COMPOSITIONS AND METHODS FOR HIGH EFFICIENCY IN VIVO GENOME EDITING

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit of priority under U.S.C. 119(e) to U.S. Provisional Patent Application No. 62/099,014, filed December 31, 2014, the entire contents of which are herein incorporated by reference.

SEQUENCE LISTING

[0002] This application contains references to nucleic acid sequences and amino acid sequences which have been submitted concurrently herewith as the sequence listing text file "SGI1850_1WO_Sequence_Listing_ST25.txt", file size 237 kilobytes (kb), created on December 30, 2015, which is incorporated by reference in its entirety pursuant to 37 C.F.R. 1.52(e) (iii)(5).

BACKGROUND

[0003] The present invention relates to genetic engineering of eukaryotic organisms and in particular to genome editing using cas/CRISPR systems.

[0004] The genome editing capability of CRISPR systems, while only recently developed, has significantly expanded the spectrum of cells and organisms that can be genetically engineered (Sander & Joung (2014) *Nature Biotechnology*). US2014/0068797, incorporated herein by reference discloses Cas9/CRISPR systems and methods of use in genome editing.

SUMMARY

[0005] The present invention provides methods for developing cell lines and microbial strains that can be used for highly efficient genome editing using an RNA-guided endonuclease, such as a Cas/CRISPR system. The cell lines and microbial strains comprise a gene encoding an RNA-guided nuclease, which can be, for example, a Cas nuclease, *e.g.*, a Cas9 nuclease, where the RNA-guided nuclease exhibits fully penetrant expression in a population of the cell line or microbial strain. The fully penetrant expression of the RNA-guided nuclease is determined by assessing the expression of a linked gene encoding a detectable marker, *e.g.*, a fluorescent protein.

[0006] The methods provided herein for isolating a fully penetrant cas-expressing cell line or microbial strain include introducing the RNA-guided nuclease gene on a nucleic acid molecule that also includes a gene encoding a detectable marker, preferably a fluorescent marker. Transformed cell lines that include the nucleic acid molecule that includes a gene encoding an RNA-guided nuclease such as a Cas protein and a detectable marker gene are

screened by flow cytometry to select a strain or cell line in which essentially all the cells of the culture express the detectable marker, which can be, for example, a fluorescent protein. A strain or line selected for culture-wide expression of the detectable marker is identified as a fully penetrant stain or line.

[0007] The invention thus provides cell lines and microbial strains that are fully penetrant for a heterologous RNA-guided nuclease such as a Cas gene, *e.g.*, a Cas9 gene. The fully penetrant Cas strains and lines provided herein demonstrate highly efficient genome editing, for example, when cells of the fully penetrant strain or cell line are transformed with a guide RNA targeting a genetic locus of interest, at least about 10%, at least about 20%, at least about 30%, at least about 40%, or at least about 50% of the cells transformed with the guide RNA (*e.g.*, a chimeric guide RNA, or a crRNA that promotes site-specific DNA editing in combination with a transactivator RNA (tracrRNA)) become genetically altered at the targeted locus. For example, in various example, when transformed with a guide RNA and donor fragment, at least about 10%, at least about 20%, at least about 30%, or at least about 40% of the cells transformed with the guide RNA incorporate the donor DNA at the targeted locus. In some examples, at least 50%, at least 60%, at least 70%, or at least 80%, at least 90%, at least 95%, or greater than 95% of the cells of a fully penetrant Cas cell line transformed with a guide RNA and donor fragment incorporate the donor DNA the targeted locus.

[0008] In one aspect, provided herein are methods for generating a high efficiency genome editing cell line that expresses an exogenous RNA-guided nuclease, in which the methods include introducing into a population of host cells a non-native nucleic acid molecule comprising a nucleic acid sequence encoding an RNA-guided nuclease and a nucleic acid sequence encoding a detectable marker to obtain one or more RNA-guided nuclease -transformed cell lines comprising the at least one non-native nucleic acid molecule; individually culturing at least one of the RNA-guided nuclease-transformed cell lines; using flow cytometry to assess the expression of the detectable marker in the RNA-guided nuclease-transformed cell line culture; and identifying a RNA-guided nuclease -transformed cell line demonstrating fully penetrant expression of the detectable marker in culture to identify a high efficiency genome editing cell line. The detectable marker can be a fluorescent protein. By "fully penetrant expression" is meant that the RNA-guided nuclease -transformed cell line, when analyzed by flow cytometry, gives rise to a single peak of fluorescence intensity, where the transformed cell fluorescence intensity peak is at a higher intensity than the peak of fluorescence exhibited by non-transformed cells, *i.e.*, is at a higher

than background intensity. As demonstrated in the examples herein, cell lines exhibiting full penetrance of a detectable marker gene physically linked to a non-native RNA-guided nuclease protein gene demonstrate highly efficient genome editing when transformed with a genome-targeting guide RNA. Highly efficient genome editing can successfully generate mutations (altered target site) in at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60% or at least 70% of the cells transformed with a donor DNA.

[0009] The methods can be performed with any cells that can be cultured, including prokaryotic cells (bacteria and archaea) and eukaryotic cells, including, without limitation, plant cells, animal cells, and protozoans, including mesomycetozoea, fungi, heterokonts, and algae.

[0010] The RNA-guided nuclease can be, for example, a Cas protein, such as a Cas9 protein, of which a large number have been identified, and can be for example a Cas9 protein of *Streptococcus pyogenes*, *Streptococcus thermophilus*, or *Neisseria meningitidis*. Other Cas proteins of interest includes, without limitation, the Cpf1 RNA-guided endonuclease (Zetsche *et al.* (2015) *Cell* 163:1-13) as well as the C2c1, C2c2, C2c3 RNA-guided nucleases (Shmakov *et al.* (2015) *Molecular Cell* 60:1-13. The nucleic acid sequence encoding the Cas protein can be codon optimized for the host cell of interest. In some instances, a Cas9 protein encoded by a nucleic acid molecule introduced into a host cell can comprise at least one mutation with respect to a wild-type Cas9 protein; for example, the Cas9 protein can be inactivated in one of the cleavage domains of the protein resulting in a "nickase" variant. Nonlimiting examples of mutations include D10A, H840A, N854A, and N863A.

[0011] The methods can be used to screen for full penetrance of proteins other than cas proteins, so that methods are provided for generating cell lines fully penetrant for expression of a gene of interest, in which the methods include introducing into a population of host cells a non-native nucleic acid molecule comprising a gene of interest and a nucleic acid sequence encoding a detectable marker to obtain one or more transformed cell lines comprising the at least one non-native nucleic acid molecule; individually culturing at least one of the transformed cell lines; using flow cytometry to assess the expression of the detectable marker in the transformed cell line culture; and identifying a transformed cell line demonstrating fully penetrant expression of the detectable marker in culture to identify a cell line having fully penetrant expression of the gene of interest. The detectable marker can be a fluorescent protein. By "fully penetrant expression" is meant that the transformed cell line, when analyzed by flow cytometry, gives rise to a single peak of fluorescence intensity, where the

transformed cell fluorescence intensity peak is shifted a higher intensity than the peak of fluorescence exhibited by non-transformed cells, *i.e.*, is at a higher than background intensity.

[0012] The gene encoding a Cas polypeptide can include, in addition to sequences encoding the cas enzyme, sequences encoding at least one nuclear localization sequence (NLS) as part of the recombinant cas protein. An NLS can optionally be at the N-terminal or C-terminal portion of the cas enzyme, or the cas enzyme can have at least one NLS at or near the N-terminus of the protein and least one NLS at or near the C-terminus of the protein. Alternatively or in addition, the nucleic acid molecule can encode a cas protein that includes an epitope tag, such as but not limited to a histidine tag, a hemagglutinin (HA) tag, a FLAG tag, or a Myc tag.

[0013] The non-native nucleic acid molecule that includes sequences encoding a cas protein can further comprise a selectable marker gene. The selectable marker can be an auxotrophic marker, or can confer resistance to an antibiotic or toxin, and the selectable marker gene can be codon-optimized for the intended host cell.

[0014] The detectable marker encoded by the nucleic acid molecule that also includes a sequence encoding a cas protein is preferably a fluorescent protein which can be any fluorescent protein, including phycoerythrin, phycocyanin, allophycocyanin, or a green, yellow, red, blue, cyan, "fruit basket" or "paintbox" (DNA 2.0) fluorescent protein. As nonlimiting examples, a fluorescent protein encoded by a nucleic acid molecule that also encodes a cas protein can be a green fluorescent protein (GFP), YFP, RFP, CFP, BFP, Cherry, Tomato, Venus, Cerulean fluorescent protein, or a variant of any thereof, including but not limited to a monomeric variant of a fluorescent protein.

[0015] The nucleic acid molecule that encodes a cas protein, *e.g.*, a Cas9 protein, can encode a detectable marker protein, e.g., a fluorescent protein such that the cas protein and detectable marker protein are regulated by the same promoter and transcribed as a single RNA. For example, the cas enzyme and detectable marker can be produced as a fusion protein. Alternatively, the Cas enzyme and detectable marker can be translated together but the translation product can include a cleavage sequence such as an FMDV 2A sequence that results in cleavage of the two polypeptide moieties so that separate cas and detectable marker proteins result. Further alternatively, an IRES can be provided in the construct between the two coding regions so that they are transcribed as a single transcript but translated as separate polypeptides. In yet another configuration, the cas protein and detectable marker can be operably linked to separate promoters. The promoters can optionally be derived from ("homologous to") the host cell species and can optionally be constitutive promoters.

[0016] A further aspect of the invention is a highly efficiency genome editing cell line. The high efficiency genome editing recombinant cell line includes an exogenous gene encoding an REN-guided endonuclease and is fully penetrant for the heterologous (introduced) RNA-guided endonuclease gene. Based on results described herein that demonstrate high efficiencies of Cas9 genome editing in strains fully penetrant for a linked fluorescent protein, the highly efficiency Cas9 genome editing cell line is said to be a "fully penetrant Cas9 cell line" based on identification of the cell line by screening for fully penetrant (culture-wide) expression of a fluorescent protein whose encoding gene is physically linked to the gene encoding the RNA-guided endonuclease gene. Without limiting the invention to a particular mechanism, it is considered that cell lines selected for penetrance using a linked fluorescence marker also exhibit Cas9 gene expression throughout the cells of the culture, resulting in the high efficiencies of targeted mutations observed. The fully penetrant Cas9 cell lines or microbial strains provided herein can have targeted mutation rates of at least 10%, at least 20%, at least 30%, at least 40%, or at least 50% using a guide RNA (gRNA) and donor fragment, where the efficiency is the percentage of cells that received the donor fragment that also have a targeted mutation.

[0017] The high efficiency genome editing cell line can include an exogenous gene encoding a fluorescent protein, or may not include an exogenous gene encoding a fluorescent protein. Using methods disclosed herein, a detectable marker gene, e.g. a gene encoding a fluorescent protein used to screen for full penetrance of a linked introduced gene such as a gene encoding an RNA-guided endonuclease, can subsequently be excised from the genome of the high efficiency genome editing cell line, for example, using a site specific recombinase such as the cre recombinase.

[0018] Further included herein is a high efficiency genome editing cell line that includes an exogenous gene encoding an RNA-guided endonuclease and an exogenous gene encoding a site-specific recombinase, such as a cre recombinase. The gene encoding a site-specific recombinase can optionally be operably linked to an inducible and/or repressible promoter. The high efficiency genome editing cell line that includes an exogenous gene encoding an RNA-guided endonuclease and an exogenous gene encoding a site-specific recombinase may or may not include an exogenous gene encoding a fluorescent protein. For example, a high efficiency genome editing cell line that includes an exogenous gene encoding an RNA-guided endonuclease and an exogenous gene encoding a site-specific recombinase may also include an exogenous gene encoding a fluorescent protein that is subsequently excised by the action of the site-specific recombinase. Further, a high efficiency genome editing cell line that

includes an exogenous gene encoding an RNA-guided endonuclease and an exogenous gene encoding a site-specific recombinase may be "markerless", *i.e.*, may lack a selectable marker. A selectable marker used to transform a strain with a construct that includes an RNA-guided endonuclease and/or an exogenous gene encoding a site-specific recombinase can subsequently be excised by the action of the site-specific recombinase.

[0019] Also provided herein is a method of altering the genome of a cell *in vivo*, where the method comprises: introducing at least one guide RNA into a fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain, wherein the guide RNA targets a site in the genome of the cell; and screening cells transformed with the guide RNA for alteration of the targeted site in the genome. Alteration of the targeted genome site can be detected, for example, by PCR or by phenotypic screen. The RNA-guided endonuclease can be a Cas protein, such as a Cas9 protein.

[0020] Optionally, a donor fragment is also transformed into the host cell with the guide RNA, where the donor fragment optionally but preferably includes a selectable marker gene. The selectable marker gene of the donor fragment is used for selection of transformants. A donor fragment can optionally include homology regions for mediating insertion into the targeted site by homologous recombination.

[0021] A fully penetrant RNA-guided endonuclease-expressing cell line or strain can be any type of cell, for example, plants or animals, metazoan or protozoan. For example, cells derived from plants, mammals, amphibians, fish, birds, marsupials, reptiles, nematodes, crustaceans, arachnids, or insects can be transformed with a construct that encodes a cas protein, where the construct preferably but optionally includes a gene regulatory sequence such as a promoter operably linked to the cas-encoding sequence. Cell lines and strains of protozoan species are also considered, such as, but not limited to microalgae, heterokonts such as labyrinthulomycetes and oomyctes, mesomycetozoea, and fungi. Archaea and bacteria can also be hosts that express cas9 for genome editing.

[0022] Also provided herein are methods of editing the genome of a host cell, comprising, transforming a fully penetrant RNA-guided endonuclease -expressing host strain with at least one guide RNA that targets a site in the genome of the host cell and at least one donor DNA to generate at least one mutation in the targeted site of the host cell genome. The method is versatile, and allows for the donor DNA to include homology arms for recombination into the target locus, or to be free of sequences homologous to the host genome. For example, the donor DNA can be circular or linear and can include a selectable marker gene and/or one or more genes encoding a regulator, a metabolic enzyme, a

transporter, an RNAi construct, an antisense RNA construct, etc. or can include a sequence bound by a DNA binding protein, transcription factor, etc.

[0023] The guide RNA can be a chimeric guide RNA or can be a guide RNA that includes crRNA having homology to a locus in the host cell genome targeted for genome alteration and, preferably, a sequence homologous to the tracr RNA ("tracr mate sequence"). A tracr RNA can be provided separately. Further, the guide RNA, tracr RNA, and/or chimeric guide RNA can be encoded by a construct transformed into the host cell.

[0024] In any of the cell lines, microbial strains, and methods herein, an RNA-guided endonuclease can be a Cas nuclease, such as, without limitation, a Cas9, Cpf1, C2c1, C2c2, or C2c3 RNA-guided nuclease, a homolog of any thereof, of a modified version of any thereof.

[0025] A host cell can be a prokaryotic cell, an animal cell, a plant cell or a single-celled eukaryotic microbe, such as a fungal cell, heterokont cell, or algal cell. A heterokont cell can be, for example, a labrynthulocycete (*e.g.*, a member of any of the genera *Aplanochytrium, Aurantiochytrium, Diplophrys*, *Japonochytrium, Labryinthula, Labryinthuloides, Schizochytrium, Thraustochytrium,* or *Ulkenia*) or can be a diatom (*e.g.*, a member of *Acnanthes*, *Amphora, Chaetoceros*, *Cyclotella, Fragilaria, Fragilariopsis, Hantzschia, Navicula, Nitzchia, Phaedactylum*, or *Thalassiosira)*. A heterokont can also be a Eustigmatophyte, such as, for example, a species of *Eustigmatos, Monodus, Nannochloropsis, Pseudostaurastrum,* or *Vischeria.*

[0026] While the methods provided refer to "genome editing" it is to be understood that "genome editing" as disclosed herein includes *in vivo* editing (e.g., mis-repair, insertion, or other target site alteration) of any DNA molecule targeted within the host cell, for example, a native chromosome, a synthetic chromosome, a naturally-occurring or synthetic episomal molecule, a viral construct etc. Without limitation, the editing can effect gene disruption by insertion of a donor fragment that "knocks out" the gene or that disrupts a noncoding sequence that results in reduced expression of the gene. Alternatively or in addition, genome editing can introduce gene expression elements such as promoters that can increase expression of a gene. Genome editing as disclosed herein can further be used to introduce genes, such as exogenous genes, into a locus. Using the genome editing methods herein, multiple genes can be introduced into a genome target site on a donor fragment. The donor fragment can optionally include a detectable marker gene, e.g., a fluorescent protein gene, that can be used to evaluate penetrance of the introduced gene or genes that are physically linked to the detectable marker gene, using the methods provided herein.

[0027] Also provided herein are methods of screening a recombinant cell lines for full penetrance of an introduced gene. The introduced gene can encode a functional RNA or polypeptide. As disclosed in the examples herein, in addition to screening for fully penetrant expression of an RNA-guided endonuclease and a site specific recombinase, the methods of screening transformants by flow cytometry to identify cell lines having a single fluorescence peak where the fluorescence peak is at a higher fluorescence intensity that the peak seen in non-transformed cells can be used to isolate cell lines having fully penetrant expression of genes encoding functional RNAs, such as RNAi molecules and polypeptides, such as enzymes. Further, the comparison of fluorescence intensity levels of different transformed cells lines can allow for selection of cell lines with higher or lower expression levels overall. Such culture-wide screening can be more reliable than other methods, such as determining levels of expressed proteins.

BRIEF DESCRIPTION OF THE DRAWINGS

[0028] **Figure 1** is a diagram of vector pSGE-6133 that includes a Cas9 protein codon optimized for *Nannochloropsis* that includes a nuclear localization sequence (NLS) and a FLAG tag. The pSGE-6133 construct also includes a chimeric CRISPR guide RNA sequence targeting the acyl-CoA oxidase gene under the control of the *Nannochloropsis* U6 promoter.

[0029] **Figure 2** is a diagram of the Chord3-KO vector that includes homology arms for the CHORD-3266 gene of *Nannochloropsis* flanking a cassette that includes a GFP gene codon optimized for *Nannochloropsis* operably linked to the *Nannochloropsis* RPL24 promoter and a hygromycin resistance gene codon optimized for *Nannochloropsis* and operably linked to the *Nannochloropsis* EIF3 promoter. The GFP gene and HygR gene are operably linked to the same bidirectional terminator at their 3' ends.

[0030] **Figure 3** depicts a strategy for disrupting the *Nannochloropsis* CHORD-3266 gene using the CRISPR system. The Chord3-KO (knockout) vector depicted in Figure 2 is designed for double homologous recombination with homology regions that flank the CHORD-3266 CRISPR target sequence in the genome. A guide RNA molecule targeting CHORD is introduced along with the knockout vector. The guide RNA and Cas9 complex are depicted as scissors. The donor fragment can be the homologous recombination fragment (HR frag) released from the Chord3-KO (knockout) vector or the intact vector can be introduced into the host cell to generated recombinants. The diagnostic PCR primers are shown aligned over the locus that includes the donor fragment, which would result in an approximately 4 kb PCR product, and the native locus, which would result in an approximately 125 bp fragment if the donor fragment did not insert.

[0031] **Figure 4** is a diagram of vector pSGE-6206 that includes a Cas9 protein codon optimized for *Nannochloropsis* that includes a nuclear localization sequence (NLS) and also includes a GFP gene.

[0032] **Figure 5 A)** shows the readout from flow cytometry performed on a host cell line transformed with construct pSGE6202 that demonstrates full penetrance (single peak, shifted with respect to control). **B)** shows the readout from flow cytometry performed on a host cell line transformed with construct pSGE6202 that does not demonstrate full penetrance (two peaks, one of which is coincident with control peak).

[0033] **Figure 6** is a Western blot with an antibody that recognizes the FLAG-tagged cas9 protein. "S" identifies proteins from cells that demonstrated a single shifted peak in flow cytometry performed to assess penetrance, and "D" identifies proteins from cells that demonstrated two peaks in flow cytometry analysis.

[0034] **Figure 7** is a diagram of a vector (pSGE-6281) that includes homology arms for the CHORD gene of *Nannochloropsis* flanking a cassette that includes a hygromycin resistance gene.

[0035] **Figure 8** depicts the strategy for developing high efficiency Cas9 genome editing lines in which colonies are transformed with a construct that includes expression cassettes for each of a selectable marker (used to isolated transformants), a Cas9 nuclease, and a fluorescent protein. Culture from individual transformants (arising from single colonies) are screened by flow cytometry for a single shifted peak indicating full penetrance of expression of Cas9. The Western step need not be included in the method.

[0036] **Figure 9** is a diagram of a vector that includes homology arms for the acyl-CoA oxidase gene of *Nannochloropsis* flanking a cassette that includes a hygromycin resistance gene.

[0037] **Figure 10** is a diagram of a vector (pSGE-6709) that includes a gene encoding a cas9 polypeptide optimized for expression in *Parachlorella*. The construct also includes a gene encoding GFP and a gene encoding a blast gene optimized for expression in *Parachlorella*. Each of the cas9, GFP and blast genes is operably linked to a separate *Parachlorella* promoter.

[0038] **Figure 11** is a Western blot of *Parachlorella* strains transformed with pSGE-6709 and confirmed to be fully penetrant by flow cytometry (6709-1, 6709-2, and 6709-3) using an antibody against cas9. WT1185 is the wild type *Parachlorella* strain.

[0039] **Figure 12** shows gels of PCR products using primer sets for detecting insertion of the bleR cassette into the CRISPR-targeted cpSRP54 locus in fully penetrant cas9-expressing

Parachlorella strain GE-15699. The product of primers 596 and 597 is the wild type (unmodified) locus; the products of primers 405/597 and 406/597 result from targeted insertion of the bleR cassette.

[0040] **Figure 13A)** is a diagram of a donor DNA construct for promoter boosting; **B)** shows insertion sites of the donor DNA in the ACCase locus upstream of the coding region.

[0041] **Figure 14 A)** provides a schematic map of the ZnCys-2845 gene locus in Nannochloropsis with arrows depicting target sites for cas9 mediated insertion of a HygR cassette. Only locus 1 failed to result in a targeted insertion. **B)** provides the level of ZnCys-2845 gene knockdown for the various targeted insertion mutants.

[0042] **Figure 15** is a schematic diagram of the vector than included an RNAi construct for attenuation expression of the ZnCys-2845 gene. The vector included a blast gene for selection and a GFP gene for assessing penetrance of the genes of the inserted RNAi construct.

[0043] **Figure 16** provides a diagram of the 22.3 kb Donor DNA that included 6 genes, each with a separate promoter.

[0044] **Figure 17** provides photographs of PCR products diagnostic for the presence of the 22.3 kb integration fragment targeted to the acyl-CoA oxidase locus, with clones 5,6,7,8,9,20,27,38, & 31 having directed integration events.

[0045] **Figure 18** is a schematic diagram of vector pSGE-6483 that includes, in addition to a Cas9 gene, GFP gene, and HygR gene, a cre recombinase gene optimized for expression in Nannochloropsis. Each of the Cas9, GFP, HygR, and cre genes was operably linked to a separate Nannochloropsis promoter. The cre recombinase gene was operably linked to the ammonia-repressible Nitrite/Sulfite Reductase promoter.

[0046] **Figure 19** shows the results of flow cytometry penetrance screens of cells transformed with pSGE-6483 and the difference in peak fluorescence intensity of cells grown in ammonia versus nitrate.

[0047] **Figure 20** is photographs of gels of RT/PCR products assessing levels of the GFP transcript under different nitrogen conditions.

[0048] **Figure 21** provides a graphical representation of levels of the Cre transcript under different nitrogen conditions in transformants A11, B11, C12, D12, E12, and F12.

[0049] **Figure 22** provides a Western blot for detection of the Cre protein under different nitrogen conditions for transformants A11, B11, C12, D12, E12, and F12.

[0050] **Figure 22** provides a Western blot for detection of the Cas9 protein under different nitrogen conditions for transformants A11, B11, C12, D12, E12, and F12.

[0051] **Figure 24** is photographs of gels of PCR products of F12 and C12 cultures to determine whether the floxed GFP and BlastR gene cassettes were intact or excised by Cre-mediated recombination.

[0052] **Figure 25** is photographs of a gel of products of PCR to demonstrate in vivo excision of floxed GFP and BlastR gene cassettes.

[0053] **Figure 26** is photographs of gels of PCR products of F12 and C12 cultures to determine whether the floxed GFP and BlastR gene cassettes were intact or excised by Cre-mediated recombination.

[0054] **Figure 27** is a schematic diagram of the floxed GFP and BlastR gene cassettes.

[0055] **Figure 28** is a diagram showing cas9 mediated insertion of a floxed disruption cassette which following confirmation of the insertion, is induced for cre expression resulting in excision of the reporter (fluorescent protein) and selectable marker, allowing for recycling of these components in further engineering steps.

[0056] **Figure 29** provides a diagram of a construct for introduction into an algal cell that encodes a Type I FAS derived from an animal species. The construct also includes a gene encoding a pantetheine phosphotransferase (PPT). The genes are operably linked to algal promoters. The construct further includes a gene encoding a fluorescent protein for assessing culture-wide expression of the exogenous FAS and PPT genes.

[0057] **Figure 30** provides a diagram of a construct for introduction into an algal cell that encodes a Type I FAS derived from a labyrinthulomycete species. The gene is operably linked to an algal promoter. The construct further includes a gene encoding a fluorescent protein for assessing culture-wide expression of the exogenous FAS gene.

[0058] **Figure 31** provides flow cytometry traces (histograms) in which the flow cytometry profile of a *Nannochloropsis* tranformant that includes a *Danio rerio* Type I FAS gene is overlaid with the flow cytometry profile of a wild type (non-transformed) algal cell culture. The figure also provides Western blots showing levels of FAS protein expression in the profiled transformed lines. Line 6201-38 (rightmost flow cytometry trace) shows no difference in its fluorescence profile relative to non-transformed cells and shows no detectable FAS protein in the Western blot (third lane from the right). Other transformed lines show fully penetrant expression with fluorescence peaks that are distinct from the wild type peak. These strains also have detectable FAS protein as evidenced by the Western blots. WE3730 is the wild type strain which does not include a Type 1 FAS protein.

[0059] **Figure 32** provides flow cytometry traces (histograms) of *Nannochloropsis* transformants in which the flow cytometry profile of a tranformant that includes a *Danio*

rerio Type I FAS gene is overlaid with the flow cytometry profile of a wild type (non-transformed) algal cell culture. The figure also provides a Western blot comparing levels of FAS protein expression in the profiled transformed lines. WE3730 is the wild type strain which does not include a Type 1 FAS protein.

[0060] **Figure 33** provides flow cytometry traces (histograms) of *Nannochloropsis* transformants in which the flow cytometry profile of a tranformant that includes a labyrinthulomycete Type I FAS gene is overlaid with the flow cytometry profile of a wild type (non-transformed) algal cell culture. The figure also provides a Western blot comparing levels of FAS protein expression in the profiled transformed lines. WE3730 is the wild type strain which does not include a Type 1 FAS protein.

[0061] **Figure 34** provides a graph of FAS activity as assayed from cell extracts of transformants. Algal transformants having the labyrinthulomycete Type I FAS gene have the highest activity.

[0062] **Figure 35** provides a graph of *in vivo* FAS rate determination using isotope tracer (^{13}C) incorporation for ChytFAS transgenic lines grown under phototrophic conditions (A) and mixotrophic conditions (B). ChytFAS strain 6167-B outperformed the wild type strain under photoautotrophic conditions (A). Strain 6167-A was also tested under mixotrophic conditions, where it outperformed wild type in FAME production (B).

[0063] **Figure 36** provides a graph of *in vivo* FAS rate determination using isotope tracer incorporation for DrFAS over-expression strains grown under photoautotrophic (A, labeled with ^{13}C bicarbonate) and acetate-boosted mixotrophic (B, labeled with ^{13}C acetate) conditions. All DrFAS transformants were able to outperform the wild type strain under mixotrophic conditions.

DETAILED DESCRIPTION

[0064] Unless otherwise defined, all terms of art, notations and other scientific terms or terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art. Many of the techniques and procedures described or referenced herein are well understood and commonly employed using conventional methodology by those skilled in the art.

[0065] The singular form “a”, “an”, and “the” include plural references unless the context clearly dictates otherwise. For example, the term “a cell” includes one or more cells,

including mixtures thereof. “A and/or B” is used herein to include all of the following alternatives: “A”, “B”, “A or B”, and “A and B”.

[0066] “About” means either: within plus or minus 10% of the provided value, or a value rounded to the nearest significant figure, in all cases inclusive of the provided value. Where ranges are provided, they are inclusive of the boundary values.

[0067] As used herein, "amino acid" refers to naturally-occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally-occurring amino acids. Naturally-occurring amino acids are those encoded by the genetic code, including D/L optical isomers, as well as those amino acids that are later modified, *e.g.*, hydroxyproline, y-carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally-occurring amino acid, *i.e.*, a carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (*e.g.*, norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally-occurring amino acid. Amino acid mimetics, as used herein, refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally-occurring amino acid.

[0068] A “nucleotide” is the basic unit of a nucleic acid molecule and typically includes a base such as adenine, guanine, cytosine, thymine, or uracil linked to a pentose sugar such as ribose or deoxyribose that is in turn linked to a phosphate group. Nucleotides can also include alternative or non-naturally occurring bases or sugars that do not occur in naturally-occurring DNA or RNA. In peptide nucleic acids one or more sugars may be substituted by amino acids, and in some nucleic acid analogs at least a portion of the phosphates may be replaced by hydroxyl groups. Although nucleotides are often used to denote the length of a single-stranded nucleic acid molecule, and “base pairs” (*i.e.*, base paired nucleotides) are often used to denote the length of double-stranded nucleic acid molecules, in the present application, “nucleotides” or “nt” may be used interchangeably with “base pairs” or “bp”, and the use of one term or the other does not meant restrict the type of nucleic acid molecule being described to being either single-stranded or double-stranded. The use of kilobases or “kb” as units of length also applies equally to single-stranded and double-stranded nucleic acid molecules.

[0069] A “nucleic acid construct”, “DNA construct” or simply “construct” is a nucleic acid molecule produced by recombinant means that includes at least two juxtaposed or

operably linked nucleic acid sequences that are not juxtaposed or operably linked to one another in nature.

[0070] An "episomal DNA molecule" or "EDM" is an independently replicating nucleic acid molecule that is not integrated into the genome of the host organism in which the EDM resides and replicates. An EDM may be stable, in which it persists for many generations or unstable, where the EDM is gradually diluted out of the population by successive cell divisions. A stable EDM may be maintained in a cell population by selective pressure (*e.g.*, the presence of an antibiotic).

[0071] A "detectable marker" is a gene or the polypeptide encoded by the gene that confers some detectable phenotype on a cell that expresses the gene. Detection can be colorimetric (for example, the blue color by expression of beta galactosidase or beta-glucuronidase in the presence of a colorimetric substrate) or by detection of luminescence or fluorescence. A detectable marker generally encodes a detectable polypeptide, for example, a green fluorescent protein or a signal producing enzyme such as luciferase, which, when contacted with an appropriate agent (a particular, wavelength of light or luciferin, respectively) generates a signal that can be detected by eye or using appropriate instrumentation (Giacomin, *Plant Sci.* 116:59-72, 1996; Scikantha, *J. Bacteriol.* 178:121, 1996; Gerdes, *FEBS Lett.* 389:44-47, 1996; see, also, Jefferson, *EMBO J.* 6:3901-3907, 1997).

[0072] The term or "selectable marker" or "selection marker" refers to a gene (or the encoded polypeptide) that confers a phenotype that allows the organism expressing the gene to survive under selective conditions. For example, a selectable marker generally is a molecule that, when present or expressed in a cell, provides a selective advantage (or, if a negative selectable marker, disadvantage) to the cell containing the marker, for example, the ability to grow in the presence of an agent that otherwise would kill the cell, or the ability to grow in the absence of a particular nutrient.

[0073] A "cDNA" is a DNA molecule that comprises at least a portion the nucleotide sequence of an mRNA molecule, with the exception that the DNA molecule substitutes the nucleobase thymine, or T, in place of uridine, or U, occurring in the mRNA sequence. A cDNA can be single-stranded or double-stranded, and can be the complement of the mRNA sequence. In preferred embodiments, a cDNA does not include one or more intron sequences that occur in the naturally-occurring gene (in the genome of an organism) that the cDNA corresponds to. For example, a cDNA can have sequences from upstream (5') of an intron of a naturally-occurring gene juxtaposed to sequences downstream (3') of the intron of the

naturally-occurring gene, where the upstream and downstream sequences are not juxtaposed in a DNA molecule (*i.e.*, the naturally occurring gene) in nature. A cDNA can be produced by reverse transcription of mRNA molecules by a polymerase (*e.g.*, a reverse transcriptase), or can be synthesized, for example, by chemical synthesis and/or by using one or more restriction enzymes, one or more ligases, one or more polymerases (including, but not limited to, high temperature tolerant polymerases that can be used in polymerase chain reactions (PCRs)), one or more recombinases, *etc.*, based on knowledge of the cDNA sequence, where the knowledge of the cDNA sequence can optionally be based on the identification of coding regions from genome sequences and/or the sequences of one or more cDNAs.

[0074] A “coding sequence” or “coding region”, as used herein in reference to an mRNA or DNA molecule, refers to the portion of the mRNA or DNA molecule that codes for a polypeptide. It typically consists of the nucleotide residues of the molecule which are matched with an anticodon region of a transfer RNA molecule during translation of the mRNA molecule or which encode a stop codon. The coding sequence may include nucleotide residues corresponding to amino acid residues which are not present in the mature protein encoded by the mRNA molecule (*e.g.*, amino acid residues in a protein export signal sequence).

[0075] “Derived from” refers to the source of a nucleotide or amino acid sequence, and typically means the sequence of the nucleic acid molecule, protein, or peptide is based on that of the referenced nucleic acid molecule, protein, or peptide. The nucleic acid molecule, protein, or peptide is either a variant having at least 60% identity (and, in various examples, at least 75%, at least 70%, at least 75%, at least 80%, or at least 85% identity) to the referenced nucleic acid molecule, protein, or peptide, and/or is a truncated or internally deleted variant of the referenced nucleic acid molecule, protein, or peptide. For example, a protein or peptide may be C-terminally or N-terminally truncated or internally deleted with respect to the protein or peptide it is derived from and may have a C-terminal, N-terminal, or internal deletion of any number of amino acids, for example, at least 1, 2, 3, 4, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 amino acids. A nucleic acid molecule may be 5’ or 3’ truncated or internally deleted with respect to the nucleic acid molecule it is derived from and may have a 5’, 3’, or internal deletion of any number of nucleotides, for example, at least 1, 2, 3, 4, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, or 200 nucleotides.

[0076] The term "endogenous," within the context of the present disclosure refers to any polynucleotide, polypeptide or protein sequence which is a natural part of a cell or organism.

[0077] An "exogenous" nucleic acid molecule or gene is a nucleic acid molecule or gene that has been introduced into a host cell. For example, an exogenous nucleic acid molecule or gene is from one species and has been introduced ("transformed") into another organism, microorganism, or cell by human intervention, for example via a recombinant nucleic acid construct. An exogenous nucleic acid can be a sequence from one species introduced into another species, *i.e.*, a heterologous nucleic acid molecule. An exogenous nucleic acid molecule can also be a sequence that is homologous with respect to the host cell or organism (*i.e.*, the nucleic acid sequence occurs naturally in that species or encodes a polypeptide that occurs naturally in the host species) and that has been reintroduced into cells of that organism. An exogenous (introduced) nucleic acid molecule that includes a sequence that is homologous (of the same species) with respect to the host organism can often be distinguished from the naturally-occurring sequence by the presence of sequences linked to the homologous nucleic acid sequence, *e.g.*, regulatory sequences that are not native to the host organism flanking an endogenous gene sequence in a recombinant nucleic acid construct. Alternatively or in addition, a stably transformed exogenous nucleic acid molecule can be detected or distinguished from a native gene by its juxtaposition to sequences in the genome where it has integrated. A nucleic acid molecule is considered exogenous if it has been introduced into a progenitor of the cell, organism, or strain under consideration.

[0078] "Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to a nucleotide sequence of interest, which can optionally be operably linked to termination signals and/or other regulatory elements. An expression cassette may also comprise sequences that enable, mediate, or enhance translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a non-translated RNA, in the sense or antisense direction. An expression cassette may be assembled entirely extracellularly (*e.g.*, by recombinant cloning techniques). However, an expression cassette may also be assembled using in part endogenous components. For example, an expression cassette may be obtained by placing (or inserting) a promoter sequence upstream of an endogenous sequence, which thereby becomes functionally linked and controlled by said promoter sequences. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus.

[0079] "Expression vector" refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector comprises sufficient *cis*-acting elements for expression; other elements for expression can be supplied by the host cell or in an *in vitro* expression system. Examples of expression vectors known in the art include cosmids, plasmids and viruses (*e.g.*, retroviruses, lentiviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide.

[0080] An "oligonucleotide", as used herein, is a nucleic acid molecule 200 or fewer nucleotides in length. An oligonucleotide can be RNA, DNA, or a combination of DNA and RNA, a nucleic acid derivative, or a synthetic nucleic acid, for example, an oligonucleotide can be a peptide nucleic acid or a locked nucleic acid, and can be single-stranded, double-stranded, or partially single-stranded and partially double-stranded. An oligonucleotide can be, for example, between about 4 and about 200 nucleotides in length, between about 6 and about 200 nucleotides in length, between about 10 and about 200 nucleotides in length, between about 15 and about 200 nucleotides in length, between about 17 and about 200 nucleotides in length, between about 20 and about 200 nucleotides in length, or between about 40 and about 200 nucleotides in length. In additional examples, an oligonucleotide can be between about 15 and about 180 nucleotides in length, between about 15 and about 160 nucleotides in length, between about 15 and about 140 nucleotides in length, between about 15 and about 120 nucleotides in length, between about 17 and about 100 nucleotides in length, between about 17 and about 80 nucleotides in length, or between about 17 and about 70 nucleotides in length, for example between about 20 and about 65 nucleotides in length.

[0081] When used in reference to a polynucleotide, a gene, a nucleic acid, a polypeptide, or an enzyme, the term "heterologous" refers to a polynucleotide, gene, a nucleic acid, polypeptide, or an enzyme not derived from the host species, e.g., from a different species with respect to the host cell. For example, a transgenic Nannochloropsis microorganism transformed with the coding sequence for a fatty acid desaturase from a Tetraselmis microorganism or from a plant is transformed with a heterologous desaturase gene. When referring to nucleic acid sequences operably linked or otherwise joined to one another ("juxtaposed") in a nucleic acid construct or molecule, "heterologous sequences", as used herein, are those that are not operably linked or are not in proximity or contiguous to each other in nature. For example, a promoter from Tetraselmis sp. is considered heterologous to a Nannochloropsis coding region sequence. Also, a sequence encoding a Nannochloropsis fatty acid desaturase operably linked to a promoter from a gene encoding a tubulin gene from

Nannochloropsis is considered to be operably linked to a heterologous promoter. Similarly, when referring to a gene regulatory sequence or to an auxiliary nucleic acid sequence used for maintaining or manipulating a gene sequence (e.g. a 5' un-translated region, 3' un-translated region, Kozak sequence, poly A addition sequence, intron sequence, splice site, ribosome binding site, internal ribosome entry sequence, genome homology region, recombination site, etc.), "heterologous" means that the regulatory sequence or auxiliary sequence is from a different source (e.g., different gene, whether from the same or different species as the host organisms) than the gene with which the regulatory or auxiliary nucleic acid sequence is juxtaposed or operably linked in a construct, genome, chromosome, or episome.

[0082] The term "hybridization", as used herein, refers generally to the ability of nucleic acid molecules to join via complementary base strand pairing. Such hybridization may occur when nucleic acid molecules are contacted under appropriate conditions. As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity, *i.e.*, when every nucleotide of one of the molecules is complementary to its base pairing partner nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional low-stringency conditions. Molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional high-stringency hybridization conditions. Conventional stringency conditions are described by Sambrook *et al.*, (1989, *supra*), and by Haymes *et al.* In: *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, D.C. (1985). Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule or fragment thereof of the present invention to serve as a primer or probe it needs only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations and temperature employed.

[0083] Appropriate stringency conditions which promote nucleic acid hybridization include, for example, 6.0× sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0× SSC at about 50°C. In addition, the temperature in the wash step can be

increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed. These conditions are known to those skilled in the art, or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1- 6.3.6. For example, low stringency conditions may be used to select nucleic acid sequences with lower sequence identities to a target nucleic acid sequence. One may wish to employ conditions such as about 0.15 M to about 0.9 M sodium chloride, at temperatures ranging from about 20°C to about 55°C. High stringency conditions may be used to select for nucleic acid sequences with higher degrees of identity to the disclosed nucleic acid sequences (Sambrook *et al.*, 1989, *supra*). In one embodiment of the present invention, high stringency conditions involve nucleic acid hybridization in about 2×SSC to about 10×SSC (diluted from a 20×SSC stock solution containing 3 M sodium chloride and 0.3 M sodium citrate, pH 7.0 in distilled water), about 2.5× to about 5× Denhardt's solution (diluted from a 50× stock solution containing 1% (w/v) bovine serum albumin, 1% (w/v) ficoll, and 1% (w/v) polyvinylpyrrolidone in distilled water), about 10 mg/mL to about 100 mg/mL fish sperm DNA, and about 0.02% (w/v) to about 0.1% (w/v) SDS, with an incubation at about 50°C to about 70°C for several hours to overnight. High stringency conditions are typically provided by 6×SSC, 5× Denhardt's solution, 100 mg/mL fish sperm DNA, and 0.1% (w/v) SDS, with incubation at 55°C for several hours. Hybridization is generally followed by several wash steps. The wash compositions generally comprise 0.5×SSC to about 10×SSC, and 0.01% (w/v) to about 0.5% (w/v) SDS with an incubation for 15-min at about 20°C to about 70°C. Typically, complementary nucleic acid segments remain hybridized after washing at least one time in 0.1×SSC at 65°C.

[0084] "Percentage of sequence identity," as used herein for the identified centromere sequences, is determined by comparing the specified centromere sequence or fragment thereof with an optimally locally aligned sequence over a comparison window defined by the specified length of the nucleotide sequence (*e.g.*, centromere fragment) set forth. In other contexts, the comparison window for percentage sequence identity between two sequences is defined by the local alignment between the two sequences. For example, an amino acid or nucleotide sequence in the comparison window may comprise additions or deletions (*e.g.*, gaps or overhangs) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. In this context, local alignment between two sequences only includes segments of each sequence that are deemed

to be sufficiently similar according to a criterion that depends on the algorithm used to perform the alignment (*e.g.* BLAST). The percentage identity is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (*Add. APL. Math.* 2:482, 1981), by the global homology alignment algorithm of Needleman and Wunsch (*J. Mol. Biol.* 48:443, 1970), by the search for similarity method of Pearson and Lipman (*Proc. Natl. Acad. Sci.* USA 85: 2444, 1988), by heuristic implementations of these algorithms (NCBI BLAST, WU-BLAST, BLAT, SIM, BLASTZ), or by inspection. GAP and BESTFIT, for example, can be employed to determine their optimal alignment of two sequences that have been identified for comparison. Typically, the default values of 5.00 for gap weight and 0.30 for gap weight length are used. The term "substantial sequence identity" between polynucleotide or polypeptide sequences refers to polynucleotide or polypeptide comprising a sequence that has at least 50% sequence identity, for example, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 96%, 97%, 98% or 99% sequence identity compared to a reference sequence using the programs. In addition, pairwise sequence homology or sequence similarity, as used refers to the percentage of residues that are similar between two sequences aligned. Families of amino acid residues having similar side chains have been well defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine).

[0085] For example, query nucleic acid and amino acid sequences can be searched against subject nucleic acid or amino acid sequences residing in public or proprietary databases. Such searches can be done using the National Center for Biotechnology Information Basic Local Alignment Search Tool (NCBI BLAST v 2.18) program. The NCBI BLAST program is available on the internet from the National Center for Biotechnology Information (blast.ncbi.nlm.nih.gov/Blast.cgi). Exemplary parameters for NCBI BLAST include: Filter options set at "default", the Comparison Matrix set to "BLOSUM62", the Gap Costs set to "Existence: 11, Extension: 1", the Word Size set to 3, the Expect (E threshold)

set to 1e-3, and the minimum length of the local alignment set to 50% of the query sequence length. Sequence identity and similarity may also be determined using GENOMEQUEST™ software (Gene-IT, Worcester, Mass. USA).

[0086] As used herein, an "isolated" nucleic acid molecule or protein is removed from its natural milieu or the context in which the nucleic acid molecule or protein exists in nature. For example, an isolated protein or nucleic acid molecule is removed from the cell or organism with which it is associated in its native or natural environment. As such, an "isolated" nucleic acid molecule typically is free of sequences that naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the cell of the organism from which the nucleic acid is derived. An isolated nucleic acid molecule or protein can be, in some instances, partially or substantially purified, but no particular level of purification is required for isolation. For example, an isolated nucleic acid molecule can be a nucleic acid sequence that has been excised from the chromosome, genome, or episome that it is integrated into in nature. Thus, an isolated nucleic acid includes, without limitation, a nucleic acid that exists as a purified molecule, or a nucleic acid molecule that is incorporated into a vector or a recombinant cell.

[0087] The terms “microbe” and “microorganism” are used interchangeably to refer to organisms that are too small to be seen with the naked eye. Microbes or microorganisms includes bacteria and protozoa, including unicellular and colonial protozoa such as, but not limited to, fungi, amoebae, mesomycetozoea, single-celled heterokonts (e.g., labyrinthylomycetes, oomyctes), and microalgae.

[0088] A "purified" nucleic acid molecule or nucleotide sequence is substantially free of cellular material and cellular components. The purified nucleic acid molecule may be free of chemicals beyond buffer or solvent, for example. "Substantially free" is not intended to mean that other components beyond the novel nucleic acid molecules are undetectable. In some circumstances "substantially free" may mean that the nucleic acid molecule or nucleotide sequence is free of at least 95% (w/w) of cellular material and components.

[0089] The term "native" is used herein to refer to nucleic acid sequences or amino acid sequences as they naturally occur in the host. The term "non-native" is used herein to refer to nucleic acid sequences or amino acid sequences that do not occur naturally in the host, or are not configured as they are naturally configured in the host. For example, non-native genes include introduced genes that are homologous with respect to the host (that is, of the same species as the host) that re-introduced into the host with a heterologous promoter and/or lacking one or more introns that occur in the native gene. A nucleic acid sequence or amino

acid sequence that has been removed from a host cell, subjected to laboratory manipulation, and introduced or reintroduced into a host cell is considered "non-native." Non-native genes further include genes endogenous to the host microorganism operably linked to one or more heterologous regulatory sequences that have been recombined into the host genome, or genes endogenous to the host organism that are in a locus of the genome other than that where they naturally occur.

[0090] In reference to a nucleic acid molecule or a polypeptide, the terms "naturally-occurring" and "wild-type" refer to a form found in nature. For example, a naturally occurring or wild-type nucleic acid molecule, nucleotide sequence or protein may be present in and isolated from a natural source, and is not intentionally modified by human manipulation.

[0091] The terms "nucleic acid molecule" and "polynucleotide molecule" are used interchangeably herein, and refer to both DNA and RNA molecule, including cDNA, genomic DNA, synthetic DNA, and DNA or RNA containing nucleic acid analogs. Polynucleotides can have any three-dimensional structure. Polynucleotides can be natural-occurring or synthetic origin. A nucleic acid molecule can be double-stranded or single-stranded. Non-limiting examples of polynucleotides include genes, gene fragments, exons, introns, messenger RNA (mRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), siRNA, micro-RNA, ribozymes, tracr RNAs, crRNAs, chimeric guide RNAs, cDNA, recombinant polynucleotides, branched polynucleotides, nucleic acid probes and nucleic acid primers. A polynucleotide may contain unconventional or modified nucleotides.

[0092] As used herein, "operably linked" is intended to mean a functional linkage between two or more sequences such that activity at or on one sequence affects activity at or on the other sequence(s). For example, an operable linkage between a polynucleotide of interest and a regulatory sequence (*e.g.*, a promoter) is a functional link that allows for expression of the polynucleotide of interest. In this sense, the term "operably linked" refers to the positioning of a regulatory region and a coding sequence to be transcribed so that the regulatory region is effective for regulating transcription or translation of the coding sequence of interest. For example, to operably link a coding sequence and a regulatory region, the translation initiation site of the translational reading frame of the coding sequence is typically positioned between one and about fifty nucleotides downstream of the regulatory region. A regulatory region can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site. Operably linked elements may be contiguous or non-contiguous. When used to refer to the joining of two protein coding regions, by “operably linked” is intended that the coding

regions are in the same reading frame. When used to refer to the effect of an enhancer, "operably linked" indicated that the enhancer increases the expression of a particular polypeptide or polynucleotides of interest. "Juxtaposed with" in the context of nucleic acid sequences, means the referenced sequences are part of the same continuous nucleic acid molecule, such as a nucleic acid construct introduced into a cell. The term "physically linked", as used herein when referring to nucleic acid sequences, means that the nucleic acid sequence are either part of the same continuous nucleic acid molecule such as a nucleic acid construct introduced into a cell, for example, or, for the purposed of the invention, are positioned on genomic DNA (e.g., a chromosome) within 200 kb of one another, and generally within 100 kb of one another, within 50 kb of one another, or within 25 kb of one another.

[0093] The term "penetrance" is used in genetics to indicate the variability of phenotype observed among organisms being genetically identical for a given gene that is known to influence the phenotype. Differences in penetrance, or the degree to which a trait is expressed in an organism, can rely on the genetic background of an individual organism or can be influenced by environmental or epigenetic factors. In the present application, "penetrance" is used to refer to the presence or absence of differences in expression level of a gene introduced into a microorganisms or cells, where the transformed gene is identical and is operably linked to (regulated by) the same promoter. In a cell population resulting from a single transformant, incomplete penetrance of expression of a transgene results in subpopulations that do not express the transgene at a level greater than background. For example, where the transgene encodes a fluorescent protein, incomplete penetrance can be observed by flow cytometry as, typically, either a single fluorescence peak that coincides with the autofluorescence peak of nontransformed cells, or two expression (fluorescence intensity) peaks, one of which coincides with the autofluorescence peak of nontransformed cells, that is, a portion of the transformed population is not expressing the transgene. Without limiting the invention to any particular mechanism, it may be that the observed differences in expression of a transgene rely at least in part on the site in the genome into which the gene has integrated, *e.g.*, "position effects" that results in inconsistent expression of the transgene throughout a clonal culture that may be due, for example, to cell cycle stages of cells at any given time throughout the culture, nutrient or environmental status of cells throughout the culture, or unknown epigenetic, stochastic, or environmental factors. "Fully penetrant" expression, where the transgene encodes a fluorescent protein, can be observed as a single

fluorescence intensity peak in flow cytometry histograms, where the single fluorescence intensity peak is greater than the autofluorescence peak of nontransformed cells.

[0094] The terms "polynucleotide sequence" and "nucleic acid sequence" as used herein interchangeably refer to a sequence of a polynucleotide molecule, and can refer, for example, to DNA or RNA sequences. The nomenclature for nucleotide bases as set forth in 37 CFR §1.822 is used herein.

[0095] A "promoter" refers to a transcription control sequence that is capable of initiating transcription in a host cell and can drive or facilitate transcription of a nucleotide sequence or fragment thereof of the instant invention. Such promoters need not be of naturally-occurring sequences. In addition, it will be understood that such promoters need not be derived from the target host cell or host organism.

[0096] “Polypeptide” and “protein” are used interchangeably herein and refer to a compound of two or more subunit amino acids, amino acid analogs, or other peptidomimetics, regardless of post-translational modification, *e.g.*, phosphorylation or glycosylation. The subunits may be linked by peptide bonds or other bonds such as, for example, ester or ether bonds. Full-length polypeptides, truncated polypeptides, point mutants, insertion mutants, splice variants, chimeric proteins, and fragments thereof are encompassed by this definition. In various embodiments the polypeptides can have at least 10 amino acids or at least 25, or at least 50 or at least 75 or at least 100 or at least 125 or at least 150 or at least 175 or at least 200 amino acids.

[0097] As used herein "progeny" means a descendant, offspring, or derivative of an organism. For example, daughter cells from a transgenic alga are progeny of the transgenic alga. Because certain modifications may occur in succeeding generations due to mutations or environmental influences, such progeny, descendant, or derivatives may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[0098] The terms "recombinant" or "engineered" as used herein in reference to a nucleic acid molecule, refer to a nucleic acid molecule that has been altered through human intervention. As non-limiting examples, a cDNA is a recombinant DNA molecule, as is any nucleic acid molecule that has been generated by *in vitro* polymerase reaction(s), or to which linkers have been attached, or that has been integrated into a vector, such as a cloning vector or expression vector. As non-limiting examples, a recombinant nucleic acid molecule: 1) has been synthesized or modified *in vitro*, for example, using chemical or enzymatic techniques (for example, by use of chemical nucleic acid synthesis, or by use of enzymes for the replication, polymerization, exonucleolytic digestion, endonucleolytic digestion, ligation,

reverse transcription, transcription, base modification (including, *e.g.*, methylation), or recombination (including homologous and site-specific recombination)) of nucleic acid molecules; 2) includes conjoined nucleotide sequences that are not conjoined in nature; 3) has been engineered using molecular cloning techniques such that it lacks one or more nucleotides with respect to the naturally occurring nucleic acid molecule sequence; and/or 4) has been manipulated using molecular cloning techniques such that it has one or more sequence changes or rearrangements with respect to the naturally occurring nucleic acid sequence. A "recombinant protein" is a protein produced by genetic engineering, for example, by expression of a genetically engineered nucleic acid molecule in a cell.

[0099] The term "regulatory region" "regulatory sequence", "regulatory element", or "regulatory element sequence", as used in the present invention, refer to a nucleotide sequence that influences transcription or translation initiation or rate, and stability and/or mobility of a transcription or translation product. Such regulatory regions need not be of naturally-occurring sequences. Regulatory sequences include but are not limited to promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5' and 3' un-translated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, introns, and combinations thereof. A regulatory region typically comprises at least a core (basal) promoter. A regulatory region also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR).

[00100] As used herein, a "synthetic chromosome construct" is a DNA construct that includes a centromere and at least one ARS. The term "synthetic chromosome" is used herein to refer to a synthetic chromosome construct that is autonomously replicating and faithfully segregating in a host cell. By "faithfully segregating" is meant that the synthetic chromosome equally partitions into two daughter cells during cell division (*i.e.*, the centromere is activated within the host cell).

[00101] As used herein, "transgenic organism" refers to an organism which comprises a heterologous polynucleotide. When applied to organisms, the terms "transgenic" or "recombinant" or "engineered" or "genetically engineered," used interchangeably herein, refer to organisms that have been manipulated by introduction into the organism of an exogenous or recombinant nucleic acid sequence. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations, although it can also be present on an episome, and may be present on a synthetic chromosome of the transgenic organism. The non-native polynucleotide may be integrated

into the genome alone or as part of a recombinant expression cassette. In additional examples, a transgenic microorganism can include an introduced exogenous regulatory sequence operably linked to an endogenous gene of the transgenic microorganism. Non-limiting examples of such manipulations include gene knockouts, targeted mutations and gene replacement, promoter replacement, deletion, or insertion, as well as introduction of transgenes into the organism. Recombinant or genetically engineered organisms can also be organisms into which constructs for gene "knock down" have been introduced. Such constructs include, but are not limited to, RNAi, microRNA, shRNA, antisense, and ribozyme constructs. Also included are organisms whose genomes have been altered by the activity of meganucleases, TALENs, zinc finger nucleases, or CRISPR nucleases. As used herein, "recombinant microorganism" or "recombinant host cell" includes progeny or derivatives of the recombinant microorganisms of the invention. Because certain modifications may occur in succeeding generations from either mutation or environmental influences, such progeny or derivatives may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[00102] For nucleic acids and polypeptides, the term "variant" is used herein to denote a polypeptide, protein, or polynucleotide molecule with some differences, generated synthetically or naturally, in their base or amino acid sequences as compared to a reference polypeptide or polynucleotide, respectively, such that the variant has at least 70% sequence identity with the reference polypeptide or polynucleotide. In other embodiments the variant can have at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with the reference polypeptide or polynucleotide. Alternatively or in addition, a variant can have one or more insertions or deletions in response to a reference polypeptide or polynucleotide. For example, protein variants may be N-terminally truncated or C-terminally truncated with respect to the reference sequence, or can have one or more internal deletions, while nucleic acid variants may have a 5' end and/or 3'end sequence truncation and/or can have one or more internal deletions. Further, a protein variant may have an additional sequence added to the N-terminus and/or C-terminus with respect to the reference sequence, or can have one or more internal additional sequences, while nucleic acid variants may have a 5' end and/or 3'end sequence addition and/or can have one or more internal sequence additions. A variant can have any desired combination of substitutions, insertions, and/or deletions with respect to a reference polypeptide or polynucleotide. Polypeptide and protein variants can further include differences in post-translational modifications (such as glycosylation, methylation. phosphorylation, *etc.*). When

the term "variant" is used in reference to a microorganism, it typically refers to a strain microbial strain having identifying characteristics of the species to which it belongs, while having at least one nucleotide sequence variation or identifiably different trait with respect to the parental strain, where the trait is genetically based (heritable).

[00103] A "vector" is any genetic element capable of serving as a vehicle of genetic transfer, expression, or replication for a foreign polynucleotide in a host cell. For example, a vector may be an artificial chromosome or a plasmid, and may be capable of stable integration into a host cell genome, or it may exist as an independent genetic element (*e.g.*, episome, plasmid). A vector may exist as a single polynucleotide or as two or more separate polynucleotides. Vectors may be single copy vectors or multicopy vectors when present in a host cell.

[00104] "RNA-guided nuclease" is used herein to refer generically to enzymes of CRISPR systems in which the referred to nuclease hydrolyzes DNA in a site-specific manner, where the targeted site is determined by an RNA molecule that interacts with the nuclease. Examples of RNA-guided nucleases include but are not limited to Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9, Cas10, Cbf1, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Cpf1, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, C2c1, C2c2, C2c3, homologs thereof, and modified versions thereof.

[00105] A "CRISPR system" or "CRISPR-cas system" refers to a Cas protein, such as but not limited to a Cas9 protein or a variant thereof, or a nucleic acid molecule encoding a Cas protein, along with one or more RNAs required for targeting and/or altering a genetic locus. For example, a CRISPR-cas system can include a Cas protein or a nucleic acid molecule encoding a Cas protein and at least one tracrRNA ("trans-activating CRISPR RNA") or gene encoding a tracr RNA and at least one crRNA or "CRISPR RNA" or gene encoding a crRNA, in which the crRNA comprises sequences homologous to a target nucleic acid sequence. The crRNA may further include a "tracr mate" sequence that is able to hybridize with the tracrRNA. Alternatively, a CRISPR system can include a cas protein (or a gene or transcript encoding a cas protein) and a gene or transcript that includes both the tracrRNA and crRNA sequences. A single RNA molecule that includes both a tracr sequence and a cr (target homologous) sequence is referred to herein as a "chimeric guide RNA" or simply a "guide RNA". A crRNA or guide RNA can further include a tracr-mate sequence (encompassing a "direct repeat" and/or a tracrRNA-processed partial direct repeat as in an endogenous CRISPR system). In some embodiments, one or more elements of a CRISPR

system is derived from a type I, type II, or type III CRISPR system. CRISPR-cas systems and their use in genome editing are disclosed in Jinek et al. (2012) *Science* 337:816-821; Brouns (2012) *Science* 337:808; Gaj et al. (2013) *Trends in Biotechnol.* 31:397-405; Hsu et al. (2013) *Cell* 157:1262-1278; Mali et al. (2013) *Science* 339:823-826; Qi et al. (2013) *Cell* 152:1173-1183; Walsh & Hochedlinger (2013) *Proc Natl Acad Sci* 110:155414-155515; Sander & Joung (2014) *Nature Biotechnology*; Sternberg et al. (2014) *Nature* 507:63-67; U.S. Patent Application Publication No. 2014/0068797; U.S. Patent No. 8,697,359; U.S. Patent Application Publication No. 20140170753; U.S. Patent Application Publication No. 20140179006; U.S. Patent No. 20140179770; U.S. Patent Application Publication No. 20140186843; and U.S. Patent Application Publication No. US 20150045546; all of which are incorporated by reference in their entireties.

[00106] In general, a CRISPR system is characterized by elements that promote the formation of a CRISPR complex at the site of a target sequence (also referred to as a protospacer in the context of an endogenous CRISPR system). In the context of formation of a CRISPR complex, "target sequence" refers to a sequence to which a guide sequence is designed to have complementarity, where hybridization between a target sequence and a guide sequence promotes the formation of a CRISPR complex. Full complementarity is not necessarily required, provided there is sufficient complementarity to cause hybridization and promote formation of a CRISPR complex. A target sequence may comprise any polynucleotide, such as DNA or RNA polynucleotides. A sequence or template that may be used for recombination into the targeted locus comprising the target sequences is referred to as an "editing template" or "editing sequence", “donor sequence” or "donor DNA". In aspects of the invention, an exogenous template polynucleotide may be referred to as a donor DNA molecule.

[00107] As used herein, a “meganuclease” also known as a “homing endonuclease” is an endodeoxynuclease with a recognition site of at least 12 base pairs. Homing endonucleases are well-known to the art (e.g. Stoddard, Quarterly Reviews of Biophysics, 2006, 38:49-95). Homing endonucleases recognize a DNA target sequence and generate a single- or double-strand break. Homing endonucleases are highly specific, recognizing DNA target sites ranging from 12 to 45 base pairs (bp) in length, usually ranging from 14 to 40 bp in length. Examples of such endonuclease include I-Sce I, I-Chu I, I-Cre I, I-Csm I, PI-Sce I, PI-Tli I, PI-Mtu I, I-Ceu I, I-Sce II, I-Sce III, HO, PI-Civ I, PI-Ctr I, PI-Aae I, PI-Bsu I, PI-Dha I, PI-Dra I, PI-Mav I, PI-Mch I, PI-Mfu I, PI-Mfl I, PI-Mga I, PI-Mgo I, PI-Min I, PI-Mka I, PI-Mle I, PI-Mma I, PI-Msh I, PI-Msm I, PI-Mth I, PI-Mtu I, PI-Mxe I, PI-Npu I, PI-Pfu I, PI-

Rma I, PI-Spb I, PI-Ssp I, PI-Fac I, PI-Mja I, PI-Pho I, PI-Tag I, PI-Thy I, PI-Tko I, PI-Tsp I, and I-Msol.

[00108] As used herein, a "zinc finger nuclease" is an engineered restriction enzyme that includes a zinc finger DNA-binding domain fused to a restriction endonuclease, such as, for example, a meganuclease or the restriction nuclease FokI. The zinc finger domain can be engineered to bind to particular DNA sequences for targeting of specific genome sites.

[00109] A "TALE" or "Transcription activator-like effector" is a DNA-binding protein that can recognize particular bases in the DNA sequence by the sequence of amino acids in its central repeat domain. TALE proteins thus can be engineered to bind particular DNA sequences and may be fused to nuclease domains (*e.g.*, a FokI nuclease) as "TALENs" or "Transcription activator-like effector nucleases".

[00110] All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

[00111] No admission is made that any reference constitutes prior art. The discussion of the references states what their authors assert, and the applicants reserve the right to challenge the accuracy and pertinence of the cited documents. It will be clearly understood that, although a number of prior art publications are referred to herein; this reference does not constitute an admission that any of these documents forms part of the common general knowledge in the art.

[00112] The discussion of the general methods given herein is intended for illustrative purposes only. Other alternative methods and embodiments will be apparent to those of skill in the art upon review of this disclosure.

CRISPR Systems

[00113] CRISPR systems include, in addition to the cas9 nuclease, a targeting RNA often denoted "crRNA" that interacts with the genome target site by complementarity with a target site sequence, a transactivating RNA that complexes with the cas9 polypeptide and also includes a region that binds (by complementarity) the targeting crRNA.

[00114] The nuclease activity cleaves target DNA to produce double strand breaks. These breaks are then repaired by the cell in one of two ways: non-homologous end joining, and homology-directed repair. In non-homologous end joining (NHEJ), the double-strand breaks are repaired by direct ligation of the break ends to one another. In this case, no new nucleic acid material is inserted into the site, although some nucleic acid material may be lost, resulting in a deletion. In homology-directed repair, a donor polynucleotide with homology to

the cleaved target DNA sequence is used as a template for repair of the cleaved target DNA sequence, resulting in the transfer of genetic information from the donor polynucleotide to the target DNA. As such, new nucleic acid material may be inserted/copied into the site. In some cases, a target DNA is contacted with a donor DNA, for example a donor DNA introduced into a host cell. The modifications of the target DNA due to NHEJ and/or homology-directed repair can lead to, for example, gene correction, gene replacement, gene tagging, transgene insertion, nucleotide deletion, gene disruption, gene mutation, etc.

[00115] In some instances, cleavage of DNA by a site-directed modifying polypeptide may be used to delete nucleic acid material from a target DNA sequence by cleaving the target DNA sequence and allowing the cell to repair the sequence in the absence of an exogenously provided donor polynucleotide.

[00116] Alternatively, if a DNA-targeting RNA and a cas polypeptide are coadministered to cells with a donor DNA, the subject methods may be used to add, i.e. insert or replace, nucleic acid material to a target DNA sequence (e.g. “knock out” by insertional mutagenesis, or "knock in" a nucleic acid that encodes for a protein, an siRNA, an miRNA, etc.), to add a tag (e.g., a fluorescent protein (e.g., a green fluorescent protein; a yellow fluorescent protein, etc.), hemagglutinin (HA), FLAG, etc.), to add a regulatory sequence to a gene (e.g. promoter, polyadenylation signal, internal ribosome entry sequence (IRES), 2A peptide, start codon, stop codon, splice signal, localization signal, etc.), to modify a nucleic acid sequence (e.g., introduce a mutation), and the like.

[00117] The invention contemplates the use of two RNA molecules (“crRNA” and “tracrRNA”) that can be cotransformed into a host strain for genome editing, or, as disclosed in the examples herein, a single guide RNA that includes a sequence complementary to a target sequence as well as a sequence that interacts with the cas9 protein. That is, a CRISPR system s used herein can comprise two separate RNA molecules (RNA polynucleotides: an "activator-RNA" and a "targeter-RNA", see below) and is referred to herein as a "double-molecule DNA-targeting RNA" or a "two-molecule DNA-targeting RNA." Alternatively, as illustrated in the examples, the DNA-targeting RNA can be a single RNA molecule (single RNA polynucleotide) and is referred to herein as a "chimeric guide RNA," a "single-guide RNA," or an "sgRNA." The term "DNA-targeting RNA" or "gRNA" is inclusive, referring both to double-molecule DNA-targeting RNAs and to single-molecule DNA-targeting RNAs (*i.e.*, sgRNAs).

[00118] An exemplary two-molecule DNA-targeting RNA comprises a crRNA-like ("CRISPR RNA" or "targeter-RNA" or "crRNA" or "crRNA repeat") molecule and a

corresponding tracrRNA-like ("trans-acting CRISPR RNA" or "activator-RNA" or "tracrRNA") molecule. A crRNA-like molecule (targeter-RNA) comprises both the DNA-targeting segment (single stranded) of the DNA-targeting RNA and a stretch ("duplex-forming segment") of nucleotides that forms one half of the dsRNA duplex of the protein-binding segment of the DNA-targeting RNA. A corresponding tracrRNA-like molecule (activator-RNA) comprises a stretch of nucleotides (duplex-forming segment) that forms the other half of the dsRNA duplex of the protein-binding segment of the DNA-targeting RNA. In other words, a stretch of nucleotides of a crRNA-like molecule are complementary to and hybridize with a stretch of nucleotides of a tracrRNA-like molecule to form the dsRNA duplex of the protein-binding domain of the DNA-targeting RNA. As such, each crRNA-like molecule can be said to have a corresponding tracrRNA-like molecule. The crRNA-like molecule additionally provides the single stranded DNA-targeting segment. Thus, a crRNA-like and a tracrRNA-like molecule (as a corresponding pair) hybridize to form a DNA-targeting RNA. The exact sequence of a given crRNA or tracrRNA molecule is characteristic of the species in which the RNA molecules are found.

[00119] The term "activator-RNA" is used herein to mean a tracrRNA-like molecule of a double-molecule DNA-targeting RNA. The term "targeter-RNA" is used herein to mean a crRNA-like molecule of a double-molecule DNA-targeting RNA. The term "duplex-forming segment" is used herein to mean the stretch of nucleotides of an activator-RNA or a targeter-RNA that contributes to the formation of the dsRNA duplex by hybridizing to a stretch of nucleotides of a corresponding activator-RNA or targeter-RNA molecule. In other words, an activator-RNA comprises a duplex-forming segment that is complementary to the duplex-forming segment of the corresponding targeter-RNA. As such, an activator-RNA comprises a duplex-forming segment while a targeter-RNA comprises both a duplex-forming segment and the DNA-targeting segment of the DNA-targeting RNA. Therefore, a subject double-molecule DNA-targeting RNA can be comprised of any corresponding activator-RNA and targeter-RNA pair.

[00120] A "host cell," as used herein, denotes an in vivo or in vitro eukaryotic cell, a prokaryotic cell (e.g., bacterial or archaeal cell), or a cell from a multicellular organism (e.g., a cell line) cultured as a unicellular entity, in which the eukaryotic or prokaryotic cells can be or have been used as recipients for a nucleic acid. “Host cells” also include the progeny of the original cell which has been transformed by the nucleic acid. It is understood that the progeny of a single cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to natural, accidental, or deliberate

mutation. A "recombinant host cell" (also referred to as a "genetically modified host cell") is a host cell into which has been introduced an exogenous nucleic acid, for example, an expression cassette or vector.

[00121] Both single-molecule guide RNAs and two RNA systems have been described in detail in the literature and for example, in US20140068797, incorporated by reference herein. Any Cas9 protein can be used in the methods herein (see, for example, the cas9 proteins provided as SEQ ID NOs:1-256 and 795-1346 in US20140068797), including chimeric cas9 proteins that may combine domains from more than one cas9 protein, as well variants and mutants of identified cas9 proteins.

[00122] For example, one mutant of the Cas9 polypeptide is a D10A (aspartate to alanine at amino acid position 10) mutation (or the corresponding mutation of any of the proteins set forth as SEQ ID NOs:1-256 and 795-1346 of US20140068797) that can cleave the complementary strand of the target DNA but has reduced ability to cleave the non-complementary strand of the target DNA (thus resulting in a single strand break (SSB) instead of a double strand break (DSB)). In some embodiments, the modified form of the Cas9 polypeptide is a H840A (histidine to alanine at amino acid position 840) mutation (or the corresponding mutation of any of the proteins set forth as SEQ ID NOs:1-256 and 795-1346) that can cleave the non-complementary strand of the target DNA but has reduced ability to cleave the complementary strand of the target DNA (thus resulting in a SSB instead of a DSB). The use of the D10A or H840A variant of Cas9 (or the corresponding mutations in any of the proteins set forth as SEQ ID NOs:1-256 and 795-1346 of US20140068797) can alter the expected biological outcome because the non-homologous end joining (NHEJ) is much more likely to occur when DSBs are present as opposed to SSBs. Other residues can be mutated to achieve the same effect (i.e. inactivate one or the other nuclease portions). As non-limiting examples, residues D10, G12, G17, E762, H840, N854, N863, H982, H983, A984, D986, and/or A987 (or the corresponding mutations of any of the proteins set forth as SEQ ID NOs:1-256 and 795-1346) can be altered (i.e., substituted) (see FIG. 3, FIG. 5, FIG. 11A, and Table 1 for more information regarding the conservation of Cas9 amino acid residues). Also, mutations other than alanine substitutions are suitable. In some embodiments when a site-directed polypeptide (e.g., site-directed modifying polypeptide) has reduced catalytic activity (e.g., when a Cas9 protein has a D10, G12, G17, E762, H840, N854, N863, H982, H983, A984, D986, and/or a A987 mutation, e.g., D10A, G12A, G17A, E762A, H840A, N854A, N863A, H982A, H983A, A984A, and/or D986A), the polypeptide can still bind to target DNA in a site-specific manner (because it is still guided to a target DNA sequence by a

DNA-targeting RNA) as long as it retains the ability to interact with the DNA-targeting RNA.

In some examples, the modified form of the Cas9 polypeptide harbors both the D10A and the H840A mutations (or the corresponding mutations of any of the proteins set forth as SEQ ID NOs:1-256 and 795-1346 of US20140068797) such that the polypeptide has a reduced ability to cleave both the complementary and the non-complementary strands of the target DNA (i.e., the variant can have no substantial nuclease activity).

Cas proteins

[00123] A Cas protein encoded by a nucleic molecule introduced into a host cell can be any cas protein, such as, for example, Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas10, Cpf1, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, C2c1, C2c2, C2c3, homologs thereof, or modified versions thereof. The Cas protein can be a Cas9 protein, such as a Cas9 protein of *S. pyogenes*, *S. thermophilus*, *S. pneumonia*, or *Neisseria meningitidis*, as nonlimiting examples. The Cas9 enzyme can cleave one or both strands of DNA at the location of a target sequence, such as within the target sequence and/or within the complement of the target sequence. For example, the cas9 enzyme can directs cleavage of one or both strands within about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 50, 100, or 200 base pairs from the first or last nucleotide of a target sequence.

[00124] In some examples, a nucleic acid molecule introduced into a host cell for generating a high efficiency genome editing cell line encodes a cas9 enzyme that is mutated to with respect to the corresponding wild-type enzyme such that the mutated cas9 enzyme lacks the ability to cleave one or both strands of a target polynucleotide containing a target sequence. For example, an aspartate-to-alanine substitution (D10A) in the RuvC I catalytic domain of Cas9 from *S. pyogenes* converts Cas9 from a nuclease that cleaves both strands to a nickase (cleaves a single strand). Other examples of mutations that render Cas9 a nickase include, without limitation, H840A, N854A, and N863A. In some embodiments, a Cas9 nickase may be used in combination with guide sequenc(es), *e.g.*, two guide sequences, which target respectively sense and antisense strands of the DNA target. This combination allows both strands to be nicked and used to induce NHEJ. Two nickase targets (within close proximity but targeting different strands of the DNA) can be used to inducing mutagenic NHEJ. Such targeting of a locus using enzymes that cleave opposite strains at staggered

positions can also reduce nontarget cleavage, as both strands must be accurately and specifically cleaved to achieve genome mutation.

[00125] As a further example, two or more catalytic domains of Cas9 (RuvC I, RuvC II, and RuvC III) may be mutated to produce a mutated Cas9 substantially lacking all DNA cleavage activity. In some embodiments, a D10A mutation is combined with one or more of H840A, N854A, or N863A mutations to produce a Cas9 enzyme substantially lacking all DNA cleavage activity. In some embodiments, a CRISPR enzyme is considered to substantially lack all DNA cleavage activity when the DNA cleavage activity of the mutated enzyme is less than about 25%, 10%, 5%, 1%, 0.1%, 0.01%, or lower with respect to its non-mutated form. Other mutations may be useful; where the Cas9 or other CRISPR enzyme is from a species other than *S. pyogenes*, mutations in corresponding amino acids may be made to achieve similar effects.

[00126] In some cases, the variant Cas9 site-directed polypeptide is a fusion polypeptide (a "variant Cas9 fusion polypeptide"), i.e., a fusion polypeptide comprising: i) a variant Cas9 site-directed polypeptide; and b) a covalently linked heterologous polypeptide (also referred to as a "fusion partner"). A heterologous nucleic acid sequence may be linked to another nucleic acid sequence (e.g., by genetic engineering) to generate a chimeric nucleotide sequence encoding a chimeric polypeptide. In some embodiments, a variant Cas9 fusion polypeptide is generated by fusing a variant Cas9 polypeptide with a heterologous sequence that provides for subcellular localization (i.e., the heterologous sequence is a subcellular localization sequence, e.g., a nuclear localization signal (NLS) for targeting to the nucleus; a mitochondrial localization signal for targeting to the mitochondria; a chloroplast localization signal for targeting to a chloroplast; an ER retention signal; and the like). In some embodiments, the heterologous sequence can provide a tag (*i.e.*, the heterologous sequence is a detectable label) for ease of tracking and/or purification (*e.g.*, a fluorescent protein, *e.g.*, green fluorescent protein (GFP), YFP, RFP, CFP, mCherry, tdTomato, and the like; a hemagglutinin (HA) tag; a FLAG tag; a Myc tag; and the like). In some embodiments, an RNA-guided nuclease can be codon-optimized for optimal expression in a host cell.

Host Cells for Highly Efficient Genome Editing

[00127] Provides herein are host cells, including cell lines and microbial strains that express an RNA-guided endonuclease and have genome editing efficiencies of at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, or at least 80%. The efficiency of genome editing is the percentage of cells that are transformed with a donor DNA that become altered at the targeted genetic locus. Typically a donor DNA (also

referred to as an editing DNA) includes a selectable marker so that cells that receive the editing construct can be selected for. The percentage of such selected transformants that have an altered targeted locus represents the efficiency of genome editing in the cell line or strain.

[00128] Targeting of a particular genetic locus is achieved by co-transforming into the cell a guide RNA that can either be a chimeric guide (that includes, in addition to the crRNA sequence having homology to the target site in the host genome, the tracrRNA sequence that interacts with the RNA-guided endonuclease) or a crRNA that includes a sequence of from about 16 to about 20 nucleotides homologous to the genomic target site and also includes a sequence that interacts with the tracrRNA (the "tracr mate sequence"). Alternatively, a chimeric guide RNA, or a crRNA plus a tracrRNA can be expressed in the host cell by transforming an expression construct into the host cell. In another variation, the host cell can express the tracrRNA from a construct engineered into the cell, and a targeting crRNA can be transformed into the cell, for example, the crRNA can co-transformed into the host cell along with the donor DNA.

[00129] The inventors have discovered that these high efficiencies can be obtained by isolating cell lines and strains that have fully penetrant, or culture-wide, expression of the introduced RNA-guided endonuclease gene. Host strains having fully penetrant expression of an RNA-guided endonuclease gene, for example, as Type II Cas gene, such as a Cas9 gene, can be isolated by introducing the gene encoding the RNA-guided endonuclease into a population of cells on the same construct with a gene encoding a detectable marker, such as a fluorescent protein, and assessing the expression level of the physically linked detectable marker gene. Cell lines or microbial strains transformed with a construct that includes a gene encoding an RNA-guided endonuclease, e.g., Cas9, and also includes a gene encoding a fluorescent protein, are analyzed by flow cytometry. A transformed cell line displaying a single fluorescence intensity peak, in which the single fluorescence peak on the flow cytometry histogram is at a higher fluorescence level than the peak displayed by control cells (cells that do not have a fluorescent protein gene), is identified as a fully penetrant cell line.

[00130] As demonstrated herein in the examples, the histogram resulting from flow cytometry of a cell culture originating from a single transformed colony, in which fluorescence is indicated on the x axis, typically on a logarithmic scale, and cell number is indicated on the y axis, provides a distribution of the expression level in the culture. It has been found that, when compared with the fluorescence level of control cells that do not express a fluorescent protein gene (e.g., nontransformed cells) which display a single peak at background (autofluorescence) level, a transformed cell line can display a single peak that

coincides with that of control cells, indicating that they are non-expressors, or can display two peaks, one of which coincides with that of control cells, indicating that the cell line is not fully penetrant for expression of the fluorescent protein gene. The examples herein demonstrate that expression of a transgene physically linked to the GFP transgene (e.g., Cas9, Cre recombinase, Type I FAS, ZnCys-2845 RNAi) demonstrates fully penetrant expression when the linked GFP gene demonstrates fully penetrant expression.

[00131] The method for isolating a fully penetrant cell line or strain analyzes a clonal cell line or strain, not a population of cells originating from independent transformation events. The flow cytometry method does not include selection of a subpopulation of the analyzed cell culture, which originates from a single clone. That is, the method in various preferred embodiments does not include cell sorting.

[00132] The method for identifying a cell line or microorganism strain having fully penetrant expression of a transgene, can be used to identify cell lines or strains having fully penetrant expression of an RNA-guided endonuclease.

Target Cells

[00133] The methods provided herein may be employed to induce DNA cleavage, DNA modification, and/or transcriptional modulation in mitotic or post-mitotic cells *in vivo* and/or *ex vivo* and/or *in vitro* (*e.g.*, to produce genetically modified cells that can be reintroduced into an individual). Because the DNA-targeting RNA provide specificity by hybridizing to target DNA, a mitotic and/or post-mitotic cell of interest in the disclosed methods may include a cell from any organism (e.g. a bacterial cell, an archaeal cell, a cell of a single-cell eukaryotic organism, a plant cell, an algal cell, a fungal cell (e.g., a yeast cell), an animal cell, a cell from an invertebrate animal (e.g. fruit fly, cnidarian, echinoderm, nematode, etc.), a cell from a vertebrate animal (e.g., fish, amphibian, reptile, bird, mammal), a cell from a mammal, a cell from a rodent, a cell from a human, etc.).

[00134] Any type of cell may be of interest (e.g. a stem cell, e.g. an embryonic stem (ES) cell, an induced pluripotent stem (iPS) cell, a germ cell; a somatic cell, e.g. a fibroblast, a hematopoietic cell, a neuron, a muscle cell, a bone cell, a hepatocyte, a pancreatic cell; an in vitro or in vivo embryonic cell of an embryo at any stage, e.g., a 1-cell, 2-cell, 4-cell, 8-cell, etc. stage zebrafish embryo; etc.). Cells may be from established cell lines or they may be primary cells, where "primary cells", "primary cell lines", and "primary cultures" are used interchangeably herein to refer to cells and cells cultures that have been derived from a subject and allowed to grow in vitro for a limited number of passages, i.e. splittings, of the culture. For example, primary cultures are cultures that may have been passaged 0 times, 1

time, 2 times, 4 times, 5 times, 10 times, or 15 times, but not enough times go through the crisis stage. Typically, the primary cell lines of the present invention are maintained for fewer than 10 passages in vitro. Target cells are in many embodiments unicellular organisms, or are grown in culture.

[00135] A host cell for genome modification can be a plant, animal, or microbial cell and may optionally be an algal cell, such as a cell of a species of *Achnanthes, Amphiprora, Amphora, Ankistrodesmus, Asteromonas, Boekelovia, Bolidomonas, Borodinella, Botrydium, Botryococcus, Bracteococcus, Chaetoceros, Carteria, Chlamydomonas, Chlorococcum, Chlorogonium, Chlorella, Chroomonas, Chrysosphaera, Cricosphaera, Crypthecodinium, Cryptomonas, Cyclotella, Dunaliella, Ellipsoidon, Emiliania, Eremosphaera, Ernodesmius, Euglena, Eustigmatos, Franceia, Fragilaria, Fragilaropsis, Gloeothamnion, Haematococcus, Halocafeteria, Heterosigma, Hymenomonas, Isochrysis, Lepocinclis, Micractinium, Monoraphidium, Nannochloris, Nannochloropsis, Navicula, Neochloris, Nephrochloris, Nephroselmis, Nitzschia, Ochromonas, Oedogonium, Oocystis, Ostreococcus, Pavlova, Parachlorella, Pascheria, Pelagomonas, Phaeodactylum, Phagus, Picochlorum, Platymonas, Pleurochrysis, Pleurococcus, Prototheca, Pseudochlorella, Pseudoneochloris, Pseudostaurastrum, Pyramimonas, Pyrobotrys, Scenedesmus, Skeletonema, Spyrogyra, Stichococcus, Tetraselmis, Thalassiosira, Tribonema, Vaucheria, Viridiella, Vischeria,* or *Volvox.*

[00136] Exemplary diatoms include members of the genera *Achnanthes, Amphora, Chaetoceros, Coscinodiscus, Cylindrotheca, Cyclotella, Cymbella*, *Fragilaria, Fragilaropsis, Hantzschia, Navicula, Nitzschia, Pseudo-Nitzschia, Phaeodactylum, Psammodictyon*, *Skeletonema, Thalassionema,* and *Thalassiosira.* Examples of eustigmatophytes that may be hosts for synthetic chromosome constructs and synthetic chromosomes as provided herein include not only *Nannochloropsis* species but also species of *Monodus, Pseudostaurastrum, Vischeria,* and *Eustigmatos*. In some examples, an alga of a species of the genus *Nannochloropsis* such as, but are not limited to, *N. gaditana, N. granulata, N. limnetica, N. oceanica, N. oculata*, and *N. salina* is transformed with a synthetic chromosome constructs as provided herein.

[00137] Alternatively or in addition, a host cell that includes a synthetic chromosome construct or synthetic chromosome of the present invention may optionally be a heterokont cell, an animal cell, a plant cell, a yeast cell, a fungal cell, or a protist. For example, heterokonts include not only eustigmatophytes and diatoms such as those listed above but also chytrid species, including labrinthulids and thraustochytrids. In some examples,

heterokont species considered for use in the invention include, but are not limited to, Bacillariophytes, Eustigmatophytes, Labrinthulids, and Thraustochytrids. In some examples, the strain may be a species of *Labryinthula, Labryinthuloides, Thraustochytrium, Schizochytrium, Aplanochytrium, Aurantiochytrium, Japonochytrium, Diplophrys*, or *Ulkenia*. For example, the strain may be a species of *Thraustochytrium, Schizochytrium, Oblongichytrium,* or *Aurantiochytrium.*

[00138] Also considered are prokaryotic host cells, for example, host cells can be of a species belonging to any of the following groups: Archaea, cyanobacteria, green-sulfur bacteria (e.g., *Chlorobium)*, green non-sulfur bacteria, purple sulfur bacteria, or purple non-sulfur bacteria or any of the following genera: *Arthrobacter, Escherichia, Bacillus, Brevibacteria, Clostridium, Corynebacteria, Desulfovibrio, Jeotgalicoccus, Kineococcus, Lactobacillus, Micrococcus, Mycobacterium, Pantoea, Pseudomonas, Rhodococcus, Rhodopseudomonas, Rhodospirillium, Rhodomicrobium, Stenotrophomonas, Vibrio, Streptomyces*, or *Zymomonas,*.

[00139] The host cells can be cells of any of the groups *Aspergillus, Mucor*, *Pichia, Pullularia, Saccharomyces, Schizosaccharomyces, Trichoderma, Rhodotorula, Yarrowia*, and alternatively can be mesomycetozoea (e.g., *Sphaeroforma*), heterokont, or algal cells.

[00140] Algal host cells can optionally be of a genus selected from the group consisting of *Achnanthes, Amphiprora, Amphora, Ankistrodesmus, Asteromonas, Boekelovia, Bolidomonas, Borodinella, Botrydium, Botryococcus, Bracteococcus, Chaetoceros, Carteria, Chlamydomonas, Chlorococcum, Chlorogonium, Chlorella, Chroomonas, Chrysosphaera, Cricosphaera, Crypthecodinium, Cryptomonas, Cyclotella, Desmodesmus, Dunaliella, Elipsoidon, Emiliania, Eremosphaera, Ernodesmius, Euglena, Eustigmatos, Franceia, Fragilaria, Fragilaropsis, Gloeothamnion, Haematococcus, Hantzschia, Heterosigma, Hymenomonas, Isochrysis, Lepocinclis, Micractinium, Monodus, Monoraphidium, Nannochloris, Nannochloropsis, Navicula, Neochloris, Nephrochloris, Nephroselmis, Nitzschia, Ochromonas, Oedogonium, Oocystis, Ostreococcus, Parachlorella, Parietochloris, Pascheria, Pavlova, Pelagomonas, Phæodactylum, Phagus, Picochlorum, Platymonas, Pleurochrysis, Pleurococcus, Prototheca, Pseudochlorella, Pseudoneochloris, Pseudostaurastrum, Pyramimonas, Pyrobotrys, Scenedesmus, Schizochlamydella, Skeletonema, Spyrogyra, Stichococcus, Tetrachlorella, Tetraselmis, Thalassiosira, Tribonema, Vaucheria, Viridiella, Vischeria,* and *Volvox*.

[00141] For example, a Cas9 expressing host as provided herein can be a diatom, such as, for example a member of any of the genera *Achnanthes, Amphora, Chaetoceros,*

Coscinodiscus, Cylindrotheca, Cyclotella, Cymbella, Fragilaria, Fragilariopsis, Hantzschia, Navicula, Nitzschia, Pavlova, Pseudo-Nitzschia, Phaeodactylum, Psammodictyon, Skeletonema, Thalassionema, and *Thalassiosira*. Eustigmatophytes that can be high efficiency cas9 Editor lines include, without limitation, species of *Eustigmatos, Monodus, Nannochloropsis, Pseudostaurastrum*, and *Vischeria*. For example, microorganisms for genetic modification or nucleic acid isolation as disclosed herein include members of the genus *Nannochloropsis*. Suitable species include but are not limited to *N. gaditana, N. granulata, N. limnetica, N. maritime, N. oceanica, N. oculata*, and *N. salina*. Some preferred species within the genus *Nannochloropsis* include, but are not limited to, *N. gaditana, N. oceanica, N. oculata*, and *N. salina*.

[00142] Other types of cells that may be of interest include e.g. a stem cell, e.g. an embryonic stem (ES) cell, an induced pluripotent stem (iPS) cell, a germ cell; a somatic cell, e.g. a fibroblast, a hematopoietic cell, a neuron, a muscle cell, a bone cell, a hepatocyte, a pancreatic cell; an in vitro or in vivo embryonic cell of an embryo at any stage, e.g., a 1-cell, 2-cell, 4-cell, 8-cell, etc. stage zebrafish embryo; etc.). Cells may be from established cell lines or they may be primary cells, where "primary cells", "primary cell lines", and "primary cultures" are used interchangeably herein to refer to cells and cells cultures that have been derived from a subject and allowed to grow in vitro for a limited number of passages, i.e. splittings, of the culture. For example, primary cultures include cultures that may have been passaged 0 times, 1 time, 2 times, 4 times, 5 times, 10 times, or 15 times, but not enough times go through the crisis stage. Primary cell lines can be are maintained for fewer than 10 passages in vitro. Target cells are in many embodiments unicellular organisms, or are grown in culture.

[00143] If the cells are primary cells, such cells may be harvest from an individual by any convenient method. For example, leukocytes may be conveniently harvested by apheresis, leukocytapheresis, density gradient separation, etc., while cells from tissues such as skin, muscle, bone marrow, spleen, liver, pancreas, lung, intestine, stomach, etc. are most conveniently harvested by biopsy. An appropriate solution may be used for dispersion or suspension of the harvested cells. Such solution will generally be a balanced salt solution, e.g. normal saline, phosphate-buffered saline (PBS), Hank's balanced salt solution, etc., conveniently supplemented with fetal calf serum or other naturally occurring factors, in conjunction with an acceptable buffer at low concentration, e.g., from 5-25 mM. Convenient buffers include HEPES, phosphate buffers, lactate buffers, etc. The cells may be used immediately, or they may be stored, frozen, for long periods of time, being thawed and

capable of being reused. In such cases, the cells will usually be frozen in 10% dimethyl sulfoxide (DMSO), 50% serum, 40% buffered medium, or some other such solution as is commonly used in the art to preserve cells at such freezing temperatures, and thawed in a manner as commonly known in the art for thawing frozen cultured cells.

Introducing Nucleic Acid into a Host Cell

[00144] A DNA-targeting RNA, or a nucleic acid comprising a nucleotide sequence encoding a transactivating RNA (tracrRNA), chimeric guide RNA (chimeric gRNA) or crispr RNA that targets a genomic locus (crRNA), can be introduced into a host cell by any of a variety of well-known methods. Introducing into a host cell a nucleic acid comprising a nucleotide sequence encoding an RNA-guide endonuclease, such as a gene encoding a Cas polypeptide, such as a Cas9 polypeptide or variant thereof, can be by any of a variety of well-known methods.

[00145] Methods of introducing a nucleic acid into a host cell are known in the art, and any known method can be used to introduce a nucleic acid (e.g., an expression construct) into a stem cell, progenitor cell, cell line, primary cell, or microbial cell. Suitable methods include, include e.g., viral or bacteriophage infection, transfection, conjugation, protoplast fusion, lipofection, electroporation, calcium phosphate precipitation, polyethyleneimine (PEI)-mediated transfection, DEAE-dextran mediated transfection, liposome-mediated transfection, particle gun technology, calcium phosphate precipitation, direct micro injection, nanoparticle-mediated nucleic acid delivery (see, e.g., Panyam et., al Adv Drug Deliv Rev. 2012 Sep. 13. pii: 50169-409X(12)00283-9. doi: 10.1016/j.addr.2012.09.023), and the like.

[00146] Genetic transformation can result in stable insertion and/or expression of transgenes or tracr RNAs, and in some cases can result in transient expression of transgenes tracr RNAs or guide RNAs. The transformation methods can also be used for the introduction of editing (donor) DNAs. Non-limiting examples of transformation methods that can be used on microorganisms including algae include agitation of cells in the presence of glass beads or silicon carbide whiskers as reported by, for example, Dunahay, *Biotechniques*, 15(3):452–460, 1993; Kindle, *Proc. Natl. Acad. Sci. U.S.A.*, 1990; Michael and Miller, *Plant J.*, 13, 427–435, 1998. Electroporation techniques have been successfully used for genetic transformation of several microalgal species including *Nannochloropsis* sp. (see, *e.g.*, Chen *et al.*, *J. Phycol.*, 44:768–76, 2008), *Chlorella* sp. (see, *e.g.*, Chen *et al.*, *Curr. Genet.*, 39:365-370, 2001; Chow and Tung, *Plant Cell Rep.* Vol.18, No. 9, 778-780, 1999), *Chlamydomonas* (Shimogawara *et al.*, *Genetics*, 148: 1821–1828, 1998), *Dunaliella* (Sun *et al.*, *Mol. Biotechnol.*, 30(3): 185-192, 2005). Micro-projectile bombardment, also referred to as

microparticle bombardment, gene gun transformation, or biolistic bombardment, has been used successfully for several algal species including, for example, diatoms species such as *Phaeodactylum* (Apt *et al.*, *Mol. Gen. Genet.*, 252:572-579, 1996), *Cyclotella* and *Navicula* (Dunahay *et al.*, *J. Phycol.*, 31:1004–1012, 1995), *Cylindrotheca* (Fischer *et al.*, *J. Phycol.*, 35:113-120, 1999), and *Chaetoceros* sp. (Miyagawa-Yamaguchi *et al.*, *Phycol. Res.* 59: 113–119, 2011), as well as green algal species such as *Chlorella* (El-Sheekh, *Biologia Plantarum,* Vol.42, No.2: 209-216, 1999), and *Volvox* species (Jakobiak *et al.*, *Protist*, 155:381-93, 2004). Additionally, *Agrobacterium*-mediated gene transfer techniques can also be useful for genetic transformation of microalgae, as has been reported by, for example, Kumar, *Plant Sci.*, 166(3):731-738, 2004, and Cheney *et al.*, *J. Phycol.*, Vol. 37, Suppl. 11, 2001.

[00147] A transformation vector or construct as described herein and/or a donor (editing) DNA as used in methods disclosed herein will typically comprise a marker gene that confers a selectable or scorable phenotype on target host cells. Common selectable markers include antibiotic resistance, fluorescent markers, and biochemical markers and are well-known in the art. Several different antibiotic resistance genes have been used successfully for selection of microalgal transformants, including blastocidin, bleomycin (see, for example, Apt *et al.*, 1996, *supra*; Fischer *et al.*, 1999, *supra*; Fuhrmann *et al.*, *Plant J.*, 19, 353- 61, 1999, Lumbreras *et al.*, *Plant J.*, 14(4):441-447, 1998; Zaslavskaia *et al.*, *J. Phycol.*, 36:379–386, 2000), spectinomycin (Cerutti *et al.*, *Genetics*, 145: 97–110, 1997; Doetsch *et al.*, *Curr. Genet.*, 39, 49-60, 2001; Fargo, *Mol. Cell. Biol.*, 19:6980-90, 1999), streptomycin (Berthold *et al.*, *Protist*, 153:401-412, 2002), paromomycin (Jakobiak *et al.*, *Protist*, *supra.*; Sizova *et al.*, *Gene*, 277:221-229, 2001), nourseothricin (Zaslavskaia *et al.*, 2000, *supra*), G418 (Dunahay *et al.*, 1995, *supra*; Poulsen and Kroger, *FEBS Lett.*, 272:3413–3423, 2005, Zaslavskaia *et al.*, 2000, *supra*), hygromycin (Berthold *et al.*, 2002, *supra*), chloramphenicol (Poulsen and Kroger, 2005, *supra*), and many others. Additional selectable markers for use in microalgae such as *Chlamydomonas* can be markers that provide resistance to kanamycin and amikacin resistance (Bateman, *Mol. Gen. Genet.* 263:404-10, 2000), zeomycin and phleomycin (*e.g.*, ZEOCIN™ pheomycin D1) resistance (Stevens, *Mol. Gen. Genet.* 251:23-30, 1996), and paramomycin and neomycin resistance (Sizova *et al.*, 2001, *supra*).

[00148] Fluorescent or chromogenic markers that have been used include luciferase (Falciatore *et al.*, *J. Mar. Biotechnol.*, 1: 239–251, 1999; Fuhrmann *et al.*, *Plant Mol. Biol.*, 2004; Jarvis and Brown, *Curr. Genet.*, 19: 317–322, 1991), β-glucuronidase (Chen *et al.*, 2001, *supra*; Cheney *et al.*, 2001, *supra*; Chow and Tung, 1999, *supra*; El-Sheekh, 1999, *supra*; Falciatore *et al.*, 1999, *supra*; Kubler *et al.*, *J. Mar. Biotechnol.*, 1:165–169, 1994), β-

galactosidase (Gan *et al.*, *J. Appl. Phycol.*, 15:345–349, 2003; Jiang *et al.*, *Plant Cell Rep.*, 21:1211–1216, 2003; Qin *et al.*, *High Technol. Lett.*, 13:87–89, 2003), and green fluorescent protein (GFP) (Cheney *et al.*, 2001, *supra*; Ender *et al.*, *Plant Cell*, 2002, Franklin *et al.*, *Plant J.*, 2002; 56, 148- 210).

[00149] A variety of known promoter sequences can be usefully deployed for transformation systems, including promoters useful in microalgal species. For example, promoters used to drive transgene expression in microalgae include various versions of the of cauliflower mosaic virus promoter 35S (CaMV35S), which has been used in both dinoflagellates and chlorophyta (Chow *et al*, *Plant Cell Rep.*, 18:778-780, 1999; Jarvis and Brown, *Curr. Genet.*, 317-321, 1991; Lohuis and Miller, *Plant J.*, 13:427-435, 1998). The SV40 promoter from simian virus has also reported to be active in several algae (Gan *et al.*, *J. Appl. Phycol.*, 151 345-349, 2003; Qin *et al.*, *Hydrobiologia* 398-399, 469-472, 1999). The promoters of RBCS2 (ribulose bisphosphate carboxylase, small subunit) (Fuhrmann *et al.*, *Plant J.*, 19:353-361, 1999) and PsaD (abundant protein of photosystem I complex; Fischer and Rochaix, *FEBS Lett.* 581:5555-5560, 2001) from *Chlamydomonas* can also be useful. The fusion promoters of HSP70A/RBCS2 and HSP70A/β2TUB (tubulin) (Schroda *et al.*, *Plant J.*, 21:121-131, 2000) can also be useful for an improved expression of transgenes, in which HSP70A promoter may serve as a transcriptional activator when placed upstream of other promoters. High-level expression of a gene of interest can also be achieved in, for example diatoms species, under the control of a promoter of an *fcp* gene encoding a diatom fucoxanthin-chlorophyll a/b binding protein (Falciatore *et al.*, *Mar. Biotechnol.*, 1:239-251, 1999; Zaslavskaia *et al.*, *J. Phycol.* 36:379-386, 2000) or the vcp gene encoding a eustigmatophyte violaxanthin-chlorophyll a/b binding protein (see U.S. Patent No. 8,318,482, incorporated by reference herein).

[00150] Inducible promoters can be useful in various aspects of the invention, including, but not limited to, expression of site-specific recombinases such as cre. For example, promoter regions of the NR genes encoding nitrate reductase can be used as inducible promoters in microorganisms including microalgae. The NR promoter activity is typically suppressed by ammonium and induced when ammonium is replaced by nitrate (Poulsen and Kroger, *FEBS Lett* 272:3413-3423, 2005), thus gene expression can be switched off or on when microalgal cells are grown in the presence of ammonium/nitrate. Additional algal promoters that can find use in the constructs and transformation systems provided herein include those disclosed in U.S. Patent No. 8,883,993; U.S. Patent Appl. Pub. No. US 2013/0023035; U.S. Patent Application Pub. No. US 2013/0323780; and U.S. Patent

Application Pub. No. US 2014/0363892, all incorporated herein by reference in their entireties.

[00151] In some embodiments, a method can involve introducing into a host cell (or a population of host cells) one or more nucleic acids comprising nucleotide sequences encoding a DNA-targeting RNA and/or a variant Cas9 site-directed polypeptide. Suitable nucleic acids comprising nucleotide sequences encoding a DNA-targeting RNA and/or a site-directed polypeptide include expression vectors, where an expression vector comprising a nucleotide sequence encoding a DNA-targeting RNA and/or a site-directed polypeptide is a "recombinant expression vector."

[00152] Depending on the host/vector system utilized, any of a number of suitable transcription and translation control elements, including constitutive and inducible promoters, transcription enhancer elements, transcription terminators, etc. may be used in the expression vector (see e.g., Bitter et al. (1987) Methods in Enzymology, 153:516-544).

[00153] In some embodiments, a nucleotide sequence encoding a DNA-targeting RNA and/or a variant Cas9 site-directed polypeptide is operably linked to a control element, e.g., a transcriptional control element, such as a promoter. The transcriptional control element may be functional in either a eukaryotic cell, e.g., a mammalian cell; or a prokaryotic cell (e.g., bacterial or archaeal cell). In some embodiments, a nucleotide sequence encoding a DNA-targeting RNA and/or a variant Cas9 site-directed polypeptide is operably linked to multiple control elements that allow expression of the nucleotide sequence encoding a DNA-targeting RNA and/or a variant Cas9 site-directed polypeptide in both prokaryotic and eukaryotic cells. [0475] A promoter can be a constitutively active promoter (i.e., a promoter that is constitutively in an active/"ON" state), it may be an inducible promoter (i.e., a promoter whose state, active/"ON" or inactive/"OFF", is controlled by an external stimulus, e.g., the presence of a particular temperature, compound, or protein.), it may be a spatially restricted promoter (i.e., transcriptional control element, enhancer, etc.) (e.g., tissue specific promoter, cell type specific promoter, etc.), and it may be a temporally restricted promoter (i.e., the promoter is in the "ON" state or "OFF" state during specific stages of embryonic development or during specific stages of a biological process, e.g., hair follicle cycle in mice).

[00154] Suitable promoters can be derived from viruses and can therefore be referred to as viral promoters, or they can be derived from any organism, including prokaryotic or eukaryotic organisms. Suitable promoters can be used to drive expression by any RNA polymerase (e.g., pol I, pol II, pol III). Exemplary promoters include, but are not limited to

the SV40 early promoter, mouse mammary tumor virus long terminal repeat (LTR) promoter; adenovirus major late promoter (Ad MLP); a herpes simplex virus (HSV) promoter, a cytomegalovirus (CMV) promoter such as the CMV immediate early promoter region (CMVIE), a rous sarcoma virus (RSV) promoter, a human U6 small nuclear promoter (U6) (Miyagishi et al., Nature Biotechnology 20, 497-500 (2002)), an enhanced U6 promoter (e.g., Xia et al., Nucleic Acids Res. 2003 Sep. 1; 31(17)), a human H1 promoter (H1), and the like.
[0477] Examples of inducible promoters include, but are not limited toT7 RNA polymerase promoter, T3 RNA polymerase promoter, Isopropyl-beta-D-thiogalactopyranoside (IPTG)-regulated promoter, lactose induced promoter, heat shock promoter, Tetracycline-regulated promoter (e.g., Tet-ON, Tet-OFF, etc.), Steroid-regulated promoter, Metal-regulated promoter, estrogen receptor-regulated promoter, etc. Inducible promoters can therefore be regulated by molecules including, but not limited to, doxycycline; RNA polymerase, e.g., T7 RNA polymerase; an estrogen receptor; an estrogen receptor fusion; etc.

Selectable Markers

[00155] A selectable marker can be, as nonlimiting examples, a gene conferring resistance to an antibiotic such as blasticidin, bleomycin, chloramphenicol, G418, gentamycin, glyphosate, hygromycin, kanamycin, neomycin, nourseothricin, paromomycin, phleomycin, puromycin, spectinomycin, streptomycin or zeomycin. A selectable marker can also confer resistance to methotrexate or DFMO, or an herbicide such as phosphinothricin, glyphosate, imidazolione, a sulfonylurea, atrazine, glufosinate, or a sulfonamide. A selectable marker can also allow autotorophic growth of an auxotrophic host strain, such as a gene encoding, for example, arginosuccinate lyase, for arginine synthesis, nitrate reductase for nitrogen assimilation (ability to utilize nitrate), thi10 for thiamine biosynthesis, or nic for nicotinamide biosynthesis.

[00156] Detectable markers or reporter genes can include genes encoding a variety of fluorescent proteins, including without limitation green, cyan, blue, yellow, orange, and red fluorescent proteins and their variants. Other markers that can be used include enzymes that produce fluorescent or chromogenic products include luciferase (Falciatore *et al.*, *J. Mar. Biotechnol.*, 1: 239–251, 1999; Fuhrmann *et al.*, *Plant Mol. Biol.*, 2004; Jarvis and Brown, *Curr. Genet.*, 19: 317–322, 1991), β-glucuronidase (Chen *et al.*, 2001, *supra*; Cheney *et al.*, 2001, *supra*; Chow and Tung, 1999, *supra*; El-Sheekh, 1999, *supra*; Falciatore *et al.*, 1999, *supra*; Kubler *et al.*, *J. Mar. Biotechnol.,* 1:165–169, 1994), and β-galactosidase (Gan *et al.*, *J. Appl. Phycol.*, 15:345–349, 2003; Jiang *et al.*, *Plant Cell Rep.*, 21:1211–1216, 2003; Qin *et al.*, *High Technol. Lett.*, 13:87–89, 2003). Further nonlimiting examples of enzymes that can

be used for detecting a colored or labeled product include aryl sulfatase (Davies *et al.* (1992) *Nucl. Acids. Res.* 20:2959-2965; Hallman and Sumper (1994) *Eur. J. Biochem.* 221:143-150), alkaline phosphatase (El-Sankary *et al.* (2001) *Drug Metab. Disposition* 29:1499-1504), and chloramphenicol acetyl transferase (Sekiya *et al.* (2000) *J. Biol. Chem.* 275:10738-10744).

[00157] A selectable marker can provide a means to obtain heterokont cells, algal cells, yeast cell, plant cells or any combination that express the marker and, therefore, include the synthetic chromosome construct, and can therefore be useful as a component of a synthetic chromosome of the present disclosure. Examples of selectable markers include genes encoding deaminase, such as the deaminase from *Aspergillus terreus*, which confers resistance to Blasticidin S (Tamura, *Biosci. Biotechnol. Biochem.* 59: 2336-2338, 1995), as well as genes conferring resistance to antibiotics such as bleomycin, gentamycin, glyphosate, hygromycin, kanamycin, neomycin, phleomycin, puromycin, spectinomycin, and streptomycin. For example, neomycin phospho-transferase confers resistance to the aminoglycosides neomycin, kanamycin and paromycin (Herrera-Estrella, *EMBO J.* 2:987-995, 1983) and the "hygro" gene confers resistance to hygromycin (Marsh, *Gene* 32:481-485, 1984). Several different antibiotic resistance genes have been used successfully for selection of microalgal transformants, including blastocydin, bleomycin (see, for example, Apt *et al.*, 1996, *supra*; Fischer *et al.*, 1999, *supra*; Fuhrmann *et al.*, *Plant J.*, 19, 353- 61, 1999, Lumbreras *et al.*, *Plant J.*, 14(4):441-447, 1998; Zaslavskaia *et al.*, *J. Phycol.*, 36:379–386, 2000), spectinomycin (Cerutti *et al.*, *Genetics*, 145: 97–110, 1997; Doetsch *et al.*, *Curr. Genet.*, 39, 49-60, 2001; Fargo, *Mol. Cell. Biol.*, 19:6980-90, 1999), streptomycin (Berthold *et al.*, *Protist*, 153:401-412, 2002), paromomycin (Jakobiak *et al.*, *Protist*, *supra.*; Sizova *et al.*, *Gene*, 277:221-229, 2001), nourseothricin (Zaslavskaia *et al.*, 2000, *supra*), G418 (Dunahay *et al.*, 1995, *supra*; Poulsen and Kroger, *FEBS Lett.*, 272:3413–3423, 2005, Zaslavskaia *et al.*, 2000, *supra*), hygromycin (Berthold *et al.*, 2002, *supra*), chloramphenicol (Poulsen and Kroger, 2005, *supra*), and others. Additional selectable markers for use in microalgae can be markers that provide resistance to kanamycin and amikacin (Bateman, *Mol. Gen. Genet.* 263:404-10, 2000), zeomycin and phleomycin (*e.g.*, ZEOCIN™ pheomycin D1) (Stevens, *Mol. Gen. Genet.* 251:23-30, 1996), and paramomycin and neomycin (Sizova *et al.*, 2001, *supra*).

[00158] Also considered are genes conferring resistance to antimetabolites, such as methotrexate, *e.g.*, genes encoding dihydrofolate reductase, (Reiss, *Plant Physiol.* (*Life Sci. Adv.*) 13:143-149, 1994); trpB, which allows cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histinol in place of histidine (Hartman, *Proc. Natl. Acad.*

Sci., USA 85:8047, 1988); mannose-6-phosphate isomerase which allows cells to utilize mannose (WO 94/20627); ornithine decarboxylase, which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine (DFMO; McConlogue, 1987, In: *Current Communications in Molecular Biology*, Cold Spring Harbor Laboratory ed.). Additional selectable markers include those that confer herbicide resistance, for example, phosphinothricin acetyltransferase gene, which confers resistance to phosphinothricin (White *et al.*, *Nucl. Acids Res.* 18:1062, 1990; Spencer *et al.*, *Theor. Appl. Genet.* 79:625-631, 1990), a mutant EPSPV-synthase, which confers glyphosate resistance (Hinchee *et al.*, *BioTechnology* 91:915-922, 1998), a mutant acetolactate synthase, which confers imidazolione or sulfonylurea resistance (Lee *et al.*, *EMBO J.* 7:1241-1248, 1988), a mutant psbA, which confers resistance to atrazine (Smeda *et al.*, *Plant Physiol.* 103:911-917, 1993), or a mutant protoporphyrinogen oxidase (see U.S. Pat. No. 5,767,373), or other markers conferring resistance to an herbicide such as glufosinate, sulfonamide, or phosphinothricin or sulfonylurea (see, for example, Maliga *et al.*, *Methods in Plant Molecular Biology*, Cold Spring Harbor Laboratory Press, 1995, page 39). Genes conferring resistance to antibiotics such as tetracycline; ampicillin, kanamycin, and chloramphenicol can be used for selection of the synthetic chromosome construct in prokaryotes such as *E. coli*.

[00159] Auxotrophic markers are selectable markers that can be used in a host having a mutation in a gene encoding a metabolic enzyme, such as, for example, arginosuccinate lyase, for arginine synthesis, nitrate reductase for nitrogen assimilation (ability to utilize nitrate), thi10 for thiamine biosynthesis, and nic for nicotinamide biosynthesis.

[00160] Negative selection markers that may be included on a synthetic chromosome construct or synthetic chromosome include, without limitation, thymidine kinase (Lupton *et al.* (1991) *Molecular and Cellular Biology* 11: 3374-3378), DAOO (Erikson *et al.* (2004) *Nature Biotechnology* 22: 455-458) URA, and sacB (Quenee *et al.* (2005) *Biotechniques* 38: 63-67).

[00161] A variety of known promoter sequences can be usefully deployed for transformation systems of microalgal and heterokont species. For example, the promoters commonly used to drive transgene expression in microalgae include various versions of the of cauliflower mosaic virus promoter 35S (CaMV35S), which has been used in both dinoflagellates and chlorophyta (Chow *et al*, *Plant Cell Rep.*, 18:778-780, 1999; Jarvis and Brown, *Curr. Genet.*, 317-321, 1991; Lohuis and Miller, *Plant J.*, 13:427-435, 1998). The SV40 promoter from simian virus has also reported to be active in several algae (Gan *et al.*, *J. Appl. Phycol.*, 151 345-349, 2003; Qin *et al.*, *Hydrobiologia* 398-399, 469-472, 1999). The

promoters of RBCS2 (ribulose bisphosphate carboxylase, small subunit) (Fuhrmann *et al.*, *Plant J.*, 19:353-361, 1999) and PsaD (abundant protein of photosystem I complex; Fischer and Rochaix, *FEBS Lett.* 581:5555-5560, 2001) from *Chlamydomonas* can also be useful. The fusion promoters of HSP70A/RBCS2 and HSP70A/β2TUB (tubulin) (Schroda *et al.*, *Plant J.*, 21:121-131, 2000) can also be useful for an improved expression of transgenes, in which HSP70A promoter may serve as a transcriptional activator when placed upstream of other promoters. High-level expression of a gene of interest can also be achieved in heterokonts, for example diatoms species, under the control of a promoter of an *fcp* gene encoding a diatom fucoxanthin-chlorophyll a/b binding protein (Falciatore *et al.*, *Mar. Biotechnol.*, 1:239-251, 1999; Zaslavskaia *et al.*, *J. Phycol.* 36:379-386, 2000) or the vcp gene encoding a eustigmatophyte violaxanthin-chlorophyll a/b binding protein (see U.S. Patent No. 8,318,482). If so desired, inducible promoters can provide rapid and tightly controlled expression of genes in transgenic microalgae. For example, promoter regions of the NR genes encoding nitrate reductase can be used as such inducible promoters. The NR promoter activity is typically suppressed by ammonium and induced when ammonium is replaced by nitrate (Poulsen and Kroger, *FEBS Lett* 272:3413-3423, 2005), thus gene expression can be switched off or on when microalgal cells are grown in the presence of ammonium/nitrate. Other regulatable promoters from *Nannochloropsis* include those disclosed in U.S. Patent Application Publication No. US2013/0023035, incorporated by reference herein. Additional *Nannochloropsis* algal promoters that can find use in the constructs and transformation systems provided herein include those disclosed in U.S. Patent No. 8,709,766; U.S. Patent Application Publication No. US2013/0323780; U.S. Patent Application 13/693,585, filed Dec. 4, 2012; and U.S. Patent Application 13/915,522, filed June 11, 2013, all incorporated by reference herein.

EXAMPLES

[00162] Example 1. Construction of a Cas9-expressing *Nannochloropsis* line.

[00163] A construct was engineered for the expression of a gene encoding the *Streptococcus pyogenes* Cas9 endonuclease using a vector based on a pCC1BAC backbone. The vector included an engineered Cas9 gene having a sequence codon optimized for *Nannochloropsis gaditana* (SEQ ID NO:1) that encoded the Cas9 protein from *Streptococcus pyogenes* (SEQ ID NO:2). A sequence encoding a Nuclear Localization Signal (NLS) peptide (SEQ ID NO:3) from SV40 that was also codon optimized for *Nannochloropsis gaditana* (SEQ ID NO:4) was linked to the 5' end of the Cas9-encoding sequence, and a sequence (SEQ ID NO:5) encoding a FLAG tag peptide (SEQ ID NO:6) was cloned 3' of the Cas9-

encoding sequence. The entire engineered Cas9 gene (SEQ ID NO:7), encoding the engineered NLS-Cas9-Cterminal FLAG protein (SEQ ID NO:8) was cloned 3' of the *N. gaditana* RPL7 promoter (SEQ ID NO:9) and 5' of the *N. gaditana* 6487 terminator (SEQ ID NO:42). The construct also included a selectable marker expression cassette, which included the blasticidin S deaminase ("blast") gene from *Aspergillus terreus* codon-optimized for *Nannochloropsis gaditana* (SEQ ID NO:10), driven by the *N. gaditana* TCTP promoter (SEQ ID NO:11). The EIF3 terminator (SEQ ID NO:12) was positioned at the 3' end of the blast gene. In addition, the vector included an expression cassette designed to drive expression of a chimeric guide RNA (SEQ ID NO:13) designed to include a 20 bp sequence for targeting the *N. gaditana* acyl-coA oxidase gene (SEQ ID NO:14), driven by the *N. gaditana* putative U6 promoter (SEQ ID NO:15) and U6 terminator (SEQ ID NO:16). A diagram of the construct, named pSGE-6133, is provided in **Figure 1**.

[00164] To target the *N. gaditana* acyl-CoA oxidase gene, the pSGE-6133 construct was linearized with SwaI restriction enzyme and transformed into *Nannochloropsis* cells by electroporation essentially according to methods known in the art (see, for example U.S. Patent Application Publication 2015/0183838, incorporated herein by reference). Blasticidin resistant colonies were obtained and colony PCR was performed on colonies to screen for the presence of the Cas9 gene. For colony screening by PCR, a small amount of cells from a colony to be screened was suspended into 100 µl of 5% Chelex 100 Resin (BioRad, Hercules, CA)/TE solution and the suspension was boiled for boiled 10 minutes at 99° C, after which the tubes were briefly spun. One microliter of the lysate supernatant was added to a PCR reaction mix, in which the PCR mixture and reactions were set up and performed according to the QIAGEN Fast Cycling PCR Master Mix Protocol (Qiagen, Germantown, MD) from the manufacturer (Handbook available at qiagen.com) using primers derived from the sequence of the engineered Cas9 construct.

[00165] Twelve of the transformed strains that were found to include the Cas9 gene were then screened by Western blot to determine the level of the Cas9 protein in the cells. Samples were removed from liquid culture of the selected strains and cells were counted using an Accuri flow cytometer. Based on the cell count, an aliquot of 2 x 10^8 cells was removed from each sample culture and centrifuged at maximum speed in a microcentrifuge. The supernatant was discarded and the pelleted cells were resuspended in 2x LDS buffer that included 100 mM DTT. The samples were boiled for 10 minutes (99° C). The lysate (10 µl) was run on a 3-8% Tris-Acetate Gel with Tris-Acetate/SDS running buffer to separate proteins, after which proteins were transferred to PVDF membrane using an iBlot Western transfer apparatus

(Invitrogen; Carlsbad, CA) according to manufacturer's instructions. For detection of the FLAG-tagged Cas9 protein, membranes were first blocked with a blocking solution of 5% milk in TBST (50 mM Tris pH7.4, 150 mM NaCl, 0.15% Tween20) and then incubated with anti-FLAG alkaline phosphatase conjugated antibody (diluted 1 to 4000 in blocking solution) overnight. The membrane was washed 3 times with TBST and the membrane was then developed with BCIP/NBT chromagen and dried to visualize the antibody-bound protein.

[00166] The strain determined to have the highest level of the Cas9 protein was GE-6571. As this strain had the highest level of expression of the Cas9 protein and also was engineered to express the chimeric guide RNA (SEQ ID NO:13) targeting the *N. gaditana* acyl-CoA oxidase gene (SEQ ID NO:48), the GE-6571 strain was analyzed for mutations within the acyl-CoA oxidase gene by colony PCR as described above along with the rest of the western-positive strains. For PCR, the primers used were ACO2-upstreamF (SEQ ID NO:17) and ACO2-downstreamR (SEQ ID NO:18) which together produced an 852 bp PCR fragment (SEQ ID NO:19) that included the targeted portion of the acyl-CoA oxidase gene. PCR fragments were Sanger sequenced using the same primers to determine the presence of any mutations. No mutations were detected at the target site of the acyl-CoA oxidase gene. Subsequent Northern blots and RT-PCR experiments failed to detect any guide RNA transcript.

[00167] Example 2. Use of Strain GE-6571 to generate targeted CHORD-3266 mutants by co-transformation of *in vitro* synthesized guide RNA and selectable donor DNA

[00168] The GE-6571 Cas9 expression strain was then tested for its ability to generate mutations in a targeted gene by co-transformation of *in vitro* synthesized chimeric guide RNA (gRNA) (SEQ ID NO:20) targeting a sequence in a *Nannochloropsis* gene encoding the CHORD-3266 polypeptide having a CHORD (cysteine and histidine rich) domain; SEQ ID NO:21) and one of the following three forms of selectable DNA; 1) a fragment that only included a hygromycin resistance (HygR) gene (SEQ ID NO:22) under the control of the *N. gaditana* EIF3 promoter (SEQ ID NO:23), and a TurboGFP gene (Evrogen, Moscow, Russia) codon optimized for *Nannochloropsis gaditana* (SEQ ID NO:24) under the control of the *N. gaditana* RPL24 promoter (SEQ ID NO:25), with both genes terminated by *N. gaditana* bidirectional terminator 2 (SEQ ID NO:26), found between the NADH-dependent fumarate reductase gene and D-tyrosyl-tRNA(Tyr) deacylase gene in the *N. gaditana* genome, 2) a circular form of a vector named "Chord3-KOvector" (SEQ ID NO:27; **Figure 2**) which included all of the elements in the fragment described above, but in this case the elements

were flanked by 2kb "up" (SEQ ID NO:28) and "down" (SEQ ID NO:29) arms which are homologous to sequences upstream and downstream of the CRISPR target sequence (SEQ ID NO:30) and contain a puc19 vector backbone, or 3) a linear DNA molecule which was released by PmeI digest from the "Chord3-KOvector" which contains all the elements of the circular homologous vector but without the puc19 backbone. The same DNA series was transformed into GE-6571 without a gRNA as a control.

[00169] The chimeric guide RNA that was designed to target the coding region of the CHORD-3266 gene included 20 nucleotides of sequence (SEQ ID NO:31) with homology to the CRISPR target in the CHORD-3266 gene (SEQ ID NO:30) upstream of the *S. pyogenes* Cas9 PAM sequence (NGG), within a 103 total chimeric guide RNA sequence (SEQ ID NO:32) that included the transactivating CRISPR (tracr) sequence. The entire chimeric guide sequence was synthesized by first making a DNA template made up of complementary DNA oligonucleotides (SEQ ID NO:33 and SEQ ID NO:34) in which the DNA sequence encoding the guide RNA molecule was included downstream of a T7 promoter sequence (SEQ ID NO:35). The oligos were annealed to create a double stranded DNA template, which was used as the template for *in vitro* transcription reactions that were performed using the MEGAshortscript™ T7 Kit (Life Technologies cat # AM1354M; Carlsbad, CA) according to the manufacturer's protocol. The resulting RNA was purified using Zymo-Spin™ V-E columns (Zymo Research; Irvine, CA; cat #C1024-25) according to manufacturer's protocol.

[00170] The GE-6571 Cas9 expression strain was transformed by electroporation using 5 µg of purified chimeric guide RNA targeting the CHORD-3266 gene and 1 µg of one of the forms of selectable donor DNA (1, 2, or 3) described previously in this example. Following electroporation, cells were plated on agar media containing hygromycin to select for transformants that incorporated the hygromycin cassette. Transformants were screened by Colony PCR using primers designed to amplify across the CHORD-CRISPR target (SEQ ID NO:36 and SEQ ID NO:37), yielding a 100 bp band if no DNA was inserted and no or very minor NHEJ mis-repair occurred, or a single 4kb band if the selectable marker and reporter cassette was inserted by NHEJ or homologous recombination (**Figure 3**). NHEJ mis-repair resulting in small insertions or deletions would likely be seen as a small shift in the 100 bp product, which should have been detectable using the 3% agarose gel electrophoresis. However, to rule out any small and hard to detect insertions or deletions due to NHEJ mis-repair, strains which initially yielded a single 100 bp band underwent an additional round of colony PCR using a different primer set in which the priming sites resided farther away from the CRISPR target site, and the PCR products were Sanger sequenced using the same

primers. Out of 555 hygromycin-resistant colonies screened for the different transformation strategies (*i.e.*, using the three different forms of selectable donor DNA as described above in this example), only 5 mutants were found, providing a mutation rate of approximately 1%. Furthermore, all 5 mutants were obtained by co-transformation of selectable DNA with homologous arms (*i.e.*, DNA insertion was by way of double recombination within the gene homology arms, for both circular and linear donor DNA forms), and no mutants were obtained using the fragment that lacked CHORD-3266 homologous arms. This fragment that did not include homology arms was never observed to have been inserted by NHEJ "knock-in", and furthermore, no mutants were caused by apparent NHEJ mis-repair. No mutants were obtained from the transformants generated by the control transformations where gRNA was omitted.

[00171] Example 3. Development of Fully Penetrant *Nannochloropsis* Cas9 Editor Lines

[00172] To improve the efficiency of making genome alterations, improved Cas9-expressing strains were produced. To do this, Nannochloropsis strains were engineered and isolated that exhibited expression of the introduced Cas9 genes in essentially 100% of the cell population of a growing culture.

[00173] The first step in generating a fully penetrant Cas9 line was to introduce a gene encoding a fluorescent protein on the vector that included the Cas9 gene. The vector pSGE-6206 (SEQ ID NO:38) (Figure 4) included the following three elements: 1) a Cas9 expression cassette which contained a Cas9 gene from Streptococcus pyogenes codon optimized for *Nannochloropsis gaditana* (SEQ ID NO:1) with an N-terminal FLAG tag (SEQ ID NO:5), nuclear localization signal (SEQ ID NO:4), and peptide linker (SEQ ID NO:39), driven by the *N. gaditana* RPL24 promoter (SEQ ID NO:25) and terminated by *N. gaditana* bidirectional terminator 2 (SEQ ID NO:26); 2) a selectable marker expression cassette, which contained the blast gene from *Aspergillus terreus* codon optimized for *N. gaditana* ("BSD"; SEQ ID NO:10), driven by the *N. gaditana* TCTP promoter (SEQ ID NO:11) and followed by the EIF3 terminator (SEQ ID NO:12); and 3) a GFP reporter expression cassette, which contained the TurboGFP gene (Evrogen, Moscow, Russia) codon-optimized for *Nannochloropsis gaditana* (SEQ ID NO:24), driven by the *N. gaditana* 4A-III promoter (SEQ ID NO:40) and followed by the *N. gaditana* bidirectional terminator 5 (SEQ ID NO:41) which occurs between the Glucosamine 6-phosphate isomerase 2 gene and the YVTN repeat like quinoprotein amine dehydrogenase gene in the *N. gaditana* genome.

[00174] An additional GFP trackable Cas9 vector (pSGE-6202) was created that was similar to pSGE-6206, except that in pSGE-6202 the Cas9 gene was driven by the N. gaditana RPL7 promoter (SEQ ID NO:9) and the N. gaditana 6487 terminator (SEQ ID NO:42), which were also used in the pSGE-6133 vector (Example 1).

[00175] Strains transformed with either pSGE-6206 or pSGE-6202 were plated onto PM74 agar medium containing 100 mg/L of blasticidin. Colonies were patched onto selection media for analysis and archiving. A small amount of biomass was taken from the patches and completely resuspended in 300 µl of 1x Instant Ocean solution (Aquatic Eco Systems, Apopka, FL). Care was taken to not add too much biomass so that a light green resuspension was obtained. This liquid was directly analyzed by flow cytometry using a BD Accuri C6 flow cytometer, using a 488nm laser and 530/10nm filter to measure GFP fluorescence per cell. 10,000-30,000 events were recorded for each sample using the slow fluidics setting. The resulting histograms were overlayed with histograms of wild type cells (*i.e.*, cells not expressing a fluorescent protein) run separately. Only strains with fully penetrant expression in culture were carried forward; this meant that the flow cytometry GFP fluorescence histogram showed a single peak or bell-shaped curve in which the fluorescence peak was fully shifted higher than the wild type autofluorescence (background fluorescence) peak when plotted on a log scale (**Figure 5A** and **B**). These strains were designated as "fully penetrant" Cas9 expressing strains, in that the expression of the GFP gene was found throughout the cells of a culture of the strain. That is, while at any given point in time the amount (and therefore fluorescence) of GFP might vary somewhat cell-to-cell, resulting in peaks or bell-shaped curves, there was no subpopulation of cells exhibiting a distinct distribution of GFP expression with respect to the shifted peak. Thus, a fully penetrant strain was one in which there was a single peak (or bell-shaped curve having a peak) where the peak was separate from and at a higher fluorescence value than the background peak of non-expressing cells (*e.g.*, cells not transformed with a GFP expression construct). Because the GFP gene was physically associated with the Cas9 gene in the introduced constructs, it was postulated that the Cas9 gene was also likely expressed throughout the cells of a culture of the strain in fully penetrant GFP strains.

[00176] Fully GFP-penetrant Cas9 strains demonstrating a single clearly shifted fluorescence peak with respect to nontransformed cells (see **Figure 5A** and **Table 1**, in which clones are scored by 'X's' according to whether they exhibited single or double peaks) were then tested by western blotting with an anti-FLAG antibody for evidence of Cas9 expression. An example of a strain (clone p1-27) that exhibited a single peak separated from the

autofluorescence peak of nontransformed cells is provided in **Figure 5A**, and compared with clone p2-02, which had two peaks, one of which coincided with the control (no GFP construct) peak (**Figure 5B**). One strain resulting from transformation with each vector (pSGE-6206 and pSGE-6202) that exhibited only a single peak by flow cytometry that recorded GFP fluorescence levels, where the single peak was shifted to a higher fluorescence level than no GFP controls, and that also demonstrated Cas9 protein expression by Western (**Figure 6**) was carried forward for genome editing tests. Strain GE-6594 was selected as a fully penetrant Cas9 strain resulting from transformation with pSGE-6202, and strain GE-6791 was selected as a fully penetrant Cas9 strain resulting from transformation with pSGE-6206.

[00177] Table 1. Nannochloropsis lines transformed with Cas9 expression vector pSGE-6202 scored for exhibiting Double or Single fluorescence peaks by flow cytometry

	Double	Single	FL-1		Double	Single	FL-1		Double	Single	FL-1
B05 p2-02	X		4111.8	G12 p3-31	X		1,449.0	F02 p1-14		X	914.78
B02 p1-10	X		3589.9	H07 p2-24	X		1,441.7	A11 p3-17		X	914.25
C04 p1-27		X	3364.2	D03 p1-20	X		1,425.8	D11 p3-20		X	912.9
B12 p3-26		X	2684.9	H06 p2-16	X		1,413.9	D02 p1-12		X	907.08
B09 p3-02		X	2661.7	H10 p3-16	X		1,404.2	G04 p1-31		X	892.9
A02 p1-09	X		2352.2	C03 p1-19	X		1,374.8	A08 p2-25		X	891.83
C02 p1-11	X		2084.9	E08 p2-29	X		1,374.3	A04 p1-25		X	888.76
E02 p1-13	X		2031.6	D09 p3-04	X		1,361.7	B06 p2-10		X	887.53
B01 p1-02	X		1969.0	B04 p1-26	X		1,349.9	F12 p3-30		X	886.9
E11 p3-21	X		1933.3	E01 p1-05	X		1,330.9	E03 p1-21		X	882.81
E07 p2-21	X		1909.3	G08 p2-31	X		1,308.8	D05 p2-04		X	880.78
B11 p3-18	X		1881.1	A06 p2-09	X		1,288.0	G01 p1-07		X	878.16
C10 p3-11	X		1775.7	H03 p1-24	X		1,280.9	C06 p2-11		X	872.85
B08 p2-26	X		1755.3	F07 p2-22	X		1,276.6	E04 p1-29		X	869.05
H01 p1-08	X		1730.2	C01 p1-03	X		1,252.3	G11 p3-23		X	867
D08 p2-28	X		1707.0	F10 p3-14	X		1,234.3	G05 p2-07		X	864.03
C05 p2-03	X		1694.5	C07 p2-19	X		1,227.7	A03 p1-17		X	861.61
D07 p2-20	X		1685.0	H11 p3-24	X		1,226.7	F01 p1-06		X	861.06
E12 p3-29	X		1588.7	C11 p3-19	X		1,214.1	G06 p2-15		X	861.02
H02 p1-16	X		1560.2	E10 p3-13	X		1,209.1	E06 p2-13		X	857.7
C08 p2-27	X		1556.6	E09 p3-05	X		1,178.2	C12 p3-27		X	854.33
F04 p1-30	X		1551.8	F05 p2-06	X		1,151.5	F09 p3-06		X	849.25
H05 p2-08	X		1547.5	E05 p2-05	X		1,115.7	F08 p2-30		X	843.08
H04 p1-32	X		1540.4	D06 p2-12	X		1,101.3	A10 p3-09		X	840.75
H08 p2-32	X		1538.1	H09 p3-08	X		1,070.7	A09 p3-01		X	834.58
F03 p1-22	X		1529.2	B03 p1-18		X	1,056.4	A12 p3-25		X	834.53
A07 p2-17	X		1523.1	G02 p1-15		X	996.8	D10 p3-12		X	826.53
B07 p2-18	X		1497.1	G03 p1-23	X		970.68	C09 p3-03		X	818.38
F06 p2-14	X		1496.7	D01 p1-04		X	956.46	G07 p2-23		X	814.46
A05 p2-01	X		1488.0	A01 p1-01		X	952.68	G10 p3-15		X	810.45
F11 p3-22	X		1465.9	B10 p3-10		X	948.74	H12 p3-32		X	803.66
D04 p1-28	X		1459.6	D12 p3-28		X	918.9	G09 p3-07		X	800.77

[00178] Example 4. High Frequency Knockout of CHORD-3266 gene using Fully Penetrant *Nannochloropsis* Cas9 Editor Lines

[00179] To test the fully penetrant *Nannochloropsis* Cas9 strains GE-6594 and GE-6791 for genome editing capability, a genome editing approach similar to that described in Example 2 was taken, using the same *in vitro* synthesized chimeric gRNA. However, in this example, which used the new fully penetrant strains, the selectable donor DNA used in the co-transformation did not include the GFP gene and associated promoter and terminator. The strains were transformed with gRNA targeting the CHORD-3266 gene (encoding a protein product having a CHORD (cysteine and histidine rich) domain) and one of the following selectable DNA molecules; 1) a HygR fragment that only included a hygromycin resistance (HygR) gene (SEQ ID NO:22) under the control of the *N. gaditana* EIF3 promoter (SEQ ID NO:23) terminated by *N. gaditana* bidirectional terminator 2 (SEQ ID NO:26) (the operably linked HygR gene, promoter, and terminator referred to herein as the HygR cassette), and flanked by 27 base pair identification sequences on the 5' (SEQ ID NO:43) and 3' (SEQ ID NO:44) ends of the gene to yield an ID-sequence-flanked HygR cassette fragment (SEQ ID NO:46), or 2) a circular form of vector pSGE-6281 (SEQ ID NO:47) (**Figure 7**) which included all of the elements in the fragment described above, but here those elements were flanked by 2kb "up" (SEQ ID NO:28) and "down" (SEQ ID NO:29) arms which were homologous to the sequences upstream and downstream of the CRISPR target (SEQ ID NO:30) in the *N. gaditana* genome, and which also contained a puc19 vector backbone. The same DNA series was transformed without gRNA as a control group.

[00180] The GE-6594 and GE-6791 Cas9 fully penetrant expression strains were transformed by electroporation using 5 μg of purified chimeric guide RNA targeting the CHORD-3266 gene and 1 μg of one of the forms of selectable DNA described above. Following electroporation, cells were plated on agar medium containing hygromycin to select for transformants that incorporated the hygromycin cassette. Transformants were screened by colony PCR as described in Example 2. The results are shown in **Table 2.**

[00181] Table **2: Rates of *in vivo* Genome Editing targeting the CHORD-3266 locus with selection in Fully Penetrant Cas9 Editor Lines**.

Cas9 Editor Strain	Donor DNA fragment	total no. transformants analyzed	no. confirmed positive for mutation at locus	% transformants with mutated target locus
GE-6791	Hyg-Frag	61	19	31
GE-6791	pSGE-6281 (arms for HR)	9	8	**89**
GE-6594	Hyg-Frag	17	6	35
GE-6594	pSGE-6281 (arms for HR)	5	5	**100**

[00182] The mutation frequency in these new Cas9 parental strains was drastically improved over the original parental strain GE-6571. Furthermore, using the homologous recombination vector pSGE-6281 as donor DNA, fully penetrant Cas9 strain GE-6791 yielded 8 clones with the donor DNA integrated into the target locus out of 9 hygromycin-resistant transformants analyzed, and fully penetrant Cas9 strain GE-6594 yielded 5 mutants having integrated DNA in the target locus out of 5 hygromycin-resistant transformants analyzed. Using the HygR cassette fragment (SEQ ID NO:46; lacking flanking sequences having homology to the targeted locus), GE-6791 yielded 19 clones with a donor fragment-disrupted target locus from 61 analyzed, and GE-6594 yielded 6 target locus integration mutants out of out of 17 hygromycin-resistant transformants analyzed. No mutants were obtained from transformants generated by control transformations where gRNA was omitted. PCR products of wild type size were Sanger sequenced to look for any small and hard to detect insertions or deletions due to NHEJ mis-repair, but none were observed.

[00183] In this example, using the fully penetrant Cas9 lines, mutants were obtained with the co-transformation of only a HygR cassette lacking homology to the targeted locus and thus target gene mutation was not dependent on the use of a homologous recombination (HR) vector. This wasn't observed in the original parent strain GE-6571 (Example 2), where integration of the donor fragment only occurred when there were homology arms on the donor fragment flanking the gene(s) of interest. This new mutant class not generated by homologous recombination was nonetheless found by colony PCR to yield a large band indicative of insertion at the targeted locus, and Sanger sequencing of the PCR products confirmed that all of these mutants had insertions of the HygR cassette at the targeted locus. Integration of the donor fragment was found to occur in either orientation, presumably

inserted during NHEJ repair (i.e., by NHEJ "knock-in"). These NHEJ integration events were sequence-confirmed by sequencing the PCR products.

[00184] The improvement in mutation frequency in the new Cas9 expressor strains over the original strain is best explained by the fact that these new strains were pre-screened and determined to be essentially 100% phenotypically penetrant for GFP prior to transformation. The original strain GE-6571 did not have a GFP cassette, and fully penetrant lines transformed with this construct were not isolated. Although GE-6571 arguably had higher Cas9 expression according to western blot (Figure 8), it was likely only partially penetrant (that is, the expression level among the population was probably not consistent). Figure 8 provides a general schema for isolating fully penetrant Cas9-expressing strains that includes transforming a strain with a construct that includes a Cas9 gene plus a selectable marker and reporter gene (preferably encoding a fluorescent protein, isolating transformants on selective media, performing a penetrance screen by flow cytometry to identify strains that have 100% penetrance of the fluorescent protein, and verifying expression of Cas9, for example, by Western blot. Interestingly, the Western blot in Figure 8 shows that GE-6571, which was not screened for penetrance and had very poor Cas9 mutational frequency (Example 2), has a higher level of Cas9 protein than the two fully penetrant Editor lines, GE-6594 and GE-6791, which show dramatically higher Cas9 mutation rates (Example 4), demonstrating that penetrance is a far more reliable screen than assessing Cas9 protein levels.

[00185] Example 5. High frequency Knockout of the Acyl-CoA Oxidase Gene using Fully Penetrant *Nannochloropsis* Cas9 Editor Lines

[00186] **To** further test the penetrant *Nannochloropsis* Cas9 Editor strains GE-6594 and GE-6791 for genome editing capability, an editing approach similar to Example 4 was taken where the CHORD-3266 gene was successfully and efficiently targeted. To target the *N. gaditana* acyl-CoA oxidase gene (SEQ ID NO:48), a chimeric guide RNA was designed to target the aco2 target sequence, which included 20 nucleotides of sequence with homology to an acyl-CoA oxidase gene sequence directly upstream of a *S. pyogenes* Cas9 PAM sequence occurring within the acyl-CoA oxidase gene (SEQ ID NO:49; 20 nucleotide target sequence plus PAM), where the 20 nucleotide targeting sequence was within a 103 base chimeric guide RNA sequence (SEQ ID NO:50) that also included the transactivating CRISPR (tracr) sequence. The entire chimeric guide sequence was synthesized by first making a DNA template made up of complementary DNA oligonucleotides (SEQ ID NO:51 and SEQ ID NO:52) in which the DNA sequence encoding the guide RNA molecule was included downstream of a T7 promoter (SEQ ID NO:35). The oligos were annealed to create a double

stranded DNA template, which was used as the template for *in vitro* transcription reactions that were performed using the MEGAshortscript™ T7 Kit (Life Technologies # AM1354M) according to the manufacturer's protocol. The resulting RNA was purified using Zymo-Spin™ V-E columns (Zymo Research #C1024-25) according to manufacturer's protocol.

[00187] The strains were transformed with the gRNA targeting aco2 and one of the following selectable DNA molecules: 1) a HygR cassette that only included a hygromycin resistance (HygR) gene (SEQ ID NO:22) under the control of the *N. gaditana* EIF3 promoter (SEQ ID NO:23) terminated by *N. gaditana* bidirectional terminator 2 (SEQ ID NO:26) (the operably linked HygR gene, promoter, and terminator referred to herein as the HygR cassette), or 2) a circular form of vector pSGE-6282 (SEQ ID NO:53) (**Figure 9**) based on a puc19 backbone which includes all of the elements in the fragment described in 1), but here those elements were flanked by 1.7kb "up" (SEQ ID NO:54) and 0.8kb "down" (SEQ ID NO:55) arms homologous to the sequences upstream and downstream of the aco2 target (SEQ ID NO:49). The homology arms omit 113 bp of DNA surrounding the aco2 target site. The same donor DNAs (1) and 2)) were transformed into Cas9 Editor strains GE-6594 and GE-6791 without gRNA as controls.

[00188] The GE-6594 and GE-6791 Cas9 expression strains were transformed by electroporation using 5 µg of purified chimeric guide RNA targeting the aco2 target site, and 1 µg of one of the forms of selectable donor DNA described above. Following electroporation, cells were plated on agar medium containing hygromycin to select for transformants that incorporated the hygromycin cassette. Transformants were screened by colony PCR as described previously (see Example 2) but using primers flanking the aco2 target (SEQ ID NO:17 and SEQ ID NO:18). The results are shown in Table 3.

[00189] Table 3: Rates of *in vivo* Genome Editing in Fully Penetrant Cas9 Editor Lines targeting the Acyl-CoA Oxidase locus.

Cas9 Editor Strain	Donor DNA fragment	total no. transformants analyzed	no. confirmed positive for mutation at locus	% transformants with mutated target locus
GE-6791	Hyg-Frag	160	90	56
GE-6791	pSGE06282 (for HR)	61	43	70
GE-6594	Hyg-Frag	96	44	46
GE-6594	pSGE06282 (for HR)	62	46	74

[00190] The mutation frequency in these new Cas9 Editor strains was drastically improved over that of the original parental strain GE-6571. Using the homologous recombination vector pSGE-6282, GE-6791 yielded 43 positive clones from 61 analyzed, and GE-6594 yielded 46 positive mutants out of 62 analyzed. Using the HygR cassette alone (without homology arms), GE-6791 yielded 90 positive clones from 160 analyzed, and GE-6594 yielded 44 positive mutants out of 96 analyzed. No mutants were obtained from the transformants generated by control transformations where gRNA was omitted. PCR products of wild type size were Sanger sequenced to look for any small and hard to detect insertions or deletions due to NHEJ mis-repair, but none were observed.

[00191] In this example, as in Example 4, mutants were again obtained with the co-transformation of only a HygR cassette fragment and not dependent on the use of an HR vector having sequences homologous to the targeted locus flanking the resistance cassette; this wasn't observed in the original parent strain GE-6571 (see Example 2). This is further evidence that the improvement in mutation frequency in the new Cas9 Editor strains over the original strain can likely be explained by the fact that these new strains were pre-screened and determined to be phenotypically fully penetrant for GFP prior to transformation.

[00192] Example 6. Development of a Fully Penetrant Cas9-expressing *Parachlorella* strain

[00193] A vector, pSGE-6709 (**Figure 10**), was engineered for the expression of the *Streptococcus pyogenes* Cas9 gene in *Parachlorella*. The vector included the following three elements: 1) a Cas9 expression cassette which contained an engineered Cas9 gene codon optimized for *Parachlorella* and containing introns from *Parachlorella,* that also included an N-terminal FLAG tag, nuclear localization signal, and peptide linker (SEQ ID NO:56) operably linked to the *Parachlorella* RPS17 promoter (SEQ ID NO:57) and terminated by the *Parachlorella* RPS17 terminator (SEQ ID NO:58); 2) a selectable marker expression cassette, which contained the blasticidin resistance gene from *Aspergillus terreus* codon optimized for *Parachlorella* and containing *Parachlorella* introns (SEQ ID NO:59), operably linked to the *Parachlorella* RPS4 promoter (SEQ ID NO:60) and terminated by the *Parachlorella* RPS4 terminator (SEQ ID NO:61); and 3) a GFP reporter expression cassette, which contained the TurboGFP gene (Evrogen, Moscow, Russia) (SEQ ID NO:24), driven by the *Parachlorella* ACP1 promoter (SEQ ID NO:62) and terminated by the *Parachlorella* ACP1 terminator (SEQ ID:63).

[00194] The vector was transformed into *Parachlorella* by biolistics. Transformation of *Parachlorella* wild type strain WT-1185 was accomplished using the BioRad Helios® Gene

Gun System essentially as described in US Patent Publication No. 2014/0154806, incorporated herein by reference. DNA for transformation was precipitated onto gold particles, the gold particles were adhered to the inside of lengths of tubing, and a burst of helium gas was fired through the tubing positioned within the Gene Gun to propel the DNA-coated gold particles into *Parachlorella* strain WT-1185 cells which were adhered on solid non-selective media (2% agar plates containing PM074 algal growth medium). The Helios® Gene Gun was used to fire two bullets per cell circle at 600 psi from a distance of 3-6 cm from the plate. The following day, cells were transferred onto selective medium for growth of transformed colonies.

[00195] Colonies were screened for full GFP penetrance as described in Example 3 by flow cytometry and identification of transformed strains that had a single fluorescence peak shifted to a higher value than the wild type fluorescence peak. Fully penetrant Cas9 strains demonstrating a clearly shifted fluorescence peak with respect to nontransformed cells were tested for Cas9 expression by anti-Cas9 western blotting for evidence of Cas9 expression (**Figure 11**). Based on these screens, isolate 6709-2 was carried forward and given strain identifier GE-15699.

[00196] Example 7. Knockout of SRP54 using Fully Penetrant *Parachlorella* Cas9 Editor Line

[00197] **To** test the new strain GE-15699 for genome editing capability, an editing approach was taken that was similar to that described in Examples 2 and 4. Chimeric gRNA (SEQ ID NO:64) was designed and synthesized *in vitro* to target the chloroplastic SRP54 gene in *Parachlorella* (SEQ ID NO:65). GE-15699 was transformed by electroporation with 1-2 µg of purified chimeric guide RNA, and 1 µg of selectable marker DNA which contained a bleomycin resistance "BleR" gene codon-optimized for *Parachlorella* and containing introns from *Parachlorella* (SEQ ID:66). The BleR gene was operably linked to the *Parachlorella* RPS4 promoter (SEQ ID:60) and terminated by the *Parachlorella* RPS4 terminator (SEQ ID:61).

[00198] Electroporation was performed by inoculating a 100mL seed culture inoculated to 1 x 10^6 cells/mL six days before transformation was used to inoculate a 1L culture to 1 x 10^6 cells/mL two days before transformation. On the day of transformation, cells were pelleted by centrifugation at 5000 x g for 20 minutes, washed three times with 0.1um filtered 385 mM sorbitol, and resuspended to 5x10^9 cells/mL in 385 mM sorbitol. Electroporation of 100 µL concentrated cells was performed in 0.2 cm cuvettes in a BioRad Gene Pulser Xcell™ under varied conditions. The DNA used for optimization of electroporation was linearized pSG6640

including the *ble* and TurboGFP expression cassettes. The TurboGFP cassette included the *Parachlorella* ACP promoter (SEQ ID NO:62) operably linked to the TurboGFP gene (SEQ ID NO:24) and the *Parachlorella* ACP terminator (SEQ ID NO:63). Immediately after electroporating pre-chilled cells and cuvettes, 1mL cold sorbitol was added and used to transfer cells into 10 mL PM074. After overnight recovery, cells were concentrated and spread onto 13cm-diameter PM074 media containing zeocin at 250 mg/L and grown under the conditions listed in the biolistics section.

[00199] After testing a range of voltages, resistances, and capacitances, the optimal electroporation conditions were determined to be 1.0-1.2 kV (5000-6000 V/cm), 200-300 ohms, and 25-50 μF. Use of larger quantities of DNA increased the resulting number of zeocin-resistant colonies, though the effect plateaued at amounts larger than 4 μg.

[00200] Following electroporation, cells were plated on agar medium (PM130) containing 250 μg/ml zeocin to select for transformants that incorporated the bleR cassette. Transformants were screened by colony PCR using primers designed to amplify across the native targeted locus (oligo-AE596; SEQ ID NO:67 and oligo-AE597; SEQ ID NO:68). The primers were designed to produce a 700 bp band in the absence of integration (*e.g.*, "knock-in" of the BleR cassette) into the locus, or a 4.3kb band if there was integration of a single BleR cassette into the targeted locus. In addition, colony PCR was also performed using primers designed to amplify a fragment extending from the cpSRP54 gene (oligo-AE597; SEQ ID NO:68) into the selectable marker (oligo-AE405; SEQ ID NO:69 and oligo-AE406; SEQ ID NO:70). Depending on orientation of the integrated ble cassette, a 1.2kb band would result from either amplification by primers 405/597 or 406/597 spanning from within the bleR cassette out to the cpSRP54 gene. The results show a high frequency (between 40 and 45% in this sample) of knock-in of the BleR cassette into the targeted locus (**Figure 12**), in the absence of homology arms. As cpSRP54 knockouts result in a pale green phenotype, these colony patches are overlaid with the PCR results in this image.

[00201] Example 8. Promoter boosting to increase expression of the native *Nannochloropsis* Accase gene using Cas9/CRISPR

[00202] The promoter region of the *N. gaditana* Accase gene was targeted to increase its promoter function. A construct was designed that included a hygromycin resistance cassette as described in Example 4, but lacking the 5' and 3' identification sequences (SEQ ID NO:45). The HygR cassette was flanked by strong promoters oriented in an outward direction (**Figure 13A**). The outwardly-directed dual promoter design was to ensure that regardless of the orientation in which the HygR cassette integrated, one of the promoters would be

positioned to enhance expression of the Accase gene when the donor fragment was targeted to the upstream region of the Accase gene (**Figure 13B**). The construct lacked homology arms for the integration region and therefore the intended mode of insertion was by NHEJ. The outward directed promoter positioned "upstream" of the HygR cassette was the TCTP promoter (SEQ ID NO:11). The outward directed promoter positioned "downstream" of the HygR cassette was RPL24 promoter (SEQ ID NO:25), giving rise to a DNA fragment termed the Dual Promoter HygR cassette (SEQ ID NO:71).

[00203] Four chimeric guide RNAs were synthesized as described in Example 2, each 20 nucleotides in length (SEQ ID Nos:72-75) to target integration of the promoter flanked hygromycin cassette (SEQ ID NO:71) into different target sites (Acc1 through Acc4) as indicated in **Figure 13B.** Transformation of *N. gaditana* Editor line GE-6791 described in Example 3 was performed using electroporation essentially as described in Example 4, where each of the four guide RNAs was individually co-transformed with the promoter flanked hygromycin cassette (SEQ ID NO:71). For each transformation, hygromycin-resistant colonies were selected and analyzed by PCR to identify whether or not the HygR cassette had integrated into the 5' region of the Accase gene. PCR products were sequenced for absolute confirmation of disrupted loci. The primers used were Accase-F (SEQ ID NO:76) and Accase-R (SEQ ID NO:77) that flanked the targeted upstream region of the Accase gene.

[00204] Two of the transformants with confirmed promoter region modification, designated ACC-KI-1 and ACC-KI-2, were selected for further analysis. In ACC-KI-1, the insert was targeted to the Acc1 guide RNA site 13 bp upstream of the deduced transcriptional start site, and in ACC-KI-2, it was targeted to the Acc2 guide RNA site 28 bp upstream of the deduced transcriptional start site. To determine the effect of the "promoter boosting" construct, Accase enzyme activity was measured exactly as described in Roessler P. (1988) Archives of Biochemistry and Biophysics 267:521-528) for the two strains ACC-KI-1 and ACC-KI-2 and the enzyme activity was compared to that of wild type cells. Increased total ACCase enzyme activity on a per total milligram protein basis in both ACC-KI-1 and ACC-KI-2 was observed (Table 4), proving that modification of a gene promoter as described gives

rise to increased expression of the gene and level of the encoded protein.

Table 4

	Activity nmol/min/mg	% increase
WE03730	0.454	0.00
ACC-KI-1	0.604	33.12
ACC-KI-2	1.129	148.63

[00205] Example 9. Knockout of the ZnCys-2845 locus in *Nannochloropsis*

[00206] The ZnCys-2845 lipid regulator gene was also knocked out using CRISPR technology. The *Nannochloropsis* Cas9 Editor line GE-6791, expressing a gene encoding the *Streptococcus pyogenes* Cas9 nuclease was used as a host for transformation with a chimeric guide RNA and donor DNA for insertional knockout.

[00207] For targeting of the ZnCys-2845 gene for disruption, a DNA construct was made (SGI-DNA, La Jolla, CA) for producing a guide RNA in which the DNA molecule included the sequence of a chimeric guide engineered downstream of a T7 promoter (SEQ ID NO:35). The chimeric guide sequence included an 18 bp target sequence (SEQ ID NO:78) homologous to a sequence within the ZnCys-2845 gene sequence that was upstream of an *S. pyogenes* cas9 PAM sequence (NGG), and also included the transactivating CRISPR (tracr) sequence. The chimeric guide sequence was synthesized by first making a DNA template made up of complementary DNA oligonucleotides (SEQ ID NO:79 and SEQ ID NO:80) that were annealed to create a double-stranded DNA template that included a T7 promoter sequence which was used in *in vitro* transcription reactions using the MEGAshortscript™ T7 Kit (Life Technologies # AM1354M) according to the manufacturer's instructions to synthesize the guide RNA. The resulting RNA was purified using Zymo-Spin™ V-E columns (Zymo Research #C1024-25) according to manufacturer's protocol.

[00208] The donor fragment for insertion into the targeted ZnCys-2845 locus (SEQ ID NO:46) included a selectable marker cassette that included the hygromycin resistance gene

(HygR, SEQ ID NO:22) downstream of the *N. gaditana* EIF3 promoter (SEQ ID NO:23) and followed by *N. gaditana* bidirectional terminator 2 (SEQ ID NO:26), with the entire promoter-hygromycin resistance gene-terminator sequence flanked by 27 base pair identification sequences on the 5' (SEQ ID NO:43 5'ID) and 3' (SEQ ID NO:44 3'ID) ends to yield the DNA fragment referred to as the "Hyg Resistance Cassette" (SEQ ID NO:46 HygR Cassette).

[00209] For targeted knockout of the ZnCys-2845 locus, Cas9 Editor line GE-6791 was transformed by electroporation using 5 μg of purified chimeric guide RNA targeting the ZnCys-2845 gene and 1 μg of the selectable donor DNA (HygR Cassette; SEQ ID NO:46) essentially as described in US 2014/0220638. Following electroporation, cells were plated on PM124 agar media containing hygromycin to select for transformants that incorporated the hygromycin resistance cassette. Transformants were patched onto a fresh plate and screened by colony PCR for insertion of the donor fragment into the ZnCys-2845 gene.

[00210] Colony PCR screening was performed as described in Example 1. The primers used to detect the insertion of the donor fragment into the targeted locus of the ZnCys-2845 gene were SEQ ID NO:81 and SEQ ID NO:82. Based on the PCR-based colony screening, knockout strains having the donor DNA (HygR cassette) inserted into the targeted ZnCys-2845 gene, GE-8564 and GE-8565 (Figure 14A), were tested in productivity assays.

[00211] ZnCys-2845 knockout strain GE-8564 and wild type progenitor strain WT-3730 were cultured in a batch productivity assay in nitrogen replete medium PM123 that included 15 mM nitrate as the sole nitrogen source available to the cells, i.e., the culture medium had no source of reduced nitrogen. Because it had been determined that the ZnCys-2845 mutant does not grow in the absence of reduced nitrogen, the production cultures were inoculated to an initial OD730 of 0.5 from seed (scale-up) cultures that were grown in PM124 medium that included 5 mM ammonium in addition to 8.8 mM nitrate.

[00212] After inoculation, ZnCys knockout strain GE-8564 and wild type strain WT-3730 were grown in triplicate cultures in a batch assay in 75 cm2 rectangular tissue culture flasks containing 175 ml of PM123 medium, which includes 15 mM nitrate as the sole nitrogen source, for seven days. The flasks were positioned with their narrowest "width" dimension against an LED light source that was programmed for a 16 h light:8 hour dark cycle, with the light intensity following a curve designed to mimic natural daylight, in which the light intensity peaked in the middle of the light period at approximately 1200 μE. Deionized H2O was added to the cultures daily to replace evaporative losses. The temperature of the cultures was regulated by a water bath set at 25°C. Cultures were inoculated on day 0 and samples (5

mls) were removed on days 3, 5, and 7 for assessing cell density, fatty acid methyl esters (FAME) as a measure of lipid, and total organic carbon (TOC).

[00213] FAME analysis was performed on 2 mL samples that were dried using a GeneVac HT-4X. To each of the the dried pellets the following were added: 500 µL of 500 mM KOH in methanol, 200 µL of tetrahydrofuran containing 0.05% butylated hydroxyl toluene, 40 µL of a 2 mg/ml C11:0 free fatty acid/C13:0 triglyceride/C23:0 fatty acid methyl ester internal standard mix and 500 µL of glass beads (425–600 µm diameter). The vials were capped with open top PTFE septa-lined caps and placed in an SPEX GenoGrinder at 1.65 krpm for 7.5 minutes. The samples were then heated at 80°C for five minutes and allowed to cool. For derivatization, 500 µL of 10% boron trifluoride in methanol was added to the samples prior to heating at 80°C for 30 minutes. The tubes were allowed to cool prior to adding 2 mL of heptane and 500 µL of 5 M NaCl. The samples were vortexed for five minutes at 2K rpm and finally centrifuged for three minutes at 1K rpm. The heptane layer was sampled using a Gerstel MPS Autosampler. Quantitation used the 80 µg of C23:0 FAME internal standard.

[00214] Total organic carbon (TOC) was determined by diluting 2 mL of cell culture to a total volume of 20 mL with DI water. Three injections per measurement were injected into a Shimadzu TOC-Vcsj Analyzer for determination of Total Carbon (TC) and Total Inorganic Carbon (TIC). The combustion furnace was set to 720°C, and TOC was determined by subtracting TIC from TC. The 4 point calibration range was from 2 ppm to 200 ppm corresponding to 20-2000 ppm for non-diluted cultures with a correlation coefficient of $r2 > 0.999$.

[00215] The results of these analyses are shown in **Tables 5-7**. Values provided for wild type and knockout GE-8564 mutant are the average of three cultures with standard deviations (sd).

[00216] Table 5. Lipid (FAME) Produced by ZnCys-2845 Knockout Mutant and Wild Type Cultures in Batch Assay with Nitrate-only Culture Medium.

Day	WT-3730 (NO3)		ZnCys-KO GE-8564 (NO_3)		
	µg/ml	sd	µg/ml	sd	% increase
3	105.03	9.71	188.56	6.52	79.53
5	140.01	13.48	223.41	0.28	59.57
7	198.49	2.04	250.76	3.22	26.33

[00217] Table 6. Biomass (TOC) Produced by ZnCys-2845 Knockout Mutant and Wild Type Cultures in Batch Assay with Nitrate-only Culture Medium.

Day	WT-3730 (NO3)		ZnCys-KO GE-8564 (NO3)		
	µg/ml	s.d.	µg/ml	s.d.	% diff
3	375.6	10.18	261.7	7.07	-30.3
4	474.6	8.34	283.95	3.61	-40.2
5	534.45	43.20	269.5	3.68	-49.6
6	644.8	48.65	311.75	3.18	-51.7
7	804.35	36.13	329.3	1. 70	-59.1

[00218] Table 7. FAME / TOC ratios of ZnCys-2845 Knockout Mutant and Wild Type Strains in Batch Assay with Nitrate-only Culture Medium.

Day	WT-3730 (NO3)		ZnCys-KO GE-8564 (NO3)		
		s.d.		s.d.	% increase
3	0.28	0.018	0.72	0.044	157
5	0.26	0.004	0.83	0.012	219
7	0.25	0.009	0.76	0.006	204

[00219] Although the FAME content of the ZnCys-2845 knockout mutant culture in nitrate-only medium was at a higher level on day 3 of the culture, which was the first day assayed, as well as on days 5 and 7 (**Table 5**), the increase in FAME per day between days 3 and 7 was less for the ZnCys-2845 knockout strain than for the wild type strain. **Table 6** demonstrates that over this time period the ZnCys-2845 gene disruption mutant cultured in nitrate-only medium increased its total organic carbon very little as compared to wild type, which showed steady growth as assessed by TOC accumulation. Thus, the ZnCys-2845 knockout strain, when cultured in a medium that included nitrate as the sole nitrogen source, behaved as though it were in nitrogen starvation. **Table 7** confirms this, demonstrating that over the course of the one week productivity assay, the FAME/TOC ratio of the ZnCys-2845 knockout strain GE-8564 was significantly elevated over the wild type FAME/TOC ratio (approximately three-fold the FAME/TOC ratio of wild type).

[00220] Example 10. Cas9 ZnCys-2845 insertional knockdown constructs

[00221] Additional mutant strains were engineered to have decreased expression of the ZnCys-2845 gene using Cas9/CRISPR genome engineering. Twelve chimeric guide RNAs

were designed to target sequences upstream of the ATG that encoded the first amino acid of the open reading frame, within an intron of the gene, in the 3' end of the gene but still within the coding sequence, or in the 3' untranslated region of the gene (**Figure 14A**). These constructs described here as "Bash Knockdown constructs" or simply "Bash constructs" because they are designed to insert the donor fragment into a site in a region of the gene where the insertion is expected to disrupt native sequences to result in the targeted gene being expressed at a lower level than in wild type. (Correspondingly, the strains that include such insertions are referred to as "Bash strains", "Bashers", or "Bash Knockdown mutants".) The twelve 18-nucleotide sequences having homology to the ZnCys-2845 gene (target site sequences) are provided in **Table 8**.

[00222] Table 8: Target and Chimeric Guide Sequences for Attenuating ZnCys-2845 Expression

"Bash" Gene Attenuation Mutant	Gene Region Targeted	Target Sequence (18 nt)
1	5' UTR	SEQ ID NO:83
2	5' UTR	SEQ ID NO:84
3	5' UTR	SEQ ID NO:85
4	5' UTR	SEQ ID NO:86
5	5' UTR	SEQ ID NO:87
6	coding region	SEQ ID NO:88
7	coding region	SEQ ID NO:89
8	C-terminus	SEQ ID NO:90
9	C-terminus	SEQ ID NO:91
10	C-terminus	SEQ ID NO:92
11	3' UTR	SEQ ID NO:93
12	3' UTR	SEQ ID NO:94

[00223] Chimeric guide DNA constructs were synthesized as two complementary strands that were annealed to produce a double-stranded construct with a T7 promoter positioned upstream of the guide sequence (that included the 18 nucleotide target sequence), and used to produce the

chimeric guide RNAs by *in vitro* transcription and purified as described in **Example 3**. Each chimeric guide RNA was individually transformed into *Nannochloropsis* Editor strain GE-6791 along with the donor fragment that included a Hyg resistance ("HygR") cassette (SEQ

ID NO:46) as described in **Example 3**. Hygromycin resistant colonies were selected and screened by colony PCR as described using primers adjacent to the targeted regions of the ZnCys-2845 gene (Primers MA-ZnCys-FP (SEQ ID NO:81) and MA-ZnCys-RP (SEQ ID NO:82) were used to confirm the knockout (GE-8564) and donor fragment insertion into introns; primers MA-5'Bash-ZnCys-FP (SEQ ID NO:95) and MA-5'Bash-ZnCys-RP (SEQ ID NO:96) were used to confirm the insertion of the donor fragment into the 5' regions of the ZnCys-2845 gene; and primers MA-3'Bash-ZnCys-FP (SEQ ID NO:97) and MA-3'Bash-ZnCys-RP (SEQ ID NO:98) were used to confirm the insertion of the donor fragment into the 3' regions of the ZNCys-2845 gene. Eleven of the twelve guide RNAs resulted in isolates that were diagnosed by colony PCR as having the Hyg gene inserted at the targeted locus.

[00224] Quantitative reverse transcription-PCR (qRT-PCR) was performed on RNA isolated from the knockdown lines to determine whether expression of the ZnCys-2845 gene was in fact reduced in these lines. The ZnCys-2845 Bash Knockdown strains were grown under standard nitrogen replete conditions (PM074 (nitrate-only) medium) and harvested during early stationary phase. Total RNA was isolated from ZnCys-2845 Bash Knockdown cells and converted to cDNA BioRad's iScript™ Reverse Transcription Supermix kit according to the manufacturer's protocol. For PCR, Ssofast EvaGreen Supermix (Bio-Rad, Hercules, CA) was used along with gene-specific primers. The PCR reaction was carried out on C1000 Thermal Cycler coupled with a CFX Real-time System (BioRad). Primer and cDNA concentrations were according to the manufacturer's recommendation. Primers for amplifying a sequence of the ZnCys-2845 transcript were SEQ ID NO:99 and SEQ ID NO:100. Transcript levels for each sample were normalized against a housekeeping gene with consistent expression levels under different culture conditions (1T5001704; SEQ ID NO:101) and relative expression levels were calculated using the ddCT method using BioRad's CFX Manager software.

[00225] **Figure 14B** shows that several of the strains had reduced levels of ZnCys-2845 transcript. Of these, strains GE-13108 (ZnCys-2845 Bash-3) and GE-13109 (ZnCys-2845 Bash-4), targeting the 5' end of the ZnCys-2845 gene, and strain GE-13112 (ZnCys-28453 Bash-12), targeting the 3' end of the ZnCys-2845 gene, were selected for productivity assays.

[00226] **Example 11. ZnCys-2845 RNAi Knockdown Construct**

[00227] In another strategy to determine whether decreasing expression of the ZnCys-2845 gene would allow the cells to accumulate more carbon than the Cas9-mediated ZnCys-2845 knockout (Example 9) while still producing increased amounts of lipid with respect to wild type, an interfering RNA (RNAi) construct (shown in **Figure 15**) was designed for

expression in *Nannochloropsis* cells. The construct included a sequence designed to form a hairpin that included a sequence homologous to a region of the ZnCys-2845 gene (SEQ ID NO:102), followed by a loop sequence and then followed by the inverse sequence to the ZnCys-2845 gene-homologous sequence, driven by the *N. gaditana* EIF3 promoter (SEQ ID NO:45) and followed by *N. gaditana* "terminator 9" (SEQ ID NO:103). The construct that included the RNAi expression cassette also included the *Nannochloropsis* codon-optimized gene encoding TurboGFP (Evrogen; Moscow, Russia) codon-optimized for *Nannochloropsis* (SEQ ID NO:24) under the control of the *Nannochloropsis* 4AIII promoter (SEQ ID NO:40) and followed by "terminator 5" (SEQ ID NO:41), as well as a gene conferring hygromycin resistance (SEQ ID NO:44) driven by the TCTP promoter (SEQ ID NO:11) and terminated by the EIF3 terminator (SEQ ID NO:12). The RNAi expression cassette for the construct was positioned between the hygromycin resistance expression cassette (which was positioned 5' of and oriented in a transcriptional direction opposite to that of the RNAi construct) and the GFP expression cassette (which was positioned 3' of the RNAi cassette and oriented in the same transcriptional direction as the RNAi cassette) The construct was linearized and transformed into wild type *Nannochloropsis gaditana* WT-3730 by electroporation as described.

[00228] Hygromycin resistant colonies were screened for the presence of the RNAi construct by PCR, and were further screened for full penetrance of GFP using flow cytometry as described in Example 3, above. Flow cytometry was performed to test the penetrance of lines 6, 7, 10, 12, 13, 21, 25, and 30 isolated from transformants that were positive for the RNAi construct and overlaid with the traces of wild type controls.

[00229] Because RNAi was employed to test different levels of gene attenuation, it was of interest to test the phenotypes of strains showing different penetrance patterns. For example, some of the RNAi construct carrying lines, such as lines 10, 13, 21, and 30, were not fully penetrant, that is, their fluorescence traces essentially coincided with that of wildtype. Interestingly, strain 25 had the most reduced RNA level with respect to wild type levels, followed by strains 7, 10, 6, and 12. A characteristic of attenuation of the ZnCys-2845 gene is the inability (or, depending on the level of attenuation of ZnCys2845 gene expression, reduced ability) to grow on media that include only nitrate as a nitrogen source. The knockout shows no growth (rightmost flask), and strain 1 and strain 12 showed very little to no growth as well. Strains 7 and 25 had reduced growth in nitrate only medium, whereas strains 10, 13, 21, and 30 demonstrated growth similar to wild type. Notably, strain 10, which appeared by RNA level to have a high level of gene attenuation (at least as high as strain 6), does not

display nearly as strong a phenotype as strain 6. This difference in phenotype, while not predictable from RNA levels, correlated well with the incomplete penetrance of GFP expression of strain 10 and the fully penetrant expression of GFP in strain 6. Thus, assessment of fluorescence of a linked fluorescent protein gene in a clonal population was a highly reliable method for isolating strains with consistent expression of a gene of interest.

[00230] Strain 7, which displayed full penetrance but a less severe reduction of growth in nitrate-only medium than the knockout strain was renamed strain GE-13103 and selected for further evaluation along with the promoter and 3' end disruption strains isolated in Example 10.

[00231] Example 12. Phenotyping of ZnCys-2845 Knockdown Constructs

[00232] To rigorously test the lipid regulator phenotype, ZnCys-2845 RNAi strain GE-13103 and ZnCys-2845 knockdown insertional "basher" strains GE-13108, GE-13109, and GE-13112 were tested in the batch productivity assay by scaling up the cultures in culture medium PM124 (which includes both NH_4 and NO_3 as nitrogen sources) and by carrying out the assay in PM123 culture medium that includes nitrate as the sole nitrogen source.

[00233] Strikingly, all gene attenuation mutants, including original knockout mutant GE-8564, produced FAME in amounts greater than wild type when cultured with nitrate as the sole nitrogen source on all days sampled (**Table 9**). However, while the original knockout strain GE-8564 had a significantly reduced rate of total organic carbon accumulation with respect to wild type (**Table 10**), in these conditions, the attenuated knockdown strains - the "bash" strains and RNAi strain having reduced expression of the ZnCys-2845 gene had rates of TOC accumulation close to or (for example in the case of GE-13112) essentially identical to, wild type (**Table 10**). Remarkably, these ZnCys-2845 knockdown mutants demonstrated FAME to TOC ratios that were significantly enhanced with respect to wild type (**Table 11**).

[00234] Table 9. FAME productivity of ZnCys-2845 Knockdown Strains Compared to Wild Type in Batch Assay with NO_3-containing Culture Medium (mg/L culture)

Day	WT	BASH-3 (GE-13108)		BASH-4 (GE-13109)		BASH-12 (GE-13112)		RNAi-7 (GE-13103)		ZnCys-KO (GE-8564)	
			% incr		% incr		% incr		% incr		% incr
3	159.22	279.72	75.68	260.14	233.36	233.36	40.64	233.36	46.56	242.05	52.02
5	191.33	446.40	133.31	377.8	368.41	368.41	55.98	368.41	92.55	360.89	88.67
7	270.37	599.06	121.57	431.41	460.69	460.69	27.96	460.69	70.39	473.53	75.14

[00235] Table 10. TOC productivity of ZnCys-2845 Knockdown Strains Compared to Wild Type in Batch Assay with NO_3-containing Culture Medium (mg/L culture)

Day	WT	BASH-3 (GE-13108)		BASH-4 (GE-13109)		BASH-12 (GE-13112)		RNAi-7 (GE-13103)		ZnCys-KO (GE-8564)	
			% diff		% diff		% diff		% diff		% diff
3	642.4	608.1	-5.34	615.05	-4.26	627.2	-2.37	497.4	-22.57	281.5	-56.18
5	920.75	827.9	-10.09	836.9	-9.11	913.95	-0.74	713.4	-22.52	408.8	-55.01
7	1188	1044.5	-12.08	1044	-12.12	1175.5	-1.05	929.2	-21.78	558.15	-53.18

[00236] Table 11. FAME/TOC ratios of ZnCys-2845 Knockdown Strains Compared to Wild Type in Batch Assay with NO_3-containing Culture Medium

Day	WT-3730		BASH-3 (GE-13108)		BASH-4 (GE-13109)		BASH-12 (GE-13112)		RNAi-7 (GE-13103)		ZnCys-KO (GE-8564)	
		s.d.		s.d.		s.d.		s.d.		s.d.		s.d.
3	0.25	0.009	0.46	0.009	0.42	0.010	0.36	0.004	0.47	0.015	0.86	0.033
5	0.21	0.001	0.54	0.006	0.45	0.003	0.33	0.011	0.52	0.023	0.88	0.040
7	0.23	0.001	0.57	0.005	0.41	0.004	0.29	0.003	0.50	0.007	0.85	0.060

[00237] Example 13. Targeted integration of transgene(s) using Fully Penetrant *Nannochloropsis* Cas9 Editor Line

[00238] Cas9 Editor Strain GE-6791 of Example 3 was also used to assess targeted integration of a transgenic pathway to a specific locus. The aco 2 CRISPR target locus within the acyl-CoA oxidase gene was again chosen (SEQ ID NO:48) as it was successfully disrupted using the HygR cassette in Example 5 and gRNA targeting the gene (SEQ ID NO:49) was already available (see Example 5). A 22.3 kb fragment obtained by Asc/Not restriction digest and gel purification of vector pSGE-6337 (SEQ ID NO:104) was chosen for targeted integration into the aco2 site. This fragment contained 6 expression cassettes intended for metabolic engineering, and the six tandemly arranged expression cassettes were flanked by a HygR cassette on one end and a GFP cassette on the other end (**Figure 16**).

[00239] The GE-6791 Cas9 expression strain was transformed by electroporation using 5 µg of purified chimeric guide RNA targeting the aco2 target site, and 1 µg of one of the pSGE-6337-Asc/Not Fragment (SEQ ID NO:104). Following electroporation, cells were plated on agar media containing hygromycin to select for transformants that incorporated the 22.3kb DNA molecule. Transformants were screened by colony PCR as described previously

(see Example 2) but using primers flanking the aco2 target (SEQ ID NO:17) (SEQ ID NO:18), as well as another reaction which included a third primer that primes off of HygR gene (SEQ ID NO:105), which is near one end of the fragment and points outward. The PCR results are shown in detail (**Figure 17**), in which colonies 5, 6, 7, 8, 9, 20, 27, 28, and 31 appear to have integrated the 22.3kb donor DNA into the targeted aco2 site.

Example 14. Nannochloropsis Editor strain expressing tracrRNA.

[00240] A *Nannochloropsis* editor strain can also be engineered by transforming wild type *Nannochloropsis* with a construct that includes: 1) a Cas9 expression cassette containing a Cas9 gene from *Streptococcus pyogenes* codon optimized for *Nannochloropsis gaditana* (SEQ ID NO:1) with an N-terminal FLAG tag (SEQ ID NO:5), nuclear localization signal (SEQ ID NO:4), and a peptide linker (SEQ ID NO:39), driven by the *N. gaditana* RPL24 promoter (SEQ ID NO:25) and terminated by *N. gaditana* bidirectional terminator 2 (SEQ ID NO:26); 2) an expression cassette designed to drive expression of a tracr RNA (SEQ ID NO:106) that includes a 20 bp sequence that hybridizes to a crRNA and a 16-22 nucleotide sequence that interacts with the Cas9 protein, driven by the *N. gaditana* putative U6 promoter (SEQ ID NO:15) and followed by the U6 terminator (SEQ ID NO:16); and 4) a selectable marker expression cassette, which contained the blast gene from *Aspergillus terreus* codon optimized for *N. gaditana* (SEQ ID NO:10), driven by the *N. gaditana* TCTP promoter (SEQ ID NO:11) and followed by the EIF3 terminator (SEQ ID NO:12); and 4) a GFP reporter expression cassette, which contained the TurboGFP gene (Evrogen, Moscow, Russia) codon-optimized for *Nannochloropsis gaditana* (SEQ ID NO:24), driven by the *N. gaditana* 4A-III promoter (SEQ ID NO:40) and followed by the *N. gaditana* bidirectional terminator 5 (SEQ ID NO:41) which occurs between the Glucosamine 6-phosphate isomerase 2 gene and the YVTN repeat like quinoprotein amine dehydrogenase gene in the *N. gaditana* genome.

[00241] Strains transformed with this construct are plated onto PM74 agar medium containing blasticidin. Colonies are patched onto selection media for analysis and archiving and optionally screened for the presence of the construct by PCR. Transformants from single colony isolates are screened by flow cytometry as described in Example 3. The resulting histograms are overlaid with histograms of wild type cells (*i.e.*, cells not expressing a fluorescent protein) run separately. Only strains with fully penetrant expression in culture are investigated further; meaning that the flow cytometry GFP fluorescence histogram show a single peak or bell-shaped curve in which the fluorescence peak was fully shifted higher than the wild type autofluorescence (background fluorescence) peak when plotted on a log scale. These strains are designated as “fully penetrant” Cas9 and tracrRNA expressing strains, in

that the expression of the physically linked GFP gene is found throughout the cells of a culture of the strain. That is, while at any given point in time the amount (and therefore fluorescence) of GFP might vary somewhat cell-to-cell, resulting in peaks or bell-shaped curves, there is no subpopulation of cells observed in these lines than exhibit a distinct distribution of GFP expression with respect to the shifted peak.

[00242] Fully GFP-penetrant Cas9 strains demonstrating a single clearly shifted fluorescence peak with respect to nontransformed cells (see for example Figures 5A and 5B and Table 1, in which clones are scored by 'X's' according to whether they exhibited single or double peaks) are then tested by western blotting with an anti-FLAG antibody for evidence of Cas9 expression and with a nucleic acid probe for the presence of the tracrRNA.

[00243] For genome editing, a fully penetrant Cas9 plus tracrRNA expressing strain is transformed with a crRNA targeting a particular genome locus as well as a donor DNA for insertion into the edited locus. The crRNA used includes a 20 nucleotide sequence targeting the acyl-CoA oxidase gene (SEQ ID NO:14) juxtaposed with a 20 nucleotide tracrRNA recognition or "tracr mate" sequence to provide the entire acyl-CoA oxidase gene targeting RNA (SEQ ID NO:107). The donor DNA included a hygromycin resistance (HygR) gene (SEQ ID NO:22) under the control of the N. gaditana EIF3 promoter (SEQ ID NO:23) terminated by N. gaditana bidirectional terminator 2 (SEQ ID NO:26) (the operably linked HygR gene, promoter, and terminator referred to herein as the HygR cassette).

[00244] Following transformation, HygR colonies are screened for the presence of the HygR cassette in the acyl-CoA oxidase gene locus.

[00245] Example 15. Chlorella Editor strain with tracr RNA expressed, cr RNA introduced

[00246] In another example, both the tracrRNA and the crRNA are transformed into fully penetrant *Parachlorella* Cas9 Editor line GE-15699 to integrate a gene cassette into a targeted locus. In this case the tracrRNA and crRNA are separate molecules. The targeting crRNA (SEQ ID NO:108) is designed to target the chloroplastic SRP54 gene whose disruption results in a reduced pigment phenotype. Both the crRNA and the transactivating RNA (SEQ ID NO:109) are chemically synthesized. The two RNAs are mixed together at a 1:1 molar ratio, at a concentration of approximately 3 μM each in 10 mM Tris, 1 mM EDTA, pH 7.5 (RNase-free). The volume can range for example, from about 20 μl to about 200 μl. The RNA solution is heated to 94-99° C in a temperature block for approximately 2 minutes, after which the temperature block is turned off. The hybridization mixture is allowed to cool in the temperature block until the block reaches 25° C or less. An amount of annealed RNAs

ranging from about 1 to about 5 µg is then added to a cuvette containing *Parachlorella* Cas9 Editor line GE-15699 cells (approximately 5 x 10^8 cells in a 0.2 cm cuvette) that have been prepared for electroporation according to Example 7. Donor DNA (approximately 1 µg) that includes the BleR cassette optimized for expression in *Parachlorella* (SEQ ID NO:66) is then added to the cuvette and the cells are electroporated according to the methods provided in Example 7. Zeocin resistant colonies are inspected visually for reduced pigment. Pale green colonies are screened by colony PCR for the presence of the donor fragment at the cpSRP54 locus using primers designed to amplify across the native targeted locus (oligo-AE596; SEQ ID NO:67 and oligo-AE597; SEQ ID NO:68).

[00247] Example 16. Markerless transformation using *Nannochloropsis* cas9 Editor Strain and Qdots

[00248] The very high efficiency of genome editing in the *Nannochloropsis* cas9 Editor Strains allows for markerless transformation. In one strategy, the photosynthetic regulator gene Lar1 (disclosed in copending U.S. Patent Application Publication No. US 2014/0220638, incorporated herein by reference) was targeted for mutation because mutation of the Lar1 gene results in an easily identifiable phenotype (reduced chlorophyll) that can be visually scored to determine if there is any improvement in mutant retrieval rate over the non-enrichment method. The Cas9 Editor strain GE- 6791was transformed with a chimeric gRNA targeting Lar1 (SEQ ID NO:109) and QDot585 "Qtracker" nanoparticles (Life Tech #Q25011MP). 5 µg of gRNA was mixed with 2 µl of pre-mixed Qtracker (according to manufacturer's instructions) and transformed into *Nannochloropsis* cells by electroporation as described previously. After transformation, cells were either: 1) directly plated onto agar media, 2) FACs sorted to enrich for Qdot positive cells and then plated, or 3) incubated with Live/Dead Blue stain (Life Technologies # L-23105) according to the manufacturer's instructions, and FACs sorted to enrich for Qdot positive cells while excluding the stained "Dead" cells and then plated.

[00249] The smallest and palest colonies were patched for PCR sequencing, where they were sequence confirmed and verified to have small insertions or deletions (averaging 1 or 2 bases) from NHEJ mis-repair. An increase in the mutant retrieval rate was increased from 0.05% when directly plating them out, to 0.13% when Qdots were FACS enriched and dead cells were excluded (Table 4). Although this increase is significant, the false positive rate was quite high. It was hypothesized that some proportion of the Qdot positive cells might have had Qdots associated with the cell wall and not necessarily residing inside the cell.

[00250] Table 12. Markerless mutation frequency using Cas9 fully penetrant Editor line

Condition	# of colonies screened	# of mutants	% rate
Direct Plating	2020	1	0.05
FACS-Qdot enriched	3310	4	0.12
FACS-Qdot enriched +LiveDeadExclusion	4690	6	0.13

[00251] Example 17. Markerless transformation using *Nannochloropsis* Cas9 Editor Strain and *in vitro* transcribed mRNA for GFP

[00252] In these experiments, instead of Qdots, the chimeric guide RNA is transformed into *Nannochloropsis* along with an in-vitro synthesized messenger RNA encoding a fluorescent protein such as TagGFP (Evrogen, Moscow, Russia). This would eliminate the high false positive rate seen in Example 9 because no fluorescent protein would be made unless the GFP mRNA was inside of the cell and in contact with its ribosome machinery. In this experiment, cells would be allowed to recover after transformation, for example, for a period of time that could be tested but might be from four to forty-eight hours, after which the cells would be sorted by flow cytometry. Cells displaying above-background fluorescence (where background fluorescence is determined by cells transformed without the GFP-encoding RNA) would be selected and plated without selection, and later screened by PCR using primers having homology to sequences flanking the targeted genomic locus. Furthermore, TagGFP, being a monomeric version of GFP, could also be translationally fused onto either the N-terminus or C-terminus of the Cas9 gene, and the Cas9 gene, instead of being integral to the host cell, might also be transiently expressed to perform its genome editing function. This would enable a non-GMO approach to Cas9 editing.

[00253] Example 18. Development of a Markerless, Reporterless *Nannochloropsis* Cas9 Editor Strain with repressible Cre recombinase expression capabilities

[00254] A vector, pSG6483, was designed and engineered for constitutive expression of a Cas9 nuclease and repressible expression of Cre recombinase in *Nannochloropsis gaditana* (**Figure 18**). The vector contained the following four elements: 1) the Cas9 expression cassette described in Example 3 ("Development of fully penetrant *Nannochloropsis* Cas9 Editor Lines"), 2) the selectable marker cassette ("HygR cassette") described in Example 3, 3) the same GFP reporter cassette described previously in Example 3, and 4) a repressible

CRE expression cassette containing the Cre recombinase from P1 Bacteriophage codon optimized for *Nannochloropsis gaditana*, which contains the same N-terminal NLS used for the Cas9 construct and also includes an *N. gaditana* intron inserted into the Cre coding region (engineered Cre gene provided as (SEQ ID NO:111). The *Nannochloropsis*-engineered Cre gene was operably linked to the "Ammonia repressible Nitrite/Sulfite Reductase" promoter (SEQ ID NO:112) at the 5' end of the Cre gene and the "Nitrite/Sulfite Reductase" terminator (SEQ ID NO:113) at the 3' end of the Cre gene. The BlastR selectable marker and GFP reporter cassettes are arranged in tandem in the construct, and together they are flanked by identical lox sites in the same orientation. Features that are flanked by loxP sites are commonly referred to as "floxed". An ammonia-repressible promoter was to repress expression of the Cre gene as much as possible until after generating antibiotic resistant colonies and establishing full phenotypic penetrance of GFP. Additionally, cloning Cre into a vector that contains lox sites proved to be problematic, as even basal levels of Cre expression in *E. coli* looped out the floxed BlastR and GFP once Cre was cloned in. To get around this hurdle, an intron was inserted into the Cre gene disrupting the catalytic and nucleophilic domains. This resulted in the final stable vector pSGE-6483 (**Figure 18**) which doesn't self-excise its floxed markers in *E.coli.*

[00255] pSGE-6483 was transformed into *Nannochloropsis gaditana* and plated onto PM128 agar media that contains ammonia but not nitrate, where the medium contained 100 mg/L of blasticidin. Colonies were re-patched onto the same selective PM128 media for analysis and archiving, and screened for full phenotypic penetrance of GFP by flow cytometry as described in Example 3. Six lines were carried forward for parallel serial culturing in either media containing ammonium as the sole nitrogen source (PM128) or media containing sodium nitrate as the sole nitrogen source (PM129), with no blasticidin selection in either medium. After 2 weeks of serial culturing, the strains were examined for loss of GFP signal by flow cytometry, excision of the floxed GFP/BlastR cassettes by diagnostic PCR, Cre expression by Western Blot and qRT-PCR, and Cas9 expression by Western Blot.

[00256] GFP histograms revealed mixed results for the different strains. Strain 6483-F12 was the only strain which showed an obvious GFP signal switch between NH_4 and NO_3 cultures. Strains B11 and C12 appeared to have lost GFP signal in both NH_4 and NO_3, while strains A11, D12, and E12 appeared to have maintained GFP signal in both NH_4 and NO_3 (**Figure 19**).

[00257] mRNA was extracted from the strains and cDNA was generated for RT-PCR and qRT-PCR experiments. RT-PCR was utilized as a fast way to detect and amplify transcripts for Cre, GFP, and a positive control gene ("1704", a gene found to have expression levels that were substantially unaffected by environmental conditions and nitrogen status of the cells) from *Nannochloropsis*. The gel image shows loss of GFP transcript in strains B11, C12, and F12 grown in NO_3 media, and an intensified signal for the Cre transcript grown in NO_3 media, except for strain E12 which had no detectable Cre transcript in either condition (**Figure 20**). qRT-PCR was used to quantify the fold changes in transcript abundance between the strains cultured in the expected repressed conditions (NH_4) versus non-repressed/induced conditions (NO_3). Varying levels of repression on NH_4 vs NO_3 was observed for all strains (**Figure 21**). The basal level of Cre expression varies amongst the strains, with F12 having the least transcript for all the strains. This data aligns well with the GFP histogram data, as F12 was the only strain to still have a GFP positive histogram after the serial culturing in NH_4, while losing the GFP signal after serial culturing in NO_3. This indicates that successful repression of Cre activity is more likely to be achieved when the introduced Cre gene is relatively depressed overall (that is, even in induced conditions), but that such low-expressing strains still adequately excise floxed sequences when Cre expression was induced.

[00258] Anti-Cre western blots were done (Figure 22), and the 38-kDa CRE protein was detected from all the cultures except E12 for which no transcript was detected by RT-PCR. Interestingly, similar amounts of Cre protein were detected in both the NH_4 and NO_3 conditions; it is possible that the differences in RNA levels detected by qRT-PCR were not reflected in the protein levels because samples were taken at different stages of growth of the cutlures. Anti-Cas9 western blots were also performed, and the Cas9 enzyme was also detected in the transformed cells (**Figure 23**).

[00259] Diagnostic PCRs were performed on both F12 cultures and the induced C12 culture to determine whether the floxed GFP and BlastR gene cassettes were intact or excised by Cre-mediated recombination, to detect the presence of the circular recombination product, and to detect the presence of the GFP and BlastR genes only (**Figure 24**). The F12-NH_4 (repressed) culture appears to be at some level of equilibrium, as both the intact floxed cassettes appear to be present (primer sets A,B,C) as well as the circular recombination product (primer set D) indicated that some level of recombination was occurring even under repressed conditions. The F12-NO_3 culture seems to have had the floxed genes mostly excised from the integration site, as primer set A failed to amplify across an entire intact

region (no 3.7kb band, difficult to discern whether a 185bp band was amplified due to excision or not), and primer sets B and C yielded extremely faint bands, while primer sets D, F, and G yielded moderately faint bands. The C12-NO_3 culture seems to be further along in the excision process, however BlastR and GFP could still be detected on their own (primers sets F, G). In order to confidently detect if the locus is altered by excision, a new primer set was used to amplify across the floxed region (**Figure 25**), in which an intact locus would yield a 4.9kb band and the excised locus would yield a 1.3kb band. The same equilibrium and/or heterogeneous culture was observed for the F12-NH_4 culture, as both the intact and excised bands are seen, while only the excised band was seen for the F12-NO_3 culture. Because faint GFP and BlastR signals were still observed in NO_3 cultures for both F12 and C12, cells from the NO_3 cultures for F12, C12, and B11 were diluted and plated out to single isolated colonies on agar plates containing NO_3 and no blasticidin to ensure strain homogeneity going forward. 3 isolated colonies from C12 and F12 were tested for the presence of the Cre, BlastR, and GFP genes by PCR (**Figure 26**). The GFP and BlastR genes seem to be gone (primer sets E and F), while the CRE gene is still readily detected (primer set G).

[00260] The F12 strain was selected for further testing as a new Cre-enabled Editor strain as it demonstrated the most repressible CRE expression. This strain was named GE-13630.

[00261] Example 19. Markerless knockouts by recycling markers in the Nannochloropsis cas9 **Editor Strain with repressible Cre recombinase capabilities**

[00262] GE-13630 was transformed with gRNA targeting the acyl-CoA oxidase gene (as described earlier in Example 5) and a floxed disruption cassette (**Figure 27**) (SEQ ID NO:115) as the donor fragment. This cassette included a hygromycin resistance gene and GFP gene, which were arranged in tandem and flanked by loxP sites in the same orientation. Outside of these loxP sites are three frames of stop codons. Upstream, they are in the direct orientation, and downstream they are in the reverse orientation. There are also unique "marks" on the far ends of the cassette for easy differentiation of the cassette, and also to serve as a DNA buffer to protect the stop codons and loxP sites from being damaged by the DNA end-repair mechanisms of *Nannochloropsis* during integration. The transformation was plated onto PM128 agar media containing 500mg/L of hygromycin. This media contains ammonium to repress Cre expression so that transformants can be identified as resistant colonies and can be isolated. Colonies were patched onto the same selective media, genotyped and analyzed for GFP expression and colony PCR (as described in Example 5). A mix of DNA signals were seen, which showed the entire 4.5kb fragment inserted as well as

the 170 bp final excision product. This indicated that excision was already underway even in the presence of ammonium. To allow excision to go to completion, the strains were taken off selection and grown in media containing nitrate (PM129), which would remove the partial repression of Cre expression and promote a complete excision process throughout the culture. Strains were then genotyped and monitored for loss of GFP signal. One strain that passed these criteria (loss of HygR-GFP fragment as observed by PCR and loss of fluorescence signal) was streaked out for homogeneity on a nitrate plate with no hygromycin selection. Four isolated colonies underwent a final genotyping, and the PCR products of the acyl-CoA oxidase gene integration locus of these strains were sequenced. This clearly showed that the acyl-CoA oxidase gene was now disrupted only by the residual 170 bp scar which included translational stops to disrupt the open reading frame of the gene. This strain was verified to be sensitive to hygromycin, consistent with excision of the floxed fragment that included the HygR gene. An overview of this stacking process is shown (**Figure 28**).

[00263] Example 20. Expression of Heterologous Type I FAS Genes in *Nannochloropsis gaditana*.

[00264] As demonstrated in Example 11, where the penetrance screen was used to select transformed strains having culture-wide desired levels of gene attenuation achieved by RNAi expression, the penetrance screen has also proven advantageous for screening transformants expressing constructs that encode molecules other than Cas9 or other genome editing nucleases. In this example, the penetrance screen was performed on isolates resulting from transformation of *Nannochloropsis* with constructs engineered to include heterologous Type I Fatty Acid Synthase genes operably linked to *Nannochloropsis* gene regulatory elements. Nucleic acid sequences encoding the zebrafish *Danio rerio* Type I Fatty Acid Synthase (Type 1 FAS) (SEQ ID NO:116) and a Type I FAS of a proprietary isolated Thraustochytrid strain (SEQ ID NO:118) were cloned into constructs designed for expression of the genes in the Eustigmatophyte alga *Nannochloropsis gaditana*, allowing isolation of strains demonstrating the functionality of heterologous Type I FAS enzymes in the cytoplasm of an alga for the first time.

[00265] The construct for expression of *C. rerio* Type I FAS, pSGE-6200 (**Figure 29**), included the gene encoding the *D. rerio* Type I FAS, termed "DrFAS", which was codon optimized for *N. gaditana* (**SEQ ID NO:116**) and operably linked to the *N. gaditana* RPL7 promoter (SEQ ID NO:Z), positioned 5' of the DrFAS coding sequence, and the *N. gaditana* 'Terminator 2' sequence (SEQ ID NO:Q), positioned at the 3' end of the DrFAS coding sequence (**SEQ ID NO:116**). The expression construct also included a nucleic acid sequence

(SEQ ID NO:117) encoding the *D. rerio* pantetheine phosphotransferase (PPT) which is required for activating the ACP domain of the DrFAS protein. The PPT gene (SEQ ID NO:117) used in the construct was also codon-optimized for *N. gaditana* and was operably linked at its 5' end to the *N. gaditana* 4AIII promoter, and at its 3' end to *N. gaditana* terminator 4. Upstream of the DrFAS and PPT genes was a cassette for the expression of the codon-optimized "blast" gene operably linked to the TCTP promoter (**SEQ ID NO:11**) at its 5' end (oriented in a direction opposite to the RPL7 promoter positioned to drive expression of the DrFAS gene), and to the EIF3 terminator at its 3' end. Downstream of the DrFAS and PPT genes was a cassette for GFP expression in which the coding sequence for TurboGFP (codon optimized for *N. gaditana*, SEQ ID NO:24) was operably linked to EIF3 promoter and *N. gaditana* terminator 5. The GFP expression cassette was oriented in the same 5' to 3' direction as the DrFAS and PPT genes.

[00266] The construct for expression of the Thraustochytrid Type I FAS, pSGE-6167 (**Figure 30**), included the gene encoding the Thraustochytrid Type I FAS, termed "ChytFAS", codon optimized for *N. gaditana* (SEQ ID NO:118) operably linked to the *N. gaditana* RPL7 promoter (SEQ ID NO:Z) 5' of the ChytFAS coding sequence, and the *N. gaditana* 'Terminator 2' sequence (SEQ ID NO:Q) at the 3' end of the DrFAS coding sequence. This construct did not include a separate PPT gene, as the Chytrid FAS includes that enzymatic activity. Upstream of the ChytFAS gene was the same blast expression cassette as provided in the DrFAS construct, also oriented such that the direction of transcription was opposite that of the FAS gene, and downstream of the ChytFAS gene was the same GFP expression cassette that was employed in the DrFAS construct, again oriented in the same direction as the FAS gene.

[00267] DNA fragments that included these expression cassettes of DrFAS expression construct pSGE-6200 and ChytFAS construct pSGE-6167 were transformed, separately, as linear molecules (with the vector backbone removed by AscI and NotI digestion of the construct and isolation of the linear fragment by gel electrophoresis) into *Nannochloropsis* by electroporation essentially as described in US 2014/0220638, incorporated herein by reference. Transformants were selected on plates that contained blastocidin and screened for the presence of the construct by PCR.

[00268] Clones that included the construct we then screened for penetrance by flow cytometry monitoring for GFP fluorescence as described in Example 3 and for FAS protein expression by Western blot using an antibody reactive against animal Type I FAS or a FLAG tag (present in some constructs) for the DrFAS transformants, or an antibody reactive against

chytrid FAS for the ChytFAS transformants. Figure 31 shows the flow cytometry traces of 6 DrFAS transformants that were found to have complete penetrance, as the transformants displayed a single fluorescence peak that was shifted with respect to the wild type fluorescence peak. In Figure 31, Western blots are shown in which it can be seen that each fully penetrant clone also demonstrated protein expression. Unlabeled lanes on the gel show protein reactivity of clones that were not determined to be fully penetrant (i.e., they displayed more than one peak, one of which coincided with wild-type, or background, fluorescence, or they displayed a single peak that was coincident with the wild type or background peak). Thus, screening for protein level alone does not result in the identification of fully penetrant lines (expression throughout the culture). Figure 32 provides the flow cytometry traces of 6 DrFAS lines that demonstrated complete penetrance and Figure 32 provides the Western blots of these lines with anti-animal FAS antibody. Interestingly, for these fully penetrant lines, protein level as assessed by Western signal intensity does correspond to the degree of separation of the transformant peak from the background (wild type) peak; for example, strains 6200-33 and 6200-37 have the most intense Western bands and the greatest separation of their flow cytometry fluorescence peaks from the wild type fluorescence peak, demonstrating that the of GFP gene expression is reflected in the degree of expression of the linked gene.

[00269] Two lines having fully penetrant ChytFAS expression were also assessed by Western for FAS protein expression (**Figure 33**). Although 6167-B had a GFP fluorescence peak shifted farther to the right (at a higher fluorescence value) than the 6167-A GFP fluorescence peak was shifted (Figure 37A), this difference was not reflected in the protein abundance as detected by Western blot. Interestingly though, strain 6167 demonstrated higher FAS activity in assays than did strain 6167A, as described below.

[00270] To analyze FAS activity in selected transformants, cell extracts of lines 6167-A and 6167-B expressing Chytrid FAS, and strains 6200-33, 6200-38, 6200-43, 6201-43, and 6201-48 expressing DrFAS, all selected as demonstrating complete penetrance (Figure 33 and Figure 34), were assayed. Malonyl-CoA dependent NADPH oxidation measured at ABS 340 nm was determined on clarified, desalted extracts in triplicate. Aliquots of cell cultures were pelleted and the pellets (approximately 200-400 µl packed volume) were resuspended in 2 ml of ice cold extraction buffer (50 mM HEPES pH 7.0 (or Tris pH 8.0), 100 mM KCl, 2 mM DTT (from fresh 1 M stock), 1 protease inhibitor cocktail from Roche at right concentration (*e.g.* 1 tablet for 10 ml). A similarly sized yeast pellet was treated the same way as a positive control extract.

[00271] The resuspensions were transferred to a 2 ml screw cap vial containing approximately 500 µl bed volume of zirconium beads. The resuspensions were bead beaten in a pre-chilled block 3 times for 1 minute to disrupt the cells. The lysed cells were centrifuged at 20,000 x g at 4° C for 20 minutes, and the supernatant and de-salted on Zeba mini-columns (Pierce, product 89882) after equilibration with extraction buffer (above). Protein concentration was measured with the Pierce BCA detection kit. The fatty acid synthase (FAS) assay was essentially according to the procedure of Lynen (1969) *Meth Enzymol* 14:17-33: a 2x buffer stock containing 0.2 M KH_2PO_4 pH 6.6, 2 mM EDTA and 0.6 mg/ml BSA was used to make a working stock assay consisting of: 0.1M KH_2PO_4 pH 6.6, 1 mM EDTA, 1 mM DTT, 40 µM Acetyl-CoA, 110 µM Malonyl-CoA (omitted in negative control assays.), 180 µM NADPH, and 1 mg/L BSA. 50 to 100 µg of total soluble protein from the extracts as prepared above were then added to each reaction mix. The change in absorbance at 340 nm per minute was measured and used to calculate the µmols oxidized NADPH per minute (**Figure 34**). Interestingly, the amount of activity demonstrated in the transformed lines correlates well with the degree to which the GFP fluorescence curves are shifted to the right (**Figure 35A**). Chytrid FAS transformed lines 6167-A and 6167-B were given strain named GE-6889 and GE6890, respectively, and DrFAS transformed lines 6200-33 was given the strain name GE-6947, DrFAS transformed lines 6200-33 was given the strain name GE-6947, DrFAS transformed lines 6200-38 was given the strain name GE-6948, DrFAS transformed lines 6200-43 was given the strain name GE-6949, DrFAS transformed lines 6201-43 was given the strain name GE-6950, DrFAS transformed lines 6201-48 was given the strain name GE-6951.

[00272] The lines were next analyzed for *in vivo* FAS rate determination under phototrophic and mixotrophic growth conditions with either ^{13}C bicarbonate or ^{13}C -labeled acetate added to the medium, respectively. Cultures (duplicates were run for each culture condition) were adapted to 16:8 light/dark cycles at ~275 µE light (light limited growth) and grown to an OD_{730} of approximately 3.0 in an Adaptis chamber. Prior to the onset of the photoperiod, cultures were centrifuged and resuspended (250 ml final vol.) to an OD_{730} of 1.0 in PM074 medium buffered with 20 mM HEPES pH 7.4 and containing either 10 mM ^{13}C sodium acetate or 20 mM ^{13}C bicarbonate. Cultures were placed in front of an LED array supplying ~275 µE light from one direction, and FAME samples were taken at 0, 1, 2, and 4 h from a 50 ml culture volume. FAME was analyzed essentially as described in U.S. Patent Application Publication US 2015/0191515, incorporated herein by reference. **Figure 35A** shows that under photoautotrophic conditions where inorganic carbon was substantially the

sole source of carbon in the culture medium, strain GE-6890, demonstrating fully penetrant expression of chytrid FAS (see **Figure 35A**), produced more newly synthesized fatty acids (represented as FAME) than controls. Newly synthesized fatty acids are fatty acids that show a high degree of labeling and have been synthesized *de novo* during the labeling experiment, where elongated fatty acids are C20:x fatty acids with one to four labeled carbons that arise from elongation of previously existing 16:x and 18:x fatty acids.

[00273] Strain GE-6890 is ChytFAS transformant line 6167-B whose penetrance profile in **Figure 33** shows a single peak shifted to the right with respect to wild type. Strain GE-6889, which is ChytFAS transformant line 6167-A, also demonstrated complete penetrance but the penetrance profile of GE-6889 (6167-A) in **Figure 33** shows a single peak that is not shifted as far to the right with respect to wild type as the fluorescence peak of GE-6890. Strain GE-6889 does not show any increase in FAME production over wild type in the radiolabeling experiment in which the strains are cultured using only an inorganic carbon source. However, when cultured under mixotrophic conditions, in which the cultures include an organic carbon source (10mM acetate) strain GE-6889 demonstrates increased fatty acid synthesis with respect to wild type cells, demonstrating that this fully penetrant strain, while demonstrating less activity than transformant GE-6890, does have increased FAS activity in mixotrophic conditions (**Figure 35B)**.

[00274] With respect to transformed strains expressing DrFAS, the same culture assay for FAS activity using under phototrophic and mixotrophic growth conditions with either ^{13}C bicarbonate or ^{13}C -labeled acetate added to the medium, respectively, was performed on cultures of fully penetrant strain GE-6947 (transformed line 6200-33), fully penetrant strain GE-6949 (transformed line 6200-43), and fully penetrant strain GE-6950 (transformed line 6201-43). These assays were performed exactly as detailed above, with duplicate cultures for each strain. **Figure 36A** shows that while cytoplasmically expressed Type I FAS did not increase photoautotrophic production of fatty acids, all three strains fully penetrant for expression of the heterologous Type I FAS construct produced more fatty acids (measured as FAME) than did wild type cells (**Figure 36B**).

CLAIMS

1. A method of generating a cell line having fully penetrant expression of an exogenous gene of interest, comprising:

introducing a non-native nucleic acid molecule comprising a gene of interest and a detectable marker gene into a population of host cells to obtain one or more transformed cell lines comprising the non-native nucleic acid molecule;

culturing at least one of the one or more transformed cell lines to provide at least one transformed cell line culture; and

using flow cytometry to identify at least one transformed cell line demonstrating fully penetrant expression of the detectable marker in culture to identify a fully penetrant expression of the exogenous gene of interest.

2. A method according to claim 1, wherein identifying a transformed cell line demonstrating fully penetrant expression of the detectable marker comprises comparing the flow cytometry trace of the at least one transformed cell line culture with the flow cytometry trace of a control culture that does not express the detectable marker, wherein a flow cytometry trace of a transformed cell line culture than demonstrates a single peak that is shifted to a higher fluorescence level than the flow cytometry trace of the control culture to identify a transformed cell line demonstrating fully penetrant expression of the gene of interest.

3. A method according to claim 1, wherein the non-native nucleic acid molecule further includes a selectable marker gene.

4. A method according to claim 3, wherein the selectable marker gene confers antibiotic resistance.

5. A method according to claim 3, wherein obtaining one or more transformed cell lines comprising the non-native nucleic acid molecule is by selecting transformed colonies on selective media.

6. A method according to claim 1, wherein the gene encoding a gene of interest and the detectable marker gene are operably linked to separate promoters.

7. A method according to claim 1, wherein the gene encoding a gene of interest and the selectable marker gene are operably linked to separate promoters.

8. A method according to any of claims 1-7, wherein a gene of interest encodes a functional RNA or polypeptide.

9. A method according to claim 8, wherein a gene of interest encodes a functional RNA selected from the group consisting of a transactivating RNA (tracrRNA), cripsr RNA (crRNA), single guide RNA, chimeric guide RNA, RNAi construct, shRNA, siRNA, antisense RNA sequence, ribozyme, or microRNA.

10. A method according to claim 8, wherein a gene of interest encodes a polypeptide selected from the group consisting of an enzyme, a ribosomal protein, a structural protein, a component of a secretion system, a transporter, a porin, a membrane receptor, a DNA-binding protein, a recombinase, an endonuclease, a transposase, a transcription factor, or a cell signaling protein.

11. A method according to any of claims 1-10, wherein the detectable marker is a fluorescent protein.

12. A method according to claim 1, wherein the detectable marker gene is flanked by sites recognized by a site-specific recombinase.

13. A method according to claim 2, wherein the selectable marker gene is flanked by sites recognized by a site-specific recombinase.

14. A method according to claim 2, wherein a sequence comprising the selectable marker gene and the detectable marker gene is flanked by sites recognized by a site-specific recombinase.

15. A method according to any of claims 1-14, wherein the non-native nucleic acid molecule comprises two or more genes of interest.

16. A method according to claim 15, comprising three, four, five, six, seven, eight, nine, ten, or more genes of interest.

17. A method according to any of claims 1-16, wherein at least one gene of interest encodes a site-specific recombinase.

18. A method according to claim 17, wherein the site-specific recombinase is operably linked to an inducible promoter.

19. A method according to claim 17 or 18, wherein the site-specific recombinase is cre, flp or Dre.

20. A method according to any of claims 17-19, wherein the detectable marker gene is flanked by sites recognized by a site-specific recombinase.

21. A method according to claim 20, further comprising inducing expression of the site-specific recombinase, whereby the detectable marker gene is excised from the nucleic acid molecule.

22. A method according to any of claims 17-19, wherein the nucleic acid molecule comprises a selectable marker gene, further wherein the selectable marker gene is flanked by sites recognized by a site-specific recombinase.

23. A method according to claim 18, further comprising inducing expression of the site-specific recombinase, whereby the selectable marker gene is recombined out of excised from the nucleic acid molecule.

24. A method according to any of claims 17-19, wherein the nucleic acid molecule comprises a selectable marker gene, wherein the nucleic acid sequence comprising the detectable marker gene and the selectable marker gene are flanked by sites recognized by a site-specific recombinase.

25. A method according to claim 24, further comprising inducing expression of the recombinase, whereby the detectable marker gene and the selectable marker gene are excised from the nucleic acid molecule.

26. The method of claim 1 wherein the host cells are eukaryotic host cells.

27. The method of claim 26 wherein the host cells are plant, mammalian, insect, arachnid, fish, reptile, amphibian, avian, crustacean, or protozoan cells.

28. The method of claim 27 wherein the host cells are fungal cells, optionally of a genus selected from the group consisting of *Aspergillus, Mucor*, *Pichia, Pullularia, Saccharomyces, Schizosaccharomyces, Trichoderma, Rhodotorula,* and *Yarrowia*.

29. The method of claim 27 wherein the host cells are mesomycetozoea, heterokont, or algal cells.

30. The method of claim 29, wherein the host cells are algal cells.

31. The method of claim 30, wherein the algal cells are of a genus selected from the group consisting of *Achnanthes, Amphiprora, Amphora, Ankistrodesmus, Asteromonas, Boekelovia, Bolidomonas, Borodinella, Botrydium, Botryococcus, Bracteococcus, Chaetoceros, Carteria, Chlamydomonas, Chlorococcum, Chlorogonium, Chlorella, Chroomonas, Chrysosphaera, Cricosphaera, Crypthecodinium, Cryptomonas, Cyclotella, Desmodesmus, Dunaliella, Elipsoidon, Emiliania, Eremosphaera, Ernodesmius, Euglena, Eustigmatos, Franceia, Fragilaria, Fragilaropsis, Gloeothamnion, Haematococcus, Hantzschia, Heterosigma, Hymenomonas, Isochrysis, Lepocinclis, Micractinium, Monodus, Monoraphidium, Nannochloris, Nannochloropsis, Navicula, Neochloris, Nephrochloris, Nephroselmis, Nitzschia, Ochromonas, Oedogonium, Oocystis, Ostreococcus, Parachlorella, Parietochloris, Pascheria, Pavlova, Pelagomonas, Phæodactylum, Phagus, Picochlorum, Platymonas, Pleurochrysis, Pleurococcus, Prototheca, Pseudochlorella, Pseudoneochloris,*

Pseudostaurastrum, Pyramimonas, Pyrobotrys, Scenedesmus, Schizochlamydella, Skeletonema, Spyrogyra, Stichococcus, Tetrachlorella, Tetraselmis, Thalassiosira, Tribonema, Vaucheria, Viridiella, Vischeria, and *Volvox*.

32. The method of claim 30, wherein the algal cells are Bacillariophyte cells, optionally of a genus selected from the group consisting of *Achnanthes, Amphora, Amphiprora, Chaetoceros, Cyclotella, Fragilaria, Fragilariopsis, Navicula, Nitzschia, Phaeodactylum, Skeletonema,* and *Thalassiosira.*

33. The method of claim 31, wherein the algal cells are Eustigmatophyte cells, optionally of a genus selected from the group consisting of *Ellipsoidion, Eustigmatos, Monodus, Nannochloropsis, Pseudostaurastrum,* and *Vischeria.*

34. The method of claim 29, wherein the host cells are Labyrinthulomycete cells, optionally of a genus selected from the group consisting of *Labryinthula, Labryinthuloides, Thraustochytrium, Schizochytrium, Aplanochytrium, Aurantiochytrium, Oblongichytrium, Japonochytrium, Diplophrys*, and *Ulkenia*.

35. A method for generating a high efficiency genome editing cell line, comprising:

introducing a non-native nucleic acid molecule comprising a nucleic acid sequence encoding an RNA-guided endonuclease and a nucleic acid sequence encoding a detectable marker into a population of host cells to obtain one or more RNA-guided endonuclease-transformed cell lines comprising the non-native nucleic acid molecule;

culturing at least one of the one or more RNA-guided endonuclease-transformed cell lines to provide at least one RNA-guided endonuclease-transformed cell line culture;

using flow cytometry to assess the at least one RNA-guided endonuclease-transformed cell line culture for expression of the detectable marker in the cells of the RNA-guided endonuclease-transformed cell line culture; and

identifying a RNA-guided endonuclease-transformed cell line demonstrating fully penetrant expression of the detectable marker in the cell line culture to identify a high efficiency genome editing cell line.

36. A method according to claim 35, wherein identifying a transformed cell line demonstrating fully penetrant expression of the detectable marker comprises comparing the flow cytometry trace of the at least one transformed cell line culture with the flow cytometry trace of a control culture that does not express the detectable marker, wherein a flow cytometry trace of a transformed cell line culture than demonstrates a single peak that is shifted to a higher fluorescence level than the flow cytometry trace of the control culture to

identify a transformed cell line demonstrating fully penetrant expression of the gene of interest.

37. The method of claim 35 wherein the RNA-guided endonuclease is heterologous with respect to the host cells.

38. The method of claim 35, wherein the RNA-guided endonuclease is a Cas protein.

39. The method of claim 38, wherein the RNA-guided endonuclease is a Type II or Type V Cas protein.

40. The method of claim 35, wherein the RNA-guided endonuclease is selected from the group consisting of Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9, Cas10, Cbf1, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Cpf1, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, C2c1, C2c2, C2c3, homologs thereof, and modified versions thereof.

41. The method of claim 39, wherein the RNA-guided endonuclease is Cas9, Cpf1, C2c1, C2c2, or C2c3.

42. The method of claim 41, wherein the RNA-guided endonuclease is Cas9.

43. The method of claim 42, wherein the Cas9 protein is a Streptococcus pyogenes, Streptococcus thermophilus, or Neisseria meningitidis Cas9 protein.

44. The method of claim 42 wherein the Cas9 protein comprises at least one mutation with respect to a wild-type Cas9 protein.

45. The method of claim 44, wherein at least one mutation is selected from the group consisting of D10A, H840A, N854A, and N863A.

46. The method of claim 35, wherein the nucleic acid sequence encoding an RNA-guided endonuclease is codon optimized for expression in the host strain.

47. The method of claim 35, wherein the RNA-guided endonuclease comprises at least one nuclear localization sequence (NLS).

48. The method of claim 35, wherein the RNA-guided endonuclease comprises at least epitope tag.

49. The method of claim 48, wherein the epitope tag is a histidine tag, a hemagglutinin (HA) tag, a FLAG tag, or a Myc tag.

50. The method of claim 35, wherein the non-native nucleic acid molecule further comprises a selectable marker.

51. The method of claim 50, wherein the selectable marker confers resistance to an antibiotic or toxin.

52. The method of claim 51, wherein the nucleic acid sequence encoding the detectable marker is codon optimized for expression in the microbial strain.

53. The method of claim 35, wherein the detectable marker is a fluorescent protein.

54. The method of claim 53, wherein the fluorescent protein is green fluorescent protein (GFP), YFP, RFP, CFP, BFP, Cherry, Tomato, Venus, Cerulean, or a variant of any thereof, including but not limited to a monomeric variant.

55. The method of claim 54, wherein the detectable marker and the Cas9 protein are produced as separate proteins.

56. The method of claim 55, wherein the gene encoding the selectable marker and the gene encoding the RNA-guided endonuclease are operably linked to different promoters.

57. The method of claim 35, wherein the host cells are prokaryotic host cells.

58. The method of claim 57, wherein the host cells are of a species belonging to any of the following groups: Archaea, cyanobacteria, green-sulfur bacteria, green non-sulfur bacteria, purple sulfur bacteria, or purple non-sulfur bacteria or any of the following genera: *Arthrobacter, Escherichia, Bacillus, Brevibacteria, Clostridium, Corynebacteria, Desulfovibrio, Jeotgalicoccus, Kineococcus, Lactobacillus, Micrococcus, Mycobacterium, Pantoea, Pseudomonas, Rhodococcus, Rhodopseudomonas, Rhodospirillium, Rhodomicrobium, Stenotrophomonas, Vibrio, Streptomyces*, or *Zymomonas,*.

59. The method of claim 35, wherein the host cells are eukaryotic host cells.

60. The method of claim 59, wherein the host cells are plant, mammalian, insect, arachnid, fish, reptile, amphibian, avian, crustacean, or protozoan cells.

61. The method of claim 59, wherein the host cells are CHO cells, COS cells, VERO cells, BHK cells, HeLa cells, Cvl cells, MDCK cells, 293 cells, 3T3 cells, or PC12 cells.

62. The method of claim 59, wherein the host cells are fungal cells, optionally of a genus selected from the group consisting of Aspergillus, Mucor, Pichia, Pullularia, Saccharomyces, Schizosaccharomyces, Trichoderma, Rhodotorula, and Yarrowia.

63. The method of claim 59, wherein the host cells are mesomycetozoea, heterokont, or algal cells.

64. The method of claim 63, wherein the host cells are algal cells, optionally of a genus selected from the group consisting of Achnanthes, Amphiprora, Amphora, Ankistrodesmus, Asteromonas, Boekelovia, Bolidomonas, Borodinella, Botrydium, Botryococcus, Bracteococcus, Chaetoceros, Carteria, Chlamydomonas, Chlorococcum, Chlorogonium, Chlorella, Chroomonas, Chrysosphaera, Cricosphaera, Crypthecodinium, Cryptomonas, Cyclotella, Desmodesmus, Dunaliella, Elipsoidon, Emiliania, Eremosphaera,

Ernodesmius, Euglena, Eustigmatos, Franceia, Fragilaria, Fragilaropsis, Gloeothamnion, Haematococcus, Hantzschia, Heterosigma, Hymenomonas, Isochrysis, Lepocinclis, Micractinium, Monodus, Monoraphidium, Nannochloris, Nannochloropsis, Navicula, Neochloris, Nephrochloris, Nephroselmis, Nitzschia, Ochromonas, Oedogonium, Oocystis, Ostreococcus, Parachlorella, Parietochloris, Pascheria, Pavlova, Pelagomonas, Phæodactylum, Phagus, Picochlorum, Platymonas, Pleurochrysis, Pleurococcus, Prototheca, Pseudochlorella, Pseudoneochloris, Pseudostaurastrum, Pyramimonas, Pyrobotrys, Scenedesmus, Schizochlamydella, Skeletonema, Spyrogyra, Stichococcus, Tetrachlorella, Tetraselmis, Thalassiosira, Tribonema, Vaucheria, Viridiella, Vischeria, and Volvox.

65. The method of claim 63, wherein the host cells are heterokont cells, optionally of a genus selected from the group consisting of Labryinthula, Labryinthuloides, Thraustochytrium, Schizochytrium, Aplanochytrium, Aurantiochytrium, Oblongichytrium, Japonochytrium, Diplophrys, and Ulkenia.

66. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain.

67. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 66, wherein the RNA-guided endonuclease is a Cas nuclease.

68. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 67, wherein the RNA-guided endonuclease is a Cas9 nuclease.

69. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to any of claims 66-68, wherein the targeted mutation rate of the fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain using a gRNA and donor fragment that comprises a selectable marker is at least 10%.

70. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 69, wherein the targeted mutation rate of the fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain using a gRNA and donor fragment that comprises a selectable marker is at least 25%.

71. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 70, wherein the targeted mutation rate of the fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain using a gRNA and donor fragment that comprises a selectable marker is approximately 50% or greater.

72. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 71, wherein the targeted mutation rate of the fully penetrant RNA-

guided endonuclease-expressing cell line or microbial strain using a gRNA and donor fragment that comprises a selectable marker is approximately 80% or greater.

73. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 72, wherein the targeted mutation rate of the fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain using a gRNA and donor fragment that comprises a selectable marker is approximately 90% or greater.

74. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to any of claims 66-73, wherein the cell line or microbial strain is a microbial strain.

75. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 74, wherein the microbial strain is a fungus, mesomycetozoea, heterokont, or alga.

76. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 74, wherein the microbial strain is a fungal strain, optionally of a genus selected from the group consisting of Aspergillus, Mucor, Pichia, Pullularia, Saccharomyces, Schizosaccharomyces, Trichoderma, Rhodotorula, and Yarrowia.

77. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 74, wherein the microbial strain is an algal strain, optionally of a genus selected from the group consisting of *Achnanthes, Amphiprora, Amphora, Ankistrodesmus, Asteromonas, Boekelovia, Bolidomonas, Borodinella, Botrydium, Botryococcus, Bracteococcus, Chaetoceros, Carteria, Chlamydomonas, Chlorococcum, Chlorogonium, Chlorella, Chroomonas, Chrysosphaera, Cricosphaera, Crypthecodinium, Cryptomonas, Cyclotella, Desmodesmus, Dunaliella, Elipsoidon, Emiliania, Eremosphaera, Ernodesmius, Euglena, Eustigmatos, Franceia, Fragilaria, Fragilaropsis, Gloeothamnion, Haematococcus, Hantzschia, Heterosigma, Hymenomonas, Isochrysis, Lepocinclis, Micractinium, Monodus, Monoraphidium, Nannochloris, Nannochloropsis, Navicula, Neochloris, Nephrochloris, Nephroselmis, Nitzschia, Ochromonas, Oedogonium, Oocystis, Ostreococcus, Parachlorella, Parietochloris, Pascheria, Pavlova, Pelagomonas, Phæodactylum, Phagus, Picochlorum, Platymonas, Pleurochrysis, Pleurococcus, Prototheca, Pseudochlorella, Pseudoneochloris, Pseudostaurastrum, Pyramimonas, Pyrobotrys, Scenedesmus, Schizochlamydella, Skeletonema, Spyrogyra, Stichococcus, Tetrachlorella, Tetraselmis, Thalassiosira, Tribonema, Vaucheria, Viridiella, Vischeria,* and *Volvox*.

78. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claim 74, wherein the microbial strain is a heterokont strain, optionally of a

genus selected from the group consisting of *Labryinthula, Labryinthuloides, Thraustochytrium, Schizochytrium, Aplanochytrium, Aurantiochytrium, Oblongichytrium, Japonochytrium, Diplophrys*, and *Ulkenia*.

79. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to any of claims 66-78, wherein the fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain does not include an exogenous selectable marker gene.

80. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to any of claims 66-79, wherein the fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain does not include an exogenous detectable marker gene.

81. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claims 79 or 80, wherein the RNA-guided endonuclease-expressing cell line or microbial strain comprises an exogenous gene encoding a site-specific recombinase.

82. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claims 79 or 80, wherein the site-specific recombinase is cre, frt, or dre.

83. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claims 79 or 80, wherein the site-specific recombinase is cre,.

84. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claims 79 or 80, wherein the exogenous gene encoding a site-specific recombinase is codon optimized from expression in the host organism.

85. A fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain according to claims 79 or 80, wherein the exogenous gene encoding a site-specific recombinase is operably linked to an inducible promoter.

86. A method of altering the genome of a cell in vivo, wherein the method comprises:

87. introducing at least one guide RNA or at least one construct for expressing at least one guide RNA into a fully penetrant RNA-guided endonuclease-expressing cell line or microbial strain, wherein the guide RNA targets a site in the genome of the cell; and

screening cells transformed with the guide RNA for alteration of the targeted site in the genome.

88. A method according to claim 86, wherein the fully penetrant RNA-guided endonuclease-expressing strain is obtained by

introducing into a cell at least one non-native nucleic acid molecule comprising at least one nucleic acid sequence encoding a RNA-guided endonuclease-expressing protein and

at least one nucleic acid sequence encoding a detectable marker to obtain transformants comprising the at least one non-native nucleic acid molecule;

culturing at least one transformant;

performing flow cytometry on a culture of at least one transformant to identify a cell line that is fully penetrant for the RNA-guided endonuclease-expressing construct.

89. A method according to claim 86 or 87, wherein the at least one guide RNA is a chimeric guide RNA.

90. A method according to claim 86 or 87, wherein the at least one guide RNA is a crRNA.

91. A method according to claim 86, wherein the fully penetrant RNA-guided endonuclease-expressing strain further comprises a construct encoding a tracrRNA.

92. A method according to claim 86, wherein the method further comprises introducing a tracrRNA into the fully penetrant RNA-guided endonuclease-expressing strain.

93. A method according to claim 91, wherein the tracrRNA comprises at least one chemical modification.

94. A method according to any of claims 86-92, wherein said screening comprises performing PCR to detect a mutation at the targeted site.

95. A method according to any of claims 86-92, wherein said screening comprises employing a phenotypic screen.

96. A method according any of claims 86 - 43, wherein the method further comprises transforming a donor DNA into the fully penetrant RNA-guided endonuclease-expressing strain for insertion into the targeted site.

97. A method according to claim 95, wherein the donor DNA molecule comprises a selectable marker.

98. A method according to claim 95, wherein the donor DNA molecule comprises one or more homology regions for recombination into the target site.

99. A method according to claim 95, wherein the donor DNA molecule does not comprise homology regions for recombination into the target site.

100. A method according to claim 95, wherein screening for alteration of the targeted site in the genome comprises identifying transformants that express the selectable marker of the donor DNA molecule.

101. A method according to claim 91 or 92, wherein tracrRNA and the crRNA are allowed to anneal prior to introducing the tracrRNA and the crRNA into the fully penetrant RNA-guided endonuclease-expressing strain.

102. A method according to any of claims 86-100, wherein the RNA-guided endonuclease is a Cas endonuclease.

103. A method according to claim 101, wherein the RNA-guided endonuclease is a Type II or Type V Cas endonuclease.

104. A method according to any of claim 102, wherein the RNA-guided endonuclease is selected from the group consisting of Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9, Cas10, Cbf1, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Cpf1, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, C2c1, C2c2, C2c3, homologs thereof, and modified versions thereof.

105. A method according to claim 103, wherein the RNA-guided endonuclease is a Cas9 RNA-guided endonuclease.

106. A method according to any of claims 86-104, wherein the cell is a plant, mammalian, insect, arachnid, fish, reptile, amphibian, avian, crustacean, or protozoan cell.

107. The method of claim 105 wherein the cell is a CHO cell, COS cell, VERO cell, BHK cell, HeLa cell, Cvl cell, MDCK cell, 293 cell, 3T3 cell, or PC12 cell.

108. The method of claim 105 wherein the cell is a fungal cell, optionally of a genus selected from the group consisting of Aspergillus, Mucor, Pichia, Pullularia, Saccharomyces, Schizosaccharomyces, Trichoderma, Rhodotorula, and Yarrowia.

109. The method of claim 105 wherein the cell is a mesomycetozoea, heterokont, or algal cell.

110. The method of claim 108, wherein the cell is an algal cell, optionally of a genus selected from the group consisting of *Achnanthes, Amphiprora, Amphora, Ankistrodesmus, Asteromonas, Boekelovia, Bolidomonas, Borodinella, Botrydium, Botryococcus, Bracteococcus, Chaetoceros, Carteria, Chlamydomonas, Chlorococcum, Chlorogonium, Chlorella, Chroomonas, Chrysosphaera, Cricosphaera, Crypthecodinium, Cryptomonas, Cyclotella, Desmodesmus, Dunaliella, Elipsoidon, Emiliania, Eremosphaera, Ernodesmius, Euglena, Eustigmatos, Franceia, Fragilaria, Fragilaropsis, Gloeothamnion, Haematococcus, Hantzschia, Heterosigma, Hymenomonas, Isochrysis, Lepocinclis, Micractinium, Monodus, Monoraphidium, Nannochloris, Nannochloropsis, Navicula, Neochloris, Nephrochloris, Nephroselmis, Nitzschia, Ochromonas, Oedogonium, Oocystis, Ostreococcus, Parachlorella, Parietochloris, Pascheria, Pavlova, Pelagomonas, Phæodactylum, Phagus, Picochlorum, Platymonas, Pleurochrysis, Pleurococcus, Prototheca, Pseudochlorella, Pseudoneochloris, Pseudostaurastrum, Pyramimonas, Pyrobotrys, Scenedesmus, Schizochlamydella,*

Skeletonema, Spyrogyra, Stichococcus, Tetrachlorella, Tetraselmis, Thalassiosira, Tribonema, Vaucheria, Viridiella, Vischeria, and *Volvox*.

111. The method of claim 108, wherein the cell is a heterokont cells, optionally of a genus selected from the group consisting of *Labryinthula, Labryinthuloides, Thraustochytrium, Schizochytrium, Aplanochytrium, Aurantiochytrium, Oblongichytrium, Japonochytrium, Diplophrys*, and *Ulkenia*.