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(54) **SOYBEAN JAG1 GENE MUTATIONS**

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(57) **ABSTRACT**

The disclosure relates to novel plants, plant parts, and nucleotide sequences in soybean plants comprising a mutated JAG1 gene, along with methods of using and making the same. Wherein the mutated JAG1 gene comprises a null mutation in the JAG1 gene encoding the polypeptide of SEQ ID NO: 10 or an allelic variant thereof and wherein the soybean plant cell lacks a loss-of-function mutation in the soybean JAG2 gene.

Specification includes a Sequence Listing.

Related U.S. Application Data

(60) Provisional application No. 63/269,663, filed on Mar. 21, 2022.

JAG1 Allele	SEQ ID NO	SEQUENCE
WT	5	GTACTCTAGAGATGGCAAACAAGTCCTCGAAGACCATACCTCTTCATCCGgtaaacttcatga Y S R D G K Q V L E D H T S S S (INTRON)
WT	6	YSRDGKQVLEDHTSSS
1:5D	7	GTACTCTAGAGATGGCAAACAAGTCCTCGAAG-----ACCTCTTCATCCGgtaaacttcatga
-2:7D	8	GTACTCTAGAGATGGCAAACAAGTCCTCGA-----ACCTCTTCATCCGgtaaacttcatga
-3:8D	9	GTACTCTAGAGATGGCAAACAAGTCCTCG-----ACCTCTTCATCCGgtaaacttcatga

[illegible]

FIGURE 1

JAG1 Allele	SEQ ID NO	SEQUENCE
WT	5	GTACTCTAGAGATGGCAAAACAAGTCCTCGAAGACCATACCTCTTCATCCCGGgtaaaacttcatga Y S R D G G K Q V L E D H T S S (INTRON)
WT	6	YSRDGKQVLEDHTSSS
1:5D	7	GTACTCTAGAGATGGCAAAACAAGTCCTCGAAG-----ACCTCTTCATCCCGgtaaaacttcatga
-2:7D	8	GTACTCTAGAGATGGCAAAACAAGTCCTCGA-----ACCTCTTCATCCCGgtaaaacttcatga
-3:8D	9	GTACTCTAGAGATGGCAAAACAAGTCCTCG-----ACCTCTTCATCCCGgtaaaacttcatga

FIGURE 2

SOYBEAN JAG1 GENE MUTATIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This international patent application claims the benefit of U.S. provisional patent application Ser. No. 63/269,663, filed Mar. 21, 2022.

INCORPORATION OF SEQUENCE LISTING

[0002] The sequence listing contained in the file named P13530W000_ST26, which is 71,751 bytes measured in operating system Windows, created on Mar. 18, 2023, and electronically filed via Patent Center on Mar. 20, 2023, is incorporated herein by reference in its entirety.

FIELD

[0003] Disclosed herein are novel plants, plant parts, and nucleotide sequences in soybean varieties comprising a mutated JAG1 gene, along with methods of making the same by growing a soybean plant or lot, and methods of using the same.

BACKGROUND

[0004] Agriculture is an essential industry for the global economy and the United States in particular. Soybean (*Glycine max*) is an important legume crop worldwide due to its ability to fix atmospheric nitrogen. Soybeans serve as a major source of animal feed protein and soybean oil has uses in a wide variety of industries, including the food and beverage, biodiesel, and other industries.

[0005] Soybean sustainability is a priority for farmers worldwide. Farming practices such as water and nutrient management help farmers improve efficiencies, boost crop productivity, conserve water, enrich soil quality, improve nutrient efficiencies of the soil, and produce sustainable soybean crops. The benefits of bioengineering for soybean farmers include increased yields and extreme weather hardness.

SUMMARY

[0006] Disclosed herein are soybean plant cells comprising a mutated JAG1 gene, wherein the mutated JAG1 gene comprises a null mutation in the JAG1 gene encoding the polypeptide of SEQ ID NO: 10 or an allelic variant thereof and wherein the soybean plant cell lacks a loss-of-function mutation in the soybean JAG2 gene. Also disclosed herein are soybean plant cells comprising a mutated JAG1 gene, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof. In certain embodiments, the soybean plant cell is homozygous for the mutated JAG1 gene. In certain embodiments, the mutated JAG1 gene comprises the polynucleotide sequence of SEQ ID NO: 7, 8, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof. In certain embodiments, the allelic variant of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, is encoded by a JAG1 gene which comprises a deletion corresponding to nucleotides 426 to 430, 424 to 430, or 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1, respectively. Soybean plants, soybean plant parts, and soybean seed comprising any of the aforementioned soybean plant cells or seed as well as soybean seed lots

comprising the soybean seed are provided. Methods of producing a soybean crop comprising planting a plurality of the aforementioned soybean seeds or an aforementioned seed lot are provided. Methods for producing a soybean by-product comprising at least one processing step of cleaning, cracking, flaking, crushing, macerating, pressing, extracting, expelling, and/or extruding an aforementioned seed lot are provided.

[0007] Polynucleotides comprising the sequence of SEQ ID NO: 7, 8, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof or encoding the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, are provided. Biological samples comprising the polynucleotides are also provided.

[0008] Methods of producing a soybean seed lot comprising: (i) growing a population of soybean plants comprising a mutated JAG1 gene to maturity, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof and wherein the soybean plants are homozygous for the mutated JAG1 gene; and (ii) harvesting seed from the population of soybean plants of step (i) at maturity, thereby producing the soybean seed lot are provided.

[0009] Methods of making a soybean plant containing a mutated JAG1 gene comprising: (a) deleting: (i) nucleotides 426 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; (ii) nucleotides 424 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; or (iii) nucleotides 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; to obtain a modified soybean plant cell comprising the mutated JAG1 gene; and (b) recovering a soybean plant from the modified soybean plant cell are provided.

DESCRIPTIONS OF THE DRAWINGS

[0010] FIG. 1 shows the wild-type genomic DNA of the soybean JAG1 gene (SEQ ID NO: 1). Exons are in uppercase, introns are in lower case, and the translation initiation and termination codons are in uppercase, bold, italics, and underlined.

[0011] FIG. 2 shows a portion of the wild type JAG1 genomic DNA containing the end of the 2nd exon and the beginning of the second intron of the soybean JAG1 gene. The annotated wild-type DNA sequence (SEQ ID NO: 5) indicates the exon and translated sequence fragment starting from Y17 (SEQ ID NO: 6), the intron region in lowercase, and the gRNA spacer complementary sequence with underlining. The deletions resulting in the frameshift mutations in the mJAG1 mutants of 1:5D (SEQ ID NO: 7), -2:7D (SEQ ID NO: 8), and -3:8D (SEQ ID NO: 9) are indicated by dashes in place of the deleted bases of the mutants.

DETAILED DESCRIPTION

Definitions

[0012] The phrase “allelic variant” as used herein refers to a polynucleotide or polypeptide sequence variant that occurs in a particular gene at particular locus in a different strain, variety, or isolate of a given organism.

[0013] The term “and/or” where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term “and/or” as used in a phrase such as “A and/or B” herein is intended to include “A and B,” “A or B,” “A” (alone), and “B” (alone). Likewise, the term “and/or” as used in a phrase such as “A, B, and/or C” is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0014] As used herein, the phrase “biological sample” refers to either intact or non-intact (e.g., milled soybean seed or soybean plant tissue, chopped soybean plant tissue, lyophilized tissue) soybean plant tissue. It may also be an extract comprising intact or non-intact seed or soybean plant tissue. The biological sample can comprise flour, meal, syrup, oil, starch, and cereals manufactured in whole or in part to contain soybean plant by-products. In certain embodiments, the biological sample is “non-regenerable” (i.e., incapable of being regenerated into a soybean plant or soybean plant part).

[0015] As used herein, the terms “correspond,” “corresponding,” and the like, when used in the context of a nucleotide position, mutation, and/or substitution in any given polynucleotide (e.g., an allelic variant of SEQ ID NO: 1) with respect to the reference polynucleotide sequence (e.g., SEQ ID NO: 1) all refer to the position of the polynucleotide residue in the given sequence that has identity to the residue in the reference nucleotide sequence when the given polynucleotide is aligned to the reference polynucleotide sequence using a pairwise alignment algorithm (e.g., CLUSTAL O 1.2.4 with default parameters).

[0016] As used herein, the terms “Cpf1” and “Cas12a” are used interchangeably to refer to the same RNA dependent DNA endonuclease (RdDe).

[0017] As used herein, the phrase “endogenous gene” refers to the native form of a gene in the genome of an organism.

[0018] As used herein, the terms “include,” “includes,” and “including” are to be construed as at least having the features to which they refer while not excluding any additional unspecified features. As used herein, the term “plant” includes reference to an immature or mature whole soybean plant, including a plant from which seed or grain or anthers have been removed. Any seed or embryo that will produce the plant is also considered to be the soybean plant.

[0019] As used herein, the phrase “loss-of-function” mutation or allele of a gene refers to a mutation or allele of a gene which exhibits decreased gene function in comparison to an unmutated or wild-type allele of the gene. “Loss-of-function” mutations thus include mutations resulting in both null (i.e., amorphic) alleles and hypomorphic alleles (i.e., reduced by not eliminated function) of a gene.

[0020] As used herein, the phrase “mutated JAG1 gene” or “mJAGT gene” refer to an endogenous soybean JAG1 gene comprising a null mutation. In certain embodiments, the mJAGT comprising the null mutation encodes the polypeptide of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or allelic variants thereof, wherein the allelic variants of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, or 30 comprise deletions corresponding to deletions of the amino acid residues encoded by nucleotides 426 to 430, 424 to 430, or 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1, respectively. In certain embodiments, the mJAGT deletion is a null

mutation that comprises a deletion corresponding to at least nucleotides 421 to 436 of SEQ ID NO: 1.

[0021] As used herein, a null mutation of a gene refers to an allele of a gene having no gene activity in comparison to the wild-type allele of the gene. Null alleles are also known as amorphic alleles.

[0022] As used herein, the term “plant” includes a whole soybean plant and any descendant, cell, tissue, part, or parts of the plant. The term “plant” thus includes reference to an immature or mature whole soybean plant, including a plant from which seed or grain or anthers have been removed.

[0023] The term “plant parts” include any part(s) of a plant, including, for example and without limitation: seed (including mature seed and immature seed); grain; stover; a plant cutting; a plant cell; a plant cell culture; or a plant organ (e.g., pollen, embryos, pods; flowers, fruits, shoots, leaves, roots, stems, and explants). A plant tissue or plant organ may be a seed, protoplast, callus, or any other group of plant cells that is organized into a structural or functional unit. A plant cell or tissue culture may be capable of regenerating a plant having the physiological and morphological characteristics of the plant from which the cell or tissue was obtained, and of regenerating a plant having substantially the same genotype as the plant. Regenerable cells in a plant cell or tissue culture may be embryos, protoplasts, meristematic cells, callus, pollen, leaves, anthers, roots, root tips, flowers, or stalks. In contrast, some plant cells are not capable of being regenerated to produce plants and are referred to herein as “non-regenerable” plant cells.

[0024] To the extent to which any of the preceding definitions is inconsistent with definitions provided in any patent or non-patent reference incorporated herein by reference, any patent or non-patent reference cited herein, or in any patent or non-patent reference found elsewhere, it is understood that the preceding definition will be used herein.

[0025] The present disclosure provides for the soybean plant cells, plant parts including seed, plants, and biological samples comprising a mJAG1 gene. These mJAG1 plants and parts can be utilized for human food, livestock feed, as a raw material in industry, or as breeding material for development of other soybean varieties. The target endogenous JAG1 gene comprises the genomic DNA of SEQ ID NO: 1 and allelic variants thereof located on soybean chromosome 20. The endogenous soybean JAG1 gene is located at nucleotides 35827671 to 35830107 of chromosome 20 of the *Glycine max* Wm82.a2.v1 set forth in the [https internet site “phytozome-next.jgi.doe.gov/report/transcript/Gmax_Wm82_a2_v1/Glyma.20G116200.1.”](https://phytozome-next.jgi.doe.gov/report/transcript/Gmax_Wm82_a2_v1/Glyma.20G116200.1) Allelic variants of an endogenous soybean JAG1 gene include variants which encode JAG1 proteins having at least 95%, 96%, 98%, 99%, or 99.5% sequence identity to SEQ ID NO: 10. Allelic variants of an endogenous soybean JAG1 gene also include variants which comprise genomic DNA having at least 95%, 96%, 98%, 99%, or 99.5% sequence identity to SEQ ID NO: 1. In certain embodiments, mJAG1 genes can encode the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof. In certain embodiments, such allelic variants of SEQ ID NO: 12, 13, or 14 can comprise an amino acid sequence having at least 95%, 96%, 98%, 99%, or 99.5% sequence identity across the entire length of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, and 30. In certain embodiments, such allelic variants of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, or

30 can comprise an amino acid sequence having at least 95%, 96%, 98%, 99%, or 99.5% sequence identity across the entire length of SEQ ID NO: 12, 13, and 14 and are encoded by a JAG1 gene which comprises a deletion corresponding to nucleotides 426 to 430, 424 to 430, or 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1, respectively. In certain embodiments, the mJAG1 gene can comprise a JAG1 gene or an aforementioned allelic variant thereof which comprises a deletion corresponding to nucleotides 426 to 430, 424 to 430, or 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1. In certain embodiments, the mJAG1 deletion is a null mutation that comprises a deletion corresponding to at least nucleotides 421 to 436 of SEQ ID NO: 1 or an allelic variant thereof.

[0026] In certain embodiments, the soybean plant cells, plants, plant parts, and seeds comprising mJAG1 null alleles of the JAG1 gene lack a loss-of-function mutation (e.g., a null mutation) in the soybean JAG2 gene. The wild-type endogenous soybean JAG2 gene, as referred to as GmJAG2, comprises the genomic DNA of SEQ ID NO: 36 or an allelic variant thereof located on soybean chromosome 10. The endogenous soybean JAG2 gene is located at nucleotides 49647129 to 49649853 of chromosome 10 of the *Glycine max* Wm82.a2.v1 genome set forth in the [https](https://www.soybase.org) internet site “soybase.org” under the gene identifier Glyma.10g273800 and comprises the coding sequence of SEQ ID NO: 37 which encodes the wild-type JAG2 protein of SEQ ID NO: 38. Soybean plant cells, plants, plant parts, and seeds lacking a loss-of-function mutation (e.g., a null mutation) in the soybean JAG2 gene can at least be identified by sequencing their genomic DNA regions correspond to SEQ ID NO:36.

[0027] In certain embodiments, the mJAG1 null alleles of the JAG1 gene provided herein will provide for soybean plants which exhibit both a narrow leaf phenotype and an increased number of seeds per kilogram of seeds harvested from the soybean plant homozygous for the null allele of the mJAG1 gene, where both the narrow leaf phenotype and increased number of seeds per kilogram of seeds harvested are in comparison to the leaf phenotype and the number of seeds per kilogram harvested from corresponding control soybean plant lacking the mJAG1 gene (e.g., a wild-type soybean plant homozygous for a wild-type JAG1 gene). In certain embodiments, the soybean plants homozygous for the mJAG1 null alleles will lack a loss-of-function mutation in the soybean JAG2 gene and will exhibit the aforementioned narrow leaf and an increased number of seeds per kilogram of seeds phenotypes in comparison to the control plant.

[0028] In certain embodiments, soybean plants homozygous for an mJAG1 gene can yield seed lots wherein the number of seeds per kilogram of seeds harvested from the soybean plant homozygous for the mJAG1 gene is increased in comparison to the number of seeds per kilogram harvested from corresponding control soybean plant lacking the mJAG1 gene (e.g., a wild-type soybean plant homozygous for a wild-type JAG1 gene). In certain embodiments, the number of seeds per kilogram of seeds harvested from the soybean plant homozygous for the mJAG1 gene is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, or 12% in comparison to the number of seeds per kilogram harvested from corresponding control soybean plant lacking the mJAG1 gene (e.g., a wild-type soybean plant homozygous for a wild-type JAG1 gene). In certain embodiments, the number of seeds per kilogram of seeds harvested from the

soybean plant homozygous for the mJAG1 gene is increased by about 1% or 2% to any one of about 5%, 6%, 7%, 8%, 9%, 10%, or 12% in comparison to the number of seeds per kilogram harvested from corresponding control soybean plant lacking the mJAG1 gene (e.g., a wild-type soybean plant homozygous for a wild-type JAG1 gene). In certain embodiments, the weight in grams per 1000 seeds harvested from the soybean plant homozygous for the mJAG1 gene is decreased by up to about 2%, 4%, 6%, 8%, 9%, 10%, or 11% in comparison to the weight in grams per 1000 seeds harvested from corresponding control soybean plant lacking the mJAG1 gene (e.g., a wild-type soybean plant homozygous for a wild-type JAG1 gene). In certain embodiments, the weight in grams per 1000 seeds harvested from the soybean plant homozygous for the mJAG1 gene is decreased by up to about 2%, 4%, 6%, 8%, 9%, 10%, or 11% in comparison to the weight in grams per 1000 seeds harvested from corresponding control soybean plant lacking the mJAG1 gene (e.g., a wild-type soybean plant homozygous for a wild-type JAG1 gene). In certain embodiments of any of the aforementioned seed lots, the mJAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12 or an allelic variant thereof. In certain embodiments, such allelic variants of SEQ ID NO: 12 can comprise an amino acid sequence having at least 95%, 96%, 98%, 99%, or 99.5% sequence identity across the entire length of SEQ ID NO: 12. In certain embodiments, such allelic variants of SEQ ID NO: 12 can comprise an amino acid sequence having at least 95%, 96%, 98%, 99%, or 99.5% sequence identity across the entire length of SEQ ID NO: 12 and are encoded by an mJAG1 gene which comprises a deletion corresponding to nucleotides 426 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1. In certain embodiments, the mJAG1 gene can comprise an mJAG1 gene or an aforementioned allelic variant thereof which comprises a deletion corresponding to nucleotides 426 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1.

[0029] Also provided here are polynucleotides comprising any of the aforementioned mJAG1 genes or fragments thereof. In certain embodiments, a polynucleotide comprising the sequence of SEQ ID NO: 7, 8, 9, 15, 16, 17, 18, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, 35, or allelic variants thereof are provided. In certain embodiments, the allelic variants of SEQ ID NO: 7, 8, or 9 will comprise sequences having at least 95%, 97%, 98%, 99%, or 99.5% sequence identity across the entire length of SEQ ID NO: 7, 8, 9, 15, 16, 17, 18, or 19 with the proviso that the sequences are not identical to across their entire length to SEQ ID NO: 1 and comprise a deletion corresponding to nucleotides 426 to 430, 424 to 430, or 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1. In certain embodiments, the allelic variants of SEQ ID NO: 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 will comprise sequences having at least 95%, 97%, 98%, 99%, or 99.5% sequence identity across the entire length of SEQ ID NO: 21, 23, 25, 27, 29, 31, 32, 33, 34, 35 with the proviso that the sequences are not identical to across their entire length to SEQ ID NO: 1 and comprise deletions in the SEQ ID NO: 1 sequence corresponding to the deletions of SEQ ID NO: 21, 23, 25, 27, or 29. In certain embodiments, the polynucleotides encode a polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof. In certain embodiments, the encoded allelic variant will comprise a

polypeptide having at least 95%, 97%, 98%, 99%, or 99.5% sequence identity across the entire length of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, or 30 with the proviso that the sequences are not identical to SEQ ID NO: 10. In certain embodiments, the polynucleotide is an isolated polynucleotide. Biological samples and soybean by-products comprising any of the aforementioned polynucleotides are also provided. In certain embodiments, the by-products are processed products are made from the mJAG1 soybean plant or its seeds, including: (a) soybean seed meal (defatted or non-defatted); (b) extracted soybean proteins, oils, sugars, syrups, and starches; (c) soy fermentation products; (d) soybean based animal feed or human food products (e.g., feed and food comprising soybean seed meal (defatted or non-defatted) and other ingredients (e.g., other cereal grains, other seed meal, other protein meal, other oil, other starch, other sugar, a binder, a preservative, a humectant, a vitamin, and/or mineral); (e) a pharmaceutical; (f) raw or processed biomass (e.g., cellulosic and/or lignocellulosic material; silage); and (g) various industrial products.

[0030] Methods of using the mJAG1 soybean plants, seeds, and seed lots to produce soybean by-products are also provided. Such methods will typically include at least one processing step of cleaning, cracking, flaking, crushing, macerating, pressing, extracting, expelling, and/or extruding the seed.

[0031] This disclosure also is directed to methods for producing a soybean plant having a mutated JAG1 gene by crossing a first parent soybean plant with a second parent soybean plant wherein the first or second parent soybean plant is a mJAG1 plant. Further, both first and second parent soybean plants can come from the mJAG1 plant. Still further, this disclosure also is directed to methods for producing mJAG1 plant-derived soybean plant by crossing a mJAG1 plant with a soybean plant, growing the progeny seed, and repeating the crossing and growing steps with the mJAG1 plant-derived soybean plant from 1 to 2 times, 1 to 3 times, 1 to 4 times, or 1 to 5 times. Thus, any such methods using a mJAG1 plant are part of this disclosure: selfing, backcrosses, hybrid production, crosses to populations, and the like. All plants produced using a mJAG1 plant as a parent are within the scope of this disclosure, including plants derived from a mJAG1 plant having a mutated JAG1 gene. Also provided are the F1 progeny soybean plant produced from the crossing of a mJAG1 containing soybean plant (e.g., a plant homozygous for the mJAG1 gene) with any other soybean plant, F1 seed, and various parts of the F1 soybean plant.

[0032] The following describes breeding methods that may be used with a mJAG1 plant in the development of further soybean plants. One such embodiment is a method for developing a mJAG1 progeny soybean plant in a soybean plant breeding program comprising: obtaining the soybean plant, or its parts, of a mJAG1 plant and utilizing said plant or plant parts as a source of breeding material; and selecting a mJAG1 progeny plant having the mutated JAG1 (mJAG1) gene. Breeding steps that may be used in the soybean plant breeding program include pedigree breeding, backcrossing, mutation breeding, and recurrent selection. In conjunction with these steps, techniques such as restriction fragment polymorphism enhanced selection, genetic marker enhanced selection (for example SSR markers), and the making of double haploids may be utilized.

[0033] Another method involves producing a population of mJAG1 progeny soybean plants, comprising crossing a mJAG1 plant with another soybean plant, thereby producing a population of soybean plants, which, on average, derive 50% of their alleles from the mJAG1 plant. A mJAG1 plant of this population may be selected and repeatedly selfed or sibbed, with a soybean variety resulting from these successive filial generations. One embodiment of this disclosure is the soybean variety produced by this method and that has obtained at least 50% of its alleles from mJAG1.

[0034] Field crops are bred through techniques that take advantage of the plant's method of pollination. According to the disclosure, a mJAG1 plant may be crossed with self-pollinated, sib-pollinated, or cross pollinated to create a pedigree soybean plant. A plant is self-pollinated if pollen from one flower is transferred to the same or another flower of the same plant. A plant is sib-pollinated when individuals within the same family or variety are used for pollination. A plant is cross-pollinated if the pollen comes from a flower on a different plant from a different family or variety. The terms "cross-pollination" and "out-cross" as used herein do not include self-pollination or sib-pollination. Soybean plants (*Glycine max*) are recognized to be naturally self-pollinated plants which, while capable of undergoing cross-pollination, rarely do so in nature. Insects are reported by some researchers to carry pollen from one soybean plant to another and it generally is estimated that less than one percent of soybean seed formed in an open planting can be traced to cross-pollination, i.e. less than one percent of soybean seed formed in an open planting is capable of producing F1 hybrid soybean plants.

[0035] Any other suitable breeding, selection, or growing methods may be used. Choice of the particular breeding or selection method with vary depending on environmental factors, population size, and the like.

[0036] In certain embodiments, soybean plant cells, plant parts (e.g., seeds), and plants comprising a mJAG1 gene and a transgenic locus are provided. In one embodiment, an mBS1 or mBS1 gene is combined with one or more soybean GM events providing tolerance to any one or a combination of glyphosate-based, glufosinate-based, HPPD inhibitor-based, sulfonylurea- or imidazolinone-based, AHAS- or ALS-inhibiting and/or auxin-type (e.g., dicamba, 2,4-D) herbicides and/or an insect resistance trait, such as Event EE-GM3 (aka FG-072, MST-FG072-3, described in WO2011063411, USDA-APHIS Petition 09-328-01p), Event SYHTOH2 (aka OH2, SYN-000H2-5, described in WO2012/082548 and 12-215-01p), Event DAS-68416-4 (aka Enlist Soybean, described in WO2011/066384 and WO2011/066360, USDA-APHIS Petition 09-349-01p), Event DAS-44406-6 (aka Enlist E3, DAS-44406-6, described in WO2012/075426 and USDA-APHIS 11-234-01p), Event MON87708 (dicamba-tolerant event of Roundup Ready 2 Xtend Soybeans, described in WO2011/034704 and USDA-APHIS Petition 10-188-01p, MON-87708-9), Event MON89788 (aka Genuity Roundup Ready 2 Yield, described in WO2006/130436 and USDA-APHIS Petition 06-178-01p), Event 40-3-2 (aka Roundup Ready, GTS 40-3-2, MON-04032-6, described in USDA-APHIS Petition 93-258-01), Event A2704-12 (aka LL27, ACS-GM005-3, described in WO2006108674 and USDA-

APHIS Petition 96-068-01p), Event 127 (aka BPS-CV127-9, described in WO2010/080829), Event A5547-127 (aka LL55, ACS-GM006-4, described in WO2006108675 and in USDA-APHIS Petition 96-068-01p), event MON87705 (MON-87705-6, Vistive Gold, published PCT patent application WO2010/037016, USDA-APHIS Petition 09-201-01p), or event DP305423 (aka DP-305423-1, published PCT patent application WO2008/054747, USDA-APHIS Petition 06-354-01p), or EE-GM5 is combined with a combination of the following events: Event MON98788×MON87708 (aka Roundup Ready 2 Xtend Soybeans, MON-87708-9×MON-89788-1), Event HOS×Event 40-3-2 (aka Plenish High Oleic Soybeans×Roundup Ready Soybeans), Event EE-GM3×EE-GM2 (aka FG-072×LL55, described in

patent applications or US national stages thereof are incorporated herein by reference in their entireties. Representative transgenic events that can be combined with an mJAG1 gene include those set forth in Table 1. Also provided herein are soybean plant cells, plant parts (e.g., seeds), and plants comprising an mJAG1 gene and a modification of any of the aforementioned transgenic events or transgenic events set forth in Table 1 below. Modifications of the transgenic events include those disclosed in WO2022/026375, WO2022/026379, WO2022/026390, WO2022/026395, WO2022/026403, US Patent Applic. Pub. No. US20220030822, and U.S. Pat. No. 11,242,534, which are each incorporated herein by reference in their entireties.

TABLE 1

Transgenic Soybean Events			
Event Name (traits) ¹	Patent or Patent Application Number(s) ²	ATCC; ³ NCIMB ⁴ Deposit Number; or Commercial Source	Trait expression cassette(s)
A5547-127 (HT)	US 20080196127 RE44962	NCIMB 41660	PAT
DAS44406-6 (HT) ⁵	U.S. Pat. No. 9,540,655	PTA-11336	Aad-12,
DAS68416-4 (IR, HT) ⁶	U.S. Pat. No. 10,400,250	PTA-10442	2mepsps, PAT
DAS81419-2 (IR, HT)	U.S. Pat. No. 9,738,904	PTA-12006	Aad-12, PAT
	U.S. Pat. No. 8,680,363	PTA-12006	cry1Ac, cry1F,
	U.S. Pat. No. 8,632,978		PAT
	U.S. Pat. No. 9,695,441		
	U.S. Pat. No. 9,738,904		
GTS 40-3-2 (HT)	US 20070136836	M690GT 0.9 RM Soybean ⁷	cp4epsps
MON87701 (IR)	U.S. Pat. No. 8,049,071	PTA-8194	cry1Ac
MON87708 (HT) ⁸	U.S. Pat. No. 9,447,428	PTA-9670	DMO
MON89788 (HT)	U.S. Pat. No. 9,944,945	PTA-6708	cp4epsps
MST-FG072-3 (HT) ⁹	U.S. Pat. No. 8,592,650	NCIMB 41659	hppdPF W336,
SYHT0H2 ¹⁰	U.S. Pat. No. 10,184,134	PTA-11226	2mepsps cAvHPPD-03

¹Traits: IR = Insect Resistance; HT = Herbicide Tolerance; AR = Antibiotic Resistance;

²Each US Patent or Patent Application Publication is incorporated herein by reference in its entirety.

³ATCC is the American Type Culture Collection, 10801 University Boulevard Manassas, VA 20110 USA (for "PTA-XXXXX" deposits).

⁴NCIMB is the National Collection of Industrial, Food and Marine Bacteria, Ferguson Building, Craibstone Estate, Bucksburn, Aberdeen AB9YA, Scotland.

⁵HT to 2,4-D; glyphosate, and glufosinate; also referred to as pDAB8264.44.06.1.

⁶Independent IR/HT and HT events combined by breeding. IR/HT event (Cry1F, Cry1Ac synpro (Cry1Ac), and PAT) is DAS81419-2, deposited with ATCC under PTA-12006, also referred to as DAS81419-2.

⁷Elk Mound Seed, 308 Railroad Street Elk Mound, WI, USA 54739.

⁸HT to dicamba.

⁹HT to both glyphosate and isoxaflutole herbicides.

¹⁰HT to glufosinate and mesotrione herbicides.

WO2011063413), Event MON 87701×MON 89788 (aka Intacta RR2 Pro Soybean, MON-87701-2×MON-89788-1), DAS-81419-2×DAS-44406-6 (aka Conkesta™ Enlist E3™ Soybean, DAS-81419-2×DAS-44406-6), Event DAS-68416-4×Event MON 89788 (aka Enlist™ RoundUp Ready® 2 Soybean, DAS-68416-4×MON-89788-1), Event MON-87769-7×Event MON-89788-1 (aka Omega-3×Genuity Roundup Ready 2 Yield Soybeans), Event MON 87705×Event MON 89788 (aka Vistive Gold, MON-87705-6×MON-89788-1), or Event MON87769×Event MON89788 (aka Omega-3×Genuity Roundup Ready 2 Yield Soybeans, MON-87769-7×MON-89788-1), where all published PCT

[0037] In certain embodiments, a mutated Jag1 gene is combined with a null mutation in the soybean TFL1b gene which is an ortholog of the *Arabidopsis* Terminal Flower 1 gene. The soybean TFL1b ortholog is found in the https internet database "soybase.org" as Glyma.19G194300 and also known as the soybean stem growth habit gene Dtl (Liu et al. Plant Physiol. 2010 May; 153(1):198-210. doi: 10.1104/pp. 109.150607. Epub 2010 Mar. 10. PMID: 20219831; PMCID: PMC2862436). The TFL1b wild-type genomic DNA is provided as SEQ ID NO: 39, the TFL1b wild-type coding sequence is provided as SEQ ID NO: 40, and the TFL1b protein is provided as SEQ ID NO: 41. Null mutations in TFL1b can be obtained by gene editing tech-

niques (e.g., by use of CRISPR/Cas9, CRISPR/Cas12, TALEN, or aZFN-mediated site-specific mutagenesis of the TFL1b gene).

[0038] Methods of producing a soybean seed lot comprising: (i) growing a population of soybean plants comprising a mJAG1 gene to maturity; and (ii) harvesting seed from the population of soybean plants of step (i) at maturity, thereby producing the soybean seed lot, wherein the soybean plants are homozygous for the mutated JAG1 gene. In certain embodiments, the seed lot is packaged in lots comprising about 50 to 60 pounds (e.g. about 22.7 to 27.2 kilograms). In certain embodiments, the seed lots comprised of seed homozygous for certain mJAG1 mutations will contain more seed than control seed lots obtained from control soybeans which comprise a wild-type JAG1 gene. In certain embodiments, up to about 2%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% more seed will be present in the seed lots comprised of seed homozygous for certain mJAG1 mutations in comparison to control seed lots obtained from control soybeans which comprise a wild-type JAG1 gene. Also provided herein are methods of treating the mJAG1 seeds and seed lots and the resultant treated mJAG1 seed and seed lots. Seeds can be treated with such fertilizers, biological agents, nematicides, insecticides, and fungicides by methods including in-furrow applications or by coating (e.g., with a drum coater, rotary coater, tumbling drum, fluidized bed, and/or spouted bed apparatus). Methods and compositions including various binders, fillers, film coats, and active ingredients such as fertilizers, surfactants, plant growth regulators, crop desiccants, fungicides, bactericides, bacteriostats, insecticides, and insect repellants for coating seeds that can be adapted for use with seeds provided herein are disclosed in U.S. patent Ser. No. 10/745, 578, which is incorporated herein by reference in its entirety.

[0039] The disclosure also provides a method of making a soybean plant containing a mutated JAG1 gene. In certain embodiments, the methods can comprise making deletions or combinations of a deletions with insertions and/or substitutions which result in an mJAG1 gene encoding a polypeptide of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof. Gene editing molecules of use in methods provided herein include molecules capable of introducing a double-strand break ("DSB") or single-strand break ("SSB") at a specific site or sequence in a double-stranded DNA, such as in genomic DNA or in a target gene located within the genomic DNA as well as accompanying guide RNA. In certain embodiments, the mJAG1 allele results from introduction of a DSB at a target site in the JAG1 gene (e.g., SEQ ID NO: 1 or an allelic variant thereof) to induce non-homologous end joining (NHEJ) at the site of the break followed by recovery of desired mJAG1 alleles. In certain embodiments, the mJAG1 allele results from introduction of a DSB at a target site in the JAG1 gene (e.g., SEQ ID NO: 1 or an allelic variant thereof) followed by homology-directed repair (HDR), microhomology-mediated end joining (MMEJ), or NHEJ to introduce a desired donor or other DNA template polynucleotide at the DSB, followed by recovery of the desired mJAG1 allele. Examples of such gene editing molecules include: (a) a nuclease comprising an RNA-guided nuclease, an RNA-guided DNA endonuclease or RNA directed DNA endonuclease (RdDe), a class I CRISPR type nuclease system, a type II Cas nuclease, a Cas9, a nCas9 nickase, a type V Cas nuclease, a Cas12a nuclease, a nCas12a nickase, a Cas12d (CasY), a Cas12e

(CasX), a Cas12b (C2c1), a Cas12c (C2c3), a Cas12i, a Cas12j, a Cas14, an engineered nuclease, a codon-optimized nuclease, a zinc-finger nuclease (ZFN) or nickase, a transcription activator-like effector nuclease (TALE-effector nuclease or TALEN) or nickase (TALE-nickase), an Argonaute, and a meganuclease or engineered meganuclease; (b) a polynucleotide encoding one or more nucleases capable of effectuating site-specific alteration (including introduction of a DSB or SSB) of a target nucleotide sequence; (c) a guide RNA (gRNA) for use with an RNA-guided nuclease, or a DNA encoding a gRNA for use with an RNA-guided nuclease; (d) optionally donor DNA template polynucleotides suitable for insertion at a break in genomic DNA by homology-directed repair (HDR) or microhomology-mediated end joining (MMEJ); and (e) optionally other DNA templates (e.g., dsDNA, ssDNA, or combinations thereof) suitable for insertion at a break in genomic DNA (e.g., by non-homologous end joining (NHEJ)). In certain embodiments, the methods can comprising: (a) deleting: (i) nucleotides 426 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; (ii) nucleotides 424 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; or (iii) nucleotides 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; to obtain a modified soybean plant cell comprising the mutated JAG1 gene; and (b) recovering a soybean plant from the modified soybean plant cell.

[0040] In certain embodiments, the mJAG1 gene and plant cells, parts including seeds, and plants comprising the mJAG1 gene are generated by CRISPR technology. CRISPR technology for editing the genes of eukaryotes is disclosed in US Patent Application Publications 2016/0138008A1 and US2015/0344912A1, and in U.S. Pat. Nos. 8,697,359, 8,771,945, 8,945,839, 8,999,641, 8,993,233, 8,895,308, 8,865,406, 8,889,418, 8,871,445, 8,889,356, 8,932,814, 8,795,965, and 8,906,616. Cpf1 endonuclease and corresponding guide RNAs and PAM sites are disclosed in US Patent Application Publication 2016/0208243 A1. Plant RNA promoters for expressing CRISPR guide RNA and plant codon-optimized CRISPR Cas9 endonuclease are disclosed in International Patent Application PCT/US2015/018104 (published as WO 2015/131101 and claiming priority to U.S. Provisional Patent Application 61/945,700). Methods of using CRISPR technology for genome editing in plants are disclosed in US Patent Application Publications US 2015/0082478A1 and US 2015/0059010A1 and in International Patent Application PCT/US2015/038767 A1 (published as WO 2016/007347 and claiming priority to U.S. Provisional Patent Application 62/023,246). In certain embodiments, an RNA-guided endonuclease that leaves a blunt end following cleavage of the target site is used. Blunt-end cutting RNA-guided endonucleases include Cas9, Cas12c, Cas12i, and Cas12h (Yan et al., 2019). In certain embodiments, an RNA-guided endonuclease that leaves a staggered single stranded DNA overhanging end following cleavage of the target site following cleavage of the target site is used. Staggered-end cutting RNA-guided endonucleases include Cas12a, Cas12b, and Cas12e. A non-limiting target Cas12 cleavage site region in the JAG1 gene set forth in SEQ ID NO: 1 and SEQ ID NO: 5 is noted in FIG. 2. Guide RNAs comprising a spacer RNA encoded by SEQ ID NO: 2 can be used in conjunction with Cas12 nucleases to

generate mJAG1 genes which: (i) encode the polypeptides of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof or an allelic variant thereof; (ii) comprise a deletion in an endogenous JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof corresponding a deletion of SEQ ID NO: 7, 8, 9, 21, 23, 25, 27, 29, 31, 32, 33, 34, 35, or an allelic variant thereof; and/or (ii) comprise deletions of nucleotides 426 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof, deletions of nucleotides 424 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell, or deletions of nucleotides 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof. All of the patent publications referenced in this paragraph are incorporated herein by reference in their entirety.

[0041] CRISPR-type genome editing can be adapted for use in the plant cells and methods provided herein in several ways. CRISPR elements, e.g., gene editing molecules comprising CRISPR endonucleases and CRISPR guide RNAs including single guide RNAs or guide RNAs in combination with tracrRNAs or scoutRNA, or polynucleotides encoding the same, are useful in effectuating genome editing without remnants of the CRISPR elements or selective genetic markers occurring in progeny. In certain embodiments, the CRISPR elements are provided directly to the eukaryotic cell (e.g., soybean plant cells), systems, methods, and compositions as isolated molecules, as isolated or semi-purified products of a cell free synthetic process (e.g., in vitro translation), or as isolated or semi-purified products of in a cell-based synthetic process (e.g., such as in a bacterial or other cell lysate). In certain embodiments, soybean plants or soybean plant cells used in the systems, methods, and compositions provided herein can comprise a transgene that expresses a CRISPR endonuclease (e.g., a Cas9, a Cpf1-type or other CRISPR endonuclease). In certain embodiments, one or more CRISPR endonucleases with unique PAM recognition sites can be used. Guide RNAs (sgRNAs or crRNAs and a tracrRNA) to form an RNA-guided endonuclease/guide RNA complex which can specifically bind sequences in the gDNA target site that are adjacent to a protospacer adjacent motif (PAM) sequence. The type of RNA-guided endonuclease typically informs the location of suitable PAM sites and design of crRNAs or sgRNAs. G-rich PAM sites, e.g., 5'-NGG are typically targeted for design of crRNAs or sgRNAs used with Cas9 proteins. Examples of PAM sequences include 5'-NGG (*Streptococcus pyogenes*), 5'-NNAGAA (*Streptococcus thermophilus* CRISPR1), 5'-NGGNG (*Streptococcus thermophilus* CRISPR3), 5'-NNGRR or 5'-NNGRR (*Staphylococcus aureus* Cas9, SaCas9), and 5'-NNNGATT (*Neisseria meningitidis*). T-rich PAM sites (e.g., 5'-TTN or 5'-TTTV, where "V" is A, C, or G) are typically targeted for design of crRNAs or sgRNAs used with Cas12 proteins. In some instances, a Cas12 nuclease such as Cas12a can also recognize a 5'-CTA PAM motif. Other examples of potential Cas12 PAM sequences include TTN, CTN, TCN, CCN, TTTN, TCTN, TTCN, CTTN, ATTN, TCCN, TTGN, GTTN, CCCN, CCTN, TTAN, TCGN, CTCN, ACTN, GCTN, TCAN, GCCN, and CCGN (wherein N is defined as any nucleotide). Cpf1 endonuclease and corresponding guide RNAs and PAM sites are disclosed in US Patent Application Publication 2016/0208243 A1, which is incor-

porated herein by reference for its disclosure of DNA encoding Cpf1 endonucleases and guide RNAs and PAM sites.

[0042] In certain embodiments, the mJAG1 gene and plant cells, parts including seeds, and plants comprising the mJAG1 gene are generated by use of zinc finger nucleases or zinc finger nickases. Zinc-finger nucleases are site-specific endonucleases comprising two protein domains: a DNA-binding domain, comprising a plurality of individual zinc finger repeats that each recognize between 9 and 18 base pairs, and a DNA-cleavage domain that comprises a nuclease domain (typically FokI). The cleavage domain dimerizes in order to cleave DNA; therefore, a pair of ZFNs are required to target non-palindromic target polynucleotides. In certain embodiments, zinc finger nuclease and zinc finger nickase design methods which have been described (Umov et al. (2010) Nature Rev. Genet., 11:636-646; Mohanta et al. (2017) Genes vol. 8, 12: 399; Ramirez et al. Nucleic Acids Res. (2012); 40(12): 5560-5568; Liu et al. (2013) Nature Communications, 4: 2565) can be adapted for use in the methods set forth herein. The zinc finger binding domains of the zinc finger nuclease or nickase provide specificity and can be engineered to specifically recognize any desired target DNA sequence. The zinc finger DNA binding domains are derived from the DNA-binding domain of a large class of eukaryotic transcription factors called zinc finger proteins (ZFPs). The DNA-binding domain of ZFPs typically contains a tandem array of at least three zinc "fingers" each recognizing a specific triplet of DNA. A number of strategies can be used to design the binding specificity of the zinc finger binding domain. One approach, termed "modular assembly", relies on the functional autonomy of individual zinc fingers with DNA. In this approach, a given sequence is targeted by identifying zinc fingers for each component triplet in the sequence and linking them into a multifinger peptide. Several alternative strategies for designing zinc finger DNA binding domains have also been developed. These methods are designed to accommodate the ability of zinc fingers to contact neighboring fingers as well as nucleotide bases outside their target triplet. Typically, the engineered zinc finger DNA binding domain has a novel binding specificity, compared to a naturally occurring zinc finger protein. Engineering methods include, for example, rational design and various types of selection. Rational design includes, for example, the use of databases of triplet (or quadruplet) nucleotide sequences and individual zinc finger amino acid sequences, in which each triplet or quadruplet nucleotide sequence is associated with one or more amino acid sequences of zinc fingers which bind the particular triplet or quadruplet sequence. See, e.g., U.S. Pat. Nos. 6,453,242 and 6,534,261, both incorporated herein by reference in their entirety. Exemplary selection methods (e.g., phage display and yeast two-hybrid systems) can be adapted for use in the methods described herein. In addition, enhancement of binding specificity for zinc finger binding domains has been described in U.S. Pat. No. 6,794,136, incorporated herein by reference in its entirety. In addition, individual zinc finger domains may be linked together using any suitable linker sequences. Examples of linker sequences are publicly known, e.g., see U.S. Pat. Nos. 6,479,626; 6,903,185; and 7,153,949, incorporated herein by reference in their entirety. The nucleic acid cleavage domain is non-specific and is typically a restriction endonuclease, such as FokI. This endonuclease must dimerize to cleave DNA.

Thus, cleavage by FokI as part of a ZFN requires two adjacent and independent binding events, which must occur in both the correct orientation and with appropriate spacing to permit dimer formation. The requirement for two DNA binding events enables more specific targeting of long and potentially unique recognition sites. FokI variants with enhanced activities have been described and can be adapted for use in the methods described herein; see, e.g., Guo et al. (2010) *J. Mol. Biol.*, 400:96-107.

[0043] In certain embodiments, the mJAG1 gene and plant cells, parts including seeds, and plants comprising the mJAG1 gene are generated by use of TAL-effector nucleases or TALENs. Transcription activator like effectors (TALEs) are proteins secreted by certain *Xanthomonas* species to modulate gene expression in host plants and to facilitate the colonization by and survival of the bacterium. TALEs act as transcription factors and modulate expression of resistance genes in the plants. Recent studies of TALEs have revealed the code linking the repetitive region of TALEs with their target DNA-binding sites. TALEs comprise a highly conserved and repetitive region consisting of tandem repeats of mostly 33 or 34 amino acid segments. The repeat monomers differ from each other mainly at amino acid positions 12 and 13. A strong correlation between unique pairs of amino acids at positions 12 and 13 and the corresponding nucleotide in the TALE-binding site has been found. The simple relationship between amino acid sequence and DNA recognition of the TALE binding domain allows for the design of DNA binding domains of any desired specificity. TALEs can be linked to a non-specific DNA cleavage domain to prepare genome editing proteins, referred to as TAL-effector nucleases or TALENs. As in the case of ZFNs, a restriction endonuclease, such as FokI, can be conveniently used. Methods for use of TALENs in plants have been described and can be adapted for use in the methods described herein, see Mahfouz et al. (2011) *Proc. Natl. Acad. Sci. USA*, 108:2623-2628; Mahfouz (2011) *GM Crops*, 2:99-103; and Mohanta et al. (2017) *Genes* vol. 8, 12: 399). TALE nickases have also been described and can be adapted for use in methods described herein (Wu et al.; *Biochem Biophys Res Commun.* (2014); 446(1):261-6; Luo et al; *Scientific Reports* 6, Article number: 20657 (2016)).

EMBODIMENTS

[0044] The present disclosure provides for soybean plants and plant parts comprising a mutated JAG1 gene, along with methods of making and using the same. Non-limiting embodiments of the disclosure are provided herein as follows:

[0045] (1) A soybean plant cell comprising a mutated JAG1 gene, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, or an allelic variant thereof, optionally wherein the plant cell is homozygous for the mutated JAG1 gene.

[0046] (2) The soybean plant cell of embodiment 1, wherein the mutated JAG1 gene comprises: (i) the polynucleotide sequence of SEQ ID NO: 7, 8, or 9; or (ii) wherein the allelic variant of SEQ ID NO: 12, 13, or 14 is encoded by a JAG1 gene which comprises a deletion corresponding to nucleotides 426 to 430, 424 to 430, or 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1, respectively.

[0047] (3) A soybean seed comprising the soybean plant cell of embodiment 1 or 2.

[0048] (4) A soybean seed lot comprising the soybean seed of embodiment 3.

[0049] (5) The soybean seed lot of embodiment 4, wherein the seed of the seed lot are homozygous for the mutated JAG1 gene, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12 or comprises the polynucleotide sequence of SEQ ID NO: 7 and wherein the number of seeds per kilogram of seeds in the seed lot is increased in comparison to the number of seeds per kilogram of a corresponding control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0050] (6) The soybean seed lot of embodiment 5, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12 or comprises the polynucleotide sequence of SEQ ID NO: 7 and wherein the number of seeds per kilogram of seeds in the seed lot is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in comparison to the number of seeds per kilogram of a corresponding control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0051] (7) A soybean plant comprising the soybean plant cell of embodiment 1 or 2.

[0052] (8) The soybean plant of embodiment 7, wherein the soybean plant is homozygous for the mutated JAG1 gene, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12 or comprises the polynucleotide sequence of SEQ ID NO: 7 and wherein the number of seeds per kilogram of seeds harvested from the soybean plant is increased in comparison to seeds harvested from corresponding control soybean plant lacking the mutated JAG1 gene.

[0053] (9) The soybean plant of embodiment 8, wherein the number of seeds per kilogram of seeds is increased by up to about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in comparison to the number of seeds per kilogram of seeds harvested from corresponding control soybean plant lacking the mutated JAG1 gene.

[0054] (10) A soybean plant part comprising the soybean plant cell of embodiment 1 or 2, wherein said part is a leaf, stem, root, or pod.

[0055] (11) A polynucleotide comprising the sequence of SEQ ID NO: 7, 8, or 9 or encoding the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, or 14.

[0056] (12) A biological sample comprising the polynucleotide of embodiment 11.

[0057] (13) The biological sample of embodiment 12, wherein the sample comprises soybean meal or soybean stover.

[0058] (14) A method of producing a soybean seed lot comprising: (i) growing a population of soybean plants comprising a mutated JAG1 gene to maturity, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, or an allelic variant thereof and wherein the soybean plants are homozygous for the mutated JAG1 gene; and (ii) harvesting seed from the population of soybean plants of step (i) at maturity, thereby producing the soybean seed lot.

[0059] (15) The method of embodiment 14, wherein the mutated JAG1 gene comprises: (i) the polynucleotide sequence of SEQ ID NO: 7, 8, or 9; or (ii) wherein the allelic

variant of SEQ ID NO: 12, 13, or 14 comprises a deletion corresponding to nucleotides 426 to 430, 424 to 430, or 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1, respectively.

[0060] (16) The method of embodiment 14, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12 or comprises the polynucleotide sequence of SEQ ID NO: 7 and wherein the number of seeds per kilogram of seeds in the seed lot is increased in comparison to a corresponding control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0061] (17) The method of embodiment 16, wherein the number of seeds per kilogram of seeds in the seed lot is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in comparison to the number of seeds per kilogram of control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0062] (18) A method of making a soybean plant containing a mutated JAG1 gene comprising: (a) deleting: (i) nucleotides 426 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; (ii) nucleotides 424 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; or (iii) nucleotides 423 to 430 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell; to obtain a modified soybean plant cell comprising the mutated JAG1 gene; and (b) recovering a soybean plant from the modified soybean plant cell.

[0063] (19) The method of embodiment 18, wherein: (a) the nucleotides of (i) are deleted and the mutated JAG1 gene comprises the polynucleotide sequence of SEQ ID NO: 7; (b) the nucleotides of (ii) are deleted and the mutated JAG1 gene comprises the polynucleotide sequence of SEQ ID NO: 8; or (c) the nucleotides of (iii) are deleted and the mutated JAG1 gene comprises the polynucleotide sequence of SEQ ID NO: 9.

[0064] (20) The method of embodiment 18 or 19, wherein the recovering comprises the steps of generating soybean callus from the modified soybean plant cell and generating the soybean plant from the soybean callus.

[0065] (21) The method of embodiment 18, 19, or 20, further comprising the step of harvesting seed comprising the deletion from the soybean plant.

[0066] (22) A method of producing a soybean crop comprising planting a plurality of soybean seeds of embodiment 3 or the seed lot of embodiment 4, 5, or 6.

[0067] (23) The method of embodiment 22, further comprising harvesting seed from soybean plants grown from the planted seed.

[0068] (24) The method of embodiment 23, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12 or comprises the polynucleotide sequence of SEQ ID NO: 7 and number of seeds per kilogram of harvested seeds is increased in comparison to the number of seeds per kilogram of soybean seeds harvested from corresponding control soybean plants grown from control soybean seeds lacking the mutated JAG1 gene.

[0069] (25) The method of embodiment 24, wherein the number of seeds per kilogram of harvested seed is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in

comparison to the number of seeds per kilogram of seeds harvested from corresponding control soybean plants grown from control soybean seeds lacking the mutated JAG1 gene.

[0070] (26) A method for producing a soybean by-product comprising at least one processing step of cleaning, cracking, flaking, crushing, macerating, pressing, extracting, expelling, and/or extruding the seed lot of embodiment 4, 5, or 6.

[0071] (27) The method of embodiment 26, wherein the by-product is soybean protein and wherein the soybean seed lot is subjected to processing steps comprising: (i) at least one of a cracking, flaking, crushing, pressing, and/or macerating step; (ii) extracting the cracked, flaked, crushed, pressed, and/or macerated soybean seed product from step (i) with an organic solvent to produce defatted soymeal; and (iii) extracting the defatted soymeal from step (ii) with an aqueous solvent to produce an aqueous fraction comprising soybean protein.

[0072] (28) The method of embodiment 26, wherein the by-product is soybean oil and wherein the soybean seed lot is pressed to produce the oil.

[0073] (29) The method of embodiment 26, wherein the by-product is soybean oil and wherein the soybean seed lot is subjected to processing steps comprising: (i) at least one of a cracking, flaking, crushing, pressing, and/or macerating step; and (ii) solvent extracting, expelling, and/or extruding step the cracked, flaked, crushed, pressed, and/or macerated soybean seed product from step (i) to produce the oil.

[0074] (30) A guide RNA molecule comprising a spacer RNA molecule encoded by SEQ ID NO: 2.

[0075] Additional non-limiting embodiments of the disclosure are also provided herein as follows:

[0076] 1. A soybean plant cell comprising a mutated JAG1 gene, wherein the mutated JAG1 gene comprises a null mutation in the JAG1 gene encoding the polypeptide of SEQ ID NO: 10 or an allelic variant thereof and wherein the soybean plant cell lacks a loss-of-function mutation in the soybean JAG2 gene.

[0077] 2. The soybean plant cell of embodiment 1, wherein the null mutation comprises a deletion of at least 1 to 16 nucleotides corresponding to nucleotides 421 to 436 of the JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof.

[0078] 3. The soybean plant cell of embodiment 1 or 2, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof.

[0079] 4. The soybean plant cell of any one of embodiments 1 to 3, wherein the plant cell is homozygous for the mutated JAG1 gene.

[0080] 5. The soybean plant cell of any one of embodiments 1 to 4, wherein the mutated JAG1 gene comprises the polynucleotide sequence of SEQ ID NO: 7, 8, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof.

[0081] 6. The soybean plant cell of any one of embodiments 1 to 5, wherein the soybean plant cell further comprises an A2704-12, A5547-127, BPS-CV127-9, DAS44406-6, DAS68416-4, DAS81419-2, DP305423, GTS 40-3-2, HOS, A5547-127, MON87701, MON87705, MON87708, MON87769, MON89788, MON98788, MST-FG072-3, or SYHTOH210 transgenic event or modification thereof; and/or wherein (ii) the soybean plant cell further comprises a null allele of the TFL1b gene.

[0082] 7. A soybean seed comprising the soybean plant cell of any one of embodiments 1 to 6.

[0083] 8. A soybean seed lot comprising the soybean seed of embodiment 7.

[0084] 9. The soybean seed lot of embodiment 8, wherein the seed lot comprises soybean seed homozygous for the mutated JAG1 gene.

[0085] 10. The soybean seed lot of embodiment 8 or 9 wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof or comprises the polynucleotide sequence of SEQ ID NO: 7, 8, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof.

[0086] 11. The soybean seed lot of any one of embodiments 8 to 10, wherein the number of seeds per kilogram of seeds in the seed lot is increased in comparison to a corresponding control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0087] 12. The soybean seed lot of any one of embodiments 8 to 10, wherein the number of seeds per kilogram of seeds in the seed lot is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in comparison to the number of seeds per kilogram of a corresponding control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0088] 13. The soybean seed lot of any one of embodiments 8 to 12, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof or comprises the polynucleotide sequence of SEQ ID NO: 7, 8, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof.

[0089] 14. A soybean plant comprising the soybean plant cell of any one of embodiments 1 to 6.

[0090] 15. The soybean plant of embodiment 14, wherein the soybean plant is homozygous for the mutated JAG1 gene.

[0091] 16. The soybean plant of embodiment 14 or 15, wherein the number of seeds per kilogram of seeds harvested from the soybean plant is increased in comparison to the number of seeds per kilogram of seeds harvested from corresponding control soybean plant lacking the mutated JAG1 gene.

[0092] 17. The soybean plant of embodiment 14 or 15, wherein the number of seeds per kilogram of seeds is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in comparison to the number of seeds per kilogram of seeds harvested from corresponding control soybean plant lacking the mutated JAG1 gene.

[0093] 18. The soybean plant of any one of embodiments 14 to 17, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof or comprises the polynucleotide sequence of SEQ ID NO: 7, 8, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof.

[0094] 19. A soybean plant part comprising the soybean plant cell of any one of embodiments 1 to 6, wherein said part is a leaf, stem, root, or pod.

[0095] 20. A polynucleotide comprising the sequence of SEQ ID NO: 7, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof or encoding the polypep-

tide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof.

[0096] 21. A biological sample comprising the polynucleotide of embodiment 20.

[0097] 22. The biological sample of embodiment 21, wherein the sample comprises soybean meal or soybean stover.

[0098] 23. A method of producing a soybean seed lot comprising: (i) growing a population of soybean plants of any one of embodiments 14 to 18 comprising a mutated JAG1 gene to maturity, wherein the soybean plants are homozygous for the mutated JAG1 gene; and (ii) harvesting seed from the population of soybean plants of step (i) at maturity, thereby producing the soybean seed lot.

[0099] 24. The method of embodiment 23, wherein the mutated JAG1 gene comprises the polynucleotide sequence of SEQ ID NO: 7, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof.

[0100] 25. The method of embodiment 23 or 24, wherein the number of seeds per kilogram of seeds in the seed lot is increased in comparison to the number of seeds per kilogram of a corresponding control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0101] 26. The method of embodiment 23 or 24, wherein the number of seeds per kilogram of seeds in the seed lot is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in comparison to the number of seeds per kilogram of the control soybean seed lot comprising soybean seeds lacking the mutated JAG1 gene.

[0102] 27. The method of any one of embodiments 23 to 26, wherein the mutated JAG1 gene encodes the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof.

[0103] 28. A method of making a soybean plant containing a mutated JAG1 gene comprising deleting at least 1 to 16 nucleotides corresponding to nucleotides 421 to 436 of the endogenous soybean JAG1 gene of SEQ ID NO: 1 or an allelic variant thereof in a wild-type soybean plant cell to obtain a modified soybean plant cell comprising the mutated JAG1 gene; and (b) recovering a soybean plant from the modified soybean plant cell.

[0104] 29. The method of embodiment 28, wherein the mutated JAG1 gene comprises the polynucleotide sequence of SEQ ID NO: 7, 8, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof.

[0105] 30. The method of embodiment 28 or 29, wherein the recovering comprises the steps of generating soybean callus from the modified soybean plant cell and generating the soybean plant from the soybean callus.

[0106] 31. The method of embodiment 30, further comprising the step of harvesting seed comprising the deletion from the soybean plant and/or further comprising the step of selecting for plants which lack a loss-of-function mutation in the soybean JAG2 gene.

[0107] 32. A method of producing a soybean crop comprising planting the seed lot of any one of embodiments 8 to 13.

[0108] 33. The method of embodiment 32, further comprising harvesting seed from soybean plants grown from the planted seed. 34 The method of embodiment 32 or 33, wherein the number of seeds per kilogram of harvested seeds is increased in comparison to the number of seeds per kilogram of soybean seeds harvested from corresponding control soybean plants grown from control soybean seeds

lacking the mutated JAG1 gene. 35. The method of embodiment 32 or 33, wherein the number of seeds per kilogram of harvested seed is increased by up to about 5%, 6%, 7%, 8%, 9%, 10%, 11%, or 12% in comparison to the number of seeds per kilogram of the seeds harvested from corresponding control soybean plants grown from control soybean seeds lacking the mutated JAG1 gene.

[0109] 36. A method for producing a soybean by-product comprising at least one processing step of cleaning, cracking, flaking, crushing, macerating, pressing, extracting, expelling, and/or extruding the seed lot of any one of embodiments 8 to 13.

[0110] 37. The method of embodiment 36, wherein the by-product is soybean protein and wherein the soybean seed lot is subjected to processing steps comprising: (i) at least one of a cracking, flaking, crushing, pressing, and/or macerating step; (ii) extracting the cracked, flaked, crushed, pressed, and/or macerated soybean seed product from step (i) with an organic solvent to produce defatted soymeal; and (iii) extracting the defatted soymeal from step (ii) with an aqueous solvent to produce an aqueous fraction comprising soybean protein.

[0111] 38. The method of embodiment 36 or 37, wherein the by-product is soybean oil and wherein the soybean seed lot is pressed to produce the oil.

[0112] 39. The method of embodiment 36 or 37, wherein the by-product is soybean oil and wherein the soybean seed lot is subjected to processing steps comprising: (i) at least one of a cracking, flaking, crushing, pressing, and/or macerating step; and (ii) solvent extracting, expelling, and/or extruding step the cracked, flaked, crushed, pressed, and/or macerated soybean seed product from step (i) to produce the oil.

[0113] 40. A guide RNA molecule comprising a Cas12 direct repeat element which is operably linked to the spacer RNA molecule encoded by SEQ ID NO: 2

Example 1. Generation of mJAG1 Soybean

[0114] The plasmid pIN1340 was created to transform soybean plants and disrupt the open reading frame of the JAGGED1 (Jag1) gene (Glyma.20g116200) (SEQ ID NO: 1) through CRISPR-mediated gene editing. This plasmid was constructed using the strategy and techniques described by Cermik et al., 2017, The Plant Cell. 29 (6) 1196-1217; DOI: 10.1105/tpc.16.00922). The pIN1340 vector has the following two functional expression cassettes between the right and left T-DNA border. A *Solanum lycopersicum* ubiquitin gene promoter and 5' untranslated region (UTR) drives the expression a CRISPR-Cas nuclease transcript. The Cas gene had a SV40 nuclear localization signal (NLS) fused to the 5' end and a nucleoplasmic NLS fused to the 3' end. The Cas coding sequence with the NLS fusions was codon optimized for soy expression as set forth in WO2021202397. The coding sequence was followed by an *Arabidopsis thaliana* heat shock gene terminator. Another expression cassette is made up of an *Arabidopsis thaliana* U6-26 promoter driving the expression of a CRISPR guide RNA comprising a crRNA fused to the RNA encoded by the JAG1_g3 (SEQ ID NO: 2) spacer designed to target the *Glycine max* JAG1 gene and followed by an RNA polymerase iii termination signal.

[0115] The other functional elements of the pIN1340 vector were derived from a standard *Agrobacterium* binary

transformation plasmid that can replicate in both *Escherichia coli* and *Agrobacterium tumefaciens*. They are a T-DNA right border sequence (SEQ ID NO: 4) followed by an expression cassette to confer glyphosate resistance to the transgenic plants. This cassette consisted of the *Arabidopsis thaliana* Ubiquitin 10 gene promoter and 5' UTR, *Agrobacterium* sp. strain CP4 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) gene and the *Pisum sativum* rib-1,5-bisphosphate carboxylase (rbcS) small subunit gene terminator. The insertion site was followed by a T-DNA left border sequence (SEQ ID NO: 3).

[0116] The plasmid pIN1340 was transformed into *Agrobacterium tumefaciens* EHA105 (Hood et al., 1993, Transgenic Research. 2: 208-218. doi:10.1007/BF01977351) by electroporation following standard techniques. Frozen glycerol stocks were prepared for use in plant transformation.

[0117] Transgenic TO soybean events were made by *Agrobacterium*-mediated transformation with vector pIN1340. Sterilized soybean seeds were imbibed in water overnight, and explants were prepared as mature cotyledon halves with trimmed hypocotyls. The explants went through the typical transformation and regeneration steps of infection and co-cultivation, shoot induction and elongation and selection, rooting, and transplanting to soil to produce T1 seeds (see, for example, Li et al, Optimization of *Agrobacterium*-Mediated Transformation in Soybean (2017) Frontiers in Plant Science v8 Article 246; Pareddy et al. Transgenic Res. 2020 June; 29(3):267-281. doi: 10.1007/s11248-020-00198-8).

[0118] T1 progeny of TO plants were grown and genotyped by AmpSeq. T1 plants with the following edits set forth in Table 2, homozygous or heterozygous as indicated in the following example, or segregating wild types, were selected for phenotyping.

TABLE 2

Gene Edits	
Description	SEQ ID NO
Wild type JAG1 DNA fragment (annotated)	5
Wild type JAG1 peptide fragment encoded by SEQ ID NO: 5	6
1:5D mJAG1 deletion	7
-2:7D mJAG1 deletion	8
-3:8D mJAG1 deletion	9
1:5D mJAG1 deletion translation product	12
-2:7D mJAG1 deletion translation product	13
-3:8D mJAG1 deletion translation product	14

[0119] The reference wild-type JAG1 DNA sequence is depicted in FIG. 1 and mJAG1 deletion sequences are depicted in FIG. 2. The three deletions produce frameshift mutations which result in the polypeptides of SEQ ID NO: 12, 13, and 14. The GmJag2 locus was sequenced as well, but no edits were found.

Example 2. Performance of mJAG1 Soybean

[0120] T1 progeny plants with the genotypes noted in the Table 3 below were grown out on a field at a sparse density, and phenotyped for seed count per plant, number of seeds per pod, total seed weight (grams) per plant, and single seed weight (seed weight/seed count).

TABLE 3

Analysis of T1 Progeny plants					
Plant ID	JAG1 Genotype	SEEDCT	NSPP	SEEDWT	Single SEEDWT
NINF1170.005	WT	523	2.43	93.42	0.179
NINF1170.006	WT	580	2.57	106.45	0.184
NINF1170.009	WT	592	2.55	112.14	0.189
NINF1170.010	WT	549	2.41	99.55	0.181
T1GM00071CB,pIN1304.520.025	WT	107	1.88	21.37	0.200
T1GM00073CB,pIN1304.440.007	WT	582	2.56	107.92	0.185
T1GM00073CB,pIN1304.440.012	WT	526	2.44	92.65	0.176
T1GM00073CB,pIN1304.440.014	WT	674	2.75	127.92	0.190
T1GM00073CB,pIN1304.440.015	WT	594	2.55	112.97	0.190
T1GM00075CB,pIN1338.533.005	WT	472	2.40	91.67	0.194
T1GM00075CB,pIN1338.533.009	WT	678	2.36	119.28	0.176
T1GM00075CB,pIN1338.533.010	WT	636	2.48	113.38	0.178
T1GM00075CB,pIN1338.533.011	WT	546	2.36	91.51	0.168
T1GM00075CB,pIN1338.533.012	WT	403	2.53	61.58	0.153
T1GM00075CB,pIN1338.533.013	WT	423	2.53	61.41	0.145
T1GM00075CB,pIN1338.533.014	WT	417	2.40	70.1	0.168
T1GM00075CB,pIN1338.533.015	WT	455	2.42	76.64	0.168
T1GM00075CB,pIN1340.300.002	1:5D/1:5D	375	2.42	64.96	0.173
T1GM00075CB,pIN1340.300.049	1:5D/1:5D	574	2.47	87.02	0.152
T1GM00075CB,pIN1340.300.052	1:5D/1:5D	519	2.40	83.89	0.162
T1GM00075CB,pIN1340.300.053	1:5D/1:5D	471	2.60	73.94	0.157
T1GM00075CB,pIN1340.300.058	1:5D/1:5D	542	2.40	89.52	0.165
T1GM00075CB,pIN1340.307.007	WT	529	2.44	96.32	0.182
T1GM00075CB,pIN1340.308.003	-3:8D/-3:8D	525	2.64	79.08	0.151
T1GM00075CB,pIN1340.308.020	-3:8D/-3:8D	473	2.53	75.49	0.160
T1GM00075CB,pIN1340.308.026	-3:8D/-3:8D	509	2.33	90.46	0.178
T1GM00075CB,pIN1340.308.030	-3:8D/-3:8D	409	2.43	69.26	0.169
T1GMIW000100.045.001	WT	407	2.45	67.7	0.166
T1GMIW000100.064.013	WT	281	2.34	52.65	0.187
T1GMIW000100.064.015	WT	221	2.13	43.65	0.198
T1GMIW000100.064.026	WT	383	2.29	69.36	0.181
T1GMIW000100.064.047	WT	459	2.37	94.58	0.206
T1GMIW000100.064.050	WT	506	2.64	97.98	0.194
T1GMIW000100.064.071	-2:7D/-2:7D	489	2.29	89.38	0.183

[0121] The data indicates that the score seed phenotypes are not significantly impacted by the mJAG1 alleles.

[0122] T1 progeny plants with the genotypes noted in Table 4 below were grown out on a field at a sparse density,

and phenotyped for leaf length and width. Leaf measurements were taken at the 5th node about 6 weeks after planting, and at the 8th node about 7 weeks after planting.

TABLE 4

Leaf Phenotypes							
Plant ID	JAG1 Genotype	5 th L_cm	5 th W_cm	5 th L/W	8 th L_cm	8 th W_cm	8 th L/W
NINF1170.005	WT	9.4	6.8	1.38	12.7	8.7	1.46
NINF1170.006	WT	9.5	6.6	1.44	11.4	7.6	1.50
NINF1170.009	WT	9.5	6.7	1.42	12.3	8.6	1.43
NINF1170.010	WT	9.6	6.7	1.43	11	7.6	1.45
T1GM00075CB,pIN1338.533.005	WT	7.3	5.5	1.33	10.3	6	1.72
T1GM00075CB,pIN1338.533.009	WT	8	5.6	1.43	11.1	7.3	1.52
T1GM00075CB,pIN1338.533.010	WT	9.3	6.1	1.52	12	7.5	1.60
T1GM00075CB,pIN1338.533.011	WT	8.8	6	1.47	10.9	7.9	1.38
T1GM00075CB,pIN1338.533.012	WT	8.4	5.9	1.42	9.7	5.6	1.73
T1GM00075CB,pIN1338.533.013	WT	8.6	5.8	1.48	10.2	6	1.70
T1GM00075CB,pIN1338.533.014	WT	7.5	5.3	1.42	9	5.4	1.67
T1GM00075CB,pIN1338.533.015	WT	7.5	5.5	1.36	9	5.8	1.55

TABLE 4-continued

Leaf Phenotypes							
Plant ID	JAG1 Genotype	5 th L_cm	5th W_cm	5th L/W	8 th L_cm	8th W_cm	8 th L/W
T1GM00075CB.pIN1340.300.002	1:5D/1:5D	10	4.8	2.08	13.5	6	2.25
T1GM00075CB.pIN1340.300.049	1:5D/1:5D	11.3	5.6	2.02	14	7	2.00
T1GM00075CB.pIN1340.300.052	1:5D/1:5D	9.4	5	1.88	13.1	6.5	2.02
T1GM00075CB.pIN1340.300.053	1:5D/1:5D	10.5	5.5	1.91	13.5	6.4	2.11
T1GM00075CB.pIN1340.300.058	1:5D/1:5D	10.3	5	2.06	13.1	6.5	2.02
T1GM00075CB.pIN1340.307.007	WT	10.2	6.3	1.62	13.2	7.6	1.74
T1GM00075CB.pIN1340.308.003	-3:8D/-3:8D	9.8	4.6	2.13	14.8	6.8	2.18
T1GM00075CB.pIN1340.308.020	-3:8D/-3:8D	9.9	4.8	2.06	13.6	5.7	2.39
T1GM00075CB.pIN1340.308.026	-3:8D/-3:8D	10.1	5	2.02	13.7	7	1.96
T1GM00075CB.pIN1340.308.030	-3:8D/-3:8D	9.5	4.7	2.02	13.3	5.3	2.51
T1GMIW000100.045.001	WT	7.6	5.2	1.46	9.7	6.5	1.49
T1GMIW000100.064.013	WT	9	6	1.50	11	6.4	1.72
T1GMIW000100.064.015	WT	8	5	1.60			
T1GMIW000100.064.026	WT	7.1	5.1	1.39	10.1	5.4	1.87
T1GMIW000100.064.047	WT	9.4	6.4	1.47	10.7	7.2	1.49
T1GMIW000100.064.050	WT	8.7	6	1.45	11.5	7.3	1.58
T1GMIW000100.064.071	-2:7D/-2:7D	10.1	5.1	1.98	12.2	6.3	1.94

[0123] The data in Table 4 indicates that the leaves of the plants homozygous for the mJAG1 mutations are narrower and elongated.

circular screen of indicated size (in inches) from a 1000 g subsample shaken for 5 minutes across 9 screens ordered in decreasing size. Collected for 1 replicate at 6 locations.

TABLE 5

Seed size					
	GENOTYPE			JAG1	Unedited
	1:5D/1:5D	-3:8D/-3:8D	-2:7D/-2:7D	Null	WT CTRL
Size Screening:	0.0	0.0	0.0	0.0	0.0
22/64 Round Screen					
Size Screening:	0.0	0.0	0.0	0.0	0.0
20/64 Round Screen					
Size Screening:	5.9	10.6	9.6	5.3	10.1
18/64 Round Screen					
Size Screening:	488.2	484.9	477.5	490.7	499.3
16/64 Round Screen					
Size Screening:	485.1	487.9	489.7	485.3	473.4
14/64 Round Screen					
Size Screening:	17.3	14.0	19.6	15.7	14.5
13/64 Round Screen					
Size Screening:	3.2	2.2	3.2	2.6	2.5
12/64 Round Screen					
Size Screening:	0.1	0.1	0.1	0.1	0.1
11/64 Round Screen					
Size Screening:	0.0	0.0	0.0	0.0	0.0
10/64 Round Screen					

Example 3. Seed Size Distribution in mJAG1 Soybean

[0124] Seed size distribution was measured using screens with round holes ranging from 3.6 (3/64 inches) to 8.7 mm (22/64 inches) in diameter at intervals of either 0.4 or 0.8 mm (Egli et al, Agronomy Journal, Volume 79, Issue 3, 463-467 1987). The screens were stacked on top of each other each sample was placed on the top screen.

[0125] For each of the sieves, the seed that remained at the top of each screen was weighed. The distribution of seed sizes is shown in Table 5 below, with the numbers indicating the weight (g) of the portion of seeds that remained on the

[0126] These results show that seeds from the 1:5D/1:5D homozygous mJAG1 plants are not of a significantly smaller size than those from the wild type controls.

Example 4. Seed Weights and Yields of mJAG1 Soybean Grown in Different Locations

[0127] Plants homozygous for the indicated mJAG1 alleles and in the same genetic background were grown at various locations, as indicated in Table 6 below. From most locations, five subsamples were collected from three replicated plots and the seeds were weighed and counted. Avg. 1000-Swt is the weight of one thousand seeds in grams. The

yield per plant or yield per plot values were largely similar for all these mutants and wild type in these trials.

TABLE 6

Seed weights and Yields					
		Allele			
		1:5D	-2:7D	-3:8D	WT
Iowa 1	Avg. 1000-Swt	150.1	152.6	153.7	156.7
	Std. dev. of 1000-Swt		3.3	3.4	3.4
	Avg. Seed/lb	3,022.0	2,972.7	2,952.3	2,895.2
	Std. dev. of Seed/lb		64.7	63.5	62.8
Iowa 2	Avg. 1000-Swt	156.4	151.0	152.6	156.4
	Std. dev. of 1000-Swt		4.0	3.1	3.3
	Avg. Seed/lb	2,899.0	3,006.7	2,973.3	2,901.2
	Std. dev. of Seed/lb		80.0	62.3	62.7
Ohio 1	Avg. 1000-Swt	152.8	163.4	164.5	167.3
	Std. dev. of 1000-Swt		2.5	2.4	7.2
	Avg. Seed/lb	2,969.0	2,777.5	2,758.0	2,715.0
	Std. dev. of Seed/lb		41.7	39.4	114.2
Illinois	Avg. 1000-Swt	144.8	148.3	150.2	150.5
	Std. dev. of 1000-Swt		2.1	2.6	3.0
	Avg. Seed/lb	3,133.0	3,058.0	3,019.7	3,014.6
	Std. dev. of Seed/lb		43.9	53.0	60.1
Indiana 1	Avg. 1000-Swt	119.1	124.6	127.0	127.2
	Std. dev. of 1000-Swt	0.8	2.0	3.6	2.6
	Avg. Seed/lb	3,810.0	3,639.3	3,574.3	3,568.0
	Std. dev. of Seed/lb	25.5	59.5	103.0	72.1
Puerto Rico 1	Avg. 1000-Swt	143.8		141.2	144.5
Rico 1	Std. dev. of 1000-Swt	3.3		15.0	14.3
	Avg. Seed/lb	3,156.2		3,242.4	3,164.9
	Std. dev. of Seed/lb	72.6		312.0	288.4
Puerto Rico 2	Avg. 1000-Swt	145.9		152.1	149.3
Rico 2	Std. dev. of 1000-Swt	1.0		4.0	1.9
	Avg. Seed/lb	3,104.5		2,979.5	3,035.0
	Std. dev. of Seed/lb	20.0		77.2	40.2
Nebraska	Avg. 1000-Swt	158.3	157.2	156.3	160.5
	Std. dev. of 1000-Swt		2.0	5.1	2.0
	Avg. Seed/lb	2,864.0	2,885.7	2,903.3	2,826.8
	Std. dev. of Seed/lb		35.5	95.4	35.9
Indiana 2	Avg. 1000-Swt	149.5		154.0	168.0
	Std. dev. of 1000-Swt	7.8			10.7
	Avg. Seed/lb	3,034.0		2,943.0	2,710.0
	Std. dev. of Seed/lb	158.4			167.1
Green house	Avg. 1000-Swt	161.8		164.5	183.3
	Std. dev. of 1000-Swt	8.0		11.6	4.3
	Avg. Seed/lb	2,808.8		2,767.8	2,476.3
	Std. dev. of Seed/lb	137.6		196.2	58.2

[0128] These results indicate a consistently lower and tighter distribution of weight of seeds from plants homozygous for the mJAG1 1:5D allele.

Example 5. Generation of Additional mJAG1 Mutations

[0129] Additional mJAG1 mutant soybean plants were generated essentially as described in Example 1. T1 progeny of T0 plants were grown and genotyped by AmpSeq. T1 and later generation plants that were homozygous the following JAG1 gene edits set forth in Table 7 were selected for phenotyping.

TABLE 7

Additional mJAG1 mutants		
Description	SEQ ID NO OF mJAG1 DNA FRAGMENT OR ENCODED mJAG1 PROTEIN	SEQ ID NO OF GENOMIC DNA WITH mJAG1 DELETION
-2:10D mJAG1 deletion	21	31
-2:10D mJAG1 deletion translation product	22	
-2:5D mJAG1 deletion	23	32
-2:5D mJAG1 deletion translation product	24	
2:1D mJAG1 deletion	25	33
2:1D mJAG1 deletion translation product	26	
1:4D mJAG1 deletion	27	34
1:4D mJAG1 deletion translation product	28	
1:7D mJAG1 deletion	29	35
1:7D mJAG1 deletion translation product	30	
Large mJAG1 Deletion	A deletion comprising at least nucleotides 421 to 436 of SEQ ID NO: 1.	
Large Deletion translation product	Not Determined	

Example 6. Seeds Per Pound of Seed for mJAG1 Soybean in 2022 Field Tests in Comparison to Checks

[0130] Plants homozygous for the indicated mJAG1 alleles and in the same genetic background were field tested in the summer of 2022 in the central United States. The number of seeds per pound of harvested seed for each mJAG1 allele was determined and compared to checks which lack the mJAG1 allele but were otherwise isogenic as indicated in Table 8 below. The number of seeds per pound of seed was increased for all mJAG1 alleles relative to checks in for the NING1295, TEND2128, TENF2132, and TENG2141T genotypes. The TENF2147L genotype with the 1:4D and 1:7D mJAG1 alleles exhibited a decrease in seed number per pound.

TABLE 8

Calculated Seeds/lb (from individual seed weight avg)						
Genotype	Allele (SEQ ID NO)	Plants	Avg for mJAG1 allele	Null Avg	Check Avg	% Check
NING1295	-2:10D (SEQ ID NO: 21)	36	3204	2937	3080	104%
	-2:5D (SEQ ID NO: 23)	33	3228	2937	3080	104.8%
	-2:7D (SEQ ID NO: 8)	34	3125	2937	3080	101.4%
	2:1D (SEQ ID NO: 25)	34	3174	2937	3080	103%
TEND2128	1:5D (SEQ ID NO: 7)	29	2863	2904	2779	103%
	-3:8D (SEQ ID NO: 9)	31	2811	2904	2779	101%
TENF2132	-2:5D (SEQ ID NO: 23)	26	2941	NA	2792	105%
	Large Deletion (ND)	34	3086	NA	2792	110.5%
TENF2147L	1:4D (SEQ ID NO: 27)	34	2894		3061	94.5%
	1:7D (SEQ ID NO: 29)	40	2864		3061	93.5%
TENG2141T	-2:5D (SEQ ID NO: 23)	42	3014		2891	104%

Example 7. Summary of Biological Sequences
Provided in Sequence Listing

[0131] The following Table 9 describes biological sequences provided herein.

TABLE 9

Biological Sequences			
SEQUENCE DESCRIPTION	SEQ ID NO	SEQUENCE TYPE	SOURCE
Wild type JAG1 genomic DNA	1	DNA	Glycine max
DNA encoding JAG1_g3 spacer	2	DNA	synthetic construct
T-DNA left border	3	DNA	synthetic construct
T-DNA right border	4	DNA	synthetic construct
Wild type JAG1 DNA fragment (annotated)	5	DNA	Glycine max
Wild type JAG1 peptide fragment encoded by SEQ ID NO: 5	6	PRT	Glycine max
1:5D mJAG1 deletion DNA fragment	7	DNA	synthetic construct
-2:7D mJAG1 deletion DNA fragment	8	DNA	synthetic construct
-3:8D mJAG1 deletion DNA fragment	9	DNA	synthetic construct
Wild-type JAG1	10	PRT	Glycine max
Wild-type JAG1 coding sequence (CDS)	11	DNA	Glycine max
1:5D mJAG1 deletion translation product (protein)	12	PRT	synthetic construct
-2:7D mJAG1 deletion translation product (protein)	13	PRT	synthetic construct
-3:8D mJAG1 deletion translation product (protein)	14	PRT	synthetic construct
1:5D mJAG1 deletion genomic sequence	15	DNA	synthetic construct
Predicted mJAG1 1:5D CDS	16	DNA	synthetic construct

TABLE 9-continued

Biological Sequences			
SEQUENCE DESCRIPTION	SEQ ID NO	SEQUENCE TYPE	SOURCE
-2:7D mJAG1 deletion genomic sequence	17	DNA	synthetic construct
-2:7D mJAG1CDS (DNA)	18	DNA	synthetic construct
-3:8D mJAG1 deletion genomic sequence	19	DNA	synthetic construct
3:8D mJAG1 CDS (DNA)	20	DNA	synthetic construct
minus 2:10D mJAG1 deletion DNA fragment	21	DNA	synthetic construct
minus 2:10D mJAG1 deletion translation product	22	PRT	synthetic construct
minus 2:5D mJAG1 deletion DNA fragment	23	DNA	synthetic construct
minus 2:5D mJAG1 deletion translation product	24	PRT	synthetic construct
2:1D mJAG1 deletion DNA fragment	25	DNA	synthetic construct
2:1D mJAG1 deletion translation product	26	PRT	synthetic construct
1:4D mJAG1 deletion DNA fragment	27	DNA	synthetic construct
1:4D mJAG1 deletion translation product	28	PRT	synthetic construct
1:7D mJAG1 deletion DNA fragment	29	DNA	synthetic construct
1:7D mJAG1 deletion translation product	30	PRT	synthetic construct
minus 2:10D mJAG1 deletion genomic DNA	31	DNA	synthetic construct
minus 2:5D mJAG1 deletion genomic DNA	32	DNA	synthetic construct
2:1D mJAG1 deletion genomic DNA	33	DNA	synthetic construct
1:4D mJAG1 deletion genomic DNA	34	DNA	synthetic construct

TABLE 9-continued

Biological Sequences			
SEQUENCE DESCRIPTION	SEQ ID		SOURCE
	NO	TYPE	
1:7D mJAG1 deletion genomic DNA	35	DNA	synthetic construct
mJAG2 wild-type (WT) genomic DNA	36	DNA	Glycine max
mJAG2 WT CDS	37	DNA	Glycine max
mJAG2 WT protein	38	PRT	Glycine max
TFL1b WT genomic DNA	39	DNA	Glycine max
TFL1b WT CDS	40	DNA	Glycine max
TFL1b WT protein	41	PRT	Glycine max

[0132] All cited patents and patent publications referred to in this application are incorporated herein by reference in their entirety. All of the materials and methods disclosed and claimed herein can be made and used without undue experimentation as instructed by the above disclosure and illustrated by the examples. Although the materials and methods of this disclosure have been described in terms of embodiments and illustrative examples, it will be apparent to those of skill in the art that substitutions and variations can be applied to the materials and methods described herein without departing from the concept, spirit, and scope of the disclosure. 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 disclosure as encompassed by the embodiments of the disclosures recited herein and the specification and appended claims.

SEQUENCE LISTING

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Sequence total quantity: 41
SEQ ID NO: 1      moltype = DNA length = 2436
FEATURE          Location/Qualifiers
source           1..2436
                 mol_type = genomic DNA
                 organism = Glycine max

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aaagctctttt atcttctacc atcactcaac cagcctctat attgcagttt caaactgaaa 120
gtctaaaattt ttttgtaaaa agcttttagtt ttatccctac ccccaacca tctgaaagaa 180
agagtgtttg cctcacatca tttttccctt ttctgtctct ctctctgtcg gtaccatgta 240
ggctcttccc cactactaca ccttcacacc cttcttttct tctctctctt tctccttctc 300
taaacccttt aactttctct cttctatgac ttgtgtgttc ctttacagga gaccagaacg 360
aaacccttta gatcttaaca atttgccga tgagtactct agagatggca aacaagtctc 420
cgaagaccat acctcttcat ccggtaaact tcatgatcat accaatatat atatatatgc 480
acgctgaaat atcaaaggaa cacttttttt ttctttctat ttaccgaatt ctatttcaca 540
atcacacacc accatgggaa gcctttcact ttccacagga aacaaagttg aacctgccc 600
gtgggttggt acccaccctt gtgggtatatt ccttgacctt gaaacagttg tcaccacact 660
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aataaaaataa gaaaaacata aaagtagtta ggtgatagaa tagaacttaa aaaaaagaaa 840
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ggtaatcgag aatggggagt taaaggcaaa gaagggtgtc atggaaagttg ctttaattgg 960
atgggtatag ttgcaggttg caggaaaaag aaaagcggtg ggaaggatgg aaaagacgag 1020
tgtgggaag tctacgagtg tagattttgt tccctcaagt tctgcaagtc tcaggctctt 1080
ggggggacaca tgaaccgcca ccgccaaggc tagtaccacc tatattatta tactttatat 1140
tttcttcttc ttttctttta ccactcttc tcacaagaac caaatctctt ctggccgtta 1200
atgatttggc catgaaagct tgcatttcca atcacaaaat gttgtgttgt tggattgctg 1260
aaattcgatc atcgagaggg ccccttcagc tgtttttttt ttttcttttt gotttgcttt 1320
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gtcaactggg ctttctgttg gactataaca ttgctgcaca aggtgccct cacttaggg 1440
atgcacccat tacttccatg cagcgattct cttctatatt cttctctctg ttcaacattt 1500
atatatttca tttctcaaat acttgttttt ctgtgggttc tttagcgttt gttaacgttg 1560
ttttttcaag gtataacaca taatttttgg gtactcagca tgacactgtt tgatactgctg 1620
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aagagatgag agattctttg ttttggtttg tgttatgttt ctgttatgtt 2160
atgtgtatc atcataaaga caccgaatcc agagagagag agaggtggtt ttgtgtttat 2220
ctacagtaac caggacagc ttttgagctc atggacacgc tcagctactt tggcttggg 2280
ttgtgggtgg gatttcttct caacatcgcc ttttgattg gtactagct agctagcttg 2340
gacaaccagt tagatttga ctgaaacttt ccaaactcct tttcctttgc atgccaaatt 2400
acaaccattt tcttctcag taatttgttc ttccaa 2436

SEQ ID NO: 2      moltype = DNA length = 23
FEATURE          Location/Qualifiers
source           1..23
                 mol_type = other DNA
                 organism = synthetic construct

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-continued

SEQUENCE: 2
 ccggatgaag aggtatggtc ttc 23

SEQ ID NO: 3 moltype = DNA length = 25
 FEATURE Location/Qualifiers
 source 1..25
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 3
 tggcaggata tattgtgggtg taaac 25

SEQ ID NO: 4 moltype = DNA length = 26
 FEATURE Location/Qualifiers
 source 1..26
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 4
 gtaaacctaa gagaaaagag cgttta 26

SEQ ID NO: 5 moltype = DNA length = 63
 FEATURE Location/Qualifiers
 source 1..63
 mol_type = genomic DNA
 organism = Glycine max

SEQUENCE: 5
 gtactctaga gatggcaaac aagtcctcga agaccatacc tcttcacccg gtaaacttca 60
 tga 63

SEQ ID NO: 6 moltype = AA length = 17
 FEATURE Location/Qualifiers
 source 1..17
 mol_type = protein
 organism = Glycine max

SEQUENCE: 6
 YSRDGKQVLE DHTSSSG 17

SEQ ID NO: 7 moltype = DNA length = 58
 FEATURE Location/Qualifiers
 source 1..58
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 7
 gtactctaga gatggcaaac aagtcctcga agacctcttc atccggtaaa ctccatga 58

SEQ ID NO: 8 moltype = DNA length = 56
 FEATURE Location/Qualifiers
 source 1..56
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 8
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SEQ ID NO: 9 moltype = DNA length = 55
 FEATURE Location/Qualifiers
 source 1..55
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 9
 gtactctaga gatggcaaac aagtcctcga cctcttcatc ccggtaaactt catga 55

SEQ ID NO: 10 moltype = AA length = 255
 FEATURE Location/Qualifiers
 source 1..255
 mol_type = protein
 organism = Glycine max

SEQUENCE: 10
 MRPERNPLDL NNLDPDEYSRD GKQVLEDHTS SSGCRKKKSG GKDGDCECGK VYECRFLCSLK 60
 FCKSQALGGH MNRHRQERET ETLNQARQLV FRCDHNIAAQ GAPHLGCCQT IGTGGYHPSG 120
 DPTVPLRFPR YFSGSSSTHM PPSPPPPPPP QRPYLYPSPT RPSVFGSSHF PLQHAYNDYY 180
 VGHVMSGGSH GHYVGGESTR SYTCIGAPVG QGGGFAGGKE GSAVQEEGLS TWGRGYSGAQ 240
 DRLDPPSAIN RFQDG 255

SEQ ID NO: 11 moltype = DNA length = 771
 FEATURE Location/Qualifiers
 source 1..771
 mol_type = other DNA

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organism = Glycine max

SEQUENCE: 11

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ggcaacaag	tectcgaaga	ccatacctct	tcatacgggt	gcaggaaaaa	gaaaagcggc	120
gggaaggatg	gaaaagacga	gtgtgggaag	gtctacgagt	gtagattttg	ttccctcaag	180
ttctgcaagt	ctcaggctct	tgggggacac	atgaaccgcc	accgccaaga	gaggggaaacg	240
gagacgctga	accaggctcg	tcaactggtc	tttcgtttgt	atcataacat	tgctgcacaa	300
ggtgcccctc	acttaggatg	ctgcccaca	ataggaacgg	ggggttatca	tcctcagga	360
gacccaacag	tgccctcaag	attcccaga	tactctcag	gttcacctc	aactcacatg	420
ccaccatccc	cgccaccgcc	gccgccaccg	caacgaccat	acctataccc	ttcacctacg	480
aggccagtgt	catttggtgc	atcacacttc	cctctccagc	atgcagtgaa	cgattactat	540
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agttacacgt	gcattgggtc	accggtgggg	caaggtggcg	gattcgctgg	tggttaaggag	660
gggtctgcag	tgcaggagga	agggttgagt	acttggggaa	ggggctattc	aggtgcacag	720
gatcgtttgg	atcctcccctc	agcgatcaat	cggtttcaag	atggtttcta	a	771

SEQ ID NO: 12 moltype = AA length = 52
FEATURE Location/Qualifiers
source 1..52
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 12

MRPERNPLDL	NNLPDEYSRD	GKQVLEDLFI	RLQEKEKRRE	GWKRRVWEG	RV	52
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SEQ ID NO: 13 moltype = AA length = 68
FEATURE Location/Qualifiers
source 1..68
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 13

MRPERNPLDL	NNLPDEYSRD	GKQVLEPLHP	VAGKRKAAGR	MEKTSVGRST	SVDFVPSSSA	60
SLRLLGDT						68

SEQ ID NO: 14 moltype = AA length = 51
FEATURE Location/Qualifiers
source 1..51
 mol_type = protein
 organism = synthetic construct

SEQUENCE: 14

MRPERNPLDL	NNLPDEYSRD	GKQVLDLFI	LQEKEKRREG	WKRRVWEG	LR V	51
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SEQ ID NO: 15 moltype = DNA length = 2431
FEATURE Location/Qualifiers
source 1..2431
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 15

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gtctaaattt	ttttgtaaaa	agcttttagt	ttatccctac	ccccacccca	tctgaaagaa	180
agagtgtttg	cctcacatca	tttttcccct	ttctgtctct	ctctctgtcg	gtaccatgta	240
ggctcttccc	cactactaca	ccttcacacc	cttctttttc	tcctcctctt	tctccttctc	300
taaacccttt	aacttttctc	ctcttatgac	tttgtttgtc	ctttacagga	gaccagaacg	360
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cgaagacctc	ttcatccggg	aaacttcatg	atcataccac	tatatatata	tatgcacgct	480
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tcgagaatgg	ggagttaaag	gcaaaagaag	gtgcatgga	agttgcttta	attggatggt	960
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gaaggtctac	gagtgtagat	ttgttcccct	caagttctgc	aagtctcagg	ctcttggggg	1080
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tcctcttttc	ttttaccact	ccttctcaca	agaacccaat	ctcttctggc	cgttaatgat	1200
ttggccatga	aagcttgcca	tttcaatcac	aaaatgttgt	gttgttggat	tgctgaaatt	1260
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ctggtctttc	ggttgatcca	taacattgct	gcacaagggt	cccctcactt	agggtatgca	1440
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tttgtgataa	tattcaatct	agatgctgcc	aaacaatagg	aacggggggg	tatcatccct	1680
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cattttcctt ctcaagtaatt tgtcttttca a 2431

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FEATURE            Location/Qualifiers
source              1..766
                    mol_type = other DNA
                    organism = synthetic construct

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ggatggaaaa gacgagtgtg ggaagggtca cgagtgtaga tttgttccc tcaagtctg 180
caagtctcag gctcttgggg gacacatgaa ccgccaccgc caagagaggg aaacggagac 240
gctgaaccag gctcgtcaac ttgtctttcg ttgtgatcat aacattgctg cacaagggtc 300
ccctcactta ggaatgtgcc aaacaatagg aacggggggg tatcatccct caggagaccc 360
aacagtgcct ctaagatttc caagataact ctcagggtca tcctcaactc acatgccacc 420
atccccgccg ccgcgcgcgc caccgcaacg accataccta tacccttcac ctacgaggcc 480
agtgtcattt gggtcacac acttcctct ccagcatgca gtgaacgatt actatgtggg 540
ccagtgatg agtggtggca gccacggaca ctatgttggg ggagagagca caaggagta 600
cacgtgcatt ggtgcaccgg tggggcaagg tggcggattc gctggtggtg aggaggggtc 660
tcagtgacag gagggaaggt tgagtgactg gggaaggggc tattcagggt cacaggatcg 720
tttgatcctt cctcagcga tcaatcggtt ttctaa 766

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SEQ ID NO: 17      moltype = DNA length = 2429
FEATURE            Location/Qualifiers
source              1..2429
                    mol_type = other DNA
                    organism = synthetic construct

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gtctaaattt ttttgtaaaa agcttttagt ttatccctac cccaccccca tctgaagaaa 180
agagtgtttg cctcacatca tttttccctt ttctgtctct ctctgtctcg gtaccatgta 240
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cgaacctctt catccggtta acttcatgat cataccaata tataatatata tgcacgctga 480
aatatcaaa gaaacatttt tttttctttc tattaccga attctatttc acaatcacac 540
accaccatgg caagcctttc acttttcaca ggaaacaaag ttgaacactg cccgtgggtt 600
gttaccatcc cctgtggtat attccttgac catgaaacag tgttcaccac actttttttt 660
cctcattttt ttattctttt tgttttgtcc ttgtatacgt ttcttttctt tttttgtttc 720
ttctcctttt cctcttctac ttctgtatag tatctcttaa aagttatgga aaaaataaaa 780
taagaaaaac ataaaagtag ttagggtgata gaatagaact taaaaaaaag aaaagtagtt 840
gtttgggggc gagcggttaag ttaattaatt gaattgattt gatggaggat ttgggtaatc 900
gagaatgggg agttaaaggg aaagaagggt gtcattgaa tgctttaat tggatgggtg 960
tagttgcagg ttgcaggaaa aagaaaagcg gcgggaagga tggaaaagac gagtgtggga 1020
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gttttttgta ttgttttgag cagagaggga aacggagacg ctgaaccagg ctcgtcaact 1380
ggtctttctg ttgtatcata acattgctgc acaagggtgc cctcacttag ggtatgcacc 1440
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tcatttctca aatacttgtt ttctgtggg ttctttagcg tttgttaacg ttgttttttc 1560
aagggtataa acataaattt tgggtactca gcatgacact gtttgatact gcgatttatt 1620
tgtgataata ttcaattcag atgctgccaa acaataggaa cgggggggta tcatccctca 1680
ggagacccaa cagtgcctct agattccca agattccca caggttcact ctcaactcac 1740
atgccaccat ccccgccacc gccgcgcgca ccgcaacgac catacctata ccttcacct 1800
acgagggcag tgtcatttgg gtcacacac ttccctctcc agcatgcagt gaacgattac 1860
tatgtgggcc ccgtgatgag tgggtggcag caccgacact atgttgagg agagagcaca 1920
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gaggggtctg cagtgcagga ggaagggttg agtacttggg gaaggggcta ttcagggtga 2040
caggatcgtt tggatcctcc ctcagcgatc aatcggtttc aagatgggtt ctaaagagat 2100
gagagattct ttgttttgag gttttttggt ttgtgttatg tttctgttat gttatgtggt 2160
atcatcataa agacacgcaa tccagagaga gagagagggt gtttttgggt tatctacagt 2220

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aaccagggac agcttttgag ctcattggaca cgtcagcta ctttggttg gagttgtggg 2280
tggtattttc tctcaacatc gccttttgta ttggtagcta gctagctagc ttggacaacc 2340
agttagattt gaactgaaac ttccaaact ccttttcctt tgcattgcaa attacaacca 2400
tttctcttct cagtaatttg tcttttcaa 2429

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SEQ ID NO: 18      moltype = DNA length = 764
FEATURE           Location/Qualifiers
source            1..764
                  mol_type = other DNA
                  organism = synthetic construct

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SEQUENCE: 18
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ggcaaaacag tctctgaacc tcttcacccg gttgcaggaa aaagaaaagc ggcgggaagg 120
atggaaaaga cgagtgtggg aaggtctacg agttagattt ttgttccctc aagttctgca 180
agtctcaggc tcttggggga cacatgaacc gccaccgcca agagagggaa acggagacgc 240
tgaaccaggc tcgtcaactg gtccttcgtt gtgatcataa cattgctgca caagggtgcc 300
ctcacttagg atgctgcaa acaataggaa cgggggggta tcctccctca ggagacccaa 360
cagtgccctc aagattccca agatacttct caggttcctc ctcaactcac atgccaccat 420
ccccgccacc gccgccgcca ccgcaacgac catacctata ccttcacct acgaggccag 480
tgtcatttgg gtcacacac tccctctccc agcatgcagt gaacgattac tatgtggccc 540
acgtgatgag tgggtggcag caccggacact atgttggagg agagagcaca aggagttaga 600
cgtgcattgg tgcaccgggt gggcaagggt gcggattcgc tgggtgtaag gaggggtctg 660
cagtgaggga ggaagggttg agtactggg gaaggggcta ttcagggtgca caggatcggt 720
tggatcctcc ctacgcgac aatcggtttc aagatgggtt ctaa 764

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SEQ ID NO: 19      moltype = DNA length = 2428
FEATURE           Location/Qualifiers
source            1..2428
                  mol_type = other DNA
                  organism = synthetic construct

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SEQUENCE: 19
gggggcgggg ggagataaga gagagagaga gaggggcaga ggaactgata gagaactttc 60
aaagctcttt atcttctacc atcactcaac cagcctctat attgcagctc caaactgaaa 120
gtctaaattt ttttgtaaaa agcttttagt ttatccctac cccaccccca tctgaaagaa 180
agagtgtttg cctcacatca tttttccctt ttctgtctct ctctctgtcg gtaccatgta 240
ggtcttcccc cactactaca ccttcacacc cttcttttct tcctcctctt tctccttctc 300
taaacctttt aacttttctt cctttatgac tttgtgttcc ctttacagga gaccagaacg 360
aaacccctta gatcttaaca atttgcctga tgagtactct agagatggca aacaagtctc 420
cgacctcttc atccggtaaa ctccatgatc ataccaatat atatatatat gcacgctgaa 480
atatcaaggg aacacttttt ttttctttct atttaccgaa ttctatttca caatcacaca 540
ccaccatggg aagcctttta cttttcacag gaaacaaagt tgaacactgc ccgtgggttg 600
ttaccatccc ctgtggtata ttcttgacc atgaaacagt gttcaccaca ctttttttcc 660
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tctccttttc ctcttctact tctgtatagt atctctttaa agttatggaa aaaaataaat 780
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gggatttctt ctcaacatcg ccttttgat ttggtagctag ctatgtagct tggacaacca 2340
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SEQ ID NO: 20      moltype = DNA length = 763
FEATURE           Location/Qualifiers
source            1..763

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mol_type = other DNA
organism = synthetic construct

SEQUENCE: 20
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tggaacagac gagtgtggga aggtctacga gtgtagattt tgttccctca agttctgcaa 180
gtctcaggct cttggggggc acatgaaccg ccaccgcaa gagagggaaa cggagacgct 240
gaaccaggct cgtcaactgg tctttcgttg tgatcataac attgctgcac aagggtgccc 300
tcacttagga tgcctgcaaa caataggaac ggggggttat catccctcag gagaccacac 360
agtgcctcta agattcccaa gatacttctc aggttcaccc tcaactcaca tgccaccatc 420
cccgccaccg ccgcgcgcac cgcaacgacc atacctatac ccttcaccta cgaggccagt 480
gtcatttggg tcacacact tcctctcca gcatgcagtg aacgattact atgtgggcca 540
cgtgatgagt ggtggcagcc acggacacta tgttggagga gagagcacia ggagttacac 600
gtgcattggg gcacgggtgg ggcaagggtg cggattcgct ggtggtaagg aggggtctgc 660
agtgcaggag gaagggttga gtacttgggg aaggggctat tcagggtgcac aggatcggtt 720
ggatcctccc tcagcgatca atcggtttca agatggtttc taa 763

SEQ ID NO: 21      moltype = DNA   length = 91
FEATURE           Location/Qualifiers
source            1..91
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 21
tactctagag atggcaaaca agtctctgat cttcatccgg taaacttcat gatcatacca 60
atatatatat atatgcacgc tgaatatatca a 91

SEQ ID NO: 22      moltype = AA   length = 67
FEATURE           Location/Qualifiers
source            1..67
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 22
MRPERNPLDL NNLPEDEYSRD GKQVLDLHPV AGKRKAAGRM EKTSVGRSTS VDFVPSSSAS 60
LRLLGDT 67

SEQ ID NO: 23      moltype = DNA   length = 96
FEATURE           Location/Qualifiers
source            1..96
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 23
tactctagag atggcaaaca agtctctgaa tacctcttca tccggtaaac ttcatgatca 60
taccaatata tatatatatg cacgctgaaa tatcaa 96

SEQ ID NO: 24      moltype = AA   length = 52
FEATURE           Location/Qualifiers
source            1..52
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 24
MRPERNPLDL NNLPEDEYSRD GKQVLEYLFI RLQEKEKRRE GWKRRVWEGRL RV 52

SEQ ID NO: 25      moltype = DNA   length = 100
FEATURE           Location/Qualifiers
source            1..100
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 25
tactctagag atggcaaaca agtctctgaa gacataacctc ttcatccggt aaacttcatg 60
atcataccaaa tatatatata tatgcacgct gaaatatcaa 100

SEQ ID NO: 26      moltype = AA   length = 70
FEATURE           Location/Qualifiers
source            1..70
                  mol_type = protein
                  organism = synthetic construct

SEQUENCE: 26
MRPERNPLDL NNLPEDEYSRD GKQVLEDIPL HPVAGKRKAA GRMEKTSVGR STSVPFVPSS 60
SASLRLLGDT 70

SEQ ID NO: 27      moltype = DNA   length = 97
FEATURE           Location/Qualifiers
source            1..97
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 27

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ataccaatat	atatatatat	gcacgcgtgaa	atatcaa			97
SEQ ID NO: 28	moltype = AA length = 69					
FEATURE	Location/Qualifiers					
source	1..69					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 28						
MRPERNPLDL	NNLPDEYSRD	GKQVLEVPLH	PVAGKRKAAG	RMEKTSVGRS	TSVDFVPSSS	60
ASLRLLGDT						69
SEQ ID NO: 29	moltype = DNA length = 94					
FEATURE	Location/Qualifiers					
source	1..94					
	mol_type = other DNA					
	organism = synthetic construct					
SEQUENCE: 29						
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ccaatatata	tatatatgca	cgcgtgaata	tcaa			94
SEQ ID NO: 30	moltype = AA length = 68					
FEATURE	Location/Qualifiers					
source	1..68					
	mol_type = protein					
	organism = synthetic construct					
SEQUENCE: 30						
MRPERNPLDL	NNLPDEYSRD	GKQVLEALHP	VAGKRKAAGR	MEKTSVGRST	SVDFVPSSSA	60
SLRLLGDT						68
SEQ ID NO: 31	moltype = DNA length = 2426					
FEATURE	Location/Qualifiers					
source	1..2426					
	mol_type = other DNA					
	organism = synthetic construct					
SEQUENCE: 31						
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aaagctcttt	atctcttacc	atcacctcaac	cagctcttat	attgcagttc	caaaactgaaa	120
gtctaaattt	ttttgtaaaa	agcttttagtt	ttatccctac	ccccacccca	tctgaaagaa	180
ggagtggttg	cctcacatca	ttttccctct	ttctgtctct	ctctctgtcg	gtaccatgta	240
ggctctcccc	cactactaca	ccttcacacc	ctctctttct	tcctctctct	tctcctttct	300
taaacctttt	aactttctct	ctctttagac	ttttgtgttc	ctttacaggga	gaccagaacg	360
aaacccttta	gatcttaaca	atttgccgga	tgagtactct	agagatggca	aacaagtcct	420
cgatcttcct	cgggtaaact	tcgatgatcat	aaccaatatat	atatatatgc	acgctgaaat	480
atcaaaaggaa	cacttttttt	ttctttctat	ttaccgaatt	ctatttcaca	atcacacacc	540
accatgggaa	gccttttact	tttcacaggga	aacaaagtgt	aacactgccc	gtgggttgtt	600
acccctccct	gtgggtatatt	ccttgaccat	gaaacagtgt	tcaccacact	ttttttctct	660
cattttttta	ttctttttgt	tttgtctctg	tatacgtttt	ttttcttttt	tgtttctctc	720
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gaaaaacata	aaagtagtta	gggtgatagaa	tagaacttaa	aaaaaagaaa	agtagtttgt	840
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aatggggagt	taaaggcaca	gaagggtgtc	atggaaagtgt	ctttaattgg	atgggtatag	960
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ttttctcaat	aacttgtttt	ctgtgggttc	tttagcgttt	gttaacgctg	ttttttcaag	1560
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tccttctcag taatttggtc ttccaa 2426

SEQ ID NO: 32 moltype = DNA length = 2431
 FEATURE Location/Qualifiers
 source 1..2431
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 32

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gtctaaattt	ttttgtaaaa	agcttttagt	ttatccctac	ccccacccca	tctgaaagaa	180
agagtgtttg	cctcacatca	ttttccccc	ttctgtctct	ctctctgtcg	gtacctatga	240
ggtcttcccc	caactaaaca	ccttcacacc	cttcttttct	tcctctctct	tctccttctc	300
taaacccctt	aacttttctc	ctcttatgac	tttgtttgtc	ctttacagga	gaccagaacg	360
aaacccctta	gatcttaaca	atttgcccca	tgagtactct	agagatggca	aacaagtcct	420
cgaatacctc	ttcatccggt	aaacttcatg	atcataccaa	tatatata	tatgcacgct	480
gaaatatcaa	aggaacactt	tttttttctt	tctatttacc	gaattctatt	tcacaatcac	540
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gaaggtctac	gagtgtagat	tttgttccct	caagttctgc	aagtctcagg	ctcttggggg	1080
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ccagtttagt	ttgaactgaa	actttccaaa	ctccttttcc	tttgcattgc	aaattacaac	2400
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SEQ ID NO: 33 moltype = DNA length = 2435
 FEATURE Location/Qualifiers
 source 1..2435
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 33

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gtctaaattt	ttttgtaaaa	agcttttagt	ttatccctac	ccccacccca	tctgaaagaa	180
agagtgtttg	cctcacatca	ttttccccc	ttctgtctct	ctctctgtcg	gtacctatga	240
ggtcttcccc	caactataca	ccttcacacc	cttcttttct	tcctctctct	tctccttctc	300
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aaacccctta	gatcttaaca	atttgcccca	tgagtactct	agagatggca	aacaagtcct	420
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tcacctacga ggccagtgtc atttgggtca tcacacttcc ctctccagca tgcagtgaac 1860
gattactatg tgggccacgt gatgagtggg gccagccacg gacactatgt tggaggagag 1920
agcacaaagg gttacacgtg cattggtgca ccggtggggc aaggtggcgg attcgtcgtt 1980
ggtaaggagg ggtctgcagt gcaggaggaa ggggtgagta cttggggaag gggctattca 2040
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agagatgaga gattctttgt ttgagtgggt ttgggtttgt gttatgtttc tgttatgtta 2160
tgtgtgtatc tcataaagtg acgcaatcca gagagagaga gaggtggttt ttggtttatc 2220
tacagtaacc agggacagct tttagactca tggacacgct cagctacttt ggcttggagt 2280
tgtgggtggg atttcttctc aacatcgctt ttgtattgg tagctagcta gctagcttgg 2340
tcaaccagtt agatttgaac tgaaccttct caaaactcct ttcttttga tgccaaatta 2400
caaccatttt cctctcagtt aatttgttct ttcaa 2435

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SEQ ID NO: 34      moltype = DNA length = 2432
FEATURE            Location/Qualifiers
source              1..2432
                    mol_type = other DNA
                    organism = synthetic construct

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SEQUENCE: 34
gggggcgggg ggagataaga gagagagaga gaggggcaga ggaactgata gagaactttc 60
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gtctaaattt tttgtaaaaa agcttttagt ttatccctac cccaccccca tctgaagaaa 180
agagtgtttg cctcacatca tttttccctt ttctgtctct ctctctgtcg gtaccatgta 240
ggttctcccc cactactaca ccttcacacc cttcttttct tctctctctt tctccttctc 300
taaacccctt aacttttctc cctttatgac ttgtttgttc ctttacagga gaccagaacg 360
aaacccctta gatcttaaca atttggccga tgagtactct agagatggca aacaagtctc 420
cgaagtacct cttcatccgg taaacttcat gatcatacca atatataat atagcacgcg 480
tgaaatatca aaggaaacac tttttttctt ttctatttac cgaattctat ttcacaatca 540
cacaccacca tgggaagcct ttcacttttc acaggaaaac aagttgaaca ctgcccgtag 600
tttgttacc atccctgtgg tatattcctt gaccatgaaa cagtggtcac cacacttttt 660
tttctctatt tttttattct tttgttttgc tctttgtata cgtttctttt ctttttttgt 720
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aaataagaaa aacataaaag tagttagggt atagaataga acttaaaaaa aagaaaagta 840
gttggtttgg ggcgagcggg aggttaatta attgaattga ttgatggag gatttgggta 900
atcgagaatg gggaggttaa ggcacaaag ggtgtcatgg aagttgcttt aattggatgg 960
ttatagttgc aggttgacag aaaaagaaaa gcggcgggaa ggttggaata gacgagtggt 1020
ggaaggtcta caggtgtaga tttgttccc tcaagttctg caagtctcag gctctggggg 1080
gacacatgaa ccgccaccgc caaggctagt accacctata ttattatact ttatatattt 1140
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tttggccatg aaagtctgtc atttcaatca caaaatgttg tgtgtgttga ttgctgaaat 1260
tcgatcatcg agagggcccc ttacagctgtt tttttttttt ctttttgcct tgccttatta 1320
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atttcatttc tcaataactt gttttctctg ggggtcttta gcgtttgtta acgttgtttt 1560
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atttgtgata atattcaatt cagatgctgc caaacaatag gaacgggggg ttatcatccc 1680
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cctacgaggg cagtgctatt tgggtcatca cacttccctc tccagcatgc agtgaacgat 1860
tactatgtgg gccacgtgat gagtgtgtgc agccacggac actatgttgg aggagagagc 1920
acaaggaggt acacgtgcac tgggtcacgc gtggggcaag gtggcggaat cgttgggtgt 1980
aaggaggggt ctgcagtga ggaggaaggg ttgagtactt ggggaagggg ctattcaggt 2040
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gatgagagat tctttgtttt agtggttttt ggtttgtgtt atgtttctgt tatgttatgt 2160
ggatatcata taaagacacg caatccagag agagagagag gtggtttttg gtttatctac 2220
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gggtgggatt tcttctcaac atcgctcttt gtattggtag ctagctagct agcttggaca 2340
accagttaga tttgaactga aactttccaa actccttttc ctttgcagtc caaattacaa 2400
ccattttctt tctcagtaat ttgttctttc aa 2432

```

```

SEQ ID NO: 35      moltype = DNA length = 2429
FEATURE            Location/Qualifiers
source              1..2429
                    mol_type = other DNA
                    organism = synthetic construct

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SEQUENCE: 35

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gggggccccg ggagataaga gagagagaga gaggggcaga ggaactgata gagaactttc 60
aaagctcttt atcttctacc atcactcaac cagcctctat attgcagtct caaactgaaa 120
gtctaaattt ttttgtaaaa agcttttagtt ttatccctac ccccaaccca tctgaaagaa 180
agagtgtttg cctcacatca tttttccctt ttctgtctct ctctctgtcg gtaccatgta 240
ggctttcccc cactactaca ccttcacacc cttcttttct tctctctctt tctccttctc 300
taaacccttt aactttctct ctcttatgac ttgttgtttc ctttacagga gaccagaacg 360
aaacccttta gatcttaaca atttgccga tgagtactct agagatggca aacaagtcct 420
cgaagctctt catcoggtaa acttcatgat cataccaata tatatatata tgcacgtga 480
aatatcaaa gaaacacttt tttttctttc tatttaccga attctatttc acaatcacac 540
accaccatgg gaagcctttc acttttcaca ggaaacaaag ttgaacactg cccgtgggtt 600
gttaccctac cctgtgttat attccttgac catgaaacag tgttcaccac actttttttt 660
cctcattttt ttattctttt tgttttgtcc ttgtatacgt tctctttctt tttttgtttc 720
ttctcctttt cctcttctac ttctgtatag tatctcttaa aggttatgga aaaaaataaa 780
taagaaaaac ataaaagttag ttagggtgata gaatagaact taaaaaaaag aaaagttagt 840
gtttgggggg gagcggttaag ttaattaatt gaattgattt gatggaggat ttgggtaatc 900
gagaatgggg agttaaaggc aaagaagggt gtcatggaag ttgctttaat tggatgggta 960
tagttgcagg ttgcaggaaa aagaaaagcg gcgggaagga tggaaaagac gagtgtggga 1020
agggtcacga gttagatttt tgttccttca agttctgcaa gtctcaggct cttgggggac 1080
acatgaacgg ccacggccaa ggctagtacc acctatatta ttatacttta tattttcttc 1140
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ggccatgaaa gcttgtcatt tcaatcacaa aatgttgtgt tgttgatttg ctgaaattcg 1260
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gaggggtctg cagtgcagga ggaagggttg agtacttggg gaaggggcta ttcaggtgca 2040
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gagagattct ttgtttgagt ggttttttgt ttgtgttatg tttctgttat gttatgtggt 2160
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aaccagggac agcttttgag ctcatggaca cgctcagcta ctttggtttg gagtgtgtgg 2280
tgggatttct tctcaacatc gcccttttga ttggtagcta gctagctagc ttggacaacc 2340
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SEQ ID NO: 36      moltype = DNA length = 4725
FEATURE           Location/Qualifiers
source            1..4725
                  mol_type = genomic DNA
                  organism = Glycine max

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SEQUENCE: 36
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tcttataaag gagtcaactga tcaactagaga tggagctagt actgtttgga ttcaaagaaa 180
tgcatctaaa gcgaacagag aataaatga tgaatgtgag acatacatca agaaaattca 240
aatccatata tgtctccagt tcatgcacat ccattgaaaa ggactatgta tatgtaactc 300
atgagatata gcaactttca aagaataaaa caacaagtg gggctcagtc tatctcaact 360
tagattgcta aaaaccctaa tgatagatac tgatagcaac ccttcttga tgcaggtcta 420
agtcccttgg gtagaatttt acaccagaa ggaggcattg agctactgtg gaccatacat 480
gacctgttct caaacatgcc cccctcttct aagcacaata accacgcaa atgtctacgt 540
accctactcc ttgtcttctg ttctttcttg tataaatgtc atctttcatt cctaggggca 600
actttaatgc tcaagatttt gtactgtaca ttgatttccc atcctttgtt ggtaaagatt 660
ttcattttga atattaattt tttttttctc aatgcatttg actgatatta ttgaaattt 720
ttttgacctt ttaattttgt gatagctcta gctagggcaa aacaacaaaa aacaagaaaa 780
ctagatgcag aagtatatca tataattatg caagatcata tttattata aaattatata 840
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taactttctc tctatctttt tctctctctt atgactttgt cgttctctta caggagacca 1560
gaacgaacc cctagatctc taacaatttg ccgatgagt actctaggga tggcaacaaa 1620
gtcctcgaag accatacttc ttcaccgggt aaacttcatg atcatatcta tctatctatc 1680

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SEQ ID NO: 37      moltype = DNA length = 774
FEATURE            Location/Qualifiers
source             1..774
                  mol_type = other DNA
                  organism = Glvcline max
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SEQ ID NO: 38      multype = AA  length = 257
FEATURE            Location/Qualifiers
source              1..257
                    mol type = protein
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organism = Glycine max
SEQUENCE: 38
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FCKSQALGGH MNRHRQERET ETLNQARQLV FRSDHIIAPQ GAPHLGCCQP IGTGGYHPSG 120
DPTVPLRFRP YFSGSSSTHM PTPPPPPPPP QQSHLYASPS RPSVFGSSHF PHQHAYNDYY 180
VGHVMSGGSH GHYVGGESTS SYTYIGAPVG QAGGFAGGGK EGSVQEEGL SWGRSYSGGA 240
QHRLDPPSAI NRPFDGDF 257

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SEQ ID NO: 39      moltype = DNA length = 2819
FEATURE           Location/Qualifiers
source            1..2819
                  mol_type = genomic DNA
                  organism = Glycine max

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SEQUENCE: 39
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tgatgggaga gaaaaaactg ggaattttta tattttttaa ttttttttac aaattttttc 120
agaactagga tgggatagaa ataaataaaa aaagtacaca ataagagttg ctaatagaat 180
aaaaaaaatt ctttattgga tgagaaatat ccatgcatcc ggtgtacagc caatcaatta 240
agaaccgatt ccaagggcc cttctgtgt ttatgaccag cggagagaga aagagagtgg 300
aaaagtggaa aggataaactc gtcacatata atgactaatg tgatttcagc acaaacatcc 360
cagacccaaa ggcaattggt gagatgagcc gaattaagag acaatatatt agtagtagtg 420
ggaggacctg cacggatgca cttgatttat ttctagcctt ttttcatttt ttgtttttcc 480
tatagaactt gtattttctc tagctaaatc taaattatgt attgcaacat attttaaagg 540
aggggcaaaa cacactcgat ctaccttcaa agaaactttt aagacattat aaatatggag 600
ccacactccc cttcttcttc agtaagatca tcaacttgta ttctcactt ccttagctcc 660
tcctcttctc tgttctctc ttacaaatgg caaaaatgcc tttagagcct ctaatatagg 720
ggagagtcac aggagaagtt cttgattctt tcaccacaag cacaaaaatg actgtgagtt 780
acaaacaaga gcaagtttac aatggccatg agctcttccc ttccactgtc aacaccaagc 840
ccaaggttga gatgagggt ggtgatatga ggtccttctt tacactggta tatatatattc 900
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ggtcacacgg tatgtctctt ttattggagt tttctttaca aatactgaat cattaagcaa 1080
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ttatctgaga gagactgtgc actggtactt aatataaaaa ttaactaact taagtagtca 1200
ttttattcat aaataacaca ccacacccac cccacatata ttgttatacc ggtttctctt 1260
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tcaaaactat gacagccagg aaggtaataa caaatactta catcacatga agaaggtaca 1440
cacatgcctt tgaattctgc aaaagtagct tgttccacca taatcccatc caccctaaaa 1500
tcaaaacaat tcaaaagggt gaataaatct cgaagtctca acaaaacatc acagaactac 1560
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gcagcagaga acgaccttgg cctccctgtg gctgctgtct acttcaatgc acagagggaa 1980
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gtagtataag tgtactaact gattatttat tacctcgtgg gtactactat gaggtgatct 2280
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tctctattgg tttttttcga tctcttcaca actaaattac gtttttgaca gaaaaaatgg 2460
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gtgatttagt tgatggaaa ctgttaatat gcactccttt aaatgcaggt gtaatcgttc 2760
caatgcccta aacatagaag ctatgaataa aaatggcggt atgttgaat caacacatt 2819

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SEQ ID NO: 40      moltype = DNA length = 522
FEATURE           Location/Qualifiers
source            1..522
                  mol_type = other DNA
                  organism = Glycine max

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SEQUENCE: 40
atggcaaaaa tgcctttaga gcctctaata gtggggagag tcataggaga agttcttgat 60
tctttcacca caagcacaaa aatgactgtg agttacaaca agaagcaagt ttacaatggc 120
catgagctct tccctttcac gttcaacacc aagcccaagg ttgagattga ggttggtgat 180
atgaggtcct tctttacact gtcacatgact gacctgtatg ttctgggcc tagtgacctc 240
tatctgagag agcacttgca ctggatagtg acagatatcc caggcacaac agatgccaca 300
tttgggaaag agttggtgag ctatgaggtc ccaaagccta atattggaat ccataggttt 360
tggtttgtcc tgttcaagca aaagcgtaga cagtggttta ctccaccac ttcaagggac 420
cacttcaaca cagcgaatt cgcagcagag aacgaccttg gcctccctgt ggctgctgtc 480

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tacttcaatg cacagaggga aacggctgca agaagacgct ag					522
SEQ ID NO: 41	moltype = AA length = 173				
FEATURE	Location/Qualifiers				
source	1..173				
	mol_type = protein				
	organism = Glycine max				
SEQUENCE: 41					
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MRSFPTLIMT DPDVPGPSDP YLREHLHWIV TDIPGTTDAT FGKELVSYEV PKPNIGIHRF					120
VFVLFKQKRR QCVTPPTS RD HFNTRKFAAE NDLGLPVA AV YFNAQRETAA RRR					173

- What is claimed is:

1.-19. (canceled)

20. A polynucleotide comprising the sequence of SEQ ID NO: 7, 15, 17, 19, 21, 23, 25, 27, 29, 31, 32, 33, 34, or 35 or an allelic variant thereof or encoding the polypeptide comprising the amino acid sequence of SEQ ID NO: 12, 13, 14, 22, 24, 26, 28, 30, or an allelic variant thereof.

21. A biological sample comprising the polynucleotide of claim **20**.

22. The biological sample of claim **21**, wherein the sample comprises soybean meal or soybean stover.
- 23.** The biological sample of claim **22**, wherein the soybean seed meal is defatted.

24. The biological sample of claim **22**, wherein the soybean seed meal is non-defatted.

25.-39. (canceled)

40. A guide RNA molecule comprising a Cas12 direct repeat element which is operably linked to the spacer RNA molecule encoded by SEQ ID NO: 2.

* * * * *