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(54) **DETECTION INSTRUMENT WITH THE USE OF POLYNUCLEOTIDES MAPPED ON BARLEY CHROMOSOME**

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(57) **ABSTRACT**

As the results of mass sequencing of cDNA clones originating in barley varieties "*H. spontaneum*", "Haruna Nijo" and "Akashinriki", a large number of sites showing single nucleotide polymorphisms (SNPs) among the varieties are found out. Because of involving nonsynonymous substitutions and likely relating to phenotypes inherent in respective varieties, these SNPs are usable for various purposes, for example, genetically distinguishing a variety, isolating a gene, producing/selecting a novel transformant and so on.

FIG. 1 (a)

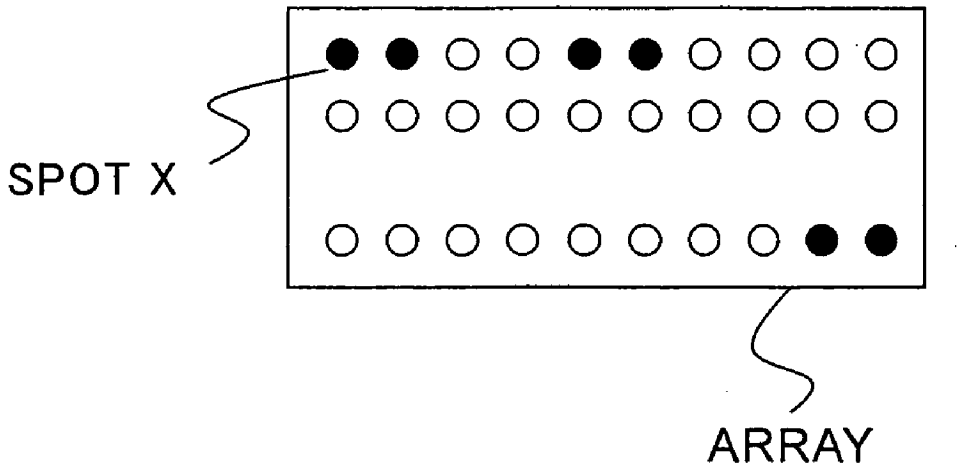


FIG. 1 (b)

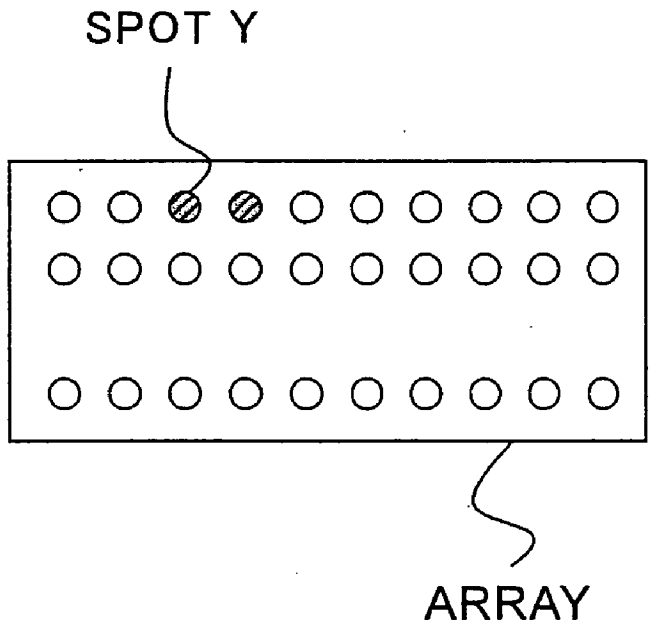
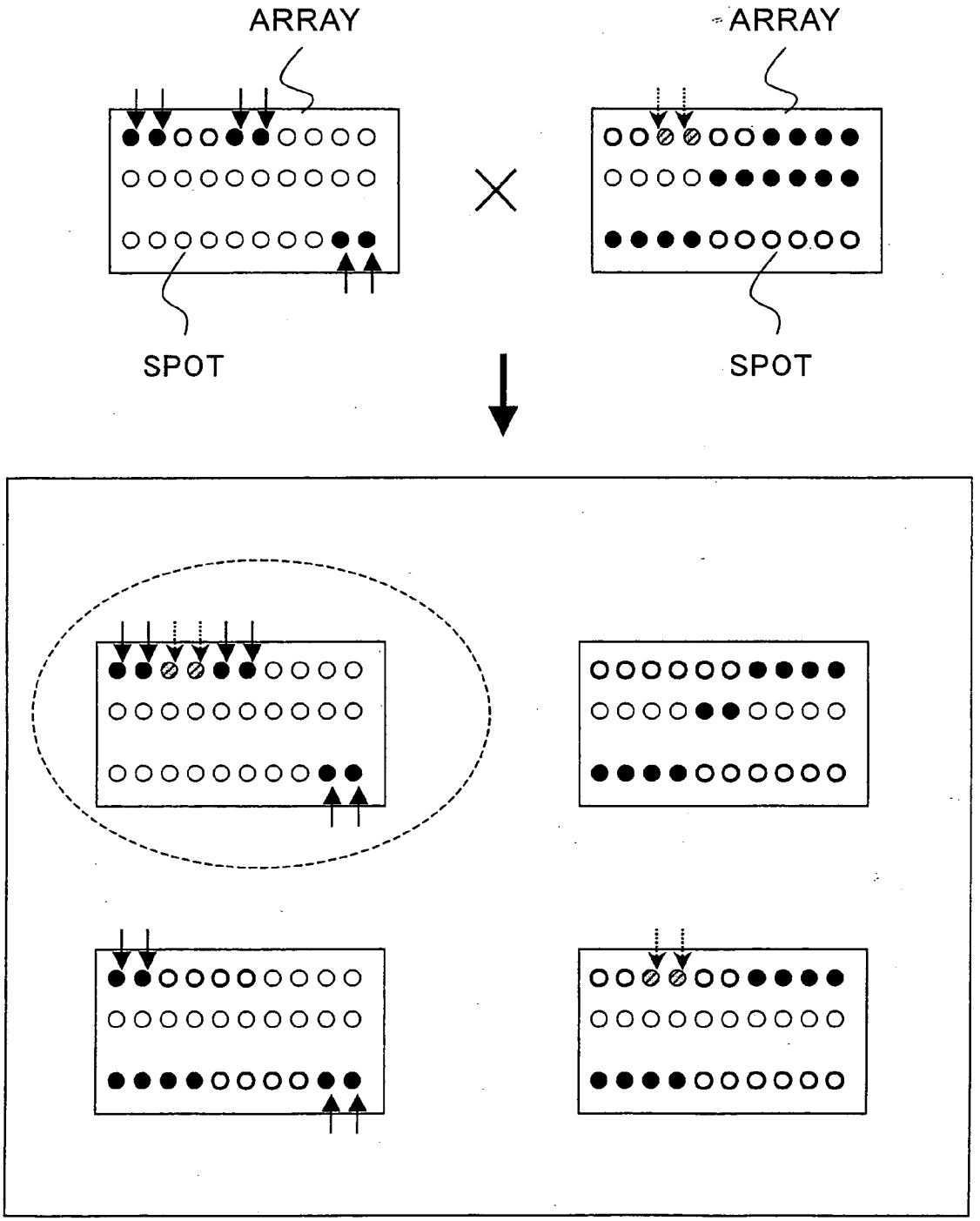


FIG. 2



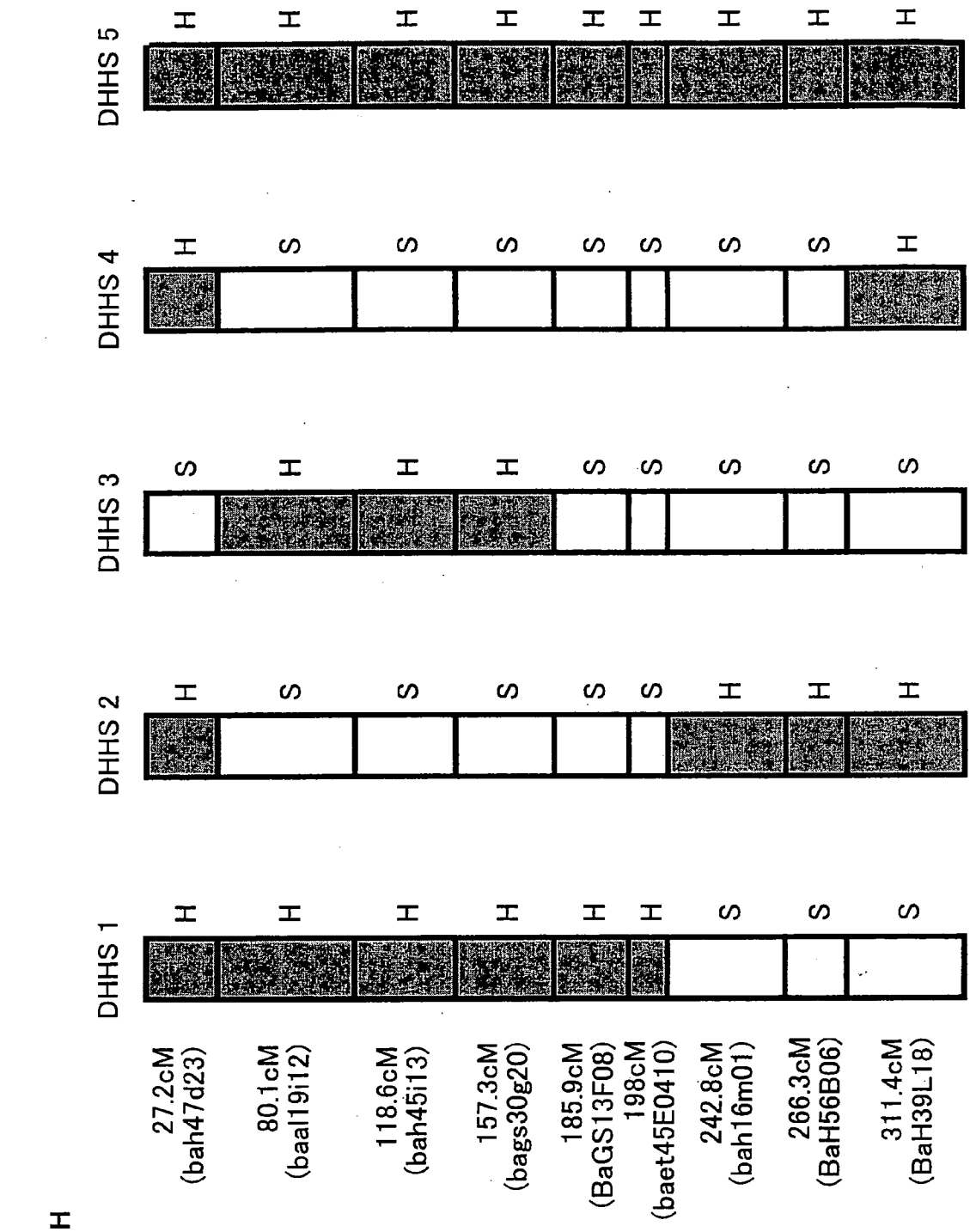

1H
DHHS 1
DHHS 2
DHHS 3
DHHS 4
DHHS 5
27.2cM (bah47d23)
80.1cM (baal19i12)
118.6cM (bah45i13)
157.3cM (bags30g20)
185.9cM (BaGS13F08)
198cM (baet45E0410)
242.8cM (bah16m01)
266.3cM (BaH56B06)
311.4cM (BaH39L18)

FIG. 3

DETECTION INSTRUMENT WITH THE USE OF POLYNUCLEOTIDES MAPPED ON BARLEY CHROMOSOME

TECHNICAL FIELD

[0001] The present invention relates to a detection instrument that uses polynucleotides mapped on barley chromosomes. Particularly, the invention relates to a detection instrument for detecting, in Triticeae species, gene expression, gene polymorphism, proteins (polypeptides), and substances that interact with proteins (polypeptides).

BACKGROUND ART

[0002] Over the last years, the entire genomes of human and many other model organisms have been sequenced. In many of these organisms, sequencing of the entire genomes has been finished already. There has also been ongoing development in the analysis of transcripts and proteins based on the sequence information of genomes. Specifically, transcriptome analysis and proteome analysis have won the recognition. The transcriptome analysis is used for the analysis of transcripts, whereby the expression of all transcripts in an organism or cells are analyzed both systematically and comprehensively. The proteome analysis is a systematic and comprehensive method of analyzing proteins, in which the properties or expression of all proteins expressed at any given location and any given time in an organism or cells are analyzed.

[0003] For the systematic and comprehensive analyses, various array techniques are often used. The array technique refers to a technique using an array, in which biosubstances, such as DNA or various proteins obtained from the organism of interest being analyzed, or synthetic substances (for example, compounds with hydrophobic groups or ion exchange groups) that interact with such biosubstances are immobilized on a support in an orderly manner.

[0004] With the array technique, the systematic and comprehensive analysis can be performed efficiently. For example, for the analysis of gene transcription control mechanism, it is required to measure transcription level of genes, which varies according to the state of the cell. For this purpose, use of a DNA micro array, one form of the array technique, allows for systematic measurement of transcription level of several thousand to several ten thousand of genes. Among such DNA micro array techniques, one that has been widely used is the DNA micro array technique developed by Affymetrix. In this technique, oligonucleotides are directly synthesized on a silica substrate using a microfabrication technique employed in the fabrication of semiconductors (see Patent Document 1, for example). Meanwhile, arrays have been developed that are modified to detect single nucleotide polymorphism (SNP) (see Non-Patent Documents 1 and 2, for example).

[0005] In order to reduce breeding time, labor, and field area, breeding of Triticeae species nowadays employs a method whereby screening is made using genetic markers as an index. Genetic markers have been used since the advent of DNA markers in the late 1980s, and the study of linkage map has advanced greatly with the use of DNA markers. Today, linkage analysis is performed in many organisms based on their high-density linkage maps. Currently, genetic markers that are strongly linked to target traits are available. By using these genetic markers, breeding can be performed more efficiently. The inventors of the present invention have been actively developing genetic markers in Triticeae species. For example, the inventors have proposed (1) a technique concerning genetic markers that are linked to genes conferring aluminum resistance to barley, and use of such genetic markers (see Patent Publication 2), and (2) a technique concerning novel primer sets that are used to detect barley chromosome nucleic acid markers on a wheat background (see Patent Publication 3), and use of such primer sets.

[0006] [Patent Publication 1]

[0007] Japanese Laid-Open Patent Publication No. 2000-228999 (published on Aug. 22, 2000)

[0008] [Patent Publication 2]

[0009] Japanese Laid-Open Patent Publication No. 2002-291474 (published on Oct. 8, 2002)

[0010] [Patent Publication 3]

[0011] Japanese Laid-Open Patent Publication No. 2003-111593 (published on Apr. 15, 2003)

[0012] [Non-Patent Publication 1]

[0013] Jobs M, Howell W M, Stromqvist L, Mayr T, Brookes A J. Related Articles, Links. DASH-2: flexible, low-cost, and high-throughput SNP genotyping by dynamic allele-specific hybridization on membrane arrays. Genome Res. 2003 May; 13(5): 916-24.

[0014] [Non-Patent Publication 2]

[0015] Matsuzaki H, Loi H, Dong S, Tsai Y Y, Fang J, Law J, Di X, Liu W M, Yang G, Liu G, Huang J, Kennedy G C, Ryder T B, Marcus G A, Walsh P S, Shriver M D, Puck J M, Jones K W, Mei R. Links. Parallel Genotyping of Over 10,000 SNPs Using a One-Primer Assay on a High-Density Oligonucleotide Array. Genome Res. 2004 March; 14(3): 414-25.

[0016] As described above, genomes of many organisms have been sequenced and many type of arrays have been marketed. However, none of these arrays is usable for the breeding of Triticeae species. Meanwhile, while breeding using genetic markers can greatly improve efficiency as compared with the conventional screening conducted in a field, the genotype of each genetic marker needs to be confirmed individually. In breeding, large numbers of agriculturally desirable traits are screened for and undesirable traits are selected out. If genotypes of these multiple genetic markers were confirmed comprehensively, it would be possible to further improve efficiency of breeding.

[0017] The present invention was made in view of the foregoing problems, and an object of the invention is to provide a detection instrument for detecting, in Triticeae species, gene expression, gene polymorphism, proteins (polypeptides), and substances that interact with proteins (polypeptides).

DISCLOSURE OF INVENTION

[0018] In order to achieve the foregoing object, the inventors of the present invention designed primers based on the EST sequences independently developed by the inventors. By finding polymorphisms between different varieties in the amplified fragments that had been amplified using the genomic DNA as a template, genetic markers were developed. The genetic markers were mapped on barley chromosomes, and a detailed genetic map was made. Upon further study, the inventors have found that, if polynucleotides with the barley EST sequences or genetic marker sequences were immobilized on a support, it would be possible to realize a gene expression detection instrument or gene polymorphism detection instrument applicable to breeding of Triticeae species. Further, the inventors also found that a protein (polypep-

tide)-interacting substance detection instrument or protein (polypeptide) detection instrument could be realized when proteins encoded by the EST sequences, or antibodies against such proteins were immobilized on a support. The present invention was accomplished based on these findings.

[0019] Specifically, the present invention provides a gene detection instrument for detecting expression or polymorphism of genes existing in a genome of Triticeae species, the gene detection instrument comprising a support on which is immobilized at least one polynucleotide selected from: (a) polynucleotides with partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley; or (b) polynucleotides with combined partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the combined partial base sequences of chromosomal DNA of barley.

[0020] It is preferable that the polynucleotide immobilized on the support comprise at least one kind of polynucleotide selected from the group consisting of: (1) polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780; (2) a polynucleotide that comprises a part of any one of the polynucleotides set forth in (1); (3) a polynucleotide whose partial sequence comprises all of or part of any one of the polynucleotides set forth in (1); and (4) a polynucleotide whose partial sequence comprises: all of or part of a base sequence of SEQ ID NO: n (where n is an odd number), or its variant base sequence, in the polynucleotides set forth in (1); and all of or part of a base sequence of SEQ ID NO: n+1, or its variant base sequence, in the polynucleotides set forth in (1). Since the polynucleotides include base sequence of barley cDNA, gene expression or gene polymorphism in Triticeae species can be detected with a gene detection instrument in which the polynucleotides are immobilized on a support.

[0021] It is preferable that two or more kinds of polynucleotides be immobilized on the support, and that regions on the support in which the polynucleotides are respectively immobilized be arranged in the same order as a chromosomal order of the polynucleotides immobilized on the support. The gene detection instrument may be adapted so that two or more kinds of polynucleotides are immobilized on the support, and that information indicative of a chromosomal order of the polynucleotides immobilized on the support is appended to regions on the support in which the polynucleotides are respectively immobilized. With the immobilizing regions arranged in the chromosomal order or with the information indicative of the chromosomal order, the locations of recombination that has occurred in crossbreeding of Triticeae species can be found with ease. As a result, efficiency of breeding can be improved.

[0022] It is preferable that the polynucleotide immobilized on the support comprise cDNA. When the polynucleotide is cDNA, gene expression can be evaluated efficiently through hybridization with polynucleotides in a sample.

[0023] According to the present invention, there is provided a gene polymorphism detection instrument for detecting polymorphism of genes existing in a genome of Triticeae species, the gene polymorphism detection instrument comprising a support on which is immobilized at least one polynucleotide selected from: polynucleotides with partial base sequences of chromosomal DNA of barley; or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley.

[0024] It is preferable that the polynucleotide immobilized on the support comprise a partial base sequence of at least one of DNA fragments amplified, using genomic DNA of Triticeae species as a template, with a primer set that comprises a combination of any two primers arbitrarily selected from: a plurality of primers designed based on a base sequence of SEQ ID NO: n (where n is an odd number) from among base sequences of SEQ ID NO: 1 through 5780; and a plurality of primers designed based on a base sequence of SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through 5780. Gene polymorphism in Triticeae species can be detected with the gene polymorphism detection instrument in which a polynucleotide with a polymorphism-containing base sequence of the amplified DNA fragments is immobilized on a support.

[0025] It is preferable that two or more kinds of polynucleotides be immobilized on the support, and that regions on the support in which the polynucleotides are respectively immobilized be arranged in the same order as a chromosomal order of the polynucleotides immobilized on the support. The gene polymorphism detection instrument may be adapted so that two or more kinds of polynucleotides are immobilized on the support, and that information indicative of a chromosomal order of the polynucleotides immobilized on the support is appended to regions on the support in which the polynucleotides are respectively immobilized. With the immobilizing regions arranged in the chromosomal order or with the information indicative of the chromosomal order, the locations of recombination that has occurred in crossbreeding of Triticeae species can be found with ease. As a result, efficiency of breeding can be improved.

[0026] It is preferable that the polynucleotide immobilized on the support comprise a synthetic oligonucleotide. With an oligonucleotide synthesized to have a sequence suitable for detection of polymorphism, the efficiency of detection can be improved.

[0027] According to the present invention, there is provided a polypeptide-interacting substance detection instrument for detecting a substance which interacts with a polypeptide that comprises a protein, or part of a protein, encoded by a gene present in the genome of Triticeae species, the polypeptide-interacting substance detection instrument comprising a support on which is immobilized at least one of polypeptides encoded by: (a) polynucleotides with partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley; or (b) polynucleotides with combined partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the combined partial base sequences of chromosomal DNA of barley.

[0028] It is preferable that the polypeptide immobilized on the support be encoded by a polynucleotide selected from the group consisting of: (1) polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780; (2) a polynucleotide that comprises a part of

any one of the polynucleotides set forth in (1); (3) a polynucleotide whose partial sequence comprises all of or part of any one of the polynucleotides set forth in (1); and (4) a polynucleotide whose partial sequence comprises: all of or part of a base sequence of SEQ ID NO: n (where n is an odd number), or its variant base sequence, in the polynucleotides set forth in (1); and all of or part of a base sequence of SEQ ID NO: n+1, or its variant base sequence, in the polynucleotides set forth in (1). Substances that interact with proteins of Triticeae species can be detected with the polypeptide-interacting substance detection instrument in which the polypeptides are immobilized on a support.

[0029] It is preferable that two or more kinds of polypeptides are immobilized on the support, and that regions on the support in which the polypeptides are respectively immobilized are arranged in the same order as a chromosomal order of the polynucleotides respectively encoding the polypeptides immobilized on the support. The polypeptide-interacting substance detection instrument may be adapted so that two or more kinds of polypeptides are immobilized on the support, and that information indicative of a chromosomal order of the polynucleotides respectively encoding the polypeptides immobilized on the support is appended to regions on the support in which the polypeptides are respectively immobilized. With the immobilizing regions arranged in the chromosomal order or with the information indicative of the chromosomal order, the locations of recombination that has occurred in crossbreeding of Triticeae species can be found with ease. As a result, efficiency of breeding can be improved.

[0030] According to the present invention, there is provided a polypeptide detection instrument for detecting a polypeptide that comprises a protein, or part of a protein, encoded by a gene present in a genome of Triticeae species, the polypeptide detection instrument comprising a support on which is immobilized at least one of antibodies against polypeptides encoded by: (a) polynucleotides with partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley; or (b) polynucleotides with combined partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the combined partial base sequences of chromosomal DNA of barley.

[0031] It is preferable that the polynucleotide encoding the polypeptide used for production of the antibody immobilized on the support comprise at least one kind of polynucleotide selected from the group consisting of: (1) polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780; (2) a polynucleotide that comprises a part of any one of the polynucleotides set forth in (1); (3) a polynucleotide whose partial sequence comprises all of or part of any one of the polynucleotides set forth in (1); and (4) a polynucleotide whose partial sequence comprises: all of or part of a base sequence of SEQ ID NO: n (where n is an odd number), or its variant base sequence, in the polynucleotides set forth in (1); and all of or part of a base sequence of SEQ ID NO: n+1, or its variant base sequence, in the polynucleotides set forth in (1). Substances that interact with proteins of Triticeae species can be detected with the polypeptide-interacting substance detection instrument in which the antibodies are immobilized on a support.

[0032] It is preferable that two or more kinds of antibodies be immobilized on the support, and that regions on the support in which the antibodies are respectively immobilized be arranged in the same order as a chromosomal order of the polynucleotides respectively encoding polypeptides used for production of the antibodies immobilized on the support. The polypeptide detection instrument may be adapted so that two or more kinds of antibodies are immobilized on the support, and that information indicative of a chromosomal order of the polynucleotides respectively encoding polypeptides used for preparation of the antibodies immobilized on the support is appended to regions on the support in which the antibodies are respectively immobilized. With the immobilizing regions arranged in the chromosomal order or with the information indicative of the chromosomal order, the locations of recombination that has occurred in crossbreeding of Triticeae species can be found with ease. As a result, efficiency of breeding can be improved.

[0033] According to the present invention, there are provided polynucleotides usable for an instrument for detecting expression or polymorphism of genes present in the genome of Triticeae species, the polynucleotides comprising: base sequences of SEQ ID NO: 1 through 5780; or base sequences of SEQ ID NO: 1 through 5780, with substitution, deletion, insertion, and/or addition of one or more bases. Further, according to the present invention, there are provided polynucleotides whose partial sequence comprises polynucleotides usable for an instrument for detecting polymorphism of genes present in the genome of Triticeae species, the polynucleotides comprising DNA fragments amplified, using genomic DNA of Triticeae species as a template, with a primer set that comprises a combination of any two primers arbitrarily selected from: a plurality of primers designed based on a base sequence of SEQ ID NO: n (where n is an odd number) from among base sequences of SEQ ID NO: 1 through 5780; and a plurality of primers designed based on a base sequence of SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through 5780.

[0034] The foregoing polynucleotides are suitable as the polynucleotides immobilized on a support of a gene detection instrument and a gene polymorphism detection instrument according to the present invention.

[0035] Additional objects, features, and strengths of the present invention will be made clear by the description below. Further, the advantages of the present invention will be evident from the following explanation in reference to the drawings.

BRIEF DESCRIPTION OF DRAWINGS

[0036] FIG. **1**(*a*) is a plan view of an array as one example of a detection instrument according to the present invention, schematically illustrating expression of genes conferring certain characteristics.

[0037] FIG. **1**(*b*) is a plan view of an array as one example of a detection instrument according to the present invention, schematically illustrating expression of genes conferring characteristics different from the characteristics represented in FIG. **1**(*a*).

[0038] FIG. **2** is a schematic view illustrating expression of genes conferring certain characteristics in a segregating population obtained from a cross between varieties that

showed the gene expression represented in FIGS. **1**(*a*) and **1**(*b*), and in specific varieties selected from the segregating population.

[0039] FIG. **3** is a view showing a result of analysis on genotypes (recombination sites) of barley hybrids that were subjected to PCR in which polynucleotides immobilized on a support of a gene polymorphism detection instrument according to the present invention were used as primers, and genomic DNA of the barley hybrids was used as a template.

BEST MODE FOR CARRYING OUT THE INVENTION

[0040] The following will describe one embodiment of the present invention. It should be appreciated that the invention is not limited in any way by the following description.

[0041] (1) Gene Detection Instrument according to the Present Invention

[0042] A gene detection instrument according to the present invention is an instrument for detecting expression or polymorphism of genes in the genomes of Triticeae species. The organisms to which a gene detection instrument of the invention is applicable may be any Triticeae species, among which barley, wheat, and rye are preferable. As will be described later, a gene detection instrument according to the present invention includes a support on which polynucleotides constituting part of barley chromosomal (1H, 2H, 3H, 4H, 5H, 6H, and 7H) DNA are immobilized. The polynucleotides immobilized on the support may solely be polynucleotides that constitute part of the barley chromosomal DNA, or other polynucleotides may additionally be immobilized on the support. Such additional polynucleotides are not particularly limited as long as they can detect expression or polymorphism of genes in the genomes of Triticeae species. For example, the additional polynucleotides may be those with the base sequences originating in non-barley organisms, or those with arbitrary base sequences that have been artificially synthesized.

[0043] In the case where the polynucleotides are immobilized in more than one region of the support, the polynucleotides immobilized in these regions may have non-overlapping base sequences or partially overlapping base sequences. Alternatively, polynucleotides with the same base sequence may be immobilized in these different regions of the support. In the case where the polynucleotides have overlapping base sequences, the polynucleotides may have partially overlapping base sequences, or the base sequence of one of the polynucleotides may be a partial sequence of the other polynucleotide.

[0044] Further, the polynucleotide immobilized in each region is not necessarily required to be of the same kind. More than one kind of polynucleotide may be immobilized in each region.

[0045] The support is not particularly limited as long as it can immobilize polynucleotides, and it may have any shape and may be made of any material. Examples of a support material generally include: inorganic materials such as glass and silicon wafer; natural polymers such as paper; synthetic polymers such as nitrocellulose and nylon; and gels using synthetic polymers or natural polymers. The shape of the support is not particularly limited as long as it provides enough area to support the polynucleotides. Generally, those with a two-dimensional plane, for example, such as a substrate with little or no flexibility, a flexible membrane, or a flexible substrate with intermediate flexibility can be preferably used. The thickness of the substrate or membrane is not particularly limited either, and it can be suitably set according to the material or use of the substrate or membrane. Various types of beads may be used as supports.

[0046] [Polynucleotides Immobilized on a Support of the Gene Detection Instrument]

[0047] In a gene detection instrument according to the present invention, at least one polynucleotide from the following polynucleotides (a) or (b) is immobilized on a support.

[0048] (a) Polynucleotides with base sequences constituting part of barley chromosomal DNA, or variants thereof with the substitution, deletion, insertion, and/or addition of one or more bases.

[0049] (b) Polynucleotides with a combination of base sequences constituting part of barley chromosomal DNA, or variants thereof with the substitution, deletion, insertion, and/or addition of one or more bases.

[0050] As used herein, a polynucleotide with a base sequence constituting part of barley chromosomal DNA is not particularly limited as long as it is a polynucleotide with a base sequence constituting part of the entire base sequences of chromosomal DNA of barley 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes. Further, a polynucleotide with a combination of base sequences constituting part of barley chromosomal DNA refers to a polynucleotide in which a base sequence constituting part of the entire base sequences of chromosomal DNA of barley 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes is joined to non-continuous base sequences constituting other parts of the chromosomes. For example, base sequences from two different parts of the chromosomes may constitute the polynucleotide, or three or more base sequences may join together to form the polynucleotide. Specifically, for example, cDNA with a plurality of exons from a protein-coding gene on barley chromosomal DNA can be regarded as a polynucleotide with a combination of base sequences constituting part of barley chromosomal DNA. However, the polynucleotide is not just limited to this specific example.

[0051] A variant with the substitution, deletion, insertion, and/or addition of one or more bases in the polynucleotide with a base sequence, or a combination of base sequences, constituting part of barley chromosomal DNA may be a polynucleotide that has been mutated on purpose, or a polynucleotide that exists in nature. For example, think of a base sequence of chromosomal DNA in a specific variety of barley. Comparing this base sequence with those of other varieties, no sequence is completely identical. Rather, these sequences are variants with the substitution, deletion, insertion, and/or addition of one or more bases.

[0052] Polynucleotides immobilized on a support of a gene detection instrument according to the present invention are preferably polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or variants with the substitution, deletion, insertion, and/or addition of one or more bases in the polynucleotides with the base sequences of SEQ ID NO: 1 through 5780. (Such polynucleotides and variants will be referred to as polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780.)

[0053] The base sequences of SEQ ID NO: 1 through 5780 are base sequences of the barley EST (expressed sequence tag) independently developed by the inventors. The inventors have previously confirmed that a polynucleotide with the base sequences of SEQ ID NO: 1 through 770, a polynucleotide with the base sequences of SEQ ID NO: 771 through 1754, a

polynucleotide with the base sequences of SEQ ID NO: 1755 through 2642, a polynucleotide with the base sequences of SEQ ID NO: 2643 through 3324, a polynucleotide with the base sequences of SEQ ID NO: 3325 through 4320, a polynucleotide with the base sequences of SEQ ID NO: 4321 through 4962, and a polynucleotide with the base sequences of SEQ ID NO: 4963 through 5780 are mapped on 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes, respectively.

[0054] The following briefly describes the inventors' EST and mapping. The inventors prepared mRNA from leaves of several different varieties of barley, and constructed cDNA libraries according to a conventional method. Plasmids with the cDNA were used as templates, and the base sequences in portions of the plasmids on the both ends of the inserts were used as primers. The base sequence that was read by a single sequence analysis on either end was adjusted, and a vector sequence was removed therefrom to obtain the barley EST sequence. Currently, about 140,000 EST sequences are available from the database of the inventors.

[0055] These EST sequences were divided into groups of about 10,000 genes based on homology of sequences at the 3' end. Using primer design software Primer 3, a primer set was designed for each EST, starting from the EST with the longest sequence. These primer sets were used to check for polymorphism in the hybrids of the mapped populations: malting barley Haruna Nijo and wild type barley H602. More specifically, first, the fragment lengths yielded by agarose gel electrophoresis were checked for polymorphism. If there were no difference in fragment length, the amplified fragments of the parents were aligned by direct sequencing. If the base sequences of the parents had differences to be recognized by restriction enzyme, the amplified fragments were digested with restriction enzyme and subjected to agarose gel electrophoresis to detect differences in fragment length. Then, using MAPMAKER/EXP, a linkage analysis was performed using the marker polymorphism information, together with the markers with known chromosomal locations. In this way, a genetic map based on the EST sequences was constructed.

[0056] It follows from this that the base sequences of SEQ ID NO: 1 through 5780 are partial sequences of barley cDNA. Thus, if polynucleotides with the base sequences of SEQ ID NO: 1 through 5780 were immobilized on the support, gene expression can be detected through hybridization with mRNA (probe based on mRNA) in a sample. Variants with the substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780 may be polynucleotides that have been mutated on purpose, or polynucleotides that exist in nature.

[0057] A polynucleotide immobilized on a support of a gene detection instrument according to the present invention may be a part of the polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780. Since the base sequence of such partial polynucleotide is a partial base sequence of barley cDNA, it can still be used to detect gene expression.

[0058] Further, a polynucleotide immobilized on a support of a gene detection instrument according to the present invention may be a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. The remaining base sequences of the polynucleotide are not limited. For example, since the base sequences of SEQ ID NO: 1 through 5780 are partial sequences of barley cDNA, these base sequences do not have the sequences on either end as originally found in the full length cDNA. Thus, a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780, and which additionally includes the cDNA sequences on the both ends or one end as originally found in the full length cDNA can be regarded as a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. Further, vectors such as plasmids and BACs (bacterial artificial chromosomes) that have incorporated all of or part of the polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780, and polynucleotides in which the partial sequence is ligated to arbitrary base sequences can also be regarded as polynucleotides whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. Such polynucleotides at least include all of or part of the polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780, i.e., part of barley cDNA, and are therefore capable of detecting gene expression.

[0059] Further, polynucleotides immobilized on a support of a gene detection instrument according to the present invention may be polynucleotides or the like whose partial sequences comprise all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n (where n is an odd number), and all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n+1, from among the base sequences of SEQ ID NO: 1 through 5780. As described above, the base sequences of SEQ ID NO: 1 through 5780 are EST sequences of barley, and comprise sequences that can be read by sequencing the cloned cDNA from the both ends only once. In other words, the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 among the base sequences of SEQ ID NO: 1 through 5780 are base sequences that are read from the both ends of the cDNA of the same clone. As such, these base sequences can realize a full length cDNA base sequence, which corresponds to all of or part of the full length cDNA. Thus, polynucleotides or the like whose partial sequences comprise all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n (where n is an odd number), and all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n+1, from among the base sequences of SEQ ID NO: 1 through 5780 can be regarded as polynucleotides with full length cDNA that comprises the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1, or polynucleotides that comprise part of the full length cDNA. Further, the foregoing polynucleotides may be polynucleotides in which vector sequences or arbitrary base sequences for example are ligated to the both ends or one end of the full length cDNA or polynucleotides that comprise part of the full length cDNA. Further, the foregoing polynucleotides may be variants that have a base substitution or other mutations in sequences other than the base sequences of SEQ ID NO: 1 through 5780, i.e., a middle section of the total cDNA unspecified by SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1. Such polynucleotides include the full length or part of barley cDNA, and are therefore capable of detecting gene expression.

[0060] The polynucleotide immobilized on a support is preferably cDNA. In this case, cDNA is not limited to full length cDNA. Rather, it may be a polynucleotide that comprises part of cDNA. Further, the polynucleotide may include other base sequences, for example, such as vector sequences, as long as it includes cDNA. Further, the polynucleotide may be a synthetic oligonucleotide that is produced by artificially synthesizing part of the cDNA base sequences.

[0061] In the case where a gene detection instrument according to the present invention is used for detection of gene expression, the substance to be detected in a sample is mRNA (probe based on mRNA). Therefore, for strong hybridization, it is preferable that the polynucleotide immobilized on a support be full length cDNA. The polynucleotide immobilized on a support may include any number of bases as long as it can detect gene expression. For example, in the case where only one polynucleotide is immobilized in each region, a polynucleotide with at least 50 bases is considered to be sufficient for detection of gene expression. When more than one polynucleotide (oligonucleotide) is immobilized in each region as in the Affymetrix system, a polynucleotide with about 25 bases is sufficient.

[0062] [Gene Detection Instrument with the Polynucleotides Immobilized in Regions that are Arranged in the Chromosomal Order]

[0063] As described above, the base sequences of SEQ ID NO: 1 through 5780 are base sequences of barley EST mapped on barley chromosomes. Further, the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 are base sequences that are read from the both ends of cDNA of the same clone, wherein n represents a base sequence on the 5' end, and n+1 represents a base sequence on the 3' end.

[0064] As used herein, the "chromosomal order" refers to the order from an arbitrary position of a chromosome. The distance by which the order is determined may be a genetic distance based on recombinations in hybrid populations, or a physical distance based on the number of bases or the length of chromosomes observed with a microscope.

[0065] As shown in Table 1-1 to Table 1-8, the chromosomal order in barley 1H chromosome (distance from the short arm end of 1H chromosome) has been specified for 385 clones including the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through SEQ ID NO: 770. The chromosomal order in barley 1H chromosome has also been specified for 3 known clones (HVM20, Bmag211, and WMCIE8).

TABLE 1-1

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
1	bah55e06	1	2	0
2	bags30b07	3	4	14
3	baak2103	5	6	17.4
4	BaAK17D13	7	8	18.5
4	basd26120	9	10	18.5
4	bah61p17	11	12	18.5
7	BaGS11O06	13	14	19.6
7	kr12H0216	15	16	19.6
7	BaGS32E23	17	18	19.6
7	basd13k20	19	20	19.6
11	BaAK24O11	21	22	20.7
11	kr26D0507	23	24	20.7
11	BaSD2D08	25	26	20.7
11	baak41n21	27	28	20.7
15	bah11b15	29	30	21.8
15	kr24B0903	31	32	21.8
17	bast50E0709	33	34	22.9
18	baal17o01	35	36	23.5
19	baak41a04	37	38	24
20	BaH28C07	39	40	24.2
21	bags16g18	41	42	24.4
22	BaSD3C22	43	44	25.1

TABLE 1-1-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
23	BaGS17B21	45	46	26.7
23	basd27b10	47	48	26.7
25	bah47d23	49	50	27.2
26	BaAK21D02	51	52	27.7
27	BaH17D02	53	54	32.1
28	baal4f12	55	56	32.7
29	BaGS11I03	57	58	33.8
29	bah56a03	59	60	33.8
29	kr16A0501	61	62	33.8
29	bah19f01	63	64	33.8
33	BaAK27F07	65	66	37
34	bah47f18	67	68	41.1
34	bah45l19	69	70	41.1
36	BaAK12I12	71	72	44.1
37	BaAL6N04	73	74	45.2
37	baal16105	75	76	45.2
37	BaSD18O20	77	78	45.2
37	BaSD3J13	79	80	45.2
41	bah63j19	81	82	49.5
41	BaH36O18	83	84	49.5
43	BaAK20A06	85	86	50.6
43	BaGS8G13	87	88	50.6
45	bah25n06	89	90	53.8
45	BaAK1P06	91	92	53.8
47	BaAK16M07	93	94	55.1
47	BaH36M15	95	96	55.1
49	BaGS12K12	97	98	62.4
50	BaAL39C22	99	100	71.9

TABLE 1-2

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
50	kr68B0303	101	102	71.9
52	baak24d09	103	104	75.8
53	BaGS11J13	105	106	76.9
54	baal38l23	107	108	79.5
54	BaAL36B15	109	110	79.5
56	bast60D0610	111	112	80.6
56	kr22D0808	113	114	80.6
56	baal19i12	115	116	80.6
56	basd23o02	117	118	80.6
56	baak1i14	119	120	80.6
56	baak24k18	121	122	80.6
56	kr18G0814	123	124	80.6
63	BaH38H09	125	126	82.3
64	BaGS8B13	127	128	85.4
64	BaH25J08	129	130	85.4
66	baak3d11	131	132	88.6
67	baal12p08	133	134	89.7
67	bags39i20	135	136	89.7
67	bags32m16	137	138	89.7
70	kr15A0402	139	140	91.3
71	baal3c01	141	142	91.9
72	baak41i03	143	144	93.9
73	BaGS29M13	145	146	95.7
74	basdl7m22	147	148	98
74	bags15g01	149	150	98
74	BaH24I06	151	152	98
77	BaH57E12	153	154	99.1
78	BaSD25C22	155	156	99.7
79	baal19m17	157	158	101.9
80	bah46p14	159	160	102.3
80	bags18d19	161	162	102.3
80	BaAK34J19	163	164	102.3
83	bags6d01	165	166	105.6
84	bags3p11	167	168	108.9

TABLE 1-2-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
84	BaAK14J21	169	170	108.9
84	baak2m05	171	172	108.9
87	baak37g19	173	174	109.4
88	BaGS31B11	175	176	109.9
88	BaAL35M08	177	178	109.9
88	BaSD16G03	179	180	109.9
88	BaH58J20	181	182	109.9
88	BaGS22B13	183	184	109.9
88	BaAK43M01	185	186	109.9
88	bah14i07	187	188	109.9
88	BaH13F14	189	190	109.9
88	baal9i16	191	192	109.9
88	basd27b20	193	194	109.9
88	BaAK2O24	195	196	109.9
88	basd18l16	197	198	109.9
88	BaAL19J14	199	200	109.9

TABLE 1-3

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
88	bags22i15	201	202	109.9
102	baak44a23	203	204	111.5
102	BaAK32N04	205	206	111.5
104	basd21e22	207	208	112
104	BaGS7K03	209	210	112
104	baak42e22	211	212	112
107	bast21D0808	213	214	113.1
107	bast75E0610	215	216	113.1
107	baet16A1002	217	218	113.1
107	basd17m16	219	220	113.1
107	bags17g08	221	222	113.1
107	baak21i01	223	224	113.1
107	baakl3n06	225	226	113.1
107	baak22o23	227	228	113.1
107	baet42E0410	229	230	113.1
116	BaGS27M04	231	232	114.2
116	BaH52H18	233	234	114.2
116	baak33k20	235	236	114.2
116	bags21f16	237	238	114.2
116	bags34e05	239	240	114.2
116	bags15d20	241	242	114.2
116	bags18g10	243	244	114.2
116	bags19a02	245	246	114.2
116	BaAK17J19	247	248	114.2
125	bags35k02	249	250	115.3
126	bah35a22	251	252	116.4
126	BaGS17H13	253	254	116.4
126	bah47n12	255	256	116.4
126	baak12p11	257	258	116.4
126	baet38B1004	259	260	116.4
126	BaGS13K12	261	262	116.4
126	BaAL25A05	263	264	116.4
133	bah27k23	265	266	117.2
134	BaAK24J12	267	268	118.3
135	BaSD14M22	269	270	119.8
135	bah17l24	271	272	119.8
137	baal29i09	273	274	120.5
137	bah16d09	275	276	120.5
137	bah60d03	277	278	120.5
137	bah45i13	279	280	120.5
137	bah11h03	281	282	120.5
137	bah47h17	283	284	120.5
143	bags35d02	285	286	122.7
143	bags37e17	287	288	122.7
143	baak14c12	289	290	122.7
143	baak34c01	291	292	122.7

TABLE 1-3-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
143	BaH35A11	293	294	122.7
148	BaAK30M16	295	296	123.8
148	BaSD11P04	297	298	123.8
148	bah12i09	299	300	123.8

TABLE 1-4

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
148	BaAL2G20	301	302	123.8
152	bags14j09	303	304	126
152	kr26E0610	305	306	126
152	bah37f01	307	308	126
152	bags29m05	309	310	126
156	BaGS17A18	311	312	126.5
157	baet34A0501	313	314	127
157	BaSD22O13	315	316	127
157	bags15a22	317	318	127
157	baet21H1016	319	320	127
157	BaH30E13	321	322	127
157	bags4e23	323	324	127
157	baak45b03	325	326	127
157	bah12o12	327	328	127
165	baak34k14	329	330	127.9
166	baal3e14	331	332	131.5
167	bags22f12	333	334	136.3
168	BaH45P03	335	336	137.2
168	basd11d13	337	338	137.2
168	Bmag211	—	—	137.2
168	HVM20	—	—	137.2
168	basd1j14	339	340	137.2
173	bags35b18	341	342	138.3
173	baal41i11	343	344	138.3
175	bags13e23	345	346	139.4
176	bah20d03	347	348	140
177	baet19F0212	349	350	140.5
177	bags12j05	351	352	140.5
179	BaSD24D17	353	354	141.6
180	BaGS24K10	355	356	142.1
181	baal9e05	357	358	142.6
181	BaGS33M23	359	360	142.6
183	bah46g14	361	362	143.1
184	bags33h05	363	364	143.6
185	baak24h12	365	366	143.9
186	BaH50N19	367	368	144.2
187	BaAK31O05	369	370	144.4
188	BaGS39L14	371	372	144.7
189	BaGS27C22	373	374	146.8
189	bags20o24	375	376	146.8
189	bags34j05	377	378	146.8
189	bah56l03	379	380	146.8
189	basd12k03	381	382	146.8
189	BaAK39I18	383	384	146.8
189	bags21h06	385	386	146.8
189	bah56k04	387	388	146.8
189	bah60e11	389	390	146.8
198	baak22i05	391	392	147.9
198	baal5i02	393	394	147.9
200	BaAK2E05	395	396	149

TABLE 1-5

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
201	baak33g12	397	398	151.2
201	bags4e05	399	400	151.2
203	bast42C0806	401	402	155.4
204	baak26c05	403	404	156.6
205	bags19a16	405	406	158.6
206	kr11F1212	407	408	159.7
206	BaH28K13	409	410	159.7
206	baak20d06	411	412	159.7
206	BaSD1I24	413	414	159.7
206	baak35l20	415	416	159.7
211	bah57m07	417	418	161.8
211	bah60k11	419	420	161.8
213	basd20o09	421	422	162.9
213	basd24i22	423	424	162.9
215	bags30g20	425	426	164
216	bags1m11	427	428	164.6
217	bags23g20	429	430	165.1
218	BaGS15B05	431	432	166.2
219	BaGS24P05	433	434	167.3
220	bags10g06	435	436	168.4
220	bah32o04	437	438	168.4
220	BaGS32P08	439	440	168.4
223	bags4e02	441	442	169.5
223	bast04H0315	443	444	169.5
223	BaGS37L06	445	446	169.5
226	basd2b18	447	448	170.6
227	bags3h12	449	450	172.1
228	bags1e21	451	452	174.6
228	BaAK27M21	453	454	174.6
230	BaSD18F05	455	456	174.9
231	BaH35B05	457	458	175.3
232	basd21h11	459	460	176.4
232	BaH32E20	461	462	176.4
234	BaGS22A20	463	464	177.5
235	BaSD14B13	465	466	179
236	bags29l04	467	468	182
236	bags22g16	469	470	182
238	BaAL4B14	471	472	184.2
238	bah61h20	473	474	184.2
240	bah15p01	475	476	186.4
240	baak41p03	477	478	186.4
242	BaSD12L06	479	480	187.7
242	BaSD23P07	481	482	187.7
242	BaGS7J05	483	484	187.7
245	bah29b06	485	486	188.3
245	BaGS31N17	487	488	188.3
247	BaGS13F08	489	490	190.4
248	BaAK39G10	491	492	195.7
249	BaAK39G03	493	494	200
249	baak2a18	495	496	200

TABLE 1-6

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
251	bags39d12	497	498	201.1
251	basd17l04	499	500	201.1
251	BaAK20B19	501	502	201.1
251	bags15j15	503	504	201.1
251	BaAK30F02	505	506	201.1
256	BaGS22A21	507	508	202.2
256	baet45E0410	509	510	202.2
256	BaGS22C14	511	512	202.2
256	bah23k12	513	514	202.2
260	BaH15O13	515	516	203.2
260	kr24F0412	517	518	203.3
260	BaGS28O21	519	520	203.3

TABLE 1-6-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
260	BaAL15N19	521	522	203.3
264	bags10j15	523	524	207.6
265	bags32j03	525	526	209.7
266	bags20e14	527	528	211.1
267	bags3c15	529	530	214
268	basd27n01	531	532	216
269	BaGS6M19	533	534	217.1
270	baak13e03	535	536	219.2
271	BaH15M10	537	538	221.5
271	bags14k12	539	540	221.5
271	bast61E0509	541	542	221.5
271	BaGS31N04	543	544	221.5
275	BaAK27D22	545	546	230
275	baal5o19	547	548	230
277	bah55b18	549	550	231.1
278	bah23i02	551	552	232.6
278	BaAK15H22	553	554	232.6
280	bags32b03	555	556	244.3
281	baak30c15	557	558	248.9
281	BaGS22A05	559	560	248.9
281	bah16m01	561	562	248.9
284	bags15e08	563	564	250
284	BaGS37D12	565	566	250
284	BaAL37N24	567	568	250
287	BaH28B09	569	570	251.1
287	bah47h08	571	572	251.1
289	BaH57N07	573	574	252.2
290	baak38o02	575	576	253.5
290	baak20f16	577	578	253.5
292	baak28n19	579	580	257.4
292	bah59j07	581	582	257.4
292	bah44j20	583	584	257.4
292	BaH47J05	585	586	257.4
296	baet39B0303	587	588	260.7
297	BaAK27D19	589	590	261.8
297	basd25g01	591	592	261.8
299	BaAL34K17	593	594	262.9
299	basd21i17	595	596	262.9

TABLE 1-7

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
301	bags15o12	597	598	264
301	baal2j10	599	600	264
303	baak44n10	601	602	264.4
304	baak21e08	603	604	264.8
305	BaGS37F14	605	606	265.2
306	BaAK41I21	607	608	266.3
306	BaGS19C07	609	610	266.3
308	BaGS15O08	611	612	268.4
308	baak40p22	613	614	268.4
310	BaH21K05	615	616	269.5
310	baal40n03	617	618	269.5
312	bags23b08	619	620	269.9
313	BaGS39L18	621	622	270.6
313	BaGS25K24	623	624	270.6
313	bags1a18	625	626	270.6
313	baal15k07	627	628	270.6
313	bags14o13	629	630	270.6
318	BaH18D15	631	632	271.7
319	bastl04F0911	633	634	272.8
319	BaGS31E03	635	636	272.8
321	BaGS19J21	637	638	273.9
322	BaGS39P08	639	640	275
323	BaH56B06	641	642	276.1
324	baal13m24	643	644	277.2

TABLE 1-7-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
324	bags15h14	645	646	277.2
324	bags35j22	647	648	277.2
324	baak20h22	649	650	277.2
328	baal34b14	651	652	278.3
328	bah16j04	653	654	278.3
328	BaH54J03	655	656	278.3
331	bast58C1206	657	658	280.4
332	BaH26M05	659	660	281.5
332	bastl20B0404	661	662	281.5
334	baak14e23	663	664	288.1
334	BaH15P22	665	666	288.1
334	BaGS17I22	667	668	288.1
337	bags15h01	669	670	292.4
338	bags7p13	671	672	294.5
339	BaGS29H13	673	674	296.7
339	bah47b01	675	676	296.7
341	bastl45E1109	677	678	299.9
341	bags32m15	679	680	299.9
341	basd12c09	681	682	299.9
344	baal27m11	683	684	301
344	basd12k01	685	686	301
344	baak41n15	687	688	301
344	bags1b01	689	690	301
348	BaH56O11	691	692	302.1
349	bah15k16	693	694	303.2
349	bags31a22	695	696	303.2

TABLE 1-8

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
349	bags21e21	697	698	303.2
349	baak32n05	699	700	303.2
353	baet02B0503	701	702	304.3
353	BaH29L05	703	704	304.3
355	baet43H1016	705	706	305.4
356	BaGS38N20	707	708	306.5
356	BaGS23O09	709	710	306.5
356	bastl26B0410	711	712	306.5
359	BaH15N14	713	714	309.6
359	baak20b06	715	716	309.6
361	BaH16I04	717	718	311.7
362	bah22p07	719	720	312.8
363	baak21j02	721	722	313.9
363	bah30o13	723	724	313.9
363	bags38f18	725	726	313.9
363	bah13o05	727	728	313.9
363	baak36b12	729	730	313.9
363	bags18o09	731	732	313.9
363	BaAK16L10	733	734	313.9
363	BaAK38E16	735	736	313.9
371	bah13e15	737	738	317.4
372	bags1f22	739	740	319.8
373	bags21o12	741	742	321.4
374	BaGS9B14	743	744	324.7
375	BaAL1N23	745	746	325.2
375	bbak1a17	747	748	325.2
377	BaH32B01	749	750	326.3
377	BaSD18L13	751	752	326.3
379	baak12p07	753	754	328.4
379	BaH58A04	755	756	328.4
381	bags1p04	757	758	329.1
381	BaAL17O03	759	760	329.1
383	baal8e17	761	762	332
384	BaH50I05	763	764	335.2
384	bastl28A0101	765	766	335.2
386	BaH39L18	767	768	336.3

TABLE 1-8-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
387	bags18e18	769	770	342.1
388	WMCIE8	—	—	362.7

[0066] As shown in Table 2-1 to Table 2-10, the chromosomal order in barley 2H chromosome (distance from the short arm end of 2H chromosome) has been specified for 492 clones including the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 771 through SEQ ID NO: 1754. The chromosomal order in barley 2H chromosome has also been specified for 8 known clones (Bmac134, cMWG682, HVM36, cMWG699, Bmag125, cMWG694, EBmac415, and MWG2076).

TABLE 2-1

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
1	BaGS20L10	771	772	0
2	BaSD15P22	773	774	15.4
2	bags7b16	775	776	15.4
4	BaAK34H02	777	778	20.7
5	BaAK22H13	779	780	21.7
6	BaGS37P19	781	782	23.2
7	BaAL19P17	783	784	24.3
8	BaH41L14	785	786	25.2
9	BaAK24H17	787	788	26.3
10	bast21A0602	789	790	26.4
10	BaAL27L20	791	792	26.4
12	Bmac134	—	—	26.7
12	cMWG682	—	—	26.7
12	bags34p10	793	794	26.7
12	basd18b14	795	796	26.7
16	bags38p20	797	798	27.8
17	BaAK41N22	799	800	28.9
17	BaAK21D17	801	802	28.9
19	BaAL29B07	803	804	30
19	baak20o16	805	806	30
21	bast42A0602	807	808	31.1
21	BaH36B07	809	810	31.1
21	BaAK26L07	811	812	31.1
21	baal12a06	813	814	31.1
25	BaSD3C20	815	816	33.3
26	bastl17G0113	817	818	34.6
27	baak11h14	819	820	39.2
28	baal12m14	821	822	40.2
29	baal33a18	823	824	41.3
30	bah28a18	825	826	43.5
30	bags39o04	827	828	43.5
30	BaH48H04	829	830	43.5
30	BaGS6B11	831	832	43.5
34	bags4p16	833	834	44.6
34	basd24j22	835	836	44.6
34	basd16p15	837	838	44.6
34	bags15k16	839	840	44.6
34	bast23D1208	841	842	44.6
39	BaAL32B22	843	844	45.3
39	BaGS39D07	845	846	45.3
41	BaH19L09	847	848	48
41	bags38a17	849	850	48
41	BaAK39I11	851	852	48
44	BaSD3I24	853	854	49.9
44	BaH35F01	855	856	49.9
46	BaAL30K02	857	858	53.9
47	bah13l23	859	860	54.9
48	BaAL26H21	861	862	55.7

TABLE 2-1-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
49	BaGS22H22	863	864	56.8
49	bags13n11	865	866	56.8

TABLE 2-2

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
51	bags1h03	867	868	62
52	baak32l16	869	870	63.2
52	baal19a12	871	872	63.2
52	BaAK45G16	873	874	63.2
55	BaGS37N19	875	876	64.3
56	baak3f03	877	878	65.4
57	bags5c02	879	880	66.4
58	BaGS35P07	881	882	67.4
58	HVM36	—	—	67.4
60	bah45e07	883	884	70.5
61	BaAK24B09	885	886	71.6
61	bags33a11	887	888	71.6
63	bah62i11	889	890	72.7
64	BaH56A24	891	892	74.9
65	BaSD21D14	893	894	77.1
66	basd1a17	895	896	78.2
66	bah17n24	897	898	78.2
68	kr70G0113	899	900	79.3
68	basd15f08	901	902	79.3
68	BaGS4J04	903	904	79.3
68	baak33f06	905	906	79.3
72	basd14f16	907	908	79.9
73	BaH59K20	909	910	80.4
73	baal35h05	911	912	80.4
73	BaGS20M01	913	914	80.4
76	BaH25N22	915	916	82.6
77	baak14a24	917	918	83.7
77	baak30d07	919	920	83.7
79	bah11n18	921	922	84.8
79	kr14C0305	923	924	84.8
79	baet18F0911	925	926	84.8
79	BaGS4J18	927	928	84.8
83	bast74C0705	929	930	85.9
83	BaAL4G17	931	932	85.9
85	bastl43H0515	933	934	86.2
85	BaH58M22	935	936	86.2
87	bags10i21	937	938	87
87	bah20h16	939	940	87
87	BaH17P13	941	942	87
87	baak41d10	943	944	87
91	BaGS14F01	945	946	88.1
91	BaAK16E24	947	948	88.1
93	BaSD18F09	949	950	92.4
93	baet42A0501	951	952	92.4
93	BaAK20L07	953	954	92.4
96	baak16e20	955	956	92.9
97	BaGS13N14	957	958	93.5
98	basd13m14	959	960	94.6
99	bags20g23	961	962	95.2
100	basd1l17	963	964	95.7

TABLE 2-3

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
100	basd26l01	965	966	95.7
100	BaAL37J18	967	968	95.7

TABLE 2-3-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
103	bags7i05	969	970	96.8
103	bah60m17	971	972	96.8
105	bags21l01	973	974	99
106	baet31E0109	975	976	101.2
107	bags34m12	977	978	102.3
107	bah50n02	979	980	102.3
107	BaH50M11	981	982	102.3
107	bast27E1010	983	984	102.3
107	bags23c12	985	986	102.3
107	bah51m11	987	988	102.3
113	baak20d17	989	990	102.8
114	bags23l21	991	992	103.4
115	BaH52K04	993	994	104.5
115	BaAL37F24	995	996	104.5
115	bags23d01	997	998	104.5
118	BaSD11K22	999	1000	105
119	baal29m02	1001	1002	105.5
119	bah17e21	1003	1004	105.5
119	bah56j18	1005	1006	105.5
119	bags38n06	1007	1008	105.5
119	baet44D1208	1009	1010	105.5
119	BaAL34O13	1011	1012	105.5
125	BaGS4N05	1013	1014	108.7
125	BaSD15P20	1015	1016	108.7
125	baal13d11	1017	1018	108.7
125	bah27g02	1019	1020	108.7
125	basd27m10	1021	1022	108.7
125	basd23f16	1023	1024	108.7
125	bah16i19	1025	1026	108.7
125	BaH50I20	1027	1028	108.7
125	BaH34M23	1029	1030	108.7
134	bah28b24	1031	1032	109.3
135	BaH50P13	1033	1034	109.8
135	basd11m16	1035	1036	109.8
137	bags10p15	1037	1038	110.9
137	bags4g01	1039	1040	110.9
137	bags10k08	1041	1042	110.9
137	bags5e16	1043	1044	110.9
141	bags18l02	1045	1046	114.1
141	baak44k02	1047	1048	114.1
141	bags35a20	1049	1050	114.1
141	BaGS26M11	1051	1052	114.1
141	basd14h21	1053	1054	114.1
141	BaSD13D12	1055	1056	114.1
147	bags38k23	1057	1058	114.3
147	BaH42E05	1059	1060	114.3
147	bastl55A0701	1061	1062	114.3
147	bags13g18	1063	1064	114.3

TABLE 2-4

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
147	BaH15D23	1065	1066	114.3
147	kr28B0604	1067	1068	114.3
147	bags10f01	1069	1070	114.3
154	BaGS33I07	1071	1072	116.4
154	BaSD27B02	1073	1074	116.4
154	BaGS30N12	1075	1076	116.4
154	basd3h13	1077	1078	116.4
154	BaGS37L19	1079	1080	116.4
159	bah16g18	1081	1082	117.5
159	bags20i15	1083	1084	117.5
161	bags35c23	1085	1086	118
162	bah56k07	1087	1088	118.5
162	bags37d02	1089	1090	118.5

TABLE 2-4-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
164	BaAK19K05	1091	1092	121.6
164	bah11i16	1093	1094	121.6
166	bags22l23	1095	1095	123.6
166	kr33A0901	1097	1098	123.6
168	bastl38C0606	1099	1100	125.4
168	baak11i13	1101	1102	125.4
168	BaH58E19	1103	1104	125.4
168	BaGS31G22	1105	1106	125.4
168	bah37h01	1107	1108	125.4
168	BaAL29P13	1109	1110	125.4
174	bags39a22	1111	1112	126
175	bah19g10	1113	1114	126.4
175	BaAL31A14	1115	1116	126.4
175	BaH50G15	1117	1118	126.4
175	BaH51M12	1119	1120	126.4
175	bags18k22	1121	1122	126.4
175	BaGS20N21	1123	1124	126.4
175	BaSD17O21	1125	1126	126.4
175	BaH37G17	1127	1128	126.4
183	bags30l22	1129	1130	128.6
184	baak22b17	1131	1132	129.7
184	bags20f22	1133	1134	129.7
186	bast72G0113	1135	1136	131.8
186	BaH30B05	1137	1138	131.8
186	BaH60B14	1139	1140	131.8
186	BaH17B16	1141	1142	131.8
190	basd12n23	1143	1144	133.9
190	BaH61A21	1145	1146	133.9
190	BaAK19H17	1147	1148	133.9
190	bah47l12	1149	1150	133.9
190	baak18p11	1151	1152	133.9
190	baet29H0715	1153	1154	133.9
190	BaH13D11	1155	1156	133.9
190	baet39D1107	1157	1158	133.9
190	BaH53E15	1159	1160	133.9
190	bags32o15	1161	1162	133.9
190	bast48A0701	1163	1164	133.9

TABLE 2-5

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
190	bast62D0907	1165	1166	133.9
190	BaH45P22	1167	1168	133.9
190	BaGS32L16	1169	1170	133.9
190	BaAK30J05	1171	1172	133.9
190	bah52a14	1173	1174	133.9
190	bah58i22	1175	1176	133.9
190	BaH56L16	1177	1178	133.9
190	bah52a21	1179	1180	133.9
190	BaSD14G11	1181	1182	133.9
190	bags6a03	1183	1184	133.9
190	bast72E0109	1185	1186	133.9
190	bags21a21	1187	1188	133.9
190	BaH58P13	1189	1190	133.9
214	bah27n22	1191	1192	134.4
215	bags20c13	1193	1194	134.9
215	bags30i14	1195	1196	134.9
215	BaAK17E11	1197	1198	134.9
215	baal1d17	1199	1200	134.9
215	bags22f06	1201	1202	134.9
215	baal10l01	1203	1204	134.9
215	baak26e17	1205	1206	134.9
215	bah16a03	1207	1208	134.9
215	BaAL11F18	1209	1210	134.9
215	BaAK29E10	1211	1212	134.9
215	bags32d21	1213	1214	134.9

TABLE 2-5-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
215	bah54j22	1215	1216	134.9
215	baak16f14	1217	1218	134.9
215	baak44c12	1219	1220	134.9
215	bah13f11	1221	1222	134.9
215	baal39m19	1223	1224	134.9
215	baak4e02	1225	1226	134.9
215	baak46f04	1227	1228	134.9
215	BaAK13N23	1229	1230	134.9
215	BaGS20E09	1231	1232	134.9
215	baal4f01	1233	1234	134.9
215	BaSD19I17	1235	1236	134.9
215	baal4l21	1237	1238	134.9
215	BaAK19P01	1239	1240	134.9
215	BaAK31O14	1241	1242	134.9
240	BaH26P22	1243	1244	135.3
241	baal13d17	1245	1246	136
242	bags22j12	1247	1248	138.3
242	bags33p05	1249	1250	138.3
242	bags38j07	1251	1252	138.3
242	kr59F0311	1253	1254	138.3
242	baal13e10	1255	1256	138.3
242	bags15d19	1257	1258	138.3
242	BaGS5K11	1259	1260	138.3
242	BaGS10J14	1261	1262	138.3
242	baak41m17	1263	1264	138.3

TABLE 2-6

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
242	bah57o03	1265	1266	138.3
242	baak41d22	1267	1268	138.3
242	bah61c16	1269	1270	138.3
242	BaAL7M13	1271	1272	138.3
242	BaAK31F11	1273	1274	138.3
242	basd22k05	1275	1276	138.3
242	basd3p19	1277	1278	138.3
242	baak17o09	1279	1280	138.3
242	baal33d23	1281	1282	138.3
242	BaAK12F04	1283	1284	138.3
242	bah53j16	1285	1286	138.3
262	BaSD2E24	1287	1288	138.5
263	bags39h08	1289	1290	138.7
264	BaSD1N02	1291	1292	139.5
264	bags20m21	1293	1294	139.5
264	baal10h19	1295	1296	139.5
264	basd12m11	1297	1298	139.5
264	bah29d24	1299	1300	139.5
264	BaGS39P09	1301	1302	139.5
264	BaGS31F17	1303	1304	139.5
264	BaGS23D08	1305	1306	139.5
264	bags39d15	1307	1308	139.5
264	BaGS34I17	1309	1310	139.5
274	BaH32N02	1311	1312	141.6
274	BaSD18H19	1313	1314	141.6
274	bast63A0101	1315	1316	141.6
274	BaH50N04	1317	1318	141.6
278	baal4a13	1319	1320	147.5
278	baal41l18	1321	1322	147.5
280	BaH31A03	1323	1324	152.2
280	bastl39A0901	1325	1326	152.2
280	baet46D0507	1327	1328	152.2
283	baal27e20	1329	1330	153.3
283	bags37l16	1331	1332	153.3
283	baak34o06	1333	1334	153.3
286	BaAL30I11	1335	1336	155.4
286	BaH62C15	1337	1338	155.4

TABLE 2-6-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
286	basd12i15	1339	1340	155.4
286	BaAK40I03	1341	1342	155.4
286	BaAK23E14	1343	1344	155.4
286	BaAL21F11	1345	1346	155.4
286	BaAK16L19	1347	1348	155.4
293	baal27a24	1349	1350	156.5
294	kr41H0315	1351	1352	157.6
294	BaH62I23	1353	1354	157.6
296	bah52i24	1355	1356	158.7
296	bastl33A0301	1357	1358	158.7
296	BaH28J15	1359	1360	158.7
299	bastl56A0301	1361	1362	159.8
299	baal39a03	1363	1364	159.8

TABLE 2-7

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
242	bah57o03	1265	1266	138.3
242	baak41d22	1267	1268	138.3
242	bah61c16	1269	1270	138.3
242	BaAL7M13	1271	1272	138.3
242	BaAK31F11	1273	1274	138.3
242	basd22k05	1275	1276	138.3
242	basd3p19	1277	1278	138.3
242	baak17o09	1279	1280	138.3
242	baal33d23	1281	1282	138.3
242	BaAK12F04	1283	1284	138.3
242	bah53j16	1285	1286	138.3
262	BaSD2E24	1287	1288	138.5
263	bags39h08	1289	1290	138.7
264	BaSD1N02	1291	1292	139.5
264	bags20m21	1293	1294	139.5
264	baal10h19	1295	1296	139.5
264	basd12m11	1297	1298	139.5
264	bah29d24	1299	1300	139.5
264	BaGS39P09	1301	1302	139.5
264	BaGS31F17	1303	1304	139.5
264	BaGS23D08	1305	1306	139.5
264	bags39d15	1307	1308	139.5
264	BaGS34I17	1309	1310	139.5
274	BaH32N02	1311	1312	141.6
274	BaSD18H19	1313	1314	141.6
274	bast63A0101	1315	1316	141.6
274	BaH50N04	1317	1318	141.6
278	baal4a13	1319	1320	147.5
278	baal41l18	1321	1322	147.5
280	BaH31A03	1323	1324	152.2
280	bastl39A0901	1325	1326	152.2
280	baet46D0507	1327	1328	152.2
283	baal27e20	1329	1330	153.3
283	bagsS7l16	1331	1332	153.3
283	baak34o06	1333	1334	153.3
286	BaAL30I11	1335	1336	155.4
286	BaH62C15	1337	1338	155.4
286	basd12i15	1339	1340	155.4
286	BaAK40I03	1341	1342	155.4
286	BaAK23E14	1343	1344	155.4
286	BaAL21F11	1345	1346	155.4
286	BaAK16L19	1347	1348	155.4
293	baal27a24	1349	1350	156.5
294	kr41H0315	1351	1352	157.6
294	BaH62I23	1353	1354	157.6
296	bah52i24	1355	1356	158.7
296	bastl33A0301	1357	1358	158.7
296	BaH28J15	1359	1360	158.7

TABLE 2-7-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
299	bastl56A0301	1361	1362	159.8
299	baal39a03	1363	1364	159.8

TABLE 2-8

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
345	kr14F0911	1459	1460	190.8
352	BaGS36A04	1461	1462	192.8
352	bags13a16	1463	1464	192.8
354	bags26e20	1465	1466	196.1
355	baet45G1214	1467	1468	197.6
356	BaAK35F14	1469	1470	202
357	BaAK23N21	1471	1472	203.2
357	basd13j22	1473	1474	203.2
359	BaAK46E10	1475	1476	208.4
359	bastl55F0812	1477	1478	208.4
361	baak46l06	1479	1480	209.4
361	BaAL2D11	1481	1482	209.4
363	baak15p17	1483	1484	210.5
364	BaGS33J16	1485	1486	211.6
364	bags7p21	1487	1488	211.6
366	BaAK22E05	1489	1490	212.7
366	bah42m05	1491	1492	212.7
368	BaAK25L01	1493	1494	213.8
369	bags39e24	1495	1496	214.9
369	BaH56N24	1497	1498	214.9
371	baak44i12	1499	1500	215.4
372	bah21j03	1501	1502	215.9
373	kr71B0103	1503	1504	217.4
373	BaGS16D15	1505	1506	217.4
375	baak21p23	1507	1508	217.9
376	BaGS6G09	1509	1510	219
376	BaSD15M02	1511	1512	219
376	basd13f02	1513	1514	219
376	BaH19F21	1515	1516	219
380	bags20b10	1517	1518	224.5
380	bah26j10	1519	1520	224.5
382	bast65G0113	1521	1522	225.5
383	baak4k13	1523	1524	226.5
383	baal19j23	1525	1526	226.5
383	bags34h11	1527	1528	226.5
386	bags37j03	1529	1530	227.6
387	baal15e13	1531	1532	230.5
387	BaAL5O10	1533	1534	230.5
389	BaGS29J10	1535	1536	234.4
390	bah22o08	1537	1538	235.7
390	bags6k13	1539	1540	235.7
392	bastl43C0705	1541	1542	236.8
393	BaAL4D10	1543	1544	237.4
393	basd12n12	1545	1546	237.4
395	bags23h03	1547	1548	240.3
395	bags6l02	1549	1550	240.3
397	bast63B0703	1551	1552	243.4
397	BaSD13E02	1553	1554	243.4
399	BaSD14P15	1555	1556	248.7
399	bah13a17	1557	1558	248.7

TABLE 2-9

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
401	BaH50L23	1559	1560	250.9
401	bags19g04	1561	1562	250.9

TABLE 2-9-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
403	bast73E0210	1563	1564	252
403	BaH50O21	1565	1566	252
403	basd21g05	1567	1568	252
406	bah33p11	1569	1570	253.1
406	baal5i19	1571	1572	253.1
406	bah16e04	1573	1574	253.1
406	baak32p24	1575	1576	253.1
406	EBmac415	—	—	253.1
411	bags38f12	1577	1578	254.2
411	basd26p18	1579	1580	254.2
413	baak45h16	1581	1582	255.3
414	bah28p12	1583	1584	257.5
415	bah19a10	1585	1586	258.6
416	baak13d11	1587	1588	258.8
417	bah49p10	1589	1590	259.1
417	baal32n15	1591	1592	259.1
419	bast09C0305	1593	1594	260.6
420	basd16l09	1595	1596	263.9
420	BaAK22H04	1597	1598	263.9
422	BaGS15J13	1599	1600	265
422	kr66G0414	1601	1602	265
424	BaSD22C07	1603	1604	266.1
424	kr71C1105	1605	1606	266.1
424	bags34i11	1607	1608	266.1
427	BaH23K17	1609	1610	267.3
428	bast39D0107	1611	1612	270.5
428	BaH44K24	1613	1614	270.5
430	BaGS18N21	1615	1616	273.5
430	baak32k15	1617	1618	273.5
432	bah61a13	1619	1620	275.7
432	bags35n11	1621	1622	275.7
432	BaAK24I03	1623	1624	275.7
435	baal4h20	1625	1626	277.5
435	BaH28N23	1627	1628	277.5
435	bags10e13	1629	1630	277.5
438	baak27i10	1631	1632	278.5
438	bags19d13	1633	1634	278.5
438	baak19d04	1635	1636	278.5
438	BaAL34O19	1637	1638	278.5
438	baal12l02	1639	1640	278.5
438	BaAK1P04	1641	1642	278.5
438	baak35m13	1643	1644	278.5
438	bags35a12	1645	1646	278.5
446	bah41n09	1647	1648	279.6
446	BaGS23I12	1649	1650	279.6
448	BaH16P20	1651	1652	280.4
448	BaAK42L17	1653	1654	280.4
450	baak36d23	1655	1656	284.2

TABLE 2-10

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
450	bast78C1006	1657	1658	284.2
452	BaH45O16	1659	1660	285
453	bah21h09	1661	1662	286.1
454	bah58p22	1663	1664	287.2
455	bags20l19	1665	1666	288.8
456	bah13i10	1667	1668	290.4
457	BaAK36B07	1669	1670	291.5
458	baak26b05	1671	1672	295.5
459	baal7c15	1673	1674	296.6
459	bah63f05	1675	1676	296.6
461	bags15j16	1677	1678	297.9
462	BaGS6N10	1679	1680	299.2
462	bah41e10	1681	1682	299.2
464	BaH54D08	1683	1684	299.7

TABLE 2-10-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
465	baak18c01	1685	1686	300.2
466	basd21o07	1687	1688	301.3
467	bah41b23	1689	1690	301.9
468	basd18g15	1691	1692	302.4
468	baak43c03	1693	1694	302.4
468	bastl30D0408	1695	1696	302.4
468	bah17p16	1697	1698	302.4
472	baal13f18	1699	1700	303.5
472	bags18i22	1701	1702	303.5
472	bags9b02	1703	1704	303.5
475	bah11e22	1705	1706	323.4
476	bah58h09	1707	1708	332.9
477	basd16e16	1709	1710	334.9
478	BaAK4C12	1711	1712	340
479	bags37a05	1713	1714	343.4
480	bags9p10	1715	1716	351.7
481	baak24m01	1717	1718	352.7
482	basd27d09	1719	1720	353.2
483	baak34a14	1721	1722	353.7
483	baak36a20	1723	1724	353.7
483	BaSD17P09	1725	1726	353.7
486	bags5m04	1727	1728	354.8
487	BaGS5E06	1729	1730	355.9
487	MWG2076	—	—	355.9
487	bags15f03	1731	1732	355.9
487	bags18j23	1733	1734	355.9
487	baal13m04	1735	1736	355.9
487	bags9o24	1737	1738	355.9
493	kr49E0610	1739	1740	356.4
494	bah12h16	1741	1742	356.9
494	baak33n16	1743	1744	356.9
494	BaGS22E05	1745	1746	356.9
497	bah26n01	1747	1748	358
497	BaGS39E07	1749	1750	358
497	BaH45O03	1751	1752	358
500	BaH38A09	1753	1754	360.2

[0067] As shown in Table 3-1 to Table 3-10, the chromosomal order in barley 3H chromosome (distance from the short arm end of 3H chromosome) has been specified for 444 clones including the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1755 through SEQ ID NO: 2642. The chromosomal order in barley 3H chromosome has also been specified for 13 known clones (MWG848, HvLTPPB, HVM9, Bmac67, Bmag136, Bmac209, HVM27, HvBRI1, HVM33, HVM60, Bmag225, Bmag13, and HVM62).

TABLE 3-1

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
1	BaAL15P01	1755	1756	0
2	BaAK42D06	1757	1758	9.8
2	bags12k16	1759	1760	9.8
2	BaAL36H19	1761	1762	9.8
2	bags1d06	1763	1764	9.8
6	bast18A0602	1765	1766	10.9
6	basd22i04	1767	1768	10.9
8	BaGS31M01	1769	1770	12
9	BaH63H24	1771	1772	12.4
10	basd15n13	1773	1774	12.8
11	MWG848	—	—	13.1
11	BaAK13C16	1775	1776	13.1
13	BaGS32C19	1777	1778	15.3

TABLE 3-1-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
13	baak36f08	1779	1780	15.3
15	bastl04C0406	1781	1782	16.4
15	bastl42D1107	1783	1784	16.4
17	BaGS31B20	1785	1786	17.5
17	baak39l17	1787	1788	17.5
19	BaAL17J24	1789	1790	20.7
19	bah15p03	1791	1792	20.7
21	baak20g06	1793	1794	21.8
21	baal22c16	1795	1796	21.8
21	baak46o05	1797	1798	21.8
24	basd15h22	1799	1800	22.9
25	BaSD19C07	1801	1802	24
26	bags22i13	1803	1804	25.7
27	baak39a14	1805	1806	26.8
28	bah31e12	1807	1808	27.9
28	BaSD15L22	1809	1810	27.9
30	BaGS20D21	1811	1812	30.1
31	bags39o21	1813	1814	30.7
31	basd21j11	1815	1816	30.7
33	BaH48C10	1817	1818	32.3
34	BaH54J07	1819	1820	33.9
35	BaSD19H23	1821	1822	36.1
35	baak35n06	1823	1824	36.1
37	bags35b22	1825	1826	39.3
37	BaAK30H06	1827	1828	39.3
37	BaAL15M07	1829	1830	39.3
40	BaGS20N02	1831	1832	40.4
40	BaAL19L12	1833	1834	40.4
42	bags25b05	1835	1836	41.5
42	HvLTPPB	—	—	41.5
42	baal1h04	1837	1838	41.5
45	baet46B0903	1839	1840	42.6
45	BaGS19F16	1841	1842	42.6
45	baak13g18	1843	1844	42.6
48	BaH45N12	1845	1846	47
49	bast74H0216	1847	1848	48.1
50	bah24l06	1849	1850	50.5

TABLE 3-2

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
51	BaAK45C14	1851	1852	53.4
51	baal5k12	1853	1854	53.4
53	kr63F0111	1855	1856	54.1
53	baak13h18	1857	1858	54.1
53	baak12j16	1859	1860	54.1
56	BaAK28J20	1861	1862	55.2
56	BaH27G14	1863	1864	55.2
56	BaH49B13	1865	1866	55.2
59	BaGS35A09	1867	1868	57.4
60	BaGS38L24	1869	1870	58.6
61	BaAK43H20	1871	1872	66.5
61	bast16A0802	1873	1874	66.5
61	basd18k01	1875	1876	66.5
64	BaH58D17	1877	1878	67.6
65	BaAK30M07	1879	1880	69.2
65	bags6a04	1881	1882	69.2
67	kr15H0915	1883	1884	69.7
67	bags26d01	1885	1886	69.7
69	basd14k04	1887	1888	70.8
69	BaSD24D11	1889	1890	70.8
69	BaH53L10	1891	1892	70.8
72	BaH60D22	1893	1894	73
72	BaSD1G06	1895	1896	73
72	BaAK21L13	1897	1898	73
72	bah57m03	1899	1900	73

TABLE 3-2-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
76	baal30b10	1901	1902	74.1
77	bah62n16	1903	1904	74.7
78	BaGS22F15	1905	1906	75.2
78	BaH50J14	1907	1908	75.2
80	bah19d23	1909	1910	75.7
81	bags38c06	1911	1912	76.2
81	BaGS25N05	1913	1914	76.2
81	bastl29B0503	1915	1916	76.2
84	baak27d01	1917	1918	77.3
84	baak43n21	1919	1920	77.3
86	BaAL4F05	1921	1922	78.4
86	baal4a06	1923	1924	78.4
88	bast17D1008	1925	1926	80
89	BaGS16B17	1927	1928	81.1
90	BaGS27P18	1929	1930	81.7
90	BaGS4J14	1931	1932	81.7
90	BaAK16B19	1933	1934	81.7
90	baal40p07	1935	1936	81.7
94	bah49c19	1937	1938	84
95	bast58C0406	1939	1940	87.4
95	BaAK35M24	1941	1942	87.4
95	bags19h13	1943	1944	87.4
95	bah57c21	1945	1946	87.4
99	BaH53P15	1947	1948	88.5
99	BaGS20A10	1949	1950	88.5

TABLE 3-3

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
99	bast02D0808	1951	1952	88.5
99	bags31c04	1953	1954	88.5
99	BaH32J06	1955	1956	88.5
99	bah60o22	1957	1958	88.5
99	BaH50C16	1959	1960	88.5
99	BaH57K23	1961	1962	88.5
99	bags21g23	1963	1964	88.5
99	HVM9	—	—	88.5
109	Bmac67	—	—	89.6
109	baak43e04	1965	1966	89.6
111	kr17G1113	1967	1968	92.8
111	bags19k19	1969	1970	92.8
111	baak38b13	1971	1972	92.8
111	baak1d12	1973	1974	92.8
111	BaH28M14	1975	1976	92.8
116	BaH48I15	1977	1978	93.9
116	basd27h23	1979	1980	93.9
116	BaAK21A11	1981	1982	93.9
119	bast04B0804	1983	1984	94.4
120	bah45f13	1985	1986	94.9
120	BaAL8J18	1987	1988	94.9
120	BaGS9D01	1989	1990	94.9
120	baal12d12	1991	1992	94.9
120	baal4i06	1993	1994	94.9
125	bah26i01	1995	1996	96.5
125	BaGS15C17	1997	1998	96.5
127	baak1k08	1999	2000	97
127	bags9b03	2001	2002	97
127	baet42G1214	2003	2004	97
127	bah18d12	2005	2006	97
127	BaSD14G02	2007	2008	97
127	bags22b22	2009	2010	97
127	bah13f10	2011	2012	97
134	baal36g05	2013	2014	97.5
135	bags33j15	2015	2016	98
135	BaAL12H04	2017	2018	98
135	BaGS16I18	2019	2020	98

TABLE 3-3-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
138	bast61D0707	2021	2022	98.5
139	bah11k22	2023	2024	99
139	baak32p21	2025	2026	99
139	bah63l21	2027	2028	99
139	BaGS38D03	2029	2030	99
143	BaSD23A04	2031	2032	100.1
144	BaSD14C15	2033	2034	101.2
144	bast63C0105	2035	2036	101.2
144	bast23C1105	2037	2038	101.2
147	bags23b01	2039	2040	102.3
147	bags29c09	2041	2042	102.3
147	bags6b06	2043	2044	102.3
147	BaAK27G06	2045	2046	102.3

TABLE 3-4

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
147	BaAK39I07	2047	2048	102.3
147	BaGS20G21	2049	2050	102.3
147	bastl22E0810	2051	2052	102.3
147	bah11m03	2053	2054	102.3
147	BaAL3C04	2055	2056	102.3
156	BaAL19H10	2057	2058	103.4
156	bags24n16	2059	2060	103.4
156	BaSD24B15	2061	2062	103.4
156	bah48n17	2063	2064	103.4
156	bags9i05	2065	2066	103.4
156	bags1l22	2067	2068	103.4
156	bah62p18	2069	2070	103.4
156	bah55n21	2071	2072	103.4
156	bah44a05	2073	2074	103.4
156	bah19c13	2075	2076	103.4
156	baal12b04	2077	2078	103.4
156	Bmag136	—	—	103.4
156	Bmac209	—	—	103.4
156	BaAK28A10	2079	2080	103.4
156	kr28B0703	2081	2082	103.4
156	bastl50C0606	2083	2084	103.4
156	BaGS36B01	2085	2086	103.4
156	BaH19A05	2087	2088	103.4
156	baal10c06	2089	2090	103.4
156	bags19p04	2091	2092	103.4
176	BaAK21A17	2093	2094	104.5
176	bah20j14	2095	2096	104.5
176	BaAK19A03	2097	2098	104.5
176	BaGS30E19	2099	2100	104.5
176	BaAK28C21	2101	2102	104.5
176	bags11o14	2103	2104	104.5
182	BaGS13P22	2105	2106	105.6
182	kr27A1101	2107	2108	105.6
182	HVM27	—	—	105.6
185	baal12i18	2109	2110	106.7
186	BaAL8G07	2111	2112	107.8
187	bast58F0412	2113	2114	108.9
187	bags3f23	2115	2116	108.9
189	baal4m06	2117	2118	109.3
190	baal32p23	2119	2120	109.7
191	basd23m17	2121	2122	110
191	bastl30E0509	2123	2124	110
191	bah44b08	2125	2126	110
191	BaGS14N10	2127	2128	110
191	BaGS32B13	2129	2130	110
191	BaH30B03	2131	2132	110
191	basd1l23	2133	2134	110
191	basd11o06	2135	2136	110

TABLE 3-4-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
191	bah17f24	2137	2138	110
191	BaAK26L17	2139	2140	110

TABLE 3-5

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
191	bags23f03	2141	2142	110
191	bags20o06	2143	2144	110
203	bags19n12	2145	2146	111.1
203	baal12a09	2147	2148	111.1
203	bast14F0612	2149	2150	111.1
203	baak13p20	2151	2152	111.1
207	BaGS16K13	2153	2154	111.9
207	baak22c16	2155	2156	111.9
209	baal40m06	2157	2158	115.4
210	BaH29I03	2159	2160	116.8
211	bah16h01	2161	2162	117.6
211	bah57a11	2163	2164	117.6
211	BaH41E23	2165	2166	117.6
211	baal11c11	2167	2168	117.6
215	BaSD14L18	2169	2170	118.1
216	bah14d17	2171	2172	118.7
216	BaGS1N17	2173	2174	118.7
216	bags27h17	2175	2176	118.7
219	bah47p22	2177	2178	119.8
219	BaH50A16	2179	2180	119.8
219	bags7b20	2181	2182	119.8
219	bags22a02	2183	2184	119.8
223	HvBRI1	—	—	120.4
224	basd12g02	2185	2186	122.6
225	basd15o18	2187	2188	123.1
226	baal25d19	2189	2190	125.3
226	bast52G0414	2191	2192	125.3
228	baal11c20	2193	2194	126.4
229	bags37k06	2195	2196	127
230	bags6e22	2197	2198	127.5
230	basd15a02	2199	2200	127.5
230	bags7b06	2201	2202	127.5
230	bah15k11	2203	2204	127.5
230	bast46C0406	2205	2206	127.5
230	bastl45E0509	2207	2208	127.5
236	baal35p14	2209	2210	128.6
237	BaH41G07	2211	2212	129.3
237	bast46H1016	2213	2214	129.3
239	bah60d12	2215	2216	131.8
239	baal39a19	2217	2218	131.8
241	baak11n24	2219	2220	132.9
241	bast14E0909	2221	2222	132.9
241	baet13G0713	2223	2224	132.9
244	HVM33	—	—	135.8
244	BaSD14L04	2225	2226	135.8
246	baak13c05	2227	2228	136
246	bast141G0513	2229	2230	136
248	BaGS39M09	2231	2232	137.6
249	baal19b12	2233	2234	138.6
250	BaAL39B05	2235	2236	144

TABLE 3-6

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
250	BaAL1J03	2237	2238	144
250	basd11k09	2239	2240	144

TABLE 3-6-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
253	BaGS33N15	2241	2242	146.1
253	baet43H0416	2243	2244	146.1
253	bah11m06	2245	2246	146.1
253	baak31a24	2247	2248	146.1
253	bags27h20	2249	2250	146.1
253	basd27c09	2251	2252	146.1
259	BaAL25O01	2253	2254	146.6
260	bags7f08	2255	2256	147.1
261	BaGS13O12	2257	2258	148.2
261	bags38b06	2259	2260	148.2
263	BaAK19J09	2261	2262	149.3
263	bags9e16	2263	2264	149.3
265	bags20n14	2265	2266	150.4
265	bah42o12	2267	2268	150.4
265	baak31k16	2269	2270	150.4
265	bags4p14	2271	2272	150.4
265	bah27a22	2273	2274	150.4
270	bags21n02	2275	2276	151.5
271	BaH62B09	2277	2278	153.7
271	BaGS19J10	2279	2280	153.7
273	bags15k18	2281	2282	154.2
274	BaAK29G03	2283	2284	154.7
274	baak23e11	2285	2286	154.7
274	bags31k04	2287	2288	154.7
274	bast56C0305	2289	2290	154.7
278	basd26c09	2291	2292	159
278	BaSD20B11	2293	2294	159
278	HVM60	—	—	159
281	BaH46F11	2295	2296	160.1
281	BaH30F03	2297	2298	160.1
281	BaSD27G02	2299	2300	160.1
284	Bmag225	—	—	161.2
284	BaAK33I12	2301	2302	161.2
286	baak32m10	2303	2304	162.3
286	BaAL4L02	2305	2306	162.3
286	kr44F0911	2307	2308	162.3
289	BaGS37A16	2309	2310	163.5
290	bags39p06	2311	2312	163.9
290	BaAL12N06	2313	2314	163.9
292	bags22p05	2315	2316	165.4
293	bags9a03	2317	2318	166.5
293	baet24F1212	2319	2320	166.5
295	baak29d10	2321	2322	167.6
295	bags13i12	2323	2324	167.6
295	BaAL16A23	2325	2326	167.6
298	bastl16B1204	2327	2328	171.6
298	bastl29F0711	2329	2330	171.6
300	BaGS32M17	2331	2332	172.1

TABLE 3-7

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
301	baal15e10	2333	2334	172.5
301	basd3g08	2335	2336	172.5
303	baal33m18	2337	2338	173.6
303	baak24e23	2339	2340	173.6
303	baak46j13	2341	2342	173.6
306	bah49o05	2343	2344	174.7
306	baal15e05	2345	2346	174.7
306	BaAK1O08	2347	2348	174.7
306	BaGS30P02	2349	2350	174.7
310	BaSD15D05	2351	2352	178.9
311	BaAL7B16	2353	2354	179.2
312	bags38n23	2355	2356	180.3
313	baak36a14	2357	2358	181.6
313	baak34g01	2359	2360	181.6

TABLE 3-7-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
313	baak12f01	2361	2362	181.6
316	BaGS30I18	2363	2364	183.7
316	bags35n24	2365	2366	183.7
316	bah37j21	2367	2368	183.7
316	bah31e13	2369	2370	183.7
320	bags22g10	2371	2372	190
320	bags22f17	2373	2374	190
322	baal30l05	2375	2376	190.9
322	bags38o10	2377	2378	190.9
324	baak40o04	2379	2380	193.1
325	BaH49L21	2381	2382	193.6
325	bastl30A0701	2383	2384	193.6
327	bags19l03	2385	2386	195.1
328	bah18m13	2387	2388	196.6
329	baak44p03	2389	2390	198.2
329	kr10H0216	2391	2392	198.2
331	bags11i04	2393	2394	199.4
332	bah52o06	2395	2396	200.5
333	bah35c14	2397	2398	200.8
333	BaAL30C02	2399	2400	200.8
335	bah11i21	2401	2402	201.9
336	BaAK36B11	2403	2404	204.1
337	BaAK20K23	2405	2406	206
337	basd14n22	2407	2408	206
339	BaAL25P17	2409	2410	207.6
339	BaH49A01	2411	2412	207.6
341	basd13p12	2413	2414	209.5
341	bags39m17	2415	2416	209.5
343	baet44D0707	2417	2418	212.8
344	BaH16P10	2419	2420	213.9
344	BaAK42J01	2421	2422	213.9
346	kr24E0709	2423	2424	215.8
346	BaAK38O08	2425	2426	215.8
348	BaAL13N01	2427	2428	217.7
349	baak12c12	2429	2430	219.8
350	BaGS31N06	2431	2432	220.9

TABLE 3-8

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
351	baal15f24	2433	2434	221.5
352	BaSD18B21	2435	2436	222
352	BaSD17G23	2437	2438	222
354	baak41k22	2439	2440	223.7
355	baak21o03	2441	2442	225.4
356	BaSD16B18	2443	2444	227
356	bast79C1105	2445	2446	227
358	BaAK4J17	2447	2448	228.1
359	BaAL37H08	2449	2450	228.6
359	BaH36L17	2451	2452	228.6
361	BaH46A12	2453	2454	229.7
361	bags11i15	2455	2456	229.7
361	baak20g24	2457	2458	229.7
364	baak20h23	2459	2460	230.8
365	baak35b18	2461	2462	231.9
365	Bmag13	—	—	231.9
365	baak41o03	2463	2464	231.9
365	baet46C0206	2465	2466	231.9
369	bags10i20	2467	2468	233
369	baal1b16	2469	2470	233
369	baal5i05	2471	2472	233
369	BaH27B05	2473	2474	233
369	bah14a11	2475	2476	233
369	basd19k10	2477	2478	233
369	bags30n17	2479	2480	233
369	bags31e24	2481	2482	233

TABLE 3-8-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
369	BaGS5B16	2483	2484	233
378	BaAL5F06	2485	2486	234.1
378	bags34a11	2487	2488	234.1
378	bags6c16	2489	2490	234.1
378	bah42g19	2491	2492	234.1
378	BaH47O14	2493	2494	234.1
383	BaH12L06	2495	2496	235.2
383	basd11a10	2497	2498	235.2
385	BaH50I12	2499	2500	237.3
385	BaH51A21	2501	2502	237.3
385	baak45p02	2503	2504	237.3
388	BaSD12P12	2505	2506	241.6
389	bags9l16	2507	2508	242.7
389	BaSD26O20	2509	2510	242.7
389	bags5d10	2511	2512	242.7
389	baal0e07	2513	2514	242.7
393	baak14e02	2515	2516	243.8
394	BaH63F14	2517	2518	244.9
394	bah33f19	2519	2520	244.9
394	bags19l10	2521	2522	244.9
397	BaH56J21	2523	2524	246
397	baal40i22	2525	2526	246
397	kr42C0105	2527	2528	246
400	bags16i19	2529	2530	246.5

TABLE 3-9

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
400	BaH54H01	2531	2532	246.5
402	kr69E0810	2533	2534	247.8
403	bags17j14	2535	2536	250
404	bags20e19	2537	2538	253
405	bast74C0206	2539	2540	255.1
405	BaAK13L10	2541	2542	255.1
407	bags20i01	2543	2544	256.2
407	basd19n14	2545	2546	256.2
407	baak42g21	2547	2548	256.2
407	BaAK39A15	2549	2550	256.2
411	basd18o21	2551	2552	257.3
411	BaAK22K17	2553	2554	257.3
413	baal6o24	2555	2556	260.9
414	BaH22C09	2557	2558	262.7
414	HVM62	—	—	262.7
416	bags23k14	2559	2560	263.8
416	baal24n12	2561	2562	263.8
418	BaGS21H17	2563	2564	268.1
418	BaSD16I09	2565	2566	268.1
418	BaAL13B22	2567	2568	268.1
421	bah41l03	2569	2570	270.2
422	bastl30F0111	2571	2572	272.5
423	BaH15L04	2573	2574	275.9
423	baak40c12	2575	2576	275.9
425	kr23D0408	2577	2578	277
425	bah57d15	2579	2580	277
427	baak31e03	2581	2582	278.1
428	BaAL13O01	2583	2584	281.8
429	BaSD26P04	2585	2586	286.3
430	bags20f18	2587	2588	287.4
431	BaH42J22	2589	2590	288.5
431	BaAL3K03	2591	2592	288.5
431	kr30B1103	2593	2594	288.5
434	baak14i02	2595	2596	289.6
434	bags28c17	2597	2598	289.6
434	baal4e21	2599	2600	289.6
434	BaGS29D05	2601	2602	289.6
438	bah54d24	2603	2604	290.7

TABLE 3-9-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
439	basd22g20	2605	2606	291.8
439	BaH62H20	2607	2608	291.8
441	bags38h17	2609	2610	292.9
441	BaAK30B23	2611	2612	292.9
441	BaAK24P09	2613	2614	292.9
441	baak23i12	2615	2616	292.9
441	BaGS22D06	2617	2618	292.9
441	BaAL34P18	2619	2620	292.9
441	BaAL39F24	2621	2622	292.9
441	BaGS4L04	2623	2624	292.9
441	bah12e02	2625	2626	292.9
441	BaAL15F23	2627	2628	292.9

TABLE 3-10

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
441	BaGS25O15	2629	2630	292.9
441	BaGS7G14	2631	2632	292.9
441	basd24i11	2633	2634	292.9
454	baak20l21	2635	2636	294
455	bags33m02	2637	2638	295
455	BaH48G21	2639	2640	295
457	bags27p13	2641	2642	300.4

[0068] As shown in Table 4-1 to Table 4-7, the chromosomal order in barley 4H chromosome (distance from the short arm end of 4H chromosome) has been specified for 341 clones including the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 2643 through SEQ ID NO: 3324. The chromosomal order in barley 4H chromosome has also been specified for 9 known clones (HVM40, MWG2033, HVM3, MWG058, Bmag353, HVM68, HVM67, sh, and VRN2).

TABLE 4-1

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
1	BaGS10N17	2643	2644	0
2	BaAK38K23	2645	2646	1.1
2	bah14a22	2647	2648	1.1
4	BaAL19O06	2649	2650	2.2
4	BaGS32P17	2651	2652	2.2
6	bah11j04	2653	2654	3.3
7	baak35b06	2655	2656	4.1
7	basd21f17	2657	2658	4.1
9	BaAK44O11	2659	2660	7
10	bastl14D0408	2661	2662	8.2
11	BaAK42C15	2663	2664	9
12	baak40n12	2665	2666	10
12	basd2j05	2667	2668	10
12	baak46n05	2669	2670	10
12	baak24g04	2671	2672	10
16	BaAL22H02	2673	2674	11
17	bah56g24	2675	2676	16.4
17	BaAL2I22	2677	2678	16.4
19	bags20c22	2679	2680	17.5
20	BaH50O22	2681	2682	18.6
20	baak32f06	2683	2684	18.6
20	bags35i24	2685	2686	18.6

TABLE 4-1-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
20	BaSD21D13	2687	2688	18.6
20	bast46D0408	2689	2690	18.6
25	bast55B1204	2691	2692	22.1
26	BaGS39M07	2693	2694	24.5
27	bags39b15	2695	2696	27.6
27	baak37p11	2697	2698	27.6
27	bah29o22	2699	2700	27.6
27	baak12k14	2701	2702	27.6
31	baet31E1010	2703	2704	28.7
32	HVM40	—	—	29.8
32	baal39h14	2705	2706	29.8
34	bags14g22	2707	2708	30.9
35	baal18m18	2709	2710	32.1
36	BaSD24E02	2711	2712	33.2
36	BaH50N14	2713	2714	33.2
36	kr70A0202	2715	2716	33.2
39	baak11d04	2717	2718	34.3
40	MWG2033	—	—	35.4
40	bags20h01	2719	2720	35.4
42	BaH39P15	2721	2722	35.9
43	BaAK46O20	2723	2724	36.4
43	baal33m06	2725	2726	36.4
43	bastl50E0309	2727	2728	36.4
43	bags20i17	2729	2730	36.4
47	BaGS22A07	2731	2732	37.5
48	bah41b09	2733	2734	37.7
49	kr18G0913	2735	2736	39
49	BaGS19O23	2737	2738	39

TABLE 4-2

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
51	bags15e12	2739	2740	39.6
52	bags29i09	2741	2742	40.1
52	baak19m23	2743	2744	40.1
54	bags14h12	2745	2746	40.6
55	bah32e15	2747	2748	41.2
55	bah11l02	2749	2750	41.2
55	bags39e16	2751	2752	41.2
55	bags10l12	2753	2754	41.2
59	BaGS31M13	2755	2756	42.3
59	baal32m10	2757	2758	42.3
59	basd12b23	2759	2760	42.3
62	baal39e15	2761	2762	43.5
63	baal16l11	2763	2764	45.8
64	BaGS31B01	2765	2766	46.9
64	BaSD17F09	2767	2768	46.9
64	BaH48L11	2769	2770	46.9
67	BaSD14M08	2771	2772	48
67	bah56c09	2773	2774	48
67	baak17g07	2775	2776	48
67	bags20k09	2777	2778	48
67	BaSD25B08	2779	2780	48
67	bast27E0309	2781	2782	48
73	baet20D0107	2783	2784	52.3
74	BaAL17L08	2785	2786	56.3
75	bah61p18	2787	2788	65.2
75	bah63d12	2789	2790	65.2
75	BaAK26A03	2791	2792	65.2
78	baak26n10	2793	2794	67.4
78	bast22B0204	2795	2796	67.4
80	BaAL3C05	2797	2798	68.5
80	BaGS38H14	2799	2800	68.5
80	BaAL4D19	2801	2802	68.5
83	BaAK20B09	2803	2804	69.6
83	BaAK37H01	2805	2806	69.6

TABLE 4-2-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
83	BaGS33P13	2807	2808	69.6
86	basd13l12	2809	2810	70.7
86	bags11m01	2811	2812	70.7
88	BaGS18H09	2813	2814	77.5
89	basd3d13	2815	2816	86.5
89	baal9m23	2817	2818	86.5
89	bags23f08	2819	2820	86.5
92	BaGS15L23	2821	2822	87.6
92	baak2k13	2823	2824	87.6
92	baak17d18	2825	2826	87.6
92	bags13a12	2827	2828	87.6
96	baak44g22	2829	2830	88.7
97	kr34F0212	2831	2832	89.8
98	baal16d11	2833	2834	92
99	bah22d04	2835	2836	93.1
99	bah48m23	2837	2838	93.1

TABLE 4-3

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
99	basd15p13	2839	2840	93.1
99	BaGS6O07	2841	2842	93.1
99	BaH37O10	2843	2844	93.1
99	bags21k10	2845	2846	93.1
99	bah56n18	2847	2848	93.1
99	baal9i11	2849	2850	93.1
99	BaAL39N06	2851	2852	93.1
99	bags9d05	2853	2854	93.1
99	BaAL19I19	2855	2856	93.1
99	basd12I11	2857	2858	93.1
99	bastl46D1008	2859	2860	93.1
99	BaH50H16	2861	2862	93.1
99	bags9n05	2863	2864	93.1
99	kr61B1103	2865	2866	93.1
115	kr27B0103	2867	2868	95.2
115	kr33H1115	2869	2870	95.2
115	baak30l02	2871	2872	95.2
115	bah55a12	2873	2874	95.2
115	BaH26K14	2875	2876	95.2
120	HVM3	—	—	96.3
120	BaAK33K19	2877	2878	96.3
120	basd18m17	2879	2880	96.3
120	BaH50G09	2881	2882	96.3
120	BaH53B03	2883	2884	96.3
120	BaH54L11	2885	2886	96.3
120	basd13i14	2887	2888	96.3
120	bah56g09	2889	2890	96.3
120	bah41b06	2891	2892	96.3
120	bags14d19	2893	2894	96.3
120	baal20f05	2895	2896	96.3
120	BaH18H12	2897	2898	96.3
120	baal9o21	2899	2900	96.3
120	bags21a02	2901	2902	96.3
120	BaAL3G19	2903	2904	96.3
120	baal7a09	2905	2906	96.3
120	BaAL29I16	2907	2906	96.3
137	bast70B0804	2909	2910	98.4
137	bags14n08	2911	2912	98.4
139	bastl14F0412	2913	2914	99.5
139	BaAK36I12	2915	2916	99.5
139	baal3f19	2917	2916	99.5
142	baal1e10	2919	2920	101.6
142	bags6k02	2921	2922	101.6
142	kr42H0315	2923	2924	101.6
145	bah39p02	2925	2926	102.7
146	BaGS9L14	2927	2928	106

TABLE 4-3-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
146	baal35l03	2929	2930	106
146	basd12m15	2931	2932	106
146	BaAK35P01	2933	2934	106
146	basd11d18	2935	2936	106

TABLE 4-4

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
146	BaH38E07	2937	2938	106
146	BaGS18H13	2939	2940	106
146	bags18g16	2941	2942	106
146	bags27f21	2943	2944	106
146	BaGS7M13	2945	2946	106
146	baal39c19	2947	2948	106
146	baak46j05	2949	2950	106
146	BaAK32D20	2951	2952	106
146	MWG058	—	—	106
146	BaGS18M02	2953	2954	106
146	bags9c05	2955	2956	106
146	baak46m13	2957	2958	106
146	bags35n16	2959	2960	106
146	bags39g08	2961	2962	106
146	baal33a06	2963	2964	106
146	BaSD17F20	2965	2966	106
146	bags22i21	2967	2968	106
168	bah32g18	2969	2970	107.1
169	BaAL37O23	2971	2972	108.2
169	bags22p03	2973	2974	108.2
171	bags38l18	2975	2976	109.3
172	BaGS35C13	2977	2978	112.6
172	bah47h04	2979	2980	112.6
174	bags30m11	2981	2982	114.7
174	BaH22L15	2983	2984	114.7
176	bags39e15	2985	2986	115.8
177	kr65H0816	2987	2988	116.9
177	basd11h11	2989	2990	116.9
177	baak2b06	2991	2992	116.9
177	Bmag353	—	—	116.9
177	bags37j11	2993	2994	116.9
177	BaAK46L15	2995	2996	116.9
183	BaSD14A23	2997	2998	122.3
183	bast25C0705	2999	3000	122.3
185	bast21B1204	3001	3002	123.3
186	bags1l16	3003	3004	129.7
186	BaAK21G02	3005	3006	129.7
188	bastl26E1109	3007	3008	130.6
188	basd13k24	3009	3010	130.6
188	BaAL13F02	3011	3012	130.6
191	bags13c10	3013	3014	134.7
191	bags11o11	3015	3016	134.7
191	BaAK36P01	3017	3018	134.7
194	bah52d09	3019	3020	135.9
194	BaGS26D18	3021	3022	135.9
196	baak33c22	3023	3024	137
196	basd1d10	3025	3026	137
196	baak11c22	3027	3028	137
196	bags34l06	3029	3030	137
196	baak33j06	3031	3032	137

TABLE 4-5

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
196	bags23a11	3033	3034	137
196	bags34f02	3035	3036	137
196	bags20p21	3037	3038	137
196	bah52m01	3039	3040	137
196	basd15d07	3041	3042	137
196	BaAL20A14	3043	3044	137
207	BaGS21B04	3045	3046	137.7
208	HVM68	—	—	138.1
209	BaAL36B07	3047	3048	139.2
209	basd11p10	3049	3050	139.2
209	BaGS33E17	3051	3052	139.2
212	kr67C0206	3053	3054	140.3
213	bags15i20	3055	3056	141.4
214	BaH15E05	3057	3058	142.5
215	BaH58K02	3059	3060	143.6
216	basd13d17	3061	3062	146.9
216	BaGS17A15	3063	3064	146.9
216	BaAK30F13	3065	3066	146.9
216	baal17m22	3067	3068	146.9
216	baak42f04	3069	3070	146.9
216	baal2n22	3071	3072	146.9
222	kr30C0705	3073	3074	148
222	BaSD19J21	3075	3076	148
222	BaH34N22	3077	3078	148
225	BaAK2I20	3079	3080	149.1
225	BaGS1E22	3081	3082	149.1
225	baak34b17	3083	3084	149.1
228	BaSD11L18	3085	3086	151.3
228	kr32A0202	3087	3088	151.3
230	bags27h21	3089	3090	151.9
231	bah62d17	3091	3092	152.4
231	bah43e22	3093	3094	152.4
231	BaAL30I23	3095	3096	152.4
231	BaSD13H20	3097	3098	152.4
231	BaSD14O04	3099	3100	152.4
236	baak34p06	3101	3102	153.5
237	bah63b08	3103	3104	156.8
238	bastl03F0812	3105	3106	157.9
239	basd14m17	3107	3108	159.2
240	BaSD2J03	3109	3110	162.2
241	bah13b17	3111	3112	171.1
242	baal32b23	3113	3114	176.5
242	bastl50D1208	3115	3116	176.5
242	BaGS9H13	3117	3118	176.5
242	baal33e04	3119	3120	176.5
246	BaAL40L16	3121	3122	177.6
247	bah44n03	3123	3124	178.7
247	bags20h05	3125	3126	178.7
247	bags20fM5	3127	3128	178.7
250	BaGS7E03	3129	3130	179.8

TABLE 4-6

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
250	bags9k13	3131	3132	179.8
252	bast55E0709	3133	3134	181.1
253	bags8a14	3135	3136	184.6
254	baak38k04	3137	3138	185.1
255	BaH33B15	3139	3140	185.6
256	bags29m17	3141	3142	186.7
257	BaSD23P08	3143	3144	187.8
257	BaH42L12	3145	3146	187.8
259	bast79G0313	3147	3148	191
259	baet46C0905	3149	3150	191
259	baal4o09	3151	3152	191
259	bah26e10	3153	3154	191

TABLE 4-6-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
263	BaH32J04	3155	3156	193.1
264	bags20l07	3157	3158	194.2
265	kr18C0505	3159	3160	195.3
266	basd11m24	3161	3162	199.7
266	basd1i15	3163	3164	199.7
266	bah45b02	3165	3166	199.7
269	bast40C0206	3167	3168	201.8
269	baal40g05	3169	3170	201.8
269	bah13i21	3171	3172	201.8
269	basd27o20	3173	3174	201.8
269	BaAK12L24	3175	3176	201.8
274	BaAL12F24	3177	3178	204
274	baak45l08	3179	3180	204
274	BaAL36N04	3181	3182	204
274	baak41d17	3183	3184	204
274	kr39E0810	3185	3186	204
274	BaGS32G16	3187	3188	204
274	BaGS25M06	3189	3190	204
274	BaH36F21	3191	3192	204
274	BaAK13B12	3193	3194	204
283	baal29j18	3195	3196	205.1
284	bast63B0604	3197	3198	206.2
284	baak11n06	3199	3200	206.2
286	kr13F1012	3201	3202	208.4
287	bags20k06	3203	3204	209.5
288	baak15p20	3205	3206	210.6
288	bah18n11	3207	3208	210.6
290	BaH23J08	3209	3210	213.9
291	baet30B1004	3211	3212	215
291	bags34p06	3213	3214	215
291	bastl33H0816	3215	3216	215
294	BaSD17I17	3217	3218	216.1
294	basd19p22	3219	3220	216.1
294	bags4e03	3221	3222	216.1
294	BaAK36A13	3223	3224	216.1
294	bags33i03	3225	3226	216.1
299	BaAK14F03	3227	3228	217.2
300	BaAK42K19	3229	3230	219.3

TABLE 4-7

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
300	bast60A1101	3231	3232	219.3
302	bah52l06	3233	3234	220.4
302	bah23h10	3235	3236	220.4
302	BaGS15O23	3237	3238	220.4
302	BaAK20E08	3239	3240	220.4
306	kr61A1202	3241	3242	222.6
307	bast03F0212	3243	3244	223.7
307	bags39m22	3245	3246	223.7
309	BaAK30O17	3247	3248	227.3
310	baak29a01	3249	3250	232.1
310	basd1e04	3251	3252	232.1
312	BaGS23K09	3253	3254	233
313	BaAL2N04	3255	3256	234.3
314	BaH42C12	3257	3258	235.5
315	bah39o14	3259	3260	236.1
316	bast26A1202	3261	3262	236.6
317	BaGS30N15	3263	3264	237.4
317	BaAL34D18	3265	3266	237.4
319	baak15k23	3267	3268	240.3
319	bags37i06	3269	3270	240.3
319	BaGS19N09	3271	3272	240.3
322	BaSD13H09	3273	3274	241.4
323	bags3h19	3275	3276	242.5
323	baak28o08	3277	3278	242.5

TABLE 4-7-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
325	BaH15K08	3279	3280	243.6
325	HVM67	—	—	243.6
325	bah17h20	3281	3282	243.6
325	BaAL5L13	3283	3284	243.6
325	BaGS31P13	3285	3286	243.6
330	BaH28A11	3287	3288	247.9
330	BaSD25E01	3289	3290	247.9
330	sh	—	—	247.9
333	baet23F0111	3291	3292	249
333	VRN2	—	—	249
333	bastl41C0806	3293	3294	249
333	basd11c04	3295	3296	249
333	bags22k17	3297	3298	249
338	bastl27A1101	3299	3300	250.2
338	bags22a16	3301	3302	250.2
340	BaAL5E04	3303	3304	250.3
341	baal39f20	3305	3306	250.5
342	baak43d13	3307	3308	250.7
342	baak41l23	3309	3310	250.7
344	baet23B0604	3311	3312	252.3
345	BaAK28I08	3313	3314	255.6
346	bastl26C1206	3315	3316	258.8
346	bah27p20	3317	3318	258.8
346	baal12d24	3319	3320	258.8
346	bastl41F0511	3321	3322	258.8
346	BaGS17E03	3323	3324	258.8

[0069] As shown in Table 5-1 to Table 5-11, the chromosomal order in barley 5H chromosome (distance from the short arm end of 5H chromosome) has been specified for 498 clones including the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 3325 through SEQ ID NO: 4320. The chromosomal order in barley 5H chromosome has also been specified for 8 known clones (MWG502, Bmac113, HVM30, Bmag223, HvLOX, MWG2077, MWG2249, and HVM6).

TABLE 5-1

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
1	baal10j04	3325	3326	0
1	BaAK33J17	3327	3328	0
1	BaAL21J19	3329	3330	0
4	bast17H0515	3331	3332	0.5
5	bags22c02	3333	3334	1
6	BaAK35A06	3335	3336	2.2
7	BaGS11K08	3337	3338	5.6
8	bastl30A0602	3339	3340	6.7
9	BaGS39H16	3341	3342	8.8
9	MWG502	—	—	8.8
11	BaAK18M22	3343	3344	9.9
12	bast26G0614	3345	3346	11.5
13	BaSD22F13	3347	3348	15.9
14	BaAK28L16	3349	3350	20.5
15	bags35o06	3351	3352	24.9
16	bags13d07	3353	3354	25.9
16	BaAL24F18	3355	3356	25.9
16	bah63l18	3357	3358	25.9
19	BaGS9H22	3359	3360	26.4
20	BaAK18A05	3361	3362	26.9
20	BaH38D03	3363	3364	26.9
20	BaH17N17	3365	3366	26.9
23	bah18d08	3367	3368	30.1
24	bags34a05	3369	3370	31.9

TABLE 5-1-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
24	bags1m23	3371	3372	31.9
24	BaH50B05	3373	3374	31.9
24	bags1h11	3375	3376	31.9
28	BaH47G19	3377	3378	32.4
29	BaAK38H10	3379	3380	32.9
29	bah47e01	3381	3382	32.9
29	bast52E0109	3383	3384	32.9
32	bags1o08	3385	3386	34
32	BaH31H16	3387	3388	34
34	baak32l14	3389	3390	36.1
34	BaH50O06	3391	3392	36.1
34	BaSD26I01	3393	3394	36.1
37	bags1h24	3395	3396	38.3
38	basd27g16	3397	3398	40.5
38	BaGS16G24	3399	3400	40.5
40	BaGS34C19	3401	3402	43.7
40	bah20k17	3403	3404	43.7
40	bah54e13	3405	3406	43.7
40	bags35i06	3407	3408	43.7
40	bah29g09	3409	3410	43.7
45	BaAK29C12	3411	3412	44.8
46	bah56c06	3413	3414	48.2
47	baal6a09	3415	3416	51.8
48	bags6j06	3417	3418	53.1
49	BaH30P15	3419	3420	54.2
50	baak30k04	3421	3422	55.3

TABLE 5-2

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
51	basd25d22	3423	3424	56
51	BaGS39M02	3425	3426	56
53	baak13n10	3427	3428	58.9
53	BaGS18J21	3429	3430	58.9
53	BaSD22G22	3431	3432	58.9
53	bags18b17	3433	3434	58.9
53	bags33j02	3435	3436	58.9
53	baak36b16	3437	3438	58.9
59	bags37f05	3439	3440	60
59	BaAL17L15	3441	3442	60
61	BaGS20H12	3443	3444	62.4
62	kr65A0802	3445	3446	64
62	BaGS13E12	3447	3448	64
64	basd3h06	3449	3450	65.2
65	basd22j16	3451	3452	66.3
65	bah39n18	3453	3454	66.3
67	bags20d19	3455	3456	67.4
67	BaGS34H19	3457	3458	67.4
69	baak42n10	3459	3460	68.5
69	BaSD24F03	3461	3462	68.5
69	BaGS23N21	3463	3464	68.5
69	BaAK45E04	3465	3466	68.5
69	bags5n23	3467	3468	68.5
74	bast52H1216	3469	3470	69.4
75	bags22f23	3471	3472	69.7
76	BaH38E02	3473	3474	70.5
76	BaH50O07	3475	3476	70.5
78	kr07C1006	3477	3478	73.3
78	baak26a02	3479	3480	73.3
78	BaAK2J22	3481	3482	73.3
78	bah45h23	3483	3484	73.3
82	bah11h09	3485	3486	74.8
82	BaAK46M16	3487	3488	74.8
84	bah55m23	3489	3490	75.2
84	bah59c05	3491	3492	75.2
84	basd11l17	3493	3494	75.2

TABLE 5-2-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
84	bah19e08	3495	3496	75.2
84	BaAK21N24	3497	3498	75.2
84	BaH50E09	3499	3500	75.2
84	BaAK17P18	3501	3502	75.2
84	BaAL7A04	3503	3504	75.2
84	bast47B0303	3505	3506	75.2
84	bah28o17	3507	3508	75.2
84	bah37k03	3509	3510	75.2
84	bastl38A0501	3511	3512	75.2
84	bags23c03	3513	3514	75.2
84	basd13j01	3515	3516	75.2
84	bags21c02	3517	3518	75.2
84	bah28l03	3519	3520	75.2
84	BaAK36B17	3521	3522	75.2

TABLE 5-3

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
84	bags6k10	3523	3524	75.2
84	BaAK32J23	3525	3526	75.2
84	bags9k18	3527	3528	75.2
84	baal18c19	3529	3530	75.2
84	baak27p14	3531	3532	75.2
84	BaGS30N21	3533	3534	75.2
84	bah55p23	3535	3536	75.2
84	bah54p22	3537	3538	75.2
84	bags34f05	3539	3540	75.2
84	Bmac113	—	—	75.2
84	bags15i11	3541	3542	75.2
84	BaH26I21	3543	3544	75.2
84	BaSD20M22	3545	3546	75.2
114	bah14a24	3547	3548	75.6
115	BaH50J11	3549	3550	76
116	bags7a20	3551	3552	76.4
116	bah25l12	3553	3554	76.4
116	bags6k09	3555	3556	76.4
116	BaGS29P21	3557	3558	76.4
116	bah58f18	3559	3560	76.4
116	bags39i18	3561	3562	76.4
122	basd22l21	3563	3564	77.1
123	bags4o22	3565	3566	77.5
124	kr27E0909	3567	3568	78
125	bastl41H0216	3569	3570	78.5
125	baak36o17	3571	3572	78.5
125	BaH31P15	3573	3574	78.5
125	kr07D0208	3575	3576	78.5
125	bags9h03	3577	3578	78.5
130	BaGS38M11	3579	3580	79.6
130	kr26C0705	3581	3582	79.6
130	bags3k24	3583	3584	79.6
130	bah53e16	3585	3586	79.6
130	bags21n10	3587	3588	79.6
130	BaGS25E06	3589	3590	79.6
130	bah38n03	3591	3592	79.6
130	BaAK38G14	3593	3594	79.6
130	baal5a06	3595	3596	79.6
130	basd26d19	3597	3598	79.6
140	BaSD26D07	3599	3600	80.7
140	BaH50G14	3601	3602	80.7
140	bah21h17	3603	3604	80.7
140	bags5d21	3605	3606	80.7
140	BaAK34D14	3607	3608	80.7
140	baak18a16	3609	3610	80.7
140	bags4b01	3611	3612	80.7
140	bags38c19	3613	3614	80.7
140	BaGS38J23	3615	3616	80.7

TABLE 5-3-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
140	kr42D0208	3617	3618	80.7
140	BaH33A16	3619	3620	80.7

TABLE 5-4

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
140	bags10e03	3621	3622	80.7
140	bags14f17	3623	3624	80.7
140	BaAK35N11	3625	3626	80.7
140	bags26n10	3627	3628	80.7
140	bags37n02	3629	3630	80.7
140	baal39l05	3631	3632	80.7
157	BaAK26L11	3633	3634	81.3
158	BaH57C19	3635	3636	81.7
158	bags7a01	3637	3638	81.7
158	bah19l15	3639	3640	81.7
158	baal4o02	3641	3642	81.7
158	bah58a12	3643	3644	81.7
158	HVM30	—	—	81.7
158	bah11b08	3645	3646	81.7
158	bags14m15	3647	3648	81.7
158	baak1e17	3649	3650	81.7
167	bags14i11	3651	3652	83.2
168	bastl04B1103	3653	3654	87
169	bags13g08	3655	3656	94.7
170	basd27p03	3657	3658	102.2
170	bast38D0707	3659	3660	102.2
172	baak35j18	3661	3662	103.7
172	baal19k05	3663	3664	103.7
174	BaH19C21	3665	3666	104.2
174	bah49g10	3667	3668	104.2
174	bags14h08	3669	3670	104.2
174	bags23g18	3671	3672	104.2
174	bags22o22	3673	3674	104.2
174	BaAL20A03	3675	3676	104.2
174	bags5e24	3677	3678	104.2
174	bags5f11	3679	3680	104.2
174	BaAK33B10	3681	3682	104.2
174	BaSD15J20	3683	3684	104.2
174	bags38b22	3685	3686	104.2
185	bah39b06	3687	3688	105.3
185	bags19j08	3689	3690	105.3
187	BaGS1G09	3691	3692	106.4
188	bah63j06	3693	3694	107.5
188	BaAL39J02	3695	3696	107.5
188	BaSD27H14	3697	3698	107.5
191	BaH50M01	3699	3700	112
192	BaSD24E13	3701	3702	113.3
193	baal5j24	3703	3704	116.7
194	bah15h18	3705	3706	117.8
194	bast62E0610	3707	3708	117.8
196	bah28k24	3709	3710	118.9
196	bah47c11	3711	3712	118.9
196	BaSD26M15	3713	3714	118.9
196	bah60o02	3715	3716	118.9
196	BaH50G06	3717	3718	118.9

TABLE 5-5

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
201	bast15G0913	3719	3720	120
201	bah62n12	3721	3722	120

TABLE 5-5-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
201	baal10n23	3723	3724	120
204	bags20c12	3725	3726	121.1
205	basd16f13	3727	3728	122.2
206	baak21h06	3729	3730	124.2
207	bags3b05	3731	3732	125.2
208	bags22p08	3733	3734	128.3
208	BaH23N06	3735	3736	128.3
208	bags29c08	3737	3738	128.3
211	BaGS11O23	3739	3740	129.4
211	baak16a11	3741	3742	129.4
213	baak15n22	3743	3744	131.6
213	BaAL18J13	3745	3746	131.6
213	bah15m02	3747	3748	131.6
213	baak38d20	3749	3750	131.6
213	BaSD12L21	3751	3752	131.6
213	kr68B1103	3753	3754	131.6
219	BaAK28L22	3755	3756	133.7
219	bags15b10	3757	3758	133.7
219	bags20h21	3759	3760	133.7
219	BaAK29K06	3761	3762	133.7
219	bags21l05	3763	3764	133.7
219	bah56j14	3765	3766	133.7
219	basd15e02	3767	3768	133.7
226	bags3j24	3769	3770	134.8
226	bags38m08	3771	3772	134.8
228	bah11m18	3773	3774	136.9
228	bags35g06	3775	3776	136.9
228	bags37b01	3777	3778	136.9
228	BaAL19F02	3779	3780	136.9
232	BaAL4D09	3781	3782	138
232	BaAK30H10	3783	3784	138
234	bags38b16	3785	3786	142.3
235	bags27f15	3787	3788	143.7
236	bags10k14	3789	3790	146.6
236	bags22f10	3791	3792	146.6
236	baak38n21	3793	3794	146.6
236	baak30e05	3795	3796	146.6
236	bastl04A0101	3797	3798	146.6
236	BaAK28P18	3799	3800	146.6
236	BaGS34E01	3801	3802	146.6
236	BaH54H04	3803	3804	146.6
236	bah13o19	3805	3806	146.6
245	BaAK29B22	3807	3808	147.7
245	BaAK27C16	3809	3810	147.7
245	BaGS22H13	3811	3812	147.7
245	BaSD27A15	3813	3814	147.7
249	BaAK27E07	3815	3816	151
250	BaGS9N02	3817	3818	152.1

TABLE 5-6

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
251	Bmag223	—	—	153.2
252	bags28o18	3819	3820	154.3
253	baal25b05	3821	3822	155.4
253	bastl30A0202	3823	3824	155.4
253	bags37d20	3825	3826	155.4
256	BaGS22K12	3827	3828	155.8
257	BaAK13G12	3829	3830	156.1
258	basd2a02	3831	3832	156.5
258	BaGS31L06	3833	3834	156.5
258	bags17j17	3835	3836	156.5
258	baal12j15	3837	3838	156.5
258	BaAK19H14	3839	3840	156.5
263	BaH34J11	3841	3842	159.8

TABLE 5-6-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
263	BaGS30I11	3843	3844	159.8
265	BaH49L06	3845	3846	161
265	baal18m24	3847	3848	161
267	baak15l06	3849	3850	163.2
267	basd18o14	3851	3852	163.2
269	bags24p22	3853	3854	164.3
269	BaAL37A09	3855	3856	164.3
269	bags5l01	3857	3858	164.3
269	BaAK12P03	3859	3860	164.3
273	baak21f10	3861	3862	164.5
274	bastl30E0410	3863	3864	164.7
274	kr25C0206	3865	3866	164.7
276	baak4j01	3867	3868	166.2
276	BaAK27E01	3869	3870	166.2
278	bah54n06	3871	3872	167.3
278	bags19p05	3873	3874	167.3
278	bast22F0311	3875	3876	167.3
281	basd1m04	3877	3878	170.6
282	bags35i04	3879	3880	171.7
282	baak41d01	3881	3882	171.7
282	baal19m08	3883	3884	171.7
282	baak13j10	3885	3886	171.7
282	baak44h11	3887	3888	171.7
287	baal19j09	3889	3890	172.2
288	baet37C1105	3891	3892	172.7
288	baak12d06	3893	3894	172.7
288	basd23f10	3895	3896	172.7
288	BaH41P07	3897	3898	172.7
292	baak1g13	3899	3900	173.8
293	basd14b04	3901	3902	174.9
294	bags22l14	3903	3904	177.1
294	bast26E1210	3905	3906	177.1
296	baet25F0911	3907	3908	180
296	BaAK32N13	3909	3910	180
298	BaSD2C09	3911	3912	180.3
299	BaGS31P01	3913	3914	180.7
299	baak30m11	3915	3916	180.7

TABLE 5-7

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
301	BaAK4N16	3917	3918	181.2
302	bastl46F1012	3919	3920	181.7
302	bags3e06	3921	3922	181.7
302	bags31o10	3923	3924	181.7
305	bags33j12	3925	3926	182.8
306	BaGS30N07	3927	3928	183.8
307	BaH37I18	3929	3930	188.1
307	baak46p24	3931	3932	188.1
309	baak46o19	3933	3934	188.7
310	basd3c19	3935	3936	189.2
310	bags30f01	3937	3938	189.2
310	BaGS20F10	3939	3940	189.2
313	BaGS32D08	3941	3942	191.4
314	BaAK23M23	3943	3944	193.6
314	bah21a16	3945	3946	193.6
314	BaAL3M08	3947	3948	193.6
314	BaAK21I09	3949	3950	193.6
314	baet33A0301	3951	3952	193.6
319	baak24k02	3953	3954	195.7
319	bah33p03	3955	3956	195.7
319	bast75D1208	3957	3958	195.7
322	BaSD12K20	3959	3960	196
323	bags34f06	3961	3962	196.4
324	bags6f09	3963	3964	196.8
324	bags7b10	3965	3966	196.8

TABLE 5-7-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
326	BaGS25H01	3967	3968	199
326	baak33m08	3969	3970	199
326	bags37e01	3971	3972	199
326	bags32n20	3973	3974	199
326	BaH47A11	3975	3976	199
326	BaGS24M06	3977	3978	199
332	bags22m23	3979	3980	200.1
332	basd18d18	3981	3982	200.1
332	bastl06F0212	3983	3984	200.1
332	BaH49O16	3985	3986	200.1
332	bags39e22	3987	3988	200.1
332	BaH38N06	3989	3990	200.1
332	BaH56P16	3991	3992	200.1
339	BaSD13O13	3993	3994	200.3
340	bags19i06	3995	3996	201.4
340	bah34f11	3997	3998	201.4
340	bags37g04	3999	4000	201.4
343	basd11k21	4001	4002	201.7
344	HvLOX	—	—	202.8
345	baak43o03	4003	4004	203.6
345	BaAL4J21	4005	4006	203.6
345	BaH51J22	4007	4008	203.6
345	bah58l03	4009	4010	203.6
345	BaGS21M18	4011	4012	203.6
345	BaGS31K06	4013	4014	203.6

TABLE 5-8

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
351	baal4o01*VRN2(sh2)	4015	4016	204
352	BaAK24H19	4017	4018	204.6
352	BaGS17D21	4019	4020	204.6
352	bah39o04	4021	4022	204.6
352	baak46e06	4023	4024	204.6
352	basd13j03	4025	4026	204.6
357	bast14H0416	4027	4028	206.8
357	BaSD18I03	4029	4030	206.8
357	bastl44H1115	4031	4032	206.8
357	bast34D0608	4033	4034	206.8
357	BaGS30F06	4035	4036	206.8
357	bags21k16	4037	4038	206.8
363	BaH48G01	4039	4040	207.9
363	bags39a24	4041	4042	207.9
363	bags15i03	4043	4044	207.9
363	bags23f02	4045	4046	207.9
363	bastl40E1010	4047	4048	207.9
368	bags17p10	4049	4050	211
369	BaH57L13	4051	4052	212.6
369	bags10e22	4053	4054	212.6
371	bags4p07	4055	4056	213.6
371	bah63a08	4057	4058	213.6
373	baak12f13	4059	4060	214.7
373	bah56j15	4061	4062	214.7
373	bah15e16	4063	4064	214.7
373	BaH50F21	4065	4066	214.7
373	basd27o16	4067	4068	214.7
378	kr66G0713	4069	4070	216.2
378	baak46c17	4071	4072	216.2
380	baet19C1206	4073	4074	216.7
380	bags34e15	4075	4076	216.7
380	baal4d18	4077	4078	216.7
380	bah13b13	4079	4080	216.7
384	BaGS26G20	4081	4082	217.2
385	BaGS28C14	4083	4084	217.7
385	kr61G1214	4085	4086	217.7
385	bags9g08	4087	4088	217.7

TABLE 5-8-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
385	bags5p01	4089	4090	217.7
385	BaAL4D04	4091	4092	217.7
385	bah26p09	4093	4094	217.7
385	bah11e02	4095	4096	217.7
385	MWG2077	—	—	217.7
385	bast41F0311	4097	4098	217.7
385	bastl54D0307	4099	4100	217.7
395	BaSD3F21	4101	4102	219.9
395	bah56f18	4103	4104	219.9
397	BaH41C21	4105	4106	221
397	basd19g21	4107	4108	221
399	kr33H0816	4109	4110	223.2
399	BaH38F16	4111	4112	223.2

TABLE 5-9

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
399	BaGS21P09	4113	4114	223.2
402	BaGS36M20	4115	4116	224.2
403	bags21m10	4117	4118	228.5
403	BaAK14G11	4119	4120	228.5
405	BaGS30L20	4121	4122	230.7
406	basd21g02	4123	4124	231.8
406	bah22m17	4125	4126	231.8
406	BaGS9H19	4127	4128	231.8
409	bah26m24	4129	4130	232.9
410	BaH56D01	4131	4132	234
411	bah53i08	4133	4134	237.1
411	bags21d10	4135	4136	237.1
411	bags9a01	4137	4138	237.1
414	baal9m13	4139	4140	238.3
414	baak20m05	4141	4142	238.3
416	baak21k16	4143	4144	238.6
417	bags34d17	4145	4146	239.4
418	baal40k24	4147	4148	240.5
419	BaGS19O14	4149	4150	243.4
419	baak35m03	4151	4152	243.4
419	baak33o23	4153	4154	243.4
419	kr57F1012	4155	4156	243.4
419	bah53i05	4157	4158	243.4
419	bags22l16	4159	4160	243.4
419	baet43C0505	4161	4162	243.4
419	BaH33H02	4163	4164	243.4
419	bastl22E1010	4165	4166	243.4
428	BaH53N24	4167	4168	244.6
429	baal8e24	4169	4170	245.9
429	BaH62H21	4171	4172	245.9
431	BaH42K01	4173	4174	250.7
432	basd26p09	4175	4176	252.1
433	bags4p18	4177	4178	253.1
433	BaH60H14	4179	4180	253.1
433	bast70D1107	4181	4182	253.1
433	bah26i23	4183	4184	253.1
437	baal39g02	4185	4186	253.6
437	bags10e02	4187	4188	253.6
439	bags22c13	4189	4190	255.1
439	bags35n03	4191	4192	255.1
439	BaAL16H03	4193	4194	255.1
442	BaAL15N07	4195	4196	255.8
443	bags18o20	4197	4198	258
444	bags37g12	4199	4200	258.4
445	bags22l12	4201	4202	259.5
446	BaAK44K01	4203	4204	260.6
446	BaAK31G07	4205	4206	260.6
446	bah53n21	4207	4208	260.6

TABLE 5-9-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
449	BaGS19C02	4209	4210	263.8
450	BaH52E20	4211	4212	265.9

TABLE 5-10

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
450	BaAL4N05	4213	4214	265.9
450	bags7p06	4215	4216	265.9
453	bast70C0905	4217	4218	270.9
453	BaSD15J01	4219	4220	270.9
455	BaH56H18	4221	4222	272.9
455	BaGS4N04	4223	4224	272.9
455	bags31o13	4225	4226	272.9
455	kr29D0107	4227	4228	272.9
459	BaAK21A15	4229	4230	274
459	bags7h14	4231	4232	274
459	basd26b20	4233	4234	274
459	baal1g06	4235	4236	274
459	bags5n14	4237	4238	274
464	BaAK34H17	4239	4240	274.5
465	bastl32H0816	4241	4242	275
465	basd18m12	4243	4244	275
465	baak31p06	4245	4246	275
465	bah52i03	4247	4248	275
469	BaAK33K05	4249	4250	276.1
469	BaAK44J08	4251	4252	276.1
469	baak18g16	4253	4254	276.1
469	baak11a11	4255	4256	276.1
473	BaH25B20	4257	4258	279.3
473	bast12G0113	4259	4260	279.3
473	baal9n02	4261	4262	279.3
473	bags20f08	4263	4264	279.3
477	BaGS9C24	4265	4266	281.5
477	BaGS22O02	4267	4268	281.5
479	baak13k16	4269	4270	282.6
479	MWG2249	—	—	282.6
479	bah41b17	4271	4272	282.6
482	bah63m11	4273	4274	283.7
482	BaGS28P07	4275	4276	283.7
482	bags1h15	4277	4278	283.7
482	kr26H0515	4279	4280	283.7
482	bags6n05	4281	4282	283.7
487	BaH24P17	4283	4284	284.1
488	bast03D0408	4285	4286	284.8
488	BaAL17G06	4287	4288	284.8
488	BaH32G11	4289	4290	284.8
488	BaGS4P17	4291	4292	284.8
488	baal31o21	4293	4294	284.8
488	BaGS36A16	4295	4296	284.8
488	bags4d11	4297	4298	284.8
488	basd13n18	4299	4300	284.8
496	basd0a08	4301	4302	285.2
497	BaGS32P24	4303	4304	285.9
498	baak12i02	4305	4306	288.2
498	kr06H0315	4307	4308	288.2
498	BaAL26B09	4309	4310	288.2

TABLE 5-11

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
498	kr32C11O5	4311	4312	288.2
498	BaH53B15	4313	4314	288.2

TABLE 5-11-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
503	bags13hO4	4315	4316	291.4
504	baal15i11	4317	4318	295.7
505	bags1m19	4319	4320	307.4
506	HVM6	—	—	331.7

[0070] As shown in Table 6-1 to Table 6-7, the chromosomal order in barley 6H chromosome (distance from the short arm end of 6H chromosome) has been specified for 321 clones including the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 4321 through SEQ ID NO: 4962. The chromosomal order in barley 6H chromosome has also been specified for 6 known clones (MWG620, Bmac316, MWG2218, HVM31, Bmac40, and MWG897).

TABLE 6-1

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
1	MWG620	—	—	0
2	basd14f03	4321	4322	12.1
2	BaH30E11	4323	4324	12.1
4	BaH59J05	4325	4326	12.6
5	BaAL39O22	4327	4328	13.1
6	baal16j24	4329	4330	14.2
7	BaAL30P12	4331	4332	15.3
7	BaGS21H12	4333	4334	15.3
9	BaAK15J05	4335	4336	16.4
9	BaGS9G15	4337	4338	16.4
9	BaAK41J04	4339	4340	16.4
12	baak43j24	4341	4342	16.9
13	bah26n19	4343	4344	17.4
13	Bmac316	—	—	17.4
13	bags38a05	4345	4346	17.4
13	BaH43D06	4347	4348	17.4
17	bags9j07	4349	4350	19.6
17	baak31p11	4351	4352	19.6
19	BaGS17P19	4353	4354	20.7
20	baal32j05	4355	4356	23.6
20	baal16l16	4357	4358	23.6
22	baal6a11	4359	4360	24.4
22	bah55p06	4361	4362	24.4
22	bags8f03	4363	4364	24.4
22	bags3m02	4365	4366	24.4
22	BaAL36L08	4367	4368	24.4
22	baet19E0309	4369	4370	24.4
22	BaSD18J06	4371	4372	24.4
29	bast48D0307	4373	4374	28.5
30	kr55D0707	4375	4376	29.8
30	BaAL4B09	4377	4378	29.8
30	bags32f21	4379	4380	29.8
33	BaGS24F04	4381	4382	31.4
33	BaGS10G07	4383	4384	31.4
35	BaGS26P07	4385	4386	31.9
35	bags12f11	4387	4388	31.9
35	MWG2218	—	—	31.9
35	BaH63O04	4389	4390	31.9
39	BaGS26D21	4391	4392	32.3
40	bags20o14	4393	4394	33
41	baak36d08	4395	4396	34.1
41	bast75H0616	4397	4398	34.1
41	basd16g17	4399	4400	34.1
41	baal4k16	4401	4402	34.1
41	bags32b14	4403	4404	34.1
46	baal4d01	4405	4406	35.2
46	baal7d23	4407	4408	35.2

TABLE 6-1-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
46	BaH62C20	4409	4410	35.2
49	BaH21K13	4411	4412	36.3
49	BaAK14J02	4413	4414	36.3

TABLE 6-2

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
51	bah22c08	4415	4416	38.1
51	baak25d07	4417	4418	38.1
53	BaAK29M05	4419	4420	40.3
54	BaGS31I08	4421	4422	44.7
54	bah12n12	4423	4424	44.7
54	baal30o06	4425	4426	44.7
54	baak13n14	4427	4428	44.7
54	bags7a09	4429	4430	44.7
54	baak32l04	4431	4432	44.7
60	bah31o16	4433	4434	45.8
60	BaAL7C19	4435	4436	45.8
62	BaAK23F04	4437	4438	46.1
63	kr40D0707	4439	4440	46.8
64	basd0g08	4441	4442	47.9
64	BaAL30H03	4443	4444	47.9
66	BaAL21B21	4445	4446	50.9
66	BaGS30E05	4447	4448	50.9
68	BaAK13G04	4449	4450	52.9
69	BaGS27N11	4451	4452	55.8
70	BaGS9A04	4453	4454	62.5
71	BaAK23M11	4455	4456	68.4
72	basd3f22	4457	4458	70.5
73	baak41p21	4459	4460	71.6
73	BaAK41K07	4461	4462	71.6
73	BaH53I11	4463	4464	71.6
73	baak26i14	4465	4466	71.6
73	BaAL18N03	4467	4468	71.6
73	baak40c08	4469	4470	71.6
73	bags17l19	4471	4472	71.6
73	BaSD25N02	4473	4474	71.6
81	BaAK37E04	4475	4476	73.8
82	baal33h17	4477	4478	75.4
83	bags20d08	4479	4480	77
84	BaGS4J01	4481	4482	78.1
84	bah48o03	4483	4484	78.1
84	bastl31A0901	4485	4486	78.1
84	bah20k22	4487	4488	78.1
84	BaGS15J17	4489	4490	78.1
84	BaAK17I01	4491	4492	78.1
84	BaAK30F08	4493	4494	78.1
84	bah47a17	4495	4496	78.1
84	basd15e10	4497	4498	78.1
93	BaH56C11	4499	4500	79.2
93	BaH18C17	4501	4502	79.2
93	BaGS20G24	4503	4504	79.2
96	bags19g17	4505	4506	81.5
97	BaAK21L02	4507	4508	84.9
98	BaH52H21	4509	4510	89.2
99	bags9l13	4511	4512	90.2
99	BaSD18C12	4513	4514	90.2

TABLE 6-3

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
101	baak23k07	4515	4516	91.1
102	bags16j16	4517	4518	91.9
103	BaSD15O17	4519	4520	93.1
104	baak12i20	4521	4522	93.6
104	BaAK3M04	4523	4524	93.6
104	BaGS4N23	4525	4526	93.6
104	baak34k24	4527	4528	93.6
104	bah15n23	4529	4530	93.6
104	baak45i02	4531	4532	93.6
104	basd13i08	4533	4534	93.6
111	BaSD17P01	4535	4536	94.7
111	HVM31	—	—	94.7
111	baak13d19	4537	4538	94.7
111	baal3h14	4539	4540	94.7
111	bags33j18	4541	4542	94.7
111	BaH45B01	4543	4544	94.7
111	baak21n07	4545	4546	94.7
111	BaH36H18	4547	4548	94.7
119	BaAL23O14	4549	4550	95.8
120	bah53f05	4551	4552	99.1
121	baak12d02	4553	4554	100.2
122	bags11h12	4555	4556	101.8
122	baet01F1212	4557	4558	101.8
124	baak17l11	4559	4560	102.3
124	basd20e17	4561	4562	102.3
124	bah29p24	4563	4564	102.3
124	bags30o05	4565	4566	102.3
124	kr68D0208	4567	4568	102.3
124	bags37l11	4569	4570	102.3
124	baal4d14	4571	4572	102.3
124	BaH58I23	4573	4574	102.3
124	bags39l04	4575	4576	102.3
124	baak29i13	4577	4578	102.3
124	bags20p18	4579	4580	102.3
124	BaAK12J13	4581	4582	102.3
124	BaH13K17	4583	4584	102.3
124	bah60p09	4585	4586	102.3
124	BaH27N11	4587	4588	102.3
124	BaGS34D11	4589	4590	102.3
124	BaGS39G07	4591	4592	102.3
124	bah22o14	4593	4594	102.3
124	bah14l20	4595	4596	102.3
124	bah42p22	4597	4598	102.3
124	BaAK21G03	4599	4600	102.3
124	BaAL35D24	4601	4602	102.3
124	baak45h14	4603	4604	102.3
124	bags28o05	4605	4606	102.3
124	BaAK31P07	4607	4608	102.3
124	bah36c06	4609	4610	102.3
124	BaGS37H24	4611	4612	102.3

TABLE 6-4

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
124	bast65B0303	4613	4614	102.3
124	BaH51A22	4615	4616	102.3
153	BaGS39K23	4617	4618	103.4
153	BaSD14O12	4619	4620	103.4
153	BaH57F12	4621	4622	103.4
153	BaGS32G02	4623	4624	103.4
153	BaAL40N06	4625	4626	103.4
153	bah11b14	4627	4628	103.4
153	bah15j14	4629	4630	103.4
153	bast21C1105	4631	4632	103.4
153	bags29f03	4633	4634	103.4
153	BaAK46B16	4635	4636	103.4

TABLE 6-4-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
153	basd11p22	4637	4638	103.4
153	baal16h16	4639	4640	103.4
165	BaSD21L07	4641	4642	104.9
165	BaH42D07	4643	4644	104.9
167	BaGS23K24	4645	4646	106.4
167	BaAK24L01	4647	4648	106.4
167	BaAL11H22	4649	4650	106.4
167	BaAL13O24	4651	4652	106.4
167	BaAL6M22	4653	4654	106.4
167	BaH56I06	4655	4656	106.4
167	BaSD19A18	4657	4658	106.4
174	BaSD20P03	4659	4660	108.2
174	BaH19B13	4661	4662	108.2
176	kr59H0416	4663	4664	110.7
177	BaGS14A02	4665	4666	112.2
177	BaH34P05	4667	4668	112.2
177	bah61o16	4669	4670	112.2
177	BaH24N07	4671	4672	112.2
177	BaAL20M22	4673	4674	112.2
177	BaAL11H20	4675	4676	112.2
177	bah54b04	4677	4678	112.2
177	BaAK14H23	4679	4680	112.2
177	BaSD20M23	4681	4682	112.2
177	BaAL15B12	4683	4684	112.2
177	baal15d09	4685	4686	112.2
177	baak39n20	4687	4688	112.2
177	BaH43N16	4689	4690	112.2
177	bags39h18	4691	4692	112.2
177	BaAL3L23	4693	4694	112.2
192	basd22c03	4695	4696	115.6
193	bast55G0913	4697	4698	117.9
193	kr47F0511	4699	4700	117.9
195	bah15l24	4701	4702	118.4
196	bast77A0402	4703	4704	118.9
196	BaH58F04	4705	4706	118.9
196	BaAK30L09	4707	4708	118.9
196	kr39G1113	4709	4710	118.9
196	baak1c16	4711	4712	118.9

TABLE 6-5

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
196	basd20e05	4713	4714	118.9
196	BaAK12F18	4715	4716	118.9
196	BaH50L11	4717	4718	118.9
196	bast50G0814	4719	4720	118.9
196	bast70D0107	4721	4722	118.9
196	baal17d05	4723	4724	118.9
196	baak46g03	4725	4726	118.9
196	bah63m17	4727	4728	118.9
209	BaH15L15	4729	4730	120
209	BaGS19N01	4731	4732	120
209	BaAK32P07	4733	4734	120
212	bags14l13	4735	4736	121.1
213	bags37o24	4737	4738	121.7
214	baal5e24	4739	4740	122.8
215	BaH46B06	4741	4742	124.5
215	bags11a16	4743	4744	124.5
215	baal27m03	4745	4746	124.5
215	BaAK1C18	4747	4748	124.5
215	BaAK38H16	4749	4750	124.5
215	BaGS37K02	4751	4752	124.5
221	bah28a10	4753	4754	125.6
221	bah27c03	4755	4756	125.6
221	BaH52B11	4757	4758	125.6
224	bah27f05	4759	4760	127.8

TABLE 6-5-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
224	bags37g15	4761	4762	127.8
224	bah59c10	4763	4764	127.8
224	bags38j06	4765	4766	127.8
224	basd14e01	4767	4768	127.8
224	BaGS24L06	4769	4770	127.8
224	bags17b02	4771	4772	127.8
224	BaH54L03	4773	4774	127.8
224	BaAK21J17	4775	4776	127.8
233	BaGS23G08	4777	4778	128.9
233	basd18e06	4779	4780	128.9
233	baak19o02	4781	4782	128.9
233	basd2o16	4783	4784	128.9
237	baak16e08	4785	4786	130
237	bags18h01	4787	4788	130
239	BaGS4L20	4789	4790	133.4
240	BaAL2M19	4791	4792	135.8
241	BaH36F15	4793	4794	139.1
242	bah58l07	4795	4796	140.2
243	baet29C0406	4797	4798	141.3
243	BaAK35B04	4799	4800	141.3
243	bags34k13	4801	4802	141.3
246	baal29i08	4803	4804	142.1
246	baak11p10	4805	4806	142.1
248	BaH30J08	4807	4808	145.1
249	bags4e12	4809	4810	147.3
250	bastl05C1206	4811	4812	148.4

TABLE 6-6

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
250	bast22G0313	4813	4814	148.4
252	basd24b08	4815	4816	149.5
252	bastl16C0206	4817	4818	149.5
252	bags33n21	4819	4820	149.5
255	baak33c11	4821	4822	151.7
255	baal13o10	4823	4824	151.7
257	BaH36P06	4825	4826	154.9
258	basd12l01	4827	4828	157.1
259	baet25H0115	4829	4830	158.2
259	bags15d14	4831	4832	158.2
259	BaGS37E09	4833	4834	158.2
259	BaAK29I15	4835	4836	158.2
259	BaAK18I01	4837	4838	158.2
264	bast62B0404	4839	4840	160.4
265	bah25l03	4841	4842	163.9
266	BaGS19I11	4843	4844	167.2
266	baal1n11	4845	4846	167.2
268	baak16l07	4847	4848	167.6
268	BaGS18P04	4849	4850	167.6
270	bags19e06	4851	4852	168.9
270	baak35n07	4853	4854	168.9
272	BaAK29K23	4855	4856	173
272	baal13c18	4857	4858	173
272	bags7d17	4859	4860	173
275	bags20j08	4861	4862	174.1
275	baal9c20	4863	4864	174.1
277	bags20l05	4865	4866	175.2
278	bah63k05	4867	4868	176.3
279	BaAK14C17	4869	4870	178.5
280	Bmac40	—	—	179.6
280	baal15i23	4871	4872	179.6
282	BaAK1N06	4873	4874	181.7
282	bags38d10	4875	4876	181.7
282	BaAK19J15	4877	4878	181.7
285	BaH50L14	4879	4880	182.8
285	BaGS37E11	4881	4882	182.8

TABLE 6-6-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
287	BaSD27E20	4883	4884	183
288	basd17f18	4885	4886	184.1
289	baal32m04	4887	4888	188.5
290	BaSD12L12	4889	4890	191.7
291	BaGS37D24	4891	4892	194
291	BaGS9K15	4893	4894	194
293	BaGS33L03	4895	4896	196
293	BaAK24G10	4897	4898	196
295	kr58F0511	4899	4900	196.5
296	BaH50F16	4901	4902	197
296	basd17d11	4903	4904	197
298	BaH37P24	4905	4906	198.1
298	bah47l21	4907	4908	198.1
298	baet45C1105	4909	4910	198.1

TABLE 6-7

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
301	baak39o18	4911	4912	199.2
301	bags20p12	4913	4914	199.2
301	bags38f23	4915	4916	199.2
304	baak14b08	4917	4918	201.4
304	bah54n10	4919	4920	201.4
306	bags3k09	4921	4922	202.5
307	bags34p08	4923	4924	203.6
308	baal1e06	4925	4926	204.7
308	baak34p14	4927	4928	204.7
308	baak14k12	4929	4930	204.7
308	BaSD13G17	4931	4932	204.7
308	MWG897	—	—	204.7
308	bags27h05	4933	4934	204.7
308	basd15m11	4935	4936	204.7
308	BaH28G09	4937	4938	204.7
308	bags21b06	4939	4940	204.7
308	basd12g17	4941	4942	204.7
318	BaH18F07	4943	4944	205
319	BaH44A23	4945	4946	205.3
320	bags3d07	4947	4948	205.6
321	BaAL6A21	4949	4950	205.9
321	BaAK24E07	4951	4952	205.9
321	BaAL29L09	4953	4954	205.9
321	kr66D1107	4955	4956	205.9
321	bastl47C0606	4957	4958	205.9
321	BaH50M03	4959	4960	205.9
327	basd27k17	4961	4962	207.3

[0071] As shown in Table 7-1 to Table 7-9, the chromosomal order in barley 7H chromosome (distance from the short arm end of 7H chromosome) has been specified for 409 clones including the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 4963 through SEQ ID NO: 5780. The chromosomal order in barley 7H chromosome has also been specified for 16 known clones (HVM4, HVCMA, cMWG704, MWG511, Bmag359, MWG2031, KT3, KT9, MWG975, EBmac764, Bmac0064, Bmag120, Bmac156, HVM49, MWG2062, and HVM5).

TABLE 7-1

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
1	basd2p19	4963	4964	0
2	BaAK38B18	4965	4966	4.7
3	bah42i06	4967	4968	6.6
3	bags6f02	4969	4970	6.6
5	BaAK39J07	4971	4972	7.2
5	BaAK1L23	4973	4974	7.2
5	baak17e10	4975	4976	7.2
5	BaH50H08	4977	4978	7.2
5	baal17e10	4979	4980	7.2
5	BaSD17C05	4981	4982	7.2
11	BaGS14P02	4983	4984	8.3
11	bastl42H0115	4985	4986	8.3
11	BaAK19C08	4987	4988	8.3
11	bastl40H1115	4989	4990	8.3
15	bags12l21	4991	4992	9.4
15	baak12j24	4993	4994	9.4
15	bags14d22	4995	4996	9.4
15	BaAK21P12	4997	4998	9.4
15	baal6b02	4999	5000	9.4
15	baak29f13	5001	5002	9.4
21	bast79C0406	5003	5004	11.3
22	BaH45M08	5005	5006	12.4
23	kr28A0301	5007	5008	16.4
23	bags19e04	5009	5010	16.4
25	BaH28L07	5011	5012	18.6
26	baak21m18	5013	5014	20.9
26	baak21l22	5015	5016	20.9
28	basd15h01	5017	5018	25.2
28	BaH19O11	5019	5020	25.2
28	BaH59A20	5021	5022	25.2
31	bags39l05	5023	5024	27.3
31	BaAK31N06	5025	5026	27.3
33	BaH58P03	5027	5028	28.4
34	bags29c18	5029	5030	29.5
35	BaAL4O04	5031	5032	30.6
35	bags37n23	5033	5034	30.6
35	BaAL39N03	5035	5036	30.6
38	BaAK14C23	5037	5038	31.7
38	kr61A1101	5039	5040	31.7
38	BaH42J17	5041	5042	31.7
41	BaH58H08	5043	5044	39.2
42	bast78A0202	5045	5046	40.4
43	BaGS21E20	5047	5048	42.5
43	bags22k18	5049	5050	42.5
45	BaGS33H15	5051	5052	45.7
45	HVM4	—	—	45.7
47	BaSD18O16	5053	5054	47.9
47	baak22j11	5055	5056	47.9
49	BaAK20K04	5057	5058	50.4
50	bags29l11	5059	5060	55.2

TABLE 7-2

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
51	BaAK17G18	5061	5062	60.3
52	baak14o13	5063	5064	61.7
53	baal8d17	5065	5066	63.2
54	BaAK37P20	5067	5068	64.2
55	bags28k04	5069	5070	71.5
56	bah34b22	5071	5072	73.8
57	BaGS37M03	5073	5074	78.3
58	BaGS18C14	5075	5076	79.5
59	bast23G0214	5077	5078	80.6
59	bah47p02	5079	5080	80.6
61	baak42a24	5081	5082	81.7
61	baak16f06	5083	5084	81.7

TABLE 7-2-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
61	bah11m12	5085	5086	81.7
64	kr66H0216	5087	5088	84.9
64	BaGS23D15	5089	5090	84.9
64	baal22c17	5091	5092	84.9
67	baak33d06	5093	5094	86
67	bags34l17	5095	5096	86
67	BaGS25G03	5097	5098	86
67	bah14j16	5099	5100	86
67	bah34a23	5101	5102	86
67	BaAK21B17	5103	5104	86
67	bast42C0406	5105	5106	86
74	baak21m13	5107	5108	87.3
75	baet45H0115	5109	5110	87.7
76	BaH38E01	5111	5112	88.1
76	bast03G0313	5113	5114	88.1
78	baak38p18	5115	5116	89.5
79	basd18g06	5117	5118	90.6
80	baak40i22	5119	5120	92
80	baal2n12	5121	5122	92
82	BaSD3C24	5123	5124	94.1
83	BaAK46M07	5125	5126	96.3
84	BaGS17N04	5127	5128	99.6
85	bags12d09	5129	5130	100.7
85	basd20c08	5131	5132	100.7
87	bags17i04	5133	5134	101.7
87	baak15p03	5135	5136	101.7
89	baak24b20	5137	5138	104.9
89	baal18g11	5139	5140	104.9
89	baal40b06	5141	5142	104.9
89	baak40g02	5143	5144	104.9
93	baal1m11	5145	5146	106.1
94	BaH26B16	5147	5148	107.9
94	baal5n08	5149	5150	107.9
96	BaSD27F05	5151	5152	109.5
96	bags9c08	5153	5154	109.5
96	baak3c01	5155	5156	109.5
99	basd1j22	5157	5158	110.6
99	BaH23N03	5159	5160	110.6

TABLE 7-3

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
99	bast46D0808	5161	5162	110.6
99	bast22A0802	5163	5164	110.6
99	bast34D0808	5165	5166	110.6
104	bast48E0509	5167	5168	114.9
104	bast26F1012	5169	5170	114.9
106	baal30e07	5171	5172	115.5
107	bags23n06	5173	5174	116.1
108	BaGS18I05	5175	5176	116.6
109	BaH52L11	5177	5178	116.8
110	baal18b16	5179	5180	117
111	bags1a17	5181	5182	118.1
111	HVCMA	—	—	118.1
111	bags8o06	5183	5184	118.1
111	baak46e14	5185	5186	118.1
115	BaGS38N08	5187	5188	118.6
115	BaH49P17	5189	5190	118.6
117	bah60l22	5191	5192	120.2
117	bags21m22	5193	5194	120.2
117	BaH54E07	5195	5196	120.2
120	BaAK39A20	5197	5198	121.3
121	bags21d11	5199	5200	123.5
122	kr39H0816	5201	5202	125.6
123	baet32B1103	5203	5204	131.1
124	BaAK31O16	5205	5206	132.1

TABLE 7-3-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
124	bags39l20	5207	5208	132.1
124	BaGS15L12	5209	5210	132.1
127	kr67D0208	5211	5212	134.3
128	BaAK1H16	5213	5214	135.4
128	BaH26F10	5215	5216	135.4
130	bags14n02	5217	5218	135.9
131	bah36f01	5219	5220	136.4
132	bast79F0711	5221	5222	137.5
132	BaGS29G21	5223	5224	137.5
134	bast79D1107	5225	5226	139.6
134	BaGS26O20	5227	5228	139.6
134	bags11h08	5229	5230	139.6
134	bags22h11	5231	5232	139.6
134	baet19D0608	5233	5234	139.6
139	bags23a14	5235	5236	140.7
139	cMWG704	—	—	140.7
139	bah62d14	5237	5238	140.7
142	BaGS37C09	5239	5240	142.6
142	bags20a01	5241	5242	142.6
144	bah53m11	5243	5244	144.5
144	BaGS26L01	5245	5246	144.5
144	bags21p23	5247	5248	144.5
144	BaAK24B01	5249	5250	144.5
144	BaAK13L03	5251	5252	144.5
149	MWG511	—	—	145.6
149	bastl56C0105	5253	5254	145.6

TABLE 7-4

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
149	basd20j22	5255	5256	145.6
149	bags28d11	5257	5258	145.6
153	BaGS4I11	5259	5260	146.7
153	BaH52G15	5261	5262	146.7
153	baak11d12	5263	5264	146.7
153	BaH42A07	5265	5266	146.7
157	BaGS38F01	5267	5268	147.2
158	BaAK32I05	5269	5270	147.7
158	bah60f18	5271	5272	147.7
160	baal2n10	5273	5274	148.8
161	BaAK14F01	5275	5276	149.9
161	bah57o01	5277	5278	149.9
161	basd12f05	5279	5280	149.9
161	bah58e21	5281	5282	149.9
161	bags1d07	5283	5284	149.9
161	BaH23J15	5285	5286	149.9
161	baak1p09	5287	5288	149.9
168	BaAK32C23	5289	5290	151
168	baal9e06	5291	5292	151
168	baal18g23	5293	5294	151
168	bastl47E0309	5295	5296	151
168	baak30o08	5297	5298	151
168	baet44C0606	5299	5300	151
174	bags39g18	5301	5302	152.1
174	BaH50P14	5303	5304	152.1
176	bags38m06	5305	5306	152.6
177	baal33e12	5307	5308	153.2
177	bags3i04	5309	5310	153.2
179	BaAL1A11	5311	5312	153.7
179	BaSD2M23	5313	5314	153.7
181	Bmag359	—	—	155.3
181	BaAK23L23	5315	5316	155.3
181	bags7a23	5317	5318	155.3
181	bah56l04	5319	5320	155.3
185	basd12k23	5321	5322	156.4
185	bast22C0105	5323	5324	156.4

TABLE 7-4-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
185	BaGS38H20	5325	5326	156.4
185	bah61p21	5327	5328	156.4
185	basd11h13	5329	5330	156.4
185	BaAL41J12	5331	5332	156.4
185	baal0f04	5333	5334	156.4
185	kr18E0810	5335	5336	156.4
185	BaH15J07	5337	5338	156.4
185	BaAL6G08	5339	5340	156.4
185	BaGS24F02	5341	5342	156.4
185	baal19m12	5343	5344	156.4
185	bah34h16	5345	5346	156.4
185	baak2e06	5347	5348	156.4
185	bast10C0406	5349	5350	156.4
185	baak12l16	5351	5352	156.4

TABLE 7-5

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
185	baak29d01	5353	5354	156.4
185	BaAK19N06	5355	5356	156.4
185	BaAK4I02	5357	5358	156.4
185	BaH49K10	5359	5360	156.4
185	baal2o03	5361	5362	156.4
185	baak28g14	5363	5364	156.4
185	bah62n05	5365	5366	156.4
185	bags16e11	5367	5368	156.4
185	bags23g13	5369	5370	156.4
210	BaSD23C05	5371	5372	157
211	BaH19F17	5373	5374	157.4
211	BaH15J02	5375	5376	157.4
211	baak20d11	5377	5378	157.4
211	BaAL6D19	5379	5380	157.4
211	baak43e16	5381	5382	157.4
216	baak40b02	5383	5384	158.5
217	bah62m03	5385	5386	159.6
218	BaGS26G17	5387	5388	161.8
219	baal6j16	5389	5390	162.9
219	bags29b09	5391	5392	162.9
219	baal20e03	5393	5394	162.9
219	BaGS9L23	5395	5396	162.9
219	bah32e22	5397	5398	162.9
219	BaAK17O14	5399	5400	162.9
225	bah56g23	5401	5402	164
225	basd22f14	5403	5404	164
227	BaH42O04	5405	5406	164.7
227	bast74F0111	5407	5408	164.7
229	BaSD21F13	5409	5410	167.3
230	BaAK26G13	5411	5412	167.4
231	BaAK44D07	5413	5414	168.2
231	bast61C0206	5415	5416	168.2
233	BaAL29L08	5417	5418	169.4
233	BaH34B20	5419	5420	169.4
233	baak21a04	5421	5422	169.4
233	BaGS37F18	5423	5424	169.4
233	baal12h12	5425	5426	169.4
233	BaAK42B16	5427	5428	169.4
233	BaAK26F12	5429	5430	169.4
233	BaH27B21	5431	5432	169.4
233	BaGS12B05	5433	5434	169.4
233	baal12h24	5435	5436	169.4
243	baal35j16	5437	5438	173.5
243	BaGS37C07	5439	5440	173.5
243	BaAK45D23	5441	5442	173.5
243	BaH42G09	5443	5444	173.5
243	BaAL40P01	5445	5446	173.5
243	kr61A0901	5447	5448	173.5

TABLE 7-5-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
249	baal4d05	5449	5450	174.6
249	basd20l03	5451	5452	174.6

TABLE 7-6

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
249	baal31b03	5453	5454	174.6
252	bags27k21	5455	5456	176.8
252	bah55n15	5457	5458	176.8
254	BaH44B17	5459	5460	177.9
254	BaSD2K11	5461	5462	177.9
256	BaAK20B23	5463	5464	180.1
256	BaGS23E20	5465	5466	180.1
256	bags33i10	5467	5468	180.1
256	bags35k06	5469	5470	180.1
260	bags22c18	5471	5472	181.2
260	MWG2031	—	—	181.2
260	BaGS22M17	5473	5474	181.2
263	baak21j24	5475	5476	184.4
263	BaH29D20	5477	5478	184.4
263	bah44f20	5479	5480	184.4
263	BaAL16O08	5481	5482	184.4
263	BaAL27L17	5483	5484	184.4
263	sKT3	—	—	184.4
263	sKT9	—	—	184.4
263	baet31B1103	5485	5486	184.4
263	MWG975	—	—	184.4
272	BaAL4A11	5487	5488	185.9
272	BaGS22I18	5489	5490	185.9
274	BaGS24K08	5491	5492	186.4
274	bah16c17	5493	5494	186.4
274	bah42m04	5495	5496	186.4
274	bags28l21	5497	5498	186.4
274	basd12f23	5499	5500	186.4
274	bah31m22	5501	5502	186.4
274	BaAL30C17	5503	5504	186.4
274	BaAK40P18	5505	5506	186.4
274	baak37n01	5507	5508	186.4
274	BaGS24O11	5509	5510	186.4
274	BaH27K19	5511	5512	186.4
274	BaGS15J07	5513	5514	186.4
286	bah19a07	5515	5516	188.9
287	BaH50I23	5517	5518	194
288	BaH56D06	5519	5520	195
288	BaAK39M05	5521	5522	195
288	bah11m16	5523	5524	195
291	bah49d03	5525	5526	196.1
291	bah62l23	5527	5528	196.1
291	BaAK38J13	5529	5530	196.1
291	BaH37N04	5531	5532	196.1
291	basd27c06	5533	5534	196.1
291	bah39g10	5535	5536	196.1
291	BaSD18P05	5537	5538	196.1
298	BaGS20A13	5539	5540	196.6
299	bah44n05	5541	5542	197.2
300	EBmac764	—	—	198.2

TABLE 7-7

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
301	BaH27L15	5543	5544	199.3
301	BaAK21I02	5545	5546	199.3

TABLE 7-7-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
303	Bmac0064	—	—	200.3
304	BaH59F07	5547	5548	210.4
304	bags9l05	5549	5550	210.4
306	BaGS13H12	5551	5552	211.7
307	BaAL19B06	5553	5554	212.9
308	BaSD15P23	5555	5556	215.1
309	bah53j21	5557	5558	217.2
309	bah21f16	5559	5560	217.2
309	baet39E0309	5561	5562	217.2
312	bags5l04	5563	5564	217.7
313	bags7g10	5565	5566	218.3
314	BaGS9D22	5567	5568	219.5
315	kr27H1216	5569	5570	221.2
315	BaAK25O11	5571	5572	221.2
317	bah18j14	5573	5574	221.7
317	bags37k14	5575	5576	221.7
317	baak26n19	5577	5578	221.7
317	bah42k03	5579	5580	221.7
317	BaH36N15	5581	5582	221.7
317	Bmag120	—	—	221.7
323	bags12i02	5583	5584	225
323	BaAK38E05	5585	5586	225
325	baet25B0604	5587	5588	226.1
325	BaAK46E21	5589	5590	226.1
327	BaGS37J12	5591	5592	229.9
328	bast60C0105	5593	5594	231
328	baak30b08	5595	5596	231
328	BaAL29N13	5597	5598	231
328	BaAL24O04	5599	5600	231
332	baak20o12	5601	5602	232.1
332	basd14k23	5603	5604	232.1
332	BaAK23L05	5605	5606	232.1
332	BaGS31G02	5607	5608	232.1
332	bags33o01	5609	5610	232.1
332	basd18g14	5611	5612	232.1
332	bah24d24	5613	5614	232.1
332	BaGS12F09	5615	5616	232.1
332	BaAK33H23	5617	5618	232.1
332	bah47p03	5619	5620	232.1
342	BaSD14F09	5621	5622	232.3
343	bah11k13	5623	5624	232.5
343	BaSD22F10	5625	5626	232.5
345	bags32a01	5627	5628	234
346	bags27o20	5629	5630	235.1
347	baak31o10	5631	5632	236.2
347	bags10f16	5633	5634	236.2
347	baal37j12	5635	5636	236.2
350	BaGS9H02	5637	5638	239.5

TABLE 7-8

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
351	BaAK40H10	5639	5640	240.3
352	bah56m09	5641	5542	240.6
353	kr66C0705	5643	5644	240.9
354	BaGS33M05	5645	5646	242
355	bast60B0204	5647	5648	243.2
356	bah56p08	5649	5650	245.4
357	baak12e19	5651	5652	246.9
357	BaGS1D05	5653	5654	246.9
359	BaH29M21	5655	5656	247.6
359	bags21c04	5657	5658	247.6
361	baak32p09	5659	5660	250.9
362	BaAL24B02	5661	5662	254.2
362	BaGS34F08	5663	5664	254.2

TABLE 7-8-continued

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
364	bast36D1208	5665	5666	255.3
364	kr25B1103	5667	5668	255.3
366	kr08D0303	5669	5670	256.4
367	baal19g05	5671	5672	257.5
367	BaH22B15	5673	5674	257.5
367	bags19c10	5675	5676	257.5
370	bags29k01	5677	5678	260.7
370	bastl54G0414	5679	5680	260.7
370	BaGS23J01	5681	5682	260.7
370	bags34b15	5683	5684	260.7
374	baak46i07	5685	5686	262.9
375	BaAL6J13	5687	5688	265
375	bah31l17	5689	5690	265
375	BaAK32A05	5691	5692	265
375	BaGS30N22	5693	5694	265
379	BaH54J20	5695	5696	266.4
380	BaGS7F20	5697	5698	269.4
381	bah63p18	5699	5700	272.8
382	bags11p11	5701	5702	274.9
383	BaH27L17	5703	5704	277.1
384	basd17e11	5705	5706	278.2
384	bags15i06	5707	5708	278.2
384	BaAK36F09	5709	5710	278.2
384	bast57A0101	5711	5712	278.2
388	baak26h17	5713	5714	280.3
388	basd13b15	5715	5716	280.3
388	bags9d11	5717	5718	280.3
391	BaH20K03	5719	5720	281.4
391	BaSD27N21	5721	5722	281.4
391	baal13a10	5723	5724	281.4
394	kr30F1212	5725	5726	282.5
394	bastl45B0903	5727	5728	282.5
394	Bmac156	—	—	282.5
394	bah60k06	5729	5730	282.5
398	BaGS32I12	5731	5732	283.6
398	BaGS4H02	5733	5734	283.6
398	bah44k12	5735	5736	283.6

TABLE 7-9

Order from the short arm end	Clones	SEQ ID NO: (5' end)	SEQ ID NO: (3' end)	Distance from the short arm end (cM)
398	bags21m21	5739	5740	283.6
398	BaSD14J15	5741	5742	283.6
404	HVM49	—	—	285.7
404	basd16e11	5743	5744	285.7
406	BaAK21N09	5745	5746	287.9
407	baal0e10	5747	5748	289
408	baak1g17	5749	5750	290.1
409	BaH14K12	5751	5752	291.2
409	BaAK31G05	5753	5754	291.2
411	MWG2062	—	—	291.5
412	BaH50G17	5755	5756	292.3
413	HVM5	—	—	293.4
413	bags38n21	5757	5758	293.4
413	bastl04B0303	5759	5760	293.4
413	baal35f12	5761	5762	293.4
417	BaH49M02	5763	5764	293.9
418	baak38f04	5765	5766	294.5
419	bah29b02	5767	5768	295
420	basd15d20	5769	5770	296.1
421	kr61C0305	5771	5772	297.1
421	BaH23B08	5773	5774	297.1
423	kr40H1115	5775	5776	298.6
424	bah51g17	5777	5778	301.4
425	BaSD22E19	5779	5780	315.4

[0072] The order on each chromosome can be specified based on the distance from the short arm end or long arm end. In the case where the order on each chromosome was specified by the distance from the short arm end, the polynucleotides mapped on 1H chromosome are first placed based on the distance from the short end, and the polynucleotides mapped on 2H and the subsequent chromosomes (3H to 7H) are placed based on the same reference (distances from the short arm end).

[0073] More specifically, in the case where the distance from the short arm end is used as a reference for positioning the polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, the polynucleotides are placed according to the order from the short arm end as shown in Table 1-1 to Table 7-9. For clones that have the same order from the short arm end, the order by which these clones are placed is not particularly limited. Once the precise order of these clones were specified by a future study, these clones will be able to be placed accordingly. Note that, the reference (origin) on the chromosome is not just limited to the short arm end of 1H chromosome. Any position on a chromosome can be used as a reference point.

[0074] When using more than one polynucleotide with base sequences from the base sequence of any one of SEQ ID NO: 1 through 5780 for example, the polynucleotides can be placed in order from the 5' end. Further, in the case where a polynucleotide with the base sequence of any one of SEQ ID NO: 1 through 5780 is used together with more than one polynucleotide with base sequences from the base sequence of any one of SEQ ID NO: 1 through 5780 for example, a polynucleotide that is closest to the 5' end is placed first. The same criteria can be used to place other polynucleotides as well.

[0075] With the polynucleotides immobilized on a support in the order they are arranged on the chromosomes, the value of a gene detection instrument according to the present invention can be greatly improved in crossbreeding of Triticeae species. More specifically, by using a gene detection instrument according to the present invention for comprehensive investigation of transcripts in hybrids of Triticeae species, the expression level or the presence or absence of polymorphism can be determined for target genes. Further, the location and extent of recombination on chromosomes can be checked to see if unnecessary recombination has occurred. This makes it easy to determine target individuals of screening and thereby improves the efficiency of breeding.

[0076] [Gene Detection Instrument with the Polynucleotides Immobilized in Regions Appended with Chromosomal Order Information]

[0077] The regions in which the polynucleotides are immobilized (hereinafter, may be referred to as "spots") may be appended with information indicative of the order in which the polynucleotides are arranged on barley chromosomes. The spots may be arranged in any way as long as they are appended with the order information. With the order information added to the spots, the data obtained from the spots can be rearranged in the chromosomal order even when the spots are randomly placed on a support. In this way, a gene detection instrument according to the present invention can improve the efficiency of breeding. Note that, the order information added to the spots can follow the foregoing criteria used to place the polynucleotides.

[0078] Adding order information enables the spots to be arranged in an arbitrary order in a gene detection instrument

of an array type, in which more than one polynucleotide is immobilized on a support such as a membrane or a glass slide. Further, the chromosomal order information of individual polynucleotides can also be added in a gene detection instrument that employs a collection of beads (bead array) in which the polynucleotide is immobilized on each bead serving as a support.

[0079] [Examples of a Gene Detection Instrument According to the Present Invention]

[0080] (i) For Detecting Gene Expression

[0081] A gene detection instrument according to the present invention can be fabricated according to a conventional gene expression array fabrication method. For example, a cDNA array can be fabricated by preparing a solution of polynucleotide that comprises cDNA (full length or partial), and by spotting it on a support with a spotter or the like. The polynucleotides immobilized on the support may be synthetic oligonucleotides with the base sequences of cDNA. Alternatively, a technique known as the Affymetrix DNA chip technique may be used, in which DNA is synthesized on a substrate.

[0082] Various conventional techniques that are designed for detection of gene expression can suitably be used in a gene detecting instrument according to the present invention. For example, cDNA or cRNA prepared from total RNA or mRNA of Triticeae species can be used for the present invention. More specifically, cDNA or cRNA is fluorescent-labeled and hybridized with the polynucleotides immobilized on the support. The expression level of genes can be evaluated by measuring the intensity of hybridization, using the fluorescence as an index. Further, cDNA or cRNA prepared from two kinds of samples may be labeled with fluorescent substances that emit different colors, and hybridized with polynucleotides immobilized on the same support. By measuring the color tone and fluorescent intensity, differences of gene expression can be evaluated.

[0083] In breeding of Triticeae species, target individuals can be screened for according to changes in the expression levels of genes that regulate target traits. Further, target individuals can also be screened for according to the expression levels of genes that are linked to target genes.

[0084] (ii) For Detecting Gene Polymorphism

[0085] Various conventional techniques that are designed for detection of gene polymorphism can suitably be used in a gene detection instrument according to the present invention.

[0086] For example, a gene detection instrument according to the present invention can be used to detect fragment length polymorphism such as RFLP (restriction fragment length polymorphism). More specifically, fragment length polymorphism can be detected by immobilizing more than one partial sequence of cDNA of the same clone on the same spot. Here, the hybridization intensity of the spot immobilizing three partial sequences is the strongest in fragments that hybridize with all of the three partial sequences, and is weaker in fragments that hybridize with two partial sequences or only one partial sequence. Thus, fragment length polymorphism can be detected by measuring fluorescence intensity or the like used as an index of hybridization intensity. In the case where fragments hybridize with distinctively different regions in the same spot, fragment length polymorphism can be detected by labeling the two fragments with different fluorescent dyes.

[0087] (2) Gene Polymorphism Detection Instrument according to the Present Invention

[0088] A gene polymorphism detection instrument according to the present invention is an instrument for detecting polymorphisms of genes in the genomes of Triticeae species. The organisms to which a gene detection instrument of the invention is applicable may be any Triticeae species, among which barley, wheat, and rye are preferable. A gene detection instrument according to the present invention includes a support on which polynucleotides constituting part of barley chromosomal (1H, 2H, 3H, 4H, 5H, 6H, and 7H) DNA are immobilized. The polynucleotides immobilized on the support may solely be polynucleotides that constitute part of barley chromosomal DNA, or other polynucleotides may additionally be immobilized on the support. Such additional polynucleotides are not particularly limited as long as they can detect expression or polymorphism of genes in the genomes of Triticeae species. For example, the additional polynucleotides may be those with the base sequences originating in non-barley organisms, or those with arbitrary base sequences that have been artificially synthesized.

[0089] In the case where the polynucleotides are immobilized in more than one region of the support, the polynucleotides immobilized in these regions may have non-overlapping base sequences or partially overlapping base sequences. Alternatively, polynucleotides of the same base sequence may be immobilized in these different regions of the support. In the case where the polynucleotides have overlapping base sequences, the polynucleotides may have partially overlapping base sequences, or the base sequence of one of the polynucleotides may be a partial sequence of the other polynucleotide.

[0090] Further, the polynucleotide immobilized in each region is not necessarily required to be of the same kind. More than one kind of polynucleotide may be immobilized in each region.

[0091] The support is not particularly limited as long as it can immobilize polynucleotides, and it may have any shape and may be made of any material. Examples of a support material generally include: inorganic materials such as glass and silicon wafer; natural polymers such as paper; synthetic polymers such as nitrocellulose and nylon; and gels using synthetic polymers or natural polymers. The shape of the support is not particularly limited as long as it provides enough area to support the polynucleotides. Generally, those with a two-dimensional plane, for example, such as a substrate with little or no flexibility, a flexible membrane, or a flexible substrate with intermediate flexibility can be preferably used. The thickness of the substrate or membrane is not particularly limited either, and it can be suitably set according to the material or use of the substrate or membrane. Various types of beads may be used as supports.

[0092] [Polynucleotides Immobilized on a Support of the Gene Polymorphism Detection Instrument]

[0093] In a gene polymorphism detection instrument according to the present invention, at least one polynucleotide from the following polynucleotides is immobilized on a support.

[0094] Polynucleotides with base sequences constituting part of barley chromosomal DNA, or variants thereof with the substitution, deletion, insertion, and/or addition of one or more bases.

[0095] As used herein, a polynucleotide with a base sequence constituting part of barley chromosomal DNA is not particularly limited as long as it is a polynucleotide with a

base sequence constituting part of the entire base sequences of chromosomal DNA of barley 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes.

[0096] A variant with the substitution, deletion, insertion, and/or addition of one or more bases in the polynucleotide with a base sequence constituting part of barley chromosomal DNA may be a polynucleotide that has been mutated on purpose, or a polynucleotide that exists in nature. For example, think of a base sequence of chromosomal DNA in a specific variety of barley. Comparing this base sequence with those of other varieties, no sequence is completely identical. Rather, these sequences are variants with the substitution, deletion, insertion, and/or addition of one or more bases.

[0097] A polynucleotide immobilized on a support of a gene polymorphism detection instrument according to the present invention is preferably a polynucleotide that constitutes part of the base sequence of at least one DNA fragment that has been amplified with a primer set that comprises two primers arbitrarily selected from a plurality of primers that have been designed based on base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from the base sequences of SEQ ID NO: 1 through 5780, using the genomic DNA of Triticeae species as a template.

[0098] The base sequences of SEQ ID NO: 1 through 5780 are base sequences of the barley EST (expressed sequence tag) independently developed by the inventors. The inventors have previously confirmed that a polynucleotide with the base sequences of SEQ ID NO: 1 through 770, a polynucleotide with the base sequences of SEQ ID NO: 771 through 1754, a polynucleotide with the base sequences of SEQ ID NO: 1755 through 2642, a polynucleotide with the base sequences of SEQ ID NO: 2643 through 3324, a polynucleotide with the base sequences of SEQ ID NO: 3325 through 4320, a polynucleotide with the base sequences of SEQ ID NO: 4321 through 4962, and a polynucleotide with the base sequences of SEQ ID NO: 4963 through 5780 are mapped on 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes, respectively.

[0099] The primers are not particularly limited as long as they are designed based on the base sequences of SEQ ID NO: 1 through 5780. As such, primer profiles, such as the number of bases and GC content are not particularly limited. Further, as described above, since the base sequence of SEQ ID NO: n (where n is an odd number) and the base sequence of SEQ ID NO: n+1 are base sequences that are read from the both ends of cDNA of the same clone, the primer set with a combination of two primers arbitrarily selected from a plurality of primers that have been designed based on these base sequences flank a specific region of the barley chromosomal DNA. For example, in amplifying DNA with the primer set using the genomic DNA of barley as a template, the base sequences of the amplified fragments will be the same as the base sequences of the cDNA when the primer set is within the same exon. On the other hand, when the primers of the primer set are in different exons, the amplified fragments will include base sequences of the intron portions.

[0100] The primers that are designed based on the base sequences of SEQ ID NO: 1 through 5780 may be primers with the base sequences of SEQ ID NO: 5781 through 17340, or primers with the complementary sequences thereof, for example. More specifically, the primers that are designed based on SEQ ID NO: 1 are primers with the base sequences of SEQ ID NO: 5781 and 5782 or the complementary sequences thereof, and the primers that are designed based on SEQ ID NO: 2 are primers with the base sequences of SEQ ID NO: 5783 and 5784 or the complementary sequences thereof. In other words, the SEQ ID NOs for the base sequences of the primers designed based on the individual base sequences of SEQ ID NO: 1 through 5780 are represented by (2×m−1)+5780 and (2×m)+5780, where m is the SEQ ID NO of the base sequence used to designed the primer.

[0101] As a specific example, amplified DNA fragments can be obtained by PCR that uses the genomic—DNA of barley as a template and is performed with a primer set including a combination of two primers arbitrarily selected from (i) primers that have been designed based on the base sequence of SEQ ID NO: 1 and having the base sequences of SEQ ID NO: 5781 through 5782 or complementary sequences thereof, and (ii) primers that have been designed based on the base sequence of SEQ ID NO: 2 and having the base sequences of SEQ ID NO: 5783 through 5784 or complementary sequences thereof. A means by which amplification is performed is not particularly limited, and PCR and other conventional methods can be used.

[0102] The polynucleotides immobilized on a support of a gene polymorphism detection instrument according to the present invention are part of the amplified DNA fragments. When amplification is performed using genomic DNA of different Triticeae species as a template and when polymorphism exists in the amplified fragments, it is preferable that the polynucleotides immobilized on the support include polymorphism-containing portions of the base sequences. The polymorphism may be amplified fragment length polymorphism or single nucleotide polymorphism (SNP), for example.

[0103] The inventors of the present invention amplified DNA fragments by using genomic DNA of Triticeae species as a template and with the use of a primer set that included a combination of two primers arbitrarily selected from (i) primers that had been designed based on the base sequence of SEQ ID NO: n (where n is an odd number), and (ii) primers that had been designed based on the base sequence of SEQ ID NO: n+1, from among the base sequences of SEQ ID NO: 1 through 5780. The inventors have found that these DNA fragments could be used as genetic markers for distinguishing different varieties of Triticeae species. That is, the inventors have specified at least 2890 genetic markers.

[0104] Specifically, the inventors have found fragment length polymorphism in the DNA fragments that were amplified by PCR that was performed with a primer set that had been designed based on SEQ ID NO: 2 and included a combination of primers with the base sequences of SEQ ID NO: 5783 and 5784, using the genomic DNA of malting barley "Haruna Nijo" (Hordeum vulgare ssp. vulgare variety Harunanijo) and the genomic DNA of wild type barley "H602" (Hordeum vulgare ssp. spontaneum H602) as templates. Further, the inventors have found SNP in the DNA fragments that were amplified by PCR that was performed with a primer set that had been designed based on SEQ ID NO: 4 and included a combination of primers with the base sequences of SEQ ID NO: 5787 and 5788, using the genomic DNA of the foregoing barley varieties as templates. It was found as a result that these DNA fragments with SNPs were CAPS (cleaved amplified polymorphic sequence) markers, which are excised by restriction enzyme in one of the varieties but not in the other varieties.

[0105] Table 8-1 through Table 14-9 show kinds of polymorphisms that were found by the inventors between Haruna Nijo and H602. Tables 8-1 through 8-8 show polymorphisms

in 1H chromosome, Tables 9-1 through 9-10 in 2H chromosome, Tables 10-1 through 10-9 in 3H chromosome, Tables 11-1 through 11-7 in 4H chromosome, Tables 12-1 through 12-10 in 5H chromosome, Tables 13-1 through 13-7 in 6H chromosome, and Tables 14-1 through 14-9 in 7H chromosome. Corresponding EST sequences of the respective clones are shown in Table 1-1 through Table 7-9. The "Primers Used" are primers that were actually used from among the primers that had been designed based on the EST sequences (SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1) corresponding to the respective clones. The primers used for each clone had the base sequences with the SEQ ID NOs shown in the tables. The DNA fragments amplified with these primer sets using the genomic DNA of Haruna Nijo and the genomic DNA of H602 as templates had polymorphisms shown in Table 8-1 through Table 14-9.

[0106] The clones are known genetic markers, which have been identified as SSR (simple sequence repeat) marker, STS (sequence tagged site) marker, dCAPS (derived cleaved amplified polymorphic sequence) marker, trait marker, CAPS marker, or size_poly (fragment length polymorphism) marker. SSR is a fragment length polymorphism based on differences in the number of repeats of recurring units of two or three bases of DNA. STS is a sequence site that has been set only for a specific location of DNA. Starting from such a specific sequence site, specific DNA fragments are amplified by PCR or the like, and electrophoresis is run for the amplified products so that polymorphism can be detected based on the presence or absence of bands, or differences in molecular weight. In dCAPS, a mismatch is induced between PCR primers and template DNA, so that polymorphism (the presence or absence of restriction enzyme site) occurs in the PCR products. Trait marker sh is an isolated gene that controls vernalization requirement. Since Haruna Nijo and H602 have polymorphism in the sequence of this gene, it can be used as a marker. CAPS and size_poly will be described later.

TABLE 8-1

Name	Primers used (SEQ ID NO:)		marker type
bah55e06	5783	5784	size_poly (codominant)
bags30b07	5787	5788	SNP
baak2l03	5791	5792	CAPS
BaAK17D13	5795	5796	SNP
basd26l20	5799	5800	SNP
bah61p17	5803	5804	SNP
BaGS11O06	5807	5808	size_poly (codominant)
kr12H0216	5811	5812	SNP
BaGS32E23	5815	5816	CAPS
basd13k20	5819	5820	CAPS
BaAK24O11	5823	5824	CAPS
kr26D0507	5827	5828	SNP
BaSD2D08	5831	5832	CAPS
baak41n21	5835	5836	SNP
bah11b15	5839	5840	CAPS
kr24B0903	5843	5844	SNP
bast50E0709	5847	5848	size_poly (codominant)
baal17o01	5851	5852	SNP
baak41a04	5855	5856	SNP
BaH28C07	5859	5860	size_poly (codominant)
bags16g18	5863	5864	SNP
BaSD3C22	5867	5868	SNP
BaGS17B21	5871	5872	CAPS
basd27b10	5875	5876	SNP
bah47d23	5879	5880	SNP
BaAK21D02	5883	5884	CAPS
BaH17D02	5887	5888	CAPS
baal4f12	5891	5892	CAPS
baGS11I03	5895	5896	CAPS

TABLE 8-1-continued

Name	Primers used (SEQ ID NO:)		marker type
bah56a03	5899	5900	size_poly (codominant)
kr16A0501	5903	5904	size_poly (codominant)
bah19f01	5907	5908	CAPS
BaAK27F07	5911	5912	CAPS
bah47f18	5915	5916	size_poly (codominant)
bah45l19	5919	5920	size_poly (codominant)
BaAK12I12	5923	5924	SNP
BaAL6N04	5927	5928	SNP
baal16l05	5931	5932	CAPS
BaSD18O20	5935	5936	size_poly (codominant)
BaSD3J13	5939	5940	SNP
bah63j19	5943	5944	size_poly (codominant)
BaH36O18	5947	5948	CAPS
BaAK20A06	5951	5952	CAPS
BaGS8G13	5955	5956	CAPS
bah25n06	5959	5960	CAPS
BaAK1P06	5963	5964	size_poly (dominant)
BaAK16M07	5967	5968	SNP
BaH36M15	5971	5972	SNP
BaGS12K12	5975	5976	size_poly (dominant)
BaAL39C22	5979	5980	SNP
kr68B0303	5983	5984	SNP

TABLE 8-2

Name	Primers used (SEQ ID NO:)		marker type
baak24d09	5987	5988	SNP
BaGS11J13	5991	5992	CAPS
baal38l23	5995	5996	CAPS
BaAL36B15	5999	6000	CAPS
bast60D0610	6003	6004	CAPS
kr22D0808	6007	6008	CAPS
baal19i12	6011	6012	SNP
basd23o02	6015	6016	CAPS
baak1j14	6019	6020	CAPS
baak24k18	6023	6024	CAPS
kr18G0814	6027	6028	SNP
BaH38H09	6031	6032	CAPS
BaGS8B13	6035	6036	SNP
BaH25J08	6039	6040	SNP
baak3d11	6043	6044	SNP
baal12p08	6047	6048	SNP
bags39i20	6051	6052	SNP
bags32m16	6055	6056	size_poly (codominant)
kr15A0402	6059	6060	SNP
baal3c01	6063	6064	SNP
baak41i03	6067	6068	SNP
BaGS29M13	6071	6072	SNP
basd17m22	6075	6076	CAPS
bags15g01	6079	6080	CAPS
BaH24I06	6083	6084	SNP
BaH57E12	6087	6088	CAPS
BaSD25C22	6091	6092	SNP
baal19m17	6095	6096	CAPS
bah46p14	6099	6100	SNP
bags18d19	6103	6104	SNP
BaAK34J19	6107	6108	SNP
bags6d01	6111	6112	CAPS
bags3P11	6115	6116	CAPS
BaAK14J21	6119	6120	CAPS
baak2m05	6123	6124	SNP
baak37g19	6127	6128	CAPS
BaGS31B11	6131	6132	SNP
BaAL35M08	6135	6136	SNP
BaSD16G03	6139	6140	CAPS
BaH58J20	6143	6144	SNP
BaGS22B13	6147	6148	SNP
BaAK43M01	6151	6152	SNP
bah14i07	6155	6156	SNP
BaH13F14	6159	6160	CAPS

TABLE 8-2-continued

Name	Primers used (SEQ ID NO:)		marker type
baal9i16	6163	6164	CAPS
basd27b20	6167	6168	CAPS
BaAK2O24	6171	6172	SNP
basd18l16	6175	6176	CAPS
BaAL19J14	6179	6180	CAPS
bags22j15	6183	6164	SNP
baak44a23	6187	6188	SNP

TABLE 8-3

Name	Primers used (SEQ ID NO:)		marker type
BaAK32N04	6191	6192	SNP
basd21e22	6195	6196	SNP
BaGS7K03	6199	6200	size_poly (codominant)
baak42e22	6203	6204	SNP
bast21D0808	6207	6208	size_poly (codominant)
bast75E0610	6211	6212	SNP
baet16A1002	6215	6216	SNP
basd17m16	6219	6220	CAPS
bags17g08	6223	6224	size_poly (codominant)
baak21i01	6227	6228	SNP
baak13n06	6231	6232	CAPS
baak22o23	6235	6236	SNP
baet42E0410	6239	6240	size_poly (codominant)
BaGS27M04	6243	6244	CAPS
BaH52H18	6247	6248	SNP
baak33k20	6251	6252	SNP
bags21f16	6255	6256	SNP
bags34e05	6259	6260	SNP
bags15d20	6263	6264	CAPS
bags18g10	6267	6268	size_poly (codominant)
bags19a02	6271	6272	SNP
BaAK17J19	6275	6276	size_poly (codominant)
bags35k02	6279	6280	SNP
bah35a22	6283	6284	SNP
BaGS17H13	6287	6288	SNP
bah47n12	6291	6292	SNP
baak12p11	6295	6296	SNP
baet38B1004	6299	6300	SNP
BaGS13K12	6303	6304	SNP
BaAL25A05	6307	6308	SNP
bah27k23	6311	6312	size_poly (codominant)
BaAK24J12	6315	6316	SNP
BaSD14M22	6319	6320	SNP
bah17l24	6323	6324	SNP
baal29j09	6327	6328	SNP
bah16d09	6331	6332	SNP
bah60d03	6335	6336	SNP
bah45i13	6339	6340	SNP
bah11h03	6343	6344	SNP
bah47h17	6347	6348	SNP
bags35d02	6351	6352	SNP
bags37e17	6355	6356	CAPS
baak14c12	6359	6360	SNP
baak34c01	6363	6364	SNP
BaH35A11	6367	6368	SNP
BaAK30M16	6371	6372	SNP
BaSD11P04	6375	6376	CAPS
bah12j09	6379	6380	CAPS
BaAL2G20	6383	6384	SNP
bags14j09	6387	6388	CAPS
kr26E0610	6391	6392	CAPS

TABLE 8-4

Name	Primers used (SEQ ID NO:)		marker type
bah37f01	6395	6396	CAPS
bags29m05	6399	6400	SNP

TABLE 8-4-continued

Name	Primers used (SEQ ID NO:)		marker type
BaGS17A18	6403	6404	CAPS
baet34A0501	6407	6408	SNP
BaSD22O13	6411	6412	CAPS
bags15a22	6415	6416	CAPS
baet21H1016	6419	6420	CAPS
BaH30E13	6423	6424	SNP
bags4e23	6427	6428	SNP
baak45b03	6431	6432	SNP
bah12o12	6435	6436	SNP
baak34k14	6439	6440	CAPS
baal3e14	6443	6444	SNP
bags22f12	6447	6448	CAPS
BaH45P03	6451	6452	CAPS
basd11d13	6455	6456	CAPS
Bmag211	—	—	SSR
HVM20	—	—	SSR
basd1j14	6459	6460	SNP
bags35b18	6463	6464	SNP
baal41i11	6467	6468	SNP
bags13e23	6471	6472	SNP
bah20d03	6475	6476	SNP
baet19F0212	6479	6480	SNP
bags12j05	6483	6484	SNP
BaSD24D17	6487	6488	SNP
BaGS24K10	6491	6492	SNP
baal9e05	6495	6496	SNP
BaGS33M23	6499	6500	SNP
bah46g14	6503	6504	SNP
bags33h05	6507	6508	SNP
baak24h12	6511	6512	SNP
BaH50N19	6515	6516	SNP
BaAK31O05	6519	6520	SNP
BaGS39L14	6523	6524	SNP
BaGS27C22	6527	6528	SNP
bags20o24	6531	6532	SNP
bags34j05	6535	6536	CAPS
bah56l03	6539	6540	CAPS
basd12k03	6543	6544	CAPS
BaAK39I18	6547	6548	CAPS
bags21h06	6551	6552	CAPS
bah56k04	6555	6556	CAPS
bah60e11	6559	6560	CAPS
baak22i05	6563	6564	CAPS
baal5i02	6567	6568	CAPS
BaAK2E05	6571	6572	CAPS
baak33g12	6575	6576	CAPS
bags4e05	6579	6580	CAPS
bast42C0806	6583	6584	SNP
baak26c05	6587	6588	SNP

TABLE 8-5

Name	Primers used (SEQ ID NO:)		marker type
bags19a16	6591	6592	SNP
kr11F1212	6595	6596	SNP
BaH28K13	6599	6600	CAPS
baak20d06	6603	6604	size_poly (codominant)
BaSD1I24	6607	6608	CAPS
baak35l20	6611	6612	SNP
bah57m07	6615	6616	SNP
bah60k11	6619	6620	SNP
basd20o09	6623	6624	SNP
basd24i22	6627	6628	SNP
bags30g20	6631	6632	SNP
bags1m11	6635	6636	SNP
bags23g20	6639	6640	SNP
BaGS15B05	6643	6644	SNP
BaGS24P05	6647	6648	SNP
bags10g06	6651	6652	SNP

TABLE 8-5-continued

Name	Primers used (SEQ ID NO:)		marker type
bah32o04	6655	6656	SNP
BaGS32P08	6659	6660	SNP
bags4e02	6663	6664	CAPS
bast04H0315	6667	6668	CAPS
BaGS37L06	6671	6672	CAPS
basd2b18	6675	6676	CAPS
bags3h12	6679	6680	SNP
bags1e21	6683	6684	SNP
BaAK27M21	6687	6688	SNP
BaSD18F05	6691	6692	size_poly (codominant)
BaH35B05	6695	6696	SNP
basd21h11	6699	6700	SNP
BaH32E20	6703	6704	SNP
BaGS22A20	6707	6708	SNP
BaSD14B13	6711	6712	CAPS
bags29l04	6715	6716	SNP
bags22g16	6719	6720	SNP
BaAL4B14	6723	6724	size_poly (codominant)
bah61h20	6727	6728	SNP
bah15p01	6731	6732	SNP
baak41p03	6735	6736	SNP
BaSD12L06	6739	6740	SNP
BaSD23P07	6743	6744	SNP
BaGS7J05	6747	6748	SNP
bah29b06	6751	6752	SNP
BaGS31N17	6755	6756	SNP
BaGS13F08	6759	6760	SNP
BaAK39G10	6763	6764	CAPS
BaAK39G03	6767	6768	CAPS
baak2a18	6771	6772	CAPS
bags39d12	6775	6776	SNP
basd17l04	6779	6780	CAPS
BaAK20B19	6783	6784	SNP
bags15j15	6787	6788	SNP
BaAK30F02	6791	6792	CAPS

TABLE 8-6

Name	Primers used (SEQ ID NO:)		marker type
BaGS22A21	6795	6796	SNP
baet45E0410	6799	6800	SNP
BaGS22C14	6803	6804	SNP
bah23k12	6807	6808	SNP
BaH15O13	6811	6812	SNP
kr24F0412	6815	6816	SNP
BaGS28O21	6819	6820	SNP
BaAL15N19	6823	6824	SNP
bags10j15	6827	6828	CAPS
bags32j03	6831	6832	SNP
bags20e14	6835	6836	SNP
bags3c15	6839	6840	CAPS
basd27n01	6843	6844	SNP
BaGS6M19	6847	6848	SNP
baak13e03	6851	6852	SNP
BaH15M10	6855	6856	CAPS
bags14k12	6859	6860	size_poly (codominant)
bast61E0509	6863	6864	CAPS
BaGS31N04	6867	6868	CAPS
BaAK27D22	6871	6872	CAPS
baal5o19	6875	6876	CAPS
bah55b18	6879	6880	CAPS
bah23i02	6883	6884	SNP
BaAK15H22	6887	6888	SNP
bags32b03	6891	6892	SNP
baak30c15	6895	6896	SNP
BaGS22A05	6899	6900	SNP
bah16m01	6903	6904	SNP
bags15e08	6907	6908	CAPS
BaGS37D12	6911	6912	SNP
BaAL37N24	6915	6916	SNP

TABLE 8-6-continued

Name	Primers used (SEQ ID NO:)		marker type
BaH28B09	6919	6920	SNP
bah47h08	6923	6924	SNP
BaH57N07	6927	6928	SNP
baak38o02	6931	6932	SNP
baak20f16	6935	6936	SNP
baak28n19	6939	6940	SNP
bah59j07	6943	6944	SNP
bah44j20	6947	6948	SNP
BaH47J05	6951	6952	CAPS
baet39B0303	6955	6956	SNP
BaAK27D19	6959	6960	SNP
basd25g01	6963	6964	SNP
BaAL34K17	6967	6968	SNP
basd21i17	6971	6972	SNP
bags15o12	6975	6976	SNP
baal2j10	6979	6980	CAPS
baak44n10	6983	6984	SNP
baak21e08	6987	6988	SNP
BaGS37F14	6991	6992	CAPS
BaAK41I21	6995	6996	SNP

TABLE 8-7

Name	Primers used (SEQ ID NO:)		marker type
BaGS19C07	6999	7000	SNP
BaGS15O08	7003	7004	SNP
baak40p22	7007	7008	SNP
BaH21K05	7011	7012	CAPS
baal40n03	7015	7016	SNP
bags23b08	7019	7020	SNP
BaGS39L18	7023	7024	SNP
BaGS25K24	7027	7028	CAPS
bags1a18	7031	7032	CAPS
baal15k07	7035	7036	size_poly (codominant)
bags14o13	7039	7040	size_poly (dominant)
BaH18D15	7043	7044	SNP
bastl04F0911	7047	7048	SNP
BaGS31E03	7051	7052	SNP
BaGS19J21	7055	7056	SNP
BaGS39P08	7059	7060	SNP
BaH56B06	7063	7064	SNP
baal13m24	7067	7068	SNP
bags15h14	7071	7072	SNP
bags35j22	7075	7076	CAPS
baak20h22	7079	7080	CAPS
baal34b14	7083	7084	SNP
bah16j04	7087	7088	CAPS
BaH54J03	7091	7092	CAPS
bast58C1206	7095	7096	SNP
BaH26M05	7099	7100	CAPS
bastl20B0404	7103	7104	SNP
baak14e23	7107	7108	CAPS
BaH15P22	7111	7112	SNP
BaGS17I22	7115	7116	SNP
bags15h01	7119	7120	SNP
bags7p13	7123	7124	SNP
BaGS29H13	7127	7128	SNP
bah47b01	7131	7132	SNP
bastl45E1109	7135	7136	CAPS
bags32m15	7139	7140	SNP
basd12c09	7143	7144	size_poly (codominant)
baal27m11	7147	7148	SNP
basd12k01	7151	7152	CAPS
baak41n15	7155	7156	size_poly (codominant)
bags1b01	7159	7160	SNP
BaH56O11	7163	7164	size_poly (codominant)
bah15k16	7167	7168	CAPS
bags31a22	7171	7172	CAPS
bags21e21	7175	7176	SNP
baak32n05	7179	7180	size_poly (codominant)

TABLE 8-7-continued

Name	Primers used (SEQ ID NO:)		marker type
baet02B0503	7183	7184	SNP
BaH29L05	7187	7188	SNP
baet43H1016	7191	7192	SNP
BaGS38N20	7195	7196	CAPS
BaGS23O09	7199	7200	CAPS

TABLE 8-8

Name	Primers used (SEQ ID NO:)		marker type
bastl26E0410	7203	7204	CAPS
BaH15N14	7207	7208	CAPS
baak20b06	7211	7212	SNP
BaH16I04	7215	7216	SNP
bah22p07	7219	7220	SNP
baak21j02	7223	7224	SNP
bah30o13	7227	7228	CAPS
bags38fl8	7231	7232	CAPS
bah13o05	7235	7236	CAPS
baak36b12	7239	7240	CAPS
bags18o09	7243	7244	CAPS
BaAK16L10	7247	7248	CAPS
BaAK38E16	7251	7252	size_poly (dominant)
bah13e15	7255	7256	CAPS
bags1f22	7259	7260	CAPS
bags21o12	7263	7264	SNP
BaGS9B14	7267	7268	SNP
BaAL1N23	7271	7272	CAPS
baaK1a17	7275	7276	SNP
BaH32B01	7279	7280	CAPS
BaSD18L13	7283	7284	CAPS
baak12p07	7287	7288	size_poly (codominant)
BaH58A04	7291	7292	CAPS
bags1p04	7295	7296	SNP
BaAL17O03	7299	7300	SNP
baal8e17	7303	7304	SNP
BaH50I05	7307	7308	CAPS
bastl28A0101	7311	7312	CAPS
BaH39L18	7315	7316	SNP
bags18e18	7319	7320	SNP
WMCIE8	—	—	SSR

TABLE 9-1

Name	Primers used (SEQ ID NO:)		marker type
BaGS20L10	7323	7324	SNP
BaSD15P22	7327	7328	SNP
bags7b16	7331	7332	SNP
BaAK34H02	7335	7336	CAPS
BaAK22H13	7339	7340	SNP
BaGS37P19	7343	7344	CAPS
BaAL19P17	7347	7348	CAPS
BaH41L14	7351	7352	SNP
BaAK24H17	7355	7356	SNP
bast21A0602	7359	7360	SNP
BaAL27L20	7363	7364	SNP
Bmac134	—	—	SSR
cMWG682	—	—	STS
bags34p10	7367	7368	SNP
basd18b14	7371	7372	size_poly (codominant)
bags38p20	7375	7376	CAPS
BaAK41N22	7379	7380	CAPS
BaAK21D17	7383	7384	CAPS
BaAL29B07	7387	7388	SNP
baak20o16	7391	7392	SNP
bast42A0602	7395	7396	CAPS
BaH36B07	7399	7400	SNP
BaAK26L07	7403	7404	CAPS

TABLE 9-1-continued

Name	Primers used (SEQ ID NO:)		marker type
baal12a06	7407	7408	CAPS
BaSD3C20	7411	7412	SNP
bastl17G0113	7415	7416	SNP
baak11h14	7419	7420	SNP
baal12m14	7423	7424	CAPS
baal33a18	7427	7428	SNP
bah28a18	7431	7432	SNP
bags39o04	7435	7436	SNP
BaH48H04	7439	7440	SNP
BaGS6B11	7443	7444	size_poly (dominant)
bags4p16	7447	7448	SNP
basd24j22	7451	7452	SNP
basd16p15	7455	7456	SNP
bags15k16	7459	7460	SNP
bast23D1208	7463	7464	SNP
BaAL32B22	7467	7468	SNP
BaGS39D07	7471	7472	size_poly (codominant)
BaH19L09	7475	7476	SNP
bags38a17	7479	7480	SNP
BaAK39I11	7483	7484	SNP
BaSD3I24	7487	7488	SNP
BaH35F01	7491	7492	CAPS
BaAL30K02	7495	7496	CAPS
bah13l23	7499	7500	SNP
BaAL26H21	7503	7504	SNP
BaGS22H22	7507	7508	CAPS
bags13n11	7511	7512	CAPS
bags1h03	7515	7516	CAPS

TABLE 9-2

Name	Primers used (SEQ ID NO:)		marker type
baak32l16	7519	7520	SNP
baal19a12	7523	7524	CAPS
BaAK45G16	7527	7528	CAPS
BaGS37N19	7531	7532	CAPS
baak3f03	7535	7536	CAPS
bags5c02	7539	7540	SNP
BaGS35P07	7543	7544	SNP
HVM36	—	—	SSR
bah45e07	7547	7548	size_poly (codominant)
BaAK24B09	7551	7552	SNP
bags33a11	7555	7556	SNP
bah62i11	7559	7560	CAPS
BaH56A24	7563	7564	SNP
BaSD21D14	7567	7568	SNP
basd1a17	7571	7572	SNP
bah17n24	7575	7576	CAPS
kr70G0113	7579	7580	SNP
basd15f08	7583	7584	SNP
BaGS4J04	7587	7588	CAPS
baak33f06	7591	7592	CAPS
basd14f16	7595	7596	CAPS
BaH59K20	7599	7600	CAPS
baal35h05	7603	7604	SNP
BaGS20M01	7607	7608	CAPS
BaH25N22	7611	7612	size_poly (codominant)
baak14a24	7615	7616	SNP
baak30d07	7619	7620	SNP
bah11n18	7623	7624	CAPS
kr14C0305	7627	7628	SNP
baet18F0911	7631	7632	CAPS
BaGS4J18	7635	7636	CAPS
bast74C0705	7639	7640	SNP
BaAL4G17	7643	7644	SNP
bastl43H0515	7647	7648	SNP
BaH58M22	7651	7652	SNP
bags10i21	7655	7656	SNP
bah20h16	7659	7660	SNP
BaH17P13	7663	7664	SNP

TABLE 9-2-continued

Name	Primers used (SEQ ID NO:)		marker type
baak41d10	7667	7668	CAPS
BaGS14F01	7671	7672	CAPS
BaAK16E24	7675	7676	SNP
BaSD18F09	7679	7680	SNP
baet42A0501	7683	7684	SNP
BaAK20L07	7687	7688	SNP
baak16e20	7691	7692	SNP
BaGS13N14	7695	7696	size_poly (codominant)
basd13m14	7699	7700	SNP
bags20g23	7703	7704	SNP
basd1l17	1707	7708	SNP
basd26l01	7711	7712	SNP
BaAL37J18	7715	7716	SNP

TABLE 9-3

Name	Primers used (SEQ ID NO:)		marker type
bags7i05	7719	7720	SNP
bah60m17	7723	7724	SNP
bags21l01	7727	7728	SNP
baet31E0109	7731	7732	SNP
bags34m12	7735	7736	SNP
bah50n02	7739	7740	SNP
BaH50M11	7743	7744	SNP
bast27E1010	7747	7748	SNP
bags23c12	7751	7752	SNP
bah51m11	7755	7756	SNP
baak20d17	7759	7760	SNP
bags23l21	7763	7764	SNP
BaH52K04	7767	7768	CAPS
BaAL37F24	7771	7772	CAPS
bags23d01	7775	7776	CAPS
BaSD11K22	7779	7780	CAPS
baal29m02	7783	7784	SNP
bah17e21	7787	7788	SNP
bah56j18	7791	7792	SNP
bags38n06	7795	7796	CAPS
baet44D1208	7799	7800	CAPS
BaAL34O13	7803	7804	SNP
BaGS4N05	7807	7808	SNP
BaSD15P20	7811	7812	SNP
baal13d11	7815	7816	CAPS
bah27g02	7819	7820	SNP
basd27m10	7823	7824	SNP
basd23f16	7827	7828	SNP
bah16i19	7831	7832	SNP
BaH50I20	7835	7836	SNP
BaH34M23	7839	7840	CAPS
bah28b24	7843	7844	SNP
BaH50P13	7847	7848	CAPS
basd11m16	7851	7852	CAPS
bags10p15	7855	7856	CAPS
bags4g01	7859	7860	CAPS
bags10k08	7863	7864	CAPS
bags5e16	7867	7868	CAPS
bags18l02	7871	7872	CAPS
baak44k02	7875	7876	CAPS
bags35a20	7879	7880	CAPS
BaGS26M11	7883	7884	CAPS
basd14h21	7887	7888	CAPS
BaSD13D12	7891	7892	CAPS
bags38k23	7895	7896	size_poly (codominant)
BaH42E05	7899	7900	CAPS
bastl55A0701	7903	7904	CAPS
bags13g18	7907	7908	SNP
BaH15D23	7911	7912	SNP
kr28B0604	7915	7916	CAPS
bags10f01	7919	7920	size_poly (codominant)

TABLE 9-4

Name	Primers used (SEQ ID NO:)		marker type
BaGS33I07	7923	7924	SNP
BaSD27B02	7927	7928	SNP
BaGS30N12	7931	7932	SNP
basd3h13	7935	7936	SNP
BaGS37L19	7939	7940	SNP
bah16g18	7943	7944	CAPS
bags20i15	7947	7948	SNP
bags35c23	7951	7952	CAPS
bah56k07	7955	7956	SNP
bags37d02	7959	7960	SNP
BaAK19K05	7963	7964	CAPS
bah11i16	7967	7968	CAPS
bags22l23	7971	7972	SNP
kr33A0901	7975	7976	SNP
bastl38C0606	7979	7980	SNP
baak11j13	7983	7984	SNP
BaH58E19	7987	7988	SNP
BaGS31G22	7991	7992	SNP
bah37h01	7995	7996	SNP
BaAL29P13	7999	8000	SNP
bags39a22	8003	8004	SNP
bah19g10	8007	8008	SNP
BaAL31A14	8011	8012	SNP
BaH50G15	8015	8016	SNP
BaH51M12	8019	8020	SNP
bags18k22	8023	8024	SNP
BaGS20N21	8027	8028	SNP
BaSD17O21	8031	8032	SNP
BaH37G17	8035	8036	SNP
bags30l22	8039	8040	SNP
baak22b17	8043	8044	CAPS
bags20f22	8047	8048	CAPS
bast72G0113	8051	8052	SNP
BaH30B05	8055	8056	SNP
BaH60B14	8059	8060	SNP
BaH17B16	8063	8064	SNP
basd12n23	8067	8068	SNP
BaH61A21	8071	8072	SNP
BaAK19H17	8075	8076	SNP
bah47l12	8079	8080	SNP
baak18p11	8083	8084	SNP
baet29H0715	8087	8088	SNP
BaH13D11	8091	8092	SNP
baet39D1107	8095	8096	SNP
BaH53E15	8099	8100	SNP
bags32o15	8103	8104	SNP
bast48A0701	8107	8108	SNP
bast62D0907	8111	8112	SNP
BaH45P22	8115	8116	SNP
BaGS32L16	8119	8120	SNP
BaAK30J05	8123	8124	SNP

TABLE 9-5

Name	Primers used (SEQ ID NO:)		marker type
bah52a14	8127	8128	SNP
bah58i22	8131	8132	SNP
BaH56L16	8135	8136	SNP
bah52a21	8139	8140	SNP
BaSD14G11	8143	8144	SNP
bags6a03	8147	8148	SNP
bast72E0109	8151	8152	SNP
bags21a21	8155	8156	SNP
BaH58P13	8159	8160	SNP
bah27n22	8163	8164	SNP
bags20c13	8167	8168	SNP
bags30i14	8171	8172	SNP
BaAK17E11	8175	8176	SNP
baal1d17	8179	8180	CAPS
bags22f06	8183	8184	CAPS

TABLE 9-5-continued

Name	Primers used (SEQ ID NO:)		marker type
baal10l01	8187	8188	SNP
baak26e17	8191	8192	SNP
bah16a03	8195	8196	CAPS
BaAL11F18	8199	8200	CAPS
BaAK29E10	8203	8204	CAPS
bags32d21	8207	8208	SNP
bah54j22	8211	8212	SNP
baak16f14	8215	8216	CAPS
baak44c12	8219	8220	CAPS
bah13f11	8223	8224	SNP
baal39m19	8227	8228	CAPS
baak4e02	8231	8232	CAPS
baak46f04	8235	8236	CAPS
BaAK13N23	8239	8240	size_poly (codominant)
BaGS20E09	8243	8244	size_poly (codominant)
baal4f01	8247	8248	CAPS
BaSD19I17	8251	8252	CAPS
baal4l21	8255	8256	SNP
BaAK19P01	8259	8260	CAPS
BaAK31O14	8263	8264	SNP
BaH26P22	8267	8268	CAPS
baal13d17	8271	8272	SNP
bags22j12	8275	8276	SNP
bags33p05	8279	8280	SNP
bags38j07	8283	8284	SNP
kr59F0311	8287	8288	CAPS
baal13e10	8291	8292	CAPS
bags15d19	8295	8296	SNP
BaGS5K11	8299	8300	CAPS
BaGS10J14	8303	8304	CAPS
baak41m17	8307	8308	CAPS
bah57o03	8311	8312	SNP
baak41d22	8315	8316	CAPS
bah61c16	8319	8320	CAPS
BaAL7M13	8323	8324	CAPS
BaAK31F11	8327	8328	CAPS

TABLE 9-6

Name	Primers used (SEQ ID NO:)		marker type
basd22k05	8331	8332	Size_poly (codominant)
basd3p19	8335	8336	Size_poly (dominant)
baak17o09	8339	8340	CAPS
baal33d23	8343	8344	CAPS
BaAK12F04	8347	8348	SNP
bah53j16	8351	8352	SNP
BaSD2E24	8355	8356	SNP
bags39h08	8359	8360	SNP
BaSD1N02	8363	8364	SNP
bags20m21	8367	8368	SNP
baal10h19	8371	8372	SNP
basd12m11	8375	8376	SNP
bah29d24	8379	8380	SNP
BaGS39P09	8383	8384	SNP
BaGS31F17	8387	8388	SNP
BaGS23D08	8391	8392	SNP
bags39d15	8395	8396	SNP
BaGS34I17	8399	8400	SNP
BaH32N02	8403	8404	SNP
BaSD18H19	8407	8408	SNP
bast63A0101	8411	8412	SNP
BaH50N04	8415	8416	SNP
baal4a13	8419	8420	SNP
baal41l18	8423	8424	SNP
BaH31A03	8427	8428	CAPS
bastl39A0901	8431	8432	CAPS
baet46D0507	8435	8436	CAPS
baal27e20	8439	8440	SNP
bags37l16	8443	8444	SNP
baak34o06	8447	8448	SNP

TABLE 9-6-continued

Name	Primers used (SEQ ID NO:)		marker type
BaAL30I11	8451	8452	SNP
BaH62C15	8455	8456	SNP
basd12i15	8459	8460	CAPS
BaAK40I03	8463	8464	CAPS
BaAK23E14	8467	8468	CAPS
BaAL21F11	8471	8472	size_poly (codominant)
BaAK16L19	8475	8476	SNP
baal27a24	8479	8480	CAPS
kr41H0315	8483	8484	SNP
BaH62I23	8487	8488	SNP
bah52i24	8491	8492	SNP
bastl33A0301	8495	8496	SNP
BaH28J15	8499	8500	CAPS
bastl56A0301	8503	8504	SNP
baal39a03	8507	8508	SNP
baal5b15	8511	8512	CAPS
baak34l03	8515	8516	SNP
BaSD20J15	8519	8520	SNP
bastl30F0711	8523	8524	SNP
baal11p07	8527	8528	size_poly (codominant)
BaH28J10	8531	8532	CAPS

TABLE 9-7

Name	Primers used (SEQ ID NO:)		marker type
baak34p05	8535	8536	CAPS
bast56G0713	8539	8540	SNP
bah27d18	8543	8544	CAPS
bastl02H0715	8547	8548	SNP
bah37e07	8551	8552	size_poly (codominant)
bags4d18	8555	8556	size_poly (codominant)
bags8i05	8559	8560	SNP
BaH50A15	8563	8564	CAPS
kr06D0907	8567	8568	size_poly (codominant)
basd18m04	8571	8572	SNP
basd2f22	8575	8576	CAPS
BaH47K06	8579	8580	CAPS
BaH28G01	8583	8584	SNP
BaSD1M13	8587	8588	SNP
bags37h19	8591	8592	SNP
bags29b01	8595	8596	CAPS
BaH21A10	8599	8600	SNP
bags23d06	8603	8604	SNP
basd2a21	8607	8608	CAPS
BaGS19G10	8611	8612	SNP
cMWG699	—	—	STS
bah11b24	8615	8616	SNP
bast39D0408	8619	8620	SNP
baak33e08	8623	8624	SNP
bags33m15	8627	8628	CAPS
BaAL33B08	8631	8632	SNP
bags39e12	8635	8636	SNP
baak41e24	8639	8640	CAPS
bah63c08	8643	8644	CAPS
bags33n09	8647	8648	SNP
Bmag125	—	—	SSR
baal32h09	8651	8652	SNP
BaAK20O17	8655	8656	SNP
BaGS32G10	8659	8660	SNP
baet33E1210	8663	8664	SNP
BaH50O08	8667	8668	SNP
bast46F0711	8671	8672	SNP
BaH16F05	8675	8676	SNP
baal17e18	8679	8680	CAPS
cMWG694	—	—	STS
bah13o11	8683	8684	SNP
basd11g04	8687	8688	CAPS
bah32c06	8691	8692	size_poly (codominant)
basd27i13	8695	8696	SNP
kr14F0911	8699	8700	size_poly (codominant)

TABLE 9-7-continued

Name	Primers used (SEQ ID NO:)		marker type
BaGS36A04	8703	8704	CAPS
bags13a16	8707	8708	CAPS
bags26e20	8711	8712	SNP
baet45G1214	8715	8716	SNP
BaAK35F14	8719	8720	CAPS
BaAK23N21	8723	8724	size_poly (codominant)

TABLE 9-8

Name	Primers used (SEQ ID NO:)		marker type
basd13j22	8727	8728	SNP
BaAK46E10	8731	8732	SNP
bastl55F0812	8735	8736	SNP
baak46l06	8739	8740	CAPS
BaAL2D11	8743	8744	size_poly (codominant)
baak15p17	8747	8748	CAPS
BaGS33J16	8751	8752	CAPS
bags7p21	8755	8756	CAPS
BaAK22E05	8759	8760	CAPS
bah42m05	8763	8764	CAPS
BaAK25L01	8767	8768	CAPS
bags39e24	8771	8772	CAPS
BaH56N24	8775	8776	size_poly (codominant)
baak44i12	8779	8780	SNP
bah21j03	8783	8784	SNP
kr71B0103	8787	8788	SNP
BaGS16D15	8791	8792	CAPS
baak21p23	8795	8796	SNP
BaGS6G09	8799	8800	SNP
BaSD15M02	8803	8804	SNP
basd13f02	8807	8808	SNP
BaH19F21	8811	8812	CAPS
bags20b10	8815	8816	CAPS
bah26j10	8819	8820	SNP
bast65G0113	8823	8824	SNP
baak4k13	8827	8828	SNP
baal19j23	8831	8832	size_poly (codominant)
bags34h11	8835	8836	SNP
bags37j03	8839	8840	SNP
baal15e13	8843	8844	size_poly (codominant)
BaAL5O10	8847	8848	size_poly (dominant)
BaGS29J10	8851	8852	CAPS
bah22o08	8855	8856	SNP
bags6k13	8859	8860	SNP
bastl43C0705	8863	8864	SNP
BaAL4D10	8867	8868	size_poly (codominant)
basd12n12	8871	8872	CAPS
bags23h03	8875	8876	SNP
bags6l02	8879	8880	CAPS
bast63B0703	8883	8884	SNP
BaSD13E02	8887	8888	SNP
BaSD14P15	8891	8892	CAPS
bah13a17	8895	8896	SNP
BaH50L23	8899	8900	SNP
bags19g04	8903	8904	CAPS
bast73E0210	8907	8908	SNP
BaH50O21	8911	8912	SNP
basd21g05	8915	8916	SNP
bah33p11	8919	8920	CAPS
baal5i19	8923	8924	SNP
bah16e04	8927	8928	SNP

TABLE 9-9

Name	Primers used (SEQ ID NO:)		marker type
baak32p24	8931	8932	SNP
EBmac415	—	—	SSR

TABLE 9-9-continued

Name	Primers used (SEQ ID NO:)		marker type
bags38f12	8935	8936	CAPS
basd26p18	8939	8940	CAPS
baak45h16	8943	8944	CAPS
bah28p12	8947	8948	CAPS
bah19a10	8951	8952	CAPS
baak13d11	8955	8956	SNP
bah49p10	8959	8960	SNP
baal32n15	8963	8964	SNP
bast09C0305	8967	8968	size_poly (codominant)
basd16l09	8971	8972	CAPS
BaAK22H04	8975	8976	SNP
BaGS15J13	8979	8980	SNP
kr66G0414	8983	8984	SNP
BaSD22C07	8987	8988	SNP
kr71C1105	8991	8992	SNP
bags34i11	8995	8996	SNP
BaH23K17	8999	9000	SNP
bast39D0107	9003	9004	SNP
BaH44K24	9007	9008	SNP
BaGS18N21	9011	9012	CAPS
baak32k15	9015	9016	SNP
bah61a13	9019	9020	SNP
bags35n11	9023	9024	SNP
BaAK24I03	9027	9028	SNP
baal4h20	9031	9032	size_poly (codominant)
BaH28N23	9035	9036	SNP
bags10e13	9039	9040	SNP
baak27i10	9043	9044	size_poly (codominant)
bags19d13	9047	9048	SNP
baak19d04	9051	9052	SNP
BaAL34O19	9055	9056	SNP
baal12l02	9059	9060	CAPS
BaAK1P04	9063	9064	SNP
baak35m13	9067	9068	SNP
bags35a12	9071	9072	CAPS
bah41n09	9075	9076	SNP
BaGS23I12	9079	9080	SNP
BaH16P20	9083	9084	SNP
BaAK42L17	9087	9088	CAPS
baak36d23	9091	9092	CAPS
bast78C1006	9095	9096	CAPS
BaH45O16	9099	9100	SNP
bah21h09	9103	9104	SNP
bah58p22	9107	9108	SNP
bags20l19	9111	9112	SNP
bah13i10	9115	9116	SNP
BaAK36B07	9119	9120	CAPS
baak26b05	9123	9124	CAPS
baal7c15	9127	9128	SNP

TABLE 9-10

Name	Primers used (SEQ ID NO:)		marker type
bah63f05	9131	9132	SNP
bags15l16	9135	9136	SNP
BaGS6N10	9139	9140	CAPS
bah41e10	9143	9144	SNP
BaH54D08	9147	9148	SNP
baak18c01	9151	9152	SNP
basd21o07	9155	9156	SNP
bah41b23	9159	9160	CAPS
basd18g15	9163	9164	size_poly (codominant)
baak43o03	9167	9168	SNP
bastl30D0408	9171	9172	CAPS
bah17p16	9175	9176	CAPS
baal13f18	9179	9180	SNP
bags18i22	9183	9184	SNP
bags9b02	9187	9188	SNP
bah11e22	9191	9192	SNP
bah58h09	9195	9196	SNP

TABLE 9-10-continued

Name	Primers used (SEQ ID NO:)		marker type
basd16e16	9199	9200	CAPS
BaAK4C12	9203	9204	SNP
bags37a05	9207	9208	SNP
bags9p10	9211	9212	CAPS
baak24m01	9215	9216	size_poly (codominant)
basd27d09	9219	9220	CAPS
baak34a14	9223	9224	size_poly (dominant)
baak36a20	9227	9228	SNP
BaSD17P09	9231	9232	CAPS
bags5m04	9235	9236	CAPS
BaGS5E06	9239	9240	CAPS
MWG2076	—	—	STS
bags15f03	9243	9244	size_poly (dominant)
bags18j23	9247	9248	size_poly (dominant)
baal13m04	9251	9252	SNP
bags9o24	9255	9256	SNP
kr49E0610	9259	9260	CAPS
bah12h16	9263	9264	SNP
baak33n16	9267	9268	SNP
BaGS22E05	9271	9272	CAPS
bah26n01	9275	9276	SNP
BaGS39E07	9279	9280	SNP
BaH45O03	9283	9284	CAPS
BaH38A09	9287	9288	SNP

TABLE 10-1

Name	Primers used (SEQ ID NO:)		marker type
BaAL15P01	9291	9292	SNP
BaAK42D06	9295	9296	size_poly (dominant)
bags12k16	9299	9300	size_poly (codominant)
BaAL36H19	9303	9304	size_poly (codominant)
bags1d06	9307	9308	SNP
bast18A0602	9311	9312	SNP
basd22i04	9315	9316	CAPS
BaGS31M01	9319	9320	CAPS
BaH63H24	9323	9324	SNP
basd15n13	9327	9328	CAPS
MWG848	—	—	STS
BaAK13C16	9331	9332	SNP
BaGS32C19	9335	9336	SNP
baak36f08	9339	9340	SNP
bastl04C0406	9343	9344	CAPS
bastl42D1107	9347	9348	SNP
BaGS31B20	9351	9352	size_poly (codominant)
baak39l17	9355	9356	CAPS
BaAL17J24	9359	9360	CAPS
bah15p03	9363	9364	CAPS
baak20g06	9367	9368	SNP
baal22c16	9371	9372	CAPS
baak46o05	9375	9376	SNP
basd15h22	9379	9380	SNP
BaSD19C07	9383	9384	SNP
bags22i13	9387	9388	CAPS
baak39a14	9391	9392	SNP
bah31e12	9395	9396	SNP
BaSD15L22	9399	9400	SNP
BaGS20D21	9403	9404	CAPS
bags39o21	9407	9408	CAPS
basd21j11	9411	9412	SNP
BaH48C10	9415	9416	SNP
BaH54J07	9419	9420	SNP
BaSD19H23	9423	9424	CAPS
baak35n06	9427	9428	CAPS
bags35b22	9431	9432	CAPS
BaAK30H06	9435	9436	CAPS
BaAL15M07	9439	9440	CAPS
BaGS20N02	9443	9444	CAPS
BaAL19L12	9447	9448	CAPS
bags25b05	9451	9452	CAPS

TABLE 10-1-continued

Name	Primers used (SEQ ID NO:)		marker type
HvLTPPB	—	—	SSR
baal1h04	9455	9456	CAPS
baet46B0903	9459	9460	SNP
BaGS19F16	9463	9464	SNP
baak13g18	9467	9468	SNP
BaH45N12	9471	9472	CAPS
bast74H0216	9475	9476	SNP
bah24l06	9479	9480	size_poly (dominant)
BaAK45C14	9483	9484	SNP

TABLE 10-2

Name	Primers used (SEQ ID NO:)		marker type
baal5k12	9487	9488	CAPS
kr63F0111	9491	9492	SNP
baak13h18	9495	9496	SNP
baak12j16	9499	9500	CAPS
BaAK28J20	9503	9504	CAPS
BaH27G14	9507	9509	CAPS
BaH49B13	9511	9512	SNP
BaGS35A09	9515	9516	CAPS
BaGS38L24	9519	9520	size_poly (dominant)
BaAK43H20	9523	9524	CAPS
bast16A0802	9527	9528	SNP
basd18k01	9531	9532	SNP
BaH58D17	9535	9536	SNP
BaAK30M07	9539	9540	CAPS
bags6a04	9543	9544	CAPS
kr15H0915	9547	9548	CAPS
bags26d01	9551	9552	SNP
basd14k04	9555	9556	SNP
BaSD24D11	9559	9560	SNP
BaH53L10	9563	9564	SNP
BaH60D22	9567	9568	size_poly (codominant)
BaSD1G06	9571	9572	size_poly (codominant)
BaAK21L13	9575	9576	size_poly (codominant)
bah57m03	9579	9580	SNP
baal30b10	9583	9584	SNP
bah62n16	9587	9588	SNP
BaGS22F15	9591	9592	SNP
BaH50J14	9595	9596	SNP
bah19d23	9599	9600	SNP
bags38c06	9603	9604	SNP
BaGS25N05	9607	9608	SNP
bastl29B0503	9611	9612	SNP
baak27d01	9615	9616	CAPS
baak43n21	9619	9620	SNP
BaAL4F05	9623	9624	size_poly (codominant)
baal4a06	9627	9628	SNP
bast17D1008	9631	9632	SNP
BaGS16B17	9635	9636	SNP
BaGS27P18	9639	9640	CAPS
BaGS4J14	9643	9644	CAPS
BaAK16B19	9647	9648	SNP
baal40p07	9651	9652	SNP
bah49c19	9655	9656	SNP
bast58C0406	9659	9660	SNP
BaAK35M24	9663	9664	SNP
bags19h13	9667	9668	SNP
bah57c21	9671	9672	SNP
BaH53P15	9675	9676	SNP
BaGS20A10	9679	9680	SNP
bast02D0808	9683	9684	SNP
bags31c04	9687	9688	SNP

TABLE 10-3

Name	Primers used (SEQ ID NO:)		marker type
BaH32J06	9691	9692	CAPS
bah60o22	9695	9696	SNP
BaH50C16	9699	9700	SNP
BaH57K23	9703	9704	CAPS
bags21g23	9707	9708	size_poly (codominant)
HVM9	—	—	SSR
Bmac67	—	—	SSR
baak43e04	9711	9712	SNP
kr17G1113	9715	9716	SNP
bags19k19	9719	9720	SNP
baak38b13	9723	9724	SNP
baak1d12	9727	9728	SNP
BaH28M14	9731	9732	SNP
BaH48I15	9735	9736	SNP
basd27h23	9739	9740	SNP
BaAK21A11	9743	9744	SNP
bast04B0804	9747	9748	SNP
bah45f13	9751	9752	SNP
BaAL8J18	9755	9756	SNP
BaGS9D01	9759	9760	SNP
baal12d12	9763	9764	CAPS
baal4i06	9767	9768	SNP
bah26i01	9771	9772	SNP
BaGS15C17	9775	9776	SNP
baak1k08	9779	9780	SNP
bags9b03	9783	9784	SNP
baet42G1214	9787	9788	SNP
bah18d12	9791	9792	SNP
BaSD14G02	9795	9796	CAPS
bags22b22	9799	9800	SNP
bah13f10	9803	9804	size_poly (codominant)
baal36g05	9807	9808	SNP
bags33j15	9811	9812	SNP
BaAL12H04	9815	9816	size_poly (codominant)
BaGS16I18	9819	9820	CAPS
bast61D0707	9823	9824	SNP
bah11k22	9827	9828	CAPS
baak32p21	9831	9832	CAPS
bah63l21	9835	9836	CAPS
BaGS38D03	9839	9840	CAPS
BaSD23A04	9843	9844	SNP
BaSD14C15	9847	9848	SNP
bast63C0105	9851	9852	SNP
bast23C1105	9855	9856	SNP
bags23b01	9859	9860	CAPS
bags29c09	9863	9864	CAPS
bags6b06	9867	9868	CAPS
BaAK27G06	9871	9872	CAPS
BaAK39D07	9875	9876	CAPS
BaGS20G21	9879	9880	CAPS
bastl22E0810	9883	9884	size_poly (codominant)

TABLE 10-4

Name	Primers used (SEQ ID NO:)		marker type
bah11m03	9887	9888	CAPS
BaAL3C04	9891	9892	CAPS
BaAL19H10	9895	9896	SNP
bags24n16	9899	9900	CAPS
BaSD24B15	9903	9904	SNP
bah48n17	9907	9908	SNP
bags9i05	9911	9912	SNP
bags1l22	9915	9916	SNP
bah62p18	9919	9920	SNP
bah55n21	9923	9924	SNP
bah44a05	9927	9928	SNP
bah19c13	9931	9932	SNP
baal12b04	9935	9936	CAPS
Bmag136	—	—	SSR
Bmac209	—	—	SSR

TABLE 10-4-continued

Name	Primers used (SEQ ID NO:)		marker type
BaAK28A10	9939	9940	size_poly (dominant)
kr28B0703	9943	9944	SNP
bastl50C0606	9947	9948	SNP
BaGS36B01	9951	9952	CAPS
BaH19A05	9955	9956	SNP
baal10c06	9959	9960	SNP
bags19p04	9963	9964	SNP
BaAK21A17	9967	9968	SNP
bah20j14	9971	9972	SNP
BaAK19A03	9975	9976	SNP
BaGS30E19	9979	9980	SNP
BaAK28C21	9983	9984	size_poly (codominant)
bags11o14	9987	9988	SNP
BaGS13P22	9991	9992	SNP
kr27A1101	9995	9996	SNP
HVM27	—	—	SSR
baal12i18	9999	10000	CAPS
BaAL8G07	10003	10004	CAPS
bast58F0412	10007	10008	SNP
bags3f23	10011	10012	CAPS
baal4m06	10015	10016	CAPS
baal32p23	10019	10020	SNP
basd23m17	10023	10024	SNP
bastl30E0509	10027	10028	SNP
bah44b0B	10031	10032	SNP
BaGS14N10	10035	10036	SNP
BaGS32B13	10039	10040	SNP
BaH30B03	10043	10044	SNP
basd1l23	10047	10048	CAPS
basd11o06	10051	10052	SNP
bah17f24	10055	10056	SNP
BaAK26L17	10059	10060	SNP
bags23f03	10063	10064	SNP
bags20o06	10067	10068	SNP
bags19n12	10071	10072	SNP
baal12a09	10075	10076	size_poly (codominant)

TABLE 10-5

Name	Primers used (SEQ ID NO:)		marker type
bast14F0612	10079	10080	SNP
baak13p20	10083	10084	CAPS
BaGS16K13	10087	10088	SNP
baak22c16	10091	10092	SNP
baal40m06	10095	10096	SNP
BaH29I03	10099	10100	CAPS
bah16h01	10103	10104	CAPS
bah57a11	10107	10108	SNP
BaH41E23	10111	10112	SNP
baal11c11	10115	10116	size_poly (dominant)
BaSD14L18	10119	10120	SNP
bah14d17	10123	10124	SNP
BaGS1N17	10127	10128	SNP
bags27h17	10131	10132	CAPS
bah47p22	10135	10136	SNP
BaH50A16	10139	10140	SNP
bags7b20	10143	10144	SNP
bags22a02	10147	10148	SNP
HvBRI1	—	—	dCAPS
basd12g02	10151	10152	SNP
basd15o18	10155	10156	SNP
baal25d19	10159	10160	SNP
bast52G0414	10163	10164	SNP
baal11c20	10167	10168	CAPS
bags37k06	10171	10172	SNP
bags6e22	10175	10176	SNP
basd15a02	10179	10180	CAPS
bags7b06	10183	10184	CAPS
bah15k11	10187	10188	CAPS
bast46C0406	10191	10192	SNP

TABLE 10-5-continued

Name	Primers used (SEQ ID NO:)		marker type
bastl45E0509	10195	10196	SNP
baal35p14	10199	10200	CAPS
BaH41G07	10203	10204	SNP
bast46H1016	10207	10208	SNP
bah60d12	10211	10212	SNP
baal39a19	10215	10216	SNP
baak11n24	10219	10220	CAPS
bast14E0909	10223	10224	SNP
baet13G0713	10227	10228	SNP
HVM33	—	—	SSR
BaSD14L04	10231	10232	CAPS
baak13c05	10235	10236	SNP
bastl41G0513	10239	10240	SNP
BaGS39M09	10243	10244	CAPS
baal19b12	10247	10248	SNP
BaAL39B05	10251	10252	SNP
BaAL1J03	10255	10256	SNP
basd11k09	10259	10260	SNP
BaGS33N15	10263	10264	SNP
baet43H0416	10267	10268	SNP
bah11m06	10271	10272	SNP

TABLE 10-6

Name	Primers used (SEQ ID NO:)		marker type
baak31a24	10275	10276	CAPS
bags27h20	10279	10280	SNP
basd27c09	10283	10284	SNP
BaAL25O01	10287	10288	SNP
bags7f08	10291	10292	CAPS
BaGS13O12	10295	10296	size_poly (codominant)
bags38b06	10299	10300	CAPS
BaAK19J09	10303	10304	SNP
bags9e16	10307	10308	size_poly (codominant)
bags20n14	10311	10312	SNP
bah42o12	10315	10316	SNP
baak31k16	10319	10320	SNP
bags4p14	10323	10324	SNP
bah27a22	10327	10328	CAPS
bags21n02	10331	10332	size_poly (codominant)
BaH62B09	10335	10336	SNP
BaGS19J10	10339	10340	SNP
bags15k18	10343	10344	SNP
BaAK29G03	10347	10348	CAPS
baak23e11	10351	10352	CAPS
bags31k04	10355	10356	CAPS
bast56C0305	10359	10360	size_poly (dominant)
basd26c09	10363	10364	SNP
BaSD20B11	10367	10368	SNP
HVM60	—	—	SSR
BaH46F11	10371	10372	SNP
BaH30F03	10375	10376	SNP
BaSD27G02	10379	10380	CAPS
Bmag225	—	—	SSR
BaAK33I12	10383	10384	SNP
baak32m10	10387	10388	CAPS
BaAL4L02	10391	10392	CAPS
kr44F0911	10395	10396	size_poly (codominant)
BaGS37A16	10399	10400	SNP
bags39p06	10403	10404	SNP
BaAL12N06	10407	10408	SNP
bags22p05	10411	10412	size_poly (codominant)
bags9a03	10415	10416	SNP
baet24F1212	10419	10420	SNP
baak29d10	10423	10424	SNP
bags13i12	10427	10428	SNP
BaAL16A23	10431	10432	SNP
bastl16B1204	10435	10436	SNP
bastl29F0711	10439	10440	SNP
BaGS32M17	10443	10444	CAPS

TABLE 10-6-continued

Name	Primers used (SEQ ID NO:)		marker type
baal15e10	10447	10448	SNP
basd3g08	10451	10452	CAPS
baal33m18	10455	10456	SNP
baak24e23	10459	10460	SNP
baak46j13	10463	10464	SNP
bah49o05	10467	10468	SNP

TABLE 10-7

Name	Primers used (SEQ ID NO:)		marker type
baal15e05	10471	10472	SNP
BaAK1O08	10475	10476	SNP
BaGS30P02	10479	10480	SNP
BaSD15D05	10483	10484	SNP
BaAL7B16	10487	10488	CAPS
bags38n23	10491	10492	SNP
baak36a14	10495	10496	SNP
baak34g01	10499	10500	CAPS
baak12f01	10503	10504	CAPS
BaGS30I18	10507	10508	CAPS
bags35n24	10511	10512	SNP
bah37j21	10515	10516	SNP
bah31e13	10519	10520	SNP
bags22g10	10523	10524	size_poly (dominant)
bags22f17	10527	10528	size_poly (codominant)
baal30l05	10531	10532	SNP
bags38o10	10535	10536	SNP
baak40o04	10539	10540	CAPS
BaH49L21	10543	10544	SNP
bastl30A0701	10547	10548	SNP
bags19l03	10551	10552	SNP
bah18m13	10555	10556	SNP
baak44p03	10559	10560	SNP
kr10H0216	10563	10564	SNP
bags11i04	10567	10568	CAPS
bah52o06	10571	10572	CAPS
bah35c14	10575	10576	size_poly (codominant)
BaAL30C02	10579	10580	size_poly (dominant)
bah11i21	10583	10584	SNP
BaAK36B11	10587	10588	size_poly (codominant)
BaAK20K23	10591	10592	SNP
basd14n22	10595	10596	SNP
BaAL25p17	10599	10600	CAPS
BaH49A01	10603	10604	size_poly (codominant)
basd13p12	10607	10608	size_poly (codominant)
bags39m17	10611	10612	size_poly (codominant)
baet44D0707	10615	10616	SNP
BaH16P10	10619	10620	SNP
BaAK42J01	10623	10624	SNP
kr24E0709	10627	10628	CAPS
BaAK38O08	10631	10632	SNP
BaAL13N01	10635	10636	CAPS
baak12c12	10639	10640	size_poly (codominant)
BaGS31N06	10643	10644	CAPS
baal15f24	10647	10648	CAPS
BaSD18B21	10651	10652	SNP
BaSD17G23	10655	10656	SNP
baak41k22	10659	10660	SNP
baak21o03	10663	10664	SNP
BaSD16B18	10667	10668	SNP
bast79C1105	10671	10672	SNP

TABLE 10-8

Name	Primers used (SEQ ID NO:)		marker type
BaAK4J17	10675	10676	SNP
BaAL37H08	10679	10680	SNP

TABLE 10-8-continued

Name	Primers used (SEQ ID NO:)		marker type
BaH36L17	10683	10684	CAPS
BaH46A12	10687	10688	size_poly (codominant)
bags11i15	10691	10692	SNP
baak20g24	10695	10696	CAPS
baak20h23	10699	10700	size_poly (codominant)
baak35b18	10703	10704	SNP
Bmag13	—	—	SSR
baak41o03	10707	10708	SNP
baet46C0206	10711	10712	CAPS
bags10i20	10715	10716	size_poly (dominant)
baal1b16	10719	10720	SNP
baal5i05	10723	10724	CAPS
BaH27B05	10727	10728	size_poly (codominant)
bah14a11	10731	10732	CAPS
basd19k10	10735	10736	size_poly (codominant)
bags30n17	10739	10740	CAPS
bags31e24	10743	10744	CAPS
BaGS5B16	10747	10748	SNP
BaAL5F06	10751	10752	SNP
bags34a11	10755	10756	CAPS
bags6c16	10759	10760	CAPS
bah42g19	10763	10764	SNP
BaH47O14	10767	10768	SNP
BaH12L06	10771	10772	SNP
basd11a10	10775	10776	CAPS
BaH50I12	10779	10780	CAPS
BaH51A21	10783	10784	SNP
baak45p02	10787	10788	CAPS
BaSD12P12	10791	10792	SNP
bags9l16	10795	10796	CAPS
BaSD26O20	10799	10800	CAPS
bags5d10	10803	10804	CAPS
baal0e07	10807	10808	CAPS
baak14e02	10811	10812	CAPS
BaH63F14	10815	10816	size_poly (codominant)
bah33f19	10819	10820	CAPS
bags19l10	10823	10824	SNP
BaH56J21	10827	10828	SNP
baal40i22	10831	10832	CAPS
kr42C0105	10835	10836	size_poly (codominant)
bags16i19	10839	10840	SNP
BaH54H01	10843	10844	SNP
kr69E0810	10847	10848	CAPS
bags17i14	10851	10852	CAPS
bags20e19	10855	10856	SNP
bast74C0206	10859	10860	SNP
BaAK13L10	10863	10864	SNP
bags20i01	10867	10868	SNP
basd19n14	10871	10872	SNP

TABLE 10-9

Name	Primers used (SEQ ID NO:)		marker type
baak42g21	10875	10876	SNP
BaAK39A15	10879	10880	CAPS
basd18o21	10883	10884	CAPS
BaAK22K17	10887	10888	SNP
baal6o24	10891	10892	SNP
BaH22C09	10895	10896	SNP
HVM62	—	—	SSR
bags23k14	10899	10900	CAPS
baal24n12	10903	10904	SNP
BaGS21H17	10907	10908	CAPS
BaSD16D09	10911	10912	SNP
BaAL13B22	10915	10916	SNP
bah41l03	10919	10920	CAPS
bastl30F0111	10923	10924	SNP
BaH15L04	10927	10928	SNP
baak40c12	10931	10932	SNP
kr23D0408	10935	10936	CAPS

TABLE 10-9-continued

Name	Primers used (SEQ ID NO:)		marker type
bah57d15	10939	10940	SNP
baak31e03	10943	10944	SNP
BaAL13O01	10947	10948	SNP
BaSD26P04	10951	10952	SNP
bags20f18	10955	10956	SNP
BaH42J22	10959	10960	SNP
BaAL3K03	10963	10964	size_poly (codominant)
kr30B1103	10967	10968	SNP
baak14i02	10971	10972	CAPS
bags28c17	10975	10976	CAPS
baal4e21	10979	10980	SNP
BaGS29D05	10983	10984	SNP
bah54d24	10987	10988	SNP
basd22g20	10991	10992	CAPS
BaH62H20	10995	10996	CAPS
bags38h17	10999	11000	SNP
BaAK30B23	11003	11004	SNP
BaAK24P09	11007	11008	SNP
baak23i12	11011	11012	CAPS
BaGS22D06	11015	11016	SNP
BaAL34P18	11019	11020	SNP
BaAL39F24	11023	11024	CAPS
BaGS4L04	11027	11028	CAPS
bah12e02	11031	11032	CAPS
BaAL15F23	11035	11036	SNP
BaGS25O15	11039	11040	SNP
BaGS7G14	11043	11044	CAPS
basd24i11	11047	11048	CAPS
baak20l21	11051	11052	size_poly (dominant)
bags33m02	11055	11056	SNP
BaH48G21	11059	11060	SNP
bags27p13	11063	11064	SNP

TABLE 11-1

Name	Primers used (SEQ ID NO:)		marker type
BaGS10N17	11067	11068	size_poly (dominant)
BaAK38K23	11071	11072	size_poly (codominant)
bah14a22	11075	11076	SNP
BaAL19O06	11079	11080	CAPS
BaGS32P17	11083	11084	SNP
bah11j04	11087	11088	CAPS
baak35b06	11091	11092	SNP
basd21f17	11095	11096	SNP
BaAK44O11	11099	11100	size_poly (dominant)
bastl14D0408	11103	11104	size_poly (codominant)
BaAK42C15	11107	11108	CAPS
baak40n12	11111	11112	CAPS
basd2j05	11115	11116	CAPS
baak46n05	11119	11120	size_poly (codominant)
baak24g04	11123	11124	CAPS
BaAL22H02	11127	11128	SNP
bah56g24	11131	11132	SNP
BaAL2I22	11135	11136	CAPS
bags20c22	11139	11140	CAPS
BaH50O22	11143	11144	CAPS
baak32f06	11147	11148	SNP
bags35i24	11151	11152	CAPS
BaSD21D13	11155	11156	SNP
bast46D0408	11159	11160	SNP
bast55B1204	11163	11164	SNP
BaGS39M07	11167	11168	size_poly (dominant)
bags39b15	11171	11172	SNP
baak37p11	11175	11176	CAPS
bah29o22	11179	11180	SNP
baak12k14	11183	11184	size_poly (codominant)
baet31E1010	11187	11188	SNP
HVM40	—	—	SSR
baal39h14	11191	11192	SNP
bags14g22	11195	11196	size_poly (codominant)

TABLE 11-1-continued

Name	Primers used (SEQ ID NO:)		marker type
baal18m18	11199	11200	SNP
BaSD24E02	11203	11204	SNP
BaH50N14	11207	11208	CAPS
kr70A0202	11211	11212	CAPS
baak11d04	11215	11216	SNP
MWG2033	—	—	STS
bags20h01	11219	11220	CAPS
BaH39P15	11223	11224	CAPS
BaAK46O20	11227	11228	CAPS
baal33m06	11231	11232	SNP
bastl50E0309	11235	11236	SNP
bags20i17	11239	11240	SNP
BaGS22A07	11243	11244	SNP
bah41b09	11247	11248	SNP
kr18G0913	11251	11252	CAPS
BaGS19O23	11255	11256	SNP
bags15e12	11259	11260	CAPS

TABLE 11-2

Name	Primers used (SEQ ID NO:)		marker type
bags29i09	11263	11264	CAPS
baak19m23	11267	11268	CAPS
bags14h12	11271	11272	SNP
bah32e15	11275	11276	SNP
bah11l02	11279	11280	CAPS
bags39e16	11283	11284	SNP
bags10l12	11287	11288	CAPS
BaGS31M13	11291	11292	CAPS
baal32m10	11295	11296	SNP
basd12b23	11299	11300	SNP
baal39e15	11303	11304	SNP
baal16l11	11307	11308	CAPS
BaGS31B01	11311	11312	SNP
BaSD17F09	11315	11316	CAPS
BaH48L11	11319	11320	SNP
BaSD14M08	11323	11324	CAPS
bah56c09	11327	11328	SNP
baak17g07	11331	11332	size_poly (codominant)
bags20k09	11335	11336	SNP
BaSD25B08	11339	11340	SNP
bast27E0309	11343	11344	SNP
baet20D0107	11347	11348	SNP
BaAL17L08	11351	11352	CAPS
bah61p18	11355	11356	CAPS
bah63d12	11359	11360	CAPS
BaAK26A03	11363	11364	CAPS
baak26n10	11367	11368	SNP
bast22B0204	11371	11372	SNP
BaAL3C05	11375	11376	SNP
BaGS38H14	11379	11380	size_poly (codominant)
BaAL4D19	11383	11384	CAPS
BaAK20B09	11387	11388	SNP
BaAK37H01	11391	11392	SNP
BaGS33P13	11395	11396	SNP
basd13l12	11399	11400	CAPS
bags11m01	11403	11404	CAPS
BaGS18H09	11407	11408	SNP
basd3d13	11411	11412	CAPS
baal9m23	11415	11416	CAPS
bags23f08	11419	11420	CAPS
BaGS15L23	11423	11424	CAPS
baak2k13	11427	11428	CAPS
baak17d18	11431	11432	SNP
bags13a12	11435	11436	SNP
baak44g22	11439	11440	CAPS
kr34F0212	11443	11444	SNP
baal16d11	11447	11448	SNP
bah22d04	11451	11452	SNP
bah48m23	11455	11456	size_poly (codominant)

TABLE 11-2-continued

Name	Primers used (SEQ ID NO:)		marker type
basd15p13	11459	11460	CAPS
BaGS6O07	11463	11464	SNP

TABLE 11-3

Name	Primers used (SEQ ID NO:)		marker type
BaH37O10	11467	11468	SNP
bags21k10	11471	11472	CAPS
bah56n18	11475	11476	CAPS
baal9i11	11479	11480	SNP
BaAL39N06	11483	11484	SNP
bags9d05	11487	11488	size_poly (codominant)
BaAL19I19	11491	11492	SNP
basd12l11	11495	11496	SNP
bastl46D1008	11499	11500	SNP
BaH50H16	11503	11504	SNP
bags9n05	11507	11508	SNP
kr61B1103	11511	11512	SNP
kr27B0103	11515	11516	SNP
kr33H1115	11519	11520	SNP
baak30l02	11523	11524	SNP
bah55a12	11527	11528	SNP
BaH26K14	11531	11532	SNP
HVM3	—	—	SSR
BaAK33K19	11535	11536	CAPS
basd18m17	11539	11540	SNP
BaH50G09	11543	11544	CAPS
BaH53B03	11547	11548	SNP
BaH54L11	11551	11552	CAPS
basd13i14	11555	11556	CAPS
bah56g09	11559	11560	CAPS
bah41b06	11563	11564	CAPS
bags14d19	11567	11568	SNP
baal20f05	11571	11572	SNP
BaH18H12	11575	11576	SNP
baal9o21	11579	11580	SNP
bags21a02	11583	11584	SNP
BaAL3G19	11587	11588	SNP
baal7a09	11591	11592	SNP
BaAL29I16	11595	11596	size_poly (codominant)
bast70B0804	11599	11600	SNP
bags14n08	11603	11604	CAPS
bastl14F0412	11607	11608	SNP
BaAK36I12	11611	11612	CAPS
baal3f19	11615	11616	SNP
baal1e10	11619	11620	SNP
bags6k02	11623	11624	SNP
kr42H0315	11627	11628	SNP
bah39p02	11631	11632	SNP
BaGS9L14	11635	11636	SNP
baal35l03	11639	11640	SNP
basd12m15	11643	11644	SNP
BaAK35P01	11647	11648	SNP
basd11d18	11651	11652	SNP
BaH38E07	11655	11656	SNP
BaGS18H13	11659	11660	SNP
bags18g16	11663	11664	SNP

TABLE 11-4

Name	Primers used (SEQ ID NO:)		marker type
bags27f21	11667	11668	SNP
BaGS7M13	11671	11672	CAPS
baal39c19	11675	11676	SNP
baak46j05	11679	11680	SNP
BaAK32D20	11683	11684	CAPS
MWG058	—	—	STS

TABLE 11-4-continued

Name	Primers used (SEQ ID NO:)		marker type
BaGS18M02	11687	11688	SNP
bags9c05	11691	11692	size_poly (dominant)
baak46m13	11695	11696	CAPS
bags35n16	11699	11700	CAPS
bags39g08	11703	11704	SNP
baal33a06	11707	11708	CAPS
BaSD17F20	11711	11712	CAPS
bags22i21	11715	11716	CAPS
bah32g18	11719	11720	SNP
BaAL37O23	11723	11724	CAPS
bags22p03	11727	11728	CAPS
bags38l18	11731	11732	SNP
BaGS35C13	11735	11736	SNP
bah47h04	11739	11740	SNP
bags30m11	11743	11744	SNP
BaH22L15	11747	11748	SNP
bags39e15	11751	11752	SNP
kr65H0816	11755	11756	CAPS
basd11h11	11759	11760	SNP
baak2b06	11763	11764	SNP
Bmag353	—	—	SSR
bags37j11	11767	11768	CAPS
BaAK46L15	11771	11772	CAPS
BaSD14A23	11775	11776	SNP
bast25C0705	11779	11780	SNP
bast21B1204	11783	11784	SNP
bags1l16	11787	11788	CAPS
BaAK21G02	11791	11792	SNP
bastl26E1109	11795	11796	SNP
basd13k24	11799	11800	SNP
BaAL13F02	11803	11804	SNP
bags13c10	11807	11808	SNP
bags11o11	11811	11812	SNP
BaAK36P01	11815	11816	SNP
bah52d09	11819	11820	SNP
BaGS26D18	11823	11824	SNP
baak33c22	11827	11828	SNP
basd1d10	11831	11832	CAPS
baak11c22	11835	11836	CAPS
bags34l06	11839	11840	SNP
baak33j06	11843	11844	CAPS
bags23a11	11847	11848	CAPS
bags34f02	11851	11852	CAPS
bags20p21	11855	11856	SNP
bah52m01	11859	11860	SNP

TABLE 11-5

Name	Primers used (SEQ ID NO:)		marker type
basd15d07	11863	11864	SNP
BaAL20A14	11867	11868	CAPS
BaGS21B04	11871	11872	CAPS
HVM68	—	—	SSR
BaAL30B07	11875	11876	SNP
basd11p10	11879	11880	CAPS
BaGS33E17	11883	11884	CAPS
kr67C0206	11887	11888	SNP
bags15j20	11891	11892	SNP
BaH15E05	11895	11896	SNP
BaH58K02	11899	11900	SNP
basd13d17	11903	11904	SNP
BaGS17A15	11907	11908	CAPS
BaAK30F13	11911	11912	SNP
baal17m22	11915	11916	CAPS
baak42f04	11919	11920	CAPS
baal2n22	11923	11924	SNP
kr30C0705	11927	11928	SNP
BaSD19J21	11931	11932	SNP
BaH34N22	11935	11936	SNP

TABLE 11-5-continued

Name	Primers used (SEQ ID NO:)		marker type
BaAK2I20	11939	11940	CAPS
BaGS1E22	11943	11944	SNP
baak34b17	11947	11948	SNP
BaSD11L18	11951	11952	CAPS
kr32A0202	11955	11956	SNP
bags27h21	11959	11960	SNP
bah62d17	11963	11964	SNP
bah43e22	11967	11968	SNP
BaAL30I23	11971	11972	SNP
BaSD13H20	11975	11976	CAPS
BaSD14O04	11979	11980	CAPS
baak34p06	11983	11984	SNP
bah63b08	11987	11988	SNP
bastl03F0812	11991	11992	SNP
basd14m17	11995	11996	SNP
BaSD2J03	11999	12000	SNP
bah13b17	12003	12004	size_poly (codominant)
baal32b23	12007	12008	SNP
bastl50D1208	12011	12012	size_poly (codominant)
BaGS9H13	12015	12016	CAPS
baal33e04	12019	12020	CAPS
BaAL40L16	12023	12024	CAPS
bah44n03	12027	12028	SNP
bags20h05	12031	12032	SNP
bags20l15	12035	12036	SNP
BaGS7E03	12039	12040	SNP
bags9k13	12043	12044	CAPS
bast55E0709	12047	12048	SNP
bags8a14	12051	12052	CAPS
baak38k04	12055	12056	SNP
BaH33B15	12059	12060	CAPS

TABLE 11-6

Name	Primers used (SEQ ID ND:)		marker type
bags29m17	12063	12064	size_poly (codominant)
BaSD23P08	12067	12068	CAPS
BaH42L12	12071	12072	SNP
bast79G0313	12075	12076	CAPS
baet46C0905	12079	12080	SNP
baal4o09	12083	12084	CAPS
bah26e10	12087	12088	SNP
BaH32J04	12091	12092	SNP
bags20l07	12095	12096	SNP
kr18C0505	12099	12100	SNP
basd11m24	12103	12104	SNP
basd1i15	12107	12108	SNP
bah45b02	12111	12112	size_poly (codominant)
bast40C0206	12115	12116	CAPS
baal40g05	12119	12120	CAPS
bah13i21	12123	12124	SNP
basd27o20	12127	12128	SNP
BaAK12L24	12131	12132	CAPS
BaAL12F24	12135	12136	CAPS
baak45l08	12139	12140	SNP
BaAL36N04	12143	12144	SNP
baak41d17	12147	12148	SNP
kr39E0810	12151	12152	CAPS
BaGS32G16	12155	12156	CAPS
BaGS25M06	12159	12160	SNP
BaH36F21	12163	12164	SNP
BaAK13B12	12167	12168	SNP
baal29j18	12171	12172	size_poly (codominant)
bast63B0604	12175	12176	SNP
baak11n06	12179	12180	SNP
kr13F1012	12183	12184	SNP
bags20k06	12187	12188	SNP
baak15p20	12191	12192	SNP

TABLE 11-6-continued

Name	Primers used (SEQ ID ND:)		marker type
bah18n11	12195	12196	size_poly (codominant)
BaH23J08	12199	12200	SNP
baet30B1004	12203	12204	SNP
bags34p06	12207	12208	size_poly (codominant)
bastl33H0816	12211	12212	SNP
BaSD17I17	12215	12216	size_poly (codominant)
basd19p22	12219	12220	CAPS
bags4e03	12223	12224	CAPS
BaAK36A13	12227	12228	CAPS
bags33i03	12231	22232	CAPS
BaAK14F03	12235	12236	CAPS
BaAK42K19	12239	12240	SNP
bast60A1101	12243	12244	SNP
bah52l06	12247	12248	SNP
bah23h10	12251	12252	SNP
BaGS15O23	12255	12256	SNP
BaAK20E08	12259	12260	SNP
kr61A1202	12263	12264	SNP

TABLE 11-7

Name	Primers used (SEQ ID NO:)		marker type
bast03F0212	12267	12268	SNP
bags39m22	12271	12272	CAPS
BaAK30O17	12275	12276	SNP
baak29a01	12279	12280	CAPS
basd1e04	12283	12284	CAPS
BaGS23K09	12287	12288	CAPS
BaAL2N04	12291	12292	SNP
BaH42C12	12295	12296	CAPS
bah39o14	12299	12300	size_poly (codominant)
bast26A1202	12303	12304	size_poly (codominant)
BaGS30N15	12307	12308	SNP
BaAL34D18	12311	12312	SNP
baak15k23	12315	12316	CAPS
bags37i06	12319	12320	SNP
BaGS19N09	12323	12324	SNP
BaSD13H09	12327	12328	SNP
bags3h19	12331	12332	CAPS
baak28o08	12335	12336	SNP
BaH15K08	12339	12340	SNP
HVM67	—	—	SSR
bah17h20	12343	12344	CAPS
BaAL5L13	12347	12348	CAPS
BaGS31P13	12351	12352	size_poly (dominant)
BaH28A11	12355	12356	SNP
BaSD25E01	12359	12360	SNP
sh	—	—	Trait
baet23F0111	12363	12364	SNP
VRN2	—	—	size_poly
bastl41C0806	12367	12368	CAPS
basd11o04	12371	12372	SNP
bags22kl7	12375	12376	SNP
bastl27A1101	12379	12380	size_poly (dominant)
bags22a16	12383	12384	CAPS
BaAL5E04	12387	12388	CAPS
baal39f20	12391	12392	CAPS
baak43d13	12395	12396	CAPS
baak41l23	12399	12400	CAPS
baet23B0604	12403	12404	CAPS
BaAK28I08	12407	12408	CAPS
bastl26C1206	12411	12412	SNP
bah27p20	12415	12416	SNP
baal12d24	12419	12420	SNP
bastl41F0511	12423	12424	SNP
BaGS17E03	12427	12428	CAPS

TABLE 12-1

Name	Primers used (SEQ ID NO:)		marker type
baal10j04	12431	12432	SNP
BaAK33J17	12435	12436	SNP
BaAL21J19	12439	12440	CAPS
bast17H0515	12443	12444	SNP
bags22c02	12447	12448	size_poly (codominant)
BaAK35A06	12451	12452	SNP
BaGS11K08	12455	12456	CAPS
bastl30A0602	12459	12460	size_poly (codominant)
BaGS39H16	12463	12464	CAPS
MWG502	—	—	STS
BaAK18M22	12467	12468	SNP
bast26G0614	12471	12472	SNP
BaSD22F13	12475	12476	SNP
BaAK28L16	12479	12480	CAPS
bags35o06	12483	12484	CAPS
bags13d07	12487	12488	CAPS
BaAL24F18	12491	12492	size_poly (codominant)
bah63l18	12495	12496	SNP
BaGS9H22	12499	12500	SNP
BaAK18A05	12503	12504	CAPS
BaH38D03	12507	12508	CAPS
BaH17N17	12511	12512	SNP
bah18d08	12515	12516	SNP
bags34a05	12519	12520	SNP
bags1m23	12523	12524	SNP
BaH50B05	12527	12528	SNP
bags1h11	12531	12532	SNP
BaH47G19	12535	12536	CAPS
BaAK38H10	12539	12540	CAPS
bah47e01	12543	12544	SNP
bast52E0109	12547	12548	SNP
bags1o08	12551	12552	SNP
BaH31H16	12555	12556	CAPS
baaK32l14	12559	12560	SNP
BaH50O06	12563	12564	SNP
BaSD26I01	12567	12568	SNP
bags1h24	12571	12572	SNP
basd27g16	12575	12576	SNP
BaGS16G24	12579	12580	CAPS
BaGS34C19	12583	12584	SNP
bah20k17	12587	12588	SNP
bah54e13	12591	12592	size_poly (codominant)
bags35i06	12595	12596	CAPS
bah29g09	12599	12600	size_poly (codominant)
BaAK29C12	12603	12604	SNP
bah56c06	12607	12608	CAPS
baal6a09	12611	12612	SNP
bags6j06	12615	12616	CAPS
BaH30P15	12619	12620	SNP
baak30k04	12623	12624	CAPS
basd25d22	12627	12628	SNP

TABLE 12-2

Name	Primers used (SEQ ID NO:)		marker type
BaGS39M02	12631	12632	CAPS
baak13n10	12635	12636	SNP
BaGS18J21	12639	12640	SNP
BaSD22G22	12643	12644	size_poly (codominant)
bags18b17	12647	12648	size_poly (codominant)
bags33j02	12651	12652	SNP
baak36b16	12655	12656	CAPS
bags37f05	12659	12660	SNP
BaAL17L15	12663	12664	SNP
BaGS20H12	12667	12668	SNP
kr65A0802	12671	12672	SNP
BaGS13E12	12675	12676	size_poly (dominant)
basd3h06	12679	12680	size_poly (codominant)

TABLE 12-2-continued

Name	Primers used (SEQ ID NO:)		marker type
basd22j16	12683	12684	SNP
bah39n18	12687	12688	SNP
bags20d19	12691	12692	SNP
BaGS34H19	12695	12696	SNP
baak42n10	12699	12700	SNP
BaSD24F03	12703	12704	SNP
BaGS23N21	12707	12708	SNP
BaAK45E04	12711	12712	SNP
bags5n23	12715	12716	SNP
bast52H1216	12719	12720	SNP
bags22f23	12723	12724	SNP
BaH38E02	12727	12728	SNP
BaH50O07	12731	12732	SNP
kr07C1006	12735	12736	SNP
baak26a02	12739	12740	SNP
BaAK2J22	12743	12744	SNP
bah45h23	12747	12748	SNP
bah11h09	12751	12752	size_poly (dominant)
BaAK46M16	12755	12756	SNP
bah55m23	12759	12760	SNP
bah59c05	12763	12764	SNP
basd11l17	12767	12768	SNP
bah19e08	12771	12772	SNP
BaAK21N24	12775	12776	SNP
BaH50E09	12779	12780	SNP
BaAK17P18	12783	12784	SNP
BaAL7A04	12787	12788	SNP
bast47B0303	12791	12792	SNP
bah28o17	12795	12796	SNP
bah37k03	12799	12800	SNP
bastl38A0501	12803	12804	SNP
bags23c03	12807	12808	SNP
basd13j01	12811	12812	SNP
bags21c02	12815	12816	SNP
bah28l03	12819	12820	CAPS
BaAK36B17	12823	12824	CAPS
bags6k10	12827	12828	SNP
BaAK32J23	12831	12832	size_poly (codominant)

TABLE 12-3

Name	Primers used (SEQ ID NO:)		marker type
bags9k18	12835	12836	SNP
baal18c19	12839	12840	CAPS
baak27p14	12843	12844	SNP
BaGS30N21	12847	12848	SNP
bah55p23	12851	12852	SNP
bah54p22	12855	12856	SNP
bags34f05	12859	12860	SNP
Bmac113	—	—	SSR
bags15i11	12863	12864	CAPS
BaH26I21	12867	12868	size_poly (codominant)
BaSD20M22	12871	12872	CAPS
bah14a24	12875	12876	SNP
BaH50J11	12879	12880	SNP
bags7a20	12883	12884	CAPS
bah25l12	12887	12888	CAPS
bags6k09	12891	12892	CAPS
BaGS29P21	12895	12896	CAPS
bah58f18	12899	12900	CAPS
bags39i18	12903	12904	CAPS
basd22l21	12907	12908	SNP
bags4o22	12911	12912	CAPS
kr27E0909	12915	12916	SNP
bastl41H0216	12919	12920	SNP
baak36o17	12923	12924	SNP
BaH31P15	12927	12928	SNP
kr07D0208	12931	12932	CAPS

TABLE 12-3-continued

Name	Primers used (SEQ ID NO:)		marker type
bags9h03	12935	12936	SNP
BaGS38M11	12939	12940	CAPS
kr26C0705	12943	12944	size_poly (dominant)
bags3k24	12947	12948	CAPS
bah53e16	12951	12952	CAPS
bags21n10	12955	12956	CAPS
BaGS25E06	12959	12960	CAPS
bah38n03	12963	12964	CAPS
BaAK38G14	12967	12968	CAPS
baal5a06	12971	12972	CAPS
basd26d19	12975	12976	CAPS
BaSD26D07	12979	12980	SNP
BaH50G14	12983	12984	CAPS
bah21h17	12987	12988	SNP
bags5d21	12991	12992	SNP
BaAK34D14	12995	12996	SNP
baak18a16	12999	13000	SNP
bags4b01	13003	13004	SNP
bags38c19	13007	13008	SNP
BaGS38J23	13011	13012	CAPS
kr42D0208	13015	13016	SNP
BaH33A16	13019	13020	CAPS
bags10e03	13023	13024	CAPS
bags14f17	13027	13028	CAPS
BaAK35N11	13031	13032	SNP

TABLE 12-4

Name	Primers used (SEQ ID NO:)		marker type
bags26n10	13035	13036	SNP
bags37n02	13039	13040	SNP
baal39l05	13043	13044	size_poly (dominant)
BaAK26L11	13047	13048	SNP
BaH57C19	13051	13052	SNP
bags7a01	13055	13056	SNP
bah19l15	13059	13060	SNP
baal4o02	13063	13064	SNP
bah58a12	13067	13068	SNP
HVM30	—	—	SSR
bah11b08	13071	13072	SNP
bags14m15	13075	13076	SNP
baak1e17	13079	13080	CAPS
bags14i11	13083	13084	size_poly (codominant)
bastl04B1103	13087	13088	SNP
bags13g08	13091	13092	SNP
basd27p03	13095	13096	SNP
bast38D0707	13099	13100	SNP
baak35j18	13103	13104	CAPS
baal19k05	13107	13108	SNP
BaH19C21	13111	13112	SNP
bah49g10	13115	13116	SNP
bags14h08	13119	13120	CAPS
bags23g18	13123	13124	SNP
bags22o22	13127	13128	SNP
BaAL20A03	13131	13132	SNP
bags5e24	13135	13136	SNP
bags5f11	13139	13140	SNP
BaAK33B10	13143	13144	SNP
BaSD15J20	13147	13148	CAPS
bags38b22	13151	13152	size_poly (codominant)
bah39b06	13155	13156	CAPS
bags19j08	13159	13160	CAPS
BaGS1G09	13163	13164	CAPS
bah63j06	13167	13168	CAPS
BaAL39J02	13171	13172	SNP
BaSD27H14	13175	13176	SNP
BaH50M01	13179	13180	SNP
BaSD24E13	13183	13184	SNP

TABLE 12-4-continued

Name	Primers used (SEQ ID NO:)		marker type
baal5j24	13187	13188	CAPS
bah15h18	13191	13192	CAPS
bast62E0610	13195	13196	CAPS
bah28k24	13199	13200	SNP
bah47c11	13203	13204	SNP
BaSD26M15	13207	13208	SNP
bah60o02	13211	13212	SNP
BaH50G06	13215	13216	SNP
bast15G0913	13219	13220	SNP
bah62n12	13223	13224	size_poly (codominant)
baal10n23	13227	13228	CAPS
bags20c12	13231	13232	SNP

TABLE 12-5

Name	Primers used (SEQ ID NO:)		marker type
basd16f13	13235	13236	SNP
baak21h06	13239	13240	CAPS
bags3b05	13243	13244	CAPS
bags22p08	13247	13248	SNP
BaH23N06	13251	13252	SNP
bags29c08	13255	13256	SNP
BaGS11O23	13259	13260	SNP
baak16a11	13263	13264	CAPS
baak15n22	13267	13268	CAPS
BaAL18J13	13271	13272	SNP
bah15m02	13275	13276	SNP
baak38d20	13279	13280	CAPS
BaSD12L21	13283	13284	CAPS
kr68B1103	13287	13288	SNP
BaAK28L22	13291	13292	CAPS
bags15b10	13295	13296	SNP
bags20h21	13299	13300	SNP
BaAK29K06	13303	13304	SNP
bags21l05	13307	13308	CAPS
bah56j14	13311	13312	SNP
basd15e02	13315	13316	CAPS
bags3j24	13319	13320	SNP
bags38m08	13323	13324	SNP
bah11m18	13327	13328	CAPS
bags35g06	13331	13332	SNP
bags37b01	13335	13336	SNP
BaAL19F02	13339	13340	SNP
BaAL4D09	13343	13344	SNP
BaAK30H10	13347	13348	CAPS
bags38b16	13351	13352	CAPS
bags27f15	13355	13356	SNP
bags10k14	13359	13360	SNP
bags22f10	13363	13364	CAPS
baak38n21	13367	13368	SNP
baak30e05	13371	13372	SNP
bastl04A0101	13375	13376	SNP
BaAK28P18	13379	13380	SNP
BaGS34E01	13383	13384	SNP
BaH54H04	13387	13388	SNP
bah13o19	13391	13392	SNP
BaAK29B22	13395	13396	CAPS
BaAK27C16	13399	13400	CAPS
BaGS22H13	13403	13404	CAPS
BaSD27A15	13407	13408	SNP
BaAK27E07	13411	13412	CAPS
BaGS9N02	13415	13416	SNP
Bmag223	—	—	SSR
bags28o18	13419	13420	CAPS
baal25b05	13423	13424	CAPS
bastl30A0202	13427	13428	SNP
bags37d20	13431	13432	CAPS

TABLE 12-6

Name	Primers used (SEQ ID NO:)		marker type
BaGS22K12	13435	13436	SNP
BaAK13G12	13439	13440	SNP
basd2a02	13443	13444	CAPS
BaGS31L06	13447	13448	CAPS
bags17j17	13451	13452	CAPS
baal12j15	13455	13456	SNP
BaAK19H14	13459	13460	CAPS
BaH34J11	13463	13464	SNP
BaGS30I11	13467	13468	SNP
BaH49L06	13471	13472	CAPS
baal18m24	13475	13476	CAPS
baak15l06	13479	13480	SNP
basd18o14	13483	13484	SNP
bags24p22	13487	13488	SNP
BaAL37A09	13491	13492	SNP
bags5l01	13495	13496	SNP
BaAK12P03	13499	13500	SNP
baak21f10	13503	13504	SNP
bastl30E0410	13507	13508	SNP
kr25C0206	13511	13512	SNP
baak4j01	13515	13516	CAPS
BaAK27E01	13519	13520	CAPS
bah54n06	13523	13524	SNP
bags19p05	13527	13528	CAPS
bast22F0311	13531	13532	SNP
basd1m04	13535	13536	SNP
bags35i04	13539	13540	CAPS
baak41d01	13543	13544	SNP
baal19m08	13547	13548	CAPS
baak13j10	13551	13552	SNP
baak44h11	13555	13556	SNP
baal19j09	13559	13560	SNP
baet37C1105	13563	13564	SNP
baak12d06	13567	13568	CAPS
basd23f10	13571	13572	SNP
BaH41P07	13575	13576	SNP
baak1g13	13579	13580	SNP
basd14b04	13583	13584	CAPS
bags22l14	13587	13588	SNP
bast26E1210	13591	13592	SNP
baet25F0911	13595	13596	SNP
BaAK32N13	13599	13600	SNP
BaSD2C09	13603	13604	size_poly (codominant)
BaGS31P01	13607	13608	SNP
baak30m11	13611	13612	SNP
BaAK4N16	13615	13616	size_poly (codominant)
bastl46F1012	13619	13620	SNP
bags3e06	13623	13624	SNP
bags31o10	13627	13628	CAPS
bags33j12	13631	13632	CAPS
BaGS30N07	13635	13636	CAPS

TABLE 12-7

Name	Primers used (SEQ ID NO:)		marker type
BaH37I18	13639	13640	CAPS
baak46p24	13643	13644	CAPS
baak46o19	13647	13648	SNP
basd3c19	13651	13652	SNP
bags30f01	13655	13656	SNP
BaGS20F10	13659	13660	CAPS
BaGS32D08	13663	13664	SNP
BaAK23M23	13667	13668	SNP
bah21a16	13671	13672	SNP
BaAL3M08	13675	13676	SNP
BaAK21I09	13679	13680	SNP
baet33A0301	13683	13684	SNP
baak24k02	13687	13688	SNP

TABLE 12-7-continued

Name	Primers used (SEQ ID NO:)		marker type
bah33p03	13691	13692	CAPS
bast75D1208	13695	13696	SNP
BaSD12K20	13699	13700	size_poly (codominant)
bags34f06	13703	13704	SNP
bags6f09	13707	13708	SNP
bags7b10	13711	13712	SNP
BaGS25H01	13715	13716	CAPS
baak33m08	13719	13720	CAPS
bags37e01	13723	13724	SNP
bags32n20	13727	13728	CAPS
BaH47A11	13731	13732	CAPS
BaGS24M06	13735	13736	SNP
bags22m23	13739	13740	SNP
basd18d18	13743	13744	SNP
bastl06F0212	13747	13748	SNP
BaH49O16	13751	13752	SNP
bags39e22	13755	13756	CAPS
BaH38N06	13759	13760	SNP
BaH56P16	13763	13764	SNP
BaSD13O13	13767	13768	SNP
bags19i06	13771	13772	CAPS
bah34f11	13775	13776	SNP
bags37g04	13779	13780	SNP
basd11k21	13783	13784	CAPS
HvLOX	—	—	SSR
baak43o03	13787	13788	SNP
BaAL4J21	13791	13792	SNP
BaH51J22	13795	13796	SNP
bah58l03	13799	13800	SNP
BaGS21M18	13803	13804	SNP
BaGS31K06	13807	13808	SNP
baal4o01* VRN2(sh2)	13811	13812	SNP
BaAK24H19	13815	13816	size_poly (codominant)
BaGS17D21	13819	13820	size_poly (codominant)
bah39o04	13823	13824	SNP
baak46e06	13827	13828	size_poly (codominant)
basd13j03	13831	13832	CAPS

TABLE 12-8

Name	Primers used (SEQ ID NO:)		marker type
bast14H0416	13835	13836	SNP
BaSD18I03	13839	13840	CAPS
bastl44H1115	13843	13844	SNP
bast34D0608	13847	13848	CAPS
BaGS30F06	13851	13852	CAPS
bags21k16	13855	13856	CAPS
BaH48G01	13859	13860	CAPS
bags39a24	13863	13864	CAPS
bags15i03	13867	13868	size_poly (dominant)
bags23f02	13871	13872	SNP
bastl40E1010	13875	13876	SNP
bags17p10	13879	13880	CAPS
BaH57L13	13883	13884	CAPS
bags10e22	13887	13888	size_poly (codominant)
bags4p07	13891	13892	CAPS
bah63a08	13895	13896	CAPS
baak12f13	13899	13900	size_poly (dominant)
bah56j15	13903	13904	CAPS
bah15e16	13907	13908	SNP
BaH50F21	13911	13912	CAPS
basd27o16	13915	13916	SNP
kr66G0713	13919	13920	SNP
baak46c17	13923	13924	SNP
baet19C1206	13927	13928	SNP
bags34e15	13931	13932	CAPS
baal4d18	13935	13936	size_poly (dominant)

TABLE 12-8-continued

Name	Primers used (SEQ ID NO:)		marker type
bah13b13	13939	13940	CAPS
BaGS26G20	13943	13944	SNP
BaGS28C14	13947	13948	SNP
kr61G1214	13951	13952	SNP
bags9g08	13955	13956	SNP
bags5p01	13959	13960	SNP
BaAL4D04	13963	13964	SNP
bah26p09	13967	13968	CAPS
bah11e02	13971	13972	SNP
MWG2077	—	—	STS
bast41F0311	13975	13976	SNP
bastl54D0307	13979	13980	SNP
BaSD3F21	13983	13984	size_poly (codominant)
bah56f18	13987	13988	size_poly (codominant)
BaH41C21	13991	13992	CAPS
basd19g21	13995	13996	CAPS
kr33H0816	13999	14000	SNP
BaH38F16	14003	14004	SNP
BaGS21P09	14007	14008	SNP
BaGS36M20	14011	14012	CAPS
bags21m10	14015	14016	CAPS
BaAK14G11	14019	14020	CAPS
BaGS30L20	14023	14024	CAPS
basd21g02	14027	14028	SNP
bah22m17	14031	14032	SNP

TABLE 12-9

Name	Primers used (SEQ ID NO:)		marker type
BaGS9H19	14035	14036	SNP
bah26m24	14039	14040	SNP
BaH56D01	14043	14044	SNP
bah53j08	14047	14048	CAPS
bags21d10	14051	14052	CAPS
bags9a01	14055	14056	CAPS
baal9m13	14059	14060	SNP
baak20m05	14063	14064	size_poly (codominant)
baak21k16	14067	14068	SNP
bags34d17	14071	14072	CAPS
baal40k24	14075	14076	CAPS
BaGS19O14	14079	14080	SNP
baak35m03	14083	14084	SNP
baak33o23	14087	14088	SNP
kr57F1012	14091	14092	SNP
bah53i05	14095	14096	size_poly (codominant)
bags22l16	14099	14100	SNP
baet43C0505	14103	14104	SNP
BaH33H02	14107	14108	CAPS
bastl22E1010	14111	14112	SNP
BaH53N24	14115	14116	SNP
baal8e24	14119	14120	SNP
BaH62H21	14123	14124	SNP
BaH42K01	14127	14128	SNP
basd26p09	14131	14132	SNP
bags4p18	14135	14136	SNP
BaH60H14	14139	14140	size_poly (codominant)
bast70D1107	14143	14144	SNP
bah26i23	14147	14148	SNP
baal39g02	14151	14152	SNP
bags10e02	14155	14156	CAPS
bags22c13	14159	14160	SNP
bags35n03	14163	14164	CAPS
BaAL16H03	14167	14168	SNP
BaAL15N07	14171	14172	CAPS
bags18o20	14175	14176	SNP
bags37g12	14179	14180	CAPS
bags22l12	14183	14184	CAPS
BaAK44K01	14187	14188	CAPS

TABLE 12-9-continued

Name	Primers used (SEQ ID NO:)		marker type
BaAK31G07	14191	14192	CAPS
bah53n21	14195	14196	CAPS
BaGS19C02	14199	14200	SNP
BaH52E20	14203	14204	SNP
BaAL4N05	14207	14208	SNP
bags7p06	14211	14212	SNP
bast70C0905	14215	14216	SNP
BaSD15J01	14219	14220	SNP
BaH56H18	14223	14224	SNP
BaGS4N04	14227	14228	SNP
bags31o13	14231	14232	SNP
kr29D0107	14235	14236	CAPS

TABLE 12-10

Name	Primers used (SEQ ID NO:)		marker type
BaAK21A15	14239	14240	size_poly (codominant)
bags7h14	14243	14244	SNP
basd26b20	14247	14248	size_poly (codominant)
baal1g06	14251	14252	size_poly (codominant)
bags5n14	14255	14256	SNP
BaAK34H17	14259	14260	size_poly (dominant)
bastl32H0816	14263	14264	SNP
basd18m12	14267	14268	size_poly (codominant)
baak31p06	14271	14272	SNP
bah52i03	14275	14276	CAPS
BaAK33K05	14279	14280	CAPS
BaAK44J08	14283	14284	SNP
baak18g16	14287	14288	SNP
baak11a11	14291	14292	SNP
BaH25B20	14295	14296	size_poly (codominant)
bast12G0113	14299	14300	CAPS
baal9n02	14303	14304	SNP
bags20f08	14307	14308	SNP
BaGS9C24	14311	14312	SNP
BaGS22O02	14315	14316	SNP
baak13k16	14319	14320	CAPS
MWG2249	—	—	STS
bah41b17	14323	14324	SNP
bah63m11	14327	14328	SNP
BaGS28P07	14331	14332	SNP
bags1h15	14335	14336	CAPS
kr26H0515	14339	14340	CAPS
bags6n05	14343	14344	size_poly (codominant)
BaH24P17	14347	14348	CAPS
bast03D0408	14351	14352	SNP
BaAL17G06	14355	14356	SNP
BaH32G11	14359	14360	CAPS
BaGS4P17	14363	14364	SNP
baal31o21	14367	14368	SNP
BaGS36A16	14371	14372	CAPS
bags4d11	14375	14376	SNP
basd13n18	14379	14380	SNP
basd0a08	14383	14384	SNP
BaGS32P24	14387	14388	SNP
baak12i02	14391	14392	CAPS
kr06H0315	14395	14396	SNP
BaAL26B09	14399	14400	SNP
kr32C1105	14403	14404	SNP
BaH53B15	14407	14408	SNP
bags13h04	14411	14412	SNP
baal15i11	14415	14416	SNP
bags1m19	14419	14420	CAPS
HVM6	—	—	SSR

TABLE 13-1

Name	Primers used (SEQ ID NO:)		marker type
MWG620	—	—	STS
basd14f03	14423	14424	CAPS
BaH30E11	14427	14428	SNP
BaH59J05	14431	14432	SNP
BaAL39O22	14435	14436	SNP
baal16i24	14439	14440	CAPS
BaAL30P12	14443	14444	CAPS
BaGS21H12	14447	14448	CAPS
BaAK15J05	14451	14452	size_poly (codominant)
BaGS9G15	14455	14456	CAPS
BaAK41J04	14459	14460	CAPS
baak43j24	14463	14464	SNP
bah26n19	14467	14468	size_poly (dominant)
Bmac316	—	—	SSR
bags38a05	14471	14472	CAPS
BaH43I06	14475	14476	CAPS
bags9j07	14479	14480	CAPS
baak31p11	14483	14484	CAPS
BaGS17P19	14487	14488	CAPS
baal32j05	14491	14492	CAPS
baal16l16	14495	14496	CAPS
baal6a11	14499	14500	CAPS
bah55p06	14503	14504	CAPS
bags8f03	14507	14508	CAPS
bags3m02	14511	14512	SNP
BaAL36L08	14515	14516	SNP
baet19E0309	14519	14520	SNP
BaSD18J06	14523	14524	size_poly (codominant)
bast48D0307	14527	14528	SNP
kr55D0707	14531	14532	SNP
BaAL4B09	14535	14536	CAPS
bags32f21	14539	14540	CAPS
BaGS24F04	14543	14544	SNP
BaGS10G07	14547	14548	CAPS
BaGS26P07	14551	14552	SNP
bags12f11	14555	14556	SNP
MWG2218	—	—	STS
BaH63O04	14559	14560	CAPS
BaGS26D21	14563	14564	CAPS
bags20o14	14567	14568	SNP
baak36d08	14571	14572	SNP
bast75H0616	14575	14576	SNP
basd16g17	14579	14580	SNP
baal4k16	14583	14584	CAPS
bags32b14	14587	14588	CAPS
baal4d01	14591	14592	CAPS
baal7d23	14595	14596	CAPS
BaH62C20	14599	14600	size_poly (codominant)
BaH21K13	14603	14604	SNP
BaAK14J02	14607	14608	SNP
bah22c08	14611	14612	SNP

TABLE 13-2

Name	Primers used (SEQ ID NO:)		marker type
baak25d07	14615	14616	CAPS
BaAK29M05	14619	14620	CAPS
BaGS31I08	14623	14624	CAPS
bah12n12	14627	14628	SNP
baal30o06	14631	14632	CAPS
baak13n14	14635	14636	CAPS
bags7a09	14639	14640	CAPS
baak32l04	14643	14644	SNP
bah31o16	14647	14648	CAPS
BaAL7C19	14651	14652	SNP
BaAK23F04	14655	14656	SNP
kr40D0707	14659	14660	CAPS
basd0g08	14663	14664	SNP
BaAL30H03	14667	14668	CAPS
BaAL21B21	14671	14672	SNP

TABLE 13-2-continued

Name	Primers used (SEQ ID NO:)		marker type
BaGS30E05	14675	14676	SNP
BaAK13G04	14679	14680	SNP
BaGS27N11	14683	14684	size_poly (dominant)
BaGS9A04	14687	14688	SNP
BaAK23M11	14691	14692	SNP
basd3f22	14695	14696	CAPS
baak41p21	14699	14700	SNP
BaAK41K07	14703	14704	CAPS
BaH53I11	14707	14708	CAPS
baak26j14	14711	14712	SNP
BaAL18N03	14715	14716	CAPS
baak40c08	14719	14720	CAPS
bags17l19	14723	14724	CAPS
BaSD25N02	14727	14728	size_poly (codominant)
BaAK37E04	14731	14732	SNP
baal33h17	14735	14736	CAPS
bags20d08	14739	14740	CAPS
BaGS4J01	14743	14744	CAPS
bah48o03	14747	14748	SNP
bastl31A0901	14751	14752	SNP
bah20k22	14755	14756	SNP
BaGS15J17	14759	14760	size_poly (dominant)
BaAK17I01	14763	14764	CAPS
BaAK30F08	14767	14768	CAPS
bah47a17	14771	14772	SNP
basd15e10	14775	14776	SNP
BaH56C11	14779	14780	SNP
BaH18C17	14783	14784	SNP
BaGS20G24	14787	14788	SNP
bags19g17	14791	14792	CAPS
BaAK21L02	14795	14796	CAPS
BaH52H21	14799	14800	SNP
bags9l13	14803	14804	CAPS
BaSD18C12	14807	14808	SNP
baak23k07	14811	14812	SNP
bags16j16	14815	14816	SNP

TABLE 13-3

Name	Primers used (SEQ ID NO:)		marker type
BaSD15O17	14819	14820	SNP
baak12i20	14823	14824	CAPS
BaAK3M04	14827	14828	CAPS
BaGS4N23	14831	14832	SNP
baak34k24	14835	14836	CAPS
bah15n23	14839	14840	CAPS
baak45i02	14843	14844	CAPS
basd13i08	14847	14848	SNP
BaSD17P01	14851	14852	SNP
HVM31	—	—	SSR
baak13d19	14855	14856	SNP
baal3h14	14859	14860	SNP
bags33j18	14863	14864	SNP
BaH45B01	14867	14868	CAPS
baak21n07	14871	14872	SNP
BaH36H18	14875	14876	size_poly (codominant)
BaAL23O14	14879	14880	CAPS
bah53f05	14883	14884	SNP
baak12d02	14887	14888	SNP
bags11h12	14891	14892	SNP
baet01F1212	14895	14896	SNP
baak17l11	14899	14900	SNP
basd20e17	14903	14904	SNP
bah29p24	14907	14908	SNP
bags30o05	14911	14912	SNP
kr68D0208	14915	14916	SNP
bags37l11	14919	14920	SNP
baal4d14	14923	14924	CAPS

TABLE 13-3-continued

Name	Primers used (SEQ ID NO:)		marker type
BaH58I23	14927	14928	SNP
bags39l04	14931	14932	SNP
baak29j13	14935	14936	CAPS
bags20p18	14939	14940	CAPS
BaAK12J13	14943	14944	CAPS
BaH13K17	14947	14948	size_poly (codominant)
bah60p09	14951	14952	SNP
BaH27N11	14955	14956	CAPS
BaGS34D11	14959	14960	CAPS
BaGS39G07	14963	14964	CAPS
bah22o14	14967	14968	SNP
bah14l20	14971	14972	SNP
bah42p22	14975	14976	SNP
BaAK21G03	14979	14980	SNP
BaAL35D24	14983	14984	SNP
baak45h14	14987	14988	SNP
bags28o05	14991	14992	SNP
BaAK31P07	14995	14996	SNP
bah36c06	14999	15000	SNP
BaGS37H24	15003	15004	SNP
bast65B0303	15007	15008	SNP
BaH51A22	15011	15012	SNP
BaGS39K23	15015	15016	SNP

TABLE 13-4

Name	Primers used (SEQ ID NO:)		marker type
BaSD14O12	15019	15020	SNP
BaH57F12	15023	15024	SNP
BaGS32G02	15027	15028	CAPS
BaAL40N06	15031	15032	SNP
bah11b14	15035	15036	SNP
bah15j14	15039	15040	SNP
bast21C1105	15043	15044	CAPS
bags29f03	15047	15048	CAPS
BaAK46B16	15051	15052	CAPS
basd11p22	15055	15056	CAPS
baal16h16	15059	15060	CAPS
BaSD21L07	15063	15064	SNP
BaH42D07	15067	15068	SNP
BaGS23K24	15071	15072	SNP
BaAK24L01	15075	15076	SNP
BaAL11H22	15079	15080	SNP
BaAL13O24	15083	15084	CAPS
BaAL6M22	15087	15088	SNP
BaH56I06	15091	15092	size_poly (codominant)
BaSD19A18	15095	15096	size_poly (dominant)
BaSD20P03	15099	15100	SNP
BaH19B13	15103	15104	SNP
kr59H0416	15107	15108	SNP
BaGS14A02	15111	15112	SNP
BaH34P05	15115	15116	SNP
bah61o16	15119	15120	SNP
BaH24N07	15123	15124	SNP
BaAL20M22	15127	15128	CAPS
BaAL11H20	15131	15132	SNP
bah54b04	15135	15136	SNP
BaAK14H23	15139	15140	size_poly (dominant)
BaSD20M23	15143	15144	SNP
BaAL15B12	15147	15148	CAPS
baal15d09	15151	15152	SNP
baak39n20	15155	15156	SNP
BaH43N16	15159	15160	SNP
bags39h18	15163	15164	CAPS
BaAL3L23	15167	15168	CAPS
basd22c03	15171	15172	SNP
bast55G0913	15175	15176	CAPS
kr47F0511	15179	15180	SNP

TABLE 13-4-continued

Name	Primers used (SEQ ID NO:)		marker type
bah15l24	15183	15184	size_poly (codominant)
bast77A0402	15187	15188	SNP
BaH58F04	15191	15192	SNP
BaAK30L09	15195	15196	SNP
kr39G1113	15199	15200	SNP
baak1c16	15203	15204	SNP
basd20e05	15207	15208	SNP
BaAK12F18	15211	15212	SNP
BaH50L11	15215	15216	CAPS
bast50G0814	15219	15220	CAPS

TABLE 13-5

Name	Primers used (SEQ ID NO:)		marker type
bast70D0107	15223	15224	SNP
baal17d05	15227	15228	SNP
baak46g03	15231	15232	SNP
bah63m17	15235	15236	SNP
BaH15L15	15239	15240	SNP
BaGS19N01	15243	15244	SNP
BaAK32P07	15247	15248	SNP
bags14l13	15251	15252	SNP
bags37o24	15255	15256	SNP
baal5e24	15259	15260	CAPS
BaH46B06	15263	15264	CAPS
bags11a16	15267	15268	CAPS
baal27m03	15271	15272	SNP
BaAK1C18	15275	15276	SNP
BaAK38H16	15279	15280	size_poly (codominant)
BaGS37K02	15283	15284	CAPS
bah28a10	15287	15288	CAPS
bah27c03	15291	15292	CAPS
BaH52B11	15295	15296	SNP
bah27f05	15299	15300	SNP
bags37g15	15303	15304	CAPS
bah59c10	15307	15308	SNP
bags38j06	15311	15312	SNP
basd14e01	15315	15316	SNP
BaGS24L06	15319	15320	size_poly (codominant)
bags17b02	15323	15324	CAPS
BaH54L03	15327	15328	CAPS
BaAK21J17	15331	15332	CAPS
BaGS23G08	15335	15336	CAPS
basd18e06	15339	15340	SNP
baak19o02	15343	15344	size_poly (codominant)
basd2o16	15347	15348	SNP
baak16e08	15351	15352	SNP
bags18h01	15355	15356	SNP
BaGS4L20	15359	15360	SNP
BaAL2M19	15363	15364	CAPS
BaH36F15	15367	15368	CAPS
bah58l07	15371	15372	CAPS
baet29C0406	15375	15376	CAPS
BaAK35B04	15379	15380	CAPS
bags34k13	15383	15384	CAPS
baal29i08	15387	15388	CAPS
baak11p10	15391	15392	CAPS
BaH30J08	15395	15396	SNP
bags4e12	15399	15400	CAPS
bastl05C1206	15403	15404	size_poly (codominant)
bast22G0313	15407	15408	SNP
basd24b08	15411	15412	CAPS
bastl16C0206	15415	15416	size_poly (codominant)
bags33n21	15419	15420	SNP
baak33c11	15423	15424	SNP

TABLE 13-6

Name	Primers used (SEQ ID NO:)		marker type
baal13o10	15427	15428	CAPS
BaH36P06	15431	15432	SNP
basd12l01	15435	15436	SNP
baet25H0115	15439	15440	SNP
bags15d14	15443	15444	CAPS
BaGS37E09	15447	15448	CAPS
BaAK29I15	15451	15452	SNP
BaAK18I01	15455	15456	SNP
bast62B0404	15459	15460	SNP
bah25l03	15463	15464	SNP
BaGS19I11	15467	15468	CAPS
baal1n11	15471	15472	SNP
baak16l07	15475	15476	SNP
BaGS18P04	15479	15480	CAPS
bags19e06	15483	15484	CAPS
baak35n07	15487	15488	CAPS
BaAK29K23	15491	15492	SNP
baal13c18	15495	15496	SNP
bags7d17	15499	15500	SNP
bags20j08	15503	15504	SNP
baal9c20	15507	15508	SNP
bags20l05	15511	15512	SNP
bah63k05	15515	15516	size_poly (codominant)
BaAK14C17	15519	15520	CAPS
Bmac40	—	—	SSR
baal15j23	15523	15524	SNP
BaAK1N06	15527	15528	CAPS
bags38d10	15531	15532	CAPS
BaAK19J15	15535	15536	CAPS
BaH50L14	15539	15540	SNP
BaGS37E11	15543	15544	SNP
BaSD27E20	15547	15548	SNP
basd17f18	15551	15552	SNP
baal32m04	15555	15556	SNP
BaSD12L12	15559	15560	CAPS
BaGS37D24	15563	15564	CAPS
BaGS9K15	15567	15568	CAPS
BaGS33L03	15571	15572	CAPS
BaAK24G10	15575	15576	SNP
kr58F0511	15579	15580	CAPS
BaH50F16	15583	15584	SNP
basd17d11	15587	15588	SNP
BaH37P24	15591	15592	SNP
bah47l21	15595	15596	SNP
baet45C1105	15599	15600	SNP
baak39o18	15603	15604	CAPS
bags20p12	15607	15608	CAPS
bags38f23	15611	15612	CAPS
baak14b08	15615	15616	SNP
bah54n10	15619	15620	SNP
bags3k09	15623	15624	CAPS

TABLE 13-7

Name	Primers used (SEQ ID NO:)		marker type
bags34p08	15627	15628	SNP
baal1e06	15631	15632	SNP
baak34p14	15635	15636	CAPS
baak14k12	15639	15640	CAPS
BaSD13G17	15643	15644	size_poly (codominant)
MWG897	—	—	STS
bags27h05	15647	15648	size_poly (codominant)
basd15m11	15651	15652	CAPS
BaH28G09	15655	15656	CAPS
bags21b06	15659	15660	CAPS
basd12g17	15663	15664	size_poly (codominant)
BaH18F07	15667	15668	CAPS
BaH44A23	15671	15672	CAPS

TABLE 13-7-continued

Name	Primers used (SEQ ID NO:)		marker type
bags3d07	15675	15676	CAPS
BaAL6A21	15679	15680	SNP
BaAK24E07	15683	15684	CAPS
BaAL29L09	15687	15688	SNP
kr66D1107	15691	15692	SNP
bastl47C0606	15695	15696	SNP
BaH50M03	15699	15700	SNP
basd27k17	15703	15704	SNP

TABLE 14-1

Name	Primers used (SEQ ID NO:)		marker type
basd2p19	15707	15708	SNP
BaAK38B18	15711	15712	size_poly (dominant)
bah42i06	15715	15716	CAPS
bags6f02	15719	15720	SNP
BaAK39J07	15723	15724	SNP
BaAK1L23	15727	15728	CAPS
baak17e10	15731	15732	SNP
BaH50H08	15735	15736	SNP
baal17e10	15739	15740	SNP
BaSD17C05	15743	15744	SNP
BaGS14P02	15747	15748	SNP
bastl42H0115	15751	15752	SNP
BaAK19C08	15755	15756	SNP
bastl40H1115	15759	15760	SNP
bags12l21	15763	15764	CAPS
baak12j24	15767	15768	CAPS
bags14d22	15771	15772	CAPS
BaAK21P12	15775	15776	SNP
baal6b02	15779	15780	CAPS
baak29f13	15783	15784	CAPS
bast79C0406	15787	15788	SNP
BaH45M08	15791	15792	SNP
kr28A0301	15795	15796	SNP
bags19e04	15799	15800	CAPS
BaH28L07	15803	15804	CAPS
baak21m18	15807	15808	CAPS
baak21l22	15811	15812	SNP
basd15h01	15815	15816	SNP
BaH19O11	15819	15820	SNP
BaH59A20	15823	15824	CAPS
bags39l05	15827	15828	SNP
BaAK31N06	15831	15832	CAPS
BaH58P03	15835	15836	SNP
bags29c18	15839	15840	CAPS
BaAL4O04	15843	15844	SNP
bags37n23	15847	15848	CAPS
BaAL39N03	15851	15852	size_poly (codominant)
BaAK14C23	15855	15856	SNP
kr61A1101	15859	15860	SNP
BaH42J17	15863	15864	SNP
BaH58H08	15867	15868	SNP
bast78A0202	15871	15872	SNP
BaGS21E20	15875	15876	CAPS
bags22k18	15879	15880	size_poly (codominant)
BaGS33H15	15883	15884	size_poly (codominant)
HVM4	—	—	SSR
BaSD18O16	15887	15888	SNP
baak22j11	15891	15892	SNP
BaAK20K04	15895	15896	SNP
bags29l11	15899	15900	SNP
BaAK17G18	15903	15904	size_poly (dominant)

TABLE 14-2

Name	Primers used (SEQ ID NO:)		marker type
baak14o13	15907	15908	SNP
baal8d17	15911	15912	size_poly (codominant)
BaAK37P20	15915	15916	CAPS
bags28k04	15919	15920	SNP
bah34b22	15923	15924	CAPS
BaGS37M03	15927	15928	SNP
BaGS18C14	15931	15932	SNP
bast23G0214	15935	15936	SNP
bah47p02	15939	15940	SNP
baak42a24	15943	15944	CAPS
baak16f06	15947	15948	CAPS
bah11m12	15951	15952	CAPS
kr66H0216	15955	15956	SNP
BaGS23D15	15959	15960	SNP
baal22c17	15963	15964	SNP
baak33d06	15967	15968	CAPS
bags34l17	15971	15972	SNP
BaGS25G03	15975	15976	CAPS
bah14j16	15979	15980	CAPS
bah34a23	15983	15984	size_poly (codominant)
BaAK21B17	15987	15988	SNP
bast42C0406	15991	15992	CAPS
baak21m13	15995	15996	SNP
baet45H0115	15999	16000	size_poly (codominant)
BaH38E01	16003	16004	SNP
bast03G0313	16007	16008	SNP
baak38p18	16011	16012	size_poly (codominant)
basd18g06	16015	16016	SNP
baak40i22	16019	16020	SNP
baal2n12	16023	16024	SNP
BaSD3C24	16027	16028	SNP
BaAK46M07	16031	16032	SNP
BaGS17N04	16035	16036	SNP
bags12d09	16039	16040	SNP
basd20c08	16043	16044	SNP
bags17i04	16047	16048	CAPS
baak15p03	16051	16052	CAPS
baak24b20	16055	16056	size_poly (codominant)
baal18g11	16059	16060	SNP
baal40b06	16063	16064	CAPS
baak40g02	16067	16068	SNP
baal1m11	16071	16072	size_poly (codominant)
BaH26B16	16075	16076	SNP
baal5n08	16079	16080	SNP
BaSD27F05	16083	16084	size_poly (codominant)
bags9c08	16087	16088	SNP
baak3c01	16091	16092	CAPS
basd1j22	16095	16096	SNP
BaH23N03	16099	16100	SNP
bast46D0808	16103	16104	SNP
bast22A0802	16107	16108	SNP

TABLE 14-3

Name	Primers used (SEQ ID NO:)		marker type
bast34D0808	16111	16112	SNP
bast48E0509	16115	16116	SNP
bast26F1012	16119	16120	SNP
baal30e07	16123	16124	SNP
bags23n06	16127	16128	CAPS
BaGS18I05	16131	16132	SNP
BaH52L11	16135	16136	CAPS
baal18b16	16139	16140	CAPS
bags1a17	16143	16144	size_poly (dominant)
HVCMA	—	—	SSR
bags8o06	16147	16148	SNP
baak46e14	16151	16152	SNP
BaGS38N08	16155	16156	SNP

TABLE 14-3-continued

Name	Primers used (SEQ ID NO:)		marker type
BaH49P17	16159	16160	SNP
bah60l22	16163	16164	CAPS
bags21m22	16167	16168	CAPS
BaH54E07	16171	16172	CAPS
BaAK39A20	16175	16176	CAPS
bags21d11	16179	16180	SNP
kr39H0816	16183	16184	SNP
baet32B1103	16187	16188	CAPS
BaAK31O16	16191	16192	CAPS
bags39l20	16195	16196	CAPS
BaGS15L12	16199	16200	CAPS
kr67D0208	16203	16204	SNP
BaAK1H16	16207	16208	SNP
BaH26F10	16211	16212	SNP
bags14n02	16215	16216	SNP
bah36f01	16219	16220	CAPS
bast79F0711	16223	16224	size_poly (codominant)
BaGS29G21	16227	16228	size_poly (codominant)
bast79D1107	16231	16232	SNP
BaGS26O20	16235	16236	SNP
bags11h08	16239	16240	CAPS
bags22h11	16243	16244	SNP
baet19D0608	16247	16248	SNP
bags23a14	16251	16252	CAPS
cMWG704	—	—	STS
bah62d14	16255	16256	size_poly (codominant)
BaGS37C09	16259	16260	SNP
bags20a01	16263	16264	SNP
bah53m11	16267	16268	SNP
BaGS26L01	16271	16272	SNP
bags21p23	16275	16276	SNP
BaAK24B01	16279	16280	SNP
BaAK13L03	16283	16284	CAPS
MWG511	—	—	CAPS
bastl56C0105	16287	16238	SNP
basd20j22	16291	16292	CAPS
bags28d11	16295	16296	SNP
BaGS4I11	16299	16300	size_poly (codominant)

TABLE 14-4

Name	Primers used (SEQ ID NO:)		marker type
BaH52G15	16303	16304	size_poly (codominant)
baak11d12	16307	16308	SNP
BaH42A07	16311	16312	SNP
BaGS38F01	16315	16316	CAPS
BaAK32I05	16319	16320	CAPS
bah60f18	16323	16324	SNP
baal2n10	16327	16328	CAPS
BaAK14F01	16331	16332	CAPS
bah57o01	16335	16336	CAPS
basd12f05	16339	16340	CAPS
bah58e21	16343	16344	CAPS
bags1d07	16347	16348	CAPS
BaH23J15	16351	16352	CAPS
baak1p09	16355	16356	CAPS
BaAK32C23	16359	16360	SNP
baal9e06	16363	16364	SNP
baal18g23	16367	16368	CAPS
bastl47E0309	16371	16372	SNP
baak30o08	16375	16376	SNP
baet44C0606	16379	16380	SNP
bags39g18	16383	16384	SNP
BaH50P14	16387	16388	CAPS
bags38m06	16391	16392	SNP
baal33e12	16395	16396	size_poly (codominant)
bags3i04	16399	16400	SNP
BaAL1A11	16403	16404	SNP

TABLE 14-4-continued

Name	Primers used (SEQ ID NO:)		marker type
BaSD2M23	16407	16408	SNP
Bmag359	—	—	SSR
BaAK23L23	16411	16412	CAPS
bags7a23	16415	16416	CAPS
bah56l04	16419	16420	CAPS
basd12k23	16423	16424	SNP
bast22C0105	16427	16428	SNP
BaGS38H20	16431	16432	SNP
bah61p21	16435	16436	SNP
basd11h13	16439	16440	SNP
BaAL41J12	16443	16444	size_poly (codominant)
baal0f04	16447	16448	SNP
kr18E0810	16451	16452	SNP
BaH15J07	16455	16456	size_poly (codominant)
BaAL6G08	16459	16460	CAPS
BaGS24F02	16463	16464	SNP
baal19m12	16467	16468	CAPS
bah34h16	16471	16472	size_poly (codominant)
baak2e06	16475	16476	SNP
bast10C0406	16479	16480	CAPS
baak12l16	16483	16484	SNP
baak29d01	16487	16488	SNP
BaAK19N06	16491	16492	SNP
BaAK4I02	16495	16496	SNP
BaH49K10	16499	16500	SNP

TABLE 14-5

Name	Primers used (SEQ ID NO:)		marker type
baal2o03	16503	16504	SNP
baak28g14	16507	16508	SNP
bah62n05	16511	16512	CAPS
bags16e11	16515	16516	SNP
bags23g13	16519	16520	SNP
BaSD23C05	16523	16524	SNP
BaH19F17	16527	16528	SNP
BaH15J02	16531	16532	size_poly (codominant)
baak20d11	16535	16536	CAPS
BaAL6D19	16539	16540	CAPS
baak43e16	16543	16544	CAPS
baak40b02	16547	16548	CAPS
bah62m03	16551	16552	CAPS
BaGS26G17	16555	16556	SNP
baal6j16	16559	16560	SNP
bags29b09	16563	16564	SNP
baal20e03	16567	16568	SNP
BaGS9L23	16571	16572	SNP
bah32e22	16575	16576	SNP
BaAK17O14	16579	16580	SNP
bah56g23	16583	16584	CAPS
basd22f14	16587	16588	CAPS
BaH42O04	16591	16592	SNP
bast74F0111	16595	16596	SNP
BaSD21F13	16599	16600	SNP
BaAK26G13	16603	16604	CAPS
BaAK44D07	16607	16608	CAPS
bast61C0206	16611	16612	size_poly (codominant)
BaAL29L08	16615	16616	SNP
BaH34B20	16619	16620	CAPS
baak21a04	16623	16624	SNP
BaGS37F18	16627	16628	SNP
baal12h12	16631	16632	SNP
BaAK42B16	16635	16636	CAPS
BaAK26F12	16639	16640	SNP
BaH27B21	16643	16644	size_poly (codominant)
BaGS12B05	16647	16648	SNP
baal12h24	16651	16652	SNP
baal35j16	16655	16656	SNP

TABLE 14-5-continued

Name	Primers used (SEQ ID NO:)		marker type
BaGS37C07	16659	16660	SNP
BaAK45D23	16663	16664	SNP
BaH42G09	16667	16668	SNP
BaAL40P01	16671	16672	SNP
kr61A0901	16675	16676	SNP
baal4d05	16679	16680	CAPS
basd20l03	16683	16684	CAPS
baal31b03	16687	16688	CAPS
bags27k21	16691	16692	CAPS
bah55n15	16695	16696	CAPS
BaH44B17	16699	16700	SNP
BaSD2K11	16703	16704	SNP

TABLE 14-6

Name	Primers used (SEQ ID NO:)		marker type
BaAK20B23	16707	16708	CAPS
BaGS23E20	16711	16712	SNP
bags33i10	16715	16716	SNP
bags35k06	16719	16720	SNP
bags22c18	16723	16724	CAPS
MWG2031	—	—	STS
BaGS22M17	16727	16728	SNP
baak21j24	16731	16732	SNP
BaH29D20	16735	16736	CAPS
bah44f20	16739	16740	CAPS
BaAL16O08	16743	16744	SNP
BaAL27L17	16747	16748	SNP
sKT3	—	—	size_poly
sKT9	—	—	size_poly
baet31B1103	16751	16752	SNP
MWG975	—	—	STS
BaAL4A11	16755	16756	CAPS
BaGS22I18	16759	16760	CAPS
BaGS24K08	16763	16764	SNP
bah16c17	16767	16768	SNP
bah42m04	16771	16772	size_poly (codominant)
bags28l21	16775	16776	SNP
basd12f23	16779	16780	size_poly (codominant)
bah31m22	16783	16784	SNP
BaAL30C17	16787	16788	SNP
BaAK40P18	16791	16792	CAPS
baak37n01	16795	16796	SNP
BaGS24O11	16799	16800	SNP
BaH27K19	16803	16804	CAPS
BaGS15J07	16807	16808	CAPS
bah19a07	16811	16812	CAPS
BaH50I23	16815	16816	SNP
BaH56D06	16819	16820	SNP
BaAK39M05	16823	16824	SNP
bah11m16	16827	16828	SNP
bah49d03	16831	16832	SNP
bah62l23	16835	16836	SNP
BaAK38J13	16839	16840	SNP
BaH37N04	16843	16844	SNP
basd27c06	16847	16848	SNP
bah39g10	16851	16852	SNP
BaSD18P05	16855	16856	size_poly (codominant)
BaGS20A13	16859	16860	SNP
bah44n05	16863	16864	CAPS
EBmac764	—	—	SSR
BaH27L15	16867	16868	SNP
BaAK21I02	16871	16872	size_poly (codominant)
Bmac0064	—	—	SSR
BaH59F07	16875	16876	SNP
bags9l05	16879	16880	SNP
BaGS13H12	16883	16884	CAPS

TABLE 14-7

Name	Primers used (SEQ ID NO:)		marker type
BaAL19B06	16887	16888	CAPS
BaSD15P23	16891	16892	CAPS
bah53j21	16895	16896	SNP
bah21f16	16899	16900	SNP
baet39E0309	16903	16904	SNP
bags5l04	16907	16908	SNP
bags7g10	16911	16912	SNP
BaGS9D22	16915	16916	SNP
kr27H1216	16919	16920	CAPS
BaAK25O11	16923	16924	CAPS
bah18j14	16927	16928	SNP
bags37k14	16931	16932	SNP
baak26n19	16935	16936	size_poly (codominant)
bah42k03	16939	16940	SNP
BaH36N15	16943	16944	CAPS
Bmag120	—	—	SSR
bags12i02	16947	16948	SNP
BaAK38E05	16951	16952	CAPS
baet25B0604	16955	16956	SNP
BaAK46E21	16959	16960	SNP
BaGS37J12	16963	16964	SNP
bast60C0105	16967	16968	CAPS
baak30b08	16971	16972	SNP
BaAL29N13	16975	16976	size_poly (codominant)
BaAL24O04	16979	16980	CAPS
baak20o12	16983	16984	SNP
basd14k23	16987	16988	SNP
BaAK23L05	16991	16992	SNP
BaGS31G02	16995	16996	CAPS
bags33o01	16999	17000	SNP
basd18g14	17003	17004	CAPS
bah24d24	17007	17008	SNP
BaGS12F09	17011	17012	SNP
BaAK33H23	17015	17016	SNP
bah47p03	17019	17020	SNP
BaSD14F09	17023	17024	SNP
bah11k13	17027	17028	CAPS
BaSD22F10	17031	17032	SNP
bags32a01	17035	17036	CAPS
bags27o20	17039	17040	SNP
baak31o10	17043	17044	SNP
bags10f16	17047	17048	SNP
baal37j12	17051	17052	CAPS
BaGS9H02	17055	17056	SNP
BaAK40H10	17059	17060	CAPS
bah56m09	17063	17064	size_poly (codominant)
kr66C0705	17067	17068	SNP
BaGS33M05	17071	17072	SNP
bast60B0204	17075	17076	size_poly (codominant)
bah56p08	17079	17080	CAPS
baak12e19	17083	17084	CAPS

TABLE 14-8

Name	Primers used (SEQ ID NO:)		marker type
BaGS1D05	17087	17088	CAPS
BaH29M21	17091	17092	CAPS
bags21c04	17095	17096	CAPS
baak32p09	17099	17100	CAPS
BaAL24B02	17103	17104	SNP
BaGS34F08	17107	17108	SNP
bast36D1208	17111	17112	SNP
kr25B1103	17115	17116	SNP
kr08D0303	17119	17120	size_poly (dominant)
baal19g05	17123	17124	SNP
BaH22B15	17127	17128	CAPS
bags19c10	17131	17132	SNP
bags29k01	17135	17136	SNP

TABLE 14-8-continued

Name	Primers used (SEQ ID NO:)		marker type
bastl54G0414	17139	17140	SNP
BaGS23J01	17143	17144	CAPS
bags34b15	17147	17148	SNP
baak46i07	17151	17152	CAPS
BaAL6J13	17155	17156	CAPS
bah31l17	17159	17160	SNP
BaAK32A05	17163	17164	SNP
BaGS30N22	17167	17168	SNP
BaH54J20	17171	17172	CAPS
BaGS7F20	17175	17176	CAPS
bah63p18	17179	17180	size_poly (codominant)
bags11p11	17183	17184	CAPS
BaH27L17	17187	17188	SNP
basd17e11	17191	17192	SNP
bags15i06	17195	17196	SNP
BaAK36F09	17199	17200	SNP
bast57A0101	17203	17204	SNP
baak26h17	17207	17208	CAPS
basd13b15	17211	17212	SNP
bags9d11	17215	17216	SNP
BaH20K03	17219	17220	size_poly (codominant)
BaSD27N21	17223	17224	size_poly (codominant)
baal13a10	17227	17228	size_poly (dominant)
kr30F1212	17231	17232	SNP
bastl45B0903	17235	17236	SNP
Bmac156	—	—	SSR
bah60k06	17239	17240	size_poly (codominant)
BaGS32I12	17243	17244	SNP
BaGS4H02	17247	17248	CAPS
bah44k12	17251	17252	size_poly (codominant)
baak27p06	17255	17256	SNP
bags21m21	17259	17260	SNP
BaSD14J15	17263	17264	CAPS
HVM49	—	—	SSR
basd16e11	17267	17268	SNP
BaAK21N09	17271	17272	SNP
baal0e10	17275	17276	size_poly (codominant)
baak1g17	17279	17280	SNP

TABLE 14-9

Name	Primers used (SEQ ID NO:)		marker type
BaH14K12	17283	17284	size_poly (codominant)
BaAK31G05	17287	17288	size_poly (codominant)
MWG2062	—	—	STS
DaH50G17	17291	17292	size_poly (codominant)
HVM5	—	—	SSR
bags38n21	17295	17296	CAPS
bastl04B0303	17299	17300	size_poly (codominant)
baal35f12	17303	17304	SNP
BaH49M02	17307	17308	CAPS
baak38f04	17311	17312	CAPS
bah29b02	17315	17316	SNP
basd15d20	17319	17320	CAPS
kr61C0305	17323	17324	CAPS
BaH23B08	17327	17328	SNP
kr40H1115	17331	17332	CAPS
bah51g17	17335	17336	SNP
BaSD22E19	17339	17340	SNP

[0107] Table 8-1 through Table 14-9 show 7 kinds of polymorphisms: CAPS, SNP, size_poly, SSR (simple sequence repeat), STS, dCAPS, and trait. SSR, STS, dCAPS, and trait are known genetic markers. The polymorphisms specified by the inventors of the present invention are classified into 3 categories: CAPS, SNP, and size_poly. The third category, size_poly, is a polymorphism based on differences in the length of amplified fragments, and it includes polymorphisms that are detected based on whether the primer sets have successfully amplified the fragments. In any case, the polymorphism can be detected by running electrophoresis for the amplified DNA fragments, and detecting differences in band positions, or the presence or absence of bands.

[0108] CAPS is a polymorphism based on the presence or absence of a restriction enzyme recognition sequence. Most CAPS are based on single nucleotide polymorphism in the restriction enzyme recognition sequence; however, CAPS also includes those based on insertion/deletion of one or more bases. In Table 8-1 through Table 14-9, the marker type designated as SNP is the marker that does not have single nucleotide polymorphism or insertion/deletion in the restriction enzyme recognition sequence. CAPS can be detected by running electrophoresis for the amplified DNA fragments after restriction enzyme treatment and then detecting the number of bands, or band positions. Non-CAPS SNPs can be detected by typing, i.e., by actually confirming the base at the site of SNP or insertion/deletion. CAPS can also be detected by SNP typing.

[0109] Table 15-1 through Table 21-6 show base sequences in the vicinity of SNP or insertion/deletion that occurs between Haruna Nijo and H602. Names of restriction enzymes and recognition sequences of the restriction enzymes are also shown. Tables 15-1 through 15-5 are for 1H chromosome, Tables 16-1 through 16-7 for 2H chromosomes, Tables 17-1 through 17-6 for 3H chromosomes, Tables 18-1 through 18-5 for 4H chromosome, Tables 19-1 through 19-6 for 5H chromosome, Tables 20-1 through 20-5 for 6H chromosome, and Tables 21-1 through 21-6 for 7H chromosome. Table 22-1 through Table 28-25 show base sequences in the vicinity of SNPs of the SNP markers (non-CAPS). Tables 22-1 through 22-20 show polymorphisms in 1H chromosome, Tables 23-1 through 23-30 in 2H chromosome, Tables 24-1 through 24-27 in 3H chromosome, Tables 25-1 through 25-18 in 4H chromosome, Tables 26-1 through 26-28 in 5H chromosome, Tables 27-1 through 27-16 in 6H chromosome, and Tables 28-1 through 28-25 in 7H chromosome. Some of these polymorphisms occur at more than one location in one fragment.

[0110] In Table 15-1 through Table 28-25, bases that represent SNP or insertion/deletion are indicated by underline. Note that, in the sequence listing, bases at SNP sites are indicated by "universal codes." Where applicable, the universal codes are also used for bases in the restriction enzyme recognition sequence.

[0111] In Table 15-1 through Table 28-25, bases with SNPs are indicated by N in cases where the base is identified only for one of Haruna Nijo and H602 but not for the other. In this case, the unidentified base is one of the remaining three bases.

[0112] Universal codes are defined as follows.

[0113] m: A or C

[0114] r: G or A

[0115] w: A or T

[0116] s: G or C

[0117] y: T or C

[0118] k: G or T

[0119] v: A, G or C

[0120] h: A, C, or T

[0121] d: A, G, or T

[0122] b: G, C, or T

[0123] n: (A, C, G, or T) or (unidentified other bases)

Lengthy table referenced here

US20090186402A1-20090723-T00001

Please refer to the end of the specification for access instructions.

[0124] As described above, a gene polymorphism detection instrument according to the present invention is realized with a support immobilized thereon polynucleotides that comprise part of the base sequences of amplified DNA fragments that have polymorphism between different varieties. The amplified DNA fragments with polymorphism are not limited to those shown in Table 8-1 through Table 14-9, as long as they are DNA fragments that have polymorphism between different varieties and that have been amplified, using the genomic DNA of Triticeae species as a template, with a primer set that comprises a combination of two primers arbitrarily selected from (i) primers that have been designed based on the base sequence of SEQ ID NO: n (where n is an odd number), and (ii) primers that have been designed based on the base sequence of SEQ ID NO: (n+1), from among the base sequences of SEQ ID NO: 1 through 5780. In the case of SNP, part of amplified DNA fragments is a polynucleotide that comprises the base sequence of a region including a SNP base. In fragment length polymorphism, part of amplified DNA fragments is a polynucleotide that includes, or does not include, the base sequence of a region, if specified, causing a fragment length difference (a base sequence portion that is present in one of the varieties but not in the other). A polynucleotide that includes such base sequence portion, and a polynucleotide that does not include such base sequence portion may be used together.

[0125] In the case where a gene polymorphism detection instrument according to the present invention is used for detection of single nucleotide polymorphism (SNP), the polynucleotide immobilized on the support is preferably a synthetic oligonucleotide. Many SNP detecting arrays currently available use synthetic oligonucleotides, and these techniques can be used for the present invention. The polynucleotide immobilized on the support may have any number of bases as long as it can detect gene expression. For example, in the case where only one synthetic oligonucleotide is immobilized in each region, an oligonucleotide with at least 50 bases is considered to be sufficient for detection of gene expression. When more than one synthetic nucleotide is immobilized in each region as in the Affymetrix system, an oligonucleotide with about 25 bases is sufficient.

[0126] [Gene Polymorphism Detection Instrument with the Polynucleotides Immobilized in Regions that are Arranged in the Chromosomal Order]

[0127] As described above, the chromosomal order of polynucleotides on barley chromosomes (1H, 2H, 3H, 4H, 5H, 6H, or 7H) (distance from the short arm end of each chromosome) has been specified in clones that have the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through SEQ ID NO: 5780. Thus, if the polynucleotides comprising part of the DNA fragments amplified with the primers that have been designed based on the respective base sequences were placed, for example, according to the order of the polynucleotides, as represented in Table 1-1 through Table 7-9, having the reference base sequences of the primers, it would be possible to place the polynucleotides according to the order in which these polynucleotides are arranged from the short arm end of 1H chromosome to the long arm end of 7H chromosome, i.e., chromosomal order. For clones that have the same order from the short arm end, the order by which these clones are placed is not particularly limited. Once the precise order of these clones were specified by a future study, these clones will be able to be placed accordingly. Note that, the reference point (origin) on the chromosome is not just limited to the short arm end of 1H chromosome. Any position on a chromosome can be used as a reference point. If the polynucleotides immobilized on the support have overlapping portions, one closest to the 5' end is placed first. When there is more than one polynucleotide having the same 5' end position, these polynucleotides are placed contiguously in any order relative to one another.

[0128] With the polynucleotides immobilized on a support in the order they are arranged on the chromosomes, the value of a gene polymorphism detection instrument according to the present invention can be greatly improved in crossbreeding of Triticeae species. More specifically, by using a gene polymorphism detection instrument according to the present invention for comprehensive investigation of gene polymorphism of Triticeae species, the genotype of a target gene of breeding can be determined. Further, the location and extent of recombination on chromosomes can be checked to see if unnecessary recombination has occurred. That is, the genotypes of the parents are directly inherited as the haplotype in portions of the chromosomes where no recombination has occurred. As a result, the genotype of a trait conferred to the selected individuals can be easily determined, with the result that the efficiency of breeding is improved.

[0129] [Gene Polymorphism Detection Instrument with the Polynucleotides Immobilized in Regions appended with Chromosomal Order Information]

[0130] The regions in which the polynucleotides are immobilized (spots) may be appended with information indicative of the order in which the polynucleotides are arranged on barley chromosomes. The spots may be arranged in any way as long as they are appended with the order information. With the order information added to the spots, the data obtained from the spots can be rearranged in the chromosomal order even when the spots are randomly placed on a support. In this way, a gene detection instrument according to the present invention can improve the efficiency of breeding. Note that, the order information added to the spots can follow the foregoing criteria used to place the polynucleotides.

[0131] Adding order information enables the spots to be arranged in an arbitrary order in a gene polymorphism detection instrument of an array type, in which more than one polynucleotide is immobilized on a support such as a membrane or a glass slide. Further, the chromosomal order information of individual polynucleotides can also be added in a gene polymorphism detection instrument that employs a collection of beads (bead array) in which the polynucleotide is immobilized on each bead serving as a support.

[0132] [Examples of a Gene Polymorphism Detection Instrument according to the Present Invention]

[0133] Various conventional techniques that are designed for detection of gene polymorphism, particularly single

nucleotide polymorphism (SNP) can be suitably used for a gene polymorphism detection instrument according to the present invention.

[0134] A representative example of such conventional techniques is GeneChip array for DNA analysis (Affymetrix). In this array, total genomic DNA is excised with restriction enzyme, and adapters that recognize cohesive ends of 4 bases are ligated. The adapters can be ligated to all fragments of any size generated by the restriction enzyme treatment. From these fragments, fragments of 250 to 1000 bp are selectively amplified by PCR and hybridized with an array that has been designed to cause a match or mismatch with SNP portions. Many other conventional SNP detecting arrays have been commercially marketed, which are also applicable to a gene polymorphism detection instrument according to the present invention. The present invention can also employ the techniques disclosed in Non-Patent Publications 1 and 2.

[0135] Alternatively, an array system can be realized with use of Gene Silicon of TOYO KOHAN. Gene Silicon is a multi-purpose chip made of a DLC (diamond like carbon)-coated semiconductor silicon substrate with an activated ester-bearing carboxyl group introduced on the surface. With the activated ester-bearing carboxyl group, Gene Silicon can immobilize DNA or proteins on the substrate.

[0136] For example, a plurality of primer sets is designed that serves as genetic markers for distinguishing barley variety A and barley variety B, and that can cause amplification in only one of the varieties when PCR is performed with the genomic DNA of these two varieties as templates. Specifically, the primers are preferably designed based on polymorphic sites of the both varieties.

[0137] One of the primers from each primer set is placed and immobilized on Gene Silicon in the chromosomal order. The array is then hybridized with genomic DNA prepared from the hybrid of a cross between variety A and variety B, and PCR reaction is performed in a reaction solution containing Cydye-dNTP.

[0138] The presence or absence of amplification in each spot can easily be confirmed by observing fluorescence emitted by the incorporation of Cydye-dNTP. Specifically, whether the genomic DNA that resides in portions of chromosomes where the genetic markers (amplified fragments) are mapped originates in which of the parents (variety A or variety B) is confirmed according to the presence or absence of amplification. In this way, locations of recombination can be found easily.

[0139] (3) Polypeptide-Interacting Substance Detection Instrument According to the Present Invention

[0140] A polypeptide-interacting substance detection instrument according to the present invention is an instrument for detecting substances that interact with proteins encoded by genes that reside in the genomes of Triticeae species, or substances that interact with polypeptides that constitutes part of the proteins. The organisms to which a polypeptide-interacting substance detection instrument of the invention is applicable may be any Triticeae species, among which barley, wheat, and rye are preferable. As will be described later, a polypeptide-interacting substance detection instrument according to the present invention includes a support on which polypeptides encoded by polynucleotides that constitute part of DNA of barley chromosomes (1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes) are immobilized. The polypeptides immobilized on the support may solely be polypeptides encoded by polynucleotides constituting part of barley chromosomal DNA, or other polypeptides may additionally be immobilized on the support. Such additional polypeptides are not particularly limited. For example, the additional polypeptides may be those encoded by polynucleotides with the base sequences originating in non-barley organisms, or those with arbitrary amino acid sequences that have been artificially synthesized.

[0141] In the case where the polypeptides are immobilized in more than one region of the support, the polypeptides immobilized in these regions may have non-overlapping amino acid sequences or partially overlapping amino acid sequences. Alternatively, polypeptides of the same amino acid sequence may be immobilized in these different regions of the support. In the case where the polypeptides have overlapping base sequences, the polypeptides may have partially overlapping amino acid sequences, or the amino acid sequence of one of the polypeptides may be a partial sequence of the other polypeptide.

[0142] Further, the polypeptide immobilized in each region is not necessarily required to be of the same kind. More than one kind of polypeptide may be immobilized in each region.

[0143] The support is not particularly limited as long as it can immobilize polypeptides, and it may have any shape and may be made of any material. Examples of a support material generally include: inorganic materials such as glass and silicon wafer; natural polymers such as paper; synthetic polymers such as nitrocellulose and nylon; and gels using synthetic polymers or natural polymers. The shape of the support is not particularly limited as long as it provides enough area to support the polypeptides. Generally, those with a two-dimensional plane, for example, such as a substrate with little or no flexibility, a flexible membrane, or a flexible substrate with intermediate flexibility can be preferably used. The thickness of the substrate or membrane is not particularly limited either, and it can be suitably set according to the material or use of the substrate or membrane. Various types of beads may be used as supports.

[0144] [Polypeptides Immobilized on a Support of the Polypeptide-Interacting Substance Detection Instrument]

[0145] In a polypeptide-interacting substance detection instrument according to the present invention, at least one polypeptide encoded by the following polynucleotides (a) or (b) is immobilized on a support.

[0146] (a) Polynucleotides with base sequences constituting part of barley chromosomal DNA, or variants thereof with the substitution, deletion, insertion, and/or addition of one or more bases.

[0147] (b) Polynucleotides with a combination of base sequences constituting part of barley chromosomal DNA, or variants thereof with the substitution, deletion, insertion, and/or addition of one or more bases.

[0148] As used herein, a polynucleotide with a base sequence constituting part of barley chromosomal DNA is not particularly limited as long as it is a polynucleotide with a base sequence constituting part of the entire base sequences of chromosomal DNA of barley 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes, and including a protein-coding region. Further, a polynucleotide with a combination of base sequences constituting part of barley chromosomal DNA refers to a polynucleotide in which a base sequence constituting part of the entire base sequences of chromosomal DNA of barley 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes is joined to non-continuous base sequences constituting other parts of these chromosomes, and in which a protein-coding

region is contained. For example, base sequences from two different parts of the chromosomes may constitute the polynucleotide, or three or more base sequences may join together to form the polynucleotide. Specifically, for example, cDNA with a plurality of exons from a protein-coding gene on barley chromosomal DNA can be regarded as a polynucleotide with a combination of base sequences constituting part of barley chromosomal DNA. However, the polynucleotide is not just limited to this specific example.

[0149] A variant with the substitution, deletion, insertion, and/or addition of one or more bases in the polynucleotide with a base sequence, or a combination of base sequences, constituting part of barley chromosomal DNA may be a polynucleotide that has been mutated on purpose, or a polynucleotide that exists in nature. For example, think of a base sequence of chromosomal DNA in a specific variety of barley. Comparing this base sequence with those of other varieties, no sequence is completely identical. Rather, these sequences are variants with the substitution, deletion, insertion, and/or addition of one or more bases. The polypeptide encoded by a polynucleotide with such variant base sequence may have the same amino acid sequence as the polypeptide encoded by a polynucleotide with a non-variant base sequence. Further, the polypeptides encoded by the polynucleotides with variant and non-variant base sequences may differ from each other with the substitution of some of the amino acids, or most of or all of the amino acid sequences may be different between these polypeptides.

[0150] Polynucleotides that encode polypeptides immobilized on a support of a polypeptide-interacting substance detection instrument according to the present invention are preferably polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or variants with the substitution, deletion, insertion, and/or addition of one or more bases in the polynucleotides with the base sequences of SEQ ID NO: 1 through 5780. (Such polynucleotides and variants will be referred to as polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780.)

[0151] The base sequences of SEQ ID NO: 1 through 5780 are base sequences of the barley EST (expressed sequence tag) independently developed by the inventors. The inventors have previously confirmed that a polynucleotide with the base sequences of SEQ ID NO: 1 through 770, a polynucleotide with the base sequences of SEQ ID NO: 771 through 1754, a polynucleotide with the base sequences of SEQ ID NO: 1755 through 2642, a polynucleotide with the base sequences of SEQ ID NO: 2643 through 3324, a polynucleotide with the base sequences of SEQ ID NO: 3325 through 4320, a polynucleotide with the base sequences of SEQ ID NO: 4321 through 4962, and a polynucleotide with the base sequences of SEQ ID NO: 4963 through 5780 are mapped on 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes, respectively.

[0152] It follows from this that the base sequences of SEQ ID NO: 1 through 5780 are partial sequences of barley cDNA. Thus, if polynucleotides with the base sequences of SEQ ID NO: 1 through 5780 contained protein-coding regions, polypeptides encoded by these polynucleotides can be immobilized on the support. Further, variants with the substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780 constitute variant base sequences of barley cDNA. Thus, if these polynucleotides with variant base sequences contained protein-coding regions, polypeptides encoded by these polynucleotides can be immobilized on the support. The polynucleotides with variant base sequences may be polynucleotides that have been mutated on purpose, or polynucleotides that exist in nature.

[0153] Polynucleotides that encode polypeptides immobilized on a support of a polypeptide-interacting substance detection instrument according to the present invention may be a part of the polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780. Since the base sequence of such partial polynucleotide is a partial base sequence of barley cDNA, a polypeptide encoded by such partial polynucleotide can be immobilized on the support if the partial polynucleotide contains a protein-coding region.

[0154] Further, polynucleotides that encode polypeptides immobilized on a support of a polypeptide-interacting substance detection instrument according to the present invention may be polynucleotides whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. The remaining base sequences of the polynucleotides are not limited. For example, since the base sequences of SEQ ID NO: 1 through 5780 are partial sequences of barley cDNA, these base sequences do not have the sequences on either end as originally found in the full length cDNA. Thus, a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780, and which additionally includes the cDNA sequences on the both ends or one end as originally found in the full length cDNA can be regarded as a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. Further, vectors such as plasmids and BACs (bacterial artificial chromosomes) that have incorporated all of or part of the polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780, and polynucleotides in which the partial sequence is ligated to arbitrary base sequences can also be regarded as polynucleotides whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. Such polynucleotides at least include all of or part of the polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780, i.e., part of barley cDNA. Therefore, polypeptides encoded by such polynucleotides can be immobilized on the support if the polynucleotides contain a protein-encoding region.

[0155] Further, polynucleotides that encode polypeptides immobilized on a support of a polypeptide-interacting substance detection instrument according to the present invention may be polynucleotides or the like whose partial sequences comprise all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n (where n is an odd number), and all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n+1, from among the base sequences of SEQ ID NO: 1 through 5780. As described above, the base sequences of SEQ ID NO: 1 through 5780 are EST sequences of barley, and comprise sequences that can be read by sequencing the cloned cDNA from the both ends only once. In other words, the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 among the base sequences of SEQ ID NO: 1 through 5780 are base sequences that are read from the both ends of the cDNA of the same clone. As such, these base sequences can realize a full length cDNA base sequence, which corresponds to all of or part of the full length cDNA. Thus, polynucleotides or the like whose partial sequences comprise all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n (where n is an odd number), and all of or part of the base sequence, or a variant thereof, of

SEQ ID NO: n+1, from among the base sequences of SEQ ID NO: 1 through 5780 can be regarded as polynucleotides with full length cDNA that comprises the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1, or polynucleotides that comprise part of the full length cDNA. Further, the polynucleotides may be polynucleotides in which vector sequences or arbitrary base sequences for example are ligated to the both ends or one end of the full length cDNA or a polynucleotide that comprises part of the full length cDNA. Further, the polynucleotides may be variants that have a base substitution or other mutations in sequences other than the base sequences of SEQ ID NO: 1 through 5780, i.e., a middle section of the total cDNA unspecified by SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1. Such polynucleotides include the full length or part of barley cDNA, enabling polypeptides encoded by the polynucleotides to be immobilized on the support. In particular, when the polynucleotides are full length cDNA or include full length cDNA, the entire proteins encoded by the genes located on the barley chromosomes can be immobilized on the support.

[0156] [Peptide-Interacting Substance Detection Instrument with the Polypeptides Immobilized in Regions that are Arranged in the Chromosomal Order]

[0157] As described above, the chromosomal order of polynucleotides on barley chromosomes (1H, 2H, 3H, 4H, 5H, 6H, or 7H) (distance from the short arm end of chromosome) has been specified in clones that have the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through SEQ ID NO: 5780. Thus, if the polypeptides encoded by the polynucleotides with the base sequences of SEQ ID NO: 1 through SEQ ID NO: 5780 were placed according to the order, as represented in Table 1-1 through Table 7-9, of the polynucleotides encoding the polypeptides, it would be possible to place the polypeptides according to the order from the short arm end of 1H chromosome to the long arm end of 7H chromosome, i.e., chromosomal order. For clones that have the same order from the short arm end, the order by which these clones are placed is not particularly limited. Once the precise order of these clones were specified by a future study, these clones will be able to be placed accordingly. Note that, the reference point (origin) on the chromosome is not just limited to the short arm end of 1H chromosome. Any position on a chromosome can be used as a reference point.

[0158] With the polypeptides immobilized on a support in the order they are arranged on the chromosomes, the location and extent of recombination on chromosomes can be checked for genes from which the expressed proteins originate. That is, the genotypes of the parents are directly inherited as the haplotype in portions of the chromosomes where no recombination has occurred. As a result, the genotype of a trait conferred to the selected individuals can be easily determined, with the result that the efficiency of breeding is improved.

[0159] [Polypeptide-Interacting Substance Detection Instrument with the Polypeptides Immobilized in Regions Appended with Chromosomal Order Information]

[0160] The regions in which the polypeptides are immobilized (spots) may be appended with information indicative of the order in which the polynucleotides encoding the polypeptides are arranged on barley chromosomes. The spots may be arranged in any way as long as they are appended with the order information. With the order information added to the spots, the data obtained from the spots can be rearranged in the chromosomal order even when the spots are randomly placed on a support. Note that, the order information added to the spots can follow the foregoing criteria used to place the polypeptides.

[0161] Adding order information enables the spots to be arranged in an arbitrary order in a polypeptide-interacting substance detection instrument of an array type, in which more than one polypeptide is immobilized on a support such as a membrane or a glass slide. Further, the chromosomal order information of individual polypeptides can also be added in a polypeptide-interacting substance detection instrument that employs a collection of beads (bead array) in which the polypeptide is immobilized on each bead serving as a support.

[0162] [Examples of a Polypeptide-Interacting Substance Detection Instrument According to the Present Invention]

[0163] Various conventional techniques that are designed for detection of protein (polypeptide)-interacting substances can suitably be used in a polypeptide-interacting substance detecting instrument according to the present invention.

[0164] For example, a biological chip, one kind of protein chip, has been commercially available from Ciphergen Biosystems, Inc. This biological chip has an activated group such as carbonyl diimidazole or epoxy on a surface of a substrate (support), allowing a user to freely immobilize target proteins or antibodies. This technique is therefore applicable to a polypeptide-interacting substance according to the present invention. Since the activated group such as carbonyl diimidazole or epoxy can immobilize antibodies or polynucleotides, the biological chip can be used for the fabrication of other detection instruments of the present invention.

[0165] (4) Polypeptide Detection Instrument according to the Present Invention

[0166] A polypeptide detection instrument according to the present invention is an instrument for detecting proteins encoded by genes that reside in the genomes of Triticeae species, or polypeptides that constitutes part of the proteins. The organisms to which a polypeptide detection instrument of the invention is applicable may be any Triticeae species, among which barley, wheat, and rye are preferable. As will be described later, a polypeptide detection instrument according to the present invention includes a support on which polypeptides encoded by polynucleotides that constitute part of DNA of barley chromosomes (1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes) are immobilized. The polypeptides immobilized on the support may solely be antibodies against the polypeptides encoded by polynucleotides constituting part of barley chromosomal DNA, or other antibodies may additionally be immobilized on the support. Such additional antibodies are not particularly limited. For example, antibodies encoded by polynucleotides with the base sequences originating in non-barley organisms may be immobilized.

[0167] As used herein, the term "antibodies" refers to immunoglobulins that can recognize and bind to specific antigens. However, the term does not necessarily mean antibody molecules as a whole, but also refers to part of antibody molecules including antigen binding sites.

[0168] It is preferable that the support include a plurality of immobilizing regions, and that different kinds of antibodies be immobilized in these regions. Further, the antibodies immobilized in each region are not necessarily required to be of the same kind. More than one kind of antibodies may be immobilized in each region.

[0169] The support is not particularly limited as long as it can immobilize antibodies, i.e., proteins, and it may have any shape and may be made of any material. Examples of a support material generally include: inorganic materials such as glass and silicon wafer; natural polymers such as paper; synthetic polymers such as nitrocellulose and nylon; and gels using synthetic polymers or natural polymers. The shape of the support is not particularly limited as long as it provides enough area to support the polynucleotides. Generally, those with a two-dimensional plane, for example, such as a substrate with little or no flexibility, a flexible membrane, or a flexible substrate with intermediate flexibility can be preferably used. The thickness of the substrate or membrane is not particularly limited either, and it can be suitably set according to the material or use of the substrate or membrane. Various types of beads may be used as supports.

[0170] [Antibodies Immobilized on a Support of the Polypeptide Detection Instrument]

[0171] In a polypeptide detection instrument according to the present invention, at least one antibody against a polypeptide encoded by a polynucleotide selected from the following polynucleotides (a) or (b) is immobilized on a support.

[0172] (a) Polynucleotides with base sequences constituting part of barley chromosomal DNA, or variants thereof with the substitution, deletion, insertion, and/or addition of one or more bases.

[0173] (b) Polynucleotides with a combination of base sequences constituting part of barley chromosomal DNA, or variants thereof with the substitution, deletion, insertion, and/or addition of one or more bases.

[0174] As used herein, a polynucleotide with a base sequence constituting part of barley chromosomal DNA is not particularly limited as long as it is a polynucleotide that has a base sequence constituting part of the entire base sequences of chromosomal DNA of barley 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes, and that includes a protein-coding region. Further, a polynucleotide with a combination of base sequences constituting part of barley chromosomal DNA refers to a polynucleotide in which a base sequence constituting part of the entire base sequences of chromosomal DNA of barley 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes is joined to non-continuous base sequences constituting other parts of these chromosomes, and in which a protein-coding region is contained. For example, base sequences from two different parts of the chromosomes may constitute the polynucleotide, or three or more base sequences may join together to form the polynucleotide. Specifically, for example, cDNA with a plurality of exons from a protein-coding gene on barley chromosomal DNA can be regarded as a polynucleotide with a combination of base sequences constituting part of barley chromosomal DNA. However, the polynucleotide is not just limited to this specific example.

[0175] A variant with the substitution, deletion, insertion, and/or addition of one or more bases in the polynucleotide with a base sequence, or a combination of base sequences, constituting part of barley chromosomal DNA may be a polynucleotide that has been mutated on purpose, or a polynucleotide that exists in nature. For example, think of a base sequence of chromosomal DNA in a specific variety of barley. Comparing this base sequence with those of other varieties, no sequence is completely identical. Rather, these sequences are variants with the substitution, deletion, insertion, and/or addition of one or more bases. The polypeptide encoded by a polynucleotide with such variant base sequence may have the same amino acid sequence as the polypeptide encoded by a polynucleotide with a non-variant base sequence. Further, the polypeptides encoded by the polynucleotides with variant and non-variant base sequences may differ from each other with the substitution of some of the amino acids, or most of or all of the amino acid sequences may be different between these polypeptides.

[0176] Polynucleotides that encode polypeptides used for production of antibodies immobilized on a support of a polypeptide detection instrument according to the present invention are preferably polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or variants with the substitution, deletion, insertion, and/or addition of one or more bases in the polynucleotides with the base sequences of SEQ ID NO: 1 through 5780. (Such polynucleotides and variants will be referred to as polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780.)

[0177] The base sequences of SEQ ID NO: 1 through 5780 are base sequences of the barley EST (expressed sequence tag) independently developed by the inventors. The inventors have previously confirmed that a polynucleotide with the base sequences of SEQ ID NO: 1 through 770, a polynucleotide with the base sequences of SEQ ID NO: 771 through 1754, a polynucleotide with the base sequences of SEQ ID NO: 1755 through 2642, a polynucleotide with the base sequences of SEQ ID NO: 2643 through 3324, a polynucleotide with the base sequences of SEQ ID NO: 3325 through 4320, a polynucleotide with the base sequences of SEQ ID NO: 4321 through 4962, and a polynucleotide with the base sequences of SEQ ID NO: 4963 through 5780 are mapped on 1H, 2H, 3H, 4H, 5H, 6H, and 7H chromosomes, respectively.

[0178] It follows from this that the base sequences of SEQ ID NO: 1 through 5780 are partial sequences of barley cDNA. Thus, if polynucleotides with the base sequences of SEQ ID NO: 1 through 5780 contained protein-coding regions, antibodies against polypeptides encoded by these polynucleotides can be immobilized on the support. Further, variants with the substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780 constitute variant base sequences of barley cDNA. Thus, if these polynucleotides with variant base sequences contained protein-coding regions, antibodies against polypeptides encoded by these polynucleotides can be immobilized on the support. The polynucleotides with variant base sequences may be polynucleotides that have been mutated on purpose, or polynucleotides that exist in nature.

[0179] Polynucleotides that encode polypeptides used for production of antibodies immobilized on a support of a polypeptide detection instrument according to the present invention may be part of the polynucleotides or the like with the base sequences of SEQ ID NO: 1 through 5780. Since the base sequence of such partial polynucleotide is a partial base sequence of barley cDNA, antibodies against polypeptides encoded by such partial polynucleotides can be immobilized on the support if the partial polynucleotides contained a protein-coding region.

[0180] Further, a polynucleotide that encodes a polypeptide used for production of an antibody immobilized on a support of a polypeptide detection instrument according to the present invention may be a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. The remaining base sequences of the polynucleotide are not limited. For example, since the base

sequences of SEQ ID NO: 1 through 5780 are partial sequences of barley cDNA, these base sequences do not have the sequences on either end as originally found in the full length cDNA. Thus, a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780, and which additionally includes the cDNA sequences on the both ends or one end as originally found in the full length cDNA can be regarded as a polynucleotide whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. Further, vectors such as plasmids and BACs (bacterial artificial chromosomes) that have incorporated all of or part of the polynucleotide or the like with the base sequences of SEQ ID NO: 1 through 5780, and polynucleotides in which the partial sequence is ligated to arbitrary base sequences can also be regarded as polynucleotides whose partial sequence comprises all of or part of the base sequences of SEQ ID NO: 1 through 5780. Such polynucleotides at least include all of or part of the polynucleotide or the like with the base sequences of SEQ ID NO: 1 through 5780, i.e., part of barley cDNA. Therefore, antibodies against polypeptides encoded by such polynucleotides can be immobilized on the support if the polynucleotides contained a protein-encoding region.

[0181] Further, polynucleotides that encode polypeptides used for production of antibodies immobilized on a support of a polypeptide detection instrument according to the present invention may be polynucleotides or the like whose partial sequences comprise all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n (where n is an odd number), and all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n+1, from among the base sequences of SEQ ID NO: 1 through 5780. As described above, the base sequences of SEQ ID NO: 1 through 5780 are EST sequences of barley, and comprise sequences that can be read by sequencing the cloned cDNA from the both ends only once. In other words, the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 among the base sequences of SEQ ID NO: 1 through 5780 are base sequences that are read from the both ends of the cDNA of the same clone. As such, these base sequences can realize a full length cDNA base sequence, which corresponds to all of or part of the full length cDNA. Thus, polynucleotides or the like whose partial sequences comprise all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n (where n is an odd number), and all of or part of the base sequence, or a variant thereof, of SEQ ID NO: n+1, from among the base sequences of SEQ ID NO: 1 through 5780 can be regarded as polynucleotides with full length cDNA that comprises the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1, or polynucleotides that comprise part of the full length cDNA. Further, the polynucleotides may be polynucleotides in which vector sequences or arbitrary base sequences for example are ligated to the both ends or one end of the full length cDNA or polynucleotides that comprise part of the full length cDNA. Further, the polynucleotides may be variants that have a base substitution or other mutations in sequences other than the base sequences of SEQ ID NO: 1 through 5780, i.e., a middle section of the total cDNA unspecified by SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1. Such polynucleotides include the full length or part of barley cDNA, and therefore antibodies against polypeptides encoded by the polynucleotides can be produced. In particular, when the polynucleotides are full length cDNA or include full length cDNA, antibodies against the entire proteins encoded by the genes located on the barley chromosomes can be produced.

[0182] [Peptide Detection Instrument with the Antibodies Immobilized in Regions that are Arranged in the Chromosomal Order of the Polynucleotides Encoding Polypeptides Used for Production of the Antibodies]

[0183] As described above, the chromosomal order of polynucleotides on barley chromosomes (1H, 2H, 3H, 4H, 5H, 6H, or 7H) (distance from the short arm end of chromosome) has been specified in clones that have the base sequences of SEQ ID NO: n (where n is an odd number) and SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through SEQ ID NO: 5780. Thus, if antibodies against the polypeptides encoded by the polynucleotides with the base sequences of SEQ ID NO: 1 through SEQ ID NO: 5780 were placed according to the order, as represented in Table 1-1 through Table 7-9, of the polynucleotides encoding the polypeptides, it would be possible to place the polypeptides according to the order from the short arm end of 1H chromosome to the long arm end of 7H chromosome, i.e., chromosomal order. For clones that have the same order from the short arm end, the order by which these clones are placed is not particularly limited. Once the precise order of these clones were specified by a future study, these clones will be able to be placed accordingly. Note that, the reference point (origin) on the chromosome is not just limited to the short arm end of 1H chromosome. Any position on a chromosome can be used as a reference point.

[0184] With the antibodies immobilized on a support in the order the polynucleotides encoding the polypeptides used for production of the antibodies are arranged on the chromosomes, the location and extent of recombination on chromosomes can be checked for genes from which the expressed proteins originate. That is, the genotypes of the parents are directly inherited as the haplotype in portions of the chromosomes where no recombination has occurred. As a result, the genotype of a trait conferred to the selected individuals can be easily determined, with the result that the efficiency of breeding is improved.

[0185] [Polypeptide Detection Instrument with the Antibodies Immobilized in Regions appended with Chromosomal Order Information of the Polynucleotides Encoding Polypeptides Used for Production of the Antibodies]

[0186] The regions in which the antibodies are immobilized (spots) may be appended with information indicative of the order in which the polynucleotides encoding the polypeptides used for production of the antibodies are arranged on barley chromosomes. The spots may be arranged in any way as long as they are appended with the order information. With the order information added to the spots, the data obtained from the spots can be rearranged in the chromosomal order even when the spots are randomly placed on a support. Note that, the order information added to the spots can follow the foregoing criteria used to place the antibodies.

[0187] Adding order information enables the spots to be arranged in an arbitrary order in a polypeptide detection instrument of an array type, in which more than one antibody is immobilized on a support such as a membrane or a glass slide. Further, the chromosomal order information of individual antibodies can also be added in a polypeptide detection instrument that employs a collection of beads (bead array) in which the antibody is immobilized on each bead serving as a support.

[0188] [Examples of a Polypeptide Detection Instrument according to the Present Invention]

[0189] Various conventional techniques that are designed for detection of protein (polypeptide) using antibodies can suitably be used in a polypeptide detecting instrument according to the present invention.

[0190] As an example of a peptide detection instrument according to the present invention, the following describes an antibody array of a bead type. The substance immobilized on the beads serving as supports is not limited to antibody. Other polypeptides or polynucleotides may be immobilized as well. As such, a gene detection instrument, a gene polymorphism detection instrument, and a polypeptide-interacting substance detection instrument according to the present invention can also be realized as bead arrays.

[0191] In an antibody array of a bead type, it is preferable that one kind of antibody be immobilized on each bead, and that each bead be appended with barley chromosomal order information of polynucleotides encoding polypeptides used for production of the antibodies. For example, by using each well of a micro titer plate as a small vessel, a plurality of beads with identification code (information of the immobilized antibodies, position information on the chromosomes, etc.) is placed in each well. By reading the identification code, information regarding identity of the immobilized antibodies can be specified. With use of a two-wavelength laser beam, 100 kinds of beads can be quantified. Further, since the technique allows for detection in a liquid phase, it is particularly effective in efficiently quantifying proteins. A representative example is Luminex, which is a fluorescent micro beads array system manufactured by HitachiSoft.

[0192] (5) Use of a Detection Instrument according to the Present Invention

[0193] Use of a detection instrument according to the present invention is not particularly limited. For example, the detection instrument can be suitably used to identify chromosome fragments including a target trait (identification of genotype), from hybrids obtained by crossing Triticeae species. Further, the detection instrument can be suitably used to screen for a variety with a target trait, from hybrids obtained by crossing Triticeae species for variety improvement. For these purposes, it is preferable that the polynucleotides or other substances immobilized on the support such as an array be arranged in the chromosomal order.

[0194] In conventional arrays, the polynucleotides or other substances immobilized on the support are randomly arranged. This enables the expression level or other profiles of the immobilized polynucleotides etc. to be individually analyzed. In hybrids, individual genes are inherited in units of blocks, from a point of cross over to the next point of cross over, on the chromosomes. Therefore, for the genotype identification or selection in variety improvement, etc., it is necessary to determine the location and extent of recombination and the presence or absence of unnecessary recombination, in addition to finding individual traits. Thus, conventional arrays with randomly arranged DNA fragments cannot be used efficiently for the screening in variety improvement, etc.

[0195] On the other hand, in a detection instrument of the present invention, the polynucleotides or other substances immobilized on the support are arranged in the chromosomal order. Thus, with a detection instrument of the present invention, the locations of recombination on the chromosomes can be found, if any, with a single round of testing. This allows for accurate selection of individuals with desirable traits from a segregating population of hybrid individuals. Further, with a detection instrument according to the present invention, chromosomal recombinations in the hybrid generation can easily be estimated. This allows a group of genes to be introduced in units of blocks, or genes in the blocks to be modified.

[0196] Further, with a detection instrument according to the present invention, the recombination patterns, i.e., the location and type of recombination on the chromosomes can be accurately grasped. Thus, by identifying conserved regions of chromosomes where recombination frequency is small in the population of hybrids or natural population, recombination can be efficiently promoted only in these regions of the chromosomes.

[0197] Referring to FIG. **1** and FIG. **2**, the following briefly describes an example of a method by which target traits are screened for using a detection instrument according to the present invention. For example, a DNA micro array was used in which polynucleotides with partial base sequences of chromosomal DNA of barley were placed and immobilized on a support in the chromosomal order. In the DNA micro array, solid spots X in FIG. **1**(*a*) indicate that genes that confer brewing characteristics are expressed, and hatched spots Y in FIG. **1**(*b*) indicates expression of genes that confer disease-resistance.

[0198] In the DNA micro array, the spots are arranged in a chromosomal order, and therefore the positions of spots X and Y are fixed. For example, in FIG. **1**(*a*), the spots X are fixed at the first, second, fifth, and sixth positions of the first row, and at the ninth and tenth positions of the bottom row. The spots Y are fixed at the third and fourth positions of the first row, as shown in FIG. **1**(*b*).

[0199] It is assumed here that segregating populations as represented by four micro arrays in the bottom of FIG. **2** were obtained from a cross between a variety expressing the brewing genes as indicated by spots X (corresponding to the upper left DNA micro array in FIG. **2**) and a variety expressing the disease-resistant genes as indicated by spots Y (corresponding to the upper right DNA micro array in FIG. **2**), for example. From the result of analysis using these DNA micro arrays, varieties expressing both the brewing genes and disease-resistant genes can be screened for from the segregating populations (variety corresponding to the upper left DNA micro array circled by a dotted line in the lower portion of FIG. **2**).

[0200] Further, whether the chromosome fragments have derived from which parent can easily be determined also for other regions of the genome. Thus, a backcross, for example, between a hybrid and the variety shown in FIG. **1**(*a*) easily allows for selection and development of varieties having all of the expressed spots as illustrated in FIG. **1**(*a*), i.e., the first, second, fifth, and sixth spots of the first row, and the ninth and tenth spots of the bottom row, as well as the third and fourth spots of the first row as shown in FIG. **1**(*b*).

[0201] In using a detection instrument according to the present invention for genotyping (whether chromosome sites originated from which parent) or detection of traits (quantitative and qualitative) linked to the genetic markers, the accuracy of data can be improved by increasing the density of the genetic markers with increased numbers of polynucleotides, polypeptides, or antibodies immobilized on a support of a detection instrument according to the present invention.

[0202] The density of polynucleotides, polypeptides, or antibodies (a distance between adjacent polynucleotides etc.) immobilized on the support is preferably no greater than 30

cM, more preferably no greater than 15 cM, or particularly preferably no greater than 10 cM, in order to confirm linkage between two adjacent markers.

[0203] For the entire barley genome, the number of polynucleotides, polypeptides, or antibodies immobilized on the support is preferably no less than 50, more preferably no less than 100, and particularly preferably no less than 150. When performing genotyping for a Mendelian segregating population of barley with a resolution as high as 1 cM, the number of polynucleotides, polypeptides, or antibodies immobilized on the support is preferably no less than 1500.

EXAMPLE

[0204] With the polynucleotides immobilized on a support of a detection instrument according to the present invention, assessment was made as to whether the genotype of each parent occurs in which part of 1H chromosome in 5 lines of hybrids (DHHS1, DHHS2, DHHS3, DHHS4, and DHHS5) obtained from a cross between malting barley (Haruna Nijo), and wild type barley (H602). That is, locations of recombination were determined.

[0205] [Genetic Markers]

[0206] Nine genetic markers mapped on 1H chromosome of barley were used. Clones: bah47d23, baa119i12, bah45i3, bags30g20, BaGS13F08, baet45e0410, bah16m01, BaH56B06, and BaH39L18.

[0207] [Primers]

[0208] Table. 29 below shows the primers used in this experiment.

TABLE 29

Clones	Forward Primer Haruna Nijo / Forward Primer H602	SEQ ID NO:	Reverse Primer	SEQ ID NO:
bah47d23	AGATGGAGGGGCCCTGTGCAT	22343	CTGTGGGAAAGCCTACATC⍰	5880
	TAGATGGAGGGGCCCTGTGTAT	22344		
baal19i12	TCAGAGAGGTGAATCTGGGTCAA	22345	GAACTGAGGCGTGCACATA	6012
	TTCAGAGAGGTGAATCTGGGTTAA	22346		
bah45i13	CCATGACCAGCAAAAGCAGTCC	22347	GCAAATCAGTTGCTGGAAC	6340
	CCATGACCAGCAAAAGCAGCCC	22348		
bags30g20	GGACTACGTACGGACTGAAATAG	22349	GGTTCCATTCCTGCAGATGT⍰	6632
	GGACTACGTACGGACTGAAACAG	22350		
BaGS13F08	TCACAAGGTAACCAAAACAATTCG⍰	22351	CTCAGGCAATGCATCAAAT⍰	6760
	ATCACAAGGTAACCAAACAATTT⍰	22352		
baet45E0410	CCGGACTTGACAAGCGGTAATTG	22353	CGGCTCTCCATAGACTGCT⍰	6800
	CGGACTTGACAAGCGGTAAGTG	22354		
bah16m01	CATGGGGGAGGTTTTGGCTCTTT	22355	AAGACCTCACTCCAAAGCG	6904
	ATGGGGGAGGTTTTGGCTCGTT	22356		
BaH56B06	CTTTTTGGTCCTCAGTCCTCATTG	22357	AGATCCGCTACTGCTTGGA⍰	7064
	TTTTTGGTCCTCAGTCCTCACTG	22358		
BaH39L18	GCTTCTAGACGCAGACAAGCTG	22359	GTATGCTTGCAGGAAGGCT⍰	7316
	AGCTTCTAGACGCAGACAAGTTG	22360		

⍰ indicates text missing or illegible when filed

[0209] As the reverse primers, the primers used to find polymorphism in 1H chromosomes, shown in Tables 8-1 through 8-8, were used. Specifically, bah47d23, baa119i12, bah45i13, bags30g20, BaGS13F08, baet45e0410, bah16m01, BaH56B06, and BaH39L18 are primers with the base sequences of SEQ ID NO: 5880, SEQ ID NO: 6012, SEQ ID NO: 6340, SEQ ID NO: 6632, SEQ ID NO: 6760, SEQ ID NO: 6800, SEQ ID NO: 6904, SEQ ID NO: 7064, and SEQ ID NO: 7316, respectively.

[0210] The forward primers were designed based on SNP-containing portions of the base sequences. Specifically, the third base from the 3' end of the primer sequence was designated as a base characterizing "Haruna Nijo" or "H602". For the first and second bases on the 3' end, the same kind of base but different from one found in the original base sequence was used. Specifically, when the base in the original sequence was A, a purine, G, was selected (and vice versa), and when the base in the original sequence was C, a pyrimidine, T, was selected (and vice versa).

[0211] For the designing of forward primers, the base sequences in the vicinity of the SNPs of the SNP markers, shown in Tables 22-1 through 22-20, mapped on 1H chromosome were used. Specifically, the forward primers (SEQ ID NO: 22343 (Haruna Nijo) and SEQ ID NO: 22344 (H602)) for bah47d23 had the base sequence of SEQ ID NO: 17380. The forward primers (SEQ ID NO: 22345 (Haruna Nijo) and SEQ ID NO: 22346 (H602)) for baa119i12 had the base sequence of SEQ ID NO: 17419. The forward primers (SEQ ID NO: 22347 (Haruna Nijo) and SEQ ID NO: 22348 (H602)) for bah45i13 had the base sequence of SEQ ID NO: 17556. The forward primers (SEQ ID NO: 22349 (Haruna Nijo) and SEQ ID NO: 22350 (H602)) for bags30g20 had the base sequence of SEQ ID NO: 17669. The forward primers (SEQ ID NO: 22351 (Haruna Nijo) and SEQ ID NO: 22352 (H602)) for BaGS13F08 had the base sequence-of SEQ ID NO:

17723. The forward primers (SEQ ID NO: 22353 (Haruna Nijo) and SEQ ID NO: 22354 (H602)) for baet45e0410 had the base sequence of SEQ ID NO: 17742. The forward primers (SEQ ID NO: 22355 (Haruna Nijo) and SEQ ID NO: 22356 (H602)) for bah16m01 had the base sequence of SEQ ID NO: 17785. The forward primers (SEQ ID NO: 22357 (Haruna Nijo) and SEQ ID NO: 22358 (H602)) for BaH56B06 had the base sequence of SEQ ID NO: 17860. The forward primers (SEQ ID NO: 22359 (Haruna Nijo) and SEQ ID NO: 22360 (H602)) for BaH39L18 had the base sequence of SEQ ID NO: 17958.

[0212] [PCR Reaction]

[0213] From each of the 5 lines of barley hybrids, genomic DNA was prepared and used as a template. Table 30 shows the composition of the PCR reaction solution. The reaction was performed under the following conditions.

94° C. for 2 minutes

Start of 5 cycles consisting of:

[0214] 94° C. for 30 seconds;

[0215] 65° C. for 30 seconds (−1° C./cycle); and

[0216] 72° C. for 1 minute

Start of 30 cycles consisting of:

[0217] 94° C. for 30 seconds;

[0218] 60° C. for 30 seconds; and

[0219] 72° C. for 1 minute

72° C. for 7 minutes

End of Reaction

[0220]

TABLE 30

Composition of PCR reaction solution

	(×1)
mQH_2O	6.86
10X Blend Taq buffer	1.00
dNTPs (2.0 mM)	1.00
Primer fwd. (50 μM)	0.02
Primer rev. (50 μM)	0.02
Blend Taq (2.5 U/μl)	0.10
DNA (10 ng/μl)	1.00
Total (μl)	10.00

[0221] [Result]

[0222] FIG. **3** shows the result. In FIG. **3**, regions indicated by "H" (black) are regions originating in Haruna Nijo, and regions indicated by "S" (blank) are regions originating in H602. As can be seen in FIG. **3**, in DHHS1, bah47d23 through BaGS13F08 were amplified by the forward primers based on the base sequences of Haruna Nijo, and baet45e0410 through BaH39L18 were amplified by the forward primers based on the base sequence of H602. In other words, in DHHS1, there were recombinations between the genetic markers based on BaGS13F08 and the genetic markers based on baet45e0410.

[0223] Similarly, in DHHS2, two recombinations were observed: one between bah47d23 and baa119i12, and one between BaGS13F08 and baet45e0410. In DHHS3, two recombinations were observed: one between bah47d23 and baa119i12, and one between bags30g20 and BaGS13F08. In DHHS4, two recombinations were observed: one between bah47d23 and baa119i12, and one between BaH56B06 and BaH39L18. In DHHS5, all clones had the genotype of H602, suggesting that the entire 1H chromosome of these individuals is very likely to be of the H602 origin.

[0224] The polynucleotides used in this Example were not immobilized on a support. However, the forward primers and reverse primers used in this Example may be immobilized, for example, on the Gene Silicon in the chromosomal order, so as to fabricate a detection instrument according to the present invention. It should be apparent to a person ordinary skill in the art that the result obtained in this Example can also be obtained with such a detection instrument.

[0225] The embodiments and concrete examples of implementation discussed in the foregoing detailed explanation serve solely to illustrate the technical details of the present invention, which should not be narrowly interpreted within the limits of such embodiments and concrete examples, but rather may be applied in many variations within the spirit of the present invention, provided such variations do not exceed the scope of the patent claims set forth below.

INDUSTRIAL APPLICABILITY

[0226] A detection instrument according to the present invention uses polynucleotides that can be used as genetic markers mapped on barley chromosomes. The detection instrument can be used to quickly and comprehensively detect gene expression, gene polymorphism, proteins (polypeptides), and protein (polypeptide)-interacting substances in Triticeae species. This greatly improves the efficiency of screening and breeding of Triticeae species. If the detection instrument were able to grow useful Triticeae species of various characteristics in a short time period, it would be possible to offer a solution to food problems.

[0227] Taken together, a detection instrument according to the present invention can be suitably used for breeding of Triticeae species, and is applicable to a wide range of agricultural fields. A detection instrument of the present invention can also be used for the basic research in agriculture and other fields of biology.

LENGTHY TABLES

The patent application contains a lengthy table section. A copy of the table is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20090186402A1). An electronic copy of the table will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20090186402A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

1. A gene detection instrument for detecting expression or polymorphism of genes existing in a genome of Triticeae species,

said gene detection instrument comprising a support on which is immobilized at least one polynucleotide selected from:

(a) polynucleotides with partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley; or

(b) polynucleotides with combined partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the combined partial base sequences of chromosomal DNA of barley.

2. A gene detection instrument as set forth in claim **1**, wherein the polynucleotide immobilized on the support comprises at least one kind of polynucleotide selected from the group consisting of:

(1) polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780;

(2) a polynucleotide that comprises a part of any one of the polynucleotides set forth in (1);

(3) a polynucleotide whose partial sequence comprises all of or part of any one of the polynucleotides set forth in (1); and

(4) a polynucleotide whose partial sequence comprises: all of or part of a base sequence of SEQ ID NO: n (where n is an odd number), or its variant base sequence, in the polynucleotides set forth in (1); and all of or part of a base sequence of SEQ ID NO: n+1, or its variant base sequence, in the polynucleotides set forth in (1).

3. A gene detection instrument as set forth in claim **1** or **2**,

wherein two or more kinds of polynucleotides are immobilized on the support, and

wherein regions on the support in which the polynucleotides are respectively immobilized are arranged in the same order as a chromosomal order of the polynucleotides immobilized on the support.

4. A gene detection instrument as set forth in claim **1** or **2**,

wherein two or more kinds of polynucleotides are immobilized on the support, and

wherein information indicative of a chromosomal order of the polynucleotides immobilized on the support is appended to regions on the support in which the polynucleotides are respectively immobilized.

5. A gene detection instrument as set forth in any one of claims **1** through **4**, wherein the polynucleotide immobilized on the support comprises cDNA.

6. A gene polymorphism detection instrument for detecting polymorphism of genes existing in a genome of Triticeae species,

said gene polymorphism detection instrument comprising a support on which is immobilized at least one polynucleotide selected from:

polynucleotides with partial base sequences of chromosomal DNA of barley; or

polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley.

7. A gene polymorphism detection instrument as set forth in claim **6**, wherein the polynucleotide immobilized on the support comprises a partial base sequence of at least one of DNA fragments amplified, using genomic DNA of Triticeae species as a template, with a primer set that comprises a combination of any two primers arbitrarily selected from:

a plurality of primers designed based on a base sequence of SEQ ID NO: n (where n is an odd number) from among base sequences of SEQ ID NO: 1 through 5780; and

a plurality of primers designed based on a base sequence of SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through 5780.

8. A gene polymorphism detection instrument as set forth in claim **6** or **7**,

wherein two or more kinds of polynucleotides are immobilized on the support, and

wherein regions on the support in which the polynucleotides are respectively immobilized are arranged in the same order as a chromosomal order of the polynucleotides immobilized on the support.

9. A gene polymorphism detection instrument as set forth in claim **6** or **7**,

wherein two or more kinds of polynucleotides are immobilized on the support, and

wherein information indicative of a chromosomal order of the polynucleotides immobilized on the support is appended to regions on the support in which the polynucleotides are respectively immobilized.

10. A gene polymorphism detection instrument as set forth in any one of claims **6** through **9**, wherein the polynucleotide immobilized on the support comprises a synthetic oligonucleotide.

11. A polypeptide-interacting substance detection instrument for detecting a substance which interacts with a polypeptide that comprises a protein, or part of a protein, encoded by a gene present in the genome of Triticeae species,

said polypeptide-interacting substance detection instrument comprising a support on which is immobilized at least one of polypeptides encoded by:

(a) polynucleotides with partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley; or

(b) polynucleotides with combined partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the combined partial base sequences of chromosomal DNA of barley.

12. A polypeptide-interacting substance detection instrument as set forth in claim **11**, wherein the polypeptide immobilized on the support is encoded by a polynucleotide selected from the group consisting of:

(1) polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780;

(2) a polynucleotide that comprises a part of any one of the polynucleotides set forth in (1);

(3) a polynucleotide whose partial sequence comprises all of or part of any one of the polynucleotides set forth in (1); and

(4) a polynucleotide whose partial sequence comprises: all of or part of a base sequence of SEQ ID NO: n (where n is an odd number), or its variant base sequence, in the polynucleotides set forth in (1); and all of or part of a base sequence of SEQ ID NO: n+1, or its variant base sequence, in the polynucleotides set forth in (1).

13. A polypeptide-interacting substance detection instrument as set forth in claim **11** or **12**,

wherein two or more kinds of polypeptides are immobilized on the support, and

wherein regions on the support in which the polypeptides are respectively immobilized are arranged in the same order as a chromosomal order of the polynucleotides respectively encoding the polypeptides immobilized on the support.

14. A polypeptide-interacting substance detection instrument as set forth in claim **11** or **12**,

wherein two or more kinds of polypeptides are immobilized on the support, and

wherein information indicative of a chromosomal order of the polynucleotides respectively encoding the polypeptides immobilized on the support is appended to regions on the support in which the polypeptides are respectively immobilized.

15. A polypeptide detection instrument for detecting a polypeptide that comprises a protein, or part of a protein, encoded by a gene present in a genome of Triticeae species,

said polypeptide detection instrument comprising a support on which is immobilized at least one of antibodies against polypeptides encoded by:

(a) polynucleotides with partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the partial base sequences of chromosomal DNA of barley; or

(b) polynucleotides with combined partial base sequences of chromosomal DNA of barley, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the combined partial base sequences of chromosomal DNA of barley.

16. A polypeptide detection instrument as set forth in claim **11**, wherein the polynucleotide encoding the polypeptide used for production of the antibody immobilized on the support comprises at least one kind of polynucleotide selected from the group consisting of:

(1) polynucleotides with the base sequences of SEQ ID NO: 1 through 5780, or polynucleotides mutated by substitution, deletion, insertion, and/or addition of one or more bases in the base sequences of SEQ ID NO: 1 through 5780;

(2) a polynucleotide that comprises a part of any one of the polynucleotides set forth in (1);

(3) a polynucleotide whose partial sequence comprises all of or part of any one of the polynucleotides set forth in (1); and

(4) a polynucleotide whose partial sequence comprises: all of or part of a base sequence of SEQ ID NO: n (where n is an odd number), or its variant base sequence, in the polynucleotides set forth in (1); and all of or part of a base sequence of SEQ ID NO: n+1, or its variant base sequence, in the polynucleotides set forth in (1).

17. A polypeptide detection instrument as set forth in claim **15** or **16**,

wherein two or more kinds of antibodies are immobilized on the support, and

wherein regions on the support in which the antibodies are respectively immobilized are arranged in the same order as a chromosomal order of the polynucleotides respectively encoding polypeptides used for production of the antibodies immobilized on the support.

18. A polypeptide detection instrument as set forth in claim **15** or **16**,

wherein two or more kinds of antibodies are immobilized on the support, and

wherein information indicative of a chromosomal order of the polynucleotides respectively encoding polypeptides used for preparation of the antibodies immobilized on the support is appended to regions on the support in which the antibodies are respectively immobilized.

19. Polynucleotides usable for an instrument for detecting expression or polymorphism of genes present in the genome of Triticeae species,

the polynucleotides comprising:

base sequences of SEQ ID NO: 1 through 5780; or

base sequences of SEQ ID NO: 1 through 5780, with substitution, deletion, insertion, and/or addition of one or more bases.

20. Polynucleotides whose partial sequence comprises polynucleotides usable for an instrument for detecting polymorphism of genes present in the genome of Triticeae species,

the polynucleotides comprising DNA fragments amplified, using genomic DNA of Triticeae species as a template, with a primer set that comprises a combination of any two primers arbitrarily selected from:

a plurality of primers designed based on a base sequence of SEQ ID NO: n (where n is an odd number) from among base sequences of SEQ ID NO: 1 through 5780; and

a plurality of primers designed based on a base sequence of SEQ ID NO: n+1 from among the base sequences of SEQ ID NO: 1 through 5780.

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