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,

a) wherein the recombinant DNA molecule is derived from a soybean plant, seed, plant part, plant cell, progeny plant, or commodity product comprising soybean event Gm_CSM63717, a representative sample of seed comprising the event having been deposited as ATCC Accession No. PTA-127604;

b) wherein the recombinant DNA molecule is comprised in a soybean plant, seed, plant part, plant cell, or progeny plant comprising soybean event Gm_CSM63717, or a commodity product produced therefrom, a representative sample of seed comprising the event having been deposited as ATCC Accession No. PTA-127604;

c) wherein 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; and/or

d) wherein the recombinant DNA molecule comprises an amplicon diagnostic for the presence of soybean event Gm_CSM63717.

3. A DNA molecule comprising

a) a polynucleotide segment of sufficient length to function as a DNA probe that hybridizes specifically under stringent hybridization conditions with soybean event Gm_CSM63717 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_CSM63717 in the sample; and/or

b) a polynucleotide segment of sufficient length to function as a DNA probe 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_CSM63717;

a 3' junction sequence between the transgenic insert of soybean event Gm_CSM63717 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_CSM63717.

4. The DNA molecule of claim 3, wherein

a) the DNA probe comprises SEQ ID NO:178;

b) wherein 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; and/or

c) wherein 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 are different from one another, and each 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_CSM63717 to produce an amplicon diagnostic for soybean event Gm_CSM63717 in a sample.

6. The pair of DNA molecules of claim 5,

a) wherein the first and the second DNA molecules comprise SEQ ID NO:176 and SEQ ID NO:177; and/or

b) wherein 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 4,201-4,202 of SEQ ID NO:10.

7. A method of detecting the presence of soybean event Gm_CSM63717 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 any one of claims 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_CSM63717 in the sample; or

II)

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

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

c) 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_CSM63717,

a 3' junction sequence between flanking soybean genomic DNA and the transgenic insert of soybean event Gm_CSM63717,

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_CSM63717; and

wherein the presence of the DNA amplicon indicates the presence of soybean event Gm_CSM63717 in the sample.

8. The method of claim 7,

a) wherein the DNA amplicon is at least 10 nucleotides in length, at least 11 nucleotides in length, at least 12 nucleotides in length, at least 13 nucleotides in length, at least 14 nucleotides in length, at least 15 nucleotides in length, at least 16 nucleotides in length, at least 17 nucleotides in length, at least 18 nucleotides in length, at least 19 nucleotides in length, at least 20 nucleotides in length, at least 25 nucleotides in length, at least 30 nucleotides in length, at least 35 nucleotides in length, at least 40 nucleotides in length, at least 45 nucleotides in length, at least 50 nucleotides in length, at least 60 nucleotides in length, at least 70 nucleotides in length, at least 80 nucleotides in length, at least 90 nucleotides in length, or at least 100 nucleotides in length; and/or

b) wherein the DNA amplicon comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:10; SEQ ID NO:9; SEQ ID NO:8; SEQ ID NO:7; SEQ ID NO:6; SEQ ID NO:5; SEQ ID NO:4; SEQ ID NO:3; SEQ ID NO:2; SEQ ID NO:1; and a fragment of any of SEQ ID NO:10, SEQ ID NO:8, SEQ ID NO:7, SEQ ID NO:6, SEQ ID NO:5, SEQ ID NO:4, SEQ ID NO:3, SEQ ID NO:2, and SEQ ID NO:1 that is

at least 10 nucleotides in length and comprises nucleotides 1,000–1,001 or 4,201-4,202 of SEQ ID NO:10.

9. A method of detecting the presence of soybean event Gm_CSM63717 in a sample of DNA 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 probe of any one of claims 3 or 4; and

b) 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 4,201-4,202 of SEQ ID NO:10; or

II)

a) contacting the sample with an antibody specific for the PPO (protoporphyrinogen oxidase) protein encoded by soybean event Gm_CSM63717; and

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

wherein the binding of the antibody indicates the presence of soybean event Gm_CSM63717 in the sample.

10. A DNA detection kit for detecting the presence of soybean event Gm_CSM63717 in a sample, wherein the kit comprises:

a) the pair of DNA primers of any one of claims 5 or 6 ; and/or

b) the DNA molecule that functions as a probe of any one of claims 3 or 4.

11. A protein detection kit for detecting the presence of soybean event Gm_CSM63717 in a sample, wherein the kit comprises an antibody specific for the PPO protein encoded by soybean event Gm_CSM63717; wherein detecting binding of the antibody to the

protein encoded by soybean event Gm_CSM63717 in a sample is diagnostic for the presence of soybean event Gm_CSM63717 in the sample.

12. A method of determining the zygosity of a soybean plant, plant part, plant seed, or plant cell comprising soybean event Gm_CSM63717, the method comprising:
I)

a) contacting a sample comprising DNA derived from the soybean plant, plant part, plant seed, or plant cell with a first primer set capable of producing a first amplicon diagnostic for the presence of soybean event Gm_CSM63717, and a second primer set capable of producing a second amplicon diagnostic for wildtype soybean genomic DNA not comprising soybean event Gm_CSM63717;

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_CSM63717, and the presence of only the first amplicon indicates that the plant, plant part, seed, or cell is homozygous for soybean event Gm_CSM63717; or
II)

a) 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_CSM63717, 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_CSM63717 but does not hybridize to soybean event Gm_CSM63717; and

b) 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_CSM63717, 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_CSM63717.

13. The method of claim 12,

a) wherein the first primer set comprises SEQ ID NO:176 and SEQ ID NO:177, and the second primer set comprises SEQ ID NO:208 and SEQ ID NO:209; and/or

b) wherein the probe set comprises SEQ ID NO:178 and SEQ ID NO:210.

14. A DNA construct comprising

a) an expression cassette, wherein the expression cassette comprises in operable linkage i) a ubiquitin 2 (UBQ) promoter, a leader sequence, and an intron sequence from Medicago truncatula, ii) a codon optimized chloroplast transit peptide coding sequence of APG6 (Albino and Pale Green 6) from Adansonia digitata, iii) a codon-optimized protoporphyrinogen oxidase coding sequence from Enterobacter cloacae, and iv) a synthetic 3' UTR sequence; and/or

b) 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%, at least 99.9%, or 100% 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 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 1,000, at least 1,500, or at least 2,000 contiguous nucleotides of SEQ ID NO:11 or SEQ ID NO:14; and/or (ii) at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 1,000, at least 1,500, or at least 2,000 contiguous nucleotides of SEQ ID NO: 12 or SEQ ID NO:15.

15. The DNA construct of claim 14,

i) wherein the DNA construct comprises SEQ ID NO:9; or

ii) wherein the DNA construct further comprises at the 5' or 3' end of said construct:

a) at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 1,000, at least 1,500, or at least 2,000 contiguous nucleotides of SEQ ID NO:11 or SEQ ID NO:14;

b) at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 1,000, at least 1,500, or at least 2,000 contiguous nucleotides of SEQ ID NO:12 or SEQ ID NO:15;

c) wherein the construct comprises at the 5' end of said construct one or more nucleotide sequences selected from SEQ ID NOs:36–105; and/or

d) wherein the construct comprises at the 3' end of said construct one or more nucleotide sequences selected from SEQ ID NOs:106–175.

16. A method for controlling volunteer soybean comprising soybean event Gm_CSM63717 in an area, the method comprising applying an herbicidally effective amount of at least one herbicide other than a PPO herbicide, wherein the herbicide application prevents growth of soybean comprising soybean event Gm_CSM63717.

17. The method of claim 16, wherein the herbicide other than a PPO herbicide is selected from the group consisting of atrazine, topramezone, clopyralid, pyrithiobac, fluometuron, (3-(3,4-dichlorophenyl)-1,1-dimethylurea) (DCMU), trifloxysulfuron, paraquat, diquat, glyphosate, glufosinate, and combinations of any thereof.

18. A method of obtaining a seed of a soybean plant or a soybean plant that is tolerant to PPO herbicides, the method comprising:

a) obtaining a population of progeny seed or plants grown therefrom, at least one of which comprises soybean event Gm_CSM63717; and

b) identifying at least a first progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63717.

19. The method of claim 18,

i) wherein identifying the progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63717 comprises:

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

b) treating the progeny plants with an effective amount of a PPO herbicide; and

c) selecting a progeny plant that is tolerant to the PPO herbicide;

ii) wherein identifying the progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63717 comprises detecting the presence of soybean event Gm_CSM63717 in a sample derived from the progeny seed or plant grown therefrom;

iii) wherein identifying the progeny seed or plant grown therefrom that comprises soybean event Gm_CSM63717 comprises detecting the presence of the PPO protein encoded by soybean event Gm_CSM63717 in a sample derived from the progeny seed or plant grown therefrom; and/or

iv) wherein the effective amount of PPO herbicide is about 0.0009 lb/acre to about 1.5 lb/acre over a growing season.

20. A method of improving tolerance to PPO herbicides in a soybean plant comprising:

a) inserting the DNA construct of any one of claims 14 or 15 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.

21. The method of claim 20, wherein the selecting comprises treating the soybean cell or plant with an effective amount of a PPO herbicide.

22. 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;

b) the DNA construct of any one of claims 14-15;

c) soybean event Gm_CSM63717, a representative sample of seed comprising soybean event Gm_CSM63717 having been deposited under ATCC Accession No. PTA-127604; and/or

d) a recombinant DNA construct integrated in chromosome 13, wherein the recombinant DNA construct confers tolerance to at least one PPO herbicide, and wherein the recombinant DNA construct is integrated in a position of said chromosome flanked by (i) at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 1,000, at least 1,500, or at least 2,000 contiguous nucleotides of SEQ ID NO:11 or SEQ ID NO:14; and/or (ii) at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 150, at least 200, at least 250, at least 300, at least 400, at least 500, at least 1,000, at least 1,500, or at least 2,000 contiguous nucleotides of SEQ ID NO: 12 or SEQ ID NO:15.

23. The soybean plant, plant seed, plant part, or plant cell of claim 22,

a) wherein the plant, plant seed, plant part, or plant cell expresses a PPO herbicide tolerance gene;

b) wherein the plant, plant seed, plant part, or plant cell is tolerant to one or more PPO herbicides;

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

d) wherein the plant, plant seed, plant part, or plant cell comprises soybean event Gm_CSM63717, a representative sample of seed comprising the event having been deposited under ATCC Accession No. PTA-127604;

e) wherein 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_CSM63717, or a soybean plant part, plant seed, or plant cell derived therefrom;

f) wherein the plant part comprises a microspore, pollen, an anther, an ovule, an ovary, a pod, a flower, an embryo, a stem, a bud, a node, a leaf, a root, or a callus;

g) wherein the soybean seed, plant, plant part, or cell is obtained by the method of any one of claims 18-19;

h) comprising at least 50 contiguous nucleotides of SEQ ID NO:11 or SEQ ID NO:14 and comprising one or more nucleotide sequences selected from SEQ ID NOs:36-105;

i) comprising at least 50 contiguous nucleotides of SEQ ID NO:12 or SEQ ID NO:15 and comprising one or more nucleotide sequences selected from SEQ ID NOs:106-175;

j) wherein the PPO herbicide is selected from the group consisting of diphenylethers, N-phenylphthalimides, oxadiazoles, oxazolidinediones, phenylpyrazoles, pyrimidinediones, thiadiazoles, triazolinones, benzoxazinone derivatives, other PPO herbicides, and combinations of any thereof; and/or

k) wherein the diphenylether is selected from the group consisting of acifluorfen, bifenox, ethoxyfen, fluorodifen, fluoronitrofen, furyloxyfen, halosafen, chlomethoxyfen, chlornitrofen, ethoxyfen-ethyl, fluoroglycofen, lactofen, nitrofen, oxyfluorfen, fomesafen, a salt of any thereof, and an ester of any thereof; the N-phenylphthalimide is selected from the group consisting of cinidon-ethyl, flumiclorac, flumiclorac-pentyl, and flumioxazin; the oxadiazole is selected from the group consisting of oxadiargyl and oxadiazon; the oxazolidinedione is pentoxazone; the phenylpyrazole is selected from the group consisting of fluazolate, pyraflufen, and pyraflufen-ethyl; the pyrimidinedione is

selected from the group consisting of benzfendizone, butafenacil, epyrifencacil (S-3100), flupropacil, flufenoximacil, saflufenacil, and tiafenacil; the thiadiazole is selected from the group consisting of fluthiacet-methyl and thidiazimin; the triazolinone is selected from the group consisting of azafenidin, bencarbazone, carfentrazone, its salts and esters, and sulfentrazone; the benzoxazinone derivative is 1,5-dimethyl-6-thioxo-3-(2,2,7-trifluoro-3,4-dihydro-3-oxo-4-prop-2-ynyl-2H-1,4-benzoxazin-6-yl)-1,3,5-triazinane-2,4-dione (trifludimoxazin)); the other PPO herbicide is selected from the group consisting of chlorphthalim, flufenpyr, flufenpyr-ethyl, flumipropyn, pyraclonil, profluazol, pyridin-2-ylmethyl [(3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}pyridin-2-yl)oxy]acetate, 2-methoxyethyl [(3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}pyridin-2-yl)oxy]acetate, 2-methoxyethyl [(3-{2-cyano-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}pyridin-2-yl)oxy]acetate, cyanomethyl [(3-{2-bromo-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}pyridin-2-yl)oxy]acetate; cyclopropylmethyl (2-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}phenoxy)acetate; methyl 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoate, methyl (2R)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy} propanoate (flufenoximacil), methyl (2S)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy} propanoate, methyl 2-{[(Z)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoate, 2-{[(Z)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoic acid, ethyl 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoate, ethyl (2R)-2-{[(E)-{2-chloro-4-fluoro-5-[3-

methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoate, ethyl (2S)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoate, 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoic acid, (2R)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoic acid, (2S)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}propanoic acid, methyl 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}-2-methylpropanoate, ethyl 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}-2-methylpropanoate, methyl 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}butanoate, methyl (2R)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy} butanoate, methyl (2S)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy} butanoate, 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}butanoic acid, (2R)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}butanoic acid, (2S)-2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}butanoic acid, ethyl 2-{[(E)-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]benzylidene}amino]oxy}butanoate, methyl 2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoate methyl (2R)-2-({(E)-[2-chloro-5-(3,5-

dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoate, methyl (2S)-2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoate, 2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoic acid, (2R)-2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoic acid, (2S)-2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoic acid, ethyl 2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoate, ethyl (2R)-2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoate, ethyl (2S)-2-({(E)-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorobenzylidene]amino}oxy)propanoate, methyl 2-{[(E)-{5-[3-amino-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorobenzylidene}amino]oxy}propanoate, methyl (2R)-2-{[(E)-{5-[3-amino-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorobenzylidene}amino]oxy} propanoate, methyl (2S)-2-{[(E)-{5-[3-amino-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorobenzylidene}amino]oxy} propanoate, 2-{[(E)-{5-[3-amino-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorobenzylidene}amino]oxy}propanoic acid, (2R)-2-{[(E)-{5-[3-amino-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorobenzylidene}amino]oxy}propanoic acid, (2S)-2-{[(E)-{5-[3-amino-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorobenzylidene}amino]oxy}propanoic acid, ethyl 3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylate, methyl 3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-methyl-4,5-

dihydro-1,2-oxazole-5-carboxylate, 3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylic acid, (5R)-3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylic acid, (5S)-3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylic acid, ethyl (5S)-3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylate, ethyl (5R)-3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylate, ethyl 3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-propyl-4,5-dihydro-1,2-oxazole-5-carboxylate, ethyl 3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-5-ethyl-4,5-dihydro-1,2-oxazole-5-carboxylate, 3-[4-chloro-2-fluoro-5-(5-{[(isopropylideneamino)oxy]carbonyl}-5-methyl-4,5-dihydro-1,2-oxazol-3-yl)phenyl]-1-methyl-6-(trifluoromethyl)pyrimidine-2,4(1H,3H)-dione, ethyl 3-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorophenyl]-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylate, methyl 3-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorophenyl]-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylate, 3-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorophenyl]-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylic acid, (5R)-3-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorophenyl]-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylic acid, (5S)-3-[2-chloro-5-(3,5-dimethyl-2,6-dioxo-4-sulfanylidene-1,3,5-triazinan-1-yl)-4-fluorophenyl]-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylic acid, 3-[4-chloro-2-fluoro-5-(5-{[(isopropylideneamino)oxy]carbonyl}-5-methyl-4,5-dihydro-1,2-oxazol-3-yl)phenyl]-1,5-dimethyl-6-sulfanylidene-1,3,5-triazinane-2,4-dione, ethyl 3-{5-[3-amino-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorophenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylate, 3-{5-[3-amino-2,6-dioxo-4-

(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]-2-chloro-4-fluorophenyl}-5-methyl-4,5-dihydro-1,2-oxazole-5-carboxylic acid, methyl 3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-3a,4,5,6-tetrahydro-6aH-cyclopenta[d][1,2] oxazole-6a-carboxylate, ethyl 3-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-3a,4,5,6-tetrahydro-6aH-cyclopenta[d][1,2] oxazole-6a-carboxylate, methyl 3-{2-bromo-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenyl}-3a,4,5,6-tetrahydro-6aH-cyclopenta[d][1,2] oxazole-6a-carboxylate, 2-ethoxy-2-oxoethyl 1-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}cyclopropanecarboxylate, {[(1-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}cyclopropyl)carbonyl]oxy}acetic acid, and 2-methoxy-2-oxoethyl 1-{2-chloro-4-fluoro-5-[3-methyl-2,6-dioxo-4-(trifluoromethyl)-3,6-dihydropyrimidin-1(2H)-yl]phenoxy}cyclopropanecarboxylate.

24. A method of producing a progeny soybean plant comprising soybean event Gm_CSM63717 comprising:

a) sexually crossing a first soybean plant that comprises soybean event Gm_CSM63717 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_CSM63717.

25. An inbred or hybrid soybean plant or seed comprising soybean event Gm_CSM63717 produced by the method of claim 24.

26. A nonliving or nonregenerable soybean plant material comprising

a) the recombinant DNA molecule of any one of claims 1 or 2 or the DNA construct of any one of claims 14or 15; or

b) soybean event Gm_CSM63717, a representative sample of seed comprising the soybean event Gm_CSM63717 having been deposited under ATCC Accession No. PTA-127604.

27. A commodity product comprising the recombinant DNA molecule of any one of claim 1 or the DNA construct of any one of claim 14 or 15.

28. The commodity product of claim 27, wherein the commodity product is produced from a transgenic soybean plant, plant part, plant seed, or plant cell comprising soybean event Gm_CSM63717.

29. The commodity product of claims 27 or 28, wherein the commodity product comprises whole or processed seeds; viable or nonviable seeds; viable plant parts (such as roots, nodes, buds or 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 soybean 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.

30. 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_CSM63717; and

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

31. A method of controlling, preventing, or reducing the development of herbicide-tolerant weeds in an area comprising

a) planting soybean comprising event Gm_CSM63717 in the area and applying an effective amount of a PPO herbicide to control weeds in the area without injury to the soybean or with less than about 10% injury to the soybean;

b) cultivating in a crop growing environment a soybean plant comprising transgenes that provide tolerance to (i) a PPO herbicide and (ii) herbicides with at least three additional herbicide modes of action, the three additional herbicide modes of action each being different from one another;

c) cultivating in a crop growing environment a soybean plant comprising the DNA construct of any one of claims 14-15 or event Gm_CSM63717, and at least three additional transgenes for providing tolerance to herbicides with at least three additional herbicide modes of action, the three additional herbicide modes of action each being different from one another and applying to the crop growing environment at least one herbicide selected from the group consisting of dicamba, glufosinate, 2,4-D, a PPO inhibitor, a β-triketone HPPD inhibitor, glyphosate, and any combination thereof, wherein the soybean plant is tolerant to the at least one herbicide; or

d) planting soybean comprising event Gm_CSM63717, event Gm_CSM63714 and/or event MON89788 in the area and applying one or more herbicides selected from the group consisting of a PPO herbicide, dicamba, glufosinate, 2, 4-D, β-triketone HPPD inhibitor, glyphosate, and combinations of any thereof to control weeds in the area without injury or with less than 10% injury to the soybean.

32. The method of claim 31, wherein the transgenes that provide tolerance to the herbicides with the at least three additional herbicide modes of action are present at a single genomic location in the soybean plant.

33. A method of reducing loci for soybean breeding by site-directed insertion of a transgene that provides tolerance to a PPO herbicide at a genomic location in a soybean plant that is within about 1-6 cM of a locus in the genome of the soybean plant that comprises transgenes for tolerance to at least three additional herbicide modes of action, the three additional herbicide modes of action each being different from one another.

34. The soybean plant, plant seed, plant part, plant cell or claim 22 or the method of claim 31

a) wherein the additional transgenes are selected from the group consisting of FT_Tv7, dicamba monooxygenase (DMO), phosphinothricin N-acetyltransferase (PAT), triketone dioxygenase (TDO), 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS), and combinations of any thereof;

b) wherein the additional transgenes provide tolerance to herbicides having modes of action selected from the group consisting of inhibitors of glutamine synthetase, inhibitors of EPSPS, β-triketone HPPD inhibitors, synthetic auxins, and combinations of any thereof;

c) wherein the FT_Tv7 transgene comprises a polynucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO:31; the DMO transgene comprises a polynucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO:29; the PAT transgene comprises a polynucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO:27; the TDO transgene comprises a polynucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO: 33, and the EPSPS transgene comprises a polynucleotide sequence encoding a protein having the amino acid sequence of SEQ ID NO:35;

d) wherein the synthetic auxin is selected from the group consisting of dicamba, 2,4-D, dichlorprop, mecoprop, 2,4,5-T (2,4,5-trichlorophenoxyacetic acid), and combinations of any thereof; the inhibitor of glutamine synthetase comprises glufosinate; the β-triketone HPPD inhibitor is selected from the group consisting of mesotrione, benzobicyclon (BBC), tembotrione, sulcotrione, tefuryltrione, and combinations of any thereof, and the inhibitor of 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) comprises glyphosate;

e) wherein the soybean plant, plant seed, plant part, or plant cell further comprises soybean event MON89788 and/or soybean event Gm_CSM63714;

f) wherein the soybean plant, plant seed, plant part, or plant cell further comprises a recombinant DNA molecule comprising a sequence selected from the group consisting of SEQ ID NO:182; SEQ ID NO:183; SEQ ID NO:184; SEQ ID NO:185; SEQ ID

NO:186; SEQ ID NO:187; SEQ ID NO:188; SEQ ID NO:189; SEQ ID NO:190; SEQ ID NO:191; 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:182 or the full length of SEQ ID NO: 183; and a complete complement of any of the foregoing; and/or

g) wherein the soybean plant, plant seed, plant part, or plant cell further comprises a recombinant DNA molecule comprising a sequence selected from the group consisting of SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197; 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:192 or the full length of SEQ ID NO:193; and a complete complement of any of the foregoing.