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(54) Title: METHODS AND COMPOSITIONS FOR BREEDING FOR PREFERRED TRAITS

(57) Abstract: The present invention relates to the field of plant breeding. More specifically, the present invention includes a method of using haploid plants for genetic mapping of traits such as disease resistance. Further, the invention includes a method for breeding corn plants containing quantitative trait loci (QTL) that are associated with resistance to Gray Leaf Spot (GLS), a fungal disease associated with *Cercospora* spp. The invention further includes a method for breeding corn plants containing QTL that are associated with Goss' Wilt, a bacterial disease associated with *Clavibacter michiganense spp.*

Cross-Reference To Related Applications

This application claims priority to U.S. Provisional Patent Application No. 60/966,706, filed August 29, 2007 and incorporated herein by reference in its' entirety.

Incorporation of Sequence Listing

[0001] A sequence listing contained in the file named "46_25_54886_0000_WO.txt" which is 2432383 bytes (measured in MS-Windows®),created on August 29, 2008 and comprising 1,361 nucleotide sequences, is electronically filed herewith and is incorporated herein by reference in its entirety.

Field of Invention

[0002] The present invention relates to the field of plant breeding. More specifically, the present invention includes a method of using haploid plants for genetic mapping of traits such as disease resistance. Further, the invention includes a method for breeding corn plants containing quantitative trait loci (QTL) that are associated with resistance to Gray Leaf Spot (GLS), a fungal disease associated with *Cercospora* spp. The invention further includes a method for breeding corn plants containing QTL that are associated with Goss' Wilt, a bacterial disease associated with *Clavibacter michiganense spp.*

Background of Invention

[0003] Plant breeding is greatly facilitated by the use of doubled haploid (DH) plants. The production of DH plants enables plant breeders to obtain inbred lines without multigenerational inbreeding, thus decreasing the time required to produce homozygous plants. DH plants provide an invaluable tool to plant breeders, particularly for generating inbred lines, QTL mapping, cytoplasmic conversions, and trait introgression. A great deal of time is spared as homozygous lines are essentially instantly generated, negating the need for multigenerational conventional inbreeding.

[0004] In particular, because DH plants are entirely homozygous, they are very amenable to quantitative genetics studies. Both additive variance and additive x additive genetic variances can be estimated from DH populations. Other applications include identification of epistasis and linkage effects. For breeders, DH populations have been particularly useful in QTL mapping, cytoplasmic conversions, and trait introgression. Moreover, there is value in testing and evaluating homozygous lines for plant breeding programs. All of the genetic variance is among progeny in a breeding cross, which improves selection gain.

[0005] However, induction of haploidization followed by diplodization requires a high input of resources. Diploidization represents a rate-limiting step as it is expensive and requires a high input of labor as well as plant material in order to generate sufficient breeding material. The present invention includes methods for the use of homozygous plant material for quantitative genetic studies. Significant time and resources can be saved by using haploid plants for QTL mapping. These plants have only one parental set of chromosomes and thus are hemizygous for all genes in their genome. This property allows for a resolution in genetic mapping which is similar to that of recombinant inbred lines (RILs) with the advantage that haploid plants can be produced in only one growing season. Further, the present invention provides an increased efficiency in allocation of diploidization resources as only those haploid plants with at least one QTL of interest can be advanced for doubling.

[0006] Methods of utilizing haploids in genetic studies have been described in the art. A statistical method to utilize pooled haploid DNA to estimate parental linkage phase and to construct genetic linkage maps has been described (Gasbarra, D. *et al.*, *Genetics* 172: 1325-1335 (2006)). An additional study has used the method of crossing haploid wheat plants with cultivars to map leaf rust resistance gene in wheat (Hiebert, C. *et al.*, *Theor Appl Genet* 110: 1453-1457 (2005)). Haploid plants and SSR markers have been used in linkage map construction of cotton (Song, X. *et al.*, *Genome* 48:378-392 (2005)). Further, AFLP marker analysis has been performed in monoploid potato (Varrieur, J., Thesis, *AFLP Marker Analysis of Monoploid Potato* (2002) To date a method of using haploid plants to genetically map loci associated with traits of interest is lacking. The present invention provides a method of using haploid plants to genetically map traits of interest.

[0007] The present invention comprises identification and introgression of QTL associated with desirable traits using haploid plants in a plant breeding program. In one aspect, the present invention includes methods and compositions for mapping disease resistance loci in corn. Two diseases which cause significant damage to corn crops are Gray Leaf Spot (GLS) caused by the fungal pathogen *Cercospora zeae-maydis* (CZ) and Goss' Wilt caused by the bacterial pathogen *Clavibacter michiganensis subsp. nebraskensis* (CN). GLS is a global problem and, in addition to prevalence in Africa, Central America and South America, it has spread across most of the U.S. cornbelt over the past 10-15 years. The fungus overwinters in field debris and requires moisture, usually in the form of heavy fogs, dews, or rains, to spread its spores and infect corn. Increasing pervasiveness has been linked to no-till practices which promote retention of fungi, such as CZ, in the soil (Paul *et al.* 2005 Phytopathology 95:388-396). Symptoms include a rectangular necrotic lesion which can coalesce to larger affected regions and symptoms usually appear later in the growing season. GLS in corn elicits an increased allocation of resources to damaged leaf tissue, leading to elevated risk for root and stalk rots, which ultimately results in even greater crop losses (Ward *et al.* 1999; Saghai-Maroof *et al.* 1996 Theor. Appl. Genet. 93:539-546). Yield-loss associated with GLS can be high if the symptoms are heavy and appear early, with reported losses exceeding 50% (Ward *et al.* 1999). Recent work has identified there are at least two sister species of CZ, as well as potentially other isolates of *Cercospora*, capable of causing GLS (Carson *et al.* 2006 Maydica 51:89-92; Carson *et al.* 2002 Plant Dis. 86:1088-109). Genomic regions on maize Chromosomes 1, 2, 3, 4, 5, 6, 7, and 8 have been associated with GLS using RFLP, AFLP and SSR markers (US Patent 5,574,210; Lehmensiek, *et al.*, TAG, (2001); Clements, *et al. Phytopathology* (2000); Gorden et al. *Crop Science* (2004); Bubeck, *et al. Crop Science*, (1993); Saghai-Maroof *et al.*, TAG (1996)). Certain genomic regions, molecular markers, and QTL associated with GLS resistance have also been reported (WO 2008/042185 A2).

[0008] Another disease of corn is Goss' Wilt which is distributed throughout the U.S. cornbelt. Symptoms include leaf freckles which are small dark green to black water soaked spots and vascular wilt which results in loss of yield. Conservation tillage practices can increase pervasiveness because CN can overwinter in debris, particularly stalks, from infected corn plants (Bradbury, J.F. (1998)). A mapping study conducted by Rocheford *et al.* reported a genomic region on maize Chromosome 4 associated with Goss' Wilt (Rocheford, *et al.*, *Journal of Heredity*, (1989)). Both GLS and Goss' Wilt are significant pathogens of corn, and a need exists for development of disease resistant lines.

[0009] Breeding for corn plants resistant to GLS and Goss' Wilt can be greatly facilitated by the use of marker-assisted selection. Of the classes of genetic markers, single nucleotide polymorphisms (SNPs) have characteristics which make them preferential to other genetic markers in detecting, selecting for, and introgressing disease resistance in a corn plant. SNPs are preferred because technologies are available for automated, high-throughput screening of SNP markers, which can decrease the time to select for and introgress disease resistance in corn plants. Further, SNP markers are ideal because the likelihood that a particular SNP allele is derived from independent origins in the extant population of a particular species is very low. As such, SNP markers are useful for tracking and assisting introgression of disease resistance alleles, particularly in the case of disease resistance haplotypes.

[0010] The present invention provides and includes a method for using haploid plants to map and fine-map QTL associated with a trait such as disease resistance in plants. The present invention also provides and includes a method for screening and selecting a corn plant comprising QTL for GLS resistance using endemic strains of CZ and single nucleotide polymorphisms (SNP) marker technology. The present invention further provides and includes a method for screening and selecting a corn plant comprising QTL for Goss' wilt resistance using endemic strains of CN and SNP marker technology.

[0011] The present invention includes methods for breeding crop plants such as maize (*Zea mays*), soybean (*Glycine max*), cotton (*Gossypium hirsutum*), peanut (*Arachis hypogaea*), barley (*Hordeum vulgare*); oats (*Avena sativa*); orchard grass (*Dactylis glomerata*); rice (*Oryza sativa*, including indica and japonica varieties); sorghum (*Sorghum bicolor*); sugar cane (*Saccharum sp*); tall fescue (*Festuca* arundinacea); turfgrass species (e.g. species: *Agrostis stolonifera, Poa pratensis, Stenotaphrum secundatum*); wheat (*Triticum aestivum*), and alfalfa (*Medicago sativa*), members of the genus *Brassica*, broccoli, cabbage, carrot, cauliflower, Chinese cabbage, cucumber, dry bean, eggplant, fennel, garden beans, gourd, leek, lettuce, melon, okra, onion, pea, pepper, pumpkin, radish, spinach, squash, sweet corn, tomato, watermelon, ornamental plants, and other fruit, vegetable, tuber, and root crops.

Summary of Invention

[0012] The present invention provides a method for the association of at least one genotype using haploid plants comprising: a) assaying a genotype of at least one haploid plant with at least one marker and b) associating the at least one marker with at least one phenotypic trait. The at least one genotype comprises at least one marker selected from the group consisting of a genetic marker, a haplotype, a nucleic acid sequence, a transcriptional profile, a metabolic profile, a nutrient composition profile, a protein expression profile, and a phenotypic character. The identified genotype can be used to make a plant breeding decision such as selecting among breeding populations, selecting progeny in one or more breeding populations, predicting progeny performance of parental lines and selecting among parental lines based on prediction of progeny performance, and advancing lines in germplasm improvement activities. Germplasm improvement activities are selected from the group consisting of line and variety development, hybrid development, transgenic event selection, making breeding crosses, testing and advancing a plant through self fertilization, purification of lines or sublines, using plants or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plants or parts thereof for mutagenesis. Plant breeding decisions can further comprise doubling at least one haploid plant based on the at least one genotype associated with at least one phenotypic trait.

[0013] The invention further provides for a method for identifying an association of a plant genotype with one or more traits of interest comprising a) screening a plurality of haploid plants displaying heritable variation for at least one trait wherein the heritable variation is linked to at least one genotype; and b) associating the at least one genotype from the haploid plants to at least one trait.

[0014] In certain embodiments, methods for the association of at least one genotype with at least one phenotype using a haploid plant comprising: a) assaying at least one genotype of at least one haploid plant with at least one genetic marker; and b) associating the at least one marker with at least one phenotypic trait are provided. In certain embodiments, the at least one genetic marker comprises a single nucleotide polymorphism (SNP), an insertion or deletion in DNA sequence (Indel), a simple sequence repeat of DNA sequence (SSR) a restriction fragment length polymorphism, a haplotype, or a tag SNP. In other embodiments, the methods can further comprise the step of using an association determined in step (b) to make a selection in a plant breeding program. In such embodiments comprising a selection, the selection can comprise any one or all of: 1) selecting among breeding populations based on the at least one genotype; 2) selecting progeny in one or more breeding populations based on the at least one genotype; 3) selecting among parental lines based on prediction of progeny performance; 4) selecting a line for advancement in a germplasm improvement activity based on the at least one genotype; and/or 5) selecting a line for advancement in a germplasm improvement activity where the germplasm improvement activity is selected from the group consisting of line development, variety development, hybrid development, transgenic event selection, making breeding crosses, testing and advancing a plant through self fertilization, purification of lines or sublines, using plants or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plants or parts thereof for mutagenesis. In certain embodiments, the methods can further comprise the step of doubling at least one haploid plant selected in said breeding program to obtain a doubled haploid plant. In such embodiments where a doubled haploid plant is obtained, the doubled haploid plant can be used for introgression of the genotype of interest into at least a second plant for use in a plant breeding program. In certain embodiments, the haploid plant in step (a) is obtained from a haploid breeding population. In certain embodiments, the haploid plant or plants comprise an intact plant, a leaf, vascular tissue, flower, pod, root, stem, seed or portion thereof. In certain embodiments, the plants are selected from the group consisting of maize (Zea mays), soybean (Glycine max), cotton (Gossypium hirsutum), peanut (Arachis hypogaea), barley (Hordeum vulgare); oats (Avena sativa); orchard grass (Dactylis glomerata); rice (Oryza sativa, including indica and japonica varieties); sorghum (Sorghum bicolor); sugar cane (Saccharum sp); tall fescue (Festuca arundinacea); turfgrass species (e.g. species: Agrostis stolonifera, Poa pratensis, Stenotaphrum secundatum); wheat (Triticum aestivum), and alfalfa (Medicago sativa), members of the genus Brassica, carrot, cucumber, dry bean, eggplant, fennel, garden beans, gourd, leek, lettuce, melon, okra, onion, pea, pepper, pumpkin, radish, spinach, squash, sweet corn, tomato, watermelon, and ornamental plants. In certain embodiments, the haploid plant is a fruit, vegetable, tuber, or root crop. In certain embodiments, the trait is selected from the group consisting of herbicide tolerance, disease resistance, insect or pest resistance, altered fatty acid, protein or carbohydrate metabolism, increased grain yield, increased oil, enhanced nutritional content, increased growth rates, enhanced stress tolerance, preferred maturity, enhanced organoleptic properties, altered morphological characteristics, sterility, a trait for industrial use, and a trait for consumer appeal.

[0015] In certain embodiments, methods for identifying an association of a plant genotype with one or more traits of interest comprising: a) screening a plurality of haploid plants displaying heritable variation for at least one trait wherein the heritable variation is linked to at least one genotype; and b) associating at least one genotype of at least one haploid plant to at least one trait are provided. In certain embodiments, the genotype comprises a genetic marker. In certain embodiments, the genetic marker comprises a single nucleotide polymorphism (SNP), an insertion or deletion in DNA sequence (Indel), a simple sequence repeat of DNA sequence (SSR) a restriction fragment length polymorphism, a haplotype, or a tag SNP. In certain embodiments, the methods can further comprising the step of using an association determined in step (b) to make a selection in a plant breeding program. In such embodiments comprising a selection, the selection can comprise any one or all of: 1) selecting among breeding populations based on the at least one genotype; 2) selecting progeny in one or more breeding populations based on the at least one genotype; 3) selecting among parental lines based on prediction of progeny performance; 4) selecting a line for advancement in a germplasm improvement activity based on the at least one genotype; and/or 5) selecting a line for advancement in a germplasm improvement activity where the germplasm improvement activity is selected from the group consisting of line development, variety development, hybrid development, transgenic event selection, making breeding crosses, testing and advancing a plant through self fertilization, purification of lines or sublines, using plants or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plants or parts thereof for mutagenesis. In certain embodiments, the methods can further comprise the step of doubling at least one haploid plant selected in the breeding program to obtain a doubled haploid plant. In certain embodiments, the doubled haploid plant is used for introgressing the genotype of interest into a plant for use in a plant breeding program. In certain embodiments, the haploid plant or plants comprise an intact plant, a leaf, vascular tissue, flower, pod, root, stem, seed or portion thereof. In certain embodiments, the plants are selected from the group consisting of maize (Zea mays), soybean (Glycine max), cotton (Gossypium hirsutum), peanut (Arachis hypogaea), barley (Hordeum vulgare); oats (Avena sativa); orchard grass (Dactylis glomerata); rice (Oryza sativa, including indica and japonica varieties); sorghum (Sorghum bicolor); sugar cane (Saccharum sp); tall fescue (Festuca arundinacea); turfgrass species (e.g. species: Agrostis stolonifera, Poa pratensis, Stenotaphrum secundatum); wheat (Triticum aestivum), and alfalfa (Medicago sativa), members of the genus Brassica, carrot, cucumber, dry bean, eggplant, fennel, garden beans, gourd, leek, lettuce, melon, okra, onion, pea, pepper, pumpkin, radish, spinach, squash, sweet corn, tomato, watermelon, and ornamental plants. In certain embodiments, the haploid plant is a fruit, vegetable, tuber, or root crop. In certain embodiments, the trait is selected from the group consisting of herbicide tolerance, disease resistance, insect or pest resistance, altered fatty acid, protein or carbohydrate metabolism, increased grain yield, increased oil, enhanced nutritional content, increased growth rates, enhanced stress tolerance, preferred maturity, enhanced organoleptic properties, altered morphological characteristics, sterility, a trait for industrial use, and a trait for consumer appeal.

[0016] In certain embodiments, methods for the association of at least one phenotype with at least one genetic marker using a haploid plant comprising: a) assaying at least one phenotype of at least one haploid plant with at least one phenotypic marker to determine the presence or absence of said phenotype; and b) associating the presence or absence of said phenotype with at least one genetic marker are provided. In certain embodiments of the methods, the haploid plant is obtained from a haploid breeding population. In certain embodiments of the methods, the at least one genetic marker can comprise a single nucleotide polymorphism (SNP), an insertion or deletion in DNA sequence (Indel), a simple sequence repeat of DNA sequence (SSR) a restriction fragment length polymorphism, a haplotype, or a tag SNP. In certain embodiments of the methods, the at least one phenotypic marker can comprise at least one of a transcriptional profile, a metabolic profile, a nutrient composition profile, a protein expression profile, protein composition, protein levels, oil composition, oil levels, carbohydrate composition, carbohydrate levels, fatty acid composition, fatty acid levels, amino acid composition, amino acid levels, biopolymers, pharmaceuticals, starch composition, starch levels, fermentable starch, fermentation yield, fermentation efficiency, energy yield, secondary compounds, metabolites, morphological characteristics, or an agronomic characteristic. In certain embodiments of these methods, the methods can further comprising the step of using an association determined in step (b) to make a selection in a plant breeding program. In certain embodiments comprising a selection, the selection can comprise any one or all of: 1) selecting among breeding populations based on the at least one genotype; 2) selecting progeny in one or more breeding populations based on the at least one genotype; 3) selecting among parental lines based on prediction of progeny performance; 4) selecting a line for advancement in a germplasm improvement activity based on the at least one genotype; and/or 5) selecting a line for advancement in a germplasm improvement activity where the germplasm improvement activity is selected from the group consisting of line development, variety development, hybrid development, transgenic event selection, making breeding crosses, testing and advancing a plant through self fertilization, purification of lines or sublines, using plants or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plants or parts thereof for mutagenesis. In certain embodiments of these methods, the methods can further comprise the step of doubling at least one haploid plant selected in said breeding program to obtain a doubled haploid plant. In certain embodiments comprising obtainment of a doubled haploid plant, the doubled haploid plant is used for introgression of the genotype of interest into at least a second plant for use in a plant breeding program.

[0017] The present invention provides a method of introgressing a GLS resistance allele into a corn plant comprising a) crossing at least one first corn plant comprising at least one nucleic acid molecule selected from the group consisting of SEQ ID NO: 1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461–1233, and SEQ ID NOs: 1360 and 1361 with at least a second corn plant in order to form a segregating population,

b) genotyping the segregating population with at least one nucleic acid marker to determine if one or more corn plants from the segregating population contains the nucleic acid molecule, and c) selecting from the segregation population at least one corn plant comprising at least one nucleic acid molecule selected from the group consisting of SEQ ID NO: 1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461–1233, SEQ ID NOs: 1360 and 1361.

[0018] The invention further provides for the elite corn plant obtained from such method. The invention further provides assays for detecting GLS resistance loci.

[0019] Various methods and compositions for identifying and obtaining corn plants with resistance to Gray Leaf Spot (GLS) are provided herein. In certain embodiments, a method of identifying a corn plant comprising at least one allele associated with Gray Leaf Spot (GLS) resistance allele in a corn plant comprising: a) genotyping at least one corn plant with at least one nucleic acid marker selected from the group consisting of SEQ ID NO:1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461–1233, 1360 and 1361. and b)selecting at least one corn plant comprising an allele of at least one of said markers associated with Gray Leaf Spot (GLS) resistance is provided. In certain embodiments of the methods, at least one corn plant genotyped in step (a) and/or the at least one corn plant selected in step (b) is a corn plant from a population generated by a cross. In embodiments where the population is generated by a cross, the cross can be effected by mechanical emasculation, chemical sterilization, or genetic sterilization of a pollen acceptor. In certain embodiments of the methods, genotyping is effected in step (a) by determining the allelic state of at least one of said corn genomic DNA markers. In certain embodiments of the methods, the selected one or more corn plants can exhibit at least partial resistance to a GLS-inducing fungus or at least substantial resistance to a GLS-inducing fungus. In certain embodiments of the methods, the population can b generated by a cross of at least one Gray Leaf Spot (GLS) resistant corn plant with at least one Gray Leaf Spot (GLS) sensitive corn plant. In certain embodiments of the methods, the population can be a segregating population or a haploid breeding population. In certain embodiments of the methods, the cross can be a back cross of at least one Gray Leaf Spot (GLS) resistant corn plant with at least one Gray Leaf Spot (GLS) sensitive corn plant to introgress GLS resistance into a corn germplasm.

[0020] Also provided herein are corn plants obtained by any of the aforementioned methods of identifying corn plants that comprise alleles of genetic loci associated with Gray Leaf Spot resistance. In certain embodiments, a corn plant obtained by any of these aforementioned methods can comprise at least one allele at least one allele of a nucleic acid marker selected from the group consisting of SEQ ID NO: 1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461–1233, 1360 and 1361, wherein said allele is associated with Gray Leaf Spot (GLS) resistance. In certain embodiments, a corn plant obtained by any of these aforementioned methods can exhibit at least partial resistance to a GLS-inducing fungus or at least substantial resistance to a GLS-inducing fungus. In certain embodiments, a corn plant obtained by any of these aforementioned methods can be a haploid corn plant. In certain embodiments, a corn plant obtained by any of the aforementioned methods and comprising at least one of the alleles can comprise at least one transgenic trait. In such embodiments, the transgenic trait can be herbicide tolerance and/or pest resistance. In embodiments where the corn plant obtained is herbicide tolerant, herbicide tolerance can be selected from the group consisting of glyphosate, dicamba, glufosinate, sulfonylurea, bromoxynil and norflurazon herbicide tolerance.

[0021] In certain embodiments, methods of introgressing a Gray Leaf Spot (GLS) resistance QTL allele into a corn plant comprising: a) screening a population with at least one nucleic acid marker to determine if one or more corn plants from the population comprise(s) an allele of said marker associated with a Gray Leaf Spot (GLS) resistance QTL selected from the group consisting of QTL numbers 1-9, 14-33, 35, 38-42, 44-52, 54-61, 63-71, 73-79, 81-92, 95-96, 99-106, 108-117, and 119-178 as provided in Figure 1; and b) selecting from said population at least one corn plant comprising an allele of said marker associated with a Gray Leaf Spot (GLS) resistance are provided. In certain embodiments of the methods, at least one of the markers can be located within 5 cM, 2 cM, or 1cM of at least one of the Gray Leaf Spot (GLS) resistance QTL. In certain embodiments of the methods, at least one of the markers can exhibit a LOD score of greater than 4.0 with at least one of said Gray Leaf Spot (GLS) resistance QTL. In certain embodiments of the methods, the population can be generated by a cross of at least one Gray Leaf Spot (GLS) resistant corn plant with at least one Gray Leaf Spot (GLS) sensitive corn plant. In certain embodiments of the methods, the population can be a haploid breeding population. In certain embodiments of the methods, the nucleic acid marker is selected from the group consisting of SEQ ID NOs: 858, 860, 862, 866, 875, 877, 881, 882, 883, and 1360.

[0022] Also provided herein are corn plants obtained by any of the aforementioned methods of identifying corn plants that comprise a Gray Leaf Spot resistance QTL. In certain embodiments, a corn plant obtained by any of these aforementioned methods can comprise a Gray Leaf Spot (GLS) resistance QTL selected from the group consisting of QTL numbers 1-9, 14-33, 35, 38-42, 44-52, 54-61, 63-71, 73-79, 81-92, 95-96, 99-106, 108-117, and 119-178 as provided in Figure 1. In certain embodiments, a corn plant obtained by any of these aforementioned methods can exhibit at least partial resistance to a GLS-inducing fungus or at least substantial resistance to a GLS-inducing fungus. In certain embodiments, a corn plant obtained by any of these aforementioned methods can be a haploid corn plant. In certain embodiments, a corn plant obtained by any of the aforementioned methods and comprising at least one of the QTL can comprise at least one transgenic trait. In such embodiments, the transgenic trait can be herbicide tolerance and/or pest resistance. In embodiments where the corn plant obtained is herbicide tolerant, herbicide tolerance can be selected from the group consisting of glyphosate, dicamba, glufosinate, sulfonylurea, bromoxynil and norflurazon herbicide tolerance.

[0023] Also provided herein are isolated nucleic acid markers for identifying polymorphisms in corn DNA. These isolated nucleic acids can be used in a variety of applications, including but not limited to the identification of corn plants that comprise alleles of genetic loci associated with Gray Leaf Spot resistance. In certain embodiments, an isolated nucleic acid molecule for detecting a molecular marker representing a polymorphism in corn DNA, wherein the nucleic acid molecule comprises at least 15 nucleotides that include or are immediately adjacent to said polymorphism, wherein said nucleic acid molecule is at least 90 percent identical to a sequence of the same number of consecutive nucleotides in either strand of DNA that include or are immediately adjacent to said polymorphism, and wherein said molecular marker is selected from the group consisting of SEQ ID NOs: 1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461-1360, and 1361. In certain embodiments, the molecular marker can be selected from the group consisting of SEQ ID NOs: 1 –26, 28- 62, 64-70, 72-120, 122-140, 142-156, 158-172, 174, 176, 178-187, 189-219, 221-223, 225-233, 235-247, 249-251, 253-377, 379, 380, 382-409, 411-439, 440-459, 461-478, 481-532, 534-581, 583-584, 586-638, 640-720, 722-726, 728-732, 734-745, 747-767, 769-772, 774-939, 941-1052, 1055-1121, 1123-1185, 1187-1233, 1304 through SEQ ID NOs: 1331, 1360, and 1361. In certain embodiments, the molecular marker is selected from the group consisting of SEQ ID NOs: 858, 860, 862, 866, 875, 877, 881, 882, 883, and 1360. In certain embodiments, the isolated nucleic acid further comprises a detectable label or provides for incorporation of a detectable label. In such embodiments that comprise or provide for incorporation of a detectable label, the detectable label is selected from the group consisting of an isotope, a fluorophore, an oxidant, a reductant, a nucleotide and a hapten. In certain embodiments, the detectable label is added to the nucleic acid by a chemical reaction or is incorporated by an enzymatic reaction. In certain embodiments, the isolated nucleic acid molecule comprises at least 16 or 17 nucleotides that include or are immediately adjacent to the polymorphism. In other embodiments, the nucleic acid molecule comprises at least 18 nucleotides that include or are immediately adjacent to the polymorphism or comprises at least 20 nucleotides that include or are immediately adjacent to the polymorphism. In certain embodiments, the isolated nucleic acid molecule hybridizes to at least one allele of the molecular marker under stringent hybridization conditions.

[0024] The present invention provides a method of introgressing a Goss' Wilt resistance allele into a corn plant comprising a) crossing at least one first corn plant comprising a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158-160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, and 1234-1303 with at least a second corn plant in order to form a segregating population, b) screening the segregating population with at least one nucleic acid marker to determine if one or more corn plants from the segregating population contains the nucleic acid molecule, and c) selecting from the segregation population at least one corn plant comprising a nucleic acid molecule selected from the group consisting of SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, and 1234-1303 .

[0025] The invention further provides for an elite corn plant obtained from such method. The invention further provides assays for detecing Goss' Wilt resistance loci.

[0026] Methods for identifying corn plants that comprise alleles of genetic loci associated with Goss' Wilt resistance are provided herein. In certain embodiments, methods of identifying a corn plant comprising at least one allele associated with Goss' Wilt resistance allele in a corn plant comprising: a) genotyping at least one corn plant with at least one nucleic acid marker selected from the group consisting of SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1302, and 1303 , and b) selecting at least one corn plant comprising an allele of at least one of the markers that is associated with resistance to Goss' Wilt are provided. In certain embodiments of the methods, the at least one corn plant genotyped in step (a) and/or the at least one corn plant selected in step (b) is a corn plant from a population generated by a cross. In embodiments of the methods where the corn plant from a population generated by a cross, the cross can be effected by mechanical emasculation, chemical sterilization, or genetic sterilization of a pollen acceptor. In certain embodiments of the methods, genotyping is effected in step (a) by determining the allelic state of at least one of the corn genomic DNA markers. In such embodiments of the methods, an allelic state can be determined by single base extension (SBE), allele-specific primer extension sequencing (ASPE), DNA sequencing, RNA sequencing, microarray-based analyses, universal PCR, allele specific extension, hybridization, mass spectrometry, ligation, extension-ligation, and/or a Flap Endonuclease-mediated assay(s). In other embodiments of the methods, the selected corn plant(s) of step (b) exhibit at least partial resistance to a Goss' Wilt-inducing bacteria or at least substantial resistance to a Goss' Wilt-inducing bacteria. In certain embodiments of the methods, the nucleic acid marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251. Alternatively, the nucleic acid marker can be selected from the group consisting of SEQ ID NOs: 234 and 1250. In embodiments where a population is generated by a cross, the population can be generated by a cross of at least one Goss' Wilt resistant corn plant with at least one Goss' Wilt sensitive corn plant. In certain embodiments of the methods where a population is generated by a cross, the cross can be a back cross of at least one Goss' Wilt resistant corn plant with at least one Goss' Wilt sensitive corn plant to introgress Goss' Wilt resistance into a corn germplasm. In embodiments where the corn plant is from a population, the population can be a segregating population. In certain embodiments of the methods, the population can be a haploid breeding population.

[0027] Also provided herein are corn plants obtained by any of the aforementioned methods of identifying corn plants that comprise alleles of genetic loci associated with Goss' Wilt resistance. In certain embodiments, a corn plant obtained by any of these aforementioned methods can comprise at least one allele of a nucleic acid marker selected from the group consisting of SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1302, and 1303, wherein the allele is associated with Goss' Wilt resistance. In certain embodiments, a corn plant obtained by any of these aforementioned methods can comprise at least one allele of a nucleic acid marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251, wherein the allele is associated with Goss' Wilt resistance. In certain embodiments, a corn plant obtained by any of these aforementioned methods can comprise at least one allele of a nucleic acid marker is selected from the group consisting of SEQ ID NOs: 234 and 1250, wherein the allele is associated with Goss' Wilt resistance. In certain embodiments, a corn plant obtained by any of these aforementioned methods exhibits at least partial resistance to a Goss' Wilt-inducing bacterium. In certain embodiments, a corn plant obtained by any of these aforementioned methods exhibits at least substantial resistance to a Goss' Wilt-inducing bacterium. In still other embodiments, a corn plant obtained by any of these aforementioned methods can be a haploid corn plant. In certain embodiments, a corn plant obtained by any of the aforementioned methods can comprise at least one transgenic trait. In such embodiments, the transgenic trait can be herbicide tolerance and/or pest resistance. In embodiments where the corn plant obtained is herbicide tolerant, herbicide tolerance can be selected from the group consisting of glyphosate, dicamba, glufosinate, sulfonylurea, bromoxynil and norflurazon herbicide tolerance. In certain embodiments, the nucleic acid marker is present as a single copy in a corn plant obtained by any of these aforementioned methods. In other embodiments, the nucleic acid marker can be present in two copies in a corn plant obtained by any of these aforementioned methods.

[0028] Also provided are methods for introgressing a Goss' Wilt resistance QTL into a corn plant. In certain embodiments, methods of introgressing a Goss' Wilt resistance QTL into a corn plant comprising: a) screening a population with at least one nucleic acid marker to determine if one or more corn plants from the population contains a Goss' Wilt resistance QTL, wherein the Goss' Wilt resistance QTL is a QTL selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, and 131 as provided in Figure 2; and b) selecting from the population at least one corn plant comprising an allele of the marker associated with Goss' Wilt resistance are provided. In certain embodiments of the methods, at least one of the markers is located within 30 cM, 25 cM, 20 cM, 15 cM, or 10 cM of the Goss' Wilt resistance QTL. In other embodiments of the methods, at least one of the markers is located within 5 cM, 2 cM, or 1 cM of the Goss' Wilt resistance QTL. In certain embodiments of the methods, at least one of the markers exhibits an LOD score of greater than 2.0, 2.5, or 3.0 with the Goss' Wilt resistance QTL. In other embodiments of the methods, at least one of the markers exhibits a LOD score of greater than 4.0 with the Goss' Wilt resistance QTL. In certain embodiments of these methods, the nucleic acid marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251., wherein the nucleic acid marker is selected from the group consisting of SEQ ID NOs: 234 and 1250. In certain embodiments of the methods, the population is a segregating population.

[0029] Also provided herein are corn plants obtained by any of the aforementioned methods of identifying corn plants that comprise a Goss' Wilt resistance QTL. In certain embodiments, a corn plant obtained by any of the aforementioned methods is provided, wherein the corn plant comprises a Goss' Wilt resistance QTL selected from the group consisting of QTL numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, and 131 as provided in Figure 2. In certain embodiments, a corn plant obtained by any of these aforementioned methods and comprising at least one of the QTL exhibits at least partial resistance to a Goss' Wilt-inducing bacterium. In certain embodiments, a corn plant obtained by any of these aforementioned methods exhibits at least substantial resistance to a Goss' Wilt-inducing bacterium. In still other embodiments, a corn plant obtained by any of these aforementioned methods and comprising at least one of the QTL can be a haploid corn plant. In certain embodiments, a corn plant obtained by any of the aforementioned methods and comprising at least one of the QTL can comprise at least one transgenic trait. In such embodiments, the transgenic trait can be herbicide tolerance and/or pest resistance. In embodiments where the corn plant obtained is herbicide tolerant, herbicide tolerance can be selected from the group consisting of glyphosate, dicamba, glufosinate, sulfonylurea, bromoxynil and norflurazon herbicide tolerance.

[0030] Also provided herein are isolated nucleic acid markers for identifying polymorphisms in corn DNA. These isolated nucleic acids can be used in a variety of applications, including but not limited to the identification of corn plants that comprise alleles of genetic loci associated with Goss' Wilt resistance. In certain embodiments, an isolated nucleic acid molecule for detecting a molecular marker representing a polymorphism in corn DNA, wherein the nucleic acid molecule comprises at least 15 nucleotides that include or are immediately adjacent to the polymorphism, wherein the nucleic acid molecule is at least 90 percent identical to a sequence of the same number of consecutive nucleotides in either strand of DNA that include or are immediately adjacent to the polymorphism, and wherein the molecular marker is selected from the group consisting of SEQ ID NOs: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719, 721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1302, and 1303 is provided. In other embodiments, the molecular marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251. In still other embodiments, the molecular marker is selected from the group consisting of SEQ ID NOs: 234 and 1250. In certain embodiments, the isolated nucleic acid further comprises a detectable label or provides for incorporation of a detectable label. In such embodiments that comprise or provide for incorporation of a detectable label, the detectable label is selected from the group consisting of an isotope, a fluorophore, an oxidant, a reductant, a nucleotide and a hapten. In certain embodiments, the detectable label is added to the nucleic acid by a chemical reaction or is incorporated by an enzymatic reaction. In certain embodiments, the isolated nucleic acid molecule comprises at least 16 or 17 nucleotides that include or are immediately adjacent to the polymorphism. In other embodiments, the nucleic acid molecule comprises at least 18 nucleotides that include or are immediately adjacent to the polymorphism or comprises at least 20 nucleotides that include or are immediately adjacent to the polymorphism. In certain embodiments, the isolated nucleic acid molecule hybridizes to at least one allele of the molecular marker under stringent hybridization conditions.

Brief description of the drawings

[0031] The accompanying drawings, which are incorporated in and form a part of the specification, illustrate the embodiments of the present invention and together with the description, serve to explain the principles of the invention.

[0032] In the drawings:

FIGURE 1. Displays markers associated with GLS resistance from association mapping studies. "*" indicates a single nucleotide deletion.

[0033] FIGURE 2. Displays markers associated with resistance to Goss' Wilt. The symbol"*" represents a single nucleotide deletion.

Detailed description of the invention

[0034] The definitions and methods provided herein define the present invention and guide those of ordinary skill in the art in the practice of the present invention. Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art. Definitions of common terms in molecular biology may also be found in Alberts et al., Molecular Biology of The Cell, 3rd Edition, Garland Publishing, Inc.: New York, 1994; Rieger et al., Glossary of Genetics: Classical and Molecular, 5th edition, Springer-Verlag: New York, 1991; and Lewin, Genes V, Oxford University Press: New York, 1994. The nomenclature for DNA bases as set forth at 37 CFR § 1.822 is used.

[0035] As used herein, a "locus" is a fixed position on a chromosome and may represent a single nucleotide, a few nucleotides or a large number of nucleotides in a genomic region.

[0036] As used herein, "polymorphism" means the presence of one or more variations of a nucleic acid sequence at one or more loci in a population of one or more individuals. The variation may comprise but is not limited to one or more base changes, the insertion of one or more nucleotides or the deletion of one or more nucleotides. A polymorphism includes a single nucleotide polymorphism (SNP), a simple sequence repeat (SSR) and indels, which are insertions and deletions. A polymorphism may arise from random processes in nucleic acid replication, through mutagenesis, as a result of mobile genomic elements, from copy number variation and during the process of meiosis, such as unequal crossing over, genome duplication and chromosome breaks and fusions. The variation can be commonly found or may exist at low frequency within a population, the former having greater utility in general plant breeding and the later may be associated with rare but important phenotypic variation.

[0037] As used herein, "marker" means a detectable characteristic that can be used to discriminate between organisms. Examples of such characteristics may include genetic markers, protein composition, protein levels, oil composition, oil levels, carbohydrate composition, carbohydrate levels, fatty acid composition, fatty acid levels, amino acid composition, amino acid levels, biopolymers, pharmaceuticals, starch composition, starch levels, fermentable starch, fermentation yield, fermentation efficiency, energy yield, secondary compounds, metabolites, morphological characteristics, and agronomic characteristics.

[0038] As used herein, "genetic marker" means polymorphic nucleic acid sequence or nucleic acid feature. A "polymorphism" is a variation among individuals in sequence, particularly in DNA sequence, or feature, such as a transcriptional profile or methylation pattern. Useful polymorphisms include single nucleotide polymorphisms (SNPs), insertions or deletions in DNA sequence (Indels), simple sequence repeats of DNA sequence (SSRs) a restriction fragment length polymorphism, a haplotype, and a tag SNP. A genetic marker, a gene, a DNA-derived sequence, a RNA-derived sequence, a promoter, a 5' untranslated region of a gene, a 3' untranslated region of a gene, microRNA, siRNA, a QTL, a satellite marker, a transgene, mRNA, ds mRNA, a transcriptional profile, and a methylation pattern may comprise polymorphisms.

[0039] As used herein, "marker assay" means a method for detecting a polymorphism at a particular locus using a particular method, e.g. measurement of at least one phenotype (such as seed color, flower color, or other visually detectable trait), restriction fragment length polymorphism (RFLP), single base extension, electrophoresis, sequence alignment, allelic specific oligonucleotide hybridization (ASO), random amplified polymorphic DNA (RAPD), microarray-based technologies, and nucleic acid sequencing technologies, etc.

[0040] As used herein, the phrase "immediately adjacent", when used to describe a nucleic acid molecule that hybridizes to DNA containing a polymorphism, refers to a nucleic acid that hybridizes to DNA sequences that directly abut the polymorphic nucleotide base position. For example, a nucleic acid molecule that can be used in a single base extension assay is "immediately adjacent" to the polymorphism.

[0041] As used herein, "interrogation position" refers to a physical position on a solid support that can be queried to obtain genotyping data for one or more predetermined genomic polymorphisms.

[0042] As used herein, "consensus sequence" refers to a constructed DNA sequence which identifies SNP and Indel polymorphisms in alleles at a locus. Consensus sequence can be based on either strand of DNA at the locus and states the nucleotide base of either one of each SNP in the locus and the nucleotide bases of all Indels in the locus. Thus, although a consensus sequence may not be a copy of an actual DNA sequence, a consensus sequence is useful for precisely designing primers and probes for actual polymorphisms in the locus.

[0043] As used herein, the term "single nucleotide polymorphism," also referred to by the abbreviation "SNP," means a polymorphism at a single site wherein said polymorphism constitutes a single base pair change, an insertion of one or more base pairs, or a deletion of one or more base pairs.

[0044] As used herein, "genotype" means the genetic component of the phenotype and it can be indirectly characterized using markers or directly characterized by nucleic acid sequencing. Suitable markers include a phenotypic character, a metabolic profile, a genetic marker, or some other type of marker. A genotype may constitute an allele for at least one genetic marker locus or a haplotype for at least one haplotype window. In some embodiments, a genotype may represent a single locus and in others it may represent a genome-wide set of loci. In another embodiment, the genotype can reflect the sequence of a portion of a chromosome, an entire chromosome, a portion of the genome, and the entire genome.

[0045] As used herein, the term "haplotype" means a chromosomal region within a haplotype window defined by at least one polymorphic molecular marker. The unique marker fingerprint combinations in each haplotype window define individual haplotypes for that window. Further, changes in a haplotype, brought about by recombination for example, may result in the modification of a haplotype so that it comprises only a portion of the original (parental) haplotype operably linked to the trait, for example, via physical linkage to a gene, QTL, or transgene. Any such change in a haplotype would be included in our definition of what constitutes a haplotype so long as the functional integrity of that genomic region is unchanged or improved.

[0046] As used herein, the term “haplotype window” means a chromosomal region that is established by statistical analyses known to those of skill in the art and is in linkage disequilibrium. Thus, identity by state between two inbred individuals (or two gametes) at one or more molecular marker loci located within this region is taken as evidence of identity-by-descent of the entire region. Each haplotype window includes at least one polymorphic molecular marker. Haplotype windows can be mapped along each chromosome in the genome. Haplotype windows are not fixed per se and, given the ever-increasing density of molecular markers, this invention anticipates the number and size of haplotype windows to evolve, with the number of windows increasing and their respective sizes decreasing, thus resulting in an ever-increasing degree confidence in ascertaining identity by descent based on the identity by state at the marker loci.

[0047] As used herein, a plant referred to as “haploid” has a single set (genome) of chromosomes and the reduced number of chromosomes (n) in the haploid plant is equal to that of the gamete.

[0048] As used herein, a plant referred to as “doubled haploid” is developed by doubling the haploid set of chromosomes. A plant or seed that is obtained from a doubled haploid plant that is selfed any number of generations may still be identified as a doubled haploid plant. A doubled haploid plant is considered a homozygous plant. A plant is considered to be doubled haploid if it is fertile, even is the entire vegetative part of the plant does not consist of the cells with the doubled set of chromosomes; that is, a plant will be considered doubled haploid if it contains viable gametes, even if it is chimeric.

[0049] As used herein, a plant referred to as “diploid” has two sets (genomes) of chromosomes and the chromosome number (2n) is equal to that of the zygote.

[0050] As used herein, the term “plant” includes whole plants, plant organs (i.e., leaves, stems, roots, etc.), seeds, and plant cells and progeny of the same. “Plant cell” includes without limitation seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, shoots, gametophytes, sporophytes, pollen, and microspores.

[0051] As used herein, a “genetic map” is the ordered list of loci known for a particular genome.

[0052] As used herein, "phenotype" means the detectable characteristics of a cell or organism which are a manifestation of gene expression.

[0053] As used herein, a "phenotypic marker" refers to a marker that can be used to discriminate phenotypes displayed by organisms.

[0054] As used herein, "linkage" refers to relative frequency at which types of gametes are produced in a cross. For example, if locus A has genes "A" or "a" and locus B has genes "B" or "b" and a cross between parent I with AABB and parent B with aabb will produce four possible gametes where the genes are segregated into AB, Ab, aB and ab. The null expectation is that there will be independent equal segregation into each of the four possible genotypes, i.e. with no linkage ¼ of the gametes will of each genotype. Segregation of gametes into a genotypes differing from ¼ are attributed to linkage.

[0055] As used herein, "linkage disequilibrium" is defined in the context of the relative frequency of gamete types in a population of many individuals in a single generation. If the frequency of allele A is p, a is p', B is q and b is q', then the expected frequency (with no linkage disequilibrium) of genotype AB is pq, Ab is pq', aB is p'q and ab is p'q'. Any deviation from the expected frequency is called linkage disequilibrium. Two loci are said to be "genetically linked" when they are in linkage disequilibrium.

[0056] As used herein, "quantitative trait locus (QTL)" means a locus that controls to some degree numerically representable traits that are usually continuously distributed.

[0057] As used herein, the term "transgene" means nucleic acid molecules in form of DNA, such as cDNA or genomic DNA, and RNA, such as mRNA or microRNA, which may be single or double stranded.

[0058] As used herein, the term "inbred" means a line that has been bred for genetic homogeneity.

[0059] As used herein, the term "hybrid" means a progeny of mating between at least two genetically dissimilar parents. Without limitation, examples of mating schemes include single crosses, modified single cross, double modified single cross, three-way cross, modified three-way cross, and double cross wherein at least one parent in a modified cross is the progeny of a cross between sister lines.

[0060] As used herein, the term "tester" means a line used in a testcross with another line wherein the tester and the lines tested are from different germplasm pools. A tester may be isogenic or nonisogenic.

[0061] As used herein, "resistance allele" means the isolated nucleic acid sequence that includes the polymorphic allele associated with resistance to the disease or condition of concern.

[0062] As used herein, the term "corn" means *Zea mays* or maize and includes all plant varieties that can be bred with corn, including wild maize species.

[0063] As used herein, the term "comprising" means "including but not limited to".

[0064] As used herein, an "elite line" is any line that has resulted from breeding and selection for superior agronomic performance.

[0065] As used herein, an "inducer" is a line which when crossed with another line promotes the formation of haploid embryos.

[0066] As used herein, "haplotype effect estimate" means a predicted effect estimate for a haplotype reflecting association with one or more phenotypic traits, wherein the associations can be made *de novo* or by leveraging historical haplotype-trait association data.

[0067] As used herein, "breeding value" means a calculation based on nucleic acid sequence effect estimates and nucleic acid sequence frequency values, the breeding value of a specific nucleic acid sequence relative to other nucleic acid sequences at the same locus (i.e., haplotype window), or across loci (i.e., haplotype windows), can also be determined. In other words, the change in population mean by fixing said nucleic acid sequence is determined. In addition, in the context of evaluating the effect of substituting a specific region in the genome, either by introgression or a transgenic event, breeding values provide the basis for comparing specific nucleic acid sequences for substitution effects. Also, in hybrid crops, the breeding value of nucleic acid sequences can be calculated in the context of the nucleic acid sequence in the tester used to produce the hybrid.

[0068] To the extent to which any of the preceding definitions is inconsistent with definitions provided in any patent or non-patent reference incorporated herein or in any reference found elsewhere, it is understood that the preceding definition will be used herein.

Haploid Mapping

[0069] The present invention provides a method of using haploid plants to identify genotypes associated with phenotypes of interest wherein the haploid plant is assayed with at least one marker and associating the at least one marker with at least one phenotypic trait. The genotype of interest can then be used to make decisions in a plant breeding program. Such decisions include, but are not limited to, selecting among new breeding populations which population has the highest frequency of favorable nucleic acid sequences based on historical genotype and agronomic trait associations, selecting favorable nucleic acid sequences among progeny in breeding populations, selecting among parental lines based on prediction of progeny performance, and advancing lines in germplasm improvement activities based on presence of favorable nucleic acid sequences. Non-limiting examples of germplasm improvement activities include line development, hybrid development, transgenic event selection, making breeding crosses, testing and advancing a plant through self fertilization, using plants for transformation, using plants for candidates for expression constructs, and using plants for mutagenesis.

[0070] Non-limiting examples of breeding decisions include progeny selection, parent selection, and recurrent selection for at least one haplotype. In another aspect, breeding decisions relating to development of plants for commercial release comprise advancing plants for testing, advancing plants for purity, purification of sublines during development, inbred development, variety development, and hybrid development. In yet other aspects, breeding decisions and germplasm improvement activities comprise transgenic event selection, making breeding crosses, testing and advancing a plant through self-fertilization, using plants for transformation, using plants for candidates for expression constructs, and using plants for mutagenesis.

[0071] It is appreciated by one skilled in the art that haploid plants can be generated from any generation of plant population and that the methods of the present invention can be used with one or more individuals, including SSD, from any generation of plant population. Non-limiting examples of plant populations include F1, F2, BC1, BC2F1, F3:F4, F2:F3, and so on, including subsequent filial generations, as well as experimental populations such as RILs and NILs. It is further anticipated that the degree of segregation within the one or more plant populations of the present invention can vary depending on the nature of the trait and germplasm under evaluation.

[0072] In still another embodiment, the present invention acknowledges that preferred haplotypes and QTL identified by the methods presented herein may be advanced as candidate genes for inclusion in expression constructs, i.e., transgenes. Nucleic acids underlying haplotypes or QTL of interest may be expressed in plant cells by operably linking them to a promoter functional in plants. In another aspect, nucleic acids underlying haplotypes or QTL of interest may have their expression modified by double-stranded RNA-mediated gene suppression, also known as RNA interference ("RNAi"), which includes suppression mediated by small interfering RNAs ("siRNA"), trans-acting small interfering RNAs ("ta-siRNA"), or microRNAs ("miRNA"). Examples of RNAi methodology suitable for use in plants are described in detail in U. S. patent application publications 2006/0200878 and 2007/0011775.

[0073] Methods are known in the art for assembling and introducing constructs into a cell in such a manner that the nucleic acid molecule for a trait is transcribed into a functional mRNA molecule that is translated and expressed as a protein product. For the practice of the present invention, conventional compositions and methods for preparing and using constructs and host cells are well known to one skilled in the art, see for example, Molecular Cloning: A Laboratory Manual, 3rd edition Volumes 1, 2, and 3 (2000) J.F. Sambrook, D.W. Russell, and N. Irwin, Cold Spring

Harbor Laboratory Press. Methods for making transformation constructs particularly suited to plant transformation include, without limitation, those described in U.S. Patent Nos. 4,971,908, 4,940,835, 4,769,061 and 4,757,011, all of which are herein incorporated by reference in their entirety. Transformation methods for the introduction of expression units into plants are known in the art and include electroporation as illustrated in U.S. Patent No. 5,384,253; microprojectile bombardment as illustrated in U.S. Patent Nos. 5,015,580; 5,550,318; 5,538,880; 6,160,208; 6,399,861; and 6,403,865; protoplast transformation as illustrated in U.S. Patent No. 5,508,184; and *Agrobacterium*-mediated transformation as illustrated in U.S. Patent Nos. 5,635,055; 5,824,877; 5,591,616; 5,981,840; and 6,384,301.

[0074] The method of the present invention can be used to identify genotypes associated with phenotypes of interest such as those associated with disease resistance, herbicide tolerance, insect or pest resistance, altered fatty acid, protein or carbohydrate metabolism, increased grain yield, increased oil, enhanced nutritional content, increased growth rates, enhanced stress tolerance, preferred maturity, enhanced organoleptic properties, altered morphological characteristics, sterility, other agronomic traits, traits for industrial uses, or traits for consumer appeal.

[0075] Production of DH plants, which entails induction of haploidization followed by diploidization, requires a high input of resources. DH plants rarely occur naturally; therefore, artificial means of production are used. First, one or more lines are crossed with an inducer parent to produce haploid seed. Inducer lines for maize include Stock 6, RWS, KEMS, KMS and ZMS, and indeterminate gametophyte (ig) mutation. Selection of haploid seed can be accomplished by various screening methods based on phenotypic or genotypic characteristics. In one approach, material is screened with visible marker genes, including GFP, GUS, anthocyanin genes such as R-nj, luciferase, YFP, CFP, or CRC, that are only induced in the endosperm cells of haploid cells, allowing for separation of haploid and diploid seed. Other screening approaches include chromosome counting, flow cytometry, genetic marker evaluation to infer copy number, etc.

[0076] Resulting haploid seed has a haploid embryo and a normal triploid endosperm. There are several approaches known in the art to achieve chromosome doubling. Haploid cells, haploid embryos, haploid seeds, haploid seedlings, or haploid plants can be treated with a doubling agent. Non-limiting examples of known doubling agents include nitrous oxide gas, anti-microtubule herbicides, anti-microtubule agents, colchicine, pronamide, and mitotic inhibitors.

[0077] The present invention includes methods for breeding crop plants such as maize (*Zea mays*), soybean (*Glycine max*), cotton (*Gossypium hirsutum*), peanut (*Arachis hypogaea*), barley (*Hordeum vulgare*); oats (*Avena sativa*); orchard grass (*Dactylis glomerata*); rice (*Oryza sativa*, including indica and japonica varieties); sorghum (*Sorghum bicolor*); sugar cane (*Saccharum sp*); tall fescue (*Festuca arundinacea*); turfgrass species (e.g. species: *Agrostis stolonifera, Poa pratensis, Stenotaphrum secundatum*); wheat (*Triticum aestivum*), and alfalfa (*Medicago sativa*), members of the genus *Brassica*, broccoli, cabbage, carrot, cauliflower, Chinese cabbage, cucumber, dry bean, eggplant, fennel, garden beans, gourd, leek, lettuce, melon, okra, onion, pea, pepper, pumpkin, radish, spinach, squash, sweet corn, tomato, watermelon, ornamental plants, and other fruit, vegetable, tuber, and root crops.

Gray Leaf Spot Resistance

[0078] The present invention provides GLS resistance loci that are located in public bins in the maize genome that were not previously associated with GLS resistance.

[0079] The present invention provides 160 GLS resistance loci that are located in public bins in the maize genome that were not previously associated with GLS resistance. QTL were assigned by dividing maize chromosomal regions into 10 cM windows. A total of 178 QTL associated with GLS were identified, of which 158 have not been previously reported. SNP markers are also provided for monitoring the introgression of the 178 GLS resistance QTL.

[0080] In the present invention, GLS resistant loci 1-9, 14-33, 35, 38-42, 44-52, 54-61, 63-71, 73-79, 81-92, 95-96, 99-106, 108-117, and 119-178 have not been previously associated with GLS and are provided. SNP markers are also provided for monitoring the introgression of GLS resistance. In the present invention, GLS resistance loci 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 177 are located on chromosome 1. SNP markers used to monitor the introgression of GLS resistance locus 1 include those selected from the group consisting of SEQ ID NOs: 1 through 9. SNP markers used to monitor the introgression of GLS resistance locus 2 include those selected from the group consisting of SEQ ID NOs: 10 through 14. SNP markers used to monitor the introgression of GLS resistance locus 3 include those selected from the group consisting of SEQ ID NOs: 15 through 22. SNP markers used to monitor the introgression of GLS resistance locus 4 include those selected from the group consisting of SEQ ID NOs: 23 through 30. SNP markers used to monitor the introgression of GLS resistance locus 5 include those selected from the group consisting of SEQ ID NOs: 31 through 37. SNP markers used to monitor the introgression of GLS resistance locus 6 include those selected from the group consisting of SEQ ID NOs: 38 through 48. SNP markers used to monitor the introgression of GLS resistance locus 7 include those selected from the group consisting of SEQ ID NOs: 49 through 58. SNP markers used to monitor the introgression of GLS resistance locus 8 include those selected from the group consisting of SEQ ID NOs: 59 through 73. SNP markers used to monitor the introgression of GLS resistance locus 9 include those selected from the group consisting of SEQ ID NOs: 74 through 86.

SNP markers used to monitor the introgression of GLS resistance locus 10 include those selected from the group consisting of SEQ ID NOs: 87 through 93. SNP markers used to monitor the introgression of GLS resistance locus 11 include those selected from the group consisting of SEQ ID NOs: 94 through 115. SNP markers used to monitor the introgression of GLS resistance locus 12 include those selected from the group consisting of SEQ ID NOs: 116 through 126. SNP markers used to monitor the introgression of GLS resistance locus 13 include those selected from the group consisting of SEQ ID NOs: 127 through 135. SNP markers used to monitor the introgression of GLS resistance locus 14 include those selected from the group consisting of SEQ ID NOs: 136 through 139. SNP markers used to monitor the introgression of GLS resistance locus 15 include those selected from the group consisting of SEQ ID NOs: 140 through 144. SNP markers used to monitor the introgression of GLS resistance locus 16 include those selected from the group consisting of SEQ ID NOs: 145 through 151. SNP markers used to monitor the introgression of GLS resistance locus 17 include those selected from the group consisting of SEQ ID NOs: 152 through 162. SNP markers used to monitor the introgression of GLS resistance locus 18 include those selected from the group consisting of SEQ ID NOs: 163 through 172. SNP markers used to monitor the introgression of GLS resistance locus 19 include those selected from the group consisting of SEQ ID NOs: 173 through 178. SNP markers used to monitor the introgression of GLS resistance locus 20 include those selected from the group consisting of SEQ ID NOs: 179 through 183. SNP markers used to monitor the introgression of GLS resistance locus 20 include those selected from the group consisting of SEQ ID NOs: 179 through 183. SNP markers used to monitor the introgression of GLS resistance locus 21 include those selected from the group consisting of SEQ ID NOs: 184 through 197. SNP markers used to monitor the introgression of GLS resistance locus 22 include those selected from the group consisting of SEQ ID NOs: 198 through 199. SNP markers used to monitor the introgression of GLS resistance locus 23 include those selected from the group consisting of SEQ ID NOs: 200 through 201. SNP markers used to monitor the introgression of GLS resistance locus 24 include those selected from the group consisting of SEQ ID NOs: 202 through 206. SNP markers used to monitor the introgression of GLS resistance locus 25 include those selected from the group consisting of SEQ ID NOs: 207 through 208. SNP markers used to monitor the introgression of GLS resistance locus 26 include those selected from the group consisting of SEQ ID NOs: 209 through 211. SNP markers used to monitor the introgression of GLS resistance locus 177 include SEQ ID NO: 1228.

[0081] In the present invention GLS resistant loci 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 178 are located on Chromosome 2. SNP markers used to monitor the introgression of GLS resistance locus 27 include those selected from the group consisting of SEQ ID NOs: 212 through 215. SNP markers used to monitor the introgression of GLS resistance locus

28 include those selected from the group consisting of SEQ ID NOs: 216 through 221 and 1229. SNP markers used to monitor the introgression of GLS resistance locus 29 include those selected from the group consisting of SEQ ID NOs: 222 through 224. SNP markers used to monitor the introgression of GLS resistance locus 30 include those selected from the group consisting of SEQ ID NOs: 225 through 231. SNP markers used to monitor the introgression of GLS resistance locus 31 include those selected from the group consisting of SEQ ID NOs: 232 through 236. SNP markers used to monitor the introgression of GLS resistance locus 32 include those selected from the group consisting of SEQ ID NOs: 237 through 242. SNP markers used to monitor the introgression of GLS resistance locus 33 include those selected from the group consisting of SEQ ID NOs: 244 through 248. SNP markers used to monitor the introgression of GLS resistance locus 34 include those selected from the group consisting of SEQ ID NOs: 249 through 260. SNP markers used to monitor the introgression of GLS resistance locus 35 include those selected from the group consisting of SEQ ID NOs: 261 through 269. SNP markers used to monitor the introgression of GLS resistance locus 36 include those selected from the group consisting of SEQ ID NOs: 270 through 291. SNP markers used to monitor the introgression of GLS resistance locus 37 include those selected from the group consisting of SEQ ID NOs: 292 through 303. SNP markers used to monitor the introgression of GLS resistance locus 38 include those selected from the group consisting of SEQ ID NOs: 304 through 311. SNP markers used to monitor the introgression of GLS resistance locus 39 include those selected from the group consisting of SEQ ID NOs: 312 through 321. SNP markers used to monitor the introgression of GLS resistance locus 40 include those selected from the group consisting of SEQ ID NOs: 322 through 330. SNP markers used to monitor the introgression of GLS resistance locus 41 include those selected from the group consisting of SEQ ID NOs: 331 through 335. SNP markers used to monitor the introgression of GLS resistance locus 42 include those selected from the group consisting of SEQ ID NOs: 336 through 341. SNP markers used to monitor the introgression of GLS resistance locus 43 include those selected from the group consisting of SEQ ID NOs: 342 through 348. SNP markers used to monitor the introgression of GLS resistance locus 44 include those selected from the group consisting of SEQ ID NOs: 349 through 351. SNP markers used to monitor the introgression of GLS resistance locus 45 include those selected from the group consisting of SEQ ID NOs: 352 through 355. SNP markers used to monitor the introgression of GLS resistance locus 46 include those selected from the group consisting of SEQ ID NOs: 356 through 360. SNP markers used to monitor the introgression of GLS resistance locus 178 include SEQ ID NO: 1229.

[0082] In the present invention GLS resistant loci 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, and 67 are located on Chromosome 3. SNP markers used to monitor the introgression of GLS resistance locus 47 include those selected from the group consisting of SEQ

ID NOs: 361 through 364. SNP markers used to monitor the introgression of GLS resistance locus 48 include those selected from the group consisting of SEQ ID NOs: 365. SNP markers used to monitor the introgression of GLS resistance locus 49 include those selected from the group consisting of SEQ ID NOs: 366. SNP markers used to monitor the introgression of GLS resistance locus 50 include those selected from the group consisting of SEQ ID NOs: 367 through 369. SNP markers used to monitor the introgression of GLS resistance locus 51 include those selected from the group consisting of SEQ ID NOs: 370 through 371. SNP markers used to monitor the introgression of GLS resistance locus 52 include those selected from the group consisting of SEQ ID NOs: 372 through 374. SNP markers used to monitor the introgression of GLS resistance locus 53 include those selected from the group consisting of SEQ ID NOs: 375. SNP markers used to monitor the introgression of GLS resistance locus 54 include those selected from the group consisting of SEQ ID NOs: 376 through 395. SNP markers used to monitor the introgression of GLS resistance locus 55 include those selected from the group consisting of SEQ ID NOs: 396 through 408. SNP markers used to monitor the introgression of GLS resistance locus 56 include those selected from the group consisting of SEQ ID NOs: 409 through 418. SNP markers used to monitor the introgression of GLS resistance locus 57 include those selected from the group consisting of SEQ ID NOs: 419 through 425. SNP markers used to monitor the introgression of GLS resistance locus 58 include those selected from the group consisting of SEQ ID NOs: 426 through 433. SNP markers used to monitor the introgression of GLS resistance locus 59 include those selected from the group consisting of SEQ ID NOs: 434 through 435. SNP markers used to monitor the introgression of GLS resistance locus 60 include those selected from the group consisting of SEQ ID NOs: 436 through 449. SNP markers used to monitor the introgression of GLS resistance locus 61 include those selected from the group consisting of SEQ ID NOs: 450 through 458. SNP markers used to monitor the introgression of GLS resistance locus 62 include those selected from the group consisting of SEQ ID NOs: 459 through 464. SNP markers used to monitor the introgression of GLS resistance locus 63 include those selected from the group consisting of SEQ ID NOs: 465 through 471. SNP markers used to monitor the introgression of GLS resistance locus 64 include those selected from the group consisting of SEQ ID NOs: 472 through 482. SNP markers used to monitor the introgression of GLS resistance locus 65 include those selected from the group consisting of SEQ ID NOs: 483 through 486. SNP markers used to monitor the introgression of GLS resistance locus 66 include those selected from the group consisting of SEQ ID NOs: 487 through 490. SNP markers used to monitor the introgression of GLS resistance locus 67 include those selected from the group consisting of SEQ ID NOs: 491 through 495.

[0083] In the present invention GLS resistant loci 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, and 87 are located on Chromosome 4. SNP markers used to monitor the introgression of GLS resistance locus 68 include those selected from the group consisting of SEQ ID NOs: 496 through 499. SNP markers used to monitor the introgression of GLS resistance locus 69 include those selected from the group consisting of SEQ ID NOs: 500 through 502. SNP markers used to monitor the introgression of GLS resistance locus 70 include those selected from the group consisting of SEQ ID NOs: 503 through 504. SNP markers used to monitor the introgression of GLS resistance locus 71 include those selected from the group consisting of SEQ ID NOs: 505 through 507. SNP markers used to monitor the introgression of GLS resistance locus 72 include those selected from the group consisting of SEQ ID NOs: 508 through 511. SNP markers used to monitor the introgression of GLS resistance locus 73 include those selected from the group consisting of SEQ ID NOs: 512 through 515. SNP markers used to monitor the introgression of GLS resistance locus 74 include those selected from the group consisting of SEQ ID NOs: 516 through 530. SNP markers used to monitor the introgression of GLS resistance locus 75 include those selected from the group consisting of SEQ ID NOs: 531 through 551. SNP markers used to monitor the introgression of GLS resistance locus 76 include those selected from the group consisting of SEQ ID NOs: 552 through 567. SNP markers used to monitor the introgression of GLS resistance locus 77 include those selected from the group consisting of SEQ ID NOs: 568 through 578. SNP markers used to monitor the introgression of GLS resistance locus 78 include those selected from the group consisting of SEQ ID NOs: 579 through 586. SNP markers used to monitor the introgression of GLS resistance locus 79 include those selected from the group consisting of SEQ ID NOs: 587 through 590. SNP markers used to monitor the introgression of GLS resistance locus 80 include those selected from the group consisting of SEQ ID NOs: 591 through 603. SNP markers used to monitor the introgression of GLS resistance locus 81 include those selected from the group consisting of SEQ ID NOs: 604 through 617. SNP markers used to monitor the introgression of GLS resistance locus 82 include those selected from the group consisting of SEQ ID NOs: 618 through 625. SNP markers used to monitor the introgression of GLS resistance locus 83 include those selected from the group consisting of SEQ ID NOs: 626 through 632. SNP markers used to monitor the introgression of GLS resistance locus 84 include those selected from the group consisting of SEQ ID NOs: 633 through 639. SNP markers used to monitor the introgression of GLS resistance locus 85 include those selected from the group consisting of SEQ ID NOs: 640 through 644. SNP markers used to monitor the introgression of GLS resistance locus 86 include those selected from the group consisting of SEQ ID NOs: 645 through 653.

[0084] SNP markers used to monitor the introgression of GLS resistance locus 87 include those selected from the group consisting of SEQ ID NOs: 654 through 656.

[0085] In the present invention GLS resistant loci 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, and 104 are located on Chromosome 5. SNP markers used to monitor the introgression of GLS resistance locus 88 include those selected from the group consisting of SEQ ID NOs: 657 through 660. SNP markers used to monitor the introgression of GLS resistance locus 89 include those selected from the group consisting of SEQ ID NOs: 661 through 668. SNP markers used to monitor the introgression of GLS resistance locus 90 include those selected from the group consisting of SEQ ID NOs: 669 through 670. SNP markers used to monitor the introgression of GLS resistance locus 91 include those selected from the group consisting of SEQ ID NOs: 671 through 674. SNP markers used to monitor the introgression of GLS resistance locus 92 include those selected from the group consisting of SEQ ID NOs: 675 through 678. SNP markers used to monitor the introgression of GLS resistance locus 93 include those selected from the group consisting of SEQ ID NOs: 679 through 692. SNP markers used to monitor the introgression of GLS resistance locus 94 include those selected from the group consisting of SEQ ID NOs: 693 through 709. SNP markers used to monitor the introgression of GLS resistance locus 95 include those selected from the group consisting of SEQ ID NOs: 710 through 721. SNP markers used to monitor the introgression of GLS resistance locus 96 include those selected from the group consisting of SEQ ID NOs: 722 through 730. SNP markers used to monitor the introgression of GLS resistance locus 97 include those selected from the group consisting of SEQ ID NOs: 731 through 738. SNP markers used to monitor the introgression of GLS resistance locus 98 include those selected from the group consisting of SEQ ID NOs: 739 through 740. SNP markers used to monitor the introgression of GLS resistance locus 99 include those selected from the group consisting of SEQ ID NOs: 741 through 748. SNP markers used to monitor the introgression of GLS resistance locus 100 include those selected from the group consisting of SEQ ID NOs: 749 through 754. SNP markers used to monitor the introgression of GLS resistance locus 101 include those selected from the group consisting of SEQ ID NOs: 755 through 760.

[0086] SNP markers used to monitor the introgression of GLS resistance locus 102 include those selected from the group consisting of SEQ ID NOs: 761 through 762. SNP markers used to monitor the introgression of GLS resistance locus 103 include those selected from the group consisting of SEQ ID NOs: 763 through 771. SNP markers used to monitor the introgression of GLS resistance locus 104 include those selected from the group consisting of SEQ ID NOs: 772 through 776.

[0087] In the present invention GLS resistant loci 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, and 117 are located on Chromosome 6. SNP markers used to monitor the introgression of GLS resistance locus 105 include those selected from the group consisting of SEQ ID NOs: 777 through 780. SNP markers used to monitor the introgression of GLS resistance locus 106 include those selected from the group consisting of SEQ ID NOs: 781 through 812. SNP markers used to monitor the introgression of GLS resistance locus 107 include those selected from the group consisting of SEQ ID NOs: 813 through 820. SNP markers used to monitor the introgression of GLS resistance locus 108 include those selected from the group consisting of SEQ ID NOs: 821 through 829 and 1232. SNP markers used to monitor the introgression of GLS resistance locus 109 include those selected from the group consisting of SEQ ID NOs: 830 through 834. SNP markers used to monitor the introgression of GLS resistance locus 110 include those selected from the group consisting of SEQ ID NOs: 835 through 845 and 1231. SNP markers used to monitor the introgression of GLS resistance locus 111 include those selected from the group consisting of SEQ ID NOs: 846 through 854. SNP markers used to monitor the introgression of GLS resistance locus 112 include those selected from the group consisting of SEQ ID NOs: 855 through 863. SNP markers used to monitor the introgression of GLS resistance locus 113 include those selected from the group consisting of SEQ ID NOs: 864 through 869. SNP markers used to monitor the introgression of GLS resistance locus 114 include those selected from the group consisting of SEQ ID NOs: 870 through 873. SNP markers used to monitor the introgression of GLS resistance locus 115 include those selected from the group consisting of SEQ ID NOs: 874 through 875. SNP markers used to monitor the introgression of GLS resistance locus 116 include those selected from the group consisting of SEQ ID NOs: 876 through 883. SNP markers used to monitor the introgression of GLS resistance locus 117 include those selected from the group consisting of SEQ ID NOs: 884 through 889 and 1360.

[0088] In the present invention GLS resistant loci 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, and 135 are located on Chromosome 7. SNP markers used to monitor the introgression of GLS resistance locus 118 include those selected from the group consisting of SEQ ID NOs: 890 through 891. SNP markers used to monitor the introgression of GLS resistance locus 119 include those selected from the group consisting of SEQ ID NOs: 892. SNP markers used to monitor the introgression of GLS resistance locus 120 include those selected from the group consisting of SEQ ID NOs: 893. SNP markers used to monitor the introgression of GLS resistance locus 121 include those selected from the group consisting of SEQ ID NOs: 894. SNP markers used to monitor the introgression of GLS resistance locus 122 include those selected from the group consisting of SEQ ID NOs: 895 through 898. SNP markers used to monitor the introgression of GLS resistance locus 123 include those selected from the group consisting of SEQ ID NOs: 899 through 907. SNP markers used to monitor the introgression of GLS resistance locus 124 include those selected from the group consisting of SEQ ID NOs: 908 through 932. SNP markers used to monitor the introgression of GLS resistance locus 125 include those selected from the group consisting of SEQ ID NOs: 933 through 939. SNP markers used to monitor the introgression of GLS resistance locus 126 include those selected from the group consisting of SEQ ID NOs: 940 through 943. SNP markers used to monitor the introgression of GLS resistance locus 127 include those selected from the group consisting of SEQ ID NOs: 944 through 953 and 1233. SNP markers used to monitor the introgression of GLS resistance locus 128 include those selected from the group consisting of SEQ ID NOs: 954 through 963. SNP markers used to monitor the introgression of GLS resistance locus 129 include those selected from the group consisting of SEQ ID NOs: 964 through 968. SNP markers used to monitor the introgression of GLS resistance locus 130 include those selected from the group consisting of SEQ ID NOs: 969 through 971. SNP markers used to monitor the introgression of GLS resistance locus 131 include those selected from the group consisting of SEQ ID NOs: 972 through 976. SNP markers used to monitor the introgression of GLS resistance locus 132 include those selected from the group consisting of SEQ ID NOs: 977. SNP markers used to monitor the introgression of GLS resistance locus 133 include those selected from the group consisting of SEQ ID NOs: 978 through 982. SNP markers used to monitor the introgression of GLS resistance locus 134 include those selected from the group consisting of SEQ ID NOs: 983 through 990. SNP markers used to monitor the introgression of GLS resistance locus 135 include those selected from the group consisting of SEQ ID NOs: 991 through 996.

[0089] In the present invention GLS resistant loci 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, and 149 are located on Chromosome 8. SNP markers used to monitor the introgression of GLS resistance locus 136 include those selected from the group consisting of SEQ ID NOs: 997 through 1000. SNP markers used to monitor the introgression of GLS resistance locus 137 include those selected from the group consisting of SEQ ID NOs: 1001 through 1003. SNP markers used to monitor the introgression of GLS resistance locus 138 include those selected from the group consisting of SEQ ID NOs: 1004 through 1010. SNP markers used to monitor the introgression of GLS resistance locus 139 include those selected from the group consisting of SEQ ID NOs: 1011 through 1015. SNP markers used to monitor the introgression of GLS resistance locus 140 include those selected from the group consisting of SEQ ID NOs: 1016 through 1022. SNP markers used to monitor the introgression of GLS resistance locus 141 include those selected from the group consisting of SEQ ID NOs: 1023 through 1031. SNP markers used to monitor the introgression of GLS resistance locus 142 include those selected from the group consisting of SEQ ID NOs: 1032 through 1046. SNP markers used to monitor the introgression of GLS resistance locus 143 include those selected from the group consisting of SEQ ID NOs: 1047 through 1050. SNP markers used to monitor the introgression of GLS resistance locus 144 include those selected from the group consisting of SEQ ID NOs: 1051 through 1060. SNP markers used to monitor the introgression of GLS resistance locus 145 include those selected from the group consisting of SEQ ID NOs: 1061 through 1062. SNP markers used to monitor the introgression of GLS resistance locus 146 include those selected from the group consisting of SEQ ID NOs: 1063 through 1069. SNP markers used to monitor the introgression of GLS resistance locus 147 include those selected from the group consisting of SEQ ID NOs: 1070 through 1072. SNP markers used to monitor the introgression of GLS resistance locus 148 include those selected from the group consisting of SEQ ID NOs: 1073 through 1075. SNP markers used to monitor the introgression of GLS resistance locus 149 include those selected from the group consisting of SEQ ID NOs: 1076 through 1078.

[0090] In the present invention GLS resistant loci 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, and 165 are located on Chromosome 9. SNP markers used to monitor the introgression of GLS resistance locus 150 include those selected from the group consisting of SEQ ID NOs: 1079 through 1081. SNP markers used to monitor the introgression of GLS resistance locus 151 include those selected from the group consisting of SEQ ID NOs: 1082 through 1086. SNP markers used to monitor the introgression of GLS resistance locus 152 include those selected from the group consisting of SEQ ID NOs: 1087. SNP markers used to monitor the introgression of GLS resistance locus 153 include those selected from the group consisting of SEQ ID NOs: 1088 through 1091. SNP markers used to monitor the introgression of GLS resistance locus 154 include those selected from the group consisting of SEQ ID NOs: 1092 through 1096. SNP markers used to monitor the introgression of GLS resistance locus 155 include those selected from the group consisting of SEQ ID NOs: 1097 through 1098. SNP markers used to monitor the introgression of GLS resistance locus 156 include those selected from the group consisting of SEQ ID NOs: 1099 through 1110. SNP markers used to monitor the introgression of GLS resistance locus 157 include those selected from the group consisting of SEQ ID NOs: 1111 through 1118. SNP markers used to monitor the introgression of GLS resistance locus 158 include those selected from the group consisting of SEQ ID NOs: 1119 through 1133 and 1127. SNP markers used to monitor the introgression of GLS resistance locus 159 include those selected from the group consisting of SEQ ID NOs: 1134 through 1142. SNP markers used to monitor the introgression of GLS resistance locus 160 include those selected from the group consisting of SEQ ID NOs: 1143 through 1150. SNP markers used to monitor the introgression of GLS resistance locus 161 include those selected from the group consisting of SEQ ID NOs: 1151 through 1157. SNP markers used to monitor the introgression of GLS resistance locus 162 include those selected from the group consisting of SEQ ID NOs: 1158 through 1159. SNP markers used to monitor the introgression of GLS resistance locus 163 include those selected from the group consisting of SEQ ID NOs: 1160 through 1164. SNP markers used to monitor the introgression of GLS resistance locus 164 include those selected from the group consisting of SEQ ID NOs: 1165. SNP markers used to monitor the introgression of GLS resistance locus 165 include those selected from the group consisting of SEQ ID NOs: 1166 through 1167.

[0091] In the present invention GLS resistant loci 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, and 176 are located on Chromosome 10. SNP markers used to monitor the introgression of GLS resistance locus 166 include those selected from the group consisting of SEQ ID NOs: 1168. SNP markers used to monitor the introgression of GLS resistance locus 167 include those selected from the group consisting of SEQ ID NOs: 1169 through 1172. SNP markers used to monitor the introgression of GLS resistance locus 168 include those selected from the group consisting of SEQ ID NOs: 1173 through 1177. SNP markers used to monitor the introgression of GLS resistance locus 169 include those selected from the group consisting of SEQ ID NOs: 1178 through 1192. SNP markers used to monitor the introgression of GLS resistance locus 170 include those selected from the group consisting of SEQ ID NOs: 1193 through 1203 and 1361. SNP markers used to monitor the introgression of GLS resistance locus 171 include those selected from the group consisting of SEQ ID NOs: 1204 through 1210. SNP markers used to monitor the introgression of GLS resistance locus 172 include those selected from the group consisting of SEQ ID NOs: 1211 through 1215. SNP markers used to monitor the introgression of GLS resistance locus 173 include those selected from the group consisting of SEQ ID NOs: 1216 through 1219. SNP markers used to monitor the introgression of GLS resistance locus 174 include those selected from the group consisting of SEQ ID NOs: 1220 through 1221. SNP markers used to monitor the introgression of GLS resistance locus 175 include those selected from the group consisting of SEQ ID NOs: 1222 through 1226. SNP markers used to monitor the introgression of GLS resistance locus 176 include SEQ ID NO: 1227. .

[0092] Exemplary marker assays for screening for GLS resistance loci are provided in Tables 5, 6, and 7. Illustrative GLS resistance locus 173 SNP marker DNA sequence SEQ ID NO: 1219 can be amplified using the primers indicated as SEQ ID NOs: 1304 through 1305 and detected with probes indicated as SEQ ID NOs: 1306 through 1307. Illustrative GLS resistance locus 57 SNP marker DNA sequence SEQ ID NO: 421 can be amplified using the primers indicated as SEQ ID NOs: 1308 through 1309 and detected with probes indicated as SEQ ID NOs: 1310 through 1311. Illustrative GLS resistance locus 64 SNP marker DNA sequence SEQ ID NO: 481 can be amplified using the primers indicated as SEQ ID NOs: 1312 through 1313 and detected with probes indicated as SEQ ID NOs: 1314 through 1315. Illustrative GLS resistance locus 176 SNP marker DNA sequence SEQ ID NO: 1127 can be amplified using the primers indicated as SEQ ID NOs: 1316 through 1317 and detected with probes indicated as SEQ ID NOs: 1318 through 1319. Illustrative oligonucleotide hybridization probes for GLS resistance locus 173 SNP marker DNA sequence SEQ ID NO: 1219 are provided as SEQ ID NO: 1320 and SEQ ID NO 1321. Illustrative oligonucleotide hybridization probes for GLS resistance locus 57 SNP marker DNA sequence SEQ ID NO: 421 are provided as SEQ ID NO: 1322 and SEQ ID NO: 1323. Illustrative oligonucleotide hybridization probes for GLS resistance locus 64 SNP marker DNA sequence SEQ ID NO: 481 are provided as SEQ ID NO: 1324 and SEQ ID NO: 1325. Illustrative oligonucleotide hybridization probes for GLS resistance locus 176 SNP marker DNA sequence SEQ ID NO: 1127 are provided as SEQ ID NO: 1326 and SEQ ID NO: 1327. An illustrative probe for single base extension assays for GLS resistance locus 173 SNP marker DNA sequence SEQ ID NO: 1219 is provided as SEQ ID NO: 1328. An illustrative probe for single base extension assays for GLS resistance locus 57 SNP marker DNA sequence SEQ ID NO: 421 is provided as SEQ ID NO: 1329. An illustrative probe for single base extension assays for GLS resistance locus 64 SNP marker DNA sequence SEQ ID NO: 481 is provided as SEQ ID NO: 1330. An illustrative probe for single base extension assays for GLS resistance locus 176 SNP marker DNA sequence SEQ ID NO: 1127 is provided as SEQ ID NO: 1331.

[0093] The present invention also provides a corn plant comprising a nucleic acid molecule selected from the group consisting of SEQ ID NO: 1 through 1233, 1360, and 1361, fragments thereof, and complements of both.

[0094] As used herein, GLS refers to any Gray Leaf Spot variant or isolate. A corn plant of the present invention can be resistant to one or more fungi capable of causing or inducing GLS. In one aspect, the present invention provides plants resistant to GLS as well as methods and compositions for screening corn plants for resistance or susceptibility to GLS, caused by the genus *Cercospora*. In a preferred aspect, the present invention provides methods and compositions for screening corn plants for resistance or susceptibility to *C. zeea-maydis*. In another aspect, the present invention provides plants resistant to and methods and compositions for screening corn plants for resistance or susceptibility to *C. zeea-maydis* strain “Type I.” In a further aspect, the present invention provides plants resistant to and methods and compositions for screening corn plants for resistance or susceptibility to *C. zeea-maydis* strain “Type II.” In an additional aspect, the present invention provides plants resistant to and methods and compositions for screening corn plants for resistance or susceptibility to *C. sorghi* var. *maydis*.

[0095] In an aspect, the plant is selected from the genus *Zea*. In another aspect, the plant is selected from the species *Zea mays*. In a further aspect, the plant is selected from the subspecies *Zea mays* L. ssp. *mays*. In an additional aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Indentata, otherwise known as dent corn. In another aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Indurata, otherwise known as flint corn. In an aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Saccharata, otherwise known as sweet corn. In another aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Amylacea, otherwise known as flour corn. In a further aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Everta, otherwise known as pop corn. *Zea* plants include hybrids, inbreds, partial inbreds, or members of defined or undefined populations.

[0096] Plants of the present invention can be a corn plant that is very resistant, resistant, substantially resistant, mid-resistant, comparatively resistant, partially resistant, mid-susceptible, or susceptible.

[0097] In a preferred aspect, the present invention provides a corn plant to be assayed for resistance or susceptibility to GLS by any method to determine whether a corn plant is very resistant, resistant, substantially resistant, mid-resistant, comparatively resistant, partially resistant, mid-susceptible, or susceptible. Phenotyping for GLS is based on visually screening plants to determine percentage of infected leaf area. The percentage of leaf area infected is used to rate plants on a scale of 1 (very resistant) to 9 (susceptible). Disease resistance is evaluated visually after pollination. The infection can be natural or from artificial inoculation.

[0098] A disease resistance QTL of the present invention may be introduced into an elite corn inbred line.

[0099] In another aspect, the corn plant can show a comparative resistance compared to a non-resistant control corn plant. In this aspect, a control corn plant will preferably be genetically similar except for the GLS resistant allele or alleles in question. Such plants can be grown under similar conditions with equivalent or near equivalent exposure to the pathogen. In this aspect, the resistant plant or plants has less than 25%, 15%, 10%, 5%, 2% or 1% of leaf area infected.

[00100] A disease resistance QTL of the present invention may be introduced into an elite corn inbred line. An “elite line” is any line that has resulted from breeding and selection for superior agronomic performance.

[00101] A GLS resistance QTL of the present invention may also be introduced into an elite corn plant comprising one or more transgenes conferring herbicide tolerance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance, modified oils production, high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistant, increased digestibility, industrial enzymes, pharmaceutical proteins, peptides and small molecules, improved processing traits, improved flavor, nitrogen fixation, hybrid seed production, reduced allergenicity, biopolymers, and biofuels among others. In one aspect, the herbicide tolerance is selected from the group consisting of glyphosate, dicamba, glufosinate, sulfonylurea, bromoxynil and norflurazon herbicides. These traits can be provided by methods of plant biotechnology as transgenes in corn.

[00102] A disease resistant QTL allele or alleles can be introduced from any plant that contains that allele (donor) to any recipient corn plant. In one aspect, the recipient corn plant can contain additional GLS resistant loci. In another aspect, the recipient corn plant can contain a transgene. In another aspect, while maintaining the introduced QTL, the genetic contribution of the plant providing the disease resistant QTL can be reduced by back-crossing or other suitable approaches. In one aspect, the nuclear genetic material derived from the donor material in the corn plant can be less than or about 50%, less than or about 25%, less than or about 13%, less than or about 5%, 3%, 2% or 1%, but that genetic material contains the GLS resistant locus or loci of interest.

[00103] It is further understood that a corn plant of the present invention may exhibit the characteristics of any relative maturity group. In an aspect, the maturity group is selected from the group consisting of RM90 – 95, RM 95 – 100, RM 100 – 105, RM 105 – 110, RM 110 – 115, and RM 115- 120.

[00104] An allele of a QTL can, of course, comprise multiple genes or other genetic factors even within a contiguous genomic region or linkage group, such as a haplotype. As used herein, an allele of a disease resistance locus can therefore encompass more than one gene or other genetic factor where each individual gene or genetic component is also capable of exhibiting allelic variation and where each gene or genetic factor is also capable of eliciting a phenotypic effect on the quantitative trait in question. In an aspect of the present invention the allele of a QTL comprises one or more genes or other genetic factors that are also capable of exhibiting allelic variation. The use of the term "an allele of a QTL" is thus not intended to exclude a QTL that comprises more than one gene or other genetic factor. Specifically, an “allele of a QTL” in the present in the invention can denote a haplotype within a haplotype window wherein a phenotype can be disease resistance. A haplotype window is a contiguous genomic region that can be defined, and tracked, with a set of one or more polymorphic markers wherein the polymorphisms indicate identity by descent. A haplotype within that window can be defined by the unique fingerprint of alleles at each marker. As used herein, an allele is one of several alternative forms of a gene occupying a given locus on a chromosome. When all the alleles present at a given locus on a chromosome are the same, that plant is homozygous at that locus. If the alleles present at a given locus on a chromosome differ, that plant is heterozygous at that locus. Plants of the present invention may be homozygous or heterozygous at any particular GLS locus or for a particular polymorphic marker.

[00105] The present invention also provides for parts of the plants of the present invention. Plant parts, without limitation, include seed, endosperm, ovule and pollen. In a particularly preferred aspect of the present invention, the plant part is a seed.

[00106] The present invention also provides a container of corn in which greater than 50%, 60%, 70%, 80%, 90%, 95%, or 99% of the seeds comprising 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, and 178 GLS resistant loci where one or more alleles at one or more of their loci are selected from the group consisting of SEQ ID NOs 1-1233, 1360, and 1361.

[00107] The container of corn seeds can contain any number, weight, or volume of seeds. For example, a container can contain at lest, or greater than, about 10, 25, 50, 100, 200, 300, 400, 500, 600, 700, 80, 90, 1000, 1500, 2000, 2500, 3000, 3500, 4000 or more seeds. In another aspect, a container can contain about, or greater than about, 1 gram, 5 grams, 10 grams, 15 grams, 20 grams, 25 grams, 50 grams, 100 grams, 250 grams, 500 grams, or 1000 grams of seeds. Alternatively, the container can contain at least, or greater than, about 0 ounces, 1 ounce, 5 ounces, 10 ounces, 1 pound, 2 pounds, 3 pounds, 4 pounds, 5 pounds, 10 pounds, 15 pounds, 20 pounds, 25 pounds, or 50 pounds or more seeds.

[00108] Containers of corn seeds can be any container available in the art. For example, a container can be a box, a bag, a can, a packet, a pouch, a tape roll, a pail, or a tube.

[00109] In another aspect, the seeds contained in the containers of corn seeds can be treated or untreated corn seeds. In one aspect, the seeds can be treated to improve germination, for example, by priming the seeds, or by disinfection to protect against seed-born pathogens. In another aspect, seeds can be coated with any available coating to improve, for example, plantability, seed emergence, and protection against seed-born pathogens. Seed coating can be any form of seed coating including, but not limited to, pelleting, film coating, and encrustments.

[00110] Plants of the present invention may also be grown in culture and regenerated. Methods for the regeneration of *Zea mays* plants from various tissue types and methods for the tissue culture of *Zea mays* are known in the art (for example, Bhaskaran *et al.* 1990 Crop Sci. 30:1328-1336). Regeneration techniques for plants such as *Zea mays* can use as the starting material a variety of tissue or cell types. With *Zea mays* in particular, regeneration processes have been developed that begin with certain differentiated tissue types such as meristems, (Sairam *et al.* 2003 *Genome* 46:323-3). Regeneration of mature *Zea mays* plants from tissue culture by organogenesis and embryogenesis has also been reported (Wang 1987 *Plant Cell. Rep.* 6:360-362; Chang 1983 *Plant Cell. Rep.* 2:18-185; Green *et al.* 1975 Crop Sci. 15:417-421). Recently, regeneration of corn from split seeds was also reported (Al-Abed *et al.* 2006 *Planta* 223:1355-1366).

[00111] The present invention also provides a disease resistant corn plant selected for by screening for disease resistance or susceptibility in the corn plant, the selection comprising interrogating genomic nucleic acids for the presence of a marker molecule that is genetically linked to an allele of a QTL associated with disease resistance in the corn plant, where the allele of a QTL is also located on a linkage group associated with disease resistant GLS.

[00112] The present invention provides a method of introgressing an allele into a corn plant comprising (A) crossing at least one first corn plant comprising a nucleic acid molecule selected from the group consisting of SEQ ID NO: 1 through 1233, and SEQ ID NOs: 1360 and 1361 with at least one second corn plant in order to form a segregating population, (B) screening the segregating population with one or more nucleic acid markers to determine if one or more corn plants from the segregating population contains the nucleic acid molecule, and (C) selecting from the segregation population one or more corn plants comprising a nucleic acid molecule selected from the group consisting of SEQ ID NO: 1 through 1233, and SEQ ID NOs: 1360 and 1361.

[00113] The present invention also includes a method of introgressing an allele into a corn plant comprising: (A) crossing at least one GLS resistant corn plant with at least one GLS sensitive corn plant in order to form a segregating population; (B) screening the segregating population with one or more nucleic acid markers to determine if one or more corn plants from the segregating population contains a GLS resistant allele, wherein the GLS resistant allele is an allele selected from the group consisting of GLS resistant locus 1-9, 14-33, 35, 38-42, 44-52, 54-61, 63-71, 73-79, 81-92, 95-96, 99-106, 108-117, and GLS resistant locus 119-178 as provided in Figure 1.

[00114] The present invention includes isolated nucleic acid molecules. Such molecules include those nucleic acid molecules capable of detecting a polymorphism genetically or physically linked to a GLS locus. Such molecules can be referred to as markers. Additional markers can be obtained that are linked to GLS resistance locus 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58,59,60,61,62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177 or GLS resistance locus 178 by available techniques. In one aspect, the nucleic acid molecule is capable of detecting the presence or absence of a marker located less than 30, 20, 10, 5, 2, or 1 centimorgans from a GLS resistance locus. In another aspect, a marker exhibits a LOD score of 2 or greater, 3 or greater, or 4 or greater with GLS, measuring using Qgene Version 2.23 (1996) and default parameters. In another aspect, the nucleic acid molecule is capable of detecting a marker in a locus selected from the group GLS resistance locus 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58,59,60,61,62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175 , 176, 177, and GLS resistance locus 178. In a further aspect, a nucleic acid molecule is selected from the group consisting of SEQ ID NO: 1 through 1233, and SEQ ID NOs: 1360 and 1361, fragments thereof, complements thereof, and nucleic acid molecules capable of specifically hybridizing to one or more of these nucleic acid molecules.

[00115] In a preferred aspect, a nucleic acid molecule of the present invention includes those that will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 1233, and SEQ ID NOs: 1360 and 1361 or SEQ ID NO: 1304 through SEQ ID NO: 1331 or complements thereof or fragments of either under moderately stringent conditions, for example at about 2.0 x SSC and about 65°C. In a particularly preferred aspect, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in

SEQ ID NO: 1 through SEQ ID NO: 1233, and SEQ ID NOs: 1360 and 1361 or SEQ ID NOs: 1304 through 1331 or complements or fragments of either under high stringency conditions. In one aspect of the present invention, a preferred marker nucleic acid molecule of the present invention has the nucleic acid sequence set forth in SEQ ID NO: 1 through SEQ ID NO: 1233, and SEQ ID NOs: 1360 and 1361 or SEQ ID NO: 1304 through SEQ ID NO: 1331 or complements thereof or fragments of either. In another aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 80% and 100% or 90% and 100% sequence identity with the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 1233, and SEQ ID NOs: 1360 and 1361 or SEQ ID NO: 1304 through SEQ ID NO: 1331 or complements thereof or fragments of either. In a further aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 95% and 100% sequence identity with the sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 1233, and SEQ ID NOs: 1360 and 1361 or SEQ ID NO: 1304 through SEQ ID NO: 1331 or complements thereof or fragments of either. In a more preferred aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 98% and 100% sequence identity with the nucleic acid sequence set forth in SEQ ID NO: 1 through SEQ ID NO: 1233, and SEQ ID NOs: 1360 and 1361 or SEQ ID NO: 1304 through SEQ ID NO: 1331 or complement thereof or fragments of either. The present invention provides a method of introgressing an allele into a corn plant comprising (A) crossing at least one first corn plant comprising a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1 through 1233, and SEQ ID NOs: 1360 and 1361 with at least one second corn plant in order to form a segregating population, (B) screening the segregating population with one or more nucleic acid markers to determine if one or more corn plants from the segregating population contains the nucleic acid molecule, and (C) selecting from the segregation population one or more corn plants comprising a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1 through 1233, and SEQ ID NOs: 1360 and 1361.

Goss' Wilt Resistance

[00116] The present invention provides Goss' Wilt resistance loci that are located in public bins in the maize genome that were not previously associated with Goss' Wilt resistance.

[00117] The present invention provides 130 Goss' Wilt resistance loci that are located in public bins in the maize genome that were not previously associated with Goss' Wilt resistance. QTL were assigned by dividing maize chromosomal regions into 10 cM windows. A total of 131 QTL were identified, with 130 not having been previously reported. SNP markers are also provided for monitoring the introgression of the 131 QTL associated with Goss' Wilt resistance.

[00118] In the present invention, Goss' Wilt resistance loci 1-53 and 55-131 have not been previously associated with Goss' Wilt and are provided. SNP markers are also provided for monitoring the introgression of Goss' Wilt resistance. In the present invention, Goss' Wilt resistance loci 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, and 20 are located on Chromosome 1. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 1 include those selected from the group consisting of SEQ ID NOs: 13 and 1274. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 2 included those selected from the group consisting of SEQ ID NOs: 1234 and 19. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 3 include those selected from the group consisting of SEQ ID NOs: 27 and 24. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 4 include SEQ ID NO: 36. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 5 included those selected from the group consisting of SEQ ID NOs: 50 and 53. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 6 include SEQ ID NOs: 90. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 7 include those selected from the group consisting of SEQ ID NOs: 94, 95, 97, 1235, 1236, 99, 101, 102, 1237, 106, 1238, 110, 111, and 1239. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 8 include those selected from the group consisting of SEQ ID NOs: 1240, 119, 121, 122, and 124. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 9 include those selected from the group consisting of SEQ ID NOs: 128, 130, 131, and 132. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 10 include those selected from the group consisting of SEQ ID NOs: 136, 138, and 1275. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 11 include SEQ ID NOs: 141. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 12 include SEQ ID NOs: 146. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 13 include those selected from the group consisting of SEQ ID NOs: 153, 1241, 159, 160, 162, and 158. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 14 include those selected from the group consisting of SEQ ID NOs: 164, 166, 169, and 172. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 15 include those selected from the group consisting of SEQ ID NOs: 175 and 177. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 16 include those selected from the group consisting of SEQ ID NOs: 1242 and 186. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 17 include SEQ ID NO: 200. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 18 include those selected from the group consisting of SEQ ID NOs: 202 and 203. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 19 include those selected from the group consisting of SEQ ID NOs: 207 and 208. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 20 include SEQ ID NO: 1243.

[00119] In the present invention Goss' Wilt resistance loci 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, and 129 are located on Chromosome 2. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 21 include SEQ ID NO: 215. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 22 include those selected from the group consisting of SEQ ID NOs: 216, 1244, 220, 218, and 1229. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 23 include those selected from the group consisting of SEQ ID NOs: 224. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 24 include those selected from the group consisting of SEQ ID NO: 228, 231, and 1276. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 25 include those selected from the group consisting of SEQ ID NOs: 232, 233, 234, 235, and 236. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 26 include those selected from the group consisting of SEQ ID NOs: 244, 248, and 1277. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 27 include those selected from the group consisting of SEQ ID NOs: 250, 252, 256, 257, 260, 1295, and 1278. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 28 include those selected from the group consisting of SEQ ID NOs: 265, 266, and 267. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 29 include those selected from the group consisting of SEQ ID NOs: 271, 273, 1245, 274, 278, 279, 282, 287, 289, and 272. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 30 include those selected from the group consisting of SEQ ID NOs: 294, 295, 296, and 299. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 31 include those selected from the group consisting of SEQ ID NOs: 1246, 317, and 320. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 32 include those selected from the group consisting of SEQ ID NOs: 332, 333, and 334. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 33 include SEQ ID NO: 337. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 34 include SEQ ID NO: 347. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 35 include SEQ ID NO: 355. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 129 include SEQ ID NO: 1294.

[00120] In the present invention Goss' Wilt resistance loci 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 122, and 123 are located on Chromosome 3. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 36 include those selected from the group consisting of

SEQ ID NOs: 362 and 363. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 37 include SEQ ID NO: 1247. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 38 include SEQ ID NO: 366. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 39 include those selected from the group consisting of SEQ ID NO: 367, 368, and 1279. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 40 include those selected from the group consisting of SEQ ID NO: 370 and 371. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 41 include those selected from the group consisting of SEQ ID NOs: 381, 382, 392, and 395. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 42 include those selected from the group consisting of SEQ ID NOs: 409, 411, and 412. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 43 include those selected from the group consisting of SEQ ID NOs: 419, 422, 423, and 1280. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 44 include those selected from the group consisting of SEQ ID NOs: 429, 430, 433 and 1281. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 45 include those selected from the group consisting of SEQ ID NOs: 438, 440, 1248, and 447. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 46 include SEQ ID NO: 1249. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 47 include those selected from the group consisting of SEQ ID NOs: 474, 476, 479, 480, and 482. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 48 include those selected from the group SEQ ID NO: 486. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 49 include SEQ ID NO: 490. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 50 include SEQ ID NO: 493. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 122 include those selected from the group consisting of SEQ ID NOs: 375 and 1296. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 123 include those selected from the group consisting of SEQ ID NOs: 401 and 408.

[00121] In the present invention Goss' Wilt resistance loci 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 124, 125, and 126 are located on Chromosome 4. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 51 include SEQ ID NO: 500. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 52 include those selected from the group consisting of SEQ ID NOs: 1250, 525, and 530. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 53 include SEQ ID NOs: 533. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 54 include those selected from the group consisting of SEQ ID NOs: 556 and 566. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 55 include those selected from the group consisting of SEQ ID NOs: 582, 585, 1251, and 1283. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 56 include those selected from the group consisting of SEQ ID NOs: 589 and 587. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 57 include those selected from the group consisting of SEQ ID NOs: 593, 594, and 599. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 58 include SEQ ID NO: 611, 1297, 1298, and 1284. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 59 include those selected from the group consisting of SEQ ID NOs: 1252, 618, 621, and 623. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 60 include those selected from the group consisting of SEQ ID NOs: 630, 632, 637, 639, and 629. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 61 include those selected from the group consisting of SEQ ID NOs: 646, 649, and 650. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 124 include SEQ ID NO: 498. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 125 include SEQ ID NO: 1282.

[00122] In the present invention Goss' Wilt resistance loci 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, and 130 are located on Chromosome 5. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 62 include SEQ ID NO: 657. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 63 include those selected from the group consisting of SEQ ID NOs: 665, 1286, and 1299. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 64 include SEQ ID NO: 669. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 65 include those selected from SEQ ID NO: 1253. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 66 include those selected from the group consisting of SEQ ID NOs: 678, 1254, and 1255. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 67 include those selected from the group consisting of SEQ ID NOs: 679, 688, and 690. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 68 include those selected from the group consisting of SEQ ID NOs: 1256, 704, 709, and 1300. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 69 include those selected from the group consisting of SEQ ID NOs: 710, 717, 719, 720, 1257, and 721. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 70 include those selected from the group SEQ ID NOs: 726, 727, and 1258. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 71 include those selected from the group consisting of SEQ ID NOs: 733 and 734. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 72 include those selected from the group consisting of SEQ ID NOs: 746 and 744. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 73 include those selected from the group consisting of SEQ ID NOs: 758 and 760. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 74 include those selected from the group consisting of SEQ ID NOs: 764, 768, and 1287. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 75 include SEQ ID NO: 773. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 130 include SEQ ID NO: 1301.

[00123] In the present invention Goss' Wilt resistance loci 76, 77, 78, 79, 80, 81, 82, 83, and 84 are located on Chromosome 6. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 76 include those selected from the group consisting of SEQ ID NOs: 1259, 792, 793, and 812. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 77 include those selected from the group consisting of SEQ ID NOs: 821 and 825. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 78 include those selected from the group consisting of SEQ ID NOs: 835, 1260, and 844. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 79 include those selected from the group consisting of SEQ ID NOs: 846, 850, and 854. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 80 include those selected from the group consisting of SEQ ID NOs: 856, 857, and 858. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 81 include SEQ ID NO: 1261. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 82 include SEQ ID NO: 874. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 83 include those selected from the group consisting of SEQ ID NOs: 876, 880, and 882. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 84 include SEQ ID NO: 885.

[00124] In the present invention Goss' Wilt resistance loci 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, and 127 are located on Chromosome 7. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 85 include SEQ ID NO: 893. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 86 include those selected from the group consisting of SEQ ID NOs: 897 and 896. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 87 include SEQ ID NO: 1262. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 88 include those selected from the group consisting of SEQ ID NOs: 915, 926, and 1288. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 89 include those selected from the group consisting of SEQ ID NOs: 940 and 942. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 90 include those selected from the group consisting of SEQ ID NOs: 949 and 951. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 91 include SEQ ID NO: 957 and 963. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 92 include those selected from the group consisting of SEQ ID NO: 964 and 1289. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 93 include those selected from the group consisting of SEQ ID NO: 974 and 976. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 94 include SEQ ID NO: 1263. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 95 include those selected from the group consisting of SEQ ID NO: 981 and 1291. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 96 include SEQ ID NOs: 983 and 990. . SNP markers used to monitor the introgression of Goss' Wilt resistance locus 127 include SEQ ID NO: 1290.

[00125] In the present invention Goss' Wilt resistance loci 97, 98, 99, 100, 101, 102, 103, and 131 are located on Chromosome 8. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 97 include those selected from the group consisting of SEQ ID NOs: 997, 999, and 1000. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 98 include those selected from the group consisting of SEQ ID NOs: 1016 and 1264. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 99 include those selected from the group consisting of SEQ ID NOs: 1027,1265, and 1303. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 100 include SEQ ID NO: 1043. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 101 include SEQ ID NO: 1049. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 102 include SEQ ID NO: 1056. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 103 include SEQ ID NO: 1075. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 131 include SEQ ID NO: 1015.

[00126] In the present invention Goss' Wilt resistance loci 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, and 115 are located on Chromosome 9. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 104 include those selected from the group consisting of SEQ ID NOs: 1266 and 1081. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 105 include SEQ ID NO: 1087. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 106 include SEQ ID NO: 1088. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 107 include SEQ ID NO: 1098. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 108 include those selected from the group consisting of SEQ ID NOs: 1099, 1100, 1104, 1105, 1108, 1110, and 1292. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 109 include those selected from the group consisting of SEQ ID NOs: 1267 and 1115. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 110 include those selected from the group consisting of SEQ ID NOs: 1122, 1268, 1131, and 1133. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 111 include those selected from the group consisting of SEQ ID NOs: 1269 and 1142. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 112 include those selected from the group consisting of SEQ ID NOs: 1143, 1145, 1146, 1148, and 1149.. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 113 include SEQ ID NO: 1270. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 114 include SEQ ID NO: 1159.

[00127] In the present invention Goss' Wilt resistance loci 115, 116, 117, 118, 119, 120, 121, and 122 are located on Chromosome 10. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 115 include SEQ ID NO: 1168. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 116 include SEQ ID NO: 1174. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 117 include those selected from the group consisting of SEQ ID NOs: 1271, 1184, and 1186. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 118 include those selected from the group consisting of SEQ ID NO: 1272 and 1196. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 119 include SEQ ID NO: 1204. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 120 include those selected from the group consisting of SEQ ID NOs: 1212 and 1215. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 121 include SEQ ID NO: 1273. SNP markers used to monitor the introgression of Goss' Wilt resistance locus 128 inlcude SEQ ID NO: 1293.

[00128] Exemplary marker assays for screening for Goss' Wilt resistance loci are provided in Tables 12, 13, and 14. Illustrative Goss' Wilt resistance locus 87 SNP marker DNA sequence SEQ ID NO: 896 can be amplified using the primers indicated as SEQ ID NOs: 1332 through 1333 and detected with probes indicated as SEQ ID NOs: 1334 through 1335. Illustrative Goss' Wilt resistance locus 91 SNP marker DNA sequence SEQ ID NO: 951 can be amplified using the primers indicated as SEQ ID NOs: 1336 through 1337 and detected with probes indicated as SEQ ID NOs: 1338 through 1339. Illustrative Goss' Wilt resistance locus 72 SNP marker DNA sequence SEQ ID NO: 733 can be amplified using the primers indicated as SEQ ID NOs: 1340 through 1341 and detected with probes indicated as SEQ ID NOs: 1342 through 1343. Illustrative Goss' Wilt resistance locus 109 SNP marker DNA sequence SEQ ID NO: 1098 can be amplified using the primers indicated as SEQ ID NOs: 1344 through 1345 and detected with probes indicated as SEQ ID NOs: 1346 through 1347. Illustrative oligonucleotide hybridization probes for Goss' Wilt resistance locus 87 SNP marker DNA sequence SEQ ID NO: 896 are provided as SEQ ID NO: 1348 and SEQ ID NO 1349. Illustrative oligonucleotide hybridization probes for Goss' Wilt resistance locus 91 SNP marker DNA sequence SEQ ID NO: 951 are provided as SEQ ID NO: 1350 and SEQ ID NO 1351. Illustrative oligonucleotide hybridization probes for Goss' Wilt resistance locus 72 SNP marker DNA sequence SEQ ID NO: 733 are provided as SEQ ID NO: 1352 and SEQ ID NO 1353. Illustrative oligonucleotide hybridization probes for Goss' Wilt resistance locus 109 SNP marker DNA sequence SEQ ID NO: 1098 are provided as SEQ ID NO: 1354 and SEQ ID NO 1355. An illustrative probe for single base extension assays for Goss' Wilt resistance locus 87 SNP marker DNA sequence SEQ ID NO: 896 is provided as SEQ ID NO: 1356. An illustrative probe for single base extension assays for Goss' Wilt resistance locus 91 SNP marker DNA sequence SEQ ID NO: 951 is provided as SEQ ID NO: 1357. An illustrative probe for single base extension assays for Goss' Wilt resistance locus 72 SNP marker DNA sequence SEQ ID NO: 733 is provided as SEQ ID NO: 1358. An illustrative probe for single base extension assays for Goss' Wilt resistance locus 109 SNP marker DNA sequence SEQ ID NO: 1098 is provided as SEQ ID NO: 1359.

[00129] As used herein, Goss' Wilt refers to any Goss' Wilt variant or isolate. A corn plant of the present invention can be resistant to one or more bacteria capable of causing or inducing Goss' Wilt. In one aspect, the present invention provides plants resistant to Goss' Wilt as well as methods and compositions for screening corn plants for resistance or susceptibility to Goss' Wilt, caused by the genus *Clavibacter*. In a preferred aspect, the present invention provides methods and compositions for screening corn plants for resistance or susceptibility to *Clavibacter michiganense spp*.

[00130] In an aspect, the plant is selected from the genus *Zea*. In another aspect, the plant is selected from the species *Zea mays*. In a further aspect, the plant is selected from the subspecies *Zea mays* L. ssp. *mays*. In an additional aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Indentata, otherwise known as dent corn. In another aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Indurata, otherwise known as flint corn. In an aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Saccharata, otherwise known as sweet corn. In another aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Amylacea, otherwise known as flour corn. In a further aspect, the plant is selected from the group *Zea mays* L. subsp. *mays* Everta, otherwise known as pop corn. *Zea* plants include hybrids, inbreds, partial inbreds, or members of defined or undefined populations.

[00131] Plants of the present invention can be a corn plant that is very resistant, resistant, substantially resistant, mid-resistant, comparatively resistant, partially resistant, mid-susceptible, or susceptible.

[00132] In a preferred aspect, the present invention provides a corn plant to be assayed for resistance or susceptibility to Goss' Wilt by any method to determine whether a corn plant is very resistant, resistant, substantially resistant, mid-resistant, comparatively resistant, partially resistant, mid-susceptible, or susceptible.

[00133] Phenotyping for Goss' Wilt is based on visually screening plants to determine percentage of infected leaf area. The percentage of leaf area infected is used to rate plants on a scale of 1 (very resistant) to 9 (susceptible).

[00134] A disease resistance QTL of the present invention may be introduced into an elite corn inbred line.

[00135] In another aspect, the corn plant can show a comparative resistance compared to a non-resistant control corn plant. In this aspect, a control corn plant will preferably be genetically similar except for the Goss' Wilt resistant allele or alleles in question. Such plants can be grown under similar conditions with equivalent or near equivalent exposure to the pathogen. In this aspect, the resistant plant or plants has less than 25%, 15%, 10%, 5%, 2% or 1% of leaf area infected.

[00136] A disease resistance QTL of the present invention may be introduced into an elite corn inbred line. An "elite line" is any line that has resulted from breeding and selection for superior agronomic performance.

[00137] A Goss' Wilt resistance QTL of the present invention may also be introduced into an elite corn plant comprising one or more transgenes conferring herbicide tolerance, increased yield, insect control, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, mycoplasma disease resistance, modified oils production, high oil production, high protein production, germination and seedling growth control, enhanced animal and human nutrition, low raffinose, environmental stress resistant, increased digestibility, industrial enzymes, pharmaceutical proteins, peptides and small molecules, improved processing traits, improved flavor, nitrogen fixation, hybrid seed production, reduced allergenicity, biopolymers, and biofuels among others. In one aspect, the herbicide tolerance is selected from the group consisting of glyphosate, dicamba, glufosinate, sulfonylurea, bromoxynil and norflurazon herbicides. These traits can be provided by methods of plant biotechnology as transgenes in corn.

[00138] A disease resistant QTL allele or alleles can be introduced from any plant that contains that allele (donor) to any recipient corn plant. In one aspect, the recipient corn plant can contain additional Goss' Wilt resistant loci. In another aspect, the recipient corn plant can contain a transgene. In another aspect, while maintaining the introduced QTL, the genetic contribution of the plant providing the disease resistant QTL can be reduced by back-crossing or other suitable approaches. In one aspect, the nuclear genetic material derived from the donor material in the corn plant can be less than or about 50%, less than or about 25%, less than or about 13%, less than or about 5%, 3%, 2% or 1%, but that genetic material contains the Goss' Wilt resistant locus or loci of interest.

[00139] It is further understood that a corn plant of the present invention may exhibit the characteristics of any relative maturity group. In an aspect, the maturity group is selected from the group consisting of RM90 – 95, RM 95 – 100, RM 100 – 105, RM 105 – 110, RM 110 – 115, and RM 115- 120.

[00140] The present invention also includes a method of introgressing an allele into a corn plant comprising: (A) crossing at least one Goss' Wilt resistant corn plant with at least one Goss' Wilt sensitive corn plant in order to form a segregating population; (B) screening the segregating population with one or more nucleic acid markers to determine if one or more corn plants from the segregating population contains a Goss' Wilt resistant allele, wherein the Goss' Wilt resistant allele is an allele selected from the group consisting of Goss' Wilt resistant locus 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61,62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 132, 124, 125, 126, 127, 128, 129, 130, and Goss' Wilt resistant locus 131.

[00141] The present invention includes isolated nucleic acid molecules. Such molecules include those nucleic acid molecules capable of detecting a polymorphism genetically or physically linked to a Goss' Wilt locus. Such molecules can be referred to as markers. Additional markers can be obtained that are linked to Goss' Wilt resistance locus 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, and Goss' Wilt resistant locus 131 by available techniques. In one aspect, the nucleic acid molecule is capable of detecting the presence or absence of a marker located less than 30, 20, 10, 5, 2, or 1 centimorgans from a Goss' Wilt resistance locus. In another aspect, a marker exhibits a LOD score of 2 or greater, 3 or greater, or 4 or greater with Goss' Wilt, measuring using Qgene Version 2.23 (1996) and default parameters. In another aspect, the nucleic acid molecule is capable of detecting a marker in a locus selected from the group Goss' Wilt resistance locus 1 through resistance locus 131. In a further aspect, a nucleic acid molecule is selected from the group consisting of SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 fragments thereof, complements thereof, and nucleic acid molecules capable of specifically hybridizing to one or more of these nucleic acid molecules.

[00142] In a preferred aspect, a nucleic acid molecule of the present invention includes those that will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500, 525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 or complements thereof or fragments of either under moderately stringent conditions, for example at about 2.0 x SSC and about 65°C. In a particularly preferred aspect, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 or complements or fragments of either under high stringency conditions. In one aspect of the present invention, a preferred marker nucleic acid molecule of the present invention has the nucleic acid sequence set forth in SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 or complements thereof or fragments of either. In another aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 80% and 100% or 90% and 100% sequence identity with the nucleic acid sequences set forth in SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158-160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 or complements thereof or fragments of either. In a further aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 95% and 100% sequence identity with the sequences set forth in SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 or complements thereof or fragments of either. In a more preferred aspect of the present invention, a preferred marker nucleic acid molecule of the present invention shares between 98% and 100% sequence identity with the nucleic acid sequence set forth in SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 or complement thereof or fragments of either.

[00143] Nucleic acid molecules or fragments thereof are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used herein, two nucleic acid molecules are capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, In: *Molecular Cloning, A Laboratory Manual, 2nd Edition*, *Cold Spring Harbor Press*, Cold Spring Harbor, New York (1989), and by Haymes *et al.*, In: *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985). Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. In order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

[00144] As used herein, a substantially homologous sequence is a nucleic acid sequence that will specifically hybridize to the complement of the nucleic acid sequence to which it is being compared under high stringency conditions. The nucleic-acid probes and primers of the present invention can hybridize under stringent conditions to a target DNA sequence. The term "stringent hybridization conditions" is defined as conditions under which a probe or primer hybridizes specifically with a target sequence(s) and not with non-target sequences, as can be determined empirically. The term "stringent conditions" is functionally defined with regard to the hybridization of a nucleic-acid probe to a target nucleic acid (i.e., to a particular nucleic-acid sequence of interest) by the specific hybridization procedure discussed in Sambrook *et al.*, 1989, at 9.52-9.55. See also, Sambrook *et al.*, 1989 at 9.47-9.52, 9.56-9.58; Kanehisa 1984 Nucl. Acids Res. 12:203-213; and Wetmur *et al.* 1968 J. Mol. Biol. 31:349-370. Appropriate stringency conditions that promote DNA hybridization are, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45° C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y., 1989, 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C.

Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

[00145] For example, hybridization using DNA or RNA probes or primers can be performed at 65°C in 6x SSC, 0.5% SDS, 5x Denhardt's, 100 μg/mL nonspecific DNA (e.g., sonicated salmon sperm DNA) with washing at 0.5x SSC, 0.5% SDS at 65°C, for high stringency.

[00146] It is contemplated that lower stringency hybridization conditions such as lower hybridization and/or washing temperatures can be used to identify related sequences having a lower degree of sequence similarity if specificity of binding of the probe or primer to target sequence(s) is preserved. Accordingly, the nucleotide sequences of the present invention can be used for their ability to selectively form duplex molecules with complementary stretches of DNA, RNA, or cDNA fragments.

[00147] A fragment of a nucleic acid molecule can be any sized fragment and illustrative fragments include fragments of nucleic acid sequences set forth in SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1303, 1332-1359 and complements thereof. In one aspect, a fragment can be between 15 and 25, 15 and 30, 15 and 40, 15 and 50, 15 and 100, 20 and 25, 20 and 30, 20 and 40, 20 and 50, 20 and 100, 25 and 30, 25 and 40, 25 and 50, 25 and 100, 30 and 40, 30 and 50, and 30 and 100. In another aspect, the fragment can be greater than 10, 15, 20, 25, 30, 35, 40, 50, 100, or 250 nucleotides.

[00148] Additional genetic markers can be used to select plants with an allele of a QTL associated with fungal disease resistance of GLS of the present invention. Examples of public marker databases include, for example: Maize Genome Database, Agricultural Research Service, United States Department of Agriculture.

Marker Technology

[00149] Genetic markers of the present invention include "dominant" or "codominant" markers. “Codominant markers” reveal the presence of two or more alleles (two per diploid individual). “Dominant markers” reveal the presence of only a single allele. The presence of the dominant marker phenotype (*e.g.*, a band of DNA) is an indication that one allele is present in either the homozygous or heterozygous condition. The absence of the dominant marker phenotype (*e.g.*, absence of a DNA band) is merely evidence that “some other” undefined allele is present. In the case of populations where individuals are predominantly homozygous and loci are predominantly dimorphic, dominant and codominant markers can be equally valuable. As populations become more heterozygous and multiallelic, codominant markers often become more informative of the genotype than dominant markers.

[00150] In another embodiment, markers, such as single sequence repeat markers (SSR), AFLP markers, RFLP markers, RAPD markers, phenotypic markers, isozyme markers, single nucleotide polymorphisms (SNPs), insertions or deletions (Indels), single feature polymorphisms (SFPs, for example, as described in Borevitz et al. 2003 Gen. Res. 13:513-523), microarray transcription profiles, DNA-derived sequences, and RNA-derived sequences that are genetically linked to or correlated with alleles of a QTL of the present invention can be utilized.

[00151] In one embodiment, nucleic acid-based analyses for the presence or absence of the genetic polymorphism can be used for the selection of seeds in a breeding population. A wide variety of genetic markers for the analysis of genetic polymorphisms are available and known to those of skill in the art. The analysis may be used to select for genes, QTL, alleles, or genomic regions (haplotypes) that comprise or are linked to a genetic marker.

[00152] Herein, nucleic acid analysis methods are known in the art and include, but are not limited to, PCR-based detection methods (for example, TaqMan assays), microarray methods, and nucleic acid sequencing methods. In one embodiment, the detection of polymorphic sites in a sample of DNA, RNA, or cDNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis, fluorescence detection methods, or other means.

[00153] A method of achieving such amplification employs the polymerase chain reaction (PCR) (Mullis *et al.* 1986 Cold Spring Harbor Symp. Quant. Biol. 51:263-273; European Patent 50,424; European Patent 84,796; European Patent 258,017; European Patent 237,362; European Patent 201,184; U.S. Patent 4,683,202; U.S. Patent 4,582,788; and U.S. Patent 4,683,194), using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

[00154] Polymorphisms in DNA sequences can be detected or typed by a variety of effective methods well known in the art including, but not limited to, those disclosed in U.S. Patents 5,468,613 and 5,217,863; 5,210,015; 5,876,930; 6,030,787; 6,004,744; 6,013,431; 5,595,890; 5,762,876; 5,945,283; 5,468,613; 6,090,558; 5,800,944; and 5,616,464, all of which are incorporated herein by reference in their entireties. However, the compositions and methods of this invention can be used in conjunction with any polymorphism typing method to type polymorphisms in corn genomic DNA samples. These corn genomic DNA samples used include but are not limited to corn genomic DNA isolated directly from a corn plant, cloned corn genomic DNA, or amplified corn genomic DNA.

[00155] For instance, polymorphisms in DNA sequences can be detected by hybridization to allele-specific oligonucleotide (ASO) probes as disclosed in U.S. Patents 5,468,613 and 5,217,863. US Patent 5,468,613 discloses allele specific oligonucleotide hybridizations where single or multiple nucleotide variations in nucleic acid sequence can be detected in nucleic acids by a process in which the sequence containing the nucleotide variation is amplified, spotted on a membrane and treated with a labeled sequence-specific oligonucleotide probe.

[00156] Target nucleic acid sequence can also be detected by probe ligation methods as disclosed in U.S. Patent 5,800,944 where sequence of interest is amplified and hybridized to probes followed by ligation to detect a labeled part of the probe.

[00157] Microarrays can also be used for polymorphism detection, wherein oligonucleotide probe sets are assembled in an overlapping fashion to represent a single sequence such that a difference in the target sequence at one point would result in partial probe hybridization (Borevitz et al., Genome Res. 13:513-523 (2003); Cui et al., Bioinformatics 21:3852-3858 (2005). On any one microarray, it is expected there will be a plurality of target sequences, which may represent genes and/or noncoding regions wherein each target sequence is represented by a series of overlapping oligonucleotides, rather than by a single probe. This platform provides for high throughput screening a plurality of polymorphisms. A single-feature polymorphism (SFP) is a polymorphism detected by a single probe in an oligonucleotide array, wherein a feature is a probe in the array. Typing of target sequences by microarray-based methods is disclosed in US Patents 6,799,122; 6,913,879; and 6,996,476.

[00158] Target nucleic acid sequence can also be detected by probe linking methods as disclosed in U.S. Patent 5,616,464 employing at least one pair of probes having sequences homologous to adjacent portions of the target nucleic acid sequence and having side chains which non-covalently bind to form a stem upon base pairing of said probes to said target nucleic acid sequence. At least one of the side chains has a photoactivatable group which can form a covalent cross-link with the other side chain member of the stem.

[00159] Other methods for detecting SNPs and Indels include single base extension (SBE) methods. Examples of SBE methods include, but are not limited, to those disclosed in U.S. Patents 6,004,744; 6,013,431; 5,595,890; 5,762,876; and 5,945,283. SBE methods are based on extension of a nucleotide primer that is immediately adjacent to a polymorphism to incorporate a detectable nucleotide residue upon extension of the primer. In certain embodiments, the SBE method uses three synthetic oligonucleotides. Two of the oligonucleotides serve as PCR primers and are complementary to sequence of the locus of corn genomic DNA which flanks a region containing the polymorphism to be assayed. Following amplification of the region of the corn genome containing the polymorphism, the PCR product is mixed with the third oligonucleotide (called an extension primer) which is designed to hybridize to the amplified DNA immediately adjacent to the polymorphism in the presence of DNA polymerase and two differentially labeled dideoxynucleosidetriphosphates. If the polymorphism is present on the template, one of the labeled dideoxynucleosidetriphosphates can be added to the primer in a single base chain extension. The allele present is then inferred by determining which of the two differential labels was added to the extension primer. Homozygous samples will result in only one of the two labeled bases being incorporated and thus only one of the two labels will be detected. Heterozygous samples have both alleles present, and will thus direct incorporation of both labels (into different molecules of the extension primer) and thus both labels will be detected.

[00160] In a preferred method for detecting polymorphisms, SNPs and Indels can be detected by methods disclosed in U.S. Patents 5,210,015; 5,876,930; and 6,030,787 in which an oligonucleotide probe having a 5’fluorescent reporter dye and a 3’quencher dye covalently linked to the 5’ and 3’ ends of the probe. When the probe is intact, the proximity of the reporter dye to the quencher dye results in the suppression of the reporter dye fluorescence, e.g. by Forster-type energy transfer. During PCR forward and reverse primers hybridize to a specific sequence of the target DNA flanking a polymorphism while the hybridization probe hybridizes to polymorphism-containing sequence within the amplified PCR product. In the subsequent PCR cycle DNA polymerase with 5’ → 3’ exonuclease activity cleaves the probe and separates the reporter dye from the quencher dye resulting in increased fluorescence of the reporter.

Marker-trait Associations

[00161] For the purpose of QTL mapping, the markers included should be diagnostic of origin in order for inferences to be made about subsequent populations. SNP markers are ideal for mapping because the likelihood that a particular SNP allele is derived from independent origins in the extant populations of a particular species is very low. As such, SNP markers are useful for tracking and assisting introgression of QTLs, particularly in the case of haplotypes.

[00162] The genetic linkage of additional marker molecules can be established by a gene mapping model such as, without limitation, the flanking marker model reported by Lander *et al.* (Lander *et al.* 1989 Genetics, 121:185-199), and the interval mapping, based on maximum likelihood methods described therein, and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL,* Whitehead Institute for Biomedical Research, Massachusetts, (1990). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY). Use of Qgene software is a particularly preferred approach.

[00163] A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an odds ratio (LOD) is then calculated as: LOD = $\log_{10}$ (MLE for the presence of a QTL/MLE given no linked QTL). The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL versus in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander *et al.* (1989), and further described by Arús and Moreno-González, *Plant Breeding*, Hayward, Bosemark, Romagosa (eds.) Chapman & Hall, London, pp. 314-331 (1993).

[00164] Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use of non-parametric methods (Kruglyak *et al.* 1995 Genetics, 139:1421-1428). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breed*, van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding,* Blackwell, Berlin, 16 (1994)). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval, and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen *et al.* (Jansen *et al.* 1994 Genetics, 136:1447-1455) and Zeng (Zeng 1994 Genetics 136:1457-1468). Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding,* van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), thereby improving the precision and efficiency of QTL mapping (Zeng 1994). These models can be extended to multi-environment experiments to analyze genotype-environment interactions (Jansen *et al.* 1995 Theor. Appl. Genet. 91:33-3).

[00165] Selection of appropriate mapping populations is important to map construction. The choice of an appropriate mapping population depends on the type of marker systems employed (Tanksley *et al.,* Molecular *mapping in plant chromosomes. chromosome structure and function: Impact of new concepts* J.P. Gustafson and R. Appels (eds.). Plenum Press, New York, pp. 157-173 (1988)). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted x exotic) and generally yield greatly reduced linkage distances. Wide crosses will usually provide segregating populations with a relatively large array of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

[00166] An F_2 population is the first generation of selfing. Usually a single F_1 plant is selfed to generate a population segregating for all the genes in Mendelian (1:2:1) fashion. Maximum genetic information is obtained from a completely classified F_2 population using a codominant marker system (Mather, Measurement of Linkage in Heredity: Methuen and Co., (1938)). In the case of dominant markers, progeny tests (e.g. F_3, BCF_2) are required to identify the heterozygotes, thus making it equivalent to a completely classified F_2 population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of F_2 individuals is often used in map construction where phenotypes do not consistently reflect genotype (*e.g.* disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations (*e.g.* F_3 or BCF_2) can be used in map construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations (F_2, F_3), where linkage groups have not been completely disassociated by recombination events (*i.e.*, maximum disequilibrium).

[00167] Recombinant inbred lines (RIL) (genetically related lines; usually $>F_5$, developed from continuously selfing F_2 lines towards homozygosity) can be used as a mapping population. Information obtained from dominant markers can be maximized by using RIL because all loci are homozygous or nearly so. Under conditions of tight linkage (*i.e.*, about <10% recombination), dominant and co-dominant markers evaluated in RIL populations provide more information per individual than either marker type in backcross populations (Reiter *et al.*1992 Proc. Natl. Acad. Sci.(USA) 89:1477-1481). However, as the distance between markers becomes larger (*i.e.*, loci become more independent), the information in RIL populations decreases dramatically.

[00168] Backcross populations (*e.g.*, generated from a cross between a successful variety (recurrent parent) and another variety (donor parent) carrying a trait not present in the former) can be utilized as a mapping population. A series of backcrosses to the recurrent parent can be made to recover most of its desirable traits. Thus a population is created consisting of individuals nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic regions from the donor parent. Backcross populations can be useful for mapping dominant markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent have contrasting polymorphic marker alleles (Reiter *et al.*1992). Information obtained from backcross populations using either codominant or dominant markers is less than that obtained from F_2 populations because one, rather than two, recombinant gametes are sampled per plant. Backcross populations, however, are more informative (at low marker saturation) when compared to RILs as the distance between linked loci increases in RIL populations (*i.e.* about .15% recombination). Increased recombination can be beneficial for resolution of tight linkages, but may be undesirable in the construction of maps with low marker saturation.

[00169] Near-isogenic lines (NIL) created by many backcrosses to produce an array of individuals that are nearly identical in genetic composition except for the trait or genomic region under interrogation can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci are expected to map to a selected region.

[00170] Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore *et al.* 1991 Proc. Natl. Acad. Sci. (U.S.A.) 88:9828-9832). In BSA, two bulked DNA samples are drawn from a segregating population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but arbitrary at unlinked regions (*i.e.* heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

Marker-assisted Breeding

[00171] Further, the present invention contemplates that preferred haploid plants comprising at least one genotype of interest are identified using the methods disclosed in US Patent Application Serial No. 60/837,864, which is incorporated herein by reference in its entirety, wherein a genotype of interest may correspond to a QTL or haplotype and is associated with at least one phenotype of interest. The methods include association of at least one haplotype with at least one phenotype, wherein the association is represented by a numerical value and the numerical value is used in the decision-making of a breeding program. Non-limiting examples of numerical values include haplotype effect estimates, haplotype frequencies, and breeding values. In the present invention, it is particularly useful to identify haploid plants of interest based on at least one genotype, such that only those lines undergo doubling, which saves resources. Resulting doubled haploid plants comprising at least one genotype of interest are then advanced in a breeding program for use in activities related to germplasm improvement.

[00172] In the present invention, haplotypes are defined on the basis of one or more polymorphic markers within a given haplotype window, with haplotype windows being distributed throughout the crop's genome. In another aspect, *de novo* and/or historical marker-phenotype association data are leveraged to infer haplotype effect estimates for one or more phenotypes for one or more of the haplotypes for a crop. Haplotype effect estimates enable one skilled in the art to make breeding decisions by comparing haplotype effect estimates for two or more haplotypes. Polymorphic markers, and respective map positions, of the present invention are provided in US Patent Applications 2005/0204780, 2005/0216545, 2005/0218305, and serial no. 11/504,538, which are incorporated herein by reference in their entirety.

[00173] In yet another aspect, haplotype effect estimates are coupled with haplotype frequency values to calculate a haplotype breeding value of a specific haplotype relative to other haplotypes at the same haplotype window, or across haplotype windows, for one or more phenotypic traits. In other words, the change in population mean by fixing the haplotype is determined. In still another aspect, in the context of evaluating the effect of substituting a specific region in the genome, either by introgression or a transgenic event, haplotype breeding values are used as a basis in comparing haplotypes for substitution effects. Further, in hybrid crops, the breeding value of haplotypes is calculated in the context of at least one haplotype in a tester used to produce a hybrid. Once the value of haplotypes at a given haplotype window are determined and high density fingerprinting information is available on specific varieties or lines, selection can be applied to these genomic regions using at least one marker in the at least one haplotype.

[00174] In the present invention, selection can be applied at one or more stages of a breeding program:

a) Among genetically distinct populations, herein defined as "breeding populations," as a pre-selection method to increase the selection index and drive the frequency of favorable haplotypes among breeding populations, wherein pre-selection is defined as selection among populations based on at least one haplotype for use as parents in breeding crosses, and leveraging of marker-trait association identified in previous breeding crosses.

b) Among segregating progeny from a breeding population, to increase the frequency of the favorable haplotypes for the purpose of line or variety development.

c) Among segregating progeny from a breeding population, to increase the frequency of the favorable haplotypes prior to QTL mapping within this breeding population.

d) For hybrid crops, among parental lines from different heterotic groups to predict the performance potential of different hybrids.

[00175] In the present invention, it is contemplated that methods of determine associations between genotype and phenotype in haploid plants can be performed based on haplotypes, versus markers alone (Fan et al. 2006 Genetics). A haplotype is a segment of DNA in the genome of an organism that is assumed to be identical by descent for different individuals when the knowledge of identity by state at one or more loci is the same in the different individuals, and that the regional amount of linkage disequilibrium in the vicinity of that segment on the physical or genetic map is high. A haplotype can be tracked through populations and its statistical association with a given trait can be analyzed. By searching the target space for a QTL association across multiple QTL mapping populations that have parental lines with genomic regions that are identical by descent, the effective population size associated with QTL mapping is increased. The increased sample size results in more recombinant progeny which increases the precision of estimating the QTL position.

[00176] Thus, a haplotype association study allows one to define the frequency and the type of the ancestral carrier haplotype. An "association study" is a genetic experiment where one tests the level of departure from randomness between the segregation of alleles at one or more marker loci and the value of individual phenotype for one or more traits. Association studies can be done on quantitative or categorical traits, accounting or not for population structure and/or stratification. In the present invention, associations between haplotypes and phenotypes for the determination of “haplotype effect estimates” can be conducted *de novo*, using mapping populations for the evaluation of one or more phenotypes, or using historical genotype and phenotype data.

[00177] A haplotype analysis is important in that it increases the statistical power of an analysis involving individual biallelic markers. In a first stage of a haplotype frequency analysis, the frequency of the possible haplotypes based on various combinations of the identified biallelic markers of the invention is determined. The haplotype frequency is then compared for distinct populations and a reference population. In general, any method known in the art to test whether a trait and a genotype show a statistically significant correlation may be used.

[00178] Methods for determining the statistical significance of a correlation between a phenotype and a genotype, in this case a haplotype, may be determined by any statistical test known in the art and with any accepted threshold of statistical significance being required. The application of particular methods and thresholds of significance are well within the skill of the ordinary practitioner of the art.

[00179] To estimate the frequency of a haplotype, the base reference germplasm has to be defined (collection of elite inbred lines, population of random mating individuals, etc.) and a representative sample (or the entire population) has to be genotyped. For example, in one aspect, haplotype frequency is determined by simple counting if considering a set of inbred individuals. In another aspect, estimation methods that employ computing techniques like the Expectation/Maximization (EM) algorithm are required if individuals genotyped are heterozygous at more than one locus in the segment and linkage phase is unknown (Excoffier et al. 1995 Mol. Biol. Evol. 12: 921-927; Li et al. 2002 Biostatistics). Preferably, a method based on the EM algorithm (Dempster et al. 1977 J. R. Stat. Soc. Ser. B 39:1-38) leading to maximum-likelihood estimates of haplotype frequencies under the assumption of Hardy-Weinberg proportions (random mating) is used (Excoffier et al. 1995 Mol. Biol. Evol. 12: 921-927). Alternative approaches are known in the art that for association studies: genome-wide association studies, candidate region association studies and candidate gene association studies (Li et al. 2006 BMC Bioinformatics 7:258). The polymorphic markers of the present invention may be incorporated in any map of genetic markers of a plant genome in order to perform genome-wide association studies.

[00180] The present invention comprises methods to detect an association between at least one haplotype in a haploid crop plant and a preferred trait, including a transgene, or a multiple trait index and calculate a haplotype effect estimate based on this association. In one aspect, the calculated haplotype effect estimates are used to make decisions in a breeding program. In another aspect, the calculated haplotype effect estimates are used in conjunction with the frequency of the at least one haplotype to calculate a haplotype breeding value that will be used to make decisions in a breeding program. A multiple trait index (MTI) is a numerical entity that is calculated through the combination of single trait values in a formula. Most often calculated as a linear combination of traits or normalized derivations of traits, it can also be the result of more sophisticated calculations (for example, use of ratios between traits). This MTI is used in genetic analysis as if it were a trait.

[00181] Any given chromosome segment can be represented in a given population by a number of haplotypes that can vary from 1 (region is fixed), to the size of the population times the ploidy level of that species (2 in a diploid species), in a population in which every chromosome has a different haplotype. Identity-by-descent among haplotype carried by multiple individuals in a non-fixed population will result in an intermediate number of haplotype and possibly a differing frequency among the different haplotypes. New haplotypes may arise through recombination at meiosis between existing haplotypes in heterozygous progenitors. The frequency of each haplotype may be estimated by several means known to one versed in the art (e.g. by direct counting, or by using an EM algorithm). Let us assume that "k" different haplotypes, identified as "h_i" (i=1,...,k), are known, that their frequency in the population is "f_i" (i=1,…,k), and for each of these haplotypes we have an effect estimate "Est_i" (i=1,…,k). If we call the " haplotype breeding value" (BV_i) the effect on that population of fixing that haplotype, then this breeding value corresponds to the change in mean for the trait(s) of interest of that population between its original state of haplotype distribution at the window and a final state at which haplotype "h_i" encounters itself at a frequency of 100%.

[00182] The haplotype breeding value of h_i in this population is calculated as:

$$BV_i = Est_i - \sum_{i=1}^{k} Est_i f_i$$

[00183] One skilled in the art will recognize that haplotypes that are rare in the population in which effects are estimated tend to be less precisely estimated, this difference of confidence may lead to adjustment in the calculation. For example one can ignore the effects of rare haplotypes, by calculating breeding value of better known haplotype after adjusting the frequency of these (by dividing it by the sum of frequency of the better known haplotypes). One could also provide confidence intervals for the breeding value of each haplotypes.

[00184] The present invention anticipates that any particular haplotype breeding value will change according to the population for which it is calculated, as a function of difference of haplotype frequencies. The term "population" will thus assume different meanings, below are two examples of special cases. In one aspect, a population is a single inbred in which one intends to replace its current haplotype h_j by a new haplotype h_i, in this case $BV_i=Est_i-Est_j$. In another aspect, a "population" is a F2 population in which the two parental haplotype h_i and h_j are originally present in equal frequency (50%), in which case $BV_i= ½ (Est_i-Est_j)$.

[00185] These statistical approaches enable haplotype effect estimates to inform breeding decisions in multiple contexts. Other statistical approaches to calculate breeding values are known to those skilled in the art and can be used in substitution without departing from the spirit and scope of this invention.

[00186] In cases where conserved genetic segments, or haplotype windows, are coincident with segments in which QTL have been identified it is possible to deduce with high probability that QTL inferences can be extrapolated to other germplasm having an identical haplotype in that haplotype window. This *a priori* information provides the basis to select for favorable QTLs prior to QTL mapping within a given population.

[00187] For example, plant breeding decisions could comprise:

a) Selection among haploid breeding populations to determine which populations have the highest frequency of favorable haplotypes, wherein haplotypes are designated as favorable based on coincidence with previous QTL mapping and preferred populations undergo doubling; or

b) Selection of haploid progeny containing the favorable haplotypes in breeding populations prior to, or in substitution for, QTL mapping within that population, wherein selection could be done at any stage of breeding and at any generation of a selection and can be followed by doubling; or

c) Prediction of progeny performance for specific breeding crosses; or

d) Selection of haploid plants for doubling for subsequent use in germplasm improvement activities based on the favorable haplotypes, including line development, hybrid development, selection among transgenic events based on the breeding value of the haplotype that the transgene was inserted into, making breeding crosses, testing and advancing a plant through self fertilization, using plant or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plant or parts thereof for mutagenesis.

[00188] In cases where haplotype windows are coincident with segments in which genes have been identified it is possible to deduce with high probability that gene inferences can be extrapolated to other germplasm having an identical genotype, or haplotype, in that haplotype window. This *a priori* information provides the basis to select for favorable genes or gene alleles on the basis of haplotype identification within a given population. For example, plant breeding decisions could comprise:

a) Selection among haploid breeding populations to determine which populations have the highest frequency of favorable haplotypes, wherein haplotypes are designated as favorable based on coincidence with previous gene mapping and preferred populations undergo doubling; or

b) Selection of haploid progeny containing the favorable haplotypes in breeding populations, wherein selection is effectively enabled at the gene level, wherein selection could be done at any stage of breeding and at any generation of a selection and can be followed by doubling; or

c) Prediction of progeny performance for specific breeding crosses; or

d) Selection of haploid plants for doubling for subsequent use in germplasm improvement activities based on the favorable haplotypes, including line development, hybrid development, selection among transgenic events based on the breeding value of the haplotype that the transgene was inserted into, making breeding crosses, testing and advancing a plant through self fertilization, using plant or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plant or parts thereof for mutagenesis.

[00189] A preferred haplotype provides a preferred property to a parent plant and to the progeny of the parent when selected by a marker means or phenotypic means. The method of the present invention provides for selection of preferred haplotypes, or haplotypes of interest, and the accumulation of these haplotypes in a breeding population.

[00190] In the present invention, haplotypes and associations of haplotypes to one or more phenotypic traits provide the basis for making breeding decisions and germplasm improvement activities. Non-limiting examples of breeding decisions include progeny selection, parent selection, and recurrent selection for at least one haplotype. In another aspect, breeding decisions relating to development of plants for commercial release comprise advancing plants for testing, advancing plants for purity, purification of sublines during development, inbred development, variety development, and hybrid development. In yet other aspects, breeding decisions and germplasm improvement activities comprise transgenic event selection, making breeding crosses, testing and advancing a plant through self-fertilization, using plants or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plants or parts thereof for mutagenesis.

[00191] In another embodiment, this invention enables indirect selection through selection decisions for at least one phenotype based on at least one numerical value that is correlated, either positively or negatively, with one or more other phenotypic traits. For example, a selection decision for any given haplotype effectively results in selection for multiple phenotypic traits that are associated with the haplotype.

[00192] In still another embodiment, the present invention acknowledges that preferred haplotypes identified by the methods presented herein may be advanced as candidate genes for inclusion in expression constructs, i.e., transgenes. Nucleic acids underlying haplotypes of interest may be expressed in plant cells by operably linking them to a promoter functional in plants. In another aspect, nucleic acids underlying haplotypes of interest may have their expression modified by double-stranded RNA-mediated gene suppression, also known as RNA interference ("RNAi"), which includes suppression mediated by small interfering RNAs ("siRNA"), trans-acting small interfering RNAs ("ta-siRNA"), or microRNAs ("miRNA"). Examples of RNAi methodology suitable for use in plants are described in detail in U. S. patent application publications 2006/0200878 and 2007/0011775.

[00193] Methods are known in the art for assembling and introducing constructs into a cell in such a manner that the nucleic acid molecule for a trait is transcribed into a functional mRNA molecule that is translated and expressed as a protein product. For the practice of the present invention, conventional compositions and methods for preparing and using constructs and host cells are well known to one skilled in the art, see for example, Molecular Cloning: A Laboratory Manual, 3rd edition Volumes 1, 2, and 3 (2000) J.F. Sambrook, D.W. Russell, and N. Irwin, Cold Spring Harbor Laboratory Press. Methods for making transformation constructs particularly suited to plant transformation include, without limitation, those described in U.S. Patent Nos. 4,971,908, 4,940,835, 4,769,061 and 4,757,011, all of which are herein incorporated by reference in their entirety. Transformation methods for the introduction of expression units into plants are known in the art and include electroporation as illustrated in U.S. Patent No. 5,384,253; microprojectile bombardment as illustrated in U.S. Patent Nos. 5,015,580; 5,550,318; 5,538,880; 6,160,208; 6,399,861; and 6,403,865; protoplast transformation as illustrated in U.S. Patent No. 5,508,184; and *Agrobacterium*-mediated transformation as illustrated in U.S. Patent Nos. 5,635,055; 5,824,877; 5,591,616; 5,981,840; and 6,384,301.

[00194] Another preferred embodiment of the present invention is to build additional value by selecting a composition of haplotypes wherein each haplotype has a haplotype effect estimate that is not negative with respect to yield, or is not positive with respect to maturity, or is null with respect to maturity, or amongst the best 50 percent with respect to a phenotypic trait, transgene, and/or a multiple trait index when compared to any other haplotype at the same chromosome segment in a set of germplasm, or amongst the best 50 percent with respect to a phenotypic trait, transgene, and/or a multiple trait index when compared to any other haplotype across the entire genome in a set of germplasm, or the haplotype being present with a frequency of 75 percent or more in a breeding population or a set of germplasm provides evidence of its high value, or any combination of these.

[00195] This invention anticipates a stacking of haplotypes from multiple windows into plants or lines by crossing parent plants or lines containing different haplotype regions. The value of the plant or line comprising in its genome stacked haplotype regions is estimated by a composite breeding value, which depends on a combination of the value of the traits and the value of the haplotype(s) to which the traits are linked. The present invention further anticipates that the composite breeding value of a plant or line is improved by modifying the components of one or each of the haplotypes. Additionally, the present invention anticipates that additional value can be built into the composite breeding value of a plant or line by selection of at least one recipient haplotype with a preferred haplotype effect estimate or, in conjunction with the haplotype frequency, breeding value to which one or any of the other haplotypes are linked, or by selection of plants or lines for stacking haplotypes by breeding.

[00196] Another embodiment of this invention is a method for enhancing breeding populations by accumulation of one or more preferred haplotypes in a set of germplasm. Genomic regions defined as haplotype windows include genetic information that contribute to one or more phenotypic traits of the plant. Variations in the genetic information at one or more loci can result in variation of one or more phenotypic traits, wherein the value of the phenotype can be measured. The genetic mapping of the haplotype windows allows for a determination of linkage across haplotypes. A haplotype of interest has a DNA sequence that is novel in the genome of the progeny plant and can in itself serve as a genetic marker for the haplotype of interest. Notably, this marker can also be used as an identifier for a gene or QTL. For example, in the event of multiple traits or trait effects associated with the haplotype, only one marker would be necessary for selection purposes. Additionally, the haplotype of interest may provide a means to select for plants that have the linked haplotype region. Selection can be performed by screening for tolerance to an applied phytotoxic chemical, such as an herbicide or antibiotic, or to pathogen resistance. Selection may be performed using phenotypic selection means, such as, a morphological phenotype that is easy to observe such as seed color, seed germination characteristic, seedling growth characteristic, leaf appearance, plant architecture, plant height, and flower and fruit morphology.

[00197] The present invention also provides for the screening of progeny haploid plants for haplotypes of interest and using haplotype effect estimates as the basis for selection for use in a breeding program to enhance the accumulation of preferred haplotypes. The method includes: a) providing a breeding population comprising at least two haploid plants wherein the genome of the breeding population comprises a plurality of haplotype windows and each of the plurality of haplotype windows comprises at least one haplotype; and b) associating a haplotype effect estimate for one or more traits for two or more haplotypes from one or more of the plurality of haplotype windows, wherein the haplotype effect estimate can then be used to calculate a breeding value that is a function of the estimated effect for any given phenotypic trait and the frequency of each of the at least two haplotypes; and c) ranking one or more of the haplotypes on the basis of a value, wherein the value is a haplotype effect estimate, a haplotype frequency, or a breeding value and wherein the value is the basis for determining whether a haplotype is a preferred haplotype, or haplotype of interest; and d) utilizing the ranking as the basis for decision-making in a breeding program; and e) at least one progeny haploid plant is selected for doubling on the basis of the presence of the respective markers associated with the haplotypes of interest, wherein the progeny haploid plant comprises in its genome at least a portion of the haplotype or haplotypes of interest of the first plant and at least one preferred haplotype of the second plant; and f) using resulting doubled haploid plants in activities related to germplasm improvement wherein the activities are selected from the group consisting of line and variety development, hybrid development, transgenic event selection, making breeding crosses, testing and advancing a plant through self fertilization, using plant or parts thereof for transformation, using plants or parts thereof for candidates for expression constructs, and using plant or parts thereof for mutagenesis.

[00198] Using this method, the present invention contemplates that haplotypes of interest are selected from a large population of plants, and the selected haplotypes can have a synergistic breeding value in the germplasm of a crop plant. Additionally, this invention provides for using the selected haplotypes in the described breeding methods to accumulate other beneficial and preferred haplotype regions and to be maintained in a breeding population to enhance the overall germplasm of the crop plant.

Plant Breeding

[00199] Plants of the present invention can be part of or generated from a breeding program. The choice of breeding method depends on the mode of plant reproduction, the heritability of the trait(s) being improved, and the type of cultivar used commercially (*e.g.*, F_1 hybrid cultivar, pureline cultivar, etc). A cultivar is a race or variety of a plant species that has been created or selected intentionally and maintained through cultivation.

[00200] Selected, non-limiting approaches for breeding the plants of the present invention are set forth below. A breeding program can be enhanced using marker assisted selection (MAS) on the progeny of any cross. It is understood that nucleic acid markers of the present invention can be used in a MAS (breeding) program. It is further understood that any commercial and non-commercial cultivars can be utilized in a breeding program. Factors such as, for example, emergence vigor, vegetative vigor, stress tolerance, disease resistance, branching, flowering, seed set, seed size, seed density, standability, and threshability etc. will generally dictate the choice.

[00201] Genotyping can be further economized by high throughput, non-destructive seed sampling. In one embodiment, plants can be screened for one or more markers, such as genetic markers, using high throughput, non-destructive seed sampling. In a preferred aspect, haploid seed is sampled in this manner and only seed with at least one marker genotype of interest is advanced for doubling. Apparatus and methods for the high-throughput, non-destructive sampling of seeds have been described which would overcome the obstacles of statistical samples by allowing for individual seed analysis. For example, U.S. Patent Application Serial No. 11/213,430 (filed August 26, 2005); U.S. Patent Application Serial No. 11/213,431 (filed August 26, 2005); U.S. Patent Application Serial No. 11/213,432 (filed August 26, 2005); U.S. Patent Application Serial No. 11/213,434 (filed August 26, 2005); and U.S. Patent Application Serial No. 11/213,435 (filed August 26, 2005), U.S. Patent Application Serial No. 11/680,611 (filed March 2, 2007), which are incorporated herein by reference in their entirety, disclose apparatus and systems for the automated sampling of seeds as well as methods of sampling, testing and bulking seeds.

[00202] For highly heritable traits, a choice of superior individual plants evaluated at a single location will be effective, whereas for traits with low heritability, selection should be based on mean values obtained from replicated evaluations of families of related plants. Popular selection methods commonly include pedigree selection, modified pedigree selection, mass selection, and recurrent selection. In a preferred aspect, a backcross or recurrent breeding program is undertaken.

[00203] The complexity of inheritance influences choice of the breeding method. Backcross breeding can be used to transfer one or a few favorable genes for a highly heritable trait into a desirable cultivar. This approach has been used extensively for breeding disease-resistant cultivars. Various recurrent selection techniques are used to improve quantitatively inherited traits controlled by numerous genes.

[00204] Breeding lines can be tested and compared to appropriate standards in environments representative of the commercial target area(s) for two or more generations. The best lines are candidates for new commercial cultivars; those still deficient in traits may be used as parents to produce new populations for further selection.

[00205] The development of new elite corn hybrids requires the development and selection of elite inbred lines, the crossing of these lines and selection of superior hybrid crosses. The hybrid seed can be produced by manual crosses between selected male-fertile parents or by using male sterility systems. Additional data on parental lines, as well as the phenotype of the hybrid, influence the breeder's decision whether to continue with the specific hybrid cross.

[00206] Pedigree breeding and recurrent selection breeding methods can be used to develop cultivars from breeding populations. Breeding programs combine desirable traits from two or more cultivars or various broad-based sources into breeding pools from which cultivars are developed by selfing and selection of desired phenotypes. New cultivars can be evaluated to determine which have commercial potential.

[00207] Backcross breeding has been used to transfer genes for a simply inherited, highly heritable trait into a desirable homozygous cultivar or inbred line, which is the recurrent parent. The source of the trait to be transferred is called the donor parent. After the initial cross, individuals possessing the phenotype of the donor parent are selected and repeatedly crossed (backcrossed) to the recurrent parent. The resulting plant is expected to have most attributes of the recurrent parent (*e.g.*, cultivar) and, in addition, the desirable trait transferred from the donor parent.

[00208] The single-seed descent procedure in the strict sense refers to planting a segregating population, harvesting a sample of one seed per plant, and using the one-seed sample to plant the next generation. When the population has been advanced from the F_2 to the desired level of inbreeding, the plants from which lines are derived will each trace to different F_2 individuals. The number of plants in a population declines each generation due to failure of some seeds to germinate or some plants to produce at least one seed. As a result, not all of the F_2 plants originally sampled in the population will be represented by a progeny when generation advance is completed.

[00209] Descriptions of other breeding methods that are commonly used for different traits and crops can be found in one of several reference books (Allard, "Principles of Plant Breeding," John Wiley & Sons, NY, U. of CA, Davis, CA, 50-98, 1960; Simmonds, "Principles of crop improvement," Longman, Inc., NY, 369-399, 1979; Sneep and Hendriksen, "Plant breeding perspectives," Wageningen (ed), Center for Agricultural Publishing and Documentation, 1979; Fehr, *In: Soybeans: Improvement, Production and Uses*, 2nd Edition, *Manograph.,* 16:249, 1987; Fehr, "Principles of variety development," *Theory and Technique,* (Vol. 1) and *Crop Species Soybean* (Vol. 2), Iowa State Univ., Macmillan Pub. Co., NY, 360-376, 1987).

[00210] An alternative to traditional QTL mapping involves achieving higher resolution by mapping haplotypes, versus individual markers (Fan *et al.* 2006 Genetics 172:663-686). This approach tracks blocks of DNA known as haplotypes, as defined by polymorphic markers, which are assumed to be identical by descent in the mapping population. This assumption results in a larger effective sample size, offering greater resolution of QTL. Methods for determining the statistical significance of a correlation between a phenotype and a genotype, in this case a haplotype, may be determined by any statistical test known in the art and with any accepted threshold of statistical significance being required. The application of particular methods and thresholds of significance are well with in the skill of the ordinary practitioner of the art.

[00211] It is further understood, that the present invention provides bacterial, viral, microbial, insect, mammalian and plant cells comprising the nucleic acid molecules of the present invention.

[00212] As used herein, a "nucleic acid molecule," be it a naturally occurring molecule or otherwise may be "substantially purified", if desired, referring to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

[00213] The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

[00214] The agents of the present invention may also be recombinant. As used herein, the term recombinant means any agent (*e.g.* DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

[00215] The agents of the present invention may be labeled with reagents that facilitate detection of the agent (*e.g.* fluorescent labels (Prober *et al.* 1987 Science 238:336-340; Albarella *et al.*, European Patent 144914), chemical labels (Sheldon *et al.*, U.S. Patent 4,582,789; Albarella *et al.*, U.S. Patent 4,563,417), modified bases (Miyoshi *et al.*, European Patent 119448).

[00216] Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Examples

Example 1: Phenotyping for GLS Reaction

[00217] In order to detect QTL associated with GLS resistance, plants were phenotyped to determine GLS reaction. The following rating scale was used for phenotypic rating for GLS was used in all studies. The percentage of leaf area infected is used to rate plants on a scale of 1 (very resistant) to 9 (susceptible). Disease resistance is evaluated visually after pollination. The infection can be natural or by artificial inoculation in the experiments.

[00218] Table 1. Description of rating scale used for GLS phenotyping. ILA= infected leaf area.

Description	Rating	Symptoms
Very Resistant	1	0% of leaf area infected; no visible lesions
Very Resistant	2	ILA< 1%; few lesions, dispersed through lower leaves
Resistant	3	1% ≤ ILA≤ 20%
Resistant	4	20% ≤ ILA≤ 40%
Mid-resistant	5	40% ≤ ILA≤ 50%; lesions reaching ear leaf, with spare lesions in the leaves above the ear
Mid-Susceptible	6	50% ≤ ILA≤ 60%; lesions reaching the leaves above the ear
Susceptible	7	60% ≤ ILA≤ 75%
Susceptible	8	75% ≤ ILA≤ 90%
Susceptible	9	> 90% of foliar area infected, with premature death of the plant before forming black layer

Example 2: GLS Resistance Mapping Study 1

[00219] To examine associations between SNP markers and GLS resistance in corn, analyzed data from a number of studies was combined. An association study was conducted to evaluate whether significant associations between one or more marker genotypes and GLS resistance are present in one or more breeding crosses. The mapping study combined data from 176 mapping populations. The number of individuals in each population ranged from 95 to 276. Segregating populations were of the following generations F2, BC1F2, BC1, and DH. The number of SNP markers used for genotyping ranged from 55 to 158. Individuals were phenotyped for traits, including GLS resistance. A total of 2499 associations between SNP markers and GLS resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. The SNP markers provided can be used to monitor the introgression of GLS resistance into a breeding population. SNP markers associated with GLS resistance, level of significance, and favorable alleles are reported in Figure 1.

Example 3: GLS Resistance Mapping Study 2

[00220] An association study was conducted to evaluate whether significant associations between one or more marker genotypes and GLS resistance are present in one or more breeding crosses. In the association study, 769 F2s from the CV128/CV162 population were screened with 117 markers. A total of 53 associations between SNP markers and GLS resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, and 8. The SNP markers provided can be used to monitor the introgression of GLS resistance into a breeding population. SNP markers associated with GLS resistance, level of significance, and favorable alleles are reported in Figure 1.

Example 4: GLS Resistance Mapping Study 3

[00221] An association study was conducted to evaluate whether significant associations between one or marker genotypes and GLS resistance are present in one or more populations. In the association study, 1177 inbred corn lines were screened with 1051 SNP markers. A total of 92 significant associations between SNP markers and GLS resistance were identified on Chromosomes 5, 6, 7, 8, 9, and 10. The SNP markers provided can be used to monitor the introgression of GLS resistance into a breeding population. SNP markers associated with GLS resistance, level of significance, and favorable alleles are reported in Figure 1.

Example 5: GLS Resistance Mapping Study 4

[00222] An association study was conducted to evaluate whether significant associations between one or marker genotypes and GLS resistance are present in one or more populations. In this association study, 1036 DH lines from 398 F1 families were screened with 2136 SNP markers. A total of 205 significant associations between SNP markers and GLS resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 8, and 10. The SNP markers provided can be used to monitor the introgression of GLS resistance into a breeding population. SNP markers associated with GLS resistance, level of significance, and favorable alleles are reported in Figure 1.

Example 6: GLS Resistance Mapping Study 5

[00223] An association study was conducted to evaluate whether significant associations between one or more marker genotypes and GLS resistance are present in one or more populations. In this association study, 495 Single seed descent (SSD) lines from 495 F1 families were screened with 1958 SNP markers. A total of 309 significant associations between SNP markers and GLS resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. The SNP markers provided can be used to monitor the introgression of GLS resistance into a breeding population. SNP markers associated with GLS resistance, level of significance, and favorable alleles are reported in Figure 1.

[00224] From the association studies of Examples 2 through 6, 1227 SNP markers were found to be associated with GLS. QTL were assigned by dividing maize chromosomal regions into 10 cM windows. A total of 176 QTL were identified by associating SNP markers with GLS resistance. The favorable alleles used for selecting for GLS resistance are also provided in Figure 1. Selection for GLS resistance is based on the genotype of GLS resistant parent.

Example 7: Exemplary marker assays for detecting GLS resistance

[00225] In one embodiment, the detection of polymorphic sites in a sample of DNA, RNA, or cDNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis, fluorescence detection methods, or other means. Exemplary primers and probes for amplifying and detecting genomic regions associated with GLS resistance are given in Table 2.

[00226] Table 2. Exemplary assays for detecting GLS resistance.

Marker	Marker SEQ ID	SNP Position	SEQ ID Forward Primer	SEQ ID Reverse Primer	SEQ ID Probe 1	SEQ ID Probe 2
NC0199588	1219	137	1304	1305	1306	1307
NC0055894	421	202	1308	1309	1310	1311
NC0028145	481	307	1312	1313	1314	1315
NC0003425	1127	280	1316	1317	1318	1319

Example 8: Oligonucleotide hybridization probes useful for detecting corn plants with GLS resistance loci.

Oligonucleotides can also be used to detect or type the polymorphisms associated with GLS resistance disclosed herein by hybridization-based SNP detection methods. Oligonucleotides capable of hybridizing to isolated nucleic acid sequences which include the polymorphism are provided. It is within the skill of the art to design assays with experimentally determined stringency to discriminate between the allelic state of the polymorphisms presented herein. Exemplary assays include Southern blots, Northern blots, microarrays, *in situ* hybridization, and other methods of polymorphism detection based on hybridization. Exemplary oligonucleotides for use in hybridization-based SNP detection are provided in Table 3. These oligonucleotides can be detectably labeled with radioactive labels, fluorophores, or other chemiluminescent means to facilitate detection of hybridization to samples of genomic or amplified nucleic acids derived from one or more corn plants using methods known in the art.

[00227] Table 3. Exemplary Oligonucleotide Hybridization Probes*.

Marker	SEQ ID Marker	SNP Position	Hybridization Probe	SEQ ID Probe
NC0199588	1219	137	CAGCGCAG**G**GCTAGCT	1320
NC0199588	1219	137	CAGCGCAG**A**GCTAGCT	1321
NC0055894	421	202	CCCAGTCG**C**AGTCCTA	1322
NC0055894	421	202	CCCAGTCG**T**AGTCCTA	1323
NC0028145	481	307	ACAGCAAC**A**AACCCAA	1324
NC0028145	481	307	ACAGCAAC**G**AACCCAA	1325
NC0003425	1127	280	ATGTGCCT**G**GTACCAG	1326
NC0003425	1127	280	ATGTGCCT**C**GTACCAG	1327

* SNP nucleotides in bold and underlined.

Example 9: Oligonucleotide probes useful for detecting corn plants with GLS resistance loci by single base extension methods

[00228] Oligonucleotides can also be used to detect or type the polymorphisms associated with GLS resistance disclosed herein by single base extension (SBE)-based SNP detection methods. Exemplary oligonucleotides for use in SBE-based SNP detection are provided in Table 4. SBE methods are based on extension of a nucleotide primer that is hybridized to sequences immediately adjacent to a polymorphism to incorporate a detectable nucleotide residue upon extension of the primer. It is also anticipated that the SBE method can use three synthetic oligonucleotides. Two of the oligonucleotides serve as PCR primers and are complementary to the sequence of the locus which flanks a region containing the polymorphism to be assayed. Exemplary PCR primers that can be used to type certain polymorphisms disclosed in this invention are provided in Table 3 in the columns labeled “Forward Primer SEQ ID” and “Reverse Primer SEQ ID”. Following amplification of the region containing the polymorphism, the PCR product is hybridized with an extension primer which anneals to the amplified DNA immediately adjacent to the polymorphism. DNA polymerase and two differentially labeled dideoxynucleoside triphosphates are then provided. If the polymorphism is present on the template, one of the labeled dideoxynucleoside triphosphates can be added to the primer in a single base chain extension. The allele present is then inferred by determining which of the two differential labels was added to the extension primer. Homozygous samples will result in only one of the two labeled bases being incorporated and thus only one of the two labels will be detected. Heterozygous samples have both alleles present, and will thus direct incorporation of both labels (into different molecules of the extension primer) and thus both labels will be detected.

[00229] **Table 4. Probes (extension primers) for Single Base Extension (SBE) assays.**

Marker	Marker SEQ ID	SNP Position	Probe (SBE)	Probe SEQ ID
NC0199588	1219	137	ATCGACGATCAGCGCAG	1328
NC0055894	421	202	GACACGGTTCCCAGTCG	1329
NC0028145	481	307	TACATATGCACAGCAAC	1330
NC0003425	1127	280	ACATGTGACATGTGCCT	1331

Example 10: Fine Mapping for GLS resistance

[00230] Three populations were developed for associating marker genotypes and GLS resistance. GLS resistant donor lines CV174 and CV173 were each backcrossed three times to I294213 to create backcross mapping populations. An additional population was developed using CV171 as the resistant source. CV171 was backcrossed two times to I294213 and selfed one generation for fine mapping. Composite interval mapping was conducted with WINQTL cartographer. SNP markers associated with GLS resistance are provided in Table 5.

[00231] **Table 5. SNP markers associated with GLS resistance.**

QTL	Marker	Chr	pos	LOD	Effect	Fav Parent	Favorable Allele	SNP Position	SEQ ID
116	NC0009667	6	139.1	6.966013	0.738745	CV171	G	226	883
83	NC0053636	6	136	6.896417	0.749228	CV171	A	202	882
117	NC0032368	6	144.3	6.226523	0.709636	CV171	G	801	1360
116	NC0002782	6	133.5	6.194592	0.858607	CV171	C	121	881
38	NC0108013	2	115.3	5.835505	0.734241	CV171	C	340	306
37	NC0151288	2	107.6	5.69125	0.868826	CV171	A	1001	303
115	NC0003201	6	127.9	3.889942	0.780583	CV171	G	74	875
38	NC0035094	2	116.9	6.76	0.666924	CV174	G	173	310
77	NC0002474	4	93.6	6.02	0.674649	CV173	C	383	571
170	NC0040011	10	54.2	2	0.503823	CV173	A	598	1361
65	NC0009079	3	194.2	1.82	0.443853	CV173	C	118	484
82	NC0038447	4	141.8	1.79	0.651293	CV173	A	526	618
89	NC0105613	5	16.6	1.59	0.375097	CV173	G	178	667
29	NC0107911	2	99.2	1.51	0.396756	CV173	T	384	289
7	NC0009159	1	66	1.49	0.423507	CV173	A	360	56
128	NC0015161	7	106.4	0.64	0.253679	CV173	G	428	962
156	NC0055759	9	62.1	0.54	0.287342	CV173	G	149	1100
148	NC0008757	8	156.3	0.16	0.312206	CV173	C	274	1075

Example 11: Phenotyping for Goss' Wilt

[00232] In order to detect QTL associated with resistance to Goss' Wilt, plants were phenotyped to determine Goss' Wilt reaction. The following rating scale was used in order to assess resistance or susceptibility to Goss' Wilt. Phenotypic evaluations of Goss' Wilt reaction is based on percentage of infected leaf area and rated according to a 1 (very resistant) to 9 (susceptible) scale (Table 6). Plants are artificially inoculated and visually rated approximately 3 to 4 weeks after pollination.

[00233] Table 6. Disease rating scale for Goss' Wilt.

Description	Rating	Symptoms
Very Resistant	1	0% of leaf area infected; no visible lesions
Very Resistant	2	ILA< 1%; few lesions, dispersed through lower leaves
Resistant	3	1% ≤ ILA≤ 20%
Resistant	4	20% ≤ ILA≤ 40%
Mid-resistant	5	40% ≤ ILA≤ 50
Mid-Susceptible	6	50% ≤ ILA≤ 60%; lesions
Susceptible	7	60% ≤ ILA≤ 75%
Susceptible	8	75% ≤ ILA≤ 90%
Susceptible	9	> 90% of foliar area infected

Example 12: Goss' Wilt Resistance Mapping Study 1

[00234] To examine associations between SNP markers and Goss' Wilt resistance, analyzed data from a number of studies was combined. An association study was conducted to evaluate whether significant associations between one or marker genotypes and Goss' Wilt resistance are present in one or more populations. In this association study, data from 10 mapping populations were combined. The number of individuals in the populations ranged from 186 to 369. The number of SNP markers used for screening ranged from 104 to 134. The populations were either F3 or BC1F2. A total of 177 significant associations between SNP markers and Goss' Wilt resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. The SNP markers provided can be used to monitor the introgression of Goss' Wilt resistance into a breeding population. Significant marker-Goss' Wilt associations are reported in Figure 2.

Example 13: Goss' Wilt Resistance Mapping Study 2

[00235] An association study was conducted to evaluate whether significant associations between one or marker genotypes and Goss' Wilt resistance are present in one or more populations. In this association study, 988 inbred lines were screened with 1051 SNP markers. A total of 53 significant associations between SNP markers and Goss' Wilt resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, 8, 9, and 10. The SNP markers provided can be used to monitor the introgression of Goss' Wilt resistance into a breeding population. SNP markers associated with Goss' Wilt resistance, level of significance, and favorable alleles are reported in Figure 2.

Example 14: Goss' Wilt Resistance Mapping Study 3

[00236] An association study was conducted to evaluate whether significant associations between one or more marker genotypes and Goss' Wilt resistance are present in one or more populations. In this study, a rating scale of 1 to 4 was used with 1 being resistant, 2 moderately resistant, 3 moderately susceptible, and 4 susceptible. In this association study, two F3 populations of 154 and 212 individuals were screened with 104 SNP markers. A total of 35 significant associations between SNP markers and Goss' Wilt resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. The SNP markers provided can be used to monitor the introgression of Goss' Wilt resistance into a breeding population. SNP markers associated with Goss' Wilt resistance, level of significance, and favorable alleles are reported in Figure 2.

Example 15: Goss' Wilt Resistance Mapping Study 4

[00237] An association study was conducted to evaluate whether significant associations between one or more marker genotypes and Goss' Wilt resistance are present in one or more populations. A population was screened with 518 SNP markers. A total of 80 significant associations between SNP markers and Goss' Wilt resistance were identified on Chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. The SNP markers provided can be used to monitor the introgression of Goss' Wilt resistance into a breeding population. SNP markers associated with Goss' Wilt resistance, level of significance, and favorable alleles are reported in Figure 2.

Example 16: Exemplary marker assays for detecting Goss' Wilt resistance.

[00238] In one embodiment, the detection of polymorphic sites in a sample of DNA, RNA, or cDNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis, fluorescence detection methods, or other means. Exemplary primers and probes for amplifying and detecting genomic regions associated with Goss' Wilt resistance are given in Table 7.

[00239] **Table 7. Exemplary assays for detecting Goss' Wilt resistance loci .**

Marker	Marker SEQ ID	SNP Position	SEQ ID Forward Primer	SEQ ID Reverse Primer	SEQ ID Probe 1	SEQ ID Probe 2
NC0027347	896	128	1332	1333	1334	1335
NC0071001	951	359	1336	1337	1338	1339
NC0017678	733	171	1340	1341	1342	1343
NC0028095	1098	116	1344	1345	1346	1347

Example 17: Oligonucleotide hybridization probes useful for detecting corn plants with Goss' Wilt resistance loci.

[00240] Oligonucleotides can also be used to detect or type the polymorphisms associated with GLS resistance disclosed herein by hybridization-based SNP detection methods. Oligonucleotides capable of hybridizing to isolated nucleic acid sequences which include the polymorphism are provided. It is within the skill of the art to design assays with experimentally determined stringency to discriminate between the allelic state of the polymorphisms presented herein. Exemplary assays include Southern blots, Northern blots, microarrays, *in situ* hybridization, and other methods of polymorphism detection based on hybridization. Exemplary oligonucleotides for use in hybridization-based SNP detection are provided in Table 8. These oligonucleotides can be detectably labeled with radioactive labels, fluorophores, or other chemiluminescent means to facilitate detection of hybridization to samples of genomic or amplified nucleic acids derived from one or more corn plants using methods known in the art.

[00241] Table 8. Exemplary Oligonucleotide Hybridization Probes*.

Marker	**Marker SEQ ID**	**SNP Position**	**Probe**	**SEQ ID Probe**
NC0027347	**896**	**128**	GCTACTAG**G**AAAATGG	1348
NC0027347	**896**	**128**	GCTACTAG**A**AAAATGG	1349
NC0071001	**951**	**359**	CAACTACC**T**AGCATTT	1350
NC0071001	**951**	**359**	CAACTACC**A**AGCATTT	1351
NC0017678	**733**	**171**	AGTCAAAG**A**TACTGCA	1352
NC0017678	**733**	**171**	AGTCAAAG**C**TACTGCA	1353
NC0028095	**1098**	**116**	TGCCCACA**T**TTGTTAT	1354
NC0028095	**1098**	**116**	TGCCCACA**C**TTGTTAT	1355

*** SNP nucleotides in bold.**

Example 18: Oligonucleotide probes useful for detecting corn plants with Goss' Wilt resistance loci by single base extension methods.

[00242] Oligonucleotides can also be used to detect or type the polymorphisms associated with GLS resistance disclosed herein by single base extension (SBE)-based SNP detection methods. Exemplary oligonucleotides for use in SBE-based SNP detection are provided in Table 9. SBE methods are based on extension of a nucleotide primer that is hybridized to sequences immediately adjacent to a polymorphism to incorporate a detectable nucleotide residue upon extension of the primer. It is also anticipated that the SBE method can use three synthetic oligonucleotides. Two of the oligonucleotides serve as PCR primers and are complementary to the sequence of the locus which flanks a region containing the polymorphism to be assayed. Exemplary PCR primers that can be used to type certain polymorphisms disclosed in this invention are provided in Table 9 in the columns labeled "Forward Primer SEQ ID" and "Reverse Primer SEQ ID". Following amplification of the region containing the polymorphism, the PCR product is hybridized with an extension primer which anneals to the amplified DNA immediately adjacent to the polymorphism. DNA polymerase and two differentially labeled dideoxynucleoside triphosphates are then provided. If the polymorphism is present on the template, one of the labeled dideoxynucleoside triphosphates can be added to the primer in a single base chain extension. The allele present is then inferred by determining which of the two differential labels was added to the extension primer. Homozygous samples will result in only one of the two labeled bases being incorporated and thus only one of the two labels will be detected. Heterozygous samples have both alleles present, and will thus direct incorporation of both labels (into different molecules of the extension primer) and thus both labels will be detected.

[00243] **Table 9. Probes (extension primers) for Single Base Extension (SBE) assays.**

Marker	Marker SEQ ID	SNP Position	Probe	SEQ ID Probe
NC0027347	896	128	TTTTGTACTGCTACTAG	1356
NC0071001	951	359	TACGGAATGCAACTACC	1357
NC0017678	733	171	GTCATGGCGAGTCAAAG	1358
NC0028095	1098	116	TGGATGCTTTGCCCACA	1359

Example 19: Haploid Mapping Study for GLS Resistance with I133314/I206447 Population

[00244] The utility of haploid plants in genetic mapping of traits of interest is demonstrated in the following example. A haploid population was developed by crossing the inbred corn lines I133314 by I206447 and then inducing the resulting F1 hybrid to produce 1945 haploid plants. This was a true hybrid population as the parents were from different heterotic groups. For mapping, 82 SNP markers were used to screen the haploid population. Phenotypic data relating to GLS reaction were collected on the population. Composite interval mapping was conducted with WINQTL cartographer, and 1000 permutations were used for the LOD cutoff estimation to examine significant associations between GLS and the SNP markers. Table 10 provides the significant marker associations found in this study. One marker, NC0055894 (SEQ ID NO: 421) was also found to be associated with GLS in two associations studies of Examples 2 and 5. QTL associated with GLS resistance were identified by genetic mapping with haploid plants. The source of the favorable allele for GLS resistance was I206447 for all makers except NC0151453 (SEQ ID NO: 1231) in which the source of the favorable allele was I133314.

[00245] Table 10. Markers useful for detecting QTL associated with GLS in the I133314/I206447 haploid mapping population.

Marker	Chr	pos	GLS QTL	LOD	Effect	Favorable Allele	SEQ ID Marker	SNP Position
NC0147103	1	39.1	177	6.15	0.17	C	1228	1001
NC0202383	2	19	2	20.38	0.30	T	1229	34
NC0201657	2	179.2	178	26.30	0.34	T	1230	342
NC0055894	3	112.4	57	6.74	0.17	T	421	202
NC0151453	6	75.1	110	17.17	-0.28	T	1231	119

Example 20: Haploid Mapping Study for GLS resistance with I294213/I283669 Population

[00246] The utility of haploid plants in genetic mapping of traits of interest is demonstrated in the following example. A haploid mapping population was developed by crossing the inbred corn lines I294213 by I283669. The resulting F1 hybrid was induced to produce 1895 haploid seed. This was a true hybrid population as the parents were from different heterotic groups. For mapping, 82 SNP markers were used to screen the haploid population. Composite interval mapping was conducted with WINQTL cartographer, and 300 permutations were used for the LOD cutoff estimation to examine significant associations between GLS and the SNP markers. Table 11 provides the significant marker associations found in this study. Five markers (SEQ ID NOs: 36, 481, 659, 1127, and 1219) were found to be associated with GLS in the association studies of Examples 2, 5, and 6. QTL associated with GLS resistance were identified by genetic mapping with haploid plants. The source of the favorable alleles was I283669 for all makers except NC0003425 (SEQ ID NO: 1127) in which the source of the favorable allele was I294213. The chromosome (Chr.) location, chromosome position (Chr. pos), and favorable allele are provided for each marker in Table 11.

[00247] Table 11. Markers useful for detecting QTL associated with GLS resistance in the I294213/I283669 haploid mapping population.

Marker	Chr	pos	GLS QTL	LOD	Effect	Favorable Allele	SEQ ID Marker	SNP Position
NC0052741	1	49.5	5	136.19	0.75	G	36	411
NC0028145	3	187.5	64	3.19	0.10	G	481	307
NC0143354	5	1.8	88	8.33	0.16	C	659	303
NC0040408	6	59.1	108	13.29	0.22	T	1232	336
NC0109097	7	93.8	127	5.93	0.13	T	1233	97
NC0003425	9	84.5	158	20.30	-0.25	G	1127	280
NC0199588	10	99.9	173	15.36	0.23	G	1219	137

Example 21: Haploid Mapping Study for Goss' Wilt with I208993/LH287 Population

[00248] The utility of haploid plants in genetic mapping of traits of interest is further demonstrated in the following example. A mapping population was developed for using haploid plants to map QTL associated with resistance to Goss' Wilt. The population was from the cross of inbred corn lines I208993 by LH287. F1 plants were induced to produce haploid seed. From the I208993/LH287 population, 1384 haploid plants were inoculated with the Goss' Wilt pathogen and phenotyped using a truncated rating scale of 1, 5, or 9. Ratings are done approximately 3 to 4 weeks after pollination. Plants rated either 1 or 9 were used in the QTL mapping. By using only the extreme values (1 or 9), environmental variation that is inherent with disease phenotyping was reduced and a bulk segregate analysis was created from which to detect major QTL. Genotyping was done using 114 SNP markers. Composite interval mapping was conducted with WINQTL cartographer and 1000 permutations were used for the LOD cutoff estimation. Table 12 provides markers useful for detecting QTL associated with resistance to Goss' Wilt in the I208993/LH287 haploid mapping population. The chromosome (Chr.) location, chromosome position (Chr. pos), and favorable (Fav.) allele are also provided in Table 12.

[00249] Table 12. Markers useful for detecting QTL associated with Goss' Wilt resistance in the I208993/LH287 haploid mapping population.

Marker	Chr	pos	Goss' Wilt QTL	Likelyhood ratio	LOD	Additive effect	Fav allele	SEQ ID	SNP Position
NC0202383	2	19	22	100.304	21.78074	0.737618	T	1229	34
NC0199732	2	37	24	113.9429	24.74239	0.779994	T	1276	138
NC0048553	2	46.8	25	103.8964	22.56081	0.758496	A	234	485
NC0201646	2	55.4	129	96.43437	20.94046	0.746649	T	1294	416
NC0201821	2	71.4	27	40.13758	8.715765	0.202738	T	1295	331
NC0019110	2	75.1	27	28.41102	6.169374	0.173568	C	1278	153
NC0004821	3	54.4	40	47.57959	10.33178	0.451741	C	371	294
NC0200643	3	70.3	122	47.48045	10.31025	0.424893	C	1296	106
NC0040461	4	51.2	125	80.02493	17.37719	0.620383	A	1282	366
NC0034462	4	67.8	52	76.55974	16.62474	0.574876	T	1250	301
NC0200535	4	132	58	29.47242	6.399855	0.142544	T	1297	411
NC0029435	4	138	58	29.25183	6.351953	0.139488	G	1298	551
NC0011194	5	29.3	63	27.51088	5.973912	-0.227689	C	1299	218
NC0016527	5	49	66	29.15712	6.331388	-0.219392	T	1255	351
NC0202055	5	76.4	68	26.18668	5.686366	-0.252002	T	1300	505
NC0147719	5	160	130	47.9265	10.40711	0.492815	G	1301	48
NC0012417	5	175	74	48.68852	10.57258	0.505586	T	768	137
NC0113381	6	83.8	79	28.96126	6.288858	-0.21407	A	850	303
NC0022200	6	93.7	80	31.16025	6.766361	-0.201408	G	1302	153
NC0010347	8	69.2	131	27.38218	5.945966	-0.144382	T	1015	160
NC0199582	8	86.3	99	26.24576	5.699195	-0.169537	A	1303	201

Example 22: Haploid Mapping Study for Goss' Wilt with I208993/LH295 Population

[00250] The utility of haploid plants in genetic mapping of traits of interest is further demonstrated in the following example. A mapping population was developed for using haploid plants to map QTL associated with resistance to Goss' Wilt. The population was from the cross of LH295 by I208993. F1 plants were induced to produce haploid seed.

[00251] From the I208993/LH295 haploid mapping population, 980 individuals were naturally exposed to the Goss' Wilt pathogen and phenotyped using a modified rating scale of 1, 5, or 9. Ratings are done approximately 3 to 4 weeks after pollination. Plants rated either 1 or 9 were used in the QTL mapping. By using only the extreme values (1 or 9), environmental variation that is inherent with disease phenotyping was reduced and a bulk segregate analysis was created from which to detect major QTL. Genotyping was done with 980 SNP markers. Table 13 provides markers useful for detecting QTL associated with Goss' Wilt in the I208993/LH295 haploid mapping population.

[00252] Table 13. Markers useful for detecting QTL associated with Goss' Wilt in the I208993/LH295 haploid mapping population

Marker	Chr	pos	Goss' Wilt QTL	Likelihood	LOD	Additive Effect	Favorable Allele	SEQ ID	SNP Position
NC0199051	1	19.3	1	28.02118	6.084721	-0.22604	G	1274	141
NC0105051	1	31.4	3	28.79147	6.251987	-0.236914	C	24	426
NC0032288	1	133.6	10	31.20763	6.77665	0.252864	C	1275	413
NC0070305	1	166.5	13	29.73574	6.457033	0.216902	A	158	532
NC0143411	2	15.4	22	31.80736	6.90688	-0.372898	C	218	401
NC0199732	2	37	24	51.17309	11.11209	-0.506613	T	1276	138
NC0013275	2	49.7	25	56.78186	12.33002	-0.677671	T	236	430
NC0199350	2	67.8	26	57.35414	12.45429	-0.577154	G	1277	226
NC0019110	2	75.1	27	51.54673	11.19323	-0.633508	C	1278	153
NC0027319	2	93.2	29	41.90672	9.099928	-0.572435	T	272	54
NC0104528	3	24.6	37	29.36476	6.376476	-0.189689	G	1247	117
NC0019963	3	40.6	39	32.03588	6.956503	-0.139199	C	368	1173
NC0077220	3	43.2	39	27.90631	6.059777	-0.133108	A	1279	149
NC0108727	3	77.4	122	32.5836	7.075438	-0.031362	C	375	241
NC0039785	3	94.5	123	30.35128	6.590696	-0.083537	T	401	512
NC0031720	3	99.7	123	46.9907	10.2039	0.199348	G	408	434
NC0200377	3	116.9	43	47.01889	10.21002	0.181809	A	1280	352
NC0199741	3	125.7	44	28.60384	6.211245	-0.315998	A	1281	294
NC0041040	3	145.4	45	36.85657	8.003303	-0.551354	A	440	497
NC0055502	4	1.8	124	36.00788	7.819012	-0.390433	C	498	105
NC0040461	4	51.2	125	42.90587	9.316891	-0.469569	A	1282	366
NC0199420	4	102.9	55	43.93528	9.540424	-0.452635	G	1283	356
NC0036240	4	112	56	38.3635	8.330528	-0.381557	A	587	441
NC0028933	4	127.6	57	29.32225	6.367245	0.144007	C	599	355
NC0147712	4	136.7	58	33.6318	7.303051	0.185174	A	1284	74
NC0028579	4	155.7	60	37.46012	8.134361	0.109588	A	629	242
NC0029487	4	171.1	126	38.35712	8.329143	0.101598	G	1285	159
NC0200359	5	11.7	63	27.52949	5.977952	-0.167336	A	1286	196
NC0040571	5	88.4	69	59.435	12.90615	-0.58299	C	721	154
NC0017678	5	103.8	71	69.69769	15.13466	-0.722151	A	733	171
NC0083876	5	124	72	29.09207	6.317263	-0.392793	T	744	513
NC0200323	5	174.8	74	27.01332	5.865868	-0.253474	A	1287	181
NC0027347	7	43.8	86	57.87354	12.56708	-0.542521	A	896	128
NC0201872	7	64.4	88	58.07534	12.6109	-0.54188	C	1288	208
NC0145922	7	80.5	89	26.87412	5.835642	-0.271008	G	940	451
NC0071001	7	99.4	90	26.59882	5.775861	-0.262452	T	951	359
NC0199879	7	112.1	92	34.51543	7.494931	-0.28773	A	1289	228
NC0200055	7	122.3	127	36.14355	7.848472	-0.277751	T	1290	116
NC0110771	7	138.5	93	32.98577	7.162769	-0.163457	A	976	490
NC0200495	7	155.9	95	27.69812	6.014571	-0.118782	G	1291	302
NC0028095	9	59.4	107	29.92602	6.498353	0.142796	C	1098	116
NC0144850	9	67	108	30.50354	6.62376	0.146897	G	1292	244
NC0030134	10	79.4	120	27.87616	6.05323	-0.317779	TCCACTAT	1215	94
NC0200312	10	85.7	128	31.10615	6.754615	-0.355789	A	1293	89

Example 23: Preselection of Haploids for doubling

[00253] The utility of haploid plants in genetic mapping of traits of interest is demonstrated in the following example. A haploid mapping population is developed by inducing a Family based pedigree, such as an F3 or BC1S1, to produce haploid seeds. The haploid seeds are planted in ear rows which represent the parents from the F3 or BC1S1 population and remnant seed is stored for doubling needs after phenotyping is completed. For mapping, SNP markers are used to screen the haploid population. Composite interval mapping is conducted to examine significant associations between a trait of interest and the SNP markers. Remnant seed can be doubled through methods known in the art. Selection of which remnant seed families to double can be based on phenotypic and genotypic data. Doubled plants can be utilized for further breeding, commercial breeding or for additional fine-mapping purposes.

Example 24: Use of haplotype effect estimates in making breeding decisions

[00254] The present invention provides methods to identify and use QTL and haplotype information by screening haploid material that enables a breeder to make informed breeding decisions. The methods and compositions of the present invention enable the determination of at least one genotype of interest from one or more haploid plants. In another aspect, a haploid plant comprising at least one genotype of interest can undergo doubling and be advanced in a breeding program. In yet another aspect, a priori QTL and haplotype information can be leveraged, as disclosed in US Patent Application Serial No. 60/837, 864, which is incorporated herein by reference in its entirety, using markers underlying at least one haplotype window, and the resulting fingerprint is used to identify the haplotypic composition of the haplotype window which is subsequently associated with one or more haplotype effect estimates for one or more phenotypic traits as disclosed therein. This information is valuable in decision-making for a breeder because it enables a selection decision to be based on estimated phenotype without having to phenotype the plant per se. Further, it is preferred to make decisions based on genotype rather than phenotype due the fact phenotype is influenced by multiple biotic and abiotic factors that can confound evaluation of any given trait and performance prediction. As used herein, the invention allows the identification of one or more preferred haploid plants such that only preferred plants undergo the doubling process, thus economizing the DH process.

[00255] In another aspect, one or more haplotypes are determined by genotyping one or more haploid plants using markers for one or more haplotype windows. The breeder is able to correspond the haplotypes with their respective haplotype effect estimates for one or more phenotypes of interest and make a decision based on the preferred haplotype. Haploid plants comprising one or more preferred haplotypes are doubled using one or more methods known in the art and then advanced in the breeding program.

[00256] In one aspect, advancement decisions in line development breeding are traditionally made based on phenotype, wherein decisions are made between two or more plants showing segregation for one or more phenotypic traits. An advantage of the present invention is the ability to make decisions based on haplotypes wherein *a priori* information is leveraged, enabling "predictive breeding." In this aspect, during line development breeding for a crop plant, sublines are evaluated for segregation at one or more marker loci. Individuals segregating at one or more haplotype windows can be identified unambiguously using genotyping and, for any given haplotype window, individuals comprising the preferred haplotype are selected. In preferred aspects, the selection decision is based on a haplotype effect estimate, a haplotype frequency, or a breeding value.

Example 25. Use of haploid seed for preselection in a high oil breeding program

[00257] The methods of the present invention can be used in a high oil corn breeding program. Haploid kernels with at least one preferred marker, such as oil content, can be selected according to the present invention. Preselection breeding methods are utilized to preselect and prescreen lines for oil and agronomic traits such as yield, using markers selected from the group consisting of genetic markers, protein composition, protein levels, oil composition, oil levels, carbohydrate composition, carbohydrate levels, fatty acid composition, fatty acid levels, amino acid composition, amino acid levels, biopolymers, pharmaceuticals, starch composition, starch levels, fermentable starch, fermentation yield, fermentation efficiency, energy yield, secondary compounds, metabolites, morphological characteristics, and agronomic characteristics.

[00258] Populations are identified for submission to the doubled haploid (DH) process. QTL and/or genomic regions of interest are identified in one or more parents in the population for targets of selection that are associated with improved agronomic traits such as yield, moisture, and testweight. In other aspects, QTL are identified that are associated with improved oil composition and/or increased oil composition. In one aspect, two or more QTL are selected.

[00259] The population undergoing haploid induction is characterized for oil content using methods known in the art, non-limiting examples of which include NIT, NIR, NMR,and MRI, wherein seed is measured in a bulk and/or on a single seed basis. Methods to measure oil content in single seeds have been described (Kotyk, J., et al., Journal of American Oil Chemists' Society 82: 855-862 (2005). In one aspect, single-kernel analysis (SKA) is conducted via magnetic resonance or other methods. In another aspect, oil content is measured using analytics methods known in the art per ear and the selected ears are bulked before undergoing SKA. The resulting data is used to select single kernels that fall within an oil range acceptable by the breeder to meet the product concept.

[00260] The selected population is sent to the DH facilities and induced. Putative haploid kernels are selected and non-destructively sampled for subsequent genotyping. Apparatus and methods for the high-throughput, non-destructive sampling of seeds have been described which would overcome the obstacles of statistical samples by allowing for individual seed analysis. For example, U.S. Patent Application Serial No. 11/213,430 (filed August 26, 2005); U.S. Patent Application Serial No. 11/213,431 (filed August 26, 2005); U.S. Patent Application Serial No. 11/213,432 (filed August 26, 2005); U.S. Patent Application Serial No. 11/213,434 (filed August 26, 2005); and U.S. Patent Application Serial No. 11/213,435 (filed August 26, 2005), U.S. Patent Application Serial No. 11/680,611 (filed March 2, 2007), which are incorporated herein by reference in their entirety, disclose apparatus and systems for the automated sampling of seeds as well as methods of sampling, testing and bulking seeds.

[00261] The seed samples are genotyped using the markers corresponding to the one or more QTL of interest. Seeds are selected based upon their genotypes for these QTL.

Seed may be selected based on preferred QTL alleles or, for the purpose of additional mapping, both ends of the distribution are selected. That is, seed is selected based on preferred and less preferred alleles for at least one QTL and/or preferred and less preferred phenotypic performance for at least one phenotype and/or preferred and less preferred predicted phenotypic performance for at least one phenotype.

[00262] Haploid kernels can also be selected and processed by methods known in the art such as NMR or MRI to characterize oil content. Kernels with preferred oil content are selected. As illustrated above, for research purposes, kernels may be selected with low, high, or average oil content in order to identify the genetic basis for oil content. In one aspect, relative oil content in germ and endosperm is characterized by taking an NMR measurement on whole kernel, wherein subsequent NMR measurements are taken on dissected germ and endosperm. In another aspect, kernels are imaged using MRI to identify the relative oil content in germ and endosperm tissue.

[00263] In another aspect, seed samples are analyzed for oil content and the genotype for at least one QTL or genomic region of interest, enabling pre-selection for high oil corn with suitable agronomic performance.

[00264] The selected haploid kernels are then doubled on the basis of analytic and/or genotypic data. In one aspect, following doubling, the putative DHs can be screened using genetic and/or analytic methods as described above.

[00265] Notably, analytic methods for detection of oil are not restricted to NMR and other relevant methods include IR-type instruments and MRI. Also, samples can be in bulk or on a single seed basis wherein the capability exists to select material based on a preferred oil content. In certain aspects, a preferred oil content is a decreased oil content which may be useful in the development of mapping populations for the detection of oil content QTL.

[00266] Selected haploids plants can be used to map for oil traits.

Example 26: Introgression of GLS resistance in breeding

[00267] Given the description of the above-described GLS resistance loci, an illustrative example is presented for the utility of said GLS resistance loci in a corn breeding program and, more specifically, in the context of development of inbred lines. GLS resistant line CV171 is used as a donor source. Corn inbred CV009 is used as the recurrent parent. Table 14 provides exemplary SNP markers and favorable alleles for selecting GLS resistant lines. Exemplary SNP markers NC0019588, NC0037947, NC0088767, NC0059114, NC0003201, NC0060514, NC0002782, NC0053636, NC0009667, and NC0032368 (SEQ ID NOs: 858, 860, 862, 866, 875, 877, 881, 882, 883, and 1360) are used to monitor introgression of GLS resistance regions from Chromosome 6. A breeder selects for lines carrying the resistance allele for one or more of said SNP markers, representing one or more GLS resistance loci.

[00268] The introgression of one or more resistance loci is achieved via repeated backcrossing to a recurrent parent accompanied by selection to retain one or more GLS resistance loci from the donor parent using the above-described markers. This backcross procedure is implemented at any stage in line development and occurs in conjunction with breeding for superior agronomic characteristics or one or more traits of interest, including transgenic and nontransgenic traits.

[00269] Alternatively, a forward breeding approach is employed wherein one or more GLS resistance loci can be monitored for successful introgression following a cross with a susceptible parent with subsequent generations genotyped for one or more GLS resistance loci and for one or more additional traits of interest, including transgenic and nontransgenic traits.

[00270] Table 14: SNP markers useful for introgression of GLS resistance from inbred CV171

Marker	Marker SEQ ID NO.	Chromosome	Favorable allele
NC0019588	858	6	C
NC0037947	860	6	G
NC0088767	862	6	A
NC0059114	866	6	T
NC0003201	875	6	G
NC0060514	877	6	CA
NC0002782	881	6	C
NC0053636	882	6	A
NC0009667	883	6	G
NC0032368	1360	6	G

Example 27: Introgression of Goss' Wilt Resistance using SNP markers

[00271] Loci associated with resistance to Goss' Wilt can be introgressed into corn plants by methods known to those skilled in the art of plant breeding. A plant breeder can use SNP markers to monitor the introgression of Goss' Wilt resistance loci and to select for lines carrying the favorable allele for one or more of said SNP markers.

[00272] In this example, the inbred line LH287 is used as a source of Goss' Wilt resistance. SNP markers used to monitor introgression of Goss' Wilt resistance loci on Chromosome 2 include NC0202383 , NC0199732, NC0048553, and NC0201646 (SEQ ID NOs: 1122, 1276, 1294, and 234). SNP used to monitor introgression of Goss' Wilt resistance loci on Chromosome 3 include NC0019963 and NC0004821 (SEQ ID NOs: 368 and 371). SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 4 include NC0040461 and NC0034462 (SEQ ID NOs: 1282 and 1250). SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 5 include NC0147719 and NC0012417 (SEQ ID NOs: 1301 and 768). The favorable allele is the allele associated with the resistant donor parent.

[00273] In a further illustration, the inbred line LH295 is used as a source of Goss' Wilt resistance. SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 2 include NC0013275, NC0199350, and NC0019110 (SEQ ID NOs: 236, 1277, and 1278). SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 3 include NC0199741 and NC0041040 (SEQ ID NOs: 1281 and 440). SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 4 include NC0040461, NC0199420, and NC0036240 (SEQ ID NOs: 1282, 1283, and 587). SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 5 include NC0040571 and NC0017678 (SEQ ID NOs: 721 and 733). SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 7 include NC0201872 and NC0145922 (SEQ ID NOs: 1288 and 940). SNP markers used to monitor the introgression of Goss' Wilt resistance loci on Chromosome 10 include NC0200312 (SEQ ID NO: 1293). A plant breeder can use SNP markers to monitor the introgression of Goss' Wilt resistance loci and to select for lines carrying the favorable allele for one or more of said SNP markers.

[00274] The introgression of one or more resistance loci is achieved via repeated backcrossing to a recurrent parent accompanied by selection to retain one or more Goss' Wilt resistance loci from the donor parent using the above-described markers. This backcross procedure is implemented at any stage in line development and occurs in conjunction with breeding for superior agronomic characteristics or one or more traits of interest, including transgenic and nontransgenic traits.

[00275] Alternatively, a forward breeding approach is employed wherein one or more Goss' Wilt resistance loci can be monitored for successful introgression following a cross with a susceptible parent with subsequent generations genotyped for one or more Goss' Wilt resistance loci and for one or more additional traits of interest, including transgenic and nontransgenic traits.

Example 28: Application of markers associated with Goss' Wilt in a corn breeding program

[00276] From the studies presented in Figure 2, it is apparent that a chromosomal region can have multiple SNP markers associated with Goss' Wilt resistance. Following are non-limiting examples of targeting at least one marker from at least on locus associated with Goss' Wilt resistance for the purpose of breeding corn resistant to Goss' Wilt. Specifically the markers of the present invention have utility for generating corn inbreds and hybrids resistant to Goss Wilt. The markers of the present invention are useful in parent selection, progeny selection, and marker-assisted introgression and backcrossing. Exemplary markers from Chromosome 1 are NC0004909 and NC0005098 (SEQ ID NOs: 175 and 177). Exemplary markers from Chromosome 3 are NC0146497 and NC0155987 (SEQ ID NOs: 479 and 480). Exemplary markers from Chromosome 4 are NC0077408, NC0003274, and NC0009280 (SEQ ID NOs: 582, 585, and 1251). Exemplary markers from Chromosome 8 are NC0010392, NC0012656, and NC0008831 (SEQ ID NOs: 1053, 1054, and 1056).

[00277] Having illustrated and described the principles of the present invention, it should be apparent to persons skilled in the art that the invention can be modified in arrangement and detail without departing from such principles. We claim all modifications that are within the spirit and scope of the appended claims.

[00278] Various patent and non-patent publications are cited herein, the disclosures of each of which are, to the extent necessary, incorporated herein by reference in their entireties.

Claims

We claim:

1. A method for the association of at least one genotype with at least one phenotype using a haploid plant comprising:

   a) assaying at least one genotype of at least one haploid plant with at least one genetic marker; and

   b) associating the at least one marker with at least one phenotypic trait.

2. The method of claim 1, wherein the at least one genetic marker comprises a single nucleotide polymorphism (SNP), an insertion or deletion in DNA sequence (Indel), a simple sequence repeat of DNA sequence (SSR) a restriction fragment length polymorphism, a haplotype, or a tag SNP.

3. A method of Claim 1, further comprising the step of using an association determined in step (b) to make a selection in a plant breeding program.

4. A method of Claim 3, wherein said selection comprises selecting among breeding populations based on the at least one genotype.

5. The method of Claim 3, wherein said selection comprises selecting progeny in one or more breeding populations based on the at least one genotype.

6. The method of Claim 3, wherein said selection comprises selecting among parental lines based on prediction of progeny performance.

7. The method of Claim 3, wherein said selection comprises selection of a line for advancement in a germplasm improvement activity based on the at least one genotype.

8. A method of Claim 3, further comprising the step of doubling at least one haploid plant selected in said breeding program to obtain a doubled haploid plant.
9. The method of Claim 9, wherein the doubled haploid plant is used for introgression of the genotype of interest into at least a second plant for use in a plant breeding program.

10. The method of claim 1, wherein said haploid plant in step (a) is obtained from a haploid breeding population.

11. A method for identifying an association of a plant genotype with one or more traits of interest comprising:

a) screening a plurality of haploid plants displaying heritable variation for at least one trait wherein the heritable variation is linked to at least one genotype; and

b) associating at least one genotype of at least one haploid plant to at least one trait.

12. The method of Claim 11, wherein the genotype comprises a genetic marker..

13. The method of Claim 11, further comprising the step of using an association determined in step (b) to make a selection in a plant breeding program.

14. The method of Claim 13, wherein said selection comprises selecting among breeding populations based on the at least one genotype.

15. The method of Claim 13, wherein said selection comprises selecting progeny in one or more breeding populations based on the at least one genotype.

16. The method of Claim 13, wherein said selection comprises selecting among parental lines based on prediction of progeny performance.

17. The method of Claim 13, wherein said selection comprises selection of a line for advancement in a germplasm improvement activity based on the at least one genotype.

18. The method of Claim 13, further comprising the step of doubling at least one haploid plant selected in said breeding program to obtain a doubled haploid plant.

19. The method of Claim 18, wherein the doubled haploid plant is used for introgressing the genotype of interest into a plant for use in a plant breeding program.

20. The method of Claim 11, wherein said haploid plant or plants comprise an intact plant, a leaf, vascular tissue, flower, pod, root, stem, seed or portion thereof.

21. The method of Claim 11, wherein the plants are selected from the group consisting of maize (Zea mays), soybean (Glycine max), cotton (Gossypium hirsutum), peanut (Arachis hypogaea), barley (Hordeum vulgare); oats (Avena sativa); orchard grass (Dactylis glomerata); rice (Oryza sativa, including indica and japonica varieties); sorghum (Sorghum bicolor); sugar cane (Saccharum sp); tall fescue (Festuca arundinacea); turfgrass species (e.g. species: Agrostis stolonifera, Poa pratensis, Stenotaphrum secundatum); wheat (Triticum aestivum), and alfalfa (Medicago sativa), members of the genus Brassica, carrot, cucumber, dry bean, eggplant, fennel, garden beans, gourd, leek, lettuce, melon, okra, onion, pea, pepper, pumpkin, radish, spinach, squash, sweet corn, tomato, watermelon, and ornamental plants.

22. The method of claim 11, wherein the haploid plant is a fruit, vegetable, tuber, or root crop.

23. The method of Claim 11, wherein the trait is selected from the group consisting of herbicide tolerance, disease resistance, insect or pest resistance, altered fatty acid, protein or carbohydrate metabolism, increased grain yield, increased oil, enhanced nutritional content, increased growth rates, enhanced stress tolerance, preferred maturity, enhanced organoleptic properties, altered morphological characteristics, sterility, a trait for industrial use, and a trait for consumer appeal.

24. A method of identifying a corn plant comprising at least one allele associated with Gray Leaf Spot (GLS) resistance allele in a corn plant comprising:

a) genotyping at least one corn plant with at least one nucleic acid marker selected from the group consisting of SEQ ID NO:1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461–1233, 1360 and 1361, and

b) selecting at least one corn plant comprising an allele of at least one of said markers associated with Gray Leaf Spot (GLS) resistance.

25. The method according to claim 24, wherein the at least one corn plant genotyped in step (a) and/or the at least one corn plant selected in step (b) is a corn plant from a population generated by a cross.

26. The method of claim 25, wherein said cross is effected by mechanical emasculation, chemical sterilization, or genetic sterilization of a pollen acceptor.

27. The method of claim 24, wherein genotyping is effected in step (a) by determining the allelic state of at least one of said corn genomic DNA markers.

28. The method according to Claim 24, wherein the selected one or more corn plants exhibit at least partial resistance to a GLS-inducing fungus or at least substantial resistance to a GLS-inducing fungus.

29. The method of claim 25 , wherein said population is generated by a cross of at least one Gray Leaf Spot (GLS) resistant corn plant with at least one Gray Leaf Spot (GLS) sensitive corn plant.

30. The method of claim 25, wherein said population is a segregating population.

31. The method of claim 25, wherein said cross is a back cross of at least one Gray Leaf Spot (GLS) resistant corn plant with at least one Gray Leaf Spot (GLS) sensitive corn plant to introgress GLS resistance into a corn germplasm.

32. The method of claim 25, wherein said population is a haploid breeding population.

33. A method of introgressing a Gray Leaf Spot (GLS) resistance QTL allele into a corn plant comprising:

a) screening a population with at least one nucleic acid marker to determine if one or more corn plants from the population comprise(s) an allele of said marker associated with a Gray Leaf Spot (GLS) resistance QTL selected from the group consisting of QTL numbers 1-9, 14-33, 35, 38-42, 44-52, 54-61, 63-71, 73-79, 81-92, 95-96, 99-106, 108-117, and 119-178 as provided in Figure 1; and

b) selecting from said population at least one corn plant comprising an allele of said marker associated with a Gray Leaf Spot (GLS) resistance.

34. The method according to Claim 33, wherein at least one of the markers is located within 5 cM of at least one of said Gray Leaf Spot (GLS) resistance QTLs.

35. The method according to Claim 34, wherein at least one of the markers is located within 2 cM of at least one of said Gray Leaf Spot (GLS) resistance QTLs.

36. The method according to Claim 35, wherein at least one of the markers is located within 1 cM of at least one of said Gray Leaf Spot (GLS) resistance QTLs.

37. The method according to Claim 33, wherein at least one of the markers exhibits a LOD score of greater than 4.0 with at least one of said Gray Leaf Spot (GLS) resistance QTLs.

38. The method according to Claim 33, wherein said population is generated by a cross of at least one Gray Leaf Spot (GLS) resistant corn plant with at least one Gray Leaf Spot (GLS) sensitive corn plant.

39. The method of claim 33, wherein said population is a haploid breeding population.

40. The method of claim 33, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 858, 860, 862, 866, 875, 877, 881, 882, 883, and 1360.

41. A corn plant obtained by the method of any one of claims 24 to 32, wherein said corn plant comprises at least one allele of a nucleic acid marker selected from the group consisting of SEQ ID NO: 1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461-1233 and SEQ ID NOs: 1360 and 1361, wherein said allele is associated with Gray Leaf Spot (GLS) resistance.

42. The corn plant of Claim 41, wherein the corn plant exhibits at least partial resistance to a GLS-inducing fungus or at least substantial resistance to a GLS-inducing fungus.

43. The corn plant of claim 41, wherein said corn plant is a haploid corn plant.

44. A corn plant obtained by the method of any one of Claims 33 to 40, wherein said corn plant comprises a Gray Leaf Spot (GLS) resistance QTL selected from the group consisting of QTL numbers 1-9, 14-33, 35, 38-42, 44-52, 54-61, 63-71, 73-79, 81-92, 95-96, 99-106, 108-117, and 119-178 as provided in Figure 1.

45. An isolated nucleic acid molecule for detecting a molecular marker representing a polymorphism in corn DNA, wherein said nucleic acid molecule comprises at least 15 nucleotides that include or are immediately adjacent to said polymorphism, wherein said nucleic acid molecule is at least 90 percent identical to a sequence of the same number of consecutive nucleotides in either strand of DNA that include or are immediately adjacent to said polymorphism, and wherein said molecular marker is selected from the group consisting of SEQ ID NOs: 1-62, 64-70, 72-156, 158-172, 174-187, 189-377, 379, 380, 382-409, 411-459, 461-1360, and 1361.

46. The isolated nucleic acid molecule of claim 45, wherein said molecular marker is selected from the group consisting of SEQ ID NOs: 858, 860, 862, 866, 875, 877, 881, 882, 883, and 1360.

47. A method of identifying a corn plant comprising at least one allele associated with Goss' Wilt resistance allele in a corn plant comprising:

a) genotyping at least one corn plant with at least one nucleic acid marker selected from the group consisting of SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1302, and 1303 , and

b) selecting at least one corn plant comprising an allele of at least one of said markers that is associated with resistance to Goss' Wilt.

48. The method according to claim 47, wherein the at least one corn plant genotyped in step (a) and/or the at least one corn plant selected in step (b) is a corn plant from a population generated by a cross.

49. The method of claim 48, wherein said cross is effected by mechanical emasculation, chemical sterilization, or genetic sterilization of a pollen acceptor.

50. The method of claim 47, wherein said genotyping is effected in step (a) by determining the allelic state of at least one of said corn genomic DNA markers.

51. The method according to Claim 47, wherein said selected corn plant(s) of step (b) exhibit at least partial resistance to a Goss' Wilt-inducing bacteria or at least substantial resistance to a Goss' Wilt-inducing bacteria.

52. The method according to claim 47, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251.

53. The method according to claim 52, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 234 and 1250.

54. The method of claim 48, wherein said population is generated by a cross of at least one Goss' Wilt resistant corn plant with at least one Goss' Wilt sensitive corn plant.

55. The method of claim 48, wherein said population is a segregating population.

56. The method of claim 48, wherein said cross is a back cross of at least one Goss' Wilt resistant corn plant with at least one Goss' Wilt sensitive corn plant to introgress Goss' Wilt resistance into a corn germplasm.

57. The method of claim 48, wherein said population is a haploid breeding population.

58. A method of introgressing a Goss' Wilt resistance QTL into a corn plant comprising:

a) screening a population with at least one nucleic acid marker to determine if one or more corn plants from the population contains a Goss' Wilt resistance QTL, wherein the Goss' Wilt resistance QTL is a QTL selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, and 131 as provided in Figure 2; and

b) selecting from said population at least one corn plant comprising an allele of said marker associated with a Goss' Wilt resistance.

59. The method according to Claim 58, wherein at least one of the markers is located within 5 cM of said Goss' Wilt resistance QTL.

60. The method according to Claim 59, wherein at least one of the markers is located within 2 cM of said Goss' Wilt resistance QTL.

61. The method according to Claim 60, wherein at least one of the markers is located within 1 cM of said Goss' Wilt resistance QTL.

62. The method according to Claim 58, where at least one of the markers exhibits a LOD score of greater than 4.0 with said Goss' Wilt resistance QTL.

63. The method according to claim 62, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251.

64. The method according to claim 63, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 234 and 1250.

65. The method of claim 58, wherein said population is a segregating population.

66. A corn plant obtained by the method of any one of Claims 47-57, wherein said corn plant comprises at least one allele of a nucleic acid marker selected from the group consisting of SEQ ID NO: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158- 160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719-721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1302, and 1303, wherein said allele is associated with Goss' Wilt resistance.

67. The corn plant according to claim 66, wherein said nucleic acid marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251.

68. The corn plant of Claim 66, wherein the corn plant exhibits at least partial resistance to a Goss' Wilt-inducing bacterium or at least substantial resistance to a Goss' Wilt-inducing bacterium.

69. The corn plant according to Claim 67, a nucleic acid marker selected from the group consisting of SEQ ID NOs: 234 and 1250.

70. The corn plant of claim 66, wherein said corn plant is a haploid corn plant.

71. A corn plant obtained by the method of any one of Claims 58-65, wherein said corn plant comprises a Goss' Wilt resistance QTL selected from the group consisting of QTL numbers

1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111,112,113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, and 131 as provided in Figure 2.

72. The isolated nucleic acid according to claim 45, wherein said molecular marker is selected from the group consisting of SEQ ID NOs: 13, 19, 24, 27, 36, 50, 53, 90, 94, 95, 97, 99, 101, 102, 106, 110, 111, 119, 121, 122, 124, 128, 130-132, 136, 138, 141, 146, 153, 158-160, 162, 164, 166, 169, 172, 175, 177, 186, 200, 202, 203, 207, 208, 215, 216, 218, 220, 224, 228, 231 – 236, 244, 248, 250, 252, 256, 257, 260, 265-267, 271-274, 278, 279, 282, 287, 289, 294-296, 299, 317, 320, 332-334, 337, 347, 355, 362, 363, 366-368, 370, 371, 375, 381, 382, 392, 395, 401, 408, 409, 411, 412, 422, 423, 429, 430, 433, 438, 440, 447, 474, 476, 479, 480, 482, 486, 490, 493, 498, 500,525, 530, 533, 556, 566, 582, 585, 587, 589, 593, 594, 599, 611, 618, 621, 623, 629, 630, 632, 637, 639, 646, 649, 650, 657, 665, 669, 678, 679, 688, 690, 704, 709, 710, 717, 719, 721, 726, 727, 733, 734, 744, 746, 758, 760, 764, 768, 773, 792, 793, 812, 821, 825, 835, 844, 846, 850, 854, 856-858, 874, 876, 880, 882, 885, 893, 896, 897, 915, 926, 940, 942, 949, 951, 957, 963, 964, 974, 976, 981, 983, 990, 997, 999, 1000, 1015, 1016, 1027, 1043, 1049, 1053, 1054, 1056, 1075, 1081, 1087, 1088, 1098-1100, 1104, 1105, 1108, 1110, 1115, 1122, 1131, 1133, 1142, 1143, 1145, 1146, 1148, 1149, 1159, 1168, 1174, 1184, 1186, 1196, 1204, 1212, 1215, 1229, 1234-1302, and 1303.

73. The isolated nucleic acid according to claim 72, wherein said molecular marker is selected from the group consisting of SEQ ID NOs: 27, 121, 141, 175, 177, 220, 224, 234, 248, 252, 381, 440, 479, 480, 533, 582, 585, 639, 721, 727, 733, 746, 768, 773, 940, 1053, 1054, 1122, 1186, 1246, 1250, and 1251.

74. The isolated nucleic acid of claim 73, wherein said molecular marker is selected from the group consisting of SEQ ID NOs: 234 and 1250.

75. A method for the association of at least one phenotype with at least one genetic marker using a haploid plant comprising:

a) assaying at least one phenotype of at least one haploid plant with at least one phenotypic marker to determine the presence or absence of said phenotype; and

b) associating the presence or absence of said phenotype with at least one genetic marker.

76. The method of claim 75, wherein said haploid plant is obtained from a haploid breeding population.

77. The method of claim 75, wherein the at least one genetic marker comprises a single nucleotide polymorphism (SNP), an insertion or deletion in DNA sequence (Indel), a simple sequence repeat of DNA sequence (SSR) a restriction fragment length polymorphism, a haplotype, or a tag SNP.

78. The method of claim 75, wherein the at least one phenotypic marker comprises at least one of a transcriptional profile, a metabolic profile, a nutrient composition profile, a protein expression profile, protein composition, protein levels, oil composition, oil levels, carbohydrate composition, carbohydrate levels, fatty acid composition, fatty acid levels, amino acid composition, amino acid levels, biopolymers, pharmaceuticals, starch composition, starch levels, fermentable starch, fermentation yield, fermentation efficiency, energy yield, secondary compounds, metabolites, morphological characteristics, and agronomic characteristics.

79. The method of Claim 75, further comprising the step of using an association determined in step (b) to make a selection in a plant breeding program.

80. The method of Claim 79, further comprising the step of doubling at least one haploid plant selected in said breeding program to obtain a doubled haploid plant.

81. The method of Claim 80, wherein the doubled haploid plant is used for introgression of the genotype of interest into at least a second plant for use in a plant breeding program.

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
1	NC0111829	1	0.3	0.034236	0.009483	G	Study 1	I283669	142	1
1	NC0024027	1	1	0.0003	0.102336	T	Study 3	--	141	2
1	NC0024027	1	1	--	--	T	Study 4	--	141	2
1	NC0024027	1	1	0.000436	0.025925	C	Study 1	CV048	141	2
1	NC0024027	1	1	0.013509	-0.0515	C	Study 1	CV082	141	2
1	NC0015697	1	1.4	0.043777	0.005404	G	Study 1	CV024	585	3
1	NC0002640	1	2.6	0.029802	0.003489	T	Study 1	CV099	383	4
1	NC0002640	1	2.6	0.011823	-0.01651	C	Study 1	CV113	383	4
1	NC0019086	1	5.7	0.013874	-0.05083	C	Study 1	CV082	401	5
1	NC0019524	1	5.8	0.009251	0.012704	C	Study 1	I283669	338	6
1	NC0033261	1	5.8	0.026044	0.064082	G	Study 1	CV128	92	7
1	NC0147181	1	6.7	0.009497	0.016068	G	Study 1	I283669	147	8
1	NC0147181	1	6.7	0.015544	0.185539	G	Study 1	CV125	147	8
1	NC0147181	1	6.7	0.001425	0.112232	G	Study 1	CV079	147	8
1	NC0147202	1	6.7	0.038382	-0.01465	T	Study 1	CV010	509	9
2	NC0111443	1	10.3	<.0001	-0.28289	A	Study 3	--	367	10
2	NC0043992	1	13.2	0.016852	-0.00981	A	Study 1	CV099	47	11
2	NC0043992	1	13.2	0.016466	0.082878	A	Study 1	CV126	47	11
2	NC0043994	1	13.2	0.008489	0.011912	C	Study 1	I283669	249	12
2	NC0043994	1	13.2	0.00067	0.021438	C	Study 1	I283669	249	12
2	NC0154927	1	18.5	0.027528	0.018791	C	Study 1	CV161	350	13
2	NC0070876	1	19.7	0.035824	0.009816	G	Study 1	I283669	438	14
2	NC0070876	1	19.7	0.000071	0.023793	G	Study 1	I283669	438	14
2	NC0070876	1	19.7	0.006703	-0.01111	C	Study 1	CV099	438	14
3	NC0066743	1	20.2	0.030831	0.005416	**	Study 1	CV024	595	15
3	NC0036199	1	20.6	0.020915	0.025886	A	Study 1	CV165	183	16
3	NC0036199	1	20.6	0.028426	0.021429	A	Study 1	CV165	183	16
3	NC0043185	1	22.6	0.025856	-0.01032	G	Study 1	CV082	230	17
3	NC0078736	1	24.3	--	--	*	Study 4	--	289	18
3	NC0078736	1	24.3	0.01126	0.089712	C	Study 1	CV079	289	18
3	NC0078736	1	24.3	0.000968	-0.01927	*	Study 1	CV093	289	18
3	NC0110473	1	24.6	0.001947	-0.01904	G	Study 1	CV093	194	19
3	NC0025418	1	26.4	0.000113	0.028173	ATC	Study 1	CV048	225	20

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
3	NC0025418	1	26.4	0.004849	0.007089	ATC	Study 1	CV137	225	20
3	NC0025418	1	26.4	0.014859	0.00354	ATC	Study 1	CV016	225	20
3	NC0025418	1	26.4	0.014859	0.00354	ATC	Study 1	CV016	225	20
3	NC0083894	1	26.5	--	--	C	Study 4	--	118	21
3	NC0147302	1	27.6	0.044474	-0.00532	T	Study 1	CV088	146	22
3	NC0147302	1	27.6	0.000008	0.025871	T	Study 1	I283669	146	22
3	NC0147302	1	27.6	0.00324	0.005147	T	Study 1	CV099	146	22
3	NC0147302	1	27.6	0.027879	-0.01508	C	Study 1	CV072	146	22
4	NC0028164	1	30.1	0.000049	0.139947	G	Study 1	CV082	237	23
4	NC0028164	1	30.1	0.000896	0.014317	G	Study 1	I283669	237	23
4	NC0028164	1	30.1	0.001984	-0.01302	G	Study 1	CV099	237	23
4	NC0028164	1	30.1	0.009606	0.007389	G	Study 1	CV099	237	23
4	NC0028164	1	30.1	0.016764	0.128532	C	Study 1	CV149	237	23
4	NC0028164	1	30.1	0.027912	0.0126	G	Study 1	CV159	237	23
4	NC0105051	1	31.4	0.019187	-0.01483	G	Study 1	CV059	426	24
4	NC0105051	1	31.4	0.015324	0.072924	C	Study 1	CV131	426	24
4	NC0105051	1	31.4	0.000114	0.019807	C	Study 1	I283669	426	24
4	NC0105051	1	31.4	0	0.043188	C	Study 1	I283669	426	24
4	NC0105051	1	31.4	0.015229	-0.02083	C	Study 1	CV064	426	24
4	NC0108303	1	31.7	0.001007	-0.08946	T	Study 1	CV050	543	25
4	NC0107227	1	34.1	0.009677	-0.33157	A	Study 1	CV130	54	26
4	NC0107227	1	34.1	0.004623	-0.01701	G	Study 1	CV093	54	26
4	NC0003563	1	34.5	--	--	G	Study 4	--	434	27
4	NC0003563	1	34.5	0.006903	0.11343	G	Study 1	CV166	434	27
4	NC0003563	1	34.5	0.021161	0.066975	G	Study 1	CV050	434	27
4	NC0003563	1	34.5	0.021183	0.119208	G	Study 1	CV125	434	27
4	NC0003563	1	34.5	0.043858	0.012263	G	Study 1	CV079	434	27
4	NC0003563	1	34.5	0.006671	0.022899	G	Study 1	CV161	434	27
4	NC0003563	1	34.5	0.031036	-0.02487	A	Study 1	I294213	434	27
4	NC0003563	1	34.5	0.019434	-0.02797	A	Study 1	CV112	434	27
4	NC0003563	1	34.5	0.02093	0.082079	G	Study 1	CV079	434	27
4	NC0113465	1	34.6	0.001084	0.024464	T	Study 1	CV048	80	28
4	NC0113465	1	34.6	0.014827	0.149222	T	Study 1	CV159	80	28

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
4	NC0113465	1	34.6	0.022392	0.013463	T	Study 1	CV159	80	28
4	NC0113465	1	34.6	0.001032	0.036529	T	Study 1	CV165	80	28
4	NC0113465	1	34.6	0.003918	0.028134	T	Study 1	CV165	80	28
4	NC0199573	1	37.2	--	--	T	Study 5	--	105	29
4	NC0144205	1	38.5	0	0.03375	T	Study 1	I283669	139	30
4	NC0144205	1	38.5	0.000055	0.013897	T	Study 1	I283669	139	30
4	NC0144205	1	38.5	0	0.029586	T	Study 1	I283669	139	30
4	NC0144205	1	38.5	0.00372	0.007952	T	Study 1	CV099	139	30
4	NC0144205	1	38.5	0.000672	0.005994	T	Study 1	CV099	139	30
5	NC0033770	1	40.3	0.001014	-0.0145	G	Study 1	CV099	75	31
5	NC0033770	1	40.3	0.010585	0.139469	C	Study 1	CV069	75	31
5	NC0033770	1	40.3	0.012479	0.143546	C	Study 1	CV160	75	31
5	NC0033770	1	40.3	0.047338	0.058002	C	Study 1	CV150	75	31
5	NC0033770	1	40.3	0.004807	0.091916	C	Study 1	CV150	75	31
5	NC0038710	1	43.8	0.040524	-0.08462	A	Study 1	CV045	360	32
5	NC0038710	1	43.8	0.01384	0.193651	A	Study 1	CV125	360	32
5	NC0110871	1	44.6	0.039621	0.164179	C	Study 1	CV073	378	33
5	NC0036685	1	45.8	0.035372	-0.11269	G	Study 1	CV053	203	34
5	NC0036685	1	45.8	0.018271	-0.19102	A	Study 1	CV069	203	34
5	NC0036685	1	45.8	0.00009	0.140649	G	Study 1	CV082	203	34
5	NC0036685	1	45.8	0.001189	0.17425	A	Study 1	CV149	203	34
5	NC0036685	1	45.8	0.048917	0.057356	A	Study 1	CV150	203	34
5	NC0036685	1	45.8	0.006246	0.089307	A	Study 1	CV150	203	34
5	NC0036685	1	45.8	0.014557	-0.02024	G	Study 1	CV063	203	34
5	NC0029694	1	46	0.000543	0.15273	C	Study 1	CV133	78	35
5	NC0029694	1	46	0.045977	-0.01474	G	Study 1	CV041	78	35
5	NC0052741	1	49.5	0.000043	0.02962	G	Study 1	CV048	411	36
5	NC0052741	1	49.5	0.000095	-0.02772	G	Study 1	CV139	411	36
5	NC0052741	1	49.5	0.013103	-0.11301	G	Study 1	CV068	411	36
5	NC0052741	1	49.5	0.012332	-0.06657	G	Study 1	CV011	411	36
5	NC0052741	1	49.5	0.005353	0.087885	G	Study 1	CV131	411	36
5	NC0052741	1	49.5	0	0.035716	G	Study 1	I283669	411	36
5	NC0052741	1	49.5	0	0.034619	G	Study 1	I283669	411	36

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
5	NC0052741	1	49.5	0.00012	0.012778	G	Study 1	I283669	411	36
5	NC0052741	1	49.5	0.025035	0.015256	G	Study 1	CV049	411	36
5	NC0052741	1	49.5	0.004544	0.123091	G	Study 1	CV125	411	36
5	NC0052741	1	49.5	0.03081	0.133684	G	Study 1	CV159	411	36
5	NC0052741	1	49.5	0.026453	0.131758	G	Study 1	CV157	411	36
5	NC0052741	1	49.5	0.000397	0.093446	G	Study 1	CV050	411	36
5	NC0052741	1	49.5	0.002057	0.156236	G	Study 1	CV125	411	36
5	NC0052741	1	49.5	0.000872	0.009598	G	Study 1	CV024	411	36
5	NC0052741	1	49.5	0.015105	-0.01269	G	Study 1	CV136	411	36
5	NC0052741	1	49.5	0.023099	0.013786	G	Study 1	CV142	411	36
5	NC0052741	1	49.5	0.02095	-0.01098	G	Study 1	CV088	411	36
5	NC0052741	1	49.5	0.038429	-0.03621	G	Study 1	CV010	411	36
5	NC0052741	1	49.5	0.021643	-0.00531	G	Study 1	CV010	411	36
5	NC0052741	1	49.5	0.000876	-0.03117	G	Study 1	CV010	411	36
5	NC0052741	1	49.5	0.00077	0.037249	G	Study 1	CV165	411	36
5	NC0052741	1	49.5	0.004239	0.027689	G	Study 1	CV165	411	36
5	NC0052741	1	49.5	0.000016	0.028741	G	Study 1	CV144	411	36
5	NC0049734	1	49.9	--	--	T	Study 5	--	462	37
6	NC0043571	1	50.3	0.045184	-0.07373	C	Study 1	CV041	336	38
6	NC0043571	1	50.3	0.011319	-0.095	C	Study 1	CV101	336	38
6	NC0038720	1	50.5	<.0001	-0.26363	C	Study 3	--	378	39
6	NC0038720	1	50.5	0.000072	-0.01561	T	Study 1	CV105	378	39
6	NC0038720	1	50.5	0.008965	0.112503	C	Study 1	CV125	378	39
6	NC0038720	1	50.5	0.004588	0.004643	C	Study 1	CV099	378	39
6	NC0148102	1	50.5	--	--	G	Study 4	--	163	40
6	NC0148102	1	50.5	0.033516	-0.05757	G	Study 1	CV050	163	40
6	NC0148102	1	50.5	0.030411	0.091659	G	Study 1	CV166	163	40
6	NC0009213	1	51.3	0.030527	-0.05804	T	Study 1	CV057	98	41
6	NC0035417	1	51.3	0.02657	0.018413	G	Study 1	CV161	176	42
6	NC0035417	1	51.3	0.000001	0.175452	G	Study 1	CV126	176	42
6	NC0035417	1	51.3	0.015318	0.086552	G	Study 1	CV079	176	42
6	NC0035417	1	51.3	0.024656	0.089317	G	Study 1	CV079	176	42
6	NC0041877	1	51.3	0.048151	0.009565	****	Study 1	CV069	77	43

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
6	NC0056126	1	51.3	<.0001	-0.14446	A	Study 3	--	250	44
6	NC0056126	1	51.3	0.020534	0.134419	A	Study 1	CV160	250	44
6	NC0152452	1	56.8	0	0.030349	G	Study 1	I283669	345	45
6	NC0152452	1	56.8	0.000201	-0.01555	G	Study 1	CV099	345	45
6	NC0152452	1	56.8	0.009202	0.004278	G	Study 1	CV099	345	45
6	NC0108891	1	58.2	--	--	T	Study 5	--	562	46
6	NC0113273	1	58.2	--	--	C	Study 5	--	111	47
6	NC0113273	1	58.2	0.010104	0.017704	C	Study 1	CV049	111	47
6	NC0113273	1	58.2	0.017765	-0.09709	C	Study 1	CV045	111	47
6	NC0113273	1	58.2	0.000455	0.02701	C	Study 1	CV144	111	47
6	NC0080697	1	58.4	--	--	G	Study 5	--	484	48
6	NC0080697	1	58.4	0.000028	0.145589	A	Study 1	CV082	484	48
6	NC0080697	1	58.4	0.0369	-0.01739	A	Study 1	CV063	484	48
6	NC0080697	1	58.4	0.028596	-0.01344	A	Study 1	CV065	484	48
7	NC0042173	1	60.2	0.002196	0.022689	TA	Study 1	CV048	91	49
7	NC0042173	1	60.2	0.006409	-0.13106	TA	Study 1	CV069	91	49
7	NC0042173	1	60.2	0.014415	-0.1113	TA	Study 1	CV068	91	49
7	NC0042173	1	60.2	0.000021	0.234914	TA	Study 1	CV069	91	49
7	NC0042173	1	60.2	0.000945	-0.12081	TA	Study 1	CV101	91	49
7	NC0042173	1	60.2	0.025031	-0.09162	TA	Study 1	CV075	91	49
7	NC0042173	1	60.2	0.013984	0.144166	TA	Study 1	CV070	91	49
7	NC0042173	1	60.2	0.000045	0.228173	**	Study 1	CV149	91	49
7	NC0113502	1	63.5	0.001208	-0.19751	C	Study 1	CV131	447	50
7	NC0113502	1	63.5	0.000173	0.018895	G	Study 1	I283669	447	50
7	NC0113502	1	63.5	0	0.02299	G	Study 1	I283669	447	50
7	NC0113502	1	63.5	0.030901	-0.00922	C	Study 1	CV010	447	50
7	NC0113502	1	63.5	0.001839	-0.08363	C	Study 1	CV050	447	50
7	NC0113502	1	63.5	0.015829	0.013654	C	Study 1	CV142	447	50
7	NC0113502	1	63.5	0.023512	-0.03917	C	Study 1	CV010	447	50
7	NC0113502	1	63.5	0.01846	-0.00539	C	Study 1	CV010	447	50
7	NC0029329	1	65.8	--	--	T	Study 4	--	497	51
7	NC0029329	1	65.8	0.044228	0.086584	C	Study 1	CV166	497	51
7	NC0029329	1	65.8	0.005862	0.162589	C	Study 1	CV070	497	51

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
7	NC0039205	1	65.8	0.000008	-0.01826	C	Study 1	CV099	233	52
7	NC0039205	1	65.8	0.016827	0.012547	C	Study 1	CV069	233	52
7	NC0039840	1	65.8	0.003155	0.131939	G	Study 1	CV133	82	53
7	NC0174834	1	65.8	--	--	C	Study 5	--	266	54
7	NC0000116	1	66	--	--	G	Study 4	--	284	55
7	NC0000116	1	66	0.026555	-0.20549	G	Study 1	CV088	284	55
7	NC0000116	1	66	0.011547	0.021667	G	Study 1	CV161	284	55
7	NC0000116	1	66	0.011475	0.014501	G	Study 1	CV142	284	55
7	NC0000116	1	66	0.000473	0.193665	G	Study 1	CV160	284	55
7	NC0000116	1	66	0.001382	0.03547	A	Study 1	CV165	284	55
7	NC0000116	1	66	0.027098	0.021496	A	Study 1	CV165	284	55
7	NC0000116	1	66	0.046525	0.009233	A	Study 1	CV012	284	55
7	NC0000116	1	66	0.046525	0.009233	A	Study 1	CV012	284	55
7	NC0009159	1	66	0	0.037243	G	Study 1	I283669	360	56
7	NC0040189	1	66.4	--	--	T	Study 4	--	325	57
7	NC0040189	1	66.4	0.000159	-0.01501	C	Study 1	CV105	325	57
7	NC0040189	1	66.4	0.000277	-0.28652	C	Study 1	CV069	325	57
7	NC0040189	1	66.4	0.000238	-0.02492	T	Study 1	CV072	325	57
7	NC0040189	1	66.4	0.000017	0.153607	C	Study 1	CV126	325	57
7	NC0200213	1	67.4	--	--	G	Study 5	--	39	58
8	NC0057022	1	70.1	0.0003	0.122684	T	Study 3	--	100	59
8	NC0014299	1	70.2	0.000533	0.207116	G	Study 1	CV157	488	60
8	NC0033819	1	70.2	0.039358	0.002775	A	Study 1	CV024	320	61
8	NC0033819	1	70.2	0.000016	0.016151	G	Study 1	I283669	320	61
8	NC0033819	1	70.2	0.014562	0.004324	G	Study 1	CV099	320	61
8	NC0033819	1	70.2	0.002104	-0.08032	A	Study 1	CV057	320	61
8	NC0038788	1	70.7	--	--	T	Study 5	--	380	62
8	NC0018320	1	72.4	0.003426	0.171713	C	Study 1	CV070	136	63
8	NC0018281	1	72.5	0.000045	-0.501	A	Study 1	CV130	248	64
8	NC0009578	1	73.5	--	--	G	Study 5	--	208	65
8	NC0009578	1	73.5	0.016603	0.017902	A	Study 1	CV048	208	65
8	NC0009578	1	73.5	0.000057	0.121862	A	Study 1	CV131	208	65
8	NC0009578	1	73.5	0	0.028927	A	Study 1	I283669	208	65

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
8	NC0146543	1	73.7	--	--	T	Study 4	--	269	66
8	NC0146543	1	73.7	0.000742	-0.12321	T	Study 1	CV101	269	66
8	NC0155962	1	73.7	--	--	G	Study 5	--	659	67
8	NC0016876	1	74.9	0.005905	0.078776	G	Study 2	--	91	68
8	NC0016876	1	74.9	0.014302	0.014671	A	Study 1	CV150	91	68
8	NC0039067	1	75.4	--	--	T	Study 4	--	172	69
8	NC0039067	1	75.4	0.000157	-0.01491	C	Study 1	CV105	172	69
8	NC0039067	1	75.4	0.000078	0.207134	C	Study 1	CV069	172	69
8	NC0039067	1	75.4	0.041629	0.006761	C	Study 1	CV102	172	69
8	NC0039812	1	77.8	0.0002	0.106174	T	Study 3	--	75	70
8	NC0039812	1	77.8	--	--	T	Study 4	--	75	70
8	NC0039812	1	77.8	0.002254	0.012704	T	Study 1	CV137	75	70
8	NC0039812	1	77.8	0.021728	0.010835	A	Study 1	I283669	75	70
8	NC0105022	1	79.5	--	--	G	Study 4	--	63	71
8	NC0105022	1	79.5	0.000714	0.014095	G	Study 1	CV137	63	71
8	NC0105022	1	79.5	0.000009	0.338016	G	Study 1	CV073	63	71
8	NC0105022	1	79.5	0.003632	0.15662	G	Study 1	CV149	63	71
8	NC0105022	1	79.5	0.003365	0.172231	G	Study 1	CV070	63	71
8	NC0105022	1	79.5	0.01818	0.013491	G	Study 1	CV142	63	71
8	NC0105022	1	79.5	0.018075	-0.01554	G	Study 1	CV077	63	71
8	NC0077749	1	79.6	0.028669	0.0143	T	Study 1	CV169	341	72
8	NC0077750	1	79.6	0	-0.26601	T	Study 1	CV069	441	73
8	NC0077750	1	79.6	0.022451	0.015363	T	Study 1	CV049	441	73
9	NC0110365	1	81.9	0.000006	0.249912	A	Study 1	CV160	427	74
9	NC0009449	1	82	--	--	G	Study 4	--	188	75
9	NC0033372	1	82	--	--	C	Study 5	--	239	76
9	NC0033372	1	82	0.000238	-0.01522	C	Study 1	CV099	239	76
9	NC0033372	1	82	0.030005	-0.00688	A	Study 1	CV089	239	76
9	NC0033372	1	82	0.03887	-0.01037	A	Study 1	CV088	239	76
9	NC0105925	1	82.1	--	--	G	Study 4	--	269	77
9	NC0105925	1	82.1	0.000023	-0.39513	A	Study 1	CV088	269	77
9	NC0105925	1	82.1	0.001341	-0.114	A	Study 1	CV101	269	77
9	NC0105925	1	82.1	0.008233	-0.11485	G	Study 1	CV075	269	77

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
9	NC0105925	1	82.1	0.000856	-0.02243	A	Study 1	CV072	269	77
9	NC0105925	1	82.1	0.009207	0.091617	A	Study 1	CV126	269	77
9	NC0113462	1	82.1	0.001028	0.204388	A	Study 1	CV157	308	78
9	NC0148156	1	83.2	--	--	C	Study 5	--	267	79
9	NC0148156	1	83.2	0	-0.38495	C	Study 1	CV069	267	79
9	NC0148156	1	83.2	0.000002	0.251324	C	Study 1	CV069	267	79
9	NC0033533	1	84.3	--	--	T	Study 4	--	113	80
9	NC0033533	1	84.3	--	--	T	Study 5	--	113	80
9	NC0033533	1	84.3	0.019404	0.052907	T	Study 1	CV006	113	80
9	NC0033533	1	84.3	0.000218	-0.09985	T	Study 1	CV050	113	80
9	NC0033533	1	84.3	0.000005	0.278326	T	Study 1	CV073	113	80
9	NC0033533	1	84.3	0.000637	0.097206	T	Study 1	CV050	113	80
9	NC0033533	1	84.3	0.047392	0.00658	T	Study 1	CV050	113	80
9	NC0033533	1	84.3	0.047315	0.108913	T	Study 1	CV164	113	80
9	NC0033533	1	84.3	0.029676	0.053936	T	Study 1	CV135	113	80
9	NC0033533	1	84.3	0.019668	-0.00716	T	Study 1	CV089	113	80
9	NC0033533	1	84.3	0.01605	0.007894	T	Study 1	CV102	113	80
9	NC0036506	1	84.6	--	--	T	Study 4	--	81	81
9	NC0036506	1	84.6	0.0278	-0.10872	T	Study 1	CV068	81	81
9	NC0036506	1	84.6	0.014213	0.094549	T	Study 1	CV082	81	81
9	NC0036506	1	84.6	0.012076	-0.09052	C	Study 1	CV041	81	81
9	NC0036506	1	84.6	0.021669	-0.04158	C	Study 1	CV010	81	81
9	NC0036506	1	84.6	0.009981	-0.01149	C	Study 1	CV010	81	81
9	NC0036506	1	84.6	0.015033	0.016512	T	Study 1	CV144	81	81
9	NC0043559	1	84.6	--	--	C	Study 4	--	300	82
9	NC0172493	1	86.9	--	--	T	Study 5	--	121	83
9	NC0173465	1	86.9	--	--	G	Study 5	--	540	84
9	NC0004287	1	88.1	0.03169	0.011529	C	Study 1	CV069	83	85
9	NC0173852	1	88.1	--	--	G	Study 5	--	556	86
10	NC0111854	1	91.4	0	-0.41188	AGT	Study 1	CV069	308	87
10	NC0111854	1	91.4	0	-0.50491	AGT	Study 1	CV088	308	87
10	NC0111854	1	91.4	0.009565	0.01692	AGT	Study 1	CV049	308	87
10	NC0111854	1	91.4	0.012466	0.135944	AGT	Study 1	CV149	308	87

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
10	NC0111854	1	91.4	0.000014	-0.56207	AGT	Study 1	CV130	308	87
10	NC0111854	1	91.4	0.017078	0.012712	AGT	Study 1	CV069	308	87
10	NC0111854	1	91.4	0.000345	0.023099	AGT	Study 1	CV169	308	87
10	NC0035579	1	94.5	--	--	G	Study 4	--	282	88
10	NC0035579	1	94.5	0	-0.29537	A	Study 1	CV069	282	88
10	NC0035579	1	94.5	0	0.312066	A	Study 1	CV069	282	88
10	NC0035579	1	94.5	0.00003	0.01724	A	Study 1	CV137	282	88
10	NC0035579	1	94.5	0.000018	0.338835	A	Study 1	CV073	282	88
10	NC0035579	1	94.5	0.003056	0.398766	A	Study 1	CV167	282	88
10	NC0035579	1	94.5	0.039875	0.012223	A	Study 1	CV150	282	88
10	NC0035579	1	94.5	0.001468	0.019444	A	Study 1	CV142	282	88
10	NC0035579	1	94.5	0.000415	0.019044	A	Study 1	CV142	282	88
10	NC0019256	1	96.4	0.007845	0.130402	G	Study 1	CV118	354	89
10	NC0025863	1	96.7	--	--	G	Study 4	--	107	90
10	NC0025863	1	96.7	0.008478	0.15461	A	Study 1	CV070	107	90
10	NC0068281	1	97.8	0.001268	-0.01406	T	Study 1	CV105	484	91
10	NC0072083	1	97.8	--	--	T	Study 4	--	416	92
10	NC0069524	1	99.9	0.003733	-0.05	A	Study 1	CV010	514	93
11	NC0016873	1	101	0.029145	-0.00653	G	Study 1	CV089	35	94
11	NC0016873	1	101	0.028498	0.008016	G	Study 1	CV102	35	94
11	NC0015205	1	101.5	--	--	G	Study 5	--	401	95
11	NC0015205	1	101.5	0.028009	0.01562	G	Study 1	CV074	401	95
11	NC0015205	1	101.5	0	0.339461	A	Study 1	CV073	401	95
11	NC0015205	1	101.5	0.006868	-0.01831	A	Study 1	CV072	401	95
11	NC0015205	1	101.5	0.034269	0.012401	A	Study 1	CV079	401	95
11	NC0015205	1	101.5	0.013942	-0.01512	G	Study 1	CV065	401	95
11	NC0057735	1	102.5	<.0001	0.31455	T	Study 3	--	556	96
11	NC0057735	1	102.5	--	--	T	Study 5	--	556	96
11	NC0011522	1	103.1	<.0001	-0.15577	A	Study 3	--	250	97
11	NC0153831	1	103.5	<.0001	0.653221	T	Study 3	--	466	98
11	NC0027375	1	103.7	0.002824	-0.05336	A	Study 1	CV010	474	99
11	NC0027375	1	103.7	0.002289	-0.01304	A	Study 1	CV010	474	99
11	NC0027375	1	103.7	0.013036	0.08742	C	Study 1	CV126	474	99

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
11	NC0027375	1	103.7	0.022507	-0.0996	A	Study 1	CV075	474	99
11	NC0028351	1	103.7	0.040047	-0.00916	A	Study 1	CV099	475	100
11	NC0038741	1	103.7	<.0001	-0.32552	A	Study 3	--	239	101
11	NC0038741	1	103.7	--	--	G	Study 4	--	239	101
11	NC0038741	1	103.7	0.001616	-0.0843	G	Study 1	CV050	239	101
11	NC0038741	1	103.7	0.000001	0.14009	A	Study 1	CV131	239	101
11	NC0038741	1	103.7	0.010888	0.199048	G	Study 1	CV132	239	101
11	NC0038741	1	103.7	0.005078	0.033261	G	Study 1	CV132	239	101
11	NC0038741	1	103.7	0.020662	0.285551	G	Study 1	CV156	239	101
11	NC0038741	1	103.7	0.00021	0.10634	G	Study 1	CV050	239	101
11	NC0066981	1	103.7	<.0001	-0.13221	C	Study 3	--	147	102
11	NC0066981	1	103.7	0	-0.51731	C	Study 1	CV088	147	102
11	NC0066981	1	103.7	0.003213	0.025264	C	Study 1	CV162	147	102
11	NC0066981	1	103.7	0.010175	-0.01374	C	Study 1	CV136	147	102
11	NC0200155	1	103.8	--	--	G	Study 5	--	394	103
11	NC0005215	1	104.8	<.0001	-0.16825	A	Study 3	--	495	104
11	NC0005215	1	104.8	--	--	T	Study 5	--	495	104
11	NC0005215	1	104.8	0.041512	0.011815	A	Study 1	CV159	495	104
11	NC0035117	1	105.1	0.00003	0.01814	G	Study 1	CV137	198	105
11	NC0035117	1	105.1	0.000009	0.266534	G	Study 1	CV160	198	105
11	NC0008984	1	105.5	--	--	T	Study 4	--	376	106
11	NC0110353	1	105.5	0.000494	0.018318	G	Study 1	CV142	134	107
11	NC0199546	1	106	--	--	C	Study 5	--	224	108
11	NC0155584	1	106.4	0.023636	0.013723	G	Study 1	CV142	190	109
11	NC0041836	1	107.7	--	--	*	Study 4	--	92	110
11	NC0014644	1	107.8	0.002	-0.11522	C	Study 3	--	485	111
11	NC0014644	1	107.8	--	--	G	Study 5	--	485	111
11	NC0014644	1	107.8	0.005112	-0.07254	G	Study 1	CV057	485	111
11	NC0014644	1	107.8	0.010697	0.153794	C	Study 1	CV070	485	111
11	NC0014644	1	107.8	0.000953	0.022739	C	Study 1	CV169	485	111
11	NC0029829	1	108	--	--	G	Study 5	--	157	112
11	NC0107044	1	108	0.032742	0.014649	C	Study 1	CV144	845	113
11	NC0111828	1	109.2	0	-0.28348	C	Study 1	CV069	584	114

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
11	NC0111828	1	109.2	0.001346	0.016741	C	Study 1	CV142	584	114
11	NC0053983	1	109.4	--	--	T	Study 5	--	471	115
11	NC0053983	1	109.4	0.035647	0.013616	T	Study 1	I283669	471	115
12	NC0008901	1	110.8	0	-0.38107	T	Study 1	CV069	119	116
12	NC0008901	1	110.8	0	0.301922	T	Study 1	CV069	119	116
12	NC0008901	1	110.8	0.000154	0.497693	T	Study 1	CV167	119	116
12	NC0008901	1	110.8	0.046663	-0.01351	T	Study 1	CV072	119	116
12	NC0143254	1	110.9	--	--	G	Study 5	--	163	117
12	NC0080733	1	111	0.003001	0.01929	T	Study 1	CV049	754	118
12	NC0033728	1	113.3	--	--	C	Study 4	--	83	119
12	NC0033728	1	113.3	0.043727	0.011941	A	Study 1	CV069	83	119
12	NC0029506	1	113.6	--	--	G	Study 5	--	808	120
12	NC0002688	1	114.6	0.030028	-0.01027	T	Study 1	CV105	69	121
12	NC0002688	1	114.6	0.000099	0.02509	C	Study 1	I283669	69	121
12	NC0002688	1	114.6	0.000827	0.025773	T	Study 1	CV169	69	121
12	NC0004176	1	116.3	0.020065	0.005269	C	Study 1	CV051	61	122
12	NC0004176	1	116.3	0.001628	0.251705	C	Study 1	CV073	61	122
12	NC0004176	1	116.3	0.027304	0.130251	C	Study 1	CV070	61	122
12	NC0050366	1	118.7	0.012475	0.183464	************	Study 1	CV129	306	123
12	NC0050366	1	118.7	0.017165	-0.06154	************	Study 1	CV057	306	123
12	NC0050366	1	118.7	0.009605	0.09125	************	Study 1	CV126	306	123
12	NC0050366	1	118.7	0.029065	0.013738	************	Study 1	CV159	306	123
12	NC0039351	1	118.8	--	--	G	Study 4	--	678	124
12	NC0039351	1	118.8	0.001394	-0.16829	G	Study 1	CV068	678	124
12	NC0039351	1	118.8	0.026093	0.048373	A	Study 1	CV006	678	124
12	NC0143864	1	118.8	--	--	C	Study 5	--	315	125
12	NC0146461	1	118.8	--	--	T	Study 5	--	41	126
13	NC0107701	1	121	0	-0.39377	G	Study 1	CV069	376	127
13	NC0107701	1	121	0.026794	0.012866	A	Study 1	CV159	376	127
13	NC0035132	1	121.5	0	-0.75003	GAGAG	Study 1	CV130	394	128
13	NC0036448	1	124.4	0.004105	-0.12039	T	Study 1	CV075	167	129
13	NC0036448	1	124.4	0.013854	-0.01675	T	Study 1	CV072	167	129
13	NC0036448	1	124.4	0.021927	-0.00704	C	Study 1	CV089	167	129

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
13	NC0034627	1	126	0	0.396474	A	Study 1	CV073	415	130
13	NC0034627	1	126	0.000852	0.197596	A	Study 1	CV160	415	130
13	NC0035547	1	126	--	--	T	Study 4	--	190	131
13	NC0035547	1	126	0.000037	-0.39867	C	Study 1	CV088	190	131
13	NC0035547	1	126	0.000483	0.015284	C	Study 1	CV137	190	131
13	NC0035547	1	126	0.000489	-0.09452	C	Study 1	CV050	190	131
13	NC0035547	1	126	0.000052	0.168203	C	Study 1	CV166	190	131
13	NC0035547	1	126	0.001475	0.093098	C	Study 1	CV050	190	131
13	NC0035547	1	126	0.040027	0.007033	C	Study 1	CV050	190	131
13	NC0035547	1	126	0.036943	0.123063	C	Study 1	CV070	190	131
13	NC0039531	1	126	0.030394	0.015354	G	Study 1	I283669	215	132
13	NC0039531	1	126	0.039109	-0.05408	C	Study 1	CV052	215	132
13	NC0111780	1	126.1	0.000029	-0.19976	A	Study 1	CV069	284	133
13	NC0028187	1	127.3	--	--	G	Study 5	--	343	134
13	NC0040655	1	128.9	0.004351	-0.018	A	Study 1	CV065	59	135
14	NC0107077	1	130.7	0.005469	-0.00887	G	Study 1	I294213	380	136
14	NC0107077	1	130.7	0.006096	-0.14266	A	Study 1	CV068	380	136
14	NC0107077	1	130.7	0.001419	0.021099	A	Study 1	CV049	380	136
14	NC0107077	1	130.7	0.006381	0.160018	A	Study 1	CV157	380	136
14	NC0107077	1	130.7	0.013837	0.013534	A	Study 1	CV007	380	136
14	NC0111987	1	132.8	0.036863	0.079081	T	Study 1	CV082	416	137
14	NC0111987	1	132.8	0.006906	-0.01323	A	Study 1	CV053	416	137
14	NC0111987	1	132.8	0.003237	0.02031	T	Study 1	CV169	416	137
14	NC0008719	1	137.1	--	--	G	Study 5	--	244	138
14	NC0008719	1	137.1	0.00266	0.162115	G	Study 1	CV069	244	138
14	NC0008719	1	137.1	0.012024	0.328433	G	Study 1	CV167	244	138
14	NC0008719	1	137.1	0.001293	0.02364	G	Study 1	CV169	244	138
14	NC0154883	1	137.4	0.048743	-0.03626	C	Study 1	CV070	991	139
14	NC0154883	1	137.4	0.020375	0.13651	C	Study 1	CV070	991	139
14	NC0154883	1	137.4	0	-0.71062	C	Study 1	CV130	991	139
15	NC0108100	1	142.1	0.031337	0.013987	GGC	Study 1	CV159	387	140
15	NC0108100	1	142.1	0.003782	0.016631	GGC	Study 1	CV159	387	140
15	NC0024096	1	145.2	0.016863	-0.25053	G	Study 1	CV088	212	141

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
15	NC0024096	1	145.2	0.043688	-0.00976	T	Study 1	CV053	212	141
15	NC0024096	1	145.2	0.035957	0.012589	T	Study 1	CV013	212	141
15	NC0024096	1	145.2	0.043183	-0.01385	G	Study 1	CV072	212	141
15	NC0155887	1	145.3	0.00504	0.098877	G	Study 1	CV126	49	142
15	NC0199385	1	145.3	--	--	T	Study 5	--	160	143
15	NC0023774	1	146.1	0.001574	0.100805	G	Study 1	CV131	388	144
15	NC0023774	1	146.1	0	0.313511	G	Study 1	CV073	388	144
15	NC0023774	1	146.1	0.00035	-0.14063	G	Study 1	CV075	388	144
15	NC0023774	1	146.1	0.004933	0.080017	A	Study 1	CV050	388	144
15	NC0023774	1	146.1	0.035029	-0.01769	A	Study 1	CV063	388	144
16	NC0147024	1	153.2	0.026141	-0.00661	C	Study 1	CV052	770	145
16	NC0107621	1	153.5	0.026884	0.176284	*******	Study 1	CV132	366	146
16	NC0107621	1	153.5	0.015765	-0.01255	*******	Study 1	CV136	366	146
16	NC0107621	1	153.5	0.000069	-0.52234	*******	Study 1	CV130	366	146
16	NC0107621	1	153.5	0.039525	0.012946	*******	Study 1	CV159	366	146
16	NC0107621	1	153.5	0.002146	0.017706	*******	Study 1	CV159	366	146
16	NC0012090	1	154.5	0.000243	0.16941	C	Study 1	CV166	289	147
16	NC0040338	1	156.3	--	--	T	Study 4	--	458	148
16	NC0040338	1	156.3	0.03526	-0.01234	T	Study 1	CV040	458	148
16	NC0038247	1	157	--	--	G	Study 5	--	267	149
16	NC0016755	1	159.7	0.025959	-0.00718	T	Study 1	I294213	141	150
16	NC0016755	1	159.7	0.005005	0.006356	C	Study 1	CV051	141	150
16	NC0016755	1	159.7	0.029313	0.172558	C	Study 1	CV073	141	150
16	NC0016755	1	159.7	0.010956	0.32269	C	Study 1	CV167	141	150
16	NC0016755	1	159.7	0.002286	-0.05528	C	Study 1	CV070	141	150
16	NC0016755	1	159.7	0.004065	-0.0194	C	Study 1	CV072	141	150
16	NC0036863	1	159.8	0.0024	0.100323	T	Study 3	--	287	151
16	NC0036863	1	159.8	--	--	T	Study 4	--	287	151
16	NC0036863	1	159.8	0.044448	-0.00908	T	Study 1	CV105	287	151
16	NC0036863	1	159.8	0.017248	0.029062	T	Study 1	CV154	287	151
17	NC0068400	1	160.5	--	--	C	Study 5	--	462	152
17	NC0041280	1	161.4	0.011076	0.011001	C	Study 1	CV137	223	153
17	NC0050719	1	161.4	0.000301	-0.13715	G	Study 1	CV075	136	154

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
17	NC0111052	1	162.2	0.004792	0.090205	G	Study 1	CV131	315	155
17	NC0111052	1	162.2	0.000069	0.247737	G	Study 1	CV073	315	155
17	NC0111052	1	162.2	0.004221	0.022368	G	Study 1	CV169	315	155
17	NC0200141	1	162.2	--	--	G	Study 5	--	743	156
17	NC0109328	1	162.9	0.008108	-0.01304	A	Study 1	CV053	552	157
17	NC0109328	1	162.9	0.011579	-0.00813	A	Study 1	CV052	552	157
17	NC0109328	1	162.9	0.023268	0.012074	G	Study 1	CV142	552	157
17	NC0070305	1	166.5	--	--	T	Study 4	--	532	158
17	NC0021568	1	167.1	0.02998	-0.00765	C	Study 1	CV080	90	159
17	NC0070702	1	167.1	0.000649	-0.02101	C	Study 1	CV065	1001	160
17	NC0004453	1	169.3	0.040369	0.089619	C	Study 1	CV093	361	161
17	NC0004453	1	169.3	0.02063	0.009746	C	Study 1	CV137	361	161
17	NC0004453	1	169.3	0.000171	0.157862	C	Study 1	CV166	361	161
17	NC0009626	1	169.6	--	--	G	Study 5	--	236	162
17	NC0009626	1	169.6	0.039686	0.058912	G	Study 1	CV128	236	162
17	NC0009626	1	169.6	0.046176	0.069951	G	Study 1	CV126	236	162
17	NC0009626	1	169.6	0.035248	0.022494	C	Study 1	CV134	236	162
18	NC0069565	1	172.1	0.010716	0.014683	G	Study 1	CV159	591	163
18	NC0105648	1	172.2	0.004942	0.017025	T	Study 1	I283669	264	164
18	NC0105648	1	172.2	0.014637	-0.01388	C	Study 1	I294213	264	164
18	NC0199667	1	173.1	--	--	T	Study 5	--	212	165
18	NC0067728	1	173.7	--	--	T	Study 4	--	218	166
18	NC0067728	1	173.7	0.015392	-0.01486	C	Study 1	CV065	218	166
18	NC0109882	1	174.1	0.024287	-0.01719	C	Study 1	CV041	295	167
18	NC0109882	1	174.1	0.013074	-0.01205	C	Study 1	CV053	295	167
18	NC0109882	1	174.1	0.011058	0.068528	C	Study 1	CV168	295	167
18	NC0004981	1	174.6	--	--	T	Study 4	--	153	168
18	NC0004981	1	174.6	0.000023	-0.5592	T	Study 1	CV130	153	168
18	NC0069344	1	176.9	0.049895	-0.00489	A	Study 1	CV018	206	169
18	NC0040092	1	177.3	--	--	G	Study 5	--	327	170
18	NC0108030	1	179.2	--	--	T	Study 4	--	95	171
18	NC0108030	1	179.2	0.021664	0.236544	T	Study 1	CV109	95	171
18	NC0108030	1	179.2	0.003403	0.080668	C	Study 1	CV116	95	171

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
18	NC0108030	1	179.2	0.002547	0.269316	T	Study 1	CV161	95	171
18	NC0108030	1	179.2	0.025776	-0.0138	C	Study 1	CV093	95	171
18	NC0027567	1	179.4	0.034385	-0.26596	G	Study 1	CV112	79	172
18	NC0027567	1	179.4	0.000191	-0.08989	G	Study 1	I294213	79	172
18	NC0027567	1	179.4	0.023899	-0.02222	G	Study 1	I294213	79	172
18	NC0027567	1	179.4	0.0123	-0.02083	C	Study 1	CV057	79	172
19	NC0016724	1	180.8	--	--	T	Study 4	--	88	173
19	NC0016724	1	180.8	0.008725	0.338865	C	Study 1	CV167	88	173
19	NC0016724	1	180.8	0.045455	-0.01228	T	Study 1	CV065	88	173
19	NC0106296	1	181	0.015245	-0.14475	G	Study 1	CV131	178	174
19	NC0106296	1	181	0.0274	0.011628	G	Study 1	CV142	178	174
19	NC0004909	1	182.1	0.008957	-0.0073	T	Study 1	CV052	324	175
19	NC0004909	1	182.1	0.047207	-0.00715	A	Study 1	CV080	324	175
19	NC0200153	1	182.8	--	--	C	Study 5	--	151	176
19	NC0005098	1	183.9	--	--	G	Study 5	--	133	177
19	NC0005098	1	183.9	0.005439	-0.16305	A	Study 1	CV131	133	177
19	NC0005098	1	183.9	0.000408	-0.02569	G	Study 1	CV041	133	177
19	NC0005098	1	183.9	0.039397	0.008647	G	Study 1	CV137	133	177
19	NC0005098	1	183.9	0.002445	0.272181	G	Study 1	CV161	133	177
19	NC0005098	1	183.9	0.004851	0.016224	A	Study 1	CV159	133	177
19	NC0032240	1	185.3	0.000253	-0.08866	T	Study 1	I294213	427	178
19	NC0032240	1	185.3	0.000535	0.145473	A	Study 1	CV166	427	178
19	NC0032240	1	185.3	0.033345	-0.01183	T	Study 1	I294213	427	178
19	NC0032240	1	185.3	0.015729	0.070549	A	Study 1	CV150	427	178
20	NC0039502	1	195.5	0.045861	0.007052	G	Study 1	CV102	41	179
20	NC0039502	1	195.5	0.034518	-0.01834	A	Study 1	CV057	41	179
20	NC0039502	1	195.5	0.034278	-0.0143	A	Study 1	CV083	41	179
20	NC0039502	1	195.5	0.017125	0.069632	G	Study 1	CV150	41	179
20	NC0111289	1	195.5	0.001864	-0.02278	********	Study 1	CV041	628	180
20	NC0111289	1	195.5	0.031502	0.023656	TGATATGC	Study 1	CV134	628	180
20	NC0015937	1	197.7	--	--	T	Study 5	--	394	181
20	NC0008982	1	198.4	--	--	G	Study 5	--	359	182
20	NC0008982	1	198.4	0.003123	-0.01418	G	Study 1	CV053	359	182

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
20	NC0008982	1	198.4	0.001701	0.088803	G	Study 1	CV116	359	182
20	NC0008982	1	198.4	0.033805	-0.07295	G	Study 1	CV017	359	182
20	NC0008982	1	198.4	0.005741	-0.00842	G	Study 1	CV052	359	182
20	NC0008982	1	198.4	0.007367	0.112934	G	Study 1	CV166	359	182
20	NC0008982	1	198.4	0.030501	0.278564	G	Study 1	CV167	359	182
20	NC0008982	1	198.4	0.005452	0.016077	A	Study 1	CV159	359	182
20	NC0040427	1	199.4	0.0019	-0.07854	T	Study 1	I294213	213	183
20	NC0040427	1	199.4	0.012537	-0.01562	T	Study 1	CV093	213	183
21	NC0113311	1	201.5	0.0007	0.116798	G	Study 3	--	98	184
21	NC0200182	1	201.9	--	--	G	Study 5	--	568	185
21	NC0013584	1	204.4	0.001272	-0.18981	C	Study 1	CV131	304	186
21	NC0013584	1	204.4	0.023005	0.047908	C	Study 1	CV067	304	186
21	NC0013584	1	204.4	0.000759	0.091944	C	Study 1	CV116	304	186
21	NC0013584	1	204.4	0.001666	-0.01037	C	Study 1	CV052	304	186
21	NC0013584	1	204.4	0.033867	0.062385	T	Study 1	CV128	304	186
21	NC0013584	1	204.4	0.024529	0.013142	T	Study 1	CV159	304	186
21	NC0013584	1	204.4	0.001223	-0.02312	T	Study 1	CV083	304	186
21	NC0111792	1	205.8	0.001994	0.137484	A	Study 1	CV093	244	187
21	NC0031264	1	205.9	0.000649	-0.01606	T	Study 1	CV053	552	188
21	NC0023209	1	206.3	--	--	G	Study 5	--	509	189
21	NC0033995	1	206.4	--	--	T	Study 5	--	199	190
21	NC0035961	1	206.7	0.026262	0.050164	T	Study 1	CV074	223	191
21	NC0035961	1	206.7	0.04561	0.058732	C	Study 1	CV120	223	191
21	NC0039896	1	207.6	--	--	C	Study 5	--	648	192
21	NC0009701	1	207.9	0.001068	-0.02499	G	Study 1	CV041	429	193
21	NC0009701	1	207.9	0.027275	-0.01135	G	Study 1	CV088	429	193
21	NC0009701	1	207.9	0.022402	-0.01456	A	Study 1	CV093	429	193
21	NC0009701	1	207.9	0.022594	-0.01534	A	Study 1	CV113	429	193
21	NC0014038	1	207.9	--	--	G	Study 5	--	78	194
21	NC0014038	1	207.9	0.043325	0.022897	G	Study 1	CV134	78	194
21	NC0016059	1	207.9	0.003762	-0.0859	G	Study 1	CV017	239	195
21	NC0016059	1	207.9	0.039384	-0.05288	T	Study 1	I294213	239	195
21	NC0016059	1	207.9	0.038043	-0.01094	G	Study 1	CV088	239	195

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
21	NC0039486	1	207.9	--	--	C	Study 5	--	201	196
21	NC0039486	1	207.9	0.010733	-0.34331	A	Study 1	CV130	201	196
21	NC0039486	1	207.9	0.004472	-0.02445	C	Study 1	CV057	201	196
21	NC0039486	1	207.9	0.012904	0.152002	A	Study 1	CV160	201	196
21	NC0188030	1	207.9	--	--	T	Study 5	--	528	197
22	NC0009082	1	212.7	0.005805	-0.14991	A	Study 1	CV131	388	198
22	NC0009082	1	212.7	0.046329	-0.00858	G	Study 1	CV095	388	198
22	NC0009082	1	212.7	0.046167	-0.01054	G	Study 1	CV136	388	198
22	NC0173402	1	217	--	--	G	Study 5	--	94	199
23	NC0015344	1	221.1	0.0004	0.093073	G	Study 3	--	420	200
23	NC0015344	1	221.1	0.011482	-0.01861	A	Study 1	CV041	420	200
23	NC0015344	1	221.1	0.006031	-0.08603	A	Study 1	CV017	420	200
23	NC0015344	1	221.1	0.038454	-0.04919	A	Study 1	CV052	420	200
23	NC0015344	1	221.1	0.009329	-0.00756	A	Study 1	CV052	420	200
23	NC0015344	1	221.1	0.010429	0.107685	G	Study 1	CV166	420	200
23	NC0015344	1	221.1	0.004057	-0.01829	A	Study 1	CV093	420	200
23	NC0015344	1	221.1	0.041054	-0.01351	A	Study 1	CV113	420	200
23	NC0199731	1	228.1	--	--	T	Study 5	--	91	201
24	NC0146570	1	237	0.030193	-0.08207	T	Study 1	CV017	232	202
24	NC0146570	1	237	0.031061	0.06269	T	Study 1	CV120	232	202
24	NC0110139	1	237.2	--	--	T	Study 4	--	224	203
24	NC0107440	1	237.6	--	--	G	Study 5	--	376	204
24	NC0107440	1	237.6	0.010223	0.013607	C	Study 1	CV069	376	204
24	NC0008996	1	238.1	0.019093	0.007248	A	Study 1	CV170	230	205
24	NC0003691	1	238.5	0.001348	0.085352	G	Study 1	CV116	364	206
24	NC0003691	1	238.5	0.027064	0.021808	G	Study 1	CV135	364	206
25	NC0013490	1	240.7	0.043432	-0.00646	T	Study 1	I294213	482	207
25	NC0013490	1	240.7	0.019669	0.068741	C	Study 1	CV128	482	207
25	NC0013490	1	240.7	0.030817	0.011039	T	Study 1	CV069	482	207
25	NC0030840	1	245.1	0.00152	0.154041	G	Study 1	CV023	413	208
25	NC0030840	1	245.1	0.013522	-0.0074	A	Study 1	CV089	413	208
25	NC0030840	1	245.1	0.033045	-0.01363	A	Study 1	CV113	413	208
26	NC0003506	1	253.1	0.031762	0.010865	C	Study 1	CV069	321	209

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
26	NC0002635	1	254.8	0.01201	0.068747	G	Study 1	CV116	188	210
26	NC0002635	1	254.8	0.032332	0.062706	G	Study 1	CV128	188	210
26	NC0002635	1	254.8	0.043003	-0.01449	G	Study 1	CV010	188	210
26	NC0002635	1	254.8	0.010337	0.013038	G	Study 1	CV069	188	210
26	NC0002635	1	254.8	0.039484	0.009954	G	Study 1	CV012	188	210
26	NC0002635	1	254.8	0.039484	0.009954	G	Study 1	CV012	188	210
26	NC0005177	1	256.5	0.007183	0.026315	A	Study 1	CV135	420	211
26	NC0005177	1	256.5	0.016622	-0.00647	T	Study 1	CV138	420	211
27	NC0196279	2	0	--	--	T	Study 5	--	333	212
27	NC0031064	2	2.9	0.021452	0.011526	C	Study 1	CV006	118	213
27	NC0009867	2	3.3	--	--	T	Study 4	--	245	214
27	NC0009867	2	3.3	0.033674	-0.00723	T	Study 1	CV122	245	214
27	NC0009867	2	3.3	0.007895	0.195296	T	Study 1	CV107	245	214
27	NC0009867	2	3.3	0.044737	0.035844	T	Study 1	CV054	245	214
27	NC0009867	2	3.3	0.018891	0.01357	T	Study 1	I283669	245	214
27	NC0009867	2	3.3	0.020274	-0.08419	T	Study 1	CV112	245	214
27	NC0009867	2	3.3	0.016588	-0.09158	T	Study 1	CV075	245	214
27	NC0009867	2	3.3	0.005336	0.148463	A	Study 1	CV164	245	214
27	NC0009867	2	3.3	0.001774	-0.02158	T	Study 1	CV108	245	214
27	NC0015766	2	7	0.028619	0.004206	G	Study 1	CV103	360	215
27	NC0015766	2	7	0.002039	-0.12908	G	Study 1	CV040	360	215
28	NC0009766	2	10.1	0.029864	0.005402	T	Study 1	CV051	328	216
28	NC0009766	2	10.1	0.004843	-0.0199	C	Study 1	CV108	328	216
28	NC0039289	2	15.2	0.019385	0.06593	C	Study 2	--	501	217
28	NC0143411	2	15.4	0.008652	0.155926	T	Study 1	CV006	401	218
28	NC0143411	2	15.4	0.004083	0.217127	T	Study 1	CV107	401	218
28	NC0143411	2	15.4	0.024699	0.005554	C	Study 1	CV051	401	218
28	NC0143411	2	15.4	0.028559	0.017561	T	Study 1	CV156	401	218
28	NC0143411	2	15.4	0.001424	-0.08095	C	Study 1	CV057	401	218
28	NC0106352	2	15.8	0.041731	-0.07369	G	Study 1	CV112	82	219
28	NC0106678	2	18.3	<.0001	-0.19456	C	Study 3	--	309	220
28	NC0106678	2	18.3	0.043579	0.073061	G	Study 1	CV082	309	220
28	NC0106678	2	18.3	0.008483	-0.10153	G	Study 1	CV075	309	220

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
28	NC0106678	2	18.3	0.012514	-0.12936	G	Study 1	CV112	309	220
28	NC0106678	2	18.3	0.006099	0.146872	C	Study 1	CV164	309	220
28	NC0106678	2	18.3	0.033291	-0.01773	C	Study 1	CV063	309	220
28	NC0082235	2	19.7	0.004634	0.207131	A	Study 1	CV107	503	221
28	NC0082235	2	19.7	0.005089	-0.12899	C	Study 1	CV067	503	221
28	NC0082235	2	19.7	0.029189	0.049392	C	Study 1	CV006	503	221
28	NC0082235	2	19.7	0.030377	-0.00624	A	Study 1	CV052	503	221
28	NC0082235	2	19.7	0.006953	0.013819	A	Study 1	CV081	503	221
28	NC0082235	2	19.7	0.010163	-0.01443	A	Study 1	CV076	503	221
28	NC0082235	2	19.7	0.04735	-0.01448	A	Study 1	CV108	503	221
29	NC0028836	2	27.1	0.001	-0.15236	C	Study 3	--	103	222
29	NC0076912	2	27.5	0.01612	-0.27869	C	Study 1	CV112	246	223
29	NC0002814	2	27.9	0.014699	0.140612	C	Study 1	CV006	92	224
30	NC0002945	2	30.7	<.0001	-0.20824	A	Study 3	--	254	225
30	NC0002945	2	30.7	0.004188	0.095382	A	Study 1	CV082	254	225
30	NC0002945	2	30.7	0.035832	-0.00777	A	Study 1	CV040	254	225
30	NC0002945	2	30.7	0.031399	0.187455	A	Study 1	CV127	254	225
30	NC0002945	2	30.7	0.004673	-0.01882	A	Study 1	CV108	254	225
30	NC0016074	2	30.7	0.003589	0.014821	G	Study 1	CV081	385	226
30	NC0080031	2	33.1	0.044514	0.058309	A	Study 2	--	164	227
30	NC0080031	2	33.1	0.013246	0.019791	G	Study 1	CV156	164	227
30	NC0002616	2	34	0.035668	-0.0122	T	Study 1	CV076	53	228
30	NC0050315	2	34	0.013291	0.067246	G	Study 1	CV084	256	229
30	NC0019127	2	35.5	0.000356	-0.09258	A	Study 1	CV057	47	230
30	NC0009706	2	35.9	0.005056	-0.11779	G	Study 1	CV040	269	231
31	NC0107479	2	42.3	0.003725	-0.1271	A	Study 1	CV067	195	232
31	NC0107479	2	42.3	0.026859	-0.01764	G	Study 1	CV057	195	232
31	NC0107479	2	42.3	0.04725	-0.01198	A	Study 1	CV065	195	232
31	NC0109140	2	44.8	0.002131	-0.09709	TAAA	Study 1	CV017	578	233
31	NC0109140	2	44.8	0.03347	-0.01219	TAAA	Study 1	CV086	578	233
31	NC0109140	2	44.8	0.007635	0.025868	TAAA	Study 1	CV165	578	233
31	NC0109140	2	44.8	0.039602	0.013041	****	Study 1	CV144	578	233
31	NC0048553	2	46.8	--	--	G	Study 5	--	485	234

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
31	NC0048553	2	46.8	0.015722	0.139889	A	Study 1	CV006	485	234
31	NC0048553	2	46.8	0.022553	0.133247	G	Study 1	CV023	485	234
31	NC0048553	2	46.8	0.007735	0.117134	A	Study 1	CV125	485	234
31	NC0048553	2	46.8	0.025805	0.010687	A	Study 1	CV069	485	234
31	NC0048553	2	46.8	0.024206	0.01286	A	Study 1	CV006	485	234
31	NC0078243	2	48.8	0.010487	-0.02209	G	Study 1	I294213	229	235
31	NC0078243	2	48.8	0.002546	0.024556	A	Study 1	CV156	229	235
31	NC0078243	2	48.8	0.042652	0.019082	A	Study 1	CV062	229	235
31	NC0078243	2	48.8	0.001722	0.026446	A	Study 1	CV161	229	235
31	NC0013275	2	49.7	--	--	T	Study 5	--	430	236
31	NC0013275	2	49.7	0.046749	0.004412	T	Study 1	CV018	430	236
31	NC0013275	2	49.7	0.026967	-0.01335	T	Study 1	CV065	430	236
32	NC0199346	2	50.8	--	--	T	Study 5	--	235	237
32	NC0199643	2	53.2	--	--	T	Study 5	--	197	238
32	NC0012259	2	54	--	--	G	Study 5	--	467	239
32	NC0002630	2	54.1	--	--	T	Study 5	--	336	240
32	NC0194506	2	54.1	--	--	T	Study 5	--	176	241
32	NC0199954	2	54.1	--	--	G	Study 5	--	741	242
32	NC0011181	2	57.2	--	--	T	Study 5	--	234	243
33	NC0020105	2	64.6	0.015052	-0.07658	A	Study 1	CV017	55	244
33	NC0020105	2	64.6	0.014794	0.024133	A	Study 1	CV062	55	244
33	NC0020105	2	64.6	0.000047	-0.03103	G	Study 1	CV083	55	244
33	NC0106391	2	65.8	--	--	C	Study 5	--	120	245
33	NC0106391	2	65.8	0.001538	0.196545	A	Study 1	CV023	120	245
33	NC0106391	2	65.8	0.01248	0.019558	C	Study 1	CV165	120	245
33	NC0106391	2	65.8	0.017695	0.103837	C	Study 1	CV125	120	245
33	NC0106391	2	65.8	0.030596	-0.30557	C	Study 1	CV130	120	245
33	NC0002812	2	65.9	0.027142	-0.01178	T	Study 1	CV086	417	246
33	NC0080704	2	68.5	0.033064	-0.10311	T	Study 1	CV067	102	247
33	NC0080704	2	68.5	0.04268	-0.01322	C	Study 1	I294213	102	247
33	NC0080705	2	68.5	0.022866	-0.00839	G	Study 1	CV122	281	248
33	NC0080705	2	68.5	0.009662	0.014631	G	Study 1	CV150	281	248
33	NC0080705	2	68.5	0.027917	0.053641	G	Study 1	CV082	281	248

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
33	NC0080705	2	68.5	0.041536	0.036595	G	Study 1	CV100	281	248
33	NC0080705	2	68.5	0.042112	-0.11905	C	Study 1	I294213	281	248
33	NC0080705	2	68.5	0.010925	0.202826	G	Study 1	CV132	281	248
33	NC0080705	2	68.5	0.009512	0.308073	G	Study 1	CV156	281	248
33	NC0080705	2	68.5	0.000103	0.0862	G	Study 1	CV074	281	248
33	NC0080705	2	68.5	0.005951	0.019505	G	Study 1	CV074	281	248
33	NC0080705	2	68.5	0.009807	0.02156	G	Study 1	CV161	281	248
33	NC0080705	2	68.5	0.017048	0.017012	G	Study 1	CV150	281	248
33	NC0080705	2	68.5	0.023501	-0.02693	C	Study 1	CV025	281	248
33	NC0080705	2	68.5	0.029172	0.035154	C	Study 1	CV066	281	248
33	NC0080705	2	68.5	0.001541	0.10332	G	Study 1	CV150	281	248
33	NC0080705	2	68.5	0.006455	0.015434	G	Study 1	CV006	281	248
34	NC0009364	2	71.6	0.023181	-0.1283	C	Study 1	I294213	410	249
34	NC0009364	2	71.6	0.043975	0.124209	C	Study 1	CV159	410	249
34	NC0009364	2	71.6	0.007523	-0.08545	C	Study 1	CV064	410	249
34	NC0009364	2	71.6	0.034367	-0.01249	C	Study 1	I294213	410	249
34	NC0009364	2	71.6	0.000518	0.033679	C	Study 1	CV165	410	249
34	NC0032200	2	71.6	0.000539	0.211843	C	Study 1	CV006	318	250
34	NC0032200	2	71.6	0.000019	-0.11059	C	Study 1	CV057	318	250
34	NC0032200	2	71.6	0.017271	-0.02113	C	Study 1	CV057	318	250
34	NC0199855	2	73.4	--	--	G	Study 5	--	140	251
34	NC0004697	2	74.8	0.027929	-0.07205	G	Study 1	CV017	175	252
34	NC0004697	2	74.8	0.006438	0.069553	G	Study 1	CV082	175	252
34	NC0004697	2	74.8	0.041907	0.150178	G	Study 1	CV129	175	252
34	NC0004697	2	74.8	0.038097	-0.00547	G	Study 1	CV097	175	252
34	NC0004697	2	74.8	0.016885	0.018692	A	Study 1	CV165	175	252
34	NC0004697	2	74.8	0.026335	0.015297	A	Study 1	CV144	175	252
34	NC0004697	2	74.8	0.000142	-0.01814	G	Study 1	CV082	175	252
34	NC0104946	2	74.8	0.003939	-0.13755	T	Study 1	CV069	269	253
34	NC0199310	2	75.7	--	--	C	Study 5	--	246	254
34	NC0009623	2	77	0.017871	0.01142	C	Study 1	CV069	73	255
34	NC0042242	2	77	0.025849	0.003257	T	Study 1	CV006	75	256
34	NC0042242	2	77	0.025849	0.003257	T	Study 1	CV006	75	256

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
34	NC0042242	2	77	0.011841	-0.0584	C	Study 1	CV022	75	256
34	NC0042242	2	77	0.03767	-0.01099	C	Study 1	CV086	75	256
34	NC0042242	2	77	0.046478	0.111267	T	Study 1	CV164	75	256
34	NC0042242	2	77	0.01429	0.008867	T	Study 1	CV164	75	256
34	NC0042242	2	77	0.045586	0.002897	T	Study 1	CV006	75	256
34	NC0042242	2	77	0.045586	0.002897	T	Study 1	CV006	75	256
34	NC0042242	2	77	0.020718	0.013547	T	Study 1	CV006	75	256
34	NC0015022	2	77.3	--	--	G	Study 4	--	143	257
34	NC0015022	2	77.3	0.016103	0.013856	G	Study 1	CV150	143	257
34	NC0015022	2	77.3	0.017635	0.238655	G	Study 1	CV109	143	257
34	NC0199362	2	77.4	--	--	T	Study 5	--	202	258
34	NC0111617	2	78.2	--	--	T	Study 4	--	149	259
34	NC0111617	2	78.2	0.032017	-0.00786	T	Study 1	CV080	149	259
34	NC0111617	2	78.2	0.000727	-0.15821	A	Study 1	I294213	149	259
34	NC0111617	2	78.2	0	0.398815	T	Study 1	CV157	149	259
34	NC0111617	2	78.2	0.001079	-0.02033	A	Study 1	I294213	149	259
34	NC0035381	2	79.6	0.009025	0.008725	T	Study 1	CV050	80	260
34	NC0035381	2	79.6	0.000021	0.095314	T	Study 1	CV074	80	260
34	NC0035381	2	79.6	0.001568	0.022668	T	Study 1	CV074	80	260
34	NC0035381	2	79.6	0.00002	-0.10971	T	Study 1	CV057	80	260
34	NC0035381	2	79.6	0.010409	-0.01653	A	Study 1	I294213	80	260
35	NC0016297	2	85	--	--	G	Study 5	--	67	261
35	NC0016297	2	85	0.000426	0.421198	A	Study 1	CV156	67	261
35	NC0016297	2	85	0.015823	0.038487	A	Study 1	CV066	67	261
35	NC0016297	2	85	0.007679	0.077492	A	Study 1	CV150	67	261
35	NC0016297	2	85	0.00088	0.108366	A	Study 1	CV150	67	261
35	NC0199396	2	86.1	--	--	G	Study 5	--	480	262
35	NC0011466	2	86.2	--	--	T	Study 4	--	214	263
35	NC0049430	2	87.7	0.028712	0.016071	T	Study 1	CV048	353	264
35	NC0049430	2	87.7	0.03503	0.009274	C	Study 1	CV012	353	264
35	NC0105002	2	88.6	--	--	T	Study 4	--	167	265
35	NC0105002	2	88.6	0.01679	0.20542	C	Study 1	CV132	167	265
35	NC0108493	2	88.6	0.000113	0.018603	A	Study 1	CV082	304	266

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
35	NC0108493	2	88.6	0.014271	-0.11131	A	Study 1	CV067	304	266
35	NC0108493	2	88.6	0.000017	-0.03103	G	Study 1	CV083	304	266
35	NC0146518	2	89.4	0.010041	-0.08236	G	Study 1	CV017	97	267
35	NC0146518	2	89.4	0.034037	0.003199	G	Study 1	CV006	97	267
35	NC0146518	2	89.4	0.034037	0.003199	G	Study 1	CV006	97	267
35	NC0104479	2	89.6	0.038531	-0.11475	T	Study 1	I294213	303	268
35	NC0104479	2	89.6	0.009926	0.333359	T	Study 1	CV167	303	268
35	NC0104479	2	89.6	0.03815	0.010826	T	Study 1	CV013	303	268
35	NC0199564	2	89.9	--	--	T	Study 5	--	129	269
36	NC0002805	2	93.1	--	--	T	Study 5	--	332	270
36	NC0053463	2	93.1	--	--	G	Study 4	--	461	271
36	NC0053463	2	93.1	0.000084	-0.10365	G	Study 1	CV057	461	271
36	NC0027319	2	93.2	0.016684	0.106488	T	Study 1	CV116	54	272
36	NC0021092	2	93.4	--	--	G	Study 4	--	94	273
36	NC0021092	2	93.4	0.00047	0.085335	G	Study 1	CV082	94	273
36	NC0021092	2	93.4	0.015668	0.007299	G	Study 1	CV082	94	273
36	NC0021092	2	93.4	0.038395	-0.00528	G	Study 1	CV097	94	273
36	NC0021092	2	93.4	0.012161	-0.00499	G	Study 1	CV100	94	273
36	NC0057604	2	94	--	--	****	Study 4	--	412	274
36	NC0057604	2	94	0.016334	0.132169	CAGG	Study 1	CV164	412	274
36	NC0057604	2	94	0.004342	0.010333	CAGG	Study 1	CV164	412	274
36	NC0170324	2	94	--	--	G	Study 5	--	228	275
36	NC0172302	2	94	--	--	G	Study 5	--	155	276
36	NC0005467	2	94.3	0.000064	0.103638	G	Study 1	CV168	72	277
36	NC0105696	2	94.3	--	--	T	Study 4	--	149	278
36	NC0105696	2	94.3	0.016869	-0.01055	C	Study 1	I294213	149	278
36	NC0105696	2	94.3	0.019211	0.007993	T	Study 1	CV050	149	278
36	NC0105696	2	94.3	0.024072	0.01775	C	Study 1	CV165	149	278
36	NC0105696	2	94.3	0.006746	-0.08421	C	Study 1	CV064	149	278
36	NC0105696	2	94.3	0.000364	-0.01542	T	Study 1	CV082	149	278
36	NC0146130	2	94.6	--	--	G	Study 4	--	96	279
36	NC0146130	2	94.6	--	--	G	Study 5	--	96	279
36	NC0146130	2	94.6	0.000752	0.206777	G	Study 1	CV006	96	279

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
36	NC0019874	2	94.7	0.002366	0.014364	A	Study 1	CV082	374	280
36	NC0023442	2	94.9	0	0.424199	C	Study 1	CV157	354	281
36	NC0032601	2	94.9	0.019734	0.043601	C	Study 1	CV100	144	282
36	NC0032601	2	94.9	0.035387	-0.02475	C	Study 1	CV025	144	282
36	NC0173589	2	95.4	--	--	G	Study 5	--	1001	283
36	NC0013347	2	96	0.028962	0.096917	A	Study 1	CV116	279	284
36	NC0079826	2	96	0.00582	0.030774	T	Study 1	CV165	364	285
36	NC0079826	2	96	0.000045	0.039125	T	Study 1	CV165	364	285
36	NC0060879	2	97.7	--	--	G	Study 4	--	363	286
36	NC0060879	2	97.7	0.007365	0.019917	G	Study 1	CV048	363	286
36	NC0060879	2	97.7	0.017321	-0.11688	G	Study 1	CV069	363	286
36	NC0108305	2	97.9	--	--	G	Study 4	--	174	287
36	NC0108305	2	97.9	0.021372	0.141804	G	Study 1	CV159	174	287
36	NC0000066	2	98.3	0.032098	-0.18014	A	Study 1	CV044	112	288
36	NC0107911	2	99.2	0.015021	0.196344	T	Study 1	CV073	384	289
36	NC0107948	2	99.2	0.000016	0.094476	G	Study 1	CV074	274	290
36	NC0107948	2	99.2	0.000392	0.024864	G	Study 1	CV074	274	290
36	NC0200140	2	99.3	--	--	G	Study 5	--	185	291
37	NC0106407	2	101.3	0.001063	-0.02421	A	Study 1	CV083	45	292
37	NC0106407	2	101.3	0.000254	-0.01638	G	Study 1	CV082	45	292
37	NC0112226	2	101.5	0.013136	0.073356	A	Study 1	CV128	237	293
37	NC0108607	2	102.1	--	--	C	Study 4	--	562	294
37	NC0108607	2	102.1	0.00878	0.112684	A	Study 1	CV116	562	294
37	NC0153941	2	102.1	0.013789	0.065078	CTT	Study 1	CV082	1176	295
37	NC0153941	2	102.1	0.003334	0.354352	***	Study 1	CV156	1176	295
37	NC0153941	2	102.1	0.010543	0.00397	CTT	Study 1	CV006	1176	295
37	NC0153941	2	102.1	0.010543	0.00397	CTT	Study 1	CV006	1176	295
37	NC0153941	2	102.1	0.007161	0.079023	***	Study 1	CV150	1176	295
37	NC0153941	2	102.1	0.001598	0.104458	***	Study 1	CV150	1176	295
37	NC0053097	2	102.6	--	--	T	Study 4	--	335	296
37	NC0053097	2	102.6	0.001765	0.083489	A	Study 1	CV168	335	296
37	NC0053097	2	102.6	0.000926	-0.15897	A	Study 1	I294213	335	296
37	NC0053097	2	102.6	0.028115	-0.02571	T	Study 1	CV025	335	296

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
37	NC0053097	2	102.6	0.009322	0.041372	A	Study 1	CV066	335	296
37	NC0053097	2	102.6	0.000335	-0.09311	A	Study 1	CV057	335	296
37	NC0053097	2	102.6	0.000568	-0.01961	A	Study 1	I294213	335	296
37	NC0053097	2	102.6	0.047188	-0.01147	T	Study 1	CV093	335	296
37	NC0000551	2	103.6	0.012721	-0.13777	T	Study 1	I294213	175	297
37	NC0000551	2	103.6	0.03013	0.03816	G	Study 1	CV054	175	297
37	NC0059782	2	103.9	--	--	C	Study 4	--	167	298
37	NC0059782	2	103.9	0.041761	0.007984	A	Study 1	CV101	167	298
37	NC0059782	2	103.9	0.006222	0.007092	A	Study 1	CV101	167	298
37	NC0059782	2	103.9	0.01123	0.183121	A	Study 1	CV129	167	298
37	NC0059782	2	103.9	0.045448	0.25546	A	Study 1	CV167	167	298
37	NC0057210	2	104.1	0.008227	0.019356	T	Study 1	CV048	191	299
37	NC0057210	2	104.1	0.003364	0.01417	C	Study 1	CV082	191	299
37	NC0057210	2	104.1	0.014946	0.01924	C	Study 1	CV165	191	299
37	NC0057210	2	104.1	0	0.379191	C	Study 1	CV157	191	299
37	NC0020609	2	104.6	0.045185	0.012025	C	Study 1	CV159	292	300
37	NC0000366	2	104.9	<.0001	0.169619	G	Study 3	--	146	301
37	NC0000366	2	104.9	0.011996	-0.00522	G	Study 1	CV100	146	301
37	NC0084829	2	104.9	--	--	C	Study 5	--	500	302
37	NC0151288	2	107.6	0.007687	-0.00568	G	Study 1	CV043	1001	303
37	NC0151288	2	107.6	0.019854	-0.01432	G	Study 1	CV060	1001	303
37	NC0151288	2	107.6	0.021757	0.00603	G	Study 1	CV101	1001	303
37	NC0151288	2	107.6	0.007549	0.020018	G	Study 1	CV150	1001	303
37	NC0151288	2	107.6	0.000048	-0.02332	G	Study 1	I294213	1001	303
37	NC0151288	2	107.6	0.000825	0.008969	A	Study 1	CV024	1001	303
38	NC0082458	2	112.4	--	--	T	Study 5	--	369	304
38	NC0082458	2	112.4	0.000964	0.014795	T	Study 1	CV012	369	304
38	NC0082458	2	112.4	0.001684	-0.1008	G	Study 1	CV017	369	304
38	NC0082458	2	112.4	0.000001	0.282159	G	Study 1	CV157	369	304
38	NC0082458	2	112.4	0.041351	0.023271	G	Study 1	CV134	369	304
38	NC0031289	2	114.8	0.002026	0.080529	C	Study 1	CV168	451	305
38	NC0031289	2	114.8	0.030818	-0.11415	C	Study 1	I294213	451	305
38	NC0031289	2	114.8	0.000286	-0.02165	C	Study 1	I294213	451	305

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
38	NC0108013	2	115.3	0.009668	0.019444	C	Study 1	CV048	340	306
38	NC0108013	2	115.3	0.000089	-0.19014	T	Study 1	I294213	340	306
38	NC0108013	2	115.3	0.003751	0.179212	C	Study 1	CV159	340	306
38	NC0108013	2	115.3	0.003346	0.234788	C	Study 1	CV073	340	306
38	NC0108013	2	115.3	0.001293	-0.27283	T	Study 1	CV044	340	306
38	NC0111247	2	115.7	--	--	T	Study 5	--	352	307
38	NC0111475	2	115.7	0.006351	0.214864	G	Study 1	CV132	283	308
38	NC0111475	2	115.7	0.045428	0.144418	G	Study 1	CV129	283	308
38	NC0111475	2	115.7	0.024183	-0.01	A	Study 1	CV082	283	308
38	NC0044080	2	116.7	--	--	T	Study 5	--	414	309
38	NC0035094	2	116.9	--	--	G	Study 5	--	173	310
38	NC0022775	2	118.1	0.000005	0.270715	G	Study 1	CV006	517	311
38	NC0022775	2	118.1	0.016671	0.006679	G	Study 1	CV141	517	311
38	NC0022775	2	118.1	0.021253	0.010334	G	Study 1	CV142	517	311
38	NC0022775	2	118.1	0.000032	0.111798	A	Study 1	CV168	517	311
38	NC0022775	2	118.1	0.015622	-0.12739	A	Study 1	I294213	517	311
38	NC0022775	2	118.1	0.042109	0.058679	G	Study 1	CV050	517	311
38	NC0022775	2	118.1	0.004502	0.009419	G	Study 1	CV050	517	311
38	NC0022775	2	118.1	0.000907	-0.18206	A	Study 1	CV119	517	311
38	NC0022775	2	118.1	0.016953	-0.01538	A	Study 1	I294213	517	311
38	NC0022775	2	118.1	0.004862	0.007812	G	Study 1	CV024	517	311
38	NC0022775	2	118.1	0.000594	-0.01982	A	Study 1	I294213	517	311
38	NC0022775	2	118.1	0.000093	0.021904	G	Study 1	CV006	517	311
39	NC0104954	2	120.4	0.030308	0.06209	G	Study 2	--	376	312
39	NC0104954	2	120.4	0.01433	0.011419	T	Study 1	CV170	376	312
39	NC0104954	2	120.4	0.000222	0.015936	T	Study 1	CV012	376	312
39	NC0104954	2	120.4	0.001632	0.249021	G	Study 1	CV132	376	312
39	NC0104954	2	120.4	0.003886	0.044662	G	Study 1	CV066	376	312
39	NC0104954	2	120.4	0.021203	-0.0158	T	Study 1	CV083	376	312
39	NC0151441	2	120.4	0.000208	0.101454	A	Study 1	CV082	313	313
39	NC0151441	2	120.4	0.017129	0.003728	G	Study 1	CV006	313	313
39	NC0151441	2	120.4	0.017129	0.003728	G	Study 1	CV006	313	313
39	NC0151441	2	120.4	0.016277	-0.0051	A	Study 1	CV010	313	313

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
39	NC0084633	2	124.6	--	--	G	Study 4	--	357	314
39	NC0084633	2	124.6	--	--	G	Study 5	--	357	314
39	NC0084633	2	124.6	0.043822	0.005129	G	Study 1	CV024	357	314
39	NC0000069	2	125.1	0.002325	0.022454	G	Study 1	CV048	162	315
39	NC0000069	2	125.1	0.002056	0.0693	A	Study 1	CV074	162	315
39	NC0000069	2	125.1	0.002922	0.021171	A	Study 1	CV074	162	315
39	NC0000069	2	125.1	0.021137	-0.0409	G	Study 1	CV010	162	315
39	NC0000069	2	125.1	0.003305	-0.00642	G	Study 1	CV010	162	315
39	NC0000069	2	125.1	0.00292	0.271173	G	Study 1	CV130	162	315
39	NC0082265	2	125.8	0.000964	0.024248	C	Study 1	CV048	479	316
39	NC0082265	2	125.8	0.028205	0.084869	C	Study 1	CV059	479	316
39	NC0082265	2	125.8	0.001851	0.008813	C	Study 1	CV141	479	316
39	NC0082265	2	125.8	0.027962	0.173506	T	Study 1	CV073	479	316
39	NC0082265	2	125.8	0.032023	-0.05577	T	Study 1	CV057	479	316
39	NC0082265	2	125.8	0.000519	0.213734	C	Study 1	CV159	479	316
39	NC0082265	2	125.8	0	0.2862	C	Study 1	CV157	479	316
39	NC0082265	2	125.8	0.041348	0.023271	C	Study 1	CV134	479	316
39	NC0082265	2	125.8	0.000443	-0.01891	T	Study 1	CV136	479	316
39	NC0082265	2	125.8	0.000002	-0.41007	T	Study 1	CV044	479	316
39	NC0082265	2	125.8	0.045664	0.011881	C	Study 1	CV159	479	316
39	NC0082265	2	125.8	0.03636	-0.01429	T	Study 1	CV083	479	316
39	NC0109393	2	127.1	0.003659	-0.01858	A	Study 1	CV060	323	317
39	NC0199804	2	127.1	--	--	T	Study 5	--	149	318
39	NC0029138	2	127.6	<.0001	0.162443	G	Study 3	--	290	319
39	NC0029138	2	127.6	--	--	G	Study 5	--	290	319
39	NC0040472	2	128.8	0	0.299027	G	Study 1	CV006	102	320
39	NC0040472	2	128.8	0.020297	-0.00458	G	Study 1	CV010	102	320
39	NC0040472	2	128.8	0.00884	-0.05495	G	Study 1	CV082	102	320
39	NC0040472	2	128.8	0.020924	0.075676	G	Study 1	CV082	102	320
39	NC0040472	2	128.8	0.000031	0.104956	G	Study 1	CV082	102	320
39	NC0040472	2	128.8	0.025058	-0.03696	G	Study 1	CV078	102	320
39	NC0040472	2	128.8	0.000039	0.022753	G	Study 1	CV006	102	320
39	NC0041850	2	128.8	0.035118	-0.02118	C	Study 1	CV146	55	321

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
39	NC0041850	2	128.8	0.008724	-0.05615	C	Study 1	CV082	55	321
39	NC0041850	2	128.8	0.000001	-0.26547	T	Study 1	CV119	55	321
39	NC0041850	2	128.8	0.044442	0.15162	C	Study 1	CV129	55	321
40	NC0009102	2	130	0.028853	-0.11616	T	Study 1	I294213	370	322
40	NC0009102	2	130	0.009332	0.011575	A	Study 1	CV142	370	322
40	NC0009102	2	130	0.026999	0.094089	T	Study 1	CV125	370	322
40	NC0009102	2	130	0.016227	0.107382	T	Study 1	CV166	370	322
40	NC0009102	2	130	0.007255	-0.08444	A	Study 1	CV064	370	322
40	NC0009102	2	130	0.009407	0.00867	A	Study 1	CV050	370	322
40	NC0009102	2	130	0.003403	0.009065	T	Study 1	CV024	370	322
40	NC0009102	2	130	0.000246	-0.02085	T	Study 1	I294213	370	322
40	NC0009102	2	130	0.000011	-0.36583	A	Study 1	CV044	370	322
40	NC0009102	2	130	0.035594	0.13242	A	Study 1	CV160	370	322
40	NC0009102	2	130	0.035871	0.062491	A	Study 1	CV148	370	322
40	NC0024089	2	130	0.000145	-0.18033	C	Study 1	I294213	136	323
40	NC0199876	2	132.1	--	--	G	Study 5	--	37	324
40	NC0009818	2	136.5	0.047731	-0.01301	T	Study 1	CV060	1	325
40	NC0009818	2	136.5	0.000709	0.295212	T	Study 1	CV127	1	325
40	NC0199317	2	138.2	--	--	G	Study 5	--	226	326
40	NC0173731	2	138.4	--	--	T	Study 5	--	621	327
40	NC0105556	2	139.5	--	--	T	Study 5	--	396	328
40	NC0105556	2	139.5	0.010472	0.012248	T	Study 1	CV082	396	328
40	NC0105556	2	139.5	0.00464	-0.05964	T	Study 1	CV082	396	328
40	NC0105556	2	139.5	0.000168	0.016899	T	Study 1	CV012	396	328
40	NC0199382	2	139.5	--	--	T	Study 5	--	91	329
40	NC0199713	2	139.5	--	--	T	Study 5	--	112	330
41	NC0108103	2	140.7	--	--	T	Study 5	--	170	331
41	NC0108103	2	140.7	0.002695	0.014301	T	Study 1	CV082	170	331
41	NC0108103	2	140.7	0.000291	-0.0785	T	Study 1	CV082	170	331
41	NC0108103	2	140.7	0.023521	0.096353	T	Study 1	CV125	170	331
41	NC0031474	2	141.4	0.045901	-0.01384	A	Study 1	CV041	842	332
41	NC0031474	2	141.4	0.026668	-0.00432	T	Study 1	CV010	842	332
41	NC0031474	2	141.4	0.002783	-0.00632	A	Study 1	CV043	842	332

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
41	NC0031474	2	141.4	0.010215	0.006765	T	Study 1	CV101	842	332
41	NC0031474	2	141.4	0.028402	-0.11553	A	Study 1	I294213	842	332
41	NC0031474	2	141.4	0.032568	0.014102	T	Study 1	CV049	842	332
41	NC0031474	2	141.4	0.005536	0.016917	T	Study 1	CV079	842	332
41	NC0031474	2	141.4	0.034255	-0.0057	T	Study 1	CV097	842	332
41	NC0031474	2	141.4	0	-0.29353	A	Study 1	CV119	842	332
41	NC0031474	2	141.4	0.011389	-0.04309	T	Study 1	CV010	842	332
41	NC0031474	2	141.4	0.00672	-0.00605	T	Study 1	CV010	842	332
41	NC0031474	2	141.4	0.000024	-0.02336	A	Study 1	I294213	842	332
41	NC0031474	2	141.4	0.026675	0.02487	T	Study 1	CV165	842	332
41	NC0031474	2	141.4	0.003599	0.028299	T	Study 1	CV165	842	332
41	NC0031474	2	141.4	0.017347	0.0112	T	Study 1	CV012	842	332
41	NC0031474	2	141.4	0.017347	0.0112	T	Study 1	CV012	842	332
41	NC0031474	2	141.4	0.015232	-0.01235	A	Study 1	I294213	842	332
41	NC0002878	2	145.1	0.0037	0.103009	C	Study 3	--	286	333
41	NC0002878	2	145.1	0.000002	-0.43414	C	Study 1	CV088	286	333
41	NC0002878	2	145.1	0.014109	0.038411	C	Study 1	CV066	286	333
41	NC0002878	2	145.1	0.010997	0.007557	C	Study 1	CV024	286	333
41	NC0005088	2	147.6	0.002898	-0.02921	T	Study 1	CV146	110	334
41	NC0005088	2	147.6	0.001976	0.022686	C	Study 1	CV048	110	334
41	NC0005088	2	147.6	0.032066	0.080362	C	Study 1	CV059	110	334
41	NC0005088	2	147.6	0.000779	-0.15924	C	Study 1	CV068	110	334
41	NC0005088	2	147.6	0.000403	0.113782	C	Study 1	CV082	110	334
41	NC0005088	2	147.6	0.000008	0.020123	C	Study 1	CV012	110	334
41	NC0005088	2	147.6	0	0.3303	C	Study 1	CV159	110	334
41	NC0005088	2	147.6	0	0.321654	C	Study 1	CV157	110	334
41	NC0005088	2	147.6	0.013174	0.219292	C	Study 1	CV127	110	334
41	NC0005088	2	147.6	0.00107	-0.11007	C	Study 1	CV064	110	334
41	NC0005088	2	147.6	0.011536	-0.04207	C	Study 1	CV078	110	334
41	NC0005088	2	147.6	0.001877	0.12908	C	Study 1	CV133	110	334
41	NC0005088	2	147.6	0.024772	0.123122	C	Study 1	CV164	110	334
41	NC0005088	2	147.6	0.02477	0.025368	C	Study 1	CV134	110	334
41	NC0005088	2	147.6	0.029722	-0.00637	C	Study 1	CV097	110	334

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
41	NC0173482	2	148.3	--	--	G	Study 5	--	1001	335
41	NC0104694	2	148.4	0.028088	0.008228	C	Study 1	CV151	253	336
42	NC0035297	2	150.7	--	--	G	Study 4	--	207	337
42	NC0035297	2	150.7	0.002939	-0.00668	G	Study 1	CV043	207	337
42	NC0035297	2	150.7	0	-0.46465	G	Study 1	CV088	207	337
42	NC0035297	2	150.7	0.016139	-0.13507	A	Study 1	I294213	207	337
42	NC0035297	2	150.7	0.021731	0.006076	A	Study 1	CV101	207	337
42	NC0035297	2	150.7	0.040244	0.022998	A	Study 1	CV165	207	337
42	NC0035297	2	150.7	0.029416	0.02124	A	Study 1	CV165	207	337
42	NC0155994	2	151.1	0.021721	-0.17461	A	Study 1	CV044	250	338
42	NC0170564	2	156.3	--	--	T	Study 5	--	55	339
42	NC0034166	2	156.6	--	--	T	Study 5	--	327	340
42	NC0019267	2	157.5	0.000012	0.251671	C	Study 1	CV006	340	341
42	NC0019267	2	157.5	0.019472	0.017327	C	Study 1	CV048	340	341
42	NC0019267	2	157.5	0.001622	0.014919	C	Study 1	CV082	340	341
42	NC0019267	2	157.5	0	-0.23732	C	Study 1	CV068	340	341
42	NC0019267	2	157.5	0	0.140418	C	Study 1	CV082	340	341
42	NC0019267	2	157.5	0.008321	0.008533	C	Study 1	CV082	340	341
42	NC0019267	2	157.5	0.011146	0.011329	C	Study 1	CV100	340	341
42	NC0019267	2	157.5	0	0.015872	C	Study 1	CV141	340	341
42	NC0019267	2	157.5	0.000836	-0.10276	C	Study 1	CV064	340	341
42	NC0019267	2	157.5	0.000953	0.297871	C	Study 1	CV130	340	341
42	NC0019267	2	157.5	0.000171	0.229627	C	Study 1	CV160	340	341
42	NC0019267	2	157.5	0.0002	-0.01735	C	Study 1	CV082	340	341
42	NC0019267	2	157.5	0.000621	0.018867	C	Study 1	CV006	340	341
43	NC0043579	2	163.8	--	--	T	Study 5	--	154	342
43	NC0043579	2	163.8	0.004419	0.322909	T	Study 1	CV124	154	342
43	NC0147548	2	163.8	--	--	G	Study 5	--	1001	343
43	NC0147548	2	163.8	0	0.016551	G	Study 1	CV141	1001	343
43	NC0005214	2	164.3	0.000014	-0.09133	C	Study 1	CV082	218	344
43	NC0005214	2	164.3	0.001151	0.137292	T	Study 1	CV166	218	344
43	NC0199851	2	165.2	--	--	C	Study 5	--	341	345
43	NC0199466	2	165.4	--	--	G	Study 5	--	74	346

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
43	NC0014467	2	167.3	0.0011	0.088551	**	Study 3	--	366	347
43	NC0014467	2	167.3	0.000117	-0.00669	**	Study 1	CV010	366	347
43	NC0014467	2	167.3	0.038914	0.075532	AT	Study 1	CV059	366	347
43	NC0014467	2	167.3	0.023789	0.047819	AT	Study 1	CV006	366	347
43	NC0014467	2	167.3	0.000033	-0.08691	**	Study 1	CV082	366	347
43	NC0014467	2	167.3	0.000001	0.155998	**	Study 1	CV082	366	347
43	NC0014467	2	167.3	0.009938	0.009692	AT	Study 1	CV151	366	347
43	NC0014467	2	167.3	0.008149	0.040634	AT	Study 1	CV066	366	347
43	NC0014467	2	167.3	0.048246	0.012347	AT	Study 1	CV079	366	347
43	NC0014467	2	167.3	0	0.284618	**	Study 1	CV157	366	347
43	NC0014467	2	167.3	0.000645	-0.1822	**	Study 1	CV119	366	347
43	NC0014467	2	167.3	0.034941	-0.00765	**	Study 1	CV116	366	347
43	NC0014467	2	167.3	0.034941	-0.00765	**	Study 1	CV116	366	347
43	NC0014467	2	167.3	0.044716	-0.01692	AT	Study 1	CV063	366	347
43	NC0003241	2	169.8	0.005198	0.15577	A	Study 1	CV006	214	348
43	NC0003241	2	169.8	0.015206	-0.00597	G	Study 1	CV056	214	348
43	NC0003241	2	169.8	0.04449	0.24082	A	Study 1	CV156	214	348
43	NC0003241	2	169.8	0.002082	0.034377	A	Study 1	CV134	214	348
44	NC0033320	2	173.6	--	--	G	Study 5	--	209	349
44	NC0033320	2	173.6	0.009771	-0.01329	C	Study 1	CV010	209	349
44	NC0008930	2	174.2	0.000002	-0.04467	A	Study 1	CV146	82	350
44	NC0008930	2	174.2	0	-0.34191	G	Study 1	CV068	82	350
44	NC0008930	2	174.2	0.00493	-0.0247	G	Study 1	CV010	82	350
44	NC0029041	2	174.2	0	-0.04086	A	Study 1	CV095	406	351
44	NC0029041	2	174.2	0.019386	-0.00402	A	Study 1	CV094	406	351
44	NC0029041	2	174.2	0.00299	-0.01268	A	Study 1	CV095	406	351
44	NC0029041	2	174.2	0.04237	-0.1692	C	Study 1	CV044	406	351
44	NC0029041	2	174.2	0.000522	0.194154	A	Study 1	CV160	406	351
45	NC0023748	2	181.9	0.029265	0.016027	A	Study 1	CV048	61	352
45	NC0023748	2	181.9	0	-0.33494	C	Study 1	CV068	61	352
45	NC0023748	2	181.9	0.005586	0.030912	A	Study 1	CV134	61	352
45	NC0023748	2	181.9	0.019941	0.010125	C	Study 1	CV145	61	352
45	NC0104359	2	182.5	--	--	C	Study 5	--	386	353

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
45	NC0104359	2	182.5	0.017561	0.010464	C	Study 1	CV012	386	353
45	NC0104359	2	182.5	0.0093	-0.00404	C	Study 1	CV094	386	353
45	NC0035238	2	185.5	0	0.150158	A	Study 1	CV082	80	354
45	NC0035238	2	185.5	0.00024	0.010939	A	Study 1	CV082	80	354
45	NC0110974	2	185.5	0.005952	0.048497	T	Study 1	CV100	522	355
45	NC0110974	2	185.5	0.001515	0.013772	T	Study 1	CV100	522	355
45	NC0110974	2	185.5	0.003305	0.008226	T	Study 1	CV141	522	355
45	NC0110974	2	185.5	0.043416	0.150624	T	Study 1	CV129	522	355
45	NC0110974	2	185.5	0.036162	0.032427	T	Study 1	CV066	522	355
45	NC0110974	2	185.5	0.042929	0.145214	T	Study 1	CV163	522	355
45	NC0110974	2	185.5	0.004411	0.017228	T	Study 1	CV079	522	355
45	NC0110974	2	185.5	0.041815	-0.11236	C	Study 1	CV119	522	355
45	NC0110974	2	185.5	0.020928	-0.15519	C	Study 1	I294213	522	355
45	NC0110974	2	185.5	0.040998	0.025217	C	Study 1	CV119	522	355
45	NC0110974	2	185.5	0.001444	-0.0543	C	Study 1	CV010	522	355
45	NC0110974	2	185.5	0.013212	-0.01307	T	Study 1	CV129	522	355
46	NC0107149	2	190.1	0.001408	-0.03228	A	Study 1	CV146	220	356
46	NC0076792	2	190.8	0.030887	0.017106	G	Study 1	CV165	195	357
46	NC0076792	2	190.8	0.000742	0.20626	G	Study 1	CV159	195	357
46	NC0011740	2	190.9	0.035279	0.120232	G	Study 1	CV006	112	358
46	NC0011740	2	190.9	0.023274	-0.00419	A	Study 1	CV010	112	358
46	NC0011740	2	190.9	0.014084	-0.00626	A	Study 1	CV056	112	358
46	NC0011740	2	190.9	0.004685	0.056636	G	Study 1	CV006	112	358
46	NC0011740	2	190.9	0.002092	-0.0744	A	Study 1	CV022	112	358
46	NC0011740	2	190.9	0.013534	-0.00894	A	Study 1	CV116	112	358
46	NC0011740	2	190.9	0.013534	-0.00894	A	Study 1	CV116	112	358
46	NC0011740	2	190.9	0.043876	-0.01181	A	Study 1	CV093	112	358
46	NC0000735	2	191.5	0.00132	0.107817	A	Study 1	CV082	94	359
46	NC0000735	2	191.5	0.015018	0.098464	A	Study 1	CV133	94	359
46	NC0000735	2	191.5	0	-0.02464	A	Study 1	CV082	94	359
46	NC0077782	2	191.5	0.000562	-0.07045	G	Study 1	CV082	280	360
47	NC0020971	3	13.9	0.048247	0.019343	A	Study 1	CV127	56	361
47	NC0020971	3	13.9	0.011424	0.014478	C	Study 1	CV159	56	361

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
47	NC0106389	3	14.2	0.044642	-0.00976	G	Study 1	CV053	207	362
47	NC0106389	3	14.2	0.01216	0.005515	G	Study 1	CV051	207	362
47	NC0106389	3	14.2	0.001438	0.166402	G	Study 1	CV125	207	362
47	NC0106389	3	14.2	0.027959	-0.09036	A	Study 1	CV045	207	362
47	NC0106389	3	14.2	0.039192	0.047284	A	Study 1	CV150	207	362
47	NC0106389	3	14.2	0.04557	0.051677	A	Study 1	CV150	207	362
47	NC0008911	3	19.9	0.008483	-0.14437	A	Study 1	CV053	205	363
47	NC0008911	3	19.9	0.029951	-0.07177	G	Study 1	CV101	205	363
47	NC0008911	3	19.9	0.048638	0.10911	G	Study 1	CV160	205	363
47	NC0051614	3	19.9	<.0001	-0.15286	C	Study 3	--	320	364
48	NC0106276	3	20	0.011321	0.017673	T	Study 1	CV140	343	365
49	NC0048700	3	31.3	0.00196	0.01503	T	Study 1	CV069	85	366
50	NC0032137	3	40.2	0.000064	0.027386	*	Study 1	CV140	216	367
50	NC0032137	3	40.2	0.0458	0.244653	A	Study 1	CV156	216	367
50	NC0032137	3	40.2	0.000335	0.187271	A	Study 1	CV125	216	367
50	NC0032137	3	40.2	0.036187	0.016821	A	Study 1	CV156	216	367
50	NC0032137	3	40.2	0.000155	0.10919	A	Study 1	CV150	216	367
50	NC0032137	3	40.2	0.000068	0.129608	A	Study 1	CV150	216	367
50	NC0032137	3	40.2	0.033677	-0.01292	A	Study 1	CV077	216	367
50	NC0032137	3	40.2	0.037026	0.017098	A	Study 1	CV069	216	367
50	NC0019963	3	40.6	0.000174	-0.20703	A	Study 1	CV053	1173	368
50	NC0019963	3	40.6	0.008851	-0.0867	C	Study 1	CV101	1173	368
50	NC0019963	3	40.6	0.03865	-0.01042	C	Study 1	CV098	1173	368
50	NC0019963	3	40.6	0.010236	-0.0122	A	Study 1	CV053	1173	368
50	NC0019963	3	40.6	0.003252	-0.00928	A	Study 1	I294213	1173	368
50	NC0019963	3	40.6	0.014632	0.016755	C	Study 1	CV165	1173	368
50	NC0019963	3	40.6	0.048093	-0.03522	A	Study 1	CV070	1173	368
50	NC0019963	3	40.6	0.043223	0.014891	A	Study 1	CV150	1173	368
50	NC0019963	3	40.6	0.004419	0.016628	A	Study 1	CV150	1173	368
50	NC0000423	3	49.9	0.0003	-0.13506	A	Study 3	--	73	369
50	NC0000423	3	49.9	0.000002	0.03237	G	Study 1	CV140	73	369
50	NC0000423	3	49.9	0.001362	-0.01547	G	Study 1	CV053	73	369
50	NC0000423	3	49.9	0.006818	0.014473	G	Study 1	CV006	73	369

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
50	NC0000423	3	49.9	0.023055	-0.05951	A	Study 1	CV082	73	369
50	NC0000423	3	49.9	0.023311	0.019632	G	Study 1	CV006	73	369
50	NC0000423	3	49.9	0.000607	0.178185	A	Study 1	CV125	73	369
50	NC0000423	3	49.9	0.001731	0.114882	A	Study 1	CV079	73	369
50	NC0000423	3	49.9	0.000326	0.145471	A	Study 1	CV079	73	369
50	NC0000423	3	49.9	0.012886	-0.01578	A	Study 1	CV063	73	369
51	NC0106329	3	53.9	0.000052	-0.22602	A	Study 1	CV053	91	370
51	NC0106329	3	53.9	0.021272	0.012684	G	Study 1	CV006	91	370
51	NC0004821	3	54.4	--	--	T	Study 5	--	294	371
51	NC0004821	3	54.4	0.000203	-0.20704	T	Study 1	CV053	294	371
51	NC0004821	3	54.4	0.000002	-0.1563	C	Study 1	CV101	294	371
51	NC0004821	3	54.4	0.011365	0.020401	C	Study 1	CV156	294	371
51	NC0004821	3	54.4	0.000026	0.121594	C	Study 1	CV150	294	371
51	NC0004821	3	54.4	0.000001	0.156172	C	Study 1	CV150	294	371
51	NC0004821	3	54.4	0.009933	-0.01624	C	Study 1	CV077	294	371
52	NC0148268	3	60.8	0.000156	0.027356	GAG	Study 1	CV140	139	372
52	NC0148268	3	60.8	0.001667	-0.08546	***	Study 1	CV082	139	372
52	NC0008520	3	62	--	--	G	Study 5	--	267	373
52	NC0049293	3	69.9	0.018849	-0.01146	A	Study 1	CV053	183	374
52	NC0049293	3	69.9	0	0.267493	C	Study 1	CV149	183	374
52	NC0049293	3	69.9	0.009754	0.175089	C	Study 1	CV149	183	374
53	NC0108727	3	77.4	--	--	G	Study 5	--	241	375
53	NC0108727	3	77.4	0.022183	-0.14469	G	Study 1	CV131	241	375
53	NC0108727	3	77.4	0.000765	-0.20123	G	Study 1	CV053	241	375
53	NC0108727	3	77.4	0.046371	-0.00672	G	Study 1	I294213	241	375
53	NC0108727	3	77.4	0	-0.20792	C	Study 1	CV101	241	375
53	NC0108727	3	77.4	0.003952	0.015425	C	Study 1	CV006	241	375
53	NC0108727	3	77.4	0.022316	0.018668	C	Study 1	CV006	241	375
53	NC0108727	3	77.4	0.000003	0.024261	C	Study 1	CV005	241	375
53	NC0108727	3	77.4	0.001818	0.016278	C	Study 1	CV006	241	375
53	NC0108727	3	77.4	0.004648	0.019024	C	Study 1	CV014	241	375
54	NC0199324	3	81.8	--	--	G	Study 5	--	115	376
54	NC0004599	3	82.9	--	--	T	Study 4	--	105	377

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
54	NC0021154	3	82.9	0.000983	0.025768	C	Study 1	CV140	55	378
54	NC0021154	3	82.9	0.030793	-0.01372	T	Study 1	CV063	55	378
54	NC0147768	3	82.9	--	--	T	Study 4	--	418	379
54	NC0028923	3	83.1	0.000004	-0.13252	G	Study 1	CV082	1052	380
54	NC0105291	3	83.2	0.014407	0.098731	C	Study 1	CV114	294	381
54	NC0106515	3	83.2	--	--	T	Study 4	--	184	382
54	NC0106515	3	83.2	0.009472	-0.06964	G	Study 1	CV050	184	382
54	NC0106515	3	83.2	0.000179	0.013858	G	Study 1	CV151	184	382
54	NC0106515	3	83.2	0.000491	0.091156	G	Study 1	CV050	184	382
54	NC0106515	3	83.2	0.022442	0.018319	G	Study 1	CV156	184	382
54	NC0106515	3	83.2	0.001193	0.035936	G	Study 1	CV165	184	382
54	NC0106515	3	83.2	0.001333	0.030989	G	Study 1	CV165	184	382
54	NC0106515	3	83.2	0	0.181127	G	Study 1	CV150	184	382
54	NC0106515	3	83.2	0	0.225564	G	Study 1	CV150	184	382
54	NC0110326	3	83.2	--	--	T	Study 4	--	263	383
54	NC0110326	3	83.2	0.00555	0.119212	T	Study 1	CV116	263	383
54	NC0110326	3	83.2	0.000909	0.12209	T	Study 1	CV079	263	383
54	NC0110326	3	83.2	0.00016	0.153677	T	Study 1	CV079	263	383
54	NC0173514	3	83.2	--	--	T	Study 5	--	628	384
54	NC0173790	3	83.2	--	--	T	Study 5	--	979	385
54	NC0021190	3	83.5	--	--	G	Study 4	--	284	386
54	NC0021190	3	83.5	0	-0.20089	G	Study 1	CV101	284	386
54	NC0021190	3	83.5	0.005804	0.014969	G	Study 1	CV006	284	386
54	NC0021190	3	83.5	0.005699	-0.01907	G	Study 1	CV077	284	386
54	NC0021190	3	83.5	0.000046	0.025734	G	Study 1	CV014	284	386
54	NC0010220	3	83.6	--	--	G	Study 4	--	291	387
54	NC0012017	3	85.7	0	0.033962	T	Study 1	CV005	135	388
54	NC0016729	3	86.8	<.0001	0.131989	T	Study 3	--	100	389
54	NC0016729	3	86.8	--	--	T	Study 4	--	100	389
54	NC0016729	3	86.8	--	--	T	Study 5	--	100	389
54	NC0145322	3	87.1	<.0001	-0.23068	C	Study 3	--	708	390
54	NC0002207	3	87.9	0.000101	0.369414	T	Study 1	CV161	494	391
54	NC0002207	3	87.9	0.015374	0.011986	C	Study 1	CV069	494	391

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
54	NC0009468	3	88	--	--	G	Study 4	--	102	392
54	NC0009470	3	88	1.61E-12	0.201223	C	Study 2	--	137	393
54	NC0194580	3	89.1	--	--	G	Study 5	--	284	394
54	NC0031647	3	89.5	--	--	T	Study 4	--	899	395
54	NC0031647	3	89.5	0.004966	-0.01206	T	Study 1	CV010	899	395
55	NC0040104	3	92.2	0.015433	0.016783	T	Study 1	CV165	143	396
55	NC0106440	3	92.3	0.022692	-0.00705	A	Study 1	CV089	450	397
55	NC0109509	3	93.7	--	--	G	Study 4	--	54	398
55	NC0035187	3	93.9	0.000817	0.018185	G	Study 1	CV006	293	399
55	NC0146158	3	94	0.000902	0.172859	**	Study 1	CV125	822	400
55	NC0146158	3	94	0.020325	0.018704	**	Study 1	CV156	822	400
55	NC0039785	3	94.5	--	--	T	Study 4	--	512	401
55	NC0039785	3	94.5	0.02233	-0.00723	T	Study 1	CV089	512	401
55	NC0082153	3	94.5	0.0027	-0.07526	A	Study 3	--	162	402
55	NC0082160	3	94.5	--	--	G	Study 5	--	334	403
55	NC0200047	3	96.1	--	--	G	Study 5	--	98	404
55	NC0200156	3	96.1	--	--	G	Study 5	--	204	405
55	NC0008900	3	97.6	4.46E-13	0.209643	A	Study 2	--	275	406
55	NC0008900	3	97.6	0.017875	-0.15091	G	Study 1	CV131	275	406
55	NC0008900	3	97.6	0.008202	-0.01946	G	Study 1	CV041	275	406
55	NC0010933	3	99.3	--	--	T	Study 5	--	508	407
55	NC0010933	3	99.3	0.015683	0.018522	T	Study 1	CV140	508	407
55	NC0010933	3	99.3	0.028218	-0.13555	T	Study 1	CV041	508	407
55	NC0010933	3	99.3	0.028498	-0.17619	G	Study 1	CV044	508	407
55	NC0031720	3	99.7	0	0.321823	G	Study 1	CV149	434	408
55	NC0031720	3	99.7	0.008492	-0.00817	G	Study 1	CV089	434	408
56	NC0009739	3	102.2	0.000431	0.322949	G	Study 1	CV161	284	409
56	NC0022590	3	104	0.042886	0.009577	T	Study 1	CV081	83	410
56	NC0022590	3	104	0.005452	0.023224	T	Study 1	CV006	83	410
56	NC0022590	3	104	0.049688	0.003247	T	Study 1	CV099	83	410
56	NC0022590	3	104	0.007023	0.012766	T	Study 1	CV145	83	410
56	NC0104504	3	104	--	--	G	Study 5	--	406	411
56	NC0104504	3	104	0.007808	-0.15689	A	Study 1	CV053	406	411

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
56	NC0104504	3	104	0.018264	-0.00921	G	Study 1	CV090	406	411
56	NC0013092	3	105.4	0.000025	0.189889	C	Study 1	CV116	369	412
56	NC0107469	3	106.3	--	--	T	Study 5	--	341	413
56	NC0108089	3	106.3	<.0001	0.209948	**	Study 3	--	274	414
56	NC0108089	3	106.3	--	--	**	Study 4	--	274	414
56	NC0108089	3	106.3	0.006447	-0.01624	**	Study 1	CV025	274	414
56	NC0154151	3	109.3	0.000443	0.093358	G	Study 1	CV168	182	415
56	NC0154151	3	109.3	0	-0.19628	A	Study 1	CV101	182	415
56	NC0154151	3	109.3	0.00069	-0.05905	A	Study 1	CV010	182	415
56	NC0154151	3	109.3	0.013453	-0.0107	A	Study 1	CV010	182	415
56	NC0154151	3	109.3	0.015414	0.009173	A	Study 1	CV151	182	415
56	NC0154151	3	109.3	0.00061	0.021724	A	Study 1	CV014	182	415
56	NC0154505	3	109.3	0.018355	-0.06512	T	Study 1	CV050	126	416
56	NC0154505	3	109.3	0.039604	0.015328	T	Study 1	CV150	126	416
56	NC0154616	3	109.3	--	--	C	Study 5	--	216	417
56	NC0155689	3	109.3	<.0001	0.385927	T	Study 3	--	231	418
57	NC0155775	3	111.4	--	--	G	Study 4	--	162	419
57	NC0155775	3	111.4	0.009072	0.105845	G	Study 1	CV114	162	419
57	NC0144126	3	111.6	0.000006	0.231245	A	Study 1	CV125	233	420
57	NC0055894	3	112.4	--	--	T	Study 4	--	202	421
57	NC0055894	3	112.4	0.028738	-0.0113	T	Study 1	CV014	202	421
57	NC0024395	3	116	0.015486	0.013618	T	Study 1	CV141	75	422
57	NC0024395	3	116	0.000373	0.126134	T	Study 1	CV079	75	422
57	NC0024395	3	116	0.000022	0.165958	T	Study 1	CV079	75	422
57	NC0024395	3	116	0	0.146535	T	Study 1	CV150	75	422
57	NC0024395	3	116	0	0.209881	T	Study 1	CV150	75	422
57	NC0079081	3	117.1	0.022233	-0.08334	C	Study 1	CV041	78	423
57	NC0079081	3	117.1	0.005235	0.023594	A	Study 1	CV006	78	423
57	NC0079081	3	117.1	0.002301	0.016044	A	Study 1	CV005	78	423
57	NC0079081	3	117.1	0.044123	-0.01155	A	Study 1	CV076	78	423
57	NC0079081	3	117.1	0.006	0.015106	A	Study 1	CV006	78	423
57	NC0111959	3	117.6	0.000511	0.158732	**	Study 1	CV116	71	424
57	NC0111959	3	117.6	0.004949	-0.07922	GT	Study 1	CV082	71	424

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
57	NC0111959	3	117.6	0.041178	-0.01013	GT	Study 1	CV014	71	424
57	NC0111959	3	117.6	0.016177	-0.01609	GT	Study 1	CV077	71	424
57	NC0023890	3	119.5	3.39E-13	0.207322	C	Study 2	--	121	425
57	NC0023890	3	119.5	0.000871	-0.20028	T	Study 1	CV041	121	425
57	NC0023890	3	119.5	0	0.267461	T	Study 1	CV149	121	425
58	NC0106349	3	120.6	--	--	G	Study 4	--	129	426
58	NC0106349	3	120.6	--	--	G	Study 5	--	129	426
58	NC0106349	3	120.6	0.0074	0.06561	G	Study 1	CV168	129	426
58	NC0106349	3	120.6	0.008712	0.118081	G	Study 1	CV118	129	426
58	NC0106349	3	120.6	0.000096	-0.15328	G	Study 1	CV101	129	426
58	NC0106349	3	120.6	0.000001	0.138245	G	Study 1	CV150	129	426
58	NC0106349	3	120.6	0	0.193598	G	Study 1	CV150	129	426
58	NC0106349	3	120.6	0.003731	0.018712	A	Study 1	CV014	129	426
58	NC0199918	3	120.6	--	--	T	Study 5	--	319	427
58	NC0000399	3	121.1	--	--	G	Study 5	--	275	428
58	NC0002905	3	123.9	--	--	T	Study 4	--	98	429
58	NC0002905	3	123.9	0.047891	-0.04422	A	Study 1	CV082	98	429
58	NC0002905	3	123.9	0.000002	0.420946	T	Study 1	CV161	98	429
58	NC0009173	3	124.2	0.017251	-0.09376	A	Study 1	CV041	101	430
58	NC0011320	3	124.2	0.000011	0.224683	C	Study 1	CV125	65	431
58	NC0144788	3	125.7	0.013531	-0.04394	G	Study 1	CV010	485	432
58	NC0144788	3	125.7	0.026704	-0.16673	A	Study 1	I294213	485	432
58	NC0008922	3	128.2	--	--	G	Study 5	--	271	433
58	NC0008922	3	128.2	0.000012	0.23008	G	Study 1	CV149	271	433
58	NC0008922	3	128.2	0.00598	0.097424	A	Study 1	CV079	271	433
58	NC0008922	3	128.2	0.000052	0.156766	A	Study 1	CV079	271	433
59	NC0040232	3	139.8	--	--	T	Study 4	--	69	434
59	NC0031450	3	139.9	0.000093	0.194748	C	Study 1	CV125	262	435
59	NC0031450	3	139.9	0.00568	0.020454	C	Study 1	CV150	262	435
60	NC0015965	3	140.8	1.14E-10	0.18974	T	Study 2	--	281	436
60	NC0015954	3	141	--	--	T	Study 4	--	254	437
60	NC0015954	3	141	0.000985	0.136399	T	Study 1	CV116	254	437
60	NC0015954	3	141	0.027735	-0.13626	A	Study 1	CV041	254	437

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
60	NC0015954	3	141	0.01645	0.026942	T	Study 1	CV165	254	437
60	NC0015954	3	141	0.002105	0.029906	T	Study 1	CV165	254	437
60	NC0015954	3	141	0.016574	0.015554	T	Study 1	CV169	254	437
60	NC0034494	3	141	0.009469	0.013891	G	Study 1	CV006	524	438
60	NC0034494	3	141	0.038421	0.024646	A	Study 1	CV155	524	438
60	NC0039763	3	145.4	0.015968	0.006325	G	Study 1	CV141	192	439
60	NC0041040	3	145.4	0.006596	-0.05752	A	Study 1	CV082	497	440
60	NC0041040	3	145.4	0.032235	-0.01237	G	Study 1	CV025	497	440
60	NC0041040	3	145.4	0.008576	0.076944	G	Study 1	CV150	497	440
60	NC0041040	3	145.4	0.000001	0.157504	G	Study 1	CV150	497	440
60	NC0077118	3	145.9	--	--	G	Study 5	--	188	441
60	NC0077118	3	145.9	0.020119	0.097199	A	Study 1	CV116	188	441
60	NC0077118	3	145.9	0.031045	0.011062	G	Study 1	I283669	188	441
60	NC0077118	3	145.9	0.000001	0.203923	A	Study 1	CV118	188	441
60	NC0015865	3	147.5	0.000248	0.195379	A	Study 1	CV149	399	442
60	NC0004013	3	148.1	0.006919	-0.01541	T	Study 1	CV076	276	443
60	NC0036695	3	148.1	0.007457	-0.23208	C	Study 1	I294213	243	444
60	NC0036695	3	148.1	0.004184	0.101278	G	Study 1	CV079	243	444
60	NC0036695	3	148.1	0.000991	0.12846	G	Study 1	CV079	243	444
60	NC0017494	3	148.4	0.003883	0.173373	G	Study 1	CV160	294	445
60	NC0199759	3	149	--	--	G	Study 5	--	288	446
60	NC0110128	3	149.5	0.046589	-0.00519	*	Study 1	CV056	217	447
60	NC0172191	3	149.5	--	--	T	Study 5	--	153	448
60	NC0173461	3	149.5	--	--	C	Study 5	--	179	449
61	NC0043810	3	151.9	0.000344	0.021577	G	Study 1	CV141	424	450
61	NC0029390	3	152.7	<.0001	0.149859	T	Study 3	--	300	451
61	NC0029390	3	152.7	1.68E-12	0.202054	C	Study 2	--	300	451
61	NC0029390	3	152.7	0.044939	0.033514	T	Study 1	CV114	300	451
61	NC0029390	3	152.7	0.002353	-0.02018	T	Study 1	CV077	300	451
61	NC0029390	3	152.7	0.028366	0.013926	C	Study 1	CV169	300	451
61	NC0199913	3	152.8	--	--	T	Study 5	--	52	452
61	NC0021772	3	154.1	0.00695	0.0315	T	Study 1	CV155	259	453
61	NC0021772	3	154.1	0.049332	0.181964	C	Study 1	CV161	259	453

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
61	NC0105966	3	154.6	0.006876	-0.02704	G	Study 1	CV146	343	454
61	NC0146188	3	154.6	0.046943	0.009359	T	Study 1	I283669	93	455
61	NC0199682	3	155.2	--	--	T	Study 5	--	173	456
61	NC0054742	3	155.3	--	--	T	Study 4	--	130	457
61	NC0054742	3	155.3	0.020843	0.022705	T	Study 1	CV135	130	457
61	NC0054742	3	155.3	0.001711	-0.23349	C	Study 1	I294213	130	457
61	NC0173894	3	156.5	--	--	G	Study 5	--	560	458
62	NC0143174	3	161.4	0.048351	0.004714	G	Study 1	CV051	424	459
62	NC0071496	3	161.7	0.016943	-0.00743	G	Study 1	CV122	139	460
62	NC0108630	3	163.5	0.0029	0.105606	G	Study 3	--	341	461
62	NC0108630	3	163.5	1.28E-07	0.175183	G	Study 2	--	341	461
62	NC0108630	3	163.5	0.045265	-0.01754	G	Study 1	I294213	341	461
62	NC0108630	3	163.5	0.042807	0.016734	A	Study 1	CV165	341	461
62	NC0004371	3	164.2	0.029475	-0.00544	C	Study 1	CV056	322	462
62	NC0004371	3	164.2	0.041613	0.009252	G	Study 1	I283669	322	462
62	NC0004371	3	164.2	0.006977	0.006361	G	Study 1	CV051	322	462
62	NC0004371	3	164.2	0.012755	0.027809	G	Study 1	CV165	322	462
62	NC0004371	3	164.2	0.00674	0.026295	G	Study 1	CV165	322	462
62	NC0151375	3	166.4	0.000164	0.193168	T	Study 1	CV125	471	463
62	NC0009473	3	168.4	0.037328	-0.04482	C	Study 1	CV082	336	464
62	NC0009473	3	168.4	0.03867	-0.12688	T	Study 1	CV025	336	464
62	NC0009473	3	168.4	0.002134	0.130502	C	Study 1	CV125	336	464
62	NC0009473	3	168.4	0.005921	-0.01616	T	Study 1	CV025	336	464
63	NC0031216	3	171.3	--	--	G	Study 5	--	195	465
63	NC0189460	3	171.8	--	--	T	Study 5	--	531	466
63	NC0105852	3	176.4	0.011254	0.158482	C	Study 1	CV160	258	467
63	NC0110780	3	176.8	0.021774	0.225985	A	Study 1	CV161	360	468
63	NC0110780	3	176.8	0.047201	0.07084	A	Study 1	CV079	360	468
63	NC0110780	3	176.8	0.00556	0.109819	A	Study 1	CV079	360	468
63	NC0055817	3	177.1	--	--	T	Study 4	--	308	469
63	NC0055817	3	177.1	0.013149	0.150169	T	Study 1	CV006	308	469
63	NC0055817	3	177.1	0.004291	-0.06239	G	Study 1	CV082	308	469
63	NC0055817	3	177.1	0.000048	0.17472	G	Study 1	CV118	308	469

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
63	NC0055817	3	177.1	0.006013	-0.13167	G	Study 1	I294213	308	469
63	NC0055817	3	177.1	0.026369	0.017815	G	Study 1	CV165	308	469
63	NC0055817	3	177.1	0.013017	0.015384	G	Study 1	CV141	308	469
63	NC0106901	3	177.6	0.000122	0.195613	T	Study 1	CV125	282	470
63	NC0030587	3	179.7	0.000141	0.095721	C	Study 1	CV168	76	471
63	NC0030587	3	179.7	0.000641	-0.01911	C	Study 1	CV040	76	471
63	NC0030587	3	179.7	0.006872	0.079336	A	Study 1	CV150	76	471
63	NC0030587	3	179.7	0.009071	0.086362	A	Study 1	CV150	76	471
63	NC0030587	3	179.7	0.008289	-0.01655	C	Study 1	CV077	76	471
63	NC0030587	3	179.7	0.000736	-0.01592	C	Study 1	I294213	76	471
64	NC0112644	3	181.8	1.51E-09	0.173132	C	Study 2	--	405	472
64	NC0112644	3	181.8	0.049167	-0.01889	T	Study 1	CV146	405	472
64	NC0112644	3	181.8	0.049934	-0.00526	C	Study 1	CV056	405	472
64	NC0112644	3	181.8	0.000759	0.086986	T	Study 1	CV168	405	472
64	NC0112644	3	181.8	0.006845	-0.1317	T	Study 1	I294213	405	472
64	NC0112644	3	181.8	0.04122	0.008138	T	Study 1	CV101	405	472
64	NC0112644	3	181.8	0.017278	0.005197	T	Study 1	CV051	405	472
64	NC0112644	3	181.8	0.041063	0.109622	T	Study 1	CV149	405	472
64	NC0112644	3	181.8	0.0378	-0.15001	T	Study 1	I294213	405	472
64	NC0112644	3	181.8	0.03852	0.014961	C	Study 1	CV074	405	472
64	NC0112644	3	181.8	0.000639	-0.01903	T	Study 1	CV040	405	472
64	NC0112644	3	181.8	0.045091	0.010415	T	Study 1	CV153	405	472
64	NC0112644	3	181.8	0.004908	0.111484	C	Study 1	CV079	405	472
64	NC0112644	3	181.8	0.000107	-0.01837	T	Study 1	I294213	405	472
64	NC0112487	3	182.9	0.0004	0.35796	G	Study 3	--	88	473
64	NC0112491	3	182.9	<.0001	-0.4002	C	Study 3	--	90	474
64	NC0112491	3	182.9	0.016096	0.150226	G	Study 1	CV006	90	474
64	NC0112491	3	182.9	0.000275	0.154988	C	Study 1	CV125	90	474
64	NC0112491	3	182.9	0.0419	0.020066	C	Study 1	CV135	90	474
64	NC0112491	3	182.9	0.034762	0.02606	C	Study 1	CV155	90	474
64	NC0112491	3	182.9	0.011429	-0.01448	G	Study 1	CV025	90	474
64	NC0056939	3	183.6	--	--	C	Study 4	--	426	475
64	NC0056939	3	183.6	--	--	C	Study 5	--	426	475

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
64	NC0056939	3	183.6	0.000334	0.018566	C	Study 1	CV005	426	475
64	NC0146534	3	183.6	--	--	T	Study 4	--	91	476
64	NC0032026	3	183.9	0.02923	0.017555	A	Study 1	CV165	1134	477
64	NC0154169	3	184.3	--	--	T	Study 5	--	74	478
64	NC0146497	3	187.4	--	--	T	Study 4	--	98	479
64	NC0146497	3	187.4	0.026386	0.056639	T	Study 1	CV168	98	479
64	NC0146497	3	187.4	0.00657	-0.01322	T	Study 1	I294213	98	479
64	NC0155987	3	187.4	--	--	T	Study 4	--	1001	480
64	NC0028145	3	187.5	0.041608	-0.00896	A	Study 1	CV013	307	481
64	NC0028145	3	187.5	0.000738	0.173307	G	Study 1	CV125	307	481
64	NC0143969	3	187.5	--	--	**	Study 4	--	100	482
64	NC0143969	3	187.5	0.041078	0.010947	TA	Study 1	CV006	100	482
64	NC0143969	3	187.5	0.013828	0.014034	**	Study 1	CV141	100	482
64	NC0143969	3	187.5	0.004572	0.165388	**	Study 1	CV160	100	482
64	NC0143969	3	187.5	0.000698	0.037604	**	Study 1	CV165	100	482
64	NC0143969	3	187.5	0.000075	0.038026	**	Study 1	CV165	100	482
65	NC0078580	3	193.9	--	--	G	Study 5	--	101	483
65	NC0009079	3	194.2	0.002594	0.128482	C	Study 1	CV125	118	484
65	NC0009079	3	194.2	0.041104	-0.00663	C	Study 1	CV089	118	484
65	NC0110756	3	197.4	0.002033	0.112545	T	Study 1	CV053	136	485
65	NC0110756	3	197.4	0.025362	0.068343	G	Study 1	CV150	136	485
65	NC0010232	3	198.7	0.000002	0.199858	T	Study 1	CV118	353	486
65	NC0010232	3	198.7	0.017304	0.128863	C	Study 1	CV149	353	486
65	NC0010232	3	198.7	0.000512	-0.01962	T	Study 1	CV025	353	486
66	NC0000055	3	201.1	0.0035	0.106003	T	Study 3	--	97	487
66	NC0190645	3	202.4	--	--	T	Study 5	--	90	488
66	NC0019414	3	204.2	0.004755	0.08091	A	Study 2	--	272	489
66	NC0019414	3	204.2	0.034246	-0.09432	C	Study 1	I294213	272	489
66	NC0019414	3	204.2	0.016056	0.005313	C	Study 1	CV051	272	489
66	NC0019414	3	204.2	0.023807	0.058043	A	Study 1	CV116	272	489
66	NC0019414	3	204.2	0.000007	0.18987	A	Study 1	CV118	272	489
66	NC0019414	3	204.2	0.002848	0.154485	A	Study 1	CV125	272	489
66	NC0019414	3	204.2	0.001511	-0.00978	C	Study 1	CV138	272	489

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
66	NC0019414	3	204.2	0.00451	0.0317	C	Study 1	CV165	272	489
66	NC0019414	3	204.2	0.001903	0.030133	C	Study 1	CV165	272	489
66	NC0019414	3	204.2	0.006783	-0.01418	C	Study 1	I294213	272	489
66	NC0003970	3	208	--	--	G	Study 5	--	355	490
66	NC0003970	3	208	0.008295	-0.06615	G	Study 1	CV052	355	490
66	NC0003970	3	208	0.021301	-0.00716	G	Study 1	CV052	355	490
66	NC0003970	3	208	0.018829	0.128122	A	Study 1	CV164	355	490
67	NC0173736	3	211	--	--	T	Study 5	--	1001	491
67	NC0104796	3	212.1	0.005392	0.15223	*	Study 1	CV164	170	492
67	NC0014041	3	217.6	0.00015	0.161921	A	Study 1	CV118	244	493
67	NC0014041	3	217.6	0.045158	-0.07707	C	Study 1	CV075	244	493
67	NC0078117	3	218.2	--	--	T	Study 5	--	215	494
67	NC0077802	3	218.7	0.043396	-0.00382	T	Study 1	I294213	201	495
67	NC0077802	3	218.7	0.001471	0.173706	G	Study 1	CV069	201	495
67	NC0077802	3	218.7	0.028323	0.017448	G	Study 1	CV165	201	495
67	NC0077802	3	218.7	0.024716	-0.00948	G	Study 1	CV095	201	495
67	NC0077802	3	218.7	0.016096	0.016356	T	Study 1	CV014	201	495
68	NC0012340	4	0.5	0.004643	0.02089	T	Study 1	CV065	402	496
68	NC0012340	4	0.5	0.035087	-0.13142	T	Study 1	CV017	402	496
68	NC0012340	4	0.5	0.000525	-0.01052	T	Study 1	CV138	402	496
68	NC0012340	4	0.5	0.04694	0.016733	A	Study 1	CV123	402	496
68	NC0012340	4	0.5	0.009471	0.021847	T	Study 1	CV069	402	496
68	NC0012340	4	0.5	0.043296	0.013107	A	Study 1	CV169	402	496
68	NC0009523	4	0.9	0.004246	0.020865	T	Study 1	CV065	434	497
68	NC0009523	4	0.9	0.001281	0.004146	A	Study 1	CV006	434	497
68	NC0009523	4	0.9	0.001281	0.004146	A	Study 1	CV006	434	497
68	NC0009523	4	0.9	0.038904	-0.03768	T	Study 1	CV041	434	497
68	NC0009523	4	0.9	0.029006	-0.02262	T	Study 1	I294213	434	497
68	NC0009523	4	0.9	0.013272	0.009077	A	Study 1	CV151	434	497
68	NC0055502	4	1.8	0.027298	0.208359	T	Study 1	CV109	105	498
68	NC0055502	4	1.8	0.006668	0.012615	C	Study 1	CV081	105	498
68	NC0055502	4	1.8	0.005363	0.022763	T	Study 1	CV069	105	498
68	NC0196391	4	6.9	--	--	C	Study 5	--	234	499

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
69	NC0002739	4	11.8	--	--	*	Study 4	--	126	500
69	NC0002739	4	11.8	0.024075	-0.01232	*	Study 1	CV136	126	500
69	NC0199824	4	13.6	--	--	G	Study 5	--	357	501
69	NC0038222	4	17.6	--	--	T	Study 5	--	95	502
70	NC0009057	4	21.7	--	--	T	Study 5	--	246	503
70	NC0009057	4	21.7	0.027692	0.014397	G	Study 1	CV011	246	503
70	NC0009057	4	21.7	0.00979	0.11185	T	Study 1	CV125	246	503
70	NC0009057	4	21.7	0.008145	0.028865	T	Study 1	CV154	246	503
70	NC0009057	4	21.7	0.00085	-0.0217	G	Study 1	CV025	246	503
70	NC0009057	4	21.7	0.007821	0.156292	G	Study 1	CV070	246	503
70	NC0009057	4	21.7	0.039053	0.012332	G	Study 1	CV079	246	503
70	NC0009057	4	21.7	0.024997	0.190896	G	Study 1	CV130	246	503
70	NC0009057	4	21.7	0.02272	0.014909	T	Study 1	CV147	246	503
70	NC0069221	4	21.9	0.006917	-0.0078	C	Study 1	CV138	170	504
71	NC0105666	4	30.4	<.0001	-0.42472	A	Study 3	--	230	505
71	NC0105666	4	30.4	0.000843	0.02179	C	Study 1	CV011	230	505
71	NC0105666	4	30.4	0.002264	-0.00858	C	Study 1	CV138	230	505
71	NC0105666	4	30.4	0.016577	-0.29806	C	Study 1	CV130	230	505
71	NC0105666	4	30.4	0.015991	0.213218	C	Study 1	CV130	230	505
71	NC0105666	4	30.4	0.01461	0.143989	C	Study 1	CV160	230	505
71	NC0110069	4	34.4	0.022632	-0.06511	G	Study 2	--	314	506
71	NC0110069	4	34.4	0.031511	-0.0061	G	Study 1	CV052	314	506
71	NC0110069	4	34.4	0.002947	0.032316	G	Study 1	CV154	314	506
71	NC0110069	4	34.4	0.002926	-0.01965	A	Study 1	CV025	314	506
71	NC0110069	4	34.4	0.035906	-0.20041	A	Study 1	CV071	314	506
71	NC0111464	4	34.4	--	--	G	Study 5	--	115	507
71	NC0111464	4	34.4	0.045859	-0.03549	A	Study 1	CV070	115	507
71	NC0111464	4	34.4	0.000008	0.258744	A	Study 1	CV070	115	507
71	NC0111464	4	34.4	0.001513	0.024966	G	Study 1	CV123	115	507
72	NC0018996	4	44.7	0.000047	0.025966	T	Study 1	CV011	213	508
72	NC0018996	4	44.7	0.006872	0.164755	C	Study 1	CV160	213	508
72	NC0019003	4	45.3	0.003694	-0.05704	G	Study 1	CV042	405	509
72	NC0034133	4	49.8	0.014484	-0.14086	C	Study 1	CV131	202	510

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
72	NC0034133	4	49.8	0.000598	-0.01869	C	Study 1	CV087	202	510
72	NC0034130	4	49.9	0.027918	0.114854	G	Study 1	CV023	126	511
72	NC0034130	4	49.9	0	-0.21546	C	Study 1	CV041	126	511
72	NC0034130	4	49.9	0.003561	0.24835	G	Study 1	CV127	126	511
72	NC0034130	4	49.9	0.030074	-0.01308	G	Study 1	CV076	126	511
73	NC0077263	4	50.6	0.000001	0.030515	A	Study 1	CV011	228	512
73	NC0024647	4	52.5	0.000006	0.029084	A	Study 1	CV011	191	513
73	NC0024647	4	52.5	0.004513	0.046544	A	Study 1	CV100	191	513
73	NC0024647	4	52.5	0.006209	0.01105	A	Study 1	CV100	191	513
73	NC0024647	4	52.5	0.000519	0.14485	G	Study 1	CV166	191	513
73	NC0024647	4	52.5	0.000286	0.282003	G	Study 1	CV132	191	513
73	NC0024647	4	52.5	0.000185	0.276161	G	Study 1	CV163	191	513
73	NC0024647	4	52.5	0.041063	-0.02025	A	Study 1	I294213	191	513
73	NC0024647	4	52.5	0.001965	-0.00892	A	Study 1	CV138	191	513
73	NC0024647	4	52.5	0.000005	0.036004	A	Study 1	CV123	191	513
73	NC0009197	4	59.7	0.000001	0.031688	*	Study 1	CV011	478	514
73	NC0037062	4	59.7	0.016846	0.010055	C	Study 1	CV170	52	515
73	NC0037062	4	59.7	0.005364	0.008903	C	Study 1	CV101	52	515
73	NC0037062	4	59.7	0	0.314486	C	Study 1	CV070	52	515
73	NC0037062	4	59.7	0.037626	0.011228	C	Study 1	CV142	52	515
73	NC0037062	4	59.7	0.000001	-0.63909	G	Study 1	CV130	52	515
73	NC0037062	4	59.7	0.037295	0.017575	C	Study 1	CV069	52	515
74	NC0001122	4	61.4	0.000001	0.031688	T	Study 1	CV011	216	516
74	NC0001122	4	61.4	0.008388	-0.1922	T	Study 1	CV069	216	516
74	NC0001122	4	61.4	0.033195	-0.03761	T	Study 1	CV070	216	516
74	NC0001122	4	61.4	0.000044	-0.02616	C	Study 1	CV025	216	516
74	NC0001122	4	61.4	0.008625	0.113033	C	Study 1	CV125	216	516
74	NC0001122	4	61.4	0.017042	0.069075	C	Study 1	CV128	216	516
74	NC0001122	4	61.4	0.028821	0.012097	T	Study 1	CV142	216	516
74	NC0001122	4	61.4	0.028663	0.132065	T	Study 1	CV160	216	516
74	NC0001122	4	61.4	0.002926	0.020327	T	Study 1	CV014	216	516
74	NC0012012	4	61.4	0.000003	0.033215	C	Study 1	CV011	129	517
74	NC0012012	4	61.4	0.045524	-0.01027	T	Study 1	CV053	129	517

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
74	NC0012012	4	61.4	0.026059	-0.0066	T	Study 1	CV052	129	517
74	NC0012012	4	61.4	0.000056	-0.06791	C	Study 1	CV010	129	517
74	NC0034325	4	63.7	0.002976	0.016907	G	Study 1	CV142	191	518
74	NC0069795	4	65.5	<.0001	0.375641	T	Study 3	--	386	519
74	NC0042575	4	65.9	0.004505	-0.08253	A	Study 2	--	107	520
74	NC0028441	4	67.1	0.014635	-0.01675	C	Study 1	CV010	125	521
74	NC0038855	4	67.1	0.021792	0.123036	C	Study 1	CV164	74	522
74	NC0038855	4	67.1	0.02141	0.059848	C	Study 1	CV135	74	522
74	NC0038855	4	67.1	0	0.620323	C	Study 1	CV130	74	522
74	NC0040371	4	67.8	--	--	C	Study 4	--	201	523
74	NC0040371	4	67.8	0.000004	0.250029	A	Study 1	CV069	201	523
74	NC0040371	4	67.8	0.000002	-0.09921	A	Study 1	CV042	201	523
74	NC0070730	4	67.8	--	--	G	Study 4	--	324	524
74	NC0010305	4	68.4	0.043563	-0.00318	T	Study 1	CV010	228	525
74	NC0010305	4	68.4	0.043563	-0.00318	T	Study 1	CV010	228	525
74	NC0010305	4	68.4	0.000544	-0.05817	T	Study 1	CV010	228	525
74	NC0035683	4	68.4	<.0001	-0.19803	C	Study 3	--	245	526
74	NC0035683	4	68.4	0.001784	-0.00911	C	Study 1	CV138	245	526
74	NC0015567	4	68.6	0.001114	0.021868	C	Study 1	CV061	235	527
74	NC0038900	4	69.3	--	--	T	Study 4	--	276	528
74	NC0038900	4	69.3	0.000202	-0.35178	T	Study 1	CV071	276	528
74	NC0009603	4	69.5	0.016775	0.026869	T	Study 1	CV154	193	529
74	NC0033483	4	69.5	--	--	T	Study 4	--	163	530
75	NC0031791	4	70.1	--	--	***********	Study 4	--	402	531
75	NC0031791	4	70.1	0.040417	0.009536	***********	Study 1	CV142	402	531
75	NC0031791	4	70.1	0.045342	-0.01281	CAGTCCCAGCT	Study 1	CV063	402	531
75	NC0020481	4	71	<.0001	0.217696	T	Study 3	--	118	532
75	NC0020481	4	71	0.021492	0.116319	A	Study 1	CV023	118	532
75	NC0020481	4	71	0.024509	0.064986	T	Study 1	CV128	118	532
75	NC0020481	4	71	0.04558	0.017471	T	Study 1	CV158	118	532
75	NC0020481	4	71	0.034415	0.018348	T	Study 1	CV162	118	532
75	NC0108120	4	71.5	0.0006	0.18251	T	Study 3	--	401	533
75	NC0108120	4	71.5	0	-0.23926	T	Study 1	CV041	401	533

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
75	NC0108120	4	71.5	0.025869	-0.10649	T	Study 1	CV067	401	533
75	NC0034464	4	73.5	0.000232	-0.10599	A	Study 2	--	125	534
75	NC0034464	4	73.5	0.000021	0.181414	A	Study 1	CV166	125	534
75	NC0034464	4	73.5	0.001398	0.228654	A	Study 1	CV163	125	534
75	NC0034464	4	73.5	0	0.433985	A	Study 1	CV070	125	534
75	NC0034464	4	73.5	0.001495	0.018969	A	Study 1	CV079	125	534
75	NC0034464	4	73.5	0	0.048971	A	Study 1	CV123	125	534
75	NC0034464	4	73.5	0.004513	0.019348	A	Study 1	CV014	125	534
75	NC0002585	4	74.4	0.048511	-0.00597	T	Study 1	CV052	223	535
75	NC0002585	4	74.4	0.013899	0.013512	T	Study 1	CV007	223	535
75	NC0005451	4	74.8	--	--	G	Study 4	--	224	536
75	NC0015096	4	74.8	0.001572	0.18765	A	Study 1	CV160	398	537
75	NC0003351	4	76	--	--	C	Study 4	--	432	538
75	NC0003351	4	76	0.005403	-0.01552	A	Study 1	CV087	432	538
75	NC0015247	4	76	--	--	T	Study 4	--	483	539
75	NC0004924	4	76.3	0.000969	-0.09708	T	Study 2	--	46	540
75	NC0113163	4	76.3	0.030834	-0.04893	C	Study 1	CV010	44	541
75	NC0199812	4	77.3	--	--	C	Study 5	--	45	542
75	NC0080778	4	77.7	--	--	G	Study 4	--	184	543
75	NC0014666	4	77.8	--	--	G	Study 4	--	108	544
75	NC0020374	4	77.8	0.00857	-0.06576	T	Study 1	CV022	397	545
75	NC0020374	4	77.8	0.045384	0.058115	T	Study 1	CV128	397	545
75	NC0078135	4	77.8	--	--	G	Study 4	--	321	546
75	NC0000415	4	78.9	0.002755	0.019343	G	Study 1	CV061	103	547
75	NC0153429	4	78.9	--	--	T	Study 5	--	235	548
75	NC0106099	4	79.8	--	--	T	Study 5	--	84	549
75	NC0106099	4	79.8	0.000876	0.021299	T	Study 1	I283669	84	549
75	NC0109551	4	79.8	0.000547	-0.10136	G	Study 2	--	100	550
75	NC0151500	4	79.8	0	-0.78401	G	Study 1	CV130	493	551
76	NC0003532	4	81.3	<.0001	0.169377	T	Study 3	--	600	552
76	NC0080475	4	82	--	--	G	Study 5	--	228	553
76	NC0084527	4	82	0	-0.44175	C	Study 1	CV069	509	554
76	NC0084527	4	82	0.000002	0.398659	C	Study 1	CV127	509	554

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
76	NC0084527	4	82	0.01718	0.022649	C	Study 1	CV127	509	554
76	NC0084527	4	82	0.000048	0.315136	C	Study 1	CV132	509	554
76	NC0084527	4	82	0.001524	0.037574	C	Study 1	CV132	509	554
76	NC0084527	4	82	0.02648	-0.007	C	Study 1	CV138	509	554
76	NC0084527	4	82	0	0.02858	C	Study 1	CV142	509	554
76	NC0084527	4	82	0.047041	-0.05815	A	Study 1	CV119	509	554
76	NC0084527	4	82	0.026658	-0.07301	A	Study 1	CV119	509	554
76	NC0084527	4	82	0.043382	0.012863	A	Study 1	CV147	509	554
76	NC0111150	4	82	0.000007	-0.02892	T	Study 1	CV025	449	555
76	NC0027345	4	82.5	0.000361	-0.10531	A	Study 2	--	237	556
76	NC0027345	4	82.5	0.000119	0.162727	G	Study 1	CV125	237	556
76	NC0027345	4	82.5	0.029972	0.279434	G	Study 1	CV167	237	556
76	NC0027345	4	82.5	0.012365	0.021041	G	Study 1	CV158	237	556
76	NC0027345	4	82.5	0.044648	0.02398	G	Study 1	CV058	237	556
76	NC0027345	4	82.5	0.017432	-0.04223	G	Study 1	CV070	237	556
76	NC0027345	4	82.5	0	0.462388	G	Study 1	CV070	237	556
76	NC0027345	4	82.5	0.002025	0.018139	G	Study 1	CV079	237	556
76	NC0104667	4	82.7	<.0001	-0.20518	GT	Study 3	--	293	557
76	NC0104667	4	82.7	0.002157	-0.29628	GT	Study 1	CV071	293	557
76	NC0104667	4	82.7	0.04141	0.014544	**	Study 1	CV169	293	557
76	NC0104906	4	82.7	0.040377	-0.11127	G	Study 1	CV119	124	558
76	NC0111329	4	82.7	0.001263	-0.18452	G	Study 1	CV131	414	559
76	NC0111329	4	82.7	0.003211	0.005229	C	Study 1	CV104	414	559
76	NC0111329	4	82.7	0.001082	0.23394	C	Study 1	CV163	414	559
76	NC0106797	4	82.9	--	--	T	Study 5	--	87	560
76	NC0106797	4	82.9	0.029875	-0.0111	G	Study 1	CV010	87	560
76	NC0038999	4	83.8	--	--	G	Study 5	--	304	561
76	NC0038999	4	83.8	0.010688	-0.0201	G	Study 1	CV041	304	561
76	NC0038999	4	83.8	0.000002	0.03003	G	Study 1	CV011	304	561
76	NC0038999	4	83.8	0.042684	-0.01097	C	Study 1	CV086	304	561
76	NC0173808	4	83.8	--	--	C	Study 5	--	418	562
76	NC0104785	4	83.9	0	0.381728	A	Study 1	CV069	436	563
76	NC0104785	4	83.9	0.000189	0.183578	A	Study 1	CV093	436	563

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
76	NC0104785	4	83.9	0.002625	0.009184	A	Study 1	CV101	436	563
76	NC0035294	4	85.2	0.024076	0.013558	G	Study 1	CV011	187	564
76	NC0039743	4	87.4	--	--	T	Study 5	--	149	565
76	NC0039743	4	87.4	0.007885	0.142618	T	Study 1	CV164	149	565
76	NC0039743	4	87.4	0.007819	0.179661	T	Study 1	CV149	149	565
76	NC0111228	4	87.9	0.000847	-0.01417	G	Study 1	CV110	130	566
76	NC0037873	4	88.3	0.004729	0.070959	G	Study 1	CV135	129	567
77	NC0038782	4	90.4	0.017817	-0.06569	A	Study 1	CV082	312	568
77	NC0022725	4	91.3	--	--	T	Study 4	--	145	569
77	NC0022725	4	91.3	0.014569	0.00739	T	Study 1	CV101	145	569
77	NC0022725	4	91.3	0	0.028689	T	Study 1	CV142	145	569
77	NC0022725	4	91.3	0.000175	0.019744	T	Study 1	CV007	145	569
77	NC0022725	4	91.3	0.003424	0.020053	T	Study 1	CV014	145	569
77	NC0069570	4	92.4	0.000016	0.177653	C	Study 1	CV125	628	570
77	NC0069570	4	92.4	0.043046	0.128082	C	Study 1	CV073	628	570
77	NC0069570	4	92.4	0	-0.74376	C	Study 1	CV130	628	570
77	NC0069570	4	92.4	0.042021	-0.01291	C	Study 1	CV063	628	570
77	NC0002474	4	93.6	0.01513	-0.14014	C	Study 1	CV131	383	571
77	NC0002474	4	93.6	0.000005	0.187697	C	Study 1	CV166	383	571
77	NC0002474	4	93.6	0.000001	0.416992	C	Study 1	CV127	383	571
77	NC0002474	4	93.6	0.000937	0.03109	C	Study 1	CV127	383	571
77	NC0002474	4	93.6	0.011535	0.170708	C	Study 1	CV149	383	571
77	NC0002474	4	93.6	0.045177	-0.01169	C	Study 1	CV076	383	571
77	NC0002474	4	93.6	0.000001	0.041355	C	Study 1	CV123	383	571
77	NC0002474	4	93.6	0.010346	-0.07446	A	Study 1	CV119	383	571
77	NC0002474	4	93.6	0.003542	-0.09518	A	Study 1	CV119	383	571
77	NC0005018	4	94.8	0.020494	0.004387	T	Study 1	CV099	646	572
77	NC0005018	4	94.8	0.000125	0.268834	C	Study 1	CV163	646	572
77	NC0005018	4	94.8	0.000002	0.276417	C	Study 1	CV070	646	572
77	NC0005018	4	94.8	0.000695	0.020594	C	Study 1	CV079	646	572
77	NC0038087	4	94.8	0.047459	-0.18799	C	Study 1	CV071	162	573
77	NC0105550	4	94.8	0.042084	-0.05111	CCTACCTTCAGAA	Study 1	CV022	241	574
77	NC0105550	4	94.8	0.001528	-0.05425	CCTACCTTCAGAA	Study 1	CV010	241	574

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
77	NC0106845	4	94.8	0	-0.21668	G	Study 1	CV041	108	575
77	NC0106845	4	94.8	0.035358	0.11341	A	Study 1	CV023	108	575
77	NC0106845	4	94.8	0.027982	0.015201	A	Study 1	CV144	108	575
77	NC0032557	4	95.1	--	--	G	Study 5	--	411	576
77	NC0032557	4	95.1	0.000083	-0.08371	C	Study 1	CV042	411	576
77	NC0040744	4	95.2	--	--	G	Study 4	--	653	577
77	NC0105197	4	99.9	0.045255	-0.03541	T	Study 1	CV070	321	578
78	NC0013363	4	104.1	0.005265	0.017998	C	Study 1	CV011	475	579
78	NC0035313	4	104.1	0.00018	0.022705	T	Study 1	I283669	656	580
78	NC0003695	4	104.2	0.002552	0.019497	A	Study 1	CV147	329	581
78	NC0077408	4	104.3	--	--	C	Study 4	--	294	582
78	NC0077408	4	104.3	0.009998	0.022562	A	Study 1	CV158	294	582
78	NC0077408	4	104.3	0.001051	0.019541	A	Study 1	CV079	294	582
78	NC0077408	4	104.3	0.016847	-0.01037	A	Study 1	CV110	294	582
78	NC0003964	4	104.4	0.001436	-0.02072	T	Study 1	CV025	171	583
78	NC0003964	4	104.4	0	0.473329	T	Study 1	CV130	171	583
78	NC0003964	4	104.4	0.007501	0.158087	G	Study 1	CV160	171	583
78	NC0040117	4	104.4	0.003724	-0.0641	T	Study 1	CV042	122	584
78	NC0003274	4	104.7	0.037642	-0.05837	G	Study 1	CV082	269	585
78	NC0003274	4	104.7	0.005747	-0.04664	G	Study 1	CV010	269	585
78	NC0009620	4	109.2	0.020291	0.004206	T	Study 1	CV104	320	586
78	NC0009620	4	109.2	0.000003	-0.17596	T	Study 1	CV041	320	586
78	NC0009620	4	109.2	0.019022	0.126255	G	Study 1	CV023	320	586
78	NC0009620	4	109.2	0.011313	-0.0632	T	Study 1	CV022	320	586
78	NC0009620	4	109.2	0.003629	0.123458	T	Study 1	CV125	320	586
78	NC0009620	4	109.2	0.023061	0.291641	T	Study 1	CV167	320	586
78	NC0009620	4	109.2	0.017828	-0.06886	G	Study 1	CV119	320	586
79	NC0036240	4	112	--	--	G	Study 5	--	441	587
79	NC0036240	4	112	0.01023	-0.01708	G	Study 1	CV025	441	587
79	NC0036240	4	112	0.024741	0.019116	G	Study 1	CV073	441	587
79	NC0036240	4	112	0.000039	0.343262	G	Study 1	CV127	441	587
79	NC0036240	4	112	0.017577	0.097681	G	Study 1	CV114	441	587
79	NC0036240	4	112	0.016853	0.131854	G	Study 1	CV164	441	587

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
79	NC0036240	4	112	0.026982	-0.00988	A	Study 1	CV082	441	587
79	NC0036239	4	112.1	--	--	G	Study 5	--	341	588
79	NC0036239	4	112.1	0.042183	-0.01559	G	Study 1	CV139	341	588
79	NC0036239	4	112.1	0.000012	0.181805	G	Study 1	CV166	341	588
79	NC0036239	4	112.1	0.000008	-0.54634	A	Study 1	CV130	341	588
79	NC0036239	4	112.1	0.003658	0.171721	G	Study 1	CV160	341	588
79	NC0036239	4	112.1	0.009936	0.016277	G	Study 1	CV147	341	588
79	NC0036239	4	112.1	0.025516	-0.00945	A	Study 1	CV110	341	588
79	NC0110078	4	115.7	0.000071	-0.31393	G	Study 1	CV069	99	589
79	NC0110078	4	115.7	0.000002	0.241478	G	Study 1	CV069	99	589
79	NC0110078	4	115.7	0.03438	0.059353	G	Study 1	CV050	99	589
79	NC0110078	4	115.7	0.033718	0.006928	G	Study 1	CV050	99	589
79	NC0110078	4	115.7	0.000695	0.242005	G	Study 1	CV163	99	589
79	NC0110078	4	115.7	0.007778	0.016302	C	Study 1	CV147	99	589
79	NC0110078	4	115.7	0.000005	0.032636	C	Study 1	CV014	99	589
79	NC0108028	4	116.8	0.04105	-0.01591	C	Study 1	CV017	278	590
79	NC0108028	4	116.8	0.002916	0.382678	C	Study 1	CV167	278	590
79	NC0108028	4	116.8	0.039163	-0.18921	T	Study 1	CV071	278	590
79	NC0108028	4	116.8	0.020054	0.022985	T	Study 1	CV165	278	590
80	NC0200096	4	120.8	--	--	T	Study 5	--	165	591
80	NC0156254	4	121	0.035897	0.007724	A	Study 1	CV151	149	592
80	NC0156254	4	121	0.000817	0.136901	A	Study 1	CV166	149	592
80	NC0156254	4	121	0.001206	0.190333	A	Study 1	CV070	149	592
80	NC0156254	4	121	0.008213	0.015944	A	Study 1	CV079	149	592
80	NC0156254	4	121	0	0.03057	A	Study 1	CV142	149	592
80	NC0156254	4	121	0.015808	0.013488	A	Study 1	CV007	149	592
80	NC0156254	4	121	0.035707	0.009546	A	Study 1	CV012	149	592
80	NC0156254	4	121	0.035707	0.009546	A	Study 1	CV012	149	592
80	NC0156263	4	121	--	--	T	Study 4	--	338	593
80	NC0156267	4	121	--	--	T	Study 4	--	321	594
80	NC0039511	4	121.5	--	--	G	Study 5	--	560	595
80	NC0039511	4	121.5	0.022372	0.009608	G	Study 1	CV170	560	595
80	NC0039511	4	121.5	0.042406	0.01691	G	Study 1	CV123	560	595

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
80	NC0188975	4	126.7	--	--	G	Study 5	--	635	596
80	NC0151518	4	127	0.006623	-0.35117	A	Study 1	CV130	104	597
80	NC0188276	4	127.5	--	--	T	Study 5	--	350	598
80	NC0028933	4	127.6	--	--	C	Study 4	--	355	599
80	NC0028933	4	127.6	0.04462	0.008424	C	Study 1	CV170	355	599
80	NC0029886	4	127.8	0.043421	-0.00968	C	Study 1	CV053	396	600
80	NC0008979	4	127.9	0.008463	-0.04644	A	Study 1	CV010	194	601
80	NC0008979	4	127.9	0.017245	0.203714	A	Study 1	CV130	194	601
80	NC0050947	4	127.9	0.047997	0.100547	*****	Study 1	CV023	236	602
80	NC0050968	4	127.9	--	--	T	Study 5	--	107	603
81	NC0070533	4	130.2	0.02702	0.003876	C	Study 1	CV104	439	604
81	NC0070533	4	130.2	0.007117	0.014204	C	Study 1	I283669	439	604
81	NC0070533	4	130.2	0.002614	0.176235	T	Study 1	CV070	439	604
81	NC0070533	4	130.2	0	0.031388	T	Study 1	CV142	439	604
81	NC0054460	4	131.7	--	--	T	Study 4	--	411	605
81	NC0054460	4	131.7	0.000002	0.251888	A	Study 1	CV069	411	605
81	NC0054460	4	131.7	0.000015	0.190583	A	Study 1	CV093	411	605
81	NC0054460	4	131.7	0.039979	0.084234	T	Study 1	CV114	411	605
81	NC0054460	4	131.7	0.045292	0.007578	A	Study 1	CV151	411	605
81	NC0054460	4	131.7	0.000058	0.109146	A	Study 1	CV050	411	605
81	NC0054460	4	131.7	0.001028	0.010642	A	Study 1	CV050	411	605
81	NC0054460	4	131.7	0.024882	0.012421	A	Study 1	CV007	411	605
81	NC0054460	4	131.7	0	0.034177	A	Study 1	CV014	411	605
81	NC0106263	4	133	--	--	G	Study 5	--	204	606
81	NC0035451	4	133.5	--	--	G	Study 5	--	650	607
81	NC0036646	4	134.7	0.007646	-0.00385	A	Study 1	CV100	54	608
81	NC0036646	4	134.7	0.007646	-0.00385	A	Study 1	CV100	54	608
81	NC0048771	4	134.7	0.0004	0.127462	C	Study 3	--	56	609
81	NC0005295	4	135.1	--	--	T	Study 4	--	266	610
81	NC0005295	4	135.1	0.002733	0.01227	C	Study 1	12053	266	610
81	NC0005295	4	135.1	0.006428	0.348799	T	Study 1	CV167	266	610
81	NC0005295	4	135.1	0.012517	0.214997	C	Study 1	CV127	266	610
81	NC0005295	4	135.1	0.033969	0.020854	C	Study 1	CV165	266	610

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
81	NC0071158	4	136.7	0.002645	0.125837	G	Study 1	CV166	775	611
81	NC0071158	4	136.7	0.01618	0.132035	G	Study 1	CV164	775	611
81	NC0071158	4	136.7	0.020795	0.010505	G	Study 1	CV012	775	611
81	NC0071158	4	136.7	0.020795	0.010505	G	Study 1	CV012	775	611
81	NC0040357	4	137.5	--	--	G	Study 4	--	202	612
81	NC0040357	4	137.5	0.013634	0.07406	A	Study 1	CV148	202	612
81	NC0067159	4	137.6	--	--	G	Study 4	--	561	613
81	NC0031964	4	138	<.0001	0.321427	T	Study 3	--	699	614
81	NC0031964	4	138	--	--	T	Study 4	--	699	614
81	NC0071447	4	138.3	<.0001	-0.27384	CG	Study 3	--	163	615
81	NC0071447	4	138.3	--	--	**	Study 4	--	163	615
81	NC0171661	4	138.7	--	--	G	Study 5	--	43	616
81	NC0004170	4	139.4	--	--	G	Study 4	--	116	617
81	NC0004170	4	139.4	0.000186	-0.01048	A	Study 1	CV138	116	617
81	NC0004170	4	139.4	0.004353	0.015603	G	Study 1	CV007	116	617
82	NC0038447	4	141.8	0.001423	0.034247	G	Study 4	--	526	618
82	NC0104975	4	142	0.000233	0.041955	G	Study 4	--	306	619
82	NC0110764	4	142	0.001688	0.187588	T	Study 1	CV070	144	620
82	NC0009491	4	144.6	0.000359	-0.25536	G	Study 1	CV069	236	621
82	NC0009491	4	144.6	0	0.031203	G	Study 1	CV142	236	621
82	NC0104484	4	147.3	0.006728	0.023916	T	Study 1	CV158	59	622
82	NC0020933	4	147.5	<.0001	0.147783	T	Study 3	--	373	623
82	NC0020933	4	147.5	--	--	T	Study 4	--	373	623
82	NC0020934	4	147.5	--	--	G	Study 4	--	173	624
82	NC0111505	4	148.2	--	--	G	Study 5	--	217	625
82	NC0111505	4	148.2	0.036763	0.128302	G	Study 1	CV159	217	625
83	NC0035950	4	153.3	0.028097	0.12962	A	Study 1	CV070	571	626
83	NC0030576	4	153.8	0.000398	0.17912	C	Study 1	CV069	873	627
83	NC0030576	4	153.8	0.049854	0.069956	C	Study 1	CV126	873	627
83	NC0030576	4	153.8	0.000002	0.026757	C	Study 1	CV142	873	627
83	NC0107293	4	155.5	--	--	C	Study 5	--	381	628
83	NC0028579	4	155.7	--	--	C	Study 4	--	242	629
83	NC0028579	4	155.7	0.018466	0.009028	C	Study 1	CV151	242	629

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
83	NC0028579	4	155.7	0.048592	0.011181	C	Study 1	CV011	242	629
83	NC0034250	4	156.3	<.0001	0.192093	T	Study 3	--	70	630
83	NC0034250	4	156.3	0.049099	0.109113	G	Study 1	CV023	70	630
83	NC0034250	4	156.3	0.00995	-0.00375	G	Study 1	CV100	70	630
83	NC0034250	4	156.3	0.00995	-0.00375	G	Study 1	CV100	70	630
83	NC0031931	4	156.4	--	--	G	Study 4	--	209	631
83	NC0031931	4	156.4	0.013771	-0.06788	G	Study 1	CV011	209	631
83	NC0031931	4	156.4	0.000014	0.027361	A	Study 1	CV014	209	631
83	NC0051079	4	156.4	--	--	G	Study 4	--	137	632
83	NC0051079	4	156.4	0.000001	0.139448	G	Study 1	CV050	137	632
83	NC0051079	4	156.4	0.005217	0.009441	G	Study 1	CV050	137	632
84	NC0199540	4	160.6	--	--	T	Study 5	--	100	633
84	NC0037175	4	161.2	--	--	C	Study 4	--	473	634
84	NC0008860	4	162	--	--	G	Study 4	--	327	635
84	NC0008860	4	162	0.0237	-0.00616	G	Study 1	I294213	327	635
84	NC0008860	4	162	0.025643	-0.0108	G	Study 1	CV087	327	635
84	NC0008860	4	162	0.000009	0.205429	A	Study 1	CV093	327	635
84	NC0008860	4	162	0.03238	-0.07148	A	Study 1	CV101	327	635
84	NC0008860	4	162	0.035811	0.074083	A	Study 1	CV162	327	635
84	NC0008860	4	162	0.000007	0.024882	A	Study 1	CV142	327	635
84	NC0002755	4	162.2	0.045316	-0.01087	C	Study 1	CV136	121	636
84	NC0037601	4	162.2	0.000674	0.118255	A	Study 1	CV126	478	637
84	NC0032049	4	162.6	0.041639	-0.08006	C	Study 1	CV075	154	638
84	NC0110455	4	169.4	0.040036	0.023981	C	Study 1	CV155	207	639
85	NC0009398	4	173.5	0.024524	-0.01469	C	Study 1	CV025	191	640
85	NC0199468	4	173.5	--	--	G	Study 5	--	231	641
85	NC0003224	4	173.6	0.000604	0.098138	C	Study 1	CV050	169	642
85	NC0003226	4	173.6	0.016723	0.004286	T	Study 1	CV104	399	643
85	NC0003226	4	173.6	0.042055	-0.0153	T	Study 1	CV112	399	643
85	NC0003226	4	173.6	0.010836	0.028464	T	Study 1	CV154	399	643
85	NC0004445	4	176.6	--	--	T	Study 4	--	274	644
85	NC0004445	4	176.6	0.046938	-0.04505	T	Study 1	CV022	274	644
85	NC0004445	4	176.6	0.021117	0.01441	C	Study 1	CV159	274	644

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
85	NC0004445	4	176.6	0.000347	0.023073	T	Study 1	CV014	274	644
85	NC0036635	4	179.7	0.01015	-0.07932	T	Study 1	CV064	596	645
86	NC0009066	4	181	0.049211	0.005578	T	Study 1	CV082	238	646
86	NC0030985	4	181.9	--	--	***********	Study 4	--	164	647
86	NC0030985	4	181.9	0.033538	0.009354	ACTGTTCCAAG	Study 1	CV142	164	647
86	NC0030985	4	181.9	0.038253	0.071991	ACTGTTCCAAG	Study 1	CV162	164	647
86	NC0030985	4	181.9	0.00436	0.100548	ACTGTTCCAAG	Study 1	CV126	164	647
86	NC0030985	4	181.9	0.009623	0.014733	ACTGTTCCAAG	Study 1	CV142	164	647
86	NC0030985	4	181.9	0.033457	-0.00632	***********	Study 1	CV138	164	647
86	NC0145280	4	183	<.0001	0.124927	C	Study 3	--	748	648
86	NC0145280	4	183	0.011246	-0.11937	C	Study 1	CV068	748	648
86	NC0145280	4	183	0.004805	-0.07397	C	Study 1	CV011	748	648
86	NC0145280	4	183	0.032174	-0.13274	C	Study 1	CV017	748	648
86	NC0148181	4	183	0.002	-0.10807	C	Study 3	--	1001	649
86	NC0148181	4	183	--	--	G	Study 4	--	1001	649
86	NC0043794	4	186.2	--	--	T	Study 5	--	197	650
86	NC0112943	4	186.4	0.024778	-0.05893	C	Study 1	CV011	134	651
86	NC0112943	4	186.4	0.042048	-0.04288	C	Study 1	CV022	134	651
86	NC0112943	4	186.4	0.042324	-0.12706	T	Study 1	CV017	134	651
86	NC0112943	4	186.4	0.043392	0.072424	C	Study 1	CV162	134	651
86	NC0112943	4	186.4	0.028007	0.012576	C	Study 1	CV142	134	651
86	NC0030211	4	186.7	0.000635	-0.01406	T	Study 1	CV099	185	652
86	NC0030211	4	186.7	0.027387	-0.06839	T	Study 1	CV064	185	652
86	NC0030211	4	186.7	0.007057	0.029412	T	Study 1	CV154	185	652
86	NC0030211	4	186.7	0.033082	-0.01412	C	Study 1	CV025	185	652
86	NC0043121	4	186.7	<.0001	0.281569	G	Study 3	--	299	653
87	NC0040159	4	190	--	--	****	Study 4	--	200	654
87	NC0040159	4	190	0.009711	0.00432	TATA	Study 1	CV104	200	654
87	NC0040159	4	190	0.01592	-0.00554	****	Study 1	CV043	200	654
87	NC0040159	4	190	0.011361	0.009413	TATA	Study 1	CV151	200	654
87	NC0035338	4	190.6	--	--	G	Study 4	--	105	655
87	NC0035338	4	190.6	0.038089	0.006182	C	Study 1	CV082	105	655
87	NC0010790	4	190.8	--	--	G	Study 5	--	74	656

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
88	NC0024265	5	1.8	0.01723	-0.00622	A	Study 1	CV056	137	657
88	NC0024265	5	1.8	0.036274	0.070527	G	Study 1	CV082	137	657
88	NC0024265	5	1.8	0.028172	-0.0101	G	Study 1	CV098	137	657
88	NC0024265	5	1.8	0.022559	-0.01376	G	Study 1	CV044	137	657
88	NC0024265	5	1.8	0.008646	0.206122	G	Study 1	CV073	137	657
88	NC0024265	5	1.8	0.001291	0.09148	G	Study 1	CV050	137	657
88	NC0024265	5	1.8	0.037561	0.006886	G	Study 1	CV050	137	657
88	NC0024265	5	1.8	0.030883	0.006409	G	Study 1	CV091	137	657
88	NC0031790	5	1.8	0.044924	0.110102	A	Study 1	CV164	551	658
88	NC0031790	5	1.8	0.020904	0.008364	A	Study 1	CV164	551	658
88	NC0143354	5	1.8	--	--	G	Study 4	--	303	659
88	NC0143354	5	1.8	0.044211	-0.01489	G	Study 1	CV021	303	659
88	NC0143354	5	1.8	0.009699	-0.08668	C	Study 1	CV101	303	659
88	NC0143354	5	1.8	0.011408	0.011148	C	Study 1	CV137	303	659
88	NC0023752	5	2.3	0.049939	0.008109	C	Study 1	CV100	65	660
89	NC0197086	5	11.6	--	--	G	Study 5	--	455	661
89	NC0014633	5	11.7	0.024737	-0.08023	G	Study 1	CV041	147	662
89	NC0014633	5	11.7	0.004154	0.050754	A	Study 1	CV100	147	662
89	NC0014633	5	11.7	0.030832	-0.01061	G	Study 1	CV087	147	662
89	NC0004808	5	12.3	0.019259	0.20192	C	Study 1	CV127	363	663
89	NC0036565	5	14.7	0.011172	0.078967	A	Study 1	CV131	211	664
89	NC0036565	5	14.7	0.005855	-0.21688	T	Study 1	I294213	211	664
89	NC0036565	5	14.7	0.006111	-0.03261	T	Study 1	I294213	211	664
89	NC0036565	5	14.7	0.003651	0.083309	A	Study 1	CV050	211	664
89	NC0036565	5	14.7	0.019528	0.007883	A	Study 1	CV050	211	664
89	NC0036565	5	14.7	0.04251	-0.17268	A	Study 1	CV047	211	664
89	NC0036565	5	14.7	0.027052	0.02151	A	Study 1	CV165	211	664
89	NC0069592	5	14.8	--	--	**	Study 4	--	439	665
89	NC0069592	5	14.8	0.021357	0.184966	AT	Study 1	CV073	439	665
89	NC0104988	5	15.9	0.040479	0.036266	TTGTA	Study 1	CV119	448	666
89	NC0105613	5	16.6	--	--	G	Study 4	--	178	667
89	NC0105613	5	16.6	0.020544	0.01634	C	Study 1	CV080	178	667
89	NC0105613	5	16.6	0.013826	-0.09745	G	Study 1	CV041	178	667

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
89	NC0105613	5	16.6	0.001024	0.019979	G	Study 1	I283669	178	667
89	NC0105613	5	16.6	0.047034	-0.01199	G	Study 1	CV044	178	667
89	NC0105613	5	16.6	0.033411	0.184423	G	Study 1	CV127	178	667
89	NC0105613	5	16.6	0.027558	0.023812	C	Study 1	CV154	178	667
89	NC0105613	5	16.6	0.025033	-0.01324	C	Study 1	CV100	178	667
89	NC0107858	5	17.1	<.0001	-0.18596	C	Study 3	--	401	668
89	NC0107858	5	17.1	0.024955	0.009371	T	Study 1	CV012	401	668
89	NC0107858	5	17.1	0.038418	-0.0128	C	Study 1	CV077	401	668
89	NC0107858	5	17.1	0.005486	0.012583	T	Study 1	CV012	401	668
89	NC0107858	5	17.1	0.005486	0.012583	T	Study 1	CV012	401	668
90	NC0011193	5	29.3	0.002149	0.090782	T	Study 1	CV131	82	669
90	NC0011193	5	29.3	0.045161	0.008304	T	Study 1	CV012	82	669
90	NC0011193	5	29.3	0.040335	0.00742	A	Study 1	CV164	82	669
90	NC0108373	5	29.5	0.012477	0.042615	T	Study 1	CV100	240	670
90	NC0108373	5	29.5	0.025189	0.009511	T	Study 1	CV100	240	670
90	NC0108373	5	29.5	0.007469	-0.01591	T	Study 1	CV100	240	670
91	NC0000091	5	30.2	<.0001	0.147445	T	Study 3	--	111	671
91	NC0000091	5	30.2	0.018784	0.027153	C	Study 1	CV165	111	671
91	NC0000091	5	30.2	0.006631	0.027022	C	Study 1	CV165	111	671
91	NC0055976	5	32.1	0.004596	0.081391	C	Study 1	CV050	332	672
91	NC0005275	5	36	0.015112	-0.00907	A	Study 1	CV040	223	673
91	NC0020668	5	36.2	0.043797	-0.10829	T	Study 1	CV071	542	674
92	NC0038726	5	40.1	0.000277	0.110285	T	Study 2	--	652	675
92	NC0038726	5	40.1	--	--	T	Study 4	--	652	675
92	NC0079943	5	40.2	0.001224	0.099001	G	Study 1	CV131	301	676
92	NC0079943	5	40.2	0.001918	-0.01933	G	Study 1	CV100	301	676
92	NC0079943	5	40.2	0.006936	0.020001	G	Study 1	CV165	301	676
92	NC0012935	5	45.7	0.042187	0.178786	G	Study 1	CV109	437	677
92	NC0012935	5	45.7	0.00522	-0.12506	G	Study 1	I294213	437	677
92	NC0012935	5	45.7	0.037904	-0.05606	A	Study 1	CV050	437	677
92	NC0012935	5	45.7	0.028096	-0.01035	A	Study 1	CV088	437	677
92	NC0109403	5	46.7	0.010929	-0.14865	TTC	Study 1	CV131	523	678
92	NC0109403	5	46.7	0.000109	0.135392	***	Study 1	CV082	523	678

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
92	NC0109403	5	46.7	0.047712	-0.10764	***	Study 1	CV071	523	678
93	NC0037588	5	60.1	0.039041	-0.12071	CACAA	Study 1	CV131	188	679
93	NC0016762	5	60.6	0.0055	-0.10018	A	Study 3	--	380	680
93	NC0016762	5	60.6	0.039943	-0.25599	C	Study 1	CV112	380	680
93	NC0109342	5	61.7	0.027159	0.053014	A	Study 1	CV082	526	681
93	NC0109342	5	61.7	0.034023	0.017582	A	Study 1	CV165	526	681
93	NC0054720	5	62	--	--	T	Study 5	--	272	682
93	NC0054720	5	62	0.003461	0.270999	T	Study 1	CV130	272	682
93	NC0079573	5	62	0.002	-0.09406	C	Study 3	--	222	683
93	NC0031205	5	62.9	3.58E-10	0.177709	T	Study 2	--	618	684
93	NC0031205	5	62.9	0.000312	0.015291	T	Study 1	CV012	618	684
93	NC0079519	5	63.1	0.012725	0.0123	C	Study 1	CV069	436	685
93	NC0018546	5	63.5	0.003896	0.169357	A	Study 1	CV023	66	686
93	NC0018546	5	63.5	0.049702	0.009776	A	Study 1	CV082	66	686
93	NC0018546	5	63.5	0.001414	-0.09224	A	Study 1	CV082	66	686
93	NC0018546	5	63.5	0.000151	0.14127	A	Study 1	CV082	66	686
93	NC0018546	5	63.5	0.048784	0.034193	A	Study 1	CV100	66	686
93	NC0018546	5	63.5	0.009855	0.017946	G	Study 1	CV112	66	686
93	NC0018546	5	63.5	0.021869	0.144981	A	Study 1	CV073	66	686
93	NC0018546	5	63.5	0.008933	-0.01584	A	Study 1	CV100	66	686
93	NC0018546	5	63.5	0.018979	0.013575	G	Study 1	CV159	66	686
93	NC0018546	5	63.5	0.032536	-0.01022	G	Study 1	CV110	66	686
93	NC0018546	5	63.5	0.036959	-0.01064	A	Study 1	CV082	66	686
93	NC0199433	5	63.5	--	--	G	Study 5	--	724	687
93	NC0009668	5	65.2	<.0001	0.166527	G	Study 3	--	107	688
93	NC0111388	5	66.6	0.020975	0.07622	C	Study 1	CV131	64	689
93	NC0111398	5	67.7	0.006721	0.01177	T	Study 1	CV012	171	690
93	NC0113139	5	68.6	0.0002	-0.18881	C	Study 3	--	269	691
93	NC0113139	5	68.6	0.002636	-0.08048	G	Study 1	CV050	269	691
93	NC0113139	5	68.6	0.029127	-0.01273	G	Study 1	CV040	269	691
93	NC0113139	5	68.6	0.007352	-0.21602	G	Study 1	CV044	269	691
93	NC0052081	5	69.4	--	--	T	Study 5	--	351	692
93	NC0052081	5	69.4	0.034698	0.011166	C	Study 1	CV006	351	692

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
94	NC0146546	5	71.2	--	--	T	Study 5	--	359	693
94	NC0008797	5	72	0.028122	0.018832	A	Study 1	CV161	247	694
94	NC0158175	5	72	--	--	T	Study 5	--	388	695
94	NC0172718	5	72	--	--	G	Study 5	--	121	696
94	NC0057859	5	72.4	<.0001	0.241238	T	Study 3	--	424	697
94	NC0057859	5	72.4	0.001707	0.282958	C	Study 1	CV130	424	697
94	NC0023808	5	73.8	0.046527	0.079429	C	Study 1	CV079	263	698
94	NC0051419	5	73.8	0.023479	-0.10937	T	Study 1	CV069	218	699
94	NC0051419	5	73.8	0.031457	-0.01099	T	Study 1	CV082	218	699
94	NC0200092	5	73.8	--	--	G	Study 5	--	290	700
94	NC0019187	5	74.1	0.004468	-0.16908	C	Study 1	CV131	186	701
94	NC0019187	5	74.1	0.029004	-0.00801	C	Study 1	CV116	186	701
94	NC0019187	5	74.1	0.029004	-0.00801	C	Study 1	CV116	186	701
94	NC0019187	5	74.1	0.018377	0.015368	C	Study 1	CV144	186	701
94	NC0082146	5	75.4	0.004773	0.166674	C	Study 1	CV023	339	702
94	NC0082146	5	75.4	0.045868	0.011502	C	Study 1	CV159	339	702
94	NC0080028	5	76.6	0.015807	0.019519	A	Study 1	CV165	267	703
94	NC0004605	5	78.5	0.026942	0.016471	T	Study 1	CV080	74	704
94	NC0107061	5	79	0.004563	0.106146	GTATGAA	Study 1	CV082	239	705
94	NC0107549	5	79	--	--	T	Study 5	--	371	706
94	NC0110919	5	79	0.029721	0.137233	T	Study 1	CV073	334	707
94	NC0110919	5	79	0.005459	0.018925	C	Study 1	CV112	334	707
94	NC0111346	5	79	8.54E-14	0.209062	C	Study 2	--	366	708
94	NC0146415	5	79.8	--	--	G	Study 4	--	336	709
94	NC0146415	5	79.8	0.017394	-0.06775	A	Study 1	CV082	336	709
95	NC0077644	5	80.4	0.044926	0.022435	C	Study 1	CV165	255	710
95	NC0077644	5	80.4	0.008524	0.025523	C	Study 1	CV165	255	710
95	NC0105854	5	81.2	--	--	G	Study 5	--	347	711
95	NC0018230	5	81.3	--	--	T	Study 4	--	322	712
95	NC0048328	5	81.3	--	--	T	Study 4	--	115	713
95	NC0022796	5	81.5	--	--	G	Study 5	--	199	714
95	NC0022796	5	81.5	0.000456	-0.27666	G	Study 1	CV044	199	714
95	NC0027874	5	81.5	--	--	T	Study 5	--	344	715

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
95	NC0019329	5	83.9	--	--	C	Study 5	--	341	716
95	NC0078535	5	83.9	--	--	G	Study 5	--	104	717
95	NC0078535	5	83.9	0.031826	-0.01643	A	Study 1	CV039	104	717
95	NC0078535	5	83.9	0.00341	0.176768	G	Study 1	CV023	104	717
95	NC0040366	5	84.1	1.12E-12	0.201703	C	Study 2	--	119	718
95	NC0040366	5	84.1	--	--	C	Study 5	--	119	718
95	NC0040366	5	84.1	0.005605	-0.01601	C	Study 1	CV088	119	718
95	NC0040366	5	84.1	0.000041	-0.01802	A	Study 1	CV095	119	718
95	NC0040366	5	84.1	0.021556	0.212947	A	Study 1	CV130	119	718
95	NC0035956	5	85.1	--	--	C	Study 5	--	246	719
95	NC0035956	5	85.1	0.02236	0.01004	C	Study 1	CV012	246	719
95	NC0035956	5	85.1	0.02882	0.076741	C	Study 1	CV126	246	719
95	NC0035956	5	85.1	0.009458	0.018563	A	Study 1	CV165	246	719
95	NC0035956	5	85.1	0.018427	0.024175	C	Study 1	CV120	246	719
95	NC0154498	5	85.2	0.028937	-0.01031	C	Study 1	CV088	84	720
95	NC0040571	5	88.4	0.036245	-0.11904	G	Study 1	CV131	154	721
95	NC0040571	5	88.4	0.040548	0.089668	G	Study 1	CV116	154	721
95	NC0040571	5	88.4	0.042321	0.102846	G	Study 1	CV118	154	721
95	NC0040571	5	88.4	0.001551	-0.08646	G	Study 1	CV050	154	721
95	NC0040571	5	88.4	0.001004	-0.0116	C	Study 1	CV080	154	721
95	NC0040571	5	88.4	0.040493	0.017044	G	Study 1	CV165	154	721
95	NC0040571	5	88.4	0.009112	0.154267	G	Study 1	CV070	154	721
95	NC0040571	5	88.4	0.000154	-0.01694	G	Study 1	CV095	154	721
95	NC0040571	5	88.4	0.002735	-0.08195	C	Study 1	I294213	154	721
95	NC0040571	5	88.4	0.043209	0.013195	G	Study 1	CV144	154	721
96	NC0110854	5	90.7	0.042512	0.009626	G	Study 1	CV069	337	722
96	NC0027864	5	93.9	0.040733	-0.05866	T	Study 1	CV082	176	723
96	NC0027864	5	93.9	0.034426	-0.01392	C	Study 1	CV095	176	723
96	NC0053792	5	93.9	--	--	T	Study 4	--	384	724
96	NC0053792	5	93.9	0.00233	-0.01399	T	Study 1	CV095	384	724
96	NC0002775	5	96	1.51E-11	0.188588	G	Study 2	--	372	725
96	NC0111999	5	96.9	--	--	G	Study 4	--	587	726
96	NC0018153	5	97	0.040563	-0.00868	G	Study 1	CV088	573	727

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
96	NC0018153	5	97	0.001553	-0.08472	A	Study 1	CV011	573	727
96	NC0018153	5	97	0.013525	0.144891	G	Study 1	CV070	573	727
96	NC0018153	5	97	0.042985	0.073017	G	Study 1	CV126	573	727
96	NC0048616	5	98.2	0.037756	-0.01023	C	Study 1	CV088	88	728
96	NC0173990	5	98.9	--	--	T	Study 5	--	438	729
96	NC0012480	5	99.4	0.042805	-0.11758	A	Study 1	CV131	137	730
96	NC0012480	5	99.4	0.000953	0.036799	C	Study 1	CV165	137	730
96	NC0012480	5	99.4	0.006982	0.026204	C	Study 1	CV165	137	730
97	NC0036637	5	100	2.58E-12	0.20134	C	Study 2	--	699	731
97	NC0199793	5	100	--	--	T	Study 5	--	92	732
97	NC0017678	5	103.8	0.004666	0.017992	A	Study 1	CV159	171	733
97	NC0009297	5	104.1	9.83E-13	0.197853	A	Study 2	--	114	734
97	NC0009297	5	104.1	0.019225	0.024065	A	Study 1	CV120	114	734
97	NC0009297	5	104.1	0.020441	0.014139	A	Study 1	CV117	114	734
97	NC0003338	5	106.2	0.046093	0.092544	C	Study 1	CV118	324	735
97	NC0003338	5	106.2	0.017526	-0.00584	C	Study 1	CV088	324	735
97	NC0003338	5	106.2	0.045399	-0.08699	C	Study 1	CV111	324	735
97	NC0003338	5	106.2	0.044603	-0.01297	C	Study 1	CV063	324	735
97	NC0038972	5	106.2	0.004529	0.318202	A	Study 1	CV124	539	736
97	NC0038972	5	106.2	0.023623	0.015004	A	Study 1	CV144	539	736
97	NC0078478	5	106.2	0.005979	-0.14672	T	Study 1	I294213	686	737
97	NC0106300	5	106.6	--	--	**	Study 4	--	329	738
98	NC0107238	5	114.7	0.032885	0.126418	A	Study 1	CV070	375	739
98	NC0008807	5	118.8	--	--	T	Study 4	--	282	740
98	NC0008807	5	118.8	0.026115	-0.00576	C	Study 1	CV088	282	740
98	NC0008807	5	118.8	0.016457	-0.02098	C	Study 1	I294213	282	740
98	NC0008807	5	118.8	0.024583	0.059631	C	Study 1	CV112	282	740
98	NC0008807	5	118.8	0.048147	-0.00906	C	Study 1	CV095	282	740
99	NC0005480	5	120	0.012229	-0.01486	A	Study 1	CV112	174	741
99	NC0016868	5	122.6	0.020135	0.07092	G	Study 1	CV131	331	742
99	NC0016868	5	122.6	0.034532	-0.01783	C	Study 1	CV064	331	742
99	NC0016868	5	122.6	0.026989	-0.00969	G	Study 1	CV109	331	742
99	NC0016868	5	122.6	0.003376	0.018262	C	Study 1	CV159	331	742

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
99	NC0017125	5	122.6	--	--	T	Study 4	--	38	743
99	NC0017125	5	122.6	0.033895	-0.09872	T	Study 1	CV069	38	743
99	NC0083876	5	124	0.023509	-0.06105	C	Study 1	CV050	513	744
99	NC0083876	5	124	0.005552	-0.06961	T	Study 1	I294213	513	744
99	NC0106716	5	125	2.27E-11	0.189503	A	Study 2	--	470	745
99	NC0106716	5	125	0.000264	-0.10179	G	Study 1	CV011	470	745
99	NC0106716	5	125	0.00216	-0.01031	G	Study 1	CV080	470	745
99	NC0106716	5	125	0.035748	0.123295	G	Study 1	CV070	470	745
99	NC0106716	5	125	0.021732	0.011995	G	Study 1	--	470	745
99	NC0106716	5	125	0.010074	0.210788	A	Study 1	CV125	470	745
99	NC0106716	5	125	0.024155	0.025295	G	Study 1	CV165	470	745
99	NC0106716	5	125	0.03505	0.020624	G	Study 1	CV165	470	745
99	NC0009434	5	125.2	0.021574	-0.12857	A	Study 1	CV131	123	746
99	NC0009434	5	125.2	0.038011	0.095313	A	Study 1	CV116	123	746
99	NC0009434	5	125.2	0.045736	0.00497	G	Study 1	--	123	746
99	NC0009434	5	125.2	0.001277	0.156453	A	Study 1	CV118	123	746
99	NC0009434	5	125.2	0.00265	0.018095	A	Study 1	CV117	123	746
99	NC0199389	5	125.8	--	--	G	Study 5	--	299	747
99	NC0010131	5	129.7	0.038207	-0.18291	T	Study 1	I294213	154	748
99	NC0010131	5	129.7	0.043775	0.057959	C	Study 1	CV050	154	748
100	NC0035377	5	132.8	0.030109	0.014921	C	Study 1	CV144	67	749
100	NC0199325	5	137.1	--	--	T	Study 5	--	69	750
100	NC0081212	5	138.2	0.017999	0.10886	G	Study 1	CV118	571	751
100	NC0154430	5	138.6	--	--	G	Study 5	--	244	752
100	NC0154899	5	138.6	0.003571	-0.0081	A	Study 1	CV088	208	753
100	NC0154899	5	138.6	0.029741	0.057171	A	Study 1	CV112	208	753
100	NC0154899	5	138.6	0.006522	0.030583	T	Study 1	CV165	208	753
100	NC0154899	5	138.6	0.015836	0.023691	T	Study 1	CV165	208	753
100	NC0085514	5	139.5	0.003	-0.08259	C	Study 3	--	126	754
100	NC0085514	5	139.5	0.003668	0.085429	C	Study 1	CV131	126	754
101	NC0053779	5	143.8	--	--	*	Study 4	--	128	755
101	NC0053779	5	143.8	0.000533	0.271906	*	Study 1	CV125	128	755
101	NC0002353	5	144.7	3.23E-10	0.178028	T	Study 2	--	123	756

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
101	NC0002353	5	144.7	0.004737	0.129085	T	Study 1	CV118	123	756
101	NC0002353	5	144.7	0.008012	-0.00904	C	Study 1	CV080	123	756
101	NC0002353	5	144.7	0.002846	0.018558	T	Study 1	CV117	123	756
101	NC0041824	5	144.7	0.039884	-0.12298	A	Study 1	CV131	54	757
101	NC0036210	5	145.2	0.016258	0.072667	T	Study 1	CV131	43	758
101	NC0111944	5	148.1	0.036985	-0.01277	A	Study 1	CV095	138	759
101	NC0143380	5	148.1	0.033619	0.06041	A	Study 1	CV050	324	760
101	NC0143380	5	148.1	0.000952	0.260294	G	Study 1	CV125	324	760
102	NC0110484	5	159.5	0.028021	0.010439	A	Study 1	CV082	215	761
102	NC0110484	5	159.5	0.036089	-0.01839	C	Study 1	I294213	215	761
102	NC0110484	5	159.5	0.049927	-0.06966	C	Study 1	CV055	215	761
102	NC0110484	5	159.5	0.004975	0.020117	A	Study 1	CV165	215	761
102	NC0104963	5	159.8	0.005412	0.080748	G	Study 1	CV131	269	762
102	NC0104963	5	159.8	0.041333	0.057004	G	Study 1	CV116	269	762
102	NC0104963	5	159.8	0.048753	-0.07455	A	Study 1	CV101	269	762
102	NC0104963	5	159.8	0.014293	0.068322	G	Study 1	CV050	269	762
102	NC0104963	5	159.8	0.029827	-0.15911	A	Study 1	CV112	269	762
103	NC0200099	5	171.1	--	--	T	Study 5	--	364	763
103	NC0104717	5	171.2	0.00789	0.077357	T	Study 2	--	298	764
103	NC0104717	5	171.2	0.006728	-0.04594	T	Study 1	CV010	298	764
103	NC0104717	5	171.2	0.005099	-0.01142	T	Study 1	CV010	298	764
103	NC0104717	5	171.2	0.023515	0.011898	C	Study 1	CV081	298	764
103	NC0104717	5	171.2	0.039112	0.009123	T	Study 1	CV012	298	764
103	NC0104717	5	171.2	0.039112	0.009123	T	Study 1	CV012	298	764
103	NC0105546	5	171.7	--	--	***	Study 4	--	104	765
103	NC0105546	5	171.7	0.044333	0.012109	AGC	Study 1	CV013	104	765
103	NC0109853	5	173.9	--	--	*****	Study 4	--	512	766
103	NC0109853	5	173.9	0.036777	-0.19442	*****	Study 1	CV088	512	766
103	NC0109853	5	173.9	0.015247	0.065208	CATTG	Study 1	CV084	512	766
103	NC0109853	5	173.9	0.04387	0.070389	*****	Study 1	CV053	512	766
103	NC0109853	5	173.9	0.023402	-0.05971	*****	Study 1	CV011	512	766
103	NC0109853	5	173.9	0.011888	-0.02129	CATTG	Study 1	I294213	512	766
103	NC0109853	5	173.9	0.04679	0.107478	*****	Study 1	CV149	512	766

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
103	NC0109853	5	173.9	0.006098	-0.00775	*****	Study 1	CV138	512	766
103	NC0109853	5	173.9	0.007444	-0.09519	CATTG	Study 1	CV055	512	766
103	NC0021585	5	175	0.012068	0.107882	G	Study 1	CV118	233	767
103	NC0021585	5	175	0.00396	0.013704	C	Study 1	CV082	233	767
103	NC0021585	5	175	0.038277	0.046828	C	Study 1	CV074	233	767
103	NC0021585	5	175	0.004712	0.020348	C	Study 1	CV074	233	767
103	NC0012417	5	175.2	0.0255	0.013991	T	Study 1	CV013	137	768
103	NC0000015	5	175.3	0.008072	0.029513	C	Study 1	CV165	373	769
103	NC0000015	5	175.3	0.018155	0.022958	C	Study 1	CV165	373	769
103	NC0200212	5	176.4	--	--	T	Study 5	--	395	770
103	NC0025270	5	177.8	0.001689	0.114529	T	Study 1	CV053	389	771
103	NC0025270	5	177.8	0.046227	-0.03578	G	Study 1	CV010	389	771
103	NC0025270	5	177.8	0.020611	-0.01026	G	Study 1	CV010	389	771
103	NC0025270	5	177.8	0.036174	-0.01226	G	Study 1	CV093	389	771
104	NC0111504	5	181	0.039978	0.011803	T	Study 1	CV159	712	772
104	NC0031084	5	181.5	0.001485	0.014991	G	Study 1	CV082	53	773
104	NC0199113	5	183.1	0.047865	-0.01488	C	Study 1	CV112	120	774
104	NC0175477	5	183.6	--	--	T	Study 5	--	297	775
104	NC0113237	5	184.1	--	--	G	Study 5	--	657	776
105	NC0108746	6	24.5	--	--	G	Study 5	--	330	777
105	NC0014417	6	25	--	--	G	Study 4	--	208	778
105	NC0014417	6	25	0.045214	0.105366	A	Study 1	CV069	208	778
105	NC0014417	6	25	0.032858	0.171458	A	Study 1	CV132	208	778
105	NC0014417	6	25	0.006327	0.095526	A	Study 1	CV162	208	778
105	NC0027615	6	25.5	0.016903	-0.14787	*	Study 1	CV017	236	779
105	NC0027615	6	25.5	0.017416	-0.07086	*	Study 1	CV100	236	779
105	NC0027615	6	25.5	0.020169	-0.10191	*	Study 1	CV100	236	779
105	NC0027615	6	25.5	0.010546	0.011145	T	Study 1	CV169	236	779
105	NC0105014	6	28.8	0.000043	-0.09171	C	Study 1	CV022	348	780
106	NC0077806	6	32.4	--	--	T	Study 5	--	86	781
106	NC0199605	6	32.4	--	--	T	Study 5	--	345	782
106	NC0153811	6	33.2	0.045604	0.003808	A	Study 1	CV113	98	783
106	NC0153811	6	33.2	0.002424	-0.01561	A	Study 1	CV087	98	783

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
106	NC0066735	6	34.3	0.013467	-0.10509	C	Study 1	CV040	564	784
106	NC0200061	6	34.4	--	--	C	Study 5	--	334	785
106	NC0013985	6	35.4	0.025269	-0.01672	A	Study 1	CV039	132	786
106	NC0033924	6	36.2	0.048558	-0.08139	C	Study 2	--	93	787
106	NC0033924	6	36.2	--	--	C	Study 5	--	93	787
106	NC0042917	6	36.4	--	--	C	Study 5	--	67	788
106	NC0069630	6	36.5	0.017027	-0.02663	A	Study 1	CV121	597	789
106	NC0069630	6	36.5	0.010676	-0.02478	A	Study 1	CV121	597	789
106	NC0069630	6	36.5	0.012692	-0.01671	A	Study 1	CV017	597	789
106	NC0105714	6	36.7	--	--	G	Study 5	--	363	790
106	NC0002870	6	38.4	0.000124	-0.11532	T	Study 2	--	398	791
106	NC0002870	6	38.4	0.032331	-0.12585	G	Study 1	I294213	398	791
106	NC0002870	6	38.4	0.01878	-0.01521	G	Study 1	CV113	398	791
106	NC0003210	6	38.4	--	--	G	Study 5	--	117	792
106	NC0025657	6	38.4	<.0001	-0.16425	C	Study 3	--	250	793
106	NC0025657	6	38.4	--	--	T	Study 5	--	250	793
106	NC0026803	6	38.4	<.0001	-0.3015	C	Study 3	--	410	794
106	NC0026803	6	38.4	0.015529	-0.20559	C	Study 1	CV071	410	794
106	NC0029828	6	38.4	--	--	T	Study 5	--	301	795
106	NC0030875	6	38.4	--	--	T	Study 4	--	335	796
106	NC0030875	6	38.4	--	--	T	Study 5	--	335	796
106	NC0030875	6	38.4	0.048601	-0.01617	C	Study 1	CV017	335	796
106	NC0042090	6	38.4	--	--	T	Study 5	--	119	797
106	NC0068941	6	38.4	--	--	G	Study 5	--	278	798
106	NC0069532	6	38.4	--	--	C	Study 5	--	54	799
106	NC0082439	6	38.4	<.0001	0.322042	T	Study 3	--	381	800
106	NC0107287	6	38.4	--	--	G	Study 5	--	278	801
106	NC0107639	6	38.4	0.004862	-0.22817	T	Study 1	CV071	206	802
106	NC0173606	6	38.4	--	--	G	Study 5	--	700	803
106	NC0173900	6	38.4	--	--	T	Study 5	--	885	804
106	NC0195587	6	38.4	0.11405	0.020232	G	Study 5	--	94	805
106	NC0110607	6	38.7	0.000584	-0.10709	T	Study 2	--	468	806
106	NC0110607	6	38.7	--	--	T	Study 5	--	468	806

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
106	NC0110607	6	38.7	0.000053	-0.09395	G	Study 1	CV022	468	806
106	NC0110607	6	38.7	0.004659	-0.17609	G	Study 1	CV017	468	806
106	NC0110607	6	38.7	0.000599	-0.01722	G	Study 1	CV087	468	806
106	NC0027095	6	38.8	--	--	G	Study 4	--	259	807
106	NC0027095	6	38.8	0.001713	-0.14448	G	Study 1	I294213	259	807
106	NC0027095	6	38.8	0.000208	-0.15721	A	Study 1	CV040	259	807
106	NC0027095	6	38.8	0.019586	0.187809	A	Study 1	CV132	259	807
106	NC0027095	6	38.8	0.036225	0.025391	A	Study 1	CV132	259	807
106	NC0027095	6	38.8	0.040489	-0.00878	G	Study 1	CV109	259	807
106	NC0027095	6	38.8	0.010238	-0.02862	G	Study 1	CV121	259	807
106	NC0027095	6	38.8	0.002924	-0.02878	G	Study 1	CV121	259	807
106	NC0110850	6	39.3	0.007236	-0.00781	C	Study 1	CV115	430	808
106	NC0025201	6	39.4	--	--	G	Study 4	--	455	809
106	NC0025201	6	39.4	--	--	G	Study 5	--	455	809
106	NC0147740	6	39.4	--	--	G	Study 4	--	916	810
106	NC0147740	6	39.4	--	--	G	Study 5	--	916	810
106	NC0199945	6	39.4	--	--	T	Study 5	--	485	811
106	NC0000439	6	39.9	0.005776	-0.08761	C	Study 1	CV064	235	812
107	NC0036067	6	41	--	--	T	Study 4	--	129	813
107	NC0036073	6	41	--	--	G	Study 4	--	388	814
107	NC0147437	6	41.2	--	--	T	Study 4	--	466	815
107	NC0037981	6	44.2	--	--	T	Study 5	--	286	816
107	NC0199296	6	44.6	--	--	G	Study 5	--	266	817
107	NC0034560	6	45.7	--	--	G	Study 5	--	680	818
107	NC0030176	6	48	--	--	T	Study 4	--	731	819
107	NC0030176	6	48	0.021089	-0.0184	T	Study 1	CV017	731	819
107	NC0106121	6	49.2	0.006782	-0.30063	C	Study 1	CV112	288	820
107	NC0106121	6	49.2	0.001916	-0.01327	C	Study 1	CV109	288	820
107	NC0106121	6	49.2	0.039963	0.011896	C	Study 1	CV069	288	820
108	NC0038040	6	52.1	--	--	G	Study 4	--	382	821
108	NC0038040	6	52.1	0.010735	0.011775	A	Study 1	--	382	821
108	NC0038040	6	52.1	0.044382	-0.01324	A	Study 1	CV108	382	821
108	NC0034523	6	53.2	0.000092	-0.1621	G	Study 1	CV040	200	822

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
108	NC0034054	6	53.4	0.00502	-0.02739	******	Study 1	CV121	129	823
108	NC0106527	6	56.4	0.031593	-0.0994	G	Study 1	I294213	356	824
108	NC0106527	6	56.4	0.004027	-0.0629	G	Study 1	CV022	356	824
108	NC0106527	6	56.4	0.046527	0.054307	G	Study 1	CV084	356	824
108	NC0106527	6	56.4	0.00828	-0.17847	G	Study 1	I294213	356	824
108	NC0106527	6	56.4	0.001497	-0.01351	G	Study 1	CV109	356	824
108	NC0004463	6	56.5	0.04077	0.054509	T	Study 1	CV116	263	825
108	NC0004463	6	56.5	0.001655	-0.09923	T	Study 1	CV064	263	825
108	NC0004463	6	56.5	0.046343	-0.0058	C	Study 1	CV115	263	825
108	NC0031945	6	56.6	0.000153	-0.11039	C	Study 2	--	416	826
108	NC0060751	6	56.6	--	--	G	Study 5	--	297	827
108	NC0060751	6	56.6	0.011905	0.089311	A	Study 1	CV079	297	827
108	NC0060751	6	56.6	0.012575	0.098597	A	Study 1	CV079	297	827
108	NC0057758	6	57.5	--	--	G	Study 4	--	46	828
108	NC0057758	6	57.5	0.020586	-0.01495	A	Study 1	CV113	46	828
108	NC0032034	6	57.6	0.001684	-0.0873	A	Study 2	--	498	829
109	NC0011591	6	60.5	4.19E-05	-0.11893	C	Study 2	--	187	830
109	NC0011591	6	60.5	0.001982	0.144404	T	Study 1	CV013	187	830
109	NC0011591	6	60.5	0.027888	0.054718	T	Study 1	CV168	187	830
109	NC0146195	6	66	--	--	G	Study 4	--	345	831
109	NC0146195	6	66	0.00766	0.250899	C	Study 1	CV109	345	831
109	NC0059008	6	66.2	0.000308	-0.10416	T	Study 2	--	83	832
109	NC0059008	6	66.2	--	--	T	Study 5	--	83	832
109	NC0003277	6	69.4	0.001946	0.020276	C	Study 1	I283669	84	833
109	NC0003277	6	69.4	0.001623	-0.01354	T	Study 1	CV109	84	833
109	NC0196774	6	69.4	--	--	G	Study 5	--	164	834
110	NC0148039	6	70.2	--	--	T	Study 4	--	76	835
110	NC0148039	6	70.2	0.028916	-0.07496	T	Study 1	CV041	76	835
110	NC0148039	6	70.2	0.029498	-0.07395	T	Study 1	CV017	76	835
110	NC0008833	6	70.9	0.000515	-0.10036	C	Study 2	--	411	836
110	NC0008833	6	70.9	0.00076	-0.14223	A	Study 1	CV040	411	836
110	NC0008833	6	70.9	0.001288	-0.10173	A	Study 1	CV064	411	836
110	NC0008838	6	77.7	<.0001	-0.14263	A	Study 3	--	293	837

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
110	NC0014694	6	77.8	--	--	C	Study 4	--	105	838
110	NC0014694	6	77.8	0.033009	-0.00354	A	Study 1	CV010	105	838
110	NC0014694	6	77.8	0.042307	-0.10126	A	Study 1	I294213	105	838
110	NC0014694	6	77.8	0.037399	-0.08549	C	Study 1	CV045	105	838
110	NC0014694	6	77.8	0.006246	0.096863	C	Study 1	CV079	105	838
110	NC0014694	6	77.8	0.000304	0.141184	C	Study 1	CV079	105	838
110	NC0014694	6	77.8	0.046772	0.010649	C	Study 1	CV007	105	838
110	NC0005064	6	78.1	--	--	G	Study 5	--	174	839
110	NC0005066	6	78.1	0.030004	-0.12874	G	Study 1	CV131	283	840
110	NC0005066	6	78.1	0.022097	0.0828	C	Study 1	CV109	283	840
110	NC0005066	6	78.1	0.001533	-0.40195	G	Study 1	CV112	283	840
110	NC0005066	6	78.1	0.044336	0.023551	C	Study 1	CV058	283	840
110	NC0005066	6	78.1	0.040902	0.017223	C	Study 1	CV161	283	840
110	NC0019518	6	78.5	0.000434	-0.1028	T	Study 2	--	375	841
110	NC0019518	6	78.5	0.001648	-0.01647	T	Study 1	CV086	375	841
110	NC0077031	6	78.8	0.000662	-0.01732	G	Study 1	CV087	105	842
110	NC0005081	6	79.3	0.0004	0.187754	G	Study 3	--	102	843
110	NC0082021	6	79.6	<.0001	0.180548	******	Study 3	--	375	844
110	NC0082021	6	79.6	0.009276	0.072698	CAGGGG	Study 1	CV116	375	844
110	NC0082021	6	79.6	0.001889	0.256305	CAGGGG	Study 1	CV125	375	844
110	NC0108196	6	79.8	<.0001	-0.1394	C	Study 3	--	119	845
110	NC0108196	6	79.8	--	--	T	Study 4	--	119	845
110	NC0108196	6	79.8	0.008691	0.128029	C	Study 1	CV013	119	845
110	NC0108196	6	79.8	0.016018	0.029521	C	Study 1	CV132	119	845
110	NC0108196	6	79.8	0.014183	0.020438	C	Study 1	CV069	119	845
110	NC0108196	6	79.8	0.014233	-0.01637	T	Study 1	CV113	119	845
111	NC0066737	6	81.9	0.029161	-0.07274	A	Study 1	CV041	281	846
111	NC0084789	6	82.2	0.006497	0.244015	T	Study 1	CV109	464	847
111	NC0084789	6	82.2	0.000752	-0.13836	C	Study 1	CV040	464	847
111	NC0145427	6	82.2	--	--	G	Study 4	--	168	848
111	NC0145427	6	82.2	--	--	G	Study 5	--	168	848
111	NC0013638	6	83.5	8.77E-05	-0.11275	G	Study 2	--	213	849
111	NC0113381	6	83.8	0.048367	-0.06296	G	Study 1	CV064	303	850

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
111	NC0113381	6	83.8	0.028475	0.010983	A	Study 1	--	303	850
111	NC0037517	6	84.9	0.019362	-0.04749	A	Study 1	CV042	449	851
111	NC0037517	6	84.9	0.001933	-0.01623	A	Study 1	CV086	449	851
111	NC0037517	6	84.9	0.001208	-0.01731	A	Study 1	CV087	449	851
111	NC0028203	6	85	0.001075	-0.01776	A	Study 1	CV087	235	852
111	NC0004030	6	85.5	0.000479	-0.1027	G	Study 2	--	312	853
111	NC0004030	6	85.5	0.009819	-0.05237	G	Study 1	CV042	312	853
111	NC0004030	6	85.5	0.045228	-0.04693	G	Study 1	CV022	312	853
111	NC0040364	6	85.5	0.005666	0.075044	G	Study 1	CV084	258	854
111	NC0040364	6	85.5	0.003055	0.081265	A	Study 1	CV116	258	854
112	NC0015070	6	91.7	--	--	G	Study 5	--	99	855
112	NC0019772	6	92.4	0.003814	-0.36712	T	Study 1	CV112	323	856
112	NC0019772	6	92.4	0.013204	0.08795	C	Study 1	CV079	323	856
112	NC0019772	6	92.4	0.000205	0.144982	C	Study 1	CV079	323	856
112	NC0110972	6	93.2	--	--	G	Study 4	--	49	857
112	NC0110972	6	93.2	0.001241	0.303679	G	Study 1	CV109	49	857
112	NC0110972	6	93.2	0.015217	0.019871	G	Study 1	CV069	49	857
112	NC0019588	6	96.7	0.003064	-0.13454	T	Study 1	CV040	361	858
112	NC0019588	6	96.7	0.029373	0.027144	C	Study 1	CV132	361	858
112	NC0107703	6	96.7	--	--	G	Study 5	--	196	859
112	NC0037947	6	97.6	--	--	G	Study 4	--	87	860
112	NC0037947	6	97.6	0.001159	0.027316	G	Study 1	CV161	87	860
112	NC0037947	6	97.6	0.030779	0.025177	A	Study 1	CV058	87	860
112	NC0037947	6	97.6	0.038051	0.017217	G	Study 1	CV069	87	860
112	NC0067075	6	98.9	0.046811	-0.07042	C	Study 1	CV041	449	861
112	NC0067075	6	98.9	0.046496	0.030867	C	Study 1	CV066	449	861
112	NC0067075	6	98.9	0.028365	0.010855	G	Study 1	--	449	861
112	NC0088767	6	99	0.001614	-0.09321	C	Study 2	--	536	862
112	NC0005319	6	99.1	0.016	-0.19278	A	Study 1	CV069	476	863
112	NC0005319	6	99.1	0.001289	-0.01686	A	Study 1	CV086	476	863
112	NC0005319	6	99.1	0.000027	0.32716	G	Study 1	CV125	476	863
113	NC0017860	6	103.5	0.000036	0.372952	A	Study 1	CV109	87	864
113	NC0017860	6	103.5	0.012963	0.134631	A	Study 1	CV013	87	864

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
113	NC0017860	6	103.5	0.008018	-0.1076	C	Study 1	CV045	87	864
113	NC0081121	6	104.4	--	--	G	Study 5	--	320	865
113	NC0059114	6	105.9	--	--	T	Study 4	--	511	866
113	NC0059114	6	105.9	0.000531	-0.06652	T	Study 1	CV042	511	866
113	NC0059114	6	105.9	0.034258	0.006562	A	Study 1	CV082	511	866
113	NC0059114	6	105.9	0.016226	-0.10082	A	Study 1	CV040	511	866
113	NC0059114	6	105.9	0.003247	0.115069	T	Study 1	CV079	511	866
113	NC0146215	6	106.6	0.003298	-0.16595	C	Study 1	CV131	217	867
113	NC0146215	6	106.6	0.001069	0.094102	C	Study 1	CV116	217	867
113	NC0146215	6	106.6	0.021072	0.02843	C	Study 1	CV132	217	867
113	NC0029924	6	109.2	0.033411	0.010365	T	Study 1	CV082	176	868
113	NC0029924	6	109.2	0.011501	0.068218	T	Study 1	CV084	176	868
113	NC0029924	6	109.2	0.029564	-0.05202	C	Study 1	CV022	176	868
113	NC0029924	6	109.2	0.044308	-0.07514	C	Study 1	CV017	176	868
113	NC0029924	6	109.2	0.046698	-0.0031	C	Study 1	CV010	176	868
113	NC0029924	6	109.2	0.046698	-0.0031	C	Study 1	CV010	176	868
113	NC0002628	6	109.6	0.026588	0.120868	C	Study 1	CV149	120	869
114	NC0054780	6	111.7	0.0007	0.107082	T	Study 3	--	477	870
114	NC0054780	6	111.7	--	--	T	Study 4	--	477	870
114	NC0054780	6	111.7	0.000479	0.314452	T	Study 1	CV109	477	870
114	NC0054780	6	111.7	0.042561	0.009282	T	Study 1	CV013	477	870
114	NC0054780	6	111.7	0.007898	0.013587	T	Study 1	CV069	477	870
114	NC0031684	6	114.5	--	--	T	Study 4	--	252	871
114	NC0031684	6	114.5	0.027686	-0.01399	T	Study 1	CV108	252	871
114	NC0031026	6	118	0.04032	0.011692	***	Study 1	CV150	326	872
114	NC0107449	6	118.1	0.00461	0.016176	T	Study 1	I283669	285	873
115	NC0023358	6	120.8	0.042831	0.090632	A	Study 1	CV013	177	874
115	NC0023358	6	120.8	0.002271	-0.10673	A	Study 1	CV041	177	874
115	NC0023358	6	120.8	0.044157	0.177117	A	Study 1	CV125	177	874
115	NC0003201	6	127.9	0.012216	0.22436	G	Study 1	CV109	74	875
115	NC0003201	6	127.9	0.043765	-0.01449	G	Study 1	CV017	74	875
115	NC0003201	6	127.9	0.025597	0.006504	G	Study 1	CV109	74	875
115	NC0003201	6	127.9	0.034669	-0.014	G	Study 1	CV108	74	875

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
116	NC0028185	6	130.1	0.022106	-0.06756	G	Study 2	--	523	876
116	NC0028185	6	130.1	0.036012	0.053674	G	Study 1	CV112	523	876
116	NC0060514	6	131.2	0.019808	-0.01729	**	Study 1	CV039	264	877
116	NC0060514	6	131.2	0.000397	-0.07039	CA	Study 1	CV042	264	877
116	NC0060514	6	131.2	0.033421	0.060061	CA	Study 1	CV116	264	877
116	NC0060514	6	131.2	0.014878	-0.05563	CA	Study 1	CV022	264	877
116	NC0060514	6	131.2	0.001088	-0.1157	**	Study 1	CV041	264	877
116	NC0060514	6	131.2	0.020466	0.097779	**	Study 1	CV118	264	877
116	NC0058629	6	131.3	--	--	T	Study 4	--	256	878
116	NC0037634	6	132.4	0.046553	0.016822	T	Study 1	--	541	879
116	NC0032509	6	132.9	0.028695	0.049476	A	Study 1	CV074	334	880
116	NC0002782	6	133.5	0.048355	-0.01117	A	Study 1	CV076	121	881
116	NC0053636	6	136	0.045675	-0.00319	G	Study 1	--	202	882
116	NC0053636	6	136	0.016849	0.01583	A	Study 1	--	202	882
116	NC0053636	6	136	0.036309	-0.05411	G	Study 1	CV011	202	882
116	NC0009667	6	139.1	0.001978	-0.09141	C	Study 2	--	226	883
116	NC0009667	6	139.1	0.039128	0.01094	C	Study 1	CV153	226	883
116	NC0009667	6	139.1	0.007861	-0.01765	G	Study 1	CV108	226	883
117	NC0194601	6	143.7	--	--	G	Study 5	--	788	884
117	NC0032370	6	144.3	0.017205	-0.0463	A	Study 1	CV042	929	885
117	NC0032370	6	144.3	0.022296	0.051491	G	Study 1	CV074	929	885
117	NC0032370	6	144.3	0.021767	0.016438	G	Study 1	CV074	929	885
117	NC0037555	6	144.7	0.00173	-0.11044	C	Study 1	CV041	390	886
117	NC0037555	6	144.7	0.042437	-0.04497	C	Study 1	CV022	390	886
117	NC0021734	6	145.4	--	--	T	Study 4	--	438	887
117	NC0021734	6	145.4	0.0401	0.013298	T	Study 1	--	438	887
117	NC0021734	6	145.4	0.03217	-0.17298	G	Study 1	CV069	438	887
117	NC0021734	6	145.4	0.00114	-0.08377	G	Study 1	CV011	438	887
117	NC0027223	6	145.8	0.026946	0.012531	C	Study 1	CV150	464	888
117	NC0027223	6	145.8	0.002304	0.15636	T	Study 1	CV093	464	888
117	NC0027223	6	145.8	0.048882	0.027138	T	Study 1	CV112	464	888
117	NC0027223	6	145.8	0.002526	-0.02085	T	Study 1	CV108	464	888
117	NC0199633	6	146	--	--	G	Study 5	--	293	889

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
118	NC0147609	7	7.1	0.032775	-0.07552	A	Study 1	CV041	57	890
118	NC0173584	7	8.5	--	--	G	Study 5	--	1001	891
119	NC0173759	7	11.2	--	--	G	Study 5	--	1001	892
120	NC0143514	7	29	--	--	G	Study 4	--	595	893
120	NC0143514	7	29	0.036853	0.087404	G	Study 1	CV166	595	893
120	NC0143514	7	29	0.015031	-0.06975	G	Study 1	I294213	595	893
120	NC0143514	7	29	0.013204	0.285677	A	Study 1	CV124	595	893
120	NC0143514	7	29	0.041477	-0.03466	G	Study 1	CV010	595	893
120	NC0143514	7	29	0.038307	-0.01725	G	Study 1	CV010	595	893
121	NC0058637	7	33.3	0.017688	-0.08092	G	Study 1	CV041	106	894
121	NC0058637	7	33.3	0.028047	-0.00579	G	Study 1	CV056	106	894
122	NC0011865	7	43.5	0.000108	0.022764	G	Study 1	I283669	382	895
122	NC0011865	7	43.5	0.009614	-0.04483	G	Study 1	CV010	382	895
122	NC0011865	7	43.5	0.007335	-0.0061	G	Study 1	CV010	382	895
122	NC0011865	7	43.5	0.04517	0.005945	A	Study 1	CV109	382	895
122	NC0027347	7	43.8	--	--	G	Study 4	--	128	896
122	NC0027347	7	43.8	0.037436	-0.01001	G	Study 1	CV053	128	896
122	NC0027347	7	43.8	0.000615	0.182675	G	Study 1	CV149	128	896
122	NC0027347	7	43.8	0.003224	-0.11165	A	Study 1	CV075	128	896
122	NC0027347	7	43.8	0.004797	0.11196	G	Study 1	CV079	128	896
122	NC0003924	7	43.9	--	--	G	Study 5	--	412	897
122	NC0003924	7	43.9	0.038352	-0.0098	G	Study 1	CV053	412	897
122	NC0003924	7	43.9	0.042761	-0.0142	G	Study 1	CV060	412	897
122	NC0003924	7	43.9	0.04264	-0.0043	C	Study 1	CV103	412	897
122	NC0003924	7	43.9	0.023825	-0.01121	C	Study 1	CV110	412	897
122	NC0107497	7	43.9	0.036812	-0.0086	G	Study 1	CV105	206	898
122	NC0107497	7	43.9	0.049261	-0.05212	G	Study 1	CV050	206	898
122	NC0107497	7	43.9	0.014936	-0.07033	C	Study 1	I294213	206	898
122	NC0107497	7	43.9	0.043823	-0.00691	C	Study 1	I294213	206	898
123	NC0084006	7	51.2	0.041474	-0.11864	C	Study 1	CV025	45	899
123	NC0034565	7	52.2	--	--	****	Study 4	--	57	900
123	NC0034565	7	52.2	0.034282	0.006756	****	Study 1	CV109	57	900
123	NC0108168	7	56	0.036799	-0.0137	C	Study 1	CV060	420	901

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
123	NC0199526	7	56	--	--	T	Study 5	--	468	902
123	NC0066143	7	57.1	0.03853	-0.07245	G	Study 1	CV101	135	903
123	NC0066143	7	57.1	0.036295	-0.0197	A	Study 1	I294213	135	903
123	NC0066143	7	57.1	0.034711	-0.01218	A	Study 1	I294213	135	903
123	NC0042164	7	57.4	0.00455	0.261062	A	Study 1	CV161	320	904
123	NC0173495	7	57.7	--	--	T	Study 5	--	540	905
123	NC0008712	7	58.1	0.011044	-0.01516	C	Study 1	I294213	418	906
123	NC0002225	7	58.5	0.006848	-0.01126	T	Study 1	CV105	121	907
123	NC0002225	7	58.5	0.010978	-0.02802	C	Study 1	CV120	121	907
123	NC0002225	7	58.5	0.048248	-0.00302	T	Study 1	CV100	121	907
123	NC0002225	7	58.5	0.048248	-0.00302	T	Study 1	CV100	121	907
124	NC0056253	7	60.4	0.013738	-0.01619	T	Study 1	CV108	94	908
124	NC0146556	7	60.4	<.0001	0.113634	T	Study 3	--	187	909
124	NC0146556	7	60.4	--	--	T	Study 5	--	187	909
124	NC0173560	7	60.4	--	--	G	Study 5	--	343	910
124	NC0027428	7	60.8	--	--	T	Study 4	--	189	911
124	NC0027428	7	60.8	0.017474	0.087543	C	Study 1	CV079	189	911
124	NC0027428	7	60.8	0.003035	0.12043	C	Study 1	CV079	189	911
124	NC0028094	7	61.9	0.0016	-0.18408	A	Study 3	--	260	912
124	NC0000558	7	62.2	--	--	T	Study 5	--	118	913
124	NC0000558	7	62.2	0.00002	0.230882	T	Study 1	CV149	118	913
124	NC0069202	7	62.5	0.0014	0.119316	G	Study 3	--	514	914
124	NC0030511	7	62.8	0.041494	-0.01482	T	Study 1	CV139	352	915
124	NC0039064	7	62.8	--	--	T	Study 4	--	317	916
124	NC0105086	7	62.8	--	--	T	Study 4	--	326	917
124	NC0108360	7	62.8	0.042224	-0.01489	G	Study 1	CV139	263	918
124	NC0108360	7	62.8	0.027426	-0.08092	A	Study 1	CV101	263	918
124	NC0108360	7	62.8	0.016278	-0.09296	G	Study 1	CV075	263	918
124	NC0108360	7	62.8	0.008016	-0.02483	G	Study 1	I294213	263	918
124	NC0108360	7	62.8	0.000108	0.209144	A	Study 1	CV149	263	918
124	NC0108360	7	62.8	0.040494	-0.01207	G	Study 1	I294213	263	918
124	NC0108360	7	62.8	0.023129	-0.01333	G	Study 1	CV100	263	918
124	NC0108360	7	62.8	0.008053	0.096373	A	Study 1	CV079	263	918

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
124	NC0108360	7	62.8	0.004609	0.114413	A	Study 1	CV079	263	918
124	NC0034215	7	63.1	--	--	T	Study 4	--	204	919
124	NC0155984	7	63.1	0.013214	-0.00427	C	Study 1	CV100	68	920
124	NC0028277	7	63.4	--	--	C	Study 5	--	42	921
124	NC0034121	7	64.1	--	--	G	Study 4	--	70	922
124	NC0078294	7	64.2	--	--	T	Study 4	--	99	923
124	NC0078294	7	64.2	0.025428	-0.08337	G	Study 1	CV101	99	923
124	NC0078294	7	64.2	0.028201	-0.16627	T	Study 1	CV112	99	923
124	NC0078294	7	64.2	0.03523	0.012348	G	Study 1	CV011	99	923
124	NC0004299	7	64.4	0.00037	0.025051	G	Study 1	--	39	924
124	NC0078783	7	64.4	--	--	T	Study 4	--	326	925
124	NC0009073	7	65.9	--	--	**	Study 4	--	191	926
124	NC0019507	7	65.9	0.0084	-0.04456	T	Study 1	CV010	237	927
124	NC0019507	7	65.9	0.017448	-0.00547	T	Study 1	CV010	237	927
124	NC0105767	7	65.9	--	--	T	Study 5	--	312	928
124	NC0068424	7	66.2	--	--	T	Study 4	--	295	929
124	NC0068426	7	66.5	0.003921	-0.18207	C	Study 1	CV041	425	930
124	NC0068426	7	66.5	0.007333	0.096674	C	Study 1	CV079	425	930
124	NC0068426	7	66.5	0.002856	0.119341	C	Study 1	CV079	425	930
124	NC0034688	7	69.4	0.029271	-0.0103	G	Study 1	CV053	203	931
124	NC0066422	7	69.4	--	--	G	Study 4	--	178	932
124	NC0066422	7	69.4	0.003677	0.12019	A	Study 1	CV166	178	932
125	NC0147598	7	70.1	0.003944	-0.01258	G	Study 1	CV105	557	933
125	NC0199886	7	71.1	--	--	T	Study 5	--	201	934
125	NC0033620	7	75.7	0.028609	-0.01026	T	Study 1	CV053	290	935
125	NC0033620	7	75.7	0.004491	0.116704	A	Study 1	CV166	290	935
125	NC0033620	7	75.7	0.045844	0.016977	A	Study 1	CV073	290	935
125	NC0033620	7	75.7	0.001747	0.180311	A	Study 1	CV160	290	935
125	NC0068434	7	76.5	--	--	T	Study 5	--	573	936
125	NC0068434	7	76.5	0.000099	0.025696	C	Study 1	--	573	936
125	NC0068434	7	76.5	0.003839	-0.18408	T	Study 1	CV041	573	936
125	NC0068434	7	76.5	0.018076	0.008093	T	Study 1	CV091	573	936
125	NC0033509	7	77.2	--	--	T	Study 5	--	154	937

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
125	NC0029362	7	78.4	0.036242	-0.01619	C	Study 1	CV041	95	938
125	NC0029362	7	78.4	0.00436	-0.01199	C	Study 1	CV110	95	938
125	NC0037827	7	78.4	--	--	T	Study 5	--	332	939
126	NC0145922	7	80.5	--	--	G	Study 5	--	451	940
126	NC0145922	7	80.5	0.003196	-0.04928	A	Study 1	CV010	451	940
126	NC0145922	7	80.5	0.019316	-0.00533	A	Study 1	CV010	451	940
126	NC0057013	7	80.7	--	--	G	Study 4	--	220	941
126	NC0057013	7	80.7	0.005695	-0.20652	A	Study 1	CV112	220	941
126	NC0057013	7	80.7	0.003597	-0.02708	A	Study 1	I294213	220	941
126	NC0057013	7	80.7	0.033104	0.054915	A	Study 1	CV112	220	941
126	NC0057013	7	80.7	0.006049	0.015585	G	Study 1	CV011	220	941
126	NC0048425	7	88.3	--	--	T	Study 4	--	484	942
126	NC0048425	7	88.3	0.002103	-0.05214	T	Study 1	CV010	484	942
126	NC0048425	7	88.3	0.018549	-0.00545	T	Study 1	CV010	484	942
126	NC0048425	7	88.3	0.045991	0.088032	C	Study 1	CV148	484	942
126	NC0048425	7	88.3	0.003862	-0.0127	T	Study 1	CV110	484	942
126	NC0035408	7	89.5	0.036009	-0.00922	C	Study 1	CV105	221	943
126	NC0035408	7	89.5	0.044378	-0.009	C	Study 1	I294213	221	943
126	NC0035408	7	89.5	0.017602	-0.10008	C	Study 1	CV067	221	943
126	NC0035408	7	89.5	0.027149	0.005198	C	Study 1	CV051	221	943
126	NC0035408	7	89.5	0.013264	-0.01707	A	Study 1	CV072	221	943
126	NC0035408	7	89.5	0.014968	-0.01438	C	Study 1	I294213	221	943
127	NC0005051	7	91.3	--	--	T	Study 5	--	98	944
127	NC0005051	7	91.3	0.041309	-0.09649	C	Study 1	CV069	98	944
127	NC0005051	7	91.3	0.010046	-0.19408	T	Study 1	CV112	98	944
127	NC0005051	7	91.3	0.01526	0.062791	T	Study 1	CV112	98	944
127	NC0043388	7	91.3	0.032728	-0.08291	G	Study 1	CV075	643	945
127	NC0199752	7	92.9	--	--	T	Study 5	--	210	946
127	NC0020649	7	93.6	0.045919	-0.01543	T	Study 1	CV041	301	947
127	NC0020649	7	93.6	0.005444	-0.00807	T	Study 1	CV052	301	947
127	NC0020649	7	93.6	0.021003	-0.02187	T	Study 1	I294213	301	947
127	NC0020649	7	93.6	0.026009	0.080346	T	Study 1	CV079	301	947
127	NC0020649	7	93.6	0.012795	0.099773	T	Study 1	CV079	301	947

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
127	NC0038914	7	96.6	0.000163	0.025088	****	Study 1	--	129	948
127	NC0038914	7	96.6	0.006651	-0.00767	ATTA	Study 1	CV052	129	948
127	NC0038914	7	96.6	0.001876	0.165881	ATTA	Study 1	CV149	129	948
127	NC0009240	7	98.5	0.049176	-0.03338	A	Study 1	CV010	379	949
127	NC0009240	7	98.5	0.035094	0.016043	A	Study 1	CV169	379	949
127	NC0155829	7	99	--	--	G	Study 5	--	416	950
127	NC0155829	7	99	0.021592	-0.09031	G	Study 1	CV075	416	950
127	NC0155829	7	99	0.008108	0.10967	A	Study 1	CV166	416	950
127	NC0155829	7	99	0.001779	0.114483	A	Study 1	CV079	416	950
127	NC0155829	7	99	0.007151	0.109911	A	Study 1	CV079	416	950
127	NC0071001	7	99.4	0.044212	0.004539	C	Study 1	CV051	359	951
127	NC0034583	7	99.5	0.021863	0.05913	T	Study 1	CV112	74	952
127	NC0070402	7	99.8	--	--	T	Study 5	--	322	953
128	NC0031157	7	100	--	--	G	Study 5	--	458	954
128	NC0173580	7	100	--	--	G	Study 5	--	919	955
128	NC0015995	7	104.6	0.007	-0.00766	C	Study 1	CV052	438	956
128	NC0015995	7	104.6	0.014316	0.005256	C	Study 1	CV051	438	956
128	NC0016008	7	104.6	0.008973	0.014024	C	Study 1	--	133	957
128	NC0199892	7	104.6	--	--	T	Study 5	--	94	958
128	NC0145260	7	104.9	0.000518	0.148069	C	Study 1	CV166	149	959
128	NC0018284	7	105.8	0.008549	-0.06565	C	Study 1	CV022	243	960
128	NC0039773	7	106.1	0.016541	-0.01643	T	Study 1	CV072	42	961
128	NC0039773	7	106.1	0.005159	0.014812	C	Study 1	--	42	961
128	NC0015161	7	106.4	--	--	G	Study 5	--	428	962
128	NC0015161	7	106.4	0.047566	0.083705	G	Study 1	CV125	428	962
128	NC0040335	7	107	<.0001	-0.15411	A	Study 3	--	407	963
128	NC0040335	7	107	0.016304	-0.00818	G	Study 1	CV122	407	963
128	NC0040335	7	107	0.001759	0.114507	G	Study 1	CV079	407	963
128	NC0040335	7	107	0.014784	0.099806	G	Study 1	CV079	407	963
129	NC0009674	7	112.1	0.00097	0.019861	G	Study 1	--	150	964
129	NC0009674	7	112.1	0.01699	0.005264	G	Study 1	CV051	150	964
129	NC0009674	7	112.1	0.022759	0.122281	G	Study 1	CV149	150	964
129	NC0030029	7	112.7	0.024426	0.09597	C	Study 1	CV125	315	965

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
129	NC0018565	7	115.2	0.00945	-0.05962	CGA	Study 1	CV022	164	966
129	NC0018565	7	115.2	0.023197	-0.08759	CGA	Study 1	CV075	164	966
129	NC0018565	7	115.2	0.020514	0.006782	CGA	Study 1	CV128	164	966
129	NC0018565	7	115.2	0.049091	-0.07093	CGA	Study 1	I294213	164	966
129	NC0027069	7	116.1	--	--	T	Study 4	--	339	967
129	NC0027069	7	116.1	0.015062	0.103812	T	Study 1	CV166	339	967
129	NC0027069	7	116.1	0.000046	0.144657	T	Study 1	CV079	339	967
129	NC0027069	7	116.1	0.001417	0.127179	T	Study 1	CV079	339	967
129	NC0003218	7	117.9	0.006576	0.018163	C	Study 1	--	342	968
129	NC0003218	7	117.9	0.00497	-0.00792	T	Study 1	CV052	342	968
129	NC0003218	7	117.9	0.048349	-0.09639	C	Study 1	CV068	342	968
129	NC0003218	7	117.9	0.022904	0.016111	T	Study 1	CV074	342	968
129	NC0003218	7	117.9	0.029603	0.005658	C	Study 1	CV024	342	968
130	NC0021967	7	122.7	--	--	C	Study 5	--	406	969
130	NC0108979	7	124.7	--	--	G	Study 5	--	232	970
130	NC0148208	7	126.9	0.02897	0.011683	C	Study 1	--	216	971
131	NC0112796	7	130.1	0.03255	0.015227	C	Study 1	CV074	145	972
131	NC0173357	7	131	--	--	T	Study 5	--	106	973
131	NC0004953	7	131.2	--	--	T	Study 4	--	154	974
131	NC0004953	7	131.2	0.038002	-0.16879	T	Study 1	I294213	154	974
131	NC0004953	7	131.2	0.020682	0.270301	A	Study 1	CV124	154	974
131	NC0004953	7	131.2	0.004498	-0.0199	A	Study 1	CV072	154	974
131	NC0004953	7	131.2	0.017215	0.137667	T	Study 1	CV160	154	974
131	NC0004953	7	131.2	0.003137	0.10733	T	Study 1	CV079	154	974
131	NC0004953	7	131.2	0.005862	0.111135	T	Study 1	CV079	154	974
131	NC0015974	7	135.9	0.016924	0.012659	G	Study 1	--	523	975
131	NC0015974	7	135.9	0.033889	0.022775	G	Study 1	CV134	523	975
131	NC0015974	7	135.9	0.048657	-0.00261	G	Study 1	CV100	523	975
131	NC0015974	7	135.9	0.048657	-0.00261	G	Study 1	CV100	523	975
131	NC0110771	7	138.5	--	--	C	Study 4	--	490	976
131	NC0110771	7	138.5	0.046346	-0.00644	A	Study 1	CV122	490	976
131	NC0110771	7	138.5	0.003219	-0.07164	A	Study 1	CV022	490	976
131	NC0110771	7	138.5	0.035734	0.130732	A	Study 1	CV073	490	976

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
131	NC0110771	7	138.5	0.019402	0.006575	A	Study 1	CV024	490	976
132	NC0199352	7	147.2	--	--	T	Study 5	--	327	977
133	NC0199339	7	150.8	--	--	C	Study 5	--	214	978
133	NC0011664	7	150.9	--	--	T	Study 5	--	84	979
133	NC0011664	7	150.9	0.023166	-0.05374	T	Study 1	CV022	84	979
133	NC0146593	7	152.9	0.004845	0.317776	C	Study 1	CV124	122	980
133	NC0146593	7	152.9	0.010074	-0.15074	C	Study 1	I294213	122	980
133	NC0146593	7	152.9	0.037992	0.074353	C	Study 1	CV079	122	980
133	NC0146593	7	152.9	0.025479	0.088883	C	Study 1	CV079	122	980
133	NC0155475	7	154.2	0.040658	0.059887	T	Study 1	CV150	77	981
133	NC0155475	7	154.2	0.036707	0.068893	T	Study 1	CV150	77	981
133	NC0143371	7	156.6	0.016396	-0.00461	G	Study 1	CV010	80	982
133	NC0143371	7	156.6	0.031174	-0.04201	T	Study 1	CV042	80	982
133	NC0143371	7	156.6	0.020148	-0.00725	T	Study 1	CV052	80	982
134	NC0151568	7	161.1	0.023028	0.009803	C	Study 1	CV170	515	983
134	NC0151568	7	161.1	0.006961	-0.00508	T	Study 1	CV010	515	983
134	NC0151568	7	161.1	0.019075	-0.0159	T	Study 1	CV072	515	983
134	NC0151568	7	161.1	0.018193	-0.12163	C	Study 1	CV112	515	983
134	NC0078091	7	164.6	0.018514	-0.04508	G	Study 1	CV042	194	984
134	NC0078091	7	164.6	0.03312	-0.00665	G	Study 1	CV052	194	984
134	NC0078091	7	164.6	0.016483	0.009193	A	Study 1	CV101	194	984
134	NC0078091	7	164.6	0.035248	0.131718	A	Study 1	CV073	194	984
134	NC0078091	7	164.6	0.04593	0.004625	A	Study 1	CV102	194	984
134	NC0078091	7	164.6	0.033482	0.069721	G	Study 1	CV150	194	984
134	NC0146620	7	165.7	0.03892	-0.0039	T	Study 1	CV010	306	985
134	NC0146620	7	165.7	0.016279	0.012687	C	Study 1	--	306	985
134	NC0038317	7	165.8	--	--	T	Study 4	--	207	986
134	NC0036490	7	166.9	--	--	T	Study 4	--	244	987
134	NC0028596	7	168.9	0.046576	0.15859	T	Study 1	CV073	121	988
134	NC0036559	7	169.2	--	--	G	Study 5	--	269	989
134	NC0038499	7	169.3	--	--	G	Study 4	--	597	990
135	NC0106258	7	170.9	--	--	G	Study 4	--	349	991
135	NC0106258	7	170.9	0.004542	-0.01835	C	Study 1	CV047	349	991

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
135	NC0106258	7	170.9	0.012527	0.279708	C	Study 1	CV124	349	991
135	NC0021038	7	171.4	--	--	T	Study 4	--	126	992
135	NC0021038	7	171.4	--	--	T	Study 5	--	126	992
135	NC0021038	7	171.4	0.00324	0.011073	A	Study 1	CV101	126	992
135	NC0021038	7	171.4	0.01175	0.138137	A	Study 1	CV164	126	992
135	NC0021038	7	171.4	0.005401	-0.01882	A	Study 1	CV072	126	992
135	NC0021038	7	171.4	0.009433	0.021273	A	Study 1	--	126	992
135	NC0021045	7	171.4	--	--	T	Study 5	--	308	993
135	NC0018157	7	171.7	--	--	T	Study 4	--	577	994
135	NC0071624	7	171.7	0.04423	-0.03853	G	Study 1	CV042	101	995
135	NC0019704	7	173.9	0.028024	0.009225	A	Study 1	CV170	183	996
135	NC0019704	7	173.9	0.048012	0.085483	T	Study 1	CV166	183	996
135	NC0019704	7	173.9	0.017618	0.267911	T	Study 1	CV124	183	996
136	NC0024672	8	33.6	0.020532	-0.05842	A	Study 1	CV022	134	997
136	NC0024672	8	33.6	0.010188	-0.00768	A	Study 1	CV138	134	997
136	NC0032600	8	37.8	--	--	T	Study 5	--	208	998
136	NC0019198	8	38.1	0.024171	0.016668	T	Study 1	CV065	316	999
136	NC0019198	8	38.1	0.048339	-0.05621	T	Study 1	I294213	316	999
136	NC0038724	8	39.6	0.000131	0.11118	A	Study 2	--	312	1000
136	NC0038724	8	39.6	--	--	C	Study 4	--	312	1000
136	NC0038724	8	39.6	0.006446	-0.19023	C	Study 1	CV069	312	1000
136	NC0038724	8	39.6	0.039369	-0.05052	A	Study 1	CV022	312	1000
136	NC0038724	8	39.6	0.002728	-0.01365	A	Study 1	CV087	312	1000
136	NC0038724	8	39.6	0.04899	0.011796	A	Study 1	CV013	312	1000
136	NC0038724	8	39.6	0.000006	-0.24759	A	Study 1	--	312	1000
137	NC0040299	8	41.2	--	--	T	Study 5	--	105	1001
137	NC0040299	8	41.2	0.044562	-0.15915	T	Study 1	I294213	105	1001
137	NC0040299	8	41.2	0.049265	-0.13762	T	Study 1	I294213	105	1001
137	NC0040299	8	41.2	0.039212	0.181986	T	Study 1	CV130	105	1001
137	NC0003792	8	41.7	0.010233	0.00618	T	Study 1	--	110	1002
137	NC0003792	8	41.7	0.045603	-0.00526	C	Study 1	CV088	110	1002
137	NC0003792	8	41.7	0.000778	-0.26121	C	Study 1	CV044	110	1002
137	NC0003792	8	41.7	0	0.178083	C	Study 1	CV079	110	1002

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
137	NC0003792	8	41.7	0.000001	0.18984	C	Study 1	CV079	110	1002
137	NC0199597	8	42.5	--	--	G	Study 5	--	700	1003
138	NC0029842	8	51.6	0.032047	0.036264	G	Study 1	CV114	261	1004
138	NC0029842	8	51.6	0.003155	-0.00834	A	Study 1	CV138	261	1004
138	NC0029842	8	51.6	0.021261	0.211863	A	Study 1	CV130	261	1004
138	NC0029842	8	51.6	0.007907	-0.07667	A	Study 1	CV106	261	1004
138	NC0008934	8	51.8	0.004712	-0.08007	T	Study 1	I294213	140	1005
138	NC0034552	8	51.8	0.043494	-0.00844	C	Study 1	CV088	258	1006
138	NC0034552	8	51.8	0.008952	-0.00704	C	Study 1	CV088	258	1006
138	NC0034552	8	51.8	0.013027	0.061094	T	Study 1	CV135	258	1006
138	NC0034552	8	51.8	0.019355	0.022981	T	Study 1	CV135	258	1006
138	NC0034552	8	51.8	0.048801	0.146979	T	Study 1	CV163	258	1006
138	NC0034552	8	51.8	0.000122	0.02322	T	Study 1	CV079	258	1006
138	NC0034552	8	51.8	0.014927	-0.19185	C	Study 1	I294213	258	1006
138	NC0034552	8	51.8	0.026279	-0.16112	C	Study 1	I294213	258	1006
138	NC0034552	8	51.8	0.000007	0.157786	T	Study 1	CV079	258	1006
138	NC0034552	8	51.8	0.000506	0.137859	T	Study 1	CV079	258	1006
138	NC0105809	8	53.4	0.042872	0.009719	G	Study 1	CV100	56	1007
138	NC0005266	8	56.5	1.83E-07	0.148108	T	Study 2	--	214	1008
138	NC0005266	8	56.5	0.011829	0.01852	C	Study 1	CV065	214	1008
138	NC0005266	8	56.5	0.047479	0.007997	C	Study 1	--	214	1008
138	NC0005266	8	56.5	0.006321	0.028785	T	Study 1	CV134	214	1008
138	NC0005266	8	56.5	0.000284	-0.02115	C	Study 1	CV025	214	1008
138	NC0005266	8	56.5	0.018161	-0.01917	C	Study 1	CV057	214	1008
138	NC0005266	8	56.5	0	-0.29464	T	Study 1	--	214	1008
138	NC0058392	8	56.6	0.042078	-0.00535	T	Study 1	CV088	291	1009
138	NC0058392	8	56.6	0.018186	0.073146	C	Study 1	CV114	291	1009
138	NC0058392	8	56.6	0.000283	-0.09407	C	Study 1	CV057	291	1009
138	NC0058392	8	56.6	0.038969	0.010819	T	Study 1	CV153	291	1009
138	NC0111628	8	57.3	0.003659	0.017693	A	Study 1	CV013	140	1010
139	NC0037392	8	60	<.0001	-0.13471	C	Study 3	--	153	1011
139	NC0037392	8	60	0.004449	-0.01945	T	Study 1	CV113	153	1011
139	NC0027485	8	60.1	0.017124	-0.01359	T	Study 1	CV087	513	1012

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
139	NC0030011	8	63.1	--	--	G	Study 5	--	326	1013
139	NC0053899	8	65.9	0.021296	0.209606	**	Study 1	CV130	473	1014
139	NC0010347	8	69.2	2.64E-06	0.13431	A	Study 2	--	160	1015
139	NC0010347	8	69.2	0.027925	0.095621	A	Study 1	CV166	160	1015
140	NC0104862	8	70	0.0001	-0.23975	C	Study 3	--	321	1016
140	NC0104862	8	70	0.006107	-0.17656	T	Study 1	CV041	321	1016
140	NC0104862	8	70	0.003291	0.158991	C	Study 1	CV164	321	1016
140	NC0029015	8	71.1	5.15E-07	0.146253	A	Study 2	--	189	1017
140	NC0029015	8	71.1	--	--	G	Study 5	--	189	1017
140	NC0029015	8	71.1	0.019315	-0.06329	G	Study 1	CV082	189	1017
140	NC0029015	8	71.1	0.009176	0.011059	G	Study 1	--	189	1017
140	NC0029015	8	71.1	0.000023	-0.11853	G	Study 1	I294213	189	1017
140	NC0029015	8	71.1	0.000429	-0.0891	G	Study 1	CV057	189	1017
140	NC0029015	8	71.1	0.02326	-0.01819	G	Study 1	CV057	189	1017
140	NC0107396	8	71.1	0.010357	0.016003	***	Study 1	CV079	75	1018
140	NC0107396	8	71.1	0	-0.3255	***	Study 1	--	75	1018
140	NC0107396	8	71.1	0.02425	0.080622	***	Study 1	CV079	75	1018
140	NC0107396	8	71.1	0.017037	0.010681	***	Study 1	CV145	75	1018
140	NC0107396	8	71.1	0.000332	-0.02505	***	Study 1	CV113	75	1018
140	NC0107396	8	71.1	0.031156	0.010586	***	Study 1	CV007	75	1018
140	NC0022765	8	72.4	--	--	T	Study 5	--	501	1019
140	NC0009659	8	72.9	0.005213	0.113132	T	Study 1	CV114	410	1020
140	NC0009659	8	72.9	0.018128	0.026174	A	Study 1	CV134	410	1020
140	NC0009659	8	72.9	0.009958	-0.00654	T	Study 1	CV138	410	1020
140	NC0082612	8	78.9	<.0001	0.128804	G	Study 3	--	309	1021
140	NC0082612	8	78.9	0.014246	-0.01	G	Study 1	I294213	309	1021
140	NC0082612	8	78.9	0.011749	0.016148	G	Study 1	CV013	309	1021
140	NC0082612	8	78.9	0.042229	0.186583	G	Study 1	CV130	309	1021
140	NC0082612	8	78.9	0.032289	-0.06256	G	Study 1	CV119	309	1021
140	NC0082612	8	78.9	0.035547	-0.06929	G	Study 1	CV119	309	1021
140	NC0027361	8	79.6	0.000054	-0.02319	C	Study 1	CV025	229	1022
141	NC0011760	8	80.3	0.008733	0.019354	C	Study 1	CV065	56	1023
141	NC0011760	8	80.3	0.004385	-0.01504	C	Study 1	CV086	56	1023

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
141	NC0011760	8	80.3	0.000648	-0.08638	G	Study 1	CV057	56	1023
141	NC0009254	8	83.9	0.004017	-0.11596	A	Study 1	CV114	146	1024
141	NC0009254	8	83.9	0.045929	-0.01608	A	Study 1	CV057	146	1024
141	NC0013946	8	84	0.0002	-0.11743	A	Study 3	--	59	1025
141	NC0015146	8	84	6.2E-07	0.142555	A	Study 2	--	426	1026
141	NC0015146	8	84	0.030707	0.066995	G	Study 1	CV114	426	1026
141	NC0015146	8	84	0.01298	-0.00404	G	Study 1	CV010	426	1026
141	NC0015146	8	84	0.01298	-0.00404	G	Study 1	CV010	426	1026
141	NC0077568	8	84	0.000005	-0.25706	G	Study 1	--	245	1027
141	NC0147465	8	84	0.004741	-0.05869	C	Study 1	CV042	288	1028
141	NC0147465	8	84	0.01496	-0.08248	C	Study 1	CV017	288	1028
141	NC0200189	8	86.9	--	--	T	Study 5	--	133	1029
141	NC0022382	8	87.8	--	--	G	Study 5	--	134	1030
141	NC0155968	8	87.9	0.00696	0.011743	C	Study 1	--	291	1031
141	NC0155968	8	87.9	0.043	-0.03588	T	Study 1	CV070	291	1031
141	NC0155968	8	87.9	0.019127	0.099464	C	Study 1	CV166	291	1031
141	NC0155968	8	87.9	0.022944	0.20092	T	Study 1	CV130	291	1031
142	NC0144363	8	91.1	0.000818	-0.08501	G	Study 1	CV057	437	1032
142	NC0144363	8	91.1	0.011915	0.007566	G	Study 1	CV099	437	1032
142	NC0145457	8	91.1	4.38E-08	0.160689	A	Study 2	--	453	1033
142	NC0056860	8	92.1	0.0012	0.095519	G	Study 3	--	289	1034
142	NC0056860	8	92.1	--	--	G	Study 4	--	289	1034
142	NC0021895	8	92.2	0.010409	0.011209	T	Study 1	--	36	1035
142	NC0021895	8	92.2	0	0.315445	T	Study 1	CV164	36	1035
142	NC0021895	8	92.2	0.011048	0.009202	T	Study 1	CV164	36	1035
142	NC0021895	8	92.2	0.000028	-0.10819	C	Study 1	I294213	36	1035
142	NC0032337	8	92.7	0.008039	-0.01406	GCTC	Study 1	CV086	237	1036
142	NC0032337	8	92.7	0.012727	-0.01862	GCTC	Study 1	CV041	237	1036
142	NC0032337	8	92.7	0.000241	-0.0254	GCTC	Study 1	CV113	237	1036
142	NC0048562	8	92.7	0.039154	0.064021	G	Study 1	CV114	217	1037
142	NC0048562	8	92.7	0.027001	0.114611	G	Study 1	CV125	217	1037
142	NC0082295	8	93.7	0.015336	0.017889	T	Study 1	CV065	251	1038
142	NC0004253	8	93.9	0.00976	-0.00684	G	Study 1	CV138	337	1039

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
142	NC0004254	8	93.9	--	--	G	Study 5	--	165	1040
142	NC0020514	8	93.9	0.035619	-0.04789	A	Study 1	CV082	368	1041
142	NC0020514	8	93.9	0.015489	-0.04469	A	Study 1	CV041	368	1041
142	NC0020514	8	93.9	0.002177	-0.01779	A	Study 1	CV025	368	1041
142	NC0004504	8	95.6	0.00267	-0.0193	A	Study 1	CV047	469	1042
142	NC0004504	8	95.6	0.000313	-0.07538	A	Study 1	CV042	469	1042
142	NC0004504	8	95.6	0.04012	0.090466	A	Study 1	CV166	469	1042
142	NC0004504	8	95.6	0.002677	-0.12136	A	Study 1	CV114	469	1042
142	NC0004504	8	95.6	0.000048	-0.24211	C	Study 1	--	469	1042
142	NC0058047	8	96.1	0.042308	-0.0085	G	Study 1	I294213	158	1043
142	NC0058047	8	96.1	0.000007	0.203552	G	Study 1	CV118	158	1043
142	NC0058047	8	96.1	0.023676	0.016044	G	Study 1	CV147	158	1043
142	NC0104858	8	96.2	0.000009	0.19853	GCT	Study 1	CV118	173	1044
142	NC0104858	8	96.2	0.025664	0.201515	GCT	Study 1	CV130	173	1044
142	NC0104858	8	96.2	0.000585	0.015009	***	Study 1	CV145	173	1044
142	NC0012023	8	96.4	0.013954	-0.08108	G	Study 1	CV017	439	1045
142	NC0152566	8	97.2	0.004123	-0.18107	G	Study 1	CV017	190	1046
142	NC0152566	8	97.2	0.000165	0.150982	G	Study 1	CV114	190	1046
142	NC0152566	8	97.2	0.000338	-0.0305	A	Study 1	CV057	190	1046
143	NC0107929	8	103.2	0.028876	-0.07807	G	Study 1	CV041	341	1047
143	NC0107929	8	103.2	0.006302	-0.02033	G	Study 1	CV041	341	1047
143	NC0105978	8	103.3	0.006537	-0.01461	A	Study 1	CV086	193	1048
143	NC0105978	8	103.3	0	0.396023	G	Study 1	CV164	193	1048
143	NC0105978	8	103.3	0.000196	0.013335	G	Study 1	CV164	193	1048
143	NC0105978	8	103.3	0.013799	-0.06298	G	Study 1	CV057	193	1048
143	NC0105978	8	103.3	0.000897	-0.02039	G	Study 1	CV100	193	1048
143	NC0105978	8	103.3	0.047039	0.019294	G	Study 1	CV143	193	1048
143	NC0105978	8	103.3	0.026698	-0.02535	A	Study 1	CV121	193	1048
143	NC0105835	8	104	0.001029	-0.08998	C	Study 1	CV082	275	1049
143	NC0082386	8	108.5	0.026076	-0.01437	A	Study 1	CV047	389	1050
143	NC0082386	8	108.5	0.019569	0.014395	G	Study 1	CV013	389	1050
144	NC0110684	8	111.2	0.038864	0.095006	C	Study 1	CV118	270	1051
144	NC0112497	8	111.7	<.0001	-0.22623	A	Study 3	--	190	1052

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
144	NC0112497	8	111.7	0.014785	-0.01589	A	Study 1	CV047	190	1052
144	NC0112497	8	111.7	0.011063	0.015643	T	Study 1	CV013	190	1052
144	NC0112497	8	111.7	0.003472	-0.01679	A	Study 1	CV025	190	1052
144	NC0010392	8	115.4	0.007479	-0.08363	C	Study 1	CV017	496	1053
144	NC0010392	8	115.4	0.027483	0.020263	A	Study 1	CV143	496	1053
144	NC0010392	8	115.4	0.016217	-0.13696	C	Study 1	--	496	1053
144	NC0010392	8	115.4	0.013996	-0.0276	C	Study 1	CV121	496	1053
144	NC0012656	8	115.6	0.001559	-0.06723	G	Study 1	CV042	156	1054
144	NC0012656	8	115.6	0.009374	-0.06717	A	Study 1	CV057	156	1054
144	NC0012656	8	115.6	0.016243	-0.01705	G	Study 1	CV113	156	1054
144	NC0020546	8	115.6	0.01566	0.018115	A	Study 1	CV065	51	1055
144	NC0020546	8	115.6	0.028685	-0.01284	A	Study 1	CV100	51	1055
144	NC0008831	8	116.3	0	0.36804	T	Study 1	CV164	206	1056
144	NC0008831	8	116.3	0.003104	0.010815	T	Study 1	CV164	206	1056
144	NC0008831	8	116.3	0.001435	0.131497	G	Study 1	CV114	206	1056
144	NC0153229	8	116.4	0.021369	0.017072	A	Study 1	CV065	49	1057
144	NC0143432	8	117.9	0.000059	-0.02134	A	Study 1	CV086	109	1058
144	NC0173479	8	118.4	--	--	G	Study 5	--	650	1059
144	NC0020537	8	118.6	<.0001	-0.24103	C	Study 3	--	140	1060
144	NC0020537	8	118.6	0.016984	-0.01612	T	Study 1	CV047	140	1060
145	NC0004586	8	125.1	0.044915	0.012812	A	Study 1	CV013	64	1061
145	NC0031630	8	125.1	0.018992	-0.08743	T	Study 1	CV041	630	1062
146	NC0010808	8	130.7	7.53E-06	0.126749	G	Study 2	--	473	1063
146	NC0200202	8	133	--	--	C	Study 5	--	198	1064
146	NC0005592	8	134.5	0.025875	0.016438	C	Study 1	CV065	305	1065
146	NC0005592	8	134.5	0.025728	-0.01178	T	Study 1	CV129	305	1065
146	NC0013100	8	138.8	0.036521	0.114127	C	Study 1	--	284	1066
146	NC0013100	8	138.8	0.045227	0.014756	A	Study 1	CV065	284	1066
146	NC0013100	8	138.8	0	0.290089	C	Study 1	CV164	284	1066
146	NC0013100	8	138.8	0.000684	-0.02249	A	Study 1	CV113	284	1066
146	NC0027810	8	139.4	0.025032	0.122741	G	Study 1	CV149	415	1067
146	NC0027810	8	139.4	0.027739	0.013242	A	Study 1	CV013	415	1067
146	NC0107286	8	139.7	0.000036	-0.14578	C	Study 1	CV041	257	1068

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
146	NC0107286	8	139.7	0.000508	-0.06864	C	Study 1	CV042	257	1068
146	NC0107286	8	139.7	0.005317	0.113675	C	Study 1	CV114	257	1068
146	NC0108962	8	139.7	0.024761	-0.00309	G	Study 1	CV120	238	1069
146	NC0108962	8	139.7	0.024761	-0.00309	G	Study 1	CV120	238	1069
147	NC0145077	8	149.2	0.0003	-0.3064	A	Study 3	--	463	1070
147	NC0145077	8	149.2	0.0277	0.051923	C	Study 1	CV082	463	1070
147	NC0145077	8	149.2	0.013547	0.100737	A	Study 1	CV114	463	1070
147	NC0145077	8	149.2	0.008563	-0.02177	C	Study 1	CV057	463	1070
147	NC0145077	8	149.2	0.044981	0.065569	A	Study 1	CV150	463	1070
147	NC0145298	8	149.2	<.0001	-0.36866	G	Study 3	--	56	1071
147	NC0154802	8	149.2	--	--	T	Study 5	--	103	1072
147	NC0154802	8	149.2	0.038649	-0.02932	T	Study 1	CV106	103	1072
148	NC0014545	8	155.1	--	--	T	Study 5	--	514	1073
148	NC0014545	8	155.1	0.034238	0.009789	T	Study 1	CV096	514	1073
148	NC0014566	8	155.1	0.019809	0.076395	T	Study 1	CV150	318	1074
148	NC0008757	8	156.3	0.005119	0.154652	C	Study 1	CV164	274	1075
148	NC0008757	8	156.3	0.002083	0.008381	C	Study 1	CV024	274	1075
148	NC0008757	8	156.3	0.023447	-0.01412	C	Study 1	CV113	274	1075
149	NC0199880	8	161.8	--	--	T	Study 5	--	319	1076
149	NC0000561	8	168.3	0.000265	-0.13825	C	Study 1	CV041	71	1077
149	NC0000561	8	168.3	0.010012	0.00744	C	Study 1	CV128	71	1077
149	NC0000561	8	168.3	0.023042	0.035476	C	Study 1	CV066	71	1077
149	NC0000561	8	168.3	0.005536	-0.03112	A	Study 1	CV121	71	1077
149	NC0000561	8	168.3	0.046099	-0.01396	C	Study 1	CV041	71	1077
149	NC0199956	8	169.9	--	--	G	Study 5	--	296	1078
150	NC0014476	9	0.8	--	--	G	Study 4	--	187	1079
150	NC0014476	9	0.8	0.02463	-0.07899	G	Study 1	CV112	187	1079
150	NC0014476	9	0.8	0.029373	-0.00467	C	Study 1	CV092	187	1079
150	NC0014476	9	0.8	0.029373	-0.00467	C	Study 1	CV092	187	1079
150	NC0014479	9	0.8	--	--	T	Study 5	--	309	1080
150	NC0054684	9	8.3	--	--	G	Study 4	--	467	1081
150	NC0054684	9	8.3	0.008863	0.115482	G	Study 1	CV093	467	1081
150	NC0054684	9	8.3	0.018107	0.012757	G	Study 1	--	467	1081

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
150	NC0054684	9	8.3	0.003018	-0.00645	C	Study 1	CV092	467	1081
150	NC0054684	9	8.3	0.003018	-0.00645	C	Study 1	CV092	467	1081
151	NC0020781	9	16	--	--	G	Study 5	--	59	1082
151	NC0020781	9	16	0.020015	-0.08048	A	Study 1	CV017	59	1082
151	NC0112118	9	16	0.009952	-0.08954	C	Study 1	CV017	601	1083
151	NC0173738	9	17.4	--	--	T	Study 5	--	661	1084
151	NC0002735	9	17.6	--	--	G	Study 4	--	86	1085
151	NC0002735	9	17.6	0.006619	-0.03316	G	Study 1	CV072	86	1085
151	NC0002735	9	17.6	0.032986	-0.05282	A	Study 1	I294213	86	1085
151	NC0002735	9	17.6	0.000153	-0.00852	G	Study 1	CV092	86	1085
151	NC0002735	9	17.6	0.000153	-0.00852	G	Study 1	CV092	86	1085
151	NC0113434	9	19.6	--	--	T	Study 4	--	352	1086
151	NC0113434	9	19.6	0.000141	-0.00871	T	Study 1	CV092	352	1086
151	NC0113434	9	19.6	0.000141	-0.00871	T	Study 1	CV092	352	1086
152	NC0049557	9	25.7	<.0001	0.203886	G	Study 3	--	464	1087
152	NC0049557	9	25.7	0.013714	-0.06091	G	Study 1	I294213	464	1087
152	NC0049557	9	25.7	0.040858	-0.0125	G	Study 1	CV013	464	1087
153	NC0012830	9	33.1	0.048968	0.019894	A	Study 1	CV152	334	1088
153	NC0012830	9	33.1	0.034933	0.015661	G	Study 1	CV048	334	1088
153	NC0012830	9	33.1	0.002312	-0.10472	A	Study 1	CV017	334	1088
153	NC0012830	9	33.1	0.007593	0.113205	G	Study 1	CV125	334	1088
153	NC0012830	9	33.1	0.007313	-0.019	A	Study 1	CV010	334	1088
153	NC0012830	9	33.1	0.016289	-0.07906	A	Study 1	CV119	334	1088
153	NC0060553	9	33.2	--	--	G	Study 5	--	299	1089
153	NC0004308	9	36	--	--	G	Study 4	--	439	1090
153	NC0148121	9	36.6	0.000579	-0.12292	T	Study 1	CV017	349	1091
154	NC0027914	9	45	0.038706	-0.00574	A	Study 1	CV022	211	1092
154	NC0027914	9	45	0.002498	0.076898	G	Study 1	CV112	211	1092
154	NC0025198	9	45.7	0.036256	-0.00704	T	Study 1	I294213	289	1093
154	NC0025198	9	45.7	0.015361	-0.01723	C	Study 1	CV010	289	1093
154	NC0025198	9	45.7	0.026887	-0.27789	T	Study 1	CV130	289	1093
154	NC0025198	9	45.7	0.005793	-0.25405	C	Study 1	CV047	289	1093
154	NC0029745	9	45.7	--	--	G	Study 4	--	1023	1094

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
154	NC0041796	9	46.5	0.038782	-0.11222	G	Study 1	I294213	59	1095
154	NC0029583	9	49.1	0.037234	0.013643	A	Study 1	--	76	1096
155	NC0029436	9	51.5	--	--	G	Study 4	--	504	1097
155	NC0029436	9	51.5	0.004685	0.120941	C	Study 1	CV125	504	1097
155	NC0029436	9	51.5	0.00267	-0.02009	G	Study 1	CV113	504	1097
155	NC0028095	9	59.4	--	--	T	Study 4	--	116	1098
155	NC0028095	9	59.4	0.004658	0.018219	C	Study 1	CV011	116	1098
155	NC0028095	9	59.4	0.043833	0.118855	C	Study 1	CV070	116	1098
156	NC0010643	9	60.6	0.018718	-0.1101	G	Study 1	CV067	184	1099
156	NC0010643	9	60.6	0.020177	-0.0121	A	Study 1	CV136	184	1099
156	NC0055759	9	62.1	0.039005	-0.00847	T	Study 1	CV095	149	1100
156	NC0018302	9	65.1	0.0038	0.098649	G	Study 3	--	290	1101
156	NC0018302	9	65.1	0.006013	-0.09183	A	Study 1	CV017	290	1101
156	NC0031233	9	66.5	0.000453	-0.31096	A	Study 1	CV047	1054	1102
156	NC0109526	9	66.5	0.005517	0.262734	C	Study 1	CV109	297	1103
156	NC0144042	9	66.5	0.00706	0.085654	C	Study 1	CV116	130	1104
156	NC0144042	9	66.5	0.000297	0.091533	C	Study 1	CV112	130	1104
156	NC0004407	9	67.2	--	--	G	Study 4	--	49	1105
156	NC0004407	9	67.2	0.03039	-0.01503	G	Study 1	CV108	49	1105
156	NC0028527	9	67.5	0.022612	-0.01429	A	Study 1	CV013	351	1106
156	NC0104195	9	68.5	0.003043	0.125578	A	Study 1	CV125	225	1107
156	NC0106791	9	68.5	--	--	T	Study 4	--	181	1108
156	NC0108984	9	68.5	--	--	G	Study 5	--	562	1109
156	NC0110377	9	68.5	0.039799	-0.06781	T	Study 1	CV119	538	1110
157	NC0031039	9	70.9	0.000112	-0.11761	C	Study 1	CV064	351	1111
157	NC0009397	9	72.6	0.020725	-0.01459	C	Study 1	CV095	311	1112
157	NC0009397	9	72.6	0.041364	-0.00846	C	Study 1	CV095	311	1112
157	NC0021430	9	74.2	0.005569	-0.1319	C	Study 1	CV067	215	1113
157	NC0112189	9	76.2	0.040855	-0.1157	G	Study 1	I294213	479	1114
157	NC0020048	9	77.5	0.0046	0.104102	G	Study 3	--	414	1115
157	NC0153427	9	77.5	--	--	T	Study 5	--	74	1116
157	NC0199943	9	79.2	--	--	G	Study 5	--	250	1117
157	NC0199722	9	79.6	--	--	G	Study 5	--	283	1118

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
158	NC0111177	9	80.1	0.000916	-0.11078	G	Study 1	CV017	365	1119
158	NC0171446	9	80.1	--	--	T	Study 5	--	462	1120
158	NC0014826	9	81.8	0.010378	0.018293	C	Study 1	CV165	51	1121
158	NC0014826	9	81.8	0.00023	-0.35545	C	Study 1	CV047	51	1121
158	NC0002383	9	83.3	0.014206	0.069466	A	Study 1	CV116	63	1122
158	NC0052822	9	83.4	--	--	G	Study 5	--	541	1123
158	NC0110125	9	83.4	0.013478	-0.01558	G	Study 1	CV013	420	1124
158	NC0174154	9	84.1	--	--	G	Study 5	--	1001	1125
158	NC0200114	9	84.1	--	--	G	Study 5	--	72	1126
158	NC0003425	9	84.5	--	--	G	Study 5	--	280	1127
158	NC0003425	9	84.5	0.004719	0.016346	C	Study 1	CV150	280	1127
158	NC0003425	9	84.5	0.032551	-0.11659	G	Study 1	I294213	280	1127
158	NC0023268	9	84.5	--	--	G	Study 5	--	117	1128
158	NC0038548	9	84.5	--	--	T	Study 5	--	312	1129
158	NC0147496	9	84.5	0.013491	-0.0346	G	Study 1	CV106	526	1130
158	NC0004123	9	84.6	--	--	T	Study 5	--	384	1131
158	NC0004123	9	84.6	0.043239	0.059168	C	Study 1	CV150	384	1131
158	NC0078438	9	84.6	0.036554	0.013475	C	Study 1	CV011	138	1132
158	NC0013086	9	87.3	0.012503	-0.01685	A	Study 1	CV021	343	1133
158	NC0013086	9	87.3	0.007289	-0.13785	A	Study 1	CV067	343	1133
158	NC0013086	9	87.3	0.030764	0.048571	A	Study 1	--	343	1133
158	NC0013086	9	87.3	0.023963	-0.18109	G	Study 1	I294213	343	1133
158	NC0013086	9	87.3	0.000523	0.145738	A	Study 1	CV125	343	1133
158	NC0013086	9	87.3	0.000226	0.01823	A	Study 1	--	343	1133
159	NC0081074	9	90.4	<.0001	-0.21669	C	Study 3	--	390	1134
159	NC0081074	9	90.4	0.038721	-0.06972	C	Study 1	CV017	390	1134
159	NC0081074	9	90.4	0.000515	-0.10568	T	Study 1	CV064	390	1134
159	NC0199525	9	90.9	--	--	G	Study 5	--	121	1135
159	NC0108275	9	91.6	0.042042	0.075411	T	Study 1	CV162	401	1136
159	NC0108275	9	91.6	0.000617	0.143921	A	Study 1	CV125	401	1136
159	NC0108275	9	91.6	0.000417	0.017898	T	Study 1	--	401	1136
159	NC0108275	9	91.6	0.02395	-0.18611	T	Study 1	CV044	401	1136
159	NC0108275	9	91.6	0.014306	-0.01569	T	Study 1	CV013	401	1136

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
159	NC0148459	9	91.7	0.044456	-0.00359	C	Study 1	CV094	258	1137
159	NC0028613	9	94.6	--	--	G	Study 5	--	167	1138
159	NC0153579	9	97.3	0.00867	0.018237	G	Study 1	CV165	1001	1139
159	NC0004890	9	98.4	<.0001	-0.17083	A	Study 3	--	104	1140
159	NC0057097	9	98.4	0.003895	-0.29326	********	Study 1	CV047	209	1141
159	NC0106442	9	98.4	0.0057	0.132784	G	Study 3	--	172	1142
159	NC0106442	9	98.4	0.030984	-0.01384	A	Study 1	CV021	172	1142
159	NC0106442	9	98.4	0.008693	0.013409	A	Study 1	--	172	1142
160	NC0041196	9	101.5	--	--	G	Study 4	--	835	1143
160	NC0041196	9	101.5	0.017498	0.013592	G	Study 1	CV150	835	1143
160	NC0041196	9	101.5	0.018747	0.029313	G	Study 1	CV132	835	1143
160	NC0041196	9	101.5	0.003921	0.110028	G	Study 1	CV162	835	1143
160	NC0041196	9	101.5	0.006328	0.190326	G	Study 1	CV149	835	1143
160	NC0041196	9	101.5	0.041725	-0.01374	G	Study 1	CV077	835	1143
160	NC0021860	9	101.8	0.035215	-0.06399	G	Study 1	CV017	90	1144
160	NC0042348	9	101.8	--	--	G	Study 4	--	103	1145
160	NC0042348	9	101.8	0.034709	-0.0155	A	Study 1	CV039	103	1145
160	NC0042348	9	101.8	0.045059	0.007284	A	Study 1	CV101	103	1145
160	NC0042348	9	101.8	0.000569	-0.10482	G	Study 1	CV064	103	1145
160	NC0042348	9	101.8	0.006059	-0.06772	G	Study 1	I294213	103	1145
160	NC0042348	9	101.8	0.003182	0.015539	A	Study 1	--	103	1145
160	NC0018417	9	102.1	0.0004	0.106203	C	Study 3	--	287	1146
160	NC0018417	9	102.1	0.042932	-0.10903	A	Study 1	I294213	287	1146
160	NC0014240	9	103.5	--	--	G	Study 5	--	525	1147
160	NC0066389	9	105.5	--	--	G	Study 4	--	161	1148
160	NC0066389	9	105.5	0.014954	0.003261	G	Study 1	CV016	161	1148
160	NC0066389	9	105.5	0.014954	0.003261	G	Study 1	CV016	161	1148
160	NC0066390	9	105.5	0.04712	-0.01314	A	Study 1	CV021	179	1149
160	NC0066390	9	105.5	0.030923	-0.00354	A	Study 1	CV094	179	1149
160	NC0066390	9	105.5	0.002599	0.015718	A	Study 1	--	179	1149
160	NC0036022	9	107.9	0.0029	0.125806	G	Study 1	CV125	78	1150
160	NC0036022	9	107.9	0.011758	-0.20572	C	Study 1	CV044	78	1150
161	NC0016689	9	110.4	0.034867	0.015865	T	Study 1	CV048	324	1151

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
161	NC0016689	9	110.4	0.028536	-0.10411	C	Study 1	CV067	324	1151
161	NC0018446	9	110.4	0.030979	-0.01502	A	Study 1	CV021	338	1152
161	NC0018446	9	110.4	0.015527	-0.0081	G	Study 1	CV080	338	1152
161	NC0018446	9	110.4	0.007553	0.010202	A	Study 1	CV101	338	1152
161	NC0018446	9	110.4	0.013718	-0.13359	G	Study 1	I294213	338	1152
161	NC0018446	9	110.4	0.01389	0.01508	A	Study 1	CV079	338	1152
161	NC0018446	9	110.4	0.008694	0.014304	A	Study 1	--	338	1152
161	NC0018446	9	110.4	0.006114	-0.01737	G	Study 1	CV013	338	1152
161	NC0035380	9	110.4	0.04682	0.088991	A	Study 1	CV013	222	1153
161	NC0199636	9	112	--	--	G	Study 5	--	264	1154
161	NC0151505	9	114.5	0.00563	0.016235	G	Study 1	CV150	117	1155
161	NC0151505	9	114.5	0.024034	-0.04788	C	Study 1	CV042	117	1155
161	NC0029176	9	116	0.041761	-0.00531	C	Study 1	CV056	176	1156
161	NC0037029	9	119.9	--	--	G	Study 5	--	396	1157
162	NC0035729	9	120.3	0.025844	0.00305	C	Study 1	CV016	102	1158
162	NC0035729	9	120.3	0.025844	0.00305	C	Study 1	CV016	102	1158
162	NC0039475	9	122.7	--	--	T	Study 4	--	267	1159
162	NC0039475	9	122.7	0.027694	-0.01578	T	Study 1	CV112	267	1159
163	NC0042929	9	130	--	--	G	Study 4	--	550	1160
163	NC0042929	9	130	0.026699	-0.12082	G	Study 1	I294213	550	1160
163	NC0042929	9	130	0.01827	0.171014	C	Study 1	CV129	550	1160
163	NC0111292	9	131.1	0.010997	0.014821	C	Study 1	CV150	168	1161
163	NC0111292	9	131.1	0.020927	0.017237	C	Study 1	CV048	168	1161
163	NC0111292	9	131.1	0.038733	-0.00523	G	Study 1	CV056	168	1161
163	NC0111292	9	131.1	0.001383	0.052787	C	Study 1	CV054	168	1161
163	NC0111292	9	131.1	0.027549	0.159768	C	Study 1	CV129	168	1161
163	NC0111292	9	131.1	0.03618	-0.01349	G	Study 1	CV013	168	1161
163	NC0009407	9	133.5	0.022785	-0.04389	G	Study 1	CV042	290	1162
163	NC0009407	9	133.5	0.037566	-0.00484	G	Study 1	CV092	290	1162
163	NC0009407	9	133.5	0.037566	-0.00484	G	Study 1	CV092	290	1162
163	NC0026895	9	133.5	0.027958	0.244518	T	Study 1	CV124	244	1163
163	NC0083647	9	136.7	<.0001	0.22023	G	Study 3	--	375	1164
163	NC0083647	9	136.7	0.02224	0.01017	A	Study 1	--	375	1164

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
164	NC0077194	9	147.7	--	--	T	Study 5	--	204	1165
164	NC0077194	9	147.7	0.007001	-0.05096	A	Study 1	CV042	204	1165
164	NC0077194	9	147.7	0.04168	0.009028	A	Study 1	--	204	1165
164	NC0077194	9	147.7	0.033341	0.134379	T	Study 1	CV073	204	1165
165	NC0049286	9	153	--	--	G	Study 4	--	149	1166
165	NC0049286	9	153	0.009925	0.190716	G	Study 1	CV129	149	1166
165	NC0049286	9	153	0.014355	-0.13436	C	Study 1	I294213	149	1166
165	NC0049286	9	153	0.00504	-0.01777	C	Study 1	CV013	149	1166
165	NC0147417	9	153.2	0.0011	-0.10846	C	Study 3	--	77	1167
165	NC0147417	9	153.2	0.003761	-0.07459	C	Study 1	CV011	77	1167
165	NC0147417	9	153.2	0.027365	0.124325	C	Study 1	CV160	77	1167
166	NC0020088	10	8.6	0.000834	-0.18941	GGAATAACT	Study 1	CV053	267	1168
166	NC0020088	10	8.6	0	0.199296	GGAATAACT	Study 1	CV053	267	1168
166	NC0020088	10	8.6	0.016207	-0.05899	GGAATAACT	Study 1	CV011	267	1168
166	NC0020088	10	8.6	0.017509	-0.10696	GGAATAACT	Study 1	CV067	267	1168
166	NC0020088	10	8.6	0.037715	0.128985	GGAATAACT	Study 1	CV073	267	1168
166	NC0020088	10	8.6	0.047779	-0.08156	GGAATAACT	Study 1	CV045	267	1168
166	NC0020088	10	8.6	0.000589	-0.24885	GGAATAACT	Study 1	I294213	267	1168
166	NC0020088	10	8.6	0.000163	0.382718	GGAATAACT	Study 1	CV161	267	1168
167	NC0153987	10	23.5	0.048224	0.008239	C	Study 1	CV081	482	1169
167	NC0153632	10	24.1	--	--	T	Study 4	--	93	1170
167	NC0153632	10	24.1	0.030649	-0.00526	T	Study 1	I294213	93	1170
167	NC0153632	10	24.1	0.000029	-0.22815	T	Study 1	CV053	93	1170
167	NC0153632	10	24.1	0	0.252924	T	Study 1	CV053	93	1170
167	NC0153632	10	24.1	0.001318	-0.01607	T	Study 1	CV053	93	1170
167	NC0153632	10	24.1	0.026518	0.063755	T	Study 1	CV131	93	1170
167	NC0153632	10	24.1	0.001902	-0.01454	T	Study 1	CV098	93	1170
167	NC0153632	10	24.1	0.027	0.099188	G	Study 1	CV093	93	1170
167	NC0153632	10	24.1	0.011133	0.039793	T	Study 1	CV066	93	1170
167	NC0153632	10	24.1	0.024937	-0.13418	T	Study 1	I294213	93	1170
167	NC0153632	10	24.1	0.019597	0.017967	G	Study 1	CV150	93	1170
167	NC0153632	10	24.1	0.037834	0.013127	G	Study 1	CV150	93	1170
167	NC0173382	10	27.7	--	--	G	Study 5	--	149	1171

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
167	NC0016033	10	29.2	0.000128	-0.22143	G	Study 1	CV053	110	1172
167	NC0016033	10	29.2	0.006965	-0.01313	G	Study 1	CV053	110	1172
167	NC0016033	10	29.2	0.033138	0.087934	G	Study 1	CV125	110	1172
168	NC0019023	10	30.3	--	--	C	Study 5	--	479	1173
168	NC0020502	10	30.3	0.000001	0.167617	G	Study 1	CV053	172	1174
168	NC0020502	10	30.3	0	0.082774	G	Study 1	CV054	172	1174
168	NC0020502	10	30.3	0.041806	0.013597	G	Study 1	CV049	172	1174
168	NC0020502	10	30.3	0.001169	0.414728	G	Study 1	CV156	172	1174
168	NC0020502	10	30.3	0.00354	0.024859	G	Study 1	CV161	172	1174
168	NC0020502	10	30.3	0.017509	0.222149	A	Study 1	CV130	172	1174
168	NC0020502	10	30.3	0.000788	0.292645	G	Study 1	CV161	172	1174
168	NC0020502	10	30.3	0.034306	0.070091	A	Study 1	CV150	172	1174
168	NC0009645	10	32.1	0.020581	-0.06974	G	Study 2	--	225	1175
168	NC0009645	10	32.1	0.041162	-0.02033	G	Study 1	I294213	225	1175
168	NC0009645	10	32.1	0.029063	-0.0134	A	Study 1	CV044	225	1175
168	NC0009645	10	32.1	0.011382	0.041189	A	Study 1	CV066	225	1175
168	NC0009645	10	32.1	0.005886	0.025674	A	Study 1	CV062	225	1175
168	NC0009645	10	32.1	0.017654	0.019373	G	Study 1	CV069	225	1175
168	NC0104672	10	32.2	--	--	C	Study 5	--	125	1176
168	NC0104672	10	32.2	0.018464	0.085446	C	Study 1	CV109	125	1176
168	NC0104672	10	32.2	0.000698	-0.13656	C	Study 1	CV045	125	1176
168	NC0111682	10	36.7	0.046957	-0.0148	C	Study 1	CV039	77	1177
169	NC0008956	10	40.8	0.000634	-0.1413	A	Study 1	CV045	447	1178
169	NC0008956	10	40.8	0.007388	0.089829	T	Study 1	CV150	447	1178
169	NC0016045	10	43.7	0.005738	-0.1294	G	Study 1	CV067	113	1179
169	NC0016045	10	43.7	0.000579	0.062844	A	Study 1	CV054	113	1179
169	NC0016045	10	43.7	0.009408	-0.11512	G	Study 1	CV100	113	1179
169	NC0028604	10	43.7	<.0001	0.138728	T	Study 3	--	248	1180
169	NC0028604	10	43.7	0.011169	-0.13561	T	Study 1	CV053	248	1180
169	NC0028604	10	43.7	0.021652	-0.10617	C	Study 1	CV067	248	1180
169	NC0028604	10	43.7	0.030098	0.075637	T	Study 1	CV053	248	1180
169	NC0028604	10	43.7	0.036209	0.016705	C	Study 1	CV069	248	1180
169	NC0005255	10	45	0.002	-0.1295	A	Study 3	--	128	1181

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
169	NC0005255	10	45	0.002613	-0.01813	C	Study 1	CV044	128	1181
169	NC0015355	10	45.2	--	--	G	Study 5	--	458	1182
169	NC0111212	10	45.9	--	--	G	Study 5	--	166	1183
169	NC0111212	10	45.9	0.001975	0.028698	G	Study 1	CV062	166	1183
169	NC0111212	10	45.9	0.004541	0.276584	G	Study 1	CV130	166	1183
169	NC0143762	10	46.7	0.016189	0.010981	A	Study 1	--	267	1184
169	NC0143762	10	46.7	0.000816	0.027097	A	Study 1	CV156	267	1184
169	NC0143762	10	46.7	0.000001	0.041456	A	Study 1	CV161	267	1184
169	NC0143762	10	46.7	0.000007	0.02589	A	Study 1	--	267	1184
169	NC0143762	10	46.7	0.014041	0.011861	A	Study 1	--	267	1184
169	NC0143762	10	46.7	0.013345	0.012708	A	Study 1	--	267	1184
169	NC0053602	10	47.3	0.0005	-0.12392	A	Study 3	--	339	1185
169	NC0053602	10	47.3	--	--	G	Study 5	--	339	1185
169	NC0053602	10	47.3	0.019961	0.025142	G	Study 1	CV134	339	1185
169	NC0147718	10	47.3	--	--	T	Study 5	--	261	1186
169	NC0148322	10	47.3	--	--	T	Study 5	--	71	1187
169	NC0173834	10	49.1	--	--	T	Study 5	--	635	1188
169	NC0199686	10	49.1	--	--	T	Study 5	--	70	1189
169	NC0109058	10	49.2	--	--	T	Study 5	--	315	1190
169	NC0109058	10	49.2	0.036137	0.042498	T	Study 1	--	315	1190
169	NC0109866	10	49.2	0.045712	0.085272	T	Study 1	CV125	112	1191
169	NC0112238	10	49.2	--	--	G	Study 5	--	394	1192
170	NC0173446	10	51.5	--	--	T	Study 5	--	1001	1193
170	NC0143388	10	51.6	0.028545	-0.06407	C	Study 1	CV082	139	1194
170	NC0143388	10	51.6	0.024809	-0.0276	T	Study 1	CV072	139	1194
170	NC0008840	10	52.1	--	--	G	Study 4	--	109	1195
170	NC0009350	10	53	0.002196	0.054987	T	Study 1	CV054	176	1196
170	NC0043776	10	53	0.000066	-0.02352	A	Study 1	CV044	74	1197
170	NC0111673	10	53	--	--	G	Study 4	--	309	1198
170	NC0111673	10	53	0.006019	-0.12385	G	Study 1	CV067	309	1198
170	NC0111673	10	53	0.00611	0.053924	G	Study 1	--	309	1198
170	NC0111673	10	53	0.000422	-0.16263	G	Study 1	CV067	309	1198
170	NC0111673	10	53	0.048729	0.176623	G	Study 1	CV127	309	1198

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
170	NC0111673	10	53	0.00581	-0.11679	A	Study 1	CV045	309	1198
170	NC0111673	10	53	0.000008	0.02637	G	Study 1	--	309	1198
170	NC0111673	10	53	0.033334	-0.01682	G	Study 1	CV041	309	1198
170	NC0009755	10	54.2	7.86E-05	-0.11882	G	Study 2	--	301	1199
170	NC0009755	10	54.2	--	--	T	Study 4	--	301	1199
170	NC0002285	10	55.4	0	0.154347	C	Study 1	CV128	313	1200
170	NC0104512	10	57.3	0	-0.04054	A	Study 1	CV021	79	1201
170	NC0003206	10	58.6	--	--	T	Study 5	--	255	1202
170	NC0003206	10	58.6	0.035917	0.020828	T	Study 1	CV152	255	1202
170	NC0003206	10	58.6	0.040862	0.178928	C	Study 1	CV132	255	1202
170	NC0003206	10	58.6	0.013859	0.070134	C	Study 1	CV050	255	1202
170	NC0003206	10	58.6	0.00553	0.014062	C	Study 1	--	255	1202
170	NC0003206	10	58.6	0.01593	0.019689	T	Study 1	CV069	255	1202
170	NC0003640	10	58.9	0.004994	0.012786	G	Study 1	--	442	1203
170	NC0003640	10	58.9	0.000024	0.023838	G	Study 1	--	442	1203
171	NC0009295	10	61.3	0.016139	0.338361	C	Study 1	CV167	133	1204
171	NC0009295	10	61.3	0.008475	0.024706	C	Study 1	CV062	133	1204
171	NC0009295	10	61.3	0	0.041387	C	Study 1	CV161	133	1204
171	NC0009295	10	61.3	0.036642	0.198994	T	Study 1	CV130	133	1204
171	NC0109090	10	61.5	0	-0.04057	*******	Study 1	CV021	336	1205
171	NC0016730	10	63.8	0.016274	-0.01773	A	Study 1	CV039	295	1206
171	NC0016730	10	63.8	0	0.149203	G	Study 1	CV128	295	1206
171	NC0016730	10	63.8	0.000197	-0.02209	A	Study 1	CV044	295	1206
171	NC0016730	10	63.8	0.038286	0.155499	A	Study 1	CV163	295	1206
171	NC0016730	10	63.8	0.020295	0.011831	A	Study 1	--	295	1206
171	NC0016730	10	63.8	0.014176	-0.01817	A	Study 1	CV041	295	1206
171	NC0107941	10	64.3	0.025811	-0.09519	A	Study 1	CV067	351	1207
171	NC0107941	10	64.3	0.003695	-0.13107	A	Study 1	CV067	351	1207
171	NC0112090	10	64.8	0.002772	0.059675	G	Study 1	--	480	1208
171	NC0173818	10	65.3	--	--	T	Study 5	--	747	1209
171	NC0011002	10	66.5	0.000389	-0.10466	A	Study 2	--	159	1210
171	NC0011002	10	66.5	--	--	C	Study 5	--	159	1210
171	NC0011002	10	66.5	0.001122	0.019282	A	Study 1	I283669	159	1210

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
172	NC0018392	10	71.5	0.036847	0.18367	T	Study 1	CV127	353	1211
172	NC0018392	10	71.5	0.002086	0.224949	T	Study 1	CV149	353	1211
172	NC0018392	10	71.5	0.005984	0.022022	T	Study 1	CV156	353	1211
172	NC0018392	10	71.5	0.000165	0.030878	T	Study 1	CV161	353	1211
172	NC0018392	10	71.5	0.023295	-0.0967	C	Study 1	CV045	353	1211
172	NC0018392	10	71.5	0.020925	-0.13661	C	Study 1	I294213	353	1211
172	NC0018392	10	71.5	0.000118	0.021301	T	Study 1	--	353	1211
172	NC0018392	10	71.5	0.00475	0.012425	T	Study 1	--	353	1211
172	NC0027447	10	75.6	--	--	G	Study 4	--	311	1212
172	NC0027447	10	75.6	0.00166	-0.18528	C	Study 1	I294213	311	1212
172	NC0027447	10	75.6	0.001821	0.01605	G	Study 1	--	311	1212
172	NC0081776	10	75.8	--	--	T	Study 4	--	136	1213
172	NC0013745	10	79	--	--	G	Study 4	--	52	1214
172	NC0030134	10	79.4	0.021242	0.008538	********	Study 1	CV151	94	1215
172	NC0030134	10	79.4	0.016376	-0.01718	********	Study 1	CV072	94	1215
172	NC0030134	10	79.4	0.003321	0.014494	TCCACTAT	Study 1	--	94	1215
173	NC0011115	10	90	0.028513	0.021923	A	Study 1	CV152	255	1216
173	NC0011115	10	90	0.000683	0.021738	G	Study 1	I283669	255	1216
173	NC0011115	10	90	0.029383	-0.06381	A	Study 1	CV082	255	1216
173	NC0011115	10	90	0.023698	0.25759	G	Study 1	CV124	255	1216
173	NC0011115	10	90	0.009069	0.179929	G	Study 1	CV149	255	1216
173	NC0011115	10	90	0.021147	0.019239	G	Study 1	CV161	255	1216
173	NC0011115	10	90	0.038035	-0.00604	A	Study 1	CV115	255	1216
173	NC0070905	10	92.1	0.00763	-0.08478	G	Study 2	--	100	1217
173	NC0070905	10	92.1	0.02693	0.212149	G	Study 1	CV130	100	1217
173	NC0067173	10	98	<.0001	-0.20298	G	Study 3	--	344	1218
173	NC0067173	10	98	0.009913	0.04922	G	Study 1	--	344	1218
173	NC0067173	10	98	0.006206	-0.0166	T	Study 1	CV044	344	1218
173	NC0067173	10	98	0.005596	0.003947	T	Study 1	CV016	344	1218
173	NC0067173	10	98	0.005596	0.003947	T	Study 1	CV016	344	1218
173	NC0199588	10	99.9	--	--	G	Study 5	--	137	1219
174	NC0154948	10	102.2	0.009826	-0.01817	**	Study 1	CV021	234	1220
174	NC0154948	10	102.2	0.022216	0.012246	**	Study 1	--	234	1220

FIGURE 1

QTL	Marker	Chr	pos	sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
174	NC0009486	10	105.5	--	--	T	Study 4	--	225	1221
174	NC0009486	10	105.5	0.018159	0.10096	T	Study 1	CV125	225	1221
174	NC0009486	10	105.5	0.01377	0.103638	T	Study 1	CV166	225	1221
174	NC0009486	10	105.5	0.040711	0.229851	T	Study 1	CV124	225	1221
174	NC0009486	10	105.5	0.028	0.025059	A	Study 1	CV154	225	1221
175	NC0008954	10	112	0.01365	0.201778	C	Study 1	CV130	345	1222
175	NC0008954	10	112	0.016656	0.013513	T	Study 1	CV159	345	1222
175	NC0008954	10	112	0.045066	0.01331	T	Study 1	CV014	345	1222
175	NC0107333	10	113.1	--	--	T	Study 4	--	174	1223
175	NC0107333	10	113.1	0.039133	0.020108	C	Study 1	CV152	174	1223
175	NC0107333	10	113.1	0.032419	-0.01396	T	Study 1	CV047	174	1223
175	NC0109666	10	113.1	0.027106	0.012937	G	Study 1	CV159	75	1224
175	NC0151488	10	114.6	0.031284	0.078602	T	Study 1	CV079	202	1225
175	NC0151488	10	114.6	0.008	0.108134	T	Study 1	CV079	202	1225
175	NC0008643	10	119.1	--	--	G	Study 4	--	281	1226
175	NC0008643	10	119.1	0.049834	0.178784	A	Study 1	CV109	281	1226
175	NC0008643	10	119.1	0.046602	0.082561	G	Study 1	CV093	281	1226
175	NC0008643	10	119.1	0.00478	0.12034	G	Study 1	CV125	281	1226
175	NC0008643	10	119.1	0.038793	-0.10742	A	Study 1	CV112	281	1226
175	NC0008643	10	119.1	0.049885	-0.10595	A	Study 1	CV119	281	1226
175	NC0008643	10	119.1	0.012644	0.01204	G	Study 1	CV069	281	1226
175	NC0008643	10	119.1	0.031391	0.006145	A	Study 1	CV109	281	1226
176	NC0111488	10	123.3	0.008636	-0.01341	A	Study 1	CV136	258	1227

FIGURE 1

Figure 2. Markers associated with resistance to Goss' Wilt. "*" represents a single nucleotide deletion.

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
1	NC0154927	1	18.5	0.04686	0.009544	C	Study 1	CV012	350	13
2	NC0001369	1	24.3	0.010408	0.011109	G	Study 1	CV012	148	1234
2	NC0110473	1	24.6	0.0006	0.108612	T	Study 2	--	194	19
3	NC0003563	1	34.5	2.95E-05	0.269505	G	Study 3	--	434	27
4	NC0052741	1	49.5	0.011696	0.085539	G	Study 3	--	411	36
5	NC0113502	1	63.5	0.001533	0.221549	G	Study 3	--	447	50
5	NC0039840	1	65.8	<.0001	0.154467	G	Study 2	--	82	53
6	NC0025863	1	96.7	0.013297	-0.00703	G	Study 1	CV085	107	90
7	NC0016873	1	101	0.024053	0.013666	G	Study 4	--	35	94
7	NC0015205	1	101.5	0.00982	-0.01944	G	Study 1	CV085	401	95
7	NC0011522	1	103.1	0.001129	0.006155	C	Study 4	--	250	97
7	NC0005280	1	103.2	0.000227	-0.04657	C	Study 4	--	141	1235
7	NC0053351	1	103.3	0.019659	-0.00398	A	Study 4	--	235	1236
7	NC0027375	1	103.7	0.005067	0.0095	C	Study 4	--	474	99
7	NC0038741	1	103.7	0.016397	0.151215	G	Study 3	--	239	101
7	NC0066981	1	103.7	0.002375	-0.04438	A	Study 4	--	147	102
7	NC0069188	1	103.7	0.00252	-0.00778	C	Study 4	--	145	1237
7	NC0008984	1	105.5	0.003146	-0.05495	C	Study 4	--	376	106
7	NC0039416	1	105.9	0.007911	0	--	Study 4	--	530	1238
7	NC0041836	1	107.7	0.000879	0.035135	*	Study 4	--	92	110
7	NC0014644	1	107.8	0.011101	-0.01058	C	Study 4	--	485	111
7	NC0037068	1	108.3	0.011592	0	--	Study 4	--	164	1239
7	NC0037068	1	108.3	0.039253	-0.00601	*********	Study 1	CV085	164	1239
8	NC0113263	1	110.1	0.005381	0.054854	G	Study 4	--	216	1240
8	NC0033728	1	113.3	0.003777	-0.0342	A	Study 4	--	83	119
8	NC0002688	1	114.6	<.0001	-0.29232	C	Study 2	--	69	121
8	NC0004176	1	116.3	0.00019	0.073238	C	Study 4	--	61	122
8	NC0039351	1	118.8	0.000128	-0.045	A	Study 4	--	678	124
8	NC0039351	1	118.8	0.015782	0.077241	G	Study 3	--	678	124
9	NC0035132	1	121.5	0.022545	-0.11069	GAGAG	Study 4	--	394	128
9	NC0035132	1	121.5	0.006728	-0.00789	*****	Study 1	CV085	394	128
9	NC0034627	1	126	0.000266	0.232974	C	Study 3	--	415	130

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
9	NC0035547	1	126	0.017288	0.040442	T	Study 4	--	190	131
9	NC0039531	1	126	0.00037	0.114735	G	Study 4	--	215	132
10	NC0107077	1	130.7	0.017758	-0.01797	A	Study 1	CV085	380	136
10	NC0107077	1	130.7	0.002565	-0.0087	A	Study 1	CV085	380	136
10	NC0008719	1	137.1	0.027094	-0.0514	A	Study 4	--	244	138
10	NC0008719	1	137.1	0.003405	-0.02195	A	Study 1	CV085	244	138
10	NC0008719	1	137.1	0.032113	-0.00605	A	Study 1	CV085	244	138
11	NC0024096	1	145.2	5.51E-05	0.254406	T	Study 3	--	212	141
11	NC0024096	1	145.2	0.012609	-0.01848	G	Study 1	CV085	212	141
11	NC0024096	1	145.2	0.004333	-0.01243	G	Study 1	CV010	212	141
11	NC0024096	1	145.2	0.006585	-0.00764	G	Study 1	CV085	212	141
12	NC0107621	1	153.5	4.36E-05	0.242328	*******	Study 3	--	366	146
13	NC0041280	1	161.4	0	-0.02301	C	Study 1	CV010	223	153
13	NC0041280	1	161.4	0.007487	-0.02045	C	Study 1	CV085	223	153
13	NC0041280	1	161.4	0.002759	-0.00882	C	Study 1	CV085	223	153
13	NC0042754	1	164	0.028177	0.04742	T	Study 4	--	76	1241
13	NC0021568	1	167.1	0	-0.02336	C	Study 1	CV010	90	159
13	NC0070702	1	167.1	0.009394	-0.08811	C	Study 4	--	1001	160
13	NC0009626	1	169.6	0	-0.02442	C	Study 1	CV010	236	162
14	NC0105648	1	172.2	0.03034	-0.00643	C	Study 1	CV085	264	164
14	NC0067728	1	173.7	0	-0.02632	T	Study 1	CV010	218	166
14	NC0069344	1	176.9	0	-0.02588	A	Study 1	CV010	206	169
14	NC0027567	1	179.4	9.27E-05	0.242128	G	Study 3	--	79	172
15	NC0004909	1	182.1	0	-0.02769	A	Study 1	CV010	324	175
15	NC0004909	1	182.1	0.022324	0.02151	A	Study 1	LH287	324	175
15	NC0005098	1	183.9	0	-0.02729	A	Study 1	CV010	133	177
16	NC0016674	1	202.2	0.0004	-0.15049	A	Study 2	--	154	1242
16	NC0013584	1	204.4	0.035163	-0.06693	C	Study 1	CV120	304	186
16	NC0013584	1	204.4	0.004577	0.027157	T	Study 1	LH287	304	186
17	NC0015344	1	221.1	<.0001	0.123021	G	Study 2	--	420	200
18	NC0146570	1	237	0.003453	0.018264	T	Study 1	CV121	232	202
18	NC0110139	1	237.2	0.013037	0.02569	T	Study 4	--	224	203
19	NC0013490	1	240.7	0.003666	0.018036	T	Study 1	CV121	482	207

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
19	NC0030840	1	245.1	0.004279	0.018013	A	Study 1	CV121	413	208
20	NC0016137	1	256.3	0.032379	0.013563	C	Study 1	CV121	482	1243
21	NC0015766	2	7	0.002324	0.020948	G	Study 4	--	360	215
22	NC0009766	2	10.1	0.037837	0.04816	T	Study 4	--	328	216
22	NC0033786	2	15.2	0.021898	-0.02638	A	Study 4	--	108	1244
22	NC0106678	2	18.3	0.000271	0.116208	G	Study 1	LH287	309	220
22	NC0106678	2	18.3	0.000271	0.116208	G	Study 1	LH287	309	220
23	NC0002814	2	27.9	0.000001	0.155237	C	Study 1	LH287	92	224
24	NC0002616	2	34	0.016239	0.074511	C	Study 1	LH287	53	228
24	NC0009706	2	35.9	0.014254	0.007758	G	Study 1	LH287	269	231
25	NC0107479	2	42.3	0.006131	0.08519	A	Study 1	LH287	195	232
25	NC0109140	2	44.8	0.016804	-0.01645	TAAA	Study 1	CV085	578	233
25	NC0048553	2	46.8	0.004592	0.008892	A	Study 1	LH287	485	234
25	NC0048553	2	46.8	0.000006	0.142232	A	Study 1	LH287	485	234
25	NC0048553	2	46.8	0.000006	0.142232	A	Study 1	LH287	485	234
25	NC0078243	2	48.8	0.028571	0.097888	G	Study 4	--	229	235
25	NC0078243	2	48.8	0.003324	-0.01908	G	Study 1	CV085	229	235
26	NC0020105	2	64.6	0.00941	-0.01685	A	Study 1	CV085	55	244
26	NC0020105	2	64.6	0.037454	0.019556	G	Study 1	LH287	55	244
26	NC0080705	2	68.5	0.005854	0.00884	G	Study 1	LH287	281	248
26	NC0080705	2	68.5	0.022582	0.071256	G	Study 1	LH287	281	248
26	NC0080705	2	68.5	0.000096	0.1266	G	Study 1	LH287	281	248
27	NC0032200	2	71.6	0.016486	0.022504	C	Study 1	LH287	318	250
27	NC0004697	2	74.8	<.0001	0.304299	G	Study 2	--	175	252
27	NC0042242	2	77	0.003374	0.097205	T	Study 1	LH287	75	256
27	NC0015022	2	77.3	0.004176	-0.04752	A	Study 4	--	143	257
27	NC0035381	2	79.6	0.024821	0.007253	T	Study 1	LH287	80	260
28	NC0105002	2	88.6	0.048425	-0.04207	C	Study 4	--	167	265
28	NC0108493	2	88.6	<.0001	-0.17752	A	Study 2	--	304	266
28	NC0146518	2	89.4	0.003188	0.009437	G	Study 1	LH287	97	267
29	NC0053463	2	93.1	0.031181	-0.05564	A	Study 4	--	461	271
29	NC0021092	2	93.4	0.01458	-0.07801	A	Study 4	--	94	273
29	NC0021092	2	93.4	<.0001	-0.23525	A	Study 2	--	94	273

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
29	NC0021405	2	93.4	0.0021	0.184068	G	Study 2	--	162	1245
29	NC0057604	2	94	0.012688	-0.07582	CAGG	Study 4	--	412	274
29	NC0105696	2	94.3	0.02062	0.071815	T	Study 4	--	149	278
29	NC0146130	2	94.6	0.004449	0.091703	G	Study 4	--	96	279
29	NC0032601	2	94.9	0.004916	-0.01262	T	Study 1	CV010	144	282
29	NC0108305	2	97.9	0.002427	0.113785	G	Study 4	--	174	287
29	NC0107911	2	99.2	0.003188	0.009437	T	Study 1	LH287	384	289
29	NC0107911	2	99.2	0.017596	0.022946	T	Study 1	LH287	384	289
29	NC0107911	2	99.2	0.018178	0.077377	T	Study 1	LH287	384	289
29	NC0107911	2	99.2	0.018178	0.077377	T	Study 1	LH287	384	289
30	NC0108607	2	102.1	0.023127	-0.00991	C	Study 1	CV010	562	294
30	NC0153941	2	102.1	0.015176	0.023873	CTT	Study 1	LH287	1176	295
30	NC0053097	2	102.6	0.004803	0.080678	T	Study 4	--	335	296
30	NC0057210	2	104.1	0.013072	-0.01105	C	Study 1	CV010	191	299
31	NC0084632	2	124.1	<.0001	-0.2503	C	Study 2	--	206	1246
31	NC0109393	2	127.1	0.021202	-0.07794	A	Study 3	--	323	317
31	NC0040472	2	128.8	0.023017	-0.00642	C	Study 1	CV085	102	320
32	NC0031474	2	141.4	0.012787	-0.00693	A	Study 1	CV085	842	332
32	NC0031474	2	141.4	0.041884	0.006559	A	Study 1	LH287	842	332
32	NC0002878	2	145.1	0.000253	-0.05653	A	Study 4	--	286	333
32	NC0005088	2	147.6	0.010516	-0.08747	C	Study 3	--	110	334
32	NC0005088	2	147.6	0.047321	0.040916	T	Study 4	--	110	334
33	NC0035297	2	150.7	6.69E-05	-0.0763	A	Study 4	--	207	337
33	NC0035297	2	150.7	0.0203	0.007441	G	Study 1	LH287	207	337
34	NC0014467	2	167.3	0.022787	-0.07608	AT	Study 3	--	366	347
34	NC0014467	2	167.3	0.006993	-0.01788	AT	Study 1	CV085	366	347
35	NC0110974	2	185.5	0.02837	-0.01488	T	Study 1	CV085	522	355
36	NC0106389	3	14.2	0.03523	0.006226	A	Study 1	CV012	207	362
36	NC0008911	3	19.9	0.001193	0.103961	G	Study 1	LH287	205	363
37	NC0104528	3	24.6	0.006011	0.008258	G	Study 1	CV012	117	1247
38	NC0048700	3	31.3	0.006464	-0.00633	A	Study 1	CV012	85	366
38	NC0048700	3	31.3	0.004943	0.091568	T	Study 1	LH287	85	366
39	NC0032137	3	40.2	0.012587	0.07729	*	Study 3	--	216	367

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
40	NC0106329	3	53.9	0.025915	0.078684	G	Study 3	--	91	370
40	NC0106329	3	53.9	0.005581	0.028641	G	Study 1	LH287	91	370
40	NC0106329	3	53.9	0.048034	0.064481	G	Study 1	LH287	91	370
41	NC0105291	3	83.2	<.0001	0.346974	T	Study 2	--	294	381
41	NC0106515	3	83.2	0.000943	0.03265	G	Study 1	LH287	184	382
41	NC0106515	3	83.2	<.0001	-0.13382	G	Study 2	--	184	382
41	NC0009468	3	88	0.007021	-0.10812	A	Study 4	--	102	392
41	NC0031647	3	89.5	0.042292	-0.1009	C	Study 4	--	899	395
42	NC0009739	3	102.2	0.004016	-0.18037	A	Study 3	--	284	409
42	NC0104504	3	104	0.0006	0.122768	G	Study 2	--	406	411
42	NC0013092	3	105.4	0.0013	-0.13783	A	Study 2	--	369	412
43	NC0155775	3	111.4	0.032869	0.001744	G	Study 4	--	162	419
43	NC0024395	3	116	0.017221	-0.01632	C	Study 1	CV085	75	422
43	NC0079081	3	117.1	0.008699	0.02747	A	Study 1	LH287	78	423
44	NC0002905	3	123.9	0.018776	-0.01573	A	Study 1	CV085	98	429
44	NC0009173	3	124.2	0.000505	0.120634	C	Study 4	--	101	430
44	NC0008922	3	128.2	0.028726	-0.08618	A	Study 4	--	271	433
45	NC0034494	3	141	0.008473	-0.16454	A	Study 3	--	524	438
45	NC0041040	3	145.4	0.0005	-0.12023	A	Study 2	--	497	440
45	NC0036694	3	148.1	<.0001	-0.14922	C	Study 2	--	180	1248
45	NC0110128	3	149.5	0.030386	0.021434	A	Study 1	LH287	217	447
46	NC0028736	3	152.7	<.0001	0.183625	G	Study 2	--	371	1249
47	NC0112491	3	182.9	0.019854	0.007439	G	Study 1	LH287	90	474
47	NC0146534	3	183.6	0.017851	-0.13867	C	Study 4	--	91	476
47	NC0146497	3	187.4	0.0007	-0.31952	A	Study 2	--	98	479
47	NC0155987	3	187.4	0.0014	-0.29056	C	Study 2	--	1001	480
47	NC0155987	3	187.4	0.03179	0.123743	T	Study 4	--	1001	480
47	NC0143969	3	187.5	0.028218	-0.11886	TA	Study 4	--	100	482
47	NC0143969	3	187.5	0.041455	0.063097	TA	Study 1	LH287	100	482
48	NC0010232	3	198.7	0.021444	0.013076	T	Study 1	CV112	353	486
49	NC0003970	3	208	0.004606	0.087194	A	Study 1	LH287	355	490
50	NC0014041	3	217.6	0.033595	0.134315	C	Study 3	--	244	493
51	NC0002739	4	11.8	0.027467	0.020664	C	Study 1	LH287	126	500

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
52	NC0034462	4	67.8	<.0001	0.285633	T	Study 2	--	301	1250
52	NC0010305	4	68.4	0.033523	0.021092	A	Study 1	LH287	228	525
52	NC0033483	4	69.5	<.0001	-0.16104	C	Study 2	--	163	530
53	NC0108120	4	71.5	<.0001	0.34256	T	Study 2	--	401	533
54	NC0027345	4	82.5	0.0295	0	--	Study 4	--	237	556
54	NC0111228	4	87.9	<.0001	-0.23052	A	Study 2	--	130	566
55	NC0077408	4	104.3	<.0001	0.26398	C	Study 2	--	294	582
55	NC0003274	4	104.7	<.0001	-0.20119	A	Study 2	--	269	585
55	NC0009280	4	104.7	<.0001	-0.36808	GCA	Study 2	--	105	1251
56	NC0110078	4	115.7	0.000557	-0.01966	C	Study 1	CV103	99	589
57	NC0156263	4	121	0.036532	0.035766	T	Study 4	--	338	593
57	NC0156267	4	121	0.02004	0.044271	T	Study 4	--	321	594
58	NC0071158	4	136.7	0.017298	-0.00696	T	Study 1	CV085	775	611
58	NC0071158	4	136.7	0.04735	-0.00629	G	Study 1	CV012	775	611
59	NC0028162	4	141.5	0.023562	-0.01486	C	Study 1	CV085	313	1252
59	NC0038447	4	141.8	0.000145	-0.2403	A	Study 3	--	526	618
59	NC0009491	4	144.6	0.045352	-0.00575	A	Study 1	CV085	236	621
59	NC0020933	4	147.5	0.0002	0.124182	T	Study 2	--	373	623
60	NC0034250	4	156.3	0.02512	-0.00638	G	Study 1	CV085	70	630
60	NC0051079	4	156.4	0.031861	-0.02094	G	Study 1	CV056	137	632
60	NC0037601	4	162.2	0.040958	-0.00658	G	Study 1	CV012	478	637
60	NC0037601	4	162.2	0.032058	-0.00565	G	Study 1	CV012	478	637
60	NC0110455	4	169.4	<.0001	0.557365	T	Study 2	--	207	639
61	NC0009066	4	181	0.03472	-0.13203	C	Study 3	--	238	646
61	NC0148181	4	183	0.016474	0	--	Study 4	--	1001	649
61	NC0043794	4	186.2	0.01927	-0.02185	G	Study 4	--	197	650
62	NC0024265	5	1.8	0.010069	-0.07556	A	Study 1	CV120	137	657
63	NC0069592	5	14.8	0.008399	-0.07734	AT	Study 1	CV120	439	665
63	NC0069592	5	14.8	0.000277	-0.00855	AT	Study 1	CV012	439	665
64	NC0011193	5	29.3	0.006766	0.090706	T	Study 3	--	82	669
64	NC0011193	5	29.3	0.004857	0.007911	T	Study 1	CV012	82	669
64	NC0011193	5	29.3	0.002346	0.013382	T	Study 1	CV012	82	669
65	NC0153131	5	34.4	0.00531	-0.00669	A	Study 1	CV012	121	1253

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
66	NC0109403	5	46.7	0.0002	-0.11371	TTC	Study 2	--	523	678
66	NC0020401	5	48	0.003351	0.097653	T	Study 3	--	175	1254
66	NC0016527	5	49	0.000006	0.01988	T	Study 1	CV012	351	1255
67	NC0037588	5	60.1	0.000154	0.230456	*****	Study 3	--	188	679
67	NC0009668	5	65.2	0	0.023591	G	Study 1	CV012	107	688
67	NC0111398	5	67.7	0	0.025687	T	Study 1	CV012	171	690
68	NC0109411	5	71.9	0.020418	0.007501	C	Study 1	CV012	114	1256
68	NC0004605	5	78.5	0.005653	-0.07337	C	Study 4	--	74	704
68	NC0146415	5	79.8	0.017437	0.039447	G	Study 4	--	336	709
69	NC0077644	5	80.4	0.013126	0.007991	A	Study 1	CV012	255	710
69	NC0077644	5	80.4	0	0.025703	A	Study 1	CV012	255	710
69	NC0078535	5	83.9	6.55E-05	-0.15465	A	Study 4	--	104	717
69	NC0035956	5	85.1	0.014	0.103388	C	Study 4	--	246	719
69	NC0154498	5	85.2	0.003588	-0.10151	C	Study 4	--	84	720
69	NC0145634	5	85.4	0.013404	0.083897	T	Study 4	--	346	1257
69	NC0040571	5	88.4	0.032454	-0.07295	C	Study 3	--	154	721
69	NC0040571	5	88.4	0.015832	0.007538	G	Study 1	CV012	154	721
69	NC0040571	5	88.4	0.000001	0.021889	G	Study 1	CV012	154	721
70	NC0111999	5	96.9	0.000695	0.015356	G	Study 1	CV012	587	726
70	NC0018153	5	97	0.0012	0.122587	G	Study 2	--	573	727
70	NC0033305	5	98.9	0.017419	0.006966	CGTG	Study 1	CV012	173	1258
71	NC0017678	5	103.8	0.03668	-0.00762	A	Study 4	--	171	733
71	NC0009297	5	104.1	0.014897	0.011512	A	Study 1	CV012	114	734
72	NC0009434	5	125.2	0.000919	0.10147	G	Study 1	LH287	123	746
73	NC0036210	5	145.2	0.004297	0.028276	T	Study 1	LH287	43	758
73	NC0036210	5	145.2	0.01061	0.078681	T	Study 1	LH287	43	758
73	NC0143380	5	148.1	0.042413	0.140185	G	Study 3	--	324	760
74	NC0104717	5	171.2	0.005668	0.087309	T	Study 1	LH287	298	764
74	NC0012417	5	175.2	0.038749	-0.07645	G	Study 4	--	137	768
75	NC0031084	5	181.5	0.024558	0.140101	G	Study 3	--	53	773
75	NC0031084	5	181.5	0.000669	0.101517	G	Study 1	LH287	53	773
75	NC0031084	5	181.5	<.0001	0.138642	G	Study 2	--	53	773
76	NC0003284	6	36.4	0.000001	0.02288	C	Study 1	CV012	439	1259

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
76	NC0003210	6	38.4	0.03556	-0.00501	C	Study 1	CV012	117	792
76	NC0025657	6	38.4	0.000027	0.019043	C	Study 1	CV012	250	793
76	NC0000439	6	39.9	0.000175	0.016391	T	Study 1	CV012	235	812
77	NC0038040	6	52.1	0.003368	-0.09931	A	Study 4	--	382	821
77	NC0004463	6	56.5	0.022561	-0.02048	C	Study 1	CV056	263	825
78	NC0148039	6	70.2	0.003442	-0.00793	T	Study 1	CV085	76	835
78	NC0148039	6	70.2	0.041391	0.004797	T	Study 1	LH287	76	835
78	NC0003726	6	78.5	0.044783	-0.01995	G	Study 1	CV056	69	1260
78	NC0082021	6	79.6	<.0001	0.191138	******	Study 2	--	375	844
79	NC0066737	6	81.9	0.0002	-0.16091	A	Study 2	--	281	846
79	NC0113381	6	83.8	0.016963	0.005846	G	Study 1	LH287	303	850
79	NC0040364	6	85.5	<.0001	-0.19557	A	Study 2	--	258	854
80	NC0019772	6	92.4	0.021285	-0.00692	T	Study 1	CV085	323	856
80	NC0110972	6	93.2	3.81E-05	0.078619	G	Study 4	--	49	857
80	NC0110972	6	93.2	0.0003	0.122193	G	Study 2	--	49	857
80	NC0019588	6	96.7	0.0007	0.104198	T	Study 2	--	361	858
80	NC0019588	6	96.7	0.019767	-0.00712	T	Study 1	CV085	361	858
80	NC0019588	6	96.7	0.004282	0.006776	T	Study 1	LH287	361	858
81	NC0081445	6	101.8	0.040744	0.011875	C	Study 1	CV112	198	1261
82	NC0023358	6	120.8	0.038628	0.014067	C	Study 1	CV121	177	874
83	NC0028185	6	130.1	0.000992	0.112587	G	Study 3	--	523	876
83	NC0032509	6	132.9	0.038095	0.006632	A	Study 1	LH287	334	880
83	NC0053636	6	136	0.0001	0.161557	G	Study 2	--	202	882
84	NC0032370	6	144.3	0.017401	0.007586	G	Study 1	LH287	929	885
85	NC0143514	7	29	0.029234	-0.00522	G	Study 1	CV012	595	893
86	NC0003924	7	43.9	0.007199	-0.00646	G	Study 1	CV012	412	897
87	NC0070341	7	51.3	0.034908	-0.00647	C	Study 4	--	741	1262
88	NC0030511	7	62.8	0.001613	-0.00768	C	Study 1	CV012	352	915
88	NC0009073	7	65.9	0.04446	0.118303	**	Study 4	--	191	926
89	NC0145922	7	80.5	0.046336	-0.00473	A	Study 1	CV012	451	940
89	NC0048425	7	88.3	0.042943	-0.06241	T	Study 1	CV120	484	942
90	NC0009240	7	98.5	0.033051	-0.00692	A	Study 1	CV012	379	949
91	NC0016008	7	104.6	0.040964	-0.00658	C	Study 1	CV012	133	957

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
91	NC0040335	7	107	0.044944	-0.00644	A	Study 1	CV012	407	963
92	NC0009674	7	112.1	0.018441	-0.04635	A	Study 4	--	150	964
93	NC0004953	7	131.2	0.023377	0.145395	T	Study 3	--	154	974
94	NC0030970	7	147.7	0.02528	-0.00717	CTG	Study 1	CV012	351	1263
95	NC0155475	7	154.2	0.037533	-0.06182	T	Study 1	CV120	77	981
95	NC0155475	7	154.2	0.023125	-0.00725	T	Study 1	CV012	77	981
96	NC0151568	7	161.1	0.013098	-0.07203	C	Study 1	CV120	515	983
96	NC0038499	7	169.3	0.028951	0.13796	G	Study 3	--	597	990
97	NC0024672	8	33.6	0.011764	0.014419	A	Study 1	CV112	134	997
97	NC0019198	8	38.1	0.002	-0.11075	C	Study 2	--	316	999
97	NC0038724	8	39.6	0.000847	0.105206	C	Study 3	--	312	1000
98	NC0104862	8	70	0.003924	0.092608	T	Study 3	--	321	1016
98	NC0020099	8	70.5	0.0002	-0.18265	C	Study 2	--	379	1264
99	NC0077568	8	84	<.0001	-0.17866	A	Study 2	--	245	1027
99	NC0110378	8	85.5	0.00803	0.092386	********	Study 3	--	300	1265
100	NC0058047	8	96.1	<.0001	-0.2066	A	Study 2	--	158	1043
101	NC0105835	8	104	0.00689	0.086467	T	Study 3	--	275	1049
102	NC0010392	8	115.4	<.0001	-0.24695	A	Study 2	--	496	1053
102	NC0012656	8	115.6	<.0001	-0.31542	A	Study 2	--	156	1054
102	NC0008831	8	116.3	0.0016	-0.133	G	Study 2	--	206	1056
103	NC0008757	8	156.3	0.01196	-0.07309	C	Study 4	--	274	1075
103	NC0008757	8	156.3	0.044648	-0.12298	C	Study 3	--	274	1075
104	NC0030508	9	8.3	0.0005	-0.10566	A	Study 2	--	885	1266
104	NC0054684	9	8.3	0.037993	-0.00909	G	Study 1	CV010	467	1081
105	NC0049557	9	25.7	0.0002	-0.21727	A	Study 2	--	464	1087
106	NC0012830	9	33.1	0.027936	-0.00966	A	Study 1	CV010	334	1088
106	NC0012830	9	33.1	0.00807	0.023919	A	Study 1	LH287	334	1088
106	NC0012830	9	33.1	0.00367	0.08419	A	Study 1	LH287	334	1088
107	NC0028095	9	59.4	0.00328	-0.04071	C	Study 4	--	116	1098
108	NC0010643	9	60.6	0.048151	0.124326	G	Study 4	--	184	1099
108	NC0055759	9	62.1	0.000377	0.031296	T	Study 1	LH287	149	1100
108	NC0144042	9	66.5	<.0001	-0.2038	A	Study 2	--	130	1104
108	NC0004407	9	67.2	0.044305	0	--	Study 4	--	49	1105

FIGURE 2

QTL	Marker	Chr	pos	Sig	effect	res allele	Mapping Study	Fav. Parent	SNP Position	SEQ ID
108	NC0106791	9	68.5	0.045643	-0.02074	C	Study 4	--	181	1108
108	NC0106791	9	68.5	<.0001	-0.2186	C	Study 2	--	181	1108
108	NC0110377	9	68.5	0.00518	0.055632	T	Study 4	--	538	1110
109	NC0148696	9	73.2	0.000779	0.030165	G	Study 1	LH287	140	1267
109	NC0020048	9	77.5	0.008116	0	--	Study 4	--	414	1115
110	NC0002383	9	83.3	0.002997	0.090942	G	Study 1	LH287	63	1122
110	NC0155793	9	84.5	0.002037	0.006672	T	Study 4	--	129	1268
110	NC0004123	9	84.6	0.041266	0	--	Study 4	--	384	1131
110	NC0013086	9	87.3	0.002474	0.028263	A	Study 1	LH287	343	1133
111	NC0145318	9	91	0.024601	-0.01431	G	Study 1	CV085	451	1269
111	NC0106442	9	98.4	0.002316	-0.0415	A	Study 4	--	172	1142
112	NC0041196	9	101.5	0.007955	0.082532	G	Study 4	--	835	1143
112	NC0042348	9	101.8	0.006537	-0.11937	A	Study 4	--	103	1145
112	NC0042348	9	101.8	0.040352	0.063111	A	Study 1	LH287	103	1145
112	NC0018417	9	102.1	0.002743	0.05722	C	Study 4	--	287	1146
112	NC0066389	9	105.5	0.010793	0.024425	G	Study 1	LH287	161	1148
112	NC0066390	9	105.5	0.048326	-0.05953	A	Study 4	--	179	1149
113	NC0110800	9	117.7	0.0002	0.237955	G	Study 2	--	406	1270
114	NC0039475	9	122.7	0.04715	0.066292	T	Study 3	--	267	1159
115	NC0020088	10	8.6	0.021211	0.021323	GGAATAACT	Study 1	LH287	267	1168
116	NC0020502	10	30.3	0.036202	0.060641	G	Study 1	LH287	172	1174
116	NC0020502	10	30.3	0.036202	0.060641	G	Study 1	LH287	172	1174
117	NC0154801	10	40	0.038609	0.065008	G	Study 1	LH287	292	1271
117	NC0154801	10	40	0.038609	0.065008	G	Study 1	LH287	292	1271
117	NC0143762	10	46.7	0.0019	0.192606	G	Study 2	--	267	1184
117	NC0147718	10	47.3	0.0002	0.262006	T	Study 2	--	261	1186
118	NC0005020	10	52.9	<.0001	0.174463	T	Study 2	--	311	1272
118	NC0009350	10	53	0.021122	0.13106	T	Study 3	--	176	1196
119	NC0009295	10	61.3	0.025103	0.129629	T	Study 3	--	133	1204
120	NC0027447	10	75.6	0.011531	0.041696	G	Study 4	--	311	1212
120	NC0030134	10	79.4	<.0001	0.167583	********	Study 2	--	94	1215
121	NC0143657	10	103.5	0.046856	0.063738	C	Study 1	LH287	871	1273
121	NC0143657	10	103.5	0.046856	0.063738	C	Study 1	LH287	871	1273

FIGURE 2

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2008/074760

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, EMBASE, BIOSIS, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LIU Z ET AL: "Mapping PrBn and other quantitative trait loci responsible for the control of homeologous chromosome pairing in oilseed rape (Brassica napus L.) haploids" GENETICS 2006 US, vol. 174, no. 3, 2006, pages 1583-1596, XP002508656 ISSN: 0016-6731 0016-6731	1,2,11, 12, 20-23, 75,77,78
Y	the whole document page 1584, column 1 page 1585, column 1, last paragraph ----- -/--	3-10, 13-19, 76,79-81

☒ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

2 February 2009

Date of mailing of the international search report

06/07/2009

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Sauer, Tincuta

C(Continuation). **DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	COLIN HIEBERT ET AL: "Locating the broad-spectrum wheat leaf rust resistance gene Lr52 (LrW) to chromosome 5B by a new cytogenetic method" THEORETICAL AND APPLIED GENETICS ; INTERNATIONAL JOURNAL OF PLANT BREEDING RESEARCH, SPRINGER, BERLIN, DE, vol. 110, no. 8, 1 May 2005 (2005-05-01), pages 1453-1457, XP019321928 ISSN: 1432-2242	1,11,12, 20-23, 75,78
Y	the whole document page 1454, column 1 figure 2 -----	2-10, 13-19, 76,77, 79-81
X	CHEBOTAR O D ET AL: "The use of maternal haploids for genetic analysis of the number of kernel rows per ear in maize" HEREDITAS 1996 SE, vol. 124, no. 2, 1996, pages 173-178, XP002508657 ISSN: 0018-0661	1,11,12, 20-23, 75,78
Y	the whole document page 173, column 1 page 175, column 2 page 178 -----	2-10, 13-19, 76,77, 79-81
X	ROTARENCO,VA: "Segregation for the marker ral gene in matroclinal haploids of maize" MAIZE GENETICS COOPERATION NEWSLETTER, vol. 74, 2000, pages 1-2, XP002508658 Retrieved from the Internet: URL:http://www.agron.missouri.edu/mnl/74/45rotarenco.html>	1,11,12, 20-23, 75,78
Y	the whole document -----	2-10, 13-19, 76,77, 79-81

-/--

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ORTIZ R. ET AL: "Use of haploids and isozyme markers for genetic analysis in the polysomic polyploid potato" J. GENET. & BREED., vol. 47, 1993, pages 283-288, XP002508659	1,2,11, 12, 20-23, 75,77,78
Y	the whole document page 284 - page 285 table 2	3-10, 13-19, 76,79-81
X	CHEBOTAR' O D ET AL: "Use of matroclinous haploids for genetic analysis of ear length and plant height in maize" GENETIKA, vol. 32, no. 6, 1996, page 1, XP002508660 ISSN: 0016-6758 abstract	1,11,12, 20-23, 75,78
Y		2-10, 13-19, 76,77, 79-81
Y	JOHN M. VARRIEUR: "AFLP MARKER ANALYSIS OF MONOPLOID POTATO"[Online] 2002, pages 1-90, XP002508661 Retrieved from the Internet: URL:http://scholar.lib.vt.edu/theses/available/etd-05242002-165327/unrestricted/ETD.pdf> [retrieved on 2008-12-18] the whole document abstract pages 2-5 pages 25-27 page 51	1-23, 75-81
Y	RÖBER, F.K., G.A. GORDILLO, H.H. GEIGER: "In vivo haploid induction in maize - Performance of new inducers and significance of doubled haploid lines in hybrid breeding" MEDICA, vol. 50, 2005, pages 275-283, XP002508662 the whole document page 275, column 1, paragraph 1	1-23, 75-81

-/--

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	PRET'OVÁ A ET AL: "Haploid formation in maize, barley, flax, and potato" PROTOPLASMA ; AN INTERNATIONAL JOURNAL OF CELL BIOLOGY, SPRINGER-VERLAG, VI, vol. 228, no. 1-3, 31 August 2006 (2006-08-31), pages 107-114, XP019430737 ISSN: 1615-6102 the whole document page 107, column 1, last paragraph page 108 page 111, column 2, paragraph 1 -----	1-23, 75-81
Y	BAJAJ ET AL: "In vitro production of haploid and their use in cell genetic and plant breeding" BIOTECHNOLOGY IN AGRICULTURE AND FORESTRY, SPRINGER VERLAG, BERLIN, DE, vol. 12, 1 January 1990 (1990-01-01), pages 3-44, XP009110068 ISSN: 0934-943X the whole document page 20 page 23 page 25 page 28 page 30 -----	1-23, 75-81
A	LEHMENSIEK A ET AL: "Genetic mapping of gray leaf spot (GLS) resistance genes in maize" THEORETICAL AND APPLIED GENETICS, SPRINGER, BERLIN, DE, vol. 103, no. 5, 1 October 2001 (2001-10-01), pages 797-803, XP002481079 ISSN: 0040-5752 the whole document -----	1-23, 75-81
A	BUBECK ET AL: "Quantitative trait loci controlling rsistance to gray leaf spot in maize" CROP SCIENCE, CROP SCIENCE SOCIETY OF AMERICA, MADISON, WI, US, vol. 33, no. 4, 1 January 1993 (1993-01-01), pages 838-847, XP002100952 ISSN: 0011-183X the whole document -----	1-23, 75-81

-/--

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	BROWN A F ET AL: "Quantitative Trait Loci in Sweet Corn Associated with Partial Resistance to Stewart's Wilt, Northern Corn Leaf Blight, and Common Rust." PHYTOPATHOLOGY MAR 2001, vol. 91, no. 3, March 2001 (2001-03), pages 293-300, XP002508663 ISSN: 0031-949X the whole document	1-23, 75-81
A	ROCHEFORD T R ET AL: "GENETIC STUDIES OF RESISTANCE IN MAIZE ZEA-MAYS L. TO GOSS'S BACTERIAL WILT AND BLIGHT CLAVIBACTER-MICHIGANENSE-SSP-NEBRASKENSE" JOURNAL OF HEREDITY, vol. 80, no. 5, 1989, XP002508664 ISSN: 0022-1503 abstract	1-23, 75-81

3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2008/074760

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers allsearchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search reportcovers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-23, 75-81

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-23, 75-81:

Method for the association of at least one genotype / genetic marker, with at least one phenotype using a haploid plant; method for identifying an association of a plant genotype with one or more traits, by screening haploid plants;

Invention (group of inventions) 2: Claims 24-46, 72-74:

Method for identifying a corn plant comprising at least one allele associated with Gray Leaf Spot resistance; method of introgressing a Gray Leaf Spot resistance QTL allele into a corn plant; a corn plant obtained by the above-mentioned methods; an isolated nucleic acid molecule for detecting a molecular marker associated with Gray Leaf Spot resistance;

Invention (group of invention) 3: Claims 47-71:

Method for identifying a corn plant comprising at least one allele associated with Goss'Wilt resistance; a corn plant obtained by the above-mentioned method.
