What is claimed is:

1. A recombinant DNA molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:10, SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, a polynucleotide having a nucleotide sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.7%, at least 99.8%, or at least 99.9% identical to the full length of SEQ ID NO:10 or the full length of SEQ ID NO: 9, and a complete complement of any of the foregoing.

2. The recombinant DNA molecule of claim 1, wherein:

    a) the recombinant DNA molecule is derived from a soybean plant, seed, plant part, plant cell, progeny plant, or commodity product comprising soybean event Gm_CSM63714, a representative sample of seed comprising the event having been deposited as ATCC Accession No. PTA-127099;

    b) the recombinant DNA molecule is comprised in a soybean plant, seed, plant part, plant cell, or progeny plant comprising soybean event Gm_CSM63714, or a commodity product produced therefrom, a representative sample of seed comprising the event having been deposited as ATCC Accession No. PTA-127099;

    c) the recombinant DNA molecule is formed by the insertion of a heterologous nucleic acid molecule into the genomic DNA of a soybean plant or soybean cell; or

    d) the recombinant DNA molecule comprises an amplicon diagnostic for the presence of soybean event Gm_CSM63714.

3. A DNA molecule comprising a polynucleotide segment of sufficient length to function as a DNA probe that:

    a) hybridizes specifically under stringent hybridization conditions with soybean event Gm_CSM63714 DNA in a sample, wherein detecting hybridization of the DNA molecule under the stringent hybridization conditions is diagnostic for the presence of soybean event Gm_CSM63714 in the sample; or

b) that is specific for detecting in a sample at least one of:

a 5’ junction sequence between flanking soybean genomic DNA and the transgenic insert of soybean event Gm_CSM63714;

a 3’ junction sequence between the transgenic insert of soybean event Gm_CSM63714 and flanking soybean genomic DNA;

SEQ ID NO:9; and

a fragment of SEQ ID NO:9 comprising a sufficient length of contiguous nucleotides of SEQ ID NO:9 to identify the sequence as a fragment of the transgenic insert of Gm_CSM63714.

4. The DNA molecule of claim 3, wherein:

a) the DNA probe comprises SEQ ID NO:16;

b) the DNA molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, and a complement of any of the foregoing; or

c) the sample is derived from a soybean plant, seed, plant part, plant cell, progeny plant, or commodity product.

5. A pair of DNA molecules comprising a first DNA molecule and a second DNA molecule, wherein the first and the second DNA molecules comprise a fragment of SEQ ID NO:10 or a complement thereof and function as DNA primers when used together in an amplification reaction with DNA comprising soybean event Gm_CSM63714 to produce an amplicon diagnostic for soybean event Gm_CSM63714 in a sample.

6. The pair of DNA molecules of claim 5, wherein:

a) the first and the second DNA molecules comprise SEQ ID NO:14 and SEQ ID NO:15; or

b) the amplicon comprises a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1;

SEQ ID NO:2;
SEQ ID NO:3;
SEQ ID NO:4;
SEQ ID NO:5;
SEQ ID NO:6;
SEQ ID NO:7;
SEQ ID NO:8;
SEQ ID NO:9;
SEQ ID NO:10; and
a fragment of any of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, wherein the fragment is at least 10 nucleotides in length and comprises nucleotides 1,000–1,001 or 11,196-11,197 of SEQ ID NO:10.

7. A method of detecting the presence of soybean event Gm_CSM63714 in a sample derived from a soybean seed, plant, plant part, plant cell, progeny plant, or commodity product, the method comprising:

I) a) contacting the sample with the DNA molecule that functions as a DNA probe of claim 3 or 4;

b) subjecting the sample and the DNA molecule that functions as a probe to stringent hybridization conditions; and

c) detecting the hybridization of the DNA molecule that functions as a probe to a DNA molecule in the sample,

wherein the hybridization of the DNA molecule that functions as a probe to the DNA molecule in the sample is diagnostic for the presence of soybean event Gm_CSM63714 in the sample; or

II) d) contacting the sample with the pair of DNA molecules of any one of claims 5 or 6;

e) performing an amplification reaction sufficient to produce a DNA amplicon; and

f) detecting the presence of the DNA amplicon,

wherein the DNA amplicon comprises at least one of:

a 5’ junction sequence between flanking soybean genomic DNA and the transgenic insert of soybean event Gm_CSM63714,

a 3’ junction sequence between flanking soybean genomic DNA and the transgenic insert of soybean event Gm_CSM63714,

SEQ ID NO: 9, and

a fragment of SEQ ID NO: 9 comprising a sufficient length of contiguous nucleotides of SEQ ID NO: 9 to identify the sequence as a fragment of the transgenic insert of Gm_CSM63714; and

wherein the presence of the DNA amplicon indicates the presence of soybean event Gm_CSM63714 in the sample;

III) g) contacting the sample with the DNA molecule of claim 3 or 4; and

h) performing a sequencing reaction to produce a target sequence,

wherein the target sequence comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, a complete complement of any thereof, and a fragment of any of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, and SEQ ID NO:10 that is at least 10 nucleotides long and comprises nucleotides 1,000–1,001 or 11,196-11,197 of SEQ ID NO:10; or

IV) i) contacting the sample with at least one antibody specific for at least one protein encoded by soybean event Gm_CSM63714; and

j) detecting binding of the antibody to the protein in the sample,

wherein the binding of the antibody indicates the presence of soybean event Gm_CSM63714 in the sample.

8. A kit for detecting the presence of soybean event Gm_CSM63714 in a sample, wherein the kit comprises:

a) the pair of DNA primers of claim 5 or 6; and/or

b) the DNA molecule that functions as a probe of claim 3 or 4; or

c) at least one antibody specific for at least one protein encoded by soybean event Gm_CSM63714; wherein detecting binding of the at least one antibody to the at least one protein encoded by soybean event Gm_CSM63714 in a sample is diagnostic for the presence of soybean event Gm_CSM63714 in the sample.

9. A soybean plant, plant seed, plant part, or plant cell comprising;

a) a recombinant DNA molecule comprising a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, a polynucleotide having a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.7%, at least 99.8%, or at least 99.9% identical to the full length of SEQ ID NO:10 or the full length of SEQ ID NO: 9, and a complete complement of any of the foregoing; or

b) soybean event Gm_CSM63714, a representative sample of seed comprising soybean event Gm_CSM63714 having been deposited under ATCC Accession No. PTA-127099.

10. The soybean plant, plant seed, plant part, or plant cell of claim 9, wherein;

a) the plant, plant seed, plant part, or plant cell expresses at least one herbicide tolerance gene selected from the group consisting of dicamba monooxygenase (DMO), phosphinothricin N-acetyltransferase (PAT), alpha-ketoglutarate-dependent non-heme iron dioxygenase variant FT_Tv7, triketone dioxygenase (TDO), and any combination thereof;

b) the plant, plant seed, plant part, or plant cell is tolerant to at least one herbicide selected from the group consisting of benzoic acid auxins, phenoxy auxins, glutamine synthetase inhibitors, β-triketone HPPD inhibitors, and combinations of any thereof

c) the plant, plant seed, plant part, or plant cell further comprises an additional transgene for tolerance to at least one additional herbicide;

d) the plant, plant seed, plant part, or plant cell comprises soybean event Gm_CSM63714, a representative sample of seed comprising the event having been deposited under ATCC Accession No. PTA-127099; or

e) the plant, plant seed, plant part, or plant cell is further defined as a progeny plant of any generation of a soybean plant comprising soybean event Gm_CSM63714, or a soybean plant part, plant seed, or plant cell derived therefrom.

11. The soybean plant, plant seed, plant part, or plant cell of claim 10, wherein:

a) the benzoic acid auxin comprises dicamba; the phenoxy auxin comprises 2,4-D; the glutamine synthetase inhibitor comprises glufosinate; and the β-triketone HPPD inhibitor is selected from the group consisting of mesotrione, benzobicyclon (BBC), tembotrione, sulcotrione, tefuryltrione, and combinations of any thereof; or

b) the at least one additional herbicide is glyphosate.

12. The soybean plant, plant seed, plant part, or plant cell of claim 11, wherein;

a) the plant, plant seed, plant part, or plant cell is tolerant to mesotrione; or

b) the plant, plant seed, plant part, or plant cell comprises a polynucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO:57; or

c) the plant part comprises a microspore, pollen, an anther, an ovule, an ovary, a flower, a pod, an embryo, a stem, a leaf, a root, or a callus.

13. A method for controlling or preventing weed growth in an area, the method comprising planting soybean comprising event Gm_CSM63714 in the area and applying an effective amount of at least one herbicide selected from the group consisting of dicamba, glufosinate, 2,4-D, a β-triketone HPPD inhibitor, and any combination thereof, to control weeds in the area without injury to the soybean or with less than about 10% injury to the soybean.

14. The method of claim 13, wherein;

a) applying the effective amount of at least one herbicide comprises applying at least two or more herbicides selected from the group consisting of dicamba, glufosinate, 2,4-D, a β-triketone HPPD inhibitor, and any combination thereof over a growing season;

b) the β-triketone HPPD inhibitor is selected from the group consisting of mesotrione, benzobicyclon (BBC), tembotrione, sulcotrione, tefuryltrione, and any combination thereof; or

c) the effective amount of dicamba is about 0.5 lb/acre to about 2 lb/acre over a growing season; wherein the effective amount of glufosinate is about 0.4 lb/acre to about 1.6 lb/acre over a growing season; wherein the effective amount of 2,4-D is about 0.5 lb/acre to about 4 lb/acre over a growing season; and/or wherein the β-triketone HPPD inhibitor comprises mesotrione and the effective amount of mesotrione is about 0.09 lb/acre to about 0.36 lb/acre over a growing season.

15. A method for controlling volunteer soybean comprising soybean event Gm_CSM63714 in an area, the method comprising applying an herbicidally effective amount of at least one herbicide other than dicamba, glufosinate, 2,4-D, or a β-triketone HPPD inhibitor, wherein the herbicide application prevents growth of soybean comprising soybean event Gm_CSM63714.

16. The method of claim 15, wherein the herbicide other than dicamba, glufosinate, 2,4-D, or a β-triketone HPPD inhibitor is selected from the group consisting of atrazine, bronioxynil (3,5-di-bromo-4-hydroxybenzonitrile), clopyralid, pyrithiobac, isoxaflutole, topramezone, fluometuron, trifloxysulfuron, monosodium methyl arsenate (MSMA), an inhibitor of protoporphyrinogen oxidase (PPO), and combinations of any thereof.

17. The method of claim 16, wherein the inhibitor of protoporphyrinogen oxidase (PPO) comprises saflufenacil, flumioxazin, sulfentrazone, or a combination of any thereof.

18. A method of obtaining a seed of a soybean plant or a soybean plant that is tolerant to benzoic acid auxins, phenoxy auxins, inhibitors of glutamine synthetase, β-triketone HPPD inhibitors, or any combination thereof, the method comprising:
    a) obtaining a population of progeny seed or plants grown therefrom, at least one of which comprises soybean event Gm_CSM63714; and

b) identifying at least a first progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63714.

19. The method of claim 18, wherein:

a) identifying the progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63714 comprises:

i) growing the progeny seed or plant to produce progeny plants;

ii) treating the progeny plants with an effective amount of at least one herbicide selected from the group consisting of a benzoic acid auxin, a phenoxy auxin, an inhibitor of glutamine synthetase, a β-triketone HPPD inhibitor, and any combination thereof; and

iii) selecting a progeny plant that is tolerant to the at least one herbicide selected from the group consisting of a benzoic acid auxin, a phenoxy auxin, an inhibitor of glutamine synthetase, a β-triketone HPPD inhibitor, and any combination thereof;

b) the benzoic acid auxin comprises dicamba; the phenoxy auxin comprises 2,4-D; the glutamine synthetase inhibitor comprises glufosinate; and the β-triketone HPPD inhibitor is selected from the group consisting of mesotrione, benzobicyclon (BBC), tembotrione, sulcotrione, tefuryltrione, and combinations of any thereof;

c) identifying the progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63714 comprises detecting the presence of soybean event Gm_CSM63714 in a sample derived from the progeny seed or plant grown therefrom; or

d) identifying the progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63714 comprises detecting the presence of at least one protein encoded by soybean event Gm_CSM63714 in a sample derived from the progeny seed or plant grown therefrom.

20. A method of determining the zygosity of a soybean plant, plant part, plant seed, or plant cell comprising soybean event Gm_CSM63714, the method comprising:

I) a) contacting a sample comprising DNA derived from the soybean plant, plant part, plant seed, or plant cell with a primer set capable of producing a first amplicon diagnostic for the presence of soybean event Gm_CSM63714 and a second amplicon

diagnostic for the wild-type soybean genomic DNA not comprising soybean event Gm_CSM63714;

b) performing a nucleic acid amplification reaction; and

c) detecting the first amplicon and the second amplicon, wherein the presence of both amplicons indicates that the plant, plant part, seed or cell is heterozygous for soybean event Gm_CSM63714, and the presence of only the first amplicon indicates that the plant, plant part, seed, or cell is homozygous for soybean event Gm_CSM63714; or

II) d) contacting a sample comprising DNA derived from the soybean plant, plant part, plant seed, or plant cell with a probe set comprising at least a first probe that specifically hybridizes to soybean event Gm_CSM63714, and at least a second probe that specifically hybridizes to soybean genomic DNA that was disrupted by insertion of the heterologous DNA of soybean event Gm_CSM63714 but does not hybridize to soybean event Gm_CSM63714; and

e) hybridizing the probe set with the sample under stringent hybridization conditions, wherein detecting hybridization of only the first probe under the hybridization conditions is diagnostic for a soybean plant, plant part, seed or plant cell homozygous for soybean event Gm_CSM63714, and wherein detecting hybridization of both the first probe and the second probe under the hybridization conditions is diagnostic for a soybean plant, plant part, seed, or plant cell heterozygous for soybean event Gm_CSM63714.

21. The method of claim 20, wherein:

a) the primer set comprises SEQ ID NO:14, SEQ ID NO:15 and SEQ ID NO:20; or

b) the probe set comprises SEQ ID NO:16 and SEQ ID NO:21.

22. A DNA construct comprising a first expression cassette, a second expression cassette, a third expression cassette and a fourth expression cassette, wherein:

I) a) the first expression cassette comprises in operable linkage i) ubiquitin (UB3) promoter, leader, and intron sequences from *Arabidopsis thaliana*, ii) a chloroplast transit peptide coding sequence of APG6 (Albino and Pale Green 6) from

Arabidopsis thaliana, iii) a codon-optimized dicamba monooxygenase coding sequence (DMO) from *Stenotrophomonas maltophilia*, and iv) a 3' UTR sequence of the aluminum-induced Sali3-2 protein from *Medicago truncatula*;

b) the second expression cassette comprises in operable linkage i) a promoter and an intron sequence derived from multiple promoter and intron sequences from *Arabidopsis thaliana*, ii) a codon-optimized phosphinothricin N-acetyltransferase (PAT) coding sequence from *Streptomyces viridochromogene*, and iii) a 3' UTR of a small heat shock protein (Hsp20) from *Medicago truncatula*;

c) the third expression cassette comprises in operable linkage i) polyubiquitin (UBQ10) promoter, leader, and intron sequences from *Arabidopsis thaliana*, ii) an alpha-ketoglutarate-dependent non-heme iron dioxygenase variant coding sequence (FT_Tv7) from *Sphingobium herbicidovorans*, and iii) a 3' UTR sequence of a putative protein from *Medicago truncatula*, and

d) the fourth expression cassette comprises in operable linkage i) promoter, leader, and intron sequences derived from multiple promoter, leader and intron sequences from *Arabidopsis thaliana*, ii) a codon-optimized coding sequence of the triketone dioxygenase (TDO) from *Oryza sativa*, and iii) a 3' UTR sequence derived from multiple 3' UTR sequences from *Zea mays*; or

II) (e) the first expression cassette comprises a dicamba monooxygenase coding sequence;

(f) the second expression cassette comprises a phospinothricin N-acetyltransferase (PAT) coding sequence; (g) the third expression cassette comprises an alpha-ketoglutarate-dependent non-heme iron dioxygenase variant coding sequence (FT_Tv7) capable of degrading 2,4-D; and (h) the fourth expression cassette comprises a triketone dioxygenase (TDO) coding sequence; and wherein the DNA construct further comprises at the 5' or 3' end of said construct (i) at least 50 contiguous nucleotides of SEQ ID NO: 11 or SEQ ID NO:98; or (ii) at least 50 contiguous nucleotides of SEQ ID NO: 12 or SEQ ID NO:99.

23. The DNA construct of claim 22, wherein the DNA construct comprises SEQ ID NO:9.

24. A method of improving tolerance to at least one herbicide selected from the group consisting of benzoic acid auxins, phenoxy auxins, inhibitors of glutamine synthetase, β-triketone HPPD inhibitors, and any combination thereof in a soybean plant comprising:
    a) inserting the DNA construct of claim 22 or 23 into the genome of a soybean cell;
    b) generating a soybean plant from the soybean cell; and
    c) selecting a soybean plant comprising the DNA construct.

25. The method of claim 24, wherein:
    a) the selecting comprises treating the soybean cell or plant with an effective amount of at least one herbicide selected from the group consisting of benzoic acid auxins, phenoxy auxins, inhibitors of glutamine synthetase, β-triketone HPPD inhibitors, and any combination thereof; or
    b) the benzoic acid auxin comprises dicamba; the pheoxy auxin comprises 2,4-D; the glutamine synthetase inhibitor comprises glufosinate; and the β-triketone HPPD inhibitor is selected from the group consisting of mesotrione, benzobicyclon (BBC), tembotrione, sulcotrione, tefuryltrione, and combinations of any thereof.

26. A soybean plant, plant seed, plant part, or plant cell tolerant to herbicides with at least three different herbicide modes of action at a single genomic location.

27. The soybean plant, plant seed, plant part, or plant cell of claim 26, wherein the soybean plant, plant seed, plant part or plant cell comprises the DNA construct of claim 22 or 23.

28. A soybean plant, plant seed, plant part, or plant cell tolerant to at least one herbicide selected from the group consisting of benzoic acid auxins, phenoxy auxins, glutamine synthetase inhibitors, β-triketone HPPD inhibitors, and any combination thereof, wherein the soybean plant, plant seed, plant part, or plant cell comprises the DNA construct of claim 22 or 23.

29. The soybean plant, plant seed, plant part, or plant cell of claim 28, wherein: the benzoic acid auxin comprises dicamba; the phenoxy auxin comprises 2,4-D; the glutamine

synthetase inhibitor comprises glufosinate; and the β-triketone HPPD inhibitor is selected from the group consisting of mesotrione, benzobicyclon (BBC), tembotrione, sulcotrione, tefuryltrione, and combinations of any thereof

30. The soybean plant, plant seed, plant part, or plant cell of any one of claims 26-29, wherein:
    a) the soybean seed, plant, plant part, or cell is obtained by the method of claim 24 or 25; or
    b) the plant, plant seed, plant part, or plant cell is tolerant to at least an additional herbicide.

31. The soybean plant, plant seed, plant part, or plant cell of claim 30, wherein the at least an additional herbicide comprises glyphosate.

32. A method of producing a progeny soybean plant comprising soybean event Gm_CSM63714 comprising:
    a) sexually crossing a first soybean plant that comprises soybean event Gm_CSM63714 with itself or a second soybean plant;
    b) collecting one or more seeds produced from the cross;
    c) growing one or more seeds to produce one or more progeny plants; and
    d) selecting at least a first progeny plant or seed comprising soybean event Gm_CSM63714.

33. An inbred or hybrid soybean plant or seed comprising soybean event Gm_CSM63714 produced by the method of claim 32.

34. A nonliving or nonregenerable soybean plant material, wherein the plant material:
    a) comprises the recombinant DNA molecule of claim 1 or 2 or the DNA construct of claim 22 or 23; or
    b) comprises soybean event Gm_CSM63714, a representative sample of seed comprising the soybean event soybean event Gm_CSM63714 having been deposited under ATCC Accession No. PTA-127099.

35. A commodity product comprising the recombinant DNA molecule of claim 1 or 2 or the DNA construct of claim 22 or 23.

36. The commodity product of claim 35, wherein:

a) the commodity product is produced from a transgenic soybean plant, plant part, plant seed, or plant cell comprising the soybean event Gm_CSM63714; or

b) the commodity product comprises whole or processed seeds; viable or nonviable seeds; viable plant parts (such as roots and leaves); viable plant cells; processed plant parts; processed plant tissues; dehydrated plant tissues; dehydrated plant parts; frozen plant tissues; frozen plant parts; food for human consumption such as soy oil, soy milk, soy flour, soy grits, soy protein, soy protein concentrate, hydrolyzed vegetable protein, textured soy protein, lecithin, curd, tofu, vegetable soybean (edamame), soy sprouts, soy film (yuba), roasted soybeans, miso, tempeh, soy sauce, or natto; plant parts processed for animal feed such as soy meal; soy fiber; biodiesel; bio-composite building materials such as particleboard, laminated plywood, or lumber products; soy oil-based solvents; soy oil-based industrial lubricants; soy ink; soy candles; soy crayons; soy-based hydraulic fluid; or soy-based foams.

37. A method of producing a commodity product, the method comprising:

a) obtaining a transgenic soybean plant, plant part, or plant seed comprising soybean event Gm_CSM63714; and

b) producing a commodity product from the transgenic soybean plant, plant part, or plant seed.

38. A method of controlling, preventing, or reducing the development of herbicide-tolerant weeds comprising:

a) cultivating in a crop growing environment a soybean plant comprising transgenes that provide tolerance to herbicides with at least three different herbicide modes of action at a single genomic location; or

b) cultivating in a crop growing environment a soybean plant comprising the DNA construct of claim 22 or 23 for providing tolerance to herbicides with at least three different herbicide modes of action at a single genomic location; and

c) applying to the crop growing environment at least one herbicide selected from the group consisting of dicamba, glufosinate, 2,4-D, a β-triketone HPPD inhibitor, and any combination thereof, wherein the soybean plant is tolerant to the at least one herbicide.

39. The method of claim 38, wherein:
    a) the at least three different herbicide modes of action are selected from the group consisting of inhibition of glutamine synthetase, inhibition of 4-hydroxyphenylpyruvate dioxygenase (HPPD), phenoxy auxins, and benzoic acid auxins; or
    b) the soybean plant further comprises at least one additional transgene for an additional herbicide mode of action.

40. The method of claim 39, wherein the at least one additional transgene is EPSPS for conferring tolerance to glyphosate.

41. The method of claim 40, wherein the EPSPS transgene comprises a polynucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO:57.

42. A method of reducing loci for soybean breeding by inserting transgenes at a single genomic location for tolerance to at least three different classes of herbicides.

43. The method of claim 42, wherein the transgenes are inserted as a single molecularly linked transgenic insert.

44. The method of claim 43, wherein the single molecularly linked transgenic insert provides a commercial level of tolerance to at least one herbicide for each herbicide mode of action.

45. The DNA construct of claim 22 or 23, further comprising at the 5’ or 3’ end of said construct:

a) at least 50 contiguous nucleotides of SEQ ID NO: 11 or SEQ ID NO:98; or
b) at least 50 contiguous nucleotides of SEQ ID NO: 12 or SEQ ID NO:99.

46. A DNA construct comprising a polynucleotide having a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.1%, at least 99.2%, at least 99.3%, at least 99.4%, at least 99.5%, at least 99.6%, at least 99.7%, at least 99.8%, or at least 99.9% identical to the full length of SEQ ID NO: 9; and wherein the DNA construct comprises at the 5' or 3' end of said construct (i) at least 50 contiguous nucleotides of SEQ ID NO: 11 or SEQ ID NO:98; or (ii) at least 50 contiguous nucleotides of SEQ ID NO: 12 or SEQ ID NO:99.

47. The DNA construct of claim 45 or 46, wherein;
a) the DNA construct comprises at least 50 contiguous nucleotides of SEQ ID NO: 11 or SEQ ID NO:98 at the 5' end of the construct and at least 50 contiguous nucleotides of SEQ ID NO: 12 or SEQ ID NO:99 at the 3' end of the construct;
b) the construct comprises at the 5' end of said construct one or more nucleotide sequences selected from SEQ ID NOs:58–77 and SEQ ID NOs:100–139; or
c) the construct comprises at the 3' end of said construct one or more nucleotide sequences selected from SEQ ID NOs:78–97 and SEQ ID NOs:140–179.

48. A soybean plant, plant cell, plant part, or plant seed comprising the DNA construct of any one of claims 45-47.

49. A soybean plant, plant cell, plant part, or plant seed comprising a recombinant DNA construct integrated in chromosome 13, wherein the recombinant DNA construct confers tolerance to at least one herbicide selected from the group consisting of benzoic acidauxins, phenoxy auxins, glutamine synthetase inhibitors, β-triketone HPPD inhibitors, and combinations of any thereof, and wherein the recombinant DNA construct is integrated in a position of said chromosome flanked by at least 50 contiguous nucleotides of SEQ ID NO:11 or SEQ ID NO:98 and 50 contiguous nucleotides of SEQ ID NO:12 or SEQ ID NO:99.

50. The soybean plant, plant cell, plant part, or plant seed of claim 49, wherein:

a) the benzoic acid auxin comprises dicamba; the phenoxy auxin comprises 2,4-D; the glutamine synthetase inhibitor comprises glufosinate; and the β-triketone HPPD inhibitor is selected from the group consisting of mesotrione, benzobicyclon (BBC), tembotrione, sulcotrione, tefuryltrione, and combinations of any thereof;

b) the at least 50 contiguous nucleotides of SEQ ID NO:11 or SEQ ID NO: 98 comprise one or more nucleotide sequences selected from SEQ ID NOs:58–77 and SEQ ID NOs:100–139; or

c) the at least 50 contiguous nucleotides of SEQ ID NO:12 or SEQ ID NO: 99 comprise one or more nucleotide sequences selected from SEQ ID NOs:78–97 and SEQ ID NOs:140–179.