Japan	Kyushu	Cultivar	
NR290	九州 56 号	KYUUSHUU 56	26477	Japan	Kyushu	Cultivar	
NR291	九州 57 号	KYUUSHUU 57	26478	Japan	Kyushu	Cultivar	
NR292	東北 51 号	TOUHOKU 51	26481	Japan	Tōhoku	Cultivar	
NR293	東北 52 号	TOUHOKU 52	26482	Japan	Tōhoku	Cultivar	
NR294	東北 53 号	TOUHOKU 53	26483	Japan	Tōhoku	Cultivar	
NR295	東北 54 号	TOUHOKU 54	26484	Japan	Tōhoku	Cultivar	
NR296	東海 25 号	TOUKAI 25	26485	Japan	Kinki	Cultivar	
NR297	東海 26 号	TOUKAI 26	26486	Japan	Kinki	Cultivar	
NR298	南九州 5 号	MINAMIKYUUSHUU 5	26491	Japan	Kyushu	Cultivar	
NR299	南九州 7 号	MINAMIKYUUSHUU 7	26493	Japan	Kyushu	Cultivar	
NR300	南九州 8 号	MINAMIKYUUSHUU 8	26494	Japan	Kyushu	Cultivar	
NR301	吾妻種	AZUMASHU	26495	Japan	Kinki	Landrace	Included
NR302	吾妻種	AZUMASHU	26496	Japan	Kinki	Landrace	
NR303	吾妻種	AZUMASHU	26497	Japan	Kinki	Landrace	
NR304	吾妻種	AZUMASHU	26498	Japan	Kinki	Landrace	
NR305	吾妻種 (28)	AZUMASHU(28)	26499	Japan	Kinki	Landrace	
NR306	吾妻種 (31)	AZUMASHU(31)	26500	Japan	Kinki	Landrace	

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR307	大朝鮮 (中野)	DAICHOUSEN(NAKANO)	26501	Overseas	Asia		
NR308	大朝鮮 (光安)	DAICHOUSEN(MIZUYASU)	26502	Overseas	Asia		
NR309	大朝鮮 (村山)	DAICHOUSEN(MURAYAMA)	26503	Overseas	Asia		
NR310	粕屋種 21 号	KASUYASHU 21	26504	Japan	Kyushu	Landrace	
NR311	唐種 (50)	TOUDANE(50)	26505	Japan	Chūgoku-Shikoku	Landrace	
NR312	唐種 (51)	TOUDANE(51)	26506	Japan	Chūgoku-Shikoku	Landrace	
NR313	唐種 (52)	TOUDANE(52)	26507	Japan	Chūgoku-Shikoku	Landrace	Included
NR314	魚成 Landrace	UONARU ZAIRAI	26508	Japan	Chūgoku-Shikoku	Landrace	
NR315	近永 Landrace	CHIKANAGA ZAIRAI	26509	Japan	Chūgoku-Shikoku	Landrace	
NR316	Landrace 種 (成妙)	ZAIRAISHU(NARITAE)	26510	Japan	Chūgoku-Shikoku	Landrace	
NR317	清満 Landrace	SEIMAN ZAIRAI	26511	Japan	Chūgoku-Shikoku	Landrace	
NR318	大川種	OOKAWASHU	26512	Japan	Kyushu	Landrace	
NR319	中野種 (矮性)	NAKANOSHU(DWARF)	26514	Japan	Kantō	Landrace	
NR320		SVALOFS ORIG	26517	Overseas	Europe		
NR321	北海 2 号	HOKKAI 2	26518	Japan	Hokkaido	Landrace	
NR322		SV.REGINA II SUMMER RAPE	26519	Overseas	Europe		Included
NR323		N.Z.CALDER SWEDE	26521	Overseas	Oceania		Included
NR324		BROAD LEAF ESSEX RAPE	26522	Overseas	Oceania		
NR325		APHIS RESISTANT RAPE	26523	Overseas	Oceania		
NR326		N.Z.WYE SWEDE(CLUB ROOT RES)	26524	Overseas	Oceania		Included
NR327		HOSTRAPS VESTAL	26525	Overseas	Europe		
NR328		HOSTRAPS PLUS	26526	Overseas	Europe		
NR329		WINTER RAPE GIESSEN	26528	Overseas	Europe		Included
NR330		EXP.SYNTHETEC VAR C(HIGH OIL)	26529	Overseas	America		
NR331		GOLDEN	26531	Overseas	America		
NR332		RAPE UNIT 13 PLANT 5	26532	Overseas	Europe		
NR333		RAPE UNIT 13 PLANT 8	26533	Overseas	Europe		Included
NR334		RAPE UNIT 15 PLANT 1	26534	Overseas	Europe		
NR335		RAPE UNIT 15 PLANT 8	26535	Overseas	Europe		Included
NR336		SCHERWITZ WINTER RAPE	26536	Overseas	Europe		
NR337		WINTER RAPE WEIBULLS MARGO	26537	Overseas	Europe		
NR338		WINTER RAPE WEIBULLS 506	26538	Overseas	Europe		
NR339		JANETZKI WINTER RAPE	26539	Overseas	Europe		
NR340	南九州 9 号	MINAMIKYUUSHUU 9	26541	Japan	Kyushu	Cultivar	
NR341	南九州 15 号	MINAMIKYUUSHUU 15	26547	Japan	Kyushu	Cultivar	
NR342	チクゼンナタネ	CHIKUZENNATANE	26556	Japan	Kyushu	Cultivar	
NR343	ダイリュウナタネ	DAIRYUUNATANE	26557	Japan	Kyushu	Cultivar	
NR344	南九州 24 号	MINAMIKYUUSHUU 24	26558	Japan	Kyushu	Cultivar	

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR345	九州 61 号	KYUSHUU 61	26561	Japan	Kyushu	Cultivar	
NR346	福系 1141-1	FUKUKEI 1141-1	26565	Japan	Kyushu	Landrace	
NR347	福系 1141-2	FUKUKEI 1141-2	26566	Japan	Kyushu	Landrace	
NR348	福系 1143-2-3	FUKUKEI 1143-2-3	26567	Japan	Kyushu	Landrace	
NR349	福系 1145-1-7	FUKUKEI 1145-1-7	26568	Japan	Kyushu	Landrace	
NR350		CUBS ROOT	26569	Overseas	Asia		
NR351		ORLE	26570	Overseas	Asia		
NR352		RAPORA	26571	Overseas	Asia		
NR353		YUDAL	26572	Overseas	Asia		
NR354	華 318	KA 318	26573	Overseas	Asia		
NR355	華 322	KA 322	26574	Overseas	Asia		
NR356	華 325	KA 325	26575	Overseas	Asia		
NR357	華 336	KA 336	26576	Overseas	Asia		
NR358		MARIS HAPLONA	26577	Overseas	Europe		Included
NR359		NILLA=1022	26578	Overseas	Europe		
NR360		NILLA(GLOSSY LEAF,RECESSIVE)	26579	Overseas	Europe		
NR361		ARTIFICIAL B.NAPUS I WINTER	26580	Overseas	Europe		
NR362		ARTIFICIAL B.NAPUS II WINTER	26581	Overseas	Europe		Included
NR363		WINTER RAPE REGAL 267/5	26582	Overseas	Europe		
NR364		WINTER RAPE MATADOR 267/3	26583	Overseas	Europe		
NR365		SVALOFS VICTORIA	26584	Overseas	Europe		
NR366		SVALOFS FENIX BANGHOLM	26585	Overseas	Europe		Included
NR367		HOST RAPE REGAL	26586	Overseas	Europe		
NR368		SVALOFS REGINA II	26587	Overseas	Europe		
NR369		REGAL	26588	Overseas	Europe		
NR370		GYLLE	26589	Overseas	Europe		
NR371		RIGO	26590	Overseas	Europe		
NR372		NORDE	26591	Overseas	Europe		Included
NR373		LINUS	26592	Overseas	Europe		Included
NR374		R JANUS	26593	Overseas	Europe		
NR375		R CRESUS	26595	Overseas	Europe		
NR376		SVALOFS GULLE	26596	Overseas	Europe		
NR377		GERMANY	26597	Overseas	Europe		
NR378		RAPOL	26598	Overseas	Europe		Included
NR379		LEMBKES	26599	Overseas	Europe		Included
NR380		FONTO	26600	Overseas	Europe		
NR381		GEBR.DIPPES	26601	Overseas	Europe		
NR382		JANETZKIS WEIHENSTEPHANER	26602	Overseas	Europe		
NR383		LIHO=PETRA	26603	Overseas	Europe		Included
NR384		SPATS ZOLLERNGOLD	26604	Overseas	Europe		Included
NR385		KOMET	26605	Overseas	Europe		
NR386		KRAPPHAUSER	26606	Overseas	Europe		

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR387		LEMBKES MALCHOWER	26607	Overseas	Europe		
NR388		QUEDLINBURGER PLATZFESTER	26608	Overseas	Europe		
NR389		OLQUELL	26609	Overseas	Europe		
NR390		MALI	26610	Overseas	Europe		Included
NR391		JANETZKIS SOMMERRAPS	26611	Overseas	Europe		
NR392		ERLE	26612	Overseas	Europe		
NR393		LIFURA	26613	Overseas	Europe		Included
NR394		LINOLA	26614	Overseas	Europe		
NR395		MATADOR	26615	Overseas	Europe		
NR396		OMI	26616	Overseas	Europe		
NR397		PETRANOVA=LIHONOVA	26617	Overseas	Europe		
NR398		ERGLU	26618	Overseas	Europe		
NR399		ARMANDER	26619	Overseas	Europe		
NR400		EXPANDER	26620	Overseas	Europe		
NR401		PANTER	26622	Overseas	Europe		
NR402		SALAMANDER	26623	Overseas	Europe		
NR403		SYNRA	26624	Overseas	Europe		
NR404		DIAMANT	26625	Overseas	Europe		
NR405		LENORA	26626	Overseas	Europe		
NR406		LESIRA	26627	Overseas	Europe		
NR407		POLNOSLASKI	26628	Overseas	Europe		Included
NR408		BRONOWSKI	26633	Overseas	Europe		
NR409		MLOCHOWSKI	26634	Overseas	Europe		Included
NR410		WIELKOPOSKI	26636	Overseas	Europe		
NR411		SZNESZOWICKI	26638	Overseas	Europe		
NR412		WARCZAWSKI	26639	Overseas	Europe		
NR413		BOROWSKI	26640	Overseas	Europe		
NR414		B.NAPUS OLEIFERA	26642	Overseas	Europe		
NR415		CESKA	26643	Overseas	Europe		
NR416		NUAPSKA	26644	Overseas	Europe		
NR417		TREBICKA	26645	Overseas	Europe		
NR418		JARNI CESKA	26646	Overseas	Europe		
NR419		FERTODI	26647	Overseas	Europe		Included
NR420	羅 1 号	RUMANIA I(RU 1)	26648	Overseas	Europe		
NR421		COLZA 18 MAROC	26649	Overseas	Europe		
NR422		CZ-YY MAROC	26650	Overseas	Europe		
NR423		TONUS	26651	Overseas	Europe		
NR424		CRESUS	26654	Overseas	Europe		
NR425		MAJOR	26655	Overseas	Europe		
NR426		TOWER	26656	Overseas	America		Included
NR427		ORO	26657	Overseas	America		
NR428		TARGET	26658	Overseas	America		
NR429		NUGGET	26659	Overseas	America		
NR430		TANKA	26660	Overseas	America		

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR431		MIDAS	26661	Overseas	America		
NR432		ZEPHYR	26663	Overseas	America		
NR433		TARGET	26664	Overseas	America		
NR434		CLUB ROOT RESISTANT RAPE	26665	Overseas	Oceania		
NR435	晩生つみな CO	BANSEI TSUMINA CO	26666	Japan	Kantō	Landrace	
NR436	川流れ	KAWA NAGARE	26667	Japan	Chūbu	Landrace	
NR437	宮内菜	MIYAUCHI NA	26668	Japan	Kantō	Landrace	
NR438		CO 4	26669	Japan	Kantō	Landrace	
NR439		BRIDGER	36289	Overseas	America		
NR440		CASCADE	36290	Overseas	America		
NR441		SHINKIRINA(KAKINA)	37340	Japan	Kantō	Landrace	
NR442	かぶれ菜	KABULENA	37341	Japan	Kantō	Landrace	Included
NR443		C O NA	37397	Japan	Kantō	Landrace	Included
NR444		JUNO	40676	Overseas	Europe		
NR445		SV 0212	40677	Overseas	Europe		
NR446		TOPAS	40678	Overseas	Europe		
NR447		GLOBAL	40679	Overseas	Europe		
NR448		EMIL	40680	Overseas	Europe		
NR449		HANNA	40681	Overseas	Europe		
NR450		OLIVIA	40682	Overseas	Europe		
NR451		OMEGA	40683	Overseas	Europe		
NR452		JUVEL	40684	Overseas	Europe		
NR453		KARAT	40685	Overseas	Europe		Included
NR454		NIKLAS	40686	Overseas	Europe		
NR455		GULLIVER	40687	Overseas	Europe		Included
NR456		DIPLOM	40688	Overseas	Europe		
NR457		LERGO	40689	Overseas	Europe		Included
NR458		ELVIRA	40690	Overseas	Europe		
NR459		BELINDA	40691	Overseas	Europe		
NR460		KORINA	40692	Overseas	Europe		
NR461		GUNDULA	40693	Overseas	Europe		
NR462		RIDANA	40694	Overseas	Europe		Included
NR463		TAMARA	40695	Overseas	Europe		
NR464		ELENA(00)	40696	Overseas	Europe		Included
NR465		SANTANA(00)	40697	Overseas	Europe		
NR466		ARABELLA(00)	40698	Overseas	Europe		
NR467		KURANDER	40699	Overseas	Europe		
NR468		MIRANDER	40700	Overseas	Europe		
NR469		PRIMOR	40701	Overseas	Europe		
NR470		ANJA	40702	Overseas	Europe		Included
NR471		MAJA	40703	Overseas	Europe		
NR472		EDITA	40704	Overseas	Europe		Included
NR473		NURA	40705	Overseas	Europe		Included
NR474		AKELA	40706	Overseas	Europe		

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR475		BARCOLI	40707	Overseas	Europe		
NR476		BISHOP	40708	Overseas	Europe		Included
NR477		CANARD	40709	Overseas	Europe		
NR478		EMERALD	40710	Overseas	Europe		
NR479		VIVA	40711	Overseas	Europe		
NR480		WINFRED	40712	Overseas	Europe		
NR481		DORAL	40713	Overseas	Europe		
NR482		GLORIA	40714	Overseas	Europe		
NR483		BINERA	40715	Overseas	Europe		
NR484		RUBIN	40716	Overseas	Europe		
NR485		CERES	40717	Overseas	Europe		
NR486		COBRA	40718	Overseas	Europe		
NR487		GARANT	40719	Overseas	Europe		
NR488		QUINTA	40720	Overseas	Europe		
NR489		ORBIS	40721	Overseas	Europe		
NR490		GERMANDER	40722	Overseas	Europe		
NR491		LIRAMA	40723	Overseas	Europe		
NR492		LINE	40724	Overseas	Europe		
NR493		OPTIMA	40725	Overseas	Europe		
NR494		RALLY	40726	Overseas	Europe		
NR495		LORAS	40727	Overseas	Europe		
NR496		LISANDRA	40728	Overseas	Europe		
NR497		BRUTOR	40729	Overseas	Europe		
NR498		DARMOR	40730	Overseas	Europe		
NR499		ALTEX	40731	Overseas	America		
NR500		ANDOR	40732	Overseas	America		
NR501		REGENT	40733	Overseas	America		
NR502		WESTAR	40734	Overseas	America		
NR503		ATR RESISTANT TOWER	40735	Overseas	America		Included
NR504	ネムロルタバカ	NEMURO RUTABAKA	41101	Japan	Hokkaido	Cultivar	Included
NR505	マジェスティク1号	MAGESTIC 1	41102	Overseas	Europe		
NR506	グリーントップ	GREEN TOP	41103	Overseas	Exotic Unknow		
NR507		N-501	46068	Japan	Kantō	Landrace	
NR508		C-463	46069	Overseas	Europe		
NR509		N-261	46070	Overseas	Europe		
NR510		N-346	46071	Overseas	America		
NR511		N-349	46072	Overseas	America		
NR512		N-404	46073	Overseas	America		Included
NR513		N-264	46074	Overseas	Oceania		
NR514		N-345	46075	Overseas	Oceania		
NR515		N-405	46076	Overseas	Oceania		
NR516	トワダナタネ	TOWADANATANE	67870	Japan	Tōhoku	Cultivar	
NR517	東北68号	TOUHOKU 68	67871	Japan	Tōhoku	Cultivar	

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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR518	東北 72 号	TOUHOKU 72	67872	Japan	Tōhoku	Cultivar	
NR519	東北 73 号	TOUHOKU 73	67873	Japan	Tōhoku	Cultivar	
NR520	青系 258	AOKEI 258	67874	Japan	Tōhoku	Cultivar	
NR521	青三系-1	AOSANKEI-1	67875	Japan	Tōhoku	Cultivar	Included
NR522	郡脂 5 号	GUNSHI 5	67876	Japan	Tōhoku	Cultivar	Included
NR523	北系 56-6-6-4	HOKUKEI 56-6-6-4	67877	Japan	Hokkaido	Cultivar	Included
NR524	Windal	WINDAL	67878	Overseas	Europe		
NR525		61・3A-14-2	67879	Overseas	Europe		
NR526		70・12・714-1	67880	Overseas	Europe		
NR527		70・34・114-3	67881	Overseas	Europe		Included
NR528	Cresor	CRESOR	67882	Overseas	Europe		
NR529		B・12・122・122・1-1	67883	Overseas	Europe		
NR530		B 23-1	67884	Overseas	Europe		Included
NR531	Ramses	RAMSES	67885	Overseas	Europe		
NR532	R39:Jetneuf-1	R39:JETNEUF-1	67886	Overseas	Europe		
NR533		RAFAL	67887	Overseas	Europe		
NR534	Blako	BLAKO	67888	Overseas	Europe		
NR535	Erra-1	ERRA-1	67889	Overseas	Europe		
NR536	Erra-2	ERRA-2	67890	Overseas	Europe		
NR537	Vertis	VERTIS	67891	Overseas	Europe		Included
NR538	北海 3 号	HOKKAI 3	67892	Japan	Hokkaido	Cultivar	
NR539	郡脂 5 号-1	GUNSHI 5-1	67893	Japan	Tōhoku	Cultivar	
NR540	郡脂 5 号-2	GUNSHI 5-2	67894	Japan	Tōhoku	Cultivar	
NR541	郡脂 5 号-3	GUNSHI 5-3	67895	Japan	Tōhoku	Cultivar	
NR542		Z・E・N	67896	Overseas	America		Included
NR543	青油 2 号	QUINGYOU 2	67897	Overseas	Asia		Included
NR544	青油 5 号	QUINGYOU 5	67898	Overseas	Asia		Included
NR545	青油 6 号	QUINGYOU 6	67899	Overseas	Asia		
NR546		D 26/79	67900	Overseas	Europe		
NR547		BK 27/78	67901	Overseas	Europe		
NR548	Prota	PROTA	67902	Overseas	Europe		
NR549	Da 5/81	DA 5/81	67903	Overseas	Europe		
NR550	Sedo 2	SEDO II	67904	Overseas	Europe		
NR551	東北 78 号	TOUHOKU 78	67905	Japan	Tōhoku	Cultivar	
NR552	東北 79 号	TOUHOKU 79	67906	Japan	Tōhoku	Cultivar	
NR553	東北 74 号	TOUHOKU 74	67907	Japan	Tōhoku	Cultivar	
NR554	東北 75 号	TOUHOKU 75	67908	Japan	Tōhoku	Cultivar	
NR555	カミキタナタネ	KAMIKITANATANE	67909	Japan	Tōhoku	Cultivar	
NR556		LAULENTIAN	76713	Overseas	America		Included



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Sample ID in this study	品種・系統名	Variety name	JP No.	Origin 1	Origin 2	Cultivar/Landrace	Corecollection
NR557		WILHELMSBURGER	76714	Overseas	America		Included
NR558		ECD 06	76715	Overseas	Europe		
NR559		ECD 07	76716	Overseas	Europe		Included
NR560		ECD 08	76717	Overseas	Europe		
NR561		ECD 09	76718	Overseas	Europe		
NR562		ECD 10	76719	Overseas	Europe		
NR563		BGR 468	80935	Overseas	America		
NR564		KRASNOSELSKAYA	128131	Overseas	Exotic Unknow		Included
NR565		BOUNTY	146914	Overseas	America		
NR566		CELEBRA	146915	Overseas	Europe		Included
NR567		DELTA	146916	Overseas	Europe		
NR568		GOLDA	146917	Overseas	Europe		Included
NR569		STALLION	146920	Overseas	Europe		Included
NR570		TRIBUTE	146921	Overseas	America		
NR571		VANGUARD	146922	Overseas	Europe		Included
NR572		AZTEC	146923	Overseas	Europe		
NR573		FALCON	146924	Overseas	Europe		
NR574		INCA	146925	Overseas	Europe		
NR575		ONYX	146926	Overseas	Exotic Unknow		
NR576		SABRINA	146927	Overseas	Europe		
NR577		MONETA	146931	Overseas	Europe		Included
NR578		HELIOS	147431	Overseas	Exotic Unknow		
NR579	高系 10 号-2	KOUKEI 10-2	207962	Japan	Chūbu	Cultivar	Included
NR580	高系 10-2 号	KOUKEI 10-2	207963	Japan	Chūbu	Cultivar	
NR581	長島 Landrace1	NAGASHIMA ZAIRAI 1	220360	Japan	Kinki	Landrace	
NR582	長島 Landrace2	NAGASHIMA ZAIRAI 2	220361	Japan	Kinki	Landrace	

Appendix 2. Primer information of the 504 SSR markers used in this study.

Marker name	Primer sequence (5'-3')		Citation
	Forward	Reverse	
BnEMS0004	CTCGTCTCTCCAACCTTCTGT	TCAACATCAACATCCACATC	Wang <i>et al.</i> (2012)
BnEMS0006	CATCTCCTCTGTCTTTATCCTT	GAATCGTGTTCGTGAGTGA	Wang <i>et al.</i> (2012)
BnEMS0008	TTCTCTCCATCTCTCTTCCA	ATGAATCGTGTGCGTGAGT	Wang <i>et al.</i> (2012)
BnEMS0020	CTCTATCCGAAGTGAATGATG	GTCGTCAACCCACACAAA	Wang <i>et al.</i> (2012)
BnEMS0031	GGACCAGAACCAGAGAGATT	TAATAACGATGAACCCTACGA	Wang <i>et al.</i> (2012)
BnEMS0048	TCACTCTACAACCTGTTTCA	TCTTTCTTTCTTCATCTCTCC	Wang <i>et al.</i> (2012)
BnEMS0056	ACGACATCCTTCTTCTTCTTC	CAGTTTATCATCAGACAATCCA	Wang <i>et al.</i> (2012)
BnEMS0112	AAAGGAACCACATTTCTCTCT	CCCATCTCTCTCTCTCTCTTC	Wang <i>et al.</i> (2012)
BnEMS0139	TTGTCGGAGATAATGAGAGAA	GAGGAGTTGGCTTGTGAG	Wang <i>et al.</i> (2012)
BnEMS0169	ATCGCTTCATCAGCAAGA	AGAGACACGACGAACACAAG	Wang <i>et al.</i> (2012)
BnEMS0214	TTGCACATCTTACTCTCTTC	TTTCTAGTCTTTATTGCGCC	Wang <i>et al.</i> (2012)
BnEMS0273	CCGCATACAAGATTGTGTTA	TCGGAATTGAAAGGTACAGT	Wang <i>et al.</i> (2012)
BnEMS0287	TCATTTCTACGGAGGAGTTG	GGAGGAGAAGAATCTAGGGA	Wang <i>et al.</i> (2012)
BnEMS0294	ATCCTCCGTTAGAGATCACA	TGGCAAACAAAATGAATGATA	Wang <i>et al.</i> (2012)
BnEMS0340	ATGGAAATGAAGAAAGACGA	CATAGAGAGGATGGCTTGAG	Wang <i>et al.</i> (2012)
BnEMS0395	AACCACAACCATAGACGAAC	TTCATTTCTCCCTTTGTCC	Wang <i>et al.</i> (2012)
BnEMS0446	GAAGAAGAGAGGCTAGGGAG	TCTGGTGAAGACAGATGTGA	Wang <i>et al.</i> (2012)
BnEMS0472	ATTATAACCGACAACAACCG	TTTAGCAGCCAAAGATAGGAG	Wang <i>et al.</i> (2012)
BnEMS0481	CTTGAGATCGTTCTCTACG	TCTAACCTCTGCTGCTCTTC	Wang <i>et al.</i> (2012)
BnEMS0525	GCATTCCTATTTGAGCAATC	GATCAAGCCAATAGATTGTA	Wang <i>et al.</i> (2012)
BnEMS0536	ATTCTTGGCTTCAATCAA	TTATTAGTTTTCAGTGGCGGT	Wang <i>et al.</i> (2012)
BnEMS0537	CTCAGACAAAGCGACCAC	CGTTAAGGAAAGGTCTGTTG	Wang <i>et al.</i> (2012)
BnEMS0612	CGGAAAGTTTGGTAAATTGAG	GAGGAGGATGATGAATCAGA	Wang <i>et al.</i> (2012)
BnEMS0619	GTTTATTTTCGCCCTGTGTC	CACAACTGATTCATCAACG	Wang <i>et al.</i> (2012)
BnEMS0620	TCTCTCAATTCCTTCAAGGA	AAGATTCATGCCACTTCAAC	Wang <i>et al.</i> (2012)
BnEMS0694	AGATTTCTCCCATCTCCAT	AAGCAGAAACCCACTAGACA	Wang <i>et al.</i> (2012)
BnEMS0718	GTCTCGAAATCTCAATACCG	GTAGATCTCGGAACCAACAG	Wang <i>et al.</i> (2012)
BnEMS0727	GAGGGATCTCATGTTCACTG	AAAGAAGACGAAAATCTAGTTGAA	Wang <i>et al.</i> (2012)
BnEMS0753	CAATCAATCTCTCAAAGCC	CCTTACCCTTCTCACTTCTCT	Wang <i>et al.</i> (2012)
BnEMS0872	TTGAAGAAGAGAAGATGGGA	CTCTCACTGGAGAATTGAGC	Wang <i>et al.</i> (2012)
BnEMS0885	TCAGGGTCACTTTCTCAATC	TTTCTGGAAAGAAGGATGAA	Wang <i>et al.</i> (2012)
BnEMS0891	CGAGTAGACGGGATTTACAG	AAAGTTAGGGTCAAGAGGAC	Wang <i>et al.</i> (2012)
BnEMS1001	CCTCCTCTCTTCTCAGTCT	ATCTGTGGATTTGAATTTGG	Wang <i>et al.</i> (2012)
BnEMS1009	AACCCTAGCTTCTCAATTC	AAGGAGGAGGAGAGGTTTAG	Wang <i>et al.</i> (2012)
BnEMS1010	AAGACAAAAGTCGGTGAAGAA	GCTACGAATCTCATCTCTCTG	Wang <i>et al.</i> (2012)
BnEMS1061	TTTACATGGAAAGAGGCAGT	ACCTATGATGAGCATGGAAC	Wang <i>et al.</i> (2012)
BnEMS1094	TTTAGTTTCATCAAACACTCTCT	CCACTATGTTAGCTTCGTCC	Wang <i>et al.</i> (2012)
BnEMS1119	ACTGGAGTTTCAATTGGATG	CATCATCTTCAGCACTAGCA	Wang <i>et al.</i> (2012)
BnEMS1132	GTCGAAAACCCAATCTGTTTA	TACAGGATATCGCTTCGTCT	Wang <i>et al.</i> (2012)
BnEMS1136	AAGGTTATAATCTGCGACGA	ATATTTGTAACCGCAAATGG	Wang <i>et al.</i> (2012)
BnEMS1150	ATCTAGAGGCGATTTCTGA	GAGATGGATCCGAGTTTGTG	Wang <i>et al.</i> (2012)
BnEMS1215	GCCAGATCAACACTCCCTTCT	ACAACAGAAGAACCGGAGGA	Wang <i>et al.</i> (2012)
BnGMS0002	TTCACATGTTTGTCTCAACG	TACCATTCTAAGGTGCCTA	Cheng <i>et al.</i> (2009)
BnGMS0014	ATCCGAAGAGAGGATAGAGG	GTATGGACGACGAATCATCT	Cheng <i>et al.</i> (2009)
BnGMS0103	GTGAGTGGAAACGTTCTAGC	AAGACTGTTACGGCTCGTC	Cheng <i>et al.</i> (2009)
BnGMS0271	ATGTTTCTCCATTTGTCTCTG	TTGTGTGTCTGGGAGAAT	Cheng <i>et al.</i> (2009)
BnGMS0281	TATAACACGGTGTGTGCTGT	CCAACAAATTTAATGCATGTT	Cheng <i>et al.</i> (2009)
BnGMS0289	CATTACAAACTCAGCGTCAA	CAGGACACTCGGTTATCAAA	Cheng <i>et al.</i> (2009)
BnGMS0293	ACGTTTCACTTGAGGATCTG	CTATACGATGTCTGGTCTGT	Cheng <i>et al.</i> (2009)
BnGMS0336	ACCGAATAACAAGTCGAACA	TTGAAACACACCCATTTACA	Cheng <i>et al.</i> (2009)
BnGMS0353	AACCAAAGAATACATCCGAA	TTGCAGAAGTTGAGACAATG	Cheng <i>et al.</i> (2009)
BnGMS0373	CAGATAAATTTGGGTAGTCA	TATGGATCTGGAAACTCGAA	Cheng <i>et al.</i> (2009)
BnGMS0386	TTGGCTCATCAATGACAATA	ACAATGTGGTAAACACGAAA	Cheng <i>et al.</i> (2009)
BnGMS0509	TGAATGTGCTTCTTCGTATG	TTCAAGCTCGTTCACTCTCT	Cheng <i>et al.</i> (2009)
BnGMS0574	ATCTATACGCACACTTCCGT	ATGGCTTTGTCTAATCGAGA	Cheng <i>et al.</i> (2009)
BnGMS0615	GGCACGGATCTTAACTAGT	TCAAGGGCTTTCATATCTTG	Cheng <i>et al.</i> (2009)
BnGMS0634	CAATTTGGGACTGAAGAAAT	CGCATTCTTCAAACAAACTC	Cheng <i>et al.</i> (2009)
BnGMS0635	CAAAGCAAATCAAACAATCA	CAATTCACGTATGATCCACA	Cheng <i>et al.</i> (2009)
BnGMS0646	TTTACGAGAGTCGGAAGAT	CATTCACATCCACTCTGATG	Cheng <i>et al.</i> (2009)
BnGMS0662	CGATCGAATTGCACTGTACT	ATGCACAGAGCTGAAGAAAT	Cheng <i>et al.</i> (2009)
BnGMS0713	CCTCCGTGATTTCTTTTCTCTG	CAGGTCCATATCATACAACTTCC	Cheng <i>et al.</i> (2009)
BnGMS0749	CGGTCTAGTTACCAGATCACC	AATCCCCTTGCCACTTATCAT	Cheng <i>et al.</i> (2009)
BnGMS0771	GTGATTTGGGATCAAAGACGA	GACGTCCGCAAACTTCTAATG	Cheng <i>et al.</i> (2009)
BnGMS0808	CTCGTGAGAAAACTGTGATGC	CATGTCCCTGGAGCTTGTG	Cheng <i>et al.</i> (2009)
BnGMS0945	AGTGTCAGCCCCTCAGAGAAC	CACATCTCTGGAAATGCAAAAC	Cheng <i>et al.</i> (2009)
BnGMS0966	ACAAAGTCGATGATCGAGGA	CTCCAATCGGTGGTGTCTTAAA	Cheng <i>et al.</i> (2009)
BnGMS0968	TACATGGCAAAGAACCCTGTC	AAGTCTCAGGAAGCACAGTCAA	Cheng <i>et al.</i> (2009)
BnGMS1004	ATGTATCTCAGCAGCCACAA	CAATCACAACAGACGTACATGC	Cheng <i>et al.</i> (2009)
BnGMS124	GGAGATTCAAGCTCAAGATG	GAGCTTTCTCAGCTTTACCA	Cheng <i>et al.</i> (2009)
BnGMS14	ATCCGAAGAGGATAGAGG	GTATGGACGCAATCATCT	Cheng <i>et al.</i> (2009)
BnGMS2	TTCACATGTTTGTCTCAACG	TACCATTCTAAGGTGCCTA	Cheng <i>et al.</i> (2009)
BnGMS205	AAGAGAGACAGCGTGTGTT	GACTCTAGGAGAGTAGACGGC	Cheng <i>et al.</i> (2009)

## Appendix 2 continue

Marker name	Primer sequence (5'-3')		Citation
	Forward	Reverse	
BnGMS239	GCGACATGGTAATTGAAAGTT	TTTAATGGGTCCATGATAGC	Cheng <i>et al.</i> (2009)
BnGMS271	ATGTTTCTCCATTTGTCCTG	GTGTGTGTTCTGGGAGAAT	Cheng <i>et al.</i> (2009)
BnGMS291	TGGGCAGTTATAGGATATGAA	ATGTCAATAACGTACTIONCGGG	Cheng <i>et al.</i> (2009)
BnGMS3	AAAGAGCCACATGAAAGTA	TGAAGTAGGCACCAAGAAGT	Cheng <i>et al.</i> (2009)
BnGMS314	TTGCTACAATTTACTTCGTTTG	GTAACCCGTATAAGTGGCTG	Cheng <i>et al.</i> (2009)
BnGMS315	TTACGGTATATTCTCGCCAT	GTCTACCAGAACACCCCTCAA	Cheng <i>et al.</i> (2009)
BnGMS317	TATTGGGTCAAGAACTTGCT	CAATGAATCCCTGTTCAAGT	Cheng <i>et al.</i> (2009)
BnGMS338	ATTATATGGCAAGCGATGTT	TCTCACAGCAGAGAACCCTT	Cheng <i>et al.</i> (2009)
BnGMS347	TCACACAAATCTCCTCTCT	AGGTATCAGCCAATGACTTC	Cheng <i>et al.</i> (2009)
BnGMS349	CCAGGAGGGAGTAAACTCTT	GGTCAATAAAACAATGGTGTG	Cheng <i>et al.</i> (2009)
BnGMS353	AACCAAAGAATACATCCGAA	TTGCAGAAGTTGAGACAATG	Cheng <i>et al.</i> (2009)
BnGMS373	CAGATAAATTTGGGTAGCTCA	TATGGATCTGGAAACTCGAA	Cheng <i>et al.</i> (2009)
BnGMS386	TTGGCTCATCAATGACAATA	ACAATGTGGTAAACACGAAA	Cheng <i>et al.</i> (2009)
BnGMS422	TGGAGAAGAAGCTATACACA	TCACACCAGGGTAAAGGTAG	Cheng <i>et al.</i> (2009)
BnGMS452	TAGATGGTCTTGACCCATA	AACATGTCTTTGATGAAGCC	Cheng <i>et al.</i> (2009)
BnGMS454	TGTATCTGGTTCATGGTTGA	ATGGAAATGGAACGTGATAG	Cheng <i>et al.</i> (2009)
BnGMS488	CGTCGCAGTCTGTAATTGT	TGTTTTAACTTCAAATATGGCTT	Cheng <i>et al.</i> (2009)
BnGMS492	AAATTATAACCAATGTCTGAAA	AGATTTAAGTGAATCGGAA	Cheng <i>et al.</i> (2009)
BnGMS513	ATGCCAGCATGAAGAGTTAG	GCTTTGTGGTCTGATTTCTC	Cheng <i>et al.</i> (2009)
BnGMS598	TGGTAGGTCATCTCTGTC	GAAGATGAAGAGGAAGGGTT	Cheng <i>et al.</i> (2009)
BnGMS602	GGAAATTTGCTTCTTACCAA	TTGTGTGTGTTTGTAAACC	Cheng <i>et al.</i> (2009)
BnGMS603	TGTATGGTCTGATGGTCTC	CGTTCCTGATGATCTCAAAT	Cheng <i>et al.</i> (2009)
BnGMS616	CGTATGGATAATGTGTTCA	ATTAACAGCAGGATAGCAA	Cheng <i>et al.</i> (2009)
BnGMS631	CCATTATTCTAGTTTACCACC	CCTCGTCTTAGTAGGTACA	Cheng <i>et al.</i> (2009)
BnGMS632	CCATTATAAGAGTGTCCATGAGT	AACGGGTTGTGACATTAAG	Cheng <i>et al.</i> (2009)
BnGMS634	CAATTTGGGACTGAAGAAAT	CGCATTCTTCAAACAAACTC	Cheng <i>et al.</i> (2009)
BnGMS646	TTTACGAGAGTCGGAAAGAT	CATTACACATCCACTCTGATG	Cheng <i>et al.</i> (2009)
BnGMS659	GCCAAATTCATTAGTAACCG	CCAAATTTGATTAAGTAGTGCT	Cheng <i>et al.</i> (2009)
BnGMS662	CGATCGAATGCACTGTACT	ATGCACAGAGCTGAAGAAAT	Cheng <i>et al.</i> (2009)
BoEMS0004	AGAGCGCAGTCCACACAC	ATGGATCAGAAAACAGTGGAG	Li <i>et al.</i> (2013)
BoEMS0016	AATCTTCGCCGCTGTTTA	TTAACCTTTATGCTAACGCC	Li <i>et al.</i> (2013)
BoEMS0049	GAATCTCGTAAATTTGATGG	CGACTAATCTTGGAGTTGG	Li <i>et al.</i> (2013)
BoGMS0026	CGAGAACAAGAGACAAGTGAG	TGATTAGACCCTGATTGAAAG	Li <i>et al.</i> (2011)
BoGMS0030	GCTAATCCAGACCAAAACA	AGAAACACCATTCAAACAAA	Li <i>et al.</i> (2011)
BoGMS0037	ACTGCTCTCCCTTCACTCT	TATCTTCCGCCTCTTCTGT	Li <i>et al.</i> (2011)
BoGMS0081	AGTCCTAATGGTGTCTTTGT	CTGTTGAGGTGTTGTCTTTT	Li <i>et al.</i> (2011)
BoGMS0112	ACTGGTCCGAATAGGTGAG	CGATAAATGGTTCATGTTCC	Li <i>et al.</i> (2011)
BoGMS0116	TGTCACCAGTCTCTCTCTC	TCAGTGTCTTCTCAAACATAA	Li <i>et al.</i> (2011)
BoGMS0168	GTCTTGATGAAGCCAGTAG	AGAGGAAGTGTCCGGGAAG	Li <i>et al.</i> (2011)
BoGMS0254	CTACGGCTTCGCTCTGTC	TACTTCCCAACCATTCTGTA	Li <i>et al.</i> (2011)
BoGMS0281	ATCCTTCTGCCTTCTCTG	TGACATCCATCCACACATT	Li <i>et al.</i> (2011)
BoGMS0282	CCCTTGTAGAGAGAGAGAGGA	AAACGAAATAAGATGACGAGA	Li <i>et al.</i> (2011)
BoGMS0299	GCAGGAATCAAACAGAAACT	TCTCTCTCTCTCTCTCTCTCT	Li <i>et al.</i> (2011)
BoGMS0342	ATGAATAACCAAGCGACAAG	TAAGCCAGAAGGCACCTGTT	Li <i>et al.</i> (2011)
BoGMS0358	GGCTCGTACACTATGCT	TTCACCAAGAAAGAGTTCATC	Li <i>et al.</i> (2011)
BoGMS0364	CCTGTCTTGTCTCATCTATTT	GCGTTAGGTGTTGTAGGATT	Li <i>et al.</i> (2011)
BoGMS0394	CCCTTACTTTGTTCAAGTTTC	CATCTCTACCACCACACA	Li <i>et al.</i> (2011)
BoGMS0420	AAATGTTATGTGTGGGTCTATT	AGAGAGAGAGAGAATGGTGAGA	Li <i>et al.</i> (2011)
BoGMS0454	GCACTGAGAGAGAAAGAGTCA	TGTTGTATGGCAAGTATGTGT	Li <i>et al.</i> (2011)
BoGMS0456	TAACAAACCGGAAAGACGA	GTGAAACCACAGAGGATAGAA	Li <i>et al.</i> (2011)
BoGMS0486	AAGGAGGAACCAATGCC	TGATAATGCCACTGATAGGAC	Li <i>et al.</i> (2011)
BoGMS0501	ATGATGAGTTTGTCTGTTAGG	AAATCTTCTCTCTTTTAC	Li <i>et al.</i> (2011)
BoGMS0505	CTGTGGTGAAGTCTATTGG	TGTTGCTCGTCAATTTCTATCT	Li <i>et al.</i> (2011)
BoGMS0507	TACGATTTCTGTTCTATTCTATC	ATCCCTGCGGTTATCAAA	Li <i>et al.</i> (2011)
BoGMS0513	CTGACCATCTATCAAACAAA	ACCGCTTTACCATTCTATC	Li <i>et al.</i> (2011)
BoGMS0525	AGTCCCATCAAGTCCAATATC	GTCGTCTTCAGCCATCAG	Li <i>et al.</i> (2011)
BoGMS0537	AAGACAACATCCCTGAAGAAC	GAGAGTCGCTGAACATAAGAA	Li <i>et al.</i> (2011)
BoGMS0545	CCTCTGTTTCTTTGCTCTTTG	GATTCATTGTGTGTGTGATGT	Li <i>et al.</i> (2011)
BoGMS0573	TTTGAGGTATTGTAGCAGATT	AGCATTGTAGTTGAGGACAG	Li <i>et al.</i> (2011)
BoGMS0576	ACCTGGAGTTGAGACGGG	CAGTGTGAGTGTCTTCTATT	Li <i>et al.</i> (2011)
BoGMS0582	CCTGAGCTTTGGAGCCTT	TCGTTATTAGATTGAGTATTTG	Li <i>et al.</i> (2011)
BoGMS0584	GAAACCCACTCGTATTAG	AAACCAACCTTCTCTTCTCA	Li <i>et al.</i> (2011)
BoGMS0594	TTGTTGCGTTTATTGTTT	GGTCCATTTACTACTTATTCCT	Li <i>et al.</i> (2011)
BoGMS0607	GTTCTTTCTTGGTTCATAC	CCGCCATTTCTATCTTTT	Li <i>et al.</i> (2011)
BoGMS0619	TCAAGACCCGCTCCAAAG	ATGTTCTGTTGCTCCAAATAG	Li <i>et al.</i> (2011)
BoGMS0624	AAGACGAAGTCAAGTCAAGGT	CGTATCATCCAGAGTATCCAG	Li <i>et al.</i> (2011)
BoGMS0660	CCTTGTCTTTGTAGGAAATG	GGTGTCTGTGCTTTGTTT	Li <i>et al.</i> (2011)
BoGMS0678	CTCTTCTTGTCTTCTCTCTC	TCTTCTTCTCTCTCTCTCT	Li <i>et al.</i> (2011)
BoGMS0687	GACAACACAACAGACGCA	GCATTTCCCATTAATTCCA	Li <i>et al.</i> (2011)
BoGMS0705	GTCACCTATCTCTCTCCATT	TAGCCACCAAGTCTGTTT	Li <i>et al.</i> (2011)
BoGMS0738	TTGAGGAAGGAACACGAA	GTGGGAGAGTGAAGGTAGTAA	Li <i>et al.</i> (2011)
BoGMS0741	CTCAAACCTCCGCTCT	TCTCTCTACTACTTTCTTCA	Li <i>et al.</i> (2011)
BoGMS0811	GCACCTGCAATCACTCAA	ACTTCTCCAAATCTCTGTCTC	Li <i>et al.</i> (2011)
BoGMS0819	AGGGAGATGGACATTTAG	GAGAGAGGGCAAAGAGATAG	Li <i>et al.</i> (2011)

Appendix 2 continue

Marker name	Primer sequence (5'-3')		Citation
	Forward	Reverse	
BoGMS0836	CATAAACACACCCGAACAAGAC	ACGCAATGACACACATACAC	Li <i>et al.</i> (2011)
BoGMS0845	CCTTTGTCTTCTTCTACTCTCC	ACCAGGCTCTTCTTTCTCT	Li <i>et al.</i> (2011)
BoGMS0867	GACTCAGACCACAAACTCA	GCAAAGAGACTTACTTACCCA	Li <i>et al.</i> (2011)
BoGMS0868	AAATCCCAACGAGATAGGTAG	AGAAAGAAAGGAAGAAAGTGG	Li <i>et al.</i> (2011)
BoGMS0927	ACCAGAGAAGGCATACATAGA	CGAAGGAGTTTGTGAGGATAA	Li <i>et al.</i> (2011)
BoGMS0929	TCAGACCCAAAGCCAGTT	TTGTGGAAGATGAAACCATT	Li <i>et al.</i> (2011)
BoGMS0934	GGTCAGAGTAAGGGATGGA	TGTAAGATGTCTGGCTAATGT	Li <i>et al.</i> (2011)
BoGMS1017	TTTGTGTGTGTGTGTGTTC	TATCTCTCGCTCGTCTCA	Li <i>et al.</i> (2011)
BoGMS1028	ACAAGTCTCTCTCACCGAA	TTCAACAACCCTCTAACATCTC	Li <i>et al.</i> (2011)
BoGMS1037	CCGTAACCTTCTCTCTCTC	GTCAGCAGCAGGATTACG	Li <i>et al.</i> (2011)
BoGMS1055	CGGATAGGAGAGGTTTCAG	TGACTTTGCTTCACTTCCA	Li <i>et al.</i> (2011)
BoGMS1065	GGGTTGATTGGGAAGTGT	CTTAGCACCATTGTTTGTATT	Li <i>et al.</i> (2011)
BoGMS1118	AGACATCAAAGCAAGACAG	TCAAACGAACTACTCTCTCAA	Li <i>et al.</i> (2011)
BoGMS1145	CTTCTCTCTTCGCATCATAAC	GTCCCTCTCTCTCTCTCT	Li <i>et al.</i> (2011)
BoGMS1218	GTAACCAGAAATCAGAATGG	GACGAAAGATGGAAGGGTAA	Li <i>et al.</i> (2011)
BoGMS1235	ATTCATCATCTCTCCGAA	TAAGGCTCATCTCAACTCTCA	Li <i>et al.</i> (2011)
BoGMS1259	ACAAGGAGAAGGAGAAGACAC	TGAGGAAGATGAAGTTGAAGA	Li <i>et al.</i> (2011)
BoGMS1264	GATTGTGGAGGTGGGTTT	TCAAGAAGAAAGAGAAAGAGAGA	Li <i>et al.</i> (2011)
BoGMS1283	TTGTCATCATCTTCTACTC	TGCTATCCACTCTTCTTCTCA	Li <i>et al.</i> (2011)
BoGMS1287	GTGAAGCAAGGCATAAATAAA	TGAGAAACAGGTCCAACCAA	Li <i>et al.</i> (2011)
BoGMS1330	AGGAGAAGAAGGAAGATACCA	AGAAAGGAAAGAAAGACCAGA	Li <i>et al.</i> (2011)
BoGMS1360	GAGACCAGAGAAGGAGGAAC	CACCTACTATCACACACTCA	Li <i>et al.</i> (2011)
BoGMS1412	GGTTTAGTGTCTTGGTTCGGT	GCGAGAGAAAAGTTGAGGTT	Li <i>et al.</i> (2011)
BoGMS1419	AAAGGTCGTATTCTCTCTCTC	GATTTGATTCTGGTGTGAAGT	Li <i>et al.</i> (2011)
BoGMS1432	AAGTCGGCACAAGGTGTT	AGGGATTTAGAGTTTCGTGTT	Li <i>et al.</i> (2011)
BoGMS1472	ACTCGCACACATACATACC	GAATAGGGAGAGAGATTGAG	Li <i>et al.</i> (2011)
BoGMS1486	AAATGTGTCTTCTGGTGATG	AGGAGGGTAAGTTGGTGATT	Li <i>et al.</i> (2011)
BoGMS1495	TAACACTGAAACACATTGGCT	GTGAGAAAGATGACGAAGATG	Li <i>et al.</i> (2011)
BoGMS1565	GATGACTTGGCGTTGATT	CTGAGAGAGAAGAAGGAGAAGA	Li <i>et al.</i> (2011)
BoGMS1567	TTCAGTAGGGAGGATAGGT	GGTTATGATGCTCGTCGG	Li <i>et al.</i> (2011)
BoGMS1615	TGCCTGAGAAGAACATGAAGAC	ACTCACTACCCATGGTTTCTT	Li <i>et al.</i> (2011)
BoGMS1652	TGCGGTCTTATAGGAGATGTGA	GGGACAATTATCATGTGGACCT	Li <i>et al.</i> (2011)
BoGMS1697	AGAGACAAACCAGCCTTGGAC	GCGATTTTCAAGAGGTTAGAGGA	Li <i>et al.</i> (2011)
BoGMS1740	CTTCCGTGGATGATGTCTTGT	AACAATGGTGTGAAAGGGTAT	Li <i>et al.</i> (2011)
BoGMS1746	GCTCGGCTAACACCTATTCTA	AGCAAGACAAGTGAGTTGGTTC	Li <i>et al.</i> (2011)
BoGMS1747	TGTTATCGGAACCTCTTGAAT	ATATAATTGACCCGTGCGTAGC	Li <i>et al.</i> (2011)
BoGMS1764	TTGGAGCATCACGAACTACAC	TGCAACGTTATCACGTTCTAT	Li <i>et al.</i> (2011)
BoGMS1795	AAGAAGTACCCGAATAGATCG	GAGATTGGAGAGATGGATTGTG	Li <i>et al.</i> (2011)
BoGMS1813	TTGTCTTCTCCGTTCCAATCT	TACAGACGAGTTGTGGATCGTC	Li <i>et al.</i> (2011)
BoGMS1897	AAGGAGGACGATCAGCTAAACC	CCCTCTCTCTCTCTTAGGG	Li <i>et al.</i> (2011)
BoGMS1909	AGGTGCAATAAGCTGTCTCTCC	AAACTCGAGCTTATCACGCTGT	Li <i>et al.</i> (2011)
BoGMS1937	TCTCTAAACCGCAGGAAATCAT	GAATGTTTGTGGAACCAAAGG	Li <i>et al.</i> (2011)
BoGMS2016	GTATCCGAACTCAAATCCGAAC	CTGTGAGAGAAGCAAACCTTT	Li <i>et al.</i> (2011)
BoGMS2026	CCTTTCGTTTCGTGATTACAAA	CCAGTAACCAGTTTAAATCCTC	Li <i>et al.</i> (2011)
BoGMS2030	AACACTAGCCAAAGGTTGTAA	AAGCAAAATGAACCATCCACTC	Li <i>et al.</i> (2011)
BoGMS2064	ATTTCGACCCACGAAAGTATT	CATCGGACGGTTCAGATATT	Li <i>et al.</i> (2011)
BoGMS2095	CCATGCTGGTAGGCAATAAGTA	TGGACCATTGGGACCATAGTAGT	Li <i>et al.</i> (2011)
BoGMS2228	CGTCCGCTTATTCAACTTTGG	TTCTCTCTTGGATTCTTCAA	Li <i>et al.</i> (2011)
BoGMS2256	AGGGAGAGAGGAAACAACTGA	ATAAGAACCCTCCGCTCTCTGCT	Li <i>et al.</i> (2011)
BoGMS2319	ACTGGTGCAGGAATGAATAGAAG	CTTTGGTGATGCCACGATAGTA	Li <i>et al.</i> (2011)
BoGMS2351	TTGGCGCTAGTCAGATCTTCTC	CCTAATGATTCCACCCTCATTC	Li <i>et al.</i> (2011)
BoGMS2360	CGATTAGTCTCGCATTATCAA	AGAATTCTCCGATACCATTCGTC	Li <i>et al.</i> (2011)
BoGMS2387	ATGTCCCTGTGAAATGTGTGTT	TTTCTCGGACAACCTTTGTGTA	Li <i>et al.</i> (2011)
BoGMS2431	CAACCACCGACTCAAATACAGA	GCACCTGCAATCTCCATACATA	Li <i>et al.</i> (2011)
BoGMS2468	CATTCCGGTTATTCAACTTTGG	CGAACGGATCGGATCTTATT	Li <i>et al.</i> (2011)
BoGMS2477	TCTGTACAGTGCCTGTCAAAT	TGACTCTTACATCAATCACGGTCT	Li <i>et al.</i> (2011)
BoGMS2499	TATACGATTGCTCTCCCTCCTC	TCGTACAGGTGAATTACGCAAG	Li <i>et al.</i> (2011)
BoGMS2504	TTTGGCCTTATCCAAATCTCTC	AGGCGACAAGTTGAATCTAAGG	Li <i>et al.</i> (2011)
BoGMS2590	GAGCAACAGTAATCAGGGTAACAA	ATTGTTCCGAAACTTCCATCTC	Li <i>et al.</i> (2011)
BoGMS2759	GATATTCGTATTGCCAGTGT	AGGATGCTTATGAATGGCTAGG	Li <i>et al.</i> (2011)
BoGMS2791	ACCGATTCTACCCGACTTAAA	TGACATACCAACTCCATCAA	Li <i>et al.</i> (2011)
BoGMS2965	AGAGACAGCTTAAACCTTCCA	TCTTAGTGGAGTACTTCGGAAC	Li <i>et al.</i> (2011)
BoGMS2992	TGTTGTTTCTCATACGTTTCG	TCACCCACACAAGTCAAATACTG	Li <i>et al.</i> (2011)
BoGMS3000	CGTGAGAGAGAGAGGGAGAGAG	CAAACCTCCTAGCCCACTCCTA	Li <i>et al.</i> (2011)
BoGMS3009	AAAGTTCGCTGCTTACTCGAC	TAAGCTGATAGCTTCCGGTTTC	Li <i>et al.</i> (2011)
BoGMS3139	CCAAATATTCAAGTTCCCATGT	GTTCTGAGGAGAGAGGCATCAT	Li <i>et al.</i> (2011)
BoGMS3309	AAGGTTGCCTTCTCTCACTT	ACAACAGATGACTGGCAAACAC	Li <i>et al.</i> (2011)
BoGMS3409	AGTTCGTTGAGCTTTTGGAA	TTCAATCTTCTTCTGTGGA	Li <i>et al.</i> (2011)
BoGMS3432	CTTGATCACAACAGAATCCTC	GCTATCTGCTCCGAGTCTAAA	Li <i>et al.</i> (2011)
BoGMS3538	TTCACCGTCTCTTCAAGTATCA	AGGAGAATCGTCAGAATCAAGC	Li <i>et al.</i> (2011)
BoGMS3581	TTCCTCATCAGGATCAACATCA	GGTTCATCATCAATGGTTTCT	Li <i>et al.</i> (2011)
BoGMS3608	TTAGACGATAGGGCTTAAACGA	ACACAAGTCAACCAGAGAAGAT	Li <i>et al.</i> (2011)
BoGMS3654	AGATGGGACTCGATGTTGAT	TTGTTGTGATGCTCTGTCACTG	Li <i>et al.</i> (2011)
BRAS019	CTCAAGACAACGACCAGTAA	GAGAAGAAATCGCCAAGA	Piquemal <i>et al.</i> (2005)

Appendix 2 continue

Marker name	Primer sequence (5'-3')		Citation
	Forward	Reverse	
BRAS084	ATTGGGTTCTGACCTTTTCTC	TTTTCCTTCATCGCTACCAC	Piquemal <i>et al.</i> (2005)
BrEMS0005	AGGAGTTCAAAGAGGAAACC	TCCTCATCTTCACCATCTTC	Li <i>et al.</i> (2013)
BrEMS0015	GATCACCCTGAAACTGAA	GCTTCTTGTAGCAGAGGAAA	Li <i>et al.</i> (2013)
BrEMS0028	TCTCTCAAGGGATTCTCATC	AATCAAGATCCGAGCCAT	Li <i>et al.</i> (2013)
BrGMS0060	GTTCTTATACTCGCGTTGGAGC	TTTAGCTTCTTCTCGAAATCGC	Xu <i>et al.</i> (2010)
BrGMS0070	TACAATGAAGATGTGATCCCGA	CGTGCCTGAGCTTATCAATACA	Xu <i>et al.</i> (2010)
BrGMS0086	ATATCCAAACACCGCACTAAAC	TTCGTCTTCATCTACGCTCAA	Xu <i>et al.</i> (2010)
BrGMS0108	TGACTCCAAACATCACCACAA	TGAAGACCAAGCGAACTTGATA	Xu <i>et al.</i> (2010)
BrGMS0140	ACTGACTCCAAACATCACCACA	TGAAGACCAAGCGAACTTGATA	Xu <i>et al.</i> (2010)
BrGMS0283	TACCATAGAGCCAAGCGGTATT	CCCTTCTTCTTCTCCTTCTC	Xu <i>et al.</i> (2010)
BrGMS0366	TTTGCCGAGTAACCTTTGTCAT	AAAGTTGGGCTTTTACTGTTCC	Xu <i>et al.</i> (2010)
BrGMS0454	ACCCTAGCCCCATAATAACCTT	TATCCACTTTGAGCGTTAAGCA	Xu <i>et al.</i> (2010)
BrGMS0485	CCTAACCTCGCAATCAAACTCG	TGAAACCGGTAAGGAGTTTGCT	Xu <i>et al.</i> (2010)
BrGMS0579	GCTTTCTTCAGATCCTCCTTGA	CCTTTCACCTGATCGTTCCTCC	Xu <i>et al.</i> (2010)
BrGMS0667	TCTTCTTCTCCTCATCCCCCTT	GGATTCTCACTTCGAGACCTA	Xu <i>et al.</i> (2010)
BrGMS0734	ATCTTCACTCGAACTCTCGCTC	AAAGCCATTGCTAATCTACACA	Xu <i>et al.</i> (2010)
BrGMS0742	ACACGTTGAAGCAAGTCACCTA	CAAAGTCCTTCCAAAACCAAAC	Xu <i>et al.</i> (2010)
BrGMS0753	CTCTTGTCGGATTTTGAGTTGA	TTGTAGGATGGTGACTGGTGAG	Xu <i>et al.</i> (2010)
BrGMS0758	AAGTTCTAGTCCGCGAGTTTT	TCAACATTCAACAACCTTACCAG	Xu <i>et al.</i> (2010)
BrGMS0899	AGATAACAATCGTTGGGCTCTGT	ATTGCTACAGTTTCGTCCATA	Xu <i>et al.</i> (2010)
BrGMS1218	GCGACAAAACCGTAAGAGAG	ATCATCGAAAGCCCCATAAGT	Xu <i>et al.</i> (2010)
BrGMS1411	GCTCCGAATCTCAAATCTAACG	AATCCCGCACTTAATCTCCAAT	Xu <i>et al.</i> (2010)
BrGMS1436	CATAATCAACAGCATGAGCTT	GTGTTTGGTATTGGGCTTCTC	Xu <i>et al.</i> (2010)
BrGMS1450	TGCTATCAACGAGACAATCCTG	AGACGATGACGATGAGAAATGTG	Xu <i>et al.</i> (2010)
BrGMS1474	ATTGTTTGTGGCCTTCTGTTC	GATTTATTTGTTGAGTTGCCGG	Xu <i>et al.</i> (2010)
BrGMS1490	ATCAAATCATCTCCTCTCCAC	ATTTACCATTCCAATTCCCA	Xu <i>et al.</i> (2010)
BrGMS1562	TTTACGTCGGTGAGACGATATG	TTCTTGGAAATCATAGCTGGACA	Xu <i>et al.</i> (2010)
BrGMS1569	TTGCTTCATTTGCTTGATGG	CCTACGTTGCAGTTTCCAATAAC	Xu <i>et al.</i> (2010)
BrGMS1713	AGGATTAGGCTGTTGAATGCTT	AGAGAGAATCGTCATGGAGGAG	Xu <i>et al.</i> (2010)
BrGMS1778	TCACCACTTCTTCAGACTCAC	GAGACAGAGATTTCGGAGGAGA	Xu <i>et al.</i> (2010)
BrGMS1786	CGCCAATAGAGTTGAGCAATAAC	CCATCGGTTCACTCAGCATA	Xu <i>et al.</i> (2010)
BrGMS1804	CACAGTTGGGTATATTTGTAAGTGC	ACGATCCCGTAGTAAAAGATT	Xu <i>et al.</i> (2010)
BrGMS1894	AAAGGGGACGTAGAACAAAGTGA	GTCACACAACCTAGGACACAGCC	Xu <i>et al.</i> (2010)
BrGMS2025	CATTGCATCTGACTCTCACCAT	CAAGCAGCCTAAGAAGGAGTGT	Xu <i>et al.</i> (2010)
BrGMS2130	GGCCACACATCACATTACCAT	TGGAGGAGGAAGCTAGAGAAGA	Xu <i>et al.</i> (2010)
BrGMS2193	AGTTTAAACCTGCGGATGATGT	GGCTGTTTGTCTGAATAGGAGTT	Xu <i>et al.</i> (2010)
BrGMS2244	CCCAAAGCGTATAGCATAGTCC	TGTGCGGTAGTCTTTAGTTTC	Xu <i>et al.</i> (2010)
BrGMS2252	GCACATGATCAGAAAGATCTCA	ATTACCTTCGGTCTCGGTTTCA	Xu <i>et al.</i> (2010)
BrGMS2375	TGGCAAGAGAGTCACATTTGTT	GATTTGTGCTGTCTCTGTGTT	Xu <i>et al.</i> (2010)
BrGMS2431	GGTTTGGGCTTCTAGGAAACAT	GATAGACCAGAGCAGACCAGAAA	Xu <i>et al.</i> (2010)
BrGMS2498	AGGAAACTTTACCGAGTGCTA	AATTGTGTTCTGTGTTGAGCAGT	Xu <i>et al.</i> (2010)
BrGMS2505	TATCCGTTAAGACAATGCAACG	CATAGTAGGCGTTAGGGTCTCTG	Xu <i>et al.</i> (2010)
BrGMS2628	TCCTTGTTGGTAAATCCTCAA	GGCGAAATTCAGTTGACATCAT	Xu <i>et al.</i> (2010)
BrGMS2767	GGGCTCCACTTTGTACTACTC	CTGGATCCAAATCCAAATCCAAT	Xu <i>et al.</i> (2010)
BrGMS2771	AGTTCTGTTCTCAGTTCTCTCC	TAAGCAATAACGGGAGCTTCTC	Xu <i>et al.</i> (2010)
BrGMS2849	CCTCTCATGAACCTGTAGTGTGA	CTCCCACCTTCTCTCTCTTA	Xu <i>et al.</i> (2010)
BrGMS2864	GGGTCCTTGGTACCATAATTGTC	TATTCTCGGTCTGTTCCACCTT	Xu <i>et al.</i> (2010)
BrGMS2901	TTTATTACGACTGCCACCAAGA	CAGATCGAGGAATAGTGACGTT	Xu <i>et al.</i> (2010)
BrGMS2969	TGTGGTCCAACAACCTAAGCAC	TTCTTCTCGCACTCATCTTCAA	Xu <i>et al.</i> (2010)
BrGMS2989	GTTACACAGGCTCAATTCTGTT	AGTCTCTGAAATTTAGCAAAGC	Xu <i>et al.</i> (2010)
BrGMS2998	AAGTGTGCAGCAGAGGAAAGA	AAAGACCCGGAGTGAACACTTA	Xu <i>et al.</i> (2010)
BrGMS3032	CGTTGCTTGTCTCCTATACAACA	AGATTCTTCTGCTCGAGTCCAC	Xu <i>et al.</i> (2010)
BrGMS3041	TCACTACGACTTCATCTACG	ACCAGAAGGTTACAGAGGTGCT	Xu <i>et al.</i> (2010)
BrGMS3080	TGTTCACTACTTGGCATGAGG	TAGATTATCACGCTGCAGGCTA	Xu <i>et al.</i> (2010)
BrGMS3093	GAGTTTGATGGCTCTCGTCTTT	CCATACCAGAACCTTGTCACCT	Xu <i>et al.</i> (2010)
BrGMS3114	TCTGATCTAAACCAAGCCAGT	AGGGCATGATAGTTGCTTCATT	Xu <i>et al.</i> (2010)
BrGMS3124	TCCCAAGGTTCTTCTCCAATAA	ATGAAACGAATTGGGTCTTAGT	Xu <i>et al.</i> (2010)
BrGMS3125	CACACACATTCGACAACCAAAT	CCTAGTACTTGAACGATGCAC	Xu <i>et al.</i> (2010)
BrGMS3126	TGTTGCTACTGAGAAAGCATCTT	GGAGAAAGTAAGAAGCTTTGAGG	Xu <i>et al.</i> (2010)
BrGMS3582	TTAACAAGACGGGCTTACG	TGCTAATCTCATAAGCCGATCA	Xu <i>et al.</i> (2010)
BrGMS3607	GCATGCATCCACTACTCCATTA	CAGGCATGAATACACACCCTTT	Xu <i>et al.</i> (2010)
BrGMS3653	AGCTGTGAGAACAGTGACATGG	GAATGGAACCAAGTGACATCAA	Xu <i>et al.</i> (2010)
BrGMS3688	GTTGAATTGCCTCCAGTGAGTT	TTTAGACGCAATGGTAAGAGCA	Xu <i>et al.</i> (2010)
BrGMS3750	GTTGGGCAAAGGTATGATGTAA	TCCATAAATCGCCAGCTATCAT	Xu <i>et al.</i> (2010)
BrGMS3755	TTATCAAGGGATTCGGTTTGAC	GATTGCAGCTTATCATCCACA	Xu <i>et al.</i> (2010)
BrGMS3784	CTTCTCTCCGACAGACATCAAT	TCTTGATCAAACCAACATACCG	Xu <i>et al.</i> (2010)
BrGMS3787	GCTAACGTTGCTCGTCACACTA	CGAATCAAAGGCACCTAAAGAT	Xu <i>et al.</i> (2010)
BrGMS3807	AACCTTGAGGACCATATCCTT	GGAGACATGGACATGATGACTG	Xu <i>et al.</i> (2010)
BrGMS3837	GCAGAACCAGATAGAATGTGTA	CCAATTTCACTGCCTAAGTGGTA	Xu <i>et al.</i> (2010)
BrGMS3857	GATAAGAGACAAGCCATTGTGC	GAGCTCGTCAGATTCTTGTGTA	Xu <i>et al.</i> (2010)
BrGMS3925	AGCAAGATCCCAAATATGCAG	GCACAACATTAGCCAGGTCATA	Xu <i>et al.</i> (2010)
BrGMS4027	ATCCGCATTGTCTCCATTAGAT	CCTGTTACAGGAGAAGAGGAA	Xu <i>et al.</i> (2010)
BrGMS4028	TGAAAACAACATCCGCTAGTGG	TTTCCGGTCAAAGTTTCTC	Xu <i>et al.</i> (2010)
BrGMS4031	CTCGAGTATTGTGTGGCGAGTA	TGCAGGATTAGTCAGAATCCAA	Xu <i>et al.</i> (2010)

Appendix 2 continue

Marker name	Primer sequence (5'-3')		Citation
	Forward	Reverse	
BrGMS4057	AGCACAGGAGTGAGACCAACAT	GCTAATGTGTCATCAGCTTTCC	Xu <i>et al.</i> (2010)
BrGMS4086	CCTTAAACTGATGCTGAATACACG	GTACACAGACTGAGAGCGAGAGA	Xu <i>et al.</i> (2010)
BrGMS4110	CAAGAATCCGACCCAAGTTTA	TGACTATGGATGATCGATTTGG	Xu <i>et al.</i> (2010)
BrGMS4149	CCCAACCTAACTGATACAAATGAG	TAGCATGGGCAATCAGGAAATA	Xu <i>et al.</i> (2010)
BrGMS4151	GAACGACGGAAATGTGAGTGTA	CATTATCCCTCGTCGAACCTT	Xu <i>et al.</i> (2010)
BrGMS4194	GCATCATCAATTGGCATATGAG	ATCTCTCGAATCGGTGTTCTTC	Xu <i>et al.</i> (2010)
BrGMS4196	CTTCTTTGGCATGTTGTACGAT	ATTGGCATCAGGGTTTCACTAA	Xu <i>et al.</i> (2010)
BrGMS4252	GCCGACCTAGTAGACCATAAG	ATTCAGATGACCATGGGTTTG	Xu <i>et al.</i> (2010)
BrGMS4289	ACAACGACGATTAGCTGTTTCA	TTTCAAAGGAAGAGGAGCAAAG	Xu <i>et al.</i> (2010)
BrGMS4320	TTGGGTAACAGATAACCCATGC	CAACTCCACCCTCTTACAGTCC	Xu <i>et al.</i> (2010)
BrGMS4450	CTCAGGTCTGTTCACCAACA	CAACAGGAAATGCGATGTGTAT	Xu <i>et al.</i> (2010)
BRMS-001	GGTGGCTCTAATTCCTCTGA	ATCTTTCTCTACCAACCCC	Suwabe <i>et al.</i> (2005)
BRMS-007	AAATTGTGTTCTTCCCAT	GTGTTAGGGAGCTGGAGAAT	Suwabe <i>et al.</i> (2005)
BRMS-008	AGGACACCAGGCACCATATA	CATTGTTGTCTTGGGAGAGC	Suwabe <i>et al.</i> (2005)
BRMS-008	AGGACACCAGGCACCATATA	CATTGTTGTCTTGGGAGAGC	Suwabe <i>et al.</i> (2005)
BRMS-014	CCGTAAGGAATTTAGGGCA	TTCCCAATTCTCAAACGGTA	Suwabe <i>et al.</i> (2005)
BRMS-016	CTAGGGTTATGGTTGAATCAGACA	TCGTATAGCTCAAATCAAATGTTC	Suwabe <i>et al.</i> (2005)
BRMS-017	GGAAAGGGAAGCTTCATATC	CTGGAAAGCATACACTTTGG	Suwabe <i>et al.</i> (2005)
BRMS-018	TCCCACGCCTCTAGCCTTC	ACCCGAGCTTTTCTGTGGCC	Suwabe <i>et al.</i> (2005)
BRMS-018	TCCCACGCCTCTAGCCTTC	ACCCGAGCTTTTCTGTGGCC	Suwabe <i>et al.</i> (2005)
BRMS-019	CCCAAACGCTTTTGACACAT	GGCACAATCCACTCAGCTTT	Suwabe <i>et al.</i> (2005)
BRMS-026	CCTATCTCCGGACTAATCAG	CTTGTAGTTTTCACATTGC	Suwabe <i>et al.</i> (2005)
BRMS-031	TGCCACCAATGACAATGACACTATC	GATGCATGGGACCACCTTACATTTT	Suwabe <i>et al.</i> (2005)
BRMS-036	GGTCCATTCTTTTTCATCTG	CATGGCAAGGGGTAACAAACAT	Suwabe <i>et al.</i> (2005)
BRMS042	TCCGAATTGGATAAGAATTCAA	GGATCAGTTATCTGCACCACAA	Suwabe <i>et al.</i> (2005)
BRMS-042	GGATCAGTTATCTGCACCACAA	TCGGAATTGGATAAGAATTCAA	Suwabe <i>et al.</i> (2005)
BRMS-043	CGATGTTTTTCTTCCAGTGTG	TTAATCCCTACCCACAATTTCC	Suwabe <i>et al.</i> (2005)
BRMS050	AACTTTGCTTCCACTGATTTTT	TTGCTTAAACGCTAAATCCATAT	Suwabe <i>et al.</i> (2005)
BRMS-050	AACTTTGCTTCCACTGATTTTT	TTGCTTAAACGCTAAATCCATAT	Suwabe <i>et al.</i> (2005)
BRMS-051	GGCCAAGCTACTGCTCAGA	GCCGAGAGTGGGAGTTATGG	Suwabe <i>et al.</i> (2005)
BRMS-056	GATCAAGGCTACGGAGAGAGAG	CGTGACGCTAGAGTAATCGAGT	Suwabe <i>et al.</i> (2005)
BRMS-058	GCAGACAAGAAATTCGCCATGTC	GACATTGGCGAAAGTCTTGAACCTGG	Suwabe <i>et al.</i> (2005)
BRMS-061	CTAGGGTTATGGTTGAATCAGACA	TCGTATAGCTCAAATCAAATGTTC	Suwabe <i>et al.</i> (2005)
BRMS-062	CTGCTGTGGAGATCGTTCATTGTAT	CCTTTTCTCTGGGTTTCTGACTT	Suwabe <i>et al.</i> (2005)
BRMS-070	AGGCCGAGGGTTAGACAAAAGAGAT	CGTTGGGAGGCTTCTTTAGTCACTT	Suwabe <i>et al.</i> (2005)
BRMS-071	CAAAGCGAGAAAGTGCAGTTGAGAG	TCCACGAAACTACTGCAGATTGAAA	Suwabe <i>et al.</i> (2005)
BRMS-075	GTTTACATATTTTCTGTATT	ACCTTAAATGTTAAGTAAGCTAAAC	Suwabe <i>et al.</i> (2005)
BRMS-079	AATTTCTACTGGGGTGGTCTATC	TTAATGGTGTGATGGCGTGACGATG	Suwabe <i>et al.</i> (2005)
BRMS-085	ACTCCACTCTCACTTCTCTAT	TTACGCTTGTTCGTGTTTTGAATA	Suwabe <i>et al.</i> (2005)
BRMS-090	AACGAACAACAACAGCAAGGAGAG	GATCTGAAAACCTAGCCGTCAATG	Suwabe <i>et al.</i> (2005)
BRMS-094	TTACCATAACCCCTTGTACAGC	TGAACGGGGAAAAGAAAAGCAAAGA	Suwabe <i>et al.</i> (2005)
BRMS-096	AGTCGAGATCTCGTTCGTGTCTCCC	TGAAGAAGGATTGAAGCTGTTGTTG	Suwabe <i>et al.</i> (2005)
BRMS-097	AAGAGCAAGAGCCAAGACAGCCTAC	TGGTGTGGAGAAAGTACATGGACGT	Suwabe <i>et al.</i> (2005)
BRMS-098	TGCTTGAGACGCTGCCACTTTGTTT	CATTCCTCCACCACCTTACATC	Suwabe <i>et al.</i> (2005)
BRMS-100	CTCTTGAGAAATCAGAGAGATTAC	GATCTTCAATATATTCATCTCTCTC	Suwabe <i>et al.</i> (2005)
BRMS-105	GAATCTCTGCAAGAAACAAATGTTA	ATCAAGTAACTCCTTTTCTCTCTC	Suwabe <i>et al.</i> (2005)
BRMS-108	ATTCAAAGACAAAGGAATGCCTGAG	GATCCTGTGCAATGGCATTAAATAAA	Suwabe <i>et al.</i> (2005)
BRMS-120	GTCAGCATACCCGCAAAACTCGCA	GGTACCGCAAGTCTCGGTCGGTTAA	Suwabe <i>et al.</i> (2005)
BRMS-124	GAGACGAGTGTGTTGTTGGCAGTTG	CGACGAGAACCAACACATAACAACC	Suwabe <i>et al.</i> (2005)
BRMS-125	GTTCTCAAAGGGAAACCGAAAAACA	GAGTTGGCAGAGATTACATGCGT	Suwabe <i>et al.</i> (2005)
BRMS-128	CCTGCATTTGGAAAAACAAACATTA	TTTACTACTTCTCTCAAATACCG	Suwabe <i>et al.</i> (2005)
BRMS-129b	TGAGGTTAGACATGGCGCTGCTTGC	TTTGTATTTGTGGTGGCGAGTTTCG	Suwabe <i>et al.</i> (2005)
BRMS-151	ACAGGAACCTGTAGAACCAGTAGG	CTTCACCAATGGCTTCTCTCAT	Suwabe <i>et al.</i> (2005)
BRMS-153	GCAATAAAACCTCCAACCTTTCTAT	AAAACACAGGAGGAAAAATTAAGAGG	Suwabe <i>et al.</i> (2005)
BRMS-158	AAAAGACAAAACCATCCAACACTA	AAGCCTTTTTGAACCTCTCTGTGAT	Suwabe <i>et al.</i> (2005)
BRMS-166	AAGTCACTACTTCCATTGAGGAACC	GATGATTGGTGGTTTGGGTTT	Suwabe <i>et al.</i> (2005)
BRMS-173	GAGGATGCAGTTGCTGTTGTT	CTTCTTCGATGGATTCAAGAGAAC	Suwabe <i>et al.</i> (2005)
BRMS-175	GTGATACTGAAAGGGAGAGAGTGAG	AATCCTCATGAGCAAATCAACTAAC	Suwabe <i>et al.</i> (2005)
BRMS-176	ATGTTACAGATGTGGAACCTATGG	AGGAAGACTGATTAACCTGTTTTGA	Suwabe <i>et al.</i> (2005)
BRMS-184	AGAACAATCTAACAAAAGACTCG	AAACAAAATAGGTCCGAAGAACTTT	Suwabe <i>et al.</i> (2005)
BRMS-185	ATCAAACAGCAGTTCTATACCAAT	TCTCTTTCTGACCCGAAGAAGAC	Suwabe <i>et al.</i> (2005)
BRMS-195	AATACTTTGTTTTCGTAAAGTGTCCGCTAA	AACCTACGCAAGATGCTTCTACTT	Suwabe <i>et al.</i> (2005)
BRMS-198	CGAGAGCAGTTAGGAAGCTTATAGA	AGAGATACTGTCTCCACCTCTT	Suwabe <i>et al.</i> (2005)
BRMS-201	GTAATAACAGTTCTGCCTCTGCTC	CTGCTGAATTAATTGCTGCTTCT	Suwabe <i>et al.</i> (2005)
BRMS-206	ATTAGACTCTTTCAAAAACGCAAAG	GATGACAACAACTTCTCTCTGTTA	Suwabe <i>et al.</i> (2005)
BRMS-218	CCAAATATGTTTTTCGTAAAGAAGGA	TCCATTACTAAACAGTTTCCCATC	Suwabe <i>et al.</i> (2005)
BRMS-221	AAAGTCTTGACGTTTGGAGGAAGAA	CAGGTTCTTATGAAGACCATGCAT	Suwabe <i>et al.</i> (2005)
BRMS-227	ACCATCTCGTATTTATTTATGAAG	GACGATTTGATAGAGGAAAGGAAT	Suwabe <i>et al.</i> (2005)
BRMS-231	ATTCATAGCAAACACGTTGTAGT	TCTGGACTTCAATTAGAGATGGTC	Suwabe <i>et al.</i> (2005)
BRMS-232	AAAACAATACGACTGATTGAACCAT	CAAATCATAGTCGAAACTAGCTAAAA	Suwabe <i>et al.</i> (2005)
BRMS-235	GGATCACAAATCGTGTCTAGTAATC	AGCATATCCATCAAGAGCTGGT	Suwabe <i>et al.</i> (2005)
BRMS-240	CAAGAGTATTTGTGGGTTGACTC	AAATAACGAACGGAGAGAGAGAG	Suwabe <i>et al.</i> (2005)
BRMS-245	CTCCTGTCTCACTATGTTTCTCT	TTGATTAGAAATAGAAGAAGAGAGA	Suwabe <i>et al.</i> (2005)
BRMS-247	TCTCTTTGAGGTTTCACTTTACG	GCTGATTAACCTTACCACCAGAG	Suwabe <i>et al.</i> (2005)

Appendix 2 continue

Marker name	Primer sequence (5'-3')		Citation
	Forward	Reverse	
BRMS-252	ACTGGACTTATGTCTGAACAAGGAC	CTGGCCAACATCAACATATAAACTA	Suwabe <i>et al.</i> (2005)
BRMS-260	AGAGATCACCAACAGAAAGTTGAAT	TTCTCGTAATTGAAACTTGGGTTTA	Suwabe <i>et al.</i> (2005)
BRMS-261	CACCTGTCATGTCTTCTCTGG	TTGTCTTTGTTTTCTTCTCATTCTG	Suwabe <i>et al.</i> (2005)
BRMS-276	GACCGTTTTGCATTTTAAGAGCATT	TCACCACCAGTATCTTCAACAATCA	Suwabe <i>et al.</i> (2005)
BRMS-298	CCACTGTTTTATGACTCCAGTGCCT	TGACCTGGTGAAGTAGTTGTCTCGT	Suwabe <i>et al.</i> (2005)
BRMS-303	ACTCAACAACCGAACAAAGAAAAACA	CGGTAGAGAACAGAGGAAGCCTAAG	Suwabe <i>et al.</i> (2005)
BRMS-312	CGCAGCAATTTAAAGCTTTCACAGTA	ATTTCAACATGTCTCAGACGCTTTTC	Suwabe <i>et al.</i> (2005)
BRMS-314	CATCATTTGTCTGTATCCGTCCTG	AATTCAGGCTATGGTAACTGTCTG	Suwabe <i>et al.</i> (2005)
BRMS-317	GCAAAAACAGATGAAGAAGATGGATG	GAGCTTATTGGGAGGCTTAACTCTG	Suwabe <i>et al.</i> (2005)
BRMS-322	CAGCAAATAATAAACTTACAACCTCA	ACAGGAAAGAGAGGAAGGTTCACTG	Suwabe <i>et al.</i> (2005)
BRMS-324	AACTTAACCGAAACGAGATAGGTG	AACTTCGAAATTCATCGACTTCCTC	Suwabe <i>et al.</i> (2005)
BRMS-327	TCGTATTTGTAGGCTCTGTTACGG	GCTTCAGCTTATCAGTCTCCTCTCC	Suwabe <i>et al.</i> (2005)
BRMS-330	TAATTTCCGTTTTCGCCTCCACTTAT	TTGCTTAAAGGATGAGTCTTGTCTG	Suwabe <i>et al.</i> (2005)
BRMS-333	ACTCTTCAGTTAGAAAAGCTAAATCT	CTCTTTCTGTGTGCTTACCGTTTTTC	Suwabe <i>et al.</i> (2005)
BRMS-336	GGAGTGATGAGCGAGTGAGTATGTT	GTTGTGATGGTAGCAGTGGCAGT	Suwabe <i>et al.</i> (2005)
BRMS-339	ATTGATTCGCTACAATGACGAGTCT	TTCTGGAAAACGACAAAATGACAAGT	Suwabe <i>et al.</i> (2005)
BRMS-342	CAACCAAAACGGGCCAATATAGTTA	TGTTTTCAAATAATCTCCCGTCTAA	Suwabe <i>et al.</i> (2005)
cnu_m250a	CAGATTTTCGAAAGGTGGTTGG	CCATCACCCGAAAATCCAAA	Kim <i>et al.</i> (2009)
cnu_m316a	TCAAGCATGTCCTTAAAACCTCGA	CGGTTACGTTTCCCATATC	Kim <i>et al.</i> (2009)
FITO017	TTTTTGTATCTCCATCATTTTTTG	TGATATGTTTGACAATTTCCCC	Iniguez-Luy <i>et al.</i> (2009)
FITO018	TGCCAAGCTTTGAGTAGCAA	TGCCTTCTCCATGCTTTCT	Iniguez-Luy <i>et al.</i> (2009)
FITO019	GTGAGACACCATCCCTCTT	TAGGAACGCTTGTAAAACCTG	Iniguez-Luy <i>et al.</i> (2009)
FITO026	TATGGCAGAGTATGTGGGA	TACAAAAGGTGTTTACCCGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO034	CTGGTTTTCTCTTCATCAG	AGCTTTTGTCTTTCTCTCTCTC	Iniguez-Luy <i>et al.</i> (2009)
FITO036	GGATTGCTGAGTTTATTCTT	TCTGGAGTAGATGCTTTGGT	Iniguez-Luy <i>et al.</i> (2009)
FITO040	GATTGTTTGTCTTAACTGTGG	GATTGTTTGTCTTAACTGTGG	Iniguez-Luy <i>et al.</i> (2009)
FITO043	AAAGTCGTGGGAAGTATCGT	AGGTGTAAGGATGGTGGTAGT	Iniguez-Luy <i>et al.</i> (2009)
FITO045	ATGGCTGTAGAAACACATTGA	CTGACAACACGAGCATCTTAC	Iniguez-Luy <i>et al.</i> (2009)
FITO050	AGCAAACTACCTGAACCTCT	TTTATCTCTGGTCTTCTCTCT	Iniguez-Luy <i>et al.</i> (2009)
FITO066	AGCCATTACCTGTGA	GAAAGACGATGCTTAGGGT	Iniguez-Luy <i>et al.</i> (2009)
FITO067	TTTCCATAAACTTCTCATT	GCTTCATCGTAATACTGCT	Iniguez-Luy <i>et al.</i> (2009)
FITO081	AACTAATCGGGAAACAACC	GAATGTCCGTCAGAATACC	Iniguez-Luy <i>et al.</i> (2009)
FITO083	CCCTTTGTTTCTTCTTTATTTCA	TCAACTATTCTATCATCTCTCCA	Iniguez-Luy <i>et al.</i> (2009)
FITO088	CCATCACTCATCTCACTCTTT	ATAAATCTCGTTGTTCGGAAGT	Iniguez-Luy <i>et al.</i> (2009)
FITO094	TTTATTTCTTTGGACTTGGG	CTACCGCATCATACATTCATT	Iniguez-Luy <i>et al.</i> (2009)
FITO095	AGATTTATCCACAGCCTC	TTTGATTTCTGGCTTCTCTC	Iniguez-Luy <i>et al.</i> (2009)
FITO098	ATGGGAAGAGAGTGAGGG	TCTAAACCTAAACTACACCTGCT	Iniguez-Luy <i>et al.</i> (2009)
FITO100	GATGAGAGAAGGAAACCCTAA	ACAGCAGGAGAAGAGAGAGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO102	TAATCATCAAACCAATGCGA	CGTCCAACACAAACACTTACT	Iniguez-Luy <i>et al.</i> (2009)
FITO110	TAACCAACAACCTCCAATGA	CAATCCGAGAACAAGATAAAA	Iniguez-Luy <i>et al.</i> (2009)
FITO120	AAATACAAAACCTCTACTCCCTG	GCTTGCTCACAGTCTTCTTC	Iniguez-Luy <i>et al.</i> (2009)
FITO122	CTATGTGATTAGTTGGTTGGG	AGCAGCGGAAGAGGAGTT	Iniguez-Luy <i>et al.</i> (2009)
FITO131	CTACACGGGGCAGGGTGA	AAATCCCATCTACTGGTTTGA	Iniguez-Luy <i>et al.</i> (2009)
FITO132	TTGGGATGTAGGAACTGA	TCACACTAAAGGTCAATCAAA	Iniguez-Luy <i>et al.</i> (2009)
FITO139	CCTCCATTACCCACAAA	CGTAGACAAAACAACACCTGA	Iniguez-Luy <i>et al.</i> (2009)
FITO146	ATTACTGAACGGACGAAA	GGAGCAGATGGAAGTTGTAG	Iniguez-Luy <i>et al.</i> (2009)
FITO156	TATGTGTGTGTGTGTGTGTGT	ATAACCTGACAACGAAGATTG	Iniguez-Luy <i>et al.</i> (2009)
FITO161	AGCCAGGGTTACACAGAGA	CCCAGAAGAGGGAGTCTAG	Iniguez-Luy <i>et al.</i> (2009)
FITO163	AGGTGGATTCTGAGTTTGAG	GTGCTGTTGAATGTAGTCTCTG	Iniguez-Luy <i>et al.</i> (2009)
FITO165	ATCTACCTATTGAGGGTTGG	CCAGGGCTACACAGAGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO190	AGTCACACATCCAGCC	GTAATCCCAGCATCCAGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO203	AAGTCGTTAGGCGAATCTG	ATTGAAGAGGAAGAAGGAGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO204	TCTGATGGAGAAGAAGAGAC	ATTGAAGAGGAAGAAGGAGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO227	GTAACAGCAGAAGCAGAAGCA	CAGGTTACGATACACAAGA	Iniguez-Luy <i>et al.</i> (2009)
FITO237	ATGAACAGCAACAACAACA	TGTCTTCTCAAGTCCAGCA	Iniguez-Luy <i>et al.</i> (2009)
FITO239	TAAGAGATTGAAGTTGGGA	GATAGTGTGAAGCAGAGAAC	Iniguez-Luy <i>et al.</i> (2009)
FITO250	TTTATTCGGTTTATTTCGGTTT	AGTATTTCTTGTATGTTTCCA	Iniguez-Luy <i>et al.</i> (2009)
FITO259	ACCAAATCTGTTCACTTCTT	ATCACCTCTCTCTCTCTATT	Iniguez-Luy <i>et al.</i> (2009)
FITO262	TCATAATAGCACAAAGTCATAGTC	GAATCAAACCAACACCTC	Iniguez-Luy <i>et al.</i> (2009)
FITO272	CTGGGTGACAGAGCAAGA	AGGCTGGTCTGAACTCC	Iniguez-Luy <i>et al.</i> (2009)
FITO279	AGAGACCTGCCACACAGA	GCATTATTACAGACCCAAAC	Iniguez-Luy <i>et al.</i> (2009)
FITO281	CACACAAAACACACACAGTT	GAAGAGAGTGAGGACGAAGAG	Iniguez-Luy <i>et al.</i> (2009)
FITO282	CAGAGGTGGAGTGAGAAAAGA	GATGAAGAATGGAACCCTAAA	Iniguez-Luy <i>et al.</i> (2009)
FITO287	TGATTAGAAGGACAGCACACT	CCTCACACCACTCGGTTC	Iniguez-Luy <i>et al.</i> (2009)
FITO289	ACTGTCATTTCTCTCTCTCTC	GTGCGGACTCTCTCTCAC	Iniguez-Luy <i>et al.</i> (2009)
FITO294	ATCACTTTCTCCAAATCACT	TACGACCTCAATCAATCAATC	Iniguez-Luy <i>et al.</i> (2009)
FITO306	AGATTGTCGGTTCTTGTATTT	CCCTGTTTCTTGTAGTGTATG	Iniguez-Luy <i>et al.</i> (2009)
FITO316	ACGGATAAAGGAGGAGAAGA	CTGGTTAGTTAGCGTTGAGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO353	ATCGTGTTCGGTGGGTT	GTGCCAATAAAGTGAAGGGA	Iniguez-Luy <i>et al.</i> (2009)
FITO355	GAACAAACCAACAGATTGAAC	GTGACGATGAGGAAGTGAA	Iniguez-Luy <i>et al.</i> (2009)
FITO373	TCCCGAACTCAAATACATAA	CCCTAAGTCCAAACTACTACAA	Iniguez-Luy <i>et al.</i> (2009)
FITO375	TAGACGAACTTGACAGCC	CGTGGAAAGAAGATGATG	Iniguez-Luy <i>et al.</i> (2009)
FITO377	CATCACGTTCCACTTATTT	TATTTGCTTTCCATCATT	Iniguez-Luy <i>et al.</i> (2009)
FITO389	CATCTCTAAACCTTCATCT	GTCCTTGACTTATGCGTT	Iniguez-Luy <i>et al.</i> (2009)

Appendix 2 continue

Marker name	Primer sequence (5'-3')		Citation
	Forward	Reverse	
FITO394	GCTGACCTCCAACACTAAACT	TGTGAAGCAAGCCTAAATG	Iniguez-Luy <i>et al.</i> (2009)
FITO398	CAGAAACTTGGAAAGAAACAA	TACTAAACGGAAACGAAACTG	Iniguez-Luy <i>et al.</i> (2009)
FITO400	AGCCACGAAGAGAGAGACTT	TAAGAGGAGAAAGAGAGCGT	Iniguez-Luy <i>et al.</i> (2009)
FITO424	AAACTGAGAATCAAGGGTT	ATGTCAAGAACAATCAACGA	Iniguez-Luy <i>et al.</i> (2009)
FITO426	TGTCATAGTCAGTCAAAGTAGG	AAAGTGGAGAGAGGCAAATAC	Iniguez-Luy <i>et al.</i> (2009)
FITO429	ATTAGGGAGGAAGCGGTG	AGACAGAGAGACGAGGAGAGA	Iniguez-Luy <i>et al.</i> (2009)
FITO434	CTTCTGTCTCTCCCTCATT	CGCTGTTATCCGACTCCA	Iniguez-Luy <i>et al.</i> (2009)
FITO472	CGTCTTGCACCTTCTATCTG	TGCCCTTGTCTTCTTCTTT	Iniguez-Luy <i>et al.</i> (2009)
FITO476	GAAACCATCCTGAAACACTC	CACACGCATCTCTCTCCTT	Iniguez-Luy <i>et al.</i> (2009)
FITO477	GAGAGAGGGAGTCTGTTTGT	TTTACGCAGTGTATGTTGG	Iniguez-Luy <i>et al.</i> (2009)
FITO482	CTTGCTCACCTCACACCC	TAAGTGGCAACAGAAACGA	Iniguez-Luy <i>et al.</i> (2009)
FITO485	GGAAATCAAACGAACATAAA	CAAGAAGAGAGGCTGAATAGA	Iniguez-Luy <i>et al.</i> (2009)
FITO486	TATTTGGTTGGGACGATTAC	CACTTTATGGAACTATCAGGGA	Iniguez-Luy <i>et al.</i> (2009)
FITO488	TTTCTAAGGCGTATCAAAGTG	ATTTCTCTCAACCAACAGAC	Iniguez-Luy <i>et al.</i> (2009)
FITO497	TGGTGTGGTATTTCTTTGT	ATTTATTCATTCTACGGG	Iniguez-Luy <i>et al.</i> (2009)
FITO503	TTTCTATGATTTGCGGGA	GAGGATGAACCCACACAAC	Iniguez-Luy <i>et al.</i> (2009)
FITO505	CTGGATGGTCTTCTGTGTTT	AGGATTTCTTTAGTGGGTTGT	Iniguez-Luy <i>et al.</i> (2009)
FITO514	TCTCAAGGTTTGTGTCTCTGT	ACGGTTGCGTCTATGTAAGT	Iniguez-Luy <i>et al.</i> (2009)
FITO520	AGCCCTTCTTCTTCTTCTTCT	GCTCTTCTTCAATGCCC	Iniguez-Luy <i>et al.</i> (2009)
FITO565	GGTCTCTCCAAAGTAATGGTC	TCAATCCTCTCTCAAATCAAG	Iniguez-Luy <i>et al.</i> (2009)
KBrB005M19R	TGGTCCGACTCCTAAGTTAATGC	CAAATCCCAATGTACAACGAACGA	Hatakeyama <i>et al.</i> (2010)
KBrB016E19R	ATGTTGAGCTGCGAATACGTTCT	GAGCAATCTTACCCTCTTCGTTG	Hatakeyama <i>et al.</i> (2010)
KBrB019C14F	GTGGAATGGAGTGTGACAAATGG	TGTTTGTGGTCTTGTCTCAAAGC	Hatakeyama <i>et al.</i> (2010)
KBrB022M07F	TTAAGCTTTGCATGTGCCTCTCTG	ATATGGGGTGATATTGGGGTGTGT	Hatakeyama <i>et al.</i> (2010)
KBrB024M19R	GCATCCTTGTTCCTGATTCCAAAC	TTAGATCCACCGGCAAAATCACT	Hatakeyama <i>et al.</i> (2010)
KBrB027H17F	GGCAGATTCATCAAGATCCAAAAC	GCTCTTCAAGGAAGGAAGATCAG	Hatakeyama <i>et al.</i> (2010)
KBrB065O24R	GTAGGGGCAGAGATATGGGGTAGG	ATGTCGTGTTGATGCGGATATTG	Hatakeyama <i>et al.</i> (2010)
KBrB070L18R	TTTGTGGTTCGAGCTGTTTCAGAG	CACAGGGAGCCGTAGAAGAAAAGA	Hatakeyama <i>et al.</i> (2010)
KBrB078P21R	GAGAAGTACAATTTTCGAGGCGTT	CAAACCAAGTCAACACCTGAAAA	Hatakeyama <i>et al.</i> (2010)
KBrB092H15F	GGGCTATGTAACATCTGGCATGG	CCGCTGGATTCTTATTCATAGTCG	Hatakeyama <i>et al.</i> (2010)
KBrH006K06R	GAGAGAGAGACGACACACTCGG	TAATCGCAATCCCCAAAAGAGAGA	Hatakeyama <i>et al.</i> (2010)
KBrH015H02R	TGAAGTAACCACGTGACATTGATGA	TCCAGATTCATATCCACATTACGCA	Hatakeyama <i>et al.</i> (2010)
KBrH057L10F	TCAAACATTTGTCAACGCACAC	GTAGCCTTCGGTCAATGCAAAGAA	Hatakeyama <i>et al.</i> (2010)
KBrH071B03R	GGACCGGCACGTATATTACCTGAA	ATCATCGAGATCCGAGAAACGAAC	Hatakeyama <i>et al.</i> (2010)
KBrH079A14F	TGCTTTCCTACCTTTTTCCCTTC	GAGTGGGACTTGGAAATTTCTCCAT	Hatakeyama <i>et al.</i> (2010)
KBrH094B16F	CCTTCTTCTCGATCTCATCTCGG	TTCGAACCTCCTTGAACGACTC	Hatakeyama <i>et al.</i> (2010)
KBrH102J11R	GGGCTTGTATCCATTCCTTAGTG	CCCATCTCAGCAAACACAGTTACG	Hatakeyama <i>et al.</i> (2010)
KBrH103G17F	ACAGACAAAAGCTTCAATTGCCACA	GAGACAAAGGCTGATTCTCCTCAA	Hatakeyama <i>et al.</i> (2010)
KBrH104H02R	ATGTGAGCTCGGGATGAGAGTAGG	TCTCGCTCCTAAACCTTTCTTCC	Hatakeyama <i>et al.</i> (2010)
KBrH107C06R	CCATCAAGTGTTTACAAACGAGCA	TGCAGGTGTTTCTTACCTCTCC	Hatakeyama <i>et al.</i> (2010)
KBrH107O12F	TCAATGTCTGGGAAGAACTCTGTG	AGATCTCTCCTCTCGCACCTCAA	Hatakeyama <i>et al.</i> (2010)
KBrH108F14R	AAGGTTCCAGCTCTGCATTTCAAG	AAGGCTTCAGTAATCCCTTCCCAG	Hatakeyama <i>et al.</i> (2010)
KBrH110H05R	TTCCACTCCCCTCTCGTCTTCTTC	CTCAGATCTGCAATCTAACAGATGAAC	Hatakeyama <i>et al.</i> (2010)
KBrH110I17R	CGCTAAGCTAGAGCTTGCCTGAA	GCGGAACAAAGAGAAATGGAGAAA	Hatakeyama <i>et al.</i> (2010)
KBrH114A18F	AACCAATTTGAGCTGAGATTTTGCC	TGCAGTTTTCATCACAACTTCCA	Hatakeyama <i>et al.</i> (2010)
KBrH120N01R	AAGCTGCCTCAAAAACAAAACCTT	AGAAACTGTATCAGTCTCCGGCCA	Hatakeyama <i>et al.</i> (2010)
KBrH123B08R	TTTCTTGAAGATCCGGACGATGT	TGTGGCACAAATGGAGTCAAATCT	Hatakeyama <i>et al.</i> (2010)
Na10-B01	CAAGTGCTGTAGGTGGGG	TGCATCGAAGAAACCAGACC	Lowe <i>et al.</i> (2002)
Na12-A07	TCAAAGCCATAAAGCAGGTG	CATCTTCAACACGCATACCG	Lowe <i>et al.</i> (2002)
Na12-B05	CAAATATCCGTCATCGGAGC	CCTGCGGGATATTGAAGACC	Lowe <i>et al.</i> (2002)
Na12-C06	AACGGATGAAGAACACATTGC	TAGGGCCTGTTATTTCGATGG	Lowe <i>et al.</i> (2002)
Ni4-F08	GAGAAAGAAGCAAACACAAAAGC	TCTCTTCTTCTCGTTGCCG	Lowe <i>et al.</i> (2002)
nia_m043a	CCATTTCGAGGTGGTTCGTA	AGAAAACGGACCTCGATTCA	Li <i>et al.</i> (2013)
OI10-B08	AAGCTGTTCGATGAAATGCC	ACTTGTGTTGCATCCATTGCC	Lowe <i>et al.</i> (2002)
OI10-C01	ATGACTGTCTAAACAGCGCC	CTTCTCCAACAAAAGCTCGG	Lowe <i>et al.</i> (2002)
OI10-D08	TCCGAACACTCTAAGTTAGCTCC	GAGCTGTATGTCTCCCGTGC	Lowe <i>et al.</i> (2002)
Ra2-G08	ATGTCCGGATAACCGAATCC	GAAGCTTTTCAATTTTAAAGTTCTCTC	Lowe <i>et al.</i> (2002)
sN2025	AAGGAGCAAACACAACGAT	GCACAAGCACTTACGGTGA	AAFC Consortium (2016)
sR11644	GCAAACCTGGTAAACCTGGA	GGGTAGACTGGTCCCGAGAT	AAFC Consortium (2016)
sR6293	CCAAACGCTTTTCTTCTG	CCAATGACGCTCCAAGATT	AAFC Consortium (2016)