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(54) **Title:** MOLECULAR MARKERS AND PHENOTYPIC SCREENING FOR METRIBUZIN TOLERANCE

(57) **Abstract:** The present invention provides methods and compositions for the identification and selection of loci modulating metribuzin herbicide tolerance in plant breeding. In addition, methods are provided for screening germplasm entries for the performance and expression of the metribuzin tolerance trait.



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INTERNATIONAL PATENT APPLICATION
MOLECULAR MARKERS AND PHENOTYPIC SCREENING FOR METRIBUZIN
TOLERANCE

Cross-Reference to Related Applications

[0001] This application claims the benefit of United States Provisional Application Serial No. 61/694,990 filed August 30, 2012, which is incorporated herein by reference in its entirety.

Incorporation of Sequence Listing

[0002] A sequence listing containing the file named "46_21_59410.txt" which is 21,685 bytes (measured in MS-Windows®) and created on August 26, 2013, contains 42 nucleotide sequences, is provided herewith via the USPTO's EFS system, and is incorporated herein by reference in its entirety.

Incorporation of Table 2

[0003] A listing of various soybean linkage group N (chromosome 3) markers is provided herewith in the Specification as Table 2. Table 2 is provided at the end of the specification following the Examples and is incorporated herein in its entirety.

Background

[0004] Distinct soybean varieties have been shown to exhibit different degrees of tolerance to the herbicide metribuzin (Wax et al. *Agron. Journal*. 68:484-486, 1976). Genetic linkage between soybean loci associated with *Phytophthora* resistance and loci associated with metribuzin tolerance have also been reported (Klein, *Journal of Heredity*, 77(4):275-277, 1986).

Summary

[0005] "Metribuzin sensitivity" is an undesirable phenotype observed in certain soybean varieties. It has been discovered that after application of metribuzin, the leaves of certain soybean plant varieties can exhibit a "metribuzin sensitivity phenotype" ranging from mild leaf chlorosis and/or necrosis to severe leaf chlorosis and/or necrosis upon exposure to metribuzin. In the most extreme cases, application of metribuzin to certain sensitive soybean varieties that exhibit severe leaf chlorosis and/or necrosis can result in plant death. However, other tolerant soybean varieties that are exposed to metribuzin in parallel with the sensitive

soybean varieties will exhibit little to no leaf chlorosis and/or necrosis and will complete their life cycle. The metribuzin sensitivity phenotype can be observed within about 7 to about 21 days after herbicide application in certain soybean varieties that are sensitive to metribuzin. The metribuzin sensitivity phenotype is undesirable as it can lead to reduced yield in certain soybean plant varieties exposed to metribuzin.

[0006] Provided herein are soybean plants comprising an introgressed genomic region associated with a metribuzin tolerance phenotype. Also provided herein are markers that reside outside of a genomic region associated with a metribuzin tolerance phenotype and that facilitate breeding activities that include, but are not limited to, introgression of this genomic region. Markers and specific alleles thereof that are associated with a metribuzin tolerance phenotype are also provided. Methods of obtaining a soybean plant that exhibits a metribuzin tolerance phenotype and methods of obtaining a soybean plant comprising in its genome at least one metribuzin tolerance locus are also provided. Methods that provide for the introgression of a genomic region associated with a metribuzin tolerance phenotype into soybean germplasm that has a genomic region associated with a metribuzin sensitivity phenotype are also provided. Identification of molecular markers associated with loci that confer the metribuzin tolerance phenotype has significant economic value. By using markers associated with the metribuzin tolerance trait, breeders can select soybean varieties with the favorable alleles (i.e. alleles that are not associated with the metribuzin sensitivity trait) for use in trait integration. They can also use the markers to help them eliminate unfavorable alleles (i.e. alleles that are associated with the metribuzin sensitivity trait) in soybeans. In certain embodiments, commercially desirable soybean lines that carry a genomic region that is associated with a “metribuzin tolerance” phenotype and tolerate dosages of metribuzin sufficient to provide for control of undesirable weeds are thus provided.

[0007] Methods for selecting a metribuzin tolerant plant from a population of plants comprising both metribuzin sensitive and metribuzin tolerant plants are provided. In certain embodiments, the plurality of soybean plants comprises a population that is obtained by: i) crossing a parent plant comprising at least one metribuzin tolerance locus with a parent plant comprising at least one metribuzin sensitivity locus; or, ii) obtaining seed or progeny from a parental plant segregating for at least one metribuzin tolerance locus. In certain embodiments, the aforementioned methods can further comprise the step of assaying for the presence of at least one additional marker, where the additional marker is either linked or unlinked to the linkage group N genomic region. In certain embodiments of the aforementioned methods, the plurality of soybean plants, the soybean plant, and/or progeny

thereof are exposed to a dosage of metribuzin sufficient to cause metribuzin sensitivity in a sensitive variety. In certain embodiments of the aforementioned methods, a plant that exhibits a metribuzin tolerance phenotype is selected.

[0008] Also provided herewith are methods for producing a soybean plant comprising in its genome at least one introgressed metribuzin tolerance locus. Also provided herewith are soybean plants comprising an introgressed metribuzin tolerance locus made by the aforementioned methods. In certain embodiments, a soybean plant comprising an introgressed metribuzin tolerance locus and one or more polymorphic loci comprising alleles or combinations of alleles that are not found in a metribuzin tolerant soybean variety and that are linked to the introgressed metribuzin tolerance locus, where the plant is produced by the aforementioned methods are provided.

[0009] Also provided are soybean plants comprising an introgressed metribuzin tolerance locus and one or more polymorphic loci comprising alleles or combinations of alleles that are not found in a metribuzin tolerant soybean variety and that are linked to the introgressed metribuzin tolerance locus.

[0010] Methods for obtaining a soybean plant comprising in its genome at least one metribuzin tolerance locus, comprising the steps of: genotyping a plurality of soybean plants with respect to at least one genetic locus in a linkage group N genomic region flanked by loci NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9); and selecting a soybean plant comprising in its genome at least one genetic locus comprising a genotype associated with metribuzin tolerance are provided herein. In certain embodiments, the genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in a sub-region of the linkage group N region flanked by loci NGMAX006077928 (SEQ ID NO: 4) and NGMAX006080885 (SEQ ID NO: 8). In certain embodiments of the aforementioned methods, the genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in the first linkage group N region or the sub-region, wherein the marker comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7). In certain embodiments, the plurality of soybean plants comprises a population that is obtained by: i) crossing a parent plant comprising at least one metribuzin tolerance locus with a parent plant comprising at least one metribuzin sensitivity locus; or, ii) obtaining seed or progeny from a parental plant segregating for at least one metribuzin tolerance locus. In certain embodiments, the population contains plants that contain a transgene that confers resistance to dicamba and/or a transgene that confers resistance to glyphosate. In certain embodiments, the methods can further comprise the step

of assaying for the presence of at least one additional marker, wherein the additional marker is either linked or unlinked to the linkage group N genomic region. In certain embodiments, the methods can comprise exposing the selected soybean plant or progeny thereof comprising the genetic locus to a dosage of metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and isolating a metribuzin tolerant plant therefrom. In certain embodiments, the selection comprises exposing a genotyped soybean plant comprising the genetic locus to a dosage of metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and isolating a metribuzin tolerant plant therefrom.

[0011] Methods for producing a soybean plant comprising in its genome at least one introgressed metribuzin tolerance locus comprising the steps of: crossing a first soybean plant with a metribuzin tolerance locus with a second soybean plant comprising: a metribuzin sensitivity locus in a first linkage group N genomic region flanked by loci NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9) and at least one linked polymorphic locus not present in the first soybean plant to obtain a population segregating for the metribuzin tolerance loci and the linked polymorphic locus; detecting at least two polymorphic nucleic acids in at least one soybean plant from the population, wherein at least one of the polymorphic nucleic acids is located in the linkage group N region and wherein at least one of the polymorphic amino acids is a linked polymorphic locus not present in the first soybean plant; and selecting a soybean plant comprising a genotype associated with metribuzin tolerance and at least one linked marker found in the second soybean plant comprising a metribuzin sensitivity locus but not found in the first soybean plant, thereby obtaining a soybean plant comprising in its genome an introgressed metribuzin tolerance locus are also provided. In certain embodiments, at least one of the first or the second soybean plants comprises a transgene that confers resistance to dicamba and/or a transgene that confers resistance to glyphosate. In certain embodiments of the methods, the population, the selected soybean plant, and/or progeny of the selected soybean plant is exposed to a dosage of metribuzin sufficient to cause a deleterious effect in a metribuzin sensitive variety. In certain embodiments of the methods, the polymorphic nucleic acid detected in step (b) is detected with marker NGMAX006079502 (SEQ ID NO: 7). In certain embodiments of the methods, the polymorphic nucleic acid detected in step (b) comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7). In certain embodiments of any of the aforementioned methods, the linked polymorphic locus is detected with a genotypic marker, a phenotypic marker, or both. In certain embodiments of any of the aforementioned methods,

the linked polymorphic locus is detected with a marker that is located within about 1000, 500, 100, 40, 20, 10, or 5 kilobases (Kb) of the metribuzin tolerance locus. In certain embodiments of any of the aforementioned methods, the linked polymorphic locus is detected with at least one marker selected from the group consisting of NGMAX006083631 (SEQ ID NO: 10), NS0202926 (SEQ ID NO: 11), NGMAX006084289 (SEQ ID NO: 12), and NGMAX006088354 (SEQ ID NO: 13).

[0012] Also provided herein are soybean plants made any of the aforementioned methods, wherein the soybean plant comprises an introgressed metribuzin tolerance locus.

[0013] Also provided herein are soybean plants comprising an introgressed metribuzin tolerance locus, wherein at least one linked marker found in the soybean plant is characteristic of germplasm comprising a metribuzin sensitivity locus and is not associated with germplasm comprising the metribuzin tolerance locus. In certain embodiments, the introgressed metribuzin tolerance locus comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).

[0014] Also provided herein are soybean plants comprising an introgressed metribuzin tolerance locus, wherein at least one linked marker found in the soybean plant is characteristic of parental germplasm comprising a metribuzin sensitivity locus but is not associated with germplasm comprising the metribuzin tolerance locus. In certain embodiments, the introgressed metribuzin tolerance locus comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7). In certain embodiments, the linked marker is selected from the group consisting of NGMAX006083631 (SEQ ID NO: 10), NS0202926 (SEQ ID NO: 11), NGMAX006084289 (SEQ ID NO: 12), and NGMAX006088354 (SEQ ID NO: 13). In certain embodiments, the linked marker comprises at least one of: a TT or a CT allele of NGMAX006083631 (SEQ ID NO: 10), an AC allele of NS0202926 (SEQ ID NO: 11), a GG allele of NGMAX006084289 (SEQ ID NO: 12), or a GG allele of NGMAX006088354 (SEQ ID NO: 13).

[0015] Methods of identifying a soybean plant that comprises a genotype associated with metribuzin tolerance, comprising: detecting in a soybean plant an allele in at least one genetic locus associated with metribuzin tolerance, wherein the genetic locus is in a linkage group N genomic region flanked by loci NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9), and denoting that the plant comprises a genotype associated with metribuzin tolerance are also provided. In certain embodiments, the methods can further comprise the step of selecting the denoted plant from a population of plants. In certain embodiments, the methods can further comprise the steps of exposing the denoted soybean plant or progeny

thereof to a dosage of metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and scoring the exposed plants for metribuzin tolerance. In certain embodiments, the selection comprises exposing the denoted soybean plant or progeny thereof comprising the genetic locus to a dosage of metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and isolating a metribuzin tolerant plant therefrom. In certain embodiments, the genotype associated with a metribuzin tolerance comprises at least one polymorphic allele of at least one marker in a sub-region of the linkage group N region that is flanked by loci NGMAX006077928 (SEQ ID NO: 4) and NGMAX006080885 (SEQ ID NO: 8). In certain embodiments, the genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in the linkage group N region or sub-region that comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).

[0016] Methods of producing a population of soybean plants with a metribuzin tolerance phenotype are also provided. In certain embodiments, these methods of producing a population of soybean plants comprising a genotype associated with a metribuzin tolerance phenotype can comprise: providing a first population of soybean plants, detecting in the soybean plants of the first population an allele in at least one metribuzin tolerance marker locus associated with a metribuzin tolerance phenotype wherein the metribuzin tolerance marker locus is in a linkage group N genomic region flanked by or including: a) NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9); or b) NGMAX006077928 (SEQ ID NO: 4) and NGMAX006080885 (SEQ ID NO: 8); selecting one or more soybean plants exhibiting an allele in the at least one metribuzin tolerance locus from the first population of soybean plants; and producing offspring from the one or more selected soybean plants. In certain embodiments, the genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in the first linkage group N region or the sub-region, wherein the marker comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7). In certain embodiments, the genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in the linkage group N region or sub-region that comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).

[0017] Further areas of applicability will become apparent from the description provided herein. It should be understood that the description and specific examples are intended for purposes of illustration only and are not intended to limit the scope of the present disclosure.

Detailed Description

Definitions

[0018] As used herein, an “allele” refers to one of two or more alternative forms of a genomic sequence at 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.

[0019] As used herein, the term “denoting” when used in reference to a plant genotype refers to any method whereby a plant is indicated to have a certain genotype. Such indications of a certain genotype include, but are not limited to, any method where a plant is physically marked or tagged. Physical markings or tags that can be used include, but not limited to, a barcode, a radio-frequency identification (RFID) tag, a label, or the like. Indications of a certain genotype also include, but are not limited to, any entry into any type of written or electronic database whereby the plant’s genotype is provided.

[0020] A “locus” is a position on a genomic sequence that is usually found by a point of reference; e.g., a short DNA sequence that is a gene, or part of a gene or intergenic region. A locus may refer to a nucleotide position at a reference point on a chromosome, such as a position from the end of the chromosome.

[0021] As used herein, “linkage group N” corresponds to the soybean linkage group N described in Choi, et al., *Genetics*, 2007 May; 176(1): 685–696. Linkage group N, as used herein, also corresponds to soybean chromosome 3 (as described on the World Wide Web at soybase.org/LG2Xsome.php). 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 at least two members. The variation can comprise but is not limited to one or more nucleotide base substitutions, the insertion of one or more nucleotides, a nucleotide sequence inversion, and/or the deletion of one or more nucleotides.

[0022] As used herein, the term “single nucleotide polymorphism,” also referred to by the abbreviation “SNP,” means a polymorphism at a single site wherein the polymorphism constitutes any or all of a single base pair change, an insertion of one or more base pairs, and/or a deletion of one or more base pairs.

[0023] As used herein, “marker” means a detectable characteristic that can be used to discriminate between organisms. Examples of such characteristics include, but are not limited to, genetic markers, biochemical markers, fermentation yield, fermentation efficiency, energy yield, secondary compounds, metabolites, morphological characteristics, and agronomic characteristics.

[0024] As used herein, “marker assay” means a method for detecting a polymorphism at a particular locus using a particular method. Marker assays thus include, but are not limited to, measurement of at least one phenotype (such as seed color, flower color, or other visually detectable trait as well as any biochemical trait), restriction fragment length polymorphism (RFLP), single base extension, electrophoresis, sequence alignment, allelic specific oligonucleotide hybridization (ASO), random amplified polymorphic DNA (RAPD), microarray-based polymorphism detection technologies, and the like.

[0025] 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.

As used herein, the term “introgressed”, when used in reference to a genetic locus, refers to a genetic locus that has been introduced into a new genetic background. Introgression of a genetic locus can thus be achieved through both plant breeding methods or by molecular genetic methods. Such molecular genetic methods include, but are not limited to, various plant transformation techniques and/or methods that provide for homologous recombination, non-homologous recombination, site-specific recombination, and/or genomic modifications that provide for locus substitution or locus conversion. In certain embodiments, introgression could thus be achieved by substitution of a metribuzin sensitivity locus with a corresponding metribuzin tolerance locus or by conversion of a locus from a metribuzin sensitivity genotype to a metribuzin tolerance genotype.

[0026] As used herein, “phenotype” means the detectable characteristics of a cell or organism which can be influenced by gene expression.

[0027] 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 $\frac{1}{4}$ of the gametes will of each genotype. Segregation of gametes into a genotypes differing from $\frac{1}{4}$ are attributed to linkage.

[0028] As used herein, the termed “linked”, when used in the context of markers and/or genomic regions, means that the markers and/or genomic regions are located on the same linkage group or chromosome.

[0029] 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 at least about 60% free, preferably at least about 75% free, more preferably at least about 90% free, and most preferably at least about 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.

[0030] As used herein, "quantitative trait locus (QTL)" means a locus that controls to some degree numerically representable traits that are usually continuously distributed. As used herein, the term "transgene" means nucleic acid molecules in the form of DNA, such as cDNA or genomic DNA, and RNA, such as mRNA or microRNA, which may be single or double stranded.

[0031] As used herein, the term "event", when used in the context of describing a transgenic plant, refers to a particular transformed plant line. In a typical transgenic breeding program, a transformation construct responsible for a trait is introduced into the genome via a transformation method. Numerous independent transformants (events) are usually generated for each construct. These events are evaluated to select those with superior performance.

[0032] As used herein, the term "soybean" means *Glycine max* and includes all plant varieties that can be bred with soybean, including wild soybean species. In certain embodiments, soybean plants from the species *Glycine max* and the subspecies *Glycine max* L. ssp. *max* or *Glycine max* ssp. *formosana* can be genotyped using the compositions and methods of the present invention. In an additional aspect, the soybean plant is from the species *Glycine soja*, otherwise known as wild soybean, can be genotyped using these compositions and methods. Alternatively, soybean germplasm derived from any of *Glycine max*, *Glycine max* L. ssp. *max*, *Glycine max* ssp. *Formosana*, and/or *Glycine soja* can be genotyped using compositions and methods provided herein.

[0033] As used herein, the term "bulk" refers to a method of managing a segregating population during inbreeding that involves growing the population in a bulk plot, harvesting the self-pollinated seed of plants in bulk, and using a sample of the bulk to plant the next generation.

[0034] As used herein, the phrase "metribuzin sensitivity" refers to undesirable phenotypic traits observed in certain soybean germplasms after exposure to metribuzin at a rate of about 0.25 pounds per acre of metribuzin acid to about 0.75 pounds per acre of metribuzin. Such

undesirable phenotypic traits include, but are not limited to, leaf chlorosis, leaf necrosis, and plant death.

[0035] As used herein, the phrase “metribuzin tolerant” refers to either the absence or reduction of undesirable phenotypic traits observed after exposure to metribuzin in “metribuzin sensitive” soybean germplasms.

[0036] As used herein, the term “comprising” means “including but not limited to.”

Description

[0037] In accordance with the present invention, Applicants have discovered genomic regions, associated markers, and associated methods for identifying and associating genotypes that effect the levels of metribuzin tolerance observed in soybean plants. Metribuzin (4-Amino-6-(1,1-dimethylethyl)-3-(methylthio)-1,2,4-triazin-5(4H)-one) is a useful broad spectrum herbicide for controlling weeds. For example, in one embodiment, a method of the invention comprises screening a plurality of germplasm entries displaying a heritable variation for at least one metribuzin tolerance trait wherein the heritable variation is linked to at least one genotype; and associating at least one genotype from the germplasm entries to at least one metribuzin tolerance trait. In another embodiment, a method of the invention comprises crossing at least two germplasm entries with a test germplasm entry for the evaluation of performance of at least one metribuzin tolerance trait in order to determine preferred crossing schemes. The methods of the present invention can be used with traditional breeding techniques as described below to more efficiently screen and identify genotypes affecting a metribuzin tolerance trait.

[0038] The use of markers to infer a phenotype of interest results in the economization of a breeding program by substituting costly, time-intensive phenotyping assays with genotyping assays. Further, breeding programs can be designed to explicitly drive the frequency of specific, favorable phenotypes by targeting particular genotypes (US Patent No. 6,399,855). Fidelity of these associations may be monitored continuously to ensure maintained predictive ability and, thus, informed breeding decisions (US Patent Application 2005/0015827). In this case, costly, time-intensive phenotyping assays required for determining if a plant or plants contains a genomic region associated with a “metribuzin tolerance” or “metribuzin sensitivity” phenotype can be supplanted by genotypic assays that provide for identification of a plant or plants that contain the desired genomic region that confers metribuzin tolerance.

A Genomic Region Associated with a Metribuzin Tolerance Phenotype

[0039] Provided herewith is a soybean genomic region that is shown herein to be associated with a desirable metribuzin tolerance phenotype when present in certain allelic forms.

[0040] A soybean genomic region provided that can be associated with a desirable metribuzin tolerance phenotype when present in certain allelic forms is located on the telomere proximal end of the short arm of soybean linkage group N (chromosome 3). A series of markers useful in practicing the methods of this invention are provided herewith in Table 1. Additional markers useful in the practice of the invention are provided herewith in Table 2 of the Specification, which is incorporated herewith by reference in its entirety. Table 2 provides the Table 1 markers, additional nucleic acid markers or loci that have been disclosed in various databases, the relative positions of the markers on a physical map of linkage group N (soybean chromosome 3), and sources for the markers.

[0041] Table 1. Markers spanning a genomic region associated with a desirable metribuzin tolerance phenotype

Marker or Locus Name	SEQ ID NO:	Map Position ¹	Allelic form(s) Associated with Metribuzin Tolerance ²
NS0206337	1	2,994,090	
NGMAX006077074	2	3,087,800	
NGMAX006077640	3	3,209,380	
NGMAX006077928	4	3239140	
NGMAX006078838	5	3,336,045	
NGMAX006079484	6	3,389,797	
NGMAX006079502	7	3,391,112	TT ³
NGMAX006080885	8	3,562,064	
NS0138011	9	3,801,236	
NGMAX006083631	10	3,901,416	
NS0202926	11	3,964,709	
NGMAX006084289	12	3,979,613	
NGMAX006088354	13	4,817,793	

¹ The relative positions of the approximate middle position of the listed markers or loci based on nucleotide positions on a physical map of soybean linkage group N (chromosome 3) of

Table 2 are provided where nucleotide position 2,987,781 is telomere proximal and nucleotide position 4,075,437 is centromere proximal. Polymorphic nucleotide bases are designated in the sequence listing provided herewith according to the WIPO Standard ST.25 (1998), Table 1, as follows: r=g or a (purine); y=t/u or c (pyrimidine); m=a or c; (amino); k=g or t/u (keto); s=g or c (strong interactions 3 H-bonds); w=a or t/u (weak interactions 2H-bonds); b=g or c or t/u (not a); d=a or g or t/u (not c); h=a or c or t/u (not g); v=a or g or c (not t, not u); and n=a or g or c or t/u (unknown, or other; any.)

² Both the maternal and paternal alleles of the single nucleotide polymorphisms that can be associated with a metribuzin tolerance phenotype are shown.

³ The identified polymorphic allele of marker is located at nucleotide 201 of SEQ ID NO: 7.

[0042] Also provided herein are sub-regions of the linkage group N region that is flanked by loci NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9) that are associated with a metribuzin tolerance phenotype. These loci flank a region that spans telomere proximal nucleotide 3,209,230 to centromere proximal nucleotide 3,801,607 in the physical map of linkage group N provided in Table 2 of the specification. A first sub-region of the linkage group N region associated with a metribuzin tolerance phenotype is flanked by loci NGMAX006077928 (SEQ ID NO: 4) and NGMAX006080885 (SEQ ID NO: 8). These loci flank a sub-region that spans telomere proximal nucleotide 3,238,990 to centromere proximal nucleotide 3,562,215 in the physical map of linkage group N provided in Table 2 of the specification. Polymorphisms located in this first sub-region that are associated with a metribuzin tolerance phenotype can be detected with markers that include, but are not limited to, NGMAX006079502 (SEQ ID NO: 7). In certain embodiments, a polymorphism in the region or the sub-region is detected with marker NGMAX006079502 (SEQ ID NO: 7). In certain embodiments, the alleles of this marker associated with metribuzin tolerance are a TT allele of NGMAX006079502 (SEQ ID NO: 7).

[0043] Additional genetic markers can be used either in conjunction with the markers provided in Table 1 and/or Table 2 or independently of the markers provided in Table 1 and/or Table 2 to practice the methods of the instant invention. Publicly available marker databases from which useful markers can be obtained include, but are not limited to, the soybase.org website on the internet (World Wide Web) that is administered by the United States Agricultural Research Service, the United States Department of Agriculture, and Iowa State University. Additional soybean markers that can be used and that have been described in the literature include, but are not limited to, Hyten et al., *BMC Genomics*. 11:38, 2010; Choi et al., *Genetics*. 176(1):685-96, 2007; Yoon et al., *Theor Appl Genet*. 2007

Mar;114(5):885-99; and Hyten et al. *Crop Sci.* 2010 50: 960-968. Given the provision herein of a genomic region on linkage group N (chromosome 3) delimited or flanked by the telomere proximal locus NGMAX006077640 (SEQ ID NO: 3) of Table 2 and the centromere proximal locus and NS0138011 (SEQ ID NO: 9) of Table 2 as well as an assortment of soybean germplasms exhibiting either a “metribuzin sensitivity” or “metribuzin tolerant” phenotype, additional markers located either within or near this genomic region that are associated with these phenotypes can be obtained by merely typing the new markers in the various germplasms provided herewith. The genomic region on linkage group N (chromosome 3) delimited or flanked by the telomere proximal locus NGMAX006077640 (SEQ ID NO: 3) of Table 2 and the centromere proximal locus NS0138011 (SEQ ID NO: 9) of Table 2 can also be mapped relative to markers provided in any publicly available or other soybean physical or genetic map to place this genetic locus on that map. In this regard, publicly available markers SAT_186, SATT152, SATT641, SATT009, and SATT149 can be used to place the linkage group N (chromosome 3) delimited or flanked by the telomere proximal locus NGMAX006077640 (SEQ ID NO: 3) of Table 2 and the centromere proximal locus NS0138011 (SEQ ID NO: 9) on publically available soybean genetic maps.

Identification of Plants Exhibiting the “Metribuzin sensitivity” or “Metribuzin Tolerance” Phenotype

[0044] To observe the presence or absence of the “metribuzin sensitivity” or metribuzin tolerance phenotypes, soybean plants are typically exposed in early to mid-vegetative growth stages to one or more doses of metribuzin. Typical doses of metribuzin that can elicit a metribuzin sensitivity phenotype can range from about a 1-fold label application rate of a commercially available metribuzin formulation (i.e. about 0.25 pounds per acre) to about a 3-fold label application rate (i.e. about 0.75 pounds per acre) of a commercially available metribuzin formulation. Commercially available formulations containing metribuzin that can be used include, but are not limited to, Authority®MTZ (FMC Corporation, Philadelphia, PA, USA); Boundary ® (Syngenta, Wilmington, Delaware, USA); Canopy® or Lexone® (Dupont, Wilmington, DE, USA); Sencor® (Bayer Crop Science, Research Triangle Park, NC, USA); or TriCor® DF (United Phosphorus, Inc., King of Prussia, PA, USA. In certain embodiments, the commercially available metribuzin formulation used is TriCor® 75DF. In certain embodiments, doses of metribuzin that can elicit a metribuzin sensitivity phenotype can range from about a 1 fold application rate of about 0.25 pounds per acre to about a three fold application rate of 0.75 pounds per acre.

[0045] The metribuzin sensitivity phenotype can be observed approximately one week to three weeks after herbicide application in certain soybean varieties that are sensitive to metribuzin. Metribuzin is typically applied during pre and post-emergent vegetative growth stages. In certain embodiments of these methods, metribuzin can be applied to the soil about 2 days prior to soybean seed planting and activated by irrigation of the planted seed to score for the presence of the metribuzin sensitivity phenotype. Genotypes provided herein are especially useful for providing metribuzin tolerance to plants exposed to metribuzin by a pre-emergence soil drench. As discussed herein, the vegetative stages of soybean are as follows: VE (emergence), VC (cotyledon stage), V1 (first trifoliate leaf), V2 (second trifoliate leaf), V3 (third trifoliate leaf), V(n) (nth trifoliate leaf), and V6 (flowering will soon start). As discussed herein, the reproductive stages of soybean are as follows: R1 (beginning bloom), R2 (full bloom), R3 (beginning pod), R4 (full pod), R5 (beginning seed), R6 (full seed), R7 (beginning maturity) and R8 (full maturity). A description of the soybean vegetative and reproductive stages can be found on the World Wide Web (internet) at ag.ndsu.edu/pubs/plantsci/rowcrops/a1174/a1174w.htm (North Dakota State University publication A-1174, June 1999, Reviewed and Reprinted August 2004).

[0046] A rating scale that evaluates the degree of metribuzin sensitivity can also be employed to identify “metribuzin sensitive” and “metribuzin tolerant” plants. An exemplary and non-limiting scale for evaluating the Metribuzin sensitivity phenotype is as follows, where a low number corresponds to a “metribuzin tolerance” phenotype and the a high number correlates to a “metribuzin sensitivity” phenotype:

A rating of 1: Little to no leaf chlorosis/necrosis

A rating of 3: Mild leaf chlorosis/necrosis; plants survive and make full recovery

A rating of 4: Moderate leaf chlorosis/necrosis; plants survive and make full recovery

A rating of 6: Moderate leaf chlorosis/necrosis; plants survive and typically recover

A rating of 7: Severe leaf chlorosis/necrosis; plants survive and typically recover;

A rating of 9: Severe chlorosis/necrosis; plants survive leading to plant death

Introgression of a Genomic Region Associated with a Metribuzin Tolerance Phenotype

[0047] Also provided herewith is unique soybean germplasm comprising an introgressed genomic region that is associated with a metribuzin tolerance phenotype and methods of obtaining the same. Marker-assisted introgression involves the transfer of a chromosomal region, defined by one or more markers, from one germplasm to a second germplasm. Offspring of a cross that contain the introgressed genomic region can be identified by the

combination of markers characteristic of the desired introgressed genomic region from a first germplasm (i.e. such as a metribuzin tolerance germplasm) and both linked and unlinked markers characteristic of the desired genetic background of a second germplasm (i.e. a metribuzin sensitivity germplasm). In addition to the markers provided herewith that identify alleles of genomic region that is associated with a metribuzin tolerance phenotype, flanking markers that fall on both the telomere proximal end of the genomic region on linkage group N (chromosome 3) and the centromere proximal end of the linkage group N (chromosome 3) genomic region are also provided in Tables 1 and 2. Table 2 is provided at the end of the specification immediately before the claims. Such flanking markers are useful in a variety of breeding efforts that include, but are not limited to, introgression of the genomic region associated with a metribuzin tolerance phenotype into a genetic background comprising markers associated with germplasm that ordinarily contains the allelic forms of the genomic region that is associated with a "Metribuzin sensitivity" phenotype. Telomere proximal flanking markers that can be used in these methods include, but are not limited to, NS0206337 (SEQ ID NO: 1), NS0262835 (SEQ ID NO: 21), NGMAX006076547 (SEQ ID NO: 18), NGMAX006076962 (SEQ ID NO: 22), NGMAX006077074 (SEQ ID NO: 2), NGMAX006077513 (SEQ ID NO: 23), SAT_186, and NGMAX006077555 (SEQ ID NO: 24), and/or polymorphisms in any of the loci listed in Table 2 of the Specification located between starting base 2,994,256 (the telomere proximal base) of locus NS0206337 (SEQ ID NO: 1) and starting base 3389647 of centromere proximal locus NGMAX006079484 (SEQ ID NO: 6). Centromere proximal flanking markers that can be used in these methods include, but are not limited to, NGMAX006082782 (SEQ ID NO: 25), NGMAX006083256 (SEQ ID NO: 26), NGMAX006083447 (SEQ ID NO: 27), NGMAX006083554 (SEQ ID NO: 28), NGMAX006083631 (SEQ ID NO: 10), NS0202926 (SEQ ID NO: 11), NGMAX006084289 (SEQ ID NO: 12), and NGMAX006088354 (SEQ ID NO: 13) and/or polymorphisms in any of the other loci listed in Table 2 that are centromere proximal to NS0138011 (SEQ ID NO: 9). Soybean plants wherein the sub regions that is flanked by loci NGMAX006077928 (SEQ ID NO: 4) and NGMAX006080885 (SEQ ID NO: 8) is introgressed can be obtained by using the NGMAX006077878 (SEQ ID NO: 19), NGMAX006078122 (SEQ ID NO: 29), NGMAX006078495 (SEQ ID NO: 30), NS0262836 (SEQ ID NO: 31), NGMAX006078838 (SEQ ID NO: 5), NGMAX006079484 (SEQ ID NO: 6), SATT152, SATT641, NGMAX006081942 (SEQ ID NO: 32), NGMAX006081999 (SEQ ID NO: 33), NGMAX006082115 (SEQ ID NO: 34), NGMAX006082688 (SEQ ID NO: 35), NGMAX006082778 (SEQ ID NO: 36), NS0118425 (SEQ ID NO: 37), NGMAX006080509

(SEQ ID NO: 38), or NGMAX006079911 (SEQ ID NO: 20) markers, or by using any of the markers located between this subregions and the telomere and/or centromere proximal portions of the genome that are provided in Table 2. Any of the aforementioned polymorphisms can be identified by sequencing loci from metribuzin sensitivity and metribuzin tolerance germplasms. Additional markers located on linkage group N (chromosome 3) and other chromosomes are disclosed in US Patent Application Publication 2009/0208964. Publicly available marker databases from which additional useful markers located on linkage group N (chromosome 3) and other chromosomes can be obtained include, but are not limited to, the soybase.org website on the internet that is administered by the United States Agricultural Research Service, the United States Department of Agriculture, and Iowa State University. Soybean plants or germplasm comprising an introgressed genomic region that is associated with a metribuzin tolerance phenotype wherein at least 10%, 25%, 50%, 75%, 90%, or 99% of the remain genomic sequences carry markers characteristic of soybean plants or germplasm that are otherwise or ordinarily comprise a genomic region associated with the Metribuzin sensitivity phenotype are thus provided.

[0048] In certain embodiments, metribuzin tolerant soybean plant are provided that comprise an introgressed linkage group N region comprising a metribuzin tolerance locus where adjacent or linked genomic regions comprise markers that are not typically linked or associated with the metribuzin tolerance locus in metribuzin tolerant strains. Non-limiting examples of alleles of linked markers that can be used to detect such introgressed metribuzin tolerance regions can include, but are not limited to, a “TT” or a “CT” allele of NGMAX006083631 (SEQ ID NO: 10), an “AC” allele of NS0202926 (SEQ ID NO: 11), a “GG” allele of NGMAX006084289 (SEQ ID NO: 12), and/or a “GG” allele of NGMAX006088354 (SEQ ID NO: 13).

Soybean plants comprising genomic region associated with the metribuzin sensitivity and metribuzin tolerance phenotypes

[0049] A non-limiting and exemplary list of soybean plants that comprise genomic regions associated with either a metribuzin sensitivity or a metribuzin tolerance phenotype are provided herewith in Table 3.

[0050] Table 3. Soybean varieties comprising a genomic region associated with a metribuzin tolerance or metribuzin sensitivity phenotype.

Branded Name¹	Metribuzin Phenotype	US Patent Number	Variety Name in Patent	ATCC Depository Accession Number²	Date of Patent Issue
TRACY	Sensitive				
BURLISON (from TRACY)	Sensitive				
H7550	Sensitive				
AG6730	Sensitive	8,203,040	A1016332	PTA-12644	19-Jun-12
AG6130	Sensitive	8207410	A1016317	PTA-12643	26-Jun-12
PAGODA	Sensitive				
DASSEL (from PAGODA)	Sensitive				
AG6931	Tolerant	2012/0030820	A1024631		
AG4730	Tolerant	8,115,076	A1016279	PTA-12275	14-Feb-12
AG4531	Tolerant	2012/0047596	A1024751		
Tracy-M	Tolerant				

¹ Branded names of Asgrow® (designated “AG”) and DEKALB® soybean varieties from Monsanto Co. 800 N. Lindbergh Blvd., St. Louis, MO, USA.

² Deposit numbers of seed available through the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, Va., USA, 20110-2209.

³ Metribuzin phenotype is the phenotype observed in the indicated germplasm containing a metribuzin sensitivity or metribuzin tolerance locus when exposed to metribuzin.

[0051] Also provided herewith are additional soybean plants that comprising a genomic region associated with a metribuzin sensitivity or metribuzin tolerance phenotype that are identified by use of the markers provided in Table 1 and/or Table 2 and/or methods provided herein. Any of the soybean plants identified in Table 3 or other soybean plants that are otherwise identified using the markers or methods provided herein can be used in methods that include, but are not limited to, methods of obtaining soybean plants with an introgressed metribuzin tolerance locus, obtaining a soybean plant that exhibits a metribuzin tolerance

phenotype, or obtaining a soybean plant comprising in its genome a genetic region associated with a metribuzin tolerance phenotype.

[0052] In certain embodiments, the soybean plants provided herein or used in the methods provided herein can comprise a transgene that confers resistance to dicamba. In certain embodiments, the dicamba tolerant soybean plants can comprise a transgene encoding a dicamba-degrading dicamba monooxygenase (DMO) enzyme that catalyzes the conversion of herbicidal dicamba (3,6-dichloro-o-anisic acid) to a non-toxic 3,6-dichlorosalicylic acid. In certain embodiments, the dicamba-degrading dicamba monooxygenase (DMOw) comprise a DMO enzyme disclosed in US Patent Nos. 7,022,896, 7,105,724, and 7,812,224, each incorporated herein by reference in their entireties. In certain embodiments, the metribuzin tolerant soybean plants can comprise a dicamba monooxygenase variant which exhibits improved catalytic parameters such as increased turnover number and/or a lower k_m for the substrate, improved catalysis at lower pH values, and/or improved catalysis at higher temperatures relative to an unaltered dicamba monooxygenase. In certain embodiments, the dicamba monooxygenase variant comprises a DMOc variant enzyme disclosed in US Patent No. 7,884,262, incorporated herein by reference in its entirety. In certain embodiments, a dicamba monooxygenase is operably linked to a chloroplast transit peptide (CTP). Operable linkage of certain CTPs to DMO is disclosed in US Patent No. 8,084,666, which is incorporated herein by reference in its entirety. In certain embodiments, it is contemplated that the soybean plants used herein can comprise one or more specific genomic insertion(s) of a dicamba tolerant transgene including, but not limited to, as those found in MON87708 soybean (deposited under ATCC accession number PTA-9670 and described in US Patent Application Publication Number 20110067134).

[0053] In certain embodiments, the soybean plants provided herein or used in the methods provided herein can comprise a transgene that confers tolerance to glyphosate. Transgenes that can confer tolerance to glyphosate include, but are not limited to, transgenes that encode glyphosate tolerant Class I EPSPS (5-enolpyruvylshikimate-3-phosphate synthases) enzymes or glyphosate tolerant Class II EPSPS (5-enolpyruvylshikimate-3-phosphate synthases) enzymes. Useful glyphosate tolerant EPSPS enzymes provided herein are disclosed in US Patent Nos. 6,803,501, RE39,247, 6,225,114, 5,188,642, and 4,971,908. In certain embodiments, the glyphosate tolerant soybean plants can comprise a transgene encoding a glyphosate oxidoreductase or other enzyme which degrades glyphosate. Glyphosate oxidoreductase enzymes had been described in US patent 5,776,760 and US Reissue patent RE38,825. In certain embodiments the soybean plant can comprise a transgene encoding a

glyphosate N-acetyltransferase gene that confers tolerance to glyphosate. In certain embodiments, the soybean plant can comprise a glyphosate n-acetyltransferase encoding transgene such as those described in US Patent No. 7,666,644. In still other embodiments, soybean plants comprising combinations of transgenes that confer glyphosate tolerance are provided. Soybean plants comprising both a glyphosate resistant EPSPS and a glyphosate N-acetyltransferase are also provided herewith. In certain embodiments, it is contemplated that the soybean plants used herein can comprise one or more specific genomic insertion(s) of a glyphosate tolerant transgene including, but not limited to, as those found in: i) MON89788 soybean (deposited under ATCC accession number PTA-6708 and described in US Patent Application Publication Number 2010/0099859), ii) GTS 40-3-2 soybean (Padgett et al., Crop Sci. 35: 1451-1461, 1995), iii) event 3560.4.3.5 soybean (seed deposited under ATCC accession number PTA-8287 and described in US Patent Publication 2009/0036308), or any combination of i (MON89788 soybean), ii (GTS 40-3-2 soybean), and iii (event 3560.4.3.5 soybean).

[0054] In certain embodiments, metribuzin tolerant soybean provided herein can further comprise transgenes that confer resistance to both dicamba and glyphosate.

[0055] In certain embodiments, it is contemplated that genotypic assays that provide for non-destructive identification of the plant or plants can be performed either in seed, the emergence stage, the "VC" stage (i.e. cotyledons unfolded), the V1 stage (appearance of first node and unifoliate leaves), the V2 stage (appearance of the first trifoliate leaf), and thereafter. In certain embodiments, non-destructive genotypic assays are performed in seed using apparatus and associated methods as described in US Patents Nos. 6,959,617; 7,134,351; 7,454,989; 7,502,113; 7,591,101; 7,611,842; and 7,685,768, which are incorporated herein by reference in their entireties. In certain embodiments, non-destructive genotypic assays are performed in seed using apparatus and associated methods as described in US Patent Application Publications 2010/0086963, 2009/0215060, and 2009/0025288, which are incorporated herein by reference in their entireties. Published US Patent Applications US 2006/0042527, US 2006/0046244, US 2006/0046264, US 2006/0048247, US 2006/0048248, US 2007/0204366, and US 2007/0207485, which are each incorporated herein by reference in their entirety, also disclose apparatus and systems for the automated sampling of seeds as well as methods of sampling, testing and bulking seeds. Thus, in a certain embodiments, any of the methods provided herein can comprise screening for markers in individual seeds of a population wherein only seed with at least one genotype of interest is advanced.

Molecular Assisted Breeding Techniques

[0056] Genetic markers that can be used in the practice of the instant invention include, but are not limited to, are Restriction Fragment Length Polymorphisms (RFLP), Amplified Fragment Length Polymorphisms (AFLP), Simple Sequence Repeats (SSR), Single Nucleotide Polymorphisms (SNP), Insertion/Deletion Polymorphisms (Indels), Variable Number Tandem Repeats (VNTR), and Random Amplified Polymorphic DNA (RAPD), and others known to those skilled in the art. Marker discovery and development in crops provides the initial framework for applications to marker-assisted breeding activities (US Patent Applications 2005/0204780, 2005/0216545, 2005/0218305, and 2006/00504538). The resulting "genetic map" is the representation of the relative position of characterized loci (DNA markers or any other locus for which alleles can be identified) along the chromosomes. The measure of distance on this map is relative to the frequency of crossover events between sister chromatids at meiosis.

[0057] As a set, polymorphic markers serve as a useful tool for fingerprinting plants to inform the degree of identity of lines or varieties (US Patent No. 6,207,367). These markers form the basis for determining associations with phenotype and can be used to drive genetic gain. The implementation of marker-assisted selection is dependent on the ability to detect underlying genetic differences between individuals.

[0058] Certain genetic markers for use in 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.

[0059] In another embodiment, markers that include, but are not limited, to 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 metribuzin tolerance loci, regions flanking metribuzin tolerance loci, regions linked to metribuzin tolerance loci, and/or regions that are unlinked to metribuzin tolerance loci can be used in certain embodiments of the instant invention.

[0060] In one embodiment, nucleic acid-based analyses for determining the presence or absence of the genetic polymorphism (i.e. for genotyping) 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, portions of genes, QTL, alleles, or genomic regions (genotypes) that comprise or are linked to a genetic marker that is linked to or correlated with metribuzin tolerance loci, regions flanking metribuzin tolerance loci, regions linked to metribuzin tolerance loci, and/or regions that are unlinked to metribuzin tolerance loci can be used in certain embodiments of the instant invention.

[0061] Nucleic acid analysis methods provided herein include, but are not limited to, PCR-based detection methods (for example, TaqMan assays), microarray methods, mass spectrometry-based methods and/or 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.

[0062] 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; US Patent 4,683,202; US Patent 4,582,788; and US 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.

[0063] Methods for typing DNA based on mass spectrometry can also be used. Such methods are disclosed in US Patents 6,613,509 and 6,503,710, and references found therein. 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 US Patent Nos. 5,468,613, 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; 5,616,464; 7,312,039; 7,238,476; 7,297,485; 7,282,355; 7,270,981 and 7,250,252 all of which are incorporated herein by

reference in their entireties. However, the compositions and methods of the present invention can be used in conjunction with any polymorphism typing method to type polymorphisms in genomic DNA samples. These genomic DNA samples used include but are not limited to genomic DNA isolated directly from a plant, cloned genomic DNA, or amplified genomic DNA.

[0064] For instance, polymorphisms in DNA sequences can be detected by hybridization to allele-specific oligonucleotide (ASO) probes as disclosed in US Patent No. 5,468,613 and 5,217,863. US Patent No. 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.

Target nucleic acid sequence can also be detected by probe ligation methods as disclosed in US Patent No. 5,800,944 where sequence of interest is amplified and hybridized to probes followed by ligation to detect a labeled part of the probe.

[0065] 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 Patent Nos. 6,799,122; 6,913,879; and 6,996,476.

[0066] Target nucleic acid sequence can also be detected by probe linking methods as disclosed in US Patent No. 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 the probes to the 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.

[0067] 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 US Patent Nos. 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 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 genomic DNA which flanks a region containing the polymorphism to be assayed. Following amplification of the region of the 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 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.

[0068] In another method for detecting polymorphisms, SNPs and Indels can be detected by methods disclosed in US Patent Nos. 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.

[0069] In another embodiment, the locus or loci of interest can be directly sequenced using nucleic acid sequencing technologies. Methods for nucleic acid sequencing are known in the art and include technologies provided by 454 Life Sciences (Branford, CT), Agencourt Bioscience (Beverly, MA), Applied Biosystems (Foster City, CA), LI-COR Biosciences

(Lincoln, NE), NimbleGen Systems (Madison, WI), Illumina (San Diego, CA), and VisiGen Biotechnologies (Houston, TX). Such nucleic acid sequencing technologies comprise formats such as parallel bead arrays, sequencing by ligation, capillary electrophoresis, electronic microchips, "biochips," microarrays, parallel microchips, and single-molecule arrays, as reviewed by R.F. Service *Science* 2006 311:1544-1546.

[0070] The markers to be used in the methods of the present invention should preferably be diagnostic of origin in order for inferences to be made about subsequent populations. Experience to date suggests that SNP markers may be 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 appear to be useful for tracking and assisting introgression of QTLs, particularly in the case of genotypes.

Examples

[0071] The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1: Metribuzin Phenotyping: Field Screening and Greenhouse Screening.

[0072] Field screening for metribuzin tolerance in soybeans was performed at the Monsanto Company Soybean Research Station near Mount Olive, NC in 2010 and 2011. Metribuzin application rate was 0.5 lbs/acre metribuzin (Sencor®, Bayer Crop Science, Research Triangle Park, NC, USA) one day prior to planting. Rows were planted as single 6' row plots with 9 seed per foot. Multiple repetitions were grown per row. Within 24 hours after planting, the trial was irrigated with 0.5" of water to help incorporate and activate the herbicide. Injury ratings were taken fourteen to twenty one (14-21) days after planting using a 1-9 scale (for example, 1 = no damage, 9 = completely killed).

[0073] Greenhouse screening for metribuzin tolerance in soybeans was performed using 10 seeds per entry planted in a pot filled with a sandy soil. Pots were then sprayed with 0.25 lbs

/ acre metribuzin then lightly soaked with water to incorporate herbicide. Metribuzin ratings were then taken seven (7), fourteen (14), and twenty one (21) days after spraying using a 1-9 scale as in the field.

Example 2: Mapping Populations to Screen for Metribuzin Tolerance

[0074] A mapping population from a cross between a metribuzin sensitive and a metribuzin tolerant plant (AG6730 x AG4531) generated 232 F2:3 rows. Tissue was sampled and genotyped with 127 SNP markers. Then, F2:4 seed from all 232 plant rows were phenotyped in the greenhouse using the method described in Example 1. A major locus was mapped using R/qtl software (<http://www.rqtl.org/>).

Example 3. Marker-Trait Association for Metribuzin Tolerance

[0075] After identifying the target region through the mapping population described in Example 2, a molecular marker was identified. An association study was done using a soybean molecular marker database. Over 200 commercial and breeding lines were characterized for metribuzin tolerance in field and greenhouse screening, as described in Example 1. The marker NGMAX006079502 was found to be tightly linked to the metribuzin tolerance trait and could be useful for marker assisted selection (MAS) to select for metribuzin tolerance and sensitivity in pre-commercial lines. Field studies demonstrate that a line containing the TT allele of NGMAX006079502 (SEQ ID NO:7) has a “metribuzin sensitivity” rating ranging from about 1.0 to about 3.7, indicating tolerance or moderate tolerance to metribuzin 10 days after spray herbicide application, whereas a line containing the CC allele of NGMAX006079502 (SEQ ID NO:7) has a “metribuzin sensitivity” rating ranging from about 7.0 to about 8.0, indicating sensitivity to metribuzin 10 days after spray herbicide application. Lines containing a heterozygous (CT) allele of NGMAX006079502 (SEQ ID NO:7) display a mixed phenotype of both tolerance and sensitivity in the field.

Example 4: Exemplary Marker Assays for Detecting Polymorphisms

[0076] 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 a metribuzin tolerance phenotype are given in Table 4.

[0077] Table 4: Exemplary Assays for Detecting Polymorphisms

Marker or Locus Name	Marker SEQ NO ID:	SNP Position	SEQ ID NO Forward Primer	SEQ ID NO Reverse Primer	SEQ ID NO Probe 1	SEQ ID NO Probe 2
NS0138011	9	385	14	15	16	17
NS0118425	37	303	39	40	41	42

Example 5: Oligonucleotide Probes Useful for Detecting Polymorphisms by Single Base Extension Methods

[0078] Oligonucleotides can also be used to detect or type the polymorphisms disclosed herein by single base extension (SBE)-based SNP detection methods. Exemplary oligonucleotides for use in SBE-based SNP detection are provided in Table 5. SBE methods are based on extension of a nucleotide primer that is hybridized to sequences 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 polymorphisms disclosed in this invention are provided in Table 4 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 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. Exemplary forward and reverse SBE probes are provided in Table 5.

[0079] Table 5: Exemplary SBE Probes for Detecting Polymorphisms

Marker or Locus Name	Marker (SEQ ID NO)	SNP Position	Probe (SBE)	Probe (SEQ ID NO)
NS0138011	9	385	AGTAGATTTTTCATTACAG	16
			AGATTGTGTCATTACAG	17
NS0118425	37	303	AGGTACATGGCTTATT	41
			AGGTACAGGGCTTAT	42

[0080] 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.

[0081] Although the materials and methods of this invention have been described in terms of various embodiments and illustrative examples, it will be apparent to those of skill in the art that variations can be applied to the materials and methods described herein without departing from the concept, spirit and scope of the invention. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

[0082] Table 2 of the Specification.

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TA41246_3847		Glycine_max_release_2	2987781	2990873	EPSP synthase [Phaseolus vulgaris (Kidney bean) (French bean)]
TC25280		LJGI.070108	2987966	2990818	similar to UniRef100_Q30CZ8 Cluster: 3-phosphoshikimate 1-carboxyvinyltransferase, n=1, Fagus sylvatica Rep: 3-phosphoshikimate 1-carboxyvinyltransferase - Fagus sylvatica (Beechnut), partial (61%)
TA4400_34305		Lotus_japonicus_release_1	2987966	2990821	Putative 5-enolpyruvylshikimate 3-phosphate synthase [Fagus sylvatica (Beechnut)]
EE124475		Arachis_hypogaea_release_5	2988836	2990821	Cluster: 3-phosphoshikimate 1-carboxyvinyltransferase, n=1, Medicago truncatula Rep: 3-phosphoshikimate 1-carboxyvinyltransferase - Medicago truncatula (Barrel medic)
TC351295		GMGI.042210	2988873	2990872	similar to UniRef100_Q946U9 3-phosphoshikimate 1-carboxyvinyltransferase - Dicliptera chinensis, partial (31%)
364540_3303_344_3_primers		cajanus_cajan	2989514	2990455	NA
364540_3303_344_3		cajanus_cajan	2989473	2990556	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC396920		GMGI.042210	2990455	2990911	similar to UniRef100_Q30CZ8 3-phosphoshikimate 1-carboxyvinyltransferase - Fagus sylvatica (Beechnut), partial (12%)
BARCSOYSSR_03_0169		Wm82_potential SSR	2992305	2992342	NA
BG726324		Glycine_max_release_2	2993161	2993597	Transketolase 7 [Craterostigma plantagineum]
Contig5194		cajanus_cajan	2993322	2993456	NA
420200_3495_3356		cajanus_cajan	2993449	2993647	NA
321475_2492_2114		cajanus_cajan	2993543	2993598	NA
TA47385_3847		Glycine_max_release_2	2993258	2993936	Transketolase= C-terminal-like [Medicago truncatula (Barrel medic)]
283539_1537_3517		cajanus_cajan	2993575	2993647	NA
BARC-028645-05979		Wm82xPI468916	2993383	2993935	NA
CA901097		Phaseolus_coccineus_release_2	2993660	2993887	Transketolase, chloroplast [Zea mays (Maize)]
419871_3332_0838		cajanus_cajan	2993675	2993950	NA
076083_1270_3130		cajanus_cajan	2993778	2993858	NA
CB543460		Phaseolus_vulgaris	2993758	2994188	UniRef100_Q7SIC9 Transketolase, chloroplastic n=1 Tax=Zea mays RepID=TKTC_MAIZE 8.00E-72
NS0206337	1		2994256	2993925	
NS0262835	21				

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC350652		GMGI.042210	2993763	2994578	homologue to UniRef100_A7QGQ5 Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vinifera (Grape), partial (36%)
Contig47295		cajanus_cajan	2994121	2994425	NA
TC415391		GMGI.042210	2993161	2995388	homologue to UniRef100_A7QGQ5 Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vinifera (Grape), partial (75%)
TA47387_3847		Glycine_max_release_2	2993421	2995388	Transketolase= C-terminal-like [Medicago truncatula (Barrel medic)]
086553_2836_0981		cajanus_cajan	2994220	2994625	NA
TA3218_3886		Phaseolus_coccineus_release_2	2993945	2994914	Putative transketolase [Oryza sativa (japonica cultivar-group)]
asembl_1387		Vigna_unguiculata	2993464	2995403	NA
TA389_3870		Lupinus_albus_release_2	2994040	2994941	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]
TA4041_34305		Lotus_japonicus_release_1	2993956	2995456	Transketolase [Polygonum tinctorium]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC32586		LJGI.070108	2993956	2995456	homologue to UniRef100_A7QGQ5 Cluster: Chromosome chr16 scaffold_94, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vinifera (Grape), partial (52%)
EG030594		Arachis_hypogaea_release_5	2994096	2995502	Cluster: Transketolase, C-terminal-like, n=1, Medicago truncatula Rep: Transketolase, C-terminal-like - Medicago truncatula (Barrel medic)
327358_3627_1811		cajanus_cajana	2994925	2995342	NA
Gm_W82_CR03.G17750		Gm_W82_CR03	2993068	2997229	Average Cons Position=LG06 29.4 cM: Q7SIC9 Transketolase, chloroplast 0 ; Q43848 Transketolase, chloroplast precursor 0

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03200		Glyma1	2993113	2997229	ID:2.2.1.1 (EC)=Transketolase.; ID:CALVIN-PWY (SoyCyc)=Activity=transketolase; Pathway=Calvin-Benson-Bassham cycle; ID:GO:0003824 (GO)=catalytic activity; ID:GO:0008152 (GO)=metabolism; ID:K00615 (KO)=E2.2.1.1, tktA, tktB; transketolase [EC:2.2.1.1] [COG:COG0021] [GO:0004802]; ID:KOG0523 (KOG)=Transketolase; ID:P21-PWY (SoyCyc)=Activity=transketolase; Pathway=pentose phosphate pathway partial; ID:PF02780 (PFAM)=Transketolase, C-terminal domain; ID:PTHR11624 (Panther)=DEHYDROGENASE RELATED; ID:PWY-5723 (SoyCyc)=Activity=transketolase; Pathway=Rubisco shunt
CB540475		Phaseolus_vulgaris	2994918	2995549	UniRef100_A9P7Z7 Putative uncharacterized protein n=1 Tax=Populus trichocarpa RepID=A9P7Z7_POPTR 7.00E-66
CB540475		Phaseolus_vulgaris_release 2	2994932	2995549	Transketolase [Polygonum tinctorium]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC127321		MTGI.071708	2994911	2995908	homologue to UniRef100_A7QGQ5 Cluster: Chromosome chr16 scaffold_94, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr16 scaffold_94, whole genome shotgun sequence - Vitis vinifera (Grape), partial (30%)
162536_1790_1692		cajanus_cajan	2995327	2995533	NA
Cfl4551d		Chafa1_1clean	2995413	2995523	NA
BE660224		GMGI.042210	2995327	2997132	similar to UniRef100_Q7SIC9 Transketolase, chloroplast - Zea mays (Maize), partial (28%)
TA74539_3847		Glycine_max_release_2	2995336	2997165	Putative transketolase [Oryza sativa (japonica cultivar-group)]
TC356209		GMGI.042210	2995467	2997215	homologue to UniRef100_Q7SIC9 Transketolase, chloroplast - Zea mays (Maize), partial (25%)
Cfl8959d		Chafa1_1clean	2996710	2996972	NA
017718_3891_1341		cajanus_cajan	3001808	3001894	NA
asmb1_1388		Vigna_unguiculata	3001905	3002039	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC363195		GMGL042210	3001739	3003321	similar to UniRef100_Q2HS72 RecA bacterial DNA recombination protein - Medicago truncatula (Barrel medic), partial (73%)
TA72645_3847		Glycine_max_release_2	3001802	3003321	RecA bacterial DNA recombination protein; Rad51= N-terminal [Medicago truncatula (Barrel medic)]
TC118321		MTGL071708	3001993	3003907	homologue to UniRef100_Q2HS72 Cluster: RecA bacterial DNA recombination protein, n=1, Medicago truncatula Rep: RecA bacterial DNA recombination protein - Medicago truncatula (Barrel medic), complete
Glyma03g03210		Glyma1	3001993	3005606	ID:KOG1434 (KOG)=Meiotic recombination protein Dmc1; ID:PF08423 (PFAM)=Rad51; ID:PTHR22942 (Panther)=RECA/RAD51/RADA DNA STRAND-PAIRING FAMILY MEMBER
Gm_W82_CR03.G17760		Gm_W82_CR03	3001993	3005606	Average Cons Position=LG06 29.5 cM: Q2HS72 RecA bacterial DNA recombination protein 1E-115

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC376154		GMGI.042210	3002839	3005687	homologue to UniRef100_Q2HS72 RecA bacterial DNA recombination protein - Medicago truncatula (Barrel medic), partial (55%)
AW203630		Glycine_max_release_2	3003133	3005645	RecA bacterial DNA recombination protein; Rad51= N-terminal [Medicago truncatula (Barrel medic)]
asmb1_1389		Vigna_unguiculata	3003153	3005658	NA
TC397626		GMGI.042210	3003192	3005712	similar to UniRef100_A7PYE0 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (41%)
GD956184		GMGI.042210	3008221	3008344	NA
AI988137		Glycine_max_release_2	3008222	3008482	NA
TC372542		GMGI.042210	3008222	3008967	similar to UniRef100_Q2HS71 SAM (And some other nucleotide) binding motif, Methyltransferase small, Tetratricopeptide-like helical - Medicago truncatula (Barrel medic), partial (19%)
Cf3692d		Chafal_1clean	3008508	3009020	NA
Cf18146d		Chafal_1clean	3011112	3011259	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03230		Glyma1	3008222	3014755	ID:KOG3191 (KOG)=Predicted N6-DNA-methyltransferase; ID:PF08242 (PFAM)=Methyltransferase domain; ID:PTHR18895 (Panther)=METHYLTRANSFERASE
Gm_W82_CR03.G17770		Gm_W82_CR03	3008221	3014755	Average Cons Position=LG06 29.5 cM: Q2HS71 SAM (And some other nucleotide) binding motif; Methyltransferase small; Tetratricopeptide-like helical 1E-120
Glyma03g03240		Glyma1	3011139	3012212	ID:PTHR10483 (Panther)=PENTATRICOPEPTIDE REPEAT-CONTAINING PROTEIN
Gm_W82_CR03.G17780		Gm_W82_CR03	3011139	3012212	Average Cons Position=LG06 29.5 cM: Q2HS71 SAM (And some other nucleotide) binding motif; Methyltransferase small; Tetratricopeptide-like helical 1E-162
TA4527_3886		Phaseolus_coccineus_release_2	3008884	3014665	Methyltransferase small domain, putative [Medicago truncatula (Barrel medic)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC354042		GMGL.042210	3008857	3014753	similar to UniRef100_Q2HS71 SAM (And some other nucleotide) binding motif, Methyltransferase small, Tetratricopeptide-like helical - Medicago truncatula (Barrel medic), partial (11%)
BARC-056039-14002		marker_map4	3017669	3018289	NA
BARC-056115-14110		marker_map4	3017705	3018289	NA
asmb1_1390		Vigna_unguiculata	3021474	3022546	NA
BI970682		Glycine_max_release_2	3021390	3024499	Glycoprotease family= putative [Medicago truncatula (Barrel medic)]
CB542218		Phaseolus_vulgaris_release_2	3021591	3024498	Glycoprotease family= putative [Medicago truncatula (Barrel medic)]
TA63194_3847		Glycine_max_release_2	3021411	3024685	Glycoprotease family= putative [Medicago truncatula (Barrel medic)]
NGMAX006076547	18		3023578	3023879	
TC405131		GMGL.042210	3021335	3030119	homologue to UniRef100_Q2HS64 Peptidase M22, glycoprotease - Medicago truncatula (Barrel medic), partial (67%)
TA63193_3847		Glycine_max_release_2	3021718	3030109	Glycoprotease family= putative [Medicago truncatula (Barrel medic)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC125199		MTGI.071708	3021786	3032333	UniRef100_Q2HS64 Cluster: Peptidase M22, glycoprotease, n=1, Medicago truncatula Rep: Peptidase M22, glycoprotease - Medicago truncatula (Barrel medic), complete
Glyma03g03250		Glymal	3021324	3034049	ID:GO:0004222 (GO)=metalloendopeptidase activity; ID:GO:0006508 (GO)=proteolysis and peptidolysis; ID:KOG2707 (KOG)=Predicted metalloprotease with chaperone activity (RNase H/HSP70 fold); ID:PF00814 (PFAM)=Glycoprotease family; ID:PTHR11735 (Panther)=O-SIALOGLYCOPROTEIN ENDOPEPTIDASE
Gm_W82_CR03.G17790		Gm_W82_CR03	3021323	3034105	Average Cons Position=LG06 29.6 cM: O22145 Putative O-sialoglycoprotein endopeptidase 0
Cf13676d		Chafa1_1clean	3024476	3031407	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC137301		MTGI.071708	3029622	3033990	similar to UniRef100_A7PYD9 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (54%)
TA63618_3847		Glycine_max_release_2	3029959	3034049	Glycoprotease family protein= expressed [Oryza sativa (japonica cultivar-group)]
TC382576		GMGI.042210	3029959	3034049	similar to UniRef100_A7PYD9 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (37%)
BG363097		Glycine_max_release_2	3031745	3033870	Putative O-sialoglycoprotein endopeptidase [Arabidopsis thaliana (Mouse-ear cress)]
Cf633d		Chafal_1clean	3042871	3043868	NA
Contig37404		cajanus_cajan	3043758	3044495	NA
AW780582		Glycine_max_release_2	3043770	3045739	Arginase [Glycine max (Soybean)]
BM524551		Glycine_soja_release_2	3043778	3047793	Arginase [Glycine max (Soybean)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03270		Glyma1	3042599	3050225	ID:ARG-PRO-PWY (SoyCyc)=Activity=arginase; Pathway=arginine degradation VI arginase 2 pathway; ID:ARGASEDEG-PWY (SoyCyc)=Activity=arginase; Pathway=arginine degradation I arginase pathway; ID:GO:0016813 (GO)=hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines; ID:GO:0046872 (GO)=metal ion binding; ID:KOG2964 (KOG)=Arginase family protein; ID:PF00491 (PFAM)=Arginase family; ID:PTHR11358 (Panther)=ARGINASE/AGMATINASE-RELATED; ID:PWY-31 (SoyCyc)=Activity=arginase; Pathway=canavanine degradation; ID:PWY-4984 (SoyCyc)=Activity=arginase; Pathway=urea cycle
TA47821_3847		Glycine_max_release_2	3042608	3050217	Arginase [Glycine max (Soybean)]
TC349067		GMGI.042210	3042608	3050222	homologue to UniRef100_O49046 Arginase - Glycine max (Soybean), complete
Gm_W82_CR03.G17800		Gm_W82_CR03	3042608	3050226	Average Cons Position=LG06 29.7 cM: O49046 Arginase 0 ; Q9ZPF5 Probable arginase 1E-149
AF035671.1		GenBank	3042649	3050212	arginase (pAG1) mRNA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TA2587_3848		Glycine_soja_release_2	3042694	3050217	Arginase [Glycine max (Soybean)]
AW201630		Glycine_max_release_2	3044392	3050203	Arginase [Glycine max (Soybean)]
TA47820_3847		Glycine_max_release_2	3044443	3050217	Arginase [Glycine max (Soybean)]
BE555381		Glycine_max_release_2	3044476	3050215	Arginase [Glycine max (Soybean)]
AW760224		Glycine_max_release_2	3045393	3050217	Arginase [Glycine max (Soybean)]
BARCSOYSSR_03_0170		Wm82_potential_SSR	3049488	3049513	NA
087411_2830_1033		cajanus_cajan	3057794	3057947	NA
BARCSOYSSR_03_0171		Wm82_potential_SSR	3060741	3060796	NA
CB829372		LJGI.070108	3064721	3066034	similar to UniRef100_A7PYD6 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (25%)
CB829372		Lotus_japonicus_release_1	3064721	3066048	Protein At1g02020 [Arabidopsis thaliana (Mouse-ear cress)]
Cf9076d		Chafal_1clean	3065839	3066273	NA
Glyma03g03280		Glyma1	3064341	3068565	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G18410		Gm_W82_CR03	3064341	3068565	Average Cons Position=LG06 29.7 cM: O23673 T7I23.2 protein 0
Cf9022d		Chafa1_1clean	3067253	3068192	NA
TC359066		GMGL.042210	3067284	3068559	similar to UniRef100_A7PYD6 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (12%)
TC372531		GMGL.042210	3068073	3068531	homologue to UniRef100_A7PYD6 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (6%)
TA75426_3847		Glycine_max_release_2	3068073	3068565	Hypothetical protein OSJNBa0040E17.29 [Oryza sativa (japonica cultivar-group)]
087411_2830_1033		cajanus_cajan	3068301	3068451	NA
TC415540		GMGL.042210	3070549	3071117	NA
TA70620_3847		Glycine_max_release_2	3070549	3071597	NA
NGMAX006076962	22		3071027	3071328	
BI786980		GMGL.042210	3071177	3071597	weakly similar to UniRef100_A7PYD5 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (22%)

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03290		Glyma1	3070549	3072650	ID:PF04483 (PFAM)=Protein of unknown function (DUF565)
Gm_W82_CR03.G18420		Gm_W82_CR03	3070422	3073399	Average Cons Position=LG06 29.8 cM: Q0DLP9 Os03g0852600 protein 1E-34
TC418355		GMGL042210	3075339	3075497	NA
Contig18691		cajanus_cajan	3075406	3075624	NA
TA55073_3847		Glycine_max_release_2	3075408	3076254	Hypothetical protein P0450A04.130 [Oryza sativa (japonica cultivar-group)]
CV543227		Phaseolus_vulgaris	3075585	3076188	UniRef100_A5ASW2 Putative uncharacterized protein (Chromosome chr14 scaffold_54, whole genome shotgun sequence) n=1 Tax=Vitis vinifera RepID=A5ASW2_VITVI 3.00E-53
238610_1965_0511		cajanus_cajan	3076032	3076243	NA
asmb1_1391		Vigna_unguiculata	3075856	3076521	NA
Cf9860d		Chafa1_1clean	3075867	3077453	NA
TA4520_3886		Phaseolus_coccineus_release_2	3076094	3077495	T12H1.6 protein [Arabidopsis thaliana (Mouse-ear cress)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03300		Glyma1	3075339	3078303	ID:GO:0008152 (GO)=metabolism; ID:GO:0008168 (GO)=methyltransferase activity; ID:PF08241 (PFAM)=Methyltransferase domain
Gm_W82_CR03.G18430		Gm_W82_CR03	3075339	3078304	Average Cons Position=LG06 29.8 cM: Q9MAA9 T12H1.6 protein 1E-122
TA55075_3847		Glycine_max_release_2	3076131	3077516	T12H1.6 protein [Arabidopsis thaliana (Mouse-ear cress)]
TC354860		GMGI.042210	3075416	3078301	NA
CA853858		Glycine_max_release_2	3076316	3077605	T12H1.6 protein [Arabidopsis thaliana (Mouse-ear cress)]
185290_3395_2875		cajanus_cajan	3079604	3079688	NA
444994_2753_3644		cajanus_cajan	3079467	3079945	NA
Contig2609_prime rs		cajanus_cajan	3079569	3079914	NA
444994_2753_3644 primers		cajanus_cajan	3079569	3079932	NA
291757_0504_1157		cajanus_cajan	3079486	3080310	NA
Contig37450		cajanus_cajan	3079464	3081239	NA
Contig37450_prime rs		cajanus_cajan	3079563	3081184	NA
Contig2609		cajanus_cajan	3079433	3081345	NA
Contig15720_prime rs		cajanus_cajan	3079543	3081269	NA
Contig15720		cajanus_cajan	3079444	3081466	NA
Contig15959		cajanus_cajan	3079586	3081351	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Contig10545		cajanus_cajan	3079604	3081484	NA
297476_1912_225 2_primers		cajanus_cajan	3079917	3081197	NA
134435_3488_171 4		cajanus_cajan	3079885	3081264	NA
297476_1912_225 2		cajanus_cajan	3079885	3081282	NA
354427_2886_207 4		cajanus_cajan	3079885	3081283	NA
400685_3217_246 4		cajanus_cajan	3079885	3081302	NA
213795_0367_400 2_primers		cajanus_cajan	3079929	3081272	NA
Contig10545_primers		cajanus_cajan	3079921	3081281	NA
213795_0367_400 2		cajanus_cajan	3079850	3081361	NA
TA50789_3847		Glycine_max_release_2	3079539	3081720	Hypothetical protein At2g45260 [Arabidopsis thaliana (Mouse-ear cress)]
Contig40445		cajanus_cajan	3079885	3081386	NA
asmbl_1393		Vigna_unguiculata	3079530	3081795	NA
CA912097		Phaseolus_coccineus_release_2	3079548	3081861	Hypothetical protein At2g45260 [Arabidopsis thaliana (Mouse-ear cress)]
TC352567		GMGI.042210	3079521	3081925	homologue to UniRef100_A7PYD3 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (52%)

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
CV537759		Phaseolus_vulgaris	3079566	3081984	UniRef100_A7PYD3 Chromosome chr15 scaffold_37, whole genome shotgun sequence n=1 Tax=Vitis vinifera RepID=A7PYD3_VITVI 1.00E-119
asmb1_1392		Vigna_unguiculata	3079530	3082028	NA
FE898754		Phaseolus_vulgaris	3079885	3081807	UniRef100_A7PYD3 Chromosome chr15 scaffold_37, whole genome shotgun sequence n=1 Tax=Vitis vinifera RepID=A7PYD3_VITVI 3.00E-71
314959_2658_0543		cajanus_cajan	3081064	3081283	NA
Glyma03g03310		Glyma1	3079477	3082885	ID:PF04859 (PFAM)=Plant protein of unknown function (DUF641)
TC388566		GMGI.042210	3079495	3082869	similar to UniRef100_A7PYD3 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), complete
286143_2148_1171		cajanus_cajan	3081239	3081430	NA
443764_2874_4020		cajanus_cajan	3081315	3081484	NA
358725_3113_3723		cajanus_cajan	3081352	3081476	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BW631067		LJGI.070108	3081192	3081649	similar to UniRef100_A7PYD3 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (31%)
Cf2278d		Chafa1_1clean	3081259	3081599	NA
020962_2290_0631		cajanus_cajan	3081485	3081697	NA
TC115824		MTGI.071708	3081192	3082028	similar to UniRef100_A7PYD3 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (58%)
Cf20941d		Chafa1_1clean	3081615	3082518	NA
Contig45852		cajanus_cajan	3082034	3082358	NA
BI425936		Glycine_max_release_2	3081947	3082470	Expressed protein [Oryza sativa (japonica cultivar-group)]
BG156189		Glycine_soja_release_2	3082080	3082515	Expressed protein [Oryza sativa (japonica cultivar-group)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BE824427		Glycine_max_release_2	3082147	3082623	Hypothetical protein At2g45260 [Arabidopsis thaliana (Mouse-ear cross)]
Pvcon6930		Phaseolus_vulgaris	3082096	3082715	UniRef100_A7PYD3 Chromosome chr15 scaffold_37, whole genome shotgun sequence n=1 Tax=Vitis vinifera RepID=A7PYD3_VITVI 3.00E-66
asmb1_1394		Vigna_unguiculata	3082089	3082756	NA
032057_1031_0927		cajanus_cajan	3082397	3082465	NA
113211_0242_1108		cajanus_cajan	3082410	3082520	NA
004558_3078_0990		cajanus_cajan	3082438	3082655	NA
Contig21707		cajanus_cajan	3082447	3082655	NA
Glyma03g03320		Glyma1	3085834	3086493	ID:GO:0004857 (GO)=enzyme inhibitor activity; ID:GO:0030599 (GO)=pectinesterase activity; ID:PF04043 (PFAM)=Plant invertase/pectin methylesterase inhibitor
Gm_W82_CR03.G18450		Gm_W82_CR03	3085834	3086493	Average Cons Position=LG06 29.8 cM: O81309 F6N15.9 protein 2E-36
NGMAX006077074	2		3087650	3087951	
TC352616		GMGI.042210	3091655	3092472	similar to UniRef100_Q89EJ0 C4-dicarboxylate transport protein - Bradyrhizobium japonicum, partial (5%)

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03330		Glyma1	3091658	3092522	ID:GO:0004857 (GO)=enzyme inhibitor activity; ID:GO:0030599 (GO)=pectinesterase activity; ID:PF04043 (PFAM)=Plant invertase/pectin methylesterase inhibitor
Gm_W82_CR03.G18460		Gm_W82_CR03	3091658	3092522	Average Cons Position=LG06 29.8 cM: O81309 F6N15.9 protein 6E-39
BM139947		Glycine_max release_2	3092245	3092450	NA
BARCSOYSSR_03_0172		Wm82_potential SSR	3099116	3099163	NA
Glyma03g03340		Glyma1	3100904	3102449	ID:GO:0016747 (GO)=transferase activity, transferring groups other than amino-acyl groups; ID:PF02458 (PFAM)=Transferase family
BARCSOYSSR_03_0173		Wm82_potential SSR	3103341	3103396	NA
Contig9906_primers		cajanus_cajana	3104938	3105569	NA
TC413526		GMGI.042210	3104626	3106429	homologue to UniRef100_Q0ZPT8 Methionine aminopeptidase - Ananas comosus (Pineapple), partial (31%)
TA60719_3847		Glycine_max release_2	3104635	3106432	Methionine aminopeptidase 1 [Ananas comosus (Pineapple)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC374413		GMGL042210	3104626	3106880	homologue to UniRef100_Q0ZPT8 Methionine aminopeptidase - Ananas comosus (Pineapple), partial (33%)
Contig9906		cajanus_cajan	3104585	3106940	NA
CB539349		Phaseolus_vulgaris_release_2	3104890	3107370	Methionine aminopeptidase 1 [Ananas comosus (Pineapple)]
034894_1456_0080		cajanus_cajan	3106877	3107085	NA
Glyma03g03350		Glyma1	3104902	3109883	ID:GO:0009987 (GO)=cellular process; ID:KOG2738 (KOG)=Putative methionine aminopeptidase; ID:PF00557 (PFAM)=metallopeptidase family M24; ID:PTHR10804 (Panther)=PROTEASE FAMILY M24 (METHIONYL AMINOPEPTIDASE, AMINOPEPTIDASE P)
Cf3363d		Chafal_1clean	3104911	3109882	NA
Pvcon6396		Phaseolus_vulgaris	3104890	3111389	UniRef100_A7PYC9 Methionine aminopeptidase n=1 Tax=Vitis vinifera RepID=A7PYC9_VITVIE-0
CA906284		Phaseolus_coccineus_release_2	3106886	3109505	Methionine aminopeptidase 1A [Arabidopsis thaliana (Mouse-ear cress)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G18480		Gm_W82_CR03	3104558	3111952	Average Cons Position=LG06 29.9 cM: Q9SLN5 Methionine aminopeptidase 1A 0 ; A7PYC9 Methionine aminopeptidase 0
297876_2793_1957		cajanus_cajan	3108527	3109322	NA
316713_3644_1516		cajanus_cajan	3109394	3109635	NA
BARCSOYSSR_03_0174		Wm82_potential_SSR	3120776	3120805	NA
Glyma03g03360		Glyma1	3120992	3124949	ID:GO:0005618 (GO)=cell wall; ID:GO:0030599 (GO)=pectinesterase activity; ID:GO:0042545 (GO)=cell wall modification; ID:PF01095 (PFAM)=Pectinesterase; ID:PWY-1081 (SoyCyc)=Activity=pectinesterase; Pathway=homogalacturonan degradation
Gm_W82_CR03.G18490		Gm_W82_CR03	3120992	3124987	Average Cons Position=LG06 30 cM: Q84R10 Putative pectinesterase 1E-149
BARCSOYSSR_03_0175		Wm82_potential_SSR	3125342	3125373	NA
BARCSOYSSR_03_0176		Wm82_potential_SSR	3125603	3125626	NA
Glyma03g03370		Glyma1	3128348	3128906	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03380		Glyma1	3129953	3130354	ID:PTHR11615:SF7 (Panther)=gb def: putative formate dehydrogenase alpha subunit [thermococcus litoralis]
Gm_W82_CR03.G18510		Gm_W82_CR03	3129953	3130354	Average Cons Position=LG06 30 cM: Q8L924 UPF0497 membrane protein At2g35760 3E-20
418082_2891_0373		cajanus_cajan	3137176	3137447	NA
375319_2742_1938		cajanus_cajan	3137533	3137620	NA
Glyma03g03390		Glyma1	3136859	3138892	ID:3.1.1.11 (EC)=Pectinesterase.; ID:GO:0005618 (GO)=cell wall; ID:GO:0030599 (GO)=pectinesterase activity; ID:GO:0042545 (GO)=cell wall modification; ID:K01051 (KO)=E3.1.1.11; pectinesterase [EC:3.1.1.11] [GO:0030599]; ID:PF01095 (PFAM)=Pectinesterase; ID:PWY-1081 (SoyCyc)=Activity=pectin esterase; Pathway=homogalacturonan degradation
Contig23415		cajanus_cajan	3138247	3138699	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC388963		GMGL042210	3138211	3138811	homologue to UniRef100_A7PYC6 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (38%)
418082_2891_0373		cajanus_cajan	3150943	3151220	NA
375319_2742_1938		cajanus_cajan	3151307	3151394	NA
BARCSOYSSR_03_0177		Wm82_potential SSR	3151786	3151827	NA
Glyma03g03400		Glyma1	3150626	3154197	ID:3.1.1.11 (EC)=Pectinesterase.; ID:GO:0005618 (GO)=cell wall; ID:GO:0030599 (GO)=pectinesterase activity; ID:GO:0042545 (GO)=cell wall modification; ID:K01051 (KO)=E3.1.1.11; pectinesterase [EC:3.1.1.11] [GO:0030599]; ID:PF01095 (PFAM)=Pectinesterase; ID:PWY-1081 (SoyCyc)=Activity=pectin esterase; Pathway=homogalacturonan degradation
Contig23415		cajanus_cajan	3153333	3153797	NA
TA72681_3847		Glycine_max_release_2	3158234	3158915	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC388963		GMGL042210	3158315	3158915	homologue to UniRef100_A7PYC6 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (38%)
Contig23415		cajanus_cajan	3158426	3158880	NA
TC135041		MTGL071708	3158575	3158878	UniRef100_Q6PQ93 Cluster: Pectin methylesterase 9, n=1, Medicago truncatula Rep: Pectin methylesterase 9 - Medicago truncatula (Barrel medic), complete
Cfl6829d		Chafa1_1clean	3158264	3159610	NA
Glyma03g03410		Glyma1	3158102	3160282	ID:3.1.1.11 (EC)=Pectinesterase.; ID:GO:0005618 (GO)=cell wall; ID:GO:0030599 (GO)=pectinesterase activity; ID:GO:0042545 (GO)=cell wall modification; ID:K01051 (KO)=E3.1.1.11; pectinesterase [EC:3.1.1.11] [GO:0030599]; ID:PF01095 (PFAM)=Pectinesterase; ID:PWY-1081 (SoyCyc)=Activity=pectin esterase; Pathway=homogalacturonan degradation
375319_2742_1938		cajanus_cajan	3159522	3159607	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
418082_2891_0373		cajanus_cajan	3159695	3159964	NA
BARCSOYSSR_03_0178		Wm82_potential SSR	3163958	3164025	NA
Glyma03g03420		Glyma1	3166793	3167020	NA
Gm_W82_CR03.G18550		Gm_W82_CR03	3166793	3167020	Average Cons Position=LG06 30.2 cM: Q8L924 UPF0497 membrane protein At2g35760 2E-13
BARCSOYSSR_03_0179		Wm82_potential SSR	3167750	3167781	NA
SATT159			3169968	3170252	
Satt159		marker_map4	3169968	3170252	NA
BARCSOYSSR_03_0180		Wm82_potential SSR	3170121	3170162	NA
305096_0951_1070		cajanus_cajan	3170506	3170717	NA
Glyma03g03430		Glyma1	3170171	3171595	NA
Gm_W82_CR03.G18560		Gm_W82_CR03	3170171	3171595	Average Cons Position=LG06 30.2 cM: Q6PQ93 Pectin methylesterase 9 1E-26 ; O04887 Pectinesterase-2 precursor 4E-24 ; Q6PQ97 Pectin methylesterase 5 2E-22 ; Q43143 Pectinesterase U1 precursor 2E-16 ; Q9FY03 Putative pectin methylesterase precursor 4E-14
Contig23415		cajanus_cajan	3170968	3171431	NA
NGMAX006077513	23		3172140	3172441	

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
NGMAX006077555	24		3181380	3181681	
Glyma03g03440		Glyma1	3192517	3192801	NA
Gm_W82_CR03.G18570		Gm_W82_CR03	3192517	3192801	Average Cons Position=LG06 30.3 cM: Q9SM60 Phosphoglucomutase, cytoplasmic 4E-25 ; P93262 Phosphoglucomutase, cytoplasmic 3E-24
BARCSOYSSR_03_0181		Wm82_potential SSR	3194639	3194700	NA
Glyma03g03450		Glyma1	3193959	3198116	ID:PTHR13856 (Panther)=VHS DOMAIN CONTAINING PROTEIN FAMILY
Gm_W82_CR03.G18580		Gm_W82_CR03	3193959	3198116	Average Cons Position=LG06 30.4 cM: Q2V732 VHS and GAT domain protein 3E-12
TA67921_3847		Glycine_max_release_2	3197245	3197763	NA
TC407739		GMGI.042210	3197272	3197763	similar to UniRef100_Q2HSP6 General substrate transporter - Medicago truncatula (Barrel medic), partial (4%)
BARCSOYSSR_03_0182		Wm82_potential SSR	3199583	3199604	NA
BARCSOYSSR_03_0183		Wm82_potential SSR	3199966	3200010	NA
Contig32455		cajanus_cajan	3200657	3200918	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Contig19141		cajanus_cajan	3200851	3201091	NA
Cf10417d		Chafal_1clean	3200836	3201120	NA
TC377879		GMGI.042210	3200720	3201287	similar to UniRef100_A7PYC6 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (27%)
418082_2891_0373		cajanus_cajan	3201086	3201309	NA
375319_2742_1938		cajanus_cajan	3201519	3201601	NA
BQ576469		GMGI.042210	3201494	3201914	similar to UniRef100_O04887 Pectinesterase-2 precursor - Citrus sinensis (Sweet orange), partial (10%)
BQ576469		Glycine_max_release_2	3201494	3202078	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]
Glyma03g03460		Glyma1	3200770	3204918	ID:GO:0005618 (GO)=cell wall; ID:GO:0030599 (GO)=pectinesterase activity; ID:GO:0042545 (GO)=cell wall modification; ID:PF01095 (PFAM)=Pectinesterase
214452_2123_1259		cajanus_cajan	3201638	3204052	NA
Pvcon9735		Phaseolus_vulgaris	3201498	3204566	UniRef100_A7PYC6 Pectinesterase n=1 Tax=Vitis vinifera RepID=A7PYC6_VITVI 1.00E-120

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TA5573_3885		Phaseolus_vulgaris_release_2	3201498	3204566	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]
TA41878_3847		Glycine_max_release_2	3201659	3204609	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]
AW706153		GMGI.042210	3203771	3204190	similar to UniRef100_A7PYC6 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (14%)
AW706153		Glycine_max_release_2	3203769	3204345	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]
Contig23415		cajanus_cajan	3204034	3204496	NA
asembl_1395		Vigna_unguiculata	3204001	3204659	NA
AI941403		Glycine_max_release_2	3204411	3204540	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]
TA41886_3847		Glycine_max_release_2	3204278	3204684	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]
BQ453360		Glycine_max_release_2	3204384	3204908	Pectinesterase-2 precursor [Citrus sinensis (Sweet orange)]
NGMAX006077640	3		3209230	3209531	
188924_1171_4036		cajanus_cajan	3211646	3211879	NA
Glyma03g03470		Glyma1	3211521	3212299	ID:PF01657 (PFAM)=Domain of unknown function DUF26

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G18800		Gm_W82_CR03	3211521	3212299	Average Cons Position=LG06 30.4 cM: Q6NKQ9 Cysteine-rich repeat secretory protein 15 precursor 3E-47
Cf5097d		Chafa1_1clean	3225804	3226039	NA
Glyma03g03480		Glyma1	3225520	3226992	ID:PF02519 (PFAM)=Auxin responsive protein
TC362898		GMGI.042210	3225774	3226757	similar to UniRef100_A7PYC4 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (51%)
BARCSOYSSR_03_0184		Wm82_potential_SSR	3226514	3226540	NA
TA61385_3847		Glycine_max_release_2	3226092	3226992	NA
TC399758		GMGI.042210	3226663	3226990	NA
NGMAX006077878	19		3232914	3233215	
NGMAX006077928	4		3238990	3239291	
NGMAX006078122	29		3253689	3253990	
TA13126_34305		Lotus_japonicus_release_1	3254515	3259837	Golgi SNARE 12 protein [Arabidopsis thaliana (Mouse-ear cress)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC24266		LJGI.070108	3254515	3259837	homologue to UniRef100_A7PYC3 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (57%)
TC365000		GMGI.042210	3254378	3260002	similar to UniRef100_A7PYC3 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (72%)
BM094071		Glycine_max_release_2	3254443	3259972	Golgi SNARE 12 protein [Arabidopsis thaliana (Mouse-ear cress)]
Cf1646d		Chafal_1clean	3254532	3261153	NA
TC120084		MTGI.071708	3254540	3261190	similar to UniRef100_A7PYC3 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (98%)

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Pvcon4074		Phaseolus_vulgaris	3254499	3261367	UniRef100_A7PYC3 Chromosome chr15 scaffold_37, whole genome shotgun sequence n=1 Tax=Vitis vinifera RepID=A7PYC3_VITVI 1.00E-112
Glyma03g03490		Glyma1	3254361	3261723	ID:GO:0006886 (GO)=intracellular protein transport; ID:GO:0016020 (GO)=membrane; ID:K08495 (KO)=; ID:KOG3208 (KOG)=SNARE protein GS28; ID:PF05008 (PFAM)=Vesicle transport v-SNARE protein; ID:PTHR21094 (Panther)=FAMILY NOT NAMED
Gm_W82_CR03.G19220		Gm_W82_CR03	3254361	3261723	Average Cons Position=LG06 30.7 cM: O22151 Golgi SNARE 12 protein 1E-101
BP048935		Lotus_japonicus_release_1	3259926	3261261	Golgi SNARE 12 protein [Arabidopsis thaliana (Mouse-ear cress)]
DB979241		GMGI.042210	3260857	3261372	similar to UniRef100_A7PYC3 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (29%)
CD399194		Glycine_max_release_2	3260921	3261324	Golgi SNARE 12 protein [Arabidopsis thaliana (Mouse-ear cress)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BARCSOYSSR_03_0185		Wm82_potential SSR	3267129	3267172	NA
BARCSOYSSR_03_0186		Wm82_potential SSR	3269087	3269130	NA
BARCSOYSSR_03_0187		Wm82_potential SSR	3270199	3270218	NA
Contig23197		cajanus_cajan	3272203	3272416	NA
415445_2756_2388		cajanus_cajan	3272279	3272416	NA
183101_0466_0966 primers		cajanus_cajan	3273791	3273999	NA
183101_0466_0966		cajanus_cajan	3273730	3274095	NA
206423_3853_3891		cajanus_cajan	3273959	3274097	NA
TC361285		GMGI.042210	3273414	3276514	similar to UniRef100_Q6SS00 YABBY-like transcription factor GRAMINIFOLIA - Antirrhinum majus (Garden snapdragon), partial (86%)
Glyma03g03500		Glyma1	3273412	3276522	ID:PF04690 (PFAM)=YABBY protein
Gm_W82_CR03.G19230		Gm_W82_CR03	3273412	3276522	Average Cons Position=LG06 30.7 cM: Q6SS00 YABBY-like transcription factor GRAMINIFOLIA 5E-96
TA52412_3847		Glycine_max_release_2	3273416	3276522	YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus (Garden snapdragon)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Cf1177d		Chafa1_1clean	3273757	3276225	NA
TA3613_3848		Glycine_soja_release_2	3273754	3276461	YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus (Garden snapdragon)]
BARCSOYSSR_03_0188		Wm82_potential SSR	3275263	3275282	NA
Cf21553d		Chafa1_1clean	3274365	3276226	NA
BP041062		LJGI.070108	3274309	3276373	homologue to UniRef100_Q6SS00 Cluster: YABBY-like transcription factor GRAMINIFOLIA, n=1, Antirrhinum majus Rep: YABBY-like transcription factor GRAMINIFOLIA - Antirrhinum majus (Garden snapdragon), partial (46%)
CD416578		Glycine_max_release_2	3274359	3276514	YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus (Garden snapdragon)]
CD414741		Glycine_max_release_2	3274379	3276514	YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus (Garden snapdragon)]
AW311204		Glycine_max_release_2	3275751	3276514	YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus (Garden snapdragon)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
CD390542		Glycine_max release_2	3276017	3276470	NA
BARCSOYSSR_03_0189		Wm82_potential_SSR	3276885	3276948	NA
Glyma03g03510		Glyma1	3282203	3283893	ID:PTHR23258 (Panther)=SERINE-THREONINE PROTEIN KINASE, PLANT-TYPE
BM094865		Glycine_max release_2	3298597	3298959	NA
BI698917		Glycine_max release_2	3298949	3299117	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
Pvcon9484		Phaseolus_vulgaris	3298902	3299318	UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 n=1 Tax=Glycine max RepID=Q2LAL4_SOYB N 2.00E-56
BARC-031833-07221		marker_map4	3298950	3299349	NA
BARC-028619-05977		Wm82xPI468916	3298952	3299501	NA
BM526084		Glycine_soja release_2	3299204	3299786	Cytochrome P450 monooxygenase CYP83A [Glycine max (Soybean)]
TC373025		GMGI.042210	3299110	3299920	UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (29%)

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC371473		GMGL.042210	3298933	3300311	homologue to UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (47%)
BE658696		Glycine_max_release_2	3298946	3300315	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
BU080942		Glycine_max_release_2	3299348	3299922	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
CA820617		GMGL.042210	3299236	3300308	UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (30%)
Glyma03g03520		Glyma1	3298597	3301147	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:K00517 (KO)=E1.14.-.-; [EC:1.14.-.-] [COG:COG2124]; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450
Glyma03g03530		Glyma1	3298597	3301147	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TA41485_3847		Glycine_max release_2	3298610	3301147	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
TC349887		GMGI.04221 0	3298612	3301147	UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), complete
BE610066		Glycine_max release_2	3299270	3300511	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
DQ340234.1		GenBank	3298639	3301147	cytochrome P450 monooxygenase CYP83E8 (CYP83E8) mRNA
Gm_W82_CR03.G 19650		Gm_W82_C R03	3298597	3301192	Average Cons Position=LG06 30.7 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-104 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-74
Gm_W82_CR03.G 19660		Gm_W82_C R03	3298597	3301192	Average Cons Position=LG06 30.7 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 0 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-162
TA2512_3848		Glycine_soja release_2	3298823	3301065	Cytochrome P450 monooxygenase CYP83A [Glycine max (Soybean)]
BQ785233		Glycine_max release_2	3299398	3301060	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TA41499_3847		Glycine_max_release_2	3299888	3300578	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
BM177920		GMGL042210	3300031	3300450	UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (19%)
BI892902		Glycine_max_release_2	3300324	3300877	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
BE806353		Glycine_max_release_2	3300458	3300769	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
BF009836		Glycine_max_release_2	3300695	3301046	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
NGMAX006078495	30		3302666	3302967	
NS0262836	31				
Glyma03g03540		Glyma1	3319774	3321759	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G19670		Gm_W82_CR03	3319774	3321759	Average Cons Position=LG06 30.8 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-141 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-109
CV535331		Phaseolus_vulgaris	3321369	3321648	UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 n=1 Tax=Glycine max RepID=Q2LAL4_SOYB N 1.00E-34
117509_1962_0397		cajanus_cajan	3321863	3321957	NA
Contig30301		cajanus_cajan	3321862	3321958	NA
Contig5456		cajanus_cajan	3321879	3321947	NA
Contig2767		cajanus_cajan	3321862	3321990	NA
BARCSOYSSR_03_0190		Wm82_potential_SSR	3325908	3325927	NA
Cf17433d		Chafal_1clean	3328712	3328856	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03550		Glyma1	3328724	3335906	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450
Gm_W82_CR03.G19680		Gm_W82_CR03	3328724	3335906	Average Cons Position=LG06 30.8 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-180 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-162
TC418102		GMGL042210	3298810	3366106	UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (32%)
ss181360642		Wm82xPI468916	3333672	3333793	NA
NGMAX006078838	5		3335895	3336196	
BARCSOYSSR_03_0191		Wm82_potential_SSR	3337556	3337597	NA
SATT152			3338479	3338729	
Satt152		marker_map4	3338479	3338729	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BARCSOYSSR_03_0192		Wm82_potential SSR	3338620	3338682	NA
BARCSOYSSR_03_0193		Wm82_potential SSR	3338831	3338878	NA
BARCSOYSSR_03_0194		Wm82_potential SSR	3343344	3343393	NA
BARCSOYSSR_03_0195		Wm82_potential SSR	3343831	3343884	NA
Gm_W82_CR03.G19690		Gm_W82_CR03	3344402	3346608	Average Cons Position=LG06 30.9 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 0 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-166
Glyma03g03560		Glyma1	3344405	3346608	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450
DT083744		Glycine_soja_release_2	3346117	3346593	Cytochrome P450 monooxygenase CYP83A [Glycine max (Soybean)]
Glyma03g03570		Glyma1	3365144	3365263	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G19700		Gm_W82_CR03	3365144	3365263	Average Cons Position=LG06 31 cM: Q9T0K5 Extensin-like protein 2E-8 ; Q9SN46 Extensin-like protein 9E-8
BARCSOYSSR_03_0196		Wm82_potential_SSR	3366060	3366097	NA
373244_3126_3343		cajanus_cajana	3372997	3373302	NA
BARCSOYSSR_03_0197		Wm82_potential_SSR	3374862	3374925	NA
BE021801		Glycine_max_release_2	3375080	3375675	RuBisCO-associated protein [Glycine max (Soybean)]
Glyma03g03580		Glyma1	3375014	3376090	NA
Gm_W82_CR03.G19710		Gm_W82_CR03	3375014	3376090	Average Cons Position=LG06 31 cM: P39657 RuBisCO- associated protein 7E-52 ; Q2HU30 2-S globulin 2E- 35
TC379722		GMGL042210	3375263	3375949	weakly similar to UniRef100_P39657 RuBisCO-associated protein - Glycine max (Soybean), partial (31%)
TA65108_3847		Glycine_max_release_2	3375299	3375949	RuBisCO-associated protein [Glycine max (Soybean)]
NGMAX006079484	6		3389647	3389948	
ss181360636		Wm82xPI468916	3390391	3390512	NA
NGMAX006079502	7		3390962	3391263	
BARCSOYSSR_03_0198		Wm82_potential_SSR	3392252	3392297	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BARCSOYSSR_03_0199		Wm82_potential SSR	3397544	3397571	NA
TC376705		GMGI.042210	3399170	3399602	similar to UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (26%)
TA68858_3847		Glycine_max_release_2	3399170	3399761	Cytochrome P450 monooxygenase CYP83H2 [Medicago truncatula (Barrel medic)]
BQ742710		GMGI.042210	3399724	3400146	weakly similar to UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (24%)
BQ742710		Glycine_max_release_2	3399724	3400170	Cytochrome P450 monooxygenase CYP83H2 [Medicago truncatula (Barrel medic)]
Glyma03g03590		Glymal	3399194	3401129	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC379046		GMGI.042210	3400601	3401037	similar to UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (29%)
TA64119_3847		Glycine_max_release_2	3400601	3401129	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]
WmFPC_Contig1249		Wm82	3269223	3539380	NA
BARCSOYSSR_03_0200		Wm82_potential SSR	3411398	3411447	NA
Gm_W82_CR03.G19720		Gm_W82_CR03	3399152	3432251	Average Cons Position=LG06 31.2 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-178 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-161
BARCSOYSSR_03_0201		Wm82_potential SSR	3416401	3416428	NA
Glyma03g03610		Glyma1	3417813	3418036	ID:PTHR23354 (Panther)=NUCLEOLAR PROTEIN 7/ESTROGEN RECEPTOR COACTIVATOR-RELATED
Glyma03g03620		Glyma1	3420542	3421382	ID:PTHR11353:SF19 (Panther)=CHAPERONIN CONTAINING T-COMPLEX PROTEIN 1, THETA SUBUNIT, TCPQ

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G19940		Gm_W82_CR03	3420542	3421382	Average Cons Position=LG06 31.2 cM: Q75HJ3 Putative TCP-1/cpn60 chaperonin family protein 2E-14
BARCSOYSSR_03_0202		Wm82_potential SSR	3428245	3428290	NA
asmbl_1396		Vigna_unguiculata	3430242	3431029	NA
Glyma03g03630		Glyma1	3430214	3432112	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450
Cf884d		Chafa1_1clean	3399773	3462808	NA
TC383713		GMGI.042210	3430945	3431920	similar to UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (41%)
TA64120_3847		Glycine_max_release_2	3430945	3432088	Cytochrome P450 monooxygenase CYP83E8 [Glycine max (Soybean)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G19950		Gm_W82_CR03	3434392	3437069	Average Cons Position=LG06 31.2 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 0 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-168
Glyma03g03640		Glyma1	3434532	3437069	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:K00517 (KO)=E1.14.-.-; [EC:1.14.-.-] [COG:COG2124]; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450
BARCSOYSSR_03_0203		Wm82_potential SSR	3441948	3441974	NA
Contig41065		cajanus_cajan	3444039	3444288	NA
Cf19649d		Chafal_1clean	3444522	3444589	NA
Glyma03g03660		Glyma1	3453314	3454353	ID:PTHR10641 (Panther)=MYB-RELATED

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G19960		Gm_W82_CR03	3453314	3454353	Average Cons Position=LG06 31.3 cM: O04498 F21M12.15 protein 1E-13 ; Q8W149 CDC5 protein 1E-13
CX529111		MTGL071708	3454177	3454324	UniRef100_A7QMU6 Cluster: Chromosome chr14 scaffold_128, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr14 scaffold_128, whole genome shotgun sequence - Vitis vinifera (Grape), partial (5%)
NGMAX006079911	20		3454832	3455133	
TA76562_3847		Glycine_max release_2	3460426	3460986	Cytochrome P450 monooxygenase CYP83H2 [Medicago truncatula (Barrel medic)]
TC353924		GMGL042210	3460363	3462296	similar to UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (55%)

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03670		Glyma1	3460363	3463031	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450
asmb1_1397		Vigna_unguiculata	3461063	3462810	NA
BM526518		Glycine_soja_release_2	3461266	3462638	Cytochrome P450 monooxygenase CYP83A [Glycine max (Soybean)]
TA74906_3847		Glycine_max_release_2	3461106	3462803	Cytochrome P450 monooxygenase CYP83H2 [Medicago truncatula (Barrel medic)]
TC350978		GMGL042210	3461205	3463031	similar to UniRef100_Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 - Medicago truncatula (Barrel medic), partial (45%)
Contig16050		cajanus_cajani	3463437	3463904	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03680		Glyma1	3463500	3463884	ID:GO:0003735 (GO)=structural constituent of ribosome; ID:GO:0005622 (GO)=intracellular; ID:GO:0005840 (GO)=ribosome; ID:GO:0006412 (GO)=protein biosynthesis; ID:PF00318 (PFAM)=Ribosomal protein S2; ID:PTHR12534 (Panther)=30S RIBOSOMAL PROTEIN S2 (PROKARYOTIC AND ORGANELLAR)
Gm_W82_CR03.G19980		Gm_W82_CR03	3463500	3463884	Average Cons Position=LG06 31.3 cM: Q2PMT2 Chloroplast 30S ribosomal protein S2 5E-66 ; A4GGA8 Ribosomal protein S2 3E-60
282842_2235_0300		cajanus_cajana	3463717	3463904	NA
SAT_186			3465323	3465611	
Sat_186		marker_map4	3465323	3465611	NA
BARCSOYSSR_03_0204		Wm82_potential_SSR	3465436	3465507	NA
Glyma03g03690		Glyma1	3466673	3467512	ID:PTHR19383 (Panther)=CYTOCHROME P450

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G19990		Gm_W82_CR03	3466673	3467512	Average Cons Position=LG06 31.3 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 2E-59 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 6E-53
Gm_W82_CR03.G19970		Gm_W82_CR03	3460310	3482068	Average Cons Position=LG06 31.4 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-174 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-174 ; Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-174 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-174
BARCSOYSSR_03_0205		Wm82_potential SSR	3480208	3480258	NA
Glyma03g03700		Glyma1	3479524	3482068	ID:PTHR19383 (Panther)=CYTOCHROME P450
TA71903_3847		Glycine_max_release_2	3481704	3482068	Cytochrome P450 monooxygenase CYP83H2 [Medicago truncatula (Barrel medic)]
Contig35199		cajanus_cajan	3494004	3494295	NA
Contig3959		cajanus_cajan	3494076	3494316	NA
048713_3862_0404		cajanus_cajan	3494085	3494309	NA
Contig13534		cajanus_cajan	3494085	3494316	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Contig26881		cajanus_cajan	3494172	3494315	NA
Glyma03g03710		Glyma1	3496238	3496656	ID:PTHR19383 (Panther)=CYTOCHROME P450
Gm_W82_CR03.G20000		Gm_W82_CR03	3496238	3496656	Average Cons Position=LG06 31.5 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-28 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 3E-24
AI855899		GMGI.042210	3498286	3498702	similar to UniRef100_O23451 Retrotransposon like protein - Arabidopsis thaliana (Mouse-ear cress), partial (18%)
Glyma03g03720		Glyma1	3496909	3507131	ID:GO:0004497 (GO)=monooxygenase activity; ID:GO:0005506 (GO)=iron ion binding; ID:GO:0009055 (GO)=electron carrier activity; ID:GO:0020037 (GO)=heme binding; ID:KOG0156 (KOG)=Cytochrome P450 CYP2 subfamily; ID:PF00067 (PFAM)=Cytochrome P450; ID:PTHR19383 (Panther)=CYTOCHROME P450

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G 20010		Gm_W82_CR03	3496909	3507191	Average Cons Position=LG06 31.5 cM: Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 0 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-176 ; Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 1E-173 ; Q2MJ14 Cytochrome P450 monooxygenase CYP83E8 1E-167
DY577297		Glycine_max_release_2	3502642	3506305	Cytochrome P450 monooxygenase CYP83H2 [Medicago truncatula (Barrel medic)]
TC390056		GMGL042210	3506393	3507131	similar to UniRef100_Q2LAL4 Cytochrome P450 monooxygenase CYP83E8 - Glycine max (Soybean), partial (43%)
BU090520		Glycine_max_release_2	3506586	3507131	Cytochrome P450 monooxygenase CYP83H2 [Medicago truncatula (Barrel medic)]
BARCSOYSSR_03 0206		Wm82_potential_SSR	3509060	3509091	NA
Glyma03g03730		Glyma1	3519958	3523194	ID:PF07160 (PFAM)=Protein of unknown function (DUF1395)
Cf6842d		Chafal_1clean	3519956	3523224	NA
NGMAX006080509	38		3523345	3523646	

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BARCSOYSSR_03_0207		Wm82_potential SSR	3532126	3532179	NA
TA57125_3847		Glycine_max_release_2	3533027	3533555	NA
Glyma03g03740		Glyma1	3533027	3534997	NA
TC382189		GMGI.042210	3533027	3534997	homologue to UniRef100_A4TTL5 Membrane protein - Magnetospirillum gryphiswaldense, partial (7%)
TA57124_3847		Glycine_max_release_2	3533481	3534997	NA
186545_1436_2413		cajanus_cajan	3539771	3539988	NA
351424_2925_3351		cajanus_cajan	3539773	3539988	NA
Contig20883		cajanus_cajan	3539773	3539988	NA
Contig14745		cajanus_cajan	3539774	3539988	NA
Contig38065		cajanus_cajan	3539781	3539989	NA
Contig6509		cajanus_cajan	3539784	3539988	NA
219748_2942_0753		cajanus_cajan	3539790	3539988	NA
293431_2369_2884		cajanus_cajan	3539793	3539988	NA
Contig27022		cajanus_cajan	3539767	3540015	NA
Contig42885		cajanus_cajan	3539793	3539992	NA
Contig4926		cajanus_cajan	3539802	3540002	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC412519		GMGI.042210	3547628	3547947	similar to UniRef100_A5KCL8 Variable surface protein Vir24-related - Plasmodium vivax, partial (5%)
303716_2876_1271		cajanus_cajan	3548384	3548512	NA
Cf17931d		Chafa1_1clean	3548408	3548488	NA
BG046534		Glycine_soja_release_2	3547861	3549153	Hypothetical protein P0018A03.7 [Oryza sativa (japonica cultivar-group)]
Cf19308d		Chafa1_1clean	3548421	3549288	NA
131874_4007_0807		cajanus_cajan	3549054	3549310	NA
BQ785172		Glycine_max_release_2	3548932	3549589	F20B17.3 [Arabidopsis thaliana (Mouse-ear cress)]
Glyma03g03750		Glyma1	3547452	3551110	ID:K08869 (KO)=; ID:KOG1235 (KOG)=Predicted unusual protein kinase; ID:PF03109 (PFAM)=ABC1 family; ID:PTHR10566 (Panther)=CHAPERONE-ACTIVITY OF BC1 COMPLEX (CABC1)-RELATED
Cf17860d		Chafa1_1clean	3549758	3550319	NA
Cf14536d		Chafa1_1clean	3550122	3550244	NA
Cf5190d		Chafa1_1clean	3550872	3551786	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
AW736224		MTGL071708	3550986	3551846	similar to UniRef100_Q9MA15 Cluster: Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplast precursor, n=2, Arabidopsis thaliana Rep: Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplast precursor - Arabidopsis thaliana (Mouse-ear cress), partial (9%)
AW459587		GMGL042210	3551428	3551782	similar to UniRef100_Q9MA15 Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplast precursor - Arabidopsis thaliana (Mouse-ear cress), partial (6%)
TA71197_3847		Glycine_max_release_2	3551413	3552423	NA
BI321376		GMGL042210	3552012	3552423	similar to UniRef100_A7SRH1 Predicted protein - Nematostella vectensis (Starlet sea anemone), partial (3%)
NGMAX006080885	8		3561914	3562215	
BARCSOYSSR_03_0208		Wm82_potential SSR	3578993	3579090	NA
225723_2718_2863		cajanus_cajan	3581358	3581429	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Contig36250		cajanus_cajan	3581439	3581816	NA
asmb1_1398		Vigna_unguiculata	3581431	3582042	NA
TA49427_3847		Glycine_max_release_2	3581425	3582129	GRAS transcription factor [Medicago truncatula (Barrel medic)]
Cf15586d		Chafal_1clean	3581734	3581838	NA
BE820512		Glycine_max_release_2	3581448	3582150	GRAS transcription factor [Medicago truncatula (Barrel medic)]
TA7292_34305		Lotus_japonicus_release_1	3581441	3582214	GRAS transcription factor [Medicago truncatula (Barrel medic)]
TC27537		LJGI.070108	3581441	3582214	weakly similar to UniRef100_A7PYF4 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (21%)
TC365523		GMGI.042210	3581299	3582452	weakly similar to UniRef100_A7PYF4 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (23%)
TC369657		GMGI.042210	3581425	3582630	weakly similar to UniRef100_A7PYF4 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (30%)

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Cf13385d		Chafa1_1clean	3581734	3582618	NA
TA49425_3847		Glycine_max_release_2	3581746	3582728	GRAS transcription factor [Medicago truncatula (Barrel medic)]
TA4094_3848		Glycine_soja_release_2	3581788	3582699	Scarecrow-like 6 [Arabidopsis thaliana (Mouse-ear cress)]
TC354455		GMGL.042210	3581939	3582741	similar to UniRef100_A7PYF4 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (22%)
Pvcon6489		Phaseolus_vulgaris	3581822	3582979	UniRef100_A7PYF4 Chromosome chr15 scaffold_37, whole genome shotgun sequence n=1 Tax=Vitis vinifera RepID=A7PYF4_VITVI 1.00E-117
TA5736_3885		Phaseolus_vulgaris_release_2	3581822	3582979	GRAS transcription factor [Medicago truncatula (Barrel medic)]
EX304728		Phaseolus_vulgaris	3582172	3582953	UniRef100_A7PYF4 Chromosome chr15 scaffold_37, whole genome shotgun sequence n=1 Tax=Vitis vinifera RepID=A7PYF4_VITVI 9.00E-62
Cf14326d		Chafa1_1clean	3582263	3582870	NA
AV419737		Lotus_japonicus_release_1	3582457	3582866	GRAS transcription factor [Medicago truncatula (Barrel medic)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
AV419737		LJGI.070108	3582470	3582866	similar to UniRef100_A7PYF4 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (15%)
Gm_W82_CR03.G20850		Gm_W82_CR03	3581403	3584467	Average Cons Position=LG06 31.8 cM: Q8LL10 Hairy meristem 1E-105
Glyma03g03760		Glyma1	3581425	3584467	ID:PF03514 (PFAM)=GRAS family transcription factor
TA49424_3847		Glycine_max release_2	3582576	3583493	GRAS transcription factor [Medicago truncatula (Barrel medic)]
asmb1_1399		Vigna_unguiculata	3582925	3583548	NA
TC384787		GMGI.042210	3582755	3583811	similar to UniRef100_A7PYF4 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (8%)
Contig33774		cajanus_cajana	3583334	3583523	NA
BM107962		Glycine_max release_2	3583135	3583811	GRAS transcription factor [Medicago truncatula (Barrel medic)]
BM526478		Glycine_soja release_2	3583674	3584202	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC399328		GMGI.042210	3583626	3584467	similar to UniRef100_A7PYF4 Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (4%)
BARCSOYSSR_03_0209		Wm82_potential_SSR	3585574	3585641	NA
BARCSOYSSR_03_0210		Wm82_potential_SSR	3597635	3597672	NA
Glyma03g03770		Glyma1	3600654	3600771	NA
BARCSOYSSR_03_0211		Wm82_potential_SSR	3602587	3602608	NA
BARCSOYSSR_03_0212		Wm82_potential_SSR	3608155	3608176	NA
BARCSOYSSR_03_0213		Wm82_potential_SSR	3608387	3608446	NA
AW598654		Glycine_max_release_2	3613044	3613631	FACT complex subunit SSRP1 [Vicia faba (Broad bean)]
183966_2432_1637		cajanus_cajan	3613341	3613924	NA
328630_4036_3779		cajanus_cajan	3614035	3614253	NA
Contig39949		cajanus_cajan	3614034	3614741	NA
Contig12168		cajanus_cajan	3614710	3614977	NA
Gm_W82_CR03.G21470		Gm_W82_CR03	3612970	3619158	Average Cons Position=LG06 31.9 cM: O04235 FACT complex subunit SSRP1 0

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03780		Glyma1	3613002	3619158	ID:GO:0003677 (GO)=DNA binding; ID:GO:0005634 (GO)=nucleus; ID:K09272 (KO)=; ID:KOG0526 (KOG)=Nucleosome-binding factor SPN, POB3 subunit; ID:PF00505 (PFAM)=HMG (high mobility group) box; ID:PTHR13711 (Panther)=SWI/SNF-RELATED CHROMATIN BINDING PROTEIN
Cf1771d		Chafa1_1clean	3613313	3618874	NA
Contig22956_primers		cajanus_cajan	3616077	3616304	NA
Contig22956		cajanus_cajan	3615797	3616789	NA
BG508541		Glycine_max_release_2	3616283	3617889	FACT complex subunit SSRP1 [Vicia faba (Broad bean)]
TC394940		GMGI.042210	3615339	3619158	homologue to UniRef100_O04235 FACT complex subunit SSRP1 - Vicia faba (Broad bean), partial (52%)
asmb1_1400		Vigna_unguiculata	3616459	3618878	NA
Contig45189_primers		cajanus_cajan	3617561	3617828	NA
Contig45189		cajanus_cajan	3617516	3617932	NA
Cf4868d		Chafa1_1clean	3629189	3629480	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03790		Glyma1	3629021	3632958	ID:PF00036 (PFAM)=EF hand; ID:PTHR10891 (Panther)=CALMODULIN
Gm_W82_CR03.G21680		Gm_W82_CR03	3629021	3632958	Average Cons Position=LG06 32 cM: Q01IH6 OSIGBa0159I10.9 protein 2E-24 ; Q9FDZ8 At1g73440 1E-22 ; Q01IH6 OSIGBa0159I10.9 protein 1E-22 ; Q9FDZ8 At1g73440 3E-22
Cf19325d		Chafa1_1clean	3630769	3632619	NA
DQ117561		Phaseolus_vulgaris_release_2	3630860	3632639	Calcium-binding EF-hand; Ubiquitin interacting motif [Medicago truncatula (Barrel medic)]
BI699366		Glycine_max_release_2	3632020	3632958	At1g73440 [Arabidopsis thaliana (Mouse-ear cress)]
BARCSOYSSR_03_0214		Wm82_potential_SSR	3632687	3632736	NA
312855_0711_3271		cajanus_cajan	3633856	3634022	NA
265958_3391_1857_primers		cajanus_cajan	3634131	3635827	NA
Cf7889d		Chafa1_1clean	3634101	3635886	NA
265958_3391_1857		cajanus_cajan	3634130	3635954	NA
Contig15510		cajanus_cajan	3633837	3636562	NA
asmb1_1401		Vigna_unguiculata	3633846	3636561	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BE658586		Glycine_max_release_2	3633896	3637470	Putative VAMP-associated protein [Arabidopsis thaliana (Mouse-ear cress)]
TC372625		GMGL042210	3633896	3637470	similar to UniRef100_A8W459 Vesicle-associated protein - Medicago truncatula (Barrel medic), partial (72%)
Glyma03g03800		Glyma1	3633770	3638147	ID:GO:0005198 (GO)=structural molecule activity; ID:KOG0439 (KOG)=VAMP-associated protein involved in inositol metabolism; ID:PF00635 (PFAM)=MSP (Major sperm protein) domain; ID:PTHR10809 (Panther)=VESICLE-ASSOCIATED MEMBRANE PROTEIN (VAMP)
Gm_W82_CR03.G21690		Gm_W82_CR03	3633770	3638151	Average Cons Position=LG06 32 cM: A8W459 Vesicle-associated protein 5E-98 ; Q7XM58 OSJNBb0020011.15 protein 3E-11
TC356639		GMGL042210	3633778	3638147	similar to UniRef100_A8W459 Vesicle-associated protein - Medicago truncatula (Barrel medic), partial (98%)
TA48856_3847		Glycine_max_release_2	3633830	3638098	F11M15.13 protein [Arabidopsis thaliana (Mouse-ear cress)]

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Pvcon2313		Phaseolus_vulgaris	3633861	3638070	UniRef100_A8W459 Vesicle-associated protein n=1 Tax=Medicago truncatula RepID=A8W459_MEDT R 1.00E-110
CA801352		Glycine_max_release_2	3636253	3636956	Putative VAMP-associated protein (At2g45140) (Putative VAMP (Vesicle-associated membrane protein)-associated protein) [Arabidopsis thaliana (Mouse-ear cress)]
CA801352		GMGI.042210	3636557	3636956	homologue to UniRef100_A8W459 Vesicle-associated protein - Medicago truncatula (Barrel medic), partial (28%)
135152_1291_2482		cajanus_cajan	3636646	3636929	NA
CA411541		Lupinus_albus_release_2	3636648	3638013	F11M15.13 protein [Arabidopsis thaliana (Mouse-ear cress)]
AW598332		Glycine_max_release_2	3636682	3638032	Putative VAMP-associated protein [Arabidopsis thaliana (Mouse-ear cress)]
CK606662		Glycine_max_release_2	3636684	3638114	F11M15.13 protein [Arabidopsis thaliana (Mouse-ear cress)]
TA4535_3886		Phaseolus_coccineus_release_2	3636737	3638091	Putative VAMP-associated protein [Arabidopsis thaliana (Mouse-ear cress)]
Contig23898		cajanus_cajan	3637449	3638104	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Contig23898_primers		cajanus_cajan	3637768	3637969	NA
Contig21922		cajanus_cajan	3644450	3644630	NA
Cf16623d		Chafa1_1clean	3644762	3644875	NA
TC33304		LJGI.070108	3644744	3645015	similar to UniRef100_A7PYF8 Cluster: Chromosome chr15 scaffold_37, whole genome shotgun sequence, n=1, Vitis vinifera Rep: Chromosome chr15 scaffold_37, whole genome shotgun sequence - Vitis vinifera (Grape), partial (28%)
TA13096_34305		Lotus_japonicus_release_1	3644744	3645016	Hypothetical protein T8B10_250 [Arabidopsis thaliana (Mouse-ear cress)]
Glyma03g03810		Glyma1	3644726	3645652	NA
asmb1_1402		Vigna_unguiculata	3645125	3645437	NA
Pvcon2861		Phaseolus_vulgaris	3645118	3645700	UniRef100_A7PYF8 Chromosome chr15 scaffold_37, whole genome shotgun sequence n=1 Tax=Vitis vinifera RepID=A7PYF8_VITVI 1.00E-131
BARCSOYSSR_03_0215		Wm82_potential_SSR	3648008	3648059	NA
BARCSOYSSR_03_0216		Wm82_potential_SSR	3648947	3648980	NA
079763_0879_0568		cajanus_cajan	3659098	3659198	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Cf19857d		Chafa1_1clean	3674397	3674718	NA
NGMAX006081942	32		3675970	3676271	
Gm_W82_CR03.G22310		Gm_W82_CR03	3674151	3678330	Average Cons Position=LG06 32.1 cM: Q7XJM6 At2g45130 protein 2E-62 ; UPI000023DC34 hypothetical protein FG01544.1 9E-11
Glyma03g03820		Glyma1	3674153	3678330	ID:PTHR10783 (Panther)=XENOTROPIC AND POLYTROPIC MURINE LEUKEMIA VIRUS RECEPTOR
Cf21636d		Chafa1_1clean	3678001	3678119	NA
NGMAX006081999	33		3688804	3689105	
214701_1085_2819		cajanus_cajan	3696674	3696867	NA
TC354431		GMGI.042210	3696212	3698076	weakly similar to UniRef100_Q40287 Anthocyanidin 3-O- glucosyltransferase - Manihot esculenta (Cassava) (Manioc), partial (25%)
TA65213_3847		Glycine_max release 2	3696212	3698092	Putative flavonol 3-O- glucosyltransferase [Arabidopsis thaliana (Mouse-ear cress)]
Glyma03g03830		Glyma1	3696212	3698853	ID:KOG1192 (KOG)=UDP- glucuronosyl and UDP- glucosyl transferase; ID:PTHR11926 (Panther)=GLUCOSYL/G LUCURONOSYL TRANSFERASES

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G 22320		Gm_W82_CR03	3696212	3698880	Average Cons Position=LG06 32.2 cM: Q40287 Anthocyanidin 3-O-glucosyltransferase 1E-100
BARCSOYSSR_03_0217		Wm82_potential SSR	3697753	3697776	NA
223169_0358_1790		cajanus_cajan	3698268	3698529	NA
BI973614		Glycine_max_release_2	3698266	3698839	NA
222017_1187_2363		cajanus_cajan	3698533	3698709	NA
214701_1085_2819		cajanus_cajan	3718709	3718902	NA
Glyma03g03840		Glyma1	3718497	3720038	ID:PTHR11926 (Panther)=GLUCOSYL/GLUCURONOSYL TRANSFERASES
Gm_W82_CR03.G 22330		Gm_W82_CR03	3718497	3720038	Average Cons Position=LG06 32.3 cM: Q9ZU72 Putative flavonol 3-O-glucosyltransferase 1E-52 ; Q9ZU71 Putative flavonol 3-O-glucosyltransferase 7E-50
CA936681		Glycine_max_release_2	3720697	3720966	NA
BG045196		Glycine_soja_release_2	3720668	3721159	AT3g50740/T3A5_120 [Arabidopsis thaliana (Mouse-ear cress)]
214701_1085_2819		cajanus_cajan	3720896	3721089	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03850		Glyma1	3720509	3723198	ID:KOG1192 (KOG)=UDP-glucuronosyl and UDP-glucosyl transferase; ID:PTHR11926 (Panther)=GLUCOSYL/G LUCURONOSYL TRANSFERASES
Gm_W82_CR03.G22340		Gm_W82_CR03	3720509	3723198	Average Cons Position=LG06 32.3 cM: Q40287 Anthocyanidin 3-O-glucosyltransferase 1E-102
BARCSOYSSR_03_0218		Wm82_potential SSR	3721975	3721994	NA
BG362737		Glycine_max_release_2	3722227	3722623	NA
223169_0358_1790		cajanus_cajan	3722497	3722758	NA
TC377946		GMGL042210	3722365	3723183	similar to UniRef100_A7QXH2 Chromosome undetermined scaffold_224, whole genome shotgun sequence - Vitis vinifera (Grape), partial (8%)
222017_1187_2363		cajanus_cajan	3722772	3722938	NA
NGMAX006082115	34		3723411	3723712	
Glyma03g03860		Glyma1	3739483	3743064	ID:PTHR11926 (Panther)=GLUCOSYL/G LUCURONOSYL TRANSFERASES

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G22350		Gm_W82_CR03	3739483	3743064	Average Cons Position=LG06 32.4 cM: Q9ZU72 Putative flavonol 3-O-glucosyltransferase 3E-30 ; Q9ZU71 Putative flavonol 3-O-glucosyltransferase 4E-28
214701_1085_2819		cajanus_cajan	3742136	3742309	NA
BARCSOYSSR_03_0219		Wm82_potential_SSR	3743233	3743280	NA
WmFPC_Contig2577		Wm82	3597056	3899983	NA
214701_1085_2819		cajanus_cajan	3767176	3767369	NA
Glyma03g03870		Glyma1	3766840	3769211	ID:KOG1192 (KOG)=UDP-glucuronosyl and UDP-glucosyl transferase; ID:PTHR11926 (Panther)=GLUCOSYL/G LUCURONOSYL TRANSFERASES
BARCSOYSSR_03_0220		Wm82_potential_SSR	3768104	3768125	NA
Gm_W82_CR03.G22360		Gm_W82_CR03	3766840	3769398	Average Cons Position=LG06 32.5 cM: Q40287 Anthocyanidin 3-O-glucosyltransferase 1E-100
223169_0358_1790		cajanus_cajan	3768626	3768887	NA
222017_1187_2363		cajanus_cajan	3768901	3769067	NA
BARCSOYSSR_03_0221		Wm82_potential_SSR	3780830	3780877	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03880		Glyma1	3780953	3782165	ID:PTHR10110:SF2 (Panther)=SODIUM/HYDROGEN EXCHANGER (NA+/H+ ANTIporter NHX)
Gm_W82_CR03.G22370		Gm_W82_CR03	3780953	3782165	Average Cons Position=LG06 32.5 cM: Q5XWR7 Sodium/hydrogen exchanger 6E-41 ; Q4VT46 Sodium/hydrogen exchanger 4E-40
NGMAX006082688	35		3783513	3783814	
120013_0199_0726		cajanus_cajan	3795534	3795754	NA
Contig10071		cajanus_cajan	3795582	3795791	NA
TC404918		GMGI.042210	3796084	3796372	similar to UniRef100_A7PKJ2 Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vinifera (Grape), partial (6%)
NS0118425	37		3797329	3796787	
Glyma03g03890		Glyma1	3795505	3806070	ID:PF03828 (PFAM)=Poly(A) polymerase; ID:PTHR23092 (Panther)=FAMILY NOT NAMED
Gm_W82_CR03.G22380		Gm_W82_CR03	3795505	3806070	Average Cons Position=LG06 32.6 cM: Q8RX81 AT4g00060/F6N15_10 0
NS0138011	9		3800866	3801607	

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BM309798		Glycine_max release_2	3800952	3802710	AT4g00060/F6N15_10 [Arabidopsis thaliana (Mouse-ear cress)]
TC415453		GMGL.04221 0	3800952	3802834	similar to UniRef100_A7PKJ2 Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vinifera (Grape), partial (3%)
TC415366		GMGL.04221 0	3800607	3805890	similar to UniRef100_A7PKJ2 Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vinifera (Grape), partial (8%)
TA59649_3847		Glycine_max release_2	3800607	3805959	AT4g00060/F6N15_10 [Arabidopsis thaliana (Mouse-ear cress)]
TC398829		GMGL.04221 0	3803354	3804019	NA
BI469325		Glycine_max release_2	3803354	3804126	NA
376070_3692_283 5		cajanus_caja n	3803828	3804020	NA
TA59648_3847		Glycine_max release_2	3804176	3806049	NA
TC370427		GMGL.04221 0	3804176	3806049	UniRef100_O28156 Uncharacterized protein AF_2124 - Archaeoglobus fulgidus, partial (7%)
GD950777		GMGL.04221 0	3804468	3805861	NA
TA59650_3847		Glycine_max release_2	3805151	3806065	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
TC349966		GMGL042210	3805151	3806073	NA
NGMAX006082778	36		3806350	3806651	
NGMAX006082782	25		3808878	3809179	
BARCSOYSSR_03_0222		Wm82_potential SSR	3817624	3817665	NA
Glyma03g03910		Glyma1	3814802	3820907	ID:GO:0004659 (GO)=prenyltransferase activity; ID:GO:0016021 (GO)=integral to membrane; ID:PF01040 (PFAM)=UbiA prenyltransferase family; ID:PTHR11048 (Panther)=PRENYLTRANSFERASES
Gm_W82_CR03.G22790		Gm_W82_CR03	3814802	3820907	Average Cons Position=LG06 32.8 cM: Q647J9 Homogentisate phytylprenyltransferase 1E-123 ; Q58FG4 Homogentisate phytylprenyltransferase 1E-120
086263_3714_2178		cajanus_cajan	3820244	3820452	NA
TA67363_3847		Glycine_max_release_2	3825407	3826540	NA
TC382671		GMGL042210	3825409	3826540	similar to UniRef100_A7PKJ1 Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vinifera (Grape), partial (23%)
059050_2801_0639		cajanus_cajan	3826082	3826873	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Cf8743d		Chafal_1clean	3826817	3827351	NA
GD676001		GMGI.042210	3827061	3827202	NA
BARC-064351-18627		marker_map4	3826875	3827418	NA
Glyma03g03920		Glyma1	3826814	3829735	ID:3.1.-.- (EC)=Acting on ester bonds.; ID:GO:0005737 (GO)=cytoplasm; ID:GO:0006281 (GO)=DNA repair; ID:GO:0006310 (GO)=DNA recombination; ID:GO:0006974 (GO)=response to DNA damage stimulus; ID:GO:0016788 (GO)=hydrolase activity, acting on ester bonds; ID:K07447 (KO)=; ID:PF03652 (PFAM)=Uncharacterised protein family (UPF0081)
Cf19457d		Chafal_1clean	3829491	3829653	NA
TA60403_3847		Glycine_max_release_2	3831923	3832830	NA
TC406296		GMGI.042210	3832100	3833014	NA
046766_3073_1326		cajanus_cajan	3832854	3833064	NA
BI973221		Glycine_max_release_2	3832711	3833221	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BI973221		GMGI.042210	3832796	3833221	similar to UniRef100_A7U5Z3 Glucan synthase catalytic, partial (0%)
Glyma03g03930		Glyma1	3831954	3839129	ID:PTHR23067 (Panther)=DOUBLE-STRANDED RNA-BINDING ZINC FINGER PROTEIN
BU544624		Glycine_max_release_2	3837285	3837804	NA
TC395926		GMGI.042210	3837285	3837973	similar to UniRef100_A6Q8J9 NADH-quinone oxidoreductase, chain K - Sulfurovum sp. (strain NBC37-1), partial (17%)
AW201693		Glycine_max_release_2	3837556	3837973	NA
CA785507		GMGI.042210	3838481	3838623	NA
Glyma03g03940		Glyma1	3845294	3846057	NA
NGMAX006083256	26		3861274	3861575	
186230_3992_3930		cajanus_cajan	3865200	3865357	NA
Gm_W82_CR03.G23030		Gm_W82_CR03	3865550	3866901	Average Cons Position=LG06 33.2 cM: Q4U316 Cys2/His2 zinc-finger transcription factor 3E-43 ; O22090 ZPT3-3 6E-43

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g03950		Glyma1	3865609	3866901	ID:GO:0005622 (GO)=intracellular; ID:GO:0008270 (GO)=zinc ion binding; ID:PF00096 (PFAM)=Zinc finger, C2H2 type; ID:PTHR11389 (Panther)=ZINC FINGER PROTEIN
TC392384		GMGL042210	3866249	3866901	similar to UniRef100_A7PKI9 Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vinifera (Grape), partial (26%)
TA2788_3848		Glycine_soja release 2	3868578	3869195	NA
DT084159		Glycine_soja release 2	3868668	3869195	NA
Glyma03g03960		Glyma1	3876581	3877716	ID:PTHR23258 (Panther)=SERINE- THREONINE PROTEIN KINASE, PLANT-TYPE
NGMAX006083447	27		3877288	3877589	
Glyma03g03970		Glyma1	3882286	3882732	NA
Gm_W82_CR03.G23450		Gm_W82_CR03	3882286	3882732	Average Cons Position=LG06 33.3 cM: Q4U314 Cys2/His2 zinc- finger transcription factor 4E-41
BARCSOYSSR_03_0223		Wm82_potential_SSR	3888578	3888641	NA
ss181361770		Wm82xPI468916	3889537	3889658	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
261825_3183_0830		cajanus_cajan	3889663	3889920	NA
061251_3291_1427		cajanus_cajan	3889901	3890022	NA
NGMAX006083554	28		3891696	3891997	
NGMAX006083631	10		3901266	3901567	
BARCSOYSSR_03_0224		Wm82_potential SSR	3906951	3907016	NA
Glyma03g03980		Glyma1	3905784	3908385	ID:PF01357 (PFAM)=Pollen allergen
Gm_W82_CR03.G23660		Gm_W82_CR03	3905784	3908385	Average Cons Position=LG06 33.5 cM: A1X8W4 Beta expansin 1 precursor 2E-79
CA908583		Phaseolus_coccineus_release_2	3905871	3908326	Putative beta-expansin [Eucalyptus globulus (Blue gum)]
BARCSOYSSR_03_0225		Wm82_potential SSR	3908619	3908672	NA
SATT009			3910203	3910364	
BARCSOYSSR_03_0226		Wm82_potential SSR	3910260	3910307	NA
Satt009		marker_map4	3910203	3910364	NA
BARCSOYSSR_03_0227		Wm82_potential SSR	3910269	3910307	NA
Contig43957		cajanus_cajan	3911076	3911325	NA
Contig33449		cajanus_cajan	3911127	3911325	NA
000154_3576_0278		cajanus_cajan	3911285	3911325	NA
003004_1235_1275		cajanus_cajan	3911285	3911325	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
006900_1493_1929		cajanus_cajan	3911285	3911325	NA
007460_3338_1291		cajanus_cajan	3911285	3911325	NA
014289_3939_0440		cajanus_cajan	3911285	3911325	NA
025966_0192_2223		cajanus_cajan	3911285	3911325	NA
026227_0909_1005		cajanus_cajan	3911285	3911325	NA
026294_1598_2544		cajanus_cajan	3911285	3911325	NA
028308_3640_0439		cajanus_cajan	3911285	3911325	NA
037852_0303_1097		cajanus_cajan	3911285	3911325	NA
040619_1093_1942		cajanus_cajan	3911285	3911325	NA
043547_3658_3419		cajanus_cajan	3911285	3911325	NA
053059_3470_1958		cajanus_cajan	3911285	3911325	NA
056612_0743_3441		cajanus_cajan	3911285	3911325	NA
059660_2583_1888		cajanus_cajan	3911285	3911325	NA
062864_3768_3193		cajanus_cajan	3911285	3911325	NA
063186_3037_2550		cajanus_cajan	3911285	3911325	NA
066572_1541_3184		cajanus_cajan	3911285	3911325	NA
070863_3199_3682		cajanus_cajan	3911285	3911325	NA
081478_2276_2703		cajanus_cajan	3911285	3911325	NA
095517_3300_2600		cajanus_cajan	3911285	3911325	NA
096113_2367_0176		cajanus_cajan	3911285	3911325	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
102296_1998_2033		cajanus_cajan	3911285	3911325	NA
102601_2987_3443		cajanus_cajan	3911285	3911325	NA
102878_3507_1146		cajanus_cajan	3911285	3911325	NA
104948_3016_0095		cajanus_cajan	3911285	3911325	NA
110539_3656_2013		cajanus_cajan	3911285	3911325	NA
112098_1843_0592		cajanus_cajan	3911285	3911325	NA
112753_1668_3825		cajanus_cajan	3911285	3911325	NA
125992_3730_1890		cajanus_cajan	3911285	3911325	NA
132002_0047_0182		cajanus_cajan	3911285	3911325	NA
153038_2371_2695		cajanus_cajan	3911285	3911325	NA
153557_3248_2660		cajanus_cajan	3911285	3911325	NA
175695_2245_1739		cajanus_cajan	3911285	3911325	NA
178644_1078_2444		cajanus_cajan	3911285	3911325	NA
208712_2112_3215		cajanus_cajan	3911285	3911325	NA
215158_3041_2690		cajanus_cajan	3911285	3911325	NA
228589_1830_3910		cajanus_cajan	3911285	3911325	NA
248892_2596_3299		cajanus_cajan	3911285	3911325	NA
261459_3344_2358		cajanus_cajan	3911285	3911325	NA
264549_3459_3346		cajanus_cajan	3911285	3911325	NA
288926_0121_3928		cajanus_cajan	3911285	3911325	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
291320_3644_1895		cajanus_cajan	3911285	3911325	NA
303787_1960_3525		cajanus_cajan	3911285	3911325	NA
Contig18363		cajanus_cajan	3911285	3911325	NA
Contig254		cajanus_cajan	3911285	3911325	NA
Contig29855		cajanus_cajan	3911285	3911325	NA
Contig38972		cajanus_cajan	3911285	3911325	NA
Contig4328		cajanus_cajan	3911285	3911325	NA
Contig6579		cajanus_cajan	3911285	3911325	NA
Contig6979		cajanus_cajan	3911285	3911325	NA
Contig911		cajanus_cajan	3911285	3911325	NA
Contig9432		cajanus_cajan	3911285	3911325	NA
036604_1796_3446		cajanus_cajan	3911285	3911331	NA
082281_3494_1612		cajanus_cajan	3911285	3911331	NA
222096_3093_3876		cajanus_cajan	3911285	3911331	NA
BARCSOYSSR_03_0228		Wm82_potential SSR	3915417	3915468	NA
397302_2219_2548		cajanus_cajan	3931040	3931321	NA
230041_2755_2778		cajanus_cajan	3931097	3931329	NA
Cf7593d		Chafa1_1clean	3931207	3931427	NA
039239_1483_0258		cajanus_cajan	3931282	3931499	NA
320914_3315_2468		cajanus_cajan	3931330	3931491	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
039239_1483_0258 primers		cajanus_cajan	3931429	3932086	NA
Glyma03g03990		Glyma1	3930986	3932577	ID:KOG1674 (KOG)=Cyclin; ID:PF00134 (PFAM)=Cyclin, N-terminal domain; ID:PTHR15615 (Panther)=FAMILY NOT NAMED
Gm_W82_CR03.G23670		Gm_W82_CR03	3930986	3932577	Average Cons Position=LG06 33.7 cM: Q9SHD3 Cyclin-U2-1 1E-79
ss181361769		Wm82xPI468916	3934845	3934966	NA
BARCSOYSSR_03_0229		Wm82_potential SSR	3935235	3935256	NA
BARCSOYSSR_03_0230		Wm82_potential SSR	3938921	3938980	NA
ss181361768		Wm82xPI468916	3944184	3944305	NA
TA56046_3847		Glycine_max_release_2	3950098	3952011	NA
TC352554		GMGL042210	3950098	3952011	similar to UniRef100_A7PKI5 Chromosome chr15 scaffold_19, whole genome shotgun sequence - Vitis vinifera (Grape), partial (30%)
Gm_W82_CR03.G23680		Gm_W82_CR03	3950090	3953935	Average Cons Position=LG06 33.8 cM: Q8GZ38 Putative bHLH transcription factor bHLH016 1E-38

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g04000		Glyma1	3950104	3953935	ID:GO:0030528 (GO)=transcription regulator activity; ID:GO:0045449 (GO)=regulation of transcription; ID:PF00010 (PFAM)=Helix-loop-helix DNA-binding domain; ID:PTHR23042 (Panther)=CIRCADIAN PROTEIN CLOCK/ARNT/BMAL/PAS
TA56045_3847		Glycine_max_release_2	3950331	3953930	NA
TC375851		GMGL.042210	3950914	3953930	similar to UniRef100_O81306 F6N15.11 protein - Arabidopsis thaliana (Mouse-ear cress), partial (25%)
BF715766		Glycine_soja_release_2	3951913	3953143	Putative bHLH transcription factor [Arabidopsis thaliana (Mouse-ear cress)]
BG043888		Glycine_soja_release_2	3953326	3953902	NA
Contig34254_primers		cajanus_cajan	3963399	3964485	NA
Contig34254		cajanus_cajan	3963346	3964851	NA
CD404584		Glycine_max_release_2	3963347	3964851	Sec61beta [Medicago truncatula (Barrel medic)]
TC374606		GMGL.042210	3963320	3965078	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g04010		Glyma1	3963336	3965289	ID:KOG3457 (KOG)=Sec61 protein translocation complex, beta subunit; ID:PF03911 (PFAM)=Sec61beta family; ID:PTHR13509 (Panther)=FAMILY NOT NAMED
Gm_W82_CR03.G23690		Gm_W82_CR03	3963336	3965289	Average Cons Position=LG06 33.9 cM: Q9M206 Transport protein subunit-like 9E-15
BM085010		Glycine_max_release_2	3964232	3964709	Sec61beta [Medicago truncatula (Barrel medic)]
TC400303		GMGI.042210	3964232	3964775	NA
Cf14447d		Chafal_1clean	3964462	3964710	NA
Cf2942d		Chafal_1clean	3964462	3964710	NA
NS0202926	11		3964906	3964512	
Contig38009		cajanus_cajan	3964588	3964869	NA

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Glyma03g04020		Glyma1	3968405	3971501	ID:GO:0004713 (GO)=protein-tyrosine kinase activity; ID:GO:0005524 (GO)=ATP binding; ID:GO:0006468 (GO)=protein amino acid phosphorylation; ID:KOG1187 (KOG)=Serine/threonine protein kinase; ID:PF07714 (PFAM)=Protein tyrosine kinase; ID:PTHR23258 (Panther)=SERINE-THREONINE PROTEIN KINASE, PLANT-TYPE
296480_1060_0054		cajanus_cajan	3970036	3970281	NA
Contig33933		cajanus_cajan	3971440	3971708	NA
BARCSOYSSR_03_0231		Wm82_potential SSR	3972030	3972069	NA
127767_0193_0529		cajanus_cajan	3972578	3972652	NA
086083_3139_0733		cajanus_cajan	3972567	3972678	NA
107263_3116_1889		cajanus_cajan	3972567	3972745	NA
Contig3427		cajanus_cajan	3972567	3972745	NA
Contig8717		cajanus_cajan	3972566	3972746	NA
339396_1511_0863		cajanus_cajan	3972612	3972746	NA
NGMAX006084289	12		3979463	3979764	

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
BARCSOYSSR_03_0232		Wm82_potential SSR	3982356	3982407	NA
Gm_W82_CR03.G24110		Gm_W82_CR03	3992073	3996230	Average Cons Position=LG06 34.2 cM: Q2YE87 NBS-LRR type disease resistance protein Rps1-k-2 0 ; Q2YE88 NBS-LRR type disease resistance protein Rps1-k- 1 0
Glyma03g04030		Glyma1	3992594	3996230	ID:GO:0005515 (GO)=protein binding; ID:KOG4658 (KOG)=Apoptotic ATPase; ID:PF00560 (PFAM)=Leucine Rich Repeat; ID:PTHR23155 (Panther)=LEUCINE- RICH REPEAT- CONTAINING PROTEIN
BARCSOYSSR_03_0233		Wm82_potential SSR	4001862	4001917	NA
Glyma03g04040		Glyma1	4017654	4019180	NA
Gm_W82_CR03.G24720		Gm_W82_CR03	4017654	4019180	Average Cons Position=LG06 34.3 cM: Q2YE87 NBS-LRR type disease resistance protein Rps1-k-2 0 ; Q2YE88 NBS-LRR type disease resistance protein Rps1-k- 1 0
Glyma03g04050		Glyma1	4027661	4027913	ID:PTHR23346 (Panther)=TRANSLATIO NAL ACTIVATOR GCN1-RELATED

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G 24730		Gm_W82_CR03	4027661	4027913	Average Cons Position=LG06 34.4 cM: Q53K35 HEAT repeat, putative 2E-14
Glyma03g04060		Glyma1	4029392	4031456	ID:PTHR11875:SF9 (Panther)=SET
Gm_W82_CR03.G 24740		Gm_W82_CR03	4029392	4031456	Average Cons Position=LG06 34.4 cM: Q9M9V0 F6A14.10 protein 2E-11 ; A9RDJ7 Nucleosome assembly protein family 8E-11
Glyma03g04070		Glyma1	4032514	4033581	ID:PTHR11043 (Panther)=ZETA-COAT PROTEIN
Gm_W82_CR03.G 24750		Gm_W82_CR03	4032514	4033581	Average Cons Position=LG06 34.5 cM: Q9MAZ9 Nonclathrin coat protein zeta1-COP 1E-13 ; A2Q5T5 Longin-like 7E-12
147515_0361_0524		cajanus_cajan	4037444	4037666	NA
AI443099		Glycine_max_release_2	4037901	4038186	NBS-LRR type disease resistance protein Rps1-k-1 [Glycine max (Soybean)]
Glyma03g04080		Glyma1	4037251	4041010	ID:GO:0005515 (GO)=protein binding; ID:KOG4658 (KOG)=Apoptotic ATPase; ID:PF00560 (PFAM)=Leucine Rich Repeat; ID:PTHR23155 (Panther)=LEUCINE-RICH REPEAT-CONTAINING PROTEIN

Locus / Display Name (1)	SEQ ID NO:	Source (3)	Start Base (4)	End Base (5)	Additional Locus Information (6)
Gm_W82_CR03.G 24760		Gm_W82_CR03	4037251	4041010	Average Cons Position=LG06 34.5 cM: Q2YE87 NBS-LRR type disease resistance protein Rps1-k-2 0 ; Q2YE88 NBS-LRR type disease resistance protein Rps1-k- 1 0
BARCSOYSSR_03_0234		Wm82_potential SSR	4050233	4050272	NA
146317_0436_0220		cajanus_cajan	4052175	4052344	NA
069073_0816_0074		cajanus_cajan	4052178	4052368	NA
Glyma03g04090		Glyma1	4065369	4065479	ID:PTHR11550 (Panther)=CTP SYNTHASE
Gm_W82_CR03.G 24770		Gm_W82_CR03	4065369	4065479	Average Cons Position=LG06 34.5 cM: Q8L6Z9 CTP synthase- like protein 3E-9
DT082886		Glycine_soja_release_2	4075130	4075437	NA

[0083] Sequences for the genes provided above can be obtained from the World Wide Web (or Internet) using the identifiers provided in Column 1 (Locus/Display Name) or Column 5 (ADDITIONAL LOCUS INFORMATION) from the following internet locations:

“soybase.org” (described in Grant et al., Nucleic Acids Research, 2010, Vol. 38, Database issue D843-D846) or soybase.org/gbrowse/cgi-bin/gbrowse/gmax1.01/ (see Hyten DL, Choi I-Y, Song Q, Specht JE, Carter TE et al. (2010) A high density integrated genetic linkage map of soybean and the development of a 1,536 Universal Soy Linkage Panel for QTL mapping. Crop Science 50:960-968. (Crop Science); and Hyten DL, Cannon SB, Song Q, Weeks N, Fickus EW et al. (2010) High-throughput SNP discovery through deep resequencing of a reduced representation library to anchor and orient scaffolds in the soybean whole genome sequence. BMC Genomics 11(1): 38);

“phytozome.net” or “phytozome.net/cgi-bin/gbrowse/soybean/?name=Gm09”;

“www.plantgdb.org” or “plantgdb.org/GmGDB/ (Assembly version Glyrna1.170 (Apr 2009)” ; and,

“ncbi.nlm.nih.gov/sites/entrez” and subsites “ncbi.nlm.nih.gov/nucest”,

“ncbi.nlm.nih.gov/dbEST”, “ncbi.nlm.nih.gov/genbank/”,

“ncbi.nlm.nih.gov/sites/genome”, “ncbi.nlm.nih.gov/unigene”, and

“ncbi.nlm.nih.gov/UniGene/UGOrg.cgi?TAXID=3847”.

We Claim:

1. A method for obtaining a soybean plant comprising in its genome at least one metribuzin tolerance locus, comprising the steps of:
 - a. genotyping a plurality of soybean plants with respect to at least one genetic locus in a linkage group N genomic region flanked by loci NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9); and
 - b. selecting a soybean plant comprising in its genome at least one genetic locus comprising a genotype associated with metribuzin tolerance.
2. The method of claim 1, wherein said genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in a sub-region of said linkage group N region flanked by loci NGMAX006077928 (SEQ ID NO: 4) and NGMAX006080885 (SEQ ID NO: 8).
3. The method of claim 1 or 2, wherein said genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in said first linkage group N region or said sub-region, wherein said marker comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).
4. The method of claim 1, wherein said plurality of soybean plants comprises a population that is obtained by: i) crossing a parent plant comprising at least one metribuzin tolerance locus with a parent plant comprising at least one metribuzin sensitivity locus; or, ii) obtaining seed or progeny from a parental plant segregating for at least one metribuzin tolerance locus.
5. The method of claim 1, wherein said population contains plants that contain a transgene that confers resistance to dicamba and/or a transgene that confers resistance to glyphosate.
6. The method of claim 1, further comprising the step of assaying for the presence of at least one additional marker, wherein said additional marker is either linked or unlinked to said linkage group N genomic region.

7. The method of claim 1, wherein said method further comprises exposing the selected soybean plant or progeny thereof comprising the genetic locus to a dosage of metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and isolating a metribuzin tolerant plant therefrom.
8. The method of claim 1, wherein said selection comprises exposing a genotyped soybean plant comprising the genetic locus to a dosage of metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and isolating a metribuzin tolerant plant therefrom.
9. A method for producing a soybean plant comprising in its genome at least one introgressed metribuzin tolerance locus comprising the steps of:
 - a. crossing a first soybean plant with a metribuzin tolerance locus with a second soybean plant comprising: a metribuzin sensitivity locus in a first linkage group N genomic region flanked by loci NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9) and at least one linked polymorphic locus not present in said first soybean plant to obtain a population segregating for the metribuzin tolerance loci and said linked polymorphic locus;
 - b. detecting at least two polymorphic nucleic acids in at least one soybean plant from said population, wherein at least one of said polymorphic nucleic acids is located in said linkage group N region and wherein at least one of said polymorphic amino acids is a linked polymorphic locus not present in said first soybean plant; and
 - c. selecting a soybean plant comprising a genotype associated with metribuzin tolerance and at least one linked marker found in said second soybean plant comprising a metribuzin sensitivity locus but not found in said first soybean plant, thereby obtaining a soybean plant comprising in its genome an introgressed metribuzin tolerance locus.
10. The method of claim 9, wherein at least one of said first or said second soybean plants comprises a transgene that confers resistance to dicamba and/or a transgene that confers resistance to glyphosate.

11. The method of claim 9, wherein said population, said selected soybean plant, and/or progeny of said selected soybean plant is exposed to a dosage of metribuzin sufficient to cause a deleterious effect in a metribuzin sensitive variety.
12. The method of claim 9, wherein said polymorphic nucleic acid detected in step (b) is detected with marker NGMAX006079502 (SEQ ID NO: 7).
13. The method of claim 9, wherein said polymorphic nucleic acid detected in step (b) comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).
14. The method of claim 9, wherein said linked polymorphic locus is detected with a genotypic marker, a phenotypic marker, or both.
15. The method of claim 14, wherein said linked polymorphic locus is detected with a marker that is located within about 1000, 500, 100, 40, 20, 10, or 5 kilobases (Kb) of said metribuzin tolerance locus.
16. The method of claim 15, wherein said linked polymorphic locus is detected with at least one marker selected from the group consisting of NGMAX006083631 (SEQ ID NO: 10), NS0202926 (SEQ ID NO: 11), NGMAX006084289 (SEQ ID NO: 12), and NGMAX006088354 (SEQ ID NO: 13).
17. A soybean plant made by the method of any one of claims 9-16, wherein said soybean plant comprises an introgressed metribuzin tolerance locus.
18. A soybean plant comprising an introgressed metribuzin tolerance locus, wherein at least one linked marker found in said soybean plant is characteristic of germplasm comprising a metribuzin sensitivity locus and is not associated with germplasm comprising the metribuzin tolerance locus.
19. The soybean plant of claim 18, wherein said introgressed metribuzin tolerance locus comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).
20. A soybean plant comprising an introgressed metribuzin tolerance locus, wherein at least one linked marker found in said soybean plant is characteristic of parental

germplasm comprising a metribuzin sensitivity locus but is not associated with
germplasm comprising the metribuzin tolerance locus.

21. The soybean plant of claim 20, wherein said introgressed metribuzin tolerance locus comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).
22. The soybean plant of claim 20 or 21, wherein said linked marker is selected from the group consisting of NGMAX006083631 (SEQ ID NO: 10), NS0202926 (SEQ ID NO: 11), NGMAX006084289 (SEQ ID NO: 12), and NGMAX006088354 (SEQ ID NO: 13).
23. The soybean plant of claim 22, wherein said linked marker comprises at least one of: a TT or a CT allele of NGMAX006083631 (SEQ ID NO: 10), an AC allele of NS0202926 (SEQ ID NO: 11), a GG allele of NGMAX006084289 (SEQ ID NO: 12), or a GG allele of NGMAX006088354 (SEQ ID NO: 13).
24. A method of identifying a soybean plant that comprises a genotype associated with metribuzin tolerance, comprising:
detecting in a soybean plant an allele in at least one genetic locus associated with metribuzin tolerance, wherein the genetic locus is in a linkage group N genomic region flanked by loci NGMAX006077640 (SEQ ID NO: 3) and NS0138011 (SEQ ID NO: 9), and denoting that said plant comprises a genotype associated with metribuzin tolerance.
25. The method of claim 24, wherein said method further comprises the step of selecting said denoted plant from a population of plants.
26. The method of claim 24, further comprising the steps of exposing the denoted soybean plant or progeny thereof to a dosage of metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and scoring the exposed plants for metribuzin tolerance.
27. The method of claim 24, wherein said selection comprises exposing the denoted soybean plant or progeny thereof comprising the genetic locus to a dosage of

metribuzin sufficient to cause a deleterious effect in a variety that is moderately sensitive or sensitive to metribuzin and isolating a metribuzin tolerant plant therefrom.

28. The method of claim 24, wherein said genotype associated with a metribuzin tolerance comprises at least one polymorphic allele of at least one marker in a sub-region of said linkage group N region that is flanked by loci NGMAX006077928 (SEQ ID NO: 4) and NGMAX006080885 (SEQ ID NO: 8).
29. The method of claim 28, wherein said genotype associated with metribuzin tolerance comprises at least one polymorphic allele of at least one marker in said linkage group N region or sub-region that comprises a TT allele of NGMAX006079502 (SEQ ID NO: 7).