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(54) **TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES**

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(57) **ABSTRACT**

Presented are methods and compositions for targeted chromosomal genomic alterations with modified single-stranded oligonucleotides. The oligonucleotides of the invention have modified nuclease-resistant termini comprising LNA, phosphorothioate linkages or 2'-O-Me base analogues or combinations of such modifications.

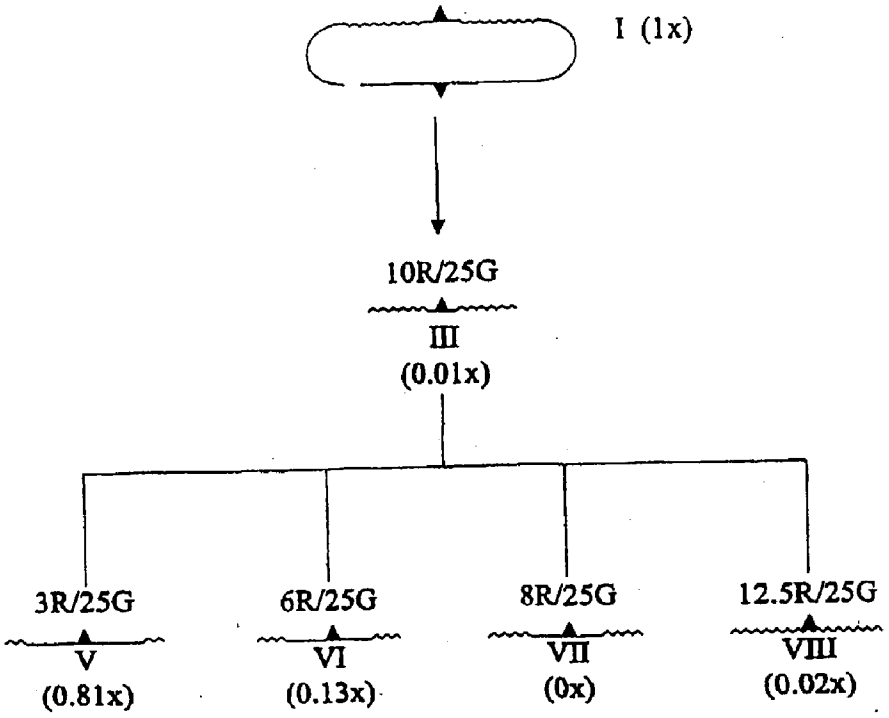


Figure 1A

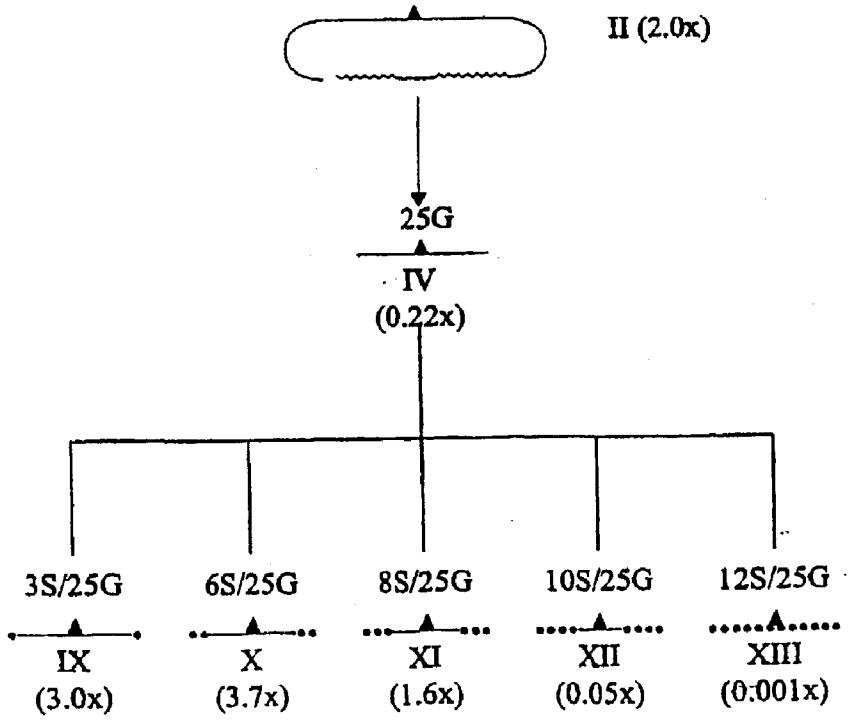


Figure 1B

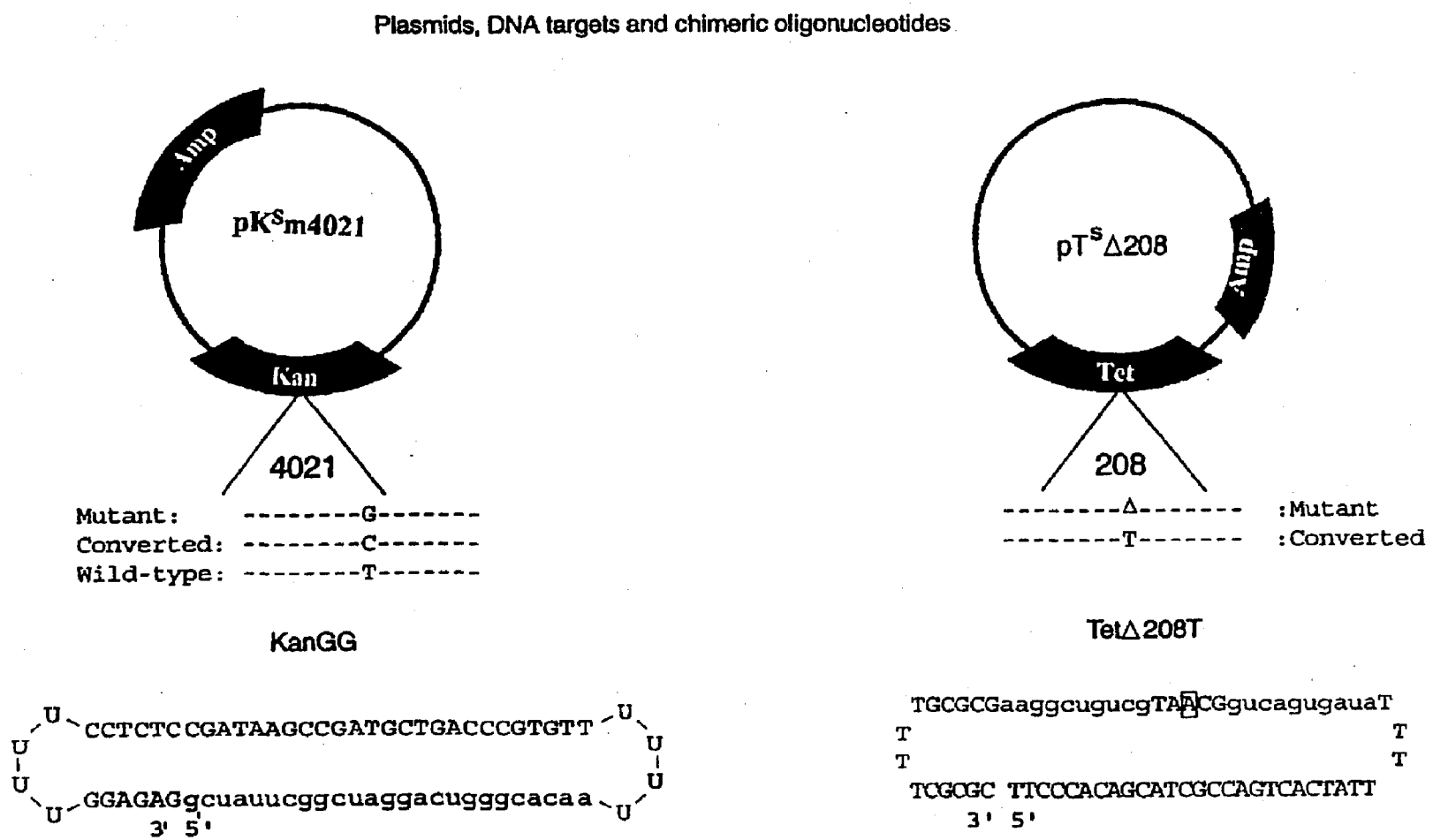

Plasmids, DNA targets and chimeric oligonucleotides
Amp
pK^Sm4021
Kan
4021
Mutant: --------G-------
Converted: --------C-------
Wild-type: --------T-------
KanGG
CCTCTCCGATAAGCCGATGCTGACCCGTGTT
GGAGAGgcuauucggcuaggacugggcacaa
3' 5'
pT^SΔ208
Amp
Tet
208
--------Δ------- :Mutant
--------T------- :Converted
TetΔ208T
TGCGCGaaggcugucgTAΔCGgucagugauaT
TCGCGC TTCCCACAGCATCGCCAGTCACTATT
3' 5'

Figure 1C

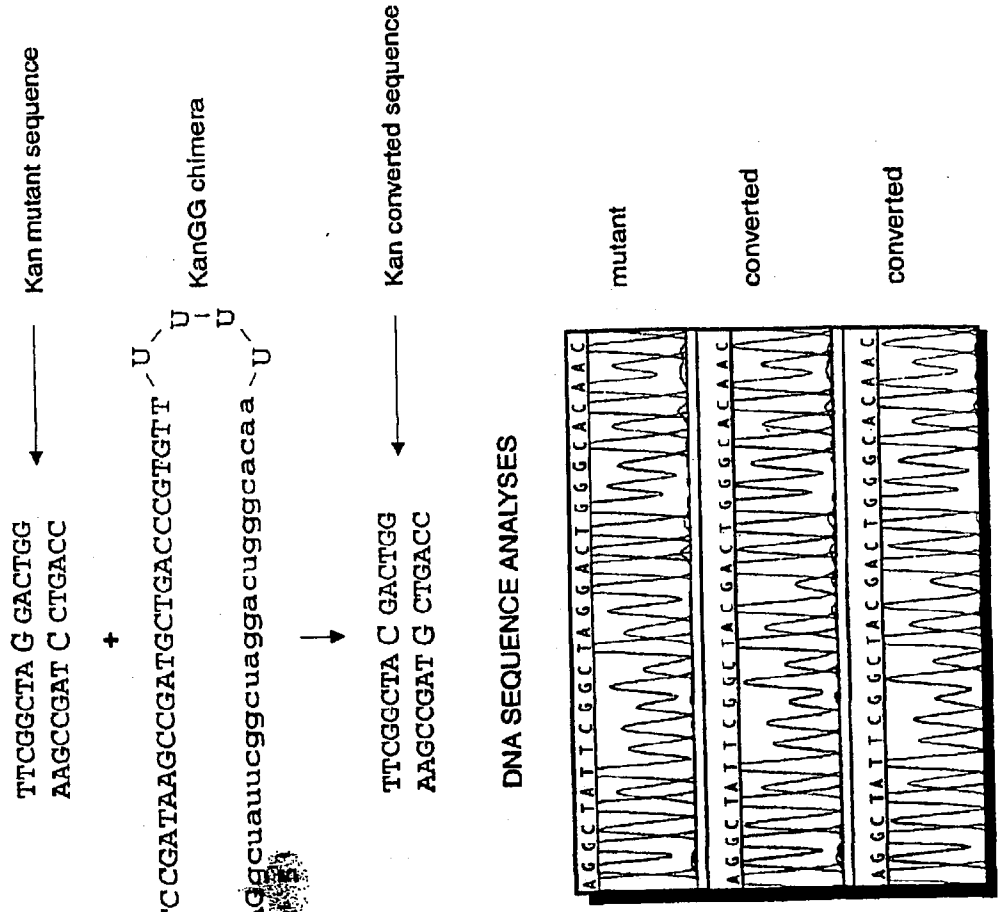

B
TTCGGCTA G GACTGG
AAGCCGAT C CTGACC
Kan mutant sequence
+
CCTCTCCGATAAGCCGATGCTGACCCGTGTT
GGAGAGgcuauucggcuaggacugggcacaa
KanGG chimera
TTCGGCTA C GACTGG
AAGCCGAT G CTGACC
Kan converted sequence
DNA SEQUENCE ANALYSES
mutant
converted
converted

Figure 1D

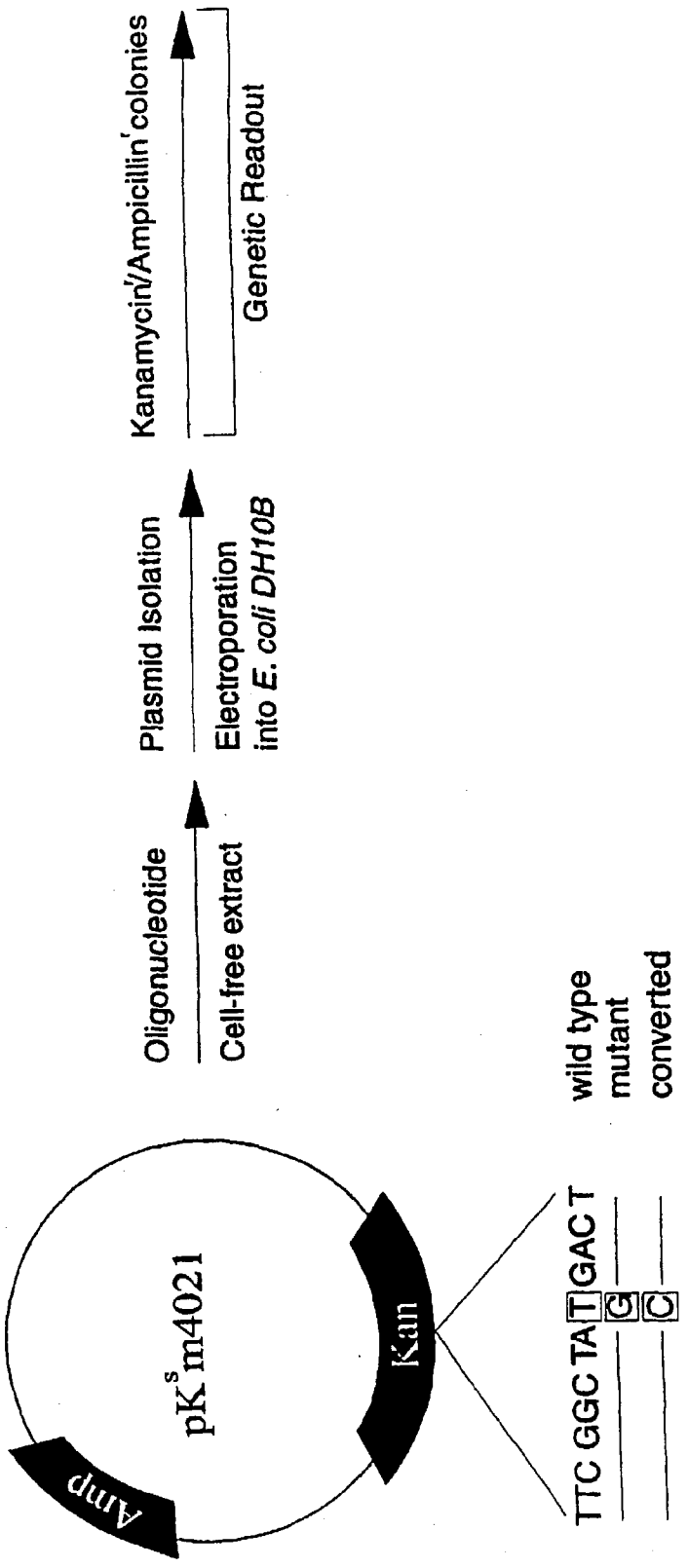
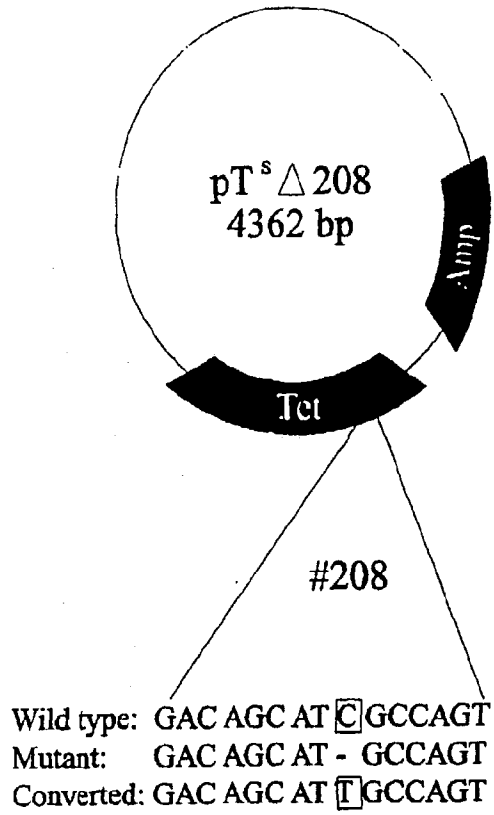

Oligonucleotide
Cell-free extract
Plasmid Isolation
Electroporation into E. coli DH10B
Kanamycin'/Ampicillin' colonies
Genetic Readout
wild type
mutant
converted
TTC GGC TA T GAC T
G
C
Kan
Amp
pK s m4021

Figure 2



Sequence analysis of Tet^r plasmid △208

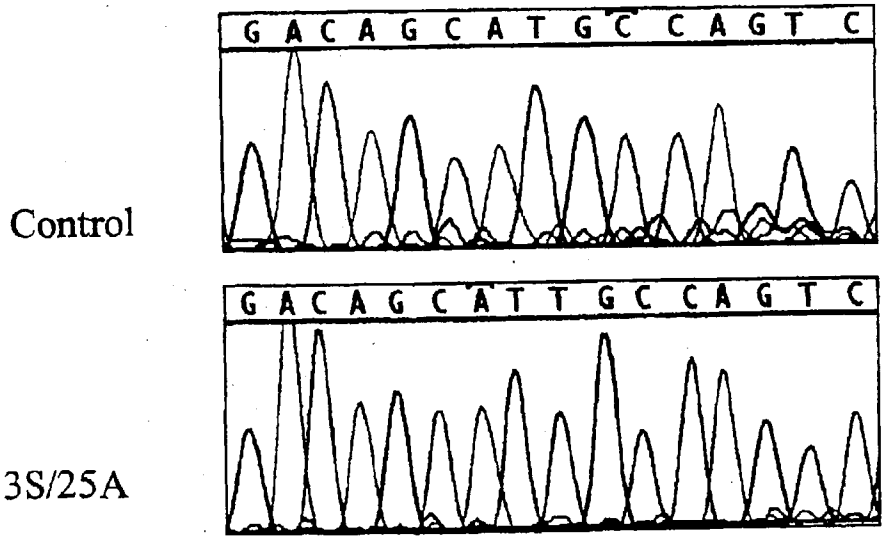


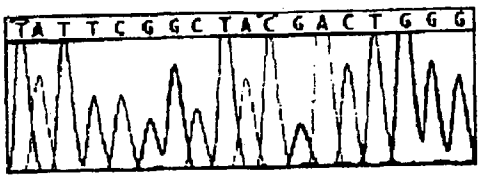
Figure 3

DNA sequence analysis of Kan^r plasmids

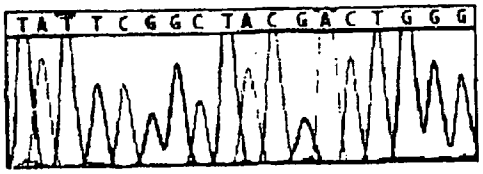
Target codon distribution

oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	----	+	----	----	----
2) 6S/25G (20)	----	+	----	----	----
3) 8S/25G (20)	----	+	----	----	----
4) 10S/25G (18)	----	+	----	+(2)	+(2)
5) 25S/25G (4)	----	----	+(2)	+(2)	----

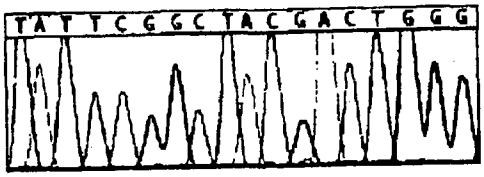
3S/25G



6S/25G



8S/25G



10S/25G



25S/25G



25S/25G



Figure 4

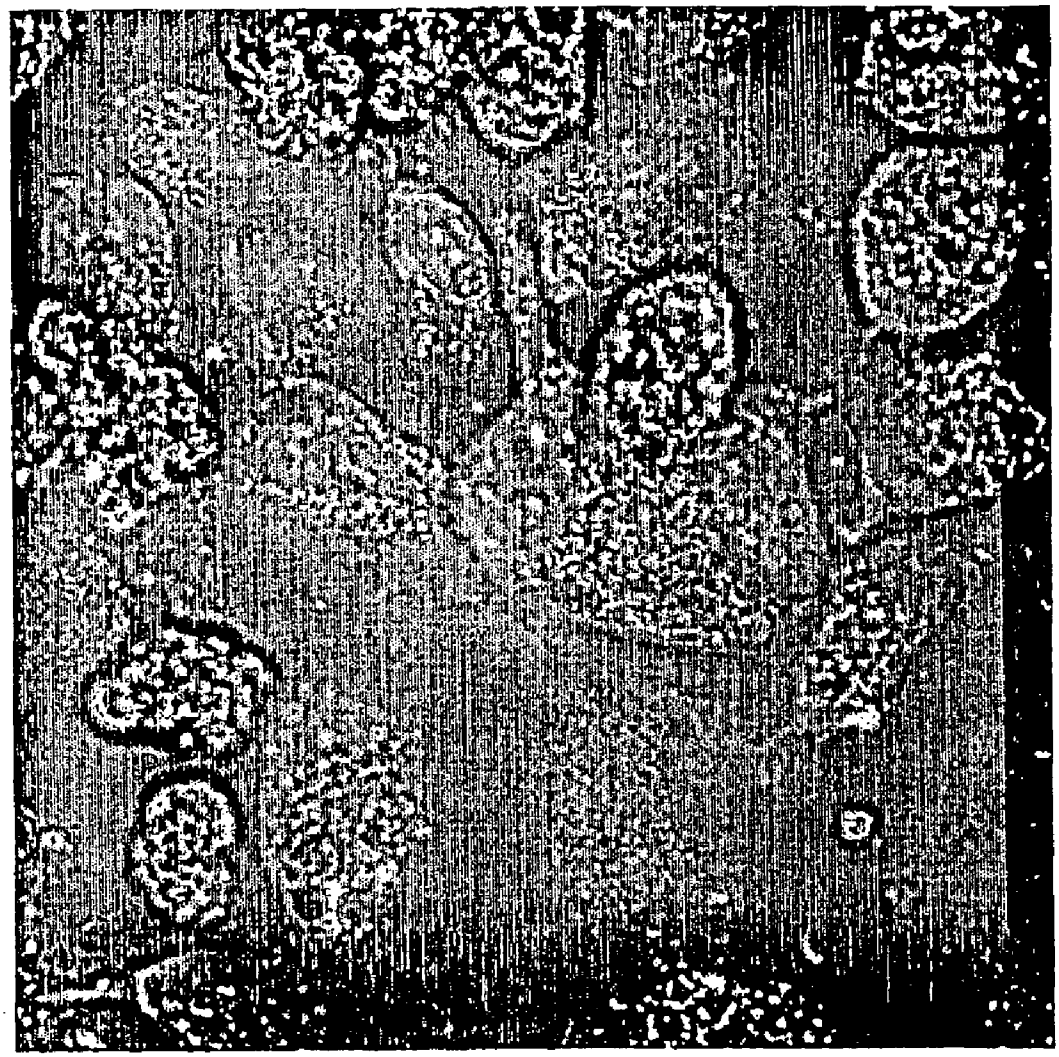


Figure 5

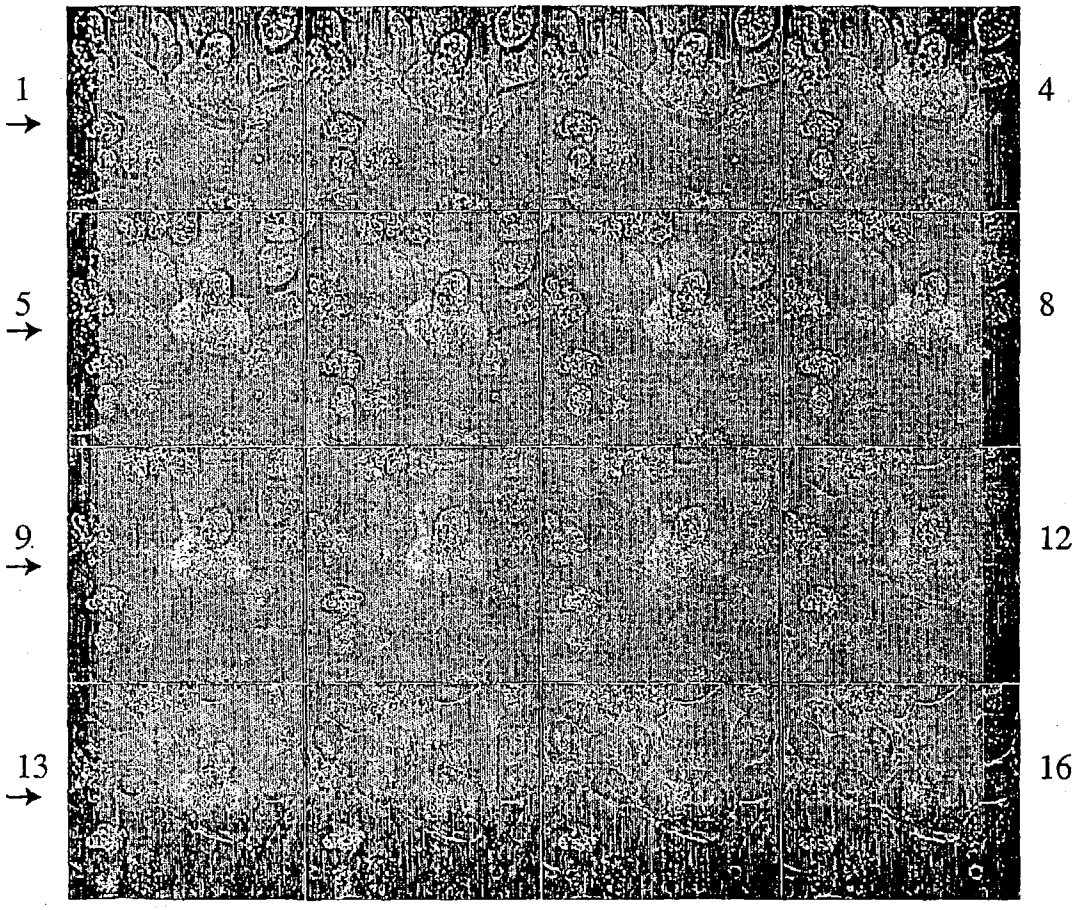
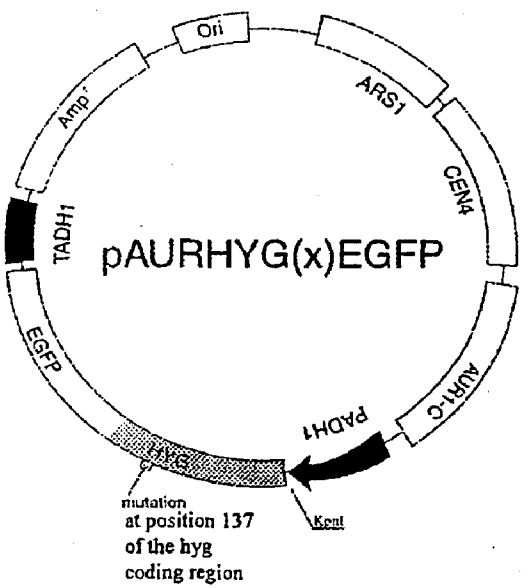


Figure 6



Sequence of normal allele: GTGGATATGTCCT
Target/existing mutant: GTGGATAATGTCCT
Desired alteration: GTGGATACGTCCT

Figure 7A

Sequence of normal allele: GTGGATATGTCCT
Target/existing mutant: GTGGATAGGTCCT
Desired alteration: GTGGATACGTCCT

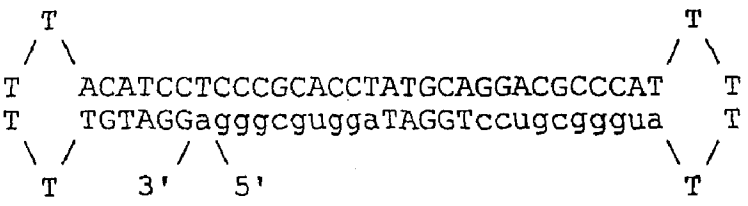
Figure 7B

HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HygE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3'

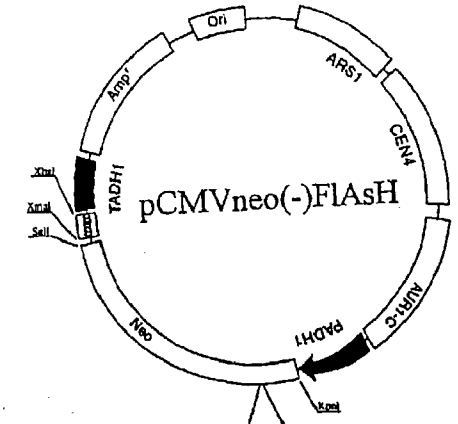
HygE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC ACG AG-3'

HygGG/Rev:



Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG A-3'

Figure 8



TTCGGCTA G GACTGG
AAGCCGAT C CTGACC

Neo/kan target mutant

TTCGGCTA C GACTGG
AAGCCGAT G CTGACC

converted

FUSION GENE FOR LIGAND BINDING

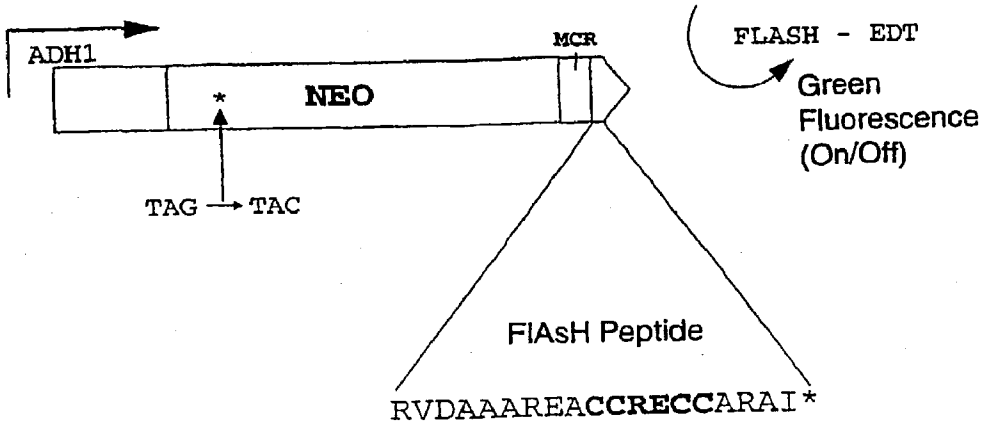


Figure 9

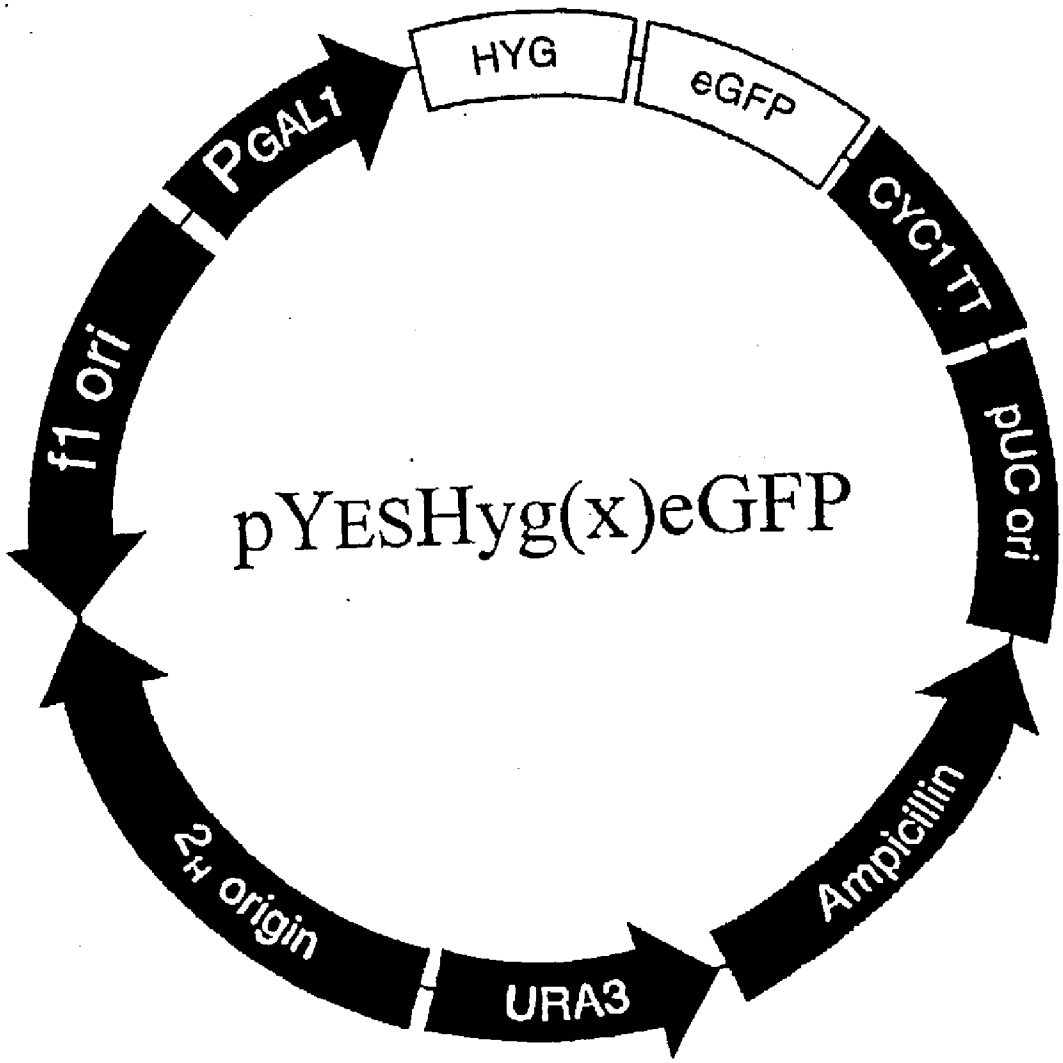

HYG
eGFP
CYC1 TT
pUC ori
Ampicillin
URA3
2μ origin
f1 ori
PGAL1
pYESHyg(x)eGFP

Figure 10

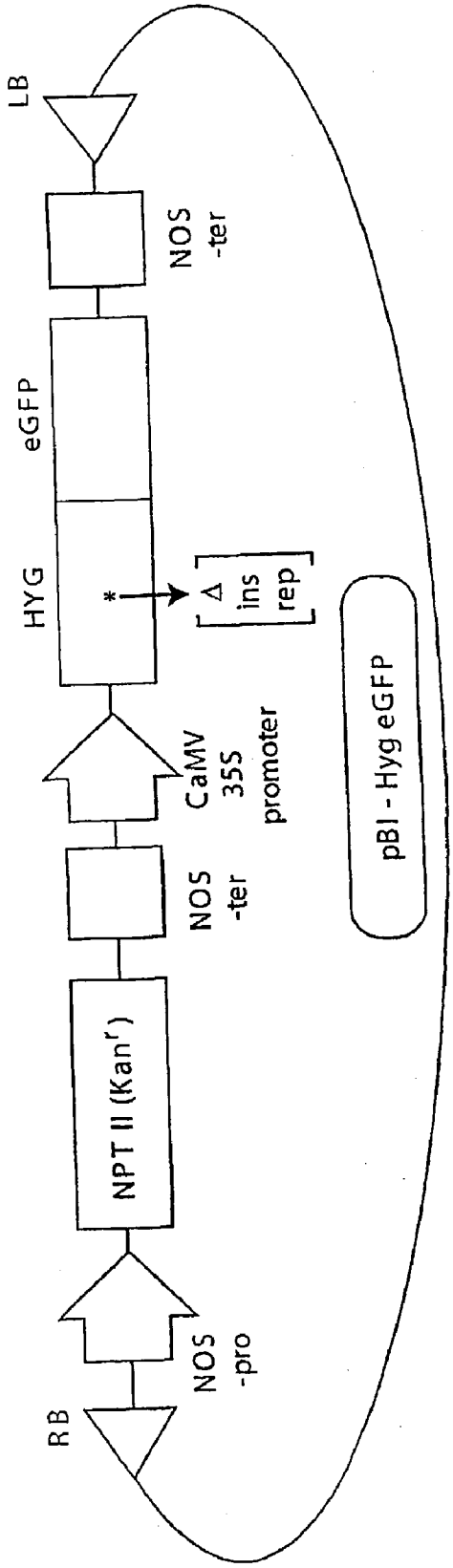

LB
NOS -ter
eGFP
HYG
*
Δ ins rep
CaMV 35S promoter
NOS -ter
NPT II (Kan^r)
NOS -pro
RB
pBI - Hyg eGFP

Figure 11

TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

FIELD OF THE INVENTION

[0001] The technical field of the invention is oligonucleotide-directed repair or alteration of plant genetic information using novel chemically modified oligonucleotides.

BACKGROUND OF THE INVENTION

[0002] A number of methods have been developed specifically to alter the genomic information of plants. These methods generally include the use of vectors such as, for example, T-DNA, carrying nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. See, for example, U.S. Pat. No. 4,459,355 which describes a method for transforming plants with a DNA vector and U.S. Pat. No. 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene-containing vectors adds one or more exogenous copies of a gene in a usually random fashion at one or more integration sites of the plant's genome at some variable frequency. The introduced gene may be foreign or may be derived from the host plant. Any gene which was originally present in the genome, which may be, for example, a normal allelic variant, mutated, defective, and/or functional copy of the introduced gene, is retained in the genome of the host plant.

[0003] These methods of gene alteration are problematic in that complications which can compromise the vigor, productivity, yield, etc. of the plant may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. The random nature of this insertion and/or the use of exogenous promoters can also cause the timing, location or strength of expression of the introduced transgene to be inappropriate or unpredictable. Another problem with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, T-DNA ends or other vector remnants, exogenous control sequences required to allow production of the transgene protein, which control sequences may be exogenous or native to the host plant and/or the transgene, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. In addition, concerns have been raised with consumption, especially by humans, of plants containing such exogenous genetic material.

[0004] More recently, simpler systems involving poly- or oligo-nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant, animal or fungal genomes. See, for example, WO 99/07865 and U.S. Pat. No. 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene alteration, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result reduces the utility of such a molecule in methods designed for targeted gene alteration.

[0005] Alternatively, other oligo- or poly-nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Pat. No. 5,422,251. The utility of these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

[0006] In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., *Nature Biotechnology* 17: 989-93 (1999). Such chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

[0007] Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., *Gene Ther.* 3:859-867 (1996). Similar efforts to target genes by homologous recombination in plants using large fragments of DNA had some success. See Kempin et al., *Nature* 389:802-803 (1997). However, the efficiency and reproducibility of the published homologous recombination approach in plants has severely limited the widespread use of this method.

[0008] Earlier experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide rather than larger fragments of DNA, wherein the oligonucleotide had no functional domains other than a region of complementary sequence to the target. See Campbell et al., *New Biologist* 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

[0009] Oligonucleotides designed for use in the targeted alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to genomic sequences that span the junction between intron sequence and exon sequence.

[0010] Artificial chromosomes can be useful for the screening purposes identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

[0011] Yeast artificial chromosomes (YACs) allow large segments of genomic DNA to be cloned and modified (Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat. Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)). Other vectors also have been developed for the cloning of large segments of genomic DNA, including cosmids, and bacteriophage P1 (Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)). YACs have certain advantages over these alternative large capacity cloning vectors (Burke et al., Science, 236:806-812 (1987)). The maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert size for a YAC.

[0012] An alternative to YACs are cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) (Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)). BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. The PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis (Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979)). In addition, BACs have been developed for transformation of plants with high-molecular weight DNA using the T-DNA system (Hamilton, *Gene* 24:107-116 (1997); Frary & Hamilton, *Transgenic Res.* 10: 121-132 (2001)).

[0013] A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

SUMMARY OF THE INVENTION

[0014] Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants are identified and the efficiency of alteration is analyzed both in vitro using a cell-free extract assay and in vivo using a yeast system and a plant system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site specific alteration of DNA is not only useful for studying function of proteins in vivo, but it is also useful for creating plants with desired phenotypes, including, for example, environmental stress tolerance, improved nutritional value, herbicide resistance, disease resistance, modified oil production, modified starch production, and altered floral morphology including selective sterility. As described herein, oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA in cells. The target genomic DNA can be nuclear chromosomal DNA as well as plastid or mitochondrial chromosomal DNA. The target DNA can also be a transgene present in the plant cell, including, for example, a previously introduced T-DNA. For screening purposes, the target plant DNA can also be extrachromosomal DNA present in plant or non-plant cells in various forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing plant DNA can be obtained from a variety of sources, including, e.g., the Arabidopsis Biological Resource Center (ABRC) at the Ohio State University, and the Rice Genome Research Program at the MAFF DNA bank in Ibaraki, Japan. The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex. In a more preferred embodiment, the target DNA to be altered is the non-transcribed strand of a transcribed gene of a genomic DNA duplex.

[0015] The low efficiency of targeted gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., *J. Am. Chem. Soc.,* 120:13252-3), we have found that it is not possible to predict which of any particular known modification would be most useful for any given alteration event, including for the construction of gene alteration oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucle-

otides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See, for example, copending applications U.S. application Ser. No. 60/208,538, U.S. application Ser. No. 60/244,989, U.S. application Ser. No. 09/818,875, international application no. PCT/US01/09761 and Gamper et al., *Nucleic Acids Research* 28: 4332-4339 (2000), the disclosures of which are incorporated herein in their entirety by reference. We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748; Wengel, WO 00/66604; and Jakobsen & Koshkin, WO 01/25478 also allow specific targeted alteration of genetic information.

[0016] The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different plants or strains, or testing cells derived from different plants or strains, or plant cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an in vitro gene repair assay. Similar results are also observed in vivo using yeast, mammalian and plant cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

DETAILED DESCRIPTION OF THE INVENTION

[0017] The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of plant genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration, including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity. For example, gene alterations that knockout a particular protein activity can be obtained using oligonucleotides designed to convert a codon in the coding region of the protein to a stop codon, thus prematurely terminating translation of the protein. Oligonucleotides that introduce stop codons in the open-reading-frame of the protein are one embodiment of the invention. Generally, oligonucleotides that introduce stop codons early in the open-reading-frame of the protein are preferred. If the open-reading-frame contains more than one methionine, oligonucleotides that introduce stop codons after the second methionine are preferred. Additionally, if the gene exhibits alternative splice sites, oligonucleotides that introduce stop codons in exons after the alternative splice site are preferred. The following table provides examples of codons that can be converted to stop codons by altering a single oligonucleotide. A skilled artisan could readily identify other codons that can be converted to stop codons by altering one, two or three of the base pairs in a given codon. Similarly, a skilled artisan could readily identify codons that can be converted to stop codons by a frameshift mutations that inserts or deletes one or two base pairs in the open-reading-frame. It is also understood that more than one stop codon can be generated in a single open-reading-frame and that these stop codons can be adjacent in the sequence or separated by intervening codons. Where more than one stop codon is introduced into a single open-reading-frame, such alterations can be generated by a single or multiple oligonucleotides and can be generated simultaneously or by sequential mutagenesis of the target nucleic acid.

Original codons*	Corresponding stop codon
GGA (glycine), **A**GA (arginine), **C**GA (arginine), T**T**A (leucine), T**C**A (serine), TG**T** (cysteine), TG**G** (tryptophan), TG**C** (cysteine)	TGA
AAG (lysine), **G**AG (glutamate), **C**AG (glutamine), T**T**G (leucine), T**C**G (serine), TG**G** (tryptophan), TA**T** (cysteine), TA**C** (tyrosine)	TAG
AAA (lysine), **G**AA (glutamate), **C**AA (glutamine), T**T**A (leucine), T**C**A (serine), TA**T** (cysteine), TA**C** (tyrosine)	TAA

*The amino acid encoded by the original codon is shown in parentheses and the base targeted for alteration to convert the codon to the corresponding stop codon is underlined and in bold

[0018] The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligonucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligo-nucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized

single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

[0019] We have discovered that single-stranded oligonucleotides having a DNA domain surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region, are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in U.S. Pat. No. 5,565,350. Preferred oligonucleotides of the invention have at least two modified bases on at least one of the termini, preferably the 3' terminus of the oligonucleotide. Oligonucleotides of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cells of different types including, for example, plant cells, fungal cells including *S. cerevisiae, Ustillago maydis, Candida albicans,* and mammalian cells. Particularly preferred are cells and cell extracts derived from plants including, for example, experimental model plants such as *Chiamydomonas reinhardtii, Physcomitrella patens,* and *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus,* e.g. *domesticus*), mangoes (*Mangifera,* e.g. *indica*), banana (*Musa,* e.g. *acuminata*), berries (such as currant, *Ribes,* e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis,* e.g. *vinifera*), bell peppers (*Capsicum,* e.g. *annuum*), cherries (such as the sweet cherry, *Prunus,* e.g. *avium*), cucumber (*Cucumis,* e.g. *sativus*), melons (*Cucumis,* e.g. *melo*), nuts (such as walnut, *Juglans,* e.g. *regia;* peanut, *Arachis hypogeae*), orange (*Citrus,* e.g. *maxima*), peach (*Prunus,* e.g. *persica*), pear (*Pyra,* e.g. *communis*), plum (*Prunus,* e.g. *domestica*), strawberry (*Fragaria,* e.g. *moschata* or *vesca*), tomato (*Lycopersicon,* e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago,* e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichoreum,* e.g. *endivia*), leek (*Allium,* e.g. *porrum*), lettuce (*Lactuca,* e.g. *sativa*), spinach (*Spinacia,* e.g. *oleraceae*), tobacco (*Nicotiana,* e.g. *tabacum*); roots, such as arrowroot (*Maranta,* e.g. *arundinacea*), beet (*Beta,* e.g. *vulgaris*), carrot (*Daucus,* e.g. *carota*), cassava (*Manihot,* e.g. *esculenta*), turnip (*Brassica,* e.g. *rapa*), radish (*Raphanus,* e.g. *sativus*), yam (*Dioscorea,* e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds, such as beans (*Phaseolus,* e.g. *vulgaris*), pea (*Pisum,* e.g. *sativum*), soybean (*Glycine,* e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum,* e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum,* e.g. *vulgare*), corn (*Zea,* e.g. *mays*), rice (*Oryza,* e.g. *sativa*), rapeseed (*Brassica napus*), millet (Panicum sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*), chickpea (*Cicer,* e.g. *arietinum*); tubers, such as kohlrabi (*Brassica,* e.g. *oleraceae*), potato (*Solanum,* e.g. *tuberosum*) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (Pinus sp.), oak (Quercus sp.), eucalyptus (Eucalyptus sp.), and the like and ornamental plants such as turfgrass (*Lolium,* e.g. *rigidum*), petunia (*Petunia,* e.g. *x hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium,* e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver,* e.g. *nudicaule*), lilac (*Syringa,* e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. Solidago spp.). Such plant cells can then be used to regenerate whole plants according to methods described herein or any method known in the art. The DNA domain of the oligonucleotides is preferably fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration event(s). On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

[0020] According to certain embodiments, one or both of the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone (including LNA derivatives and analogs) modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. The oligonucleotides of the invention are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA (including LNA derivatives or analogs), phosphorothioate linkages, or 2'-O-methyl analog incorporation into an oligonucleotide can not yet be predicted because the proteins involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

[0021] In the examples, oligonucleotides of defined sequence are provided for alteration of genes in particular plants. Provided the teachings of the instant application, one of skill in the art could readily design oligonucleotides to introduce analogous alterations in homologous genes from any plant. Furthermore, in the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. In some embodiments, longer nucleic acids of up to 240 bases which comprise the sequences

disclosed herein may be used. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for alteration of particular plant genes contain phosphorothioate linkages, 2'-O-methyl analog or LNA (including LNA derivatives and analogs) or any combination of these modifications just as the assay oligonucleotides do.

[0022] The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs (including LNA derivatives and analogs), phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

[0023] The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4 analogs are preferred. The optimal number and type of backbone modifications for any particular oligo-nucleotide useful for altering target DNA may be determined empirically by comparing the alteration efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

[0024] Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligo-nucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

[0025] Efficiency of conversion is defined herein as the percentage of recovered substrate molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired the desire change. The oligonucleotides of the invention in different embodiments can alter DNA two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin oligonucleotide such as disclosed in U.S. Pat. No. 5,565,350.

[0026] In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

[0027] The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligo-nucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either strand of DNA and can include any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

[0028] Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene alteration activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Pat. No. 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular

triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide-dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the same sequence alteration. Similarly, molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

[0029] The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

[0030] Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, preferably, using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, Iowa 52241) (http://www.idtdna.com); this program is available for use on the world wide web at http://www.idtdna.com/program/oligoanalyzer/oligoanalyzer.asp.

[0031] For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, Wis. 53715, Phone: (608) 258-7420 (http://www.dnastar.com/products/PrimerSelect.html).

[0032] If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

[0033] Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligo-nucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e. the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

[0034] The oligonucleotides of the invention can include more than a single base change. In an oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

[0035] The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. For plant cells, biolistic or particle bombardment methods are typically used. According to certain preferred embodiments of the present invention, isolated plant cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Alternatively, plant target DNA may be modified in vitro or in another cell type, including for example, yeast or bacterial cells and then introduced into a plant cell as, for example, a T-DNA. Plant cells thus modified may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place in vivo following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

[0036] The single-stranded, modified oligonucleotides of the present invention have numerous applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the genetic complement of the

organism. Such agents may, for example, be used to develop plants with improved traits by rationally changing the sequence of selected genes in isolated cells and using these modified cells to regenerate whole plants having the altered gene. See, e.g., U.S. Pat. No. 6,046,380 and U.S. Pat. No. 5,905,185 incorporated herein by reference. Such plants produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of plants having particular modified or inactivated genes. Altered plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used to introduce molecular markers, including, for example, SNPs, RFLPs, AFLPs and CAPs.

[0037] The purified oligonucleotide compositions may be formulated in accordance with routine procedures depending on the target. For example, purified oligonucleotide can be used directly in a standard reaction mixture to introduce alterations into targeted DNA in vitro or where cells are the target as a composition adapted for bathing cells in culture or for microinjection into cells in culture. The purified oligonucleotide compositions may also be provided on coated microbeads for biolistic delivery into plant cells. Where necessary, the composition may also include a solubilizing agent. Generally, the ingredients will be supplied either separately or mixed together in single-use form, for example, as a dry, lyophilized powder or water-free concentrate. In general, dosage required for efficient targeted gene alteration will range from about 0.001 to 50,000 μg/kg target tissue, preferably between 1 to 250 μg/kg, and most preferably at a concentration of between 30 and 60 micromolar.

[0038] For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein. For biolistic delivery, microbeads are generally coated with resuspended oligonucleotides, which range of oligonucleotide to microbead concentration can be similarly adjusted to improve efficiency as determined using one of the assay methods described herein, starting with about 0.05 to 1 microgram of oligonucleotide to 25 microgram of 1.0 micrometer gold beads or similar microcarrier.

[0039] Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an additional reagent or article of manufacture. The additional reagent or article of manufacture may comprise a delivery mechanism, cell extract, a cell, or a plasmid, such as one of those disclosed in the Figures herein, for use in an assay of the invention. Alternatively, the invention includes a kit comprising an isogenic set of cells in which each cell in the kit comprises a different altered amino acid for a target protein encoded by a targeted altered gene within the cell produced according to the methods of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0040] **FIG. 1**. Flow diagram for the generation of modified single-stranded oligonucleotides. The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene. The numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G). **FIG. 1**(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left; SEQ ID NO: 2673) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments (right; SEQ ID NO: 2674). **FIG. 1**(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide (SEQ ID NO: 2673) is used. In **FIG. 1**(D), the Kan mutant sequence corresponds to SEQ ID NO: 2675 and SEQ ID NO: 2676; the Kan converted sequence corresponds to SEQ ID NO: 2677 and SEQ ID NO: 2678; the mutant sequence in the sequence trace corresponds to SEQ ID NO: 2679 and the converted sequences in the sequence trace correspond to SEQ ID NO: 2680.

[0041] **FIG. 2**. Genetic readout system for correction of a point mutation in plasmid pK^sm4021. A mutant kanamycin gene harbored in plasmid pK^sm4021 is the target for correction by oligonucleotides. The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts. The wild type sequence corresponds to SEQ ID NO: 2681.

[0042] **FIG. 3**: Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides. (A) Plasmid $pT^s\Delta 208$ contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair. The wild type sequence corresponds to SEQ ID NO: 2682, the mutant sequence corresponds to SEQ ID NO: 2683 and the converted sequence corresponds to SEQ ID NO: 2684. The control sequence in the sequence trace corresponds to SEQ

ID NO: 2685 and the 3S/25A sequence in the sequence trace corresponds to SEQ ID NO: 2686.

[0043] **FIG. 4**. DNA sequences of representative kan^r colonies. Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues. The sequences in the sequence traces have been assigned numbers as follows: 3S/25G, 6S/25G and 8S/25G correspond to SEQ ID NO: 2687, 10S/25G corresponds to SEQ ID NO: 2688, 25S/25G on the lower left corresponds to SEQ ID NO: 2689 and 25S/25G on the lower right corresponds to SEQ ID NO: 2690.

[0044] **FIG. 5**. Gene correction in HeLa cells. Representative oligonucleotides of the invention are co-transfected with the pCMVneo(−)FIAsH plasmid (shown in **FIG. 9**) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

[0045] **FIG. 6**. Z-series imaging of corrected cells. Serial cross-sections of the HeLa cell represented in **FIG. 5** are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

[0046] **FIG. 7**. Hygromycin-eGFP target plasmids. (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. In **FIG. 7**A, the sequence of the normal allele corresponds to SEQ ID NO: 2691, the sequence of the targe/existing mutation corresponds to SEQ ID NO: 2692 and the sequence of the desired alteration corresponds to SEQ ID NO: 2693. (B) Plasmid pAURHYG(rep)GFP contains a base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function. In **FIG. 7**B, the sequence of the normal allele correspond to SEQ ID NO: 2691, the sequence of the targe/existing mutation corresponds to SEQ ID NO: 2694 and the sequence of the desired alteration corresponds to SEQ ID NO: 2693.

[0047] **FIG. 8**. Oligonucleotides for correction of hygromycin resistance gene. The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined. In **FIG. 8**, the sequence of HygE3T/25 corresponds to SEQ ID NO: 2695, the sequence of HygE3T/74 corresponds to SEQ ID NO: 2696, the sequence of HygE3T/74a corresponds to SEQ ID NO: 2697, the sequence of HygGG/Rev corresponds to SEQ ID NO: 2698 and the sequence of Kan70T corresponds to SEQ ID NO: 2699.

[0048] **FIG. 9**. pAURNeo(−)FIAsH plasmid. This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence. In **FIG. 9**, the sequence of the Neo/kan target mutant corresponds to SEQ ID NO: 2675 and SEQ ID NO: 2676, the converted sequence corresponds to SEQ ID NO: 2677 and SEQ ID NO: 2678 and the FIAsH peptide sequence corresponds to SEQ ID NO: 2700.

[0049] **FIG. 10**. pYESHyg(x)eGFP plasmid. This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in **FIG. 7**, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

[0050] **FIG. 11**. pBI-HygeGFP plasmid. This plasmid is a construct based on the plasmids pBI101, pBI 101.2, pBI101.3 or pBI 121 available from Clontech in which HygeGFP replaces the beta-glucuronidase gene of the Clontech plasmids. The different Clontech plasmids vary by a reading frame shift relative to the polylinker, or the presence of the Cauliflower mosaic virus promoter.

[0051] The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

EXAMPLE 1

Assay Method for Base Alteration and Preferred Oligonucleotide Selection

[0052] In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see **FIG. 1** for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK^sm4021 (**FIG. 2**) or the tetracycline gene of $pT^s\Delta 208$ (**FIG. 3**). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in **FIG. 1**C and **FIG. 1D**. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(−)FIAsH (**FIG. 9**), bearing the kan^s gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferasea (kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FIAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, Wis.). The resulting construct replicates in *S. cerevisiae* at low copy number, confers

resistance to aureobasidinA and constitutively expresses either the Neo+/FIAsH fusion product (after alteration) or the truncated Neo−/FIAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy.

[0053] Additional constructs can be made to test additional gene alteration events or for specific use in different expression systems. For example, alternative comparable plant plasmids or integration vectors such as, e.g. those based on T-DNA, can be constructed for stable expression in plant cells according to the disclosures herein. Such constructs would use a plant specific promoter such as, e.g., cauliflower mosaic virus 35S promoter, to replace the promoters directing expression of the neo, hyg or aureobasidinA resistance gene disclosed herein, including for example, in **FIGS. 7B, 9** and **10** herein. Moreover, the green fluorescent protein (GFP) sequence used herein may be modified to increase expression in plant cells such as Arabidopsis and the other plants disclosed herein as described in Haseloff et al., Proc. Natl.Acad. Sci. 94(6): 2122-7 (1997), Rouwendal et al. Plant Mol. Biol. 33(6): 989-99 (1997) and Hu et al. FEBS Lett. 369(2-3): 331-4 (1995). Codon usage for optimal expression of GFP in plants results from increasing the frequency of codons with a C or a G in the third position from 32 to about 60%. Specific constructs are disclosed and can be used as follows with such plant specific alterations.

[0054] We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T1374→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHYGeGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3'; SEQ ID NO: 2701) to primer Hygrepr (5'GACCTATCCACGCCCTCC-3'; SEQ ID NO: 2702), HygΔr (5'-GACTATCCACGCCCTCC-3'; SEQ ID NO: 2703), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'; SEQ ID NO: 2704), respectively. We generate a 300 bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrepf (5'-CTGGGATAGGTCCTGCGG-3'; SEQ ID NO: 2705), HygΔf (5'-CGTGGATAGTCCTGCGG-3'; SEQ ID NO: 2706), Hyginsf (5'-CGTGGATAATGTCCTGCGG-3'; SEQ ID NO: 2707), respectively to primer HygEGFPr (5'-AAATCACGCCATGTAGTG-3'; SEQ ID NO: 2708). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94° C. for 10 seconds, annealing at 55° C. for 20 seconds and elongation at 68° C. for 1 minute. We digest 10 μg of vector pHYGeGFP and 5 μg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHYGeGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

[0055] Oligonucleotide synthesis and cells. Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper et al., *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 μg/ml per A_{260} unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2 mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, Md.); DH10B cells contain a mutation in the RECA gene (recA).

[0056] Cell-free extracts. Although this portion of this example is directed to mammalian systems, similar extracts from plants can be prepared as disclosed elsewhere in this application and used as disclosed in this example. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately 2×10^8 cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM $MgCl_2$; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000×g. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage. We then immediately aliquote and freeze the supernatant at −80° C. We determine the protein concentration in the extract by the Bradford assay.

[0057] We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis,* and *Candida albicans.* For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30° C. We then centrifuge the cultures at 5000×g, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1 mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000×g for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000×g for 15 minutes. We then

add glycerol to the clarified extract to a concentration of 10% (v/v) and freeze aliquots at −80° C. We determine the protein concentration of the extract by the Bradford assay.

[0058] Reaction mixtures of 50 μl are used, consisting of 10-30 μg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 μg chimeric double-hairpin oligonucleotide or 0.55 μg single-stranded molecule (3S/25G or 6S/25G, see **FIG. 1**), and 1 μg of plasmid DNA (see **FIGS. 2 and 3**) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM $MgCl_2$, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30° C. for 45 min. The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4° C. for 30 min., is washed with 70% ethanol, resuspended in 50 μl H_2O, and is stored at −20° C. 5 μl of plasmid from the resuspension (~100 ng) was transfected in 20 μl of DH10B cells by electroporation (400 V, 300 μF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37° C. for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 μg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37° C. Cells are then spun down at 3750×g and the pellet is resuspended in 500 μl SOC. 200 μl is added undiluted to each of two kanamycin (50 μg/ml) agar plates and 200 μl of a 10^5 dilution is added to an ampicillin (100 μg/ml) plate. After overnight 37° C. incubation, bacterial colonies are counted using an Accucount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10^{-5} to correct for the amp dilution.

[0059] The following procedure can also be used. 5 μl of resuspended reaction mixtures (total volume 50 μl) are used to transform 20 μl aliquots of electro-competent DH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37° C. for 1 hour at which time 50 μg/ml kanamycin or 12 μg/ml tetracycline is added for an additional 3 hours. Prior to plating, the bacteria are pelleted and resuspended in 200 μl of SOC. 100 μl aliquots are plated onto kan or tet agar plates and 100 μl of a $10^{31\ 4}$ dilution of the cultures are concurrently plated on agar plates containing 100 μg/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads. Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

[0060] Chimeric single-stranded oligonucleotides. In **FIG. 1** the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligo-nucleotides that contain (**FIG. 1A**) 2'-O-methyl RNA nucleotides or (**FIG. 1B**) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene.

[0061] Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan^s system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and **FIG. 1**B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining the optimum oligonucleotide for a particular alteration event.

[0062] The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and **FIG. 2**A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

[0063] Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple experiments are processed and the isolated plasmid DNA is sequenced. As seen in **FIG. 4**, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base changes. In these illustrative examples, the second base of the codon is changed (see **FIG. 3**). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

[0064] In **FIG. 1**, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the examplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phos-

phorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

[0065] Correction of a mutant kanamycin gene in cultured mammalian cells. Although this portion of this example is directed to cultured mammalian cells, comparable methods may be used using cultured plant cells or protoplasts of those cells from the plant species disclosed herein. The experiments are performed using different eukaryotic cells including plant and mammalian cells, including, for example, 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37° C. and 5% CO_2 in a humidified incubator to a density of 2×10^5 cells/ml in an 8 chamber slide (Lab-Tek). After replacing the regular DMEM with Optimem, the cells are co-transfected with 10 μg of plasmid pAURNeo(−) FIAsH and 5 μg of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10 μg lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37° C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan^s gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence (SEQ ID NO: 2717) in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FIAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FIAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

[0066] Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid $pkan^sm4021$ (see **FIG. 1**). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (**FIG. 3**) in the tet gene contained in plasmid pTetΔ208. Table 4 illustrates data from repair of the $pkan^sm4021$ point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan^r or tet^r and fold increases (single strand versus double hairpin) are presented for kan^r in Table 1.

[0067] **FIG. 5A** is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). **FIG. 5B** represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

[0068] Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold in certain embodiments when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

[0069] This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK^sm4021 contains a mutation (T→G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

[0070] The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Pat. No. 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan^s mutation, gene repair is observed (I in **FIG. 1A**). Chimera II (**FIG. 1B**) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan^s mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

[0071] Frame shift mutations are repaired. By using plasmid $pT^sΔ208$, described in **FIG. 1**(C) and **FIG. 3**, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested

for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. **FIG. 3** illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. **FIG. 3** represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

[**0072**] Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides. From a comparison of molecules VII and XI, it is apparent that gene repair is more subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

[**0073**] Oligonucleotides can target multiple nucleotide alterations within the same template. The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK^{s}m4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence TTCGATAAGCCTATGCTGACCCGTG (SEQ ID NO: 2709) corrects the original mutation present in the kanamycin resistance gene of pK^{s}m4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence TTCGGCTACGACTGGGCACAACAGACAATTGGC (SEQ ID NO: 2710) with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oigo2 directs correction of the mutation in pK^{s}m4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

[**0074**] We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK^{s}M4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-TTGTGCCCAGTCGTATCCGAATAGC-3' (SEQ ID NO: 2711); a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGA-3' (SEQ ID NO: 2712); and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-GCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTAGCCGMTAGCCT-3' (SEQ ID NO: 2713). The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

[**0075**] We assay correction of the original mutation in pK^{s}m4021 by monitoring kanamycin resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp5091 which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to determine whether the additional, silent alteration has also been introduced. The results of an analysis are presented below:

	Oligo 1 (25-mer)	Oligo 2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

[**0076**] Nuclease sensitivity of unmodified DNA oligonucleotide. Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

[**0077**] Plant extracts direct repair. The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract or extracts made from other plant cells disclosed herein. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM $MgCl_2$; 10 mM DTT; and 10% [v/v] glycerol). Some plant cell-free extracts also include about 1% (w/v) PVP. We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000×g for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by Bradford assay. We dispense 100 μg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at −80° C.

[**0078**] We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant

improvement in gene repair occurred when modified single-stranded molecules were used.

[0079] Tables are attached hereto.

TABLE I

Gene repair activity is directed by single-stranded oligonucleotides.

Oligonucleotide	Plasmid	Extract (ug)	kan^r colonies	Fold increase
I	pK^{S}m4021	10	300	
I	↓	20	418	1.0 ×
II	↓	10	537	
II	↓	20	748	1.78 ×
III	↓	10	3	
III	↓	20	5	0.01 ×
IV	↓	10	112	
IV	↓	20	96	0.22 ×
V	↓	10	217	
V	↓	20	342	0.81 ×
VI	↓	10	6	
VI	↓	20	39	0.093 ×
VII	↓	10	0	
VII	↓	20	0	0 ×
VIII	↓	10	3	
VIII	↓	20	5	0.01 ×
IX	↓	10	936	
IX	↓	20	1295	3.09 ×
X	↓	10	1140	
X	↓	20	1588	3.7 ×
XI	↓	10	480	
XI	↓	20	681	1.6 ×
XII	↓	10	18	
XII	↓	20	25	0.059 ×
XIII	↓	10	0	
XIII	↓	20	4	0.009 ×
—	↓	20	0	
I	↓	—	0	

[0080] Plasmid pK^{S}m4021 (1 μg), the indicated oligonucleotide (1.5 μg chimeric oligonucleotide or 0.55 μg single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20 μg of HUH7 cell-free extract were incubated 45 min at 37° C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan^r colonies counted. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of three experiments (standard deviation usually less than +/−15%). Fold increase is defined relative to 418 kan^r colonies (second reaction) and in all reactions was calculated using the 20 μg sample.

TABLE II

Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.

A. Oligonucleotide	Plasmid	Extract	kan^r colonies
IX (3S/25G)	↓	HUH7	637
X (6S/25G)	↓	HUH7	836
IX	↓	MEF2$^{-/-}$	781
X	↓	MEF2$^{-/-}$	676
IX	↓	MEF3$^{-/-}$	582
X	↓	MEF3$^{-/-}$	530
IX	↓	MEF$^{+/+}$	332
X	↓	MEF$^{+/+}$	497
—	↓	MEF2$^{-/-}$	10
—	↓	MEF3$^{-/-}$	5
—	↓	MEF$^{+/+}$	14

[0081] Chimeric oligonucleotide (1.5 μg) or modified single-stranded oligonucleotide (0.55 μg) was incubated with 1 μg of plasmid pK^{S}m4021 and 20 μg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 (2$^{-/-}$) or MSH3 (3$^{-/-}$) deleted. MEF$^{+/+}$ indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies.

TABLE III

Frameshift mutation repair is directed by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	tet^r colonies
Tet IX (3S/25A; 0.5 μg)	pT^{S}Δ208 (1 μg)	—	0
—	↓	20 μg	0
Tet IX (0.5 μg)	↓	↓	48
Tet IX (1.5 μg)	↓	↓	130
Tet IX (2.0 μg)	↓	↓	68
Tet I (chimera; 1.5 μg)	↓	↓	48

[0082] Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide. The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of pT^{s}Δ208. The oligonucleotides are equivalent to structures I and IX in **FIG. 2**.

TABLE IV

Plant cell-free extracts support gene repair by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	kan^r colonies
II (chimera)	pK^{S}m402l	30 μg Canola	337
IX (3S/25G)	↓	Canola	763
X (6S/25G)	↓	Canola	882
II	↓	Musa	203
IX	↓	Musa	343
X	↓	Musa	746
—	↓	Canola	0
—	↓	Musa	0
IX	↓	— Canola	0
X	↓	— Musa	0

[0083] Canola or Musa cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 μg) and modified single-stranded oligonucleotides IX and X (0.55 μg) were used to correct pK^{S}m4021. Total number of kan^r colonies are present per 10^7 ampicillin resistant colonies and represent an average of four independent experiments.

TABLE V

Gene repair activity in cell-free extracts prepared from yeast (*Saccharomyces cerevisiae*)

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	$kan^r/amp^r \times 10^6$
Wild type	$pKan^s m4021$	1 μg		0.36
Wild type	↓		1 μg	0.81
ΔRAD52	↓	1 μg		10.72
ΔRAD52	↓		1 μg	17.41
ΔPMS1	↓	1 μg		2.02
ΔPMS1	↓		1 μg	3.23

In this experiment, the kan^s gene in $pKan^s 4021$ is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/25G).

EXAMPLE 2

Yeast Cell Targeting Assay Method for Base Alteration and Preferred Oligonucleotide Selection

[0084] In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (**FIG. 7**), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (**FIG. 7**) and pAURHYG(Δ)GFP which has a single base deletion. We also use the plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

[0085] We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, Calif.). We digest 10 μg pAUR123 vector DNA, as well as, 10 μg of each pHyg(x-)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

[0086] We use this system to assay the ability of five oligonucleotides (shown in **FIG. 8**) to support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74α, is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence. Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2-O-methylated modified oligonucleotide may be used as a control. Alternatively, oligonucleotides containing one, two, three, four, five, six, eight, ten or more LNA modifications on at least one of the two termini (and preferrably the 3' terminus) may be used in different embodiments.

[0087] Oligonucleotide synthesis and cells. We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 MAT α at low copy number under aureobasidin selection. Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30° C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30° C. until the OD_{600} was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4° C. at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4° C. at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4° C. at 5000 rpm for 5 minutes and resuspend the cells in 120 μl 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 μl of cells with 5 μg of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes. We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 μF, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30° C. with shaking at 300 rpm for 6 hours. We then spread 200 μl of this culture on selective plates containing 300 μg/ml hygromycin and spread 200 μl of a 10^5 dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30° C. for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10^5 aureobasidinA resistant colonies.

[0088] Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in **FIG. 8** to correct a frameshift mutation in vivo using LSY678 yeast

cells containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

[0089] We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAG-GAGGGCGTGGGTACGTCCTGCGGG-TAAATAGCTGCGCCGATGGTTTCTAC-3' (SEQ ID NO: 2714); a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCT-TCGATGTAGGAGGGCGTGGATACGTCCT-GCGGGTAAACAGCTGCGCCGATGGTTTCTAC-3' (SEQ ID NO: 2715); and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTCGT-GCTTTCAGCTTCGATGTAGGAGGGCGTG-GATACGTCCTGCGGGTAAATAGCTGCGC-CGACGGTTTCTAC (SEQ ID NO: 2716). The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

[0090] Oligonucleotides targeting the sense strand direct gene correction more efficiently. We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74α, with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6 μg, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74α and HygE3T/74). Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74α relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in **FIG. 10**.

[0091] Optimization of oligonucleotide concentration. To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0 μg. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

[0092] Tables are attached hereto.

TABLE 6

Correction of an insertion mutation in pAURHYG(ins)GFP by HygGG/Rev, HygE3T/25 and HygE3T/74

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin ($/10^5$)	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

[0093]

TABLE 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

	Colonies per hygromycin plate	
Amount of Oligonucleotide (μg)	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

*The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

[0094]

TABLE 8

Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.

Oligonucleotide	Plasmid tested (contained in LSY678)	
Tested (5 μg)	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

[0095]

TABLE 9

Optimization of oligonucleotide concentration in electroporated yeast cells.

Amount (μg)	Colonies on hygromycin	Colonies on aureobasidin ($/10^5$)	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

EXAMPLE 3

Cultured Cell Manipulation

[0096] Although disclosure in this example is directed to use of stem cells or human blood cells and microinjection, the microinjection procedures may also be used with cultured plant cells or protoplasts using any plant species, including those disclosed herein. Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, Calif.). Lin^-CD38^- cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, Calif.). Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection. S Medium contains Iscoves' Modified Dulbecc's Medium without phenol red (IMDM) with 100 μg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 μg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM; Stem Cell Technologies), 40 μg/ml low-density lipoprotein (LDL; Sigma, St. Louis, Mo.), 50 mM HEPEs buffer and 50 μM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, N.J.). After microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

[0097] 35 mm dishes are coated overnight at 4° C. with 50 μg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, Wis.) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C. prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 μm to 0.3 μm outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C. and injected using an electronically interfaced Eppendorf Micromanipulator and Transjector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are flourescently labeled allow determination of the amount of oligonucleotide delivered to the cells.

[0098] For in vitro erythropoiesis from Lin^-CD38^- cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythoid progeny. CD34+ cells can convert a normal A (β^A) to sickle T (β^S) mutation in the β-globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

[0099] Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

[0100] Biolistic delivery of oligonucleotide into plant cells may be accomplished according to the following method. One milliliter of packed cell volume of plant cell suspensions are subcultured onto plates containing solid medium [with Murashige and Skoog salts from Gibco/BRL, 500 mg/liter Mes, 1 mg/liter thiamin, 100 mg/liter myo-inositol, 180 mg/liter KH2PO4, 2.21 mg/liter 2,4-dichlorophenoxyacetic acid (2,4-D), and 30 g/liter sucrose (pH 5.7) and having 8 g/liter agar-agar from Sigma added before autoclaving]. By using a helium-driven particle gun such as that from BioRad and following manufacturers directions, oligonucleotides may be introduced to cells after precipitation onto 1 micrometer or comparable gold microcarriers (Bio-Rad). To precipitate onto microcarriers, 35 microliters of a particle suspension (60 mg of microcarriers per ml of 100% ethanol) is transferred to a 1.5 ml microcentrifuge tube, which is agitated on a vortex mixer. Then 40 microliter of resuspended oligonucleotide (60 ng/microliter water) is added; then 75 microliter of ice-cold 2.5 M CaCl2 is added; then 75 microliter of ice-cold 0.1 M spermidine is added. The tube is mixed vigorously or a vortex mixer for 10 min at room temperature. The particles are allowed to settle for 10 min and are centrifuged at 11,750 g for 30 sec. The supernatant is removed and the particles are resuspended in 50 microliter of 100% ethanol. An aliquot of 10 microliter of the resuspended particles are applied to each macroprojectile which is used to bombard each plate once at 900 psi (1 psi=6.89 kPa) with a gap distance (distance from

power source to macroprojectile) of 1 cm and a target distance (distance from microprojectile launch site to target material) of 10 cm.

[0101] An alternative method of delivery can be used as follows. Cultured cells are suspended in liquid N6 medium and then plated on a VWR Scientific glass fiber filter. About 0.4 microgram of oligonucleotide are precipitated with 15 microliter of 2.5 mM CaCl2 and 5 microliter of 0.1 M spermidine onto 25 microgram of 1.0 micrometer gold particles. Microprojectile bombardment is performed by using a Bio-Rad PDS-1000 He particle delivery system or comparable machine following manufacturers instructions. Alterations in oligonucleotide concentrations can be employed to determine the optimum concentration of oligonucleotide according to the procedures described herein for any particular oligonucleotide of the invention.

[0102] Alternatively, the oligonucleotide of the invention may be delivered to a plant cell by electroporation of a protoplast derived from a plant part. The protoplasts may be formed by enzymatic treatment of a plant part, particularly a leaf, according to techniques such as those in Gallois et al., Methods in Molecular Biology 55: 89-107 by Humana Press. Such conditions for electroporation use about 3×10^5 protoplasts in a total volume of about 0.3 ml with a concentration of oligonucleotide of between 0.6 to 4 microgram per ml.

EXAMPLE 4

Plant Cells

[0103] The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon.

[0104] Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

[0105] For introduction of a T-DNA, including the T-DNA in the plasmid of **FIG. 11**, into a plant cell, *Agrobacterium tumefaciens* is used. These techniques are routine standard techniques known in the art. For example, one method follows. We transform *A. tumefaciens* is transformed by electroporation (using a BioRad Gene Pulser™). Competent *A. tumefaciens* is prepared using a method similar to that of preparing competent *E. coli* by suspending a freshly grown culture three times in ice-cold water and a final resuspension in 10% glycerol. Electroporation conditions are a 0.2 cm gap cuvette at a setting of 25 μF,200 Ω and2.5 kV.

[0106] *A. tumefaciens* containing a plasmid with a T-DNA is then used to introduce the T-DNA into a plant cell using routine standard techniques known in the art. For example, we transform Arabidopsis by vacuum infiltration or by dipping flowers in an Agrobacterium solution containing a surfactant, e.g. L-77. Seeds are then collected, grown and screened for presence of the T-DNA. Alternatively, Agrobacterium can be used to transform callus tissue and the callus tissue can then be used to regenerate transformed plants.

[0107] All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

[0108] Notes on the Tables Presented Below:

[0109] Each of the following tables presents, for the specified gene, a plurality of mutations that are known to confer a relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the genome according to the present invention.

[0110] The left-most column identifies each alteration or mutation and the phenotype that the alteration/mutation confers.

[0111] For most entries, the mutation/alteration is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

[0112] The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the genome or in cloned DNA including DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

[0113] All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

[0114] The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair/altering nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair/alteration. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair/alteration nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

[0115] The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

EXAMPLE 5

Engineering Herbicide Resistant Plants

[0116] Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

[0117] Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

[0118] Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-aminophenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

[0119] The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

TABLE 10

Genome-Altering Oligos Conferring Glyphosate Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Glyphosate Resistance	AAGCGTCGGAGATTGTACTTCAAC-	1
	CCATTTAGAGAAATCTCCGGTC	
EPSPS	TTATTAAGCTTCCTGCCTCCAAGTCTCTATCAAATCGGATCCTGC	
Arabidopsis thaliana	TTCTCGCTGCTCTGTCTGAGGTATATATCAC	
Gly97Ala	GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT	2
GGC-GCC	TGATAGAGACTTGGAGGCAGGAAGCTTAATAAGACCGGAGATTT	
	CTCTAATGGGTTGAAGTACAATCTCCGACGCTT	
	GCTTCCTG**C**CTCCAAGT	3
	ACTTGGAG**G**CAGGAAGC	4
Glyphosate Resistance	AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTC	5
EPSPS	TCATTAAGCTACCCGCATCCAAATCTCTCTCCAATCGGATCCTCC	
Brassica napus	TTCTTGCCGCTCTATCTGAGGTACATATACT	
Gly93AIa	AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT	6
GGA-GCA	GGAGAGAGATTTGGATGCGGGTAGCTTAATGAGACCCGAGATTT	
	CTCTGATTGGTTGAAGCACAATCTCTGAAGCTT	
	GCTACCCG**C**ATCCAAAT	7
	ATTIGGAT**G**CGGGTAGC	8
Glyphosate Resistance	AGCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC	9
EPSPS 1	ACTGTTAAATTGCCTGCTTCTAAATC-	
	CCTTTCCAATCGTATTCTCC	
Nicotiana tabacum	TTCTTGCTGCCCTTTCTAAGGGAAGGACTGT	
Gly95Ala	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATT	10
GGT-GCT	GGAAAGGGATTTAGAA**G**CAGGCAATTTAACAGTGCCTGATATATC	
	TTTGATGGGTTGCAGCACAATCTCGTIGGGCT	
	ATTGCCTG**C**TTCTAAAT	11
	ATTTAGAA**G**CAGGCAAT	12
Glyphosate Resistance	ATTGTTTCCTTGGTACGAAATGTCCTCCTGTTCGAATTGTCAGCA	13
EPSPS 2	AGGGAGGCCTTCCCGCAGGGAAGGTAAAGCTCTCTGGATCAATT	
Nicotiana tabacum	AGCAGCCAGTACTTGACTGCTCTGCTTATGGC	
Gly62Ala	GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGA	14
GGA-GCA	GAGCTTTACCTTCCCT**G**CGGGAAGGCCTCCCTTGCTGACAATTC	
	GAACAGGAGGACATTTCGTACCAAGGAAACAAT	
	CCTTCCCG**C**AGGGAAGG	15
	CCTTCCCG**C**GGGAAGG	16
Glyphosate Resistance	ATTGTTTCCTTGGCACTGACTGGCCACCTGTTCGTGTCAATGGAA	17
EPSPS	TCGGAGGGCTACCTG**C**TGGCAAGGTCAAGCTGTCTGGCTCCATC	
Zea mays	AGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	
Gly168Ala	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA	18

TABLE 10-continued

Genome-Altering Oligos Conferring Glyphosate Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
GGT-GCT	CAGCTTGACCTTGCCA**G**CAGGTAGCCCTCCGATTCCATTGACAC	
	GAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	
	GCTACCTG**C**TGGCAAGG	19
	CCTTGCCA**G**CAGGTAGC	20
Glyphosate Resistance	ACTGTTTCCTTGGCACTGAATGCCCACCTGTTCGTGTCAAGGGA	21
EPSPS	ATTGGAGGACTTCCTG**C**TGGCAAGGTTAAGCTCTCTGGTTCCAT	
Cryza sativa	CAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	
Gly115Ala	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGA	22
GGT-GCT	GAGCTTAACCTTGCCAGCAGGAAGTCCTCCAATTCCCTTGACAC	
	GAACAGGTGGGCATTCAGTGCCAAGGAAACAGT	
	ACTTCCTG**C**TGGCAAGG	23
	CCTTGCCA**G**CAGGAAGT	24
Glyphosate Resistance	AGCCTTCTGAGATAGTGTTGCAACCCATTAAAGAGATTTCAGGCA	25
EPSPS	CTGTTAAATTGCCTGCCTCTAAATCAT-	
	TATCTAATAGAATTCTCCT	
Petunia x hybrida	TCTTGCTGCCTTATCTGAAGGMCAACTGT	
Gly93Ala	ACAGTTGTTCCTTCAGATAAGGCAGCAAGAAGGAGAATTCTATTA	26
GGC-GCC	GATAATGATTTAGAGGCAGGCAATTTAACAGTGCCTGAAATCTCT	
	TTAATGGGTTGCAACACTATCTCAGAAGGCT	
	ATTGCCTGCCTCTAAAT	27
	ATTTAGAG**G**CAGGCAAT	28
Glyphosate Resistance	AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTA	29
EPSPS	CTGTTAAATTACCCG	
	CTTCGAAATCCCTTTCCAATCGTATTCTCCT	
Lycopersicon	TCTTGCTGCCCTTTCTGAGGGAAGGACTGT	
esculentum	ACAGTCCTTCCCTCAGAAAGGGCAGCAAGAAGGAGAATACGATT	30
Gly97Ala	GGAAAGGGATTTCGAA**G**CGGGTAATTTAACAGTACCAGATATATC	
GGT-GCT	TTTGATGGGTNCTAGCACAATCTGATGGGGTT	
	ATTACCCG**C**TTCGAAAT	31
	ATTTCGAA**G**CGGGTAAT	32
Glyphosate Resistance	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTCGKATCAACGGGA	33
EPSPS	TTGGAGGGCTACCTGCTGGCAAGGTTAAGCTGTCTGGTTCCAIT	
Lolium rigidum	AGCAGCCAATACTTGAGTTCCTTGCTGATGGC	
Gly107Ala	GCCATCAGCAAGGAACTCAAGTATTGGCTGCTGATGGAACCAGA	34
GGT-GCT	CAGCTTAACCTTGCCA**G**CAGGTAGCCCTCCAATGCCGTTGATCG	
	AACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	
	GCTACCTG**C**TGGCAAGG	35
	CCTTGCCA**G**CAGGTAGC	36

[0120]

TABLE 11

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA	37
Resistance	ATCACAGGACAAGTC**T**CTCGTCGTATGATTGGTACAGATGCGTTT	
ALS	CAAGAGACTCCGATTGTTGAGGTAACGCGTT	
Arabidopsis thaliana	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC	38
Pro197Ser	CAATCATACGACGAG**A**GACTTGTCCTGTGATTGCTACAAGAGGAA	
CCT-TCT	CACTATCTAACAACGCATCGGCTAATCCGCT	
	GACAAGTCTC**T**CGTCGT	39
	ACGACGAG**A**GACTTGTC	40
Sulfonylurea	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA	41
Resistance	ATCACAGGACAAGTCC**AG**CGTCGTATGATTGGTACAGATGCGTTT	
ALS	CAAGAGACTCCGATTGTTGAGGTAACGCGTT	
Arabidopsis thaliana	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC	42

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Pro197GLN	CAATCATACGACG**C**TGGACTTGTCCTGTGATTGCTACAAGAGGAA	
CCT-CAG	CACTATCTAACAACGCATCGGCTAATCCGCT	
	ACAAGTCC**AG**CGTCGTC	43
	TACGACG**CT**GGACTTGT	44
Sulfonylurea	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA	45
Resistance	ATCACAGGACAAGTCC**AA**CGTCGTATGATTGGTACAGATGCGTTT	
ALS	CAAGAGACTCCGATTGTTGAGGTAACGCGTT	
Arabidopsis thaliana	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC	46
Pro197GLN	CAATCATACGACG**TT**GGACTTGTCCTGTGATTGCTACAAGAGGAA	
CCT-CAA	CACTATCTAACAACGCATCGGCTAATCCGCT	
	ACAAGTCC**AA**CGTCGTA	47
	TACGACG**TT**GGACTTGT	48
Imidazolinone	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT	49
Resistance	TGCCGATGATCCCGA**AC**GGTGGCACTTTCAACGATGTCATAACGG	
ALS	AAGGAGATGGCCGGATTAAATACTGAGAGAT	
Arabidopsis thaliana	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT	50
Ser653Asn	TGAAAGTGCCACC**GT**TCGGGATCATCGGCAACACATGTTCTTGGT	
AGT-AAC	GCGGACAAATCACATCCAACAGGTAAGGTC	
	GATCCCGA**AC**GGTGGCA	51
	TGCCACC**GT**TCGGGATC	52
Imidazolinone	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT	53
Resistance	TGCCGATGATCCCGA**AT**GGTGGCACTTTCAACGATGTCATAACGG	
ALS	AAGGAGATGGCCGGATTAAATACTGAGAGAT	
Arabidopsis thaliana	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT	54
Ser653Asn	TGAAAGTGCCACC**AT**TCGGGATCATCGGCAACACATGTTCTTGGT	
AGT-AAT	GCGGACAAATCACATCCAACAGGTAAGGTC	
	GATCCCGA**AT**GGTGGCA	55
	TGCCACC**AT**TCGGGATC	56
Sulfonylurea	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC	57
Resistance	CATCACGGGCCAGGTC**T**CCCGCCGCATGATCGGCACCGACGCCT	
ALS	TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	
Oryza saliva	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG	58
Pro171Ser	CCGATCATGCGGCGGG**A**GACCTGGCCCGTGATGGCGACCATCG	
CCC-TCC	GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	
	GCCAGGTC**T**CCCGCCGC	59
	GCGGCGGG**A**GACCTGGC	60
Sulfonylurea	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC	61
Resistance	ATCACGGGCCAGGTCC**AA**CGCCGCATGATCGGCACCGACGCCTT	
ALS	CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	
Oryza saliva	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT	
	62	
Pro171Gln	GCCGATCATGCGGCG**TT**GGACCTGGCCCGTGATGGCGACCATCG	
CCC-CAA	GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	
	CCAGGTCC**AA**CGCCGCA	63
	TGCGGCG**TT**GGACCTGG	64
Sulfonylurea	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC	65
Resistance	ATCACGGGCCAGGTCC**AG**CGCCGCATGATCGGCACCGACGCCTT	
ALS	CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	
Oryza saliva	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT	66
Pro171Gln	GCCGATCATGCGGCG**CT**GGACCTGGCCCGTGATGGCGACCATCG	
CCC-CAG	GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	
	CCAGGTCC**AG**CGCCGCA	67
	TGCGGCG**CT**GGACCTGG	68
Imidazolinone	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC	69
Resistance	TGCCTATGATCCCAA**A**TGGGGGCGCATTCAAGGACATGATCCTGG	
ALS	ATGGTGATGGCAGGACTGTGTATTAATCTAT	
Oryza saliva	ATAGATTAATACACAGTCCTGCGATCACCATCCAGGATCATGTCCT	70
Ilee627Asn	TGAATGCGCCCCCA**T**TTGGGATCATAGGCAGCACATGCTCCTGGT	
ATT-AAT	GCGGGACGATGATATCCAACAAGTATGGCC	
	GATCCCAA**A**TGGGGGCG	71
	CGCCCCCA**T**TTGGGATC	72

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS *Zea mays* Pro165Ser CCG-TCG	TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC	73
	CATCACGGGACAGGTG**T**CGCGACGCATGATTGGCACCGACGCCT	
	TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGT	74
	GCCAATCATGCGTCGCG**A**CACCTGTCCCGTGATGGCGACCATGG	
	GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	
	GACAGGTG**T**CGCGACGC	75
	GCGTCGCG**A**CACCTGTC	76
Sulfonylurea Resistance ALS *Zea mays* Pro165Gln CCG-CAG	CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC	77
	ATCACGGGACAGGTGC**A**GCGACGCATGATTGGCACCGACGCCTT	
	CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGG	78
	TGCCAATCATGCGTCGC**T**GCACCTGTCCCGTGATGGCGACCATG	
	GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGG	
	ACAGGTGC**A**GCGACGCA	79
	TGCGTCGC**T**GCACCTGT	80
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT	81
	TGCCTATGATCCCTA**AT**GGTGGGGCTTTCAAGGATATGATCCTGG	
	ATGGTGATGGCAGGACTGTGTACTGATCTAA	
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT	82
	TGAAAGCCCCACC**AT**TAGGGATCATAGGCAACACATGCTCCTGGT	
	GTGGGACGATTATATCCAAGAGGTACGGCC	
	GATCCCTA**AT**GGTGGGG	83
	CCCCACC**AT**TAGGGATC	84
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAC	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT	85
	TGCCTATGATCCCTA**AC**GGTGGGGCTTTCAAGGATATGATCCTGG	
	ATGGTGATGGCAGGACTGTGTACTGATCTAA	
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT	86
	TGAAAGCCCCACC**GT**TAGGGATCATAGGCAACACATGCTCCTGGT	
	GTGGGACGATTATATCCAAGAGGTACGGCC	
	GATCCCTA**AC**GGTGGGG	87
	CCCCACC**GT**TAGGGATC	88
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Ser CCG-TCC	TCCGCGCTCGCCGACGCCGTCCTCGACTCCATCCCCATGGTGGC	89
	CATCACGGGGCAGGTC**T**CGCGCCGCATGATCGGCACGGACGCCT	
	TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGTG	90
	CCGATCATGCGGCGCG**A**GACCTGCCCCGTGATGGCCACCATGG	
	GGATGGAGTVGAGGAGGGCCTCGGCGACCCCCCA	
	GGCAGGTC**T**CGCGCCGC	91
	GCGGCGCG**A**GACCTGCC	92
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Gln CCG-CAG	CCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCC	93
	ATCACGGGGCAGGTCC**A**GCGCCGCATGATCGGCACGGACGCCTT	
	CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGT	94
	GCCGATCATGCGGCGC**T**GGACCTGCCCCGTGATGGCCACCATGG	
	GGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGG	
	GCAGGTCC**A**GCGCCGCA	95
	TGCGGCGC**T**GGACCTGC	96
Imidazolinone Resistance ALS *Lolium multiflorum* Ser623Asn AGC-AAC	CTGGGCCATACTTGTTGGATATCATCGTCCCTCACCAGGAGCATG	97
	TGCTGCCTATGATCCCTA**A**CGGTGGTGCTTTCAAGGACATTATCA	
	TGGAAGGTGATGGCAGGATTTCGTATTAAAC	
	GTTTAATACGAAATCCTGCCATCACCTTCCATGATAATGTCGTTGA	98
	AAGCACCACCG**T**TAGGGATCATAGGCAGCACATGCTCCTGGTGA	
	GGGACGATGATATCCAACAAGTATGGCCCAG	
	GATCCCTA**A**CGGTGGTG	99
	CACCACCG**T**TAGGGATC	100
Sulfonylurea Resistance ALS *Hordeum vulgare* Pro68Ser CCA-TCA	TCCGCGCTCGCCGACGGTCTCCTCGACTCCATCGCCATGGTCGC	101
	CATCACGGGCCAGGTC**T**CACGCCGCATGATCGGCACGGACGCGT	
	TCCAGGAGACGCCCATAGTGGAGGTCACGCGCT	
	AGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTG	102
	CGGATCATGCGGCGTG**A**GACCTGGCCCGTGATGGCGACCATGG	
	GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGGA	

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCCAGGTCTCACGCCGC	103
	GCGGCGTGAGACCTGGC	104
Sulfonyurea	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCC	105
Resistance	ATCACGGGCCAGGTCCAACGCCGCATGATCGGCACGGACGCGTT	
ALS	CCAGGAGACGCCCATAGTGGAGGTCACGCGCTC	
Hordeum vulgare	GAGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGT	106
Pro68Gln	GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATGG	
CCA-CAA	GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGG	
	CCAGGTCCAACGCCGCA	107
	TGCGGCGTTGGACCTGG	108
Imidazolinone	CCCAGGGCCGTACCTGCTGGATATCATTGTCCCGCATCAGGAGC	109
Resistance	ACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTCAAGGACATGA	
ALS	TCATGGAGGGTGATGGCAGGACCTCGTACTGA	
Hordeum vulgare	TCAGTACGAGGTCCTGCCATTCACCCTCCATGATCATGTCCTTGAA	110
Ser524Asn	AGCACCACCGTTTGGGATCATAGGCAGCACGTGCTCCTGATGCG	
AGC-AAC	GGACAATGATATCCAGCAGGTACGGCCCTGGG	
	GATCCCAAACGGTGGTG	111
	CACCACCGTTTGGGATC	112
Sulfonylurea	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG	113
Resistance	ATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTC	
ALS	CAGGAAACTCCAATTGTTGAGGTAACAAGGT	
Gossypium hirsutum	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC	114
Pro186Ser	CGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGG	
CCT-TCT	ATACTATCGAGCATTGCATCAGCGAGACCACT	
	GTCAAGTCTCTCGTCGG	115
	CCGACGAGAGACTTGAC	116
Sulfonylurea	GTGGTCTCGCTGATGCAATGGTCGATAGTATCCCTCTCGTGGCGA	117
Resistance	TCACTGGTCAAGTCCAACGTCGGATGATCGGTACCGATGCTTTCC	
ALS	AGGAAACTCCAATTGTTGAGGTAACAAGGTC	
Gossypium hirsutum	GACCTTGTTACCTCAACAATTGGAGTTICCTGGAAAGCATCGGTA	118
Pro186Gln	CCGATCATCCGACGTTGGACTTGACCAGTGATCGCCACGAGAGG	
CCT-CAA	GATACTATCGAGCATTGCATCAGCGAGACCAC	
	TCAAGTCCAACGTCGGA	119
	TCCGACGTTGGACTTGA	120
Sulfonylurea	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA	121
Resistance	TCACIGGTCAAGTCCAGCGTCGGATGATCGGTACCGATGCTTTCC	
ALS	AGGAAACTCCAATTGTTGAGGTAACAAGGTC	
Gossypium hirsutum	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA	122
Pro186Gln	CCGATCATCCGACGCTGGACTTGACCAGTGATCGCCACGAGAGG	
CCT-CAG	GATACTATCGAGCATTGCATCAGCGAGACCAC	
	TCAAGTCCAGCGTCGGA	123
	TCCGACGCTGGACTTGA	124
Imidazolinone	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCT	125
Resistance	GCCTATGATCCCCAATGGAGGCGCTTTCAAAGATGTGATCACAGA	
ALS	GGGTGATGGAAGAACACAATATTGACCTCA	
Gossypium hirsutum	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTT	126
Ser642Asn	TGAAAGCGCCTCCATTGGGGATCATAGGCAGGACATGTTCTTGAT	
AGT-AAT	GTGGGACAATCACATCCAACAAGTAAGGTC	
	GATCCCCAATGGAGGCG	127
	CGCCTCCATTGGGGATC	128
Sulfonylurea	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA	129
Resistance	TTACTGGGCAAGTTTCCCGGCGTATGATTGGTACTGATGCTTTTCA	
ALS	AGAGACTCCAATTGTTGAGGTAACTCGAT	
Amaranthus retroflexus	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC	130
	AATCATACGCCGGGAAACTTGCCCAGTAATGGCGACAAGAGGGA	
Pro192Ser	CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	
CCC-TCC	GGCAAGTTTCCCGGCGT	131
	ACGCCGGGAAAGTTGCC	132
Sulfonylurea	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT	133
Resistance	TACTGGGCAAGTTCAACGGCGTATGATTGGTACTGATGCTTTTCA	
ALS	AGAGACTCCAATTGTTGAGGTAACTCGATC	

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Amaranthus	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC	134
retroflexus	CAATCATACGCCG**TT**GAACTTGCCCAGTAATGGCGACAAGAGGGA	
Pro192Gln	CTGAGTCAAGAAGTGCATCAGCAAGACCAG	
CCC-CAA	GCAAGTTC**AA**CGGCGTA	135
	TACGCCG**TT**GAACTTGC	136
Sulfonylurea	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT	137
Resistance	TACTGGGCAAG+TC**AG**CGGCGTATGATTGGTACTGATGCTTTTCA	
ALS	AGAGACTCCAATTGTTGAGGTAACTCGATC	
Amaranthus	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC	138
retroflexus	CAATCATACGCCG**CT**GAACTTGCCCAGTAATGGCGACAAGAGGG	
Pro192Gln	ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	
CCC-CAG	GCAAGTTC**AG**CGGCGTA	139
	TACGCCG**CT**GAACTTGC	140
Imidazolinone	GACCGTATCTTGCTGGATGTTAATCG-	141
	TACCACATCAGGAGCATGTGC	
Resistance	TGCCTAIGATCCCT**A**ACGGTGCCGCCTTCAAGGACACCATAACAG	
ALS	AGGGTGATGGAAGAAGGGGTTATTAGTTGGT	
Amaranthus	ACCAACTAATAAGCCCTTCTTCCAT-	142
	TCACCCTCTGTTATGGTGTCCT	
retroflexus	TGAAGGCGGCACCG**T**TAGGGATCATAGGCAGCACATGCTCCTGA	
Ser652Asn	TGTGGTACGATTACATCCAGCAGATACGGTC	
AGC-AAC	GATCCCTA**A**CGGTGCCG	143
	CGGCACCG**T**TAGGGATC	144
Sulfonylurea	AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC	145
Resistance	TATAACAGGTCAAGTG**T**CACGTAGGATGATAGGTACTGATGCTTTT	
ALS 1	CAGGAAACTCCTATTGTITGAGGTAACTAGAT	
Nicotiana tabacum	ATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTACC	146
Pro194Ser	TATCATCCTACGTG**A**CACTTGACCTGTTATAGCAACAATGGGGAC	
CCA-TCA	GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	
	GTCAAGTG**T**CACGTAGG	147
	CCTACGTG**A**CACTTGAC	148
Sulfonylurea	GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT	149
Resistance	ATAACAGGTCAAGTGC**AA**CGTAGGATGATAGGTACTGATGCTTTT	
ALS 1	CAGGAAACTCCTATTGTTGAGGTAACTAGATC	
Nicotiana tabacum	GATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTAC	150
Pro194Gln	CTATCATCCTACGT**T**GCACTTGACCTGTTATAGCAACAATGGGGA	
CCA-CAA	CGCTATCCAGTAGCGCGTCAGCGAGGCCGC	
	TCAAGTGC**A**ACGTAGGA	151
	TCCTACGT**T**GCACTTGA	152
Imidazolinone	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTTT	153
Resistance	ACCTATGATTCCCA**A**TGGCGGAGCTTTCAAAGATGTGATCACAGA	
ALS 1	GGGTGACGGGAGAAGTTCCTATTGAGTTTG	
Nicotiana tabacum	CAAACTGAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT	154
Ser650Asn	TGAAAGCTCCGCCA**T**TGGGAATCATAGGTAAAACATGTTCCTGAT	
AGT-AAT	GAGGTACAATCACATCCAACAAGTATGGCC	
	GATTCCCA**A**TGGCGGAG	155
	CTCCGCCA**T**TGGGAATC	156
Sulfonylurea	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC	157
Resistance	TATAACCGGTCAAGTG**T**CACGTAGGATGATCGGTACTGATGCTTT	
ALS 2	TCAGGAAACTCCGATTGTTGAGGTAACTAGAT	
Nicotiana tabacum	ATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTACC	158
Pro191Ser	GATCATCCTACGTG**A**CACTTGACCGGTTATAGCAACAATGGGGAC	
CCA-TCA	GCTATCCAGTAGGGCGTCCGCGAGGCCACT	
	GICAAGTG**T**CACGTAGG	159
	CCTACGTG**A**CACTTGAC	160
Sulfonylurea	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT	161
Resistance	ATAACCGGTCAAGTGC**A**ACGTAGGATGATCGGTACTGATGCTTTT	
ALS 2	CAGGAAACTCCGATTGTTGAGGTAACTAGATC	
Nicotiana tabacum	GATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTAC	162
Pro191Gln	CGATCATCCTACGT**T**GCACTTGACCGGTTATAGCAACAATGGGGA	

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
CCA-CAA	CGCTATCCAGTAGGGCGTCCGCGAGGCCAC	
	TCAAGTGC**A**ACGTAGGA	163
	TCCTACGT**T**GCACTTGA	164
Imidazolinone	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTCT	165
Resistance	ACCTATGATTCCCA**A**TGGCGGGGCTTTCAAAGATGTGATCACAGA	
ALS 2	GGGTGACGGGAGAAGTTCCTATTGACTTTG	
Nicotiana tabacum	CAAAGTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT	166
Ser647Asn	TGAAAGCCCCGCCA**T**TGGGAATCATAGGTAGAACATGTTCCTGAT	
AGT-AAT	GAGGTACAATCACATCCAACAAGTATGGCC	
	GATTCCCA**A**TGGCGGGG	167
	CCCCGCCA**T**TGGGAATC	168
Sulfonylurea	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTA	169
Resistance	TTACTGGTCAAGTT**T**CCAGGAGAATGATTGGAACAGATGCGTTTC	
ALS	AAGAAACCCCTATTGTTGAGGTAACACGTT	
Xanthium spp.	AACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC	170
Pro175Ser	AATCATTCTCCTGG**A**AACTTGACCAGTAATAGCAACCATTGGAACA	
CCC-TCC	CTGTCTAATAAAGCATCAGCAAGACCACT	
	GTCAAGTT**T**CCAGGAGA	171
	TCTCCTGG**A**AACTTGAC	172
Sulfonylurea	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT	173
Resistance	TACTGGTCAAGTTC**AA**AGGAGAATGATTGGAACAGATGCGTTTCA	
ALS	AGAAACCCCTATTGTTGAGGTAACACGTTC	
Xanthium spp.	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTC	174
Pro175Gln	CAATCATTCTCCT**TT**GAACTTGACCAGTAATAGCAACCATTGGAAC	
CCC-CAA	ACTGTCTAATAAAGCATCAGCAAGACCAC	
	TCAAGTTC**AA**AGGAGAA	175
	TTCTCCT**TT**GAACTTGA	176
Sulfonylurea	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT	177
Resistance	TACTGGTCAAGTTC**AG**AGGAGAATGATTGGAACAGATGCGTTTCA	
ALS	AGAAACCCCTATTGTTGAGGTAACACGTTC	
Xanthium spp.	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTC	178
Pro175Gln	CAATCATTCTCCT**CT**GAACTTGACCAGTAATAGCAACCATTGGAAC	
CCC-CAG	ACTGTCTAATAAAGCATCAGCAAGACCAC	
	TCAAGTTC**AG**AGGAGAA	179
	TTCTCCT**CT**GAACTTGA	180
Imidazolinone	GGGCCTTACTTGTTGGATGTGATCGTGCCCCATCAAGAACATGTG	181
Resistance	TTGCCCATGATCCCG**AA**TGGTGGAGGTTTCATGGATGTGATCACC	
ALS	GAAGGCGACGGCAGAATGAAATATTGAGCTT	
Xanthium spp.	AAGCTCAATATTTCATTCTGCCGTCGCCTTCGGTGATCACATCCAT	182
Ala631Asn	GAAACCTCCACCA**TT**CGGGATCATGGGCAACACATGTTCTTGATG	
GCT-AAT	GGGCACGATCACATCCAACAAGTAAGGCCC	
	TGATCCCG**AA**TGGTGGA	183
	TCCACCA**TT**CGGGATCA	184
Sulfonylurea	TCCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCG	185
Resistance	ATCACGGGGCAGGTG**T**CGCGGCGAATGATTGGGACGGATGCTTT	
ALS	TCAGGAGACTCCTATTGTTGAGGTAACACGGT	
Bassia scoparia	ACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC	186
Pro189Ser	CAATCATTCGCCGCG**A**CACCTGCCCCGTGATCGCCACCAGTGGA	
CCG-TCG	ACGGAATCGAGCAAAGCATCAGCAAACCCGGA	
	GGCAGGTG**T**CGCGGCGA	187
	TCGCCGCG**A**CACCTGCC	188
Sulfonylurea	CCGGGTTTGGTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCGA	189
Resistance	TCACGGGGCAGGTGC**A**GCGGCGAATGATTGGGACGGATGCTTTT	
ALS	CAGGAGACTCCTATTGTTGAGGTAACACGGTC	
Bassia scoparia	GACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTC	190
Pro189Gln	CCAATCATTCGCCGC**T**GCACCTGCCCCGTGATCGCCACCAGTGG	
CCG-CAG	AACGGAATCGAGCAAAGCATCAGCAAACCCGG	
	GCAGGTGC**A**GCGGCGAA	191
	TTCGCCGC**T**GCAGCTGC	192

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone	GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC	193
Resistance	TGCCTATGATTCCTA**A**TGGTGCAGCCTTCAAGGATATCATTAACGA	
ALS	AGGTGATGGAAGAACAAGTTATTGATGTTC	
Bassia scoparia	GAACATCAATAACTTGTTCTTCCATCAC-CTTCGTTAATGATATCCTT	194
Ser649Asn	GAAGGCTGCACCA**T**TAGGAATCATAGGCAGCACATGCTCCTGATG	
AGT-AAT	AGGTACAATCACATCAAGCAGGTAAGGTC	
	GATTCGTA**A**TGGTGCAG	195
	CTGCACCA**T**TAGGAATC	196
Sulfonylurea	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCC	197
Resistance	ATTACAGGACAGGTC**T**CTCGCCGGATGATCGGTACTGACGCCTTC	
ALS 1	CAAGAGACACCAATCGTTGAGGTAACGAGGT	
Brassica napus	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC	198
Pro182Ser	CGATCATCCGGCGAG**A**GACCTGTCCTGTAATGGCGACAAGAGGA	
CCT-TCT	ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	
	GACAGGTC**T**CTCGCCGG	199
	CCGGCGAG**A**GACCTGTC	200
Sulfonylurea	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCA	201
Resistance	TTACAGGACAGGTCC**AA**CGCCGGATGATCGGTACTGACGCCTTC	
ALS 1	CAAGAGACACCAATCGTTGAGGTAACGAGGTC	
Brassica napus	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA	202
Pro182Gln	CCGATCATCCGGCG**TT**GGACCTGTCCTGTAATGGCGACAAGAGG	
CCT-CAA	AACACTGTCAAGCATCGCGTCTGCTAACCCGC	
	ACAGGTCC**AA**CGCCGGA	203
	TCCGGCG**TT**GGACCTGT	204
Sulfonylurea	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCA	205
Resistance	TTACAGGACAGGTCC**AG**CGCCGGATGATCGGTACTGACGCCTTC	
ALS 1	CAAGAGACACCAATCGTTGAGGTAACGAGGTC	
Brassica napus	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA	206
Pro182Gln	CCGATCATCCGGCG**CT**GGACCTGTCCTGTAATGGCGACAAGAGG	
CCT-CAG	AACACTGTCAAGCATCGCGTCTGCTAACCCGC	
	ACAGGTCC**AG**CGCCGGA	207
	TCCGGCG**CT**GGACCTGT	208
Imidazolinone	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT	209
Resistance	TACCGATGATCCCAA**A**TGGTGGCACTTTCAAAGATGTAATAACAG	
ALS 1	AAGGGGATGGTCGCACTAAGTACTGAGAGAT	
Brassica napus	ATCTCTCAGTACTTAGTGCGACCATC-CCCTTCTGTTATTACATCTTT	210
Ser638Asn	GAAAGTGCCACCA**T**TTGGGATCATCGGTAACACATGTTCTTGGTG	
AGT-AAT	CGGACATATCACATCCAACAGGTATGGTC	
	GATCCCAA**A**TGGTGGCA	211
	TGCCACCA**T**TTGGGATC	212
Sulfonylurea	CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGC	213
Resistance	CATTACAGGACAGG**TT**CCTCGCCGGATGATCGGTACTGACGCCTT	
ALS 2	CCAAGAGACACCAATCGTTGAGGTAACGAGG	
Brassica napus	CCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACC	214
Pro126Ser	GATCATCCGGCGAGG**AA**CCTGTCCTGTAATGGCGACAAGAGGAA	
CCC-TCC	CACTGTCAAGCATCGCGTCTGCTAACCCGCTG	
	GGACAGGT**T**CCTCGCCG	215
	CGGCGAGG**A**ACCTGTCC	216
Sulfonylurea	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCC	217
Resistance	ATTACAGGACAGGTC**A**CTCGCCGGATGATCGGTACTGACGCCTTC	
ALS 2	CAAGAGACACCAATCGTTGAGGTAACGAGGT	
Brassica napus	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC	218
Pro126Gln	CGATCATCCGGCGAG**T**GACCTGTCCTGTAATGGCGACAAGAGGA	
CCC-CAG	ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	
	GACAGGTC**A**CTCGCCGG	219
	CCGGCGAG**T**GACCTGTC	220
Imidazolinone	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT	221
Resistance	TACCGATGATCCCAA**AT**GGTGGCACTTTCAAAGATGTAATAACAG	
ALS 2	AAGGGGATGGTCGCACTAAGTACTGAGAGAT	

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Brassica napus	ATCTCTCAGTACTTAGTGCGACCATC-CCCTTCTGTTATTACATCTTT	222
Ser582Asn	GAAAGTGCCACCA**T**TTGGGATCATCGGTAACACATGTTCTTGGTG	
AGT-AAT	CGGACATATCACATCCAACAGGTATGGTC	
	GATCCCAA**A**TGGTGGCA	223
	TGCCACCA**T**TTGGGATC	224
Sulfonylurea	AGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGC	225
Resistance	CATCACAGGACAGGTC**T**CTCGCCGGATGATCGGTACTGACGCGT	
ALS 3	TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT	
Brassica napus	ACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTAC	226
Pro179Ser	CGATCATCCGGCGAG**A**GACCTGTCCTGTGATGGCGACGAGAGGA	
CCT-TCT	ACACTGTCAAGCATCGCGTCGGCTAACCCGCT	
	GACAGGTC**T**CTCGCCGG	227
	CCGGCGAG**A**GACCTGTC	228
Sulfonylurea	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC	229
Resistance	ATCACAGGACAGGTCC**AA**CGCCGGATGATCGGTACTGACGCGTT	
ALS 3	CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	
Brassica napus	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA	230
Pro179Gln	CCGATCATCCGGCG**TT**GGACCTGTCCTGTGATGGCGACGAGAGG	
CCT-CAA	AACACTGTCAAGCATCGCGTCGGCTAACCCGC	
	ACAGGTCC**AA**ee CGCCGGA	231
	TCCGGCG**TT**GGACCTGT	232
Sulfonylurea	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC	233
Resistance	ATCACAGGACAGGTCC**AG**CGCCGGATGATCGGTACTGACGCGTT	
ALS 3	CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	
Brassica napus	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA	234
Pro179Gln	CCGATCATCCGGCG**CT**GGACCTGTCCTGTGATGGCGACGAGAGG	
CCT-CAG	AACACTGTCAAGCATCGCGTCGGCTAACCCGC	
	ACAGGTCC**AG**CGCCGGA	235
	TCCGGCG**CT**GGACCTGT	236
Imidazolinone	GACCGTACCTGTTGGATGTCATCTGTCCGCACCAAGAACATGTGT	237
Resistance	TACOGATGATCCCAA**A**TGGTGGCACTTTCAAAGATGTAATAACCG	
ALS 3	AAGGGGATGGTCGCACTAAGTACTGAGAGAT	
Brassica napus	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCGGTTATTACATCTT	238
Ser635Asn	TGAAAGTGCCACCA**T**TTGGGATCATCGGTAACACATGTTCTTGGT	
AGT-AAT	GCGGACAGATGACATCCAACAGGTACGGTC	
	GATCCCAA**A**TGGTGGCA	239
	TGCCACCA**T**TTGGGATC	240
Sultonylurea	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC	241
Resistance	CATCACGGGCCAGGTC**T**CCCGCCGCATGATCGGCACCGACGCCT	
ALS	TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	
Oryza sativa	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG	242
Pro171 Ser	CCGATCATGCGGCGGG**A**GACCTGGCCCGTGATGGCGACCATCG	
CCC-TCC	GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	
	GCCAGGTC**T**CCCGCCGC	243
	GCGGCGGG**A**GACCTGGC	244
Sulfonylurea	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC	245
Resistance	ATCACGGGCCAGGTCC**AA**CGCCGCATGATCGGCACCGACGCCTT	
ALS	CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	
Oryza sativa	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT	246
Pro171Gln	GCCGATCATGCGGCG**T**ee TGGACCTGGCCCGTGATGGCGAC-CATCG	
CCC-CAA	GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	
	CCAGGTCC**AA**CGCCGCA	247
	TGCGGCG**TT**GGACCTGG	248
Sulfonylurea	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC	249
Resistance	ATCACGGGCCAGGTCC**AG**CGCCGCATGATCGGCACCGACGCCTT	
ALS	CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	
Oryza sativa	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT 250	
Pro171Gln	GCCGATCATGCGGCG**CT**GGACCTGGCCCGTGATGGGGACCATCG	
CCC-CAG	GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCAGGTCC**AG**CGCCGCA	251
	TGCGGCG**CT**GGACCTGG	252
Imidazolinone	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC	253
Resistance	TGCCTATGATCCCAA**AT**GGGGGCGCATTCAAGGACATGATCCTGG	
ALS	ATGGTGATGGCAGGACTGTGTATTAATCTAT	
Oryza sativa	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT	254
Ser627Asn	TGAATGCGCCCCCA**TT**TGGGATCATAGGCAGCACATGCICCTGGI	
AGT-AAT	GCGGGACGATGATATCCAACAAGTATGGCC	
	GATCCCAA**AT**GGGGGCG	255
	CGCCCCGA**TT**TGGGATC	256
Sulfonylurea	TCTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGC	257
Resistance	CATCACGGGACAGGTG**T**CGCGACGCATGATTGGCACCGACGCCT	
ALS	TTCAGGAGACGCCCATCGTCGAGGTCACCCGCT	
Zea mays	AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTG	258
Pro165Ser	CCAATCATGCGTCGCG**A**CACCTGTCCCGTGATGGCGACCATGGG	
CCG-TCG	GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	
	GACAGGTG**T**CGCGACGC	259
	GCGTCGCG**A**CACCTGTC	260
Sulfonylurea	CTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCC	261
Resistance	ATCACGGGACAGGTGC**A**GCGACGCATGATTGGCACCGACGCCTT	
ALS	TCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	
Zea mays	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGT	
	262	
Pro165Gln	GCCAATCATGCGTCGC**T**GCACCTGTCCCGTGATGGCGACCATGG	
CCG-CAG	GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	
	ACAGGTGC**A**GCGACGCA	263
	TGCGTCGC**T**GCACCTGT	264
Imidazolinone	GGCCGTACCTCTTGGATATAATCGTCCCGCACCAGGAGCATGTGT	265
Resistance	TGCCTATGATCCCTA**AT**GGTGGGGCTTTCAAGGATATGATCCTGG	
ALS	ATGGTGATGGCAGGACTGTGTATTGATCCGT	
Zea mays	ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCC	266
Ser621Asn	TTGAAAGCCCCACC**AT**TAGGGATCATAGGCAACACATGCTCCTGG	
AGT-AAT	TGCGGGACGATTATATCCAAGAGGTACGGCC	
	GATCCCTA**AT**GGTGGGG	267
	CCCCACCA**TT**AGGGATC	268
Sulfonylurea	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG	269
Resistance	ATCACTGGICAAGTC**T**CTCGTCGGATGATCGGTACCGATGCTTTC	
ALS	CAGGAAACTCCAATTGTTGAGGTAACAAGGT	
Gossypium hirsutum	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC	270
Pro186Ser	CGATCATCCGACGAG**A**GACTTGACCAGTGATCGCCACGAGAGGG	
CCT-TCT	ATACTATGGAGCATTGCATCAGCGAGACCACT	
	GTCAAGTCTC**T**CGTCGG	271
	CCGACGAGAG**A**CTTGAC	272
Sulfonylurea	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA	273
Resistance	TCACTGGTCAAGTCC**AA**CGTCGGATGATCGGTACCGATGCTTTCC	
ALS	AGGAAACTCCAATTGTTGAGGTAACAAGGTC	
Gossypium hirsutum	GACCTTGTTACCTTAACAATTGGAGTTTCCTGGAAAGCATCGGTA	274
Pro186Gln	CCGATCATCCGACG**TT**GGACTTGACCAGTGATCGCCACGAGAGG	
CCT-CAA	GATACTATCGAGCATTGCATCAGCGAGACCAC	
	TCAAGTCC**AA**CGTCGGA	275
	TTCCGACG**TT**GGACTTGA	276
Sulfonylurea	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGCCGA	277
Resistance	TCACTGGTCAAGTCC**AG**CGTCGGATGATCGGTACCGATGCTTTCC	
ALS	AGGAAACTCCAATTGTTGAGGTAACAAGGTC	
Gossypium hirsutum	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA	278
Pro186Gln	CCGATCATCCGACG**CT**GGACTTGACCAGTGATCGCCACGAGAGG	
CCT-CAG	GATACTATCGAGCATTGCATCAGCGAGACCAC	
	TCAAGTCC**AG**CGTCGGA	279
	TCCGACG**CT**GGACTTGA	280
Imidazolinone	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCT	281
Resistance	GCCTATGATCCCCA**AT**GGAGGGGCTTTCAAAGATGTGATCACAGA	

TABLE 11-continued

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
ALS	GGGTGATGGAAGAACACAATATTGACCTCA	
Gossypium hirsutum	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTT	282
Ser642Asn	TGAAAGCCCCTCCA**T**TGGGGATCATAGGCAGGACATGTTCTTGAT	
AGT-AAT	GTGGGACAATCACATCCAACAAGTAAGGTC	
	GATCCCCA**A**TGGAGGGG	283
	CCCCTCCA**T**ee TGGGGATC	284
Sulfonylurea	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA	285
Resistance	TTACTGGGCAAGTT**T**CCCGGCGTATGATTGGTACTGATGCTTTTCA	
ALS	AGAGACTCCAATTGTTGAGGTAACTCGAT	
Amaranthus powellii	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC	286
Pro192Ser	AATCATACGCCGGG**A**AACTTGCCCAGTAATGGCGACAAGAGGGA	
CCC-TCC	CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	
	GGCAAGTT**T**CCCGGCGT	287
	ACGCCGGG**A**AACTTGCC	288
Sulfonymurea	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT	289
Resistance	TACTGGGC**AA**GTTCAACGGCGTATGATTGGTACTGATGCTTTTCA	
ALS	AGAGACTCCAATTGTTGAGGTAACTCGATC	
Amaranthus powellii	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC	290
Pro192Gln	CAATCATACGCCG**TT**GAACTTGCCCAGTAATGGCGACAAGAGGGA	
CCC-CAA	CTGAGTCAAGAAGTGCATCAGCAAGACCAG	
	GCAAGTTC**AA**CGGCGTA	291
	TACGCCG**TT**GAACTTGC	292
Sulfonylurea	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT	293
Resistance	TACTGGGCAAGTTC**AG**CGGCGTATGATTGGTACTGATGCTTTTCA	
ALS	AGAGACTCCAATTGTTGAGGTAACTCGATC	
Amaranthus powellii	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC	294
Pro192Gln	CAATCATACGCCG**CT**GAACTTGCCCAGTAATGGCGACAAGAGGG	
CCC-CAG	ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	
	GCAAGTTC**AG**CGGCGTA	295
	TACGCCG**CT**GAACTTGC	296
Imidazolinone	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC	297
Resistance	TGCCTATGATCCCTA**A**CGGTGCCGCCTTCAAGGACACCATAACAG	
ALS	AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	
Amaranthus powellii	ACCAACTAATAAGCCCTTCTTCCATCACCCTCTGTTATGGIGTCCT	298
Ser652Asn	TGAAGGCGGCACCG**TT**AGGGATCATAGGCAGCACATGCTCCTGA	
AGC-AAC	TGTGGTACGATTACATCCAGCAGATACGGTG	
	GATCCCTA**A**CGGTGCCG	299
	CGGCACCG**TT**AGGGATC	300

[0121]

TABLE 12

Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide	TCTTGCGCCCTCTTTCTGAATCTGCTGCAAATGCACTCTCAAAACT	301
Resistant	ATATTACCCACCA**AT**G**G**CAGCAGTATCTATCTCGTACCCGAAAGA	
PPO	AGCAATCCGAACAGAATGTTTGATAGATGG	
Arabidopsis thaliana	CCATCTATCAAACATTCTGTTCGGATTGCTTCTTTCGGGTACGAGA	302
Val365Met	TAGATACTGCTG**C**CA**T**TGGTGGGTAATATAGTTTTGAGAGTGCATT	
GTT-ATG	TGCAGCAGATTCAGAAAGAGGGCGCAAGA	
	CCCACCA**AT**G**G**CAGCAG	303
	CTGCTGC**CAT**TGGTGGG	304
Porphyric Herbicide	TATTACGTCCTCTTTCGGTTGCCGCAGCAGATGCACTTTCAAATTT	305
Resistant	CTACTAICCCCCA**AT**G**G**GAGCAGTCACAATTTCATATCCTCAAGAA	
PPO	GCTATTCGTGATGAGCGTCTGGTTGATGG	

TABLE 12-continued

Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Nicotiana tabacum	CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAA	306
Val376Met	ATTGTGACTGCTCC**CATT**GGGGGATAGTAGAAATTTGAAAGTGCA	
GTT-ATG	TCTGCTGCGGCAACCGAAAGAGGACGTAATA	
	TCCCCC**AATG**GGAGCAG	307
	CTGCTCC**CATT**GGGGGA	308
Porphyric Herbicide	TGTTGCGTCCGCTTTCGTTGGGTGCAGCAGATGCATTGTCAAAAT	309
Resistant	TTTATTATCCTCCG**ATG**GCAGCTGTATCAATTTCATATCCAAAAGA	
PPO	CGGAATTCGTGCTGACCGGCTGATTGATGG	
Cichorium intybus	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTTGGATATGAA	310
Val383Met	ATTGATACAGCTGC**CAT**CGGAGGATAATAAAATTTTGACAATGCAT	
GTT-ATG	CTGCTGCACCCAACGAAAGCGGACGCAACA	
	TCCTCCG**ATG**GCAGCTG	311
	CAGCTGC**CAT**CGGAGGA	312
Porphyric Herbicide	TCCTTCGTCCACTTTCAGATGTCGCCGCAGAATCTCTTTCAAAATT	313
Resistant	TCATTATCCACC**AATG**GCAGCTGTGTCACTTTCCTATCCTAAAGAA	
PPO	GCAATTAGATCAGAGTGCTTGATTGACGG	
Spinacia oleracea	CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTTAGGATAGGAAA	314
Val390Met	GTGACACAGCTGC**CAT**TGGTGGATAATGAAATTTTGAAAGAGATT	
GTT-ATG	CTGCGGCGACATCTGAAAGTGGACGAAGGA	
	TCCACC**AATG**GCAGCTG	315
	CAGCTGC**CATT**GGTGGA	316
Porphyric Herbicide	TTTTGCGTCCACTTTCAAGCGATGCTGCAGATGCTCTATCAAGATT	317
Resistant	CTATTATCCACCG**ATG**GCTGCIGTAACTGTTTCGTATCCAAAGGAA	
PPO	GCAATTAGAAAAGAATGCTTAATTGATGG	
Zea mays	CGATCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATACGAAAC	318
Val363Met	AGTTACAGCAGC**CAT**CGGTGGATAATAGAATCTTGATAGAGCATC	
GTT-ATG	TGCAGCATCGCTTGAAAGTGGACGCAAAA	
	TCCACCG**ATG**GCTGCTG	319
	CAGCAGC**CAT**CGGTGGA	320
Porphyric Herbicide	TCTTGCGGCCACTTTCAAGTGATGGAGCAGATGCTCTGTCAATATT	321
Resistant	CTATTATCCACC**AATG**GCTGCTGTAACTGTTTCATATCCAAAAGAA	
PPO	GCAATTAGAAAAGAATGCTTAATTGACGG	
Oryza sativa	CCGTCAATTAAGCATTCTTTTCTAATTGCTTCTTTTGGATATGAAAC	322
Val364Met	AGTTACAGCAGC**CATT**GGTGGATAATAGAATATTGACAGAGCATC	
GTT-ATG	TGCTGCATCACTTGAAAGTGGCCGCAAGA	
	TCCACC**AATG**GCTGCTG	323
	CAGCAGCCA**TT**GGTGGA	324
Porphyric Herbicide	CTGGTCAAGGAGCAGGCGCCCGCCGCCGCCGAGGCCCTGGGCT	325
Resistant	CCTTCGACTACCCGCCG**A**TGGGCGCCGTGACGCTGTCGTACCCG	
PPO	CTGAGCGCCGTGCGGGAGGAGCGCAAGGCCTCGG	
Chlamydomonas	CCGAGGCCTTGCGCTCCTCCCGCACGGCGCTCAGCGGGTACGAC	326
reinhardtii	AGCGTCACGGCGCCC**AT**CGGCGGGTAGTCGAAGGAGCCCAGGG	
Val389Met	CCTCGGCGGCGGCGGGCGCCTGCTCCTTGACCAG	
GTG-ATG	ACCCGCCG**A**TGGGCGCC	327
	GGCGCCC**AT**CGGGGGGT	328

[0122]

TABLE 13

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	329
D1 Protein	TTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTT	
Arabidopsis thaliana	AGCGGCTTGGCCGGTAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA	330
AGT-ACT	CGAGAATIGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAAT	

TABLE 13-continued

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AACCGTGAGCAGCTACAATGTTGTAAGTTT	
	ATATGCTA**C**TTTCAACA	331
	TGTTGAAA**G**TAGCATAT	332
Triazine Resistant	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	333
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC	
Nicotiana tabacum	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAG**G**CCAAGCAGCTAGGAAGAAGTGTAACGAA	334
AGT-ACT	CGAGAGtTGTIGAAA**G**TAGCATATTGGAAGATCAAtCGGCCAAAA	
	TAACCATGAGCGGCTACGATGTTATAAGTTT	
	ATATGCTA**C**TTTCAACA	335
	TGTTGAAA**G**TAGCATAT	336
Triazine Resistant	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	337
D1Protein	CTTCCAATATGCTA**C**TTTTAACAACTCTCGCTCTTTACATTTCTTCT	
Populus deltoides	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG	338
AGT-ACT	CGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCGGCTACGATATTATAAGTTT	
	ATATGCTA**C**TTTTAACA	339
	TGTTAAAA**G**TAGCATAT	340
Triazine Resistant	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	341
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC	
Petunia x hybrida	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA	342
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCGGCTACGATATTATAAGTTT	
	ATATGCTA**C**TTTCAACA	343
	TGTTGAAA**G**TAGCATAT	344
Triazine Resistant	AAACTTATAAIATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT	345
D1Protein	CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCC	
Magnolia pyramidata	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA	346
AGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCAGCTACGATATTATAAGTTT	
	ATATGCTA**C**TTTCAACA	347
	TGTTGAAA**G**TAGCATAT	348
Triazine Resistant	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT	349
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACATTTCTTCC	
Medicago sativa	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA	350
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAAGCATGAGCTGCTACAATATTATAGGTTT	
	ATATGCTA**C**TTTCAACA	351
	TGTTGAAA**G**TAGCATAT	1352
Triazine Resistant	AAACCTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTGAT	353
D1Protein	CTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCT	
Glycine max	TAGCTGCTTGGCCTGTAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA	354
AGT-ACT	CGAGAATTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCAGCTACAATATTATAGGTTT	
	ATATGCAA**C**TTTCAACA	355
	TGTTGAAA**G**TTGCATAT	356
Triazine Resistant	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	357
D1Protein	CTTCCAATATGCT**AC**TTTCAACAATTCTCGTTCTTTACATTTCTTCT	
Brassica napus	TAGCGGCTTGGCCGGTAGTAGGTATTTG	
Gly264Thr	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA	358
GGT-ACT	CGAGAAITGTTGAAA**GT**AGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCGTGAGCAGCTACAATGTTGTAAGTTT	
	ATATGCT**AC**TTTCAACA	359
	TGTTGAAA**GT**AGCATAT	360
Triazine Resistant	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAT	361
D1Protein	CTTCCAATATGCTA**C**TTTTAACAACTCTCGTTCTTTACACTTCTTCT	
Oryza sativa	TGGCTGCTTGGCCTGTAGTAGGGATTTG	
Ser264Thr	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA	362
AGT-ACT	CGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATTAATCGGCCAAAAT	
	AACCATGAGCGGCCACAATATTATAAGTTT	
	ATATGCTA**C**TTTTAACA	363
	TGTTAAAA**G**TAGCATAT	364
Triazine Resistant	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAT	365
D1Protein	CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACACTTCTTCT	
Zea mays	TGGCTGCTtGGCCTGTAGTAGGGATCtG	

TABLE 13-continued

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Ser264Thr	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA	366
AGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATTAATCGACCAAAAT	
	AACCGTGAGCAGCCACAATATTATAAGTCT	
	ATATGCTA**C**TTTCAACA	367
	TGTTGAAA**G**TAGCATAT	368
Triazine Resistant	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	369
D1Protein	TTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTT	
Arabidopsis thaliana	AGCGGCTTGGCCGGTAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA	370
AGT-ACT	CGAGAATTGITGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAAT	
	AACCGTGAGCAGCTACAATGTTGTAAGTTT	
	ATATGCTA**C**TTTCAACA	371
	TGTTGAAA**G**TAGCATAT	372
Triazine Resistant	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	373
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC	
Nicotiana tabacum	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA	374
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCGGCTACGATGTTATAAGTTT	
	ATATGCTA**C**TTTCAACA	375
	TGTTGAAA**G**TAGCATAT	376
Triazine Resistant	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	377
D1Protein	CTTCCAATATGCTA**C**TTTTAACAACTCTCGCTCTTTACATTTCTTCT	
Papulus deltoides	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGGTAAGAAGAAATGTAAAGAG	378
AGT-AGT	CGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCGGCTACGATATTATAAGTTT	
	ATATGCTA**C**TTTTAACA	379
	TGTTAAAA**G**TAGCATAT	380
Triazine Resistant	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	381
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC	
Petunia x hybrida	TAGCTGGTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA	382
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCGGCTACGATATTATAAGTTT	
	ATATGCTA**C**TTTCAACA	383
	TGTTGAAA**G**TAGCATAT	384
Triazine Resistant	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT	385
D1Protein	CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCC	
Magnolia pyramidata	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA	386
AGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCAGCTACGATATTATAAGTTT	
	ATATGCTA**C**TTTCAACA	387
	TGTTGAAA**G**TAGCATAT	388
Triazine Resistant	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT	389
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACATTTGTTCC	
Medicago sativa	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA	390
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCTGCTACAATATTATAGGTTT	
	ATATGCTA**C**TTTCAACA	391
	TGTTGAAA**G**TAGCATAT	392
Triazine Resistant	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT	393
D1Protein	CTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCT	
Glycine max	TAGCTGCTTGGCCTGTAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA	394
AGT-ACT	CGAGAATTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGGCAAAA	
	TAACCATGAGCAGCTACAATATTATAGGTTT	
	ATATGCAA**C**TTTCAACA	395
	TGTTGAAA**G**TTGCATAT	396
Triazine Resistant	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	397
D1Protein	CTTCCAATATGCT**AC**TTTCAACAATTCTCGTTCTTTACATTTCTTCT	
Brassica napus	TAGCGGCTTGGCCGGTAGTAGGTATTTG	
Gly264Thr	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA	398
GGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCGTGAGCAGCTACAATGTTGTAAGTTT	
	ATATGCT**AC**TTTCAACA	399
	TGTTGAAA**GT**AGCATAT	400

TABLE 13-continued

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAT	401
D1Protein	CTTCCAATATGCTA**C**TTTTAACAACTCTCGTTCTTTACACTTCTTCT	
Oryza sativa	TGGCTGCTTGGCCTGTAGTAGGGATTTG	
Ser264Ihr	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA	402
AGT-ACT	CGAGAGTTGTTAAAA**G**TAGCATATTGGAAGATTAATCGGCCAAAAT	
	AACCATGAGCGGCCACAATATTATAAGTTT	
	ATATGCTA**C**TTTTAACA	403
	TGTTAAAA**G**TAGCATAT	404
Triazine Resistant	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAT	405
D1Protein	CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACACTTCTTCT	
Zea mays	TGGCTGCTTGGCCTGTAGTAGGGATCTG	
Ser264Thr	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA	406
AGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATTAATCGACCAAAAT	
	AACCGTGAGCAGCCACAATATTATAAGTCT	
	ATATGCTA**C**TTTCAACA	407
	TGTTGAAA**G**TAGCATAT	408
Triazine Resistant	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	409
D1Protein	TTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTT	
Arabidopsis thaliana	AGCGGCTTGGCCGGTAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA	410
AGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAAT	
	AACCGTGAGCAGCTACAATGTTGTAAGTTT	
	ATATGCTA**C**TTTCAACA	411
	TGTTGAAA**G**TAGCATAT	412
Triazine Resistant	AAACCTACAATATTGTGGCTGCTCACGGTTATTTCGGCCGATTGAT	413
D1Protein	CTTCCAGTATGCTA**C**TTTCAACAACTCCCGTTCTTTACATTTCTTCT	
Picea abies	TAGCTGCTTGGCCCGTAGCAGGTATCTG	
Ser264Thr	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA	414
AGT-ACT	CGGGAGTTGTTGAAA**G**TAGCATACTGGAAGATCAATCGGCCGAAA	
	TAACCGTGAGCAGCCACAATATTGTAGGTTT	
	GTATGCTA**C**TTTCAACA	415
	TGTTGAAA**G**TAGCATAC	416
Triazine Resistant	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	417
D1Protein	CTTCCAATATGCTA**C**TTTCAACAATTCTCGCTCTTTACATTTCTTCC	
Vicia faba	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG	418
AGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCGTGAGCAGCTACAATATTATAGGTTT	
	ATATGCTA**C**TTTCAACA	419
	TGTTGAAA**G**TAGCATAT	420
Triazine Resistant	AGACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAAT	421
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCT	
Hordeum vulgare	TGGCTGCTTGGCCTGTAGTAGGAATCTG	
Ser264Thr	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA	422
AGT-ACT	CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAA	
	TAACCATGAGCAGCCACAATATTATAAGTCT	
	ATATGCTACTTTCAACA	423
	TGTTGAAAGTAGCATAT	424
Triazine Resistant	AAACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAAT	425
D1Protein	CTTCCAATATGCTACTTTCAACAACTCTCGTTCTTTACACTTCTTCT	
Triticum aestivum	TGGCTGCTTGGCCTGTAGTAGGAATCTG	
Ser264Thr	CAGATTCCTACTACAGGCCMGCAGCCAAGAAGAAGTGTAAAGAA	426
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATTAATCGGCCAAAA	
	TAACCATGAGCAGCCACAATATTATAAGTTT	
	ATATGCTA**C**TTTCAACA	427
	TGTTGAAA**G**TAGCATAT	428
Triazine Resistant	AAACTTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTAATC	429
D1Protein	TTCCAATATGCAA**C**TTTCMCAATTCTCGTTCTTTACATTTCTTCCT	
Vigna unguiculata	AGCTGCTTGGCCTGTAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA	430
AGT-ACT	CGAGAATTGTTGAAA**G**TTGCATATTGGAAGATTAATCGGCCAAAAT	
	AACCATGAGCAGCTACAATATTATAAGTTT	
	ATATGCAA**C**TTTCAACA	431
	TGTTGAAA**G**TTGCATAT	432
Triazine Resistant	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	433
D1Protein	CTTCCAATATGCAA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCT	
Lotus japonicus	TAGCTGCTTGGCCTGTTGTAGGTATCTG	
Ser264Thr	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA	434
AGT-ACT	CGAGAGTTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCGTGAGCAGCTACAATATTATAGGTTT	

TABLE 13-continued

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATATGCAA**C**TTTCAACA	435
	TGTTGAAA**G**TTGCATAT	436
Triazine Resistant	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	437
D1Protein	CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCT	
Sinapis alba	TAGCGGCTTGGCCGGTAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA	438
AGT-ACT	CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCGTGAGCAGCTACAATGTTGTAAGTTT	
	ATATGCTA**C**TTTCAACA	439
	TGTTGAAA**G**TAGCATAT	440
Triazine Resistant	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT	441
D1Protein	CTTCCAATATGCTA**C**TTTCAACAATTCTCGCTCTTTACATTTCTTCC	
Pisum sativum	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTIAGGAAGAAATGTAAAGAG	442
AGt-ACT	CGAGAATTGTTGAAAGTAGCAtATTGGAAGATCAATCGGCCAAAA	
	TAACCGTGAGCAGCTACAATATTATAGGTTT	
	ATATGCTA**C**TTTCAACA	443
	TGTTGAAA**G**TAGCATAT	444
Triazine Resistant	AAACTTATAATATCGTAGGTGCTCATGGTTATTTTGGTCGATTGAT	445
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCT	
Spinacia oleracea	TAGCTGCTTGGCCTGIAGTAGGTATTTG	
Ser264Thr	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA	446
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGACCAAAA	
	TAACCATGAGCAGGTACGATATTATAAGTTT	
	ATATGCTA**C**TTTCAACA	447
	TGTTGAAA**G**TAGCATAT	448
Triazine Resistant	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	449
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC	
Nicotiana debneyi	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGAtACCtACTACAGGCGAAGCAGCtAGGAAGAAGTGTAACGAA	450
AGT-ACT	CGAGAGtTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCGGCTACGATGTTATAAGTTT	
	ATATGCTA**C**TTTCAACA	451
	TGTTGAAA**G**TAGCATAT	452
Triazine Resistant	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	453
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC	
Solanum nigrum	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
Ser264Thr	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA	454
AGT-ACT	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
	TAACCATGAGCGGCTACGATATTATAAGTTT	
	ATATGCTA**C**TTTCAACA	455
	TGTTGAAA**G**TAGCATAT	456
Triazine Resistant	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT	457
D1Protein	CTTCCAATATGCTA**C**TTTCAACAACTCTCGTICGTTACACTTCTTCC	
Nicotiana plumbaginifolia	TAGCTGCTTGGCCTGTAGTAGGTATCTG	
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA	458
Ser264Thr	CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA	
AGT-ACT	TAACCATGAGCGGCTACGATGTTATAAGTTT	
	ATATGCTA**C**TTTCAACA	459
	TGTTGAAA**G**TAGCATAT	460

EXAMPLE 6

Engineering Male- or Female-Sterile Plants

[0123] Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, AGAMOUS (AG), APETALA1 (AP1), and APETALA3 (AP3) and PISTILLATA (PI) in *Arabidopsis thaliana,* and DEFICIENS A (DEFA), GLOBOSA (GLO), SQUAMOSA (SQUA), and PLENA (PLE) in *Antirrhinum majus.* Genetic studies have shown that the DEFA, GLO and AP3 genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus,* and maize.

[0124] Altering the expression of these genes results in altered floral morphology. For example, mutations in AP3 and PI result in male-sterile flowers because petals develop in place of stamens.

[0125] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

TABLE 14

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile	TTGTCCTCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAG	461
AP3	AGAAGAATATGGCG**T**GAGGGAAGATCCAGATCAAGAGGATAGAGA	
Arabidopsis thaliana	ACCAGACAAACAGACAAGTGACGTATTCAA	
Arg3Term	TTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATC	462
AGA-TGA	TGGATCTTCCCTC**A**CGCCATATTCTTCTCTCTTIGTTTAATCTTTTT	
	GTTGAAGAGATTTGGTGGAGAGGACAA	
	ATATGGCG**T**GAGGGAAG	463
	CTTCCCTC**A**CGCCATAT	464
Male-sterile	TCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGA	465
AP3	ATATGGCGAGAGGG**T**AGATCCAGATCAAGAGGATAGAGAACCAGA	
Arabidopsis thaliana	CAAACAGACAAGTGACGTATTCAAAGAGAA	
Lys5Term	TTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTC	466
AAG-TAG	TTGATCTGGATCT**A**CCCTCTCGCCATATTCTTCTCTCTTTGTTTAAT	
	CTTTTTGTTGAAGAGATTTGGTGGAGA	
	CGAGAGGG**T**AGATCCAG	467
	CTGGATCT**A**CCGTCTCG	468
Male-sterile	CCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG	469
AP3	CGAGAGGGAAGATC**T**AGATCAAGAGGATAGAGAAGCAGACAAACA	
Arabidopsis thaliana	GACAAGTGACGTATTCAAAGAGAAGGAATG	
Gln7Term	CATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCT	470
CAG-TAG	ATCCTCTTGATCT**A**GATCTTCCCTCTCGCCATATTCTTCTCTCTTTG	
	TTTAATCTTTTTGTTGAAGAGATTTGG	
	GGAAGATC**T**AGATCAAG	471
	CTTGATCT**A**GATCTTCC	472
Male-sterile	CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAG	473
AP3	GGAAGATCCAGATC**T**AGAGGATAGAGAACCAGACAAACAGAGAAG	
Arabidopsis thaliana	TGACGTATTCAAAGAGAAGGAATGGTTTAT	
Lys9Term	ATAAACCATTCGTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGG	474
AAG-TAG	TTCTCTATCCTCT**A**GATCTGGATCTTCCCTCTCGCCATATTCTTCTC	
	TCTTTGTTTAATCTTTTTGTTGAAGAG	
	TCCAGATC**T**AGAGGATA	475
	TATCCTCT**A**GATCTGGA	476
Male-sterile	AGAGGGAAGATCGAGATGAAGAGGATAGAGAACGAGAGGAACCG	477
AP3	ACAAGTGACGTATTCT**T**AGAGAAGAAATGGTTTGTTCAAGAAAGCT	
Brassica oleracea	CACGAGCTTACAGTTTTATGTGATGCTAGGG	
Lys23Term	CCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAACAA	478
AAG-TAG	ACCATTTCTTCTCT**A**AGAATACGTCACTTGTCGGTTGGTCTGGTTC	
	TCTATCCTCTTGATCTGGATCTTCCCTCT	
	CGTATTCT**T**AGAGAAGA	479
	TCTTCTCT**A**AGAATACG	480
Male-sterile	GGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAA	481
AP3	GTGACGTATTCTAAG**T**GAAGAAATGGTTTGTTCAAGAAAGCTCACG	
Brassica oleracea	AGCTTACAGTTTTATGTGATGCTAGGGTTT	
Arg24Term	AAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAA	482
AGA-TGA	CAAACCATTTCTTC**A**CTTAGAATACGTCACTTGTGGGTTGGTCTGG	
	TTCTCTATCCTCTTGATCTGGATCTTCCC	
	ATTCTAAG**T**GAAGAAAT	483
	ATTTCTTC**A**CTTAGAAT	484
Male-sterile	AAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAGTG	485
AP3	ACGTATTCTAAGAGA**T**GAAATGGTTTGTTCAAGAAAGCTCACGAGC	
Brassica oleracea	TTACAGTTTTATGTGATGCTAGGGTTTCGA	
Arg25Term	TCGAAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTT	486
AGA-TGA	GAACAAACCATTTC**A**TCTCTTAGAATACGTCACTTGTCGGTTGGTC	
	TGGTTCTCTATGCTCTTGATCTGGATCTT	
	CTAAGAGA**T**GAAATGGT	487
	ACCATTTC**A**TCTCTTAG	488
Male-sterile	TCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTA	489
AP3	AGAGAAGAAATGGTT**A**GTTCAAGAAAGCTCACGAGCTTACAGTTTT	
Brassica oleracea	ATGTGATGCTAGGGTTTCGATTATCATGTT	
Leu28Term	AACATGATAATCGAAACCCTAGCATCACATAAAACTGTAAGCTCGT	490
TTG-TAG	GAGCTTTCTTGAAC**T**AACCATTTCTTCTCTTAGAATACGTCACTTGT	
	CGGTTGGTCTGGTTCTCTATCCTCTTGA	

TABLE 14-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAATGGTTAGTTCAAGA	491
	TCTTGAACTAACCATTT	492
Male-sterile	GGCTCGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA	493
AP3	CAGGCAGGTCACCTAGTCCAAGAGAAGAAATGGTTTGTTCAAGAA	
Brassica napus	AGCACACGAGCTCTCTGTTCTCTGTGATGCT	
Tyr21Term	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACC	494
TAC-TAG	ATTTCTTCTCTTGGACTAGGTGACCTGCCTGTTTGTTTGGTTCTCTA	
	TCCTCTTAATCTGGATCTTCCCTCGAGCC	
	GTCACCTAGTCCAAGAG	495
	CTCTTGGACTAGGTGAC	496
Male-sterile	CGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGG	497
AP3	CAGGTCACCTACTCCTAGAGAAGAAATGGTTTGTTCAAGAAAGCAC	
Brassica napus	ACGAGCTCTCTGTTCTCTGTGATGCTAAAG	
Lys23Term	CTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAA	498
AAG-TAG	ACCATTTCTTCTCTAGGAGTAGGTGACCTGCCTGTTTGTTTGGTTC	
	TCTATCCTCTTAATCTGGATCTTCCCTCG	
	CCTACTCCTAGAGAAGA	499
	TCTTCTCTAGGAGTAGG	500
Male-sterile	GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAG	501
AP3	GTCACCTACTCCAAGTGAAGAAATGGTTTGTTCAAGAAAGCACACG	
Brassica napus	AGCTCTCTGTTCTCTGTGATGCTAAAGTTT	
Arg24Term	AAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAA	502
AGA-TGA	CAAACCATTTGTTCACTTGGAGTAGGTGACCTGCCTGTTTGTTTGG	
	TTCTCTATCCTCTTAATCTGGATCTTCCC	
	ACTCCAAGTGAAGAAAT	503
	ATTTCTTCACTTGGAGT	504
Male-sterile	AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTC	505
AP3	ACCTACTCCAAGAGATGAAATGGTTTGTTCAAGAAAGCACACGAG	
Brassica napus	CTCTCTGTTCTCTGTGATGCTAAAGTTTCCA	
Arg25Term	TGGAAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTT	506
AGA-TGA	GAACAAACCATTTCATCTCTTGGAGTAGGTGACCTGCCTGTTTGTT	
	TGGTTCTCTATCCTCTTAATCTGGATCTT	
	CCAAGAGATGAAATGGT	507
	ACCATTTCATCTCTTGG	508
Male-sterile	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGG	509
DEFA	TAGTGGTTCGATGGCTTGAGGGAAGATCCAGATTAAGAGGATAGA	
Antirrhinum majus	GAACCAAACAAACAGGCAGGTCACCTACTCCA	
Arg3Term	TGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAAT	510
CGA-TGA	CTGGATCTTCCCTCAAGCCATCGAACCACTACCACTACTGCTCTTG	
	TTTTCTTCTTCCAGCTTTCCTTTCTCTCC	
	CGATGGCTTGAGGGAAG	511
	CTTCCCTCAAGCCATCG	512
Male-sterile	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT	513
DEFA	TCCATGGCTCGAGGGTAGATCCAGATTAAGAGGATAGAGAACCAA	
Antirrhinum majus	ACAAACAGGCAGGTCACCTACTCCAAGAGAA	
Lys5Term	TTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCT	514
AAG-TAG	CTTAATCTGGATCTACCCTCGAGCCATCGAACCACTAGCACTACTG	
	CTCTTGTTTTCTTCTTCCAGCTTTCCTTT	
	CTCGAGGGTAGATCCAG	515
	CTGGATCTACCCTCGAG	516
Male-sterile	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATG	517
DEFA	GCTCGAGGGAAGATCTAGATTAAGAGGATAGAGAACCAAACAAAC	
Antirrhinum majus	AGGCAGGTCACCTACTCCAAGAGAAGAAATG	
Gln7Term	CATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTC	518
CAG-TAG	TATCCTCTTAATCTAGATCTTCCCTCGAGCCATCGAACCACTACCA	
	CTACTGCTCTTGTTTTCTTCTTCCAGCTT	
	GGAAGATCTAGATTAAG	519
	CTTAATCTAGATCTTCC	520
Male-sterile	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGA	521
DEFA	GGGAAGATCCAGATTTAGAGGATAGAGAACCAAACAAACAGGCAG	
Antirrhinum majus	GTCACCTACTCCAAGAGAAGAAATGGTTTGT	
Lys9Term	ACAAACCATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTG	522
AAG-TAG	GTTCTCTATCCTCTAAATCTGGATCTTCCCTCGAGCCATCGAACCA	

TABLE 14-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTACCACTACTGCTCTTGTTTTCTTCTTC	
	TCCAGATTTAGAGGATA	523
	TATCCTCTAAATCTGGA	524
Male-sterile	TCAGTAATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAAC	525
AP3	TATGGCTCGTGGGTAGATCCAGATCAAGAGAATAGAGAACCAAAC	
Nicotiana tabacum	AAACAGACAAGTCACTTATTCTAAGAGAA	
Lys5Term	TTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCTATTCTC	526
AAG-TAG	TTGATCTGGATCTACCCACGAGCCATAGTTTTTTTTTCTTTTTGCTC	
	AAAGTTTGAGATCTTAAGAATTACTGA	
	CTCGTGGGTAGATCCAG	527
	CTGGATCTACCCACGAG	528
Male-sterile	ATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAAACTATGGC	529
AP3	TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAAACAAACAG	
Nicotiana tabacum	ACAAGTCACTTATTCTAAGAGAAGAAATG	
Gln7Term	CATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCT	530
CAG-TAG	ATTCTCTTGATCTAGATCTTCCCACGAGCCATAGTTTTTTTTTCTTT	
	TTGCTCAAAGTTTGAGATCTTAAGAAT	
	GGAAGATCTAGATCAAG	531
	CTTGATCTAGATCTTCC	532
Male-sterile	AAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTG	533
AP3	GGAAGATCCAGATCTAGAGAATAGAGAACCAAACAAACAGACAAG	
Nicotiana tabacum	TCACTTATTCTAAGAGAAGAAATGGACTTT	
Lys9Term	AAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGG	534
AAG-TAG	TTCTCTATTCTCTAGATCTGGATCTTCCCACGAGCCATAGTTTTTTT	
	TTCTTTTTGCTCAAAGTTTGAGATCTT	
	TCCAGATCTAGAGAATA	535
	TATTCTCTAGATCTGGA	536
Male-sterile	ATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTGGGA	537
AP3	AGATCCAGATCAAGTGAATAGAGAACCAAACAAACAGACAAGTCA	
Nicotiana tabacum	CTTATTCTAAGAGAAGAAATGGACTTTTCA	
Arg10Term	TGAAAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTT	538
AGA-TGA	TGGTTCTCTATTCAACTTGATCTGGATCTTCCCACGAGCCATAGTTT	
	TTTTTTCTTTTTGCTCAAAGTTTGAGAT	
	AGATCAAGTGAATAGAG	539
	CTCTATTCACTTGATCT	540
Male-sterile	GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA	541
AP3	CAGACAAGTAACTTAGTCAAAACGAAGGGATGGTCTTTTCAAGAAG	
Medicago sativa	GCCAATGAGCTCACTGTTCTTTGTGATGCT	
Tyr21Term	AGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCA	542
TAC-TAG	TCCCTTCGTTTTGACTAAGTTACTTGTCTGTTCGTTGTGTTCTCTAT	
	TCTCTTGATCTGGATCTTTCCTCGAGCC	
	GTAACTTAGTCAAAACG	543
	CGTTTTGACTAAGTTAC	544
Male-sterile	CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACA	545
AP3	GACAAGTAACTTACTGAAAACGAAGGGATGGTCTTTTCAAGAAGG	
Medicago sativa	CCAATGAGCTCACTGTTCTTTGTGATGCTAA	
Ser22Term	TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGAC	546
TCA-TGA	CATCCCTTCGTTTTCAGTAAGTTACTTGTCTGTTCGTTGTGTTCTCT	
	ATTCTCTTGATCTGGATCTTTCCTCGAG	
	AACTTACTGAAAACGAA	547
	TTCGTTTTCAGTAAGTT	548
Male-sterile	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA	549
AP3	CAAGTAACTTACTCATAACGAAGGGATGGTCTTTTCAAGAAGGCCA	
Medicago sativa	ATGAGCTCACTGTTCTTTGTGATGCTAAGG	
Lys23Term	CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAG	550
AAA-TAA	ACCATCCCTTCGTTATGAGTAAGTTACTTGTCTGTTCGTTGTGTTCT	
	CTATTCTCTTGATCTGGATCTTTCCTCG	
	CTTACTCATAACGAAGG	551
	CCTTCGTTATGAGTAAG	552
Male-sterile	GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA	553
AP3	GTAACTTACTCAAAATGAAGGGATGGTCTTTTCAAGAAGGCCAATG	
Medicago sativa	AGCTCACTGTTCTTTGTGATGCTAAGGTTT	

TABLE 14-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Arg24Term	AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAA	554
CGA-TGA	AAGACCATCCCTTC**A**TTTTGAGTAAGTTACTTGTCTGTTCGTTGTGT	
	TCTCTATTCTCTTGATCTGGATCTTTCC	
	ACTCAAAA**T**GAAGGGAT	555
	ATCCCTTC**A**TTTTGAGT	556
Male-sterile	GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT	557
DEF4	AGGCAAGTGACTTA**G**TCAAAGAGAAGAAATGGGCTATTCAAGAAG	
Solanum tuberosum	GCTAATGAACTTACAGTTCTTTGTGATGCT	
Tyr21Term	AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCA	558
TAT-TAG	TTTCTTCTCTTTGA**C**TAAGTCACTTGCCTATTTGTTTGGTTTTCTATT	
	TTCTTGATCTGGATCTTACCACGAGCC	
	GTGACTTA**G**TCAAAGAG	559
	CTCTTTGA**C**TAAGTCAC	560
Male-sterile	CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG	561
DEF4	GCAAGTGACTTATT**G**AAAGAGAAGAAATGGGCTATTCAAGAAGGC	
Solanum tuberosum	TAATGAACTTACAGTTCTTTGTGATGCTAA	
Ser22Term	TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCC	562
TCA-TGA	CATTTCTTCTCTTT**C**AATAAGTCACTTGCCTATTTGTTTGGTTTTCTA	
	TTTTCTTGATCTGGATCTTACCACGAG	
	GACTTATT**G**AAAGAGAA	563
	TTCTCTTT**C**AATAAGTC	564
Male-sterile	CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGG	565
DEF4	CAAGTGACTTATTCA**T**AGAGAAGAAATGGGCTATTCAAGAAGGCTA	
Solanum tuberosum	ATGAACTTACAGTTCTTTGTGATGCTAAAG	
Lys23Term	CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAG	566
AAG-TAG	CCCATTTCTTCTCT**A**TGAATAAGTCACTTGCCTATTTGTTTGGTTTT	
	CTATTTTCTTGATCTGGATCTTACCACG	
	CTTATTCA**T**AGAGAAGA	567
	TCTTCTCT**A**TGAATAAG	568
Male-sterile	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAA	569
DEF4	GTGACTTATTCAAAG**T**GAAGAAATGGGCTATTCAAGAAGGCTAATG	
Solanum tuberosum	AACTTACAGTTCTTTGTGATGCTAAAGTTT	
Arg24Term	AAACTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAAT	570
AGA-TGA	AGCCCATTTCTTC**A**CTTTGAATAAGTCACTTGCCTATTTGTTTGGTT	
	TTCTATTTTCTTGATCTGGATCTTACC	
	ATTCAAAG**T**GAAGAAAT	571
	ATTTCTTC**A**GTTTGAAT	572
Male-sterile	GCTAATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTAT	573
AP3	GATTTCTAGTACT**T**GAAAACTTCATGAGTTTATAAGTCCCTCTATCA	
Lycopersicon	CGACCAAACAATTGTTCGATCTGTACC	
esculentum	GGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAA	574
Gly27Term	CTCATGAAGTTTTC**A**AGTACTAGAAATCATAACAATTGAAACTTTAG	
GGA-TGA	CATCACAAAGAACAGTAAGTTCATTAGC	
	CTAGTACT**T**GAAAACTT	575
	AAGTTTTC**A**AGTACTAG	576
Male-sterile	AATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGAT	577
AP3	TTCTAGTACTGGA**T**AACTTCATGAGTTTATAAGTCCCTCTATCACGA	
Lycopersicon	CCAAACAATTGTTCGATCTGTACCAGA	
esculentum	TCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTAT	578
Lys28Term	AAACTCATGAAGTT**A**TCCAGTACTAGAAATCATAACAATTGAAACTT	
AAA-TAA	TAGCATCACAAAGAACAGTAAGTTCATT	
	GTACTGGA**T**AACTTCAT	579
	ATGAAGTT**A**TCCAGTAC	580
Male-sterile	ACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTAC	581
AP3	TGGAAAACTTCAT**T**AGTTTATAAGTCCCTCTATCACGACCAAACAAT	
Lycopersicon	TGTTCGATCTGTACCAGAAGACTATTG	
esculentum	CAATAGTCTTCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGA	582
Glu31Term	GGGACTTATAAACT**A**ATGAAGTTTTCCAGTACTAGAAATCATAACA	
GAG-TAG	ATTGAAACTTTAGCATCACAAAGAACAGT	
	AACTTCAT**T**AGTTTATA	583
	TATAAACT**A**ATGAAGTT	584

TABLE 14-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile	ATTGTTATGATTTCTAGTACTGGAAAACTTCATGAGTTTATAAGTCC	585
AP3	CTCTATCACGACC**T**AACAATTGTTCGATCTGTACCAGAAGACTATT	
Lycopersicon	GGAGTTGATATTTGGACTACTCACTATG	
esculentum	CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTCTGGTACAG	586
Lys40Term	ATCGAACAATTGTT**A**GGTCGTGATAGAGGGACTTATAAACTCATGA	
AAA-TAA	AGTTTTCCAGTACTAGAAATCATAACAAT	
	TCACGACC**T**AACAATTG	587
	CAATTGTT**A**GGTCGTGA	588
Male-sterile	GGGGCGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA	589
AP3	ACAGGCAGGTGACCTA**G**TCCAAGCGCCGGTCGGGGATCATGAAG	
Triticum aestivum	AAGGCGCGGGAGCTCACCGTGCTCTGCGACGCC	
Tyr21Term	GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCC	590
TAC-TAG	CCGACCGGCGCTTGGA**C**TAGGTCACCTGCCTGTTGGTGGCGTTCT	
	CGATCCGCTTTATCTCAATCTTCCCCCGCCCC	
	GTGACCTA**G**TCCAAGCG	591
	CGCTTGGA**C**TAGGTCAC	592
Male-sterile	CGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG	593
AP3	GCAGGTGACCTACTCC**T**AGCGCCGGTCGGGGATCATGAAGAAGG	
Triticum aestivum	CGCGGGAGCTCACCGTGCTCTGCGACGCCCAGG	
Lys23Term	CCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATG	594
AAG-TAG	ATCCCCGACCGGCGCT**A**GGAGTAGGTCACCTGCCTGTTGGTGGC	
	GTTCTCGATCCGCTTTATCTCAATCTTCCCCCG	
	CCTACTCC**T**AGCGCCGG	595
	CCGGCGCT**A**GGAGTAGG	596
Male-sterile	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT	597
AP3	ACTCGAAGCGCCGGT**A**GGGGATCATGAAGAAGGCGCGGGAGCTC	
Triticum aestivum	ACCGTGCTCTGCGACGCCCAGGTCGCCATCAT	
Ser26Term	ATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGC	598
TCG-TAG	CTTCTTCATGATCCCC**T**ACCGGCGCTTGGAGTAGGTCACCTGCCT	
	GTTGGTGGCGTTGTCGATCCGCTTTATCTCAA	
	GCGCCGGT**A**GGGGATCA	599
	TGATCCCC**T**ACCGGCGC	600
Male-sterile	CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG	601
AP3	CCGGTCGGGGATCATG**T**AGAAGGCGCGGGAGCTCACCGTGCTCT	
Triticum aestivum	GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	
Lys30Term	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG	602
AAG-TAG	AGCTCCCGCGCCTTCT**A**CATGATCCCCGACCGGCGCTTGGAGTAG	
	GTCACCTGCCTGTTGGTGGCGTTGTCGATCCG	
	GGATCATG**T**AGAAGGCG	603
	CGCCTTCT**A**CATGATCC	604
Male-sterile	GGGGCGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA	605
Silky1	ACCGCCAGGTGACCTA**G**TCCAAGCGCCGGACGGGGATCATGAAG	
Zea mays	AAGGCACGCGAGCTCACCGTGCTCTGCGACGCC	
Tyr21Term	GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATGATCCC	606
TAG-TAG	CGTCCGGCGCTTGGA**C**TAGGTCACCTGGCGGTTGGTGGCGTTCT	
	CGATCGGCTTGATCTCGATCTTGCCGCGCCCC	
	GTGACCTA**G**TCCAAGCG	607
	CGCTTGGA**C**TAGGTCAC	608
Male-sterile	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG	609
Silky1	CCAGGTGACCTACTCC**T**AGCGCCGGACGGGGATCATGAAGAAGG	
Zea mays	CACGCGAGCTCACCGTGCTCTGCGACGCCCAGG	
Lys23Term	CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATG	610
AAG-TAG	ATCCCCGTCCGGCGCT**A**GGAGTAGGTCACCTGGCGGTTGGTGGC	
	GTTCTCGATCCGCTTGATCTCGATCTTGCCGCG	
	CCTACTCC**T**AGCGCCGG	611
	CCGGCGCT**A**GGAGTAGG	612
Male-sterile	CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG	613
Silky1	CCGGACGGGGATCATG**T**AGAAGGCACGCGAGCTCACCGTGCTCT	
Zea mays	GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	
Lys30Term	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG	614
AAG-TAG	AGCTCGCGTGCCTTCT**A**CATGATCCCGGTCCGGCGCTTGGAGTAG	
	GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	

TABLE 14-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGATCATGTAGAAGGCA	615
	TGCCTTCTACATGATCC	616
Male-sterile	ATCGAGAACGCCACCAACCGCCAGGTGACGTACTCCAAGCGCCG	617
Silky1	GACGGGGATCATGAAGTAGGCACGCGAGCTCACCGTGCTCTGCG	
Zea mays	ACGCCCAGGTCGCCATCATCATGTTCTCCTCCA	
Lys31Term	TGGAGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACG	618
AAG-TAG	GTGAGCTCGCGTGCCTACTTCATGATCCCCGTCCGGCGCTTGGAG	
	TAGGTCACCTGGCGGTTGGTGGCGTTCTCGAT	
	TCATGAAGTAGGCACGC	619
	GCGTGCCTACTTCATGA	620
Male-sterile	GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC	621
AP3	GGCCATGGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACG	
Oryza sativa	CGACCAACAGGCAGGTGACCTACTCGAAGCGCC	
Lys5Term	GGCGCTTGGAGTAGGTCACCTGCCTGTTGGTCGCGTTCTCGATCC	622
AAG-TAG	GCTTGATCTCGATCTAGCCCGTCCCCATGGCGGCCCCCTGCAGCA	
	GCTATCTCTCTCGCCGGACAATGCAGCTAGC	
	GGAGGGGCTAGATCGAG	623
	CTCGATCTAGCCCCTCC	624
Male-sterile	TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT	625
AP3	GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACGCGACCA	
Oryza sativa	ACAGGCAGGTGACCTACTCGAAGCGCCGCACGG	
Glu7Term	CCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCT	626
GAG-TAG	CGATCCGCTTGATCTAGATCTTGCCCCTCCCCATGGCCGCCCCCT	
	GCAGCAGCTATCTCTCTCGCCGGACAATGCA	
	GCAAGATCTAGATCAAG	627
	CTTGATCTAGATCTTGC	628
Male-sterile	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGA	629
AP3	GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG	
Oryza sativa	CAGGTGACCTACTCGAAGCGCCGCACGGGGATCA	
Lys9Term	TGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCG	630
AAG-TAG	CGTTCTCGATCCGCTAGATCTCGATCTTGCCCCTCCCCATGGCCG	
	CCCCCTGCAGCAGCTATCTCTCTCGCCGGAC	
	TCGAGATCTAGCGGATC	631
	GATCCGCTAGATCTCGA	632
Male-sterile	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGA	633
AP3	TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT	
Oryza sativa	ACTCGAAGCGCCGCACGGGGATCATGAAGAAGG	
Glu12Term	CCTTCTTCATGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCC	634
GAG-TAG	TGTTGGTCGCGTTCTAGATCCGCTTGATCTCGATCTTGCCCCTCCC	
	CATGGCGGCCCCCTGCAGCAGCTATCTCTC	
	AGCGGATCTAGAACGCG	635
	CGCGTTCTAGATCCGCT	636

[0126]

TABLE 15

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile	TCTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCA	637
AG	GCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCCTCTCC	
Arabidopsis thaliana	CTTGAGGAAATCTGGGAGAGGAAAGATCGAA	
Tyr35Term	TTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCT	638
TAG-TAG	CCTAGGTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAAA	
	ACGTTTAGGGCAAAATTTGATTAGTACAGA	

TABLE 15-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ACGGCGTAGCAATCGGA	639
	TCCGATTGCTACGCCGT	640
Male-sterile AG *Arabidopsis thaliana* Gln36Term CAA-TAA	CTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAG	641
	CAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCCTCTCCCT	
	TGAGGAAATCTGGGAGAGGAAAGATCGAAA	
	TTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCC	642
	TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAA	
	AACGTTTAGGGCAAAATTTGATTAGTACAG	
	CGGCGTACTAATCGGAG	643
	CTCCGATTAGTACGCCG	644
Male-sterile AG *Arabidopsis thaliana* Ser37Term TCG-TAG	ACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAAT	645
	CACGGCGTACCAATAGGAGCTAGGAGGAGATTCCTCTCCCTTGA	
	GGAAATCTGGGAGAGGAAAGATCGAAATCAA	
	TTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAAT	646
	CTCCTCCTAGCTCCTATTGGTACGCCGTGATTGCTGCTCCAAAGC	
	CAAAAACGTTTAGGGCAAAATTTGATTAGT	
	GTACCAATAGGAGCTAG	647
	CTAGCTCCTATTGGTAC	648
Male-sterile AG *Arabidopsis thalana* Glu38Term GAG-TAG	TAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCA	649
	CGGCGTACCAATCGTAGCTAGGAGGAGATTCCTCTCCCTTGAGGA	
	AATCTGGGAGAGGAAAGATCGAAATCAAAC	
	GTTTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGA	650
	ATCTCCTCCTAGCTACGATTGGTACGCCGTGATTGCTGCTCCAAA	
	GCCAAAAACGTTTAGGGCAAAATTTGATTA	
	ACCAATCGTAGCTAGGA	651
	TCCTAGCTACGATTGGT	652
Male-sterile AG *Brassica napus* Glu3Term GAA-TAA	CTCTCCCACTTCTTTTCGGTGGTTTATTCATTTGGTGACGATATCA	653
	CAGAAGCAATGGATTAAGGTGGGAGTAGTCACGATGCAGAGAGT	
	AGCAAGAAGATAGGTAGAGGGAAGATAGAGA	
	TCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTCTGCATCGTGA	654
	CTACTCCCACCTTAATCCATTGCTTCTGTGATATCGTCACCAAATG	
	AATAAACCACCGAAAAGAAGTGGGAGAG	
	CAATGGATTAAGGTGGG	655
	CCCACCTTAATCCATTG	656
Male-sterile AG *Brassica napus* Glu11Term GAG-TAG	TATTCATTTGGTGACGATATCACAGAAGCAATGGATGAAGGTGGG	657
	AGTAGTCACGATGCATAGAGTAGCAAGAAGATAGGTAGAGGGAA	
	GATAGAGATAAAGAGGATAGAGAACACAACAA	
	TTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATC	658
	TTCTTGCTACTCTATGCATCGTGACTACTCCCACCTTCATCCATTG	
	CTTCTGTGATATCGTCACCAAATGAATA	
	ACGATGCATAGAGTAGC	659
	GCTACTCTATGCATCGT	660
Male-sterile AG *Brassica napus* Lys14Term AAG-TAG	GGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCA	661
	CGATGCAGAGAGTAGCTAGAAGATAGGTAGAGGGAAGATAGAGA	
	TAAAGAGGATAGAGAACACAACAAATCGTCAAG	
	CTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCT	662
	GTACCTATCTTCTAGCTACTCTCTGCATCGTGACTACTCCCACCTT	
	CATCCATTGCTTCTGTGATATCGTCACC	
	AGAGTAGCTAGAAGATA	663
	TATCTTCTAGCTAGTCT	664
Male-sterile AG *Brassica napus* Lys15Term AAG-TAG	GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGA	665
	TGCAGAGAGTAGCAAGTAGATAGGTAGAGGGAAGATAGAGATAAA	
	GAGGATAGAGAACACAACAAATCGTCAAGTAA	
	TTACTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTC	666
	CCTCTACCTATCTACTTGCTACTCTCTGCATCGTGACTACTCCCAC	
	CTTCATCCATTGCTTCTGTGATATCGTC	
	GTAGCAAGTAGATAGGT	667
	ACCTATCTACTTGCTAC	668
Male-sterile AG *Lycopersicon esculentum*	CAACCAAAAAACTTAAAAATCTTCTCTTTCCTTTCCTTACAAGGTGA	669
	AGTAATGGACTTCTAAAGTGATCTAACCAGAGAGATCTCACCACAA	
	AGGAAACTAGGAAGGGGGAAAATTGAGA	
	TCTCAATTTTCCCCCTTCCTAGTTTCCTTTGTGGTGAGATCTCTCT	670

TABLE 15-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Glu4Term	GGTTAGATCACTTT**A**GAAGTCCATTACTTCACCTTGTAAGGAAAGG	
CAA-TAA	AAAGAGAAGATTTTTAAGTTTTTTGGTTG	
	TGGACTTC**T**AAAGTGAT	671
	ATCACTTT**A**GAAGTCCA	672
Male-sterile	AAAATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCC	673
AG	AAAGTGATCTAACC**T**GAGAGATCTCACCACAAAGGAAACTAGGAA	
Lycopersicon	GGGGGAAAATTGAGATCAAAAGGATCGAAA	
esculentum	TTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTTTGT	674
Arg9Term	GGTGAGATCTCTC**A**GGTTAGATCACTTTGGAAGTCCATTACTTCAC	
AGA-TGA	CTTGTAAGGAAAGGAAAGAGAAGATTTT	
	ATCTAACC**T**GAGAGATC	675
	GATCTCTC**A**GGTTAGAT	676
Male-sterile	ATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAA	677
AG	GTGATCTAACCAGA**T**AGATCTCACCACAAAGGAAACTAGGAAGGG	
Lycopersicon	GGAAAATTGAGATCAAAAGGATCGAAAACA	
esculentum	TGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTT	678
Glu10Term	TGTGGTGAGATCT**A**TCTGGTTAGATCACTTTGGAAGTCCATTACTT	
GAG-TAG	CACCTTGTAAGGAAAGGAAAGAGAAGAT	
	TAACCAGA**T**AGATCTCA	679
	TGAGATCT**A**TCTGGTTA	680
Male-sterile	CTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT	681
AG	AACCAGAGAGATCT**G**ACCACAAAGGAAACTAGGAAGGGGGAAAA	
Lycopersicon	TTGAGATCAAAAGGATCGAAAACACGACGAA	
esculentum	TTCGTCGTGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAG	682
Ser12Term	TTTCCTTTGTGGT**C**AGATCTCTGTGGTTAGATCACTTTGGAAGTCC	
TCA-TGA	ATTACTTCACCTTGTAAGGAAAGGAAAG	
	AGAGATCT**G**ACCACAAA	683
	TTTGTGGT**C**AGATCTCT	684
Male-sterile	GTACTCTCTATTTTCATCTTCCAACCCTTTCTTTCCTTACCAGGTGA	685
NAG1	AAGTATGGACTTC**T**AAAGTGATCTAACAAGAGAGATCTCTCCACAA	
Nicotiana tabacum	AGGAAACTGGGAAGAGGAAAGATTGAGA	
Gln4Term	TCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCTCTCTT	686
CAA-TAA	GTTAGATCACTTT**A**GAAGTCCATACTTTCACCTGGTAAGGAAAGAA	
	AGGGTTGGAAGATGAAAATAGAGAGTAC	
	TGGACTTC**T**AAAGTGAT	687
	ATCACTTT**A**GAAGTCCA	688
Male-sterile	ATCTTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCC	689
NAG1	AAAGTGATCTAACA**T**GAGAGATCTCTCCACAAAGGAAACTGGGAA	
Nicotiana tabacum	GAGGAAAGATTGAGATCAAACGGATCGAAA	
Arg9Term	TTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTTGT	690
AGA-TGA	GGAGAGATCTCTC**A**TGTTAGATCACTTTGGAAGTCCATACTTTCAC	
	CTGGTAAGGAAAGAAAGGGTTGGAAGAT	
	ATCTAACA**T**GAGAGATC	691
	GATCTCTC**A**TGTTAGAT	692
Male-sterile	TTCCAACCCTTTCTTTCCTTAGCAGGTGAAAGTATGGACTTCCAAA	693
NAG1	GTGATCTAACAAGA**T**AGATCTCTCCACAAAGGAAACTGGGAAGAG	
Nicotiana tabacum	GAAAGATTGAGATCAAACGGATCGAAAACA	
Glu10Term	TGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTT	694
GAG-TAG	TGTGGAGAGATCT**A**TCTTGTTAGATGACTTTGGAAGTCCATACTTT	
	CACCTGGTAAGGAAAGAAAGGGTTGGAA	
	TAACAAGA**T**AGATCTCT	695
	AGAGATCT**A**TCTTGTTA	696
Male-sterile	CTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACAA	697
NAG1	GAGAGATCTCTCCA**T**AAAGGAAACTGGGAAGAGGAAAGATTGAGA	
Nicotiana tabacum	TCAAACGGATCGAAAACACAACGAATCGTC	
Gln14Term	GACGATTCGTTGTGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTT	698
CAA-TAA	CCCAGTTTCCTTT**A**TGGAGAGATCTCTCTTGTTAGATCACTTTGGA	
	AGTCCATACTTTCACCTGGTAAGGAAAG	
	TCTCTCCA**T**AAAGGAAA	699
	TTTCCTTT**A**TGGAGAGA	700
Male-sterile	GCCTATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAA	701
AG	AGAAGATTGGGAAGG**T**GAAAGATCGAGATCAAGCGGATCGAAAA	

TABLE 15-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Rosa hybrida	CACCACCAATCGTCAAGTCACCTTCTGCAAAA	
Gly22Term	TTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCCGCT	702
GGA-TGA	TGATCTGGATCTTTC**A**CCTTCCCAATCTTCTTTGGGCATCAGCGTC	
	CAGGACCGTGTTGGGTTTGTTTTCATAGGC	
	TGGGAAGG**T**GAAAGATC	703
	GATCTTTC**A**CCTTCCCA	704
Male-sterile	TATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGA	705
AG	AGATTGGGAAGGGGA**T**AGATCGAGATCAAGCGGATCGAAAACAC	
Rosa hybrida	CACCAATCGTCAAGTCACCTTCTGCAAAAGGC	
Lys23Term	GCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCC	706
AAG-TAG	GCTTGATCTCGATCT**A**TCCCCTTCCCAATCTTCTTTGGGCATCAGC	
	GTCCAGGACCGTGTTGGGTTTGTTTTCATA	
	GAAGGGGA**T**AGATCGAG	707
	CTCGATCT**A**TCCCCTTC	708
Male-sterile	AACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTG	709
AG	GGAAGGGGAAAGATC**T**AGATCAAGCGGATCGAAAACACCACCAA	
Rosa hybrida	TCGTCAAGTCACCTTCTGCAAAAGGCGCAATG	
Glu25Term	CATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTT	710
GAG-TAG	CGATCCGCTTGATCT**A**GATCTTTCCCCTTCCCAATCTTCTTTGGGC	
	ATCAGCGTCCAGGACCGTGTTGGGTTTGTT	
	GAAAGATC**T**AGATCAAG	711
	CTTGATCT**A**GATCTTTC	712
Male-sterile	CCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAG	713
AG	GGGAAAGATCGAGATC**T**AGCGGATCGAAAACACCACCAATCGTCA	
Rosa hybrida	AGTCACCTTCTGCAAAAGGCGCAATGGTTTGC	
Lys27	GCAAACCATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGG	714
AAG-TAG	TGTTTTCGATCCGCT**A**GATCTCGATCTTTCCCCTTCCCAATCTTCT	
	TTGGGCATCAGCGTCCAGGACCGTGTTGGG	
	TCGAGATC**T**AGCGGATC	715
	GATCCGCT**A**GATCTCGA	716
Male-sterile	CAATTGCGTGTTTTTATTTTTTTTGTTTTTGACTAAGTAGAAATGGC	717
far	GTCTCTAAGCGAT**T**AATCGACCGAGGTATCGCGCGAGAGGAAAAT	
Antirrhinum majus	CGGGAGAGGAAAGATCGAGATCAAACGGA	
Gln7Term	TCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTCTCGGGCGA	718
CAA-TAA	TACCTCGGTCGATT**A**ATCGCTTAGAGACGCCATTTCTACTTAGTCA	
	AAAAGAAAAAAAATAAAAACAGGCAATTG	
	TAAGCGAT**T**AATCGACC	719
	GGTCGATT**A**ATCGCTTA	720
Male-sterile	GTTTTTATTTTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAG	721
far	CGATCAATCGACC**T**AGGTATCGCCCGAGAGGAAAATCGGGAGAG	
Antirrhinum majus	GAAAGATCGAGATCAAACGGATCGAAAACA	
Glu10Term	TGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTC	722
GAG-TAG	TCGGGCGATACCT**A**GGTCGATTGATCGCTTAGAGACGCCATTTCT	
	ACTTAGTCAAAAAGAAAAAAAATAAAAAC	
	AATCGACC**T**AGGTATCG	723
	CGATACCT**A**GGTCGATT	724
Male-sterile	TTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGA	725
far	CCGAGGTATCGCCC**T**AGAGGAAAATCGGGAGAGGAAAGATCGAG	
Antirrhinum majus	ATCAAACGGATCGAAAACAAAACAAATCAAC	
Glu14Term	GTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTC	726
GAG-TAG	CCGATTTTCCTCT**A**GGGCGATACCTCGGTCGATTGATCGCTTAGA	
	GACGCCATTTCTACTTAGTCAAAAAGAAA	
	TATCGCCC**T**AGAGGAAA	727
	TTTCCTCT**A**GGGCGATA	728
Male-sterile	TTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAG	729
far	GTATCGCCCGAGAGG**T**AAATCGGGAGAGGAAAGATCGAGATCAA	
Antirrhinum majus	ACGGATCGAAAACAAAACAAATCAACAGGTTA	
Lys16Term	TAACCTGTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTT	730
AAA-TAA	CCTCTCCCGATTT**A**CCTCTCGGGCGATACCTCGGTCGATTGATCG	
	CTTAGAGACGCCATTTCTACTTAGTCAAA	
	CCGAGAGG**T**AAATCGGG	731
	CCCGATTT**A**CCTCTCGG	732

TABLE 15-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile	TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA	733
AG	AGGAAAGGGTAAGT**A**GCAAATAAAGGGGATGTTCCAGAATCAAGA	
Cucumis sativus	AGAGAAGATGTCAGACTCGCCTCAGAGGAA	
Leu21Term	TTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACA	734
TTG-TAG	TCCCCTTTATTTGC**T**ACTTACCCTTTCCTTCTTCCTTAATCATTCTT GTGAGTGGTGACTGATAATGCTTGGACA	
	GGGTAAGT**A**GCAAATAA	735
	TTATTTGC**T**ACTTACCC	736
Male-sterile	TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAA	737
AG	GGAAAGGGTAAGTTG**T**AAATAAAGGGGATGTTCCAGAATCAAGAA	
Cucumis sativus	GAGAAGATGTCAGACTCGCCTCAGAGGAAGA	
Gln22Term	TCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAA	738
CAA-TAA	CATCCCCTTTATTT**A**CAACTTACCCTTTCCTTCTTCCTTAATCATTC TTGTGAGTGGTGACTGATAATGCTTGGA	
	GTAAGTTG**T**AAATAAAG	739
	CTTTATTT**A**CAACTTAC	740
Male-sterile	CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG	741
AG	GGTAAGTTGCAAAT**A**TAGGGGATGTTCCAGAATCAAGAAGAGAAG	
Cucumis sativus	ATGTCAGACTCGCCTCAGAGGAAGATGGGAA	
Lys24Term	TTCCCATCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATT	742
AAG-TAG	CTGGAACATCCCCT**A**TATTTGCAACTTACCCTTTCCTTCTTCCTTAA TCATTCTTGTGAGTGGTGACTGATAATG	
	TGCAAATA**T**AGGGGATG	743
	CATCCCCT**A**TATTTGCA	744
Male-sterile	CCACTCACAAGAATGATTAAGGAAGAAGGAAAGGGTAAGTTGCAA	745
AG	ATAAAGGGGATGTTC**T**AGAATCAAGAAGAGAAGATGTCAGACTCG	
Cucumis sativus	CCTCAGAGGAAGATGGGAAGAGGAAAGATTG	
Gln28Term	CAATCTTTCCTCTTCCCATCTTCCTCTGAGGCGAGTCTGACATCTT	746
CAG-TAG	CTCTTCTTGATTCT**A**GAACATCCCCTTTATTTGCAACTTACCCTTTC CTTCTTCCTTAATCATTCTTGTGAGTGG	
	GGATGTTC**T**AGAATCAA	747
	TTGATTCT**A**GAACATCC	748
Male-sterile	CCACCACCACCACCACCACCACCACACCATGCTCAACATGAT	749
AG	GACTGATCTGAGCTG**A**GGGCCGTCGTCCAAGGTCAAGGAGCAGG	
Zea mays	TGGCGGCGGCGCCGACGGGCTCCGGCGACAGG	
Cys10Term	CCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCTGCTCCTTGA	750
TGC-TGA	CCTTGGACGACGGCCC**T**CAGCTCAGATCAGTCATCATGTTGAGCA TGGTGTGGTGGTGGTGGTGGTGGTGGTGG	
	CTGAGCTG**A**GGGCCGTC	751
	GACGGCCC**T**CAGCTCAG	752
Male-sterile	ACCACCACCACCACCACCACACCATGCTCAACATGATGACTGATC	753
AG	TGAGCTGCGGGCCGT**A**GTCCAAGGTCAAGGAGCAGGTGGCGGC	
Zea mays	GGCGCCGACGGGCTCCGGCGACAGGCAGGGGCA	
Ser13Term	TGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCT	754
TCG-TAG	GCTCCTTGACCTTGGAC**T**ACGGCCCGCAGCTCAGATCAGTCATCA TGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGT	
	CGGGCCGT**A**GTCCAAGG	755
	CCTTGGAC**T**ACGGCCCG	756
Male-sterile	CACCACCACCACCACACCATGCTCAACATGATGACTGATCTGAGC	757
AG	TGCGGGCCGTCGTCC**T**AGGTCAAGGAGCAGGTGGCGGCGGCGC	
Zea mays	CGACGGGCTCCGGCGACAGGCAGGGGCAGGGGA	
Lys15Term	TCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGC	758
AAG-TAG	CACCTGCTCCTTGACCT**A**GGACGACGGCCCGCAGCTCAGATCAG TCATCATGTTGAGCATGGTGTGGTGGTGGTGGTG	
	CGTCGTCC**T**AGGTCAAG	759
	CTTGACCT**A**GGACGACG	760
Male-sterile	CACCACCACACCATGCTCAACATGATGACTGATCTGAGCTGCGGG	761
AG	CCGTCGTCCAAGGTC**T**AGGAGCAGGTGGCGGCGGCGCCGACGG	
Zea mays	GCTCCGGCGACAGGCAGGGGCAGGGGAGAGGCA	
Lys17Term	TGCCTCTCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCC	762
AAG-TAG	GCCGCCACCTGCTCCT**A**GACCTTGGACGACGGCCCGCAGCTCAG ATCAGTCATCATGTTGAGCATGGTGTGGTGGTG	

TABLE 15-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCAAGGTCTAGGAGCAG	763
	CTGCTCCTAGACCTTGG	764
Male-sterile	TCCTACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA	765
AG	AGAGCATGCACATCTGAGAAGAGGAGGCTACACCATCCACAGTAA	
Zea mays	CAGGCATCATGTCGACCCTGACTTCGGCGG	
Arg4Term	CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT	766
CGA-TGA	GTAGCCTCCTCTTCTCAGATGTGCATGCTCTTGTTCCTATCACACA	
	GATTTTGAGGTCTGAAGGAGAAAAGGTAGGA	
	TGCACATCTGAGAAGAG	767
	CTCTTCTCAGATGTGCA	768
Male-sterile	TACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA	769
AG	GCATGCACATCCGATAAGAGGAGGCTACACCATCCACAGTAACAG	
Zea mays	GCATCATGTCGACCCTGACTTCGGCGGGGC	
Glu5Term	GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT	770
GAA-TAA	GGTGTAGCCTCCTCTTATCGGATGTGCATGCTCTTGTTCCTATCAC	
	ACAGATTTTGAGGTCTGAAGGAGAAAAGGTA	
	ACATCCGATAAGAGGAG	771
	CTCCTCTTATCGGATGT	772
Male-sterile	CTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA	773
AG	TGCACATCCGAGAATAGGAGGCTACACCATCCACAGTAACAGGCA	
Zea mays	TCATGTCGACCCTGACTTCGGCGGGGCAGC	
Glu6Term	GCTGCCCCGCCGAAGTGAGGGTCGACATGATGCCTGTTACTGTG	774
GAG-TAG	GATGGTGTAGCCTCCTATTCTCGGATGTGCATGCTCTTGTTCCTAT	
	CACACAGATTTTGAGGTCTGAAGGAGAAAAG	
	TCCGAGAATAGGAGGCT	775
	AGCCTCCTATTCTCGGA	776
Male-sterile	TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATG	777
AG	CACATCCGAGAAGAGTAGGCTACACCATCCACAGTAACAGGCATC	
Zea mays	ATGTCGACCCTGACTTCGGCGGGGCAGCAGA	
Glu7Term	TCTGCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT	778
GAG-TAG	GTGGATGGTGTAGCCTACTCTTCTCGGATGTGCATGCTCTTGTTC	
	CTATCACACAGATTTTGAGGTCTGAAGGAGAA	
	GAGAAGAGTAGGCTACA	779
	TGTAGCCTACTCTTCTC	780
Male-sterile	GCTGGGTCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGC	781
AG	GAGAAGATGGGGAGGGGGTAGATCGAGATAAAGCGGATCGAGAA	
Oryza sativa	CACGACGAACCGGCAGGTGACCTTCTGCAAGCGCC	
Lys5Term	GGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATC	782
AAG-TAG	CGCTTTATCTCGATCTACCCCCTCCCCATCTTCTCGCTGCTCCCC	
	GCCGCCACCGCCGCCGACGATCCTGACCCAGC	
	GGAGGGGGTAGATCGAG	783
	CTCGATCTACCCCCTCC	784
Male-sterile	TCAGGATCGTCGGCGGGGGTGGCGGCGGGGAGCAGCGAGAAGA	785
AG	TGGGGAGGGGGAAGATCTAGATAAAGCGGATCGAGAACACGACG	
Oryza sativa	AACCGGCAGGTGACCTTCTGCAAGCGCCGCAATG	
GTu7Term	CATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCT	786
GAG-TAG	CGATCCGCTTTATCTAGATCTTCCCCCTCCCCATCTTCTCGCTGCT	
	CCCCGCCGCCACCGCCGCCGACGATCCTGA	
	GGAAGATCTAGATAAAG	787
	CTTTATCTAGATCTTCC	788
Male-sterile	TCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGG	789
AG	AGGGGGAAGATCGAGATATAGCGGATCGAGAACACGACGAACCG	
Oryza sativa	GCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCC	
Lys9Term	GGAGGCCATTGCCGCGCTTGCAGAAGGTCACCTGCCGGTTCGTC	790
AAG-TAG	GTGTTCTCGATCCGCTATATCTCGATCTTCCCCCTCCCCATCTTCT	
	CGCTGCTCCCCGCCGCCACCGCCGCCGACGA	
	TCGAGATATAGCGGATC	791
	GATCCGCTATATCTCGA	792
Male-sterile	GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAG	793
AG	ATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGAC	
Oryza sativa	CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	
Glu12Term	CCTTCTTCAGGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGC	794

TABLE 15-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
GAG-TAG	CGGTTCGTCGTGTTCT**A**GATCCGCTTTATCTCGATCTTCCCCCTCC	
	CCATCTTCTCGCTGCTCCCCGCCGCCACCGC	
	AGCGGATC**T**AGAACACG	795
	CGTGTTCT**A**GATCCGCT	796

[0127]

TABLE 16

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile	GGGAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAA	797
P1	TAGACAAGTTACATA**G**TCAAAGAGAAGAAATGGTATCATCAAAAAA	
Cucumis sativus	GCCAAAGAAATTACTGTTCTTTGCGATGCT	
Tyr21Term	AGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCAT	798
TAT-TAG	TTCTTCTCTTTGA**C**TATGTAACTTGTCTATTGCTTGAGTTCTCTATTC	
	TTTTTATTTCTATTTTCCCTCTTCCC	
	GTTACATA**G**TCAAAGAG	799
	CTCTTTGA**C**TATGTAAC	800
Male-sterile	GAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATA	801
P1	GACAAGTTACATATT**G**AAAGAGAAGAAATGGTATCATCAAAAAAGC	
Cucumis sativus	CAAAGAAATTACTGTTCTTTGCGATGCTCA	
Ser22Term	TGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATAC	802
TCA-TGA	CATTTCTTCTCTTT**C**AATATGTAACTTGTCTATTGCTTGAGTTCTCTA	
	TTGTTTTTATTTCTATTTTCCCTCTTC	
	TACATATT**G**AAAGAGAA	803
	TTCTCTTT**C**AATATGTA	804
Male-sterile	AGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGAC	805
P1	AAGTTAGATATTCA**T**AGAGAAGAAATGGTATCATCAAAAAAGCCAA	
Cucumis sativus	AGAAATTACTGTTCTTTGCGATGCTCAAG	
Lys23Term	CTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATA	806
AAG-TAG	CCATTTCTTCTCT**A**TGAATATGTAACTTGTCTATTGCTTGAGTTCTC	
	TATTCTTTTTATTTCTATTTTCCCTCT	
	CATATTCA**T**AGAGAAGA	807
	TCTTCTCT**A**TGAATATG	808
Male-sterile	GGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAG	809
P1	TTACATATTCAAAG**T**GAAGAAATGGTATCATCAAAAAAGCCAAAGA	
Cucumis sativus	AATTACTGTTCTTTGCGATGCTCAAGTTT	
Arg24Term	AAACTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATG	810
AGA-TGA	ATACCATTTCTTC**A**CTTTGAATATGTAACTTGTCTATTGCTTGAGTT	
	CTCTATTCTTTTTATTTCTATTTTCCC	
	ATTCAAAG**T**GAAGAAAT	811
	ATTTCTTC**A**CTTTGAAT	812
Male-sterile	GGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTGAAGTAA	813
P1	CAGGCAGGTGACCTA**G**TCCAAGAGGAGGAATGGGATTATCAAGAA	
Malus domestica	GGCAAAGGAGATCACTGTTCTATGTGATGCT	
Tyr21Term	AGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATCCCA	814
TAG-TAG	TTCCTCCTCTTGGA**C**TAGGTGACCTGCCTGTTACTTGAGTTCTCAA	
	TCCTCTTGATCTCAACCTTCCCACGTCGC	
	GTGACCTA**G**TGCAAGAG	815
	CTCTTGGA**C**TAGGTCAC	816
Male-sterile	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG	817
P1	CAGGTGACCTACTCC**T**AGAGGAGGAATGGGATTATCAAGAAGGCA	
Malus domestica	AAGGAGATCACTGTTCTATGTGATGCTAAAG	
Lys23Term	CTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATC	818
AAG-TAG	CCATTCCTCCTCT**A**GGAGTAGGTCACCTGCCTGTTACTTGAGTTCT	
	CAATCCTCTTGATCTCAACCTTCCCACG	

TABLE 16-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCTACTCCTAGAGGAGG	819
	CCTCCTCTAGGAGTAGG	820
Male-sterile	AGGATTGAGAAGTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG	821
P1	AGGAATGGGATTATCTAGAAGGCAAAGGAGATGACTGTTCTATGT	
Malus domestica	GATGCTAAAGTATCTCTTATCATTTATTCTA	
Lys30Term	TAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGAT	822
AAG-TAG	CTCCTTTGCCTTCTAGATAATCGCATTCCTCCTCTTGGAGTAGGTC	
	ACCTGCCTGTTACTTGAGTTCTCAATCCT	
	GGATTATCTAGAAGGCA	823
	TGCCTTCTAGATAATCC	824
Male-sterile	ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG	825
P1	AATGGGATTATCAAGTAGGCAAAGGAGATCACTGTTCTATGTGATG	
Malus domestica	CTAAAGTATCTCTTATCATTTATTCTAGCT	
Lys31Term	AGCTAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGT	826
AAG-TAG	GATCTCCTTTGCCTACTTGATAATGCCATTCCTCCTCTTGGAGTAG	
	GTCACCTGCCTGTTACTTGAGTTCTCAAT	
	TTATCAAGTAGGCAAAG	827
	CTTTGCCTACTTGATAA	828
Male-sterile	CATTTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA	829
globosa	AAACAAAAAAATGTGAAGAGGAAAAATTGAGATCAAAAGAATTGAG	
Antirrhinum majus	AACTCAAGCAACAGGCAGGTTACTTACT	
Gly2Term	AGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCA	830
GGA-TGA	ATTTTTCCTCTTCACATTTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTG	
	TTTGCAGATAACTATTGTAAAAATG	
	AAAAAATGTGAAGAGGA	831
	TCCTCTTCACATTTTTT	832
Male-sterile	TTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAA	833
globosa	CAAAAAAATGGGATGAGGAAAAATTGAGATCAAAAGAATTGAGAAC	
Antirrhinum majus	TCAAGCAACAGGCAGGTTACTTACTCAA	
Arg3Term	TTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATC	834
AGA-TGA	TCAATTTTTCCTCATCCCATTTTTTTGTTTTTGTTTTTCTCTCTTGTTT	
	TTGTTTGCAGATAACTATTGTAAAA	
	AAATGGGATGAGGAAAA	835
	TTTTCCTCATCCCATTT	836
Male-sterile	TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACA	837
globosa	AAAAAATGGGAAGATGAAAAATTGAGATCAAAAGAATTGAGAACTC	
Antirthinum majus	AAGCAACAGGCAGGTTACTTACTCAAAGA	
Gly4Term	TCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTG	838
GGA-TGA	ATCTCAATTTTTCATCTTCCCATTTTTTTGTTTTTGTTTTTCTCTCTTG	
	TTTTTGTTTGCAGATAACTATTGTA	
	TGGGAAGATGAAAAATT	839
	AATTTTTCATCTTCCCA	840
Male-sterile	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAA	841
globosa	AAATGGGAAGAGGATAAATTGAGATCAAAAGAATTGAGAACTCAAG	
Antirrhinum majus	CAACAGGCAGGTTACTTACTCAAAGAGAA	
Lys5Term	TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTGTT	842
AAA-TAA	TTGATCTCAATTTATCCTCTTCCCATTTTTTTGTTTTTGTTTTTCTCT	
	CTTGTTTTTGTTTGCAGATAACTATT	
	GAAGAGGATAAATTGAG	843
	CTCAATTTATCCTCTTC	844
Male-sterile	GCTGAGCTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGC	845
P1	AGTATGGGGCGCGGCTAGATCAAGATCAAGAGGATCGAGAACTCT	
Zea mays	ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	
Lys5Term	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC	846
AAG-TAG	TCTTGATCTTGATCTAGCCGCGCCCCATACTGCGTTCTCCACTCCC	
	AAACAGATCCAAGGGCAGCAAGAGCTCAGC	
	GGCGCGGCTAGATGAAG	847
	CTTGATCTAGCCGCGCC	848
Male-sterile	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG	849
P1	GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC	
Zea mays	CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	
Lys7Term	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC	850

TABLE 16-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
AAG-TAG	TCGATCCTCTTGATCT**A**GATCTTGCCGCGCCCCATACTGCGTTCTC	
	CACTCCCAAACAGATCCAAGGGCAGCAAGAG	
	GCAAGATC**T**AGATCAAG	851
	CTTGATCT**A**GATCTTGC	852
Male-sterile	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG	853
P1	GGGCGCGGCAAGATC**T**AGATCAAGAGGATCGAGAACTCTACCAAC	
Zea mays	CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	
Lys9Term	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC	854
AAG-TAG	TCGATCCTCTTGATCT**A**GATCTTGCCGCGCCCCATACTGCGTTCTC	
	CACTCCCAAACAGATCCAAGGGCAGCAAGAG	
	GCAAGATC**T**AGATCAAG	855
	GTTGATCT**A**GATCTTGC	856
Male-sterile	GATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGAT	857
P1	CAAGATCAAGAGGATC**T**AGAACTCTACCAACCGGCAGGTGACCTT	
Zea mays	CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	
Glu12Term	CCTTCTTGACGAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC	858
GAG-TAG	CGGTTGGTAGAGTTCT**A**GATCCTCTTGATCTTGATCTTGCCGCGCC	
	CCATACTGCGTTCTCCACTCCCAAACAGATC	
	AGAGGATC**T**AGAACTCT	859
	AGAGTTCT**A**GATGCTCT	860
Male-sterile	GCTGAGCTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGG	861
P1	AGTATGGGGCGCGGC**T**AGATCGAGATCAAGAGGATCGAGAACTCT	
Zea mays	ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	
Lys5Term	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC	862
AAG-TAG	TCTTGATCTCGATCT**A**GCCGCGCCCCATACTCCGTTCTCCACTCCC	
	TAACAGATTCAAGGGCAGCAAGAGCTCAGC	
	GGCGCGGC**T**AGATCGAG	863
	CTCGATCT**A**GCCGCGCC	864
Male-sterile	CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATG	865
P1	GGGCGCGGCAAGATC**T**AGATCAAGAGGATCGAGAACTCTACCAAC	
Zea mays	CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	
Glu7Term	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC	866
GAG-TAG	TCGATCCTCTTGATCT**A**GATCTTGCCGCGCCCCATACTCCGTTCTC	
	CACTCCCTAACAGATTCAAGGGCAGCAAGAG	
	GCAAGATC**T**AGATCAAG	867
	CTTGATCT**A**GATCTTGC	868
Male-sterile	CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCG	869
P1	CGGCAAGATCGAGATC**T**AGAGGATCGAGAACTCTACCAACCGGCA	
Zea mays	GGTGACCTTCTCCAAGCGCCGGGCCGGACTGG	
Lys9Term	CCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTA	870
AAG-TAG	GAGTTCTCGATCCTCT**A**GATCTCGATCTTGCCGCGCCCCATACTC	
	CGTTCTCCACTCCCTAACAGATTCAAGGGCAG	
	TCGAGATC**T**AGAGGATC	871
	GATCCTCT**A**GATCTCGA	872
Male-sterile	AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT	873
P1	GGAGATGAAGAGGATC**T**AGAACTCTACCAACCGGCAGGTGACCTT	
Zea mays	CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	
Glu12Term	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC	874
GAG-TAG	CGGTTGGTAGAGTTCT**A**GATCCTCTTGATCTCGATCTTGCCGCGC	
	CCCATACTCCGTTCTCCACTCCCTAACAGATT	
	AGAGGATC**T**AGAACTCT	875
	AGAGTTCT**A**GATCCTCT	876
Male-sterile	TTGCTGCTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGG	877
P1	CGGGATGGGGCGCGGG**T**AGATCGAGATCAAGAGGATCGAGAACT	
Oryza sativa	CCACCAACCGCCAGGTGACCTTCTCCAAGCGCA	
Lys5Term	TGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCC	878
AAG-TAG	TCTTGATGTCGATGT**A**CCCGCGCCCCATCCCGCCTCCTCCTCCTC	
	CTCCTCCTTCCTCCAGCTAGCTTAGCAGCAA	
	GGCGCGGG**T**AGATCGAG	879
	CTCGATCT**A**CCCGCGCC	880
Male-sterile	CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGCGGGA	881
P1	TGGGGCGCGGGAAGATC**T**AGATCAAGAGGATCGAGAACTCCACC	

TABLE 16-continued

Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Oryza sativa	AACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG	
Glu7Term	CGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCT	882
GAG-TAG	CGATCCTCTTGATCT**A**GATCTTCCCGCGCCCCATCCCGCCTCCTC	
	CTCCTCCTCCTCCTTCCTCCAGCTAGCTTAG	
	GGAAGATC**T**AGATCAAG	883
	CTTGATCT**A**GATCTTCC	884
Male-sterile	TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGC	885
P1	GCGGGAAGATCGAGATC**T**AGAGGATCGAGAACTCCACCAACCGC	
Oryza sativa	CAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC	
Lys9Term	GGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTG	886
AAG-TAG	GAGTTCTCGATCCTCT**A**GATCTCGATCTTCCCGCGCCCCATCCCG	
	CCTCCTCCTCCTCCTCCTCCTTCCTCCAGCTA	
	TCGAGATC**T**AGAGGATC	887
	GATCCTCT**A**GATCTCGA	888
Male-sterile	GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAG	889
P1	ATCGAGATCAAGAGGATC**T**AGAACTCCACCAACCGCCAGGTGACC	
Oryza sativa	TTCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG	
Glu12Term	CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGC	890
GAG-TAG	GGTTGGTGGAGTTCT**A**GATCCTCTTGATCTCGATCTTCCCGCGCC	
	CCATCCCGCCTCCTCCTCCTCCTCCTTC	
	AGAGGATC**T**AGAACTCC	891
	GGAGTTCT**A**GATCCTCT	892

EXAMPLE 7

Engineering Plants for Abiotic Stress Tolerance

[0128] Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy meals, and extreme temperature, are major factors limiting plant growth and productivity. The worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

[0129] Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing levels of alcohol dehydrogenase can confer enhances flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

[0130] Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

[0131] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

TABLE 17

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance	CGTCTTTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT	893
P5CS	GTGACCGATAGCAGT**GC**TAGAGATAAGGATTTCAGGAAGCAACTT	
Arabidopsis thaliana	AGTGAAACTGTCAAAGCGATGCTGAGGATGA	
Phe128Ala	TCATCCTCAGCATCGCTTTGACAGTTTCACTAAGTTGCTTCCTGAA	894
TTT-GCT	ATCCTTATGTCTA**GC**ACTGCTATCGGTCACAAGCATTTGAGCAACC	
	GTCACATCCAACTACCACACAAAAAGACG	
	ATAGCAGT**GC**TAGAGAT	895
	ATCTCTA**GC**ACTGCTAT	896

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance	GAGAGTATGTTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG	897
P5CS 1	GTGAATGACAGTAGT**GC**CAGAGACAAGGAGTTCAGGAAGCAACTT	
Brassica napus	AATGAGACAGTGAAGTCCATGCTTGATTTGA	
Phe128Ala	TCAAATCAAGCATGGACTTCACTGTCTCATTAAGTTGCTTCCTGAA	898
TTC-GCC	CTCCTTGTCTCTG**GC**ACTACTGTCATTCACCAGCAGCTGAGCAGC	
	CGTCACATCCAGCTGGTCAAACATAGTGTC	
	ACAGTAGT**GC**CAGAGAC	899
	GTCTCTG**GC**ACTACTGT	900
Salt Tolerance	GAGACTATGTTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG	901
P505 2	GTGACTGATAGCAGT**G**TCAGAGATAAGGATTTCAGGAAGCAACTT	
Brassica napus	AGTGAGACAGTCAAAGCTATGCTGAAAATGA	
Phe129Ala	TCATTTTCAGCATAGCTTTGACTGTCTCACTAAGTTGCTTCCTGAA	902
TTC-GCC	ATCCTTATCTCTGA**C**ACTGCTATCAGTCACCAGCATTTGAGCCACC	
	GTCACATCCATCTGGTCAAACATAGTCTC	
	ATAGCAGT**G**TCAGAGAT	903
	ATCTCTGA**C**ACTGCTAT	904
Salt Tolerance	GATATGTTGTTTAACCAACTGGATGTCTCGTCATCTCAACTTCTTG	905
P5GS	TCACCGACAGTGAT**GC**TGAGAACCCAAAGTTCCGGGAGCAACTCA	
Oryza sativa	CTGAAACTGTTGAGTCATTATTAGATCTTA	
Phe128Ala	TAAGATCTAATAATGACTCAACAGTTTCAGTGAGTTGCTCCCGGAA	906
TTT-GCT	CTTTGGGTTCTCA**GC**ATCACTGTCGGTGACAAGAAGTTGAGATGA	
	CGAGACATCCAGTTGGTTAAACAACATATC	
	ACAGTGAT**GC**TGAGAAC	907
	GTTCTCA**GC**ATCACTGT	908
Salt Tolerance	GATATTTTGTTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTTG	909
P5CS	TTACTGACAATGAT**GC**TAGAGACCAAGATTTTAGAAAGCAACTTTC	
Medicago sativa	TGAAACTGTGAGATCACTTCTAGCACTAA	
Phe128Ala	TTAGTGCTAGAAGTGATCTCACAGTTTCAGAAAGTTGCTTTCTAAA	910
TTT-GCT	ATCTTGGTCTCTA**GC**ATCATTGTCAGTAAGAAGAAGCTGAGCAGAT	
	GTCACATCCAGCTGACTAAACAAAATATC	
	ACAATGAT**GC**TAGAGAC	911
	GTCTCTA**GC**ATCATTGT	912
Salt Tolerance	GATACATTGTTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC	913
P5CS	GTTACTGATAATGAT**GC**TAGGGATCCAGAATTCAGGAAGCAACTT	
Actinidia deliciosa	ACTGAAACTGTAGAATCACTATTGAATTTGA	
Phe128Ala	TCAAATTCAATAGTGATTCTACAGTTTCAGTAAGTTGCTTCCTGAAT	914
TTT-GCT	TCTGGATCCCTA**GC**ATCATTATCAGTAACGAGTAGCTGAGCTGAT	
	GTCACATCCAGCTGACTAAACAATGTATC	
	ATAATGAT**GC**TAGGGAT	915
	ATCCCTA**GC**ATCATTAT	916
Salt Tolerance	GACACACTCTTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT	917
P5CS	GTAACAGATAATGAC**GC**CAGAAGTCCAGAATTTAGAAAACAACTTA	
Cichorium intybus	CTGAAACAGTCGATTCTTTATTATCTTATA	
Phe122Ala	TATAAGATAATAAAGAATCGACTGTTTCAGTAAGTTGTTTTCTAAAT	918
TTC-GCC	TCTGGACTTCTG**GC**GTCATTATCTGTTACAAGAAGCTGTGCTGAT	
	GTCACATCCAGTTGACTGAAGAGTGTGTC	
	ATAATGAC**GC**CAGAAGT	919
	ACTTCTG**GC**GTCATTAT	920
Salt Tolerance	GATTCTTTGTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGG	921
P5CS	TGACTGATAATGAC**GC**TAGAGATCCAGATTTTAGGAGACAACTCA	
Lycopersicon	ATGACACAGTAAATTCGTTGCTTTCTCTAA	
esculentum	TTAGAGAAAGCAACGAATTTACTGTGTCATTGAGTTGTCTCCTAAA	922
Phe12BAla	ATCTGGATCTCTA**GC**GTCATTATCAGTCACCAGAAGCTGAGCTGA	
TTT-GCT	TGTCACATCCAACTGACTGAACAAAGAATC	
	ATAATGAC**GC**TAGAGAT	923
	ATCTCTA**GC**GTCATTAT	924
Salt Tolerance	GATACCATGTTCAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTG	925
P5CS	TGAATGATGGATTT**GC**TAGGGATGCTGGCTTCAGAAAACAACTTT	
Vigna unguiculata	CGGACACAGTGAACGCGTTATTAGATTTAA	
Phe162Ala	TTAAATCTAATAACGCGTTCACTGTGTCCGAAAGTTGTTTTCTGAA	926
TTT-GCT	GCCAGCATCCCTA**GC**AAATCCATCATTCACAAGAAGTTGGGAAGA	
	AGTCACATCAAGCTGGCTGAACATGGTATC	

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATGGATTT**GC**TAGGGAT	927
	ATCCCTA**GC**AAATCCAT	928
Salt Tolerance	GACACCTTGTTTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTT	929
P5CS	GTGACGGACAACGAC**GC**TAGAGATCCAAGTTTTAGAACACAACTA	
Mesembryanthemum	ACTGAAACAGTGTATCAGTTGTTGGATCTAA	
crystallinum	TTAGATCCAACAACTGATACACTGTTTCAGTTAGTTGTGTTCTAAA	930
Phe125Ala	ACTTGGATCTCTA**GC**GTCGTTGTCCGTCACAAGCAGCTGAGCAGC	
TTT-GCT	AGTCAGATCCAACTGACTAAACAAGGTGTC	
	ACAACGAC**GC**TAGAGAT	931
	ATCTCTA**GC**GTCGTTGT	932
Salt Tolerance	GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT	933
P5CS	GTGACTGATAATGAT**GC**TAGGGATGAAGCTTTCCGAAATCAACTTA	
Vitis vinifera	CTCAAACAGTGGATTCATTGTTAGCTTTGA	
Phe130Ala	TCAAAGCTAACAATGAATCCACTGTTTGAGTAAGTTGATTTCGGAA	934
TTT-GCT	AGCTTCATCCCTA**GC**ATCATTATCAGTCACAAGAAGCTGAGCTGAT	
	GTCACATCCAGCTGGCTAAATAATGTGTC	
	ATAATGAT**GC**TAGGGAT	935
	ATCCCTA**GC**ATCATTAT	936
Salt Tolerance	GATACGCTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT	937
P5CS	GTGACGGATAACGAT**GC**TCGAGATAAGGATTTCAGGAAGCAGCTT	
Vigna aconitifolia	ACTGAGACTGTGAAGTCGCTGTTGGGGCTGA	
Phe129Ala	TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCCTGA	938
TTT-GCT	AATCCTTATCTCGA**GC**ATCGTTATCCGTCACAAGAAGCTGAGCCG	
	ATGTCACATCGAGCTGAGTGAACAGCGTATC	
	ATAACGAT**GC**TCGAGAT	939
	ATCTCGA**GC**ATCGTTAT	940
Salt Tolerance	AGAGATGTTCTTAGTTCCAAAGAAATCTCACCTCTCAGTTTCTCCG	941
HKT1	TCTTCACAACAGTT**GT**CACGTTTGCAAACTGCGGATTTGTCCCCAC	
Arabidopsis thaliana	GAATGAGAACATGATCATCTTTCGCAAAA	
Ser207Val	TTTTGCGAAAGATGATCATGTTCTCATTCGTGGGGACAAATCCGC	942
TCC-GTC	AGTTTGCAAACGTG**AC**AACTGTTGTGAAGACGGAGAAAGTGAGAG	
	GTGAGATTTCTTTGGAACTAAGAACATCTCT	
	CAACAGTT**GT**CACGTTT	943
	AAACGTG**AC**AACTGTTG	944
Salt Tolerance	CGAATGAGAACATGATCATCTTTCGCAAAAACTCTGGTCTCATCTG	945
HKT1	GCTCCTAATCCCTC**T**AGTACTGATGGGAAACACTTTGTTCCCTTGC	
Arabidopsis thaliana	TTCTTGGTTTTGCTCATATGGGGACTTTA	
Gln237Leu	TAAAGTCCCCATATGAGCAAAACCAAGAAGCAAGGGAACAAAGTG	946
CAA-CTA	TTTCCCATCAGTACT**A**GAGGGATTAGGAGCCAGATGAGACCAGAG	
	TTTTTGCGAAAGATGATCATGTTCTCATTCG	
	AATCCCTC**T**AGTACTGA	947
	TCAGTACT**A**GAGGGATT	948
Salt Tolerance	AGTCTCTAGAAGGAATGAGTTCGTACGAGAAGTTGGTTGGATCGT	949
HKT1	TGTTTCAAGTGGTGA**G**TTCGCGACACACCGGAGAAACTATAGTAG	
Arabidopsis thaliana	ACCTCTCTACACTTTCCCCAGCTATCTTGGT	
Asn332Ser	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTTCT	950
AAT-AGT	CCGGTGTGTCGCGAA**C**TCACCACTTGAAACAACGATCCAACCAAC	
	TTCTCGTACGAACTCATTCCTTCTAGAGACT	
	AGTGGTGA**G**TTCGCGAC	951
	GTCGCGAA**C**TCACCACT	952
Salt Tolerance	AGAGATGTGCTAAAGAAGAAAGGTCTCAAAATGGTGACCTTTTCC	953
HKT1	GTCTTCACCACCGTG**GT**GACCTTTGCCAGTTGTGGGTTTGTCCCG	
Eucalyptus	ACCAATGAAAACATGATTATCTTCAGCAAAA	
camaldulensis	TTTTGCTGAAGATAATCATGTTTTCATTGGTCGGGACAAACCCACA	954
Ser256Val	ACTGGCAAAGGTC**AC**CACGGTGGTGAAGACGGAAAAGGTCACCA	
TCG-GTG	TTTTGAGACCTTTCTTCTTTAGCACATCTCT	
	CCACCGTG**GT**GACCTTT	955
	AAAGGTC**AC**CACGGTGG	956
Salt Tolerance	CCAATGAAAACATGATTATCTTCAGCAAAAACTCTGGCCTCCTCCT	957
HKT1	GATTCTCATCCCTC**T**GGCCCTTCTTGGGAACATGCTGTTCCCATC	
Eucalyptus	GAGCCTACGTTTGACGCTTTGGCTCATCGG	
camaldulensis	CCGATGAGCCAAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT	958

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Gln286Leu	GTTCCCAAGAAGGGCCA**G**AGGGATGAGAATCAGGAGGAGGCCA	
CAG-CTG	GAGTTTTTGCTGAAGATAATCATGTTTTCATTGG	
	CATCCCTC**T**GGCCCTTC	959
	GAAGGGCC**A**GAGGGATG	960
Salt Tolerance	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCGCGC	961
HKT1	TGTTTCAGTGCGTGA**G**CAGCAGACATACCGGCGAGACGGTCGTC	
Eucalyptus	GATCTGTCCACAGTTGCTCCCGCCATCTTGGT	
camaldulensis	ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC	962
Asn381Ser	GCCGGTATGTCTGCTG**C**TCACGCACTGAAACAGCGCGCCCACGA	
AAC-AGC	TTTTCTCACAGGAGCTTAGTCCATTCAACGATT	
	GTGCGTGA**G**CAGCAGAC	963
	GTCTGCTG**C**TCACGCAC	964
Salt Tolerance	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCA	965
HKT1	TTCTCGGTCACGGTC**GT**CTCGTTTGCGAATGTGGGGCTCGTGCC	
Oryza sativa	GACAAATGAGAACATGGCAATCTTCTCCAAGA	
Ser238Val	TCTTGGAGAAGATTGCCATGTTCTCATTTGTCGGCACGAGCCCCA	966
TCC-GTC	CATTCGCAAACGAG**AC**GACCGTGACCGAGAATGAGAAGAGTGCA	
	ATGTTGATCCCTTTCTTCTTCAGTGGAGCTTT	
	TCACGGTC**GT**CTCGTTT	967
	AAACGAG**AC**GACCGTGA	968
Salt Tolerance	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCCTCC	969
HKT1	TCCTGTTCATCGGCC**T**GATTGTTGCAGGCAATACACTTTACCCTCT	
Oryza sativa	CTTCCTAAGGCTATTGATATGGTTCCTGGG	
Gln268Leu	CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTA	970
CAG-CTG	TTGCCTGCAAGAATC**A**GGCCGATGAACAGGAGGAGGAGGCCCGG	
	GTTCTTGGAGAAGATTGCCATGTTCTCATTTG	
	CATCGGCC**T**GATTCTTG	971
	CAAGAATC**A**GGCCGATG	972
Salt Tolerance	CAGTCTTTGATGGACTCAGCTCTTACCAGAAGATTATCAATGCATT	973
HKT1	GTTCATGGCAGTGA**G**CGCAAGGCACTCGGGGGAGAACTCCATCG	
Oryza sativa	ACTGCTCACTCATCGCCCCTGCTGTTCTAGT	
Asn363Ser	ACTAGAACAGCAGGGGCGATGAGTGAGCAGTCGATGGAGTTCTC	974
AAC-AGC	CCCCGAGTGCCTTGCG**C**TCACTGCCATGAACAATGCATTGATAAT	
	CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	
	GGCAGTGA**G**CGCAAGGC	975
	GCCTTGCG**C**TCACTGCC	976
Salt Tolerance	GTGCCCCACTGAACAAGAAAGGGATCAACATCGTGCTCTTCTCAC	977
HKT1	TATCAGTCACCGTTG**T**CTCCTGTGCGAATGCAGGACTCGTGCCCA	
Triticum aestivum	CAAATGAGAACATGGTCATCTTCTCAAAGAA	
Ala240Val	TTCTTTGAGAAGATGACCATGTTCTCATTTGTGGGCACGAGTCCT	978
GCC-GTC	GCATTCGCACAGGAG**A**CAACGGTGAGTGATAGTGAGAAGAGCAC	
	GATGTTGATCCCTTTCTTGTTCAGTGGGGCAC	
	CACCGTTG**T**CTCCTGTG	979
	CACAGGAG**A**CAACGGTG	980
Salt Tolerance	CAAATGAGAACATGGTCATCTTCTCAAAGAATTCAGGCCTCTTGTT	981
HKT1	GCTGCTGAGTGGCC**T**GATGCTCGCAGGCAATACATTGTTCCCTCT	
Triticum aestivum	CTTCCTGAGGCTACTGGTGTGGTTCCTGGG	
Gln270Leu	CCCAGGAACCACACCAGTAGCCTCAGGAAGAGAGGGAACAATGT	982
CAG-CTG	ATTGCCTGCGAGCATC**A**GGCCACTCAGCAGCAACAAGAGGCCTG	
	AATTCTTTGAGAAGATGACCATGTTCTCATTTG	
	GAGTGGCC**T**GATGCTCG	983
	CGAGCATC**A**GGCCACTC	984
Salt Tolerance	CAGTCTTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT	985
HKT1	CTTCATGGTGGTGA**G**TGCGAGGCACTCAGGGGAGAATTCCATCG	
Triticum aestivum	ACTGCTCGCTCATGTCCCCTGCCATTATAGT	
Asn365Ser	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC	986
AAT-AGT	CCTGAGTGCCTCGCA**C**TCACCACCATGAAGAATGCATTGACAGTC	
	TTCTGATAAGAGCTGAGCCCATCAAAGACTG	
	GGTGGTGA**G**TGCGAGGC	987
	GCCTCGCA**C**TCACCACC	988
Freezing Tolerance	TTTTTTTTGTTTTCGTTTTCAAAAAGAAAATCTTTGAATTTTATGGCA	989
praline oxidase	ACCGGTCTTCTC**T**GAACAAACTTTATCCGGCGATCTTACCGTTTAG	

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
precursor	CCGCTTTTAGCCCGGTGGGTCCTCCCA	
Arabidopsis thaliana	TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGC	990
Arg7Term	GGGATAAAGTTTGTTC**A**GAGAAGACGGGTTGCCATAAAATTCAAA	
CGA-TGA	GATTTTGTTTTTGAAAACGAAAACAAAAAAAA	
	GTCTTCTC**T**GAACAAAC	991
	GTTTGTTC**A**GAGAAGAC	992
Freezing Tolerance	TCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCAGAA	993
proline oxidase	CAAACTTTATCCGG**T**GATCTTACCGTTTACCGGCTTTTAGCCCGGT	
precursor	GGGTCCTCCCACCGTGACTGCTTCCACCG	
Arabidopsis thaliana	CGGTGGAAGCAGTCACGGTGGGAGGACCCAGCGGGCTAAAAGC	994
Arg13Term	GGGTAAACGGTAAGATC**A**CCGGATAAAGTTTGTTCTGAGAAGACG	
CGA-TGA	GGTTGCCATAAAATTCAAAGATTTTGTTTTTGA	
	TTATCCGG**T**GATCTTAC	995
	GTAAGATC**A**CCGGATAA	996
Freezing Tolerance	AAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTT	997
praline oxidase	ATCCGGCGATCTTA**G**CGTTTACCCGCTTTTAGCCCGGTGGGTCCT	
precursor	CCCACCGTGACTGCTTCCACCGCCGTCGTC	
Arabidopsis thaliana	GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG	998
Tyr15Term	CTAAAAGCGGGTAAACG**C**TAAGATCGCCGGATAAAGTTTGTTCGG	
TAG-TAG	AGAAGAGGGGTTGCCATAAAATTCAAAGATTTT	
	CGATCTTA**G**CGTTTACC	999
	GGTAAACG**C**TAAGATCG	1000
Freezing Tolerance	CTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTTATCCG	1001
praline oxidase	GCGATCTTACCGTT**A**ACCCGCTTTTAGCCCGGTGGGTCCTCCCAC	
precursor	CGTGACTGCTTCCACCGCCGTCGTCCCGGA	
Arabidopsis thaliana	TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCA	1002
Leu17Term	CCGGGCTAAAAGCGGGT**T**AACGGTAAGATCGGCGGATAAAGTTT	
TTA-TAA	GTTCGGAGAAGACGGGTTGCCATAAAATTCAAAG	
	TTACCGTT**A**ACCCGCTT	1003
	AAGCGGGT**T**AACGGTAA	1004
Freezing Tolerance	CCGGTGGGTCCTCCCACCGTGACTGCTTCCAGCGCCGTGGTCCC	1005
proline oxidase	GGAGATTCTCTCCTTT**T**GACAACAAGCACCGGAACCACCTCTTCA	
precursor	CCACCCAAAACCCACCGAGCAATCTCACGATG	
Arabidopsis thaliana	CATCGTGAGATTGCTCGGTGGGTTTTGGGTGGTGAAGAGGTGGT	1006
Gly42Term	TCCGGTGCTTGTTGTC**A**AAAGGAGAGAATCTCCGGGACGACGGC	
GGA-TGA	GGTGGAAGCAGTCACGGTGGGAGGACCCACCGG	
	TCTCCTTT**T**GACAACAA	1007
	TTGTTGTC**A**AAAGGAGA	1008
Lead Tolerance	ACATGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCT	1009
cyclic nucleotide-	AAACTATGAATTTC**T**GACAAGAGAAGTTTGTAAGGTCAGTGTTCCA	
regulated ion channel	GATTTGTCTCATTGAATTCTAAGTCGTGA	
Arabidopsis thaliana	TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTAC	1010
Arg4Term	AAACTTCTCTTGTC**A**GAAATTCATAGTTTGAGACTAATAAGATTCAA	
CGA-TGA	TACAAACAGAGATTTCACTGCTTCATGT	
	TGAATTTC**T**GACAAGAG	1011
	CTCTTGTC**A**GAAATTCA	1012
Lead Tolerance	TGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAA	1013
cyclic nucleotide-	CTATGAATTTCCGA**T**AAGAGAAGTTTGTAAGGTCAGTGTTCCAGAT	
regulated ion channel	TTGTCTCATTGAATTCTAAGTCGTGAAGC	
Arabidopsis thaliana	GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCT	1014
Gln5Term	TACAAACTTCTCTT**A**TCGGAAATTCATAGTTTGAGACTAATAAGATT	
CAA-TAA	CAATACAAACAGAGATTTCACTGCTTCA	
	ATTTCCGA**T**AAGAGAAG	1015
	CTTCTCTT**A**TCGGAAAT	1016
Lead Tolerance	AGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTAT	1017
cyclic nucleotide-	GAATTTCCGACAA**T**AGAAGTTTGTAAGGTCAGTGTTCCAGATTTGT	
regulated ion channel	CTCATTGAATTCTAAGTCGTGAAGCTTA	
Arabidopsis thaliana	TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGA	1018
Glu6Term	CCTTACAAACTTCT**A**TTGTCGGAAATTCATAGTTTGAGACTAATAA	
GAG-TAG	GATTCAATACAAACAGAGATTTCACTGCT	
	TCCGACAA**T**AGAAGTTT	1019
	AAACTTCT**A**TTGTCGGA	1020

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Lys7Term AAG-TAG	AGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTATGAA	1021
	TTTCCGACAAGAGTAGTTTGTAAGGTCAGTGTTCCAGATTTGTCTC	
	ATTGAATTCTAAGTCGTGAAGCTTAATT	
	AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACAC	1022
	TGACCTTACAAACTACTCTTGTCGGAAATTCATAGTTTGAGACTAA	
	TAAGATTCAATACAAACAGAGATTTCACT	
	GACAAGAGTAGTTTGTA	1023
	TACAAACTACTCTTGTC	1024
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTCGATTCTTCTTCACTTTC	1025
	TCGGATCAGGTTTTAAGATTGGAAGTCGGATAAGACTTCCTCCGA	
	CGTGGAATATTCCGGTAAAAACGAGATTC	
	GAATCTCGTTTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATC	1026
	CGACTTCCAATCTTAAAACCTGATCCGAGAAAGTGAAGAAGAATC	
	GAATTAAGCTTCACGACTTAGAATTCAATG	
	TCAGGTTTTAAGATTGG	1027
	CCAATCTTAAAACCTGA	1028
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln5Term CAA-TAA	TGGAAGTCAATCCCCCACGTTGAGCAGGTTGATGCATTGGGTAAA	1029
	GTTATGAATCACCGCTAAGACGAGTTTGTGAGGTTTCAGGATTGG	
	AAATCAGAGAGAAGCTCTGAGGGAAATTTTC	
	GAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTGAAACCT	1030
	CACAAACTCGTCTTAGCGGTGATTCATAACTTTAGCCAATGCATCA	
	ACCTGCTCAACGTGGGGGATTGACTTCCA	
	ATCACCGCTAAGACGAG	1031
	CTCGTCTTAGCGGTGAT	1032
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gly7Term GAG-TAG	TCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG	1033
	AATCACCGCCAAGACTAGTTTGTGAGGTTTCAGGATTGGAAATCA	
	GAGAGAAGCTCTGAGGGAAATTTTCATGCTA	
	TAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTG	1034
	AAACCTCACAAACTAGTCTTGGCGGTGATTCATAACTTTAGCCAAT	
	GCATCAACCTGCTCAACGTGGGGGATTGA	
	GCCAAGACTAGTTTGTG	1035
	CACAAACTAGTCTTGGC	1036
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC	1037
	GAGTTTGTGAGGTTTTAGGATTGGAAATCAGAGAGAAGCTCTGAG	
	GGAAATTTTCATGCTAAAGGTGGAGTCCACC	
	GGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTC	1038
	TGATTTCCAATCCTAAAACCTCACAAACTCGTCTTGGCGGTGATTC	
	ATAACTTTAGCCAATGCATCAACCTGCTC	
	TGAGGTTTTAGGATTGG	1039
	CCAATCCTAAAACCTCA	1040
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGT	1041
	GAGGTTTCAGGATTGTAAATCAGAGAGAAGCTCTGAGGGAAATTT	
	TCATGCTAAAGGTGGAGTCCACCGAAGTAAA	
	TTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAG	1042
	CTTCTCTCTGATTTACAATCCTGAAACCTCACAAACTCGTCTTGGC	
	GGTGATTCATAACTTTAGCCAATGCATCA	
	CAGGATTGTAAATCAGA	1043
	TCTGATTTACAATCCTG	1044
Lead Tolerance cyclic nucleotide-gated calmoduin-binding ion channel (CBP4) *Nicotiana Tabacum* Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTG	1045
	AGGTTTCAGGATTGGTAATCAGAGAGAAGCTGTGAGGGAAATTTT	
	CATGCTAAAGGTGGAGTCCACCGAAGTAAAG	
	CTTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGA	1046
	GCTTCTCTCTGATTACCAATCCTGAAACCTCACAAACTCGTCTTGG	
	CGGTGATTCATAACTTTAGCCAATGCATC	
	AGGATTGGTAATCAGAG	1047
	CTCTGATTACCAATCCT	1048
Lead Tolerance calmoduin binding transport protein *Hordeum vulgare* Glu2Term GAA-TAA	CTTGAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGG	1049
	TGGAGATAATGATGTAAAGAGAGGACAGATATGTTAGATTTCAGG	
	ACTGCAAATCAGAGCAATCTGTTATCTCAG	
	CTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATGTAACATA	1050
	TCTGTCCTCTCTTTACATCATTATCTCCACCAGGCGAACAGTTAGC	
	AGCTAAGAGTGGTAGATCAATTCTTCAAG	

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TAATGATGTAAAGAGAG	1051
	CTCTCTTTACATCATTA	1052
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Arg3Term AGA-TGA	GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTG GAGATAATGATGGAATGAGAGGACAGATATGTTAGATTTCAGGAC TGCAAATCAGAGCAATCTGTTATCTCAGAGA	1053
	TCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAAC ATATCTGTCCTCTCATTCCATCATTATCTCCACCAGGCGAACAGTT AGCAGCTAAGAGTGGTAGATCAATTCTTC	1054
	TGATGGAATGAGAGGAC	1055
	GTCCTCTCATTCCATCA	1056
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Glu4Term GAG-TAG	GAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAG ATAATGATGGAAAGATAGGACAGATATGTTAGATTTCAGGACTGC AAATCAGAGCAATCTGTTATCTCAGAGAACG	1057
	CGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCT AACATATCTGTCCTATCTTTCCATCATTATCTCCACCAGGCGAACA GTTAGCAGCTAAGAGTGGTAGATCAATTC	1058
	TGGAAAGATAGGACAGA	1059
	TCTGTCCTATCTTTCCA	1060
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Arg6Term AGA-TGA	ATCTACCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATG ATGGAAAGAGAGGACTGATATGTTAGATTTCAGGACTGCAAATCA GAGCAATCTGTTATCTCAGAGAACGCAGTTT	1061
	AAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTG AAATCTAACATATCAGTCCTCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAAGAGTGGTAGAT	1062
	GAGAGGACTGATATGTT	1063
	AACATATCAGTCCTCTC	1064
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Tyr7Term TAT-TAG	CCACTCTTAGCTGCTAACTGTTCGCCTGGTGGAGATAATGATGGA AAGAGAGGACAGATAGGTTAGATTTCAGGAGTGCAAATCAGAGCA ATCTGTTATCTCAGAGAACGCAGTTTCACCA	1065
	TGGTGAAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCA GTCCTGAAATCTAACCTATCTGTCCTCTCTTTCCATCATTATCTCCA CCAGGCGAACAGTTAGCAGCTAAGAGTGG	1066
	GACAGATAGGTTAGATT	1067
	AATCTAACCTATCTGTC	1068
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Glu2Term GAG-TAG	ATCCTTCTCTGAGAAAAAACAACAGATCCGAATTTTATCTTTAATCA GCCGGAAAAAATGTAGAAAGCGATCGAGAGACAACGCGTTCTTCT TGAGCATCTCCGACCTTCTTCTTCTTCTT	1069
	AAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGTTGT CTCTCGATCGCTTTCTACATTTTTTCCGGCTGATTAAAGATAAAATT CGGATCTGTTGTTTTTTCTCAGAGAAGGAT	1070
	AAAAAATGTAGAAAGCG	1071
	CGCTTTCTACATTTTTT	1072
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Lys3Term AAA-TAA	CTTCTCTGAGAAAAAACAACAGATCCGAATTTTATCTTTAATCAGC CGGAAAAAATGGAGTAAGCGATCGAGAGACAACGCGTTCTTCTTG AGCATCTCCGACCTTCTTCTTCTTCTTCGC	1073
	GCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGT TGTCTCTCGATCGCTTACTCCATTTTTTCCGGCTGATTAAAGATAA AATTCGGATCTGTTGTTTTTTTCTCAGAGAAG	1074
	AAATGGAGTAAGCGATC	1075
	GATCGCTTACTCCATTT	1076
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Glu6Term GAG-TAG	GAAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAA TGGAGAAAGCGATCTAGAGACAACGCGTTCTTCTTGAGCATCTCC GACCTTCTTCTTCTTCTTCGCACAATTACG	1077
	CGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGA AGAACGCGTTGTCTCTAGATCGCTTTCTCCATTTTTTCCGGCTGAT TAAAGATAAAATTCGGATCTGTTGTTTTTTC	1078
	AAGCGATCTAGAGACAA	1079
	TTGTCTCTAGATCGCTT	1080
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Arg7Term	AAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGG AGAAAGCGATCGAGTGACAACGCGTTCTTCTTGAGCATCTCCGAC CTTCTTCTTCTTCTTCGCACAATTACGAGG	1081
	CCTCGTAATTGTGGGAAGAAGAAGAAGAAGGTCGGAGATGCTCAA GAAGAACGCGTTGTCACTCGATCGCTTTCTCCATTTTTTCCGGCT	1082

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
AGA-TGA	GATTAAAGATAAAATTCGGATCTGTTGTTTT	
	CGATCGAG**T**GACAACGC	1083
	GCGTTGTC**A**CTCGATCG	1084
2,4-DB resistance	ACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGA	1085
3-ketoacyl-CoA	AAGCGATCGAGAGA**T**AACGCGTTCTTCTTGAGCATCTCCGACCTT	
thiolase	CTTCTTCTTCTTCGCACAATTACGAGGCTT	
Arabidopsis thaliana	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGC	1086
Gln8Term	TCAAGAAGAACGCGTT**A**TCTCTCGATCGCTTTCTCCATTTTTTCCG	
CAA-TAA	GCTGATTAAAGATAAAATTCGGATCTGTTGT	
	TCGAGAGA**T**AACGCGTT	1087
	AACGCGTT**A**TCTCTCGA	1088
2,4-DB resistance	GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCCTTCTTCTTCTT	1089
glyoxysomal beta-	CCTCTCACAGCTTT**T**AAGGCTCTCTCTCTGCTTCAGCTTGCTTGGC	
ketoacyol-thiolase	TGGGGACAGTGCTGCGTATCAGAGGACCT	
precursor	AGGTCGTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAA	1090
Brassica napus	GCAGAGAGAGAGCCTT**A**AAAGCTGTGAGAGGAAGAAGAAGAAGG	
Glu26Term	ACGGAGATGTTCAAGAAGAACTCTTTGTCTCTC	
GAA-TAA	ACAGCTTT**T**AAGGCTCT	1091
	AGAGCCTT**A**AAAGCTGT	1092
2,4-DB resistance	TTGAACATCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGG	1093
glyoxysomal beta-	CTCTCTCTCTGCTT**G**AGCTTGCTTGGCTGGGGACAGTGCTGCGTA	
ketoacyol-thiolase	TCAGAGGACCTCTCTCTATGGAGATGATGT	
precursor	ACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCC	1094
Brassica napus	CCAGCCAAGCAAGCT**C**AAGCAGAGAGAGAGCCTTCAAAGCTGTG	
Ser32Term	AGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	
TCA-TGA	CTCTGCTT**G**AGCTTGCT	1095
	AGCAAGCT**C**AAGCAGAG	1096
2,4-DB resistance	TCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTC	1097
glyoxysomal beta-	TCTGCTTCAGCTTG**A**TTGGCTGGGGACAGTGCTGCGTATCAGAG	
ketoacyol-thiolase	GACCTCTCTCTATGGAGATGATGTAGTCATT	
precursor	AATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGC	1098
Brassica napus	ACTGTCCCCAGCCAA**T**CAAGCTGAAGCAGAGAGAGAGCCTTCAAA	
Cys34Term	GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	
TGC-TGA	TCAGCTTG**A**TTGGCTGG	1099
	CCAGCCAA**T**CAAGCTGA	1100
2,4-DB resistance	TCCGTCCTTCTTCTTGTTCCTCTCACAGCTTTGAAGGCTCTCTCTC	1101
glyoxysomal beta-	TGCTTCAGCTTGCT**A**GGCTGGGGACAGTGCTGCGTATCAGAGGA	
ketoacyol-thiolase	CCTCTCTCTATGGAGATGATGTAGTCATTGT	
precursor	ACAATGACTACATCATCTCCATAGAGAGAGGTCGTCTGATACGCA	1102
Brassica napus	GCACTGTCCCCAGCC**T**AGCAAGCTGAAGCAGAGAGAGAGCCTTC	
Leu35Term	AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGA	
TTG-TAG	AGCTTGCT**A**GGCTGGGG	1103
	CCCCAGCC**T**AGCAAGCT	1104
2,4-DB resistance	TCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGG	1105
glyoxysomal beta-	GGACAGTGCTGCGTA**G**CAGAGGACCTCTCTCTATGGAGATGATGT	
ketoacyol-thiolase	AGTCATTGTTGCGGCACATAGGACTGCACTA	
precursor	TAGTGCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA	1106
Brassica napus	GAGAGAGGTCGTCTG**C**TACGCAGCACTGTCCCCAGCCAAGCAAG	
Tyr42Term	CTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGA	
TAT-TAG	GCTGCGTA**G**CAGAGGAC	1107
	GTCCTCTG**C**TACGCAGC	1108
2,4-DB resistance	CAACAGACAGGAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTC	1109
3-ketoacyl-CoA	TTCTTCTCACAATTA	
	Gee GAGTCCGCTCTTGCCGCATCAGTATGTGCT	
thiolase B	GCAGGGGATAGCGCCGCATATCATAGGGCT	
Mangifera indica	AGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGC	1110
Tyr25Term	GGCAAGAGCGGACTC**C**TAATTGTGAGAAGAAGAATTAGAAGGGC	
TAC-TAG	GGAGATGCTGGAGCAACACTTGCTGTCTGTTG	
	CACAATTA**G**GAGTCCGC	1111
	GCGGACTC**C**TAATTGTG	1112
2,4-DB resistance	AACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTT	1113
3-ketoacyol-CoA	CTTCTCACAATTAC**T**AGTCCGCTCTTGCCGCATCAGTATGTGCTGC	

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
thiolase B	AGGGGATAGCGCCGCATATCATAGGGCTT	
Magnifera indica	AAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATG	1114
Glu26Term	CGGCAAGAGCGGACT**A**GTAATTGTGAGAAGAAGAATTAGAAGGG	
GAG-TAG	CGGAGATGCTGGAGCAACACTTGCTGTCTGTT	
	ACAATTAC**T**AGTCCGCT	1115
	AGCGGACT**A**GTAATTGT	1116
2,4-DB resistance	TCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTC	1117
3-ketoacy o-CoA	CGCTCTTGCCGCAT**G**AGTATGTGCTGCAGGGGATAGCGCCGCAT	
thioblase B	ATCATAGGGCTTCTGTTTATGGAGACGATGT	
Mangifera indica	ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCC	1118
Ser32Term	CCTGCAGCACATACT**C**ATGCGGCAAGAGCGGACTCGTAATTGTGA	
TCA-TGA	GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	
	TGCCGCAT**G**AGTATGTG	1119
	CACATACT**C**ATGCGGCA	1120
2,4-DB resistance	TCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTT	1121
3-ketoacyl-CoA	GCCGCATCAGTATG**A**GCTGCAGGGGATAGCGCCGGATATCATAG	
thiolase B	GGCTTCTGTTTATGGAGACGATGTGGTGATT	
Mangifera indica	AATCACCACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGC	1122
Cys34Term	GCTATCCCCTGCAGC**T**CATACTGATGCGGCAAGAGCGGACTCGT	
TGT-TGA	AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	
	TCAGTATG**A**GCTGCAGG	1123
	CCTGCAGC**T**CATACTGA	1124
2,4-DB resistance	TCACAATTACGAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGG	1125
3-ketoacyl-CoA	GGATAGCGCCGCATA**G**CATAGGGCTTGTGTTTATGGAGACGATGT	
thiolase B	GGTGATTGTGGCAGGTCATCGTACTGCACTT	
Mangifera indica	AAGTGCAGTAGGATGAGCTGCCACAATCACCACATCGTCTCCATA	1126
Tyr42Term	AACAGAAGCCCTATG**C**TATGCGGCGCTATCCCCTGCAGCACATAC	
TAT-TAG	TGATGCGGCAAGAGCGGACTCGTAATTGTGA	
	GCCGCATA**G**CATAGGGC	1127
	GCCCTATG**C**TATGCGGC	1128
2,4-DB resistance	GAAGGCGATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCC	1129
3-ketoacyl-CoA	TTCTTCTTCCGCTTA**G**ACAAATGAATCTTCGCTCTCTGCATCGGTT	
thiolase	TGTGCAGCTGGGGATAGTGCTTCGTATCAA	
Cucumis sativus	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG	1130
Tyr22Term	CGAAGATTCATTTGT**C**TAAGCGGAAGAAGAAGGCCGGAGATGATG	
TAG-TAG	TAGCAAAATGCTCTGGCTGTTGATCGCCTTC	
	TCCGCTTA**G**ACAAATGA	1131
	TCATTTGT**C**TAAGCGGA	1132
2,4-DB resistance	ATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTT	1133
3-ketoacyl-CoA	CCGCTTACACAAAT**T**AATCTTCGCTCTCTGCATCGGTTTGTGCAGC	
thiolase	TGGGGATAGTGCTTCGTATCAAAGGACAT	
Cucumis sativus	ATGTCCTTTGATACGAAGCAGTATCCCCAGCTGCACAAACCGATG	1134
Glu25Term	CAGAGAGCGAAGATT**A**ATTTGTGTAAGCGGAAGAAGAAGGCCGG	
GAA-TAA	AGATGATGTAGCAAAATGCTCTGCCTGTTGAT	
	ACACAAAT**T**AATCTTCG	1135
	CGAAGATT**A**ATTTGTGT	1136
2,4-DB resistance	GGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTTCCGCTTA	1137
3-ketoacyl-CoA	CACAAATGAATCTT**A**GCTCTCTGCATCGGTTTGTGCAGCTGGGGA	
thiolase	TAGTGCTTCGTATCAAAGGACATCGGTGTT	
Cucumis sativus	AACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAA	1138
Ser27Term	ACCGATGCAGAGAGC**T**AAGATTCATTTGTGTAAGCGGAAGAAGAA	
TCG-TAG	GGCCGGAGATGATGTAGCAAAATGCTCTGCC	
	TGAATCTT**A**GCTCTCTG	1139
	CAGAGAGC**T**AAGATTCA	1140
2,4-DB resistance	TGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATC	1141
3-ketoacyl-CoA	TTCGCTCTCTGCATA**G**GTTTGTGCAGCTGGGGATAGTGCTTCGTA	
thiolase	TCAAAGGACATCGGTGTTTGGAGATGATGT	
Cucumis sativus	ACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCC	1142
Ser31Term	CAGCTGCACAAACC**T**ATGCAGAGAGCGAAGATTCATTTGTGTAAG	
TCG-TAG	CGGAAGAAGAAGGCCGGAGATGATGTAGCA	
	CTCTGCAT**A**GGTTTGTG	1143
	CACAAACC**T**ATGCAGAG	1144

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance	TCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCGCTC	1145
3-ketoacyl-CoA	TCTGCATCGGTTTG**A**GCAGCTGGGGATAGTGCTTCGTATCAAAGG	
thiolase	ACATCGGTGTTTGGAGATGATGTCGTGATT	
Cucumis sativus	AATCACGACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCA	1146
Cys33Term	CTATCCCCAGCTGC**T**CAAACCGATGCAGAGAGCGAAGATTCATTT	
TGT-TGA	GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	
	TCGGTTTG**A**GCAGCTGG	1147
	CCAGCTGC**T**CAAACCGA	1148
2A-DB resistance	GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC	1149
3-ketoacyl-CoA	TTCATCTTCGGCTT**AG**ACCCATGAATCTTCGCTCTCTGCATCGGTT	
thiolase	TGTGCAGCTGGGGATAGTGCGTCGTATCAA	
Cucurbita sp.	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG	1150
Tyr22Term	CGAAGATTCATGGCT**C**TAAGCCGAAGATGAAGGCCGGAGATGAT	
TAT-TAG	GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	
	TCGGCTTA**G**AGCCATGA	1151
	TCATGGCT**C**TAAGCCGA	1152
2,4-DB resistance	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT	1153
3-ketoacyl-CoA	CGGCTTATAGCCAT**T**AATCTTCGCTCTCTGCATCGGTTTGTGCAGC	
thiolase	TGGGGATAGTGCGTCGTATCAAAGAACGT	
Cucurbita sp.	ACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATG	1154
Glu25Term	CAGAGAGCGAAGATT**A**ATGGCTATAAGCCGAAGATGAAGGCCGG	
GAA-TAA	AGATGATGTAGCAGAATGCTCTGCCTGTTGAT	
	ATAGCCAT**T**AATCTTCG	1155
	CGAAGATT**A**ATGGCTAT	1156
2,4-DB resistance	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTT	1157
3-ketoacyl-CoA	ATAGCCATGAATCTT**A**GCTCTCTGCATCGGTTTGTGCAGCTGGGG	
thiolase	ATAGTGCGTCGTATCAAAGAACGTCGGTGTT	
Cucurbita sp.	AACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAA	1158
Ser27Term	ACCGATGCAGAGAGCTAAGATTCATGGCTATAAGCCGAAGATGAA	
TCG-TAG	GGCCGGAGATGATGTAGCAGAATGCTCTGCC	
	TGAATCTT**A**GCTCTCTG	1159
	CAGAGAGC**T**AAGATTCA	1160
2,4-DB resistance	TGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATC	1161
3-ketoacyl-CoA	TTCGCTCTCTGCAT**A**GGTTTGTGCAGCTGGGGATAGTGCGTCGTA	
thiolase	TCAAAGAACGTCGGTGTTTGGAGATGATGT	
Cucurbita sp.	ACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCC	1162
Ser31Term	CAGCTGCACAAACC**T**ATGCAGAGAGCGAAGATTCATGGCTATAAG	
TCG-TAG	CCGAAGATGAAGGCCGGAGATGATGTAGCA	
	CTCTGCAT**A**GGTTTGTG	1163
	CACAAACC**T**ATGCAGAG	1164
2,4-DB resistance	TCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTC	1165
3-ketoacyl-CoA	TCTGCATCGGTTTG**A**GCAGCTGGGGATAGTGCGTCGTATCAAAGA	
thiolase	ACGTCGGTGTTTGGAGATGATGTCGTGATA	
Cucurbita sp.	TATCACGACATCATCTCCAAACACCGACGTTCTTTGATACGACGCA	1166
Cys33Term	CTATCCCCAGCTGC**T**CAAACCGATGCAGAGAGCGAAGATTCATGG	
TGT-TGA	CTATAAGCCGAAGATGAAGGCCGGAGATGA	
	TCGGTTTG**A**GCAGCTGG	1167
	CCAGCTGC**T**CAAACCGA	1168
2,4 DB resistance	TCATAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTG	1169
Pex14	CTATGGCAACTCAT**T**AGCAAACGCAACCTCCTTCCGATTTTCCCGC	
Arabidopsis thaliana	TCTTGCCGATGAAAATTCCCAGATTCCAG	
Gln5Term	CTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAA	1170
CAG-TAG	GGAGGTTGCGTTTGCT**AA**TGAGTTGCCATAGCAGCTCACTAACCT	
	TGGAAGAATCCAAGCGGCAAAAGAGACTATGA	
	CAACTCAT**T**AGCAAACG	1171
	CGTTTGCT**AA**TGAGTTG	1172
2,4 DB resistance	TAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTA	1173
Pex14	TGGCAACTCATCAG**T**AAACGCAACCTCCTTCCGATTTTCCCGCTCT	
Arabidopsis thaliana	TGCCGATGAAAATTCCCAGATTGCAGGTT	
Gln6Term	AACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGG	1174
CAA-TAA	AAGGAGGTTGCGTTT**A**CTGATGAGTTGCCATAGCAGCTCACTAAC	
	CTTGGAAGAATCCAAGCGGCAAAAGAGACTA	

TABLE 17-continued

Genome-Altering Oligos Conferring Stress Tolerance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTCATCAG**T**AAACGCAA	1175
	TTGCGTTT**A**CTGATGAG	1176
2,4 DB resistance	CTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCA	1177
Pex14	ACTCATCAGCAAACG**T**AACCTCCTTCCGATTTTCCCGCTCTTGCCG	
Arabidopsis thaliana	ATGAAAATTCCGAGATTCCAGGTTCAATTT	
Gln8Term	AAATTGAACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAA	1178
CAA-TAA	AATCGGAAGGAGGTT**A**CGTTTGCTGATGAGTTGCCATAGCAGCTC	
	ACTAACCTTGGAAGAATCCAAGCGGCAAAAG	
	AGCAAACG**T**AACCTCCT	1179
	AGGAGGTT**A**CGTTTGCT	1180
2,4 DB resistance	GCTGCTATGGCAACTGATGAGCAAACGCAACCTCCTTCCGATTTT	1181
Pex14	CCCGCTCTTGCCGAT**T**AAAATTCCCAGATTCCAGGTTCAATTTACA	
Arabidopsis thaliana	CCTTCTAATCATTATTTCTTAATTTTTCTT	
Glu19Term	AAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGG	1182
GAA-TAA	AATCTGGGAATTTT**AA**TCGGCAAGAGCGGGAAAATCGGAAGGAG	
	GTTGCGTTTGCTGATGAGTTGCCATAGCAGC	
	TTGCCGAT**T**AAAATTCC	1183
	GGAATTTT**AA**TCGGCAA	1184
2,4 DB resistance	GCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTT	1185
Pex14	GCCGATGAAAATTCC**T**AGATTCCAGGTTCAATTTACACCTTCTAAT	
Arabidopsis thaliana	CATTATTTCTTAATTTTTCTTTGGTGGATT	
Gln22Term	AATCCACCAAAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAAT	1186
CAG-TAG	TGAACCTGGAATCT**A**GGAATTTTCATCGGCAAGAGCGGGAAAATC	
	GGAAGGAGGTTGCGTTTGCTGATGAGTTGC	
	AAAATTCC**T**AGATTCCA	1187
	TGGAATCT**A**GGAATTTT	1188

EXAMPLE 8

Production of Albino Mutants for the Analysis of Photosynthetic Processes

[0132] Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

[0133] The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

TABLE 18

Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
White leaves	TTCTTTCCTGTGAAATTATCTGCTCAAATCTTTGGTTCCTGACGGAG	1189
Immutans	ATGGCGGCGATTT**G**AGGCATCTCCTCTGGTACGTTGACGATTTCA	
Arabidopsis thaliana	CGGCCTTTGGTTACTCTTCGACGCTCTAG	
Ser5Term	CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA	1190
TCA-TGA	CCAGAGGAGATGCCT**C**AAATCGCCGCCATCTCCGTCAGGAACCAA	
	AGATTTGAGCAGATAATTTCACAGGAAAGAA	
	GGCGATTT**G**AGGCATCT	1191
	AGATGCCT**C**AAATCGCC	1192
White leaves	GCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCA	1193
Immutans	TCTCCTCTGGTACGT**A**AGACGATTTCACGGCCTTTGGTTACTCTTCG	
Arabidopsis thaliana	ACGCTCTAGAGCCGCCGTTTCGTACAGCTC	

TABLE 18-continued

Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Leu12Term	GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAAA	
	1194	
TTG-TAG	GGCCGTGAAATCGTC**T**ACGTACCAGAGGAGATGCCTGAAATCGCC	
	GCCATCTCCGTCAGGAACCAAAGATTTGAGC	
	TGGTACGT**A**GACGATTT	1195
	AAATCGTC**T**ACGTACCA	1196
White leaves	TTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCATCTCCTCTG	1197
Immutans	GTACGTTGACGATTTGACGGCCTTTGGTTACTCTTCGACGCTCTAG	
Arabidopsis thaliana	AGCCGCCGTTTCGTACAGCTCCTCTCACCG	
Ser15Term	CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAG	1198
TCA-TGA	AGTAACCAAAGGCCGT**C**AAATCGTCAACGTACCAGAGGAGATGCC	
	TGAAATCGCCGCCATCTCCGTCAGGAACCAAA	
	GACGATTT**G**ACGGCCTT	1199
	AAGGCCGT**C**AAATCGTC	1200
White leaves	GCGGCGATTTCAGGCATCTCCTCTGGTACGTTGACGATTTCACGG	1201
Immutans	CCTTTGGTTACTCTT**T**GACGCTCTAGAGCCGCCGTTTCGTACAGCT	
Arabidopsis thaliana	CCTCTCACCGATTGCTTCATCATCTTCCTC	
Arg22Term	GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG	1202
CGA-TGA	GCGGCTCTAGAGCGTC**A**AAGAGTAACCAAAGGCCGTGAAATCGTC	
	AACGTACCAGAGGAGATGCCTGAAATCGCCGC	
	TTACTCTT**T**GACGCTCT	1203
	AGAGCGTC**A**AAGAGTAA	1204
White leaves	TCAGGCATCTCCTCTGGTACGTTGACGATTTCACGGCCTTTGGTTA	1205
Immutans	CTCTTCGACGCTCT**T**GAGCCGCCGTTTCGTACAGCTCCTCTCACC	
Arabidopsis thaliana	GATTGCTTCATCATCTTCCTCTCTCTTCTC	
Arg25Term	GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG	1206
AGA-TGA	TACGAAACGGCGGCTC**A**AGAGCGTCGAAGAGTAACCAAAGGCCG	
	TGAAATCGTCAACGTACCAGAGGAGATGCCTGA	
	GACGCTCT**T**GAGCCGCC	1207
	GGCGGCTC**A**AGAGCGTC	1208
White leaves	GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATT	1209
Immutans	TCTGCTATGAGTTTTT**T**GAACCTCAGTTTCTTCATATTCTTGTTTTAG	
Lycopersicon	AGCTAGGAGTTTTGAGAAGTCATCAGTTT	
esculentum	AAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATGA	1210
Gly11Term	AGAAACTGAGGTTC**A**AAAACTCATAGCAGAAATCGAAATCGCCATT	
GGA-TGA	CTTGATCCTTCTTCCTTCCCACAAGAATC	
	TGAGTTTT**T**GAACCTCA	1211
	TGAGGTTC**A**AAAACTCA	1212
White leaves	GTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTA	1213
Immutans	TGAGTTTTGGAACCT**G**AGTTTCTTCATATTCTTGTTTTAGAGCTAGG	
Lycopersicon	AGTTTTGAGAAGTCATCAGTTTTATGCAA	
esculentum	TTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAG	1214
Ser13Term	AATATGAAGAAACT**C**AGGTTCCAAAACTCATAGCAGAAATCGAAAT	
TCA-TGA	CGCCATTCTTGATCCTTCTTCCTTCCCAC	
	TGGAACCT**G**AGTTTCTT	1215
	AAGAAACT**C**AGGTTCCA	1216
White leaves	AAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGG	1217
Immutans	AACCTCAGTTTCTTGATATTCTTGTTTTAGAGCTAGGAGTTTTGAGA	
Lycopersicon	AGTCATCAGTTTTATGCAATTCCCAGAA	
esculentum	TTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTC	1218
Ser16Term	TAAAACAAGAATAT**C**AAGAAACTGAGGTTCCAAAACTCATAGCAGA	
TCA-TGA	AATCGAAATCGCCATTCTTGATCCTTCTT	
	AGTTTCTT**G**ATATTCTT	1219
	AAGAATAT**C**AAGAAACT	1220
White leaves	AGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACC	1221
Immutans	TCAGTTTCTTCATA**G**TCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTC	
Lycopersicon	ATCAGTTTTATGCAATTCCCAGAACCCA	
esculentum	TGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTA	1222
Tyr17Term	GCTCTAAAACAAGA**C**TATGAAGAAACTGAGGTTCCAAAACTCATAG	
TAT-TAG	CAGAAATCGAAATCGCCATTCTTGATCCT	
	TCTTCATA**G**TCTTGTTT	1223
	AAACAAGA**C**TATGAAGA	1224

TABLE 18-continued

Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
White leaves	AAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACCTCAGTT	1225
Immutans	TCTTCATATTCTTG**A**TTTAGAGCTAGGAGTTTTGAGAAGTCATCAGT	
Lycopersicon	TTTATGCAATTCCCAGAACCCATGTCGG	
esculentum	CCGACATGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAA	1226
Cys19Term	CTCCTAGCTCTAAA**T**CAAGAATATGAAGAAACTGAGGTTCCAAAAC	
TGT-TGA	TCATAGCAGAAATCGAAATCGCCATTCTT	
	TATTCTTG**A**TTTAGAGC	1227
	GCTCTAAA**T**CAAGAATA	1228
White leaves	CGCGTCCGATAAAAAAATCAAGAATGGCGATTTCCATATCTGCTAT	1229
Immutans	GAGTTTTCGAACTT**G**AGTTTCTTCTTCATATTCAGCATTTTTGTGCA	
Capsicum annuum	ATTCCAAGAACCCATTTTGTTTGAATTC	
Ser13Term	GAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCTGAAT	1230
TCA-TGA	ATGAAGAAGAAACT**C**AAGTTCGAAAACTCATAGCAGATATGGAAAT	
	CGCCATTCTTGATTTTTTTATCGGACGCG	
	TCGAACTT**G**AGTTTCTT	1231
	AAGAAACT**C**AAGTTCGA	1232
White leaves	AAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAAC	1233
Immutans	TTCAGTTTCTTCTTC**G**ATATTCAGCATTTTTGTGCAATTCCAAGAACC	
Capsicum annuum	CATTTTGTTTGAATTCTCTATTTTCACT	
Ser17Term	AGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCACA	1234
TCA-TGA	AAAATGCTGAATAT**C**AAGAAGAAACTGAAGTTCGAAAACTCATAGC	
	AGATATGGAAATCGCCATTCTTGATTTTT	
	TTCTTCTT**G**ATATTCAG	1235
	CTGAATAT**C**AAGAAGAA	1236
White leaves	CAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGT	1237
Immutans	TTCTTCTTCATATT**G**AGCATTTTTGTGCAATTCCAAGAACCCATTTT	
Capsicum annuum	GTTTGAATTCTCTATTTTCACTTAGGAA	
Ser19Term	TTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAAT	1238
TCA-TGA	TGCACAAAAATGCT**C**AATATGAAGAAGAAACTGAAGTTCGAAAACT	
	CATAGCAGATATGGAAATCGCCATTCTTG	
	TTCATATT**G**AGCATTTT	1239
	AAAATGCT**C**AATATGAA	1240
White leaves	CGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCA	1241
Immutans	TATTCAGCATTTT**A**GTGCAATTCCAAGAACCCATTTTGTTTGAATTC	
Capsicum annuum	TCTATTTTCACTTAGGAATTCTCATAG	
Leu21Term	CTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGT	1242
TTG-TAG	TCTTGGAATTGCAC**T**AAAATGCTGAATATGAAGAAGAAACTGAAGT	
	TCGAAAACTCATAGCAGATATGGAAATCG	
	AGCATTTT**A**GTGCAATT	1243
	AATTGCAC**T**AAAATGCT	1244
White leaves	TTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATT	1245
Immutans	CAGCATTTTTGTG**A**AATTCCAAGAACCCATTTTGTTTGAATTCTCTA	
Capsicum annuum	TTTTCACTTAGGAATTCTCATAGAACT	
Cys22Term	AGTTCTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAAT	1246
TGC-TGA	GGGTTCTTGGAATT**T**CACAAAAATGCTGAATATGAAGAAGAAACTG	
	AAGTTCGAAAACTCATAGCAGATATGGAA	
	TTTTTGTG**A**AATTCCAA	1247
	TTGGAATT**T**CACAAAAA	1248
White leaves	TTCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTCGAGG	1249
Immutans	AGTCCTTCCCCTTCAGG**T**AGACGGCTCCTCCTGACGAGCCACTGG	
Oryza sativa	TCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG	
Glu22Term	CGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCTCGT	1250
GAG-TAG	CAGGAGGAGCCGTCT**A**CCTGAAGGGGAAGGACTCCTCGACGGCC	
	ACCTCGGTCTGCTCCTTCTCCCTCGTGCCGAA	
	CCTTCAGG**T**AGACGGCT	1251
	AGCCGTCT**A**CCTGAAGG	1252
White leaves	GAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGGGA	1253
Immutans	GACGGCTCCTCCTGAC**T**AGCCACTGGTCACCGCCGAGGAGAGCT	
Oryza sativa	GGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT	
Glu28Term	AAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCTCCTCGG	1254
CAG-TAG	CGGTGACCAGTGGCT**A**GTCAGGAGGAGCCGTCTCCCTGAAGGGG	
	AAGGACTCCTCGACGGCCACCTCGGTCTGCTC	

TABLE 18-continued

Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTCCTGACTAGCCACTG	1255
	CAGTGGCTAGTCAGGAG	1256
White leaves	GTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGA	1257
Immutans	GCCACTGGTCACCGCCTAGGAGAGCTGGGTGGTTAAGCTCGAGC	
Oryza sativa	AGTCCGTGAACATTTTCCTCACGGAGTCAGTCA	
Glu34Term	TGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAA	1258
GAG-TAG	CCACCCAGCTCTCCTAGGCGGTGACCAGTGGCTCGTCAGGAGGA	
	GCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC	
	TCACCGCCTAGGAGAGC	1259
	GCTCTCCTAGGCGGTGA	1260
White leaves	GAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCC	1261
Immutans	ACTGGTCACCGCCGAGTAGAGCTGGGTGGTTAAGCTCGAGCAGT	
Oryza sativa	CCGTGAACATTTTCCTCACGGAGTCAGTCATCA	
Glu35Term	TGATGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCT	1262
GAG-TAG	TAACCACCCAGCTCTACTCGGCGGTGACCAGTGGCTCGTCAGGA	
	GGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC	
	CCGCCGAGTAGAGCTGG	1263
	CCAGCTCTACTCGGCGG	1264
White leaves	CTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCAC	1265
Immutans	CGCCGAGGAGAGCTGAGTGGTTAAGCTCGAGCAGTCCGTGAACA	
Oryza sativa	TTTTCCTCACGGAGTCAGTCATCACGATACTT	
Trp37Term	AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTCACGGACTG	1266
TGG-TGA	CTCGAGCTTAACCACTCAGCTCTCCTCGGCGGTGACCAGTGGCTC	
	GTCAGGAGGAGCCGTCTCCCTGAAGGGGAAG	
	GAGAGCTGAGTGGTTAA	1267
	TTAACCACTCAGCTCTC	1268
White leaves	TCCGGAGGAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCG	1269
Immutans	GCGAGGACGGCGACTGAGTCGTCAGATTCGAGCAGTCCTTCAAC	
Triticum aestivum	GTATTCCTCACGGATACTGTCATCTTTATACTC	
Trp22Term	GAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTG	1270
TGG-TGA	CTCGAATCTGACGACTCAGTCGCCGTCCTCGCCGGCGAGGGTGA	
	GCTCCTCGTCGAATCCCCCTTCCTCCTCCGGA	
	GGCGACTGAGTCGTCAG	1271
	CTGACGACTCAGTCGCC	1272
White leaves	GAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGG	1273
Immutans	ACGGCGACTGGGTCGTCTGATTCGAGCAGTCCTTCAACGTATTCC	
Triticum aestivum	TCACGGATACTGTCATCTTTATACTCGATATTC	
Arg25Term	GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAA	1274
AGA-TGA	GGACTGCTCGAATCAGACGACCCAGTCGCCGTCCTCGCCGGCGA	
	GGGTGAGCTCCTCGTCGAATCCCCCTTCCTC	
	GGGTCGTCTGATTCGAG	1275
	CTCGAATCAGACGACCC	1276
White leaves	GGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCG	1277
Immutans	ACTGGGTCGTCAGATTCTAGCAGTCCTTCAACGTATTCCTCACGGA	
Triticum aestivum	TACTGTCATCTTTATACTCGATATTCTGTATC	
Glu21Term	GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATAC	1278
GAG-TAG	GTTGAAGGACTGCTAGAATCTGACGACCCAGTCGCCGTCCTCGCC	
	GGCGAGGGTGAGCTCCTCGTCGAATCCCCC	
	TCAGATTCTAGCAGTCC	1279
	GGACTGCTAGAATCTGA	1280
White leaves	GGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTG	1281
Immutans	GGTCGTCAGATTCGAGTAGTCCTTCAACGTATTCCTCACGGATACT	
Triticum aestivum	GTCATCTTTATACTCGATATTCTGTATCGTG	
Gln28Term	CACGATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAA	1282
CAG-TAG	TACGTTGAAGGACTACTCGAATCTGACGACCCAGTCGCCGTCCTC	
	GCCGGCGAGGGTGAGCTCCTCGTCGAATCC	
	GATTCGAGTAGTCCTTC	1283
	GAAGGACTACTCGAATC	1284
White leaves	CGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATA	1285
Immutans	CTCGATATTCTGTAGCGTGACCGCGACTACGCAAGGTTCTTCGTG	
Triticum aestivum	CTCGAGACCATCGCCAGGGTGCCCTATTTC	
Tyr46Term	GAAATAGGGCACCCTGGCGATGGTCTCGAGCACGAAGAACCTTG	1286

TABLE 18-continued

Oligonucleotides to produce albino plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
TAT-TAG	CGTAGTCGCGGTCACGCTACAGAATATCGAGTATAAAGATGACAG	
	TATCCGTGAGGAATACGTTGAAGGACTGCTCG	
	ATTCTGTA**G**CGTGACCG	1287
	CGGTCACG**C**TACAGAAT	1288

EXAMPLE 9

Altering Amino Acid Content of Plants

[0134] Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

[0135] Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

[0136] An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

[0137] The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

TABLE 19

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction	TATCCTCCAGGATCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCT	1289
CGS	GAGCATTAAAGCCC**A**TAGAAACTGTAGCAACATCGGTGTTGCACA	
Arabidopsis thaliana	GATCGTGGCGGCTAAGTGGTCCAACAACCC	
Arg77His	GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGAT	1290
CGT-CAT	GTTGCTACAGTTTCTA**T**GGGCTTTAATGCTCAGCTGACGGACGAA	
	ATTAGGAGGAAATCTTAAGATCCTGGAGGATA	
	TAAAGCCC**A**TAGAAACT	1291
	AGTTTCTA**T**GGGCTTTA	1292
Met Overproduction	TCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGC	1293
CGS	CCGTAGAAACTGTA**A**CAACATCGGTGTTGCACAGATCGTGGCGG	
Arabidopsis thaliana	CTAAGTGGTCCAACAACCCATCCTCCGCGTT	
Ser81Asn	AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTG	1294
AGC-AAC	TGCAACACCGATGTTG**T**TACAGTTTCTACGGGCTTTAATGCTCAGC	
	TGACGGACGAAATTAGGAGGAAATCTTAAGA	
	AAACTGTA**A**CAACATCG	1295
	CGATGTTG**T**TACAGTTT	1296
Met Overproduction	TTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAA	1297
CGS	ACTGTAGCAACATC**A**GTGTTGCACAGATCGTGGCGGCTAAGTGGT	
Arabidopsis thaliana	CCAACAACCCATCCTCCGCGTTACCTTCGG	
Gly84Ser	CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCC	1298
GGT-AGT	ACGATCTGTGCAACAC**T**GATGTTGCTACAGTTTCTACGGGCTTTAA	
	TGCTCAGCTGACGGACGAAATTAGGAGGAAA	

TABLE 19-continued

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAACATC**A**GTGTTGCA	1299
	TGCAACAC**T**GATGTTGC	1300
Met Overproduction	TTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAA	1301
CGS	CTGTAGCAACATCG**A**TGTTGCACAGATCGTGGCGGCTAAGTGGTC	
Arabidopsis thaliana	CAACAACCCATCCTCCGCGTTACCTTCGGC	
Gly84Asp	GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGC	1302
GGT-GAT	CACGATCTGTGCAACA**T**CGATGTTGCTACAGTTTCTACGGGCTTTA	
	ATGCTCAGCTGACGGACGAAATTAGGAGGAA	
	CAACATCG**A**TGTTGCAC	1303
	GTGCAACA**T**CGATGTTG	1304
Met Overproduction	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC	1305
CGS	TCAGCACCAAGGCCC**A**CCGCAACTGCAGCAACATCGGCGTCGCG	
Fragraria vesca	CAGATCGTCGCGGCTTCGTGGTCCAACAAAGA	
Arg73His	TCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGAT	1306
CGC-CAC	GTTGCTGCAGTTGCGG**T**GGGCCTTGGTGCTGAGCTGGCGGACGA	
	AGTTGGGAGGGAAGCGGAGGATGAGTGACGATA	
	CAAGGCCC**A**CCGCAACT	1307
	AGTTGCGG**T**GGGCCTTG	1308
Met Overproduction	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGG	1309
CGS	CCCGCCGCAACTGCA**A**CAACATCGGCGTCGCGCAGATCGTCGCG	
Fragraria vesca	GCTTCGTGGTCCAACAAAGACTCCGACCTTTC	
Ser77Asn	GAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTG	1310
AGC-AAC	CGCGACGCCGATGTTG**T**TGCAGTTGCGGCGGGCCTTGGTGCTGA	
	GCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGA	
	CAACTGCA**A**CAACATCG	1311
	CGATGTTG**T**TGCAGTTG	1312
Met Overproduction	TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG	1313
CGS	CAACTGCAGCAACATC**A**GCGTCGCGCAGATCGTCGCGGCTTCGT	
Fragraria vesca	GGTCCAACAAAGACTCCGACCTTTCGGCGGTGC	
Gly80Ser	GCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCG	1314
GGC-AGC	ACGATCTGCGCGACGC**T**GATGTTGGTGCAGTTGCGGCGGGCCTT	
	GGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	
	GCAACATC**A**GCGTCGCG	1315
	CGCGACGC**T**GATGTTGC	1316
Met Overproduction	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGC	1317
CGS	AACTGCAGCAACATCG**A**CGTCGCGCAGATCGTCGCGGCTTCGTG	
Fragraria vesca	GTCCAACAAAGACTCCGACCTTTCGGCGGTGCC	
Gly80Asp	GGCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGC	1318
GGC-GAC	GACGATCTGCGCGACG**T**CGATGTTGCTGCAGTTGCGGCGGGCCT	
	TGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGA	
	CAACATCG**A**CGTCGCGC	1319
	GCGCGACG**T**CGATGTTG	1320
Met Overproduction	TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGC	1321
CGS	TAAGCACCAAGGCG**A**GCCGCAACTGCAGCAACATCGGCGTCGCG	
Glycine max	CAAATCGTCGCCGCTTCGTGGTCGAACAACAG	
Arg68His	CTGTTGTTCGACCACGAAGCGGCGACGATTTGCGCGACGCCGAT	1322
CGC-CAC	GTTGCTGCAGTTGCGGC**T**CGCCTTGGTGCTTAGCTGGCGCTGGA	
	AGTTGGGAGGGAAGCGGAGGATGAGGGAGGAGA	
	CCAAGGCG**A**GCCGCAAC	1323
	GTTGCGGC**T**CGCCTTGG	1324
Met Overproduction	TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGG	1325
CGS	CGCGCCGCAACTGCA**A**CAACATCGGCGTCGCGCAAATCGTCGCC	
Glycine max	GCTTCGTGGTCGAACAACAGCGACAACTCTCC	
Ser72Asn	GGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCGACGATTTG	1326
AGC-AAC	CGCGACGCCGATGTTG**T**TGCAGTTGCGGCGCGCCTTGGTGCTTA	
	GCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGA	
	CAACTGCA**A**CAACATCG	1327
	CGATGTTG**T**TGCAGTTG	1328
Met Overproduction	TTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCG	1329
CGS	CAACTGCAGCAACATC**A**GCGTCGCGCAAATCGTCGCCGCTTCGT	
Glycine max	GGTCGAACAACAGCGACAACTCTCCGGCCGCCG	
Gly75Ser	CGGCGGCCGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCG	1330

TABLE 19-continued

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
GGC-AGC	ACGATTTGCGCGACGC**T**GATGTTGCTGCAGTTGCGGCGCGCCTT	
	GGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	
	GCAACATC**A**GCGTCGCG	1331
	CGCGACGC**T**GATGTTGC	1332
Met Overproduction	TCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGC	1333
CGS	AACTGCAGCAACATCG**A**CGTCGCGCAAATCGTCGCCGCTTCGTG	
Glycine max	GTCGAACAACAGCGACAACTCTCCGGCCGCCGG	
Gly75Asp	CCGGCGGCGGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGC	1334
GGC-GAC	GACGATTTGCGCGACG**T**CGATGTTGCTGCAGTTGCGGCGCGCCT	
	TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGA	
	CAACATCG**A**CGTCGCGC	1335
	GCGCGACG**T**CGATGTTG	1336
Met Overproduction	TGTCTTCTCTGATTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCT	1337
CGS	AAGCATTAAGGCT**CAC**AGGAATTGCAGCAATATTGGCGTGGCTCA	
Solanum tuberosum	AGTTGTGGCGGCTTCCTGGTCTAACAACCA	
Arg70His	TGGTTGTTAGACCAGGAAGCCGCCACAACTTGAGCCACGCCAATA	1338
AGG-CAC	TTGCTGCAATTCCT**GTG**AGCCTTAATGCTTAGCTGCCTCACGAAAT	
	TAGGAGGAAACCTGAAAATCAGAGAAGACA	
	TAAGGCT**CAC**AGGAATT	1339
	AATTCCT**GTG**AGCCTTA	1340
Met Overproduction	TTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGC	1341
CGS	TAGGAGGAATTGCA**A**CAATATTGGCGTGGCTCAAGTTGTGGCGG	
Solanum tuberosum	CTTCCTGGTCTAACAACCAAGCCGGTCCTGA	
Ser74Asn	TCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCCACAACTTG	1342
AGC-AAC	AGCCACGCCAATATTGTTGCAATTCCTCCTAGCCTTAATGCTTAGC	
	TGCCTCACGAAATTAGGAGGAAACCTGAAAA	
	GAATTGCA**A**CAATATTG	1343
	CAATATTG**T**TGCAATTC	1344
Met Overproduction	TTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGG	1345
CGS	AATTGCAGCAATATT**A**GCGTGGCTCAAGTTGTGGCGGCTTCCTGG	
Solanum tuberosum	TCTAACAACCAAGCCGGTCCTGAATTCACTC	
Gly77Ser	GAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCC	1346
GGC-AGC	ACAACTTGAGCCACGC**T**AATATTGCTGCAATTCCTCCTAGCCTTAA	
	TGCTTAGCTGCCTCACGAAATTAGGAGGAAA	
	GCAATATT**A**GCGTGGGT	1347
	AGCCACGC**T**AATATTGC	1348
Met Overproduction	TTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGGA	1349
CGS	ATTGCAGCAATATTG**A**CGTGGCTCAAGTTGTGGCGGCTTCCTGGT	
Solanum tuberosum	CTAACAACCAAGCCGGTCCTGAATTCACTCC	
Gly77Asp	GGAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGC	1350
GGC-GAC	CACAACTTGAGCCACG**T**CAATATTGCTGCAATTCCTCCTAGCCTTA	
	ATGCTTAGCTGCCTCACGAAATTAGGAGGAA	
	CAATATTG**A**CGTGGCTC	1351
	GAGCCACG**T**CAATATTG	1352
Met Overproduction	CTTCCTCTCTTATCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCT	1353
CGS	CAGCACCAAGGCTCGCC**A**CAACTGCAGCAACATTGGTGTCGCAC	
Mesembryanthemum crystallinum	AGGTCGTCGCTGCCTCCTGGTCCAACAACTC	
	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT	1354
Arg73His	GTTGCTGCAGTTG**T**GGCGAGCCTTGGTGCTGAGCTGACGGACAA	
CGC-CAC	AGTTGGGAGGAAAGCGAAGGATAAGAGAGGAAG	
	GGCTCGCC**A**CAACTGCA	1355
	TGCAGTTG**T**GGCGAGCC	1356
Met Overproduction	TCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGG	1357
CGS	CTCGCCGCAACTGCAACAACATTGGTGTCGCACAGGTCGTCGCT	
Mesembryanthemum crystallinum	GCCTCCTGGTCCAACAACTCCGATGCCGGCGC	
	GCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCT	1358
Ser77Asn	GTGCGACACCAATG**T**TGTTGCAGTTGCGGCGAGCCTTGGTGCTG	
AGC-AAC	AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA	
	CAACTGCA**A**CAACATTG	1359
	CAATGTTG**T**TGCAGTTG	1360
Met Overproduction	TTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGC	1361
CGS	AACTGCAGCAACATT**A**GTGTCGCACAGGTCGTCGCTGCCTCCTG	

TABLE 19-continued

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Mesembryanthemum	GTCCAACAACTCCGATGCCGGCGCCACCTCTT	
crystallinum	AAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGC	1362
Gly80Ser	GACGACCTGTGCGACAC**T**AATGTTGCTGCAGTTGCGGCGAGCCT	
GGT-AGT	TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	
	GCAACATT**A**GTGTCGCA	1363
	TGCGACAC**T**AATGTTGC	1364
Met Overproduction	TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCA	1365
CGS	ACTGCAGCAACATTG**A**TGTCGCACAGGTCGTCGCTGCCTCCTGGT	
Mesembryanthemum	CCAACAACTCCGATGCCGGCGCCACCTCTTG	
crystallinum	CAAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAG	1366
Gly80Asp	CGACGACCTGTGCGACA**T**CAATGTTGCTGCAGTTGCGGCGAGCC	
GGT-GAT	TTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	
	CAACATTG**A**TGTCGCAC	1367
	GTGCGACA**T**CAATGTTG	1368
Met Overproduction	CCTCTGCTACCATCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGC	1369
CGS	TTAGCACCAAGGCACACGGCAACTGCAGCAACATCGGCGTCGCG	
Zea mays	CAGATCGTCGCCGCCGCGTGGTCCGACTGCCC	
Arg41His	GGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGA	1370
CGC-CAC	TGTTGCTGCAGTTGCGG**T**GTGCCTTGGTGCTAAGCTGGCGGACA	
	AAGTTTGGCGGAAAGCGGAGGATGGTAGCAGAGG	
	CAAGGCAC**A**CCGCAACT	1371
	AGTTGCGG**T**GTGCCTTG	1372
Met Overproduction	TCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGG	1373
CGS	CACGCCGCAACTGCA**A**CAACATCGGCGTCGCGCAGATCGTCGCC	
Zea mays	GCCGCGTGGTCCGACTGCCCCGCCGCTCGCCC	
Ser45Asn	GGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGGCGACGATCT	1374
AGC-AAC	GCGCGACGCCGATGTTG**T**TGCAGTTGCGGCGTGCCTTGGTGCTA	
	AGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGA	
	CAACTGCA**A**CAACATCG	1375
	CGATGTTG**T**TGCAGTTG	1376
Met Overproduction	TTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC	1377
CGS	AACTGCAGCAACATC**A**GCGTCGCGCAGATCGTCGCCGCCGCGTG	
Zea mays	GTCCGACTGCCCCGCCGCTCGCCCCCACTTAG	
Gly48Ser	CTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGG	1378
GGC-AGC	CGACGATCTGCGCGACGC**T**GATGTTGCTGCAGTTGCGGCGTGCC	
	TTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAA	
	GCAACATC**A**GCGTCGCG	1379
	CGCGACGC**T**GATGTTGC	1380
Met Overproduction	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCA	1381
CGS	ACTGCAGCAACATCG**A**CGTCGCGCAGATCGTCGCCGCCGCGTGG	
Zea mays	TCCGACTGCCCCGCCGCTCGCCCCCACTTAGG	
Gly48Asp	CCTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCG	1382
GGC-GAC	GCGACGATCTGCGCGACG**T**CGATGTTGCTGCAGTTGCGGCGTGC	
	CTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAA	
	CAACATCG**A**CGTCGCGG	1383
	GCGCGACG**T**CGATGTTG	1384
Met Overproduction	GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATACAG	1385
TS	GAAGTTTCAAGGATCGTGGAATGACTGTTTTGGTTAGTCAAGTTAA	
Arabidopsis thaliana	TCGTCTGAGAAAGATGAAACGACCTGTGGT	
Leu205Arg	ACCACAGGTCGTTTCATCTTTCTCAGACGATTAACTTGACTAACCA	1386
CTT-CGT	AAACAGTCATTCCA**C**GATCCTTGAAACTTCCTGTATGACTAATCCC	
	ACAGTGTTTCACCCACAGATCATTCATAC	
	CAAGGATC**G**TGGAATGA	1387
	TCATTCCA**C**GATCCTTG	1388
Met Overproduction	GCATGACTGATTTGTGGGTCAAACACTGTGGGATTAGCCATACTG	1389
TS	GTAGTTTTAAGGATCGTGGGATGACTGTTTTGGTGAGTCAAGTTAA	
Solanum tuberosum	TCGCTTGCGGAAAATGCATAAACCGGTTGT	
Leu198Arg	ACAACCGGTTTATGCATTTTCCGCAAGCGATTAACTTGACTCACCA	1390
CTT-CGT	AAACAGTCATCCCACGATCCTTAAAACTACCAGTATGGCTAATCCC	
	ACAGTGTTTGACCCACAAATCAGTCATGC	
	TAAGGATC**G**TGGGATGA	1391
	TCATCCCA**C**GATCCTTA	1392

TABLE 19-continued

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lys Overproduction	TCATTGGGCACACAGTGAACTGCTTTGGCTCTAGAATCAAAGTGA	1393
DHPS	TAGGCAACACAGGAA**A**CAACTCAACCAGAGAAGCCGTCCACGCA	
Zea mays	ACAGAACAGGGATTTGCTGTTGGCATGCATGC	
Ser157Asn	GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGCGTGGACGGCT	1394
AGC-AAC	TCTCTGGTTGAGTTG**T**TTCCTGTGTTGCCTATCACTTTGATTCTAG	
	AGCCAAAGCAGTTCACTGTGTGCCCAATGA	
	CACAGGAA**A**CAACTCAA	1395
	TTGAGTTG**T**TTCCTGTG	1396
Lys Overproduction	GCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCA	1397
DHPS	GAGAAGCCGTCCACG**A**AACAGAACAGGGATTTGCTGTTGGCATG	
Zea mays	CATGCGGCTCTCCACATCAATCCTTACTACGG	
Ala166Val	CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC	1398
GCA-GAA	AAATCCCTGTTCTGTT**T**CGTGGACGGCTTCTCTGGTTGAGTTGCTT	
	CCTGTGTTGCCTATCACTTTGATTCTAGAGC	
	CGTCCACG**A**AACAGAAC	1399
	GTTCTGTT**T**CGTGGACG	1400
Lys Overproduction	GGCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACC	1401
DHPS	AGAGAAGCCGTCCAC**A**CAACAGAACAGGGATTTGCTGTTGGCAT	
Zea mays	GCATGCGGCTCTCCACATCAATCCTTACTACG	
Ala166Thr	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCA	1402
GCA-ACA	AATCCCTGTTCTGTTG**T**GTGGACGGCTTCTCTGGTTGAGTTGCTTC	
	CTGTGTTGCCTATCACTTTGATTCTAGAGCC	
	CCGTCCAC**A**CAACAGAA	1403
	TTCTGTTG**T**GTGGACGG	1404
Lys Overproduction	TTATTGGGCATACAGTTAACTGCTTTGGCACTAAAATTAAAGTGGT	1405
DHPS	CGGCAACACAGGAA**A**TAACTCAACAAGGGAGGCTATTCACGCAAC	
Oryza sativa	TGAGCAGGGATTCGCTGTAGGTATGCACGC	
Ser24Asn	GCGTGCATACCTACAGCGAATCCCTGCTCAGTTGCGTGAATAGCC	1406
AGT-AAT	TCCCTTGTTGAGTTA**T**TTCCTGTGTTGCCGACCACTTTAATTTTAGT	
	GCCAAAGCAGTTAACTGTATGCCCAATAA	
	CACAGGAA**A**TAACTCAA	1407
	TTGAGTTA**T**TTCCTGTG	1408
Lys Overproduction	GCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACAA	1409
DHPS	GGGAGGCTATTCACGTAACTGAGCAGGGATTCGCTGTAGGTATG	
Oryza sativa	CACGCGGCTCTCCACATCAATCCTTACTACGG	
Ala133Val	CCGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGC	1410
GCA-GTA	GAATCCCTGCTCAGTT**A**CGTGAATAGCCTCCCTTGTTGAGTTACTT	
	CCTGTGTTGCCGACCACTTTAATTTTAGTGC	
	TATTCACG**T**AACTGAGC	1411
	GCTCAGTT**A**CGTGAATA	1412
Lys Overproduction	GGCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACA	1413
DHPS	AGGGAGGCTATTCACACAACTGAGCAGGGATTCGCTGTAGGTAT	
Oryza sativa	GCACGCGGCTCTCCACATCAATCCTTACTACG	
Ala133Thr	CGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCG	1414
GCA-ACA	AATCCCTGCTCAGTTG**T**GTGAATAGCCTCCCTTGTTGAGTTACTTC	
	CTGTGTTGCCGACCACTTTAATTTTAGTGCC	
	CTATTCAC**A**CAACTGAG	1415
	CTCAGTTG**T**GTGAATAG	1416
Lys Overproduction	TCATCGGGCATACTGTTAACTGCTTTGGAGCCAACATTAAAGTGAT	1417
DHPS 1	AGGCAACACGGGAA**A**TAACTCAACCAGAGAAGCTGTTCACGCGA	
Triticum aestivum	CAGAGCAGGGATTTGCTGTTGGCATGCATGC	
Ser65Asn	GCATGCATGCCAACAGCAAATCCCTGCTCTGTCGCGTGAACAGCT	1418
AGT-AAT	TCTCTGGTTGAGTTA**T**TTCCCGTGTTGCCTATCACTTTAATGTTGG	
	CTCCAAAGCAGTTAACAGTATGCCCGATGA	
	CACGGGAA**A**TAACTCAA	1419
	TTGAGTTA**T**TTCCCGTG	1420
Lys Overproduction	GAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACCA	1421
DHPS 1	GAGAAGCTGTTCACGTGACAGAGCAGGGATTTGCTGTTGGCATG	
Triticum aestivum	CATGCAGCTCTTCATGTCAATCCTTACTACGG	
Ala174Val	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA	1422
GCG-GTG	AATCCCTGCTCTGTC**A**CGTGAACAGCTTCTCTGGTTGAGTTACTTC	
	CCGTGTTGCCTATCACTTTAATGTTGGCTC	

TABLE 19-continued

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTTCACGTGACAGAGC	1423
	GCTCTGTCACGTGAACA	1424
Lys Overproduction	GGAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACC	1425
DHPS 1	AGAGAAGCTGTTCACACGACAGAGCAGGGATTTGCTGTTGGCAT	
Triticum aestivum	GCATGCAGCTCTTCATGTCAATCCTTACTACG	
Ala174Thr	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA	1426
GCG-ACG	ATCCCTGCTCTGTCGTGTGAACAGCTTCTCTGGTTGAGTTACTTCC	
	CGTGTTGCCTATCACTTTAATGTTGGCTCC	
	CTGTTCACAGGACAGAG	1427
	CTCTGTCGTGTGAACAG	1428
Lys Overproduction	TCATCGGGCACACTGTTAACTGCTTTGGAACTAACATTAAAGTGAT	1429
DHPS 2	AGGCAACACGGGAAATAACTCAACTAGAGAAGCGATTCACGCTTC	
Triticum aestivum	AGAGCAGGGATTTGCTGTTGGCATGCATGC	
Ser154Asn	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT	1430
AGT-AAT	TCTCTAGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTAGT	
	TCCAAAGCAGTTAACAGTGTGCCCGATGA	
	CACGGGAAATAACTCAA	1431
	TTGAGTTATTTCCCGTG	1432
Lys Overproduction	GAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTA	1433
DHPS 2	GAGAAGCGATTCACGTTTCAGAGCAGGGATTTGCTGTTGGCATGC	
Triticum aestivum	ATGCAGCTCTCCATGTCAATCCTTACTATGG	
Ala163Val	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA	1434
GCT-GTT	AATCCCTGCTCTGAAACGTGAATCGCTTCTCTAGTTGAGTTACTTC	
	CCGTGTTGCCTATCACTTTAATGTTAGTTC	
	GATTCACGTTTCAGAGC	1435
	GCTCTGAAACGTGAATC	1436
Lys Overproduction	GGAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACT	1437
DHPS 2	AGAGAAGCGATTCACACTTCAGAGCAGGGATTTGCTGTTGGCATG	
Triticum aestivum	CATGCAGCTCTCCATGTCAATCCTTACTATG	
Ala163Thr	CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA	1438
GCT-ACT	ATCCCTGCTCTGAAGTGTGAATCGCTTCTCTAGTTGAGTTACTTCC	
	CGTGTTGCCTATCACTTTAATGTTAGTTCC	
	CGATTCACACTTCAGAG	1439
	CTCTGAAGTGTGAATCG	1440
Lys Overproduction	CTCATTGGGCATACTGTGAACTGCTTTGGCTCTAGAATTAAAGTGA	1441
DHPS	TAGGCAACACAGGAAATAACTCAACCAGAGAAGCTGTTCACGCAA	
Coix lacryma-jobi	CAGAGCAGGGATTTGCTGTTGGCATGCATG	
Ser154Asn	CATGCATGCCAACAGCAAATCCCTGCTCTGTTGCGTGAACAGCTT	1442
AGT-AAT	CTCTGGTTGAGTTATTTCCTGTGTTGCCTATCACTTTAATTCTAGA	
	GCCAAAGCAGTTCACAGTATGCCCAATGAG	
	CACAGGAAATAACTCAA	1443
	TTGAGTTATTTCCTGTG	1444
Lys Overproduction	GCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACCA	1445
DHPS	GAGAAGCTGTTCACGTAACAGAGCAGGGATTTGCTGTTGGCATGC	
Coix lacryma-jobi	ATGCAGCTCTCCACATCAATCCTTACTATGG	
Ala163Val	CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA	1446
GCA-GTA	AATCCCTGCTCTGTTACGTGAACAGCTTCTCTGGTTGAGTTACTTC	
	CTGTGTTGCCTATCACTTTAATTCTAGAGC	
	TGTTCACGTAACAGAGC	1447
	GCTCTGTTACGTGAACA	1448
Lys Overproduction	GGCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACC	1449
DHPS	AGAGAAGCTGTTCACACAACAGAGCAGGGATTTGCTGTTGGCATG	
Coix lacryma-jobi	CATGCAGCTCTCCACATCAATCCTTACTATG	
Ala163Thr	CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA	1450
GCA-ACA	ATCCCTGCTCTGTTGTGTGAACAGCTTCTCTGGTTGAGTTACTTCC	
	TGTGTTGCCTATCACTTTAATTCTAGAGCC	
	CTGTTCACACAACAGAG	1451
	CTCTGTTGTGTGAACAG	1452
Lys Overproduction	TCATTGGTCACACAGTCAATTGTTTTGGAGGGTCCATCAAAGTCAT	1453
DHPS	CGGGAACACTGGAAACAACTCCACAAGGGAAGCAATCCATGCAA	
Nicotiana tabacum	CTGAACAGGGATTTGCTGTAGGTATGCATGC	
Ser136Asn	GCATGCATACCTACAGCAAATCCCTGTTCAGTTGCATGGATTGCTT	1454

TABLE 19-continued

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
AGC-AAC	CCCTTGTGGAGTTGTTTCCAGTGTTCCCGATGACTTTGATGGACC	
	CTCCAAAACAATTGACTGTGTGACCAATGA	
	CACTGGAAACAACTCCA	1455
	TGGAGTTGTTTCCAGTG	1456
Lys Overproduction	GAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAA	1457
DHPS	GGGAAGCAATCCATGTAACTGAACAGGGATTTGCTGTAGGTATGC	
Nicotiana tabacum	ATGCAGCTCTTCACATTAATCCCTACTATGG	
Ala145Val	CCATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCA	1458
GCA-GTA	AATCCCTGTTCAGTTACATGGATTGCTTCCCTTGTGGAGTTGCTTC	
	CAGTGTTCCCGATGACTTTGATGGACCCTC	
	AATCCATGTAACTGAAC	1459
	GTTCAGTTACATGGATT	1460
Lys Overproduction	GGAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCAC	1461
DHPS	AAGGGAAGCAATCCATACAACTGAACAGGGATTTGCTGTAGGTAT	
Nicotiana tabacum	GCATGCAGCTCTTCACATTAATCCCTACTATG	
Ala145Thr	CATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAA	1462
GCA-ACA	ATCCCTGTTCAGTTGTATGGATTGCTTCCCTTGTGGAGTTGCTTCC	
	AGTGTTCCCGATGACTTTGATGGACCCTCC	
	CAATCCATACAACTGAA	1463
	TTCAGTTGTATGGATTG	1464
Lys Overproduction	TTATAGGCCATACCGTTAACTGTTTTGGCGGAAGCATCAAAGTCAT	1465
DHPS	TGGAAACACTGGAAACAATTCGACTAGAGAAGCAATCCACGCGAC	
Arabidopsis thaliana	TGAACAAGGATTCGCGGTTGGAATGCATGC	
Ser142Asn	GCATGCATTCCAACCGCGAATCCTTGTTCAGTCGCGTGGATTGCT	1466
AGC-AAC	TCTCTAGTCGAATTGTTTCCAGTGTTTCCAATGACTTTGATGCTTC	
	CGCCAAAACAGTTAACGGTATGGCCTATAA	
	CACTGGAAACAATTCGA	1467
	TCGAATTGTTTCCAGTG	1468
Lys Overproduction	GCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTA	1469
DHPS	GAGAAGCAATCCACGTGACTGAACAAGGATTCGCGGTTGGAATG	
Arabidopsis thaliana	CATGCTGCTCTTCATATAAACCCTTACTATGG	
Ala151Val	CCATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCG	1470
GCG-GTG	AATCCTTGTTCAGTCACGTGGATTGCTTCTCTAGTCGAATTGCTTC	
	CAGTGTTTCCAATGACTTTGATGCTTCCGC	
	AATCCACGTGACTGAAC	1471
	GTTCAGTCACGTGGATT	1472
Lys Overproduction	GGCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACT	1473
DHPS	AGAGAAGCAATCCACACGACTGAACAAGGATTCGCGGTTGGAAT	
Arabidopsis thaliana	GCATGCTGCTCTTCATATAAACCCTTACTATG	
Ala151Thr	CATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGA	1474
GCG-ACG	ATCCTTGTTCAGTCGTGTGGATTGCTTCTCTAGTCGAATTGCTTCC	
	AGTGTTTCCAATGACTTTGATGCTTCCGCC	
	CAATCCACACGACTGAA	1475
	TTCAGTCGTGTGGATTG	1476
Lys Overproduction	TTATTGCTCATACAGTCAACTGTTTTGGTGGGAAAATTAAGGTTAT	1477
DHPS	TGGAAATACTGGAAACAACTCCACCAGGGAAGCAATTCATGCCAC	
Glycine max	TGAGCAGGGTTTTGCTGTTGGAATGCATGC	
Ser103Asn	GCATGCATTCCAACAGCAAAACCCTGCTCAGTGGCATGAATTGCT	1478
AGC-AAC	TCCCTGGTGGAGTTGTTTCCAGTATTTCCAATAACCTTAATTTTCC	
	CACCAAAACAGTTGACTGTATGAGCAATAA	
	TACTGGAAACAACTCCA	1479
	TGGAGTTGTTTCCAGTA	1480
Lys Overproduction	GTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCA	1481
DHPS	GGGAAGCAATTCATGTCACTGAGCAGGGTTTTGCTGTTGGAATGC	
Glycine max	ATGCTGCCCTTCACATAAACCCTTACTATGG	
Ala112Val	CCATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCA	1482
GCC-GTC	AAACCCTGCTCAGTGACATGAATTGCTTCCCTGGTGGAGTTGCTT	
	CCAGTATTTCCAATAACCTTAATTTTCCCAC	
	AATTCATGTCACTGAGC	1483
	GCTCAGTGACATGAATT	1484
Lys Overproduction	GGTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACC	1485
DHPS	AGGGAAGCAATTCATACCACTGAGCAGGGTTTTGCTGTTGGAATG	

TABLE 19-continued

Genome-Altering Oligos Conferring Amino Acid Overproduction

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Glycine max	CATGCTGCCCTTCACATAAACCCTTACTATG	
Ala112Thr	CATAGTAAGGGTTTATGTGAAGGGCAGCATGGATTCCAACAGCAA	1486
GCC-ACC	AACCCTGCTCAGTGG**T**ATGAATTGCTTCCCTGGTGGAGTTGCTTC	
	CAGTATTTCCAATAACCTTAATTTTCCCACC	
	CAATTCAT**A**CCACTGAG	1487
	CTCAGTGG**T**ATGAATTG	1488
Trp Overproduction	CTTGCAGGAGACATATTTCAGATCGTGCTGAGTCAACGTTTTGAG	1489
AS	CGGCGAACATTTGCA**A**ACCCCTTTGAAGTTTATAGAGCACTAAGA	
Arabidopsis thaliana	GTTGTGAATCCAAGTCCGTATATGGGTTATT	
Asp341Asn	AATAACCCATATACGGACTTGGATTCACAACTCTTAGTGCTCTATA	1490
GAG-AAC	AACTTCAAAGGGGT**T**TGCAAATGTTCGCCGCTCAAAACGTTGACT	
	CAGCACGATCTGAAATATGTCTCCTGCAAG	
	CATTTGCA**A**ACCCCTTT	1491
	AAAGGGGT**T**TGCAAATG	1492
Trp Overproduction	GCTGCAGGAGACATATTTCAAATCGTTTTAAGTCAACGCTTTGAGA	1493
AS	GAAGAACATTTGCT**A**ACCCATTTGAAGTGTACAGAGCATTAAGAAT	
Nicotiana tabacum	TGTGAATCCAAGCCCATATATGACTTACA	
Asp326Asn	TGTAAGTCATATATGGGCTTGGATTCACAATTCTTAATGCTCTGTA	1494
GAC-AAC	CACTTCAAATGGGT**T**AGCAAATGTTCTTCTCTCAAAGCGTTGACTT	
	AAAACGATTTGAAATATGTCTCCTGCAGC	
	CATTTGCT**A**ACCCATTT	1495
	AAATGGGT**T**AGCAAATG	1496
Trp Overproduction	CTAGCTGGTGACATTTTTCAAGTAGTCTTAAGCCAGCGTTTTGAGA	1497
AS	GGCGTACATTTGCT**A**ACCCCTTTGAGGTGTACCGTGCATTGCGTA	
Oryza sativa	TTGTCAATCCTAGTCCTTATATGGCCTATC	
Asp323Asn	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT	1498
GAC-AAC	ACACCTCAAAGGGGT**T**AGCAAATGTACGCCTCTCAAAACGCTGGC	
	TTAAGACTACTTGAAAAATGTCACCAGCTAG	
	CATTTGCT**A**ACCCCTTT	1499
	AAAGGGGT**T**AGCAAATG	1500
Trp Overproduction	CTTGCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTTGAAA	1501
AS	GGCGAACGTTCGCA**A**ACCCATTTGAAATCTATAGATCACTGAGGA	
Ruta graveolens	TTGTTAATCCAAGCCCATATATGACTTATT	
Asp354Asn	AATAAGTCATATATGGGCTTGGATTAACAATCCTCAGTGATCTATA	1502
GAC-AAC	GATTTCAAATGGGT**T**TGCGAACGTTCGCCTTTCAAAACGCTGACTT	
	AGTACGATCTGGAATATGTCACCAGCAAG	
	CGTTCGCA**A**ACCCATTT	1503
	AAATGGGT**T**TGCGAACG	1504
Trp Overproduction	CTGGCTGGGGACATATTCCAGCTTGTCCTAAGTCAGCGTTTTGAA	1505
AS	CGGCGAACATTTGCA**A**ATCCATTTGAAGTCTACCGAGCATTGAGA	
Catharanthus roseus	ATTGTCAACCCAAGTCCATATATGACTTATT	
Asp354Asn	AATAAGTCATATATGGACTTGGGTTGACAATTCTCAATGCTCGGTA	1506
GAT-AAT	GACTTCAAATGGAT**T**TGCAAATGTTCGCCGTTCAAAACGCTGACTT	
	AGGACAAGCTGGAATATGTCCCCAGCCAG	
	CATTTGCA**A**ATCCATTT	1507
	AAATGGAT**T**TGCAAATG	1508

EXAMPLE 10

Production of Modified Starch in Plants

[0138] A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

[0139] The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of α-1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional α-1,6-glycosidic linkages. In plants from which starch is typi-

cally isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

[0140] In maize, various mutants in starch metabolism are known, for example waxy, sugary, shrunken and opaque-2. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

[0141] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

TABLE 20

Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT	1509
ADPGPP	ATTCTTGGAGGTGGA**AA**AGGAACTCGACTCTTTCCTCTCACAAAA	
Arabidopsis thaliana	CGCCGCGCCAAGCCTGCCGTTCCTATCGGGG	
Ala99Lys	CCCCGATAGGAACGGCAGGCTTGGCGCGGCGTTTTGTGAGAGGA	1510
GCA-AAA	AAGAGTCGAGTTCCT**TT**TCCACCTCCAAGAATAATGGAAGCAACT	
	GTCCTTGGATCCCTTTTCTCAGTCTCAAGTTC	
	GAGGTGGA**AA**AGGAACT	1511
	AGTTCCT**TT**TCCACCTC	1512
Increased Starch	CAAAACGCCGCGCCAAGCCTGCCGTTCCTATCGGGGGAGCCTAT	1513
ADPGPP	AGGTTGATAGATGTAC**T**AATGAGCAATTGTATTAACAGCGGAATCA	
Arabidopsis thaliana	ACAAAGTCTACATACTCACACAATATAACTC	
Pro127Leu	GAGTTATATTGTGTGAGTATGTAGACTTTGTTGATTCCGCTGTTAA	1514
CCA-CTA	TACAATTGCTCATT**A**GTACATCTATCAACCTATAGGCTCCCCCGAT	
	AGGAACGGCAGGCTTGGCGCGGCGTTTTG	
	AGATGTAC**T**AATGAGCA	1515
	TGCTCATT**A**GTACATCT	1516
Increased Starch	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC	1517
ADPGPP	TTACAACTCCAAT**AAT**CTTGGCTTTGGAGATGGCTATGTTGAGGTT	
Arabidopsis thaliana	CTTGCGGCCACTCAAACGCCAGGAGAATC	
Gly162Asn	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA	1518
GGA-AAT	TCTCCAAAGCCAAG**ATT**ATTGGAGTTGTAAGCACGGGGTAAATGC	
	CTGTTCAATGATGCTGAGTTATATTGTGTGA	
	CTCCAAT**AAT**CTTGGCT	1519
	AGCCAAG**ATT**ATTGGAG	1520
Increased Starch	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC	1521
ADPGPP	TTACAACTCCAAT**AAC**CTTGGCTTTGGAGATGGCTATGTTGAGGTT	
Arabidopsis thaliana	CTTGCGGCCACTCAAACGCCAGGAGAATC	
Gly162Asn	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA	1522
GGA-AAC	TCTCCAAAGCCAAG**GTT**ATTGGAGTTGTAAGCACGGGCTAAATGC	
	CTGTTCAATGATGCTGAGTTATATTGTGTGA	
	CTCCAAT**AAC**CTTGGCT	1523
	AGCCAAG**GTT**ATTGGAG	1524
Increased Starch	GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT	1525
ADPGPP	TCTAGGAGGAGGCAA**A**GGAGCTAAACTCTTCCCTCTTACAATGAG	
Arabidopsis thaliana	AGCCGCAACACCAGCTGTAAATATTCATCTT	
Asn100Lys	AAGATGAATATTTACAGCTGGTGTTGCGGCTCTCATTGTAAGAGG	1526
AAT-AAA	GAAGAGTTTAGCTCC**T**TTGCCTCCTCCTAGAATGATTGCAGCCAC	
	ATTTTGCGGGTCTACCTTTCTTCTCTCAAAC	
	GGAGGCAA**A**GGAGCTAA	1527
	TTAGCTCC**T**TTGCCTCC	1528
Increased Starch	CTTGTGTCTTCAAATTATGTTAGGTTCCTGTTGGTGGATGCTACAG	1529
ADPGPP	GCTGATCGATATCC**T**GATGAGTAACTGTATTAACAGCTGCATCAAC	
Arabidopsis thaliana	AAGATATTTGTGCTGACACAGTTCAACTC	
Pro128Leu	GAGTTGAACTGTGTCAGCACAAATATCTTGTTGATGCAGCTGTTAA	1530
CCG-CTG	TACAGTTACTCATC**A**GGATATCGATCAGCCTGTAGCATCCACCAA	
	CAGGAACCTAACATAATTTGAAGACACAAG	
	CGATATCC**T**GATGAGTA	1531
	TACTCATC**A**GGATATCG	1532
Increased Starch	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC	1533
ADPGPP	TTATTTTGGGAAT**AAT**ATAAACTTTGGAGGTGGTTTCGTAGAGGTA	
Arabidopsis thaliana	CAAACACTATGACAATAATAACTCTCAGC	

TABLE 20-continued

Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Gly163Asn	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC	1534
GGC-AAT	CTCCAAAGTTTAT**ATT**ATTCCCAAAATAAGTTCGTGCTAAATGTCG	
	ATTAAGGGAAGCTGAGTTGAACTGTGTCA	
	TGGGAAT**AAT**ATAAACT	1535
	AGTTTAT**ATT**ATTCCCA	1536
Increased Starch	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC	1537
ADPGPP	TTATTTTGGGAAT**AAC**ATAAACTTTGGAGGTGGTTTCGTAGAGGTA	
Arabidopsis thaliana	CAAACACTATGACAATAATAACTCTCAGC	
Gly163Asn	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC	1538
GGC-AAC	CTCCAAAGTTTAT**GTT**ATTCCCAAAATAAGTTCGTGCTAAATGTCG	
	ATTAAGGGAAGCTGAGTTGAACTGTGTCA	
	TGGGAAT**AAC**ATAAACT	1539
	AGTTTAT**GTT**ATTCCCA	1540
Increased Starch	TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCA	1541
ADPGPP	TTCTAGGTGGTGGT**AAA**GGAACTCGTCTTTTTCCTCTTACAAGCA	
Lycopersicon	GAAGAGCTAAACCAGCTGTTCCTATTGGTGG	
esculentum	CCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTGTAAGAGGA	1542
Val94Lys	AAAAGACGAGTTCC**TTT**ACCACCACCTAGAATGACAGAGGCAACA	
GTT-AAA	GCTTTTGGATCTGCCGTTGGTTGTTCCTCAA	
	TGGTGGT**AAA**GGAACTC	1543
	GAGTTCC**TTT**ACCACCA	1544
Increased Starch	CAAGCAGAAGAGCTAAACCAGCTGTTCCTATTGGTGGTTGTTACC	1545
ADPGPP	GGCTAATTGATGTAC**A**AATGAGTAACTGCATTAACAGTGGCATAC	
Lycopersicon	GGAAAATTTTCATCTTAACACAGTTCAATTC	
esculentum	GAATTGAACTGTGTTAAGATGAAAATTTTCCGTATGCCACTGTTAA	1546
Pro122Leu	TGCAGTTACTCATT**T**GTACATCAATTAGCCGGTAACAACCACCAAT	
CCA-CAA	AGGAACAGCTGGTTTAGCTCTTCTGGTTG	
	TGATGTAC**A**AATGAGTA	1547
	TACTCATT**T**GTACATCA	1548
Increased Starch	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTA	1549
ADPGPP	TAATTTTGGAAAT**AAT**GTGGGTTTTGGAGATGGATTTGTGGAGGTT	
Lycopersicon	TTAGCTGCAACCCAGACTCCAGGGGATGC	
esculentum	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA	1550
Gly158Asn	TCTCCAAAACCCAC**ATT**ATTTCCAAAATTATACGTGCGGGCAAGGT	
GGA-AAT	GACGATTGAGGGAAAAGGAATTGAACTGTG	
	TGGAAAT**AAT**GTGGGTT	1551
	AACCCAC**ATT**ATTTCCA	1552
Increased Starch	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTA	1553
ADPGPP	TAATTTTGGAAAT**AAC**GTGGGTTTTGGAGATGGATTTGTGGAGGT	
Lycopersicon	TTTAGCTGCAACCCAGACTCCAGGGGATGC	
esculentum	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA	1554
Gly158Asn	TCTCCAAAACCCAC**GTT**ATTTCCAAAATTATACGTGCGGGCAAGGT	
GGA-AAC	GACGATTGAGGGAAAAGGAATTGAACTGTG	
	TGGAAAT**AAC**GTGGGTT	1555
	AACCCAC**GTT**ATTTCCA	1556
Increased Starch	ACGTAGATTTGGAAAAAAGAGACCCAAGTACAGTTGTAGCAATTAT	1557
ADPGPP	ACTAGGTGGAGGT**AAA**GGAACTCGTCTCTTCCCTCTCACCAAGCG	
Cicer arietinum	ACGAGCCAAGCCTGCTGTTCCAATTGGAGG	
Ala101Lys	CCTCCAATTGGAACAGCAGGCTTGGCTCGTCGCTTGGTGAGAGG	1558
GCT-AAA	GAAGAGACGAGTTCC**TTT**ACCTCCACCTAGTATAATTGCTACAACT	
	GTACTTGGGTCTCTTTTTTCCAAATCTACGT	
	TGGAGGT**AAA**GGAACTC	1559
	GAGTTCC**TTT**ACCTCCA	1560
Increased Starch	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA	1561
ADPGPP	GGCTGATAGATGTAC**T**AATGAGTAACTGCATCAATAGTGGGATCA	
Cicer arietinum	ACAAAGTATACATTCTCACTCAATTTAATTC	
Pro129Leu	GAATTAAATTGAGTGAGAATGTATACTTTGTTGATCCCACTATTGA	
	1562	
CCA-CTA	TGCAGTTACTCATT**A**GTACATCTATCAGCCTATAAGCACCTCCAAT	
	TGGAACAGCAGGCTTGGCTCGTCGCTTGG	
	AGATGTAC**T**AATGAGTA	1563
	TACTCATT**A**GTACATCT	1564

TABLE 20-continued

Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA	1565
ADPGPP	TAACTCTGGTACT**AAT**GTCACTTTTGGAGATGGCTATGTTGAGGTT	
Cicer arietinum	CTTGCAGCAACTCAAACTCCAGGGGAGCA	
Gly165Asn	TGCTCCCGTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA	1566
GGA-AAT	TCTCCAAAAGTGAC**ATT**AGTACCAGAGTTATAAGCACGTGCAATAT	
	GCCTGTTGAGTGAGGCTGAATTAAATTGAG	
	TGGTACT**AAT**GTCACTT	1567
	AAGTGAC**ATT**AGTACCA	1568
Increased Starch	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA	1569
ADPGPP	TAACTCTGGTACT**AAC**GTCACTTTTGGAGATGGCTATGTTGAGGTT	
Cicer arietinum	CTTGCAGCAACTCAAACTCCAGGGGAGCA	
Gly165Asn	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA	1570
GGA-AAC	TCTCCAAAAGTGAC**GTT**AGTACCAGAGTTATAAGCACGTGCAATAT	
	GCCTGTTGAGTGAGGCTGAATTAAATTGAG	
	TGGTACT**AAC**GTCACTT	1571
	AAGTGAC**GTT**AGTACCA	1572
Increased Starch	ATATTGGAGAGGCGTCGGGCAAACCCTAAGAATGTGGCTGCAATC	
	1573	
ADPGPP	ATACTGCCAGGCGGT**AA**AGGGACACACCTATTCCCTCTCACCAAT	
Ipomoea batatas	CGAGCTGCAACCCCTGCTGTTCCACTTGGAG	
Ala94Lys	CTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGG	1574
GCA-AAA	AATAGGTGTGTCCCT**TT**ACCGCCTGGCAGTATGATTGCAGCCACA	
	TTCTTAGGGTTTGCCCGACGCCTCTCCAATAT	
	CAGGCGGT**AA**AGGGACA	1575
	TGTCCCT**TT**ACCGCCTG	1576
Increased Starch	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATA	1577
ADPGPP	GGTTGATCGACATTC**T**AATGAGCAACTGCATCAACAGCGGGGTTA	
Ipomoea batatas	ACAAGATCTTTGTGCTGACCCAGTTCAATTC	
Pro122Leu	GAATTGAACTGGGTCAGCACAAAGATCTTGTTAACCCCGCTGTTG	1578
CCA-CTA	ATGCAGTTGCTCATT**A**GAATGTCGATCAACCTATAGCATCCTCCAA	
	GTGGAACAGCAGGGGTTGCAGCTCGATTGG	
	CGACATTC**T**AATGAGCA	1579
	TGCTCATT**A**GAATGTCG	1580
Increased Starch	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC	1581
ADPGPP	CGTCTTTGGCAAT**AAT**GTGAGCTTCGGAGATGGATTTGTTGAGGT	
Ipomoea batatas	GCTGGCTGCAACCCAAACACAAGGGGAAAC	
Gly157Asn	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA	1582
GGT-AAT	TCTCCGAAGCTCAC**ATT**ATTGCCAAAGACGGTACGGGAAATGTGA	
	CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	
	TGGCAAT**AAT**GTGAGCT	1583
	AGCTCAC**ATT**ATTGCCA	1584
Increased Starch	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC	1585
ADPGPP	CGTCTTTGGCAAT**AAC**GTGAGCTTCGGAGATGGATTTGTTGAGGT	
Ipomoea batatas	GCTGGCTGCAACCCAAACACAAGGGGAAAC	
Gly157Asn	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA	1586
GGT-AAC	TCTCCGAAGCTCAC**GTT**ATTGCCAAAGACGGTACGGGAAATGTGA	
	CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	
	TGGCAAT**AAC**GTGAGCT	1587
	AGCTCAC**GTT**ATTGCCA	1588
Increased Starch	CATTCCGGAGGAACTTTGCGGATCCAAATGAGGTTGCTGCTGTTA	1589
ADPGPP	TATTGGGTGGTGGCA**AA**GGGACTCAACTTTTTCCTCTCACAAGCA	
Oryza sativa	CAAGGGCCACGCCTGCTGTTCCTATTGGAGG	
Thr96Lys	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTGTGAGAGG	1590
ACC-AAA	AAAAAGTTGAGTCCC**TT**TGCCACCACCCAATATAACAGCAGCAAC	
	CTCATTTGGATCCGCAAAGTTCCTCCGGAATG	
	TGGTGGCA**AA**GGGACTC	1591
	GAGTCCC**TT**TGCCACCA	1592
Increased Starch	CAAGCACAAGGGCCACGCCTGCTGTTCCTATTGGAGGATGCTATA	1593
ADPGPP	GGCTTATCGATATCC**T**CATGAGCAACTGTTTCAACAGTGGCATAAA	
Oryza sativa	CAAGATATTCATAATGACTCAATTCAACTC	
Pro124Leu	GAGTTGAATTGAGTCATTATGAATATCTTGTTTATGCCACTGTTGA	1594
CCC-CTC	AACAGTTGCTCATG**A**GGATATCGATAAGCCTATAGCATCCTCCAAT	
	AGGAACAGCAGGCGTGGCCCTTGTGCTTG	

TABLE 20-continued

Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGATATCC**T**CATGAGCA	1595
	TGCTCATG**A**GGATATCG	1596
Increased Starch	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC	1597
ADPGPP	GTACCTTGGTGGT**AAT**ATCAACTTTACTGATGGTTCTGTTGAGGTA	
Oryza sativa	TTAGCCGCTACACAAATGCCTGGGGAGGC	
Gly159Asn	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA	1598
GGA-AAT	TCAGTAAAGTTGAT**ATT**ACCACCAAGGTACGTACGATGAATGTGA	
	CGATTAAGAGATGCTGAGTTGAATTGAGTCA	
	TGGTGGT**AAT**ATCAACT	1599
	AGTTGAT**ATT**ACCACCA	1600
Increased Starch	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC	1601
ADPGPP	GTACCTTGGTGGT**AAC**ATCAACTTTACTGATGGTTCTGTTGAGGTA	
Oryza sativa	TTAGCCGCTACACAAATGCCTGGGGAGGC	
Gly159Asn	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA	1602
GGA-AAC	TCAGTAAAGTTGAT**GTT**ACCACCAAGGTACGTACGATGAATGTGA	
	CGATTAAGAGATGCTGAGTTGAATTGAGTCA	
	TGGTGGT**AAC**ATCAACT	1603
	AGTTGAT**GTT**ACCACCA	1604
Increased Starch	GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC	1605
ADPGPP	ATACTCGGCGGCGGCA**AA**GGGACTCAGCTCTTCCCACTCACGAG	
Triticum aestivum	CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	
Thr80Lys	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG	1606
ACC-AAA	GAAGAGCTGAGTCCC**TT**TGCCGCCGCCGAGTATGACGGCCGCAA	
	CCTCGTTCGGATCGCTTAATCCTCCTGAAGGAC	
	CGGCGGCA**AA**GGGACTC	1607
	GAGTCCC**TT**TGCCGCCG	1608
Increased Starch	CGAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA	1609
ADPGPP	GGCTCATCGACATTC**T**CATGAGCAACTGCTTCAACAGTGGCATCA	
Triticum aestivum	ACAAGATATTCGTCATGACCCAGTTCAACTC	
Pro108Leu	GAGTTGAACTGGGTCATGACGAATATCTTGTTGATGCCACTGTTG	1610
CCC-CTC	AAGCAGTTGCTCATG**A**GAATGTCGATGAGCCTGTAACATCCTCCA	
	ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	
	CGACATTC**T**CATGAGCA	1611
	TGCTCATG**A**GAATGTCG	1612
Increased Starch	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA	1613
ADPGPP	CCTACCTCGGCGGG**AAT**ATCAATTTCACTGATGGATCCGTTGAGG	
Triticum aestivum	TATTGGCCGCGACGCAAATGCCCGGGGAGGC	
Gly143Asn	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC	1614
GGA-AAT	ATCAGTGAAATTGAT**ATT**CCCGCCGAGGTAGGTGCGGTGAATGTG	
	ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	
	CGGCGGG**AAT**ATCAATT	1615
	AATTGAT**ATT**CCCGCCG	1616
Increased Starch	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA	1617
ADPGPP	CCTACCTCGGCGGG**AAC**ATCAATTTCACTGATGGATCCGTTGAGG	
Triticum aestivum	TATTGGCCGCGACGCAAATGCCCGGGGAGGC	
Gly143Asn	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC	1618
GGA-AAC	ATCAGTGAAATTGAT**GTT**CCCGCCGAGGTAGGTGCGGTGAATGTG	
	ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	
	CGGCGGG**AAC**ATCAATT	1619
	AATTGAT**GTT**CCCGCCG	1620
Increased Starch	CCTCCCGAAAGAATTATGCTGATGCAAGCCACGTTTCTGCTGTCA	1621
ADPGPP	TTTTGGGTGGAGGCA**AA**GGAGTTCAACTCTTTCCTCTGACAAGCA	
Oryza sativa	CAAGGGCTACCCCCGCTGTTCCTGTTGGAGG	
Thr95Lys	CCTCCAACAGGAACAGCGGGGGTAGCCCTTGTGCTTGTCAGAGG	1622
ACT-AAA	AAAGAGTTGAACTCC**TT**TGCCTCCACCCAAAATGACAGCAGAAAC	
	GTGGCTTGCATCAGCATAATTCTTTCGGGAGG	
	TGGAGGCA**AA**GGAGTTC	1623
	GAACTCC**TT**TGCCTCCA	1624
Increased Starch	CAAGCACAAGGGCTACCCCCGCTGTTCCTGTTGGAGGATGTTACA	1625
ADPGPP	GGCTTATTGACATCC**T**TATGAGCAATTGCTTCAATAGCGGAATAAA	
Oryza sativa	TAAAATATTTGTGATGACTCAGTTCAATTC	
Pro123Leu	GAATTGAACTGAGTCATCACAAATATTTTATTTATTCCGCTATTGAA	1626

TABLE 20-continued

Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
CCT-CTT	GCAATTGCTCATA**A**GGATGTCAATAAGCCTGTAACATCCTCCAACA	
	GGAACAGCGGGGGTAGCCCTTGTGCTTG	
	TGACATCC**T**TATGAGCA	1627
	TGCTCATA**A**GGATGTCA	1628
Increased Starch	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA	1629
ADPGPP	TACCTTGGTGGG**AAT**ATCAACTTTACTGATGGGTCTGTGCAGGTA	
Oryza sativa	TTGGCTGCTACACAAATGCCTGACGAACC	
Gly158Asn	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA	1630
GGG-AAT	TCAGTAAAGTTGAT**ATT**CCCACCAAGGTATGTATGATGGATATGGC	
	GATTAAGAGAAGCAGAATTGAACTGAGTCA	
	TGGTGGG**AAT**ATCAACT	1631
	AGTTGATATTCCCACCA	1632
Increased Starch	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA	1633
ADPGPP	TACCTTGGTGGG**AAC**ATCAACTTTACTGATGGGTCTGTGCAGGTA	
Oryza sativa	TTGGCTGCTACACAAATGCCTGACGAACC	
Gly158Asn	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA	1634
GGG-AAC	TCAGTAAAGTTGAT**GTT**CCCACCAAGGTATGTATGATGGATATGG	
	CGATTAAGAGAAGCAGAATTGAACTGAGTCA	
	TGGTGGG**AAC**ATCAACT	1635
	AGTTGAT**GTT**CCCACCA	1636
Increased Starch	CCTTCCGCAGGAATTACGCCGATCCGAACGAGGTCGCGGCCGTC	1637
ADPGPP	ATACTCGGCGGTGGCAAAGGGACTCAGCTCTTCCCTCTCACAAG	
Triticum pestivum	CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	
Thr99Lys	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTTGTGAGAGG	1638
ACC-AAA	GAAGAGCTGAGTCCC**TT**TGCCACCGCCGAGTATGACGGCCGCGA	
	CCTCGTTCGGATCGGCGTAATTCCTGCGGAAGG	
	CGGTGGC**AA**AGGGACTC	1639
	GAGTCCC**TT**TGCCACCG	1640
Increased Starch	CAAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA	1641
ADPGPP	GGCTCATCGATATTC**T**CATGAGCAACTGCTTCAATAGTGGCATCAA	
Triticum aestivum	CAAGATATTCGTCATGACGCAGTTCAACTC	
Pro127Leu	GAGTTGAACTGCGTCATGACGAATATCTTGTTGATGCCACTATTGA	1642
CCC-CTC	AGCAGTTGCTCATG**A**GAATATCGATGAGCCTGTAACATCCTCCAA	
	TAGGAACAGCAGGTGTGGCCCTTGTGCTTG	
	CGATATTC**T**CATGAGCA	1643
	TGCTCATG**A**GAATATCG	1644
Increased Starch	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA	1645
ADPGPP	CCTACCTCGGCGGG**AAT**ATCAATTTCACTGATGGATCTGTTGAGG	
Triticum aestivum	TATTGGCCGCGACGCAAATGCCCGGGGAGGC	
Gly162Asn	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC	1646
GGA-AAT	ATCAGTGAAATTGAT**ATT**CCCGCCGAGGTAGGTGCGGTGAATGTG	
	ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	
	CGGCGGG**AAT**ATCAATT	1647
	AATTGAT**ATT**CCCGCCG	1648
Increased Starch	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA	1649
ADPGPP	CCTACCTCGGCGGG**AAC**ATCAATTTCACTGATGGATCTGTTGAGG	
Triticum aestivum	TATTGGCCGCGACGCAAATGCCCGGGGAGGC	
Gly162Asn	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC	1650
GGA-AAC	ATCAGTGAAATTGAT**GTT**CCCGCCGAGGTAGGTGCGGTGAATGTG	
	ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	
	CGGCGGG**AAC**ATCAATT	1651
	AATTGAT**GTT**CCCGCCG	1652
Increased Starch	CTTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA	1653
ADPGPP	TTTTGGGTGGTGGTA**AA**GGGACTCAGCTTTTCCCTCTCACAAGCA	
Zea mays	CAAGGGCCACCCCTGCTGTTCCTATTGGAGG	
Thr96Lys	CCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTGTGAGAGG	1654
ACC-AAA	GAAAAGCTGAGTCCC**TT**TACCACCACCCAAAATGACGGCAGCGAG	
	TTCATTAGGATCAGCATAATTCCTCCGAAAAG	
	TGGTGGTA**AA**GGGACTC	1655
	GAGTCCC**TT**TACCACCA	1656
Increased Starch	CAAGCACAAGGGCCACCCCTGCTGTTCCTATTGGAGGATGTTACA	1657
ADPGPP	GGCTTATTGATATCC**T**CATGAGCAACTGTTTCAACAGTGGCATAAA	

TABLE 20-continued

Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Zea mays	CAAGATATTTGTTATGACTCAGTTCAACTC	
Pro124Leu	GAGTTGAACTGAGTCATAACAAATATCTTGTTTATGCCACTGTTGA	1658
CCC-CTC	AACAGTTGCTCATG**A**GGATATCAATAAGCCTGTAACATCCTCCAAT	
	AGGAACAGCAGGGGTGGCCCTTGTGCTTG	
	TGATATCC**T**CATGAGCA	1659
	TGCTCATG**A**GGATATCA	1660
Increased Starch	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC	1661
ADPGPP	CTATCTTGGTGGG**AAT**ATCAACTTCACTGATGGATCTGTTGAGGT	
Zea mays	GCTGGCTGCAACACAAATGCCTGGGGAGGC	
Gly159Asn	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA	1662
GGG-AAT	TCAGTGAAGTTGAT**ATT**CCCACCAAGATAGGTACGATGAATGTGA	
	CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	
	TGGTGGG**AAT**ATCAACT	1663
	AGTTGAT**ATT**CCCACCA	1664
Increased Starch	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC	1665
ADPGPP	CTATCTTGGTGGG**AAC**ATCAACTTCACTGATGGATCTGTTGAGGT	
Zea mays	GCTGGCTGCAACACAAATGCCTGGGGAGGC	
Gly159Asn	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA	1666
GGG-AAC	TCAGTGAAGTTGAT**GTT**CCCACCAAGATAGGTACGATGAATGTGA	
	CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	
	TGGTGGG**AAC**ATCAACT	1667
	AGTTGAT**GTT**CCCACCA	1668
Increased Starch	CTTGAGAGGCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT	1669
ADPGPP	CATTCTAGGAGGGGGA**AA**GGGAACTCGTCTTTTCCCCCTCACCAA	
Solanum tuberosum	ACGTCGTGCTAAGCCTGCCGTTCCAATGGGAG	
Ala58Lys	CTCCCATTGGAACGGCAGGCTTAGCACGACGTTTGGTGAGGGGG	1670
GCG-AAG	AAAAGACGAGTTCCC**TT**TCCCCCTCCTAGAATGATTGCTACTACTG	
	TCCTTGCATCGCCCTTCTTTTGCCTCTCAAG	
	GAGGGGGA**AA**GGGAACT	1671
	AGTTCCC**TT**TCCCCCTC	1672
Increased Starch	CCAAACGTCGTGCTAAGCCTGCCGTTCCAATGGGAGGAGCATATA	1673
ADPGPP	GGCTAATTGATGTAC**T**AATGAGCAACTGTATTAACAGTGGCATCAA	
Solanum tuberosum	CAAAGTATACATTCTCACTCAATTCAACTC	
Pro86Leu	GAGTTGAATTGAGTGAGAATGTATACTTTGTTGATGCCACTGTTAA	1674
CCA-CTA	TACAGTTGCTCATT**A**GTACATCAATTAGCCTATATGCTCCTCCCAT	
	TGGAACGGCAGGCTTAGCACGACGTTTGG	
	TGATGTAC**T**AATGAGCA	1675
	TGCTCATT**A**GTACATCA	1676
Increased Starch	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA	1677
ADPGPP	CAACTTTGGCAAT**AAT**GTCACATTCGAGAGTGGCTATGTCGAGGT	
Solanum tuberosum	CTTAGCAGCAACTCAAACACCAGGTGAATT	
Gly122Asn	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA	1678
GGG-AAT	CTCTCGAATGTGAC**ATT**ATTGCCAAAGTTGTAAGCACGAGCTATAT	
	GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	
	TGGCAAT**AAT**GTCACAT	1679
	ATGTGAC**ATT**ATTGCCA	1680
Increased Starch	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA	1681
ADPGPP	CAACTTTGGCAAT**AAC**GTCACATTCGAGAGTGGCTATGTCGAGGT	
Solanum tuberosum	CTTAGCAGCAACTCAAACACCAGGTGAATT	
Gly122Asn	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA	1682
GGG-AAC	CTCTCGAATGTGAC**GTT**ATTGCCAAAGTTGTAAGCACGAGCTATAT	
	GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	
	TGGCAAT**AAC**GTCACAT	1683
	ATGTGACGTTATTGCCA	1684
Increased Starch	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT	1685
ADPGPP	GCTGGGTGGTGGT**AAA**GGGACTCGCCTCTTTCCTCTTACTAGCAG	
Beta vulgaris	GAGAGCTAAGCCAGCAGTGCCAATTGGAGG	
Ala98Lys	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA	1686
GCT-AAA	AAGAGGCGAGTCCC**TTT**ACCACCACCCAGCACAATTGCAGCCACA	
	TTTTTTGGGTCAGCTTTTGGAGATTCAAATA	
	TGGTGGT**AAA**GGGACTC	1687
	GAGTCCC**TTT**ACCACCA	1688

TABLE 20-continued

Genome-Altering Oligos Conferring Increased Starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT	1689
ADPGPP	GCTGGGTGGTGGT**AAC**GGGACTCGCCTCTTTCCTCTTACTAGCAG	
Beta vulgaris	GAGAGCTAAGCCAGCAGTGCCAATTGGAGG	
Ala98Lys	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA	1690
GCT-AAC	AAGAGGCGAGTCCC**GTT**ACCACCACCCAGCACAATTGCAGCCAC	
	ATTTTTTGGGTCAGCTTTTGGAGATTCAAATA	
	TGGTGGT**AAC**GGGACTC	1691
	GAGTCCC**GTT**ACCACCA	1692
Increased Starch	CTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGGGTGTTAC	1693
ADPGPP	AGGCTGATTGATGTGC**T**TATGAGCAACTGCATCAACAGTGGCATT	
Beta vulgaris	AGAAAGATTTTCATTCTTACCCAGTTCAATTC	
Pro126Leu	GAATTGAACTGGGTAAGAATGAAAATCTTTCTAATGCCACTGTTGA	1694
CCT-CTT	TGCAGTTGCTCATA**A**GCACATCAATCAGCCTGTAACACCCTCCAA	
	TTGGCACTGCTGGCTTAGCTCTCCTGCTAG	
	TGATGTGC**T**TATGAGCA	1695
	TGCTCATA**A**GCACATCA	1696
Increased Starch	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA	1697
ADPGPP	TAATTTTGGAGAT**AAT**GTGAATTTTGGGGATGGCTTTGTGGAGGTT	
Beta vulgaris	TTTGCTGCTACACAAACACCTGGAGAATC	
Gly162Asn	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA	1698
GGT-AAT	TCCCCAAAATTCAC**ATT**ATCTCCAAAATTATAGGTTCGAGCAAGAT	
	GACGATTAAGCGAAAACGAATTGAACTGGG	
	TGGAGAT**AAT**GTGAATT	1699
	AATTCAC**ATT**ATCTCCA	1700
Increased Starch	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA	1701
ADPGPP	TAATTTTGGAGAT**AAC**GTGAATTTTGGGGATGGCTTTGTGGAGGT	
Beta vulgaris	TTTTGCTGCTACACAAACACCTGGAGAATC	
Gly162Asn	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA	1702
GGT-AAC	TCCCCAAAATTCAC**GTT**ATCTCCAAAATTATAGGTTCGAGCAAGAT	
	GACGATTAAGCGAAAACGAATTGAACTGGG	
	TGGAGAT**AAC**GTGAATT	1703
	AATTCAC**GTT**ATCTCCA	1704

[0142]

TABLE 21

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch	GAATCCAGGTAAACGGGTAGTTCAT-	1705
	AATGGCAACTGTGACTGCTT	
GBSS	CTTCTAACTTTGTGT	
	GAAGAACTTCACTTTTCAACAATCATGGTGCT	
Arabidopsis thaliana	TCTTCATGCTCTGATGTCGCTCAGATTAC	
Ser12Term	GTAATCTGAGCGACATCAGAGCATGAA-	1706
	GAAGCACCATGATTGTTG	
TCA-TGA	AAAAGTGAAGTTCTT	
	CACACAAAGTTAGAAGAAGCAGTCACAGTTG	
	CCATTATGAACTACCCGTTTACCTGGATTC	
	CTTTGTGT**G**AAGAACTT	1707
	AAGTTCTT**C**ACACAAAG	1708
Waxy starch	ATCCAGGTAAACGGGTAGTTCATAATG-	1709
	GCAACTGTGACTGCTTCTT	
GBSS	CTAACTTTGTGTCA	
	TGAACTTCACTTTTCAACAATCATGGTGCTTCT	
Arabidopsis thaliana	TCATGCTCTGATGTCGCTCAGATTACCT	
Arg13Term	AGGTAATCTGAGCGACATCAGAGCAT-	1710
	GAAGAAGCACCATGATTGT	
AGA-TGA	TGAAAAGTGAAGTTC	
	ATGACACAAAGTTAGAAGAAGCAGTCACAGT	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCCATTATGAACTACCCGTTTACCTGGAT	
	TTGTGTCA**T**GAACTTCA	1711
	TGAAGTTC**A**TGACACAA	1712
Waxy starch	TAAACGGGTAGTTCATAATGGCAACTGT-GACTGCTTCTTCTAACTT	1713
GBSS	TGTGTCAAGAACTTGACTTTTCAACAAT-CATGGTGCTTCTTCATGCT	
Arabidopsis thaliana	CTGATGTCGCTCAGATTACCTTAAAAGG	
Ser15Term	CCTTTTAAGGTAATCTGAGCGACATCA-GAGCATGAAGAAGCACCAT	1714
TCA-TGA	GATTGTTGAAAAGT	
	CAAGTTCTTGACACAAAGTTAGAAGAAGCAGT	
	CACAGTTGCCATTATGAACTACCCGTTTA	
	AAGAACTT**G**ACTTTTCA	1715
	TGAAAAGT**C**AAGTTCTT	1716
Waxy starch	TGACTGCTTCTTCTAACTTTGTGTCAA-GAACTTGACTTTTCAACAAT	1717
GBSS	CATGGTGCTTCTT	
	GATGCTCTGATGTCGCTCAGATTACCTTAAAAG	
Arabidopsis thaliana	GCCAATCCTTGACTCATTGTGGGTTAAG	
Ser24Term	CTTAACCCACAATGAGTCAAGGATTGGC-CTTTTAAGGTAATCTGAG	1718
TCA-TGA	CGACATCAGAGCAT	
	CAAGAAGCACCATGATTGTTGAAAAGTGAAG	
	TTCTTGACACAAAGTTAGAAGAAGCAGTCA	
	TGCTTCTT**G**ATGCTCTG	1719
	CAGAGCAT**C**AAGAAGCA	1720
Waxy starch	TGCTTCTTCTAACTTTGTGTCAAGAACT-TCACTTTTCAACAATCATG	1721
GBSS	GTGCTTCTTCATG	
	ATCTGATGTCGCTCAGATTACCTTAAAAGGCCA	
Arabidopsis thaliana	ATCCTTGACTCATTGTGGGTTAAGGTCA	
Cys25Term	TGACCTTAACCCACAATGAGTCAAGGAT-TGGCCTTTTAAGGTAATC	1722
TGC-TGA	TGAGCGACATCAGATCATGAAGAAGCAC-CATGATTGTTGAAAAGT	
	GAAGTTCTTGACACAAAGTTAGAAGAAGCA	
	TCTTCATG**A**TCTGATGT	1723
	ACATCAGA**T**CATGAAGA	1724
Waxy starch	GTAACAGCTTCACAGTTGGTGTCACAT-GTCCATGGTGGAGCAACG	1725
GBSS	TCTTCACCGGATACT	
	TAAACAAACTTGGCCCAGGTTGGCCTCAGG	
Antirrhinum majus	AACCAGCAATTCACTCACAATGGGTTGAGAT	
Lys24Term	ATCTCAAGCCATTGTGAGTGAATTGCTG-GTTCGTGAGGCCAACCTG	1726
AAA-TAA	GGCCAAGTTTGTTT	
	AAGTATCGGGTGAAGACGTTGCTCCACCATG	
	GACATGTGACACCAACTGTGAAGGTGTTAC	
	CGGATACT**T**AAACAAAC	1727
	GTTTGTTT**A**AGTATCCG	1728
Waxy starch	CACAGTTGGTGTCACATGTCCATGGTG-GAGCAAGGTCTTCACCGG	1729
GBSS	ATAGTAAAACAAACT	
	AGGGCGAGGTTGGCCTCAGGAACCAGCAAT	
Antirrhinum majus	TCACTCACAATGGGTTGAGATCAATAAACAT	
Leu27Term	ATGTTTATTGATCTCAACCCATTGT-GAGTGAATTGCTGGTTCCTGA	1730
TTG-TAG	GGCCAACCTGGGCC	
	TAGTTTGTTTTAGTATCGGGTGAAGACGTTG	
	CTCCACCATGGACATGTGACACCAACTGTG	
	AACAAACT**A**GGCCCAGG	1731
	CCTGGGCC**T**AGTTTGTT	1732
Waxy starch	TTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT	1733
GBSS	AAAACAAACTTGGCC	
	TAGGTTGGCCTCAGGAACCAGCAATTCACT	
Antirrhinum majus	CACAATGGGTTGAGATCAATAAACATGGTTG	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Gln29Term	CAACCATGTTTATTGATCTCAACCCAT-	1734
	TGTGAGTGAATTGCTGGTT	
GAG-TAG	CCTGAGGCCAACCT	
	AGGCCAAGTTTGTTTTAGTATCCGGTGAAGA	
	CGTTGCTCCACCATGGACATGTGACACCAA	
	ACTTGGCC**T**AGGTTGGC	1735
	GCCAACCT**A**GGCCAAGT	1736
Waxy starch	GGTGGAGCAACGTCTTCACCGGATAC-	1737
	TAAAACAAACTTGGCCCAG	
GBSS	GTTGGCCTCAGGAACTAGCAATTCACT-	
	CACAATGGGTTGAGATCA	
Antirrhinum majus	ATAAACATGGTTGATAAGCTTCAAATGAGGA	
Gln35Term	TCCTCATTTGAAGCTTATCAACCATGTT-	1738
	TATTGATGTCAACCCATTG	
GAG-TAG	TGAGTGAATTGCT	
	AGTTCCTGAGGCCAACCTGGGCCAAGTTTGTTT	
	TAGTATCCGGTGAAGACGTTGCTCCACC	
	TCAGGAAC**T**AGCAATTC	1739
	GAATTGCT**A**GTTCCTGA	1740
Waxy starch	GGAGCAACGTCTTCACCGGATACTAAAA-	1741
	CAAACTTGGCCCAGGTT	
GBSS	GGCCTCAGGAACCAG	
	TAATTCACTCACAATGGGTTGAGATCAATAA	
Antirrhinum majus	ACATGGTTGATAAGCTTCAAATGAGGAACA	
Gln36Term	TGTTCCTCATTTGAAGCTTATCAACCAT-	1742
	GTTTATTGATCTCAACCCA	
CAA-TAA	TTGTGAGTGAATT	
	ACTGGTTCCTGAGGCCAACCTGGGCCAAGTTT	
	GTTTTAGTATCCGGTGAAGACGTTGCTCC	
	GGAACCAG**T**AATTCACT	1743
	AGTGAATT**A**CTGGTTCC	1744
Waxy starch	GTGATGGCGACTATAACTGCCTCA-	1745
	CACTTTGTTTCTCATGTCTGTG	
GBSS	GGGGTGCCACTTCT	
	TGAGAATCAAAAGTGGGGTTGGGTCAATTAG	
Ipomoea batatas	CCCTGAGGAGCCAAGCTGTGACTCACAATG	
Gly20Term	CATTGTGAGTCACAGCTTGGCTCCT-	1746
	CAGGGCTAATTGACCCAACC	
GGA-TGA	CCACTTTTGATTCTC	
	AAGAAGTGGCACCCCCACAGACATGAGAAA	
	CAAAGTGTGAGGCAGTTATAGTCGCCATCAC	
	CCACTTCT**T**GAGAATCA	1747
	TGATTCTC**A**AGAAGTGG	1748
Waxy starch	ATGGCGACTATAACTGCCTCA-	1749
	CACTTTGTTTCTCATGTCTGTGGGG	
GBSS	GTGCCACTTCTGGA	
	TAATCAAAAGTGGGGTTGGGTCAATTAGCCC	
Ipomoea batatas	TGAGGAGCCAAGCTGTGACTCACAATGGGT	
Glu21Term	ACCCATTGTGAGTCACAGCTTGGCTCCT-	1750
	CAGGGCTAATTGACCCA	
GAA-TAA	ACCCCACTTTTGATT	
	ATCCAGAAGTGGCACCCCCACAGACATGAG	
	AAACAAAGTGTGAGGCAGTTATAGTCGCCAT	
	CTTCTGGA**T**AATCAAAA	1751
	TTTTGATT**A**TCCAGAAG	1752
Waxy starch	CGACTATAACTGCCTCA-	1753
	CACTTTGTTTCTCATGTCTGTGGGGGTGC	
GBSS	CACTTCTGGAGAAT	
	GAAAAGTGGGGTTGGGTCAATTAGCCCTGAG	
Ipomoea batatas	GAGCCAAGCTGTGACTCACAATGGGTTGAG	
Ser22Term	CTCAACCCATTGTGAGTCACAGCTTG-	1754
	GCTCCTCAGGGCTAATTGA	
TCA-TGA	CCCAACCCCACTTTT	
	CATTCTCCAGAAGTGGCACCCCCACAGACAT	
	GAGAAACAAAGTGTGAGGCAGTTATAGTCG	
	TGGAGAAT**G**AAAAGTGG	1755
	CCACTTTT**C**ATTCTCCA	1756

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch	ACTATAACTGCCTCACACTTTGTTTCT-CATGTCTGTGGGGGTGCCA	1757
GBSS	CTTCTGGAGAATCA	
	TAAGTGGGGTTGGGTCAATTAGCCCTGAGGA	
Ipomoea batatas	GCCAAGCTGTGACTCACAATGGGTTGAGAC	
Lys23Term	GTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATT	1758
AAA-TAA	GACCCAACCCCACTT	
	ATGATTCTCCAGAAGTGGCACCCCCACAGA	
	CATGAGAAACAAAGTGTGAGGCAGTTATAGT	
	GAGAATCA**T**AAGTGGGG	1759
	CCCCACTT**A**TGATTCTC	1760
Waxy starch	CCTCACACTTTGTTTCTCATGTCT-GTGGGGGTGCCACTTCTGGAGA	1761
G BSS	ATCAAAAGTGGGGT	
	AGGGTCAATTAGCCCTGAGGAGCCAAGCTGT	
Ipomoea batatas	GACTCACAATGGGTTGAGACCTGTGAACAA	
Leu26Term	TTGTTCACAGGTCTCAACCCATTGT-GAGTCACAGCTTGGCTCCTCA	1762
TTG-TAG	GGGCTAATTGACCC	
	TACCCCACTTTTGATTCTCCAGAAGTGGCACC	
	CCCACAGACATGAGAAACAAAGTGTGAGG	
	AGTGGGGT**A**GGGTCAAT	1763
	ATTGACCC**T**ACCCCACT	1764
Waxy starch	CATCGGCGATTGTTGCTCCTTACT-GCTCTCTCACAGAATGGCAACG	1765
GBSS	GTGACGGGGTCTTA	
	GGTGGTGTCGAGAAGCGCGTGCTTCAATTCC	
Astragalus	CAGGGAAGAACAGAAGCCAAAGTGAATTCA	
membranaeus	TGAATTCACTTTGGCTTCTGTTCTTC-CCTGGGAATTGAAGCACGCG	1766
Tyr8Term	CTTCTCGACACCAC	
	CTAAGACCCCGTCACCGTTGCCATTCTGTGA	
TAT-TAG	GAGAGCAGTAAGGAGCAACAATCGCCGATG	
	GGGTCTTA**G**GTGGTGTC	1767
	GACACCAC**C**TAAGACCC	1768
Waxy starch	ATTGTTGCTCCTTACTGCTCTCTCACA-GAATGGCAACGGTGACGG	1769
GBSS	GGTCTTATGTGGTGT	
	AGAGAAGCGCGTGCTTCAATTCCCAGGGAA	
Astragalus	GAACAGAAGCCAAAGTGAATTCACCTCAGAA	
membranaeus	TTCTGAGGTGAATTCACTTTGGCTTCT-GTTCTTCCCTGGGAATTGA	1770
Ser11Term	AGCACGCGCTTCTCTACACCACATAA-GACCCCGTCACCGTTGCCA	
TCG-TAG	TTCTGTGAGAGAGCAGTAAGGAGCAACAAT	
	TGTGGTGT**A**GAGAAGCG	1771
	CGCTTCTC**T**ACACCACA	1772
Waxy starch	TGTTGCTCCTTACTGCTCTCTCACA-GAATGGCAACGGTGACGGGG	1773
GBSS	TCTTATGTGGTGTCGTGAAGCGCGTGCT-TCAATTCCCAGGGAAGA	
Astragalus	ACAGAAGCCAAAGTGAATTCACCTCAGAAGA	
membranaeus	TCTTCTGAGGTGAATTCACTTTGGCT-TCTGTTCTTCCCTGGGAATT	1774
Arg12Term	GAAGCACGCGCTTC	
	ACGACACCACATAAGACCCCGTCACCGTTGC	
AGA-TGA	CATTCTGTGAGAGAGCAGTCAGGAGCAACA	
	TGGTGTCG**T**GAAGCGCG	1775
	CGCGCTTC**A**CGACACCA	1776
Waxy starch	ACTGCTCTCTCACAGAATGGCAACGGT-GACGGGGTCTTATGTGGT	1777
GBSS	GTCGAGAAGCGCGTG	
	ATTCAATTCCCAGGGAAGAACAGAAGCCAA	
Astragalus	AGTGAATTCACCTCAGAAGATAAATCTGAAT	
membranaeus	ATTGAGATTTATCTTCTGAGGTGAAT-TCACTTTGGCTTCTGTTCTTC	1778
Cys15Term	CCTGGGAATTGAATCACGCGCTTCTCGA-CACCACATAAGACCCCG	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
TGC-TGA	TCACCGTTGCCATTCTGTGAGAGAGCAGT	
	AGCGCGTG**A**TTCAATTC	1779
	GAATTGAA**T**CACGCGCT	1780
Waxy starch	CACAGAATGGCAACGGTGACGGGGTCT-TATGTGGTGTCGAGAAG	1781
GBSS	CGCGTGGTTCAATTCCTAGGGAAGAACA-GAAGCCAAAGTGAATTC	
Astragalus	ACCTCAGAAGATAAATCTCAATAGCCAAGCAT	
membranaeus	ATGCTTGGCTATTGAGATTTATCTTCT-GAGGTGAATTCACTTTGGCT	1782
Gln19Term	TCTGTTCTTCCCTAGGAATTGAAG-CACGCGCTTCTCGACACCACAT	
CAG-TAG	AAGACCCCGTCACCGTTGCCATTCTGTG	
	TCAATTCC**T**AGGGAAGA	1783
	TCTTCCCT**A**GGAATTGA	1784
Waxy starch	TGTAGCTTGGTAGATTCCCCTTTTTGTC-GACCACACATCACATGGC	1785
GBSS	AAGCATCACAGCTT	
	GACACCACTTTGTGTCAAGAAGCCAAACTTCA	
Solanum tuberosum	CTAGACACCAAATCAACCTTGTCACAGAT	
Ser7Term	ATCTGTGACAAGGTTGATTTGGT-GTCTAGTGAAGTTTGGCTTCTTG	1786
TCA-TGA	ACACAAAGTGGTGT	
	CAAGCTGTGATGCTTGCCATGTGATGTGTGG	
	TCTACAAAAAGGGGAATCTACCAAGCTACA	
	CACAGCTT**G**ACACCACT	1787
	AGTGGTGT**C**AAGCTGTG	1788
Waxy starch	TCCCCTTTTTGTAGACCACACATCA-CATGGCAAGCATCACAGCTTC	1789
GBSS	ACACCACTTTGTGT	
	GAAGAAGCCAAACTTCACTAGACACCAAATCA	
Solanum tuberosum	ACCTTGTCACAGATAGGACTCAGGAACCA	
Ser12Term	TGGTTCCTGAGTCCTATCTGTGACAAG-GTTGATTTGGTGTCTAGTG	1790
TCA-TGA	AAGTTTGGCTTCTT	
	CACACAAAGTGGTGTGAAGCTGTGATGCTTGC	
	CATGTGATGTGTGGTCTACAAAAAGGGGA	
	CTTTGTGT**G**AAGAAGCC	1791
	GGCTTCTT**C**ACACAAAG	1792
Waxy starch	CCCTTTTTGTAGACCACACATCACATG-GCAAGCATCACAGCTTCAC	1793
GBSS	ACCACTTTGTGTCATGAAGCCAAACT-TCACTAGACACCAAATCAAC	
Solanum tuberosum	CTTGTCACAGATAGGACTCAGGAACCATA	
Arg13Term	TATGGTTCCTGAGTCCTATCTGTGA-CAAGGTTGATTTGGTGTCTAG	1794
AGA-TGA	TGAAGTTTGGCTTC	
	ATGACACAAAGTGGTGTGAAGCTGTGATGCTT	
	GCCATGTGATGTGTGGTCTACAAAAAGGG	
	TTGTGTCA**T**GAAGCCAA	1795
	TTGGCTTC**A**TGACACAA	1796
Waxy starch	TTGTAGACCACACATCACATGGCAAG-CATCACAGCTTCACACCACT	1797
GBSS	TTGTGTCAAGAAGCTAAACTTCACTAGA-CACCAAATCAACCTTGTC	
Solanum tuberosum	ACAGATAGGACTCAGGAACCATACTCTGA	
Gln15Term	TCAGAGTATGGTTCCTGAGTCCTATCT-GTGACAAGGTTGATTTGGT	1798
CAA-TAA	GTCTAGTGAAGTTT	
	AGCTTCTTGACACAAAGTGGTGTGAAGCTGTG	
	ATGCTTGCCATGTGATGTGTGGTCTACAA	
	CAAGAAGC**T**AAACTTCA	1799
	TGAAGTTT**A**GCTTCTTG	1800
Waxy starch	CCACACATCACATGGCAAGCATCA-CAGCTTCACACCACTTTGTGTC	1801

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
GBSS	AAGAAGCCAAACTT	
	GACTAGACACCAAATCAACCTTGTCACAGATA	
Solanum tuberosum	GGACTCAGGAACCATACTCTGACTCACAA	
Sen17Term	TTGTGAGTCAGAGTCTGGTTCCTGAGTC-	1802
	CTATCTGTGACAAGGTTG	
TCA-TGA	ATTTGGTGTCTAGT	
	CAAGTTTGGCTTGTTGACACAAAGTGGTGTGA	
	AGCTGTGATGCTTGCCATGTGATGTGTGG	
	CCAAACTTGACTAGACA	1803
	TGTCTAGTCAAGTTTGG	1804
Waxy starch	GTCGATCACTCTTCTCTCACCGCCGAAA-	1805
	CAGATTTTGACACAAAAA	
GBSS	TGGCAACAATAACG	
	TGATCTTCAATGCCGACGAGAACCGCGTGCT	
Pisum sativum	TCAATTACCAAGGAAGATCAGCAGAGTCTA	
Gly6Term	TAGACTCTGCTGATCTTCCTTGGTCAT-	1806
	TGAAGCACGCGGTTCTCGT	
GGA-TGA	CGGCATTGAAGATC	
	ACGTTATTGTTGCCATTTTTGTGTCAAAATCT	
	GTTTCGGCGGTGAGAGAAGAGTGATCGAC	
	CAATAACGTGATCTTCA	1807
	TGAAGATCACGTTATTG	1808
Waxy starch	ACTCTTCTCTCACCGCCGAAACA-	1809
	GATTTTGACACAAAAATGGCAAC	
GBSS	AATAACGGGATCTT	
	GAATGCCGACGAGAACCGCGTGCTTCAATTA	
Pisum sativum	CCAAGGAAGATCAGCAGAGTCTAAACTGAA	
Ser8Term	TTCAGTTTAGACTCTGCTGATCTTCCT-	1810
	TGGTCATTGAAGCACGCGG	
TCA-TGA	TTCTCGTCGGCATT	
	CAAGATCCCGTTATTGTTGCCATTTTTGTGTCA	
	AAATCTGTTTCGGCGGTGAGAGAAGAGT	
	GGGATCTTGAATGCCGA	1811
	TCGGCATTCAAGATCCC	1812
Waxy starch	ACCGCCGAAACAGATTTTGACA-	1813
	CAAAAATGGCAACAATAACGGGA	
GBSS	TCTTCAATGCCGACG	
	TGAACCGCGTGCTTCAATTACCAAGGAAGA	
Pisum sativum	TCAGCAGAGTCTAAACTGAATTTGCCTCAGA	
Arg12Term	TCTGAGGCAAATTCAGTTTAGACTCT-	1814
	GCTGATCTTCCTTGGTCATT	
AGA-TGA	GAAGCACGCGGTTC	
	ACGTCGGCATTGAAGATCCCGTTATTGTTGC	
	CATTTTTGTGTCAAAATCTGTTTCGGCGGT	
	TGCCGACGTGAACCGCG	1815
	CGCGGTTCACGTCGGCA	1816
Waxy starch	AGATTTTGACACAAAAATGGCAA-	1817
	CAATAACGGGATCTTCAATGCCG	
GBSS	ACGAGAACCGCGTG	
	ATTCAATTACCAAGGAAGATCAGCAGAGTCT	
Pisum sativum	AAACTGAATTTGCCTCAGATACACTTCAAT	
Cys15Term	ATTGAAGTGTCTCTGAGGCAAAT-	1818
	TCAGTTTAGACTCTGCTGATCTT	
TGC-TGA	CCTTGGTCATTGAA	
	TCACGCGGTTCTCGTCGGCATTGAAGATCCC	
	GTTATTGTTGCCATTTTTGTGTCAAAATCT	
	ACCGCGTGATTCAATTA	1819
	TAATTGAATCACGCGGT	1820
Waxy starch	CACAAAAATGGCAACAATAACGGGATCT-	1821
	TCAATGCCGACGAGAAC	
GBSS	CGCGTGCTTCAATTA	
	GCAAGGAAGATCAGCAGAGTCTAAACTGAA	
Pisum sativum	TTTGCCTCAGATACACTTCAATAACAACCAA	
Tyr18Term	TTGGTTGTTATTGAAGTGTATCTGAG-	1822
	GCAAATTCAGTTTAGACTCT	
TAC-TAG	GCTGATCTTCCTTG	
	CTAATTGAAGCACGCGGTTCTCGTCGGCATTG	
	AAGATCCCGTTATTGTTGCCATTTTTGTG	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTCAATTA**G**CAAGGAAG	1823
	CTTCCTTG**C**TAATTGAA	1824
Waxy starch	TCTACACCGGAGAGAGCACCATG-	1825
	GCAACTGTAATAGCTGCACATT	
GBSS	TCGTTTCCAGGAGCT	
	GACACTTGAGCATCCATGCATTAGAGACTAA	
Manihot esculenta	GGCTAATAATTTGTCTCACACTGGACCCTG	
Ser14Term	CAGGGTCCAGTGTGAGACAAATTATT-	1826
	AGCCTTAGTCTCTAATGCAT	
TCA-TGA	GGATGCTCAAGTGT	
	CAGCTCCTGGAAACGAAATGTGCAGCTATTA	
	CAGTTGCCATGGTGCTCTCTCCGGTGTAGA	
	CAGGAGCT**G**ACACTTGA	1827
	TCAAGTGT**C**AGCTCCTG	1828
Waxy starch	CCGGAGAGAGCACCATGGCAACTGTAAT-	1829
	AGCTGCACATTTCGTTT	
GBSS	CCAGGAGCTCACACT	
	AGAGCATCCATGCATTAGAGACTAAGGCTA	
Manihot esculenta	ATAATTTGTCTCACACTGGACCCTGGACCCA	
Leu16Term	TGGGTCCAGGGTCCAGTGTGAGACAAAT-	1830
	TATTAGCCTTAGTCTCTA	
TTG-TAG	ATGCATGGATGCTC	
	TAGTGTGAGCTCCTGGAAACGAAATGTGCAG	
	CTATTACAGTTGCCATGGTGCTCTCTCCGG	
	CTCACACT**A**GAGCATCC	1831
	GGATGCTC**T**AGTGTGAG	1832
Waxy starch	TGGCAACTGTAATAGCTGCA-	1833
	CATTTCGTTTCCAGGAGCTCACACTT	
GBSS	GAGCATCCATGCAT	
	GAGAGACTAAGGCTAATAATTTGTCTCACACT	
Manihot esculenta	GGACCCTGGACCCAAACTATCACTCCCAA	
Leu21Term	TTGGGAGTGATAGTTTGGGTCCAGGGTC-	1834
	CAGTGTGAGACAAATTA	
TTA-TGA	TTAGCCTTAGTCTCT	
	CATGCATGGATGCTCAAGTGTGAGCTCCTGG	
	AAACGAAATGTGCAGCTATTACAGTTGCCA	
	CCATGCAT**G**AGAGACTA	1835
	TAGTCTCT**C**ATGCATGG	1836
Waxy starch	GCAACTGTAATAGCTGCA-	1837
	CATTTCGTTTCCAGGAGCTCACACTTGA	
GBSS	GCATCCATGCATTA	
	TAGACTAAGGCTAATAATTTGTCTCACACTGG	
Manihot esculenta	ACCCTGGACCCAAACTATCACTCCCAATG	
Glu22Term	CATTGGGAGTGATAGTTTGGGTC-	1838
	CAGGGTCCAGTGTGAGACAAAT	
GAG-TAG	TATTAGCCTTAGTCT	
	ATAATGCATGGATGCTCAAGTGTGAGCTCCT	
	GGAAACGAAATGTGCAGCTATTACAGTTGC	
	ATGCATTA**T**AGACTAAG	1839
	CTTAGTCT**A**TAATGCAT	1840
Waxy starch	GTCATAGCTGCACATTTCGTTTCCAG-	1841
	GAGCTCACACTTGAGCATCC	
GBSS	ATGCATTAGAGACT	
	TAGGCTAATAATTTGTCTCACACTGGACCCTG	
Manihot esculenta	GACCCAAACTATCACTCCCAATGGTTTAA	
Lys24Term	TTAAACCATTGGGAGTGAT-	1842
	AGTTTGGGTCCAGGGTCCAGTGTGAG	
AAG-TAG	ACAAATTATTAGCCT	
	AAGTCTCTAATGCATGGATGCTCAAGTGTGA	
	GCTCCTGGAAACGAAATGTGCAGCTATTAC	
	TAGAGACT**T**AGGCTAAT	1843
	ATTAGCCT**A**AGTCTCTA	1844
Waxy starch	ACAACTCCTCCGTCACCGGTATAAG-	1845
	CATGGCAACGGTATCGATGG	
GBSS	CATCGTGCGTGGCGT	
	GAAAAGGCGCGTGGAGTACAGAGACAAAA	
Phaseolus vulgaris	GTGAAATCTTCGGGTCAGATGAGCCTGAACCG	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Ser12Term	CGGTTCAGGCTCATCTGACCCGAA-	1846
	GATTTCACTTTTGTCTCTGTCC	
TCA-TGA	TCCACGCGCCTTTT	
	CACGCCACGCACGATGCCATCGATACCGTTG	
	CCATGCTTATACCGGTGACGGAGGAGTTGT	
	CGTGGCGT**G**AAAAGGCG	1847
	CGCCTTTT**C**ACGCCACG	1848
Waxy starch	CACCGGTCTAAGCATGGCAACGGTATC-	1849
	GATGGCATCGTGCGTGGC	
GBSS	GTCAAAAGGCGCGTG	
	AAGTACAGAGACAAAAGTGAAATCTTCGGG	
Phaseolus vulgaris	TCAGATGAGCCTGAACCGTCATGAATTGAAA	
Trp16Term	TTTCAATTCATGACGGTTCAGGCT-	1850
	CATCTGACCCGAAGATTTCACT	
TGG-TGA	TTTGTCTCTGTACT	
	TCACGCGCCTTTTGACGCCACGCACGATGCCA	
	TCGATACCGTTGGCATGCTTATACCGGTG	
	GGCGCGTG**A**AGTACAGA	1851
	TCTGTACT**T**CACGCGCC	1852
Waxy starch	ATAAGCATGGCAACGGTCTCGATG-	1853
	GCATCGTGCGTGGCGTCAAAA	
GBSS	GGCGCGTGGAGTACA	
	TAGACAAAAGTGAAATCTTCGGGTCAGATG	
Phaseolus vulgaris	AGCCTGAACCGTCATGAATTGAAATACGATG	
Glu19Term	CATCGTATTTCAATTCATGACGGTTCAG-	1854
	GCTCATCTGACCCGAAGA	
GAG-TAG	TTTCACTTTTGTCT	
	ATGTACTCCACGCGCCTTTTGACGCCACGCAC	
	GATGCCATCGATACCGTTGCCATGCTTAT	
	GGAGTACA**T**AGACAAAA	1855
	TTTTGTCT**A**TGTACTCC	1856
Waxy starch	ATGGCAACGGTATCGATGGCATCGTGCGTGGGGTCAAAAGGCGC	1857
GBSS	GTGGAGTACAGAGACA	
	TAAGTGAAATCTTCGGGTCAGATGAGCCT	
Phaseolus vulgaris	GAACCGTCATGAATTGAAATACGATGGGTTGA	
Lys21Term	TCAACCCATCGTATTTCAATTCATGACG-	1858
	GTTCAGGCTCATCTGACC	
AAA-TAA	CGAAGATTTCACTT	
	ATGTCTCTGTACTCCACGCGCCTTTTGACGCC	
	ACGCACGATGCCATCGATACCGTTGCCAT	
	CAGAGACA**T**AAGTGAAA	1859
	TTTCACTT**A**TGTCTCTG	1860
Waxy starch	ACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAG	1861
GBSS	TACAGAGACAAAAGTG	
	TAATCTTCGGGTCAGATGAGCCTGAACCG	
Phaseolus vulgaris	TCATGAATTGAAATACGATGGGTTGAGATCTC	
Lys23Term	GAGATCTCAACCCATCGTATTTCAAT-	1862
	TCATGACGGTTCAGGCTCAT	
AAA-TAA	CTGACCCGAAGATT	
	ACACTTTTGTCTCTGTACTCCACGCGCCTTTT	
	GACGCCACGCACGATGCCATCGATACCGT	
	CAAAAGTG**T**AATCTTCG	1863
	CGAAGATT**A**CACTTTTG	1864
Waxy starch	GCGCCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGG	1865
GBSS	GTTCCATTCCTAATTA	
	GTGTTCTTATCAAACAAACAGTGTTGGTTCA	
Triticum aestivum	CTGAAACTGTCGCCTCACATCCAATTCCAG	
Tyr7Term	CTGGAATTGGATGTGAGGCGA-	1866
	CAGTTTCAGTGAACCAACACTGTT	
TAT-TAG	TGTTTGATAAGAACA	
	CTAATTAGGAATGGAACCCATTGGTGCAGCC	
	TCTCAATGACGACCTTTTCGAGCTAGGCGC	
	CCTAATTA**G**TGTTCTTA	1867
	TAAGAACA**C**TAATTAGG	1868
Waxy starch	CCTAGCTCGAAAAGGTCGTCATTGAGAG-	1869
	GCTGCACCAATGGGTTC	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
GBSS	CATTCCTAATTATTG	
	ATCTTATCAAACAAACAGTGTTGGTTCACTGA	
Triticum aestivum	AACTGTCGCCTCACATCCAATTCCAGCAA	
Cys8Term	TTGCTGGAATTGGATGTGAGGCGA-	1870
	CAGTTTCAGTGAACCAACACT	
TGT-TGA	GTTTGTTTGATAAGA	
	TCAATAATTAGGAATGGAACCCATTGGTGCA	
	GCCTCTCAATGACGACCTTTTCGAGCTAGG	
	AATTATTGATCTTATCA	1871
	TGATAAGATCAATAATT	1872
Waxy starch	TCGAAAAGGTCGTCATTGAGAGGCTG-	1873
	CACCAATGGGTTCCATTCC	
GBSS	TAATTATTGTTCTTA	
	GCAAACAAACAGTGTTGGTTCACTGAAACTGT	
Triticum aestivum	CGCCTCACATCCAATTCCAGCAATCTTGT	
Tyr10Term	ACAAGATTGCTGGAATTGGATGTGAGGC-	1874
	GACAGTTTCAGTGAACC	
TAT-TAG	AACACTGTTTGTTTG	
	CTAAGAACAATAATTAGGAATGGAACCCATT	
	GGTGCAGCCTCTCAATGACGACCTTTTCGA	
	TGTTCTTAGCAAACAAA	1875
	TTTGTTTGCTAAGAACA	1876
Waxy starch	CGAAAAGGTCGTCATTGAGAGGCTGCAC-	1877
	CAATGGGTTCCATTCCT	
GBSS	AATTATTGTTCTTAT	
	TAAACAAACAGTGTTGGTTCACTGAAACTGTC	
Triticum aestivum	GCCTCACATCCAATTCCAGCAATCTTGTA	
Gln11Term	TACAAGATTGCTGGAATTGGATGTGAG-	1878
	GCGACAGTTTCAGTGAAC	
CAA-TAA	CAACACTGTTTGTTT	
	AATAAGAACAATAATTAGGAATGGAACCCATT	
	GGTGCAGCCTCTCAATGACGACCTTTTCG	
	GTTCTTATTAAACAAAC	1879
	GTTTGTTTAATAAGAAC	1880
Waxy starch	AGGCTGCACCAATGGGTTCCATTC-	1881
	CTAATTATTGTTCTTATCAAACA	
GBSS	AACAGTGTTGGTT	
	GACTGAAACTGTCGCCTCACATCCAATTCCAGC	
Triticum aestivum	AATCTTGTCACAATGAAGTTATGTTCCT	
Ser17Term	AGGAACATAACTTCATTGTTACAAGAT-	1882
	TGCTGGAATTGGATGTGAG	
TCA-TGA	GCGACAGTTTCAGT	
	CAACCAACACTGTTTGTTTGATAAGAACAATA	
	ATTAGGAATGGAACCCATTGGTGCAGCCT	
	TGTTGGTTGACTGAAAC	1883
	GTTTCAGTCAACCAACA	1884
Waxy starch	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT	1885
GBSS	CCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCCGGAGCCCGGCG	
Triticum aestivum	GATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA	
Gln28Term	TAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTC	1886
CAG-TAG	CGGGGCCTCACGCCCT	
	AGAAACCTGCACGCCGGAACCTGTCGGT	
	GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	
	CAGGTTTCTAGGGCGTG	1887
	CACGCCCTAGAAACCTG	1888
Waxy starch	GGTTTCCAGGGCGTGAGGCCCCGGAGC-	1889
	CCGGCGGATGCGGCTCT	
GBSS	CGGCATGAGGACCGTC	
	TGAGCTAGCGCCGCCCCAACGCAAAGCC	
Triticum aestivum	GGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	
Gly46Term	AGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGCGTT	1890
GGA-TGA	GGGGCGGCGCTAGCTCAGACGGTCCTCATGCCGAGAGCCGCATC	
	CGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	
	GGACCGTCTGAGCTAGC	1891
	GCTAGCTCAGACGGTCC	1892
Waxy starch	CGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAG	1893

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
GBSS	CTAGCGCCGCCCCAACG	
	TAAAGCCGGAAAGCGCACCGCGGGACC	
Triticum aestivum	CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCG	
Gln53Term	CGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG	1894
CAA-TAA	GTGCGCTTTCCGGCTTTACGTTGGGGCGGCGCTAGCTCCGACGG	
	TCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCG	
	CCCCAACGTAAAGCCGG	1895
	CCGGCTTTACGTTGGGG	1896
Waxy starch	GCGGATGCGGCTCTCGGCATGAGGAC-	1897
	CGTCGGAGCTAGCGCCGC	
GBSS	CCCAACGCAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGC	
Triticum aestivum	CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCG	
Lys56Term	CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAGGCACCGCCG	1898
AAA-TAA	GGTCCCGCGGTGCGCTTACCGGCTTTGCGTTGGGGCGGCGCTAG	
	CTCCGACGGTCCTCATGCCGAGAGCCGCATCCGC	
	AAAGCCGGTAAGCGCAC	1899
	GTGCGCTTACCGGCTTT	1900
Waxy starch	CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCGGCATGAACCT	1901
GBSS	CGTGTTCGTCGGCGCC	
	TAGATGGCGCCCTGGACCAAGACCGGCG	
Triticum aestivum	GCCTCGGCGACGTCCTCGGGGGCCTCCCCCCAG	
Glu85Term	CTGGGGGGAGGCCCCCGAGGACGTCGCCGAGGCCGCCGGTCTT	1902
GAG-TAG	GCTCCAGGGCGCCATCT	
	AGGCGCCGACGAACACGAGGTTCATGC	
	CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAG	
	TCGGCGCCTAGATGGCG	1903
	CGCCATCTAGGCGCCGA	1904
Waxy starch	GTGGTCTCTCGCTGCAGGTAGCCACACCCTGCGCGCGCGATGGC	1905
GBSS	GGCTCTGGTCACGTCGTAGCTCGCCACCTCCGGCACCGTCCTCG	
Triticum aestivum	GCATCACCGACAGGTTCCGGCGTGCAGGTTTTC	
Gln8Term	GAAAACCTGCACGCCGGAACCTGTCGGT-	1906
	GATGCCGAGGACGGTG	
CAG-TAG	CCGGAGGTGGCGAGCTACGACGTGACCAGAGCCGCCATCGCGC	
	GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC	
	TCACGTCGTAGCTCGCC	1907
	GGCGAGCTACGACGTGA	1908
Waxy starch	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT	1909
GBSS	CCGGCGTGCAGGTTTT	
	TAGGGTGTGAGGCCCCGGAGCCCGGCAG	
Triticum aestivum	ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	
Gln28Term	TCGCTCCGGTCGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC	1910
GAG-TAG	CGGGGCCTCACACCCT	
	AAAAACCTGCACGCCGGAACCTGTCGGT	
	GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	
	CAGGTTTTTAGGGTGTG	1911
	CACACCCTAAAAACCTG	1912
Waxy starch	CCCCGGAGCCCGGCAGATGCGCCGCTCG-	1913
	GCATGAGGACTACCGG	
GBSS	AGCGAGCGCCGCCCCG	
	TAGCAACAAAGCCGGAAAGCGCACCGCG	
Triticum aestivum	GGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	
Lys52Term	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC	1914
AAG-TAG	TTTCCGGCTTTGTTGCT	
	ACGGGGCGGCGCTCGCTCCGGTAGTCCT	
	CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	
	CCGCCCCGTAGCAACAA	1915
	TTGTTGCTACGGGGCGG	1916
Waxy starch	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG	1917
GBSS	CGAGCGCCGCCCCGAAG	
	TAACAAAGCCGGAAAGCGCACCGCGG	
Triticum aestivum	GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	
Gln53Term	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG	1918
CAA-TAA	CGCTTTCCGGCTTTGTT	
	ACTTCGGGGCGGCGCTCGCTCCGGTAGT	
	CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCCCGAAGTAACAAAGC	1919
	GCTTTGTTACTTCGGGG	1920
Waxy starch	AGCCCGGCAGATGCGCCGCTCGGCAT-	1921
	GAGGACTACCGGAGCGAG	
GBSS	CGCCGCCCCGAAGCAA	
	TAAAGCCGGAAAGCGCACCGCGGGACCC	
Triticum aestivum	GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	
Gln54Term	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG	1922
CAA-TAA	GTGCGCTTTCCGGCTTT	
	ATTGCTTCGGGGCGGCGCTCGCTCCGGT	
	AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	
	CGAAGCAATAAAGCCGG	1923
	CCGGCTTTATTGCTTCG	1924
Waxy starch	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT	1925
GBSS	CCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCCGGAACCCGGCG	
Triticum durum	GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	
Gln28Term	TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTC	1926
CAG-TAG	CGGGGCCTCACGCCCT	
	AGAAACCTGCACGCCGGAACCTGTCGGT	
	GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	
	CAGGTTTCTAGGGCGTG	1927
	CACGCCCTAGAAACCTG	1928
Waxy starch	CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGG	1929
GBSS	AGCGAGCGCCGCCCCG	
	TAGCAAAGCCGGAAAGCGCACCGCGGG	
Triticum durum	AGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	
Lys52Term	TGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCGGTG	1930
AAG-TAG	CGCTTTCCGGCTTTGCT	
	ACGGGGCGGCGCTCGCTCCGATAGTCCT	
	CATGACGAGGGCCGCATCCGCCGGGTTCCGGGG	
	CCGCCCCGTAGCAAAGC	1931
	GCTTTGCTACGGGGCGG	1932
Waxy starch	CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC	1933
GBSS	GAGCGCCGCCCCGAAG	
	TAAAGCCGGAAAGCGCACCGCGGGAGC	
Triticum durum CGGCGGT-GCCTCTCCATGGTGGT-GCGCGCCACGG		
Gln53Term	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCG	1934
CAA-TAA	GTGCGCTTTCCGGCTTT	
	ACTTCGGGGCGGCGCTCGCTCCGATAGT	
	CCTCATGACGAGGGCCGCATCCGCCGGGTTCCG	
	CCCCGAAGTAAAGCCGG	1935
	CCGGCTTTACTTCGGGG	1936
Waxy starch	GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC	1937
GBSS	CCCGAAGCAAAGCCGG	
	TAAGCGCACCGCGGGAGCCGGCGGTGC	
Triticum durum	CTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCG	
Lys56Term	CGCCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCG	1938
AAA-TAA	GCTCCCGCGGTGCGCTTACCGGCTTTGCTTCGGGGCGGGGCTCG	
	CTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	
	AAAGCCGGTAAGCGCAC	1939
	GTGCGCTTACCGGCTTT	1940
Waxy starch	TATCGGAGCGAGCGCCGCCCCGAAG-	1941
	CAAAGCCGGAAAGCGCACC	
GBSS	GCGGGAGCCGGCGGTGACTCTCCATGGTGGTGCGCGCCACGGG	
Triticum durum	CAGCGGCGGCATGAACCTCGTGTTCGTCGGCGCC	
Cys64Term	GGCGCCGACGAACACGAGGTTCATGC-	1942
	CGCCGCTGCCCGTGGCGC	
TGC-TGA	GCACCACCATGGAGAGTCACCGCCGGCTCCCGCGGTGCGCTTTC	
	CGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATA	
	CGGCGGTGACTCTCCAT	1943
	ATGGAGAGTCACCGCCG	1944
Waxy starch	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT	1945

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
GBSS	CCGGCGTGCAGGTTTT	
	TAGGGTGTGAGGCCCCGGAGCCCGGCAG	
Triticum turgidum	ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	
Gln28Term	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCGGGGCTC	1946
CAG-TAG	CGGGGCCTCACACCCT	
	AAAAACGTGCACGCCGGAACCTGTCGGT	
	GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	
	CAGGTTTT**T**AGGGTGTG	1947
	CACACCCT**A**AAAACCTG	1948
Waxy starch	CCCCGGAGCCCGGCAGATGCGCCGCTCG-	1949
	GCATGAGGACTACCGG	
GBSS	AGCGAGCGCCGCCCCG	
	TAGCAACAAAGCCGGAAAGCGCACCGCG	
Triticum turgidum	GGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	
Lys52Term	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC	1950
AAG-TAG	TTTCCGGCTTTGTTGCT	
	ACGGGGCGGCGCTCGCTCCGGTAGTCCT	
	CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	
	CCGCCCCG**T**AGCAACAA	1951
	TTGTTGCT**A**CGGGGCGG	1952
Waxy starch	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG	1953
GBSS	CGAGCGCCGCCCCGAAG	
	TAACAAAGCCGGAAAGCGCACCGCGG	
Triticum turgidum	GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	
Gln53Term	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG	1954
CAA-TAA	CGCTTTCCGGCTTTGTT	
	ACTTCGGGGCGGCGCTCGCTCCGGTAGT	
	CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	
	CCCCGAAG**T**AACAAAGC	1955
	GCTTTGTT**A**CTTCGGGG	1956
Waxy starch	AGCCCGGCAGATGCGCCGCTCGGCAT-	1957
	GAGGACTACCGGAGCGAG	
GBSS	CGCCGCCCCGAAGCAA	
	TAAAGCCGGAAAGCGCACCGCGGGACCC	
Triticum turgidum	GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	
Gln54Term	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG	1958
CAA-TAA	GTGCGCTTTCCGGCTTT	
	ATTGCTTCGGGGCGGCGCTCGCTCCGGT	
	AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	
	CGAAGCAA**T**AAAGCCGG	1959
	CCGGCTTT**A**TTGCTTCG	1960
Waxy starch	GATGCGCCGCTCGGCATGAGGACTACCG-	1961
	GAGCGAGCGCCGCCCC	
GBSS	GAAGCAACAAAGCCGG	
	TAAGCGCACCGCGGGACCCGGCGGTGC	
Triticum turgidum	CTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCG	
Lys57Term	CGGCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCG	1962
AAA-TAA	GGTCCCGCGGTGCGCTT**A**CCGGCTTTGTTGCTTCGGGGCGGCGC	
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATC	
	AAAGCCGG**T**AAGCGCAC	1963
	GTGCGCTT**A**CCGGCTTT	1964
Waxy starch	CAGCTCGCCACCTCCGCCACCGTCCTCG-	1965
	GCATCACCGACAGGTTC	
GBSS	CGCCATGCAGGTTTC	
	TAGGGCGTGAGGCCCCGGAGCCCGGCAGA	
Aegilops speltoides	TGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	
Gln28Term	TCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC	1966
CAG-TAG	CGGGGCCTCACGCCCT	
	AGAAACCTGCATGGCGGAACCTGTCGGT	
	GATGCCGAGGACGGTGGCGGAGGTGGCGAGCTG	
	CAGGTTTC**T**AGGGCGTG	1967
	CACGCCCT**A**GAAACCTG	1968
Waxy starch	GGTTTCCAGGGCGTGAGGCCCCGGAGC-	1969
	CCGGCAGATGCGCCGCT	
GBSS	CGGCATGAGGACTGTC	
	TGAGCGAGCGCCGCCCCGAAGCAACAAA	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Aegilops speltoides	GCCGGAAAGCGCACCGCGGGACCCGGCGGTGCC	
Gly46Term	GGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTTC	1970
GGA-TGA	GGGGCGGCGCTCGCTC**A**GACAGTCCTCATGCCGAGCGGCGCATC	
	TGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	
	GGACTGTC**T**GAGCGAGC	1971
	GCTCGCTC**A**GACAGTCC	1972
Waxy starch	CCCCGGAGCCCGGCAGATGCGCCGCTCG-GCATGAGGACTGTCGG	1973
GBSS	AGCGAGCGCCGCCCCG	
	TAGCAACAAAGCCGGAAAGCGCACCGCG	
Aegilops speltoides	GGACCCGGCGGTGCCTCTCGATGGTGGTGCGCG	
Lys52Term	CGCGCACCACCATCGAGAGGCACCGC-CGGGTCCCGCGGTGCGCT	1974
AAG-TAG	TTCCGGCTTTGTTGCT	
	ACGGGGCGGCGCTCGCTCCGACAGTCCTC	
	ATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	
	CCGCCCCG**T**AGCAACAA	1975
	TTGTTGCT**A**CGGGGCGG	1976
Waxy starch	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAG	1977
GBSS	CGAGCGCCGCCCCGAAG	
	TAACAAAGCCGGAAAGCGCACCGCGG	
Aegilops speltoides	GACCCGGCGGTGCCTCTCGATGGTGGTGCGCGCCA	
Gln53Term	TGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTG	1978
CAA-TAA	CGCTTTCCGGCTTTGTT	
	ACTTCGGGGCGGCGCTCGCTCCGACAGT	
	CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	
	CCCCGAAG**T**AACAAAGC	1979
	GCTTTGTT**A**CTTCGGGG	1980
Waxy starch	AGCCCGGCAGATGCGCCGCTCGGCAT-GAGGACTGTCGGAGCGAG	1981
GBSS	CGCCGCCCCGAAGCAA	
	TAAAGCCGGAAAGCGCACCGCGGGACCC	
Aegilops speltoides	GGCGGTGCCTCTCGATGGTGGTGCGCGCCACCG	
Gln54Term	CGGTGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCG	1982
CAA-TAA	GTGCGCTTTCCGGCTTT	
	ATTGCTTCGGGGCGGCGCTCGCTCCGAC	
	AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	
	CGAAGCAA**T**AAAGCCGG	1983
	CCGGCTTT**A**TTGCTTCG	1984
Waxy starch	AGTGCAGAGATCTTCCACAGCAA-CAGCTAGACAACCACCATGTCG	1985
GBSS	GCTCTCACCACGTCC**T**AGCTCGCCACCTCGGCCACCGGCTTCGG	
Oryza glaberrima	CATCGCTGACAGGTCGGCGCCGTCGTCGCTGC	
Gln8Term	GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT	1986
GAG-TAG	GGCCGAGGTGGCGAGCT**A**GGACGTGGTGAGAGCCGACATGGTG	
	GTTGTCTAGCTGTTGCTGTGGAAGATCTCTGCACT	
	CCACGTCC**T**AGCTCGCC	1987
	GGCGAGCT**A**GGACGTGG	1988
Waxy starch	TCCACAGCAACAGCTAGACAACCACCAT-GTCGGCTCTCACCACGT	1989
GBSS	CCCAGCTCGCCACCT**A**GGCCACCGGCTTCGGCATCGCTGACAGG	
Oryza glaberrima	TCGGCGCCGTCGTCGCTGCTCCGCCACGGGTT	
Ser12Term	AACCCGTGGCGGAGCAGCGACGACG-GCGCCGACCTGTCAGCGAT	1990
TCG-TAG	GCCGAAGCCGGTGGCC**T**AGGTGGCGAGCTGGGACGTGGTGAGA	
	GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	
	CGCCACCT**A**GGCCACCG	1991
	CGGTGGCC**T**AGGTGGCG	1992
Waxy starch	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC	1993
GBSS	GGCATCGCTGACAGGT**A**GGCGCCGTCGTCGCTGCTCCGCCACGG	
Oryza glaberrima	GTTCCAGGGCCTCAAGCCCCGCAGCCCCGCCGG	
Ser22Term	CCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACCCGTGGCGGA	1994
TCG-TAG	GCAGCGACGACGGCGCC	
	TACCTGTCAGCGATGCCGAAGCCGGTG	
	GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGACAGGTAGGCGCCGT	1995
	ACGGCGCCTACCTGTCA	1996
Waxy starch	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCT	1997
GBSS	GACAGGTCGGCGCCGT	
	AGTCGCTGCTCCGCCACGGGTTCCAGGG	
Oryza glaberrima	CCTCAAGCCCCGCAGCCCCGCCGGCGGCGACGC	
Ser25Term	GCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACC	1998
TCG-TAG	CGTGGCGGAGCAGCGAC	
	TACGGCGCCGACCTGTCAGCGATGCCG	
	AAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	
	GGCGCCGTAGTCGCTGC	1999
	GCAGCGACTACGGCGCC	2000
Waxy starch	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC	2001
GBSS	AGGTCGGCGCCGTCGTAGCTGCTCCGCCACGGGTTCCAGGGCCT	
Oryza glaberrima	CAAGCCCCGCAGCCCCGCCGGCGGCGACGCGAC	
Ser26Term	GTCGCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGA	2002
TCG-TAG	ACCCGTGGCGGAGCAGC	
	TACGACGGCGCCGACCTGTCAGCGATG	
	CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	
	GCCGTCGTAGCTGCTCC	2003
	GGAGCAGCTACGACGGC	2004
Waxy starch	TCCACAGCAAGAGCTAAACAGCCGAC-	2005
	CGTGTGCACCACCATGTCG	
GBSS	GCTGTCACCACGTCCTAGCTCGCCACCTCGGCCACCGGCTTCGG	
Oryza sativa	CATCGCCGACAGGTCGGCGCCGTCGTCGCTGG	
Gln8Term	GCAGCGACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGT	2006
CAG-TAG	GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG	
	GTGCACACGGTCGGCTGTTTAGCTCTTGCTGTGGA	
	CCACGTCCTAGCTCGCC	2007
	GGCGAGCTAGGACGTGG	2008
Waxy starch	CTAAACAGCCGACCGTGTGCACCACCAT-	2009
	GTCGGCTCTCACCACGT	
GBSS	CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCCGACAGG	
Oryza sativa	TCGGCGCCGTCGTCGCTGCTTCGCCACGGGTT	
Ser12Term	AACCCGTGGCGAAGCAGCGACGACG-	2010
	GCGCCGACCTGTCGGCGAT	
TCG-TAG	GCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGA	
	GCCGACATGGTGGTGCACACGGTCGGCTGTTTAG	
	CGCCACCTAGGCCACCG	2011
	CGGTGGCCTAGGTGGCG	2012
Waxy starch	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC	2013
GBSS	GGCATCGCCGACAGGTAGGCGCCGTCGTCGCTGCTTCGCCACGG	
Oryza sativa	GTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGG	
Ser22Term	CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAA	2014
TCG-TAG	GGAGCGACGACGGCGCC	
	TACCTGTCGGCGATGCCGAAGCCGGTG	
	GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	
	CGACAGGTAGGCGCCGT	2015
	ACGGCGCCTACCTGTCG	2016
Waxy starch	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCC	2017
GBSS	GACAGGTCGGCGCCGT	
	AGTCGCTGCTTCGCCACGGGTTCCAGGG	
Oryza sativa	CCTCAAGCCCCGTAGCCCAGCCGGCGGGGACGC	
Ser25Term	GCGTCCCCGCCGGCTGGGCTACGGGGCT-	2018
	TGAGGCCCTGGAACCC	
TCG-TAG	GTGGCGAAGCAGCGAC	
	TACGGCGCCGACCTGTCGGCGATGCCGA	
	AGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	
	GGCGCCGTAGTCGCTGC	2019
	GCAGCGACTACGGCGCC	2020
Waxy starch	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGAC	2021
GBSS	AGGTCGGCGCCGTCGTAGCTGCTTCGCCACGGGTTCCAGGGCCT	
Oryza sativa	CAAGCCCCGTAGCCCAGCCGGCGGGGACGCATC	
Ser26Term	GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA	2022

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
TCG-TAG	CCCGTGGCGAAGCAGC	
	TACGACGGCGCCGACCTGTCGGCGATGC	
	CGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	
	GCCGTCGTAGCTGCTTC	2023
	GAAGCAGCTACGACGGC	2024
Waxy starch	GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCATGGC	2025
GBSS	GGCTCTGGCCACGTCCTAGCTCGCCACCTCCGGCACCGTCCTCG	
Hordeum vulgare	GCGTCACCGACAGATTCCGGCGTCCAGGTTTTC	
Gln8Term	GAAAACCTGGACGCCGGAATCTGTCGGT-	2026
	GACGCCGAGGACGGTG	
GAG-TAG	CCGGAGGTGGCGAGCTAGGACGTGGCCAGAGCCGGCATGGCGC	
	CGCGCACAGGGTGTGGCTACCTGCAGTGAGAGAC	
	CCACGTCCTAGCTCGCC	2027
	GGCGAGCTAGGACGTGG	2028
Waxy starch	ATGGCGGCTCTGGCCACGTCCCAGCTCGCCACGTCCGGCACCGT	2029
GBSS	CCTCGGCGTCACCGAC	
	TGATTCCGGCGTCCAGGTTTTGAGGGCCT	
Hordeum vulgare	CAGGCCCCGGAACCCGGCGGATGCGGCGCTTG	
Arg21Term	CAAGCGCGGCATCCGCCGGGTTC-	2030
	CGGGGCCTGAGGCCGTGAAAA	
AGA-TGA	CCTGGACGCCGGAATCAGTCGGTGACGCCGAGGACGGTGCCGG	
	AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	
	TCACCGACTGATTCCGG	2031
	CCGGAATCAGTCGGTGA	2032
Waxy starch	CAGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATT	2033
GBSS	CCGGCGTCCAGGTTTT	
	TAGGGCCTCAGGCCCCGGAACCCGGCGG	
Hordeum vulgare	ATGCGGCGCTTGGTCTGAGGACTATCGGAGCAA	
Gln28Term	TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCC	2034
CAG-TAG	GGGGCCTGAGGCCCT	
	AAAAACCTGGACGCCGGAATCTGTCGGTG	
	ACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	
	CAGGTTTTTAGGGCCTC	2035
	GAGGCCCTAAAAACCTG	2036
Waxy starch	GGTTTTCAGGGCCTCAGGCCGCGGAAC-	2037
	CCGGCGGATGCGGCGCT	
GBSS	TGGTATGAGGACTATCTGAGCAAGCGC-	
	CGCCCCGAAGCAAAGGC	
Hordeum vulgare	GGAAAGCGGACCGCGGGAGCCGGCGGTGCCTCT	
Gly46Term	AGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTC	2038
GGA-TGA	GGGGCGGCGCTTGCTCAGATAGTCCTCATACCAAGCGCCGCATC	
	CGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACC	
	GGACTATCTGAGCAAGC	2039
	GCTTGCTCAGATAGTCC	2040
Waxy starch	CCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGG	2041
GBSS	AGCAAGCGCCGCCCCG	
	TAGCAAAGCCGGAAAGCGCACCGCGGG	
Hordeum vulgare	AGCCGGCGGTGCCTCTCCGTGGTGGTGAGCGCCA	
Lys52Term	TGGCGCTCACCACCACGGAGAGGCAC-	2042
	CGCCGGCTCCCGCGGTGC	
AAG-TAG	GCTTTGCGGCTTTGCT	
	ACGGGGCGGCGCTTGCTCCGATAGTCCTC	
	ATACCAAGCGCCGCATCCGCCGGGTTCCGGGG	
	CCGCCCCGTAGCAAAGC	2043
	GCTTTGCTACGGGGCGG	2044
Waxy starch	ACGTCTTTTCTCTCTCTCCTACGCAGTG-	2045
	GATTAATCGGCATGGCGG	
GBSS	CTCTGGCCACGTCG	
	TAGCTCGTCGCAACGCGGGCCGGCCTGGGC	
Zea mays	GTCCCGGACGCGTCCACGTTCCGCCGCGGCG	
Gln8Term	CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGC	2046
GAG-TAG	GCGCGTTGCGACGAGCT	
	ACGACGTGGCCAGAGCCGCCATGCCGA	
	TTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT	
	CCACGTCGTAGCTCGTC	2047
	GACGAGCTACGACGTGG	2048

TABLE 21-continued

Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch	GTCGCAACGCGCGCCGGCCTGGGCGTC-CCGGACGCGTCCACGTT	2049
GBSS	CCGCCGCGGCGCCGCGTAGGGCCTGAGGGGGGCCCGGGCGTCG	
Zea mays	GCGGGGGCGGACACGCTCAGCATGCGGACCAGCG	
Gln30Term	CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGCCCGG	2050
CAG-TAG	GCCCCCCTCAGGCCCTACGCGGCGCCGCGGCGGAACGTGGACG	
	CGTCCGGGACGCCCAGGCCGGCGCGCGTTGCGAC	
	GCGCCGCGTAGGGCCTG	2051
	CAGGCCCTACGCGGCGC	2052
Waxy starch	TCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCGCAGGGCCT	2053
GBSS	GAGGGGGGCCCGGGCGTAGGCGGCGGCGGACACGCTCAGCATG	
Zea mays	CGGACCAGCGCGCGCGCGGCGCCCAGGCACCAGCA	
Ser38Term	TGCTGGTGCCTGGGCGCCGCGCGCGCTGGTCCGCATGCTGAG	2054
TCG-TAG	CGTGTCCGCCGCCGCCTACGCCCGGGCCCCCCTCAGGCCCTGCG	
	CGGCGCCGCGGCGGAACGTGGACGCGTCCGGGA	
	CCGGGCGTAGGCGGCGG	2055
	CCGCCGCCTACGCCCGG	2056
Waxy starch	GCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGC	2057
GBSS	GCGCGGCGCCCAGGCAC	
	TAGCAGCAGGCGCGCCGCGGGGGCAG	
Zea mays	GTTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCA	
Ser57Term	TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCCCC	2058
GAG-TAG	GCGGCGCGCCTGCTGCTAGTGCCTGGGCGCCGCGCGCGCGCTG	
	GTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGC	
	CCAGGCACTAGCAGCAG	2059
	CTGCTGCTAGTGCCTGG	2060
Waxy starch	TCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCG	2061
GBSS	CGGCGCCCAGGCACCAGTAGCAGGCGCGCCGCGGGGGCAGGTT	
Zea mays	CCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGA	
Gln58Term	TCATGCCGGGGCTGGCGCACACGAC-GAGCGACGGGAACCTGCCC	2062
CAG-TAG	CCGCGGCGCGCCTGCTACTGGTGCCTGGGCGCCGCGCGCGCGC	
	TGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGA	
	GGCACCAGTAGCAGGCG	2063
	CGCCTGCTACTGGTGCC	2064

EXAMPLE 11

Altering Fatty Acid Content of Plants

[0143] Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

[0144] Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearoyl- and oleoyl-ACP.

[0145] A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearoyl-acyl carrier protein (stearoyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

[0146] The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

TABLE 22

Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate	TTTGGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGC	2065
Acyl-ACP-thioesterase	CACCTCTGCTACGT**A**GTCATTCTTTCCTGTACCATCTTCTTCACTTG	
Arabidopsis thaliana	ATCCTAATGGAAAAGGCAATAAGATTGG	
Ser8Term	CCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTA	2066
TCG-TAG	CAGGAAAGAATGAC**T**ACGTCGCAGAGGTGGCCACCATGACGAGG	
	AGATGAAGCGTTCAAAGACACTGCCACCAAA	
	TGCTACGT**A**GTCATTCT	2067
	AGAATGAC**T**ACGTAGCA	2068
Reduced palmitate	GGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGCCA	2069
Acyl-ACP-thioesterase	CCTCTGCTACGTCGT**G**ATTCTTTCCTGTACCATCTTCTTCACTTGAT	
Arabidopsis thaliana	CCTAATGGAAAAGGCAATAAGATTGGGTC	
Ser9Term	GACCCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATG	2070
TCA-TGA	GTACAGGAAAGAAT**C**ACGACGTAGCAGAGGTGGCCACCATGACG	
	AGGAGATGAAGCGTTCAAAGACACTGCCACC	
	TACGTCGT**G**ATTCTTTC	2071
	GAAAGAAT**C**ACGACGTA	2072
Reduced palmitate	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCATTCTTTCC	2073
Acyl-ACP-thioesterase	TGTACCATCTTCTT**G**ACTTGATCCTAATGGAAAAGGCAATAAGATT	
Arabidopsis thaliana	GGGTCTACGAATCTTGCTGGACTCAATTC	
Ser17Term	GAATTGAGTCCAGCAAGATTCGTCGACCCAATCTTATTGCCTTTTC	2074
TCA-TGA	CATTAGGATCAAGT**C**AAGAAGATGGTCCAGGAAAGAATGACGACG	
	TAGCAGAGGTGGCCACCATGACGAGGAGAT	
	ATCTTCTT**G**ACTTGATC	2075
	GATCAAGT**C**AAGAAGAT	2076
Reduced palmitate	GTGGCCACCTCTGCTACGTCGTCATTCTTTCCTGTACCATCTTCTT	2077
Acyl-AGP-thioesterase	CACTTGATCCTAAT**T**GAAAAGGCAATAAGATTGGGTCTACGAATCT	
Arabidopsis thaliana	TGCTGGACTCAATTCTGCACCTAACTCTG	
Gly22Term	CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATTCGTCGACCCAA	2078
GGA-TGA	TCTTATTGCCTTTTC**A**ATTAGGATCAAGTGAAGAAGATGGTCCAGG	
	AAAGAATGACGACGTAGCAGAGGTGGCCAC	
	ATCCTAAT**T**GAAAAGGC	2079
	GCCTTTTC**A**ATTAGGAT	2080
Reduced palmitate	GCTTGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGC	2081
Acyl-ACP-thioesterase	TACTGCCGCCACGT**G**ATCATTCTTTCCGTTGACTTCCCCTTCTGGG	
Garcinia mangostana	GATGCCAAATCGGGCAATCCCGGAAAAGG	
Ser8Term	CCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAAGTC	2082
TCA-TGA	AACGGAAAGAATGAT**C**ACGTGGCGGCAGTAGCAACCATTGTGGCC	
	ACAATTAACCAATCAGATCACAAATTCAAGC	
	CGCCACGT**G**ATCATTCT	2083
	AGAATGAT**C**ACGTGGCG	2084
Reduced palmitate	TGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTAC	2085
Acyl-ACP-thioesterase	TGCCGCCACGTCAT**G**ATTCTTTCCGTTGACTTCCCCTTCTGGGGAT	
Garcinia mangostana	GCCAAATCGGGCAATCCCGGAAAAGGGTC	
Ser9Term	GACCCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAA	2086
TCA-TGA	GTCAACGGAAAGAAT**C**ATGACGTGGCGGCAGTAGCAACCATTGTG	
	GCCACAATTAACCAATCAGATCACAAATTCA	
	CACGTCAT**G**ATTCTTTC	2087
	GAAAGAAT**C**ATGACGTG	2088
Reduced palmitate	CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT	2089
Acyl-ACP-thioesterase	CATCATTCTTTCCGT**A**GACTTCCCCTTCTGGGGATGCCAAATCGGG	
Garcinia mangostana	CAATCCCGGAAAAGGGTCGGTGAGTTTTGG	
Leu13Term	CCAAAACTCACCGACCCTTTTCCGGGATTGCCCGATTTGGCATCC	2090
TTG-TAG	CCAGAAGGGGAAGTC**T**ACGGAAAGAATGATGACGTGGCGGCAGT	
	AGCAACCATTGTGGCCACAATTAACCAATCAG	
	CTTTCCGT**A**GACTTCCC	2091
	GGGAAGTC**T**ACGGAAAG	2092
Reduced palmitate	ATGGTTGCTACTGCCGCCACGTCATCATTCTTTCCGTTGACTTCCC	2093
Acyl-ACP-thioesterase	CTTCTGGGGATGCC**T**AATCGGGCAATCCCGGAAAAGGGTCGGTG	
Garcinia mangostana	AGTTTTGGGTCAATGAAGTCGAAATCCGCGG	
Lys21Term	CCGCGGATTTCGACTTCATTGACCCAAAACTCACCGACCCTTTTCC	2094
AAA-TAA	GGGATTGCCCGATT**A**GGCATCCCCAGAAGGGGAAGTCAACGGAA	
	AGAATGATGACGTGGCGGCAGTCGCAACCAT	

TABLE 22-continued

Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGGATGCC**T**AATCGGGC	2095
	GCCCGATT**A**GGCATCCC	2096
Reduced palmitate	GGGATTTCAGCACGAAATTGAAGTTGTTTTTAAAAACCATGGTTGC	2097
Acyl-ACP-thioesterase	TACTGCTGTGACAT**A**GGCGTTTTTCCCAGTCACTTCTTCACCTGAC	
Gossypium hirsutum	TCCTCTGACTCGAAAAACAAGAAGCTCGG	
Ser8Term	CCGAGCTTCTTGTTTTTCGAGTCAGAGGAGTCAGGTGAAGAAGTG	2098
TCG-TAG	ACTGGGAAAAACGCC**T**ATGTCACAGCAGTAGCAACCATGGTTTTTA	
	AAAACAACTTCAATTTCGTGCTGAAATCCC	
	TGTGACAT**A**GGCGTTTT	2099
	AAAACGCC**T**ATGTCACA	2100
Reduced palmitate	TGTTTTTAAAAACCATGGTTGCTACTGCTGTGACATCGGCGTTTTT	2101
Acyl-ACP-thioesterase	CCCAGTCACTTCTT**G**ACCTGACTCCTCTGACTCGAAAAACAAGAAG	
Gossypium hirsutum	CTCGGAAGCATCAAGTCGAAGCCATCGGT	
Ser16Term	ACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTCGAGT	2102
TCA-TGA	CAGAGGAGTCAGGT**C**AAGAAGTGACTGGGAAAAACGCCGATGTCA	
	CAGCAGTAGCAACCATGGTTTTTAAAAACA	
	CACTTCTT**G**ACCTGACT	2103
	AGTCAGGT**C**AAGAAGTG	2104
Reduced palmitate	TTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACC	2105
Acyl-ACP-thioesterase	TGACTCCTCTGACT**A**GAAAAACAAGAAGCTCGGAAGCATCAAGTC	
Gossypium hirsutum	GAAGCCATCGGTTTCTTCTGGAAGTTTGCA	
Ser22Term	TGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCG	2106
TCG-TAG	AGCTTCTTGTTTTTC**T**AGTCAGAGGAGTCAGGTGAAGAAGTGACTG	
	GGAAAAACGCCGATGTCACAGCAGTCGCAA	
	CTCTGACT**A**GAAAAACA	2107
	TGTTTTTC**T**AGTCAGAG	2108
Reduced palmitate	GCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTG	2109
Acyl-ACP-thioesterase	ACTCCTCTGACTCG**T**AAAACAAGAAGCTCGGAAGCATCAAGTCGA	
Gossypium hirsutum	AGCCATCGGTTTGTTCTGGAAGTTTGCAAG	
Lys23Term	CTTGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCC	2110
AAA-TAA	GAGCTTCTTGTTTTT**A**CGAGTCAGAGGAGTCAGGTGAAGAAGTGAC	
	TGGGAAAAACGCCGATGTCACAGCAGTAGC	
	CTGACTCG**T**AAAACAAG	2111
	CTTGTTTT**A**GGAGTCAG	2112
Reduced palmitate	CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTG	2113
Acyl-ACP-thioesterase	CATTCTTCCCCGTGT**A**GTCCCCGGTCACCTCCTCTAGACCAGGAA	
Cuphea hookeriana	AGCCCGGAAATGGGTCATCGAGCTTCAGCCC	
Ser14Term	GGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCCTGGTCTAGAG	2114
TCG-TAG	GAGGTGACCGGGGAC**T**ACACGGGGAAGAATGCAGAGCTTGCAGC	
	GGTAGCCACCATTGTCTTTCAACGAGCGGGAG	
	CCCCGTGT**A**GTCCCCGG	2115
	CCGGGGAC**T**ACACGGGG	2116
Reduced palmitate	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCC	2117
Acyl-ACP-thioesterase	CCGGTCACCTCCTCT**T**GACCAGGAAAGCCCGGAAATGGGTCATCG	
Cuphea hookeriana	AGCTTCAGCCCCATCAAGCCCAAATTTGTCG	
Arg21Term	CGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTC	2118
AGA-TGA	CGGGCTTTCCTGGTC**A**AGAGGAGGTGACCGGGGACGACACGGG	
	GAAGAATGCAGAGCTTGCAGCGGTAGCCACCAT	
	CCTCCTCT**T**GACCAGGA	2119
	TCCTGGTC**A**AGAGGAGG	2120
Reduced palmitate	GCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTC	2121
Acyl-ACP-thioesterase	ACCTCCTCTAGACCA**T**GAAAGCCCGGAAATGGGTCATCGAGCTTC	
Cuphea hookeriana	AGCCCCATCAAGCCCAAATTTGTCGCCAATG	
Gly23Term	CATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACC	2122
GGA-TGA	CATTTCCGGGCTTTC**A**TGGTCTAGAGGAGGTGACCGGGGACGAC	
	ACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	
	CTAGACCA**T**GAAAGCCC	2123
	GGGCTTTC**A**TGGTCTAG	2124
Reduced palmitate	ACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACC	2125
Acyl-ACP-thioesterase	TCCTCTAGACCAGGA**T**AGCCCGGAAATGGGTCATGGAGCTTCAGC	
Cuphea hookeriana	CCCATCAAGCCCAAATTTGTCGCCAATGGCG	
Lys24Term	CGCCATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATG	2126

TABLE 22-continued

Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
AAG-TAG	ACCCATTTCCGGGCT**A**TCCTGGTCTAGAGGAGGTGACCGGGGAC	
	GACACGGGGAAGAATGCAGAGCTTGCAGCGGT	
	GACCAGGA**T**AGCCCGGA	2127
	TCCGGGCT**A**TCCTGGTC	2128
Reduced palmitate	GCCACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGAC	2129
Acyl-ACP-thioesterase	ACCTCCTCTAGGCCG**T**GAAAGCTGGGAAATGGGTCATCGAGCTTG	
Cuphea lanceolata	AGCCCCCTCAAGCCCAAATTTGTCGCCAATG	
Gly23Term	CATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACC	2130
GGA-TGA	CATTTCCGAGCTTTC**A**CGGCCTAGAGGAGGTGTCCGGGGACGGC	
	AGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	
	CTAGGCCG**T**GAAAGCTC	2131
	GAGCTTTC**A**CGGCCTAG	2132
Reduced palmitate	ACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACC	2133
Acyl-ACP-thioesterase	TCCTCTAGGCCGGGA**T**AGCTCGGAAATGGGTCATCGAGCTTGAGC	
Cuphea lanceolata	CCCCTCAAGCCCAAATTTGTCGCCAATGCCG	
Lys24Term	CGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGAT	2134
AAG-TAG	GACCCATTTCCGAGCT**A**TCCCGGCCTAGAGGAGGTGTCCGGGGA	
	CGGCAGGGGGAAGAATGCAGAACTTGCAGCGGT	
	GGCCGGGA**T**AGCTCGGA	2135
	TCCGAGCT**A**TCCCGGCC	2136
Reduced palmitate	GCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCT	2137
Acyl-ACP-thioesterase	AGGCCGGGAAAGCTC**T**GAAATGGGTCATCGAGCTTGAGCCCCCT	
Cuphea lanceolata	CAAGCCCAAATTTGTCGCCAATGCCGGGTTGA	
Gly26Term	TCAACCCGGCATTGGCGACAAATTTGGGGTTGAGGGGGCTCAAGC	2138
GGA-TGA	TCGATGACCCATTTC**A**GAGCTTTCCCGGCCTAGAGGAGGTGTCCG	
	GGGACGGCAGGGGGAAGAATGCAGAACTTGC	
	GAAAGCTC**T**GAAATGGG	2139
	CCCATTTC**A**GAGCTTTC	2140
Reduced palmitate	CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAA	2141
Acyl-ACP-thioesterase	AGCTCGGAAATGGGT**G**ATCGAGCTTGAGCCCCCTCAAGCCCAAAT	
Cuphea lanceolata	TTGTCGCCAATGCCGGGTTGAAGGTTAAGGC	
Ser29Term	GCCTTAACCTTCAACCCGGCATTGGCGACAAATTTGGGCTTGAGG	2142
TCA-TGA	GGGCTCAAGCTCGAT**C**ACCCATTTCCGAGCTTTCCCGGCCTAGAG	
	GAGGTGTCCGGGGACGGCAGGGGGAAGAATG	
	AAATGGGT**G**ATCGAGCT	2143
	AGCTCGAT**C**ACCCATTT	2144
Reduced palmitate	CGTTTAAGTGGATCGGACATTTAAGTGTTTTAATCATGGTAGCTAT	2145
Acyl-ACP-thioesterase	GAGTGCTACTGCGT**A**GCTGTTTCCGGTTTCTTCCCCAAAACCTCAC	
Helianthus annuus	TCTGGAGCCAAGACATCTGATAAGCTTGG	
Ser9Term	CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTTGGGGAA	2146
TCG-TAG	GAAACCGGAAACAGC**T**ACGCAGTCGCACTCATAGCTACCATGATT	
	AAAACACTTAAATGTCCGATCCACTTAAACG	
	TACTGCGT**A**GCTGTTTC	2147
	GAAACAGC**T**ACGCAGTA	2148
Reduced palmitate	AGTGTTTTAATCATGGTCGCTATGAGTGCTACTGCGTCGCTGTTTC	2149
Acyl-ACP-thioesterase	CGGTTTCTTCCCCA**T**AACCTCACTCTGGAGCCAAGACATCTGATAA	
Helianthus annuus	GCTTGGAGGTGAACCAGGTAGTGTTGCTG	
Lys17Term	CAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCTTGGC	2150
AAA-TAA	TCCAGAGTGAGGTT**A**TGGGGAAGAAACCGGAAACAGCGACGCAG	
	TAGCACTCATAGCTACCATGATTAAAACACT	
	CTTCCCCA**T**AACCTCAC	2151
	GTGAGGTT**A**TGGGGAAG	2152
Reduced palmitate	ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCC	2153
Acyl-ACP-thioesterase	CAAAACCTCACTCT**T**GAGCCAAGACATCTGATAAGCTTGGAGGTG	
Helianthus annuus	AACCAGGTAGTGTTGCTGTGCGCGGAATCA	
Gly21Term	TGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATC	2154
GGA-TGA	AGATGTCTTGGCTC**A**AGAGTGAGGTTTTGGGGAAGAAACCGGAAA	
	CAGCGACGCAGTAGCACTCATAGCTACCAT	
	CTCACTCT**T**GAGCCAAG	2155
	CTTGGCTC**A**AGAGTGAG	2156
Reduced palmitate	GCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCCCAAAAC	2157
Acyl-ACP-thioesterase	CTCACTCTGGAGCCT**A**GACATCTGATAAGCTTGGAGGTGAACCAG	

TABLE 22-continued

Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Helianthus annuus	GTAGTGTTGCTGTGCGCGGAATCAAGACAA	
Lys23Term	TTGTCTTGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAG	2158
AAG-TAG	CTTATCAGATGTCT**A**GGCTCCAGAGTGAGGTTTTGGGGAAGAAAC	
	CGGAAACAGCGACGCAGTCGCACTCATAGC	
	CTGGAGCC**T**AGACATCT	2159
	AGATGTCT**A**GGCTCCAG	2160
Reduced palmitate	ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCC	2161
Acyl-ACP-thioesterase	CCAGGAGCCTCCCCT**T**AACCTGGGAAGTTAGGCAACTGGTCATCG	
Cuphea palustris	AGTTTGAGCCCTTCCTTGAAGCCCAAGTCAA	
Lys21Term	TTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATGACCAGTTGC	2162
AAA-TAA	CTAACTTCCCAGGTT**A**AGGGGAGGCTCCTGGGGATGGAACAGGG	
	AAGCATGCAGAACTTGCTGCAGCAGCCACCAT	
	CCTCCCCT**T**AACCTGGG	2163
	CCCAGGTT**A**AGGGGAGG	2164
Reduced palmitate	GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCC	2165
Acyl-ACP-thioesterase	TCCCCTAAACCTGGG**T**AGTTAGGCAACTGGTCATCGAGTTTGAGC	
Cuphea palustris	CCTTCCTTGAAGCCCAAGTCAATCCCCAATG	
Lys24Term	CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATG	2166
AAG-TAG	ACCAGTTGCCTAACT**A**CCCAGGTTTAGGGGAGGCTCCTGGGGATG	
	GAACAGGGAAGCATGCAGAACTTGCTGCAGC	
	AACCTGGG**T**AGTTAGGC	2167
	GCCTAACT**A**CCCAGGTT	2168
Reduced palmitate	TGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGG	2169
Acyl-ACP-thioesterase	GAAGTTAGGCAACTG**A**TCATCGAGTTTGAGCCCTTCCTTGAAGCC	
Cuphea palustris	CAAGTCAATCCCCAATGGCGGATTTCAGGTT	
Trp28Term	AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGG	2170
TGG-TGA	GCTCAAACTCGATGA**T**CAGTTGCCTAACTTCCCAGGTTTAGGGGA	
	GGCTCCTGGGGATGGAACAGGGAAGCATGCA	
	GGCAACTG**A**TCATCGAG	2171
	CTCGATGA**T**CAGTTGCC	2172
Reduced palmitate	CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGGA	2173
Acyl-ACP-thioesterase	AGTTAGGCAACTGGT**G**ATCGAGTTTGAGCCCTTCCTTGAAGCCCA	
Cuphea palustris	AGTCAATCCCCAATGGCGGATTTCAGGTTAA	
Ser29Term	TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAA	2174
TCA-TGA	GGGCTCAAACTCGAT**C**ACCAGTTGCCTAACTTCCCAGGTTTAGGG	
	GAGGCTCCTGGGGATGGAACAGGGAAGCATG	
	CAACTGGT**G**ATCGAGTT	2175
	AACTCGAT**C**ACCAGTTG	2176
Reduced paimitate	ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACC	2175
Acyl-ACP-thioesterase	CCGGGAATCTCCCCT**T**AACCCGGGAAGTTCGGTAATGGTGGCTTT	
Cuphea hookeriana	CAGGTTAAGGCAAACGCCAATGCCCATCCTA	
Lys21Term	TAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTAC	2178
AAA-TAA	CGAACTTCCCGGGTT**A**AGGGGAGATTCCCGGGGTTGGAACGGAG	
	AAGAATGCAGAACTTGCTGCGGCAGCCACCAT	
	TCTCCCCT**T**AACCCGGG	2179
	CCCGGGTT**A**AGGGGAGA	2180
Reduced palmitate	GCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATC	2181
Acyl-ACP-thioesterase	TCCCCTAAACCCGGG**T**AGTTCGGTAATGGTGGCTTTCAGGTTAAG	
Cuphea hookeriana	GCAAACGCCAATGCCCATCCTAGTCTAAAGT	
Lys24Term	ACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGC	2182
AAG-TAG	CACCATTACCGAACT**A**CCCGGGTTTAGGGGAGATTCCCGGGGTTG	
	GAACGGAGAAGAATGCAGAACTTGCTGCGGC	
	AACCCGGG**T**AGTTCGGT	2183
	ACCGAACT**A**CCCGGGTT	2184
Reduced palmitate	TTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTC	2185
Acyl-ACP-thioesterase	GGTAATGGTGGCTTTT**T**AGGTTAAGGCAAACGCCAATGCCCATCCT	
Cuphea hookeriana	AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	
Gln31Term	CTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGG	2186
CAG-TAG	CGTTTGCCTTAACCT**A**AAAGCCACCATTACCGAACTTCCCGGGTTT	
	AGGGGAGATTCCCGGGGTTGGAACGGAGAA	
	GTGGCTTTT**T**AGGTTAAG	2187
	CTTAACCT**A**AAAGCCAC	2188

TABLE 22-continued

Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate	GTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAAT	2189
Acyl-ACP-thioesterase	GGTGGCTTTCAGGTTTAGGCAAACGCCAATGCCCATCCTAGTCTA	
Cuphea hookeriana	AAGTCTGGCAGCCTCGAGACTGAAGATGACA	
Lys33Term	TGTCATCTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGG	2190
AAG-TAG	CATTGGCGTTTGCCTAAACCTGAAAGCCACCATTACCGAACTTCCC	
	GGGTTTAGGGGAGATTCCCGGGGTTGGAAC	
	TTCAGGTTTAGGCAAAC	2191
	GTTTGCCTAAACCTGAA	2192
Reduced palmitate	ATGTTGAAGCTCTCGTGTAATGCGACTGATAAGTTACAGACCCTCT	2193
Acyl-ACP-thioesterase	TCTCGCATTCTCATTAACCGGATCCGGCACACCGGAGAACCGTCT	
Brassica rapa	CCTCCGTGTCGTGCTCTCATCTGAGGAAAC	
Gln21Term	GTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGT	2194
CAA-TAA	GTGCCGGATCCGGTTAATGAGAATGCGAGAAGAGGGTCTGTAACT	
	TATCAGTCGCATTACACGAGAGCTTCAACAT	
	ATTCTCATTAACCGGAT	2195
	ATCCGGTTAATGAGAAT	2196
Reduced palmitate	GCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATCAACCGG	2197
Acyl-ACP-thioesterase	ATCCGGCACACCGGTGAACCGTCTCCTCCGTGTCGTGCTCTCATC	
Brassica rapa	TGAGGAAACCGGTTCTCGATCCTTTGCGAG	
Arg28Term	CTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACGACA	2198
AGA-TGA	CGGAGGAGACGGTTCACCGGTGTGCCGGATCCGGTTGATGAGAA	
	TGCGAGAAGAGGGTCTGTAACTTATCAGTCGC	
	CACACCGGTGAACCGTC	2199
	GACGGTTCACCGGTGTG	2200
Reduced palmitate	CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAA	2201
Acyl-ACP-thioesterase	CCGTCTCCTCCGTGTAGTGCTCTCATCTGAGGAAACCGGTTCTCG	
Brassica rapa	ATCCTTTGCGAGCGATCGTATCTGCTGATCA	
Ser24Term	TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTC	2202
TCG-TAG	CTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTGTGC	
	CGGATCCGGTTGATGAGAATGCGAGAAGAGGG	
	CTCCGTGTAGTGCTCTC	2203
	GAGAGCACTACACGGAG	2204
Reduced palmitate	CTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGT	2205
Acyl-ACP-thioesterase	CTCCTCCGTGTCGTGATCTCATCTGAGGAAACCGGTTCTCGATCC	
Brassica rapa	TTTGCGAGCGATCGTATCTGCTGATCAAGGA	
Cys25Term	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG	2206
TGC-TGA	TTTCCTCAGATGAGATCACGACACGGAGGAGACGGTTCTCCGGTG	
	TGCCGGATCCGGTTGATGAGAATGCGAGAAG	
	GTGTCGTGATCTCATCT	2207
	AGATGAGATCACGACAC	2208
Reduced palmitate	ATTCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGG	2209
Acyl-ACP-thioesterase	GCATCAAAAATGTAGAAGCTTTCGTGTAATGTGACTAACAACTTAC	
Brassica napus	ACACCTTCTCCTTCTTCTCCGATTCCTC	
Leu2Term	GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACA	2210
TTG-TAG	TTACACGAAAGCTTCTACATTTTTGATGCCCTTTTTTTTTTATGGTTC	
	CTGAGGTTTTGGTTTATAGAAGAAGAAT	
	AAAAATGTAGAAGCTTT	2211
	AAAGCTTCTACATTTTT	2212
Reduced palmitate	TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGG	2213
Acyl-ACP-thioesterase	CATCAAAAATGTTGTAGCTTTCGTGTAATGTGACTAACAACTTACAC	
Brassica napus	ACCTTCTCCTTCTTCTCCGATTCCTCCC	
Lys3Term	GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCA	2214
AAG-TAG	CATTACACGAAAGCTACAACATTTTTGATGCCCTTTTTTTTTTATGG	
	TTCCTGAGGTTTTGGTTTATAGAAGAAGA	
	AAATGTTGTAGCTTTCG	2215
	CGAAAGCTACAACATTT	2216
Reduced palmitate	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAA	2217
Acyl-ACP-thioesterase	AATGTTGAAGCTTTAGTGTAATGTGACTAACAACTTACACACCTTCT	
Brassica napus	CCTTCTTCTCCGATTCCTCCCTTTTCAT	
Ser5Term	ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTT	2218
TCG-TAG	GTTAGTCACATTACACTAAAGCTTCAACATTTTTGATGCCCTTTTTT	
	TTTTATGGTTCCTGAGGTTTTGGTTTATAG	

TABLE 22-continued

Oligonucleotides to produce plants with reduced palmitate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAAGCTTT**A**GTGTAATG	2219
	CATTACAC**T**AAAGCTTC	2220
Reduced palmitate	AAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGGCATCAAAAATG	2221
Acyl-ACP-thioesterase	TTGAAGCTTTCGTG**A**AATGTGACTAACAACTTACACACCTTCTCCTT	
Brassica napus	CTTCTCCGATTCCTCCCTTTTCATCCCG	
Cys6Term	CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTA	2222
TGT-TGA	AGTTGTTAGTCACATT**T**CACGAAAGCTTCAACATTTTTGATGCCCTT	
	TTTTTTTTATGGTTCCTGAGGTTTTGGTTT	
	CTTTCGTG**A**AATGTGAC	2223
	GTCACATT**T**CACGAAAG	2224

[0147]

TABLE 23

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCATTCATCATATC	2225
stearoyl-ACP	CAGAAATGGCTCTA**T**AGTTTAACCCTTTGGTGGCATCTCAGCCTTA	
desaturase	CAAATTCCCTTCCTCGACTCGTCCGCCAA	
Arabidopsis thaliana	TTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCC	2226
Lys4 Term	ACCAAAGGGTTAAACT**A**TAGAGCCATTTCTGGATATGATGAATGAA	
AAG-TAG	TCCTTCTTTTCTACAGAGCTAGAGCTCTCCC	
	TGGCTCTA**T**AGTTTAAC	2227
	GTTAAACT**A**TAGAGCCA	2228
Increased stearate	CTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCT	2229
stearoyl-ACP	AAAGTTTAACCCTT**A**GGTGGCATCTCAGCCTTACAAATTCCCTTCC	
desaturase	TCGACTCGTCCGCCAACTCCTCTTTCAG	
Arabidopsis thaliana	CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTA	2230
Leu8 Term	AGGCTGAGATGCCACC**T**AAGGGTTAAACTTTAGAGCCATTTCTGG	
TTG-TAG	ATATGATGAATGAATCCTTCTTTTCTACAGAG	
	TAACCCTT**A**GGTGGCAT	2231
	ATGCCACC**T**AAGGGTTA	2232
Increased stearate	AGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACC	2233
stearoyl-ACP	CTTTGGTGGCATCT**T**AGCCTTACAAATTCCCTTCCTCGACTCGTCC	
desaturase	GCCAACTCCTTCTTTCAGATCTCCCAAGT	
Arabidopsis thaliana	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA	2234
Gln12 Term	GGGAATTTGTAAGGCT**A**AGATGCCACCAAAGGGTTAAACTTTAGA	
CAG-TAG	GCCATTTCTGGATATGATGAATGAATCCTTCT	
	TGGCATCT**T**AGCCTTAC	2235
	GTAAGGCT**A**AGATGCCA	2236
Increased stearate	TCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTTTGGTG	2237
stearoyl-ACP	GCATCTCAGCCTTA**G**AAATTCCCTTCCTCGACTCGTCCGCCAACTC	
desaturase	CTTCTTTCAGATCTCCCAAGTTCCTCTGC	
Arabidopsis thaliana	GCAGAGGAACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG	2238
Phe14 Term	TCGAGGAAGGGAATTT**C**TAAGGCTGAGATGCCACCAAAGGGTTAA	
TAC-TAG	ACTTTAGAGCCATTTCTGGATATGATGAATGA	
	CAGCCTTA**G**AAATTCCC	2239
	GGGAATTT**C**TAAGGCTG	2240
Increased stearate	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA	2241
stearoyl-ACP	AAAGAAAATGGCAT**A**GAAGCTTAACCCTTTGGCATCTCAGCCTTAC	
desaturase	AAACTCCCTTCCTCGGCTCGTCCGCCAAT	
Brassica napus	ATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGC	2242
Leu3 Term	CAAAGGGTTAAGCTTC**T**ATGCCATTTTCTTTTTTTTGATACGAGGTT	

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
TTG-TAG	TGATGTTCTTTCAGACACGAGCGAGCTCTC	
	AATGGCAT**A**AGAAGCTTA	2243
	TAAGCTTC**T**ATGCCATT	2244
Increased stearate	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAA	2245
stearoyl-ACP	AGAAAATGGCATTG**T**AGCTTAACCCTTTGGCATCTCAGCCTTACAA	
desaturase	ACTCCCTTCCTCGGCTCGTCCGCCAATCT	
Brassica napus	AGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGAT	2246
Lys4 Term	GCCAAAGGGTTAAGCT**A**CAATGCCATTTTCTTTTTTTTGATACGAG	
AAG-TAG	GTTTGATGTTCTTTCAGACACGAGCGAGCTC	
	TGGCATTG**T**AGCTTAAC	2247
	GTTAAGCT**A**CAATGCCA	2248
Increased stearate	TCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATT	2249
stearoyl-ACP	GAAGCTTAACCCTT**A**GGCATCTCAGCCTTACAAACTCCCTTCCTCG	
desaturase	GCTCGTCCGCCAATCTCTACTCTCAGATC	
Brassica napus	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTT	2250
Leu8 Term	GTAAGGCTGAGATGCC**T**AAGGGTTAAGCTTCAATGCCATTTTCTTT	
TTG-TAG	TTTTTGATACGAGGTTTGATGTTCTTTCAGA	
	TAACCCTT**A**GGCATCTC	2251
	GAGATGCC**T**AAGGGTTA	2252
Increased stearate	AACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTGAAGCTTA	2253
stearoyl-ACP	ACCCTTTGGCATCT**T**AGCCTTACAAACTCCCTTCCTCGGCTCGTCC	
desaturase	GCCAATCTCTACTCTCAGATCTCCCAAGT	
Brassica napus	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA	2254
Gln11 Term	GGGAGTTTGTAAGGCT**A**AGATGCCAAAGGGTTAAGCTTCAATGCC	
CAG-TAG	ATTTTCTTTTTTTTGATACGAGGTTTGATGTT	
	TGGCATCT**T**AGCCTTAC	2255
	GTAAGGCT**A**AGATGCCA	2256
Increased stearate	AACCAAAAGAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCA	2257
stearoyl-ACP	ATCCTTTCCTTTCT**T**AAACCCAAAAGTTACCTTCTTTCGCTCTTCCA	
desaturase	CCAATGGCCAGTACCAGATCTCCTAAGT	
Ricinus communis	ACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAG	2258
Gln27 Term	GTAACTTTTGGGTTT**A**AGAAAGGATTGAGCTTGAGAGCCAT	
CAA-TAA	TGTTTTTTTTCTTACCTTTTTCTTTTGGTT	
	TCCTTTCT**T**AAACCCAA	2259
	TTGGGTTT**A**AGAAAGGA	2260
Increased stearate	AAGAAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTT	2261
stearoyl-ACP	TCCTTTCTCAAACC**T**AAAAGTTACCTTCTTTCGCTCTTCCACCAATG	
desaturase	GCCAGTACCAGATCTCCTAAGTTCTACA	
Ricinus communis	TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGA	2262
Gln29 Term	AAGAAGGTAACTTTT**A**GGTTTGAGAAAGGAAAGGATTGAGCTTGA	
CAA-TAA	GAGCCATTGTTTTTTTTCTTACCTTTTTCTT	
	CTCAAACC**T**AAAAGTTA	2263
	TAACTTTT**A**GGTTTGAG	2264
Increased stearate	AAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCC	2265
stearoyl-ACP	TTTCTCAAACCCAA**T**AGTTACCTTCTTTCGCTCTTCCACCAATGGCC	
desaturase	AGTACCAGATCTCCTAAGTTCTACATGG	
Ricinus communis Lys30 TermCGAAAGAAGG-TAACT **A**TTGGGTTTGAGAAAGGAAAGGATTGAGCT	CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAG	2266
AAG-TAG	TGAGAGCCATTGTTTTTTTTCTTACCTTTTT	
	AAACCCAA**T**AGTTACCT	2267
	AGGTAACT**A**TTGGGTTT	2268
Increased stearate	TCTCAAACCCAAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCA	2269
stearoyl-ACP	GTACCAGATCTCCT**T**AGTTCTACATGGCCTCTACCCTCAAGTCTGG	
desaturase	TTCTAAGGAAGTTGAGAATCTCAAGAAGC	
Ricinus communis	GCTTCTTGAGATTCTCAACTTCCTTAGAACCAGACTTGAGGGTAGA	2270
Lys46 Term	GGCCATGTAGAACT**A**AGGAGATCTGGTACTGGCCATTGGTGGAG	
AAG-TAG	AGCGAAAGAAGGTAACTTTTGGGTTTGAGA	
	GATCTCCT**T**AGTTCTAC	2271
	GTAGAACT**A**AGGAGATC	2272

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate	TCTTCTGATTCATTTAATCTTTACTCATCAATGGCTCTGAGACTGAA	2273
stearoyl-ACP	CCCTATCCCCACC**T**AAACCTTCTCCCTCCCCCAAATGGCCAGTCTC	
desaturase	AGATCTCCCAGGTTCCGCATGGCCTCTA	
Glycine max	TAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTGG	2274
Gln11 Term	GGGAGGGAGAAGGTTT**A**GGTGGGGATAGGGTTCAGTCTCAGAGC	
CAA-TAA	CATTGATGAGTAAAGATTAAATGAATCAGAAGA	
	TCCCCACC**T**AAACCTTC	2275
	GAAGGTTT**A**GGTGGGGA	2276
Increased stearate	CTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCCAAA	2277
stearoyl-ACP	CCTTCTCCCTCCCC**T**AAATGGCCAGTCTCAGATCTCCCAGGTTCC	
desaturase	GCATGGCCTCTACCCTCCGCTCCGGTTCCA	
Glycine max	TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGAT	2278
Gln17 Term	CTGAGACTGGCCATTT**A**GGGGAGGGAGAAGGTTTGGGTGGGGAT	
CAA-TAA	AGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG	
	CCCTCCCC**T**AAATGGCC	2279
	GGCCATTT**A**GGGGAGGG	2280
Increased stearate	GCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCC	2281
stearoyl-ACP	CAAATGGCCAGTCTC**T**GATCTCCCAGGTTCCGCATGGCCTCTACC	
desaturase	CTCCGCTCCGGTTCCAAAGAGGTTGAAAATA	
Glycine max	TATTTTCAACCTCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGC	2282
Arg22 Term	GGAACCTGGGAGATC**A**GAGACTGGCCATTTGGGGGAGGGAGAAG	
AGA-TGA	GTTTGGGTGGGGATAGGGTTCAGTCTCAGAGC	
	CCAGTCTC**T**GATCTCCC	2283
	GGGAGATC**A**GAGACTGG	2284
Increased stearate	CAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACC	2285
stearoyl-ACP	CTCCGCTCCGGTTCC**T**AAGAGGTTGAAAATATTAAGAAGCCATTCA	
desaturase	CTCCTCCCAGAGAAGTGCATGTTCAAGTAA	
Glycine max	TTACTTGAACATGCACTTCTCTGGGAGGAGTGAATGGCTTCTTAAT	2286
Lys37 Term	ATTTTCAACCTCTT**A**GGAACCGGAGCGGAGGGTAGAGGCCATGCG	
AAA-TAA	GAACCTGGGAGATCTGAGACTGGCCATTTG	
	CCGGTTCC**T**AAGAGGTT	2287
	AACCTCTT**A**GGAACCGG	2288
Increased stearate	CAACAAGCACACACAAGAACAACATCAACAATGGCGATTCGCATC	2289
stearoyl-ACP	AATACGGCGACGTTT**T**AATCAGACCTGTACCGTTCATTCGCGTTTC	
desaturase	CTCAACCGAAACCTCTCAGATCTCCCAAAT	
Helianthus annuus	ATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAAC	2290
Gln11 Term	GGTACAGGTCTGATT**A**AAACGTCGCCGTATTGATGCGAATCGCCA	
CAA-TAA	TTGTTGATGTTGTTCTTGTGTGTGCTTGTTG	
	CGACGTTT**T**AATCAGAC	2291
	GTCTGATT**A**AAACGTCG	2292
Increased stearate	AAGCACACACAAGAAGCAACATCAACAATGGCGATTCGCATCAATAC	2293
stearoyl-ACP	GGCGACGTTTCAAT**G**AGACCTGTACCGTTCATTCGCGTTTCCTCAA	
desaturase	CCGAAACCTCTCAGATCTCCCAAATTCGC	
Helianthus annuus	GCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAAT	2294
Ser12 Term	GAACGGTACAGGTCT**C**ATTGAAACGTCGCCGTATTGATGCGAATC	
TCA-TGA	GCCATTGTTGATGTTGTTCTTGTGTGTGCTT	
	GTTTCAAT**G**AGACCTGT	2295
	ACAGGTCT**C**ATTGAAAC	2296
Increased stearate	AAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTT	2297
stearoyl-ACP	CAATCAGACCTGTA**G**CGTTCATTCGCGTTTCCTCAACCGAAACCTC	
desaturase	TCAGATCTCCCAAATTCGCCATGGCTTCC	
Helianthus annuus	GGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGG	2298
Tyr15 Term	AAACGCGAATGAACG**C**TACAGGTCTGATTGAAACGTCGCCGTATT	
TAC-TAG	GATGCGAATCGCCATTGTTGATGTTGTTCTT	
	GACCTGTA**G**CGTTCATT	2299
	AATGAACG**C**TACAGGTC	2300
Increased stearate	CAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTTCAATC	2301
stearoyl-ACP	AGACCTGTACCGTT**G**ATTCGCGTTTCCTCAACCGAAACCTCTCAGA	
desaturase	TCTCCCAAATTCGCCATGGCTTCCACCAT	
Helianthus annuus	ATGGTGGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGT	2302
Ser17 Term	TGAGGAAACGCGAAT**C**AACGGTACAGGTCTGATTGAAACGTCGCC	

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
TCA-TGA	GTATTGATGCGAATCGCCATTGTTGATGTTG	
	GTACCGTT**G**ATTCGCGT	2303
	ACGCGAAT**C**AACGGTAC	2304
Increased stearate	ACACACAACACACACTCAATCACACACACATCATCATCTTCTTCATC	2305
stearoyl-ACP	AACGATGGCGCTT**T**GAATGAGTCCGGTGACGCTTCAACGGGAGAT	
desaturase	ATATCCTTCATACACTTTTCATCAATCGA	
Helianthus annuus	TCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTGAAGCGT	2306
Arg4 Term	CACCGGACTCATTC**A**AAGCGCCATCGTTGATGAAGAAGATGATGA	
CGA-TGA	TGTGTGTGTGATTGAGTGTGTGTTGTGTGT	
	TGGCGCTT**T**GAATGAGT	2307
	ACTCATTC**A**AAGCGCCA	2308
Increased stearate	ACACACACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGA	2309
stearoyl-ACP	GTCCGGTGACGCTT**T**AACGGGAGATATATCCTTCATACACTTTTCA	
desaturase	TCAATCGAAAAATCTCAGATCTCCTAAAT	
Helianthus annuus	ATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGG	2310
Gln11 Term	ATATATCTCCCGTT**A**AAGCGTCACCGGACTCATTCGAAGCGCCATC	
CAA-TAA	GTTGATGAAGAAGATGATGATGTGTGTGT	
	TGACGCTT**T**AACGGGAG	2311
	CTCCCGTT**A**AAGCGTCA	2312
Increased stearate	ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGG	2313
stearoyl-ACP	TGACGCTTCAACGG**T**AGATATATCCTTCATACACTTTTCATCAATCG	
desaturase	AAAAATCTCAGATCTCCTAAATTCGCGA	
Helianthus annuus	TCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTA	2314
Glu13 Term	TGAAGGATATATCT**A**CCGTTGAAGCGTCACCGGACTCATTCGAAG	
GAG-TAG	CGCCATCGTTGATGAAGAAGATGATGATGT	
	TTCAACGG**T**AGATATAT	2315
	ATATATCT**A**CCGTTGAA	2316
Increased stearate	ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTT	2317
stearoyl-ACP	CAACGGGAGATATA**G**CCTTCATACACTTTTCATCAATCGAAAAATC	
desaturase	TCAGATCTCCTAAATTCGCGATGGCTTCC	
Helianthus annuus	GGAAGCCATCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGA	2318
Tyr15 Term	AAAGTGTATGAAGG**C**TATATCTCCCGTTGAAGCGTCACCGGACTC	
TAT-TAG	ATTCGAAGCGCCATCGTTGATGAAGAAGAT	
	GAGATATA**G**CCTTCATA	2319
	TATGAAGG**C**TATATCTC	2320
Increased stearate	AACTCAGCCAGCTTGCCCCCAAACAACAGCGCAGAAAAACCTTCA	2321
stearoyl-ACP	ACAACAATGGCTCTC**T**AGCTCAACCCAGTCACCACCTTCCCTTCAA	
desaturase	CACGCTCCCTCAACAACTTCTCCTCCAGAT	
Linum usitatissimum	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTG	2322
Lys4 Term	GTGACTGGGTTGAGCT**A**GAGAGCCATTGTTGTTGAAGGTTTTTCT	
AAG-TAG	GCGCTGTTGTTTGGGGGCAAGCTGGCTGAGTT	
	TGGCTCTC**T**AGCTCAAC	2323
	GTTGAGCT**A**GAGAGCCA	2324
Increased stearate	GCGCAGAAAAACCTTCAACAACAATGGCTCTCAAGCTCAACCCAG	2325
stearoyl-ACP	TCACCACCTTCCCTT**G**AACACGCTCCCTCAACAACTTCTCCTCCAG	
desaturase	ATCTCCTCGCACCTTTCTCATGGCTGCTTC	
Linum usitatissimum	GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTT	2326
Ser13 Term	GTTGAGGGAGCGTGTT**C**AAGGGAAGGTGGTGACTGGGTTGAGCT	
TCA-TGA	TGAGAGCCATTGTTGTTGAAGGTTTTTCTGCGC	
	CTTCCCTT**G**AACACGCT	2327
	AGCGTGTT**C**AAGGGAAG	2328
Increased stearate	CTCAAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCA	2329
stearoyl-ACP	ACAACTTCTCCTCC**T**GATCTCCTCGCACCTTTCTCATGGCTGCTTC	
desaturase	CACTTTCAATTCCACCTCCACCAAGTAAG	
Linum usitatissimum	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAA	2330
Arg23 Term	AGGTGCGAGGAGATC**A**GGAGGAGAAGTTGTTGAGGGAGCGTGTT	
AGA-TGA	GAAGGGAAGGTGGTGACTGGGTTGAGCTTGAG	
	TCTCCTCC**T**GATCTCCT	2331
	AGGAGATC**A**GGAGGAGA	2332
Increased stearate	TCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCA	2333
stearoyl-ACP	ATTCCACCTCCACC**T**AGTAAGCATCTCCTCCTCCTCGGAATCTCCG	
desaturase	CCGATTTCTTTTAAGCGATTGATCGTAGA	

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Linum usitatissimum	TCTACGATCAATCGCTTAAAAGAAATCGGCGGAGATTCCGAGGAG	2334
Lys411 Term	GAGGAGATGCTTACT**A**GGTGGAGGTGGAATTGAAAGTGGAAGCA	
AAG-TAG	GCCATGAGAAAGGTGCGAGGAGATCTGGAGGA	
	CCTCCACC**T**AGTAAGCA	2335
	TGCTTACT**A**GGTGGAGG	2336
Increased stearate	ATGGCACTGAAACTTTGCTTTCCACCCCACAAGATGCCTTCCTTCC	2337
stearoyl-ACP	CCGATGCTCGTATC**T**GATCTCACAGGGTTTTCATGGCTTCAACTAT	
desaturase	TCATTCTCCTTCTATGGAGGTCGGAAAAG	
Olea europaeap	CTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA	2338
Arg21 Term	AACCCTGTGAGATC**A**GATACGAGCATCGGGGAAGGAAGGCATCTT	
AGA-TGA	GTGGGGTGGAAAGCAAAGTTTCAGTGCCAT	
	CTCGTATC**T**GATCTCAC	2339
	GTGAGATC**A**GATACGAG	2340
Increased stearate	CCCACAAGATGCCTTCCTTCCCCGATGCTCGTATCAGATCTCACAG	2341
stearoyl-ACP	GGTTTTCATGGCTT**G**AACTATTCATTCTCCTTCTATGGAGGTCGGA	
desaturase	AAAGTTAAAAAGCCTTTCACGCCTCCACG	
Olea europaeap	CGTGGAGGCGTGAAAGGCTTTTTAACTTTTCCGACCTCCATAGAA	2342
Ser29 Term	GGAGAATGAATAGTT**C**AAGCCATGAAAACCCTGTGAGATCTGATAC	
TCA-TGA	GAGCATCGGGGAAGGAAGGCATCTTGTGGG	
	CATGGCTT**G**AACTATTC	2343
	GAATAGTT**C**AAGCCATG	2344
Increased stearate	GATGCTCGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTC	2345
stearoyl-ACP	ATTCTCCTTCTATG**T**AGGTCGGAAAAGTTAAAAAGCCTTTCACGCC	
desaturase	TCCACGAGAGGTACATGTTCAAGTAACCC	
Olea europaeap	GGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTT	2346
Glu37 Term	TAACTTTTCCGACCT**A**CATGAAGGAGAATGAATAGTTGAAGCCAT	
GAG-TAG	GAAAACCCTGTGAGATCTGATACGAGCATC	
	CTTCTATG**T**AGGTCGGA	2347
	TCCGACCT**A**CATAGAAG	2348
Increased stearate	CGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTCATTCTC	2349
stearoyl-ACP	CTTCTATGGAGGTC**T**GAAAAGTTAAAAAGCCTTTCACGCCTCCACG	
desaturase	AGAGGTACATGTTCAAGTAACCCATTCCT	
Olea europaeap	AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAG	2350
Gly39 Term	GCTTTTTAACTTTTC**A**GACCTCCATAGAAGGAGAATGAATAGTTGA	
GGA-TGA	AGCCATGAAAACCCTGTGAGATCTGATACG	
	TGGAGGTC**T**GAAAAGTT	2351
	AACTTTTC**A**GACCTCCA	2352
Increased stearate	TTCTCGTTTTTGTCGTCCCCTCTGCTCTCTCTCTCTATCAGGCACG	2353
stearoyl-ACP	GAGAAATGGCACTG**T**AACTCAGTCCAGTCATGTTTCAATCTCAGAA	
desaturase	GCTTCCATTTCTTGCCTCCTATCCGCCTT	
Persea americana	AAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTGAAACA	2354
Lys4 Term	TGACTGGACTGAGTT**A**CAGTGCCATTTCTCCGTGCCTGATAGAGA	
AAA-TAA	GAGAGAGCAGAGGGGACGACAAAAACGAGAA	
	TGGCACTG**T**AACTCAGT	2355
	ACTGAGTT**A**CAGTGCCA	2356
Increased stearate	CTGCTCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCA	2357
stearoyl-ACP	GTCCAGTCATGTTT**T**AATCTCAGAAGCTTCCATTTCTTGCCTCCTAT	
desaturase	CCGCCTTCCAATCTCAGATCTCCGAGGG	
Persea americana	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT	2358
Gln11 Term	GGAAGCTTCTGAGATT**A**AAACATGACTGGACTGAGTTTCAGTGCC	
CAA-TAA	ATTTCTCCGTGCCTGATAGAGAGAGAGAGCAG	
	TCATGTTT**T**AATCTCAG	2359
	CTGAGATT**A**AAACATGA	2360
Increased stearate	TCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA	2361
stearoyl-ACP	GTCATGTTTCAATCT**T**AGAAGCTTCCATTTCTTGCCTCCTATCCGCC	
desaturase	TTCCAATCTCAGATCTCCGAGGGTTTTCA	
Persea americana	TGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA	2362
Gln13 Term	GAAATGGAAGCTTCT**A**AGATTGAAACATGACTGGACTGAGTTTCAG	
CAG-TAG	TGCCATTTCTCCGTGCCTGATAGAGAGAGA	
	TTCAATCT**T**AGAAGCTT	2363
	AAGCTTCT**A**AGATTGAA	2364

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC	2365
stearoyl-ACP	ATGTTTCAATCTCAG**T**AGCTTCCATTTCTTGCCTCCTATCCGCCTTC	
desaturase	CAATCTCAGATCTCCGAGGGTTTTCATGG	
Persea americana	CCATGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAG	2366
Lys14 Term	GCAAGAAATGGAAGCT**A**CTGAGATTGAAACATGACTGGACTGAGT	
AAG-TAG	TTCAGTGCCATTTCTCCGTGCCTGATAGAGAG	
	AATCTCAG**T**AGCTTCCA	2367
	TGGAAGCT**A**CTGAGATT	2368
Increased stearate	CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTCGCGGCGTCCC	2369
stearoyl-ACP	ACACCGCATCGCCGTA**G**TCCTGCGGCGGCGTGGCGCAGAGGAG	
desaturase	GAGCAATGGGATGTCGAAGATGGTGGCCATGGCC	
Oryza sativa	GGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCTGCGC	2370
Tyr12 Term	CACGCCGCCGCAGGA**C**TACGGCGATGCGGTGTGGGACGCCGCG	
TAC-TAG	AACGCCATGAGCAGCGGCAGCGAGATCTCGGGG	
	TCGCCGTA**G**TCCTGCGG	2371
	CCGCAGGA**C**TACGGCGA	2372
Increased stearate	CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTACTCC	2373
stearoyl-ACP	TGCGGCGGCGTGGCG**T**AGAGGAGGAGCAATGGGATGTCGAAGAT	
desaturase	GGTGGCCATGGCCTCCACCATCAACAGGGTCA	
Oryza sativa	TGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTCGACATCC	2374
Gln19 Term	CATTGCTCCTCCTCT**A**CGCCACGCCGCCGCAGGAGTACGGCGAT	
CAG-TAG	GCGGTGTGGGACGCCGCGAACGCCATGAGCAG	
	GCGTGGCG**T**AGAGGAGG	2375
	CCTCCTCT**A**CGCCACGC	2376
Increased stearate	CCCACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGG	2377
stearoyl-ACP	AGGAGCAATGGGATGT**A**GAAGATGGTGGCCATGGCCTCCACCAT	
desaturase	CAACAGGGTCAAGACTGCTAAGAAGCCCTACAC	
Oryza sativa	GTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCC	2378
Ser26 Term	ATGGCCACCATCTTC**T**ACATCCCATTGCTCCTCCTCTGCGCCACGC	
TCG-TAG	CGCCGCAGGAGTACGGCGATGCGGTGTGGG	
	TGGGATGT**A**GAAGATGG	2379
	CCATCTTC**T**ACATCCCA	2380
Increased stearate	CACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGGAG	2381
stearoyl-ACP	GAGCAATGGGATGTCG**T**AGATGGTGGCCATGGCCTCCACCATCAA	
desaturase	CAGGGTCAAGACTGCTAAGAAGCCCTACACTC	
Oryza sativa	GAGTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGG	2382
Lys27 Term	CCATGGCCACCATCT**A**CGACATCCCATTGCTCCTCCTCTGCGCCA	
AAG-TAG	CGCCGCCGCAGGAGTACGGCGATGCGGTGTG	
	GGATGTCG**T**AGATGGTG	2383
	CACCATCT**A**CGACATCC	2384
Increased stearate	TTCTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGA	2385
stearoyl-ACP	GAGAAGCAATGGCGT**A**GAAGCTTCACCACACGGCCTTCAATCCTT	
desaturase	CCATGGCGGTTACCTCTTCGGGACTTCCTCG	
Simmondsia chinensis	CGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGC	2386
Leu3 Term	CGTGTGGTGAAGCTTC**T**ACGCCATTGCTTCTCTCTCCTAAGTGCTT	
TTG-TAG	CTGTTGGTAACCGCTCAACCTAGAGAGAGAA	
	AATGGCGT**A**GAAGCTTC	2387
	GAAGCTTC**T**ACGCCATT	2388
Increased stearate	CTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGA	2389
stearoyl-ACP	GAGCAATGGCGTTG**T**AGCTTCACCACACGGCCTTCAATCCTTCC	
desaturase	ATGGCGGTTACCTCTTCGGGACTTCCTCGAT	
Simmondsia chinensis	ATCGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAG	2390
Lys4 Term	GCCGTGTGGTGAAGCT**A**CAACGCCATTGCTTCTCTCTCCTAAGTG	
AAG-TAG	CTTCTGTTGGTAACCGCTCAACCTAGAGAGAG	
	TGGCGTTG**T**AGCTTCAC	2391
	GTGAAGCT**A**CAACGCCA	2392
Increased stearate	AAGCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCAT	2393
stearoyl-ACP	GGCGGTTACCTCTT**A**GGGACTTCCTCGATCGTATCACCTCAGATCT	
desaturase	CACCGCGTTTTCATGGCTTCTTCTACAAT	
Simmondsia chinensis	ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATAC	2394
Ser19 Term	GATCGAGGAAGTCCC**T**AAGAGGTAACCGCCATGGAAGGATTGAAG	

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
TCG-TAG	GCCGTGTGGTGAAGCTTCAACGCCATTGCTT	
	TACCTCTT**A**GGGACTTC	2395
	GAAGTCCC**T**AAGAGGTA	2396
Increased stearate	GCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATG	2397
stearoyl-ACP	GCGGTTACCTCTTCG**T**GACTTCCTCGATCGTATCACCTCAGATCTC	
desaturase	ACCGCGTTTTCATGGCTTCTTCTACAATTG	
Simmondsia chinensis	CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGAT	2398
Gly20 Term	ACGATCGAGGAAGTC**A**CGAAGAGGTAACCGCCATGGAAGGATTG	
GGA-TGA	AAGGCCGTGTGGTGAAGCTTCAACGCCATTGC	
	CCTCTTCG**T**GACTTCCT	2399
	AGGAAGTC**A**CGAAGAGG	2400
Increased stearate	TGGCTCTGAATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCG	2401
stearoyl-ACP	ATTGCCGTCTTTCT**G**ACCTCGTCAAACGCCTTCTCGCAGATCTCCC	
desaturase	AAATTCTTCATGGCTTCCACTCTCAGCAG	
Spinacia oleracea	CTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAA	2402
Ser21 Term	GGCGTTTGACGAGGT**C**AGAAAGACGGCAATCGACGACACTGAAAT	
TCA-TGA	GGTGTGGAAACGGGGTTGAGATTCAGAGCCA	
	GTCTTTCT**G**ACCTCGTC	2403
	GACGAGGT**C**AGAAAGAC	2404
Increased stearate	AATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCGATTGCCGT	2405
stearoyl-ACP	CTTTCTCACCTCGT**T**AAACGCCTTCTCGCAGATCTCCCAAATTCTT	
desaturase	CATGGCTTCCACTCTCAGCAGCTCTTCTC	
Spinacia oleracea	GAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATC	2406
Gln24 Term	TGCGAGAAGGCGTTT**A**ACGAGGTGAGAAAGACGGCAATCGACGA	
CAA-TAA	CACTGAAATGGTGTGGAAACGGGGTTGAGATT	
	CACCTCGT**T**AAACGCCT	2407
	AGGCGTTT**A**ACGAGGTG	2408
Increased stearate	TCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTC	2409
stearoyl-ACP	AAACGCCTTCTCGC**T**GATCTCCCAAATTCTTCATGGCTTCCACTCT	
desaturase	CAGCAGCTCTTCTCCTAAGGAAGCGGAAA	
Spinacia oleracea	TTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGA	2410
Arg29 Term	AGAATTTGGGAGATC**A**GCGAGAAGGCGTTTGACGAGGTGAGAAA	
AGA-TGA	GACGGCAATCGACGACACTGAAATGGTGTGGA	
	CTTCTCGC**T**GATCTCCC	2411
	GGGAGATC**A**GCGAGAAG	2412
Increased stearate	TTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTT	2413
stearoyl-ACP	CTCGCAGATCTCCC**T**AATTCTTCATGGCTTCCACTCTCAGCAGCTC	
desaturase	TTCTCCTAAGGAAGCGGAAAGCCTGAAGA	
Spinacia oleracea	TCTTCAGGCTTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGG	2414
Lys32 Term	AAGCCATGAAGAATT**A**GGGAGATCTGCGAGAAGGCGTTTGACGAG	
AAA-TAA	GTGAGAAAGACGGCAATCGACGACACTGAAA	
	GATCTCCC**T**AATTCTTC	2415
	GAAGAATT**A**GGGAGATC	2416
Increased stearate	AAATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATAT	2417
stearoyl-ACP	CAATGGGGTGTCGT**G**AAAATCTCACAAAATGTTACCATTTCCTTGT	
desaturase	TCTTCAGCCAGATCTGAGCGAGTTTTCAT	
Solanum tuberosum	ATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAAC	2418
Leu10 Term	ATTTTGTGAGATTTT**C**ACGACACCCCATTGATATTCAGTGCCATTGT	
TTA-TGA	TGATGCTCTGTTTTTCACCTCGACTATTT	
	GGTGTCGT**G**AAAATCTC	2419
	GAGATTTT**C**ACGACACC	2420
Increased stearate	ATAGTCGAGGTGAAAACAGAGCATCAACAATGGCACTGAATATCA	2421
stearoyl-ACP	ATGGGGTGTCGTTA**T**AATCTCACAAAATGTTACCATTTCCTTGTTCT	
desaturase	TCAGCCAGATCTGAGCGAGTTTTCATGG	
Solanum tuberosum	CCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTA	2422
Lys11 Term	ACATTTTGTGAGATT**A**TAACGACACCCCATTGATATTCAGTGCCATT	
AAA-TAA	GTTGATGCTCTGTTTTTCACCTCGACTAT	
	TGTCGTTA**T**AATCTCAC	2423
	GTGAGATT**A**TAACGACA	2424
Increased stearate	GTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTG	2425
stearoyl-ACP	TCGTTAAAATCTCAC**T**AAATGTTACCATTTCCTTGTTCTTCAGCCAG	
desaturase	ATCTGAGCGAGTTTTCATGGCTTCAACCA	

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Solanum tuberosum	TGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAG	2426
Lys14 Term	GAAATGGTAACATTT**A**GTGAGATTTTAACGACACCCCATTGATATT	
AAA-TAA	CAGTGCCATTGTTGATGCTCTGTTTTTCAC	
	AATCTCAC**T**AAATGTTA	2427
	TAACATTT**A**GTGAGATT	2428
Increased stearate	ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTAAA	2429
stearoyl-ACP	ATCTCACAAAATGT**G**ACCATTTCCTTGTTCTTCAGCCAGATCTGAG	
desaturase	CGAGTTTTCATGGCTTCAACCATTCATCG	
Solanum tuberosum	CGATGAATGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAA	2430
Leu16 Term	GAACAAGGAAATGGT**C**ACATTTTGTGAGATTTTAACGACACCCCAT	
TTA-TGA	TGATATTCAGTGCCATTGTTGATGCTCTGT	
	CAAAATGT**G**ACCATTTC	2431
	GAAATGGT**C**ACATTTTG	2432
Increased stearate	TGGCTCTGAGGCTGAACCCTAACCCTTCACAGAAGCTCTTTCTCTC	2433
stearoyl-ACP	TCCTTCTTCATCAT**G**ATCTTCTTCTTCTTCATCGTTCTCGCTTCCTC	
desaturase	AAATGGCTAGCCTCAGATCTCCAAGGTT	
Arachis hypogaea	AACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGAT	2434
Ser21 Term	GAAGAAGAAGAAGAT**C**ATGATGAAGAAGGAGAGAGAAAGAGCTTC	
TCA-TGA	TGTGAAGGGTTAGGGTTCAGCCTCAGAGCCA	
	TTCATCAT**G**ATCTTCTT	2435
	AAGAAGAT**C**ATGATGAA	2436
Increased stearate	ACCCTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCA	2437
stearoyl-ACP	TCTTCTTCTTCTT**G**ATCGTTCTCGCTTCCTCAAATGGCTAGCCTCA	
desaturase	GTCTCCAAGGTTCCGCATGGCCTCCAC	
Arachis hypogaea	GTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTTGA	2438
Ser26 Term	GGAAGCGAGAACGAT**C**AAGAAGAAGAAGATGATGATGAAGAAGGA	
TCA-TGA	GAGAGAAAGAGCTTCTGTGAAGGGTTAGGGT	
	TTCTTCTT**G**ATCGTTCT	2439
	AGAACGAT**C**AAGAAGAA	2440
Increased stearate	CTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCT	2441
stearoyl-ACP	TCTTCTTCTTCAT**A**GTTCTCGCTTCCTCAAATGGCTAGCCTCAGAT	
desaturase	CTCCAAGGTTCCGCATGGCCTCCACCCT	
Arachis hypogaea	AGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCAT	2442
Ser27 Term	TTGAGGAAGCGAGAAC**T**ATGAAGAAGAAGAAGATGATGATGAAGA	
TCG-TAG	AGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAG	
	TTCTTCAT**A**GTTCTCGC	2443
	GCGAGAAC**T**ATGAAGAA	2444
Increased stearate	CTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCT	2445
stearoyl-ACP	TCTTCATCGTTCT**A**GCTTCCTCAAATGGCTAGCCTCAGATCTCCAA	
desaturase	GGTTCCGCATGGCCTCCACCCTCCGCAC	
Arachis hypogaea	GTGCGGAGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCT	2446
Ser29 Term	AGCCATTTGAGGAAGC**T**AGAACGATGAAGAAGAAGAAGATGATGA	
TCG-TAG	TGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG	
	ATCGTTCT**A**GCTTCCTC	2447
	GAGGAAGC**T**AGAACGAT	2448
Increased stearate	AAAGTTAAAAGCCGTCCAAAACCCAAACCAGGAAAGGCAAACGAA	2449
stearoyl-ACP	AAGAAAAAATGGCTT**A**GAATTTTAATGCCATCGCCTCGAAATCTCA	
desaturase	GAAGCTCCCTTGCTTTGCTCTTCCACCAAA	
Gossypium hirsutum	TTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTCGAGGCG	2450
Leu3 Term	ATGGCATTAAAATTC**T**AAGCCATTTTTTCTTTTCGTTTGCCTTTCCT	
TTG-TAG	GGTTTGGGTTTTGGACGGCTTTTAACTTT	
	AATGGCTT**A**GAATTTTA	2451
	TAAAATTC**T**AAGCCATT	2452
Increased stearate	CCCAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTT	2453
stearoyl-ACP	TAATGCCATCGCCT**A**GAAATCTCAGAAGCTCCCTTGCTTTGCTCTT	
desaturase	CCACCAAAGGCCACCCTTAGATCTCCCAA	
Gossypium hirsutum	TTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGG	2454
Ser1-Term	GAGCTTCTGAGATTTC**T**AGGCGATGGCATTAAAATTCAAAGCCATT	
TCG-TAG	TTTTCTTTTCGTTTGCCTTTCCTGGTTTGGG	
	CATCGCCT**A**GAAATCTC	2455
	GAGATTTC**T**AGGCGATG	2456

TABLE 23-continued

Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Lys11 Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTA ATGCCATCGCCTCG**T**AATCTCAGAAGCTCCCTTGCTTTGCTCTTCC ACCAAAGGCCACCCTTAGATCTCCCAAGT	2457
	ACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAG GGAGCTTCTGAGATT**A**CGAGGCGATGGCATTAAAATTCAAAGCCAA TTTTTTCTTTTCGTTTGCCTTTCCTGGTTTG	2458
	TCGCCTCG**T**AATCTCAG	2459
	CTGAGATT**A**CGAGGCGA	2460
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Gln13 Term CAG-TAG	AGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCA TCGCCTCGAAATCT**T**AGAAGCTCCCTTGCTTTGCTCTTCCACCAAA GGCCACCCTTAGATCTCCCAAGTTTTCCA	2461
	TGGAAAACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAA AGCAAGGGAGCTTCT**A**AGATTTCGAGGCGATGGCATTAAAATTCA AAGCCATTTTTTCTTTTCGTTTGCCTTTCCT	2462
	CGAAATCT**T**AGAAGCTC	2463
	GAGCTTCT**A**AGATTTCG	2464

[0148]

TABLE 24

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reducing linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser4 Term TCG-TAG	AATAGAACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGC TCCAATGGCGAGCT**A**GGTTTTATCAGAATGTGGTTTTAGACCTCTC CCCAGATTCTACCCTAAACACACAACCTC	2465
	GAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTAAAACCA CATTCTGATAAAACC**T**AGCTCGCCATTGGAGCCTCTTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCGTTCTATT	2466
	GGCGAGCT**T**GGTTTTAT	2467
	ATAAAACC**A**AGCTCGCC	2468
Reducing linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Leu6 Term TTA-TGA	ACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTTT**G**ATCAGAATGTGGTTTTAGACCTCTCCCCAG ATTCTACCCTAAACACACAACCTCTTTTGC	2469
	GCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGAT**C**AAACCGAGCTCGCCATTGGAGCCTCTTCCC AAGAAGAAAAGAGGAAAAAGTCTCTGTCGT	2470
	CTCGGTTT**G**ATCAGAAT	2471
	ATTCTGAT**C**AAACCGAG	2472
Reducing linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser7 Term TCA-TGA	ACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTTTAT**G**AGAATGTGGTTTTAGACCTCTCCCCAGATTC TACCCTAAACACACAACCTCTTTTGCCTC	2473
	GAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCT**C**ATAAAACCGAGCTCGCCATTGGAGCCTCTT CCAAGAAGAAAAGAGGAAAAAGTCTCTGT	2474
	GGTTTTAT**G**AGAATGTG	2475
	CACATTCT**C**ATAAAACC	2476
Reducing linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Glu8 Term GAA-TAA	AGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTTTATCA**T**AATGTGGTTTTAGACCTCTCCCCAGATTCTA CCCTAAACACACAACCTCTTTTGCCTCTA	2477
	TAGAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATT**A**TGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCCAAGAAGAAAAGAGGAAAAAGTCTCT	2478
	TTTTATCA**T**AATGTGGT	2479
	ACCACATT**A**TGATAAAA	2480
Reducing linolenic acid omega-3 fatty acid	TCATCATCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTC TAGCAATGGCGAACT**A**GGTCTTATCCGAATGTGGCATAAGACCTC	2481

TABLE 24-continued

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
desaturase	TCCCCAGAATCTACACCACACCCAGATCCAC	
Brassica juncea	GTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCA	2482
Leu4 Term	CATTCGGATAAGACC**T**AGTTCGCCATTGCTAGAGCTCTTTTGCTCT	
TTG-TAG	CTCTCTCTCCCCAGAAGAAGAAGATGATGA	
	GGCGAACT**A**GGTCTTAT	2483
	ATAAGACC**T**AGTTCGCC	2484
Reducing linolenic acid	TCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAA	2485
omega-3 fatty acid	TGGCGAACTTGGTCT**G**ATCCGAATGTGGCATAAGACCTCTCCCCA	
desaturase	GAATCTACACCACACCCAGATCCACTTTCCT	
Brassica juncea	AGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTT	2486
Leu6 Term	ATGCCACATTCGGAT**C**AGACCAAGTTCGCCATTGCTAGAGCTCTTT	
TTA-TGA	TGCTCTCTCTCTCTCCCCAGAAGAAGAAGA	
	CTTGGTCT**G**ATCCGAAT	2487
	ATTCGGAT**C**AGACCAAG	2488
Reducing linolenic acid	TTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCG	2489
omega-3 fatty acid	AACTTGGTCTTATCC**T**AATGTGGCATAAGACCTCTCCCCAGAATCT	
desaturase	ACACCACACCCAGATCCACTTTCCTCTCCA	
Brassica juncea	TGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGA	2490
Glu8 Term	GGTCTTATGCCACATT**A**GGATAAGACCAAGTTCGCCATTGCTAGA	
GAA-TAA	GCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAA	
	TCTTATCC**T**AATGTGGC	2491
	GCCACATT**A**GGATAAGA	2492
Reducing linolenic acid	CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACT	2493
omega-3 fatty acid	TGGTCTTATCCGAATG**A**GGCATAAGACCTCTCCCCAGAATCTACAC	
desaturase	CACACCCAGATCCACTTTCCTCTCCAACACC	
Brassica juncea	GGTGTTGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGG	2494
Cys9 Term	GGAGAGGTCTTATGCC**T**CATTCGGATAAGACCAAGTTCGCCATTG	
TGT-TGA	CTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAG	
	TCCGAATG**A**GGCATAAG	2495
	CTTATGCC**T**CATTCGGA	2496
Reducing linolenic acid	ATAACAGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAA	2497
omega-3 fatty acid	TGGCTGCTGGTTG**A**GTATTATCAGAATGTGGTTTAAGGCCTCTCCC	
desaturase	AAGAATCTACTCACGACCCAGAATTGGT	
Ricinus communis	ACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACC	2498
Trp5 Term	ACATTCTGATAATAC**T**CAACCAGCAGCCATTGAAAACCCAGAAGCT	
TGG-TGA	AAAAATGCAAGAATTCAGCAATTCTGTTAT	
	GCTGGTTG**A**GTATTATC	2499
	GATAATAC**T**CAACCAGC	2500
Reducing linolenic acid	AGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCT	2501
omega-3 fatty acid	GCTGGTTGGGTAT**G**ATCAGAATGTGGTTTAAGGCCTCTCCCAAGA	
desaturase	ATCTACTCACGACCCAGAATTGGTTTTAC	
Ricinus communis	GTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTT	2502
Leu7 Term	AAACCACATTCTGAT**C**ATACCCAACCAGCAGCCATTGAAAACCCAG	
TTA-TGA	AAGCTAAAAATGCAAGAATTCAGCAATTCT	
	TTGGGTAT**GATCAGAAT**	2503
	ATTCTGAT**C**ATACCCAA	2504
Reducing linolenic acid	ATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCT	2505
omega-3 fatty acid	GGTTGGGTATTATG**A**GAATGTGGTTTAAGGCCTCTCCCAAGAATCT	
desaturase	ACTCACGACCCAGAATTGGTTTTACATC	
Ricinus communis	GATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGC	2506
Ser8 Term	CTTAAACCACATTCT**C**ATAATACCCAACCAGCAGCCATTGAAAACC	
TCA-TGA	CAGAAGCTAAAAATGCAAGAATTCAGCAAT	
	GGTATTATG**A**GAATGTG	2507
	CACATTCT**C**ATAATACC	2508
Reducing linolenic acid	TGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTG	2509
omega-3 fatty acid	GTTGGGTATTATC**A**TAATGTGGTTTAAGGCCTCTCCCAAGAATCTA	
desaturase	CTCACGACCCAGAATTGGTTTTACATCGA	
Ricinus communis	TCGATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGFGGAGAG	2510
Glu9 Term	CGCCTTAAACCACATT**A**TGATAATACCCAACCAGCAGCCATTGAAAA	
GAA-TAA	CCCAGAAGCTAAAAATGCAAGAATTCAGCA	
	TATTATCA**T**AATGTGGT	2511
	ACCACATT**A**TGATAATA	2512

TABLE 24-continued

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reducing linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg22 Term AGA-TGA	GCAAGTTGGTTTTATCAGAATGTGGTCTTAGACCACTCCCAAGAA	2513
	TCTACCCTAAGCCC**T**GAACTGGGGCAGCCACTTCTGCCTCCTCTC	
	ACATTAAGTTGAGAATTTCACGTACAGATC	
	GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGAGGCAGAAGT	2514
	GGCTGCCCCAGTTC**A**GGGCTTAGGGTAGFATTCTTGGGAGTGGTCT	
	AAGACCACATTCTGATAAAACCCAACTTGC	
	CTAAGCCC**T**GAACTGGG	2515
	CCCAGTTC**A**GGGCTTAG	2516
Reducing linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Lys34 Term AAG-TAG	CTCCCAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCT	2517
	GCCTCCTCTCACATT**T**AGTTGAGAATTTCACGTACAGATCTGAGTG	
	GTTCTGCAATTTCTTTGTCTAATACTAAT	
	TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG	2518
	TGAAATTCTCAACT**A**AATGTGAGAGGAGGCAGAAGTGGCTGCCCC	
	AGTTCTGGGCTTAGGGTAGATTCTTGGGAG	
	CTCACATT**T**AGTTGAGA	2519
	TCTCAACT**A**AATGTGAG	2520
Reducing linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Leu35 Term TTG-TAG	CAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCT	2521
	CCTCTCACATTAAGT**A**GAGAATTTCACGTACAGATCTGAGTGGTTC	
	TGCAATTTCTTTGTCTAATACTAATAAAGA	
	TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT	2522
	ACGTGAAATTCTC**T**ACTTAATGTGAGAGGAGGCAGAAGTGGCTGC	
	CCCAGTTCTGGGCTTAGGGTAGATTCTTG	
	CATTAAGT**A**GAGAATTT	2523
	AAATTCTC**T**ACTTAATG	2524
Reducing linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg36 Term AGA-TGA	AGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCC	2525
	TCTCACATTAAGTTG**T**GAATTTCACGTACAGATCTGAGTGGTTCTG	
	CAATTTCTTTGTCTAATACTAATAAAGAGA	
	TCTCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT	2526
	GTACGTGAAATTC**A**CAACTTAATGTGAGAGGAGGCAGAAGTGGCT	
	GCCCCAGTTCTGGGCTTAGGGTAGATTCT	
	TTAAGTTG**T**GAATTTCA	2527
	TGAAATTC**A**CAACTTAA	2528
Reducing linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Arg22 Term AGA-TGA	GCGAGTTGGGTTTTATCAGAATGTGGTCTGAGGCCACTCCCGAGG	2529
	GTCTATCCTAAGCCA**T**GAACTGGCCACCCTTTGTTGAATTCCAATC	
	CCACAAAGCTGAGATTTTCAAGAACAGATC	
	GATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAACAA	2530
	AGGGTGGCCAGTTC**A**TGGCTTAGGATAGACCCTCGGGAGTGGCC	
	TCAGACCACATTCTGATAAAACCCAACTCGC	
	CTAAGCCA**T**GAACTGGC	2531
	GCCAGTTC**A**TGGCTTAG	2532
Reducing linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu27 Term TTG-TAG	CAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAA	2533
	GAACTGGCCACCCTT**A**GTTGAATTCCAATCCCACAAAGCTGAGATT	
	TTCAAGAACAGATCTTGGAAATGGTTCTTC	
	GAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGG	2534
	GATTGGAATTCAAC**T**AAGGGTGGCCAGTTCTTGGCTTAGGATAGA	
	CCCTCGGGAGTGGCCTCAGACCACATTCTG	
	CCACCCTT**A**GTTGAATT	2535
	AATTCAAC**T**AAGGGTGG	2536
Reducing linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu28 Term TTG-TAG	AATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAA	2537
	CTGGCCACCCTTTGT**A**GAATTCCAATCCCACAAAGCTGAGATTTTC	
	AAGAACAGATCTTGGAAATGGTTCTTCATT	
	AATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGT	2538
	GGGATTGGAATTC**T**ACAAAGGGTGGCCAGTTCTTGGCTTAGGATA	
	GACCCTCGGGAGTGGCCTCAGACCACATT	
	CCCTTTGT**A**GAATTCCA	2539
	TGGAATTC**T**ACAAAGGG	2540
Reducing linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Lys34 Term	CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTTG	2541
	AATTCCAATCCCACA**T**AGCTGAGATTTTCAAGAACAGATCTTGGAA	
	ATGGTTCTTCATTCTGTTTGTCGAGTGGGA	
	TCCCACTCGACAAACAGAATGAAGAACCATTTCCAAGATCTGTTCT	2542
	TGAAAATCTCAGCT**A**TGTGGGATTGGAATTCAACAAAGGGTGGCC	

TABLE 24-continued

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
AAG-TAG	AGTTCTTGGCTTAGGATAGACCCTCGGGAG	
	ATCCCACA**T**AGCTGAGA	2543
	TCTCAGCT**A**TGTGGGAT	2544
Reducing linolenic acid	CATCAGAGCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATG	2545
omega-3 fatty acid	GAAGTCTATGAGTTA**G**GTCGTCAGAGAGCTAGCCATCGTGTTCGC	
desaturase	ACTAGCTGCTGGAGCTGCTTACCTCAACAAT	
Brassica napus	ATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGC	2546
Tyr3 Term	TAGCTCTCTGACGAC**C**TAACTCATAGACTTCCATGGATTCTTAACC	
TAC-TAG	CAGCAATGCTTAGGTATCGCCGCTCTGATG	
	ATGAGTTA**G**GTCGTCAG	2547
	CTGACGAC**C**TAACTCAT	2548
Reducing linolenic acid	GCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCT	2549
omega-3 fatty acid	ATGAGTTACGTCGTC**T**GAGAGCTAGCCATCGTGTTCGCACTAGCT	
desaturase	GCTGGAGCTGCTTACCTCAACAATTGGCTTG	
Brassica napus	CAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACA	2550
Arg6 Term	CGATGGCTAGCTCTC**A**GACGACGTAACTCATAGACTTCCATGGAT	
AGA-TGA	CTTAACCCAGCAATGCTTAGGTATCGCCGC	
	ACGTCGTC**T**GAGAGCTA	2551
	TAGCTCTC**A**GACGACGT	2552
Reducing linolenic acid	GCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGA	2553
omega-3 fatty acid	GTTACGTCGTCAGA**T**AGCTAGCCATCGTGTTCGCACTAGCTGCTG	
desaturase	GAGCTGCTTACCTCAACAATTGGCTTGTTT	
Brassica napus	AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGA	2554
Glu7 Term	ACACGATGGCTAGCT**A**TCTGACGACGTAACTCATAGACTTCCATG	
GAG-TAG	GATTCTTAACCCAGCAATGCTTAGGTATCGC	
	TCGTCAGA**T**AGCTAGCC	2555
	GGCTAGCT**A**TCTGACGA	2556
Reducing linolenic acid	CCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGTG	2557
omega-3 fatty acid	TTCGCACTAGCTGCT**T**GAGCTGCTTACCTCAACAATTGGCTTGTTT	
desaturase	GGCCTCTCTATTGGATTGCTCAAGGAACCA	
Brassica napus	TGGTTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTT	2558
Gly17 Term	GAGGTAAGCAGCTC**A**AGCAGCTAGTGCGAACACGATGGCTAGCT	
GGA-TGA	CTCTGACGACGTAACTCATAGACTTCCATGG	
	TAGCTGCT**T**GAGCTGCT	2559
	AGCAGCTC**A**AGCAGCTA	2560
Reducing linolenic acid	GCAAGTTGGGTTCTATCAGAATGTGGTCTTAGACCACTACCAAGAA	2561
omega-3 fatty acid	TATACCCAAAGCCC**T**GAATAGGGTCTTCTTCCGTTTGCGCCACCAA	
desaturase	TTTAAATCTGAGAAGAATTTCACCTTCAC	
Solanum tuberosum	GTGAAGGTGAAATTCTTCTCAGATTTAAATTGGTGGCGCAAACGGA	2562
Arg22 Term	AGAAGACCCTATTC**A**GGGCTTTGGGTATATTCTTGGTAGTGGTCTA	
AGA-TGA	AGACCACATTCTGATAGAACCCAACTTGC	
	CAAAGCCC**T**GAATAGGG	2563
	CCCTATTC**A**GGGCTTTG	2564
Reducing linolenic acid	TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGG	2565
omega-3 fatty acid	GTCTTCTTCCGTTTG**A**GCCACCAATTTAAATCTGAGAAGAATTTCA	
desaturase	CCTTCACCTATACGAACAGATCGGAATTGT	
Solanum tuberosum	ACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAATTCTTCTCAGA	2566
Cys29 Term	TTTAAATTGGTGGC**T**CAAACGGAAGAAGACCCTATTCTGGGCTTTG	
TGC-TGA	GGTATATTCTTGGTAGTGGTCTAAGACCA	
	TCCGTTTG**A**GCCACCAA	2567
	TTGGTGGC**T**CAAACGGA	2568
Reducing linolenic acid	CACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGT	2569
omega-3 fatty acid	TTGCGCCACCAATT**G**AAATCTGAGAAGAATTTCACCTTCACCTATA	
desaturase	CGAACAGATCGGAATTGTTGGGCATTGAG	
Solanum tuberosum	CTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAA	2570
Leu33 Term	TTCTTCTCAGATTT**C**AATTGGTGGCGCAAACGGAAGAAGACCCTAT	
TTA-TGA	TCTGGGTTTGGGTATATTCTTGGTAGTG	
	CACCAATT**G**AAATCTGA	2571
	TCAGATTT**C**AATTGGTG	2572
Reducing linolenic acid	AGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCA	2573
omega-3 fatty acid	CCAATTTAAATCTG**T**GAAGAATTTCACCTTCACCTATACGAACAGAT	
desaturase	CGGAATTGTTGGGCATTGAGGGTAAGTG	

TABLE 24-continued

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Solanum tuberosum	CACTTACCCTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGA	2574
Arg36 Term	AGGTGAAATTCTTC**A**CAGATTTAAATTGGTGGCGCAAACGGAAGAA	
AGA-TGA	GACCCTATTCTGGGCTTTGGGTATATTCT	
	TAAATCTG**T**GAAGAATT	2575
	AATTCTTC**A**CAGATTTA	2576
Reducing linolenic acid	CTCTTTATTATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACC	2577
omega-3 fatty acid	TATGGCAAGTTG**A**GTGATTTCAGAATGTGGGCTAAGGCCACTTCC	
desaturase	AAGAATCTATGCCAGGCCCAGAAGTGGA	
Petroselinum crispum	TCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCC	2578
Trp4 Term	ACATTCTGAAATCAC**T**CAACTTGCCATAGGTGACTCAGAACTCAAA	
TGG-TGA	AAAAACAAAGAAGAGGAGGATAATAAAGAG	
	GCAAGTTG**A**GTGATTTC	2579
	GAAATCAC**T**CAACTTGC	2580
Reducing linolenic acid	TATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCA	2581
omega-3 fatty acid	AGTTGGGTGATTT**G**AGAATGTGGGCTAAGGCCACTTCCAAGAATC	
desaturase	TATGCCAGGCCCAGAAGTGGAGCTTCATG	
Petroselinum crispum	CATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGC	2582
Ser7 Term	CTTAGCCCACATTCT**C**AAATCACCCAACTTGCCATAGGTGACTCAG	
TCA-TGA	AACTCAAAAAAAACAAAGAAGAGGAGGATA	
	GGTGATTT**G**AGAATGTG	2583
	CACATTCT**C**AAATCACC	2584
Reducing linolenic acid	TCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAG	2585
omega-3 fatty acid	TTGGGTGATTTCA**T**AATGTGGGCTAAGGCCACTTCCAAGAATCTAT	
desaturase	GCCAGGCCCAGAAGTGGAGCTTCATGTT	
Petroselinum crispum	AACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTG	2586
Glu8 Term	GCCTTAGCCCACATT**A**TGAAATCACCCAACTTGCCATAGGTGACTC	
GAA-TAA	AGAACTCAAAAAAAACAAAGAAGAGGAGGA	
	TGATTTCA**T**AATGTGGG	2587
	CCCACATT**A**TGAAATCA	2588
Reducing linolenic acid	CTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGG	2589
omega-3 fatty acid	TGATTTCAGAAT**G**AGGGCTAAGGCCACTTCCAAGAATCTATGCCA	
desaturase	GGCCCAGAAGTGGAGCTTCATGTTTCAAC	
Petroselinum crispum	GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGG	2590
Cys9 Term	AAGTGGCCTTAGCCC**T**CATTCTGAAATCACCCAACTTGCCATAGGT	
TGT-TGA	GACTCAGAACTCAAAAAAAACAAAGAAGAG	
	TCAGAATG**A**GGGCTAAG	2591
	CTTAGCCC**T**CATTCTGA	2592
Reducing linolenic acid	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTA	2593
omega-3 fatty acid	ATGGTTTTCATGCT**T**AAGAAGAAGAAGAAGAAGAGGATTTCGACTT	
desaturase	AAGCAATCCTCCTCCATTCAATATTGGTC	
Vernicia fordii	GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTC	2594
Lys21 Term	TTCTTCTTCTTCTT**A**AGCATGAAAACCATTAACGCCATTTAGAATTG	
AAA-TAA	GGGTGTCTTTGTACTGTTGCTGCTTCAT	
	TTCATGCT**T**AAGAAGAA	2595
	TTCTTCTT**A**AGCATGAA	2596
Reducing linolenic acid	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATG	2597
omega-3 fatty acid	GTTTTCATGCTAAA**T**AAGAAGAAGAAGAAGAGGATTTCGACTTAAG	
desaturase	CAATCCTCCTCCATTCAATATTGGTCAGA	
Vernicia fordii	TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC	2598
Glu22 Term	TTCTTCTTCTTCTT**A**TTTAGCATGAAAACCATTAACGCCATTTAGAA	
GAA-TAA	TTGGGGTGTCTTTGTACTGTTGCTGCTT	
	ATGCTAAA**T**AAGAAGAA	2599
	TTCTTCTT**A**TTTAGCAT	2600
Reducing linolenic acid	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT	2601
omega-3 fatty acid	TTCATGCTAAAGAA**T**AAGAAGAAGAAGAGGATTTCGACTTAAGCAA	
desaturase	TCCTCCTCCATTCAATATTGGTCAGATCC	
Vernicia fordii	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC	2602
Glu23 Term	CTCTTCTTCTTCTT**A**TTCTTTAGCATGAAAACCATTAACGCCATTTA	
GAA-TAA	GAATTGGGGTGTCTTTGTACTGTTGCTG	
	CTAAAGAA**T**AAGAAGAA	2603
	TTCTTCTT**A**TTCTTTAG	2604

TABLE 24-continued

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reducing linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu24 Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT	2605
	TTCATGCTAAAGAA**T**AAGAAGAAGAAGGATTTCGACTTAAGCAA	
	TCCTCCTCCATTCAATATTGGTCAGATCC	
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC	2606
	CTCTTCTTCTTCTT**A**TTCTTTAGCATGAAAACCATTAACGCCATTTA	
	GAATTGGGGTGTCTTTGTACTGTTGCTG	
	CTAAAGAA**T**AAGAAGAA	2607
	TTCTTCTT**A**TTCTTTAG	2608
Reducing linolenic acid omega-3 fatty acid desaturase *Glycine max* Tyr21 Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA	2609
	AGAAGATCAAGCTTA**G**TTTGATCCAAGTGCTCCACCACCCTTCAAG	
	ATTGCAAATATCAGAGCAGCAATTCCAAAA	
	TTTTGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGA	2610
	GCACTTGGATCAAA**C**TAAGCTTGATCTTCTTTCCCTGCACCATTAC	
	CAACATGTTGTAGAGGCTGTGCTTGGACC	
	CAAGCTTA**G**TTTGATCC	2611
	GGATCAAA**C**TAAGCCTG	2612
Reducing linolenic acid omega-3 fatty acid desaturase *Glycine max* Lys31 Term AAG-TAG	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTTTGATCCAAGT	2613
	GCTCCACCACCCTTC**T**AGATTGCAAATATCAGAGCAGCAATTCCAA	
	AACATTGCTGGGAGAAGAACACATTGAGAT	
	ATCTCAATGTGTTCTTCTCCCAGCAATGTTTTGGAATTGCTGCTCT	2614
	GATATTTGCAATCT**A**GAAGGGTGGTGGAGCACTTGGATCAAAATAA	
	GCTTGATCTTCTTTCCCTGCACCATTACC	
	CACCCTTC**T**AGATTGCA	2615
	TGCAATCT**A**GAAGGGTG	2616
Reducing linolenic acid omega-3 fatty acid desaturase *Glycine max* Arg36 Term AGA-TGA	AAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTCA	2617
	AGATTGCAAATATC**T**GAGCAGCAATTCCAAAACATTGCTGGGAGAA	
	GAACACATTGAGATCTCTGAGTTATGTTC	
	GAACATAACTCAGAGATCTCAATGTGTTCTTCTCCCAGCAATGTTTT	2618
	GGAATTGCTGCTC**A**GATATTTGCAATCTTGAAGGGTGGTGGAGCA	
	CTTGGATCAAAATAAGCTTGATCTTCTTT	
	CAAATATC**T**GAGCAGCA	2619
	TGCTGCTC**A**GATATTTG	2620
Reducing linolenic acid omega-3 fatty acid desaturase *Glycine max* Leu41 Term AAA-TAA	TATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCA	2621
	GAGCAGCAATTCCA**T**AACATTGCTGGGAGAAGAACACATTGAGAT	
	CTCTGAGTTATGTTCTGAGGGATGTGTTGG	
	CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT	2622
	CTCCCAGCAATGTT**A**TGGAATTGCTGCTCTGATATTTGCAATCTTG	
	AAGGGTGGTGGAGCACTTGGATCAAAATA	
	CAATTCCA**T**AACATTGC	2623
	GCAATGTT**A**TGGAATTG	2624
Reducing linolenic acid omega-3 fatty acid desaturase *Zea mays* Glu8 Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGC	2625
	CCGGCTCGTGCTCTCC**T**AGTGCTCGGGCCTCGCGCCCGTCCGCC	
	GCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGC	
	GCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGG	2626
	GCGCGAGGCCCGAGCACT**A**GGAGAGCACGAGCCGGGCCATTGC	
	CGCCGTCAGCGGGGCGGGTGCGGGTGCGGGTGGATG	
	TGCTCTCC**T**AGTGCTCG	2627
	CGAGCACT**A**GGAGAGCA	2628
Reducing linolenic acid omega-3 fatty acid desaturase *Zea mays* Cys9 Term TGC-TGA	ACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGG	2629
	CTCGTGCTCTCCGAGTG**A**TCGGGCCTCGCGCCCGTCCGCCGCCT	
	GCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA	
	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGG	2630
	ACGGGCGCGAGGCCCG**A**TCACTCGGAGAGCACGAGCCGGGCCA	
	TTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGT	
	TCCGAGTG**A**TCGGGCCT	2631
	AGGCCCG**A**TCACTCGGA	2632
Reducing linolenic acid omega-3 fatty acid desaturase *Zea mays* Ser10 Term	CCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCT	2633
	CGTGCTCTCCGAGTGCT**A**GGGCCTCGCGCCCGTCCGCCGCCTGC	
	GCGCCGGCCGGGGCGCCATTGCGGCGCGGTCACC	
	GGTGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGC	2634
	GGACGGGCGCGAGGCCC**T**AGCACTCGGAGAGCACGAGCCGGGC	

TABLE 24-continued

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
TCG-TAG	CATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGG	
	CGAGTGCT**A**GGGCCTCG	2635
	CGAGGCCC**T**AGCACTCG	2636
Reducing linolenic acid	GCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGG	2637
omega-3 fatty acid	CGCCATTGCGGCGCGGT**G**ACCCCCCGCGCTCTCCGCGGCGCCG	
desaturase	CGCCGTCGTCCCGCGTCCGCGTCCATCCACCGCGA	
Zea mays	TCGCGGTGGATGGACGCGGACGCGGGACGACGGCGCGGCGCCG	2638
Ser29 Term	CGGAGAGCGCGGGGGGT**C**ACCGCGCCGCAATGGCGCCCCGGCC	
TCA-TGA	GGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGC	
	GGCGCGGT**G**ACCCCCCG	2639
	CGGGGGGT**C**ACCGCGCC	2640
Reducing linolenic acid	CCCCCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGC	2641
omega-3 fatty acid	CCCCGCAATGAGGCCG**T**AGCAGGAGGCGAGCTGCAAGGCCACCG	
desaturase	AGGACCACCGCTCCGAGTTCGACGCCGCCAAGC	
Triticum aestivum	GCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTG	2642
Glu8 Term	CAGCTCGCCTCCTGCT**A**CGGCCTCATTGCGGGGGCCATGGCCGC	
GAG-TAG	GGATGGATCTGTGCGTGTGCGTGGGGGAGGGGG	
	TGAGGCCG**T**AGCAGGAG	2643
	CTCCTGCT**A**CGGCCTCA	2644
Reducing linolenic acid	CCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCC	2645
omega-3 fatty acid	CGCAATGAGGCCGGAG**T**AGGAGGCGAGCTGCAAGGCCACCGAG	
desaturase	GACCACCGCTCCGAGTTCGACGCCGCCAAGCCGC	
Triticum aestivum	GCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCC	2646
Gln9 Term	TTGCAGCTCGCCTCCT**A**CTCCGGCCTCATTGCGGGGGCCATGGC	
CAG-TAG	CGCGGATGGATCTGTGCGTGTGCGTGGGGGAGG	
	GGCCGGAG**T**AGGAGGCG	2647
	CGCCTCCT**A**CTCCGGCC	2648
Reducing linolenic acid	CCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGC	2649
omega-3 fatty acid	AATGAGGCCGGAGCAG**T**AGGCGAGCTGCAAGGCCACCGAGGACC	
desaturase	ACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGC	
Triticum aestivum	GCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGT	2650
Glu10 Term	GGCCTTGCAGCTCGCCT**A**CTGCTCCGGCCTCATTGCGGGGGCCA	
GAG-TAG	TGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGG	
	CGGAGCAG**T**AGGCGAGC	2651
	GCTCGCCT**A**CTGCTCCG	2652
Reducing linolenic acid	ACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGG	2653
omega-3 fatty acid	AGCAGGAGGCGAGCTG**A**AAGGCCACCGAGGACCACCGCTCCGA	
desaturase	GTTCGACGCCGCCAAGCCGCCGCCCTTCCGCATC	
Triticum aestivum	GATGCGGAAGGGCGGCGGCTTGGCGGCGTCGAACTCGGAGCGG	2654
Cys13 TermTGGTCCTCGGTG-GCCTTTCAGCTCGCCTCCT-GCTCCGGCCTCATT		
TGC-TGA	GCGGGGGCCATGGCCGCGGATGGATCTGTGCGT	
	GCGAGCTG**A**AAGGCCAC	2655
	GTGGCCTT**T**CAGCTCGC	2656
Reducing linolenic acid	CTTCACAAATCACAAATCGGAATCAGATCCACCACGACACCCCGG	2657
omega-3 fatty acid	CGGCAATGGCGGCGT**A**GGCGACCCAGGAGGCCGACTGCAAGGC	
desaturase	TTCCGAGGACGCCCGTCTCTTCTTCGACGCCGC	
Oryza sativa	GCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGCCTTGCAGTC	2658
Ser4 Term	GGCCTCCTGGGTCGCC**T**ACGCCGCCATTGCCGCCGGGGTGTCGT	
TCG-TAG	GGTGGATCTGATTCCGATTTGTGATTTGTGAAG	
	GGCGGCGT**A**GGCGACCC	2659
	GGGTCGCC**T**ACGCCGCC	2660
Reducing linolenic acid	ATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATG	2661
omega-3 fatty acid	GCGGCGTCGGCGACC**T**AGGAGGCCGACTGCAAGGCTTCCGAGGA	
desaturase	CGCCCGTCTCTTCTTCGACGCCGCCAAGCCCC	
Oryza sativa	GGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC	2662
Gln7 Term	CTTGCAGTCGGCCTCCT**A**GGTCGCCGACGCCGCCATTGCCGCCG	
CAG-TAG	GGGTGTCGTGGTGGATCTGATTCCGATTTGTGAT	
	CGGCGACC**T**AGGAGGCC	2663
	GGCCTCCT**A**GGTCGCCG	2664

TABLE 24-continued

Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reducing linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Glu8 Term GAG-TAG	ACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGC	2665
	GGCGTCGGCGACCCAG**T**AGGCCGACTGCAAGGCTTCCGAGGACG	
	CCCGTCTCTTCTTCGACGCCGCCAAGCCCCCGC	
	GCGGGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGA	2666
	AGCCTTGCAGTCGGCC**T**ACTGGGTCGCCGACGCCGCCATTGCCG	
	CCGGGGTGTCGTGGTGGATCTGATTCCGATTTGT	
	CGACCCAG**T**AGGCCGAC	2667
	GTCGGCC**T**ACTGGGTCG	2668
Reducing linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Cys10 Term TGC-TGA	TCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTCGGCGA	2669
	CCCAGGAGGCCGACTG**A**AAGGCTTCCGAGGACGCCCGTCTCTTC	
	TTCGACGCCGCCAAGCCCCCGCCCTTCCGCATC	
	GATGCGGAAGGGCGGGGGCTTGGCGGCGTCGAAGAAGAGACGG	2670
	GCGTCCTCGGAAGCCTTT**T**CAGTCGGCCTCCTGGGTCGCCGACGC	
	CGCCATTGCCGCCGGGGTGTCGTGGTGGATCTGA	
	GCCGACTG**A**AAGGCTTC	2671

What is claimed is:

1. An oligonucleotide for targeted alteration of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications of the oligonucleotide, said chemical modifications selected from the group consisting of an o-methyl modification, an LNA modification including LNA derivatives and analogs, two or more phosphorothioate linkages on a terminus, and a combination of any two or more of these modifications.

2. The oligonucleotide according to claim one that comprises two or more phosphorothioate linkages on at least the 3' terminus.

3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.

4. The oligonucleotide according to claim one that comprises an LNA nucleotide, including an LNA derivative or analog.

5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.

6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.

7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 1-2672.

8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in callus, comprising administering to the callus an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, **9** or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A plant organism comprising the cell according to claim 14.

16. A plant or plant part produced by the method of claim 11.

17. A method of determining whether an oligonucleotide is optimized for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a second oligonucleotide, said second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2'-O-methylated oligonucleotide and a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

18. The method of claim 17 in which the alteration is produced in a plant cell extract.

19. The method of claim 17 in which the alteration is produced in a cell.

20. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of an oligonucleotide that lacks the mismatch, a fully modified phosphorothiolated oligonucleotide, a fully modified 2-O-methylated oligonucleotide and a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

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