

TARGETED CHROMOSOMAL GENOMIC ALTERATIONS IN PLANTS USING MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

Field Of The Invention

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

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, United States Patent 4,459,355 which describes a method for transforming plants with a DNA vector and United States Patent 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.

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.

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. Patent 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.

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. Patent 5,422,251. The utility of these oligonucleotides for directing targeted gene alteration is compromised by a high frequency of nonspecific base changes.

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.

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.

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.

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.

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.

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.

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)).

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

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.

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., nucleotides 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 United States application no. 60/208,538, United States application no. 60/244,989, United States application 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.

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

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), T**G**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

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 oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligonucleotides 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.

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 US Patent 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 *Chlamydomonas 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.

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.

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.

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.

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 oligonucleotide 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.

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 oligonucleotide 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.

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 US Patent 5,565,350.

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.

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 oligonucleotides 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.

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. Patent 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.

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.

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, IA 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.

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, WI 53715, Phone: (608) 258-7420 (http://www.dnastar.com/products/PrimerSelect.html).

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

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 oligonucleotide 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.

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.

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.

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. Patent 6,046,380 and U.S. Patent 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.

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.

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.

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

Figure 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). Figure 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). Figure 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 Figure 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.

Figure 2. *Genetic readout system for correction of a point mutation in plasmid* pK^{s}m4021. A mutant kanamycin gene harbored in plasmid pK^{s}m4021 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.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid pT^{s}Δ208 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.

Figure 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.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(-)FIAsH plasmid (shown in Figure 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.

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

Figure 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 Figure 7A, the sequence of the normal allele corresponds to SEQ ID NO: 2691, the sequence of the target/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 Figure 7B, the sequence of the normal allele correspond to SEQ ID NO: 2691, the sequence of the target/existing mutation corresponds to SEQ ID NO: 2694 and the sequence of the desired alteration corresponds to SEQ ID NO: 2693.

Figure 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 Figure 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.

Figure 9. *pAURNeo(-)FlAsH plasmid.* This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence. In Figure 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 FlAsH peptide sequence corresponds to SEQ ID NO: 2700.

Figure 10. pYESHyg(x)eGFP plasmid. This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 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.

Figure 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.

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

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 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 $pK^{s}m4021$ (Figure 2) or the tetracycline gene of $pT^{s}\Delta 208$ (Figure 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 Figures 1C and Figure 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(-)FlAsH (Figure 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 FlAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FlAsH fusion product (after alteration) or the truncated Neo-/FlAsH 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.

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 Figures 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.

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 T137➞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 300bp 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.

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, 2mM 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 (*rec*A).

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 $2x10^8$ 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 12000x*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.

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 5000xg, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM 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 3000x*g* for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000x*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.

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 Figure 1), and 1 µg of plasmid DNA (see Figures 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_20, 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 x 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.

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 µ1 of SOC. 100 µl aliquots are plated onto kan or tet agar plates and 100 µl of a 10^{-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).

Chimeric single-stranded oligonucleotides. In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 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.

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 Figure 1B, 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.

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 Figure 2A, 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.

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 Figure 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 Figure 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.

In Figure 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 phosphorothioate 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).

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(-)FlAsH 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 (FlAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FlAsH-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).

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 $pkan^s m4021$ (see Figure 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 (Figure 3) in the tet gene contained in plasmid pTetΔ208. Table 4 illustrates data from repair of the $pkan^s m4021$ 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.

Figure 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). Figure 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".

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.

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^{s}m4021 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.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 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 Figure 1A). Chimera II (Figure 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.

Frame shift mutations are repaired. By using plasmid pT^{s}Δ208, described in Figure 1(C) and Figure 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. Figure 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. Figure 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.

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.

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. Oligo2 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).

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'-CATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTA GCCGAATAGCCTCTCCACCCAAGCGGCCGGAGA-3' (SEQ ID NO: 2712); and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-GCTGACAGCCGGAACACGG CGGCATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTAGCCGAATAGCCT-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.

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 Tsp509I 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:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

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).

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 x *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.

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.

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^Sm4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
-		20	0	
I		-	0	

Plasmid pK^Sm4021 (1μg), 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 20μg 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

Chimeric oligonucleotide (1.5 μg) or modified single-stranded oligonucleotide (0.55 μg) was incubated with 1μg of plasmid $pK^{s}m4021$ and 20μg 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)	$pT^4\Delta208$ (1μg)	-	0
-		20μg	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

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 $pT^4\Delta208$. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

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

Oligonucleotide	Plasmid	Extract	kan^r colonies
II (chimera)	pK^Sm4021	30µg 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

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 (0.55µg) were used to correct pK^Sm4021. 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°m4021	1µg		0.36
Wild type			1µg	0.81
ΔRAD52		1µg		10.72
ΔRAD52			1µg	17.41
ΔPMS1		1µg		2.02
ΔPMS1			1µg	3.23

In this experiment, the kan° gene in pKan°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

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 (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 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.

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, CA). 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.

We use this system to assay the ability of five oligonucleotides (shown in Figure 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 2-0-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.

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 *MATα* 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.

Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in Figure 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.

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'-CTCGTGCTTTCAGCT TCGATGTAGGAGGGCGTGG**G**TA**C**GTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTAC-3' (SEQ ID NO: 2714); a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTAAA**C**AGCTGCGCCGATG GTTTCTAC-3' (SEQ ID NO: 2715); and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTA AATAGCTGCGCCGA**C**GGTTTCTAC (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.

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 Figure 10.

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.

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	—	—

Table 7

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

Amount of Oligonucleotide (µg)	Colonies per hygromycin plate	
	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.

Table 8

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

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

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

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, CA). 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, CA). 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 Dulbecco'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, NJ). After microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

35 mm dishes are coated overnight at 4° C with 50 µg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) 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.

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.

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.

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 macro-projectile 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.

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.

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 x 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

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

. 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.

For introduction of a T-DNA, including the T-DNA in the plasmid of Figure 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 and 2.5 kV.

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.

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.

Notes on the tables presented below:

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.

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

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.

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.

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.

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.

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

Example 5

Engineering herbicide resistant plants

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.

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.

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-amino-phenyl)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.

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 EPSPS *Arabidopsis thaliana* Gly97Ala GGC-GCC	AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTTCCTGCCTCCAAGTCTCTATCAAATCGGATCCTGC TTCTCGCTGCTCTGTCTGAGGTATATATCAC	1
	GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT TGATAGAGACTTGGAGGCAGGAAGCTTAATAAGACCGGAGATTT CTCTAATGGGTTGAAGTACAATCTCCGACGCTT	2
	GCTTCCTGCCTCCAAGT	3
	ACTTGGAGGCAGGAAGC	4
Glyphosate Resistance EPSPS *Brassica napus* Gly93Ala GGA-GCA	AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTC TCATTAAGCTACCCGCATCCAAATCTCTCTCCAATCGGATCCTCC TTCTTGCCGCTCTATCTGAGGTACATATACT	5
	AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT GGAGAGAGATTTGGATGCGGGTAGCTTAATGAGACCCGAGATTT CTCTGATTGGTTGAAGCACAATCTCTGAAGCTT	6
	GCTACCCGCATCCAAAT	7
	ATTTGGATGCGGGTAGC	8
Glyphosate Resistance EPSPS 1 *Nicotiana tabacum* Gly95Ala GGT-GCT	AGCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC ACTGTTAAATTGCCTGCTTCTAAATCCCTTTCCAATCGTATTCTCC TTCTTGCTGCCCTTTCTAAGGGAAGGACTGT	9
	ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTAGAAGCAGGCAATTTAACAGTGCCTGATATATC TTTGATGGGTTGCAGCACAATCTCGTTGGGCT	10
	ATTGCCTGCTTCTAAAT	11
	ATTTAGAAGCAGGCAAT	12
Glyphosate Resistance EPSPS 2 *Nicotiana tabacum* Gly62Ala GGA-GCA	ATTGTTTCCTTGGTACGAAATGTCCTCCTGTTCGAATTGTCAGCA AGGGAGGCCTTCCCGCAGGGAAGGTAAAGCTCTCTGGATCAATT AGCAGCCAGTACTTGACTGCTCTGCTTATGGC	13
	GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGA GAGCTTTACCTTCCCTGCGGGAAGGCCTCCCTTGCTGACAATTC GAACAGGAGGACATTTCGTACCAAGGAAACAAT	14
	CCTTCCCGCAGGGAAGG	15
	CCTTCCCTGCGGGAAGG	16
Glyphosate Resistance EPSPS *Zea mays* Gly168Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTCGTGTCAATGGAA TCGGAGGGCTACCTGCTGGCAAGGTCAAGCTGTCTGGCTCCATC AGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	17
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA CAGCTTGACCTTGCCAGCAGGTAGCCCTCCGATTCCATTGACAC GAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	18

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTACCTGCTGGCAAGG	19
	CCTTGCCAGCAGGTAGC	20
Glyphosate Resistance EPSPS *Oryza sativa* Gly115Ala GGT-GCT	ACTGTTTCCTTGGCACTGAATGCCCACCTGTTCGTGTCAAGGGA ATTGGAGGACTTCCTGCTGGCAAGGTTAAGCTCTCTGGTTCCAT CAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC	21
	GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGA GAGCTTAACCTTGCCAGCAGGAAGTCCTCCAATTCCCTTGACAC GAACAGGTGGGCATTCAGTGCCAAGGAAACAGT	22
	ACTTCCTGCTGGCAAGG	23
	CCTTGCCAGCAGGAAGT	24
Glyphosate Resistance EPSPS *Petunia x hybrida* Gly93Ala GGC-GCC	AGCCTTCTGAGATAGTGTTGCAACCCATTAAAGAGATTTCAGGCA CTGTTAAATTGCCTGCCTCTAAATCATTATCTAATAGAATTCTCCT TCTTGCTGCCTTATCTGAAGGAACAACTGT	25
	ACAGTTGTTCCTTCAGATAAGGCAGCAAGAAGGAGAATTCTATTA GATAATGATTTAGAGGCAGGCAATTTAACAGTGCCTGAAATCTCT TTAATGGGTTGCAACACTATCTCAGAAGGCT	26
	ATTGCCTGCCTCTAAAT	27
	ATTTAGAGGCAGGCAAT	28
Glyphosate Resistance EPSPS *Lycopersicon esculentum* Gly97Ala GGT-GCT	AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTA CTGTTAAATTACCCGCTTCGAAATCCCTTTCCAATCGTATTCTCCT TCTTGCTGCCCTTTCTGAGGGAAGGACTGT	29
	ACAGTCCTTCCCTCAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTCGAAGCGGGTAATTTAACAGTACCAGATATATC TTTGATGGGTNCTAGCACAATCTCATGGGGTT	30
	ATTACCCGCTTCGAAAT	31
	ATTTCGAAGCGGGTAAT	32
Glyphosate Resistance EPSPS *Lolium rigidum* Gly107Ala GGT-GCT	ATTGTTTCCTTGGCACTGACTGCCCACCTGTTCGKATCAACGGCA TTGGAGGGCTACCTGCTGGCAAGGTTAAGCTGTCTGGTTCCATC AGCAGCCAATACTTGAGTTCCTTGCTGATGGC	33
	GCCATCAGCAAGGAACTCAAGTATTGGCTGCTGATGGAACCAGA CAGCTTAACCTTGCCAGCAGGTAGCCCTCCAATGCCGTTGATCG AACAGGTGGGCAGTCAGTGCCAAGGAAACAAT	34
	GCTACCTGCTGGCAAGG	35
	CCTTGCCAGCAGGTAGC	36

Table 11

Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Ser CCT-TCT	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA ATCACAGGACAAGTCTCTCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	37
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGAGAGACTTGTCCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	38
	GACAAGTCTCTCGTCGT	39
	ACGACGAGAGACTTGTC	40
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Gln CCT-CAG	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA ATCACAGGACAAGTCCAGCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	41
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGCTGGACTTGTCCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	42
	ACAAGTCCAGCGTCGTC	43
	TACGACGCTGGACTTGT	44
Sulfonylurea Resistance ALS *Arabidopsis thaliana* Pro197Gln CCT-CAA	AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCCTCTTGTAGCA ATCACAGGACAAGTCCAACGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT	45
	AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGTTGGACTTGTCCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT	46
	ACAAGTCCAACGTCGTA	47
	TACGACGTTGGACTTGT	48
Imidazolinone Resistance ALS *Arabidopsis thaliana* Ser653Asn AGT-AAC	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAACGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	49
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACCGTTCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	50
	GATCCCGAACGGTGGCA	51
	TGCCACCGTTCGGGATC	52

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS *Arabidopsis thaliana* Ser653Asn AGT-AAT	GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAATGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT	53
	ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACCATTCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC	54
	GATCCCGAATGGTGGCA	55
	TGCCACCATTCGGGATC	56
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCTCCCGCCGCATGATCGGCACCGACGCCT TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	57
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGGAGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	58
	GCCAGGTCTCCCGCCGC	59
	GCGGCGGGAGACCTGGC	60
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGCCAGGTCCAACGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	61
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	62
	CCAGGTCCAACGCCGCA	63
	TGCGGCGTTGGACCTGG	64
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGCCAGGTCCAGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	65
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGCTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	66
	CCAGGTCCAGCGCCGCA	67
	TGCGGCGCTGGACCTGG	68
Imidazolinone Resistance ALS *Oryza sativa* Ile627Asn ATT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAAATGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	69
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCATTTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	70
	GATCCCAAATGGGGGCG	71

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCCCCATTTGGGATC	72
Sulfonylurea Resistance ALS *Zea mays* Pro165Ser CCG-TCG	TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	73
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGT GCCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA	74
	GACAGGTGTCGCGACGC	75
	GCGTCGCGACACCTGTC	76
Sulfonylurea Resistance ALS *Zea mays* Pro165Gln CCG-CAG	CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGCAGCGACGCATGATTGGCACCGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	77
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGG TGCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATG GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGG	78
	ACAGGTGCAGCGACGCA	79
	TGCGTCGCTGCACCTGT	80
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAATGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	81
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACCATTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	82
	GATCCCTAATGGTGGGG	83
	CCCCACCATTAGGGATC	84
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAC	GGCCGTACCTCTTGGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTAACGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA	85
	TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACCGTTAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC	86
	GATCCCTAACGGTGGGG	87
	CCCCACCGTTAGGGATC	88
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Ser CCG-TCG	TCCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTCTCGCGCCGCATGATCGGCACGGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT	89
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGTG CCGATCATGCGGCGCGAGACCTGCCCCGTGATGGCCACCATGG GGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA	90

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGCAGGTCTCGCGCCGC	91
	GCGGCGCGAGACCTGCC	92
Sulfonylurea Resistance ALS *Lolium multiflorum* Pro167Gln CCG-CAG	CCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCC ATCACGGGGCAGGTCCAGCGCCGCATGATCGGCACGGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	93
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGT GCCGATCATGCGGCGCTGGACCTGCCCCGTGATGGCCACCATGG GGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGG	94
	GCAGGTCCAGCGCCGCA	95
	TGCGGCGCTGGACCTGC	96
Imidazolinone Resistance ALS *Lolium multiflorum* Ser623Asn AGC-AAC	CTGGGCCATACTTGTTGGATATCATCGTCCCTCACCAGGAGCATG TGCTGCCTATGATCCCTAACGGTGGTGCTTTCAAGGACATTATCA TGGAAGGTGATGGCAGGATTTCGTATTAAAC	97
	GTTTAATACGAAATCCTGCCATCACCTTCCATGATAATGTCCTTGA AAGCACCACCGTTAGGGATCATAGGCAGCACATGCTCCTGGTGA GGGACGATGATATCCAACAAGTATGGCCCAG	98
	GATCCCTAACGGTGGTG	99
	CACCACCGTTAGGGATC	100
Sulfonylurea Resistance ALS *Hordeum vulgare* Pro68Ser CCA-TCA	TCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGC CATCACGGGCCAGGTCTCACGCCGCATGATCGGCACGGACGCGT TCCAGGAGACGCCCATAGTGGAGGTCACGCGCT	101
	AGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTG CCGATCATGCGGCGTGAGACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGGA	102
	GCCAGGTCTCACGCCGC	103
	GCGGCGTGAGACCTGGC	104
Sulfonylurea Resistance ALS *Hordeum vulgare* Pro68Gln CCA-CAA	CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCC ATCACGGGCCAGGTCCAACGCCGCATGATCGGCACGGACGCGTT CCAGGAGACGCCCATAGTGGAGGTCACGCGCTC	105
	GAGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGG	106
	CCAGGTCCAACGCCGCA	107
	TGCGGCGTTGGACCTGG	108

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Imidazolinone Resistance ALS *Hordeum vulgare* Ser524Asn AGC-AAC	CCCAGGGCCGTACCTGCTGGATATCATTGTCCCGCATCAGGAGC ACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTCAAGGACATGA TCATGGAGGGTGATGGCAGGACCTCGTACTGA	109
	TCAGTACGAGGTCCTGCCATCACCCTCCATGATCATGTCCTTGAA AGCACCACCGTTTGGGATCATAGGCAGCACGTGCTCCTGATGCG GGACAATGATATCCAGCAGGTACGGCCCTGGG	110
	GATCCCAAACGGTGGTG	111
	CACCACCGTTTGGGATC	112
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTC CAGGAAACTCCAATTGTTGAGGTAACAAGGT	113
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	114
	GTCAAGTCTCTCGTCGG	115
	CCGACGAGAGACTTGAC	116
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAACGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	117
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGTTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	118
	TCAAGTCCAACGTCGGA	119
	TCCGACGTTGGACTTGA	120
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAGCGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	121
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGCTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	122
	TCAAGTCCAGCGTCGGA	123
	TCCGACGCTGGACTTGA	124
Imidazolinone Resistance ALS *Gossypium hirsutum* Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCT GCCTATGATCCCCAATGGAGGCGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	125
	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTT TGAAAGCGCCTCCATTGGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	126
	GATCCCCAATGGAGGCG	127

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCCTCCATTGGGGATC	128
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTTTCCCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACTCGAT	129
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGGAAACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	130
	GGCAAGTTTCCCGGCGT	131
	ACGCCGGGAAACTTGCC	132
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCAACGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACTCGATC	133
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCGTTGAACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	134
	GCAAGTTCAACGGCGTA	135
	TACGCCGTTGAACTTGC	136
Sulfonylurea Resistance ALS *Amaranthus retroflexus* Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCAGCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACTCGATC	137
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCGCTGAACTTGCCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	138
	GCAAGTTCAGCGGCGTA	139
	TACGCCGCTGAACTTGC	140
Imidazolinone Resistance ALS *Amaranthus retroflexus* Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTAACGGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	141
	ACCAACTAATAAGCCCTTCTTCCATCACCCTCTGTTATGGTGTCCT TGAAGGCGGCACCGTTAGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC	142
	GATCCCTAACGGTGCCG	143
	CGGCACCGTTAGGGATC	144

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 *Nicotiana tabacum* Pro194Ser CCA-TCA	AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGTGTCACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAACTAGAT	145
	ATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTACC TATCATCCTACGTGACACTTGACCTGTTATAGCAACAATGGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT	146
	GTCAAGTGTCACGTAGG	147
	CCTACGTGACACTTGAC	148
Sulfonylurea Resistance ALS 1 *Nicotiana tabacum* Pro194Gln CCA-CAA	GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGTGCAACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAACTAGATC	149
	GATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTAC CTATCATCCTACGTTGCACTTGACCTGTTATAGCAACAATGGGGA CGCTATCCAGTAGCGCGTCAGCGAGGCCGC	150
	TCAAGTGCAACGTAGGA	151
	TCCTACGTTGCACTTGA	152
Imidazolinone Resistance ALS 1 *Nicotiana tabacum* Ser650Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTTT ACCTATGATTCCCAATGGCGGAGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCCTATTGAGTTTG	153
	CAAACTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCTCCGCCATTGGGAATCATAGGTAAAACATGTTCCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	154
	GATTCCCAATGGCGGAG	155
	CTCCGCCATTGGGAATC	156
Sulfonylurea Resistance ALS 2 *Nicotiana tabacum* Pro191Ser CCA-TCA	AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACCGGTCAAGTGTCACGTAGGATGATCGGTACTGATGCTTT TCAGGAAACTCCGATTGTTGAGGTAACTAGAT	157
	ATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTACC GATCATCCTACGTGACACTTGACCGGTTATAGCAACAATGGGGAC GCTATCCAGTAGGGCGTCCGCGAGGCCACT	158
	GTCAAGTGTCACGTAGG	159
	CCTACGTGACACTTGAC	160
Sulfonylurea Resistance ALS 2 *Nicotiana tabacum* Pro191Gln CCA-CAA	GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACCGGTCAAGTGCAACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAACTAGATC	161
	GATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTAC CGATCATCCTACGTTGCACTTGACCGGTTATAGCAACAATGGGGA CGCTATCCAGTAGGGCGTCCGCGAGGCCAC	162
	TCAAGTGCAACGTAGGA	163

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTACGTTGCACTTGA	164
Imidazolinone Resistance ALS 2 *Nicotiana tabacum* Ser647Asn AGT-AAT	GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTCT ACCTATGATTCCCAATGGCGGGGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCCTATTGACTTTG	165
	CAAAGTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCCCCGCCATTGGGAATCATAGGTAGAACATGTTCCTGAT GAGGTACAATCACATCCAACAAGTATGGCC	166
	GATTCCCAATGGCGGGG	167
	CCCCGCCATTGGGAATC	168
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Ser CCC-TCC	AGTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTA TTACTGGTCAAGTTTCCAGGAGAATGATTGGAACAGATGCGTTTC AAGAAACCCCTATTGTTGAGGTAACACGTT	169
	AACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC AATCATTCTCCTGGAAACTTGACCAGTAATAGCAACCATTGGAACA CTGTCTAATAAAGCATCAGCAAGACCACT	170
	GTCAAGTTTCCAGGAGA	171
	TCTCCTGGAAACTTGAC	172
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Gln CCC-CAA	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTTCAAAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTC	173
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTC CAATCATTCTCCTTTGAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	174
	TCAAGTTCAAAGGAGAA	175
	TTCTCCTTTGAACTTGA	176
Sulfonylurea Resistance ALS *Xanthium* spp. Pro175Gln CCC-CAG	GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTTCAGAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTC	177
	GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTC CAATCATTCTCCTCTGAACTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC	178
	TCAAGTTCAGAGGAGAA	179
	TTCTCCTCTGAACTTGA	180
Imidazolinone Resistance ALS *Xanthium* spp. Ala631Asn GCT-AAT	GGGCCTTACTTGTTGGATGTGATCGTGCCCCATCAAGAACATGTG TTGCCCATGATCCCGAATGGTGGAGGTTTCATGGATGTGATCACC GAAGGCGACGGCAGAATGAAATATTGAGCTT	181
	AAGCTCAATATTTCATTCTGCCGTCGCCTTCGGTGATCACATCCAT GAAACCTCCACCATTCGGGATCATGGGCAACACATGTTCTTGATG GGGCACGATCACATCCAACAAGTAAGGCCC	182

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATCCCGAATGGTGGA	183
	TCCACCATTCGGGATCA	184
Sulfonylurea Resistance ALS *Bassia scoparia* Pro189Ser CCG-TCG	TCCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCG ATCACGGGGCAGGTGTCGCGGCGAATGATTGGGACGGATGCTTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT	185
	ACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CAATCATTCGCCGCGACACCTGCCCCGTGATCGCCACCAGTGGA ACGGAATCGAGCAAAGCATCAGCAAACCCGGA	186
	GGCAGGTGTCGCGGCGA	187
	TCGCCGCGACACCTGCC	188
Sulfonylurea Resistance ALS *Bassia scoparia* Pro189Gln CCG-CAG	CCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCGA TCACGGGGCAGGTGCAGCGGCGAATGATTGGGACGGATGCTTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC	189
	GACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTC CCAATCATTCGCCGCTGCACCTGCCCCGTGATCGCCACCAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG	190
	GCAGGTGCAGCGGCGAA	191
	TTCGCCGCTGCACCTGC	192
Imidazolinone Resistance ALS *Bassia scoparia* Ser649Asn AGT-AAT	GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC TGCCTATGATTCCTAATGGTGCAGCCTTCAAGGATATCATTAACGA AGGTGATGGAAGAACAAGTTATTGATGTTC	193
	GAACATCAATAACTTGTTCTTCCATCACCTTCGTTAATGATATCCTT GAAGGCTGCACCATTAGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC	194
	GATTCCTAATGGTGCAG	195
	CTGCACCATTAGGAATC	196
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Ser CCT-TCT	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCC ATTACAGGACAGGTCTCTCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGT	197
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC CGATCATCCGGCGAGAGACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	198
	GACAGGTCTCTCGCCGG	199
	CCGGCGAGAGACCTGTC	200

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Gln CCT-CAA	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCA TTACAGGACAGGTCCAACGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGTC	201
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCGTTGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	202
	ACAGGTCCAACGCCGGA	203
	TCCGGCGTTGGACCTGT	204
Sulfonylurea Resistance ALS 1 *Brassica napus* Pro182Gln CCT-CAG	GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCCA TTACAGGACAGGTCCAGCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGTC	205
	GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCGCTGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC	206
	ACAGGTCCAGCGCCGGA	207
	TCCGGCGCTGGACCTGT	208
Imidazolinone Resistance ALS 1 *Brassica napus* Ser638Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAAATGGTGGCACTTTCAAAGATGTAATAACAG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	209
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTTT GAAAGTGCCACCATTTGGGATCATCGGTAACACATGTTCTTGGTG CGGACATATCACATCCAACAGGTATGGTC	210
	GATCCCAAATGGTGGCA	211
	TGCCACCATTTGGGATC	212
Sulfonylurea Resistance ALS 2 *Brassica napus* Pro126Ser CCC-TCC	CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGC CATTACAGGACAGGTTCCTCGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGG	213
	CCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACC GATCATCCGGCGAGGAACCTGTCCTGTAATGGCGACAAGAGGAA CACTGTCAAGCATCGCGTCTGCTAACCCGCTG	214
	GGACAGGTTCCTCGCCG	215
	CGGCGAGGAACCTGTCC	216
Sulfonylurea Resistance ALS 2 *Brassica napus* Pro126Gln CCC-CAG	AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCTCTTGTCGCC ATTACAGGACAGGTCACTCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGT	217
	ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC CGATCATCCGGCGAGTGACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT	218
	GACAGGTCACTCGCCGG	219

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGGCGAGTGACCTGTC	220
Imidazolinone Resistance ALS 2 *Brassica napus* Ser582Asn AGT-AAT	GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAAATGGTGGCACTTTCAAAGATGTAATAACAG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	221
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTTT GAAAGTGCCACCATTTGGGATCATCGGTAACACATGTTCTTGGTG CGGACATATCACATCCAACAGGTATGGTC	222
	GATCCCAAATGGTGGCA	223
	TGCCACCATTTGGGATC	224
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Ser CCT-TCT	AGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGC CATCACAGGACAGGTCTCTCGCCGGATGATCGGTACTGACGCGT TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT	225
	ACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTAC CGATCATCCGGCGAGAGACCTGTCCTGTGATGGCGACGAGAGGA ACACTGTCAAGCATCGCGTCGGCTAACCCGCT	226
	GACAGGTCTCTCGCCGG	227
	CCGGCGAGAGACCTGTC	228
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Gln CCT-CAA	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC ATCACAGGACAGGTCCAACGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	229
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCGTTGGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	230
	ACAGGTCCAACGCCGGA	231
	TCCGGCGTTGGACCTGT	232
Sulfonylurea Resistance ALS 3 *Brassica napus* Pro179Gln CCT-CAG	GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCC ATCACAGGACAGGTCCAGCGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC	233
	GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCGCTGGACCTGTCCTGTGATGGCGACGAGAGG AACACTGTCAAGCATCGCGTCGGCTAACCCGC	234
	ACAGGTCCAGCGCCGGA	235
	TCCGGCGCTGGACCTGT	236
Imidazolinone Resistance ALS 3 *Brassica napus* Ser635Asn AGT-AAT	GACCGTACCTGTTGGATGTCATCTGTCCGCACCAAGAACATGTGT TACCGATGATCCCAAATGGTGGCACTTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT	237
	ATCTCTCAGTACTTAGTGCGACCATCCCCTTCGGTTATTACATCTT TGAAAGTGCCACCATTTGGGATCATCGGTAACACATGTTCTTGGT GCGGACAGATGACATCCAACAGGTACGGTC	238

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GATCCCAAATGGTGGCA	239
	TGCCACCATTTGGGATC	240
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Ser CCC-TCC	TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGCCAGGTCTCCCGCCGCATGATCGGCACCGACGCCT TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT	241
	AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGGAGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA	242
	GCCAGGTCTCCCGCCGC	243
	GCGGCGGGAGACCTGGC	244
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAA	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGCCAGGTCCAACGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	245
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	246
	CCAGGTCCAACGCCGCA	247
	TGCGGCGTTGGACCTGG	248
Sulfonylurea Resistance ALS *Oryza sativa* Pro171Gln CCC-CAG	CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGCCAGGTCCAGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC	249
	GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGCTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG	250
	CCAGGTCCAGCGCCGCA	251
	TGCGGCGCTGGACCTGG	252
Imidazolinone Resistance ALS *Oryza sativa* Ser627Asn AGT-AAT	GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAAATGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT	253
	ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCATTTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC	254
	GATCCCAAATGGGGGCG	255
	CGCCCCCATTTGGGATC	256

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Sulfonylurea Resistance ALS *Zea mays* Pro165Ser CCG-TCG	TCTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT TTCAGGAGACGCCCATCGTCGAGGTCACCCGCT	257
	AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTG CCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGGG GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA	258
	GACAGGTGTCGCGACGC	259
	GCGTCGCGACACCTGTC	260
Sulfonylurea Resistance ALS *Zea mays* Pro165Gln CCG-CAG	CTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGCAGCGACGCATGATTGGCACCGACGCCTT TCAGGAGACGCCCATCGTCGAGGTCACCCGCTC	261
	GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGT GCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATGG GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG	262
	ACAGGTGCAGCGACGCA	263
	TGCGTCGCTGCACCTGT	264
Imidazolinone Resistance ALS *Zea mays* Ser621Asn AGT-AAT	GGCCGTACCTCTTGGATATAATCGTCCCGCACCAGGAGCATGTGT TGCCTATGATCCCTAATGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTATTGATCCGT	265
	ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCC TTGAAAGCCCCACCATTAGGGATCATAGGCAACACATGCTCCTGG TGCGGGACGATTATATCCAAGAGGTACGGCC	266
	GATCCCTAATGGTGGGG	267
	CCCCACCATTAGGGATC	268
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Ser CCT-TCT	AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTC CAGGAAACTCCAATTGTTGAGGTAACAAGGT	269
	ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT	270
	GTCAAGTCTCTCGTCGG	271
	CCGACGAGAGACTTGAC	272
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAA	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAACGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	273
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGTTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	274
	TCAAGTCCAACGTCGGA	275

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACGTTGGACTTGA	276
Sulfonylurea Resistance ALS *Gossypium hirsutum* Pro186Gln CCT-CAG	GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCCAGCGTCGGATGATCGGTACCGATGCTTTCC AGGAAACTCCAATTGTTGAGGTAACAAGGTC	277
	GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGCTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC	278
	TCAAGTCCAGCGTCGGA	279
	TCCGACGCTGGACTTGA	280
Imidazolinone Resistance ALS *Gossypium hirsutum* Ser642Asn AGT-AAT	GACCTTACTTGTTGGATGTGATTGTCCCACATCAAGAACATGTCCT GCCTATGATCCCCAATGGAGGGGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA	281
	TGAGGTCAATATTGTGTTCTTCCATCACCCTCTGTGATCACATCTT TGAAAGCCCCTCCATTGGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC	282
	GATCCCCAATGGAGGGG	283
	CCCCTCCATTGGGGATC	284
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Ser CCC-TCC	TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTTICCCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACTCGAT	285
	ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGGAAACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA	286
	GGCAAGTTICCCGGCGT	287
	ACGCCGGGAAACTTGCC	288
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Gln CCC-CAA	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCAACGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACTCGATC	289
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCGTTGAACTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG	290
	GCAAGTTCAACGGCGTA	291
	TACGCCGTTGAACTTGC	292
Sulfonylurea Resistance ALS *Amaranthus powellii* Pro192Gln CCC-CAG	CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCAGCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACTCGATC	293
	GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCGCTGAACTTGCCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG	294

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCAAGTTCAGCGGCGTA	295
	TACGCCGCTGAACTTGC	296
Imidazolinone Resistance ALS *Amaranthus powellii* Ser652Asn AGC-AAC	GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTAACGGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT	297
	ACCAACTAATAAGCCCTTCTTCCATCACCCTCTGTTATGGTGTCCT TGAAGGCGGCACCGTTAGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC	298
	GATCCCTAACGGTGCCG	299
	CGGCACCGTTAGGGATC	300

Table 12
Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO *Arabidopsis thaliana* Val365Met GTT-ATG	TCTTGCGCCCTCTTTCTGAATCTGCTGCAAATGCACTCTCAAAACT ATATTACCCACCAATGGCAGCAGTATCTATCTCGTACCCGAAAGA AGCAATCCGAACAGAATGTTTGATAGATGG	301
	CCATCTATCAAACATTCTGTTCGGATTGCTTCTTTCGGGTACGAGA TAGATACTGCTGCCATTGGTGGGTAATATAGTTTTGAGAGTGCATT TGCAGCAGATTCAGAAAGAGGGCGCAAGA	302
	CCCACCAATGGCAGCAG	303
	CTGCTGCCATTGGTGGG	304
Porphyric Herbicide Resistant PPO *Nicotiana tabacum* Val376Met GTT-ATG	TATTACGTCCTCTTTCGGTTGCCGCAGCAGATGCACTTTCAAATTT CTACTATCCCCCAATGGGAGCAGTCACAATTTCATATCCTCAAGAA GCTATTCGTGATGAGCGTCTGGTTGATGG	305
	CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAA ATTGTGACTGCTCCCATTGGGGGATAGTAGAAATTTGAAAGTGCA TCTGCTGCGGCAACCGAAAGAGGACGTAATA	306
	TCCCCCAATGGGAGCAG	307
	CTGCTCCCATTGGGGGA	308
Porphyric Herbicide Resistant PPO *Cichorium intybus* Val383Met GTT-ATG	TGTTGCGTCCGCTTTCGTTGGGTGCAGCAGATGCATTGTCAAAAT TTTATTATCCTCCGATGGCAGCTGTATCAATTTCATATCCAAAAGA CGCAATTCGTGCTGACCGGCTGATTGATGG	309
	CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTTGGATATGAA ATTGATACAGCTGCCATCGGAGGATAATAAAATTTTGACAATGCAT CTGCTGCACCCAACGAAAGCGGACGCAACA	310
	TCCTCCGATGGCAGCTG	311
	CAGCTGCCATCGGAGGA	312
Porphyric Herbicide Resistant PPO *Spinacia oleracea* Val390Met GTT-ATG	TCCTTCGTCCACTTTCAGATGTCGCCGCAGAATCTCTTTCAAAATT TCATTATCCACCAATGGCAGCTGTGTCACTTTCCTATCCTAAAGAA GCAATTAGATCAGAGTGCTTGATTGACGG	313
	CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTTAGGATAGGAAA GTGACACAGCTGCCATTGGTGGATAATGAAATTTTGAAAGAGATT CTGCGGCGACATCTGAAAGTGGACGAAGGA	314
	TCCACCAATGGCAGCTG	315
	CAGCTGCCATTGGTGGA	316

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Porphyric Herbicide Resistant PPO *Zea mays* Val363Met GTT-ATG	TTTTGCGTCCACTTTCAAGCGATGCTGCAGATGCTCTATCAAGATT CTATTATCCACCGATGGCTGCTGTAACTGTTTCGTATCCAAAGGAA GCAATTAGAAAAGAATGCTTAATTGATGG	317
	CCATCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATACGAAAC AGTTACAGCAGCCATCGGTGGATAATAGAATCTTGATAGAGCATC TGCAGCATCGCTTGAAAGTGGACGCAAAA	318
	TCCACCGATGGCTGCTG	319
	CAGCAGCCATCGGTGGA	320
Porphyric Herbicide Resistant PPO *Oryza sativa* Val364Met GTT-ATG	TCTTGCGGCCACTTTCAAGTGATGCAGCAGATGCTCTGTCAATATT CTATTATCCACCAATGGCTGCTGTAACTGTTTCATATCCAAAAGAA GCAATTAGAAAAGAATGCTTAATTGACGG	321
	CCGTCAATTAAGCATTCTTTTCTAATTGCTTCTTTTGGATATGAAAC AGTTACAGCAGCCATTGGTGGATAATAGAATATTGACAGAGCATC TGCTGCATCACTTGAAAGTGGCCGCAAGA	322
	TCCACCAATGGCTGCTG	323
	CAGCAGCCATTGGTGGA	324
Porphyric Herbicide Resistant PPO *Chlamydomonas reinhardtii* Val389Met GTG-ATG	CTGGTCAAGGAGCAGGCGCCCGCCGCCGCCGAGGCCCTGGGCT CCTTCGACTACCCGCCGATGGGCGCCGTGACGCTGTCGTACCCG CTGAGCGCCGTGCGGGAGGAGCGCAAGGCCTCGG	325
	CCGAGGCCTTGCGCTCCTCCCGCACGGCGCTCAGCGGGTACGAC AGCGTCACGGCGCCCATCGGCGGGTAGTCGAAGGAGCCCAGGG CCTCGGCGGCGGCGGGCGCCTGCTCCTTGACCAG	326
	ACCCGCCGATGGGCGCC	327
	GGCGCCCATCGGCGGGT	328

Table 13

Genome-Altering Oligos Conferring Triazine Resistance

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	329
	CAAATACCTACTACCGCCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	330

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATATGCTACTTTCAACA	331
	TGTTGAAAGTAGCATAT	332
Triazine Resistant D1 Protein *Nicotiana tabacum* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	333
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	334
	ATATGCTACTTTCAACA	335
	TGTTGAAAGTAGCATAT	336
Triazine Resistant D1 Protein *Populus deltoides* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTTAACAACTCTCGCTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	337
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	338
	ATATGCTACTTTTAACA	339
	TGTTAAAAGTAGCATAT	340
Triazine Resistant D1 Protein *Petunia x hybrida* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	341
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	342
	ATATGCTACTTTCAACA	343
	TGTTGAAAGTAGCATAT	344
Triazine Resistant D1 Protein *Magnolia pyramidata* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	345
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT	346
	ATATGCTACTTTCAACA	347
	TGTTGAAAGTAGCATAT	348
Triazine Resistant D1 Protein *Medicago sativa* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	349
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT	350
	ATATGCTACTTTCAACA	351

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTTGAAAGTAGCATAT	352
Triazine Resistant D1 Protein *Glycine max* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCAACTTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	353
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTTGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACAATATTATAGGTTT	354
	ATATGCAACTTTCAACA	355
	TGTTGAAAGTTGCATAT	356
Triazine Resistant D1 Protein *Brassica napus* Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	357
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT	358
	ATATGCTACTTTCAACA	359
	TGTTGAAAGTAGCATAT	360
Triazine Resistant D1 Protein *Oryza sativa* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAT CTTCCAATATGCTACTTTTAACAACTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG	361
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAAGTAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT	362
	ATATGCTACTTTTAACA	363
	TGTTAAAAGTAGCATAT	364
Triazine Resistant D1 Protein *Zea mays* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	365
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATTAATCGACCAAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	366
	ATATGCTACTTTCAACA	367
	TGTTGAAAGTAGCATAT	368
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	369
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	370
	ATATGCTACTTTCAACA	371
	TGTTGAAAGTAGCATAT	372

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Nicotiana tabacum* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	373
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	374
	ATATGCTACTTTCAACA	375
	TGTTGAAAGTAGCATAT	376
Triazine Resistant D1 Protein *Populus deltoides* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTTAACAACTCTCGCTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG	377
	CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	378
	ATATGCTACTTTTAACA	379
	TGTTAAAAGTAGCATAT	380
Triazine Resistant D1 Protein *Petunia x hybrida* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	381
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	382
	ATATGCTACTTTCAACA	383
	TGTTGAAAGTAGCATAT	384
Triazine Resistant D1 Protein *Magnolia pyramidata* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	385
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT	386
	ATATGCTACTTTCAACA	387
	TGTTGAAAGTAGCATAT	388
Triazine Resistant D1 Protein *Medicago sativa* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	389
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT	390
	ATATGCTACTTTCAACA	391
	TGTTGAAAGTAGCATAT	392

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Glycine max* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCAA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	393
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACAATATTATAGGTTT	394
	ATATGCAA**C**TTTCAACA	395
	TGTTGAAA**G**TTGCATAT	396
Triazine Resistant D1 Protein *Brassica napus* Gly264Thr GGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCT**AC**TTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	397
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT	398
	ATATGCT**AC**TTTCAACA	399
	TGTTGAAA**GT**AGCATAT	400
Triazine Resistant D1 Protein *Oryza sativa* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAT CTTCCAATATGCTA**C**TTTTAACAACTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG	401
	CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAA**GT**AGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT	402
	ATATGCTA**C**TTTTAACA	403
	TGTTAAAA**G**TAGCATAT	404
Triazine Resistant D1 Protein *Zea mays* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAT CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG	405
	CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATTAATCGACCAAAAT AACCGTGAGCAGCCACAATATTATAAGTCT	406
	ATATGCTA**C**TTTCAACA	407
	TGTTGAAA**G**TAGCATAT	408
Triazine Resistant D1 Protein *Arabidopsis thaliana* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG	409
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA**G**TAGCATATTGGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT	410
	ATATGCTA**C**TTTCAACA	411
	TGTTGAAA**G**TAGCATAT	412

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Picea abies* Ser264Thr AGT-ACT	AAACCTACAATATTGTGGCTGCTCACGGTTATTTCGGCCGATTGAT CTTCCAGTATGCTACTTTCAACAACTCCCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCCGTAGCAGGTATCTG	413
	CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGGGAGTTGTTGAAAGTAGCATACTGGAAGATCAATCGGCCGAAA TAACCGTGAGCAGCCACAATATTGTAGGTTT	414
	GTATGCTACTTTCAACA	415
	TGTTGAAAGTAGCATAC	416
Triazine Resistant D1 Protein *Vicia faba* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAATTCTCGCTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	417
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT	418
	ATATGCTACTTTCAACA	419
	TGTTGAAAGTAGCATAT	420
Triazine Resistant D1 Protein *Hordeum vulgare* Ser264Thr AGT-ACT	AGACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	421
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAA TAACCATGAGCAGCCACAATATTATAAGTCT	422
	ATATGCTACTTTCAACA	423
	TGTTGAAAGTAGCATAT	424
Triazine Resistant D1 Protein *Triticum aestivum* Ser264Thr AGT-ACT	AAACTTATAATATTGTGGCTGCTCATGGTTATTTTGGCCGATTAAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG	425
	CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAA TAACCATGAGCAGCCACAATATTATAAGTTT	426
	ATATGCTACTTTCAACA	427
	TGTTGAAAGTAGCATAT	428
Triazine Resistant D1 Protein *Vigna unguiculata* Ser264Thr AGT-ACT	AAACTTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTAATC TTCCAATATGCAACTTTCAACAATTCTCGTTCTTTACATTTCTTCCT AGCTGCTTGGCCTGTAGTAGGTATTTG	429
	CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTTGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAAGTTT	430
	ATATGCAACTTTCAACA	431
	TGTTGAAAGTTGCATAT	432

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Lotus japonicus* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCAA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTTGTAGGTATCTG	433
	CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAA**G**TTGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT	434
	ATATGCAA**C**TTTCAACA	435
	TGTTGAAA**G**TTGCATAT	436
Triazine Resistant D1 Protein *Sinapis alba* Ser264Thr AGT-ACT	AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG	437
	CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT	438
	ATATGCTA**C**TTTCAACA	439
	TGTTGAAA**G**TAGCATAT	440
Triazine Resistant D1 Protein *Pisum sativum* Ser264Thr AGT-ACT	AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTCAACAATTCTCGCTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	441
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT	442
	ATATGCTA**C**TTTCAACA	443
	TGTTGAAA**G**TAGCATAT	444
Triazine Resistant D1 Protein *Spinacia oleracea* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGTCGATTGAT CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG	445
	CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGACCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT	446
	ATATGCTA**C**TTTCAACA	447
	TGTTGAAA**G**TAGCATAT	448
Triazine Resistant D1 Protein *Nicotiana debneyi* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA**C**TTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	449
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAA**G**TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	450
	ATATGCTA**C**TTTCAACA	451
	TGTTGAAA**G**TAGCATAT	452

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Triazine Resistant D1 Protein *Solanum nigrum* Ser264Thr AGT-ACT	AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	453
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT	454
	ATATGCTACTTTCAACA	455
	TGTTGAAAGTAGCATAT	456
Triazine Resistant D1 Protein *Nicotiana plumbaginifolia* Ser264Thr AGT-ACT	AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTACTTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG	457
	CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT	458
	ATATGCTACTTTCAACA	459
	TGTTGAAAGTAGCATAT	460

Example 6
Engineering male- or female-sterile plants

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.

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.

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 AP3 *Arabidopsis thaliana* Arg3Term AGA-TGA	TTGTCCTCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAG AGAAGAATATGGCGTGAGGGAAGATCCAGATCAAGAGGATAGAGA ACCAGACAAACAGACAAGTGACGTATTCAA	461
	TTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATC TGGATCTTCCCTCACGCCATATTCTTCTCTCTTTGTTTAATCTTTTT GTTGAAGAGATTTGGTGGAGAGGACAA	462
	ATATGGCGTGAGGGAAG	463
	CTTCCCTCACGCCATAT	464
Male-sterile AP3 *Arabidopsis thaliana* Lys5Term AAG-TAG	TCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGA ATATGGCGAGAGGGTAGATCCAGATCAAGAGGATAGAGAACCAGA CAAACAGACAAGTGACGTATTCAAAGAGAA	465
	TTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCTATCCTC TTGATCTGGATCTACCCTCTCGCCATATTCTTCTCTCTTTGTTTAAT CTTTTTGTTGAAGAGATTTGGTGGAGA	466
	CGAGAGGGTAGATCCAG	467

	CTGGATCTACCCTCTCG	468
Male-sterile AP3 *Arabidopsis thaliana* Gln7Term CAG-TAG	CCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG CGAGAGGGAAGATCTAGATCAAGAGGATAGAGAACCAGACAAACA GACAAGTGACGTATTCAAAGAGAAGGAATG	469
	CATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCT ATCCTCTTGATCTAGATCTTCCCTCTCGCCATATTCTTCTCTCTTTG TTTAATCTTTTTGTTGAAGAGATTTGG	470
	GGAAGATCTAGATCAAG	471
	CTTGATCTAGATCTTCC	472
Male-sterile AP3 *Arabidopsis thaliana* Lys9Term AAG-TAG	CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAG GGAAGATCCAGATCTAGAGGATAGAGAACCAGACAAACAGACAAG TGACGTATTCAAAGAGAAGGAATGGTTTAT	473
	ATAAACCATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGG TTCTCTATCCTCTAGATCTGGATCTTCCCTCTCGCCATATTCTTCTC TCTTTGTTTAATCTTTTTGTTGAAGAG	474
	TCCAGATCTAGAGGATA	475
	TATCCTCTAGATCTGGA	476
Male-sterile AP3 *Brassica oleracea* Lys23Term AAG-TAG	AGAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCG ACAAGTGACGTATTCTTAGAGAAGAAATGGTTTGTTCAAGAAAGCT CACGAGCTTACAGTTTTATGTGATGCTAGGG	477
	CCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAACAA ACCATTTCTTCTCTAAGAATACGTCACTTGTCGGTTGGTCTGGTTC TCTATCCTCTTGATCTGGATCTTCCCTCT	478
	CGTATTCTTAGAGAAGA	479
	TCTTCTCTAAGAATACG	480
Male-sterile AP3 *Brassica oleracea* Arg24Term AGA-TGA	GGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAA GTGACGTATTCTAAGTGAAGAAATGGTTTGTTCAAGAAAGCTCACG AGCTTACAGTTTTATGTGATGCTAGGGTTT	481
	AAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTTGAA CAAACCATTTCTTCACTTAGAATACGTCACTTGTCGGTTGGTCTGG TTCTCTATCCTCTTGATCTGGATCTTCCC	482
	ATTCTAAGTGAAGAAAT	483
	ATTTCTTCACTTAGAAT	484
Male-sterile AP3 *Brassica oleracea* Arg25Term AGA-TGA	AAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAGTG ACGTATTCTAAGAGATGAAATGGTTTGTTCAAGAAAGCTCACGAGC TTACAGTTTTATGTGATGCTAGGGTTTCGA	485
	TCGAAACCCTAGCATCACATAAAACTGTAAGCTCGTGAGCTTTCTT GAACAAACCATTTCATCTCTTAGAATACGTCACTTGTCGGTTGGTC TGGTTCTCTATCCTCTTGATCTGGATCTT	486
	CTAAGAGATGAAATGGT	487
	ACCATTTCATCTCTTAG	488

Male-sterile AP3 *Brassica oleracea* Leu28Term TTG-TAG	TCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTA AGAGAAGAAATGGTTAGTTCAAGAAAGCTCACGAGCTTACAGTTTT ATGTGATGCTAGGGTTTCGATTATCATGTT	489
	AACATGATAATCGAAACCCTAGCATCACATAAAACTGTAAGCTCGT GAGCTTTCTTGAACTAACCATTTCTTCTCTTAGAATACGTCACTTGT CGGTTGGTCTGGTTCTCTATCCTCTTGA	490
	AAATGGTTAGTTCAAGA	491
	TCTTGAACTAACCATTT	492
Male-sterile AP3 *Brassica napus* Tyr21Term TAC-TAG	GGCTCGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGCAGGTCACCTAGTCCAAGAGAAGAAATGGTTTGTTCAAGAA AGCACACGAGCTCTCTGTTCTCTGTGATGCT	493
	AGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACC ATTTCTTCTCTTGGACTAGGTGACCTGCCTGTTTGTTTGGTTCTCTA TCCTCTTAATCTGGATCTTCCCTCGAGCC	494
	GTCACCTAGTCCAAGAG	495
	CTCTTGGACTAGGTGAC	496
Male-sterile AP3 *Brassica napus* Lys23Term AAG-TAG	CGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGG CAGGTCACCTACTCCTAGAGAAGAAATGGTTTGTTCAAGAAAGCAC ACGAGCTCTCTGTTCTCTGTGATGCTAAAG	497
	CTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAA ACCATTTCTTCTCTAGGAGTAGGTGACCTGCCTGTTTGTTTGGTTC TCTATCCTCTTAATCTGGATCTTCCCTCG	498
	CCTACTCCTAGAGAAGA	499
	TCTTCTCTAGGAGTAGG	500
Male-sterile AP3 *Brassica napus* Arg24Term AGA-TGA	GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGTGAAGAAATGGTTTGTTCAAGAAAGCACACG AGCTCTCTGTTCTCTGTGATGCTAAAGTTT	501
	AAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAA CAAACCATTTCTTCACTTGGAGTAGGTGACCTGCCTGTTTGTTTGG TTCTCTATCCTCTTAATCTGGATCTTCCC	502
	ACTCCAAGTGAAGAAAT	503
	ATTTCTTCACTTGGAGT	504
Male-sterile AP3 *Brassica napus* Arg25Term AGA-TGA	AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTC ACCTACTCCAAGAGATGAAATGGTTTGTTCAAGAAAGCACACGAG CTCTCTGTTCTCTGTGATGCTAAAGTTTCCA	505
	TGGAAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTT GAACAAACCATTTCATCTCTTGGAGTAGGTGACCTGCCTGTTTGTT TGGTTCTCTATCCTCTTAATCTGGATCTT	506
	CCAAGAGATGAAATGGT	507
	ACCATTTCATCTCTTGG	508

Male-sterile DEFA *Antirrhinum majus* Arg3Term CGA-TGA	GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGG TAGTGGTTCGATGGCTIGAGGGAAGATCCAGATTAAGAGGATAGA GAACCAAACAAACAGGCAGGTCACCTACTCCA	509
	TGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCTCTTAAT CTGGATCTTCCCTCAAGCCATCGAACCACTACCACTACTGCTCTTG TTTTCTTCTTCCAGCTTTCCTTTCTCTCC	510
	CGATGGCTIGAGGGAAG	511
	CTTCCCTCAAGCCATCG	512
Male-sterile DEFA *Antirrhinum majus* Lys5Term AAG-TAG	AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGGTAGATCCAGATTAAGAGGATAGAGAACCAA ACAAACAGGCAGGTCACCTACTCCAAGAGAA	513
	TTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTCTATCCT CTTAATCTGGATCTACCCTCGAGCCATCGAACCACTACCACTACTG CTCTTGTTTTCTTCTTCCAGCTTTCCTTT	514
	CTCGAGGGTAGATCCAG	515
	CTGGATCTACCCTCGAG	516
Male-sterile DEFA *Antirrhinum majus* Gln7Term CAG-TAG	AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATG GCTCGAGGGAAGATCTAGATTAAGAGGATAGAGAACCAAACAAAC AGGCAGGTCACCTACTCCAAGAGAAGAAATG	517
	CATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTGGTTCTC TATCCTCTTAATCTAGATCTTCCCTCGAGCCATCGAACCACTACCA CTACTGCTCTTGTTTTCTTCTTCCAGCTT	518
	GGAAGATCTAGATTAAG	519
	CTTAATCTAGATCTTCC	520
Male-sterile DEFA *Antirrhinum majus* Lys9Term AAG-TAG	GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGA GGGAAGATCCAGATTTAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGAGAAGAAATGGTTTGT	521
	ACAAACCATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGTTTG GTTCTCTATCCTCTAAATCTGGATCTTCCCTCGAGCCATCGAACCA CTACCACTACTGCTCTTGTTTTCTTCTTC	522
	TCCAGATTTAGAGGATA	523
	TATCCTCTAAATCTGGA	524
Male-sterile AP3 *Nicotiana tabacum* Lys5Term AAG-TAG	TCAGTAATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAAC TATGGCTCGTGGGTAGATCCAGATCAAGAGAATAGAGAACCAAAC AAACAGACAAGTCACTTATTCTAAGAGAA	525
	TTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCTATTCTC TTGATCTGGATCTACCCACGAGCCATAGTTTTTTTTTCTTTTTGCTC AAAGTTTGAGATCTTAAGAATTACTGA	526
	CTCGTGGGTAGATCCAG	527
	CTGGATCTACCCACGAG	528

Male-sterile AP3 *Nicotiana tabacum* Gln7Term CAG-TAG	ATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGC TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAAACAAACAG ACAAGTCACTTATTCTAAGAGAAGAAATG	529
	CATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGGTTCTCT ATTCTCTTGATCTAGATCTTCCCACGAGCCATAGTTTTTTTTTCTTT TTGCTCAAAGTTTGAGATCTTAAGAAT	530
	GGAAGATCTAGATCAAG	531
	CTTGATCTAGATCTTCC	532
Male-sterile AP3 *Nicotiana tabacum* Lys9Term AAG-TAG	AAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTG GGAAGATCCAGATCTAGAGAATAGAGAACCAAACAAACAGACAAG TCACTTATTCTAAGAGAAGAAATGGACTTT	533
	AAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTTTGG TTCTCTATTCTCTAGATCTGGATCTTCCCACGAGCCATAGTTTTTTT TTCTTTTTGCTCAAAGTTTGAGATCTT	534
	TCCAGATCTAGAGAATA	535
	TATTCTCTAGATCTGGA	536
Male-sterile AP3 *Nicotiana tabacum* Arg10Term AGA-TGA	ATCTCAAACTTTGAGCAAAAAGAAAAAAAAACTATGGCTCGTGGGA AGATCCAGATCAAGTGAATAGAGAACCAAACAAACAGACAAGTCA CTTATTCTAAGAGAAGAAATGGACTTTTCA	537
	TGAAAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGTT TGGTTCTCTATTCACTTGATCTGGATCTTCCCACGAGCCATAGTTT TTTTTTCTTTTTGCTCAAAGTTTGAGAT	538
	AGATCAAGTGAATAGAG	539
	CTCTATTCACTTGATCT	540
Male-sterile AP3 *Medicago sativa* Tyr21Term TAC-TAG	GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA CAGACAAGTAACTTAGTCAAAACGAAGGGATGGTCTTTTCAAGAAG GCCAATGAGCTCACTGTTCTTTGTGATGCT	541
	AGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCA TCCCTTCGTTTTGACTAAGTTACTTGTCTGTTCGTTGTGTTCTCTAT TCTCTTGATCTGGATCTTTCCTCGAGCC	542
	GTAACTTAGTCAAAACG	543
	CGTTTTGACTAAGTTAC	544
Male-sterile AP3 *Medicago sativa* Ser22Term TCA-TGA	CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACA GACAAGTAACTTACTGAAAACGAAGGGATGGTCTTTTCAAGAAGG CCAATGAGCTCACTGTTCTTTGTGATGCTAA	545
	TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGAC CATCCCTTCGTTTTCAGTAAGTTACTTGTCTGTTCGTTGTGTTCTCT ATTCTCTTGATCTGGATCTTTCCTCGAG	546
	AACTTACTGAAAACGAA	547
	TTCGTTTTCAGTAAGTT	548

Male-sterile AP3 *Medicago sativa* Lys23Term AAA-TAA	CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACTTACTCATAACGAAGGGATGGTCTTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTTGTGATGCTAAGG	549
	CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAG ACCATCCCTTCGTTATGAGTAAGTTACTTGTCTGTTCGTTGTGTTCT CTATTCTCTTGATCTGGATCTTTCCTCG	550
	CTTACTCATAACGAAGG	551
	CCTTCGTTATGAGTAAG	552
Male-sterile AP3 *Medicago sativa* Arg24Term CGA-TGA	GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACTTACTCAAAATGAAGGGATGGTCTTTTCAAGAAGGCCAATG AGCTCACTGTTCTTTGTGATGCTAAGGTTT	553
	AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAA AAGACCATCCCTTCATTTTGAGTAAGTTACTTGTCTGTTCGTTGTGT TCTCTATTCTCTTGATCTGGATCTTTCC	554
	ACTCAAAATGAAGGGAT	555
	ATCCCTTCATTTTGAGT	556
Male-sterile DEF4 *Solanum tuberosum* Tyr21Term TAT-TAG	GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTAGTCAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACTTACAGTTCTTTGTGATGCT	557
	AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCA TTTCTTCTCTTTGACTAAGTCACTTGCCTATTTGTTTGGTTTTCTATT TTCTTGATCTGGATCTTACCACGAGCC	558
	GTGACTTAGTCAAAGAG	559
	CTCTTTGACTAAGTCAC	560
Male-sterile DEF4 *Solanum tuberosum* Ser22Term TCA-TGA	CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATTGAAAGAGAAGAAATGGGCTATTCAAGAAGGC TAATGAACTTACAGTTCTTTGTGATGCTAA	561
	TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCC CATTTCTTCTCTTTCAATAAGTCACTTGCCTATTTGTTTGGTTTTCTA TTTTCTTGATCTGGATCTTACCACGAG	562
	GACTTATTGAAAGAGAA	563
	TTCTCTTTCAATAAGTC	564
Male-sterile DEF4 *Solanum tuberosum* Lys23Term AAG-TAG	CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGG CAAGTGACTTATTCATAGAGAAGAAATGGGCTATTCAAGAAGGCTA ATGAACTTACAGTTCTTTGTGATGCTAAAG	565
	CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAG CCCATTTCTTCTCTATGAATAAGTCACTTGCCTATTTGTTTGGTTTT CTATTTTCTTGATCTGGATCTTACCACG	566
	CTTATTCATAGAGAAGA	567
	TCTTCTCTATGAATAAG	568

Male-sterile DEF4 *Solanum tuberosum* Arg24Term AGA-TGA	GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAA GTGACTTATTCAAAGTGAAGAAATGGGCTATTCAAGAAGGCTAATG AACTTACAGTTCTTTGTGATGCTAAAGTTT	569
	AAACTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAAT AGCCCATTTCTTCACTTTGAATAAGTCACTTGCCTATTTGTTTGGTT TTCTATTTTCTTGATCTGGATCTTACC	570
	ATTCAAAGTGAAGAAAT	571
	ATTTCTTCACTTTGAAT	572
Male-sterile AP3 *Lycopersicon esculentum* Gly27Term GGA-TGA	GCTAATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTAT GATTTCTAGTACTTGAAAACTTCATGAGTTTATAAGTCCCTCTATCA CGACCAAACAATTGTTCGATCTGTACC	573
	GGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAA CTCATGAAGTTTTCAAGTACTAGAAATCATAACAATTGAAACTTTAG CATCACAAAGAACAGTAAGTTCATTAGC	574
	CTAGTACTTGAAAACTT	575
	AAGTTTTCAAGTACTAG	576
Male-sterile AP3 *Lycopersicon esculentum* Lys28Term AAA-TAA	AATGAACTTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGAT TTCTAGTACTGGATAACTTCATGAGTTTATAAGTCCCTCTATCACGA CCAAACAATTGTTCGATCTGTACCAGA	577
	TCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTAT AAACTCATGAAGTTATCCAGTACTAGAAATCATAACAATTGAAACTT TAGCATCACAAAGAACAGTAAGTTCATT	578
	GTACTGGATAACTTCAT	579
	ATGAAGTTATCCAGTAC	580
Male-sterile AP3 *Lycopersicon esculentum* Glu31Term GAG-TAG	ACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTAC TGGAAAACTTCATTAGTTTATAAGTCCCTCTATCACGACCAAACAAT TGTTCGATCTGTACCAGAAGACTATTG	581
	CAATAGTCTTCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGA GGGACTTATAAACTAATGAAGTTTTCCAGTACTAGAAATCATAACA ATTGAAACTTTAGCATCACAAAGAACAGT	582
	AACTTCATTAGTTTATA	583
	TATAAACTAATGAAGTT	584
Male-sterile AP3 *Lycopersicon esculentum* Lys40Term AAA-TAA	ATTGTTATGATTTCTAGTACTGGAAAACTTCATGAGTTTATAAGTCC CTCTATCACGACCTAACAATTGTTCGATCTGTACCAGAAGACTATT GGAGTTGATATTTGGACTACTCACTATG	585
	CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTCTGGTACAG ATCGAACAATTGTTAGGTCGTGATAGAGGGACTTATAAACTCATGA AGTTTTCCAGTACTAGAAATCATAACAAT	586
	TCACGACCTAACAATTG	587
	CAATTGTTAGGTCGTGA	588

Male-sterile AP3 *Triticum aestivum* Tyr21Term TAC-TAG	GGGGCGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCTAGTCCAAGCGCCGGTCGGGGATCATGAAG AAGGCGCGGGAGCTCACCGTGCTCTGCGACGCC	589
	GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCC CCGACCGGCGCTTGGACTAGGTCACCTGCCTGTTGGTGGCGTTCT CGATCCGCTTTATCTCAATCTTCCCCCGCCCC	590
	GTGACCTAGTCCAAGCG	591
	CGCTTGGACTAGGTCAC	592
Male-sterile AP3 *Triticum aestivum* Lys23Term AAG-TAG	CGGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGACCTACTCCTAGCGCCGGTCGGGGATCATGAAGAAGG CGCGGGAGCTCACCGTGCTCTGCGACGCCCAGG	593
	CCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATG ATCCCCGACCGGCGCTAGGAGTAGGTCACCTGCCTGTTGGTGGC GTTCTCGATCCGCTTTATCTCAATCTTCCCCCG	594
	CCTACTCCTAGCGCCGG	595
	CCGGCGCTAGGAGTAGG	596
Male-sterile AP3 *Triticum aestivum* Ser26Term TCG-TAG	TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACTCCAAGCGCCGGTAGGGGATCATGAAGAAGGCGCGGGAGCTC ACCGTGCTCTGCGACGCCCAGGTCGCCATCAT	597
	ATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGC CTTCTTCATGATCCCCTACCGGCGCTTGGAGTAGGTCACCTGCCT GTTGGTGGCGTTCTCGATCCGCTTTATCTCAA	598
	GCGCCGGTAGGGGATCA	599
	TGATCCCCTACCGGCGC	600
Male-sterile AP3 *Triticum aestivum* Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG CCGGTCGGGGATCATGTAGAAGGCGCGGGAGCTCACCGTGCTCT GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	601
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCCCGCGCCTTCTACATGATCCCCGACCGGCGCTTGGAGTAG GTCACCTGCCTGTTGGTGGCGTTCTCGATCCG	602
	GGATCATGTAGAAGGCG	603
	CGCCTTCTACATGATCC	604
Male-sterile Silky1 *Zea mays* Tyr21Term TAC-TAG	GGGGCGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA ACCGCCAGGTGACCTAGTCCAAGCGCCGGACGGGGATCATGAAG AAGGCACGCGAGCTCACCGTGCTCTGCGACGCC	605
	GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATGATCCC CGTCCGGCGCTTGGACTAGGTCACCTGGCGGTTGGTGGCGTTCT CGATCCGCTTGATCTCGATCTTGCCGCGCCCC	606
	GTGACCTAGTCCAAGCG	607
	CGCTTGGACTAGGTCAC	608

Male-sterile Silky1 *Zea mays* Lys23Term AAG-TAG	CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCCTAGCGCCGGACGGGGATCATGAAGAAGG CACGCGAGCTCACCGTGCTCTGCGACGCCCAGG	609
	CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATG ATCCCCGTCCGGCGCTAGGAGTAGGTCACCTGGCGGTTGGTGGC GTTCTCGATCCGCTTGATCTCGATCTTGCCGCG	610
	CCTACTCCTAGCGCCGG	611
	CCGGCGCTAGGAGTAGG	612
Male-sterile Silky1 *Zea mays* Lys30Term AAG-TAG	CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATGTAGAAGGCACGCGAGCTCACCGTGCTCT GCGACGCCCAGGTCGCCATCATCATGTTCTCCT	613
	AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCGCGTGCCTTCTACATGATCCCCGTCCGGCGCTTGGAGTAG GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG	614
	GGATCATGTAGAAGGCA	615
	TGCCTTCTACATGATCC	616
Male-sterile Silky1 *Zea mays* Lys31Term AAG-TAG	ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAGTAGGCACGCGAGCTCACCGTGCTCTGCG ACGCCCAGGTCGCCATCATCATGTTCTCCTCCA	617
	TGGAGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACG GTGAGCTCGCGTGCCTACTTCATGATCCCCGTCCGGCGCTTGGAG TAGGTCACCTGGCGGTTGGTGGCGTTCTCGAT	618
	TCATGAAGTAGGCACGC	619
	GCGTGCCTACTTCATGA	620
Male-sterile AP3 *Oryza sativa* Lys5Term AAG-TAG	GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAAGCGCC	621
	GGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCTCGATCC GCTTGATCTCGATCTAGCCCCTCCCCATGGCCGCCCCCTGCAGCA GCTATCTCTCTCGCCGGACAATGCAGCTAGC	622
	GGAGGGGCTAGATCGAG	623
	CTCGATCTAGCCCCTCC	624
Male-sterile AP3 *Oryza sativa* Glu7Term GAG-TAG	TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACGCGACCA ACAGGCAGGTGACCTACTCGAAGCGCCGCACGG	625
	CCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCGCGTTCT CGATCCGCTTGATCTAGATCTTGCCCCTCCCCATGGCCGCCCCCT GCAGCAGCTATCTCTCTCGCCGGACAATGCA	626
	GCAAGATCTAGATCAAG	627
	CTTGATCTAGATCTTGC	628

Male-sterile AP3 *Oryza sativa* Lys9Term AAG-TAG	GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGA GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAAGCGCCGCACGGGGATCA	629
	TGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTCG CGTTCTCGATCCGCTAGATCTCGATCTTGCCCCTCCCCATGGCCG CCCCCTGCAGCAGCTATCTCTCTCGCCGGAC	630
	TCGAGATCTAGCGGATC	631
	GATCCGCTAGATCTCGA	632
Male-sterile AP3 *Oryza sativa* Glu12Term GAG-TAG	GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGA TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT ACTCGAAGCGCCGCACGGGGATCATGAAGAAGG	633
	CCTTCTTCATGATCCCCGTGCGGCGCTTCGAGTAGGTCACCTGCC TGTTGGTCGCGTTCTAGATCCGCTTGATCTCGATCTTGCCCCTCCC CATGGCCGCCCCCTGCAGCAGCTATCTCTC	634
	AGCGGATCTAGAACGCG	635
	CGCGTTCTAGATCCGCT	636

Table 15
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Arabidopsis thaliana* Tyr35Term TAC-TAG	TCTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCA GCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCCTCTCC CTTGAGGAAATCTGGGAGAGGAAAGATCGAA	637
	TTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAAA ACGTTTAGGGCAAAATTTGATTAGTACAGA	638
	ACGGCGTAGCAATCGGA	639
	TCCGATTGCTACGCCGT	640
Male-sterile AG *Arabidopsis thaliana* Gln36Term CAA-TAA	CTGTACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAG CAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCCTCTCCCT TGAGGAAATCTGGGAGAGGAAAGATCGAAA	641
	TTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAA AACGTTTAGGGCAAAATTTGATTAGTACAG	642
	CGGCGTACTAATCGGAG	643
	CTCCGATTAGTACGCCG	644

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Arabidopsis thaliana* Ser37Term TCG-TAG	ACTAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAAT CACGGCGTACCAATAGGAGCTAGGAGGAGATTCCTCTCCCTTGA GGAAATCTGGGAGAGGAAAGATCGAAATCAA	645
	TTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGAAT CTCCTCCTAGCTCCTATTGGTACGCCGTGATTGCTGCTCCAAAGC CAAAAACGTTTAGGGCAAAATTTGATTAGT	646
	GTACCAATAGGAGCTAG	647
	CTAGCTCCTATTGGTAC	648
Male-sterile AG *Arabidopsis thaliana* Glu38Term GAG-TAG	TAATCAAATTTTGCCCTAAACGTTTTTGGCTTTGGAGCAGCAATCA CGGCGTACCAATCGTAGCTAGGAGGAGATTCCTCTCCCTTGAGGA AATCTGGGAGAGGAAAGATCGAAATCAAAC	649
	GTTTGATTTCGATCTTTCCTCTCCCAGATTTCCTCAAGGGAGAGGA ATCTCCTCCTAGCTACGATTGGTACGCCGTGATTGCTGCTCCAAA GCCAAAAACGTTTAGGGCAAAATTTGATTA	650
	ACCAATCGTAGCTAGGA	651
	TCCTAGCTACGATTGGT	652
Male-sterile AG *Brassica napus* Glu3Term GAA-TAA	CTCTCCCACTTCTTTTCGGTGGTTTATTCATTTGGTGACGATATCA CAGAAGCAATGGATTAAGGTGGGAGTAGTCACGATGCAGAGAGT AGCAAGAAGATAGGTAGAGGGAAGATAGAGA	653
	TCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTCTGCATCGTGA CTACTCCCACCTTAATCCATTGCTTCTGTGATATCGTCACCAAATG AATAAACCACCGAAAAGAAGTGGGAGAG	654
	CAATGGATTAAGGTGGG	655
	CCCACCTTAATCCATTG	656
Male-sterile AG *Brassica napus* Glu11Term GAG-TAG	TATTCATTTGGTGACGATATCACAGAAGCAATGGATGAAGGTGGG AGTAGTCACGATGCATAGAGTAGCAAGAAGATAGGTAGAGGGAA GATAGAGATAAAGAGGATAGAGAACACAACAA	657
	TTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATC TTCTTGCTACTCTATGCATCGTGACTACTCCCACCTTCATCCATTG CTTCTGTGATATCGTCACCAAATGAATA	658
	ACGATGCATAGAGTAGC	659
	GCTACTCTATGCATCGT	660
Male-sterile AG *Brassica napus* Lys14Term AAG-TAG	GGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCA CGATGCAGAGAGTAGCTAGAAGATAGGTAGAGGGAAGATAGAGA TAAAGAGGATAGAGAACACAACAAATCGTCAAG	661
	CTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCT CTACCTATCTTCTAGCTACTCTCTGCATCGTGACTACTCCCACCTT CATCCATTGCTTCTGTGATATCGTCACC	662
	AGAGTAGCTAGAAGATA	663
	TATCTTCTAGCTACTCT	664

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Brassica napus* Lys15Term AAG-TAG	GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGA TGCAGAGAGTAGCAAGTAGATAGGTAGAGGGAAGATAGAGATAAA GAGGATAGAGAACACAACAAATCGTCAAGTAA	665
	TTACTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTC CCTCTACCTATCTACTTGCTACTCTCTGCATCGTGACTACTCCCAC CTTCATCCATTGCTTCTGTGATATCGTC	666
	GTAGCAAGTAGATAGGT	667
	ACCTATCTACTTGCTAC	668
Male-sterile AG *Lycopersicon esculentum* Glu4Term CAA-TAA	CAACCAAAAAACTTAAAAATCTTCTCTTTCCTTTCCTTACAAGGTGA AGTAATGGACTTCTAAAGTGATCTAACCAGAGAGATCTCACCACAA AGGAAACTAGGAAGGGGGAAAATTGAGA	669
	TCTCAATTTTCCCCCTTCCTAGTTTCCTTTGTGGTGAGATCTCTCT GGTTAGATCACTTTAGAAGTCCATTACTTCACCTTGTAAGGAAAGG AAAGAGAAGATTTTTAAGTTTTTTGGTTG	670
	TGGACTTCTAAAGTGAT	671
	ATCACTTTAGAAGTCCA	672
Male-sterile AG *Lycopersicon esculentum* Arg9Term AGA-TGA	AAAATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAACCTGAGAGATCTCACCACAAAGGAAACTAGGAA GGGGGAAAATTGAGATCAAAAGGATCGAAA	673
	TTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTTTGT GGTGAGATCTCTCAGGTTAGATCACTTTGGAAGTCCATTACTTCAC CTTGTAAGGAAAGGAAAGAGAAGATTTT	674
	ATCTAACCTGAGAGATC	675
	GATCTCTCAGGTTAGAT	676
Male-sterile AG *Lycopersicon esculentum* Glu10Term GAG-TAG	ATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAACCAGATAGATCTCACCACAAAGGAAACTAGGAAGGG GGAAAATTGAGATCAAAAGGATCGAAAACA	677
	TGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAGTTTCCTT TGTGGTGAGATCTATCTGGTTAGATCACTTTGGAAGTCCATTACTT CACCTTGTAAGGAAAGGAAAGAGAAGAT	678
	TAACCAGATAGATCTCA	679
	TGAGATCTATCTGGTTA	680
Male-sterile AG *Lycopersicon esculentum* Ser12Term TCA-TGA	CTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT AACCAGAGAGATCTGACCACAAAGGAAACTAGGAAGGGGGAAAA TTGAGATCAAAAGGATCGAAAACACGACGAA	681
	TTCGTCGTGTTTTCGATCCTTTTGATCTCAATTTTCCCCCTTCCTAG TTTCCTTTGTGGTCAGATCTCTCTGGTTAGATCACTTTGGAAGTCC ATTACTTCACCTTGTAAGGAAAGGAAAG	682
	AGAGATCTGACCACAAA	683

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTTGTGGTCAGATCTCT	684
Male-sterile NAG1 *Nicotiana tabacum* Gln4Term CAA-TAA	GTACTCTCTATTTTCATCTTCCAACCCTTTCTTTCCTTACCAGGTGA AAGTATGGACTTCTAAAGTGATCTAACAAGAGAGATCTCTCCACAA AGGAAACTGGGAAGAGGAAAGATTGAGA	685
	TCTCAATCTTTCCTCTTCCCAGTTTCCTTTGTGGAGAGATCTCTCTT GTTAGATCACTTTAGAAGTCCATACTTTCACCTGGTAAGGAAAGAA AGGGTTGGAAGATGAAAATAGAGAGTAC	686
	TGGACTTCTAAAGTGAT	687
	ATCACTTTAGAAGTCCA	688
Male-sterile NAG1 *Nicotiana tabacum* Arg9Term AGA-TGA	ATCTTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCC AAAGTGATCTAACATGAGAGATCTCTCCACAAAGGAAACTGGGAA GAGGAAAGATTGAGATCAAACGGATCGAAA	689
	TTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTTTGT GGAGAGATCTCTCATGTTAGATCACTTTGGAAGTCCATACTTTCAC CTGGTAAGGAAAGAAAGGGTTGGAAGAT	690
	ATCTAACATGAGAGATC	691
	GATCTCTCATGTTAGAT	692
Male-sterile NAG1 *Nicotiana tabacum* Glu10Term GAG-TAG	TTCCAACCCTTTCTTTCCTTACCAGGTGAAAGTATGGACTTCCAAA GTGATCTAACAAGATAGATCTCTCCACAAAGGAAACTGGGAAGAG GAAAGATTGAGATCAAACGGATCGAAAACA	693
	TGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTTCCCAGTTTCCTT TGTGGAGAGATCTATCTTGTTAGATCACTTTGGAAGTCCATACTTT CACCTGGTAAGGAAAGAAAGGGTTGGAA	694
	TAACAAGATAGATCTCT	695
	AGAGATCTATCTTGTTA	696
Male-sterile NAG1 *Nicotiana tabacum* Gln14Term CAA-TAA	CTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACAA GAGAGATCTCTCCATAAAGGAAACTGGGAAGAGGAAAGATTGAGA TCAAACGGATCGAAAACACAACGAATCGTC	697
	GACGATTCGTTGTGTTTTCGATCCGTTTGATCTCAATCTTTCCTCTT CCCAGTTTCCTTTATGGAGAGATCTCTCTTGTTAGATCACTTTGGA AGTCCATACTTTCACCTGGTAAGGAAAG	698
	TCTCTCCATAAAGGAAA	699
	TTTCCTTTATGGAGAGA	700
Male-sterile AG *Rosa hybrida* Gly22Term GGA-TGA	GCCTATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAA AGAAGATTGGGAAGGTGAAAGATCGAGATCAAGCGGATCGAAAA CACCACCAATCGTCAAGTCACCTTCTGCAAAA	701
	TTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCCGCT TGATCTCGATCTTTCACCTTCCCAATCTTCTTTGGGCATCAGCGTC CAGGACCGTGTTGGGTTTGTTTTCATAGGC	702
	TGGGAAGGTGAAAGATC	703
	GATCTTTCACCTTCCCA	704

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Rosa hybrida* Lys23Term AAG-TAG	TATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGA AGATTGGGAAGGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTTCTGCAAAAGGC	705
	GCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTTCGATCC GCTTGATCTCGATCTATCCCCTTCCCAATCTTCTTTGGGCATCAGC GTCCAGGACCGTGTTGGGTTTGTTTTCATA	706
	GAAGGGGATAGATCGAG	707
	CTCGATCTATCCCCTTC	708
Male-sterile AG *Rosa hybrida* Glu25Term GAG-TAG	AACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTG GGAAGGGGAAAGATCTAGATCAAGCGGATCGAAAACACCACCAA TCGTCAAGTCACCTTCTGCAAAAGGCGCAATG	709
	CATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTTT CGATCCGCTTGATCTAGATCTTTCCCCTTCCCAATCTTCTTTGGGC ATCAGCGTCCAGGACCGTGTTGGGTTTGTT	710
	GAAAGATCTAGATCAAG	711
	CTTGATCTAGATCTTTC	712
Male-sterile AG *Rosa hybrida* Lys27 AAG-TAG	CCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCACCAATCGTCA AGTCACCTTCTGCAAAAGGCGCAATGGTTTGC	713
	GCAAACCATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTTTCGATCCGCTAGATCTCGATCTTTCCCCTTCCCAATCTTCT TTGGGCATCAGCGTCCAGGACCGTGTTGGG	714
	TCGAGATCTAGCGGATC	715
	GATCCGCTAGATCTCGA	716
Male-sterile far *Antirrhinum majus* Gln7Term CAA-TAA	CAATTGCCTGTTTTTATTTTTTTTCTTTTTGACTAAGTAGAAATGGC GTCTCTAAGCGATTAATCGACCGAGGTATCGCCCGAGAGGAAAAT CGGGAGAGGAAAGATCGAGATCAAACGGA	717
	TCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTCTCGGGCGA TACCTCGGTCGATTAATCGCTTAGAGACGCCATTTCTACTTAGTCA AAAAGAAAAAAAAATAAAAACAGGCAATTG	718
	TAAGCGATTAATCGACC	719
	GGTCGATTAATCGCTTA	720
Male-sterile far *Antirrhinum majus* Glu10Term GAG-TAG	GTTTTTATTTTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAG CGATCAATCGACCTAGGTATCGCCCGAGAGGAAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA	721
	TGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTCCCGATTTTCCTC TCGGGCGATACCTAGGTCGATTGATCGCTTAGAGACGCCATTTCT ACTTAGTCAAAAAGAAAAAAAATAAAAAC	722
	AATCGACCTAGGTATCG	723
	CGATACCTAGGTCGATT	724

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile far *Antirrhinum majus* Glu14Term GAG-TAG	TTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGA CCGAGGTATCGCCCTAGAGGAAAATCGGGAGAGGAAAGATCGAG ATCAAACGGATCGAAAACAAAACAAATCAAC	725
	GTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTC CCGATTTTCCTCTAGGGCGATACCTCGGTCGATTGATCGCTTAGA GACGCCATTTCTACTTAGTCAAAAAGAAA	726
	TATCGCCCTAGAGGAAA	727
	TTTCCTCTAGGGCGATA	728
Male-sterile far *Antirrhinum majus* Lys16Term AAA-TAA	TTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAG GTATCGCCCGAGAGGTAAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAAACAAATCAACAGGTTA	729
	TAACCTGTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTT CCTCTCCCGATTTACCTCTCGGGCGATACCTCGGTCGATTGATCG CTTAGAGACGCCATTTCTACTTAGTCAAA	730
	CCGAGAGGTAAATCGGG	731
	CCCGATTTACCTCTCGG	732
Male-sterile AG *Cucumis sativus* Leu21Term TTG-TAG	TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA AGGAAAGGGTAAGTAGCAAATAAAGGGGATGTTCCAGAATCAAGA AGAGAAGATGTCAGACTCGCCTCAGAGGAA	733
	TTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACA TCCCCTTTATTTGCTACTTACCCTTTCCTTCTTCCTTAATCATTCTT GTGAGTGGTGACTGATAATGCTTGGACA	734
	GGGTAAGTAGCAAATAA	735
	TTATTTGCTACTTACCC	736
Male-sterile AG *Cucumis sativus* Gln22Term CAA-TAA	TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAA GGAAAGGGTAAGTTGTAAATAAAGGGGATGTTCCAGAATCAAGAA GAGAAGATGTCAGACTCGCCTCAGAGGAAGA	737
	TCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAA CATCCCCTTTATTTACAACTTACCCTTTCCTTCTTCCTTAATCATTC TTGTGAGTGGTGACTGATAATGCTTGGA	738
	GTAAGTTGTAAATAAAG	739
	CTTTATTTACAACTTAC	740
Male-sterile AG *Cucumis sativus* Lys24Term AAG-TAG	CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG GGTAAGTTGCAAATATAGGGGATGTTCCAGAATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAGATGGGAA	741
	TTCCCATCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATT CTGGAACATCCCCTATATTTGCAACTTACCCTTTCCTTCTTCCTTAA TCATTCTTGTGAGTGGTGACTGATAATG	742
	TGCAAATATAGGGGATG	743
	CATCCCCTATATTTGCA	744

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Cucumis sativus* Gln28Term CAG-TAG	CCACTCACAAGAATGATTAAGGAAGAAGGAAAGGGTAAGTTGCAA ATAAAGGGGATGTTCTAGAATCAAGAAGAGAAGATGTCAGACTCG CCTCAGAGGAAGATGGGAAGAGGAAAGATTG	745
	CAATCTTTCCTCTTCCCATCTTCCTCTGAGGCGAGTCTGACATCTT CTCTTCTTGATTCTAGAACATCCCCTTTATTTGCAACTTACCCTTTC CTTCTTCCTTAATCATTCTTGTGAGTGG	746
	GGATGTTCTAGAATCAA	747
	TTGATTCTAGAACATCC	748
Male-sterile AG *Zea mays* Cys10Term TGC-TGA	CCACCACCACCACCACCACCACCACCACACCATGCTCAACATGAT GACTGATCTGAGCTGAGGGCCGTCGTCCAAGGTCAAGGAGCAGG TGGCGGCGGCGCCGACGGGCTCCGGCGACAGG	749
	CCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCTGCTCCTTGA CCTTGGACGACGGCCCTCAGCTCAGATCAGTCATCATGTTGAGCA TGGTGTGGTGGTGGTGGTGGTGGTGGTGG	750
	CTGAGCTGAGGGCCGTC	751
	GACGGCCCTCAGCTCAG	752
Male-sterile AG *Zea mays* Ser13Term TCG-TAG	ACCACCACCACCACCACCACACCATGCTCAACATGATGACTGATC TGAGCTGCGGGCCGTAGTCCAAGGTCAAGGAGCAGGTGGCGGC GGCGCCGACGGGCTCCGGCGACAGGCAGGGGCA	753
	TGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGCCACCT GCTCCTTGACCTTGGACTACGGCCCGCAGCTCAGATCAGTCATCA TGTTGAGCATGGTGTGGTGGTGGTGGTGGTGGT	754
	CGGGCCGTAGTCCAAGG	755
	CCTTGGACTACGGCCCG	756
Male-sterile AG *Zea mays* Lys15Term AAG-TAG	CACCACCACCACCACACCATGCTCAACATGATGACTGATCTGAGC TGCGGGCCGTCGTCCTAGGTCAAGGAGCAGGTGGCGGCGGCGC CGACGGGCTCCGGCGACAGGCAGGGGCAGGGGA	757
	TCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCCGCCGC CACCTGCTCCTTGACCTAGGACGACGGCCCGCAGCTCAGATCAG TCATCATGTTGAGCATGGTGTGGTGGTGGTGGTG	758
	CGTCGTCCTAGGTCAAG	759
	CTTGACCTAGGACGACG	760
Male-sterile AG *Zea mays* Lys17Term AAG-TAG	CACCACCACACCATGCTCAACATGATGACTGATCTGAGCTGCGGG CCGTCGTCCAAGGTCTAGGAGCAGGTGGCGGCGGCGCCGACGG GCTCCGGCGACAGGCAGGGGCAGGGGAGAGGCA	761
	TGCCTCTCCCCTGCCCCTGCCTGTCGCCGGAGCCCGTCGGCGCC GCCGCCACCTGCTCCTAGACCTTGGACGACGGCCCGCAGCTCAG ATCAGTCATCATGTTGAGCATGGTGTGGTGGTG	762
	CCAAGGTCTAGGAGCAG	763
	CTGCTCCTAGACCTTGG	764

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Zea mays* Arg4Term CGA-TGA	TCCTACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATCTGAGAAGAGGAGGCTACACCATCCACAGTAA CAGGCATCATGTCGACCCTGACTTCGGCGG	765
	CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTCTCAGATGTGCATGCTCTTGTTCCTATCACACA GATTTTGAGGTCTGAAGGAGAAAAGGTAGGA	766
	TGCACATCTGAGAAGAG	767
	CTCTTCTCAGATGTGCA	768
Male-sterile AG *Zea mays* Glu5Term GAA-TAA	TACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCGATAAGAGGAGGCTACACCATCCACAGTAACAG GCATCATGTCGACCCTGACTTCGGCGGGGC	769
	GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTGTAGCCTCCTCTTATCGGATGTGCATGCTCTTGTTCCTATCAC ACAGATTTTGAGGTCTGAAGGAGAAAAGGTA	770
	ACATCCGATAAGAGGAG	771
	CTCCTCTTATCGGATGT	772
Male-sterile AG *Zea mays* Glu6Term GAG-TAG	CTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCGAGAATAGGAGGCTACACCATCCACAGTAACAGGCA TCATGTCGACCCTGACTTCGGCGGGGCAGC	773
	GCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTGTAGCCTCCTATTCTCGGATGTGCATGCTCTTGTTCCTAT CACACAGATTTTGAGGTCTGAAGGAGAAAAG	774
	TCCGAGAATAGGAGGCT	775
	AGCCTCCTATTCTCGGA	776
Male-sterile AG *Zea mays* Glu7Term GAG-TAG	TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATG CACATCCGAGAAGAGTAGGCTACACCATCCACAGTAACAGGCATC ATGTCGACCCTGACTTCGGCGGGGCAGCAGA	777
	TCTGCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTGTAGCCTACTCTTCTCGGATGTGCATGCTCTTGTTC CTATCACACAGATTTTGAGGTCTGAAGGAGAA	778
	GAGAAGAGTAGGCTACA	779
	TGTAGCCTACTCTTCTC	780
Male-sterile AG *Oryza sativa* Lys5Term AAG-TAG	GCTGGGTCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGC GAGAAGATGGGGAGGGGGTAGATCGAGATAAAGCGGATCGAGAA CACGACGAACCGGCAGGTGACCTTCTGCAAGCGCC	781
	GGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCTCGATC CGCTTTATCTCGATCTACCCCCTCCCCATCTTCTCGCTGCTCCCC GCCGCCACCGCCGCCGACGATCCTGACCCAGC	782
	GGAGGGGGTAGATCGAG	783
	CTCGATCTACCCCCTCC	784

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile AG *Oryza sativa* Glu7Term GAG-TAG	TCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGA TGGGGAGGGGGAAGATCTAGATAAAGCGGATCGAGAACACGACG AACCGGCAGGTGACCTTCTGCAAGCGCCGCAATG	785
	CATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTCGTGTTCT CGATCCGCTTTATCTAGATCTTCCCCCTCCCCATCTTCTCGCTGCT CCCCGCCGCCACCGCCGCCGACGATCCTGA	786
	GGAAGATCTAGATAAAG	787
	CTTTATCTAGATCTTCC	788
Male-sterile AG *Oryza sativa* Lys9Term AAG-TAG	TCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGG AGGGGGAAGATCGAGATATAGCGGATCGAGAACACGACGAACCG GCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCC	789
	GGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGCCGGTTCGTC GTGTTCTCGATCCGCTATATCTCGATCTTCCCCCTCCCCATCTTCT CGCTGCTCCCCGCCGCCACCGCCGCCGACGA	790
	TCGAGATATAGCGGATC	791
	GATCCGCTATATCTCGA	792
Male-sterile AG *Oryza sativa* Glu12Term GAG-TAG	GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAG ATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGAC CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG	793
	CCTTCTTCAGGAGGCCATTGCGGCGCTTGCAGAAGGTCACCTGC CGGTTCGTCGTGTTCTAGATCCGCTTTATCTCGATCTTCCCCCTCC CCATCTTCTCGCTGCTCCCCGCCGCCACCGC	794
	AGCGGATCTAGAACACG	795
	CGTGTTCTAGATCCGCT	796

Table 16
Oligonucleotides to produce male-sterile plants

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Cucumis sativus* Tyr21Term TAT-TAG	GGGAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAA TAGACAAGTTACATAGTCAAAGAGAAGAAATGGTATCATCAAAAAA GCCAAAGAAATTACTGTTCTTTGCGATGCT	797
	AGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCAT TTCTTCTCTTTGACTATGTAACTTGTCTATTGCTTGAGTTCTCTATTC TTTTTATTTCTATTTTCCCTCTTCCC	798

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTACATAGTCAAAGAG	799
	CTCTTTGACTATGTAAC	800
Male-sterile PI *Cucumis sativus* Ser22Term TCA-TGA	GAAGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATA GACAAGTTACATATTGAAAGAGAAGAAATGGTATCATCAAAAAAGC CAAAGAAATTACTGTTCTTTGCGATGCTCA	801
	TGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATAC CATTTCTTCTCTTTCAATATGTAACTTGTCTATTGCTTGAGTTCTCTA TTCTTTTTATTTCTATTTTCCCTCTTC	802
	TACATATTGAAAGAGAA	803
	TTCTCTTTCAATATGTA	804
Male-sterile PI *Cucumis sativus* Lys23Term AAG-TAG	AGAGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGAC AAGTTACATATTCATAGAGAAGAAATGGTATCATCAAAAAAGCCAA AGAAATTACTGTTCTTTGCGATGCTCAAG	805
	CTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATA CCATTTCTTCTCTATGAATATGTAACTTGTCTATTGCTTGAGTTCTC TATTCTTTTTATTTCTATTTTCCCTCT	806
	CATATTCATAGAGAAGA	807
	TCTTCTCTATGAATATG	808
Male-sterile PI *Cucumis sativus* Arg24Term AGA-TGA	GGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAG TTACATATTCAAAGTGAAGAAATGGTATCATCAAAAAAGCCAAAGA AATTACTGTTCTTTGCGATGCTCAAGTTT	809
	AAACTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATG ATACCATTTCTTCACTTTGAATATGTAACTTGTCTATTGCTTGAGTT CTCTATTCTTTTTATTTCTATTTTCCC	810
	ATTCAAAGTGAAGAAAT	811
	ATTTCTTCACTTTGAAT	812
Male-sterile PI *Malus domestica* Tyr21Term TAC-TAG	GGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAA CAGGCAGGTGACCTAGTCCAAGAGGAGGAATGGGATTATCAAGAA GGCAAAGGAGATCACTGTTCTATGTGATGCT	813
	AGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATCCCA TTCCTCCTCTTGGACTAGGTCACCTGCCTGTTACTTGAGTTCTCAA TCCTCTTGATCTCAACCTTCCCACGTCCC	814
	GTGACCTAGTCCAAGAG	815
	CTCTTGGACTAGGTCAC	816

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Malus domestica* Lys23Term AAG-TAG	CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG CAGGTGACCTACTCCTAGAGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTCTATGTGATGCTAAAG	817
	CTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATC CCATTCCTCCTCTAGGAGTAGGTCACCTGCCTGTTACTTGAGTTCT CAATCCTCTTGATCTCAACCTTCCCACG	818
	CCTACTCCTAGAGGAGG	819
	CCTCCTCTAGGAGTAGG	820
Male-sterile PI *Malus domestica* Lys30Term AAG-TAG	AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATCTAGAAGGCAAAGGAGATCACTGTTCTATGT GATGCTAAAGTATCTCTTATCATTTATTCTA	821
	TAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGAT CTCCTTTGCCTTCTAGATAATCCCATTCCTCCTCTTGGAGTAGGTC ACCTGCCTGTTACTTGAGTTCTCAATCCT	822
	GGATTATCTAGAAGGCA	823
	TGCCTTCTAGATAATCC	824
Male-sterile PI *Malus domestica* Lys31Term AAG-TAG	ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAGTAGGCAAAGGAGATCACTGTTCTATGTGATG CTAAAGTATCTCTTATCATTTATTCTAGCT	825
	AGCTAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGT GATCTCCTTTGCCTACTTGATAATCCCATTCCTCCTCTTGGAGTAG GTCACCTGCCTGTTACTTGAGTTCTCAAT	826
	TTATCAAGTAGGCAAAG	827
	CTTTGCCTACTTGATAA	828
Male-sterile globosa *Antirrhinum majus* Gly2Term GGA-TGA	CATTTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAAATGTGAAGAGGAAAAATTGAGATCAAAAGAATTGAG AACTCAAGCAACAGGCAGGTTACTTACT	829
	AGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATCTCA ATTTTTCCTCTTCACATTTTTTTGTTTTTGTTTTTCTCTCTTGTTTTTG TTTGCAGATAACTATTGTAAAAATG	830
	AAAAAATGTGAAGAGGA	831
	TCCTCTTCACATTTTTT	832
Male-sterile globosa *Antirrhinum majus* Arg3Term AGA-TGA	TTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAA CAAAAAAATGGGATGAGGAAAAATTGAGATCAAAAGAATTGAGAAC TCAAGCAACAGGCAGGTTACTTACTCAA	833
	TTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATC TCAATTTTTCCTCATCCCATTTTTTTGTTTTTGTTTTTCTCTCTTGTTT TTGTTTGCAGATAACTATTGTAAAA	834

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAATGGGATGAGGAAAA	835
	TTTTCCTCATCCCATTT	836
Male-sterile globosa *Antirrhinum majus* Gly4Term GGA-TGA	TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACA AAAAAATGGGAAGATGAAAAATTGAGATCAAAAGAATTGAGAACTC AAGCAACAGGCAGGTTACTTACTCAAAGA	837
	TCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTG ATCTCAATTTTTCATCTTCCCATTTTTTTGTTTTTGTTTTTCTCTCTTG TTTTTGTTTGCAGATAACTATTGTA	838
	TGGGAAGATGAAAAATT	839
	AATTTTTCATCTTCCCA	840
Male-sterile globosa *Antirrhinum majus* Lys5Term AAA-TAA	AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAA AAATGGGAAGAGGATAAATTGAGATCAAAAGAATTGAGAACTCAAG CAACAGGCAGGTTACTTACTCAAAGAGAA	841
	TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTT TTGATCTCAATTTATCCTCTTCCCATTTTTTTGTTTTTGTTTTTCTCT CTTGTTTTTGTTTGCAGATAACTATT	842
	GAAGAGGATAAATTGAG	843
	CTCAATTTATCCTCTTC	844
Male-sterile PI *Zea mays* Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGC AGTATGGGGCGCGGCTAGATCAAGATCAAGAGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	845
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTTGATCTAGCCGCGCCCCATACTGCGTTCTCCACTCCC AAACAGATCCAAGGGCAGCAAGAGCTCAGC	846
	GGCGCGGCTAGATCAAG	847
	CTTGATCTAGCCGCGCC	848
Male-sterile PI *Zea mays* Lys7Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	849
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG	850
	GCAAGATCTAGATCAAG	851
	CTTGATCTAGATCTTGC	852

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Zea mays* Lys9Term AAG-TAG	CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	853
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG	854
	GCAAGATCTAGATCAAG	855
	CTTGATCTAGATCTTGC	856
Male-sterile PI *Zea mays* Glu12Term GAG-TAG	GATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGAT CAAGATCAAGAGGATCTAGAACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	857
	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTTGATCTTGCCGCGCC CCATACTGCGTTCTCCACTCCCAAACAGATC	858
	AGAGGATCTAGAACTCT	859
	AGAGTTCTAGATCCTCT	860
Male-sterile PI *Zea mays* Lys5Term AAG-TAG	GCTGAGCTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGG AGTATGGGGCGCGGCTAGATCGAGATCAAGAGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC	861
	GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTCGATCTAGCCGCGCCCCATACTCCGTTCTCCACTCCC TAACAGATTCAAGGGCAGCAAGAGCTCAGC	862
	GGCGCGGCTAGATCGAG	863
	CTCGATCTAGCCGCGCC	864
Male-sterile PI *Zea mays* Glu7Term GAG-TAG	CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG	865
	CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTCCGTTCTC CACTCCCTAACAGATTCAAGGGCAGCAAGAG	866
	GCAAGATCTAGATCAAG	867
	CTTGATCTAGATCTTGC	868
Male-sterile PI *Zea mays* Lys9Term AAG-TAG	CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCG CGGCAAGATCGAGATCTAGAGGATCGAGAACTCTACCAACCGGCA GGTGACCTTCTCCAAGCGCCGGGCCGGACTGG	869
	CCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTA GAGTTCTCGATCCTCTAGATCTCGATCTTGCCGCGCCCCATACTC CGTTCTCCACTCCCTAACAGATTCAAGGGCAG	870

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCGAGATCTAGAGGATC	871
	GATCCTCTAGATCTCGA	872
Male-sterile PI *Zea mays* Glu12Term GAG-TAG	AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CGAGATCAAGAGGATCTAGAACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG	873
	CCTTCTTGACCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTCGATCTTGCCGCGC CCCATACTCCGTTCTCCACTCCCTAACAGATT	874
	AGAGGATCTAGAACTCT	875
	AGAGTTCTAGATCCTCT	876
Male-sterile PI *Oryza sativa* Lys5Term AAG-TAG	TTGCTGCTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGG CGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGATCGAGAACT CCACCAACCGCCAGGTGACCTTCTCCAAGCGCA	877
	TGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCC TCTTGATCTCGATCTACCCGCGCCCCATCCCGCCTCCTCCTCCTC CTCCTCCTTCCTCCAGCTAGCTTAGCAGCAA	878
	GGCGCGGGTAGATCGAG	879
	CTCGATCTACCCGCGCC	880
Male-sterile PI *Oryza sativa* Glu7Term GAG-TAG	CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGA TGGGGCGCGGGAAGATCTAGATCAAGAGGATCGAGAACTCCACC AACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG	881
	CGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCT CGATCCTCTTGATCTAGATCTTCCCGCGCCCCATCCCGCCTCCTC CTCCTCCTCCTCCTTCCTCCAGCTAGCTTAG	882
	GGAAGATCTAGATCAAG	883
	CTTGATCTAGATCTTCC	884
Male-sterile PI *Oryza sativa* Lys9Term AAG-TAG	TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGC GCGGGAAGATCGAGATCTAGAGGATCGAGAACTCCACCAACCGC CAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC	885
	GGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTG GAGTTCTCGATCCTCTAGATCTCGATCTTCCCGCGCCCCATCCCG CCTCCTCCTCCTCCTCCTCCTTCCTCCAGCTA	886
	TCGAGATCTAGAGGATC	887
	GATCCTCTAGATCTCGA	888

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Male-sterile PI *Oryza sativa* Glu12Term GAG-TAG	GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAG ATCGAGATCAAGAGGATCTAGAACTCCACCAACCGCCAGGTGACC TTCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG	889
	CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGC GGTTGGTGGAGTTCTAGATCCTCTTGATCTCGATCTTCCCGCGCC CCATCCCGCCTCCTCCTCCTCCTCCTCCTTC	890
	AGAGGATCTAGAACTCC	891
	GGAGTTCTAGATCCTCT	892

Example 7

Engineering plants for abiotic stress tolerance

Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, 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.

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.

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.

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 P5CS *Arabidopsis thaliana* Phe128Ala TTT-GCT	CGTCTTTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGTGCTAGAGATAAGGATTTCAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA	893
	TCATCCTCAGCATCGCTTTGACAGTTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTAGCACTGCTATCGGTCACAAGCATTTGAGCAACC GTCACATCCAACTACCACACAAAAAGACG	894
	ATAGCAGTGCTAGAGAT	895
	ATCTCTAGCACTGCTAT	896
Salt Tolerance P5CS 1 *Brassica napus* Phe128Ala TTC-GCC	GAGACTATGTTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGTGCCAGAGACAAGGAGTTCAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTTGA	897
	TCAAATCAAGCATGGACTTCACTGTCTCATTAAGTTGCTTCCTGAA CTCCTTGTCTCTGGCACTACTGTCATTCACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC	898
	ACAGTAGTGCCAGAGAC	899
	GTCTCTGGCACTACTGT	900
Salt Tolerance P5CS 2 *Brassica napus* Phe129Ala TTC-GCC	GAGACTATGTTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGTGTCAGAGATAAGGATTTCAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAAATGA	901
	TCATTTTCAGCATAGCTTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTGACACTGCTATCAGTCACCAGCATTTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC	902
	ATAGCAGTGTCAGAGAT	903
	ATCTCTGACACTGCTAT	904
Salt Tolerance P5CS *Oryza sativa* Phe128Ala TTT-GCT	GATATGTTGTTTAACCAACTGGATGTCTCGTCATCTCAACTTCTTG TCACCGACAGTGATGCTGAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA	905
	TAAGATCTAATAATGACTCAACAGTTTCAGTGAGTTGCTCCCGGAA CTTTGGGTTCTCAGCATCACTGTCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTTAAACAACATATC	906
	ACAGTGATGCTGAGAAC	907
	GTTCTCAGCATCACTGT	908

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance P5CS *Medicago sativa* Phe128Ala TTT-GCT	GATATTTTGTTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTTG TTACTGACAATGATGCTAGAGACCAAGATTTTAGAAAGCAACTTTC TGAAACTGTGAGATCACTTCTAGCACTAA	909
	TTAGTGCTAGAAGTGATCTCACAGTTTCAGAAAGTTGCTTTCTAAA ATCTTGGTCTCTAGCATCATTGTCAGTAACAAGAAGCTGAGCAGAT GTCACATCCAGCTGACTAAACAAAATATC	910
	ACAATGATGCTAGAGAC	911
	GTCTCTAGCATCATTGT	912
Salt Tolerance P5CS *Actinidia deliciosa* Phe128Ala TTT-GCT	GATACATTGTTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGATGCTAGGGATCCAGAATTCAGGAAGCAACTT ACTGAAACTGTAGAATCACTATTGAATTTGA	913
	TCAAATTCAATAGTGATTCTACAGTTTCAGTAAGTTGCTTCCTGAAT TCTGGATCCCTAGCATCATTATCAGTAACGAGTAGCTGAGCTGAT GTCACATCCAGCTGACTAAACAATGTATC	914
	ATAATGATGCTAGGGAT	915
	ATCCCTAGCATCATTAT	916
Salt Tolerance P5CS *Cichorium intybus* Phe122Ala TTC-GCC	GACACACTCTTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGACGCCAGAAGTCCAGAATTTAGAAAACAACTTA CTGAAACAGTCGATTCTTTATTATCTTATA	917
	TATAAGATAATAAAGAATCGACTGTTTCAGTAAGTTGTTTTCTAAAT TCTGGACTTCTGGCGTCATTATCTGTTACAAGAAGCTGTGCTGAT GTCACATCCAGTTGACTGAAGAGTGTGTC	918
	ATAATGACGCCAGAAGT	919
	ACTTCTGGCGTCATTAT	920
Salt Tolerance P5CS *Lycopersicon esculentum* Phe128Ala TTT-GCT	GATTCTTTGTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGACGCTAGAGATCCAGATTTTAGGAGACAACTCA ATGACACAGTAAATTCGTTGCTTTCTCTAA	921
	TTAGAGAAAGCAACGAATTTACTGTGTCATTGAGTTGTCTCCTAAA ATCTGGATCTCTAGCGTCATTATCAGTCACCAGAAGCTGAGCTGA TGTCACATCCAACTGACTGAACAAAGAATC	922
	ATAATGACGCTAGAGAT	923
	ATCTCTAGCGTCATTAT	924
Salt Tolerance P5CS *Vigna unguiculata* Phe162Ala TTT-GCT	GATACCATGTTCAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTG TGAATGATGGATTTGCTAGGGATGCTGGCTTCAGAAAACAACTTT CGGACACAGTGAACGCGTTATTAGATTTAA	925
	TTAAATCTAATAACGCGTTCACTGTGTCCGAAAGTTGTTTTCTGAA GCCAGCATCCCTAGCAAATCCATCATTCACAAGAAGTTGGGAAGA AGTCACATCAAGCTGGCTGAACATGGTATC	926
	ATGGATTTGCTAGGGAT	927

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	ATCCCTAGCAAATCCAT	928
Salt Tolerance P5CS *Mesembryanthemum crystallinum* Phe125Ala TTT-GCT	GACACCTTGTTTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGACGCTAGAGATCCAAGTTTTAGAACACAACTA ACTGAAACAGTGTATCAGTTGTTGGATCTAA	929
	TTAGATCCAACAACTGATACACTGTTTCAGTTAGTTGTGTTCTAAA ACTTGGATCTCTAGCGTCGTTGTCCGTCACAAGCAGCTGAGCAGC AGTCAGATCCAACTGACTAAACAAGGTGTC	930
	ACAACGACGCTAGAGAT	931
	ATCTCTAGCGTCGTTGT	932
Salt Tolerance P5CS *Vitis vinifera* Phe130Ala TTT-GCT	GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGATGCTAGGGATGAAGCTTTCCGAAATCAACTTA CTCAAACAGTGGATTCATTGTTAGCTTTGA	933
	TCAAAGCTAACAATGAATCCACTGTTTGAGTAAGTTGATTTCGGAA AGCTTCATCCCTAGCATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC	934
	ATAATGATGCTAGGGAT	935
	ATCCCTAGCATCATTAT	936
Salt Tolerance P5CS *Vigna aconitifolia* Phe129Ala TTT-GCT	GATACGCTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGATGCTCGAGATAAGGATTTCAGGAAGCAGCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA	937
	TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCCTGA AATCCTTATCTCGAGCATCGTTATCCGTCACAAGAAGCTGAGCCG ATGTCACATCGAGCTGAGTGAACAGCGTATC	938
	ATAACGATGCTCGAGAT	939
	ATCTCGAGCATCGTTAT	940
Salt Tolerance HKT1 *Arabidopsis thaliana* Ser207Val TCC-GTC	AGAGATGTTCTTAGTTCCAAAGAAATCTCACCTCTCACTTTCTCCG TCTTCACAACAGTTGTCACGTTTGCAAACTGCGGATTTGTCCCCAC GAATGAGAACATGATCATCTTTCGCAAAA	941
	TTTTGCGAAAGATGATCATGTTCTCATTCGTGGGGACAAATCCGC AGTTTGCAAACGTGACAACTGTTGTGAAGACGGAGAAAGTGAGAG GTGAGATTTCTTTGGAACTAAGAACATCTCT	942
	CAACAGTTGTCACGTTT	943
	AAACGTGACAACTGTTG	944
Salt Tolerance HKT1 *Arabidopsis thaliana* Gln237Leu CAA-CTA	CGAATGAGAACATGATCATCTTTCGCAAAAACTCTGGTCTCATCTG GCTCCTAATCCCTCTAGTACTGATGGGAAACACTTTGTTCCCTTGC TTCTTGGTTTTGCTCATATGGGGACTTTA	945
	TAAAGTCCCCATATGAGCAAAACCAAGAAGCAAGGGAACAAAGTG TTTCCCATCAGTACTAGAGGGATTAGGAGCCAGATGAGACCAGAG TTTTTGCGAAAGATGATCATGTTCTCATTCG	946

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCCCTCTAGTACTGA	947
	TCAGTACTAGAGGGATT	948
Salt Tolerance HKT1 *Arabidopsis thaliana* Asn332Ser AAT-AGT	AGTCTCTAGAAGGAATGAGTTCGTACGAGAAGTTGGTTGGATCGT TGTTTCAAGTGGTGAGTTCGCGACACACCGGAGAAACTATAGTAG ACCTCTCTACACTTTCCCCAGCTATCTTGGT	949
	ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTTCT CCGGTGTGTCGCGAACTCACCACTTGAAACAACGATCCAACCAAC TTCTCGTACGAACTCATTCCTTCTAGAGACT	950
	AGTGGTGAGTTCGCGAC	951
	GTCGCGAACTCACCACT	952
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Ser256Val TCG-GTG	AGAGATGTGCTAAAGAAGAAAGGTCTCAAAATGGTGACCTTTTCC GTCTTCACCACCGTGGTGACCTTTGCCAGTTGTGGGTTTGTCCCG ACCAATGAAAACATGATTATCTTCAGCAAAA	953
	TTTTGCTGAAGATAATCATGTTTTCATTGGTCGGGACAAACCCACA ACTGGCAAAGGTCACCACGGTGGTGAAGACGGAAAAGGTCACCA TTTTGAGACCTTTCTTCTTTAGCACATCTCT	954
	CCACCGTGGTGACCTTT	955
	AAAGGTCACCACGGTGG	956
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Gln286Leu CAG-CTG	CCAATGAAAACATGATTATCTTCAGCAAAAACTCTGGCCTCCTCCT GATTCTCATCCCTCTGGCCCTTCTTGGGAACATGCTGTTCCCATC GAGCCTACGTTTGACGCTTTGGCTCATCGG	957
	CCGATGAGCCAAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCCAAGAAGGGCCAGAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTTGCTGAAGATAATCATGTTTTCATTGG	958
	CATCCCTCTGGCCCTTC	959
	GAAGGGCCAGAGGGATG	960
Salt Tolerance HKT1 *Eucalyptus camaldulensis* Asn381Ser AAC-AGC	AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCGCGC TGTTTCAGTGCGTGAGCAGCAGACATACCGGCGAGACGGTCGTC GATCTGTCCACAGTTGCTCCCGCCATCTTGGT	961
	ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC GCCGGTATGTCTGCTGCTCACGCACTGAAACAGCGCGCCCACGA TTTTCTCACAGGAGCTTAGTCCATTCAACGATT	962
	GTGCGTGAGCAGCAGAC	963
	GTCTGCTGCTCACGCAC	964

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Salt Tolerance HKT1 *Oryza sativa* Ser238Val TCC-GTC	AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCA TTCTCGGTCACGGTC**GT**CTCGTTTGCGAATGTGGGGCTCGTGCC GACAAATGAGAACATGGCAATCTTCTCCAAGA	965
	TCTTGGAGAAGATTGCCATGTTCTCATTTGTCGGCACGAGCCCCA CATTCGCAAACGAG**AC**GACCGTGACCGAGAATGAGAAGAGTGCA ATGTTGATCCCTTTCTTCTTCAGTGGAGCTTT	966
	TCACGGTC**GT**CTCGTTT	967
	AAACGAG**AC**GACCGTGA	968
Salt Tolerance HKT1 *Oryza sativa* Gln268Leu CAG-CTG	CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCCTCC TCCTGTTCATCGGCC**T**GATTCTTGCAGGCAATACACTTTACCCTCT CTTCCTAAGGCTATTGATATGGTTCCTGGG	969
	CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTA TTGCCTGCAAGAATC**A**GGCCGATGAACAGGAGGAGGAGGCCCGG GTTCTTGGAGAAGATTGCCATGTTCTCATTTG	970
	CATCGGCC**T**GATTCTTG	971
	CAAGAATC**A**GGCCGATG	972
Salt Tolerance HKT1 *Oryza sativa* Asn363Ser AAC-AGC	CAGTCTTTGATGGACTCAGCTCTTACCAGAAGATTATCAATGCATT GTTCATGGCAGTGA**G**CGCAAGGCACTCGGGGGAGAACTCCATCG ACTGCTCACTCATCGCCCCTGCTGTTCTAGT	973
	ACTAGAACAGCAGGGGCGATGAGTGAGCAGTCGATGGAGTTCTC CCCCGAGTGCCTTGCG**C**TCACTGCCATGAACAATGCATTGATAAT CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG	974
	GGCAGTGA**G**CGCAAGGC	975
	GCCTTGCG**C**TCACTGCC	976
Salt Tolerance HKT1 *Triticum aestivum* Ala240Val GCC-GTC	GTGCCCCACTGAACAAGAAAGGGATCAACATCGTGCTCTTCTCAC TATCAGTCACCGTTG**T**CTCCTGTGCGAATGCAGGACTCGTGCCCA CAAATGAGAACATGGTCATCTTCTCAAAGAA	977
	TTCTTTGAGAAGATGACCATGTTCTCATTTGTGGGCACGAGTCCT GCATTCGCACAGGAG**A**CAACGGTGACTGATAGTGAGAAGAGCAC GATGTTGATCCCTTTCTTGTTCAGTGGGGCAC	978
	CACCGTTG**T**CTCCTGTG	979
	CACAGGAG**A**CAACGGTG	980
Salt Tolerance HKT1 *Triticum aestivum* Gln270Leu CAG-CTG	CAAATGAGAACATGGTCATCTTCTCAAAGAATTCAGGCCTCTTGTT GCTGCTGAGTGGCC**T**GATGCTCGCAGGCAATACATTGTTCCCTCT CTTCCTGAGGCTACTGGTGTGGTTCCTGGG	981
	CCCAGGAACCACACCAGTAGCCTCAGGAAGAGAGGGAACAATGT ATTGCCTGCGAGCATC**A**GGCCACTCAGCAGCAACAAGAGGCCTG AATTCTTTGAGAAGATGACCATGTTCTCATTTG	982
	GAGTGGCC**T**GATGCTCG	983

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGAGCATCAGGCCACTC	984
Salt Tolerance HKT1 *Triticum aestivum* Asn365Ser AAT-AGT	CAGTCTTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT CTTCATGGTGGTGAGTGCGAGGCACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCTGCCATTATAGT	985
	ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCCTCGCACTCACCACCATGAAGAATGCATTGACAGTC TTCTGATAAGAGCTGAGCCCATCAAAGACTG	986
	GGTGGTGAGTGCGAGGC	987
	GCCTCGCACTCACCACC	988
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Arg7Term CGA-TGA	TTTTTTTTGTTTTCGTTTTCAAAAACAAAATCTTTGAATTTTATGGCA ACCCGTCTTCTCTGAACAAACTTTATCCGGCGATCTTACCGTTTAC CCGCTTTTAGCCCGGTGGGTCCTCCCA	989
	TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGC CGGATAAAGTTTGTTCAGAGAAGACGGGTTGCCATAAAATTCAAA GATTTTGTTTTTGAAAACGAAAACAAAAAAAA	990
	GTCTTCTCTGAACAAAC	991
	GTTTGTTCAGAGAAGAC	992
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Arg13Term CGA-TGA	TCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTCAGAA CAAACTTTATCCGGTGATCTTACCGTTTACCCGCTTTTAGCCCGGT GGGTCCTCCCACCGTGACTGCTTCCACCG	993
	CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGC GGGTAAACGGTAAGATCACCGGATAAAGTTTGTTCTGAGAAGACG GGTTGCCATAAAATTCAAAGATTTTGTTTTTGA	994
	TTATCCGGTGATCTTAC	995
	GTAAGATCACCGGATAA	996
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Tyr15Term TAC-TAG	AAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTT ATCCGGCGATCTTAGCGTTTACCCGCTTTTAGCCCGGTGGGTCCT CCCACCGTGACTGCTTCCACCGCCGTCGTC	997
	GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACGCTAAGATCGCCGGATAAAGTTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATTTT	998
	CGATCTTAGCGTTTACC	999
	GGTAAACGCTAAGATCG	1000

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Leu17Term TTA-TAA	CTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAAACTTTATCCG GCGATCTTACCGTTAACCCGCTTTTAGCCCGGTGGGTCCTCCCAC CGTGACTGCTTCCACCGCCGTCGTCCCGGA	1001
	TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCA CCGGGCTAAAAGCGGGTTAACGGTAAGATCGCCGGATAAAGTTT GTTCGGAGAAGACGGGTTGCCATAAAATTCAAAG	1002
	TTACCGTTAACCCGCTT	1003
	AAGCGGGTTAACGGTAA	1004
Freezing Tolerance proline oxidase precursor *Arabidopsis thaliana* Gly42Term GGA-TGA	CCGGTGGGTCCTCCCACCGTGACTGCTTCCACCGCCGTCGTCCC GGAGATTCTCTCCTTTTGACAACAAGCACCGGAACCACCTCTTCA CCACCCAAAACCCACCGAGCAATCTCACGATG	1005
	CATCGTGAGATTGCTCGGTGGGTTTTGGGTGGTGAAGAGGTGGT TCCGGTGCTTGTTGTCAAAAGGAGAGAATCTCCGGGACGACGGC GGTGGAAGCAGTCACGGTGGGAGGACCCACCGG	1006
	TCTCCTTTTGACAACAA	1007
	TTGTTGTCAAAAGGAGA	1008
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Arg4Term CGA-TGA	ACATGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTC AAACTATGAATTTCTGACAAGAGAAGTTTGTAAGGTCAGTGTTCCA GATTTGTCTCATTGAATTCTAAGTCGTGA	1009
	TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTAC AAACTTCTCTTGTCAGAAATTCATAGTTTGAGACTAATAAGATTCAA TACAAACAGAGATTTCACTGCTTCATGT	1010
	TGAATTTCTGACAAGAG	1011
	CTCTTGTCAGAAATTCA	1012
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Gln5Term CAA-TAA	TGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAA CTATGAATTTCCGATAAGAGAAGTTTGTAAGGTCAGTGTTCCAGAT TTGTCTCATTGAATTCTAAGTCGTGAAGC	1013
	GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCT TACAAACTTCTCTTATCGGAAATTCATAGTTTGAGACTAATAAGATT CAATACAAACAGAGATTTCACTGCTTCA	1014
	ATTTCCGATAAGAGAAG	1015
	CTTCTCTTATCGGAAAT	1016
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Glu6Term GAG-TAG	AGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTAT GAATTTCCGACAATAGAAGTTTGTAAGGTCAGTGTTCCAGATTTGT CTCATTGAATTCTAAGTCGTGAAGCTTA	1017
	TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGA CCTTACAAACTTCTATTGTCGGAAATTCATAGTTTGAGACTAATAA GATTCAATACAAACAGAGATTTCACTGCT	1018

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCGACAATAGAAGTTT	1019
	AAACTTCTATTGTCGGA	1020
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Lys7Term AAG-TAG	AGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACTATGAA TTTCCGACAAGAGTAGTTTGTAAGGTCAGTGTTCCAGATTTGTCTC ATTGAATTCTAAGTCGTGAAGCTTAATT	1021
	AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACAC TGACCTTACAAACTACTCTTGTCGGAAATTCATAGTTTGAGACTAA TAAGATTCAATACAAACAGAGATTTCACT	1022
	GACAAGAGTAGTTTGTA	1023
	TACAAACTACTCTTGTC	1024
Lead Tolerance cyclic nucleotide-regulated ion channel *Arabidopsis thaliana* Gln12Term CAA-TAA	CATTGAATTCTAAGTCGTGAAGCTTAATTCGATTCTTCTTCACTTTC TCGGATCAGGTTTTAAGATTGGAAGTCGGATAAGACTTCCTCCGA CGTGGAATATTCCGGTAAAAACGAGATTC	1025
	GAATCTCGTTTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATC CGACTTCCAATCTTAAAACCTGATCCGAGAAAGTGAAGAAGAATC GAATTAAGCTTCACGACTTAGAATTCAATG	1026
	TCAGGTTTTAAGATTGG	1027
	CCAATCTTAAAACCTGA	1028
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln5Term CAA-TAA	TGGAAGTCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAA GTTATGAATCACCGCTAAGACGAGTTTGTGAGGTTTCAGGATTGG AAATCAGAGAGAAGCTCTGAGGGAAATTTTC	1029
	GAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTGAAACCT CACAAACTCGTCTTAGCGGTGATTCATAACTTTAGCCAATGCATCA ACCTGCTCAACGTGGGGGATTGACTTCCA	1030
	ATCACCGCTAAGACGAG	1031
	CTCGTCTTAGCGGTGAT	1032
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gly7Term GAG-TAG	TCAATCCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG AATCACCGCCAAGACTAGTTTGTGAGGTTTCAGGATTGGAAATCA GAGAGAAGCTCTGAGGGAAATTTTCATGCTA	1033
	TAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCCAATCCTG AAACCTCACAAACTAGTCTTGGCGGTGATTCATAACTTTAGCCAAT GCATCAACCTGCTCAACGTGGGGGATTGA	1034
	GCCAAGACTAGTTTGTG	1035
	CACAAACTAGTCTTGGC	1036

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Gln12Term CAG-TAG	GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC GAGTTTGTGAGGTTTTAGGATTGGAAATCAGAGAGAAGCTCTGAG GGAAATTTTCATGCTAAAGGTGGAGTCCACC	1037
	GGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTC TGATTTCCAATCCTAAAACCTCACAAACTCGTCTTGGCGGTGATTC ATAACTTTAGCCAATGCATCAACCTGCTC	1038
	TGAGGTTTTAGGATTGG	1039
	CCAATCCTAAAACCTCA	1040
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Trp14Term TGG-TGA	TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGT GAGGTTTCAGGATTGTAAATCAGAGAGAAGCTCTGAGGGAAATTT TCATGCTAAAGGTGGAGTCCACCGAAGTAAA	1041
	TTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAG CTTCTCTCTGATTTACAATCCTGAAACCTCACAAACTCGTCTTGGC GGTGATTCATAACTTTAGCCAATGCATCA	1042
	CAGGATTGTAAATCAGA	1043
	TCTGATTTACAATCCTG	1044
Lead Tolerance cyclic nucleotide-gated calmodulin-binding ion channel (CBP4) *Nicotiana Tabacum* Lys15Term AAA-TAA	GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTG AGGTTTCAGGATTGGTAATCAGAGAGAAGCTCTGAGGGAAATTTT CATGCTAAAGGTGGAGTCCACCGAAGTAAAG	1045
	CTTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGA GCTTCTCTCTGATTACCAATCCTGAAACCTCACAAACTCGTCTTGG CGGTGATTCATAACTTTAGCCAATGCATC	1046
	AGGATTGGTAATCAGAG	1047
	CTCTGATTACCAATCCT	1048
Lead Tolerance calmodulin binding transport protein *Hordeum vulgare* Glu2Term GAA-TAA	CTTGAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTCGCCTGG TGGAGATAATGATGTAAAGAGAGGACAGATATGTTAGATTTCAGG ACTGCAAATCAGAGCAATCTGTTATCTCAG	1049
	CTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAACATA TCTGTCCTCTCTTTACATCATTATCTCCACCAGGCGAACAGTTAGC AGCTAAGAGTGGTAGATCAATTCTTCAAG	1050
	TAATGATGTAAAGAGAG	1051
	CTCTCTTTACATCATTA	1052

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
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 AAGAGAGGACAGATAGGTTAGATTTCAGGACTGCAAATCAGAGCA 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

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAAATGTAGAAAGCG	1071
	CGCTTTCTACATTTTTT	1072
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Lys3Term AAA-TAA	CTTCTCTGAGAAAAAACAACAGATCCGAATTTTATCTTTAATCAGC CGGAAAAAATGGAGTAAGCGATCGAGAGACAACGCGTTCTTCTTG AGCATCTCCGACCTTCTTCTTCTTCTTCGC	1073
	GCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGT TGTCTCTCGATCGCTTACTCCATTTTTTCCGGCTGATTAAAGATAA AATTCGGATCTGTTGTTTTTTCTCAGAGAAG	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 AGA-TGA	AAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGG AGAAAGCGATCGAGTGACAACGCGTTCTTCTTGAGCATCTCCGAC CTTCTTCTTCTTCTTCGCACAATTACGAGG	1081
	CCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAA GAAGAACGCGTTGTCACTCGATCGCTTTCTCCATTTTTTCCGGCT GATTAAAGATAAAATTCGGATCTGTTGTTTT	1082
	CGATCGAGTGACAACGC	1083
	GCGTTGTCACTCGATCG	1084
2,4-DB resistance 3-ketoacyl-CoA thiolase *Arabidopsis thaliana* Gln8Term CAA-TAA	ACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGA AAGCGATCGAGAGATAACGCGTTCTTCTTGAGCATCTCCGACCTT CTTCTTCTTCTTCGCACAATTACGAGGCTT	1085
	AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGC TCAAGAAGAACGCGTTATCTCTCGATCGCTTTCTCCATTTTTTCCG GCTGATTAAAGATAAAATTCGGATCTGTTGT	1086
	TCGAGAGATAACGCGTT	1087
	AACGCGTTATCTCTCGA	1088

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Glu26Term GAA-TAA	GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCCTTCTTCTTCTT CCTCTCACAGCTTTTAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGC TGGGGACAGTGCTGCGTATCAGAGGACCT	1089
	AGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAA GCAGAGAGAGAGCCTTAAAAGCTGTGAGAGGAAGAAGAAGAAGG ACGGAGATGTTCAAGAAGAACTCTTTGTCTCTC	1090
	ACAGCTTTTAAGGCTCT	1091
	AGAGCCTTAAAAGCTGT	1092
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Ser32Term TCA-TGA	TTGAACATCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGG CTCTCTCTCTGCTTGAGCTTGCTTGGCTGGGGACAGTGCTGCGTA TCAGAGGACCTCTCTCTATGGAGATGATGT	1093
	ACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCC CCAGCCAAGCAAGCTCAAGCAGAGAGAGAGCCTTCAAAGCTGTG AGAGGAAGAAGAAGAAGGACGGAGATGTTCAA	1094
	CTCTGCTTGAGCTTGCT	1095
	AGCAAGCTCAAGCAGAG	1096
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Cys34Term TGC-TGA	TCTCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTC TCTGCTTCAGCTTGATTGGCTGGGGACAGTGCTGCGTATCAGAG GACCTCTCTCTATGGAGATGATGTAGTCATT	1097
	AATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGC ACTGTCCCCAGCCAATCAAGCTGAAGCAGAGAGAGAGCCTTCAAA GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA	1098
	TCAGCTTGATTGGCTGG	1099
	CCAGCCAATCAAGCTGA	1100
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Leu35Term TTG-TAG	TCCGTCCTTCTTCTTCTTCCTCTCACAGCTTTGAAGGCTCTCTCTC TGCTTCAGCTTGCTAGGCTGGGGACAGTGCTGCGTATCAGAGGA CCTCTCTCTATGGAGATGATGTAGTCATTGT	1101
	ACAATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCA GCACTGTCCCCAGCCTAGCAAGCTGAAGCAGAGAGAGAGCCTTC AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGA	1102
	AGCTTGCTAGGCTGGGG	1103
	CCCCAGCCTAGCAAGCT	1104

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance glyoxysomal beta-ketoacyol-thiolase precursor *Brassica napus* Tyr42Term TAT-TAG	TCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGG GGACAGTGCTGCGTAGCAGAGGACCTCTCTCTATGGAGATGATGT AGTCATTGTTGCGGCACATAGGACTGCACTA	1105
	TAGTGCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA GAGAGAGGTCCTCTGCTACGCAGCACTGTCCCCAGCCAAGCAAG CTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGA	1106
	GCTGCGTAGCAGAGGAC	1107
	GTCCTCTGCTACGCAGC	1108
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Tyr25Term TAC-TAG	CAACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTC TTCTTCTCACAATTAGGAGTCCGCTCTTGCCGCATCAGTATGTGCT GCAGGGGATAGCGCCGCATATCATAGGGCT	1109
	AGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACTCCTAATTGTGAGAAGAAGAATTAGAAGGGC GGAGATGCTGGAGCAACACTTGCTGTCTGTTG	1110
	CACAATTAGGAGTCCGC	1111
	GCGGACTCCTAATTGTG	1112
2,4-DB resistance 3-ketoacyol-CoA thiolase B *Magnifera indica* Glu26Term GAG-TAG	AACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTT CTTCTCACAATTACTAGTCCGCTCTTGCCGCATCAGTATGTGCTGC AGGGGATAGCGCCGCATATCATAGGGCTT	1113
	AAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACTAGTAATTGTGAGAAGAAGAATTAGAAGGG CGGAGATGCTGGAGCAACACTTGCTGTCTGTT	1114
	ACAATTACTAGTCCGCT	1115
	AGCGGACTAGTAATTGT	1116
2,4-DB resistance 3-ketoacy\ol-CoA thiolase B *Mangifera indica* Ser32Term TCA-TGA	TCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTC CGCTCTTGCCGCATGAGTATGTGCTGCAGGGGATAGCGCCGCAT ATCATAGGGCTTCTGTTTATGGAGACGATGT	1117
	ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCC CCTGCAGCACATACTCATGCGGCAAGAGCGGACTCGTAATTGTGA GAAGAAGAATTAGAAGGGCGGAGATGCTGGA	1118
	TGCCGCATGAGTATGTG	1119
	CACATACTCATGCGGCA	1120

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Cys34Term TGT-TGA	TCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTT GCCGCATCAGTATGAGCTGCAGGGGATAGCGCCGCATATCATAG GGCTTCTGTTTATGGAGACGATGTGGTGATT	1121
	AATCACCACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGC GCTATCCCCTGCAGCTCATACTGATGCGGCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA	1122
	TCAGTATGAGCTGCAGG	1123
	CCTGCAGCTCATACTGA	1124
2,4-DB resistance 3-ketoacyl-CoA thiolase B *Mangifera indica* Tyr42Term TAT-TAG	TCACAATTACGAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGG GGATAGCGCCGCATAGCATAGGGCTTCTGTTTATGGAGACGATGT GGTGATTGTGGCAGCTCATCGTACTGCACTT	1125
	AAGTGCAGTACGATGAGCTGCCACAATCACCACATCGTCTCCATA AACAGAAGCCCTATGCTATGCGGCGCTATCCCCTGCAGCACATAC TGATGCGGCAAGAGCGGACTCGTAATTGTGA	1126
	GCCGCATAGCATAGGGC	1127
	GCCCTATGCTATGCGGC	1128
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Tyr22Term TAC-TAG	GAAGGCGATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCC TTCTTCTTCCGCTTAGACAAATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCTTCGTATCAA	1129
	TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCATTTGTCTAAGCGGAAGAAGAAGGCCGGAGATGATG TAGCAAAATGCTCTGCCTGTTGATCGCCTTC	1130
	TCCGCTTAGACAAATGA	1131
	TCATTTGTCTAAGCGGA	1132
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTT CCGCTTACACAAATTAATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCTTCGTATCAAAGGACAT	1133
	ATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAATTTGTGTAAGCGGAAGAAGAAGGCCGG AGATGATGTAGCAAAATGCTCTGCCTGTTGAT	1134
	ACACAAATTAATCTTCG	1135
	CGAAGATTAATTTGTGT	1136

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Ser27Term TCG-TAG	GGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTTCCGCTTA CACAAATGAATCTTAGCTCTCTGCATCGGTTTGTGCAGCTGGGGA TAGTGCTTCGTATCAAAGGACATCGGTGTT	1137
	AACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCATTTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAAATGCTCTGCC	1138
	TGAATCTTAGCTCTCTG	1139
	CAGAGAGCTAAGATTCA	1140
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATC TTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCTTCGTA TCAAAGGACATCGGTGTTTGGAGATGATGT	1141
	ACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATTTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA	1142
	CTCTGCATAGGTTTGTG	1143
	CACAAACCTATGCAGAG	1144
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucumis sativus* Cys33Term TGT-TGA	TCATCTCCGGCCTTCTTCTTCCGCTTACACAAATGAATCTTCGCTC TCTGCATCGGTTTGAGCAGCTGGGGATAGTGCTTCGTATCAAAGG ACATCGGTGTTTGGAGATGATGTCGTGATT	1145
	AATCACGACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATTT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA	1146
	TCGGTTTGAGCAGCTGG	1147
	CCAGCTGCTCAAACCGA	1148
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Tyr22Term TAT-TAG	GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTTCGGCTTAGAGCCATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCGTCGTATCAA	1149
	TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCATGGCTCTAAGCCGAAGATGAAGGCCGGAGATGAT GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC	1150
	TCGGCTTAGAGCCATGA	1151
	TCATGGCTCTAAGCCGA	1152

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Glu25Term GAA-TAA	ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT CGGCTTATAGCCATTAATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCGTCGTATCAAAGAACGT	1153
	ACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAATGGCTATAAGCCGAAGATGAAGGCCGG AGATGATGTAGCAGAATGCTCTGCCTGTTGAT	1154
	ATAGCCATTAATCTTCG	1155
	CGAAGATTAATGGCTAT	1156
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Ser27Term TCG-TAG	GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTT ATAGCCATGAATCTTAGCTCTCTGCATCGGTTTGTGCAGCTGGGG ATAGTGCGTCGTATCAAAGAACGTCGGTGTT	1157
	AACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCATGGCTATAAGCCGAAGATGAA GGCCGGAGATGATGTAGCAGAATGCTCTGCC	1158
	TGAATCTTAGCTCTCTG	1159
	CAGAGAGCTAAGATTCA	1160
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Ser31Term TCG-TAG	TGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATC TTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCGTCGTA TCAAAGAACGTCGGTGTTTGGAGATGATGT	1161
	ACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATGGCTATAAG CCGAAGATGAAGGCCGGAGATGATGTAGCA	1162
	CTCTGCATAGGTTTGTG	1163
	CACAAACCTATGCAGAG	1164
2,4-DB resistance 3-ketoacyl-CoA thiolase *Cucurbita sp.* Cys33Term TGT-TGA	TCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTC TCTGCATCGGTTTGAGCAGCTGGGGATAGTGCGTCGTATCAAAGA ACGTCGGTGTTTGGAGATGATGTCGTGATA	1165
	TATCACGACATCATCTCCAAACACCGACGTTCTTTGATACGACGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATGG CTATAAGCCGAAGATGAAGGCCGGAGATGA	1166
	TCGGTTTGAGCAGCTGG	1167
	CCAGCTGCTCAAACCGA	1168
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln5Term CAG-TAG	TCATAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTG CTATGGCAACTCATTAGCAAACGCAACCTCCTTCCGATTTTCCCGC TCTTGCCGATGAAAATTCCCAGATTCCAG	1169
	CTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAA GGAGGTTGCGTTTGCTAATGAGTTGCCATAGCAGCTCACTAACCT TGGAAGAATCCAAGCGGCAAAAGAGACTATGA	1170

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAACTCATTAGCAAACG	1171
	CGTTTGCTAATGAGTTG	1172
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln6Term CAA-TAA	TAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAGTAAACGCAACCTCCTTCCGATTTTCCCGCTCT TGCCGATGAAAATTCCCAGATTCCAGGTT	1173
	AACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGG AAGGAGGTTGCGTTTACTGATGAGTTGCCATAGCAGCTCACTAAC CTTGGAAGAATCCAAGCGGCAAAAGAGACTA	1174
	CTCATCAGTAAACGCAA	1175
	TTGCGTTTACTGATGAG	1176
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln8Term CAA-TAA	CTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCA ACTCATCAGCAAACGTAACCTCCTTCCGATTTTCCCGCTCTTGCCG ATGAAAATTCCCAGATTCCAGGTTCAATTT	1177
	AAATTGAACCTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAA AATCGGAAGGAGGTTACGTTTGCTGATGAGTTGCCATAGCAGCTC ACTAACCTTGGAAGAATCCAAGCGGCAAAAG	1178
	AGCAAACGTAACCTCCT	1179
	AGGAGGTTACGTTTGCT	1180
2,4 DB resistance Pex14 *Arabidopsis thaliana* Glu19Term GAA-TAA	GCTGCTATGGCAACTCATCAGCAAACGCAACCTCCTTCCGATTTT CCCGCTCTTGCCGATTAAAATTCCCAGATTCCAGGTTCAATTTACA CCTTCTAATCATTATTTCTTAATTTTTCTT	1181
	AAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGG AATCTGGGAATTTTAATCGGCAAGAGCGGGAAAATCGGAAGGAG GTTGCGTTTGCTGATGAGTTGCCATAGCAGC	1182
	TTGCCGATTAAAATTCC	1183
	GGAATTTTAATCGGCAA	1184
2,4 DB resistance Pex14 *Arabidopsis thaliana* Gln22Term CAG-TAG	GCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTT GCCGATGAAAATTCCTAGATTCCAGGTTCAATTTACACCTTCTAAT CATTATTTCTTAATTTTTCTTTGGTGGATT	1185
	AATCCACCAAAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAAT TGAACCTGGAATCTAGGAATTTTCATCGGCAAGAGCGGGAAAATC GGAAGGAGGTTGCGTTTGCTGATGAGTTGC	1186
	AAAATTCCTAGATTCCA	1187
	TGGAATCTAGGAATTTT	1188

Example 8

Production of albino mutants for the analysis of photosynthetic processes

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.

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 Immutans *Arabidopsis thaliana* Ser5Term TCA-TGA	TTCTTTCCTGTGAAATTATCTGCTCAAATCTTTGGTTCCTGACGGAG ATGGCGGCGATTTGAGGCATCTCCTCTGGTACGTTGACGATTTCA CGGCCTTTGGTTACTCTTCGACGCTCTAG	1189
	CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGCCTCAAATCGCCGCCATCTCCGTCAGGAACCAA AGATTTGAGCAGATAATTTCACAGGAAAGAA	1190
	GGCGATTTGAGGCATCT	1191
	AGATGCCTCAAATCGCC	1192
White leaves Immutans *Arabidopsis thaliana* Leu12Term TTG-TAG	GCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCA TCTCCTCTGGTACGTAGACGATTTCACGGCCTTTGGTTACTCTTCG ACGCTCTAGAGCCGCCGTTTCGTACAGCTC	1193
	GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAAA GGCCGTGAAATCGTCTACGTACCAGAGGAGATGCCTGAAATCGCC GCCATCTCCGTCAGGAACCAAAGATTTGAGC	1194
	TGGTACGTAGACGATTT	1195
	AAATCGTCTACGTACCA	1196
White leaves Immutans *Arabidopsis thaliana* Ser15Term TCA-TGA	TTTGGTTCCTGACGGAGATGGCGGCGATTTCAGGCATCTCCTCTG GTACGTTGACGATTTGACGGCCTTTGGTTACTCTTCGACGCTCTAG AGCCGCCGTTTCGTACAGCTCCTCTCACCG	1197
	CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAG AGTAACCAAAGGCCGTCAAATCGTCAACGTACCAGAGGAGATGCC TGAAATCGCCGCCATCTCCGTCAGGAACCAAA	1198
	GACGATTTGACGGCCTT	1199
	AAGGCCGTCAAATCGTC	1200
White leaves Immutans *Arabidopsis thaliana* Arg22Term CGA-TGA	GCGGCGATTTCAGGCATCTCCTCTGGTACGTTGACGATTTCACGG CCTTTGGTTACTCTTTGACGCTCTAGAGCCGCCGTTTCGTACAGCT CCTCTCACCGATTGCTTCATCATCTTCCTC	1201
	GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG GCGGCTCTAGAGCGTCAAAGAGTAACCAAAGGCCGTGAAATCGTC AACGTACCAGAGGAGATGCCTGAAATCGCCGC	1202
	TTACTCTTTGACGCTCT	1203
	AGAGCGTCAAAGAGTAA	1204

White leaves Immutans *Arabidopsis thaliana* Arg25Term AGA-TGA	TCAGGCATCTCCTCTGGTACGTTGACGATTTCACGGCCTTTGGTTA CTCTTCGACGCTCTTGAGCCGCCGTTTCGTACAGCTCCTCTCACC GATTGCTTCATCATCTTCCTCTCTCTTCTC	1205
	GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG TACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCG TGAAATCGTCAACGTACCAGAGGAGATGCCTGA	1206
	GACGCTCTTGAGCCGCC	1207
	GGCGGCTCAAGAGCGTC	1208
White leaves Immutans *Lycopersicon esculentum* Gly11Term GGA-TGA	GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATT TCTGCTATGAGTTTTTGAACCTCAGTTTCTTCATATTCTTGTTTTAG AGCTAGGAGTTTTGAGAAGTCATCAGTTT	1209
	AAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAGAATATGA AGAAACTGAGGTTCAAAAACTCATAGCAGAAATCGAAATCGCCATT CTTGATCCTTCTTCCTTCCCACAAGAATC	1210
	TGAGTTTTTGAACCTCA	1211
	TGAGGTTCAAAAACTCA	1212
White leaves Immutans *Lycopersicon esculentum* Ser13Term TCA-TGA	GTGGGAAGGAAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTA TGAGTTTTGGAACCTGAGTTTCTTCATATTCTTGTTTTAGAGCTAGG AGTTTTGAGAAGTCATCAGTTTTATGCAA	1213
	TTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTCTAAAACAAG AATATGAAGAAACTCAGGTTCCAAAACTCATAGCAGAAATCGAAAT CGCCATTCTTGATCCTTCTTCCTTCCCAC	1214
	TGGAACCTGAGTTTCTT	1215
	AAGAAACTCAGGTTCCA	1216
White leaves Immutans *Lycopersicon esculentum* Ser16Term TCA-TGA	AAGAAGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGG AACCTCAGTTTCTTGATATTCTTGTTTTAGAGCTAGGAGTTTTGAGA AGTCATCAGTTTTATGCAATTCCCAGAA	1217
	TTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTAGCTC TAAAACAAGAATATCAAGAAACTGAGGTTCCAAAACTCATAGCAGA AATCGAAATCGCCATTCTTGATCCTTCTT	1218
	AGTTTCTTGATATTCTT	1219
	AAGAATATCAAGAAACT	1220
White leaves Immutans *Lycopersicon esculentum* Tyr17Term TAT-TAG	AGGATCAAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACC TCAGTTTCTTCATAGTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTC ATCAGTTTTATGCAATTCCCAGAACCCA	1221
	TGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAACTCCTA GCTCTAAAACAAGACTATGAAGAAACTGAGGTTCCAAAACTCATAG CAGAAATCGAAATCGCCATTCTTGATCCT	1222
	TCTTCATAGTCTTGTTT	1223
	AAACAAGACTATGAAGA	1224

White leaves Immutans *Lycopersicon esculentum* Cys19Term TGT-TGA	AAGAATGGCGATTTCGATTTCTGCTATGAGTTTTGGAACCTCAGTT TCTTCATATTCTTGATTTAGAGCTAGGAGTTTTGAGAAGTCATCAGT TTTATGCAATTCCCAGAACCCATGTCGG	1225
	CCGACATGGGTTCTGGGAATTGCATAAAACTGATGACTTCTCAAAA CTCCTAGCTCTAAATCAAGAATATGAAGAAACTGAGGTTCCAAAAC TCATAGCAGAAATCGAAATCGCCATTCTT	1226
	TATTCTTGATTTAGAGC	1227
	GCTCTAAATCAAGAATA	1228
White leaves Immutans *Capsicum annuum* Ser13Term TCA-TGA	CGCGTCCGATAAAAAAATCAAGAATGGCGATTTCCATATCTGCTAT GAGTTTTCGAACTTGAGTTTCTTCTTCATATTCAGCATTTTTGTGCA ATTCCAAGAACCCATTTTGTTTGAATTC	1229
	GAATTCAAACAAAATGGGTTCTTGGAATTGCACAAAAATGCTGAAT ATGAAGAAGAAACTCAAGTTCGAAAACTCATAGCAGATATGGAAAT CGCCATTCTTGATTTTTTTATCGGACGCG	1230
	TCGAACTTGAGTTTCTT	1231
	AAGAAACTCAAGTTCGA	1232
White leaves Immutans *Capsicum annuum* Ser17Term TCA-TGA	AAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAAC TTCAGTTTCTTCTTGATATTCAGCATTTTTGTGCAATTCCAAGAACC CATTTTGTTTGAATTCTCTATTTTCACT	1233
	AGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAATTGCACA AAAATGCTGAATATCAAGAAGAAACTGAAGTTCGAAAACTCATAGC AGATATGGAAATCGCCATTCTTGATTTTT	1234
	TTCTTCTTGATATTCAG	1235
	CTGAATATCAAGAAGAA	1236
White leaves Immutans *Capsicum annuum* Ser19Term TCA-TGA	CAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGT TTCTTCTTCATATTGAGCATTTTTGTGCAATTCCAAGAACCCATTTT GTTTGAATTCTCTATTTTCACTTAGGAA	1237
	TTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGGAAT TGCACAAAAATGCTCAATATGAAGAAGAAACTGAAGTTCGAAAACT CATAGCAGATATGGAAATCGCCATTCTTG	1238
	TTCATATTGAGCATTTT	1239
	AAAATGCTCAATATGAA	1240
White leaves Immutans *Capsicum annuum* Leu21Term TTG-TAG	CGATTTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCA TATTCAGCATTTTAGTGCAATTCCAAGAACCCATTTTGTTTGAATTC TCTATTTTCACTTAGGAATTCTCATAG	1241
	CTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGT TCTTGGAATTGCACTAAAATGCTGAATATGAAGAAGAAACTGAAGT TCGAAAACTCATAGCAGATATGGAAATCG	1242
	AGCATTTTAGTGCAATT	1243
	AATTGCACTAAAATGCT	1244

White leaves Immutans *Capsicum annuum* Cys22Term TGC-TGA	TTCCATATCTGCTATGAGTTTTCGAACTTCAGTTTCTTCTTCATATT CAGCATTTTTGTGAAATTCCAAGAACCCATTTTGTTTGAATTCTCTA TTTTCACTTAGGAATTCTCATAGAACT	1245
	AGTTCTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAAT GGGTTCTTGGAATTTCACAAAAATGCTGAATATGAAGAAGAAACTG AAGTTCGAAAACTCATAGCAGATATGGAA	1246
	TTTTTGTGAAATTCCAA	1247
	TTGGAATTTCACAAAAA	1248
White leaves Immutans *Oryza sativa* Glu22Term GAG-TAG	TTCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTCGAGG AGTCCTTCCCCTTCAGGTAGACGGCTCCTCCTGACGAGCCACTGG TCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG	1249
	CGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCTCGT CAGGAGGAGCCGTCTACCTGAAGGGGAAGGACTCCTCGACGGCC ACCTCGGTCTGCTCCTTCTCCCTCGTGCCGAA	1250
	CCTTCAGGTAGACGGCT	1251
	AGCCGTCTACCTGAAGG	1252
White leaves Immutans *Oryza sativa* Glu28Term CAG-TAG	GAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGGGA GACGGCTCCTCCTGACTAGCCACTGGTCACCGCCGAGGAGAGCT GGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT	1253
	AAATGTTCACGGACTGCTCGAGCTTAACCACCCAGCTCTCCTCGG CGGTGACCAGTGGCTAGTCAGGAGGAGCCGTCTCCCTGAAGGGG AAGGACTCCTCGACGGCCACCTCGGTCTGCTC	1254
	CTCCTGACTAGCCACTG	1255
	CAGTGGCTAGTCAGGAG	1256
White leaves Immutans *Oryza sativa* Glu34Term GAG-TAG	GTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGA GCCACTGGTCACCGCCTAGGAGAGCTGGGTGGTTAAGCTCGAGC AGTCCGTGAACATTTTCCTCACGGAGTCAGTCA	1257
	TGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCTTAA CCACCCAGCTCTCCTAGGCGGTGACCAGTGGCTCGTCAGGAGGA GCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC	1258
	TCACCGCCTAGGAGAGC	1259
	GCTCTCCTAGGCGGTGA	1260
White leaves Immutans *Oryza sativa* Glu35Term GAG-TAG	GAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCC ACTGGTCACCGCCGAGTAGAGCTGGGTGGTTAAGCTCGAGCAGT CCGTGAACATTTTCCTCACGGAGTCAGTCATCA	1261
	TGATGACTGACTCCGTGAGGAAAATGTTCACGGACTGCTCGAGCT TAACCACCCAGCTCTACTCGGCGGTGACCAGTGGCTCGTCAGGA GGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC	1262
	CCGCCGAGTAGAGCTGG	1263
	CCAGCTCTACTCGGCGG	1264

White leaves Immutans *Oryza sativa* Trp37Term TGG-TGA	CTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCAC CGCCGAGGAGAGCTGAGTGGTTAAGCTCGAGCAGTCCGTGAACA TTTTCCTCACGGAGTCAGTCATCACGATACTT	1265
	AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTCACGGACTG CTCGAGCTTAACCACTCAGCTCTCCTCGGCGGTGACCAGTGGCTC GTCAGGAGGAGCCGTCTCCCTGAAGGGGAAG	1266
	GAGAGCTGAGTGGTTAA	1267
	TTAACCACTCAGCTCTC	1268
White leaves Immutans *Triticum aestivum* Trp22Term TGG-TGA	TCCGGAGGAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCG GCGAGGACGGCGACTGAGTCGTCAGATTCGAGCAGTCCTTCAAC GTATTCCTCACGGATACTGTCATCTTTATACTC	1269
	GAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTG CTCGAATCTGACGACTCAGTCGCCGTCCTCGCCGGCGAGGGTGA GCTCCTCGTCGAATCCCCCTTCCTCCTCCGGA	1270
	GGCGACTGAGTCGTCAG	1271
	CTGACGACTCAGTCGCC	1272
White leaves Immutans *Triticum aestivum* Arg25Term AGA-TGA	GAGGAAGGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGG ACGGCGACTGGGTCGTCTGATTCGAGCAGTCCTTCAACGTATTCC TCACGGATACTGTCATCTTTATACTCGATATTC	1273
	GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAA GGACTGCTCGAATCAGACGACCCAGTCGCCGTCCTCGCCGGCGA GGGTGAGCTCCTCGTCGAATCCCCCTTCCTC	1274
	GGGTCGTCTGATTCGAG	1275
	CTCGAATCAGACGACCC	1276
White leaves Immutans *Triticum aestivum* Glu27Term GAG-TAG	GGGGGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCG ACTGGGTCGTCAGATTCTAGCAGTCCTTCAACGTATTCCTCACGGA TACTGTCATCTTTATACTCGATATTCTGTATC	1277
	GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATAC GTTGAAGGACTGCTAGAATCTGACGACCCAGTCGCCGTCCTCGCC GGCGAGGGTGAGCTCCTCGTCGAATCCCCC	1278
	TCAGATTCTAGCAGTCC	1279
	GGACTGCTAGAATCTGA	1280
White leaves Immutans *Triticum aestivum* Gln28Term CAG-TAG	GGATTCGACGAGGAGCTCACCCTCGCCGGCGAGGACGGCGACTG GGTCGTCAGATTCGAGTAGTCCTTCAACGTATTCCTCACGGATACT GTCATCTTTATACTCGATATTCTGTATCGTG	1281
	CACGATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAA TACGTTGAAGGACTACTCGAATCTGACGACCCAGTCGCCGTCCTC GCCGGCGAGGGTGAGCTCCTCGTCGAATCC	1282
	GATTCGAGTAGTCCTTC	1283
	GAAGGACTACTCGAATC	1284

White leaves Immutans *Triticum aestivum* Tyr46Term TAT-TAG	CGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATA CTCGATATTCTGTAGCGTGACCGCGACTACGCAAGGTTCTTCGTG CTCGAGACCATCGCCAGGGTGCCCTATTTC	1285
	GAAATAGGGCACCCTGGCGATGGTCTCGAGCACGAAGAACCTTG CGTAGTCGCGGTCACGCTACAGAATATCGAGTATAAAGATGACAG TATCCGTGAGGAATACGTTGAAGGACTGCTCG	1286
	ATTCTGTAGCGTGACCG	1287
	CGGTCACGCTACAGAAT	1288

Example 9

Altering amino acid content of plants

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.

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.

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.

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 CGS *Arabidopsis thaliana* Arg77His CGT-CAT	TATCCTCCAGGATCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCT GAGCATTAAAGCCCATAGAAACTGTAGCAACATCGGTGTTGCACA GATCGTGGCGGCTAAGTGGTCCAACAACCC	1289
	GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGAT GTTGCTACAGTTTCTATGGGCTTTAATGCTCAGCTGACGGACGAA ATTAGGAGGAAATCTTAAGATCCTGGAGGATA	1290
	TAAAGCCCATAGAAACT	1291
	AGTTTCTATGGGCTTTA	1292
Met Overproduction CGS *Arabidopsis thaliana* Ser81Asn AGC-AAC	TCTTAAGATTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGC CCGTAGAAACTGTAACAACATCGGTGTTGCACAGATCGTGGCGG CTAAGTGGTCCAACAACCCATCCTCCGCGTT	1293
	AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTG TGCAACACCGATGTTGTTACAGTTTCTACGGGCTTTAATGCTCAGC TGACGGACGAAATTAGGAGGAAATCTTAAGA	1294
	AAACTGTAACAACATCG	1295
	CGATGTTGTTACAGTTT	1296
Met Overproduction CGS *Arabidopsis thaliana* Gly84Ser GGT-AGT	TTTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAA ACTGTAGCAACATCAGTGTTGCACAGATCGTGGCGGCTAAGTGGT CCAACAACCCATCCTCCGCGTTACCTTCGG	1297
	CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCC ACGATCTGTGCAACACTGATGTTGCTACAGTTTCTACGGGCTTTAA TGCTCAGCTGACGGACGAAATTAGGAGGAAA	1298
	GCAACATCAGTGTTGCA	1299
	TGCAACACTGATGTTGC	1300
Met Overproduction CGS *Arabidopsis thaliana* Gly84Asp GGT-GAT	TTCCTCCTAATTTCGTCCGTCAGCTGAGCATTAAAGCCCGTAGAAA CTGTAGCAACATCGATGTTGCACAGATCGTGGCGGCTAAGTGGTC CAACAACCCATCCTCCGCGTTACCTTCGGC	1301
	GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGC CACGATCTGTGCAACATCGATGTTGCTACAGTTTCTACGGGCTTTA ATGCTCAGCTGACGGACGAAATTAGGAGGAA	1302
	CAACATCGATGTTGCAC	1303
	GTGCAACATCGATGTTG	1304

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Fragraria vesca* Arg73His CGC-CAC	TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC TCAGCACCAAGGCCCACCGCAACTGCAGCAACATCGGCGTCGCG CAGATCGTCGCGGCTTCGTGGTCCAACAAAGA	1305
	TCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGAT GTTGCTGCAGTTGCGGTGGGCCTTGGTGCTGAGCTGGCGGACGA AGTTGGGAGGGAAGCGGAGGATGAGTGACGATA	1306
	CAAGGCCCACCGCAACT	1307
	AGTTGCGGTGGGCCTTG	1308
Met Overproduction CGS *Fragraria vesca* Ser77Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGG CCCGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCG GCTTCGTGGTCCAACAAAGACTCCGACCTTTC	1309
	GAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTG CGCGACGCCGATGTTGTTGCAGTTGCGGCGGGCCTTGGTGCTGA GCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGA	1310
	CAACTGCAACAACATCG	1311
	CGATGTTGTTGCAGTTG	1312
Met Overproduction CGS *Fragraria vesca* Gly80Ser GGC-AGC	TTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG CAACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGT GGTCCAACAAAGACTCCGACCTTTCGGCGGTGC	1313
	GCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCG ACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGGGCCTT GGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA	1314
	GCAACATCAGCGTCGCG	1315
	CGCGACGCTGATGTTGC	1316
Met Overproduction CGS *Fragraria vesca* Gly80Asp GGC-GAC	TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCGC AACTGCAGCAACATCGACGTCGCGCAGATCGTCGCGGCTTCGTG GTCCAACAAAGACTCCGACCTTTCGGCGGTGCC	1317
	GGCACCGCCGAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGC GACGATCTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGGGCCT TGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGA	1318
	CAACATCGACGTCGCGC	1319
	GCGCGACGTCGATGTTG	1320
Met Overproduction CGS *Glycine max* Arg68His CGC-CAC	TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGC TAAGCACCAAGGCGAGCCGCAACTGCAGCAACATCGGCGTCGCG CAAATCGTCGCCGCTTCGTGGTCGAACAACAG	1321
	CTGTTGTTCGACCACGAAGCGGCGACGATTTGCGCGACGCCGAT GTTGCTGCAGTTGCGGCTCGCCTTGGTGCTTAGCTGGCGCTGGA AGTTGGGAGGGAAGCGGAGGATGAGGGAGGAGA	1322
	CCAAGGCGAGCCGCAAC	1323

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTGCGGCTCGCCTTGG	1324
Met Overproduction CGS *Glycine max* Ser72Asn AGC-AAC	TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGG CGCGCCGCAACTGCAACAACATCGGCGTCGCGCAAATCGTCGCC GCTTCGTGGTCGAACAACAGCGACAACTCTCC	1325
	GGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCGACGATTTG CGCGACGCCGATGTTGTTGCAGTTGCGGCGCGCCTTGGTGCTTA GCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGA	1326
	CAACTGCAACAACATCG	1327
	CGATGTTGTTGCAGTTG	1328
Met Overproduction CGS *Glycine max* Gly75Ser GGC-AGC	TTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCG CAACTGCAGCAACATCAGCGTCGCGCAAATCGTCGCCGCTTCGT GGTCGAACAACAGCGACAACTCTCCGGCCGCCG	1329
	CGGCGGCCGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGCG ACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCTT GGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA	1330
	GCAACATCAGCGTCGCG	1331
	CGCGACGCTGATGTTGC	1332
Met Overproduction CGS *Glycine max* Gly75Asp GGC-GAC	TCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGC AACTGCAGCAACATCGACGTCGCGCAAATCGTCGCCGCTTCGTG GTCGAACAACAGCGACAACTCTCCGGCCGCCGG	1333
	CCGGCGGCCGGAGAGTTGTCGCTGTTGTTCGACCACGAAGCGGC GACGATTTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGCGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGA	1334
	CAACATCGACGTCGCGC	1335
	GCGCGACGTCGATGTTG	1336
Met Overproduction CGS *Solanum tuberosum* Arg70His AGG-CAC	TGTCTTCTCTGATTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCT AAGCATTAAGGCTCACAGGAATTGCAGCAATATTGGCGTGGCTCA AGTTGTGGCGGCTTCCTGGTCTAACAACCA	1337
	TGGTTGTTAGACCAGGAAGCCGCCACAACTTGAGCCACGCCAATA TTGCTGCAATTCCTGTGAGCCTTAATGCTTAGCTGCCTCACGAAAT TAGGAGGAAACCTGAAAATCAGAGAAGACA	1338
	TAAGGCTCACAGGAATT	1339
	AATTCCTGTGAGCCTTA	1340
Met Overproduction CGS *Solanum tuberosum* Ser74Asn AGC-AAC	TTTTCAGGTTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGC TAGGAGGAATTGCAACAATATTGGCGTGGCTCAAGTTGTGGCGG CTTCCTGGTCTAACAACCAAGCCGGTCCTGA	1341
	TCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCCACAACTTG AGCCACGCCAATATTGTTGCAATTCCTCCTAGCCTTAATGCTTAGC TGCCTCACGAAATTAGGAGGAAACCTGAAAA	1342

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTGCAACAATATTG	1343
	CAATATTGTTGCAATTC	1344
Met Overproduction CGS *Solanum tuberosum* Gly77Ser GGC-AGC	TTTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGG AATTGCAGCAATATTAGCGTGGCTCAAGTTGTGGCGGCTTCCTGG TCTAACAACCAAGCCGGTCCTGAATTCACTC	1345
	GAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCC ACAACTTGAGCCACGCTAATATTGCTGCAATTCCTCCTAGCCTTAA TGCTTAGCTGCCTCACGAAATTAGGAGGAAA	1346
	GCAATATTAGCGTGGCT	1347
	AGCCACGCTAATATTGC	1348
Met Overproduction CGS *Solanum tuberosum* Gly77Asp GGC-GAC	TTCCTCCTAATTTCGTGAGGCAGCTAAGCATTAAGGCTAGGAGGA ATTGCAGCAATATTGACGTGGCTCAAGTTGTGGCGGCTTCCTGGT CTAACAACCAAGCCGGTCCTGAATTCACTCC	1349
	GGAGTGAATTCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGC CACAACTTGAGCCACGTCAATATTGCTGCAATTCCTCCTAGCCTTA ATGCTTAGCTGCCTCACGAAATTAGGAGGAA	1350
	CAATATTGACGTGGCTC	1351
	GAGCCACGTCAATATTG	1352
Met Overproduction CGS *Mesembryanthemum crystallinum* Arg73His CGC-CAC	CTTCCTCTCTTATCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCT CAGCACCAAGGCTCGCCACAACTGCAGCAACATTGGTGTCGCAC AGGTCGTCGCTGCCTCCTGGTCCAACAACTC	1353
	GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTGTGGCGAGCCTTGGTGCTGAGCTGACGGACAA AGTTGGGAGGAAAGCGAAGGATAAGAGAGGAAG	1354
	GGCTCGCCACAACTGCA	1355
	TGCAGTTGTGGCGAGCC	1356
Met Overproduction CGS *Mesembryanthemum crystallinum* Ser77Asn AGC-AAC	TCCTTCGCTTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGG CTCGCCGCAACTGCAACAACATTGGTGTCGCACAGGTCGTCGCT GCCTCCTGGTCCAACAACTCCGATGCCGGCGC	1357
	GCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTGTTGCAGTTGCGGCGAGCCTTGGTGCTG AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA	1358
	CAACTGCAACAACATTG	1359
	CAATGTTGTTGCAGTTG	1360

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Met Overproduction CGS *Mesembryanthemum crystallinum* Gly80Ser GGT-AGT	TTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGC AACTGCAGCAACATTAGTGTCGCACAGGTCGTCGCTGCCTCCTG GTCCAACAACTCCGATGCCGGCGCCACCTCTT	1361
	AAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGC GACGACCTGTGCGACACTAATGTTGCTGCAGTTGCGGCGAGCCT TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA	1362
	GCAACATTAGTGTCGCA	1363
	TGCGACACTAATGTTGC	1364
Met Overproduction CGS *Mesembryanthemum crystallinum* Gly80Asp GGT-GAT	TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCA ACTGCAGCAACATTGATGTCGCACAGGTCGTCGCTGCCTCCTGGT CCAACAACTCCGATGCCGGCGCCACCTCTTG	1365
	CAAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAG CGACGACCTGTGCGACATCAATGTTGCTGCAGTTGCGGCGAGCC TTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA	1366
	CAACATTGATGTCGCAC	1367
	GTGCGACATCAATGTTG	1368
Met Overproduction CGS *Zea mays* Arg41His CGC-CAC	CCTCTGCTACCATCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGC TTAGCACCAAGGCACACCGCAACTGCAGCAACATCGGCGTCGCG CAGATCGTCGCCGCCGCGTGGTCCGACTGCCC	1369
	GGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGA TGTTGCTGCAGTTGCGGTGTGCCTTGGTGCTAAGCTGGCGGACA AAGTTTGGCGGAAAGCGGAGGATGGTAGCAGAGG	1370
	CAAGGCACACCGCAACT	1371
	AGTTGCGGTGTGCCTTG	1372
Met Overproduction CGS *Zea mays* Ser45Asn AGC-AAC	TCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGG CACGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCC GCCGCGTGGTCCGACTGCCCCGCCGCTCGCCC	1373
	GGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGGCGACGATCT GCGCGACGCCGATGTTGTTGCAGTTGCGGCGTGCCTTGGTGCTA AGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGA	1374
	CAACTGCAACAACATCG	1375
	CGATGTTGTTGCAGTTG	1376
Met Overproduction CGS *Zea mays* Gly48Ser GGC-AGC	TTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCCGCCGCGTG GTCCGACTGCCCCGCCGCTCGCCCCCACTTAG	1377
	CTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCGG CGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGTGCC TTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAA	1378
	GCAACATCAGCGTCGCG	1379

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGCGACGCTGATGTTGC	1380
Met Overproduction CGS *Zea mays* Gly48Asp GGC-GAC	TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCA ACTGCAGCAACATCGACGTCGCGCAGATCGTCGCCGCCGCGTGG TCCGACTGCCCCGCCGCTCGCCCCCACTTAGG	1381
	CCTAAGTGGGGGCGAGCGGCGGGGCAGTCGGACCACGCGGCG GCGACGATCTGCGCGACGTCGATGTTGCTGCAGTTGCGGCGTGC CTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAA	1382
	CAACATCGACGTCGCGC	1383
	GCGCGACGTCGATGTTG	1384
Met Overproduction TS *Arabidopsis thaliana* Leu205Arg CTT-CGT	GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATACAG GAAGTTTCAAGGATCGTGGAATGACTGTTTTGGTTAGTCAAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT	1385
	ACCACAGGTCGTTTCATCTTTCTCAGACGATTAACTTGACTAACCA AAACAGTCATTCCACGATCCTTGAAACTTCCTGTATGACTAATCCC ACAGTGTTTCACCCACAGATCATTCATAC	1386
	CAAGGATCGTGGAATGA	1387
	TCATTCCACGATCCTTG	1388
Met Overproduction TS *Solanum tuberosum* Leu198Arg CTT-CGT	GCATGACTGATTTGTGGGTCAAACACTGTGGGATTAGCCATACTG GTAGTTTTAAGGATCGTGGGATGACTGTTTTGGTGAGTCAAGTTAA TCGCTTGCGGAAAATGCATAAACCGGTTGT	1389
	ACAACCGGTTTATGCATTTTCCGCAAGCGATTAACTTGACTCACCA AAACAGTCATCCCACGATCCTTAAAACTACCAGTATGGCTAATCCC ACAGTGTTTGACCCACAAATCAGTCATGC	1390
	TAAGGATCGTGGGATGA	1391
	TCATCCCACGATCCTTA	1392
Lys Overproduction DHPS *Zea mays* Ser157Asn AGC-AAC	TCATTGGGCACACAGTGAACTGCTTTGGCTCTAGAATCAAAGTGA TAGGCAACACAGGAAACAACTCAACCAGAGAAGCCGTCCACGCA ACAGAACAGGGATTTGCTGTTGGCATGCATGC	1393
	GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGCGTGGACGGCT TCTCTGGTTGAGTTGTTTCCTGTGTTGCCTATCACTTTGATTCTAG AGCCAAAGCAGTTCACTGTGTGCCCAATGA	1394
	CACAGGAAACAACTCAA	1395
	TTGAGTTGTTTCCTGTG	1396
Lys Overproduction DHPS *Zea mays* Ala166Val GCA-GAA	GCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCA GAGAAGCCGTCCACGAAACAGAACAGGGATTTGCTGTTGGCATG CATGCGGCTCTCCACATCAATCCTTACTACGG	1397
	CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC AAATCCCTGTTCTGTTTCGTGGACGGCTTCTCTGGTTGAGTTGCTT CCTGTGTTGCCTATCACTTTGATTCTAGAGC	1398

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CGTCCACGAAACAGAAC	1399
	GTTCTGTTTCGTGGACG	1400
Lys Overproduction DHPS *Zea mays* Ala166Thr GCA-ACA	GGCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACC AGAGAAGCCGTCCACACAACAGAACAGGGATTTGCTGTTGGCAT GCATGCGGCTCTCCACATCAATCCTTACTACG	1401
	CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCA AATCCCTGTTCTGTTGTGTGGACGGCTTCTCTGGTTGAGTTGCTTC CTGTGTTGCCTATCACTTTGATTCTAGAGCC	1402
	CCGTCCACACAACAGAA	1403
	TTCTGTTGTGTGGACGG	1404
Lys Overproduction DHPS *Oryza sativa* Ser124Asn AGT-AAT	TTATTGGGCATACAGTTAACTGCTTTGGCACTAAAATTAAAGTGGT CGGCAACACAGGAAATAACTCAACAAGGGAGGCTATTCACGCAAC TGAGCAGGGATTCGCTGTAGGTATGCACGC	1405
	GCGTGCATACCTACAGCGAATCCCTGCTCAGTTGCGTGAATAGCC TCCCTTGTTGAGTTATTTCCTGTGTTGCCGACCACTTTAATTTTAGT GCCAAAGCAGTTAACTGTATGCCCAATAA	1406
	CACAGGAAATAACTCAA	1407
	TTGAGTTATTTCCTGTG	1408
Lys Overproduction DHPS *Oryza sativa* Ala133Val GCA-GTA	GCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACAA GGGAGGCTATTCACGTAACTGAGCAGGGATTCGCTGTAGGTATG CACGCGGCTCTCCACATCAATCCTTACTACGG	1409
	CCGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGC GAATCCCTGCTCAGTTACGTGAATAGCCTCCCTTGTTGAGTTACTT CCTGTGTTGCCGACCACTTTAATTTTAGTGC	1410
	TATTCACGTAACTGAGC	1411
	GCTCAGTTACGTGAATA	1412
Lys Overproduction DHPS *Oryza sativa* Ala133Thr GCA-ACA	GGCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACA AGGGAGGCTATTCACACAACTGAGCAGGGATTCGCTGTAGGTAT GCACGCGGCTCTCCACATCAATCCTTACTACG	1413
	CGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCG AATCCCTGCTCAGTTGTGTGAATAGCCTCCCTTGTTGAGTTACTTC CTGTGTTGCCGACCACTTTAATTTTAGTGCC	1414
	CTATTCACACAACTGAG	1415
	CTCAGTTGTGTGAATAG	1416
Lys Overproduction DHPS 1 *Triticum aestivum* Ser165Asn AGT-AAT	TCATCGGGCATACTGTTAACTGCTTTGGAGCCAACATTAAAGTGAT AGGCAACACGGGAAATAACTCAACCAGAGAAGCTGTTCACGCGA CAGAGCAGGGATTTGCTGTTGGCATGCATGC	1417

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCATGCATGCCAACAGCAAATCCCTGCTCTGTCGCGTGAACAGCT TCTCTGGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTGG CTCCAAAGCAGTTAACAGTATGCCCGATGA	1418
	CACGGGAAATAACTCAA	1419
	TTGAGTTATTTCCCGTG	1420
Lys Overproduction DHPS 1 *Triticum aestivum* Ala174Val GCG-GTG	GAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACCA GAGAAGCTGTTCACGTGACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTTCATGTCAATCCTTACTACGG	1421
	CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTCACGTGAACAGCTTCTCTGGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTGGCTC	1422
	TGTTCACGTGACAGAGC	1423
	GCTCTGTCACGTGAACA	1424
Lys Overproduction DHPS 1 *Triticum aestivum* Ala174Thr GCG-ACG	GGAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACC AGAGAAGCTGTTCACACGACAGAGCAGGGATTTGCTGTTGGCAT GCATGCAGCTCTTCATGTCAATCCTTACTACG	1425
	CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTCGTGTGAACAGCTTCTCTGGTTGAGTTACTTCC CGTGTTGCCTATCACTTTAATGTTGGCTCC	1426
	CTGTTCACACGACAGAG	1427
	CTCTGTCGTGTGAACAG	1428
Lys Overproduction DHPS 2 *Triticum aestivum* Ser154Asn AGT-AAT	TCATCGGGCACACTGTTAACTGCTTTGGAACTAACATTAAAGTGAT AGGCAACACGGGAAATAACTCAACTAGAGAAGCGATTCACGCTTC AGAGCAGGGATTTGCTGTTGGCATGCATGC	1429
	GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT TCTCTAGTTGAGTTATTTCCCGTGTTGCCTATCACTTTAATGTTAGT TCCAAAGCAGTTAACAGTGTGCCCGATGA	1430
	CACGGGAAATAACTCAA	1431
	TTGAGTTATTTCCCGTG	1432
Lys Overproduction DHPS 2 *Triticum aestivum* Ala163Val GCT-GTT	GAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTA GAGAAGCGATTCACGTTTCAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCATGTCAATCCTTACTATGG	1433
	CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAAACGTGAATCGCTTCTCTAGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTAGTTC	1434
	GATTCACGTTTCAGAGC	1435
	GCTCTGAAACGTGAATC	1436

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Lys Overproduction DHPS 2 *Triticum aestivum* Ala163Thr GCT-ACT	GGAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACT AGAGAAGCGATTCACACTTCAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCATGTCAATCCTTACTATG	1437
	CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGAAGTGTGAATCGCTTCTCTAGTTGAGTTACTTCC CGTGTTGCCTATCACTTTAATGTTAGTTCC	1438
	CGATTCACACTTCAGAG	1439
	CTCTGAAGTGTGAATCG	1440
Lys Overproduction DHPS *Coix lacryma-jobi* Ser154Asn AGT-AAT	CTCATTGGGCATACTGTGAACTGCTTTGGCTCTAGAATTAAAGTGA TAGGCAACACAGGAAATAACTCAACCAGAGAAGCTGTTCACGCAA CAGAGCAGGGATTTGCTGTTGGCATGCATG	1441
	CATGCATGCCAACAGCAAATCCCTGCTCTGTTGCGTGAACAGCTT CTCTGGTTGAGTTATTTCCTGTGTTGCCTATCACTTTAATTCTAGA GCCAAAGCAGTTCACAGTATGCCCAATGAG	1442
	CACAGGAAATAACTCAA	1443
	TTGAGTTATTTCCTGTG	1444
Lys Overproduction DHPS *Coix lacryma-jobi* Ala163Val GCA-GTA	GCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACCA GAGAAGCTGTTCACGTAACAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCACATCAATCCTTACTATGG	1445
	CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTTACGTGAACAGCTTCTCTGGTTGAGTTACTTC CTGTGTTGCCTATCACTTTAATTCTAGAGC	1446
	TGTTCACGTAACAGAGC	1447
	GCTCTGTTACGTGAACA	1448
Lys Overproduction DHPS *Coix lacryma-jobi* Ala163Thr GCA-ACA	GGCTCTAGAATTAAAGTGATAGGCAACACAGGAAGTAACTCAACC AGAGAAGCTGTTCACACAACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCACATCAATCCTTACTATG	1449
	CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTTGTGTGAACAGCTTCTCTGGTTGAGTTACTTCC TGTGTTGCCTATCACTTTAATTCTAGAGCC	1450
	CTGTTCACACAACAGAG	1451
	CTCTGTTGTGTGAACAG	1452
Lys Overproduction DHPS *Nicotiana tabacum* Ser136Asn AGC-AAC	TCATTGGTCACACAGTCAATTGTTTTGGAGGGTCCATCAAAGTCAT CGGGAACACTGGAAACAACTCCACAAGGGAAGCAATCCATGCAA CTGAACAGGGATTTGCTGTAGGTATGCATGC	1453
	GCATGCATACCTACAGCAAATCCCTGTTCAGTTGCATGGATTGCTT CCCTTGTGGAGTTGTTTCCAGTGTTCCCGATGACTTTGATGGACC CTCCAAAACAATTGACTGTGTGACCAATGA	1454
	CACTGGAAACAACTCCA	1455

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGAGTTGTTTCCAGTG	1456
Lys Overproduction DHPS *Nicotiana tabacum* Ala145Val GCA-GTA	GAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAA GGGAAGCAATCCATGTAACTGAACAGGGATTTGCTGTAGGTATGC ATGCAGCTCTTCACATTAATCCCTACTATGG	1457
	CCATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCA AATCCCTGTTCAGTTACATGGATTGCTTCCCTTGTGGAGTTGCTTC CAGTGTTCCCGATGACTTTGATGGACCCTC	1458
	AATCCATGTAACTGAAC	1459
	GTTCAGTTACATGGATT	1460
Lys Overproduction DHPS *Nicotiana tabacum* Ala145Thr GCA-ACA	GGAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCAC AAGGGAAGCAATCCATACAACTGAACAGGGATTTGCTGTAGGTAT GCATGCAGCTCTTCACATTAATCCCTACTATG	1461
	CATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAA ATCCCTGTTCAGTTGTATGGATTGCTTCCCTTGTGGAGTTGCTTCC AGTGTTCCCGATGACTTTGATGGACCCTCC	1462
	CAATCCATACAACTGAA	1463
	TTCAGTTGTATGGATTG	1464
Lys Overproduction DHPS *Arabidopsis thaliana* Ser142Asn AGC-AAC	TTATAGGCCATACCGTTAACTGTTTTGGCGGAAGCATCAAAGTCAT TGGAAACACTGGAAACAATTCGACTAGAGAAGCAATCCACGCGAC TGAACAAGGATTCGCGGTTGGAATGCATGC	1465
	GCATGCATTCCAACCGCGAATCCTTGTTCAGTCGCGTGGATTGCT TCTCTAGTCGAATTGTTTCCAGTGTTTCCAATGACTTTGATGCTTC CGCCAAAACAGTTAACGGTATGGCCTATAA	1466
	CACTGGAAACAATTCGA	1467
	TCGAATTGTTTCCAGTG	1468
Lys Overproduction DHPS *Arabidopsis thaliana* Ala151Val GCG-GTG	GCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTA GAGAAGCAATCCACGTGACTGAACAAGGATTCGCGGTTGGAATG CATGCTGCTCTTCATATAAACCCTTACTATGG	1469
	CCATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCCTTGTTCAGTCACGTGGATTGCTTCTCTAGTCGAATTGCTTC CAGTGTTTCCAATGACTTTGATGCTTCCGC	1470
	AATCCACGTGACTGAAC	1471
	GTTCAGTCACGTGGATT	1472
Lys Overproduction DHPS *Arabidopsis thaliana* Ala151Thr GCG-ACG	GGCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACT AGAGAAGCAATCCACACGACTGAACAAGGATTCGCGGTTGGAAT GCATGCTGCTCTTCATATAAACCCTTACTATG	1473
	CATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCCTTGTTCAGTCGTGTGGATTGCTTCTCTAGTCGAATTGCTTCC AGTGTTTCCAATGACTTTGATGCTTCCGCC	1474

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAATCCACACGACTGAA	1475
	TTCAGTCGTGTGGATTG	1476
Lys Overproduction DHPS *Glycine max* Ser103Asn AGC-AAC	TTATTGCTCATACAGTCAACTGTTTTGGTGGGAAAATTAAGGTTAT TGGAAATACTGGAAACAACTCCACCAGGGAAGCAATTCATGCCAC TGAGCAGGGTTTTGCTGTTGGAATGCATGC	1477
	GCATGCATTCCAACAGCAAAACCCTGCTCAGTGGCATGAATTGCT TCCCTGGTGGAGTTGTTTCCAGTATTTCCAATAACCTTAATTTTCC CACCAAAACAGTTGACTGTATGAGCAATAA	1478
	TACTGGAAACAACTCCA	1479
	TGGAGTTGTTTCCAGTA	1480
Lys Overproduction DHPS *Glycine max* Ala112Val GCC-GTC	GTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCA GGGAAGCAATTCATGTCACTGAGCAGGGTTTTGCTGTTGGAATGC ATGCTGCCCTTCACATAAACCCTTACTATGG	1481
	CCATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCA AAACCCTGCTCAGTGACATGAATTGCTTCCCTGGTGGAGTTGCTT CCAGTATTTCCAATAACCTTAATTTTCCCAC	1482
	AATTCATGTCACTGAGC	1483
	GCTCAGTGACATGAATT	1484
Lys Overproduction DHPS *Glycine max* Ala112Thr GCC-ACC	GGTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACC AGGGAAGCAATTCATACCACTGAGCAGGGTTTTGCTGTTGGAATG CATGCTGCCCTTCACATAAACCCTTACTATG	1485
	CATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCAA AACCCTGCTCAGTGGTATGAATTGCTTCCCTGGTGGAGTTGCTTC CAGTATTTCCAATAACCTTAATTTTCCCACC	1486
	CAATTCATACCACTGAG	1487
	CTCAGTGGTATGAATTG	1488
Trp Overproduction AS *Arabidopsis thaliana* Asp341Asn GAC-AAC	CTTGCAGGAGACATATTTCAGATCGTGCTGAGTCAACGTTTTGAG CGGCGAACATTTGCAAACCCCTTTGAAGTTTATAGAGCACTAAGA GTTGTGAATCCAAGTCCGTATATGGGTTATT	1489
	AATAACCCATATACGGACTTGGATTCACAACTCTTAGTGCTCTATA AACTTCAAAGGGGTTTGCAAATGTTCGCCGCTCAAAACGTTGACT CAGCACGATCTGAAATATGTCTCCTGCAAG	1490
	CATTTGCAAACCCCTTT	1491
	AAAGGGGTTTGCAAATG	1492
Trp Overproduction AS *Nicotiana tabacum* Asp326Asn GAC-AAC	GCTGCAGGAGACATATTTCAAATCGTTTTAAGTCAACGCTTTGAGA GAAGAACATTTGCTAACCCATTTGAAGTGTACAGAGCATTAAGAAT TGTGAATCCAAGCCCATATATGACTTACA	1493

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGTAAGTCATATATGGGCTTGGATTCACAATTCTTAATGCTCTGTA CACTTCAAATGGGTTAGCAAATGTTCTTCTCTCAAAGCGTTGACTT AAAACGATTTGAAATATGTCTCCTGCAGC	1494
	CATTTGCTAACCCATTT	1495
	AAATGGGTTAGCAAATG	1496
Trp Overproduction AS *Oryza sativa* Asp323Asn GAC-AAC	CTAGCTGGTGACATTTTTCAAGTAGTCTTAAGCCAGCGTTTTGAGA GGCGTACATTTGCTAACCCCTTTGAGGTGTACCGTGCATTGCGTA TTGTCAATCCTAGTCCTTATATGGCCTATC	1497
	GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAAGGGGTTAGCAAATGTACGCCTCTCAAAACGCTGGC TTAAGACTACTTGAAAAATGTCACCAGCTAG	1498
	CATTTGCTAACCCCTTT	1499
	AAAGGGGTTAGCAAATG	1500
Trp Overproduction AS *Ruta graveolens* Asp354Asn GAC-AAC	CTTGCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTTGAAA GGCGAACGTTCGCAAACCCATTTGAAATCTATAGATCACTGAGGA TTGTTAATCCAAGCCCATATATGACTTATT	1501
	AATAAGTCATATATGGGCTTGGATTAACAATCCTCAGTGATCTATA GATTTCAAATGGGTTTGCGAACGTTCGCCTTTCAAAACGCTGACTT AGTACGATCTGGAATATGTCACCAGCAAG	1502
	CGTTCGCAAACCCATTT	1503
	AAATGGGTTTGCGAACG	1504
Trp Overproduction AS *Catharanthus roseus* Asp354Asn GAT-AAT	CTGGCTGGGGACATATTCCAGCTTGTCCTAAGTCAGCGTTTTGAA CGGCGAACATTTGCAAATCCATTTGAAGTCTACCGAGCATTGAGA ATTGTCAACCCAAGTCCATATATGACTTATT	1505
	AATAAGTCATATATGGACTTGGGTTGACAATTCTCAATGCTCGGTA GACTTCAAATGGATTTGCAAATGTTCGCCGTTCAAAACGCTGACTT AGGACAAGCTGGAATATGTCCCCAGCCAG	1506
	CATTTGCAAATCCATTT	1507
	AAATGGATTTGCAAATG	1508

Example 10

Production of modified starch in plants

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.

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

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.

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 ADPGPP *Arabidopsis thaliana* Ala99Lys GCA-AAA	GAACTTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGGAGGTGGAAAAGGAACTCGACTCTTTCCTCTCACAAAA CGCCGCGCCAAGCCTGCCGTTCCTATCGGGG	1509
	CCCCGATAGGAACGGCAGGCTTGGCGCGGCGTTTTGTGAGAGGA AAGAGTCGAGTTCCTTTTCCACCTCCAAGAATAATGGAAGCAACT GTCCTTGGATCCCTTTTCTCAGTCTCAAGTTC	1510
	GAGGTGGAAAAGGAACT	1511
	AGTTCCTTTTCCACCTC	1512
Increased Starch ADPGPP *Arabidopsis thaliana* Pro127Leu CCA-CTA	CAAAACGCCGCGCCAAGCCTGCCGTTCCTATCGGGGGAGCCTAT AGGTTGATAGATGTACTAATGAGCAATTGTATTAACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC	1513
	GAGTTATATTGTGTGAGTATGTAGACTTTGTTGATTCCGCTGTTAA TACAATTGCTCATTAGTACATCTATCAACCTATAGGCTCCCCCGAT AGGAACGGCAGGCTTGGCGCGGCGTTTTG	1514
	AGATGTACTAATGAGCA	1515
	TGCTCATTAGTACATCT	1516
Increased Starch ADPGPP *Arabidopsis thaliana* Gly162Asn GGA-AAT	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACTCCAATAATCTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	1517
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAGATTATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	1518
	CTCCAATAATCTTGGCT	1519
	AGCCAAGATTATTGGAG	1520
Increased Starch ADPGPP *Arabidopsis thaliana* Gly162Asn GGA-AAC	TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACTCCAATAACCTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC	1521
	GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAGGTTATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA	1522
	CTCCAATAACCTTGGCT	1523
	AGCCAAGGTTATTGGAG	1524

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Arabidopsis thaliana* Asn100Lys AAT-AAA	GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT TCTAGGAGGAGGCAAAGGAGCTAAACTCTTCCCTCTTACAATGAG AGCCGCAACACCAGCTGTAAATATTCATCTT	1525
	AAGATGAATATTTACAGCTGGTGTTGCGGCTCTCATTGTAAGAGG GAAGAGTTTAGCTCCTTTGCCTCCTCCTAGAATGATTGCAGCCAC ATTTTGCGGGTCTACCTTTCTTCTCTCAAAC	1526
	GGAGGCAAAGGAGCTAA	1527
	TTAGCTCCTTTGCCTCC	1528
Increased Starch ADPGPP *Arabidopsis thaliana* Pro128Leu CCG-CTG	CTTGTGTCTTCAAATTATGTTAGGTTCCTGTTGGTGGATGCTACAG GCTGATCGATATCCTGATGAGTAACTGTATTAACAGCTGCATCAAC AAGATATTTGTGCTGACACAGTTCAACTC	1529
	GAGTTGAACTGTGTCAGCACAAATATCTTGTTGATGCAGCTGTTAA TACAGTTACTCATCAGGATATCGATCAGCCTGTAGCATCCACCAA CAGGAACCTAACATAATTTGAAGACACAAG	1530
	CGATATCCTGATGAGTA	1531
	TACTCATCAGGATATCG	1532
Increased Starch ADPGPP *Arabidopsis thaliana* Gly163Asn GGC-AAT	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAATATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	1533
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC CTCCAAAGTTTATATTATTCCCAAAATAAGTTCGTGCTAAATGTCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	1534
	TGGGAATAATATAAACT	1535
	AGTTTATATTATTCCCA	1536
Increased Starch ADPGPP *Arabidopsis thaliana* Gly163Asn GGC-AAC	TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAACATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC	1537
	GCTGAGAGTTATTATTGTCATAGTGTTTGTACCTCTACGAAACCAC CTCCAAAGTTTATGTTATTCCCAAAATAAGTTCGTGCTAAATGTCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA	1538
	TGGGAATAACATAAACT	1539
	AGTTTATGTTATTCCCA	1540
Increased Starch ADPGPP *Lycopersicon esculentum* Val94Lys GTT-AAA	TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCA TTCTAGGTGGTGGTAAAGGAACTCGTCTTTTTCCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCCTATTGGTGG	1541
	CCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTGTAAGAGGA AAAAGACGAGTTCCTTTACCACCACCTAGAATGACAGAGGCAACA GCTTTTGGATCTGCCGTTGGTTGTTCCTCAA	1542
	TGGTGGTAAAGGAACTC	1543

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTTCCTTTACCACCA	1544
Increased Starch ADPGPP *Lycopersicon esculentum* Pro122Leu CCA-CAA	CAAGCAGAAGAGCTAAACCAGCTGTTCCTATTGGTGGTTGTTACC GGCTAATTGATGTACAAATGAGTAACTGCATTAACAGTGGCATAC GGAAAATTTTCATCTTAACACAGTTCAATTC	1545
	GAATTGAACTGTGTTAAGATGAAAATTTTCCGTATGCCACTGTTAA TGCAGTTACTCATTTGTACATCAATTAGCCGGTAACAACCACCAAT AGGAACAGCTGGTTTAGCTCTTCTGCTTG	1546
	TGATGTACAAATGAGTA	1547
	TACTCATTTGTACATCA	1548
Increased Starch ADPGPP *Lycopersicon esculentum* Gly158Asn GGA-AAT	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGGAAATAATGTGGGTTTTGGAGATGGATTTGTGGAGGTT TTAGCTGCAACCCAGACTCCAGGGGATGC	1549
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACATTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	1550
	TGGAAATAATGTGGGTT	1551
	AACCCACATTATTTCCA	1552
Increased Starch ADPGPP *Lycopersicon esculentum* Gly158Asn GGA-AAC	CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGGAAATAACGTGGGTTTTGGAGATGGATTTGTGGAGGT TTTAGCTGCAACCCAGACTCCAGGGGATGC	1553
	GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACGTTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG	1554
	TGGAAATAACGTGGGTT	1555
	AACCCACGTTATTTCCA	1556
Increased Starch ADPGPP *Cicer arietinum* Ala101Lys GCT-AAA	ACGTAGATTTGGAAAAAAGAGACCCAAGTACAGTTGTAGCAATTAT ACTAGGTGGAGGTAAAGGAACTCGTCTCTTCCCTCTCACCAAGCG ACGAGCCAAGCCTGCTGTTCCAATTGGAGG	1557
	CCTCCAATTGGAACAGCAGGCTTGGCTCGTCGCTTGGTGAGAGG GAAGAGACGAGTTCCTTTACCTCCACCTAGTATAATTGCTACAACT GTACTTGGGTCTCTTTTTTCCAAATCTACGT	1558
	TGGAGGTAAAGGAACTC	1559
	GAGTTCCTTTACCTCCA	1560

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Cicer arietinum* Pro129Leu CCA-CTA	CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA GGCTGATAGATGTACTAATGAGTAACTGCATCAATAGTGGGATCA ACAAAGTATACATTCTCACTCAATTTAATTC	1561
	GAATTAAATTGAGTGAGAATGTATACTTTGTTGATCCCACTATTGA TGCAGTTACTCATTAGTACATCTATCAGCCTATAAGCACCTCCAAT TGGAACAGCAGGCTTGGCTCGTCGCTTGG	1562
	AGATGTACTAATGAGTA	1563
	TACTCATTAGTACATCT	1564
Increased Starch ADPGPP *Cicer arietinum* Gly165Asn GGA-AAT	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAATGTCACTTTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAACTCCAGGGGAGCA	1565
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACATTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	1566
	TGGTACTAATGTCACTT	1567
	AAGTGACATTAGTACCA	1568
Increased Starch ADPGPP *Cicer arietinum* Gly165Asn GGA-AAC	CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAACGTCACTTTTGGAGATGGCTATGTTGAGGTT CTTGCAGCAACTCAAACTCCAGGGGAGCA	1569
	TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACGTTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAAATTGAG	1570
	TGGTACTAACGTCACTT	1571
	AAGTGACGTTAGTACCA	1572
Increased Starch ADPGPP *Ipomoea batatas* Ala94Lys GCA-AAA	ATATTGGAGAGGCGTCGGGCAAACCCTAAGAATGTGGCTGCAATC ATACTGCCAGGCGGTAAAGGGACACACCTATTCCCTCTCACCAAT CGAGCTGCAACCCCTGCTGTTCCACTTGGAG	1573
	CTCCAAGTGGAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGG AATAGGTGTGTCCCTTTACCGCCTGGCAGTATGATTGCAGCCACA TTCTTAGGGTTTGCCCGACGCCTCTCCAATAT	1574
	CAGGCGGTAAAGGGACA	1575
	TGTCCCTTTACCGCCTG	1576
Increased Starch ADPGPP *Ipomoea batatas* Pro122Leu CCA-CTA	CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATA GGTTGATCGACATTCTAATGAGCAACTGCATCAACAGCGGGGTTA ACAAGATCTTTGTGCTGACCCAGTTCAATTC	1577
	GAATTGAACTGGGTCAGCACAAAGATCTTGTTAACCCCGCTGTTG ATGCAGTTGCTCATTAGAATGTCGATCAACCTATAGCATCCTCCAA GTGGAACAGCAGGGGTTGCAGCTCGATTGG	1578
	CGACATTCTAATGAGCA	1579

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTCATTAGAATGTCG	1580
Increased Starch ADPGPP *Ipomoea batatas* Gly157Asn GGT-AAT	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAATAATGTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	1581
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCACATTATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	1582
	TGGCAATAATGTGAGCT	1583
	AGCTCACATTATTGCCA	1584
Increased Starch ADPGPP *Ipomoea batatas* Gly157Asn GGT-AAC	TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAATAACGTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC	1585
	GTTTCCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCACGTTATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA	1586
	TGGCAATAACGTGAGCT	1587
	AGCTCACGTTATTGCCA	1588
Increased Starch ADPGPP *Oryza sativa* Thr96Lys ACC-AAA	CATTCCGGAGGAACTTTGCGGATCCAAATGAGGTTGCTGCTGTTA TATTGGGTGGTGGCAAAGGGACTCAACTTTTTCCTCTCACAAGCA CAAGGGCCACGCCTGCTGTTCCTATTGGAGG	1589
	CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTGTGAGAGG AAAAAGTTGAGTCCCTTTGCCACCACCCAATATAACAGCAGCAAC CTCATTTGGATCCGCAAAGTTCCTCCGGAATG	1590
	TGGTGGCAAAGGGACTC	1591
	GAGTCCCTTTGCCACCA	1592
Increased Starch ADPGPP *Oryza sativa* Pro124Leu CCC-CTC	CAAGCACAAGGGCCACGCCTGCTGTTCCTATTGGAGGATGCTATA GGCTTATCGATATCCTCATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTCATAATGACTCAATTCAACTC	1593
	GAGTTGAATTGAGTCATTATGAATATCTTGTTTATGCCACTGTTGA AACAGTTGCTCATGAGGATATCGATAAGCCTATAGCATCCTCCAAT AGGAACAGCAGGCGTGGCCCTTGTGCTTG	1594
	CGATATCCTCATGAGCA	1595
	TGCTCATGAGGATATCG	1596
Increased Starch ADPGPP *Oryza sativa* Gly159Asn GGA-AAT	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGTAATATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	1597
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGATATTACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	1598

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGGTGGTAATATCAACT	1599
	AGTTGATATTACCACCA	1600
Increased Starch ADPGPP *Oryza sativa* Gly159Asn GGA-AAC	TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGTAACATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC	1601
	GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGATGTTACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA	1602
	TGGTGGTAACATCAACT	1603
	AGTTGATGTTACCACCA	1604
Increased Starch ADPGPP *Triticum aestivum* Thr80Lys ACC-AAA	GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGCGGCAAAGGGACTCAGCTCTTCCCACTCACGAG CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	1605
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCCTTTGCCGCCGCCGAGTATGACGGCCGCAA CCTCGTTCGGATCGCTTAATCCTCCTGAAGGAC	1606
	CGGCGGCAAAGGGACTC	1607
	GAGTCCCTTTGCCGCCG	1608
Increased Starch ADPGPP *Triticum aestivum* Pro108Leu CCC-CTC	CGAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA GGCTCATCGACATTCTCATGAGCAACTGCTTCAACAGTGGCATCA ACAAGATATTCGTCATGACCCAGTTCAACTC	1609
	GAGTTGAACTGGGTCATGACGAATATCTTGTTGATGCCACTGTTG AAGCAGTTGCTCATGAGAATGTCGATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG	1610
	CGACATTCTCATGAGCA	1611
	TGCTCATGAGAATGTCG	1612
Increased Starch ADPGPP *Triticum aestivum* Gly143Asn GGA-AAT	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGGAATATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	1613
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGATATTCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	1614
	CGGCGGGAATATCAATT	1615
	AATTGATATTCCCGCCG	1616
Increased Starch ADPGPP *Triticum aestivum* Gly143Asn GGA-AAC	TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGGAACATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	1617

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGATGTTCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA	1618
	CGGCGGGAACATCAATT	1619
	AATTGATGTTCCCGCCG	1620
Increased Starch ADPGPP *Oryza sativa* Thr95Lys ACT-AAA	CCTCCCGAAAGAATTATGCTGATGCAAGCCACGTTTCTGCTGTCA TTTTGGGTGGAGGCAAAGGAGTTCAACTCTTTCCTCTGACAAGCA CAAGGGCTACCCCCGCTGTTCCTGTTGGAGG	1621
	CCTCCAACAGGAACAGCGGGGGTAGCCCTTGTGCTTGTCAGAGG AAAGAGTTGAACTCCTTTGCCTCCACCCAAAATGACAGCAGAAAC GTGGCTTGCATCAGCATAATTCTTTCGGGAGG	1622
	TGGAGGCAAAGGAGTTC	1623
	GAACTCCTTTGCCTCCA	1624
Increased Starch ADPGPP *Oryza sativa* Pro123Leu CCT-CTT	CAAGCACAAGGGCTACCCCCGCTGTTCCTGTTGGAGGATGTTACA GGCTTATTGACATCCTTATGAGCAATTGCTTCAATAGCGGAATAAA TAAAATATTTGTGATGACTCAGTTCAATTC	1625
	GAATTGAACTGAGTCATCACAAATATTTTATTTATTCCGCTATTGAA GCAATTGCTCATAAGGATGTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTTGTGCTTG	1626
	TGACATCCTTATGAGCA	1627
	TGCTCATAAGGATGTCA	1628
Increased Starch ADPGPP *Oryza sativa* Gly158Asn GGG-AAT	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA TACCTTGGTGGGAATATCAACTTTACTGATGGGTCTGTGCAGGTA TTGGCTGCTACACAAATGCCTGACGAACC	1629
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGATATTCCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA	1630
	TGGTGGGAATATCAACT	1631
	AGTTGATATTCCCACCA	1632
Increased Starch ADPGPP *Oryza sativa* Gly158Asn GGG-AAC	TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA TACCTTGGTGGGAACATCAACTTTACTGATGGGTCTGTGCAGGTA TTGGCTGCTACACAAATGCCTGACGAACC	1633
	GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGATGTTCCCACCAAGGTATGTATGATGGATATGG CGATTAAGAGAAGCAGAATTGAACTGAGTCA	1634
	TGGTGGGAACATCAACT	1635
	AGTTGATGTTCCCACCA	1636

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased Starch ADPGPP *Triticum aestivum* Thr99Lys ACC-AAA	CCTTCCGCAGGAATTACGCCGATCCGAACGAGGTCGCGGCCGTC ATACTCGGCGGTGGCAAAGGGACTCAGCTCTTCCCTCTCACAAG CACAAGGGCCACACCTGCTGTTCCTATTGGAGG	1637
	CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTTGTGAGAGG GAAGAGCTGAGTCCCTTTGCCACCGCCGAGTATGACGGCCGCGA CCTCGTTCGGATCGGCGTAATTCCTGCGGAAGG	1638
	CGGTGGCAAAGGGACTC	1639
	GAGTCCCTTTGCCACCG	1640
Increased Starch ADPGPP *Triticum aestivum* Pro127Leu CCC-CTC	CAAGCACAAGGGCCACACCTGCTGTTCCTATTGGAGGATGTTACA GGCTCATCGATATTCTCATGAGCAACTGCTTCAATAGTGGCATCAA CAAGATATTCGTCATGACGCAGTTCAACTC	1641
	GAGTTGAACTGCGTCATGACGAATATCTTGTTGATGCCACTATTGA AGCAGTTGCTCATGAGAATATCGATGAGCCTGTAACATCCTCCAA TAGGAACAGCAGGTGTGGCCCTTGTGCTTG	1642
	CGATATTCTCATGAGCA	1643
	TGCTCATGAGAATATCG	1644
Increased Starch ADPGPP *Triticum aestivum* Gly162Asn GGA-AAT	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGGAATATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	1645
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGATATTCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	1646
	CGGCGGGAATATCAATT	1647
	AATTGATATTCCCGCCG	1648
Increased Starch ADPGPP *Triticum aestivum* Gly162Asn GGA-AAC	TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGGAACATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC	1649
	GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGATGTTCCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA	1650
	CGGCGGGAACATCAATT	1651
	AATTGATGTTCCCGCCG	1652
Increased Starch ADPGPP *Zea mays* Thr96Lys ACC-AAA	CTTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA TTTTGGGTGGTGGTAAAGGGACTCAGCTTTTCCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCCTATTGGAGG	1653
	CCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTGTGAGAGG GAAAAGCTGAGTCCCTTTACCACCACCCAAAATGACGGCAGCGAC TTCATTAGGATCAGCATAATTCCTCCGAAAAG	1654
	TGGTGGTAAAGGGACTC	1655

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAGTCCCTTTACCACCA	1656
Increased Starch ADPGPP *Zea mays* Pro124Leu CCC-CTC	CAAGCACAAGGGCCACCCCTGCTGTTCCTATTGGAGGATGTTACA GGCTTATTGATATCCTCATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTTGTTATGACTCAGTTCAACTC	1657
	GAGTTGAACTGAGTCATAACAAATATCTTGTTTATGCCACTGTTGA AACAGTTGCTCATGAGGATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGGTGGCCCTTGTGCTTG	1658
	TGATATCCTCATGAGCA	1659
	TGCTCATGAGGATATCA	1660
Increased Starch ADPGPP *Zea mays* Gly159Asn GGG-AAT	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGGAATATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	1661
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGATATTCCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	1662
	TGGTGGGAATATCAACT	1663
	AGTTGATATTCCCACCA	1664
Increased Starch ADPGPP *Zea mays* Gly159Asn GGG-AAC	TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGGAACATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC	1665
	GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGATGTTCCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA	1666
	TGGTGGGAACATCAACT	1667
	AGTTGATGTTCCCACCA	1668
Increased Starch ADPGPP *Solanum tuberosum* Ala58Lys GCG-AAG	CTTGAGAGGCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGGAAAGGGAACTCGTCTTTTCCCCCTCACCAA ACGTCGTGCTAAGCCTGCCGTTCCAATGGGAG	1669
	CTCCCATTGGAACGGCAGGCTTAGCACGACGTTTGGTGAGGGGG AAAAGACGAGTTCCCTTTCCCCCTCCTAGAATGATTGCTACTACTG TCCTTGCATCGCCCTTCTTTTGCCTCTCAAG	1670
	GAGGGGGAAAGGGAACT	1671
	AGTTCCCTTTCCCCCTC	1672
Increased Starch ADPGPP *Solanum tuberosum* Pro86Leu CCA-CTA	CCAAACGTCGTGCTAAGCCTGCCGTTCCAATGGGAGGAGCATATA GGCTAATTGATGTACTAATGAGCAACTGTATTAACAGTGGCATCAA CAAAGTATACATTCTCACTCAATTCAACTC	1673
	GAGTTGAATTGAGTGAGAATGTATACTTTGTTGATGCCACTGTTAA TACAGTTGCTCATTAGTACATCAATTAGCCTATATGCTCCTCCCAT TGGAACGGCAGGCTTAGCACGACGTTTGG	1674

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGATGTACTAATGAGCA	1675
	TGCTCATTAGTACATCA	1676
Increased Starch ADPGPP *Solanum tuberosum* Gly122Asn GGG-AAT	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAATAATGTCACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	1677
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGACATTATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	1678
	TGGCAATAATGTCACAT	1679
	ATGTGACATTATTGCCA	1680
Increased Starch ADPGPP *Solanum tuberosum* Gly122Asn GGG-AAC	CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAATAACGTCACATTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT	1681
	AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGACGTTATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTTAAGTGAGGCTGAGTTGAATTGAG	1682
	TGGCAATAACGTCACAT	1683
	ATGTGACGTTATTGCCA	1684
Increased Starch ADPGPP *Beta vulgaris* Ala98Lys GCT-AAA	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAAAGGGACTCGCCTCTTTCCTCTTACTAGCAG GAGAGCTAAGCCAGCAGTGCCAATTGGAGG	1685
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCCTTTACCACCACCCAGCACAATTGCAGCCACA TTTTTTGGGTCAGCTTTTGGAGATTCAAATA	1686
	TGGTGGTAAAGGGACTC	1687
	GAGTCCCTTTACCACCA	1688
Increased Starch ADPGPP *Beta vulgaris* Ala98Lys GCT-AAC	TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGTAACGGGACTCGCCTCTTTCCTCTTACTAGCAG GAGAGCTAAGCCAGCAGTGCCAATTGGAGG	1689
	CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCCGTTACCACCACCCAGCACAATTGCAGCCAC ATTTTTTGGGTCAGCTTTTGGAGATTCAAATA	1690
	TGGTGGTAACGGGACTC	1691
	GAGTCCCGTTACCACCA	1692
Increased Starch ADPGPP *Beta vulgaris* Pro126Leu CCT-CTT	CTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGGGTGTTAC AGGCTGATTGATGTGCTTATGAGCAACTGCATCAACAGTGGCATT AGAAAGATTTTCATTCTTACCCAGTTCAATTC	1693

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAATTGAACTGGGTAAGAATGAAAATCTTTCTAATGCCACTGTTGA TGCAGTTGCTCATAAGCACATCAATCAGCCTGTAACACCCTCCAA TTGGCACTGCTGGCTTAGCTCTCCTGCTAG	1694
	TGATGTGCTTATGAGCA	1695
	TGCTCATAAGCACATCA	1696
Increased Starch ADPGPP *Beta vulgaris* Gly162Asn GGT-AAT	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAATGTGAATTTTGGGGATGGCTTTGTGGAGGTT TTTGCTGCTACACAAACACCTGGAGAATC	1697
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCACATTATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	1698
	TGGAGATAATGTGAATT	1699
	AATTCACATTATCTCCA	1700
Increased Starch ADPGPP *Beta vulgaris* Gly162Asn GGT-AAC	CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAACGTGAATTTTGGGGATGGCTTTGTGGAGGT TTTTGCTGCTACACAAACACCTGGAGAATC	1701
	GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCACGTTATCTCCAAAATTATAGGTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG	1702
	TGGAGATAACGTGAATT	1703
	AATTCACGTTATCTCCA	1704

Table 21
Oligonucleotides to produce plants with waxy starch

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Arabidopsis thaliana* Ser12Term TCA-TGA	GAATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTT CTTCTAACTTTGTGTGAAGAACTTCACTTTTCAACAATCATGGTGCT TCTTCATGCTCTGATGTCGCTCAGATTAC	1705
	GTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTG AAAAGTGAAGTTCTTCACACAAAGTTAGAAGAAGCAGTCACAGTTG CCATTATGAACTACCCGTTTACCTGGATTC	1706
	CTTTGTGTGAAGAACTT	1707
	AAGTTCTTCACACAAAG	1708
Waxy starch GBSS *Arabidopsis thaliana* Arg13Term AGA-TGA	ATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTT CTAACTTTGTGTCATGAACTTCACTTTTCAACAATCATGGTGCTTCT TCATGCTCTGATGTCGCTCAGATTACCT	1709
	AGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGT TGAAAAGTGAAGTTCATGACACAAAGTTAGAAGAAGCAGTCACAGT TGCCATTATGAACTACCCGTTTACCTGGAT	1710
	TTGTGTCATGAACTTCA	1711
	TGAAGTTCATGACACAA	1712
Waxy starch GBSS *Arabidopsis thaliana* Ser15Term TCA-TGA	TAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTT TGTGTCAAGAACTTGACTTTTCAACAATCATGGTGCTTCTTCATGCT CTGATGTCGCTCAGATTACCTTAAAAGG	1713
	CCTTTTAAGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCAT GATTGTTGAAAAGTCAAGTTCTTGACACAAAGTTAGAAGAAGCAGT CACAGTTGCCATTATGAACTACCCGTTTA	1714
	AAGAACTTGACTTTTCA	1715
	TGAAAAGTCAAGTTCTT	1716
Waxy starch GBSS *Arabidopsis thaliana* Ser24Term TCA-TGA	TGACTGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAAT CATGGTGCTTCTTGATGCTCTGATGTCGCTCAGATTACCTTAAAAG GCCAATCCTTGACTCATTGTGGGTTAAG	1717
	CTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATCTGAG CGACATCAGAGCATCAAGAAGCACCATGATTGTTGAAAAGTGAAG TTCTTGACACAAAGTTAGAAGAAGCAGTCA	1718
	TGCTTCTTGATGCTCTG	1719
	CAGAGCATCAAGAAGCA	1720

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Arabidopsis thaliana* Cys25Term TGC-TGA	TGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATG GTGCTTCTTCATGATCTGATGTCGCTCAGATTACCTTAAAAGGCCA ATCCTTGACTCATTGTGGGTTAAGGTCA	1721
	TGACCTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATC TGAGCGACATCAGATCATGAAGAAGCACCATGATTGTTGAAAAGT GAAGTTCTTGACACAAAGTTAGAAGAAGCA	1722
	TCTTCATGATCTGATGT	1723
	ACATCAGATCATGAAGA	1724
Waxy starch GBSS *Antirrhinum majus* Lys24Term AAA-TAA	GTAACAGCTTCACAGTTGGTGTCACATGTCCATGGTGGAGCAACG TCTTCACCGGATACTTAAACAAACTTGGCCCAGGTTGGCCTCAGG AACCAGCAATTCACTCACAATGGGTTGAGAT	1725
	ATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCTG GGCCAAGTTTGTTTAAGTATCCGGTGAAGACGTTGCTCCACCATG GACATGTGACACCAACTGTGAAGCTGTTAC	1726
	CGGATACTTAAACAAAC	1727
	GTTTGTTTAAGTATCCG	1728
Waxy starch GBSS *Antirrhinum majus* Leu27Term TTG-TAG	CACAGTTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGG ATACTAAAACAAACTAGGCCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAATGGGTTGAGATCAATAAACAT	1729
	ATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGA GGCCAACCTGGGCCTAGTTTGTTTTAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG	1730
	AACAAACTAGGCCCAGG	1731
	CCTGGGCCTAGTTTGTT	1732
Waxy starch GBSS *Antirrhinum majus* Gln29Term CAG-TAG	TTGGTGTCACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT AAAACAAACTTGGCCTAGGTTGGCCTCAGGAACCAGCAATTCACT CACAATGGGTTGAGATCAATAAACATGGTTG	1733
	CAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTT CCTGAGGCCAACCTAGGCCAAGTTTGTTTTAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA	1734
	ACTTGGCCTAGGTTGGC	1735
	GCCAACCTAGGCCAAGT	1736
Waxy starch GBSS *Antirrhinum majus* Gln35Term CAG-TAG	GGTGGAGCAACGTCTTCACCGGATACTAAAACAAACTTGGCCCAG GTTGGCCTCAGGAACTAGCAATTCACTCACAATGGGTTGAGATCA ATAAACATGGTTGATAAGCTTCAAATGAGGA	1737
	TCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTG TGAGTGAATTGCTAGTTCCTGAGGCCAACCTGGGCCAAGTTTGTTT TAGTATCCGGTGAAGACGTTGCTCCACC	1738

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCAGGAACTAGCAATTC	1739
	GAATTGCTAGTTCCTGA	1740
Waxy starch GBSS *Antirrhinum majus* Gln36Term CAA-TAA	GGAGCAACGTCTTCACCGGATACTAAAACAAACTTGGCCCAGGTT GGCCTCAGGAACCAGTAATTCACTCACAATGGGTTGAGATCAATAA ACATGGTTGATAAGCTTCAAATGAGGAACA	1741
	TGTTCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCA TTGTGAGTGAATTACTGGTTCCTGAGGCCAACCTGGGCCAAGTTT GTTTTAGTATCCGGTGAAGACGTTGCTCC	1742
	GGAACCAGTAATTCACT	1743
	AGTGAATTACTGGTTCC	1744
Waxy starch GBSS *Ipomoea batatas* Gly20Term GGA-TGA	GTGATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTG GGGGTGCCACTTCTTGAGAATCAAAAGTGGGGTTGGGTCAATTAG CCCTGAGGAGCCAAGCTGTGACTCACAATG	1745
	CATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACC CCACTTTTGATTCTCAAGAAGTGGCACCCCCACAGACATGAGAAA CAAAGTGTGAGGCAGTTATAGTCGCCATCAC	1746
	CCACTTCTTGAGAATCA	1747
	TGATTCTCAAGAAGTGG	1748
Waxy starch GBSS *Ipomoea batatas* Glu21Term GAA-TAA	ATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGG GTGCCACTTCTGGATAATCAAAAGTGGGGTTGGGTCAATTAGCCC TGAGGAGCCAAGCTGTGACTCACAATGGGT	1749
	ACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCA ACCCCACTTTTGATTATCCAGAAGTGGCACCCCCACAGACATGAG AAACAAAGTGTGAGGCAGTTATAGTCGCCAT	1750
	CTTCTGGATAATCAAAA	1751
	TTTTGATTATCCAGAAG	1752
Waxy starch GBSS *Ipomoea batatas* Ser22Term TCA-TGA	CGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGC CACTTCTGGAGAATGAAAAGTGGGGTTGGGTCAATTAGCCCTGAG GAGCCAAGCTGTGACTCACAATGGGTTGAG	1753
	CTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGA CCCAACCCCACTTTTCATTCTCCAGAAGTGGCACCCCCACAGACAT GAGAAACAAAGTGTGAGGCAGTTATAGTCG	1754
	TGGAGAATGAAAAGTGG	1755
	CCACTTTTCATTCTCCA	1756

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Ipomoea batatas* Lys23Term AAA-TAA	ACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCA CTTCTGGAGAATCATAAGTGGGGTTGGGTCAATTAGCCCTGAGGA GCCAAGCTGTGACTCACAATGGGTTGAGAC	1757
	GTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATT GACCCAACCCCACTTATGATTCTCCAGAAGTGGCACCCCCACAGA CATGAGAAACAAAGTGTGAGGCAGTTATAGT	1758
	GAGAATCATAAGTGGGG	1759
	CCCCACTTATGATTCTC	1760
Waxy starch GBSS *Ipomoea batatas* Leu26Term TTG-TAG	CCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGA ATCAAAAGTGGGGTAGGGTCAATTAGCCCTGAGGAGCCAAGCTGT GACTCACAATGGGTTGAGACCTGTGAACAA	1761
	TTGTTCACAGGTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCA GGGCTAATTGACCCTACCCCACTTTTGATTCTCCAGAAGTGGCACC CCCACAGACATGAGAAACAAAGTGTGAGG	1762
	AGTGGGGTAGGGTCAAT	1763
	ATTGACCCTACCCCACT	1764
Waxy starch GBSS *Astragalus membranaeus* Tyr8Term TAT-TAG	CATCGGCGATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACG GTGACGGGGTCTTAGGTGGTGTCGAGAAGCGCGTGCTTCAATTCC CAGGGAAGAACAGAAGCCAAAGTGAATTCA	1765
	TGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCG CTTCTCGACACCACCTAAGACCCCGTCACCGTTGCCATTCTGTGA GAGAGCAGTAAGGAGCAACAATCGCCGATG	1766
	GGGTCTTAGGTGGTGTC	1767
	GACACCACCTAAGACCC	1768
Waxy starch GBSS *Astragalus membranaeus* Ser11Term TCG-TAG	ATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGG GGTCTTATGTGGTGTAGAGAAGCGCGTGCTTCAATTCCCAGGGAA GAACAGAAGCCAAAGTGAATTCACCTCAGAA	1769
	TTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATTGA AGCACGCGCTTCTCTACACCACATAAGACCCCGTCACCGTTGCCA TTCTGTGAGAGAGCAGTAAGGAGCAACAAT	1770
	TGTGGTGTAGAGAAGCG	1771
	CGCTTCTCTACACCACA	1772

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Astragalus membranaeus* Arg12Term AGA-TGA	TGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGG TCTTATGTGGTGTCGTGAAGCGCGTGCTTCAATTCCCAGGGAAGA ACAGAAGCCAAAGTGAATTCACCTCAGAAGA	1773
	TCTTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTCCCTGGGAATT GAAGCACGCGCTTCACGACACCACATAAGACCCCGTCACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA	1774
	TGGTGTCGTGAAGCGCG	1775
	CGCGCTTCACGACACCA	1776
Waxy starch GBSS *Astragalus membranaeus* Cys15Term TGC-TGA	ACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGT GTCGAGAAGCGCGTGATTCAATTCCCAGGGAAGAACAGAAGCCAA AGTGAATTCACCTCAGAAGATAAATCTCAAT	1777
	ATTGAGATTTATCTTCTGAGGTGAATTCACTTTGGCTTCTGTTCTTC CCTGGGAATTGAATCACGCGCTTCTCGACACCACATAAGACCCCG TCACCGTTGCCATTCTGTGAGAGAGCAGT	1778
	AGCGCGTGATTCAATTC	1779
	GAATTGAATCACGCGCT	1780
Waxy starch GBSS *Astragalus membranaeus* Gln19Term CAG-TAG	CACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTCGAGAAG CGCGTGCTTCAATTCCTAGGGAAGAACAGAAGCCAAAGTGAATTC ACCTCAGAAGATAAATCTCAATAGCCAAGCAT	1781
	ATGCTTGGCTATTGAGATTTATCTTCTGAGGTGAATTCACTTTGGCT TCTGTTCTTCCCTAGGAATTGAAGCACGCGCTTCTCGACACCACAT AAGACCCCGTCACCGTTGCCATTCTGTG	1782
	TCAATTCCTAGGGAAGA	1783
	TCTTCCCTAGGAATTGA	1784
Waxy starch GBSS *Solanum tuberosum* Ser7Term TCA-TGA	TGTAGCTTGGTAGATTCCCCTTTTTGTAGACCACACATCACATGGC AAGCATCACAGCTTGACACCACTTTGTGTCAAGAAGCCAAACTTCA CTAGACACCAAATCAACCTTGTCACAGAT	1785
	ATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTCTTG ACACAAAGTGGTGTCAAGCTGTGATGCTTGCCATGTGATGTGTGG TCTACAAAAAGGGGAATCTACCAAGCTACA	1786
	CACAGCTTGACACCACT	1787
	AGTGGTGTCAAGCTGTG	1788
Waxy starch GBSS *Solanum tuberosum* Ser12Term TCA-TGA	TCCCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC ACACCACTTTGTGTGAAGAAGCCAAACTTCACTAGACACCAAATCA ACCTTGTCACAGATAGGACTCAGGAACCA	1789
	TGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTG AAGTTTGGCTTCTTCACACAAAGTGGTGTGAAGCTGTGATGCTTGC CATGTGATGTGTGGTCTACAAAAAGGGGA	1790

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTTTGTGTGAAGAAGCC	1791
	GGCTTCTTCACACAAAG	1792
Waxy starch GBSS *Solanum tuberosum* Arg13Term AGA-TGA	CCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCAC ACCACTTTGTGTCATGAAGCCAAACTTCACTAGACACCAAATCAAC CTTGTCACAGATAGGACTCAGGAACCATA	1793
	TATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAG TGAAGTTTGGCTTCATGACACAAAGTGGTGTGAAGCTGTGATGCTT GCCATGTGATGTGTGGTCTACAAAAAGGG	1794
	TTGTGTCATGAAGCCAA	1795
	TTGGCTTCATGACACAA	1796
Waxy starch GBSS *Solanum tuberosum* Gln15Term CAA-TAA	TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACT TTGTGTCAAGAAGCTAAACTTCACTAGACACCAAATCAACCTTGTC ACAGATAGGACTCAGGAACCATACTCTGA	1797
	TCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGT GTCTAGTGAAGTTTAGCTTCTTGACACAAAGTGGTGTGAAGCTGTG ATGCTTGCCATGTGATGTGTGGTCTACAA	1798
	CAAGAAGCTAAACTTCA	1799
	TGAAGTTTAGCTTCTTG	1800
Waxy starch GBSS *Solanum tuberosum* Ser17Term TCA-TGA	CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTC AAGAAGCCAAACTTGACTAGACACCAAATCAACCTTGTCACAGATA GGACTCAGGAACCATACTCTGACTCACAA	1801
	TTGTGAGTCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTG ATTTGGTGTCTAGTCAAGTTTGGCTTCTTGACACAAAGTGGTGTGA AGCTGTGATGCTTGCCATGTGATGTGTGG	1802
	CCAAACTTGACTAGACA	1803
	TGTCTAGTCAAGTTTGG	1804
Waxy starch GBSS *Pisum sativum* Gly6Term GGA-TGA	GTCGATCACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAA TGGCAACAATAACGTGATCTTCAATGCCGACGAGAACCGCGTGCT TCAATTACCAAGGAAGATCAGCAGAGTCTA	1805
	TAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGGTTCTCGT CGGCATTGAAGATCACGTTATTGTTGCCATTTTTGTGTCAAAATCT GTTTCGGCGGTGAGAGAAGAGTGATCGAC	1806
	CAATAACGTGATCTTCA	1807
	TGAAGATCACGTTATTG	1808

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Pisum sativum* Ser8Term TCA-TGA	ACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAATGGCAAC AATAACGGGATCTTGAATGCCGACGAGAACCGCGTGCTTCAATTA CCAAGGAAGATCAGCAGAGTCTAAACTGAA	1809
	TTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGG TTCTCGTCGGCATTCAAGATCCCGTTATTGTTGCCATTTTTGTGTCA AAATCTGTTTCGGCGGTGAGAGAAGAGT	1810
	GGGATCTTGAATGCCGA	1811
	TCGGCATTCAAGATCCC	1812
Waxy starch GBSS *Pisum sativum* Arg12Term AGA-TGA	ACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGA TCTTCAATGCCGACGTGAACCGCGTGCTTCAATTACCAAGGAAGA TCAGCAGAGTCTAAACTGAATTTGCCTCAGA	1813
	TCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTTCCTTGGTAATT GAAGCACGCGGTTCACGTCGGCATTGAAGATCCCGTTATTGTTGC CATTTTTGTGTCAAAATCTGTTTCGGCGGT	1814
	TGCCGACGTGAACCGCG	1815
	CGCGGTTCACGTCGGCA	1816
Waxy starch GBSS *Pisum sativum* Cys15Term TGC-TGA	AGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCG ACGAGAACCGCGTGATTCAATTACCAAGGAAGATCAGCAGAGTCT AAACTGAATTTGCCTCAGATACACTTCAAT	1817
	ATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCTGCTGATCTT CCTTGGTAATTGAATCACGCGGTTCTCGTCGGCATTGAAGATCCC GTTATTGTTGCCATTTTTGTGTCAAAATCT	1818
	ACCGCGTGATTCAATTA	1819
	TAATTGAATCACGCGGT	1820
Waxy starch GBSS *Pisum sativum* Tyr18Term TAC-TAG	CACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAAC CGCGTGCTTCAATTAGCAAGGAAGATCAGCAGAGTCTAAACTGAA TTTGCCTCAGATACACTTCAATAACAACCAA	1821
	TTGGTTGTTATTGAAGTGTATCTGAGGCAAATTCAGTTTAGACTCT GCTGATCTTCCTTGCTAATTGAAGCACGCGGTTCTCGTCGGCATTG AAGATCCCGTTATTGTTGCCATTTTTGTG	1822
	TTCAATTAGCAAGGAAG	1823
	CTTCCTTGCTAATTGAA	1824
Waxy starch GBSS *Manihot esculenta* Ser14Term TCA-TGA	TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATT TCGTTTCCAGGAGCTGACACTTGAGCATCCATGCATTAGAGACTAA GGCTAATAATTTGTCTCACACTGGACCCTG	1825
	CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCAT GGATGCTCAAGTGTCAGCTCCTGGAAACGAAATGTGCAGCTATTA CAGTTGCCATGGTGCTCTCTCCGGTGTAGA	1826

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAGGAGCTGACACTTGA	1827
	TCAAGTGTCAGCTCCTG	1828
Waxy starch GBSS *Manihot esculenta* Leu16Term TTG-TAG	CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTCGTTT CCAGGAGCTCACACTAGAGCATCCATGCATTAGAGACTAAGGCTA ATAATTTGTCTCACACTGGACCCTGGACCCA	1829
	TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTA ATGCATGGATGCTCTAGTGTGAGCTCCTGGAAACGAAATGTGCAG CTATTACAGTTGCCATGGTGCTCTCTCCGG	1830
	CTCACACTAGAGCATCC	1831
	GGATGCTCTAGTGTGAG	1832
Waxy starch GBSS *Manihot esculenta* Leu21Term TTA-TGA	TGGCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTT GAGCATCCATGCATGAGAGACTAAGGCTAATAATTTGTCTCACACT GGACCCTGGACCCAAACTATCACTCCCAA	1833
	TTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTA TTAGCCTTAGTCTCTCATGCATGGATGCTCAAGTGTGAGCTCCTGG AAACGAAATGTGCAGCTATTACAGTTGCCA	1834
	CCATGCATGAGAGACTA	1835
	TAGTCTCTCATGCATGG	1836
Waxy starch GBSS *Manihot esculenta* Glu22Term GAG-TAG	GCAACTGTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGA GCATCCATGCATTATAGACTAAGGCTAATAATTTGTCTCACACTGG ACCCTGGACCCAAACTATCACTCCCAATG	1837
	CATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAAT TATTAGCCTTAGTCTATAATGCATGGATGCTCAAGTGTGAGCTCCT GGAAACGAAATGTGCAGCTATTACAGTTGC	1838
	ATGCATTATAGACTAAG	1839
	CTTAGTCTATAATGCAT	1840
Waxy starch GBSS *Manihot esculenta* Lys24Term AAG-TAG	GTAATAGCTGCACATTTCGTTTCCAGGAGCTCACACTTGAGCATCC ATGCATTAGAGACTTAGGCTAATAATTTGTCTCACACTGGACCCTG GACCCAAACTATCACTCCCAATGGTTTAA	1841
	TTAAACCATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAG ACAAATTATTAGCCTAAGTCTCTAATGCATGGATGCTCAAGTGTGA GCTCCTGGAAACGAAATGTGCAGCTATTAC	1842
	TAGAGACTTAGGCTAAT	1843
	ATTAGCCTAAGTCTCTA	1844

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Phaseolus vulgaris* Ser12Term TCA-TGA	ACAACTCCTCCGTCACCGGTATAAGCATGGCAACGGTATCGATGG CATCGTGCGTGGCGTGAAAAGGCGCGTGGAGTACAGAGACAAAA GTGAAATCTTCGGGTCAGATGAGCCTGAACCG	1845
	CGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTAC TCCACGCGCCTTTTCACGCCACGCACGATGCCATCGATACCGTTG CCATGCTTATACCGGTGACGGAGGAGTTGT	1846
	CGTGGCGTGAAAAGGCG	1847
	CGCCTTTTCACGCCACG	1848
Waxy starch GBSS *Phaseolus vulgaris* Trp16Term TGG-TGA	CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGC GTCAAAAGGCGCGTGAAGTACAGAGACAAAAGTGAAATCTTCGGG TCAGATGAGCCTGAACCGTCATGAATTGAAA	1849
	TTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACT TTTGTCTCTGTACTTCACGCGCCTTTTGACGCCACGCACGATGCCA TCGATACCGTTGCCATGCTTATACCGGTG	1850
	GGCGCGTGAAGTACAGA	1851
	TCTGTACTTCACGCGCC	1852
Waxy starch GBSS *Phaseolus vulgaris* Glu19Term GAG-TAG	ATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAA GGCGCGTGGAGTACATAGACAAAAGTGAAATCTTCGGGTCAGATG AGCCTGAACCGTCATGAATTGAAATACGATG	1853
	CATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGA TTTCACTTTTGTCTATGTACTCCACGCGCCTTTTGACGCCACGCAC GATGCCATCGATACCGTTGCCATGCTTAT	1854
	GGAGTACATAGACAAAA	1855
	TTTTGTCTATGTACTCC	1856
Waxy starch GBSS *Phaseolus vulgaris* Lys21Term AAA-TAA	ATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGC GTGGAGTACAGAGACATAAGTGAAATCTTCGGGTCAGATGAGCCT GAACCGTCATGAATTGAAATACGATGGGTTGA	1857
	TCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACC CGAAGATTTCACTTATGTCTCTGTACTCCACGCGCCTTTTGACGCC ACGCACGATGCCATCGATACCGTTGCCAT	1858
	CAGAGACATAAGTGAAA	1859
	TTTCACTTATGTCTCTG	1860
Waxy starch GBSS *Phaseolus vulgaris* Lys23Term AAA-TAA	ACGGTATCGATGGCATCGTGCGTGGCGTCAAAAGGCGCGTGGAG TACAGAGACAAAAGTGTAATCTTCGGGTCAGATGAGCCTGAACCG TCATGAATTGAAATACGATGGGTTGAGATCTC	1861
	GAGATCTCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCAT CTGACCCGAAGATTACACTTTTGTCTCTGTACTCCACGCGCCTTTT GACGCCACGCACGATGCCATCGATACCGT	1862

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAAAAGTGTAATCTTCG	1863
	CGAAGATTACACTTTTG	1864
Waxy starch GBSS *Triticum aestivum* Tyr7Term TAT-TAG	GCGCCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGG GTTCCATTCCTAATTAGTGTTCTTATCAAACAAACAGTGTTGGTTCA CTGAAACTGTCGCCTCACATCCAATTCCAG	1865
	CTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTT TGTTTGATAAGAACACTAATTAGGAATGGAACCCATTGGTGCAGCC TCTCAATGACGACCTTTTCGAGCTAGGCGC	1866
	CCTAATTAGTGTTCTTA	1867
	TAAGAACACTAATTAGG	1868
Waxy starch GBSS *Triticum aestivum* Cys8Term TGT-TGA	CCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTC CATTCCTAATTATTGATCTTATCAAACAAACAGTGTTGGTTCACTGA AACTGTCGCCTCACATCCAATTCCAGCAA	1869
	TTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACT GTTTGTTTGATAAGATCAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTTCGAGCTAGG	1870
	AATTATTGATCTTATCA	1871
	TGATAAGATCAATAATT	1872
Waxy starch GBSS *Triticum aestivum* Tyr10Term TAT-TAG	TCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCC TAATTATTGTTCTTAGCAAACAAACAGTGTTGGTTCACTGAAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT	1873
	ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACC AACACTGTTTGTTTGCTAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCGA	1874
	TGTTCTTAGCAAACAAA	1875
	TTTGTTTGCTAAGAACA	1876
Waxy starch GBSS *Triticum aestivum* Gln11Term CAA-TAA	CGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCCT AATTATTGTTCTTATTAAACAAACAGTGTTGGTTCACTGAAACTGTC GCCTCACATCCAATTCCAGCAATCTTGTA	1877
	TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAAC CAACACTGTTTGTTTAATAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCG	1878
	GTTCTTATTAAACAAAC	1879
	GTTTGTTTAATAAGAAC	1880

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum aestivum* Ser17Term TCA-TGA	AGGCTGCACCAATGGGTTCCATTCCTAATTATTGTTCTTATCAAACA AACAGTGTTGGTTGACTGAAACTGTCGCCTCACATCCAATTCCAGC AATCTTGTAACAATGAAGTTATGTTCCT	1881
	AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAG GCGACAGTTTCAGTCAACCAACACTGTTTGTTTGATAAGAACAATA ATTAGGAATGGAACCCATTGGTGCAGCCT	1882
	TGTTGGTTGACTGAAAC	1883
	GTTTCAGTCAACCAACA	1884
Waxy starch GBSS *Triticum aestivum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCCGGAGCCCGGCG GATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA	1885
	TAGCTCCGACGGTCCTCATGCCGAGAGCCGCATCCGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	1886
	CAGGTTTCTAGGGCGTG	1887
	CACGCCCTAGAAACCTG	1888
Waxy starch GBSS *Triticum aestivum* Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCCGGAGCCCGGCGGATGCGGCTCT CGGCATGAGGACCGTCTGAGCTAGCGCCGCCCCAACGCAAAGCC GGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT	1889
	AGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGCGTT GGGGCGGCGCTAGCTCAGACGGTCCTCATGCCGAGAGCCGCATC CGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	1890
	GGACCGTCTGAGCTAGC	1891
	GCTAGCTCAGACGGTCC	1892
Waxy starch GBSS *Triticum aestivum* Gln53Term CAA-TAA	CGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAG CTAGCGCCGCCCCAACGTAAAGCCGGAAAGCGCACCGCGGGACC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCG	1893
	CGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTACGTTGGGGCGGCGCTAGCTCCGACGG TCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCG	1894
	CCCCAACGTAAAGCCGG	1895
	CCGGCTTTACGTTGGGG	1896
Waxy starch GBSS *Triticum aestivum* Lys56Term AAA-TAA	GCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGC CCCAACGCAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCG	1897
	CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGCGTTGGGGCGGCGCTAG CTCCGACGGTCCTCATGCCGAGAGCCGCATCCGC	1898

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAGCCGGTAAGCGCAC	1899
	GTGCGCTTACCGGCTTT	1900
Waxy starch GBSS *Triticum aestivum* Glu85Term GAG-TAG	CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCGGCATGAACCT CGTGTTCGTCGGCGCCTAGATGGCGCCCTGGAGCAAGACCGGCG GCCTCGGCGACGTCCTCGGGGGCCTCCCCCCAG	1901
	CTGGGGGGAGGCCCCCGAGGACGTCGCCGAGGCCGCCGGTCTT GCTCCAGGGCGCCATCTAGGCGCCGACGAACACGAGGTTCATGC CGCCGCTGCCGGTGGCGCGCACCACCATGGAGAG	1902
	TCGGCGCCTAGATGGCG	1903
	CGCCATCTAGGCGCCGA	1904
Waxy starch GBSS *Triticum aestivum* Gln8Term CAG-TAG	GTCGTCTCTCGCTGCAGGTAGCCACACCCTGCGCGCGCGATGGC GGCTCTGGTCACGTCGTAGCTCGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGCAGGTTTTC	1905
	GAAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCTACGACGTGACCAGAGCCGCCATCGCGC GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC	1906
	TCACGTCGTAGCTCGCC	1907
	GGCGAGCTACGACGTGA	1908
Waxy starch GBSS *Triticum aestivum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTTTTAGGGTGTGAGGCCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	1909
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	1910
	CAGGTTTTTAGGGTGTG	1911
	CACACCCTAAAAACCTG	1912
Waxy starch GBSS *Triticum aestivum* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGG AGCGAGCGCCGCCCCGTAGCAACAAAGCCGGAAAGCGCACCGCG GGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	1913
	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGGTAGTCCT CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	1914
	CCGCCCCGTAGCAACAA	1915
	TTGTTGCTACGGGGCGG	1916

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum aestivum* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	1917
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	1918
	CCCCGAAGTAACAAAGC	1919
	GCTTTGTTACTTCGGGG	1920
Waxy starch GBSS *Triticum aestivum* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAG CGCCGCCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	1921
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGGT AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	1922
	CGAAGCAATAAAGCCGG	1923
	CCGGCTTTATTGCTTCG	1924
Waxy starch GBSS *Triticum durum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCCGGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA	1925
	TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	1926
	CAGGTTTCTAGGGCGTG	1927
	CACGCCCTAGAAACCTG	1928
Waxy starch GBSS *Triticum durum* Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCCGTAGCAAAGCCGGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	1929
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCGGTG CGCTTTCCGGCTTTGCTACGGGGCGGCGCTCGCTCCGATAGTCCT CATGACGAGGGCCGCATCCGCCGGGTTCCGGGG	1930
	CCGCCCCGTAGCAAAGC	1931
	GCTTTGCTACGGGGCGG	1932
Waxy starch GBSS *Triticum durum* Gln53Term CAA-TAA	CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCCGAAGTAAAGCCGGAAAGCGCACCGCGGGAGC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	1933
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGCTCCCGCG GTGCGCTTTCCGGCTTTACTTCGGGGCGGCGCTCGCTCCGATAGT CCTCATGACGAGGGCCGCATCCGCCGGGTTCCG	1934

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCCCGAAGTAAAGCCGG	1935
	CCGGCTTTACTTCGGGG	1936
Waxy starch GBSS *Triticum durum* Lys56Term AAA-TAA	GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC CCCGAAGCAAAGCCGGTAAGCGCACCGCGGGAGCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCG	1937
	CGCCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCG GCTCCCGCGGTGCGCTTACCGGCTTTGCTTCGGGGCGGCGCTCG CTCCGATAGTCCTCATGACGAGGGCCGCATCCGC	1938
	AAAGCCGGTAAGCGCAC	1939
	GTGCGCTTACCGGCTTT	1940
Waxy starch GBSS *Triticum durum* Cys64Term TGC-TGA	TATCGGAGCGAGCGCCGCCCCGAAGCAAAGCCGGAAAGCGCACC GCGGGAGCCGGCGGTGACTCTCCATGGTGGTGCGCGCCACGGG CAGCGGCGGCATGAACCTCGTGTTCGTCGGCGCC	1941
	GGCGCCGACGAACACGAGGTTCATGCCGCCGCTGCCCGTGGCGC GCACCACCATGGAGAGTCACCGCCGGCTCCCGCGGTGCGCTTTC CGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATA	1942
	CGGCGGTGACTCTCCAT	1943
	ATGGAGAGTCACCGCCG	1944
Waxy starch GBSS *Triticum turgidum* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTTTTAGGGTGTGAGGCCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA	1945
	TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	1946
	CAGGTTTTTAGGGTGTG	1947
	CACACCCTAAAAACCTG	1948
Waxy starch GBSS *Triticum turgidum* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGG AGCGAGCGCCGCCCCGTAGCAACAAAGCCGGAAAGCGCACCGCG GGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG	1949
	CGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGGTAGTCCT CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	1950
	CCGCCCCGTAGCAACAA	1951
	TTGTTGCTACGGGGCGG	1952

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Triticum turgidum* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA	1953
	TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	1954
	CCCCGAAGTAACAAAGC	1955
	GCTTTGTTACTTCGGGG	1956
Waxy starch GBSS *Triticum turgidum* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAG CGCCGCCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG	1957
	CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGGT AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	1958
	CGAAGCAATAAAGCCGG	1959
	CCGGCTTTATTGCTTCG	1960
Waxy starch GBSS *Triticum turgidum* Lys57Term AAA-TAA	GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCC GAAGCAACAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCG	1961
	CGGCGCTGCCCGTGGCGCGCACCACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGTTGCTTCGGGGCGGCGC TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATC	1962
	AAAGCCGGTAAGCGCAC	1963
	GTGCGCTTACCGGCTTT	1964
Waxy starch GBSS *Aegilops speltoides* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGCCACCGTCCTCGGCATCACCGACAGGTTC CGCCATGCAGGTTTCTAGGGCGTGAGGCCCCGGAGCCCGGCAGA TGCGCCGCTCGGCATGAGGACTGTCGGAGCGA	1965
	TCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCATGGCGGAACCTGTCGGT GATGCCGAGGACGGTGGCGGAGGTGGCGAGCTG	1966
	CAGGTTTCTAGGGCGTG	1967
	CACGCCCTAGAAACCTG	1968
Waxy starch GBSS *Aegilops speltoides* Gly46Term GGA-TGA	GGTTTCCAGGGCGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCT CGGCATGAGGACTGTCTGAGCGAGCGCCGCCCCGAAGCAACAAA GCCGGAAAGCGCACCGCGGGACCCGGCGGTGCC	1969
	GGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTTC GGGGCGGCGCTCGCTCAGACAGTCCTCATGCCGAGCGGCGCATC TGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC	1970

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GGACTGTCTGAGCGAGC	1971
	GCTCGCTCAGACAGTCC	1972
Waxy starch GBSS *Aegilops speltoides* Lys52Term AAG-TAG	CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGG AGCGAGCGCCGCCCCGTAGCAACAAAGCCGGAAAGCGCACCGCG GGACCCGGCGGTGCCTCTCGATGGTGGTGCGCG	1973
	CGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTGCGCT TTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGACAGTCCTC ATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG	1974
	CCGCCCCGTAGCAACAA	1975
	TTGTTGCTACGGGGCGG	1976
Waxy starch GBSS *Aegilops speltoides* Gln53Term CAA-TAA	CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCGATGGTGGTGCGCGCCA	1977
	TGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGACAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG	1978
	CCCCGAAGTAACAAAGC	1979
	GCTTTGTTACTTCGGGG	1980
Waxy starch GBSS *Aegilops speltoides* Gln54Term CAA-TAA	AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGAG CGCCGCCCCGAAGCAATAAAGCCGGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCGATGGTGGTGCGCGCCACCG	1981
	CGGTGGCGCGCACCACCATCGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGAC AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT	1982
	CGAAGCAATAAAGCCGG	1983
	CCGGCTTTATTGCTTCG	1984
Waxy starch GBSS *Oryza glaberrima* Gln8Term CAG-TAG	AGTGCAGAGATCTTCCACAGCAACAGCTAGACAACCACCATGTCG GCTCTCACCACGTCCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCTGACAGGTCGGCGCCGTCGTCGCTGC	1985
	GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTTGTCTAGCTGTTGCTGTGGAAGATCTCTGCACT	1986
	CCACGTCCTAGCTCGCC	1987
	GGCGAGCTAGGACGTGG	1988

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Oryza glaberrima* Ser12Term TCG-TAG	TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCTGACAGG TCGGCGCCGTCGTCGCTGCTCCGCCACGGGTT	1989
	AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA	1990
	CGCCACCTAGGCCACCG	1991
	CGGTGGCCTAGGTGGCG	1992
Waxy starch GBSS *Oryza glaberrima* Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGTAGGCGCCGTCGTCGCTGCTCCGCCACGG GTTCCAGGGCCTCAAGCCCCGCAGCCCCGCCGG	1993
	CCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACCCGTGGCGGA GCAGCGACGACGGCGCCTACCTGTCAGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	1994
	TGACAGGTAGGCGCCGT	1995
	ACGGCGCCTACCTGTCA	1996
Waxy starch GBSS *Oryza glaberrima* Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTCGGCGCCGTAGTCGCTGCTCCGCCACGGGTTCCAGGG CCTCAAGCCCCGCAGCCCCGCCGGCGGCGACGC	1997
	GCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACC CGTGGCGGAGCAGCGACTACGGCGCCGACCTGTCAGCGATGCCG AAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	1998
	GGCGCCGTAGTCGCTGC	1999
	GCAGCGACTACGGCGCC	2000
Waxy starch GBSS *Oryza glaberrima* Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTCGGCGCCGTCGTAGCTGCTCCGCCACGGGTTCCAGGGCCT CAAGCCCCGCAGCCCCGCCGGCGGCGACGCGAC	2001
	GTCGCGTCGCCGCCGGCGGGGCTGCGGGGCTTGAGGCCCTGGA ACCCGTGGCGGAGCAGCTACGACGGCGCCGACCTGTCAGCGATG CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	2002
	GCCGTCGTAGCTGCTCC	2003
	GGAGCAGCTACGACGGC	2004
Waxy starch GBSS *Oryza sativa* Gln8Term CAG-TAG	TCCACAGCAAGAGCTAAACAGCCGACCGTGTGCACCACCATGTCG GCTCTCACCACGTCCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCCGACAGGTCGGCGCCGTCGTCGCTGC	2005
	GCAGCGACGACGGCGCCGACCTGTCGGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTGCACACGGTCGGCTGTTTAGCTCTTGCTGTGGA	2006

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACGTCCTAGCTCGCC	2007
	GGCGAGCTAGGACGTGG	2008
Waxy starch GBSS *Oryza sativa* Ser12Term TCG-TAG	CTAAACAGCCGACCGTGTGCACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCCGACAGG TCGGCGCCGTCGTCGCTGCTTCGCCACGGGTT	2009
	AACCCGTGGCGAAGCAGCGACGACGGCGCCGACCTGTCGGCGAT GCCGAAGCCGGTGGCCTAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTGCACACGGTCGGCTGTTTAG	2010
	CGCCACCTAGGCCACCG	2011
	CGGTGGCCTAGGTGGCG	2012
Waxy starch GBSS *Oryza sativa* Ser22Term TCG-TAG	CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCCGACAGGTAGGCGCCGTCGTCGCTGCTTCGCCACGG GTTCCAGGGCCTCAAGCCCCGTAGCCCAGCCGG	2013
	CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAA GCAGCGACGACGGCGCCTACCTGTCGGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG	2014
	CGACAGGTAGGCGCCGT	2015
	ACGGCGCCTACCTGTCG	2016
Waxy starch GBSS *Oryza sativa* Ser25Term TCG-TAG	CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCC GACAGGTCGGCGCCGTAGTCGCTGCTTCGCCACGGGTTCCAGGG CCTCAAGCCCCGTAGCCCAGCCGGCGGGGACGC	2017
	GCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCC GTGGCGAAGCAGCGACTACGGCGCCGACCTGTCGGCGATGCCGA AGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG	2018
	GGCGCCGTAGTCGCTGC	2019
	GCAGCGACTACGGCGCC	2020
Waxy starch GBSS *Oryza sativa* Ser26Term TCG-TAG	CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGAC AGGTCGGCGCCGTCGTAGCTGCTTCGCCACGGGTTCCAGGGCCT CAAGCCCCGTAGCCCAGCCGGCGGGGACGCATC	2021
	GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA CCCGTGGCGAAGCAGCTACGACGGCGCCGACCTGTCGGCGATGC CGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG	2022
	GCCGTCGTAGCTGCTTC	2023
	GAAGCAGCTACGACGGC	2024

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Hordeum vulgare* Gln8Term CAG-TAG	GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCATGGC GGCTCTGGCCACGTCCTAGCTCGCCACCTCCGGCACCGTCCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTTC	2025
	GAAAACCTGGACGCCGGAATCTGTCGGTGACGCCGAGGACGGTG CCGGAGGTGGCGAGCTAGGACGTGGCCAGAGCCGCCATGGCGC CGCGCACAGGGTGTGGCTACCTGCAGTGAGAGAC	2026
	CCACGTCCTAGCTCGCC	2027
	GGCGAGCTAGGACGTGG	2028
Waxy starch GBSS *Hordeum vulgare* Arg21Term AGA-TGA	ATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACCGT CCTCGGCGTCACCGACTGATTCCGGCGTCCAGGTTTTCAGGGCCT CAGGCCCCGGAACCCGGCGGATGCGGCGCTTG	2029
	CAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAA CCTGGACGCCGGAATCAGTCGGTGACGCCGAGGACGGTGCCGG AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT	2030
	TCACCGACTGATTCCGG	2031
	CCGGAATCAGTCGGTGA	2032
Waxy starch GBSS *Hordeum vulgare* Gln28Term CAG-TAG	CAGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATT CCGGCGTCCAGGTTTTTAGGGCCTCAGGCCCCGGAACCCGGCGG ATGCGGCGCTTGGTATGAGGACTATCGGAGCAA	2033
	TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCC GGGGCCTGAGGCCCTAAAAACCTGGACGCCGGAATCTGTCGGTG ACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG	2034
	CAGGTTTTTAGGGCCTC	2035
	GAGGCCCTAAAAACCTG	2036
Waxy starch GBSS *Hordeum vulgare* Gly46Term GGA-TGA	GGTTTTCAGGGCCTCAGGCCCCGGAACCCGGCGGATGCGGCGCT TGGTATGAGGACTATCTGAGCAAGCGCCGCCCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT	2037
	AGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTC GGGGCGGCGCTTGCTCAGATAGTCCTCATACCAAGCGCCGCATC CGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACC	2038
	GGACTATCTGAGCAAGC	2039
	GCTTGCTCAGATAGTCC	2040
Waxy starch GBSS *Hordeum vulgare* Lys52Term AAG-TAG	CCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGG AGCAAGCGCCGCCCCGTAGCAAAGCCGGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGAGCGCCA	2041
	TGGCGCTCACCACCACGGAGAGGCACCGCCGGCTCCCGCGGTGC GCTTTCCGGCTTTGCTACGGGGCGGCGCTTGCTCCGATAGTCCTC ATACCAAGCGCCGCATCCGCCGGGTTCCGGGG	2042

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCGCCCCGTAGCAAAGC	2043
	GCTTTGCTACGGGGCGG	2044
Waxy starch GBSS *Zea mays* Gln8Term CAG-TAG	ACGTCTTTTCTCTCTCTCCTACGCAGTGGATTAATCGGCATGGCGG CTCTGGCCACGTCGTAGCTCGTCGCAACGCGCGCCGGCCTGGGC GTCCCGGACGCGTCCACGTTCCGCCGCGGCG	2045
	CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGC GCGCGTTGCGACGAGCTACGACGTGGCCAGAGCCGCCATGCCGA TTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT	2046
	CCACGTCGTAGCTCGTC	2047
	GACGAGCTACGACGTGG	2048
Waxy starch GBSS *Zea mays* Gln30Term CAG-TAG	GTCGCAACGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGTT CCGCCGCGGCGCCGCGTAGGGCCTGAGGGGGGCCCGGGCGTCG GCGGCGGCGGACACGCTCAGCATGCGGACCAGCG	2049
	CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGCCCGG GCCCCCCTCAGGCCCTACGCGGCGCCGCGGCGGAACGTGGACG CGTCCGGGACGCCCAGGCCGGCGCGCGTTGCGAC	2050
	GCGCCGCGTAGGGCCTG	2051
	CAGGCCCTACGCGGCGC	2052
Waxy starch GBSS *Zea mays* Ser38Term TCG-TAG	TCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCGCAGGGCCT GAGGGGGGCCCGGGCGTAGGCGGCGGCGGACACGCTCAGCATG CGGACCAGCGCGCGCGCGGCGCCCAGGCACCAGCA	2053
	TGCTGGTGCCTGGGCGCCGCGCGCGCGCTGGTCCGCATGCTGAG CGTGTCCGCCGCCGCCTACGCCCGGGCCCCCCTCAGGCCCTGCG CGGCGCCGCGGCGGAACGTGGACGCGTCCGGGA	2054
	CCGGGCGTAGGCGGCGG	2055
	CCGCCGCCTACGCCCGG	2056
Waxy starch GBSS *Zea mays* Ser57Term CAG-TAG	GCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGC GCGCGGCGCCCAGGCACTAGCAGCAGGCGCGCCGCGGGGGCAG GTTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCA	2057
	TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCCCC GCGGCGCGCCTGCTGCTAGTGCCTGGGCGCCGCGCGCGCGCTG GTCCGCATGCTGAGCGTGTCCGCCGCCGCCGACGC	2058
	CCAGGCACTAGCAGCAG	2059
	CTGCTGCTAGTGCCTGG	2060

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Waxy starch GBSS *Zea mays* Gln58Term CAG-TAG	TCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCG CGGCGCCCAGGCACCAGTAGCAGGCGCGCCGCGGGGGCAGGTT CCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGA	2061
	TCATGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCC CCGCGGCGCGCCTGCTACTGGTGCCTGGGCGCCGCGCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGA	2062
	GGCACCAGTAGCAGGCG	2063
	CGCCTGCTACTGGTGCC	2064

Example 11

Altering fatty acid content of plants

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.

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.

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.

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 Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser8Term TCG-TAG	TTTGGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGTAGTCATTCTTTCCTGTACCATCTTCTTCACTTG ATCCTAATGGAAAAGGCAATAAGATTGG	2065
	CCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGACTACGTAGCAGAGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAAA	2066

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGCTACGTAGTCATTCT	2067
	AGAATGACTACGTAGCA	2068
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser9Term TCA-TGA	GGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGCCA CCTCTGCTACGTCGTGATTCTTTCCTGTACCATCTTCTTCACTTGAT CCTAATGGAAAAGGCAATAAGATTGGGTC	2069
	GACCCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATG GTACAGGAAAGAATCACGACGTAGCAGAGGTGGCCACCATGACG AGGAGATGAAGCGTTCAAAGACACTGCCACC	2070
	TACGTCGTGATTCTTTC	2071
	GAAAGAATCACGACGTA	2072
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Ser17Term TCA-TGA	ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCATTCTTTCC TGTACCATCTTCTTGACTTGATCCTAATGGAAAAGGCAATAAGATT GGGTCTACGAATCTTGCTGGACTCAATTC	2073
	GAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTC CATTAGGATCAAGTCAAGAAGATGGTACAGGAAAGAATGACGACG TAGCAGAGGTGGCCACCATGACGAGGAGAT	2074
	ATCTTCTTGACTTGATC	2075
	GATCAAGTCAAGAAGAT	2076
Reduced palmitate Acyl-ACP-thioesterase *Arabidopsis thaliana* Gly22Term GGA-TGA	GTGGCCACCTCTGCTACGTCGTCATTCTTTCCTGTACCATCTTCTT CACTTGATCCTAATTGAAAAGGCAATAAGATTGGGTCTACGAATCT TGCTGGACTCAATTCTGCACCTAACTCTG	2077
	CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATTCGTAGACCCAA TCTTATTGCCTTTTCAATTAGGATCAAGTGAAGAAGATGGTACAGG AAAGAATGACGACGTAGCAGAGGTGGCCAC	2078
	ATCCTAATTGAAAAGGC	2079
	GCCTTTTCAATTAGGAT	2080
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Ser8Term TCA-TGA	GCTTGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGC TACTGCCGCCACGTGATCATTCTTTCCGTTGACTTCCCCTTCTGGG GATGCCAAATCGGGCAATCCCGGAAAAGG	2081
	CCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAAGTC AACGGAAAGAATGATCACGTGGCGGCAGTAGCAACCATTGTGGCC ACAATTAACCAATCAGATCACAAATTCAAGC	2082
	CGCCACGTGATCATTCT	2083
	AGAATGATCACGTGGCG	2084

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Ser9Term TCA-TGA	TGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTAC TGCCGCCACGTCATGATTCTTTCCGTTGACTTCCCCTTCTGGGGAT GCCAAATCGGGCAATCCCGGAAAAGGGTC	2085
	GACCCTTTTCCGGGATTGCCCGATTTGGCATCCCCAGAAGGGGAA GTCAACGGAAAGAATCATGACGTGGCGGCAGTAGCAACCATTGTG GCCACAATTAACCAATCAGATCACAAATTCA	2086
	CACGTCATGATTCTTTC	2087
	GAAAGAATCATGACGTG	2088
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Leu13Term TTG-TAG	CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT CATCATTCTTTCCGTAGACTTCCCCTTCTGGGGATGCCAAATCGGG CAATCCCGGAAAAGGGTCGGTGAGTTTTGG	2089
	CCAAAACTCACCGACCCTTTTCCGGGATTGCCCGATTTGGCATCC CCAGAAGGGGAAGTCTACGGAAAGAATGATGACGTGGCGGCAGT AGCAACCATTGTGGCCACAATTAACCAATCAG	2090
	CTTTCCGTAGACTTCCC	2091
	GGGAAGTCTACGGAAAG	2092
Reduced palmitate Acyl-ACP-thioesterase *Garcinia mangostana* Lys21Term AAA-TAA	ATGGTTGCTACTGCCGCCACGTCATCATTCTTTCCGTTGACTTCCC CTTCTGGGGATGCCTAATCGGGCAATCCCGGAAAAGGGTCGGTG AGTTTTGGGTCAATGAAGTCGAAATCCGCGG	2093
	CCGCGGATTTCGACTTCATTGACCCAAAACTCACCGACCCTTTTCC GGGATTGCCCGATTAGGCATCCCCAGAAGGGGAAGTCAACGGAA AGAATGATGACGTGGCGGCAGTAGCAACCAT	2094
	GGGATGCCTAATCGGGC	2095
	GCCCGATTAGGCATCCC	2096
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser8Term TCG-TAG	GGGATTTCAGCACGAAATTGAAGTTGTTTTTAAAAACCATGGTTGC TACTGCTGTGACATAGGCGTTTTTCCCAGTCACTTCTTCACCTGAC TCCTCTGACTCGAAAAACAAGAAGCTCGG	2097
	CCGAGCTTCTTGTTTTTCGAGTCAGAGGAGTCAGGTGAAGAAGTG ACTGGGAAAAACGCCTATGTCACAGCAGTAGCAACCATGGTTTTTA AAAACAACTTCAATTTCGTGCTGAAATCCC	2098
	TGTGACATAGGCGTTTT	2099
	AAAACGCCTATGTCACA	2100
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser16Term TCA-TGA	TGTTTTTAAAAACCATGGTTGCTACTGCTGTGACATCGGCGTTTTT CCCAGTCACTTCTTGACCTGACTCCTCTGACTCGAAAAACAAGAAG CTCGGAAGCATCAAGTCGAAGCCATCGGT	2101
	ACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTCGAGT CAGAGGAGTCAGGTCAAGAAGTGACTGGGAAAAACGCCGATGTCA CAGCAGTAGCAACCATGGTTTTTAAAAACA	2102

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CACTTCTTGACCTGACT	2103
	AGTCAGGTCAAGAAGTG	2104
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Ser22Term TCG-TAG	TTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACC TGACTCCTCTGACTAGAAAAACAAGAAGCTCGGAAGCATCAAGTC GAAGCCATCGGTTTCTTCTGGAAGTTTGCA	2105
	TGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCG AGCTTCTTGTTTTTCTAGTCAGAGGAGTCAGGTGAAGAAGTGACTG GGAAAAACGCCGATGTCACAGCAGTAGCAA	2106
	CTCTGACTAGAAAAACA	2107
	TGTTTTTCTAGTCAGAG	2108
Reduced palmitate Acyl-ACP-thioesterase *Gossypium hirsutum* Lys23Term AAA-TAA	GCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTG ACTCCTCTGACTCGTAAAACAAGAAGCTCGGAAGCATCAAGTCGA AGCCATCGGTTTCTTCTGGAAGTTTGCAAG	2109
	CTTGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCC GAGCTTCTTGTTTTACGAGTCAGAGGAGTCAGGTGAAGAAGTGAC TGGGAAAAACGCCGATGTCACAGCAGTAGC	2110
	CTGACTCGTAAAACAAG	2111
	CTTGTTTTACGAGTCAG	2112
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Ser14Term TCG-TAG	CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTG CATTCTTCCCCGTGTAGTCCCCGGTCACCTCCTCTAGACCAGGAA AGCCCGGAAATGGGTCATCGAGCTTCAGCCC	2113
	GGGCTGAAGCTCGATGACCCATTTCCGGGCTTTCCTGGTCTAGAG GAGGTGACCGGGGACTACACGGGGAAGAATGCAGAGCTTGCAGC GGTAGCCACCATTGTCTTTCAACGAGCGGGAG	2114
	CCCCGTGTAGTCCCCGG	2115
	CCGGGGACTACACGGGG	2116
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Arg21Term AGA-TGA	ATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCC CCGGTCACCTCCTCTTGACCAGGAAAGCCCGGAAATGGGTCATCG AGCTTCAGCCCCATCAAGCCCAAATTTGTCG	2117
	CGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTC CGGGCTTTCCTGGTCAAGAGGAGGTGACCGGGGACGACACGGG GAAGAATGCAGAGCTTGCAGCGGTAGCCACCAT	2118
	CCTCCTCTTGACCAGGA	2119
	TCCTGGTCAAGAGGAGG	2120

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Gly23Term GGA-TGA	GCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTC ACCTCCTCTAGACCATGAAAGCCCGGAAATGGGTCATCGAGCTTC AGCCCCATCAAGCCCAAATTTGTCGCCAATG	2121
	CATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACC CATTTCCGGGCTTTCATGGTCTAGAGGAGGTGACCGGGGACGAC ACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC	2122
	CTAGACCATGAAAGCCC	2123
	GGGCTTTCATGGTCTAG	2124
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys24Term AAG-TAG	ACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACC TCCTCTAGACCAGGATAGCCCGGAAATGGGTCATCGAGCTTCAGC CCCATCAAGCCCAAATTTGTCGCCAATGGCG	2125
	CGCCATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATG ACCCATTTCCGGGCTATCCTGGTCTAGAGGAGGTGACCGGGGAC GACACGGGGAAGAATGCAGAGCTTGCAGCGGT	2126
	GACCAGGATAGCCCGGA	2127
	TCCGGGCTATCCTGGTC	2128
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Gly23Term GGA-TGA	GCCACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGAC ACCTCCTCTAGGCCGTGAAAGCTCGGAAATGGGTCATCGAGCTTG AGCCCCCTCAAGCCCAAATTTGTCGCCAATG	2129
	CATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACC CATTTCCGAGCTTTCACGGCCTAGAGGAGGTGTCCGGGGACGGC AGGGGGAAGAATGCAGAACTTGCAGCGGTGGC	2130
	CTAGGCCGTGAAAGCTC	2131
	GAGCTTTCACGGCCTAG	2132
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Lys24Term AAG-TAG	ACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACC TCCTCTAGGCCGGGATAGCTCGGAAATGGGTCATCGAGCTTGAGC CCCCTCAAGCCCAAATTTGTCGCCAATGCCG	2133
	CGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGAT GACCCATTTCCGAGCTATCCCGGCCTAGAGGAGGTGTCCGGGGA CGGCAGGGGGAAGAATGCAGAACTTGCAGCGGT	2134
	GGCCGGGATAGCTCGGA	2135
	TCCGAGCTATCCCGGCC	2136
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Gly26Term GGA-TGA	GCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCT AGGCCGGGAAAGCTCTGAAATGGGTCATCGAGCTTGAGCCCCCT CAAGCCCAAATTTGTCGCCAATGCCGGGTTGA	2137
	TCAACCCGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGC TCGATGACCCATTTCAGAGCTTTCCCGGCCTAGAGGAGGTGTCCG GGGACGGCAGGGGGAAGAATGCAGAACTTGC	2138

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GAAAGCTCTGAAATGGG	2139
	CCCATTTCAGAGCTTTC	2140
Reduced palmitate Acyl-ACP-thioesterase *Cuphea lanceolata* Ser29Term TCA-TGA	CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAA AGCTCGGAAATGGGTGATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGGTTGAAGGTTAAGGC	2141
	GCCTTAACCTTCAACCCGGCATTGGCGACAAATTTGGGCTTGAGG GGGCTCAAGCTCGATCACCCATTTCCGAGCTTTCCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGGAAGAATG	2142
	AAATGGGTGATCGAGCT	2143
	AGCTCGATCACCCATTT	2144
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Ser9Term TCG-TAG	CGTTTAAGTGGATCGGACATTTAAGTGTTTTAATCATGGTAGCTAT GAGTGCTACTGCGTAGCTGTTTCCGGTTTCTTCCCCAAAACCTCAC TCTGGAGCCAAGACATCTGATAAGCTTGG	2145
	CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTTGGGGAA GAAACCGGAAACAGCTACGCAGTAGCACTCATAGCTACCATGATT AAAACACTTAAATGTCCGATCCACTTAAACG	2146
	TACTGCGTAGCTGTTTC	2147
	GAAACAGCTACGCAGTA	2148
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Lys17Term AAA-TAA	AGTGTTTTAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTC CGGTTTCTTCCCCATAACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTTGCTG	2149
	CAGCAACACTACCTGGTTCACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGTTATGGGGAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAAAACACT	2150
	CTTCCCCATAACCTCAC	2151
	GTGAGGTTATGGGGAAG	2152
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Gly21Term GGA-TGA	ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCC CAAAACCTCACTCTTGAGCCAAGACATCTGATAAGCTTGGAGGTG AACCAGGTAGTGTTGCTGTGCGCGGAATCA	2153
	TGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAGCTTATC AGATGTCTTGGCTCAAGAGTGAGGTTTTGGGGAAGAAACCGGAAA CAGCGACGCAGTAGCACTCATAGCTACCAT	2154
	CTCACTCTTGAGCCAAG	2155
	CTTGGCTCAAGAGTGAG	2156

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Helianthus annuus* Lys23Term AAG-TAG	GCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCCCAAAAC CTCACTCTGGAGCCTAGACATCTGATAAGCTTGGAGGTGAACCAG GTAGTGTTGCTGTGCGCGGAATCAAGACAA	2157
	TTGTCTTGATTCCGCGCACAGCAACACTACCTGGTTCACCTCCAAG CTTATCAGATGTCTAGGCTCCAGAGTGAGGTTTTGGGGAAGAAAC CGGAAACAGCGACGCAGTAGCACTCATAGC	2158
	CTGGAGCCTAGACATCT	2159
	AGATGTCTAGGCTCCAG	2160
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Lys21Term AAA-TAA	ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCC CCAGGAGCCTCCCCTTAACCTGGGAAGTTAGGCAACTGGTCATCG AGTTTGAGCCCTTCCTTGAAGCCCAAGTCAA	2161
	TTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATGACCAGTTGC CTAACTTCCCAGGTTAAGGGGAGGCTCCTGGGGATGGAACAGGG AAGCATGCAGAACTTGCTGCAGCAGCCACCAT	2162
	CCTCCCCTTAACCTGGG	2163
	CCCAGGTTAAGGGGAGG	2164
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Lys24Term AAG-TAG	GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCC TCCCCTAAACCTGGGTAGTTAGGCAACTGGTCATCGAGTTTGAGC CCTTCCTTGAAGCCCAAGTCAATCCCCAATG	2165
	CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACTCGATG ACCAGTTGCCTAACTACCCAGGTTTAGGGGAGGCTCCTGGGGATG GAACAGGGAAGCATGCAGAACTTGCTGCAGC	2166
	AACCTGGGTAGTTAGGC	2167
	GCCTAACTACCCAGGTT	2168
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Trp28Term TGG-TGA	TGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGG GAAGTTAGGCAACTGATCATCGAGTTTGAGCCCTTCCTTGAAGCC CAAGTCAATCCCCAATGGCGGATTTCAGGTT	2169
	AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGG GCTCAAACTCGATGATCAGTTGCCTAACTTCCCAGGTTTAGGGGA GGCTCCTGGGGATGGAACAGGGAAGCATGCA	2170
	GGCAACTGATCATCGAG	2171
	CTCGATGATCAGTTGCC	2172
Reduced palmitate Acyl-ACP-thioesterase *Cuphea palustris* Ser29Term TCA-TGA	CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGGA AGTTAGGCAACTGGTGATCGAGTTTGAGCCCTTCCTTGAAGCCCA AGTCAATCCCCAATGGCGGATTTCAGGTTAA	2173
	TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAA GGGCTCAAACTCGATCACCAGTTGCCTAACTTCCCAGGTTTAGGG GAGGCTCCTGGGGATGGAACAGGGAAGCATG	2174

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CAACTGGTGATCGAGTT	2175
	AACTCGATCACCAGTTG	2176
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys21Term AAA-TAA	ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACC CCGGGAATCTCCCCTTAACCCGGGAAGTTCGGTAATGGTGGCTTT CAGGTTAAGGCAAACGCCAATGCCCATCCTA	2177
	TAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTAC CGAACTTCCCGGGTTAAGGGGAGATTCCCGGGGTTGGAACGGAG AAGAATGCAGAACTTGCTGCGGCAGCCACCAT	2178
	TCTCCCCTTAACCCGGG	2179
	CCCGGGTTAAGGGGAGA	2180
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys24Term AAG-TAG	GCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATC TCCCCTAAACCCGGGTAGTTCGGTAATGGTGGCTTTCAGGTTAAG GCAAACGCCAATGCCCATCCTAGTCTAAAGT	2181
	ACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGC CACCATTACCGAACTACCCGGGTTTAGGGGAGATTCCCGGGGTTG GAACGGAGAAGAATGCAGAACTTGCTGCGGC	2182
	AACCCGGGTAGTTCGGT	2183
	ACCGAACTACCCGGGTT	2184
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Gln31Term CAG-TAG	TTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTC GGTAATGGTGGCTTTTAGGTTAAGGCAAACGCCAATGCCCATCCT AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG	2185
	CTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGG CGTTTGCCTTAACCTAAAAGCCACCATTACCGAACTTCCCGGGTTT AGGGGAGATTCCCGGGGTTGGAACGGAGAA	2186
	GTGGCTTTTAGGTTAAG	2187
	CTTAACCTAAAAGCCAC	2188
Reduced palmitate Acyl-ACP-thioesterase *Cuphea hookeriana* Lys33Term AAG-TAG	GTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAAT GGTGGCTTTCAGGTTTAGGCAAACGCCAATGCCCATCCTAGTCTA AAGTCTGGCAGCCTCGAGACTGAAGATGACA	2189
	TGTCATCTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGG CATTGGCGTTTGCCTAAACCTGAAAGCCACCATTACCGAACTTCCC GGGTTTAGGGGAGATTCCCGGGGTTGGAAC	2190
	TTCAGGTTTAGGCAAAC	2191
	GTTTGCCTAAACCTGAA	2192

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Gln21Term CAA-TAA	ATGTTGAAGCTCTCGTGTAATGCGACTGATAAGTTACAGACCCTCT TCTCGCATTCTCATTAACCGGATCCGGCACACCGGAGAACCGTCT CCTCCGTGTCGTGCTCTCATCTGAGGAAAC	2193
	GTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGT GTGCCGGATCCGGTTAATGAGAATGCGAGAAGAGGGTCTGTAACT TATCAGTCGCATTACACGAGAGCTTCAACAT	2194
	ATTCTCATTAACCGGAT	2195
	ATCCGGTTAATGAGAAT	2196
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Arg28Term AGA-TGA	GCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATCAACCGG ATCCGGCACACCGGTGAACCGTCTCCTCCGTGTCGTGCTCTCATC TGAGGAAACCGGTTCTCGATCCTTTGCGAG	2197
	CTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACGACA CGGAGGAGACGGTTCACCGGTGTGCCGGATCCGGTTGATGAGAA TGCGAGAAGAGGGTCTGTAACTTATCAGTCGC	2198
	CACACCGGTGAACCGTC	2199
	GACGGTTCACCGGTGTG	2200
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Ser24Term TCG-TAG	CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAA CCGTCTCCTCCGTGTAGTGCTCTCATCTGAGGAAACCGGTTCTCG ATCCTTTGCGAGCGATCGTATCTGCTGATCA	2201
	TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTC CTCAGATGAGAGCACTACACGGAGGAGACGGTTCTCCGGTGTGC CGGATCCGGTTGATGAGAATGCGAGAAGAGGG	2202
	CTCCGTGTAGTGCTCTC	2203
	GAGAGCACTACACGGAG	2204
Reduced palmitate Acyl-ACP-thioesterase *Brassica rapa* Cys25Term TGC-TGA	CTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGT CTCCTCCGTGTCGTGATCTCATCTGAGGAAACCGGTTCTCGATCC TTTGCGAGCGATCGTATCTGCTGATCAAGGA	2205
	TCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGG TTTCCTCAGATGAGATCACGACACGGAGGAGACGGTTCTCCGGTG TGCCGGATCCGGTTGATGAGAATGCGAGAAG	2206
	GTGTCGTGATCTCATCT	2207
	AGATGAGATCACGACAC	2208
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Leu2Term TTG-TAG	ATTCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGG GCATCAAAAATGTAGAAGCTTTCGTGTAATGTGACTAACAACTTAC ACACCTTCTCCTTCTTCTCCGATTCCTC	2209
	GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACA TTACACGAAAGCTTCTACATTTTTGATGCCCTTTTTTTTTTATGGTTC CTGAGGTTTTGGTTTATAGAAGAAGAAT	2210

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AAAAATGTAGAAGCTTT	2211
	AAAGCTTCTACATTTTT	2212
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Lys3Term AAG-TAG	TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGG CATCAAAAATGTTGTAGCTTTCGTGTAATGTGACTAACAACTTACAC ACCTTCTCCTTCTTCTCCGATTCCTCCC	2213
	GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCA CATTACACGAAAGCTACAACATTTTTGATGCCCTTTTTTTTTTATGG TTCCTGAGGTTTTGGTTTATAGAAGAAGA	2214
	AAATGTTGTAGCTTTCG	2215
	CGAAAGCTACAACATTT	2216
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Ser5Term TCG-TAG	CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAA AATGTTGAAGCTTTAGTGTAATGTGACTAACAACTTACACACCTTCT CCTTCTTCTCCGATTCCTCCCTTTTCAT	2217
	ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTT GTTAGTCACATTACACTAAAGCTTCAACATTTTTGATGCCCTTTTTT TTTTATGGTTCCTGAGGTTTTGGTTTATAG	2218
	GAAGCTTTAGTGTAATG	2219
	CATTACACTAAAGCTTC	2220
Reduced palmitate Acyl-ACP-thioesterase *Brassica napus* Cys6Term TGT-TGA	AAACCAAAACCTCAGGAACCATAAAAAAAAAAGGGCATCAAAAATG TTGAAGCTTTCGTGAAATGTGACTAACAACTTACACACCTTCTCCTT CTTCTCCGATTCCTCCCTTTTCATCCCG	2221
	CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTA AGTTGTTAGTCACATTTCACGAAAGCTTCAACATTTTTGATGCCCTT TTTTTTTTATGGTTCCTGAGGTTTTGGTTT	2222
	CTTTCGTGAAATGTGAC	2223
	GTCACATTTCACGAAAG	2224

Table 23
Oligonucleotides to produce plants with increased stearate

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Lys4Term AAG-TAG	GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCATTCATCATATC CAGAAATGGCTCTATAGTTTAACCCTTTGGTGGCATCTCAGCCTTA CAAATTCCCTTCCTCGACTCGTCCGCCAA	2225
	TTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCC ACCAAAGGGTTAAACTATAGAGCCATTTCTGGATATGATGAATGAA TCCTTCTTTTCTACAGAGCTAGAGCTCTCCC	2226
	TGGCTCTATAGTTTAAC	2227
	GTTAAACTATAGAGCCA	2228
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Leu8Term TTG-TAG	CTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCT AAAGTTTAACCCTTAGGTGGCATCTCAGCCTTACAAATTCCCTTCC TCGACTCGTCCGCCAACTCCTTCTTTCAG	2229
	CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTA AGGCTGAGATGCCACCTAAGGGTTAAACTTTAGAGCCATTTCTGG ATATGATGAATGAATCCTTCTTTTCTACAGAG	2230
	TAACCCTTAGGTGGCAT	2231
	ATGCCACCTAAGGGTTA	2232
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Gln12Term CAG-TAG	AGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACC CTTTGGTGGCATCTTAGCCTTACAAATTCCCTTCCTCGACTCGTCC GCCAACTCCTTCTTTCAGATCTCCCAAGT	2233
	ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA GGGAATTTGTAAGGCTAAGATGCCACCAAAGGGTTAAACTTTAGA GCCATTTCTGGATATGATGAATGAATCCTTCT	2234
	TGGCATCTTAGCCTTAC	2235
	GTAAGGCTAAGATGCCA	2236
Increased stearate stearoyl-ACP desaturase *Arabidopsis thaliana* Phe14Term TAC-TAG	TCATTCATCATATCCAGAAATGGCTCTAAAGTTTAACCCTTTGGTG GCATCTCAGCCTTAGAAATTCCCTTCCTCGACTCGTCCGCCAACTC CTTCTTTCAGATCTCCCAAGTTCCTCTGC	2237
	GCAGAGGAACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG TCGAGGAAGGGAATTTCTAAGGCTGAGATGCCACCAAAGGGTTAA ACTTTAGAGCCATTTCTGGATATGATGAATGA	2238
	CAGCCTTAGAAATTCCC	2239
	GGGAATTTCTAAGGCTG	2240

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Brassica napus* Leu3Term TTG-TAG	GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA AAAGAAAATGGCATAGAAGCTTAACCCTTTGGCATCTCAGCCTTAC AAACTCCCTTCCTCGGCTCGTCCGCCAAT	2241
	ATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGATGC CAAAGGGTTAAGCTTCTATGCCATTTTCTTTTTTTTGATACGAGGTT TGATGTTCTTTCAGACACGAGCGAGCTCTC	2242
	AATGGCATAGAAGCTTA	2243
	TAAGCTTCTATGCCATT	2244
Increased stearate stearoyl-ACP desaturase *Brassica napus* Lys4Term AAG-TAG	GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAAAA AGAAAATGGCATTGTAGCTTAACCCTTTGGCATCTCAGCCTTACAA ACTCCCTTCCTCGGCTCGTCCGCCAATCT	2245
	AGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAGGCTGAGAT GCCAAAGGGTTAAGCTACAATGCCATTTTCTTTTTTTTGATACGAG GTTTGATGTTCTTTCAGACACGAGCGAGCTC	2246
	TGGCATTGTAGCTTAAC	2247
	GTTAAGCTACAATGCCA	2248
Increased stearate stearoyl-ACP desaturase *Brassica napus* Leu8Term TTG-TAG	TCTGAAAGAACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATT GAAGCTTAACCCTTAGGCATCTCAGCCTTACAAACTCCCTTCCTCG GCTCGTCCGCCAATCTCTACTCTCAGATC	2249
	GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTT GTAAGGCTGAGATGCCTAAGGGTTAAGCTTCAATGCCATTTTCTTT TTTTTGATACGAGGTTTGATGTTCTTTCAGA	2250
	TAACCCTTAGGCATCTC	2251
	GAGATGCCTAAGGGTTA	2252
Increased stearate stearoyl-ACP desaturase *Brassica napus* Gln11Term CAG-TAG	AACATCAAACCTCGTATCAAAAAAAAGAAAATGGCATTGAAGCTTA ACCCTTTGGCATCTTAGCCTTACAAACTCCCTTCCTCGGCTCGTCC GCCAATCTCTACTCTCAGATCTCCCAAGT	2253
	ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA GGGAGTTTGTAAGGCTAAGATGCCAAAGGGTTAAGCTTCAATGCC ATTTTCTTTTTTTTGATACGAGGTTTGATGTT	2254
	TGGCATCTTAGCCTTAC	2255
	GTAAGGCTAAGATGCCA	2256
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Gln27Term CAA-TAA	AACCAAAAGAAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCA ATCCTTTCCTTTCTTAAACCCAAAAGTTACCTTCTTTCGCTCTTCCA CCAATGGCCAGTACCAGATCTCCTAAGT	2257
	ACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAG GTAACTTTTGGGTTTAAGAAAGGAAAGGATTGAGCTTGAGAGCCAT TGTTTTTTTTCTTACCTTTTTCTTTTGGTT	2258

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCCTTTCTTAAACCCAA	2259
	TTGGGTTTAAGAAAGGA	2260
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Gln29Term CAA-TAA	AAGAAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTT TCCTTTCTCAAACCTAAAAGTTACCTTCTTTCGCTCTTCCACCAATG GCCAGTACCAGATCTCCTAAGTTCTACA	2261
	TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGA AAGAAGGTAACTTTTAGGTTTGAGAAAGGAAAGGATTGAGCTTGA GAGCCATTGTTTTTTTTCTTACCTTTTTCTT	2262
	CTCAAACCTAAAAGTTA	2263
	TAACTTTTAGGTTTGAG	2264
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Lys30Term AAG-TAG	AAAAAGGTAAGAAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCC TTTCTCAAACCCAATAGTTACCTTCTTTCGCTCTTCCACCAATGGCC AGTACCAGATCTCCTAAGTTCTACATGG	2265
	CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAG CGAAAGAAGGTAACTATTGGGTTTGAGAAAGGAAAGGATTGAGCT TGAGAGCCATTGTTTTTTTTCTTACCTTTTT	2266
	AAACCCAATAGTTACCT	2267
	AGGTAACTATTGGGTTT	2268
Increased stearate stearoyl-ACP desaturase *Ricinus communis* Lys46Term AAG-TAG	TCTCAAACCCAAAAGTTACCTTCTTTCGCTCTTCCACCAATGGCCA GTACCAGATCTCCTTAGTTCTACATGGCCTCTACCCTCAAGTCTGG TTCTAAGGAAGTTGAGAATCTCAAGAAGC	2269
	GCTTCTTGAGATTCTCAACTTCCTTAGAACCAGACTTGAGGGTAGA GGCCATGTAGAACTAAGGAGATCTGGTACTGGCCATTGGTGGAAG AGCGAAAGAAGGTAACTTTTGGGTTTGAGA	2270
	GATCTCCTTAGTTCTAC	2271
	GTAGAACTAAGGAGATC	2272
Increased stearate stearoyl-ACP desaturase *Glycine max* Gln11Term CAA-TAA	TCTTCTGATTCATTTAATCTTTACTCATCAATGGCTCTGAGACTGAA CCCTATCCCCACCTAAACCTTCTCCCTCCCCCAAATGGCCAGTCTC AGATCTCCCAGGTTCCGCATGGCCTCTA	2273
	TAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTGG GGGAGGGAGAAGGTTTAGGTGGGGATAGGGTTCAGTCTCAGAGC CATTGATGAGTAAAGATTAAATGAATCAGAAGA	2274
	TCCCCACCTAAACCTTC	2275
	GAAGGTTTAGGTGGGGA	2276

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Glycine max* Gln17Term CAA-TAA	CTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCCAAA CCTTCTCCCTCCCCTAAATGGCCAGTCTCAGATCTCCCAGGTTCC GCATGGCCTCTACCCTCCGCTCCGGTTCCA	2277
	TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGAT CTGAGACTGGCCATTTAGGGGAGGGAGAAGGTTTGGGTGGGGAT AGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG	2278
	CCCTCCCCTAAATGGCC	2279
	GGCCATTTAGGGGAGGG	2280
Increased stearate stearoyl-ACP desaturase *Glycine max* Arg22Term AGA-TGA	GCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCC CAAATGGCCAGTCTCTGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCAAAGAGGTTGAAAATA	2281
	TATTTTCAACCTCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGC GGAACCTGGGAGATCAGAGACTGGCCATTTGGGGGAGGGAGAAG GTTTGGGTGGGGATAGGGTTCAGTCTCAGAGC	2282
	CCAGTCTCTGATCTCCC	2283
	GGGAGATCAGAGACTGG	2284
Increased stearate stearoyl-ACP desaturase *Glycine max* Lys37Term AAA-TAA	CAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCTAAGAGGTTGAAAATATTAAGAAGCCATTCA CTCCTCCCAGAGAAGTGCATGTTCAAGTAA	2285
	TTACTTGAACATGCACTTCTCTGGGAGGAGTGAATGGCTTCTTAAT ATTTTCAACCTCTTAGGAACCGGAGCGGAGGGTAGAGGCCATGCG GAACCTGGGAGATCTGAGACTGGCCATTTG	2286
	CCGGTTCCTAAGAGGTT	2287
	AACCTCTTAGGAACCGG	2288
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Gln11Term CAA-TAA	CAACAAGCACACACAAGAACAACATCAACAATGGCGATTCGCATC AATACGGCGACGTTTTAATCAGACCTGTACCGTTCATTCGCGTTTC CTCAACCGAAACCTCTCAGATCTCCCAAAT	2289
	ATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAAC GGTACAGGTCTGATTAAAACGTCGCCGTATTGATGCGAATCGCCA TTGTTGATGTTGTTCTTGTGTGTGCTTGTTG	2290
	CGACGTTTTAATCAGAC	2291
	GTCTGATTAAAACGTCG	2292
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Ser12Term TCA-TGA	AAGCACACACAAGAACAACATCAACAATGGCGATTCGCATCAATAC GGCGACGTTTCAATGAGACCTGTACCGTTCATTCGCGTTTCCTCAA CCGAAACCTCTCAGATCTCCCAAATTCGC	2293
	GCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAAT GAACGGTACAGGTCTCATTGAAACGTCGCCGTATTGATGCGAATC GCCATTGTTGATGTTGTTCTTGTGTGTGCTT	2294

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTTTCAATGAGACCTGT	2295
	ACAGGTCTCATTGAAAC	2296
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Tyr15Term TAC-TAG	AAGAACAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTT CAATCAGACCTGTAGCGTTCATTCGCGTTTCCTCAACCGAAACCTC TCAGATCTCCCAAATTCGCCATGGCTTCC	2297
	GGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGG AAACGCGAATGAACGCTACAGGTCTGATTGAAACGTCGCCGTATT GATGCGAATCGCCATTGTTGATGTTGTTCTT	2298
	GACCTGTAGCGTTCATT	2299
	AATGAACGCTACAGGTC	2300
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Ser17Term TCA-TGA	CAACATCAACAATGGCGATTCGCATCAATACGGCGACGTTTCAATC AGACCTGTACCGTTGATTCGCGTTTCCTCAACCGAAACCTCTCAGA TCTCCCAAATTCGCCATGGCTTCCACCAT	2301
	ATGGTGGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGT TGAGGAAACGCGAATCAACGGTACAGGTCTGATTGAAACGTCGCC GTATTGATGCGAATCGCCATTGTTGATGTTG	2302
	GTACCGTTGATTCGCGT	2303
	ACGCGAATCAACGGTAC	2304
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Arg4Term CGA-TGA	ACACACAACACACACTCAATCACACACACATCATCATCTTCTTCATC AACGATGGCGCTTTGAATGAGTCCGGTGACGCTTCAACGGGAGAT ATATCCTTCATACACTTTTCATCAATCGA	2305
	TCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTGAAGCGT CACCGGACTCATTCAAAGCGCCATCGTTGATGAAGAAGATGATGA TGTGTGTGTGATTGAGTGTGTGTTGTGTGT	2306
	TGGCGCTTTGAATGAGT	2307
	ACTCATTCAAAGCGCCA	2308
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Gln11Term CAA-TAA	ACACACACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGA GTCCGGTGACGCTTTAACGGGAGATATATCCTTCATACACTTTTCA TCAATCGAAAAATCTCAGATCTCCTAAAT	2309
	ATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGG ATATATCTCCCGTTAAAGCGTCACCGGACTCATTCGAAGCGCCATC GTTGATGAAGAAGATGATGATGTGTGTGT	2310
	TGACGCTTTAACGGGAG	2311
	CTCCCGTTAAAGCGTCA	2312

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Glu13Term GAG-TAG	ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGG TGACGCTTCAACGGTAGATATATCCTTCATACACTTTTCATCAATCG AAAAATCTCAGATCTCCTAAATTCGCGA	2313
	TCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTA TGAAGGATATATCTACCGTTGAAGCGTCACCGGACTCATTCGAAG CGCCATCGTTGATGAAGAAGATGATGATGT	2314
	TTCAACGGTAGATATAT	2315
	ATATATCTACCGTTGAA	2316
Increased stearate stearoyl-ACP desaturase *Helianthus annuus* Tyr15Term TAT-TAG	ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTT CAACGGGAGATATAGCCTTCATACACTTTTCATCAATCGAAAAATC TCAGATCTCCTAAATTCGCGATGGCTTCC	2317
	GGAAGCCATCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGA AAAGTGTATGAAGGCTATATCTCCCGTTGAAGCGTCACCGGACTC ATTCGAAGCGCCATCGTTGATGAAGAAGAT	2318
	GAGATATAGCCTTCATA	2319
	TATGAAGGCTATATCTC	2320
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Lys4Term AAG-TAG	AACTCAGCCAGCTTGCCCCCAAACAACAGCGCAGAAAAACCTTCA ACAACAATGGCTCTCTAGCTCAACCCAGTCACCACCTTCCCTTCAA CACGCTCCCTCAACAACTTCTCCTCCAGAT	2321
	ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTG GTGACTGGGTTGAGCTAGAGAGCCATTGTTGTTGAAGGTTTTTCT GCGCTGTTGTTTGGGGGCAAGCTGGCTGAGTT	2322
	TGGCTCTCTAGCTCAAC	2323
	GTTGAGCTAGAGAGCCA	2324
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Ser13Term TCA-TGA	GCGCAGAAAAACCTTCAACAACAATGGCTCTCAAGCTCAACCCAG TCACCACCTTCCCTTGAACACGCTCCCTCAACAACTTCTCCTCCAG ATCTCCTCGCACCTTTCTCATGGCTGCTTC	2325
	GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTT GTTGAGGGAGCGTGTTCAAGGGAAGGTGGTGACTGGGTTGAGCT TGAGAGCCATTGTTGTTGAAGGTTTTTCTGCGC	2326
	CTTCCCTTGAACACGCT	2327
	AGCGTGTTCAAGGGAAG	2328
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Arg23Term AGA-TGA	CTCAAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCA ACAACTTCTCCTCCTGATCTCCTCGCACCTTTCTCATGGCTGCTTC CACTTTCAATTCCACCTCCACCAAGTAAG	2329
	CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAA AGGTGCGAGGAGATCAGGAGGAGAAGTTGTTGAGGGAGCGTGTT GAAGGGAAGGTGGTGACTGGGTTGAGCTTGAG	2330

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TCTCCTCCTGATCTCCT	2331
	AGGAGATCAGGAGGAGA	2332
Increased stearate stearoyl-ACP desaturase *Linum usitatissimum* Lys41Term AAG-TAG	TCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCA ATTCCACCTCCACCTAGTAAGCATCTCCTCCTCCTCGGAATCTCCG CCGATTTCTTTTAAGCGATTGATCGTAGA	2333
	TCTACGATCAATCGCTTAAAAGAAATCGGCGGAGATTCCGAGGAG GAGGAGATGCTTACTAGGTGGAGGTGGAATTGAAAGTGGAAGCA GCCATGAGAAAGGTGCGAGGAGATCTGGAGGA	2334
	CCTCCACCTAGTAAGCA	2335
	TGCTTACTAGGTGGAGG	2336
Increased stearate stearoyl-ACP desaturase *Olea europaea* Arg21Term AGA-TGA	ATGGCACTGAAACTTTGCTTTCCACCCCACAAGATGCCTTCCTTCC CCGATGCTCGTATCTGATCTCACAGGGTTTTCATGGCTTCAACTAT TCATTCTCCTTCTATGGAGGTCGGAAAAG	2337
	CTTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCCTGTGAGATCAGATACGAGCATCGGGGAAGGAAGGCATCTT GTGGGGTGGAAAGCAAAGTTTCAGTGCCAT	2338
	CTCGTATCTGATCTCAC	2339
	GTGAGATCAGATACGAG	2340
Increased stearate stearoyl-ACP desaturase *Olea europaea* Ser29Term TCA-TGA	CCCACAAGATGCCTTCCTTCCCCGATGCTCGTATCAGATCTCACAG GGTTTTCATGGCTTGAACTATTCATTCTCCTTCTATGGAGGTCGGA AAAGTTAAAAAGCCTTTCACGCCTCCACG	2341
	CGTGGAGGCGTGAAAGGCTTTTTAACTTTTCCGACCTCCATAGAA GGAGAATGAATAGTTCAAGCCATGAAAACCCTGTGAGATCTGATAC GAGCATCGGGGAAGGAAGGCATCTTGTGGG	2342
	CATGGCTTGAACTATTC	2343
	GAATAGTTCAAGCCATG	2344
Increased stearate stearoyl-ACP desaturase *Olea europaea* Glu37Term GAG-TAG	GATGCTCGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTC ATTCTCCTTCTATGTAGGTCGGAAAAGTTAAAAAGCCTTTCACGCC TCCACGAGAGGTACATGTTCAAGTAACCC	2345
	GGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTT TAACTTTTCCGACCTACATAGAAGGAGAATGAATAGTTGAAGCCAT GAAAACCCTGTGAGATCTGATACGAGCATC	2346
	CTTCTATGTAGGTCGGA	2347
	TCCGACCTACATAGAAG	2348

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Olea europaea* Gly39Term GGA-TGA	CGTATCAGATCTCACAGGGTTTTCATGGCTTCAACTATTCATTCTC CTTCTATGGAGGTCTGAAAAGTTAAAAAGCCTTTCACGCCTCCACG AGAGGTACATGTTCAAGTAACCCATTCCT	2349
	AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAG GCTTTTTAACTTTTCAGACCTCCATAGAAGGAGAATGAATAGTTGA AGCCATGAAAACCCTGTGAGATCTGATACG	2350
	TGGAGGTCTGAAAAGTT	2351
	AACTTTTCAGACCTCCA	2352
Increased stearate stearoyl-ACP desaturase *Persea americana* Lys4Term AAA-TAA	TTCTCGTTTTTGTCGTCCCCTCTGCTCTCTCTCTCTATCAGGCACG GAGAAATGGCACTGTAACTCAGTCCAGTCATGTTTCAATCTCAGAA GCTTCCATTTCTTGCCTCCTATCCGCCTT	2353
	AAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTGAAACA TGACTGGACTGAGTTACAGTGCCATTTCTCCGTGCCTGATAGAGA GAGAGAGCAGAGGGGACGACAAAAACGAGAA	2354
	TGGCACTGTAACTCAGT	2355
	ACTGAGTTACAGTGCCA	2356
Increased stearate stearoyl-ACP desaturase *Persea americana* Gln11Term CAA-TAA	CTGCTCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCA GTCCAGTCATGTTTTAATCTCAGAAGCTTCCATTTCTTGCCTCCTAT CCGCCTTCCAATCTCAGATCTCCGAGGG	2357
	CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT GGAAGCTTCTGAGATTAAAACATGACTGGACTGAGTTTCAGTGCC ATTTCTCCGTGCCTGATAGAGAGAGAGAGCAG	2358
	TCATGTTTTAATCTCAG	2359
	CTGAGATTAAAACATGA	2360
Increased stearate stearoyl-ACP desaturase *Persea americana* Gln13Term CAG-TAG	TCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA GTCATGTTTCAATCTTAGAAGCTTCCATTTCTTGCCTCCTATCCGCC TTCCAATCTCAGATCTCCGAGGGTTTTCA	2361
	TGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA GAAATGGAAGCTTCTAAGATTGAAACATGACTGGACTGAGTTTCAG TGCCATTTCTCCGTGCCTGATAGAGAGAGA	2362
	TTCAATCTTAGAAGCTT	2363
	AAGCTTCTAAGATTGAA	2364
Increased stearate stearoyl-ACP desaturase *Persea americana* Lys14Term AAG-TAG	CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC ATGTTTCAATCTCAGTAGCTTCCATTTCTTGCCTCCTATCCGCCTTC CAATCTCAGATCTCCGAGGGTTTTCATGG	2365
	CCATGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAG GCAAGAAATGGAAGCTACTGAGATTGAAACATGACTGGACTGAGT TTCAGTGCCATTTCTCCGTGCCTGATAGAGAG	2366

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	AATCTCAGTAGCTTCCA	2367
	TGGAAGCTACTGAGATT	2368
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Tyr12Term TAC-TAG	CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTCGCGGCGTCCC ACACCGCATCGCCGTAGTCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCGAAGATGGTGGCCATGGCC	2369
	GGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCTGCGC CACGCCGCCGCAGGACTACGGCGATGCGGTGTGGGACGCCGCG AACGCCATGAGCAGCGGCAGCGAGATCTCGGGG	2370
	TCGCCGTAGTCCTGCGG	2371
	CCGCAGGACTACGGCGA	2372
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Gln19Term CAG-TAG	CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTACTCC TGCGGCGGCGTGGCGTAGAGGAGGAGCAATGGGATGTCGAAGAT GGTGGCCATGGCCTCCACCATCAACAGGGTCA	2373
	TGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTCGACATCC CATTGCTCCTCCTCTACGCCACGCCGCCGCAGGAGTACGGCGAT GCGGTGTGGGACGCCGCGAACGCCATGAGCAG	2374
	GCGTGGCGTAGAGGAGG	2375
	CCTCCTCTACGCCACGC	2376
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Ser26Term TCG-TAG	CCCACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGG AGGAGCAATGGGATGTAGAAGATGGTGGCCATGGCCTCCACCAT CAACAGGGTCAAGACTGCTAAGAAGCCCTACAC	2377
	GTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCC ATGGCCACCATCTTCTACATCCCATTGCTCCTCCTCTGCGCCACGC CGCCGCAGGAGTACGGCGATGCGGTGTGGG	2378
	TGGGATGTAGAAGATGG	2379
	CCATCTTCTACATCCCA	2380
Increased stearate stearoyl-ACP desaturase *Oryza sativa* Lys27Term AAG-TAG	CACACCGCATCGCCGTACTCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCGTAGATGGTGGCCATGGCCTCCACCATCAA CAGGGTCAAGACTGCTAAGAAGCCCTACACTC	2381
	GAGTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGG CCATGGCCACCATCTACGACATCCCATTGCTCCTCCTCTGCGCCA CGCCGCCGCAGGAGTACGGCGATGCGGTGTG	2382
	GGATGTCGTAGATGGTG	2383
	CACCATCTACGACATCC	2384

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Leu3Term TTG-TAG	TTCTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGA GAGAAGCAATGGCGTAGAAGCTTCACCACACGGCCTTCAATCCTT CCATGGCGGTTACCTCTTCGGGACTTCCTCG	2385
	CGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGC CGTGTGGTGAAGCTTCTACGCCATTGCTTCTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTCAACCTAGAGAGAGAA	2386
	AATGGCGTAGAAGCTTC	2387
	GAAGCTTCTACGCCATT	2388
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Lys4Term AAG-TAG	CTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGA GAAGCAATGGCGTTGTAGCTTCACCACACGGCCTTCAATCCTTCC ATGGCGGTTACCTCTTCGGGACTTCCTCGAT	2389
	ATCGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTACAACGCCATTGCTTCTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTCAACCTAGAGAGAG	2390
	TGGCGTTGTAGCTTCAC	2391
	GTGAAGCTACAACGCCA	2392
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Ser19Term TCG-TAG	AAGCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCAT GGCGGTTACCTCTTAGGGACTTCCTCGATCGTATCACCTCAGATCT CACCGCGTTTTCATGGCTTCTTCTACAAT	2393
	ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATAC GATCGAGGAAGTCCCTAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTTCAACGCCATTGCTT	2394
	TACCTCTTAGGGACTTC	2395
	GAAGTCCCTAAGAGGTA	2396
Increased stearate stearoyl-ACP desaturase *Simmondsia chinensis* Gly20Term GGA-TGA	GCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATG GCGGTTACCTCTTCGTGACTTCCTCGATCGTATCACCTCAGATCTC ACCGCGTTTTCATGGCTTCTTCTACAATTG	2397
	CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGAT ACGATCGAGGAAGTCACGAAGAGGTAACCGCCATGGAAGGATTG AAGGCCGTGTGGTGAAGCTTCAACGCCATTGC	2398
	CCTCTTCGTGACTTCCT	2399
	AGGAAGTCACGAAGAGG	2400
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Ser21Term TCA-TGA	TGGCTCTGAATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCG ATTGCCGTCTTTCTGACCTCGTCAAACGCCTTCTCGCAGATCTCCC AAATTCTTCATGGCTTCCACTCTCAGCAG	2401
	CTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAA GGCGTTTGACGAGGTCAGAAAGACGGCAATCGACGACACTGAAAT GGTGTGGAAACGGGGTTGAGATTCAGAGCCA	2402

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GTCTTTCTGACCTCGTC	2403
	GACGAGGTCAGAAAGAC	2404
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Gln24Term CAA-TAA	AATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCGATTGCCGT CTTTCTCACCTCGTTAAACGCCTTCTCGCAGATCTCCCAAATTCTT CATGGCTTCCACTCTCAGCAGCTCTTCTC	2405
	GAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATC TGCGAGAAGGCGTTTAACGAGGTGAGAAAGACGGCAATCGACGA CACTGAAATGGTGTGGAAACGGGGTTGAGATT	2406
	CACCTCGTTAAACGCCT	2407
	AGGCGTTTAACGAGGTG	2408
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Arg29Term AGA-TGA	TCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTC AAACGCCTTCTCGCTGATCTCCCAAATTCTTCATGGCTTCCACTCT CAGCAGCTCTTCTCCTAAGGAAGCGGAAA	2409
	TTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGA AGAATTTGGGAGATCAGCGAGAAGGCGTTTGACGAGGTGAGAAA GACGGCAATCGACGACACTGAAATGGTGTGGA	2410
	CTTCTCGCTGATCTCCC	2411
	GGGAGATCAGCGAGAAG	2412
Increased stearate stearoyl-ACP desaturase *Spinacia oleracea* Lys32Term AAA-TAA	TTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTT CTCGCAGATCTCCCTAATTCTTCATGGCTTCCACTCTCAGCAGCTC TTCTCCTAAGGAAGCGGAAAGCCTGAAGA	2413
	TCTTCAGGCTTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGG AAGCCATGAAGAATTAGGGAGATCTGCGAGAAGGCGTTTGACGAG GTGAGAAAGACGGCAATCGACGACACTGAAA	2414
	GATCTCCCTAATTCTTC	2415
	GAAGAATTAGGGAGATC	2416
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Leu10Term TTA-TGA	AAATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATAT CAATGGGGTGTCGTGAAAATCTCACAAAATGTTACCATTTCCTTGT TCTTCAGCCAGATCTGAGCGAGTTTTCAT	2417
	ATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAAC ATTTTGTGAGATTTTCACGACACCCCATTGATATTCAGTGCCATTGT TGATGCTCTGTTTTTCACCTCGACTATTT	2418
	GGTGTCGTGAAAATCTC	2419
	GAGATTTTCACGACACC	2420

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Lys11Term AAA-TAA	ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCA ATGGGGTGTCGTTATAATCTCACAAAATGTTACCATTTCCTTGTTCT TCAGCCAGATCTGAGCGAGTTTTCATGG	2421
	CCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTA ACATTTTGTGAGATTATAACGACACCCCATTGATATTCAGTGCCATT GTTGATGCTCTGTTTTTCACCTCGACTAT	2422
	TGTCGTTATAATCTCAC	2423
	GTGAGATTATAACGACA	2424
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Lys14Term AAA-TAA	GTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTG TCGTTAAAATCTCACTAAATGTTACCATTTCCTTGTTCTTCAGCCAG ATCTGAGCGAGTTTTCATGGCTTCAACCA	2425
	TGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAAGAACAAG GAAATGGTAACATTTAGTGAGATTTTAACGACACCCCATTGATATT CAGTGCCATTGTTGATGCTCTGTTTTTCAC	2426
	AATCTCACTAAATGTTA	2427
	TAACATTTAGTGAGATT	2428
Increased stearate stearoyl-ACP desaturase *Solanum tuberosum* Leu16Term TTA-TGA	ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCGTTAAA ATCTCACAAAATGTGACCATTTCCTTGTTCTTCAGCCAGATCTGAG CGAGTTTTCATGGCTTCAACCATTCATCG	2429
	CGATGAATGGTTGAAGCCATGAAAACTCGCTCAGATCTGGCTGAA GAACAAGGAAATGGTCACATTTTGTGAGATTTTAACGACACCCCAT TGATATTCAGTGCCATTGTTGATGCTCTGT	2430
	CAAAATGTGACCATTTC	2431
	GAAATGGTCACATTTTG	2432
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser21Term TCA-TGA	TGGCTCTGAGGCTGAACCCTAACCCTTCACAGAAGCTCTTTCTCTC TCCTTCTTCATCATGATCTTCTTCTTCTTCATCGTTCTCGCTTCCTC AAATGGCTAGCCTCAGATCTCCAAGGTT	2433
	AACCTTGGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGAT GAAGAAGAAGAAGATCATGATGAAGAAGGAGAGAGAAAGAGCTTC TGTGAAGGGTTAGGGTTCAGCCTCAGAGCCA	2434
	TTCATCATGATCTTCTT	2435
	AAGAAGATCATGATGAA	2436
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser26Term TCA-TGA	ACCCTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCA TCTTCTTCTTCTTGATCGTTCTCGCTTCCTCAAATGGCTAGCCTCA GATCTCCAAGGTTCCGCATGGCCTCCAC	2437
	GTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCATTTGA GGAAGCGAGAACGATCAAGAAGAAGAAGATGATGATGAAGAAGGA GAGAGAAAGAGCTTCTGTGAAGGGTTAGGGT	2438

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TTCTTCTTGATCGTTCT	2439
	AGAACGATCAAGAAGAA	2440
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser27Term TCG-TAG	CTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCT TCTTCTTCTTCATAGTTCTCGCTTCCTCAAATGGCTAGCCTCAGAT CTCCAAGGTTCCGCATGGCCTCCACCCT	2441
	AGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAACTATGAAGAAGAAGAAGATGATGATGAAGA AGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAG	2442
	TTCTTCATAGTTCTCGC	2443
	GCGAGAACTATGAAGAA	2444
Increased stearate stearoyl-ACP desaturase *Arachis hypogaea* Ser29Term TCG-TAG	CTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCT TCTTCATCGTTCTAGCTTCCTCAAATGGCTAGCCTCAGATCTCCAA GGTTCCGCATGGCCTCCACCCTCCGCAC	2445
	GTGCGGAGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCT AGCCATTTGAGGAAGCTAGAACGATGAAGAAGAAGAAGATGATGA TGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG	2446
	ATCGTTCTAGCTTCCTC	2447
	GAGGAAGCTAGAACGAT	2448
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Leu3Term TTG-TAG	AAAGTTAAAAGCCGTCCAAAACCCAAACCAGGAAAGGCAAACGAA AAGAAAAAATGGCTTAGAATTTTAATGCCATCGCCTCGAAATCTCA GAAGCTCCCTTGCTTTGCTCTTCCACCAAA	2449
	TTTGGTGGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTCGAGGCG ATGGCATTAAAATTCTAAGCCATTTTTTCTTTTCGTTTGCCTTTCCT GGTTTGGGTTTTGGACGGCTTTTAACTTT	2450
	AATGGCTTAGAATTTTA	2451
	TAAAATTCTAAGCCATT	2452
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Ser1-Term TCG-TAG	CCCAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTT TAATGCCATCGCCTAGAAATCTCAGAAGCTCCCTTGCTTTGCTCTT CCACCAAAGGCCACCCTTAGATCTCCCAA	2453
	TTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAGG GAGCTTCTGAGATTTCTAGGCGATGGCATTAAAATTCAAAGCCATT TTTTCTTTTCGTTTGCCTTTCCTGGTTTGGG	2454
	CATCGCCTAGAAATCTC	2455
	GAGATTTCTAGGCGATG	2456

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Lys11Term AAA-TAA	CAAACCAGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTA ATGCCATCGCCTCGTAATCTCAGAAGCTCCCTTGCTTTGCTCTTCC ACCAAAGGCCACCCTTAGATCTCCCAAGT	2457
	ACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAAAGCAAG GGAGCTTCTGAGATTACGAGGCGATGGCATTAAAATTCAAAGCCA TTTTTTCTTTTCGTTTGCCTTTCCTGGTTTG	2458
	TCGCCTCGTAATCTCAG	2459
	CTGAGATTACGAGGCGA	2460
Increased stearate stearoyl-ACP desaturase *Gossypium hirsutum* Gln13Term CAG-TAG	AGGAAAGGCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCA TCGCCTCGAAATCTTAGAAGCTCCCTTGCTTTGCTCTTCCACCAAA GGCCACCCTTAGATCTCCCAAGTTTTCCA	2461
	TGGAAAACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAAGAGCAA AGCAAGGGAGCTTCTAAGATTTCGAGGCGATGGCATTAAAATTCA AAGCCATTTTTTCTTTTCGTTTGCCTTTCCT	2462
	CGAAATCTTAGAAGCTC	2463
	GAGCTTCTAAGATTTCG	2464

Table 24
Oligonucleotides to produce plants with reduced linolenic acid

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser4Term TCG-TAG	AATAGAACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGC TCCAATGGCGAGCTAGGTTTTATCAGAATGTGGTTTTAGACCTCTC CCCAGATTCTACCCTAAACACACAACCTC	2465
	GAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTAAAACCA CATTCTGATAAAACCTAGCTCGCCATTGGAGCCTCTTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCGTTCTATT	2466
	GGCGAGCTTGGTTTTAT	2467
	ATAAAACCAAGCTCGCC	2468
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Leu6Term TTA-TGA	ACGACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTTTGATCAGAATGTGGTTTTAGACCTCTCCCCAG ATTCTACCCTAAACACACAACCTCTTTTGC	2469
	GCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGATCAAACCGAGCTCGCCATTGGAGCCTCTTCCC AAGAAGAAAAGAGGAAAAAGTCTCTGTCGT	2470
	CTCGGTTTGATCAGAAT	2471
	ATTCTGATCAAACCGAG	2472
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Ser7Term TCA-TGA	ACAGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTTTATGAGAATGTGGTTTTAGACCTCTCCCCAGATTC TACCCTAAACACACAACCTCTTTTGCCTC	2473
	GAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCTCATAAAACCGAGCTCGCCATTGGAGCCTCTT CCCAAGAAGAAAAGAGGAAAAAGTCTCTGT	2474
	GGTTTTATGAGAATGTG	2475
	CACATTCTCATAAAACC	2476
Reduced linolenic acid omega-3 fatty acid desaturase *Arabidopsis thaliana* Glu8Term GAA-TAA	AGAGACTTTTTCCTCTTTTCTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTTTATCATAATGTGGTTTTAGACCTCTCCCCAGATTCTA CCCTAAACACACAACCTCTTTTGCCTCTA	2477
	TAGAGGCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATTATGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCCAAGAAGAAAAGAGGAAAAAGTCTCT	2478
	TTTTATCATAATGTGGT	2479
	ACCACATTATGATAAAA	2480

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Leu4Term TTG-TAG	TCATCATCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTC TAGCAATGGCGAACTAGGTCTTATCCGAATGTGGCATAAGACCTC TCCCCAGAATCTACACCACACCCAGATCCAC	2481
	GTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCA CATTCGGATAAGACCTAGTTCGCCATTGCTAGAGCTCTTTTGCTCT CTCTCTCTCCCCAGAAGAAGAAGATGATGA	2482
	GGCGAACTAGGTCTTAT	2483
	ATAAGACCTAGTTCGCC	2484
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Leu6Term TTA-TGA	TCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAA TGGCGAACTTGGTCTGATCCGAATGTGGCATAAGACCTCTCCCCA GAATCTACACCACACCCAGATCCACTTTCCT	2485
	AGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTT ATGCCACATTCGGATCAGACCAAGTTCGCCATTGCTAGAGCTCTTT TGCTCTCTCTCTCTCCCCAGAAGAAGAAGA	2486
	CTTGGTCTGATCCGAAT	2487
	ATTCGGATCAGACCAAG	2488
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Glu8Term GAA-TAA	TTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCG AACTTGGTCTTATCCTAATGTGGCATAAGACCTCTCCCCAGAATCT ACACCACACCCAGATCCACTTTCCTCTCCA	2489
	TGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGA GGTCTTATGCCACATTAGGATAAGACCAAGTTCGCCATTGCTAGA GCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAA	2490
	TCTTATCCTAATGTGGC	2491
	GCCACATTAGGATAAGA	2492
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica juncea* Cys9Term TGT-TGA	CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACT TGGTCTTATCCGAATGAGGCATAAGACCTCTCCCCAGAATCTACAC CACACCCAGATCCACTTTCCTCTCCAACACC	2493
	GGTGTTGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGG GGAGAGGTCTTATGCCTCATTCGGATAAGACCAAGTTCGCCATTG CTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAG	2494
	TCCGAATGAGGCATAAG	2495
	CTTATGCCTCATTCGGA	2496
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Trp5Term TGG-TGA	ATAACAGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAA TGGCTGCTGGTTGAGTATTATCAGAATGTGGTTTAAGGCCTCTCCC AAGAATCTACTCACGACCCAGAATTGGT	2497
	ACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACC ACATTCTGATAATACTCAACCAGCAGCCATTGAAAACCCAGAAGCT AAAAATGCAAGAATTCAGCAATTCTGTTAT	2498

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	GCTGGTTGAGTATTATC	2499
	GATAATACTCAACCAGC	2500
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Leu7Term TTA-TGA	AGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCT GCTGGTTGGGTATGATCAGAATGTGGTTTAAGGCCTCTCCCAAGA ATCTACTCACGACCCAGAATTGGTTTTAC	2501
	GTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTT AAACCACATTCTGATCATACCCAACCAGCAGCCATTGAAAACCCAG AAGCTAAAAATGCAAGAATTCAGCAATTCT	2502
	TTGGGTATGATCAGAAT	2503
	ATTCTGATCATACCCAA	2504
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Ser8Term TCA-TGA	ATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCT GGTTGGGTATTATGAGAATGTGGTTTAAGGCCTCTCCCAAGAATCT ACTCACGACCCAGAATTGGTTTTACATC	2505
	GATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGC CTTAAACCACATTCTCATAATACCCAACCAGCAGCCATTGAAAACC CAGAAGCTAAAAATGCAAGAATTCAGCAAT	2506
	GGTATTATGAGAATGTG	2507
	CACATTCTCATAATACC	2508
Reduced linolenic acid omega-3 fatty acid desaturase *Ricinus communis* Glu9Term GAA-TAA	TGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTG GTTGGGTATTATCATTAATGTGGTTTAAGGCCTCTCCCAAGAATCTA CTCACGACCCAGAATTGGTTTTACATCGA	2509
	TCGATGTAAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAG GCCTTAAACCACATTATGATAATACCCAACCAGCAGCCATTGAAAA CCCAGAAGCTAAAAATGCAAGAATTCAGCA	2510
	TATTATCATAATGTGGT	2511
	ACCACATTATGATAATA	2512
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg22Term AGA-TGA	GCAAGTTGGGTTTTATCAGAATGTGGTCTTAGACCACTCCCAAGAA TCTACCCTAAGCCCTGAACTGGGGCAGCCACTTCTGCCTCCTCTC ACATTAAGTTGAGAATTTCACGTACAGATC	2513
	GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGAGGCAGAAGT GGCTGCCCCAGTTCAGGGCTTAGGGTAGATTCTTGGGAGTGGTCT AAGACCACATTCTGATAAAACCCAACTTGC	2514
	CTAAGCCCTGAACTGGG	2515
	CCCAGTTCAGGGCTTAG	2516

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Lys34Term AAG-TAG	CTCCCAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCT GCCTCCTCTCACATTTAGTTGAGAATTTCACGTACAGATCTGAGTG GTTCTGCAATTTCTTTGTCTAATACTAATA	2517
	TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG TGAAATTCTCAACTAAATGTGAGAGGAGGCAGAAGTGGCTGCCCC AGTTCTGGGCTTAGGGTAGATTCTTGGGAG	2518
	CTCACATTTAGTTGAGA	2519
	TCTCAACTAAATGTGAG	2520
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Leu35Term TTG-TAG	CAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCT CCTCTCACATTAAGTAGAGAATTTCACGTACAGATCTGAGTGGTTC TGCAATTTCTTTGTCTAATACTAATAAAGA	2521
	TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT ACGTGAAATTCTCTACTTAATGTGAGAGGAGGCAGAAGTGGCTGC CCCAGTTCTGGGCTTAGGGTAGATTCTTG	2522
	CATTAAGTAGAGAATTT	2523
	AAATTCTCTACTTAATG	2524
Reduced linolenic acid omega-3 fatty acid desaturase *Nicotiana tabacum* Arg36Term AGA-TGA	AGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCC TCTCACATTAAGTTGTGAATTTCACGTACAGATCTGAGTGGTTCTG CAATTTCTTTGTCTAATACTAATAAAGAGA	2525
	TCTCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT GTACGTGAAATTCACAACTTAATGTGAGAGGAGGCAGAAGTGGCT GCCCCAGTTCTGGGCTTAGGGTAGATTCT	2526
	TTAAGTTGTGAATTTCA	2527
	TGAAATTCACAACTTAA	2528
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Arg22Term AGA-TGA	GCGAGTTGGGTTTTATCAGAATGTGGTCTGAGGCCACTCCCGAGG GTCTATCCTAAGCCATGAACTGGCCACCCTTTGTTGAATTCCAATC CCACAAAGCTGAGATTTTCAAGAACAGATC	2529
	GATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAACAA AGGGTGGCCAGTTCATGGCTTAGGATAGACCCTCGGGAGTGGCC TCAGACCACATTCTGATAAAACCCAACTCGC	2530
	CTAAGCCATGAACTGGC	2531
	GCCAGTTCATGGCTTAG	2532
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu27Term TTG-TAG	CAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAA GAACTGGCCACCCTTAGTTGAATTCCAATCCCACAAAGCTGAGATT TTCAAGAACAGATCTTGGAAATGGTTCTTC	2533
	GAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGG GATTGGAATTCAACTAAGGGTGGCCAGTTCTTGGCTTAGGATAGA CCCTCGGGAGTGGCCTCAGACCACATTCTG	2534

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CCACCCTTAGTTGAATT	2535
	AATTCAACTAAGGGTGG	2536
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Leu28Term TTG-TAG	AATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAA CTGGCCACCCTTTGTAGAATTCCAATCCCACAAAGCTGAGATTTTC AAGAACAGATCTTGGAAATGGTTCTTCATT	2537
	AATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGT GGGATTGGAATTCTACAAAGGGTGGCCAGTTCTTGGCTTAGGATA GACCCTCGGGAGTGGCCTCAGACCACATT	2538
	CCCTTTGTAGAATTCCA	2539
	TGGAATTCTACAAAGGG	2540
Reduced linolenic acid omega-3 fatty acid desaturase *Sesamum indicum* Lys34Term AAG-TAG	CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTTG AATTCCAATCCCACATAGCTGAGATTTTCAAGAACAGATCTTGGAA ATGGTTCTTCATTCTGTTTGTCGAGTGGGA	2541
	TCCCACTCGACAAACAGAATGAAGAACCATTTCCAAGATCTGTTCT TGAAAATCTCAGCTATGTGGGATTGGAATTCAACAAAGGGTGGCC AGTTCTTGGCTTAGGATAGACCCTCGGGAG	2542
	ATCCCACATAGCTGAGA	2543
	TCTCAGCTATGTGGGAT	2544
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Tyr3Term TAC-TAG	CATCAGAGCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATG GAAGTCTATGAGTTAGGTCGTCAGAGAGCTAGCCATCGTGTTCGC ACTAGCTGCTGGAGCTGCTTACCTCAACAAT	2545
	ATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGC TAGCTCTCTGACGACCTAACTCATAGACTTCCATGGATTCTTAACC CAGCAATGCTTAGGTATCGCCGCTCTGATG	2546
	ATGAGTTAGGTCGTCAG	2547
	CTGACGACCTAACTCAT	2548
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Arg6Term AGA-TGA	GCGGCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCT ATGAGTTACGTCGTCTGAGAGCTAGCCATCGTGTTCGCACTAGCT GCTGGAGCTGCTTACCTCAACAATTGGCTTG	2549
	CAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACA CGATGGCTAGCTCTCAGACGACGTAACTCATAGACTTCCATGGATT CTTAACCCAGCAATGCTTAGGTATCGCCGC	2550
	ACGTCGTCTGAGAGCTA	2551
	TAGCTCTCAGACGACGT	2552

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Glu7Term GAG-TAG	GCGATACCTAAGCATTGCTGGGTTAAGAATCCATGGAAGTCTATGA GTTACGTCGTCAGATAGCTAGCCATCGTGTTCGCACTAGCTGCTG GAGCTGCTTACCTCAACAATTGGCTTGTTT	2553
	AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGA ACACGATGGCTAGCTATCTGACGACGTAACTCATAGACTTCCATG GATTCTTAACCCAGCAATGCTTAGGTATCGC	2554
	TCGTCAGATAGCTAGCC	2555
	GGCTAGCTATCTGACGA	2556
Reduced linolenic acid omega-3 fatty acid desaturase *Brassica napus* Gly17Term GGA-TGA	CCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGTG TTCGCACTAGCTGCTTGAGCTGCTTACCTCAACAATTGGCTTGTTT GGCCTCTCTATTGGATTGCTCAAGGAACCA	2557
	TGGTTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTT GAGGTAAGCAGCTCAAGCAGCTAGTGCGAACACGATGGCTAGCT CTCTGACGACGTAACTCATAGACTTCCATGG	2558
	TAGCTGCTTGAGCTGCT	2559
	AGCAGCTCAAGCAGCTA	2560
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Arg22Term AGA-TGA	GCAAGTTGGGTTCTATCAGAATGTGGTCTTAGACCACTACCAAGAA TATACCCAAAGCCCTGAATAGGGTCTTCTTCCGTTTGCGCCACCAA TTTAAATCTGAGAAGAATTTCACCTTCAC	2561
	GTGAAGGTGAAATTCTTCTCAGATTTAAATTGGTGGCGCAAACGGA AGAAGACCCTATTCAGGGCTTTGGGTATATTCTTGGTAGTGGTCTA AGACCACATTCTGATAGAACCCAACTTGC	2562
	CAAAGCCCTGAATAGGG	2563
	CCCTATTCAGGGCTTTG	2564
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Cys29Term TGC-TGA	TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGG GTCTTCTTCCGTTTGAGCCACCAATTTAAATCTGAGAAGAATTTCA CCTTCACCTATACGAACAGATCGGAATTGT	2565
	ACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAATTCTTCTCAGA TTTAAATTGGTGGCTCAAACGGAAGAAGACCCTATTCTGGGCTTTG GGTATATTCTTGGTAGTGGTCTAAGACCA	2566
	TCCGTTTGAGCCACCAA	2567
	TTGGTGGCTCAAACGGA	2568
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Leu33Term TTA-TGA	CACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGT TTGCGCCACCAATTGAAATCTGAGAAGAATTTCACCTTCACCTATA CGAACAGATCGGAATTGTTGGGCATTGAG	2569
	CTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGAAGGTGAAA TTCTTCTCAGATTTCAATTGGTGGCGCAAACGGAAGAAGACCCTAT TCTGGGCTTTGGGTATATTCTTGGTAGTG	2570

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CACCAATTGAAATCTGA	2571
	TCAGATTTCAATTGGTG	2572
Reduced linolenic acid omega-3 fatty acid desaturase *Solanum tuberosum* Arg36Term AGA-TGA	AGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCA CCAATTTAAATCTGTGAAGAATTTCACCTTCACCTATACGAACAGAT CGGAATTGTTGGGCATTGAGGGTAAGTG	2573
	CACTTACCCTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGA AGGTGAAATTCTTCACAGATTTAAATTGGTGGCGCAAACGGAAGAA GACCCTATTCTGGGCTTTGGGTATATTCT	2574
	TAAATCTGTGAAGAATT	2575
	AATTCTTCACAGATTTA	2576
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Trp4Term TGG-TGA	CTCTTTATTATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACC TATGGCAAGTTGAGTGATTTCAGAATGTGGGCTAAGGCCACTTCC AAGAATCTATGCCAGGCCCAGAAGTGGA	2577
	TCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGCCTTAGCCC ACATTCTGAAATCACTCAACTTGCCATAGGTGACTCAGAACTCAAA AAAAACAAAGAAGAGGAGGATAATAAAGAG	2578
	GCAAGTTGAGTGATTTC	2579
	GAAATCACTCAACTTGC	2580
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Ser7Term TCA-TGA	TATCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCA AGTTGGGTGATTTGAGAATGTGGGCTAAGGCCACTTCCAAGAATC TATGCCAGGCCCAGAAGTGGAGCTTCATG	2581
	CATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTGGC CTTAGCCCACATTCTCAAATCACCCAACTTGCCATAGGTGACTCAG AACTCAAAAAAAAACAAAGAAGAGGAGGATA	2582
	GGTGATTTGAGAATGTG	2583
	CACATTCTCAAATCACC	2584
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Glu8Term GAA-TAA	TCCTCCTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAG TTGGGTGATTTCATAATGTGGGCTAAGGCCACTTCCAAGAATCTAT GCCAGGCCCAGAAGTGGAGCTTCATGTT	2585
	AACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGGAAGTG GCCTTAGCCCACATTATGAAATCACCCAACTTGCCATAGGTGACTC AGAACTCAAAAAAAAACAAAGAAGAGGAGGA	2586
	TGATTTCATAATGTGGG	2587
	CCCACATTATGAAATCA	2588

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Petroselinum crispum* Cys9Term TGT-TGA	CTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGG TGATTTCAGAATGAGGGCTAAGGCCACTTCCAAGAATCTATGCCA GGCCCAGAAGTGGAGCTTCATGTTTCAAC	2589
	GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGG AAGTGGCCTTAGCCCTCATTCTGAAATCACCCAACTTGCCATAGGT GACTCAGAACTCAAAAAAAACAAAGAAGAG	2590
	TCAGAATGAGGGCTAAG	2591
	CTTAGCCCTCATTCTGA	2592
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Lys21Term AAA-TAA	ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTA ATGGTTTTCATGCTTAAGAAGAAGAAGAAGAAGAGGATTTCGACTT AAGCAATCCTCCTCCATTCAATATTGGTC	2593
	GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTC TTCTTCTTCTTCTTAAGCATGAAAACCATTAACGCCATTTAGAATTG GGGTGTCTTTGTACTGTTGCTGCTTCAT	2594
	TTCATGCTTAAGAAGAA	2595
	TTCTTCTTAAGCATGAA	2596
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu22Term GAA-TAA	AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATG GTTTTCATGCTAAATAAGAAGAAGAAGAAGAGGATTTCGACTTAAG CAATCCTCCTCCATTCAATATTGGTCAGA	2597
	TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC TTCTTCTTCTTCTTATTTAGCATGAAAACCATTAACGCCATTTAGAA TTGGGGTGTCTTTGTACTGTTGCTGCTT	2598
	ATGCTAAATAAGAAGAA	2599
	TTCTTCTTATTTAGCAT	2600
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu23Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	2601
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTATTCTTTAGCATGAAAACCATTAACGCCATTTA GAATTGGGGTGTCTTTGTACTGTTGCTG	2602
	CTAAAGAATAAGAAGAA	2603
	TTCTTCTTATTCTTTAG	2604
Reduced linolenic acid omega-3 fatty acid desaturase *Vernicia fordii* Glu24Term GAA-TAA	CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTCGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC	2605
	GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTATTCTTTAGCATGAAAACCATTAACGCCATTTA GAATTGGGGTGTCTTTGTACTGTTGCTG	2606

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	CTAAAGAATAAGAAGAA	2607
	TTCTTCTTATTCTTTAG	2608
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Tyr21Term TAT-TAG	GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA AGAAGATCAAGCTTAGTTTGATCCAAGTGCTCCACCACCCTTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAAA	2609
	TTTTGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGA GCACTTGGATCAAACTAAGCTTGATCTTCTTTCCCTGCACCATTAC CAACATGTTGTAGAGGCTGTGCTTGGACC	2610
	CAAGCTTAGTTTGATCC	2611
	GGATCAAACTAAGCTTG	2612
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Lys31Term AAG-TAG	GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTTTGATCCAAGT GCTCCACCACCCTTCTAGATTGCAAATATCAGAGCAGCAATTCCAA AACATTGCTGGGAGAAGAACACATTGAGAT	2613
	ATCTCAATGTGTTCTTCTCCCAGCAATGTTTTGGAATTGCTGCTCT GATATTTGCAATCTAGAAGGGTGGTGGAGCACTTGGATCAAAATAA GCTTGATCTTCTTTCCCTGCACCATTACC	2614
	CACCCTTCTAGATTGCA	2615
	TGCAATCTAGAAGGGTG	2616
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Arg36Term AGA-TGA	AAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTCA AGATTGCAAATATCTGAGCAGCAATTCCAAAACATTGCTGGGAGAA GAACACATTGAGATCTCTGAGTTATGTTC	2617
	GAACATAACTCAGAGATCTCAATGTGTTCTTCTCCCAGCAATGTTTT GGAATTGCTGCTCAGATATTTGCAATCTTGAAGGGTGGTGGAGCA CTTGGATCAAAATAAGCTTGATCTTCTTT	2618
	CAAATATCTGAGCAGCA	2619
	TGCTGCTCAGATATTTG	2620
Reduced linolenic acid omega-3 fatty acid desaturase *Glycine max* Leu41Term AAA-TAA	TATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCA GAGCAGCAATTCCATAACATTGCTGGGAGAAGAACACATTGAGAT CTCTGAGTTATGTTCTGAGGGATGTGTTGG	2621
	CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT CTCCCAGCAATGTTATGGAATTGCTGCTCTGATATTTGCAATCTTG AAGGGTGGTGGAGCACTTGGATCAAAATA	2622
	CAATTCCATAACATTGC	2623
	GCAATGTTATGGAATTG	2624

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Glu8Term GAG-TAG	CATCCACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGC CCGGCTCGTGCTCTCCTAGTGCTCGGGCCTCGCGCCCGTCCGCC GCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGC	2625
	GCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGG GCGCGAGGCCCGAGCACTAGGAGAGCACGAGCCGGGCCATTGC CGCCGTCAGCGGGGCGGGTGCGGGTGCGGGTGGATG	2626
	TGCTCTCCTAGTGCTCG	2627
	CGAGCACTAGGAGAGCA	2628
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Cys9Term TGC-TGA	ACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGG CTCGTGCTCTCCGAGTGATCGGGCCTCGCGCCCGTCCGCCGCCT GCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA	2629
	TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGG ACGGGCGCGAGGCCCGATCACTCGGAGAGCACGAGCCGGGCCA TTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGT	2630
	TCCGAGTGATCGGGCCT	2631
	AGGCCCGATCACTCGGA	2632
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Ser10Term TCG-TAG	CCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCT CGTGCTCTCCGAGTGCTAGGGCCTCGCGCCCGTCCGCCGCCTGC GCGCCGGCCGGGGCGCCATTGCGGCGCGGTCACC	2633
	GGTGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGC GGACGGGCGCGAGGCCCTAGCACTCGGAGAGCACGAGCCGGGC CATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGG	2634
	CGAGTGCTAGGGCCTCG	2635
	CGAGGCCCTAGCACTCG	2636
Reduced linolenic acid omega-3 fatty acid desaturase *Zea mays* Ser29Term TCA-TGA	GCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGG CGCCATTGCGGCGCGGTGACCCCCCGCGCTCTCCGCGGCGCCG CGCCGTCGTCCCGCGTCCGCGTCCATCCACCGCGA	2637
	TCGCGGTGGATGGACGCGGACGCGGGACGACGGCGCGGCGCCG CGGAGAGCGCGGGGGGTCACCGCGCCGCAATGGCGCCCCGGCC GGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGC	2638
	GGCGCGGTGACCCCCCG	2639
	CGGGGGGTCACCGCGCC	2640
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Glu8Term GAG-TAG	CCCCCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGC CCCCGCAATGAGGCCGTAGCAGGAGGCGAGCTGCAAGGCCACCG AGGACCACCGCTCCGAGTTCGACGCCGCCAAGC	2641
	GCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTG CAGCTCGCCTCCTGCTACGGCCTCATTGCGGGGGCCATGGCCGC GATTGGATCTGTGCGTGTGCGTGGGGGAGGGGG	2642

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
	TGAGGCCGTAGCAGGAG	2643
	CTCCTGCTACGGCCTCA	2644
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Gln9Term CAG-TAG	CCTCCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCC CGCAATGAGGCCGGAGTAGGAGGCGAGCTGCAAGGCCACCGAG GACCACCGCTCCGAGTTCGACGCCGCCAAGCCGC	2645
	GCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCC TTGCAGCTCGCCTCCTACTCCGGCCTCATTGCGGGGGCCATGGC CGCGGATGGATCTGTGCGTGTGCGTGGGGGAGG	2646
	GGCCGGAGTAGGAGGCG	2647
	CGCCTCCTACTCCGGCC	2648
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Glu10Term GAG-TAG	CCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGC AATGAGGCCGGAGCAGTAGGCGAGCTGCAAGGCCACCGAGGACC ACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGC	2649
	GCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGT GGCCTTGCAGCTCGCCTACTGCTCCGGCCTCATTGCGGGGGCCA TGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGG	2650
	CGGAGCAGTAGGCGAGC	2651
	GCTCGCCTACTGCTCCG	2652
Reduced linolenic acid omega-3 fatty acid desaturase *Triticum aestivum* Cys13Term TGC-TGA	ACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGG AGCAGGAGGCGAGCTGAAAGGCCACCGAGGACCACCGCTCCGA GTTCGACGCCGCCAAGCCGCCGCCCTTCCGCATC	2653
	GATGCGGAAGGGCGGCGGCTTGGCGGCGTCGAACTCGGAGCGG TGGTCCTCGGTGGCCTTTCAGCTCGCCTCCTGCTCCGGCCTCATT GCGGGGGCCATGGCCGCGGATGGATCTGTGCGT	2654
	GCGAGCTGAAAGGCCAC	2655
	GTGGCCTTTCAGCTCGC	2656
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Ser4Term TCG-TAG	CTTCACAAATCACAAATCGGAATCAGATCCACCACGACACCCCGG CGGCAATGGCGGCGTAGGCGACCCAGGAGGCCGACTGCAAGGC TTCCGAGGACGCCCGTCTCTTCTTCGACGCCGC	2657
	GCCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGCCTTGCAGTC GTCCTCCTGGGTCGCCTACGCCGCCATTGCCGCCGGGGTGTCGT GGTGGATCTGATTCCGATTTGTGATTTGTGAAG	2658
	GCCGGCGTAGGCGACCC	2659
	GGGTCGCCTACGCCGCC	2660

Phenotype, Gene, Plant & Targeted Alteration	Altering Oligos	SEQ ID NO:
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Gln7Term CAG-TAG	ATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATG GCGGCGTCGGCGACCTAGGAGGCCGACTGCAAGGCTTCCGAGGA CGCCCGTCTCTTCTTCGACGCCGCCAAGCCCC	2661
	GGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAGTCGGCCTCCTAGGTCGCCGACGCCGCCATTGCCGCCG GGGTGTCGTGGTGGATCTGATTCCGATTTGTGAT	2662
	CGGCGACCTAGGAGGCC	2663
	GGCCTCCTAGGTCGCCG	2664
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Glu8Term GAG-TAG	ACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAGTAGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCTTCGACGCCGCCAAGCCCCCGC	2665
	GCGGGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGCAGTCGGCCTACTGGGTCGCCGACGCCGCCATTGCCG CCGGGGTGTCGTGGTGGATCTGATTCCGATTTGT	2666
	CGACCCAGTAGGCCGAC	2667
	GTCGGCCTACTGGGTCG	2668
Reduced linolenic acid omega-3 fatty acid desaturase *Oryza sativa* Cys10Term TGC-TGA	TCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTCGGCGA CCCAGGAGGCCGACTGAAAGGCTTCCGAGGACGCCCGTCTCTTC TTCGACGCCGCCAAGCCCCCGCCCTTCCGCATC	2669
	GATGCGGAAGGGCGGGGGCTTGGCGGCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTTTCAGTCGGCCTCCTGGGTCGCCGACGC CGCCATTGCCGCCGGGGTGTCGTGGTGGATCTGA	2670
	GCCGACTGAAAGGCTTC	2671
	GAAGCCTTTCAGTCGGC	2672

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.