METHODS AND COMPOSITIONS FOR INACTIVATING GLUTAMINE SYNTHETASE GENE EXPRESSION

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[0001] Not applicable.

TECHNICAL FIELD

[0002] The present disclosure is in the fields of genome engineering, cell culture, generation of cell lines and protein production.

BACKGROUND

[0003] Glutamine synthetase (GS) is a critical enzyme in the synthesis of the amino acid L-glutamine. See, Meister, A. in Glutamine Metabolism, Enzymology and Regulation (eds. J. Mora & R. Palacios) 1-40 (Academic Press, N.Y.; 1980). A *GS*-negative cell line is therefore auxotrophic for L-glutamine. *GS* is frequently used as a selection marker gene in CHO cell based recombinant protein expression systems (Wurm *et al.* (2004) *Nature Biotechnology* 22: 1393-1398), though the absence of a *GS*-negative CHO line requires the use of the GS inhibitor methionine sulfoximine to achieve selection.

[0004] In addition, dihydrofolate reductase (DHFR, 5,6,7,8-tetrahydrofolate:NADP+oxidoreductase) is an essential enzyme in both eukaryotes and prokaryotes and catalyzes the NADPH-dependent reduction of dihydrofolate to tetrahydrofolate, an essential carrier of one-carbon units in the biosynthesis of thymidylate, purine nucleotides, glycine and methyl compounds.

[0005] DHFR-deficient cells have long been used for production of recombinant proteins. DHFR-deficient cells will only grow in medium supplemented by certain factors involved in folate metabolism or if DHFR is provided to the cell, for example as a transgene. Cells into which a *DHFR* transgene has been stably integrated can be selected for by growing the cells in unsupplemented medium. Moreover, exogenous sequences are typically co-integrated when introduced into a cell using a single polynucleotide. Accordingly, when the *DHFR* transgene also

includes a sequence encoding a protein of interest, selected cells will express both DHFR and the protein of interest. Furthermore, in response to inhibitors such as methotrexate (MTX), the *DHFR* gene copy number can be amplified. Accordingly, sequences encoding a protein of interest that are co-integrated with exogenous *DHFR* can be amplified by gradually exposing the cells to increasing concentrations of methotrexate, resulting in overexpression of the recombinant protein of interest. However, despite the wide use of *DHFR*-deficient cell systems for recombinant protein expression, currently available *DHFR*-deficient cell lines do not grow as well as the parental *DHFR*-competent cells from which they are derived.

[0006] Thus, mammalian cells with single and multi-gene knockouts have enormous utility in research, drug discovery, and cell-based therapeutics. However, conventional methods for the targeted elimination of an investigator-specified gene rely upon the process of homologous recombination or gene targeting. Mansour *et al.* (1988) *Nature* 336:348-352; Vasquez *et al.* (2001) *Proc Natl Acad Sci USA* 98:8403-8410; Rago *et al.* (2007) *Nature Protocols* 2:2734-2746; Kohli *et al.* (2004) *Nucleic Acids Research* 32, e3. While capable of generating a defined biallelic knockout, for many cell types this technique has proven too inefficient and thus too laborious for routine application. See, *e.g*, Yamane-Ohnuki *et al.* (2004) *Biotechnol Bioeng* 87:614-622. These methods for targeted gene deletion require sequential rounds of homologous recombination and drug selection to isolate rare desired events – a process sufficiently laborious to limit application to individual loci. Consequently, the generation of mammalian cell lines modified at multiple target loci has been largely unexplored.

[0007] Zinc-finger nucleases (ZFNs) have been used for targeted cleavage and gene inactivation. *See*, for example, United States Patent Publications 20030232410; 20050208489; 20050026157; 20050064474; 20060188987; 20060063231; 2008/0015164 and U.S. Serial No. 12/218,035 and International Publication WO 07/014275, the disclosures of which are incorporated by reference in their entireties for all purposes. Formed via the fusion of an engineered zinc-finger DNA binding domain specific for a designated target sequence and the catalytic domain of *Fok I* (a restriction endonuclease from *Flavobacterium okeanokoites*), ZFNs provide the ability to place a double-strand DNA break (DSB) at a chosen genomic address. The removal of this site-specific DSB is carried out by the cell's own DNA repair machinery either via a homology-directed repair process when donor DNA is

provided, or via non-homologous end joining (NHEJ). See, *e.g.*, Urnov *et al.* (2005) *Nature* 435:646-651 (2005); Moehle *et al.* (2007) *Proc Natl Acad Sci U S A* 104:3055-3060 (2007); Bibikova, *et al.* (2001) *Mol Cell Biol* 21:289-297; Bibikova *et al.* (2003) *Science* 300:764; Porteus *et al.* (2005) *Nature Biotechnology* 23:967-973; Lombardo *et al.* (2007) *Nature Biotechnology* 25:1298-1306; Perez *et al.* (2008) *Nature Biotechnology* 26:808-816; Bibikova *et al.* (2002) *Genetics* 161:1169-1175; Lloyd *et al.* (2005) *Proc Natl Acad Sci U S A* 102:2232-2237; Morton *et al.* (2006) *Proc Natl Acad Sci U S A* 103:16370-16375.

[0008] While both homology-directed repair and NHEJ processes result in the modification of the target locus, the NHEJ-driven approach obviates the need for donor DNA design and synthesis yet results in a high frequency of disrupted alleles and the error-prone nature of the NHEJ-mediated DSB repair can be exploited to achieve the knockout of a targeted gene in mammalian cells following simple transient transfection of a DNA construct encoding the ZFNs. See, *e.g.*, Santiago *et al.* (2008) *Proc Natl Acad Sci U S A* 105:5809-5814. ZFN technology has allowed the isolation of several independent knockout cell lines from a screening effort of less than one 96-well plate of single-cell derived clones. As no donor DNA or selection strategy was employed, the resultant single-gene knock out line is a suitable starting cell line for subsequent genetic modification.

SUMMARY

[0009] Disclosed herein are compositions for the partial or complete inactivation of a *GS* gene. Also disclosed herein are methods of making and using these compositions (reagents), for example to inactivate *GS* in a cell to produce cell lines in which a *GS* gene is inactivated. *GS* disrupted cell lines are useful, for example, in production of recombinant proteins.

[0009a] In the first aspect, the present invention refers to a zinc finger DNA-binding domain comprising four, five or six zinc finger recognition regions as shown in a single row of the following table:

ZFN name Target sequence	F1	F2	F3	F4	F5	F6
ZFN 9075 gaATGGTGCAGGCTgc (SEQ ID NO:1)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSDTLSN (SEQ ID NO:4)	RKDVRIT (SEQ ID NO:5)	N/A	N/A
ZFN 9372 gtTCCCAGGAATGGG CTTGGgg (SEQ ID NO:6)	RSDHLST (SEQ ID NO:7)	QSSDLRR (SEQ ID NO:8)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)
ZFN 8361 ctGGGTTGATGGTActg gagaaggactg (SEQ ID NO:13)	QSGALAR (SEQ ID NO:14)	RSDALTQ (SEQ ID NO:15)	RSDSLSA (SEQ ID NO:16)	RSAHLSR (SEQ ID NO:17)	N/A	N/A
ZFN 8365 taTACATGGCTTGGact ttctcaccctg (SEQ ID NO:18)	RSDHLST (SEQ ID NO:7)	QSSDLRR (SEQ ID NO:8)	RSDSLSV (SEQ ID NO:19)	DNANRTK (SEQ ID NO:20)	N/A	N/A
ZFN 9076 gaATGGTGCAGGCTgc cataccaacttt (SEQ ID NO:21)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSSALTR (SEQ ID NO:22)	RSDALTQ (SEQ ID NO:15)	N/A	N/A
ZFN 9179 ggAATGGTgCAGGCTg ccataccaactt (SEQ ID NO:23)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	QSSHLTR (SEQ ID NO:24)	TSSNRKT (SEQ ID NO:25)	N/A	N/A
ZFN 7858 gaATGGTGCAGGCTgc (SEQ ID NO:1)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSDSLLR (SEQ ID NO:26)	RSDALTQ (SEQ ID NO:15)	N/A	N/A
ZFN 7889 gtTCCCAGGAATGGgc (SEQ ID NO:27)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)	N/A	N/A
ZFN 9373 gtTCCCAGGAATGGgC TTGGGgtcaaag (SEQ ID NO:28)	RSDHLSQ (SEQ ID NO:9)	RNADRIT (SEQ ID NO:29)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)

[0010] In one example, zinc finger proteins, engineered to bind in a *GS* gene, are provided. Any of the zinc finger proteins described herein may include 1, 2, 3, 4, 5, 6 or more zinc fingers, each zinc finger having a recognition helix that binds to a target subsite in a *GS* gene. In certain examples, the zinc finger proteins comprises 4, 5 or 6 fingers (wherein the individual zinc fingers are designated F1, F2, F3, F4, F5 and F6) and comprise the amino acid sequence of the recognition helices shown in Table 1.

[0010a] In the second aspect, the present invention refers to a polynucleotide encoding the zinc finger DNA-binding domain or fusion protein as defined above.

[0011] In another example, zinc finger proteins, engineered to bind in a *DHFR* gene, are provided. Any of the zinc finger proteins described herein may include 1, 2, 3, 4, 5, 6 or more zinc fingers, each zinc finger having a recognition helix that binds to a target subsite in a *DHFR* gene. In certain examples, the zinc finger proteins comprise 4, 5 or 6 fingers (wherein the individual zinc fingers are designated F1, F2, F3, F4, F5 and F6) and comprise the amino acid sequence of the recognition helices shown in Table 2.

[0011a] In the third aspect, the present invention refers to a fusion protein comprising a zinc finger DNA-binding domain as defined above and at least one cleavage domain or at least one cleavage half-domain.

[0012] In another example, fusion proteins comprising any of the zinc finger proteins described herein and at least one cleavage domain or at least one cleavage half-domain, are also provided. In certain examples, the cleavage half-domain is a wild-type *FokI* cleavage half-domain. In other examples, the cleavage half-domain is an engineered *FokI* cleavage half-domain.

[0013] In yet another example, a polynucleotide encoding any of the proteins described herein is provided.

[0013a] In the fourth aspect, the present invention refers to an isolated cell comprising a protein as defined above or a polynucleotide as defined above.

[0014] In yet another example, also provided is an isolated cell comprising any of the proteins and/or polynucleotide as described herein. In certain examples, *GS* is inactivated (partially or fully) in the cell. Any of the cells described herein may include additional genes that have been inactivated, for example, using zinc finger nucleases designed to bind to a target site in the selected gene. In certain examples, provided herein are cells or cell lines in which *FUT8*, dihydrofolate reductase (*DHFR*) and glutamine synthetase (*GS*) have been inactivated.

[0014a] In the fifth aspect, the present invention refers to a cell line in which glutamine synthetase (GS) is partially or fully inactivated by a fusion protein as defined above or a polynucletide encoding the fusion protein.

[0015] In addition, methods of using the zinc finger proteins and fusions thereof in methods of inactivating *GS* in a cell or cell line are provided.

[0015a] In the sixth aspect, the present invention refers to a method of inactivating an endogenous cellular *GS* gene in a cell, the method comprising:

(a) introducing, into a cell, a first nucleic acid encoding a first polypeptide, wherein the first polypeptide comprises:

(i) a zinc finger DNA-binding domain as defined above that binds to a first target site in an endogenous *GS* gene; and

(ii) a cleavage domain; such that the polypeptide is expressed in the cell, whereby the polypeptide binds to the target site and cleaves the *GS* gene.

[0016] Thus, in another example, provided herein is a method for inactivating a cellular *GS* gene (*e.g.*, an endogenous *GS* gene) in a cell, the method comprising: (a) introducing, into a cell, a first nucleic acid encoding a first polypeptide, wherein the first polypeptide comprises: (i) a zinc finger DNA-binding domain that is engineered to bind to a first target site in an endogenous *GS* gene; and (ii) a cleavage domain; such that the polypeptide is expressed in the cell, whereby the polypeptide binds to the target site and cleaves the *GS* gene. In certain examples, the method further comprise introducing a nucleic acid encoding a second polypeptide, wherein the second polypeptide comprises: (i) a zinc finger DNA-binding domain that is engineered to bind to a second target site in the *GS* gene; and (ii) a cleavage domain; such that the second polypeptide is expressed in the cell, whereby the first and second

polypeptides bind to their respective target sites and cleave the *GS* gene. The first and second polypeptides may be encoded by the first nucleic acid or by different nucleic acids. In certain examples, one or more additional polynucleotide or polypeptides are introduced into the cells, for example polynucleotides encoding additional zinc finger proteins.

[0016a] In the seventh aspect, the present invention refers to a method of producing a recombinant protein of interest in a host cell, the method comprising the steps of:

(a) providing a host cell comprising an endogenous *GS* gene;

(b) inactivating the endogenous *GS* gene of the host cell by the method as defined above; and

(c) introducing an expression vector comprising a transgene, the transgene comprising a sequence encoding a protein of interest into the host cell, thereby producing the recombinant protein.

[0017] In yet another example, the disclosure provides a method of producing a recombinant protein of interest in a host cell, the method comprising the steps of: (a) providing a host cell comprising an endogenous *GS* gene; (b) inactivating the endogenous *GS* gene of the host cell by any of the methods described herein; and (c) introducing an expression vector comprising a transgene, the transgene comprising a sequence encoding a protein of interest, into the host cell, thereby producing the recombinant protein. In certain examples, the protein of interest comprises an antibody, *e.g.*, a monoclonal antibody.

[0017a] In the eighth aspect, the present invention refers to a cell line in which a *GS* gene is partially or fully inactivated, wherein the cell line is produced by

(a) inactivating the GS gene in a cell as defined above; and

(b) culturing the cell under conditions suitable for generating a cell line in which the *GS* gene is partially or fully inactivated.

[0018] In any of the cells and methods described herein, the cell or cell line can be for example, but not limited to a COS, CHO (*e.g.*, CHO-S, CHO-K1, CHO-DG44, CHO-DUXB11, CHO-DUKX, CHOK1SV), VERO, MDCK, WI38, V79, B14AF28-G3, BHK, HaK, NS0, SP2/0-Ag14, HeLa, HEK293 (*e.g.*, HEK293-F, HEK293-H, HEK293-T), NIH3T3, perC6, insect cell such as *Spodoptera fugiperda* (Sf), or fungal cell such as *Saccharomyces*, *Pichia* and *Schizosaccharomyces*.

BRIEF DESCRIPTION OF THE DRAWINGS

[0019] **Figure 1,** panels A to E, show ZFN-mediated disruption of the glutamine synthetase gene in CHO cells and generation of single knockout *GS*$^{-/-}$ cell lines. FIG. 1A is a schematic depicting the actively-transcribed *GS* gene, which contains 7 exons. The start codon ATG located in exon 2. FIG. 1A also shows that the target sequence for ZFN pair ZFN9372/ZFN9075 is located in exon 6 as indicated and that the target sequence of ZFN pair 8361/8365 is located in exon 2. Additional ZFNs (9076, 9179, 7858, 7889, 9373) targeted to exon 6 are also shown. FIG. 1B are gels showing ZFN-mediated disruption of the endogenous CHO *GS* gene using ZFN pair 9372/9075 linked to either the wild-type or an obligate heterodimer EL/KK variant of the catalytic domain of *Fok I* in CHO-K1 cells (left panel) or CHO-S cells (right panel), as determined by the Surveyor™ Nuclease Assay. FIG. 1C depicts exemplary DNA sequences of the target *GS* locus for the indicated cell lines along with their growth properties in the absence of exogenously added L-glutamine ("L-

Glu Growth"; '+': growth in the absence of L-glutamine indistinguishable from wild-type CHO; '-': no growth in the absence of L-glutamine). The ZFN target sequences are underlined. The protein translation is shown under the wild-type sequence. Capital letters indicate exonic sequences, small letters indicate intronic sequences, '-' indicate deletions, bold letters indicate insertions. FIG. 1D depicts Western blot analysis of selected CHO-S (left panel) and CHO-K1 (right panel) cell lines using an anti-GS monoclonal antibody (top panels). As a loading control, blots were re-probed with an anti-DHFR antibody (bottom panels). FIG. 1E shows graphs depicting growth and viability of selected CHO-K1 *GS*$^{-/-}$ cell lines that had been grown for period of approximately 3 months. The viability (smooth line on the top of the graph) and viable cell density (jagged line) of these cell lines is shown for a 30 day period following the initial 3 month period, where cells were grown in L-glutamine-supplemented medium, splitting the cells every 2-3 days. L-glutamine was withdrawn at the time indicated by the arrow.

[0020] **Figure 2**, panels A to F, depict ZFN-mediated disruption of the *DHFR* gene in CHO cells and generation of double knockout *DHFR*$^{-/-}$*GS*$^{-/-}$ cell lines. FIG. 2A shows the genomic organization of the *DHFR* gene in CHO cells and the location of the target sites for ZFN pairs 9461/7844 (in exon 1, see, U.S. Patent Application No. 20080015164) and 9476/9477 (in intron 1 located 240-bp 3' of the exon 1 ZFN 9461/7844 cleavage site). FIG. 2B depicts the level of gene modification using ZFN pair 9461/7844 (left panel) and ZFN pair 9476/9477 (right panel), as measured using the Surveyor™ Nuclease Assay. FIG. 2 C depicts PCR analysis of *GS*$^{-/-}$ clone B3 genomic DNA 2 days after concurrent transfection of plasmids encoding both ZFN pairs, which resulted in a deletion of approximately 240 bp in the *DHFR* locus (small arrow in lane 7). Serving as controls were cells transfected with empty vector (Lane 1), a GFP control vector (Lane 2), the exonic ZFN pair only (ZFN9461/ZFN7844, Lane 3), the intronic ZFN pair only (ZFN9476/ZFN9477, Lane 4), the "inner" ZFNs relative to the deletion (ZFN7844 and ZFN9477, Lane5), and the "outer" ZFNs relative to the deletion (ZFN9461 and ZFN9476, Lane 6). FIG. 2D depicts results of *DHFR* genotyping analysis of single-cell lines. For homozygous clones, the common sequence for both alleles is shown. For compound heterozygous clones the sequence of each unique allele is shown. FIG. 2E depicts Western blot analysis with the indicated antibodies (DHFR, GS and β-tubulin) of whole cell lysates from the cell lines indicated above each lane. Cell lines 1F1.6 and 2B12.8 (*DHFR* / *GS* knockout)

were analyzed while the parental *GS*$^{-/-}$ cell line B3, wild-type CHO cells (WT), and the DHFR-deficient CHO cell line DG44 (see Urlab *et al.* (1983) *Cell* 33:405-412) served as controls. FIG 2F depicts growth of the 1F1.6 and 2B12.8 cell lines and the dependence of these lines on exogenously provided hypoxanthine, thymidine and glutamine.

[0021] **Figure 3**, panels A to D, show ZFN-mediated disruption of the *FUT8* gene in CHO cells and generation of triple knockout *FUT8*$^{-/-}$*DHFR*$^{-/-}$*GS*$^{-/-}$ cell lines. FIG. 3A is a schematic depicting ZFNs targeted to the critical and highly conserved region encoding the *FUT8* Fut motif II located in exon 10. See, also, U.S. Patent Application No. 12/218,0135. FIG. 3B depicts the level of gene modification 2 days after transient transfection of the ZFN pair 12176/12172 into the *DHFR*$^{-/-}$*GS*$^{-/-}$ clone 1F1.6, as measured using the Surveyor™ Nuclease Assay. FIG. 3C depicts fluorescent-LCA binding activity of the triple-KO clones 35F2 and 14C1 (lines on left side of panel) by FACS analysis. F-LCA stained wild-type CHO-S cells (line on right side of panel) served as positive controls, and unstained cells (dotted line) served as negative controls. FIG. 3D shows the genotype (for both alleles) of the triple-knockout cell lines 35F2 and 14C1 at the *FUT8* locus where the sequence shown is for both alleles. Capital letters indicate exon 10 sequences, small letters indicates intron sequences, italic letters indicate Fut motif II sequences, bold letters indicate sequence insertions, '-' indicates deletions. The protein translation is also shown under the wild-type sequence. Underline indicates the ZFN binding sites.

[0022] **Figure 4**, panels A to C, depict an exemplary ZFN design and its target site in the CHO *GS* gene. FIG. 4A is a schematic representation of the functional intron-containing glutamine synthetase gene in CHO cells. It contains 7 exons, the start codon ATG is located in exon 2, and the target sequence of ZFN pair ZFN9372/ZFN9075, located in exon 6, is also indicated. The nucleotide sequence of the region of interest around exon 6 is shown. Capital letters indicate exon 6 sequences, small letters indicate intron sequences. The target sequences of ZFN9372 and ZFN9075 are underlined. FIG. 4B is a schematic representation of ZFN9372 and ZFN9075 binding to their double-stranded target sequence (underlined). FIG. 4C depicts the target sequences and zinc-finger designs of ZFN9372 and ZFN9075. The core DNA target sequences (capital letters) and 2 flanking bases (small letters) are shown. ZFN9075 contains 4 zinc-finger DNA-binding domains, and ZFN9372 contains 6 zinc-finger domains. The amino acid residues at positions '-1' to '+6' of

the recognition α-helix of each of the zinc-finger DNA-binding domains for the indicated target DNA triplets are shown.

[0023] **Figure 5** shows exemplary results of sequencing of the genomic *GS* locus from ZFN transfected cells. "C" refers to the count (number of times the indicated sequence was observed) and "G" refers to the genotype. The ZFN target sequences are underlined. Bold letters indicate sequence insertions, '-' indicates deletions.

[0024] **Figure 6** is a graph depicting L-glutamine-dependent growth of a homozygous $GS^{-/-}$ cell line (Clone B3). In the presence of L-glutamine, CHO-S $GS^{-/-}$ clone B3 (triangle) grows as well as wild-type CHO-S (diamond). In the absence of exogenous L-glutamine, the Clone B3 (circle) stopped growing and all cells died within 4 days, whereas the wild-type CHO cells (square) continued to grow at a reduced rate.

[0025] **Figure 7**, panels A to C, depict exemplary ZFN designs and their target sites in the CHO *DHFR* gene. FIG. 7A shows the nucleotide sequence of the *DHFR* region targeted by the indicated ZFN pairs in CHO cells. Capital letters indicate exon sequences, small letters indicate intron sequences. FIG. 7B is a schematic representation of the ZFNs targeting *DHFR* when the ZFNs are bound to their double-stranded target sequences (underlined). The two ZFNs labeled "inner" target sequences are internal to the region to be deleted, while the two ZFNs labeled "outer" target sequences are outside of the expected deletion junction. FIG 7C shows the target sequences and zinc-finger designs of exemplary ZFNs targeting the CHO *DHFR* gene. The core DNA target sequences (capital letters) and 2 flanking bases (small letters) are shown. All ZFNs contain 4 zinc-finger DNA-binding domains. The amino acid residues at positions '-1' to '+6' of the recognition α-helix for each of the zinc-finger DNA-binding domains for the indicated target DNA triplet are shown.

[0026] **Figure 8** shows exemplary results of sequencing of the genomic *DHFR* locus from ZFN transfected cells. "C" refers to the count (number of times the indicated sequence was observed) and "G" refers to the genotype. The ZFN target sequences are underlined. Bold letters indicate sequence insertions, '-' indicates deletions. Bold letters indicate sequence insertions. Italics indicate sequence changes. Capital letters indicate exonic sequence, small letters indicate intronic sequence.

[0027] **Figure 9**, panels A to C, depict ZFN target sites and finger designs targeted to the CHO *FUT8* gene. FIG. 9A depicts a schematic of the ZFN binding

sites within exon 10 of the *FUT8* gene as well as the nucleotide sequence of the target region within exon 10. Capital letters indicate exon 10 sequences, small letters indicate intronic sequences. The target sequences of ZFN12176 and ZFN12172 are underlined. The nucleotides comprising the fucosyltransferase motif II are shown in italics. FIG. 9B is a schematic representation of ZFN12176 and ZFN12172 binding to their double-stranded target sequence (underlined). FIG 9C depicts the target sequences and zinc-finger designs of ZFN12176 and ZFN12172. The core DNA target sequences (capital letters) and 2 flanking bases (small letters) are shown. ZFN12176 contains 5 zinc-finger DNA-binding domains, and ZFN12172 contains 6 zinc-finger domains. The amino acid residues at positions '-1' to '+6' of the recognition α-helix for each of the zinc-finger DNA-binding domains for the indicated target DNA triplet are shown.

[0028] **Figure 10**, panels A to C, show ZFN targeting of *CCR5*, *GR* and *AAVS1* loci. FIG. 10A is a schematic showing the location of ZFN targeting sites in C-C chemokine receptor 5 (*CCR5*), glucocorticoid receptor (*GR*), and adeno-associated virus integration site (*AAVS1*) loci, respectively. FIG. 10B depicts ZFN-mediated simultaneous disruption, as measured by Surveyor™ Nuclease Assay, of *CCR5* (left panel), *GR* (middle panel), and *AAVS1* (right panel) loci as measured 20 days after transient co-transfection of pairs of ZFNs linked to either the wild-type, ZFN-*Fok I* (wt) or an obligate heterodimer EL/KK variant, ZFN-*Fok I*(EL/KK), of the catalytic domain of Fok into K562 cells. Treatments for each lane are as following: lane1, *CCR5* ZFN-*FokI* (wt); lane 2, *GR* ZFN-*Fok I*(wt); lane 3, *AAVS1* ZFN-*Fok I*(wt); lane 4, *CCR5* ZFN-*Fok I*(EL/KK); lane 5, *GR* ZFN-*Fok I*(EL/KK); lane 6, *AAVS1* ZFN-*Fok I*(EL/KK); lane 7, *CCR5* ZFN-*FokI*(wt) + *GR* ZFN-*FokI*(wt) + *AAVS1* ZFN-*FokI*(wt); lane 8, *CCR5* ZFN-*FokI*(EL/KK) + *GR* ZFN-*FokI*(EL/KK) + *AAVS1* ZFN-*FokI*(EL/KK). FIG. 10C depicts the genotype of a single triple knockout clone wherein the target *CCR5*, *GR*, *AAVS1* loci for the indicated cell lines are shown. The ZFN target sequences are underlined. '-' indicate deletions, bold letters indicate insertions.

[0029] **Figure 11**, panels A and B, show sequence alignments of CHO *GS* genomic sequences as determined herein with the indicated species. FIG. 11A shows alignment of exon 2 sequence. The target sites for ZFN8361 and ZFN8365 are underlined. FIG. 11B shows alignment of exon 6 sequence. The target sites for ZFN9075 and ZFN9372 are underlined.

[0030] **Figure 12**, panels A to D, show ZFN-mediated disruption in human and mouse cells. FIGs. 12A and B show disruption of *GS* in human K562 mediated by ZFNs targeted to exon 2 of CHO *GS* (FIG. 12A) and exon 6 of CHO *GS* (FIG. 12B). FIGs. 12C and D show disruption of *GS* in mouse Neuro2a cells mediated by ZFNs targeted to exon 2 of CHO *GS* (FIG. 12C) and exon 6 of CHO *GS* (FIG. 12D).

[0031] **Figure 13**, panels A to C, show the complete genomic sequence of CHO *GS* locus (SEQ ID NO:55). Introns and exons are designated as shown.

[0032] **Figure 14**, panels A to C, show the results of *GS*-specific gene targeting in HEK293 cells. FIG 14A depicts the percent of NHEJ activity in cells treated with *GS*-specific ZFNs (labeled GS) in comparison with cells transfected with a GFP donor molecule (labeled GFP). FIG 14B shows that 2 clones, g17 and g52, derived from a pool of cells treated with the *GS*-specific ZFNs, do not express *GS* as assayed by Western blot. FIG 14C is a graph showing growth over 7 days of the *GS* knock out clones and demonstrates the requirement for glutamine supplementation for growth.

DETAILED DESCRIPTION

[0033] Described herein are compositions and methods for partial or complete inactivation of a *GS* gene. Also disclosed are methods of making and using these compositions (reagents), for example to inactivate a GS gene in a target cell. Inactivation of GS, alone or in combination with other genes such as *DHFR* and *FUT8* in a target cell can be used to produce cell lines for expression of recombinant proteins, for example monoclonal antibodies that elicit enhanced antibody-dependent cellular cytotoxicity (ADCC).

General

[0034] Practice of the methods, as well as preparation and use of the compositions disclosed herein employ, unless otherwise indicated, conventional techniques in molecular biology, biochemistry, chromatin structure and analysis, computational chemistry, cell culture, recombinant DNA and related fields as are within the skill of the art. These techniques are fully explained in the literature. *See*, for example, Sambrook *et al.* MOLECULAR CLONING: A LABORATORY MANUAL, Second edition, Cold Spring Harbor Laboratory Press, 1989 and Third edition, 2001; Ausubel *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons,

New York, 1987 and periodic updates; the series METHODS IN ENZYMOLOGY, Academic Press, San Diego; Wolffe, CHROMATIN STRUCTURE AND FUNCTION, Third edition, Academic Press, San Diego, 1998; METHODS IN ENZYMOLOGY, Vol. 304, "Chromatin" (P.M. Wassarman and A. P. Wolffe, eds.), Academic Press, San Diego, 1999; and METHODS IN MOLECULAR BIOLOGY, Vol. 119, "Chromatin Protocols" (P.B. Becker, ed.) Humana Press, Totowa, 1999.

Definitions

[0035] The terms "nucleic acid," "polynucleotide," and "oligonucleotide" are used interchangeably and refer to a deoxyribonucleotide or ribonucleotide polymer, in linear or circular conformation, and in either single- or double-stranded form. For the purposes of the present disclosure, these terms are not to be construed as limiting with respect to the length of a polymer. The terms can encompass known analogues of natural nucleotides, as well as nucleotides that are modified in the base, sugar and/or phosphate moieties (*e.g.*, phosphorothioate backbones). In general, an analogue of a particular nucleotide has the same base-pairing specificity; *i.e.*, an analogue of A will base-pair with T.

[0036] The terms "polypeptide," "peptide" and "protein" are used interchangeably to refer to a polymer of amino acid residues. The term also applies to amino acid polymers in which one or more amino acids are chemical analogues or modified derivatives of a corresponding naturally-occurring amino acids.

[0037] "Binding" refers to a sequence-specific, non-covalent interaction between macromolecules (*e.g.*, between a protein and a nucleic acid). Not all components of a binding interaction need be sequence-specific (*e.g.*, contacts with phosphate residues in a DNA backbone), as long as the interaction as a whole is sequence-specific. Such interactions are generally characterized by a dissociation constant (K_d) of 10^{-6} M^{-1} or lower. "Affinity" refers to the strength of binding: increased binding affinity being correlated with a lower K_d.

[0038] A "binding protein" is a protein that is able to bind non-covalently to another molecule. A binding protein can bind to, for example, a DNA molecule (a DNA-binding protein), an RNA molecule (an RNA-binding protein) and/or a protein molecule (a protein-binding protein). In the case of a protein-binding protein, it can bind to itself (to form homodimers, homotrimers, *etc.*) and/or it can bind to one or more molecules of a different protein or proteins. A binding protein can have more than one type of binding

activity. For example, zinc finger proteins have DNA-binding, RNA-binding and protein-binding activity.

[0039] A "zinc finger DNA binding protein" (or binding domain) is a protein, or a domain within a larger protein, that binds DNA in a sequence-specific manner through one or more zinc fingers, which are regions of amino acid sequence within the binding domain whose structure is stabilized through coordination of a zinc ion. The term zinc finger DNA binding protein is often abbreviated as zinc finger protein or ZFP.

[0040] Zinc finger binding domains can be "engineered" to bind to a predetermined nucleotide sequence. Non-limiting examples of methods for engineering zinc finger proteins are design and selection. A designed zinc finger protein is a protein not occurring in nature whose design/composition results principally from rational criteria. Rational criteria for design include application of substitution rules and computerized algorithms for processing information in a database storing information of existing ZFP designs and binding data. See, for example, US Patents 6,140,081; 6,453,242; and 6,534,261; see also WO 98/53058; WO 98/53059; WO 98/53060; WO 02/016536 and WO 03/016496.

[0041] A "selected" zinc finger protein is a protein not found in nature whose production results primarily from an empirical process such as phage display, interaction trap or hybrid selection. See *e.g.*, US 5,789,538; US 5,925,523; US 6,007,988; US 6,013,453; US 6,200,759; WO 95/19431; WO 96/06166; WO 98/53057; WO 98/54311; WO 00/27878; WO 01/60970; WO 01/88197 and WO 02/099084.

[0042] The term "sequence" refers to a nucleotide sequence of any length, which can be DNA or RNA; can be linear, circular or branched and can be either single-stranded or double stranded. The term "donor sequence" refers to a nucleotide sequence that is inserted into a genome. A donor sequence can be of any length, for example between 2 and 10,000 nucleotides in length (or any integer value therebetween or thereabove), preferably between about 100 and 1,000 nucleotides in length (or any integer therebetween), more preferably between about 200 and 500 nucleotides in length.

[0043] A "homologous, non-identical sequence" refers to a first sequence which shares a degree of sequence identity with a second sequence, but whose sequence is not identical to that of the second sequence. For example, a polynucleotide comprising the wild-type sequence of a mutant gene is homologous and non-identical to the sequence of the mutant gene. In certain embodiments, the

degree of homology between the two sequences is sufficient to allow homologous recombination therebetween, utilizing normal cellular mechanisms. Two homologous non-identical sequences can be any length and their degree of non-homology can be as small as a single nucleotide (*e.g.*, for correction of a genomic point mutation by targeted homologous recombination) or as large as 10 or more kilobases (*e.g.*, for insertion of a gene at a predetermined ectopic site in a chromosome). Two polynucleotides comprising the homologous non-identical sequences need not be the same length. For example, an exogenous polynucleotide (*i.e.*, donor polynucleotide) of between 20 and 10,000 nucleotides or nucleotide pairs can be used.

[0044] Techniques for determining nucleic acid and amino acid sequence identity are known in the art. Typically, such techniques include determining the nucleotide sequence of the mRNA for a gene and/or determining the amino acid sequence encoded thereby, and comparing these sequences to a second nucleotide or amino acid sequence. Genomic sequences can also be determined and compared in this fashion. In general, identity refers to an exact nucleotide-to-nucleotide or amino acid-to-amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Two or more sequences (polynucleotide or amino acid) can be compared by determining their percent identity. The percent identity of two sequences, whether nucleic acid or amino acid sequences, is the number of exact matches between two aligned sequences divided by the length of the shorter sequences and multiplied by 100. An approximate alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981). This algorithm can be applied to amino acid sequences by using the scoring matrix developed by Dayhoff, Atlas of Protein Sequences and Structure, M.O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA, and normalized by Gribskov, Nucl. Acids Res. 14(6):6745-6763 (1986). An exemplary implementation of this algorithm to determine percent identity of a sequence is provided by the Genetics Computer Group (Madison, WI) in the "BestFit" utility application. Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, for example, another alignment program is BLAST, used with default parameters. For example, BLASTN and BLASTP can be used using the following default parameters: genetic code = standard; filter = none; strand = both; cutoff = 60; expect = 10; Matrix = BLOSUM62; Descriptions = 50 sequences;

sort by = HIGH SCORE; Databases = non-redundant, GenBank + EMBL + DDBJ + PDB + GenBank CDS translations + Swiss protein + Spupdate + PIR. Details of these programs can be found on the GenBank website. With respect to sequences described herein, the range of desired degrees of sequence identity is approximately 80% to 100% and any integer value therebetween. Typically the percent identities between sequences are at least 70-75%, preferably 80-82%, more preferably 85-90%, even more preferably 92%, still more preferably 95%, and most preferably 98% sequence identity.

[0045] Alternatively, the degree of sequence similarity between polynucleotides can be determined by hybridization of polynucleotides under conditions that allow formation of stable duplexes between homologous regions, followed by digestion with single-stranded-specific nuclease(s), and size determination of the digested fragments. Two nucleic acid, or two polypeptide sequences are substantially homologous to each other when the sequences exhibit at least about 70%-75%, preferably 80%-82%, more preferably 85%-90%, even more preferably 92%, still more preferably 95%, and most preferably 98% sequence identity over a defined length of the molecules, as determined using the methods above. As used herein, substantially homologous also refers to sequences showing complete identity to a specified DNA or polypeptide sequence. DNA sequences that are substantially homologous can be identified in a Southern hybridization experiment under, for example, stringent conditions, as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, *e.g.*, Sambrook et al., *supra*; Nucleic Acid Hybridization: A Practical Approach, editors B.D. Hames and S.J. Higgins, (1985) Oxford; Washington, DC; IRL Press).

[0046] Selective hybridization of two nucleic acid fragments can be determined as follows. The degree of sequence identity between two nucleic acid molecules affects the efficiency and strength of hybridization events between such molecules. A partially identical nucleic acid sequence will at least partially inhibit the hybridization of a completely identical sequence to a target molecule. Inhibition of hybridization of the completely identical sequence can be assessed using hybridization assays that are well known in the art (*e.g.*, Southern (DNA) blot, Northern (RNA) blot, solution hybridization, or the like, see Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, (1989) Cold Spring Harbor, N.Y.). Such assays can be conducted using varying degrees of selectivity, for

example, using conditions varying from low to high stringency. If conditions of low stringency are employed, the absence of non-specific binding can be assessed using a secondary probe that lacks even a partial degree of sequence identity (for example, a probe having less than about 30% sequence identity with the target molecule), such that, in the absence of non-specific binding events, the secondary probe will not hybridize to the target.

[0047] When utilizing a hybridization-based detection system, a nucleic acid probe is chosen that is complementary to a reference nucleic acid sequence, and then by selection of appropriate conditions the probe and the reference sequence selectively hybridize, or bind, to each other to form a duplex molecule. A nucleic acid molecule that is capable of hybridizing selectively to a reference sequence under moderately stringent hybridization conditions typically hybridizes under conditions that allow detection of a target nucleic acid sequence of at least about 10-14 nucleotides in length having at least approximately 70% sequence identity with the sequence of the selected nucleic acid probe. Stringent hybridization conditions typically allow detection of target nucleic acid sequences of at least about 10-14 nucleotides in length having a sequence identity of greater than about 90-95% with the sequence of the selected nucleic acid probe. Hybridization conditions useful for probe/reference sequence hybridization, where the probe and reference sequence have a specific degree of sequence identity, can be determined as is known in the art (see, for example, Nucleic Acid Hybridization: A Practical Approach, editors B.D. Hames and S.J. Higgins, (1985) Oxford; Washington, DC; IRL Press).

[0048] Conditions for hybridization are well-known to those of skill in the art. Hybridization stringency refers to the degree to which hybridization conditions disfavor the formation of hybrids containing mismatched nucleotides, with higher stringency correlated with a lower tolerance for mismatched hybrids. Factors that affect the stringency of hybridization are well-known to those of skill in the art and include, but are not limited to, temperature, pH, ionic strength, and concentration of organic solvents such as, for example, formamide and dimethylsulfoxide. As is known to those of skill in the art, hybridization stringency is increased by higher temperatures, lower ionic strength and lower solvent concentrations.

[0049] With respect to stringency conditions for hybridization, it is well known in the art that numerous equivalent conditions can be employed to establish a particular stringency by varying, for example, the following factors: the length and

nature of the sequences, base composition of the various sequences, concentrations of salts and other hybridization solution components, the presence or absence of blocking agents in the hybridization solutions (e.g., dextran sulfate, and polyethylene glycol), hybridization reaction temperature and time parameters, as well as, varying wash conditions. The selection of a particular set of hybridization conditions is selected following standard methods in the art (see, for example, Sambrook, et al., Molecular Cloning: A Laboratory Manual, Second Edition, (1989) Cold Spring Harbor, N.Y.).

[0050] "Recombination" refers to a process of exchange of genetic information between two polynucleotides. For the purposes of this disclosure, "homologous recombination (HR)" refers to the specialized form of such exchange that takes place, for example, during repair of double-strand breaks in cells. This process requires nucleotide sequence homology, uses a "donor" molecule to template repair of a "target" molecule (*i.e.*, the one that experienced the double-strand break), and is variously known as "non-crossover gene conversion" or "short tract gene conversion," because it leads to the transfer of genetic information from the donor to the target. Without wishing to be bound by any particular theory, such transfer can involve mismatch correction of heteroduplex DNA that forms between the broken target and the donor, and/or "synthesis-dependent strand annealing," in which the donor is used to resynthesize genetic information that will become part of the target, and/or related processes. Such specialized HR often results in an alteration of the sequence of the target molecule such that part or all of the sequence of the donor polynucleotide is incorporated into the target polynucleotide.

[0051] "Cleavage" refers to the breakage of the covalent backbone of a DNA molecule. Cleavage can be initiated by a variety of methods including, but not limited to, enzymatic or chemical hydrolysis of a phosphodiester bond. Both single-stranded cleavage and double-stranded cleavage are possible, and double-stranded cleavage can occur as a result of two distinct single-stranded cleavage events. DNA cleavage can result in the production of either blunt ends or staggered ends. In certain embodiments, fusion polypeptides are used for targeted double-stranded DNA cleavage.

[0052] An "cleavage half-domain" is a polypeptide sequence which, in conjunction with a second polypeptide (either identical or different) forms a complex having cleavage activity (preferably double-strand cleavage activity). The terms "first

and second cleavage half-domains;" "+ and – cleavage half-domains" and "right and left cleavage half-domains" are used interchangeably to refer to pairs of cleavage half-domains that dimerize.

[0053] An "engineered cleavage half-domain" is a cleavage half-domain that has been modified so as to form obligate heterodimers with another cleavage half-domain (*e.g.*, another engineered cleavage half-domain). *See, also,* U.S. Patent Publication Nos. 2005/0064474; 2007/0218528 and 2008/0131962, incorporated herein by reference in their entireties.

[0054] "Chromatin" is the nucleoprotein structure comprising the cellular genome. Cellular chromatin comprises nucleic acid, primarily DNA, and protein, including histones and non-histone chromosomal proteins. The majority of eukaryotic cellular chromatin exists in the form of nucleosomes, wherein a nucleosome core comprises approximately 150 base pairs of DNA associated with an octamer comprising two each of histones H2A, H2B, H3 and H4; and linker DNA (of variable length depending on the organism) extends between nucleosome cores. A molecule of histone H1 is generally associated with the linker DNA. For the purposes of the present disclosure, the term "chromatin" is meant to encompass all types of cellular nucleoprotein, both prokaryotic and eukaryotic. Cellular chromatin includes both chromosomal and episomal chromatin.

[0055] A "chromosome," is a chromatin complex comprising all or a portion of the genome of a cell. The genome of a cell is often characterized by its karyotype, which is the collection of all the chromosomes that comprise the genome of the cell. The genome of a cell can comprise one or more chromosomes.

[0056] An "episome" is a replicating nucleic acid, nucleoprotein complex or other structure comprising a nucleic acid that is not part of the chromosomal karyotype of a cell. Examples of episomes include plasmids and certain viral genomes.

[0057] An "accessible region" is a site in cellular chromatin in which a target site present in the nucleic acid can be bound by an exogenous molecule which recognizes the target site. Without wishing to be bound by any particular theory, it is believed that an accessible region is one that is not packaged into a nucleosomal structure. The distinct structure of an accessible region can often be detected by its sensitivity to chemical and enzymatic probes, for example, nucleases.

[0058] A "target site" or "target sequence" is a nucleic acid sequence that defines a portion of a nucleic acid to which a binding molecule will bind, provided sufficient conditions for binding exist. For example, the sequence 5'-GAATTC-3' is a target site for the Eco RI restriction endonuclease.

[0059] An "exogenous" molecule is a molecule that is not normally present in a cell, but can be introduced into a cell by one or more genetic, biochemical or other methods. "Normal presence in the cell" is determined with respect to the particular developmental stage and environmental conditions of the cell. Thus, for example, a molecule that is present only during embryonic development of muscle is an exogenous molecule with respect to an adult muscle cell. Similarly, a molecule induced by heat shock is an exogenous molecule with respect to a non-heat-shocked cell. An exogenous molecule can comprise, for example, a functioning version of a malfunctioning endogenous molecule or a malfunctioning version of a normally-functioning endogenous molecule.

[0060] An exogenous molecule can be, among other things, a small molecule, such as is generated by a combinatorial chemistry process, or a macromolecule such as a protein, nucleic acid, carbohydrate, lipid, glycoprotein, lipoprotein, polysaccharide, any modified derivative of the above molecules, or any complex comprising one or more of the above molecules. Nucleic acids include DNA and RNA, can be single- or double-stranded; can be linear, branched or circular; and can be of any length. Nucleic acids include those capable of forming duplexes, as well as triplex-forming nucleic acids. See, for example, U.S. Patent Nos. 5,176,996 and 5,422,251. Proteins include, but are not limited to, DNA-binding proteins, transcription factors, chromatin remodeling factors, methylated DNA binding proteins, polymerases, methylases, demethylases, acetylases, deacetylases, kinases, phosphatases, integrases, recombinases, ligases, topoisomerases, gyrases and helicases. An exogeneous molecule can also be the same type of molecule as an endogenous molecule but derived from a different species than the cell is derived from. For example, a human nucleic acid sequenced may be introduced into a cell line originally derived from a mouse or hamster.

[0061] An exogenous molecule can be the same type of molecule as an endogenous molecule, *e.g.*, an exogenous protein or nucleic acid. For example, an exogenous nucleic acid can comprise an infecting viral genome, a plasmid or episome introduced into a cell, or a chromosome that is not normally present in the cell.

Methods for the introduction of exogenous molecules into cells are known to those of skill in the art and include, but are not limited to, lipid-mediated transfer (*i.e.*, liposomes, including neutral and cationic lipids), electroporation, direct injection, cell fusion, particle bombardment, calcium phosphate co-precipitation, DEAE-dextran-mediated transfer and viral vector-mediated transfer. An exogenous molecule can also refer to a nucleic acid from a different species, for example, a human gene inserted into a hamster genome.

[0062] By contrast, an "endogenous" molecule is one that is normally present in a particular cell at a particular developmental stage under particular environmental conditions. For example, an endogenous nucleic acid can comprise a chromosome, the genome of a mitochondrion, chloroplast or other organelle, or a naturally-occurring episomal nucleic acid. Additional endogenous molecules can include proteins, for example, transcription factors and enzymes.

[0063] A "fusion" molecule is a molecule in which two or more subunit molecules are linked, preferably covalently. The subunit molecules can be the same chemical type of molecule, or can be different chemical types of molecules. Examples of the first type of fusion molecule include, but are not limited to, fusion proteins (for example, a fusion between a ZFP DNA-binding domain and a cleavage domain) and fusion nucleic acids (for example, a nucleic acid encoding the fusion protein described *supra*). Examples of the second type of fusion molecule include, but are not limited to, a fusion between a triplex-forming nucleic acid and a polypeptide, and a fusion between a minor groove binder and a nucleic acid.

[0064] Expression of a fusion protein in a cell can result from delivery of the fusion protein to the cell or by delivery of a polynucleotide encoding the fusion protein to a cell, wherein the polynucleotide is transcribed, and the transcript is translated, to generate the fusion protein. Trans-splicing, polypeptide cleavage and polypeptide ligation can also be involved in expression of a protein in a cell. Methods for polynucleotide and polypeptide delivery to cells are presented elsewhere in this disclosure.

[0065] A "gene," for the purposes of the present disclosure, includes a DNA region encoding a gene product (see *infra*), as well as all DNA regions which regulate the production of the gene product, whether or not such regulatory sequences are adjacent to coding and/or transcribed sequences. Accordingly, a gene includes, but is not necessarily limited to, promoter sequences, terminators, translational regulatory

sequences such as ribosome binding sites and internal ribosome entry sites, enhancers, silencers, insulators, boundary elements, replication origins, matrix attachment sites and locus control regions.

[0066] "Gene expression" refers to the conversion of the information, contained in a gene, into a gene product. A gene product can be the direct transcriptional product of a gene (*e.g.*, mRNA, tRNA, rRNA, antisense RNA, shRNAs, micro RNAs (miRNAs) ribozyme, structural RNA or any other type of RNA) or a protein produced by translation of a mRNA. Gene products also include RNAs which are modified, by processes such as capping, polyadenylation, methylation, and editing, and proteins modified by, for example, methylation, acetylation, phosphorylation, ubiquitination, ADP-ribosylation, myristilation, and glycosylation.

[0067] "Modulation" of gene expression refers to a change in the activity of a gene. Modulation of expression can include, but is not limited to, gene activation and gene repression. Gene inactivation refers to any reduction in gene expression as compared to a cell that does not include a ZFP as described herein. Thus, gene inactivation may be complete (knock-out) or partial (*e.g.*, a hypomorph in which a gene exhibits less than normal expression levels or a product of a mutant gene that shows partial reduction in the activity it influences).

[0068] "Eucaryotic" cells include, but are not limited to, fungal cells (such as yeast), plant cells, animal cells, mammalian cells and human cells (*e.g.*, T-cells).

[0069] A "region of interest" is any region of cellular chromatin, such as, for example, a gene or a non-coding sequence within or adjacent to a gene, in which it is desirable to bind an exogenous molecule. Binding can be for the purposes of targeted DNA cleavage and/or targeted recombination. A region of interest can be present in a chromosome, an episome, an organellar genome (*e.g.*, mitochondrial, chloroplast), or an infecting viral genome, for example. A region of interest can be within the coding region of a gene, within transcribed non-coding regions such as, for example, leader sequences, trailer sequences or introns, or within non-transcribed regions, either upstream or downstream of the coding region. A region of interest can be as small as a single nucleotide pair or up to 2,000 nucleotide pairs in length, or any integral value of nucleotide pairs.

[0070] The terms "operative linkage" and "operatively linked" (or "operably linked") are used interchangeably with reference to a juxtaposition of two or more

components (such as sequence elements), in which the components are arranged such that both components function normally and allow the possibility that at least one of the components can mediate a function that is exerted upon at least one of the other components. By way of illustration, a transcriptional regulatory sequence, such as a promoter, is operatively linked to a coding sequence if the transcriptional regulatory sequence controls the level of transcription of the coding sequence in response to the presence or absence of one or more transcriptional regulatory factors. A transcriptional regulatory sequence is generally operatively linked in *cis* with a coding sequence, but need not be directly adjacent to it. For example, an enhancer is a transcriptional regulatory sequence that is operatively linked to a coding sequence, even though they are not contiguous.

[0071] With respect to fusion polypeptides, the term "operatively linked" can refer to the fact that each of the components performs the same function in linkage to the other component as it would if it were not so linked. For example, with respect to a fusion polypeptide in which a ZFP DNA-binding domain is fused to a cleavage domain, the ZFP DNA-binding domain and the cleavage domain are in operative linkage if, in the fusion polypeptide, the ZFP DNA-binding domain portion is able to bind its target site and/or its binding site, while the cleavage domain is able to cleave DNA in the vicinity of the target site.

[0072] A "functional fragment" of a protein, polypeptide or nucleic acid is a protein, polypeptide or nucleic acid whose sequence is not identical to the full-length protein, polypeptide or nucleic acid, yet retains the same function as the full-length protein, polypeptide or nucleic acid. A functional fragment can possess more, fewer, or the same number of residues as the corresponding native molecule, and/or can contain one ore more amino acid or nucleotide substitutions. Methods for determining the function of a nucleic acid (*e.g.*, coding function, ability to hybridize to another nucleic acid) are well-known in the art. Similarly, methods for determining protein function are well-known. For example, the DNA-binding function of a polypeptide can be determined, for example, by filter-binding, electrophoretic mobility-shift, or immunoprecipitation assays. DNA cleavage can be assayed by gel electrophoresis. See Ausubel *et al.*, *supra*. The ability of a protein to interact with another protein can be determined, for example, by co-immunoprecipitation, two-hybrid assays or complementation, both genetic and biochemical. See, for example,

Fields *et al.* (1989) *Nature* **340**:245-246; U.S. Patent No. 5,585,245 and PCT WO 98/44350.

[0073] The term "antibody" as used herein includes antibodies obtained from both polyclonal and monoclonal preparations, as well as, the following: hybrid (chimeric) antibody molecules (see, for example, Winter et al., Nature (1991) 349:293-299; and U.S. Pat. No. 4,816,567); F(ab')2 and F(ab) fragments; Fv molecules (non-covalent heterodimers, see, for example, Inbar et al., Proc Natl Acad Sci USA (1972) 69:2659-2662; and Ehrlich et al., Biochem (1980) 19:4091-4096); single-chain Fv molecules (sFv) (see, for example, Huston et al., Proc Natl Acad Sci USA (1988) 85:5879-5883); dimeric and trimeric antibody fragment constructs; minibodies (see, e.g., Pack et al., Biochem (1992) 31:1579-1584; Cumber et al., J Immunology (1992) 149B: 120-126); humanized antibody molecules (see, for example, Riechmann et al., Nature (1988) 332:323-327; Verhoeyan et al., Science (1988) 239:1534-1536; and U.K. Patent Publication No. GB 2,276,169, published 21 Sep. 1994); and, any functional fragments obtained from such molecules, wherein such fragments retain immunological binding properties of the parent antibody molecule.

[0074] As used herein, the term "monoclonal antibody" refers to an antibody composition having a homogeneous antibody population. The term is not limited regarding the species or source of the antibody, nor is it intended to be limited by the manner in which it is made. The term encompasses whole immunoglobulins as well as fragments such as Fab, F(ab')2, Fv, and other fragments, as well as chimeric and humanized homogeneous antibody populations that exhibit immunological binding properties of the parent monoclonal antibody molecule.

Zinc finger nucleases

[0075] Described herein are zinc finger nucleases (ZFNs) that can be used for inactivation of a *GS* gene. ZFNs comprise a zinc finger protein (ZFP) and a nuclease (cleavage) domain.

A. Zinc finger proteins

[0076] Zinc finger binding domains can be engineered to bind to a sequence of choice. *See*, for example, Beerli *et al.* (2002) *Nature Biotechnol.* **20**:135-141; Pabo *et al.* (2001) *Ann. Rev. Biochem.* **70**:313-340; Isalan *et al.* (2001) *Nature Biotechnol.*

19:656-660; Segal *et al.* (2001) *Curr. Opin. Biotechnol.* 12:632-637; Choo *et al.* (2000) *Curr. Opin. Struct. Biol.* 10:411-416. An engineered zinc finger binding domain can have a novel binding specificity, compared to a naturally-occurring zinc finger protein. Engineering methods include, but are not limited to, rational design and various types of selection. Rational design includes, for example, using databases comprising triplet (or quadruplet) nucleotide sequences and individual zinc finger amino acid sequences, in which each triplet or quadruplet nucleotide sequence is associated with one or more amino acid sequences of zinc fingers which bind the particular triplet or quadruplet sequence. See, for example, co-owned U.S. Patents 6,453,242 and 6,534,261, incorporated by reference herein in their entireties.

[0077] Exemplary selection methods, including phage display and two-hybrid systems, are disclosed in US Patents 5,789,538; 5,925,523; 6,007,988; 6,013,453; 6,410,248; 6,140,466; 6,200,759; and 6,242,568; as well as WO 98/37186; WO 98/53057; WO 00/27878; WO 01/88197 and GB 2,338,237. In addition, enhancement of binding specificity for zinc finger binding domains has been described, for example, in co-owned WO 02/077227.

[0078] Selection of target sites; ZFPs and methods for design and construction of fusion proteins (and polynucleotides encoding same) are known to those of skill in the art and described in detail in U.S. Patent Application Publication Nos. 20050064474 and 20060188987, incorporated by reference in their entireties herein.

[0079] In addition, as disclosed in these and other references, zinc finger domains and/or multi-fingered zinc finger proteins may be linked together using any suitable linker sequences, including for example, linkers of 5 or more amino acids in length. See, also, U.S. Patent Nos. 6,479,626; 6,903,185; and 7,153,949 for exemplary linker sequences 6 or more amino acids in length. The proteins described herein may include any combination of suitable linkers between the individual zinc fingers of the protein. Examples of additional linker structures are found in U.S. Provisional Application No. 61/130,099, filed May 28, 2008 and entitled Compositions For Linking DNA-Binding Domains And Cleavage Domains.

[0080] Table 1 describes a number of zinc finger binding domains that have been engineered to bind to nucleotide sequences in the *GS* gene. See, also, Fig. 1 and Fig. 3. Each row describes a separate zinc finger DNA-binding domain. The DNA target sequence for each domain is shown in the first column and the second through fifth columns show the amino acid sequence of the recognition region (amino acids -1

through +6, with respect to the start of the helix) of each of the zinc fingers (F1 through F4, F5 or F6) in the protein. Nucleotides shown in uppercase denote triplets that are directly targeted by a zinc finger and nucleotides shown in lower case denotes bases that are not directly targeted by a zinc finger (for example due to longer linkers between fingers which can result in "skipping" a base). Also provided in the first column is an identification number for the proteins.

Table 1: Zinc finger nucleases targeted to *GS*

ZFN name Target sequence	F1	F2	F3	F4	F5	F6
ZFN 9075 gaATGGTGCAGGCTgc (SEQ ID NO:1)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSDTLSN (SEQ ID NO:4)	RKDVRIT (SEQ ID NO:5)	N/A	N/A
ZFN 9372 gtTCCCAGGAATGGG CTTGGgg (SEQ ID NO:6)	RSDHLST (SEQ ID NO:7)	QSSDLRR (SEQ ID NO:8)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)
ZFN 8361 ctGGGTTGATGGTActg gagaaggactg (SEQ ID NO:13)	QSGALAR (SEQ ID NO:14)	RSDALTQ (SEQ ID NO:15)	RSDSLSA (SEQ ID NO:16)	RSAHLSR (SEQ ID NO:17)	N/A	N/A
ZFN 8365 taTACATGGCTTGGact ttctcaccctg (SEQ ID NO:18)	RSDHLST (SEQ ID NO:7)	QSSDLRR (SEQ ID NO:8)	RSDSLSV (SEQ ID NO:19)	DNANRTK (SEQ ID NO:20)	N/A	N/A
ZFN 9076 gaATGGTGCAGGCTgc cataccaacttt (SEQ ID NO:21)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSSALTR (SEQ ID NO:22)	RSDALTQ (SEQ ID NO:15)	N/A	N/A
ZFN 9179 ggAATGGTgCAGGCTg ccataccaactt (SEQ ID NO:23)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	QSSHLTR (SEQ ID NO:24)	TSSNRKT (SEQ ID NO:25)	N/A	N/A
ZFN 7858 gaATGGTGCAGGCTgc (SEQ ID NO:1)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSDSLLR (SEQ ID NO:26)	RSDALTQ (SEQ ID NO:15)	N/A	N/A
ZFN 7889 gtTCCCAGGAATGGgc (SEQ ID NO:27)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)	N/A	N/A
ZFN 9373 gtTCCCAGGAATGGgC TTGGGgtcaaag (SEQ ID NO:28)	RSDHLSQ (SEQ ID NO:9)	RNADRIT (SEQ ID NO:29)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)

[0081] As described below, in certain embodiments, a four-, five-, or six-finger binding domain as shown in Table 1 is fused to a cleavage half-domain, such as, for example, the cleavage domain of a Type IIs restriction endonuclease such as *Fok*I. One or more pairs of such zinc finger/nuclease half-domain fusions are used for

targeted cleavage, as disclosed, for example, in U.S. Patent Publication Nos. 20050064474 and 20070218528.

[0082] For targeted cleavage, the near edges of the binding sites can separated by 5 or more nucleotide pairs, and each of the fusion proteins can bind to an opposite strand of the DNA target. All pairwise combinations of the proteins shown in Table 1 can be used for targeted cleavage of a *GS* gene. Following the present disclosure, ZFNs can be targeted to any sequence in a *GS* gene.

B. Cleavage Domains

[0083] The ZFNs also comprise a nuclease (cleavage domain, cleavage half-domain). The cleavage domain portion of the fusion proteins disclosed herein can be obtained from any endonuclease or exonuclease. Exemplary endonucleases from which a cleavage domain can be derived include, but are not limited to, restriction endonucleases and homing endonucleases. *See*, for example, 2002-2003 Catalogue, New England Biolabs, Beverly, MA; and Belfort *et al.* (1997) *Nucleic Acids Res.* **25**:3379-3388. Additional enzymes which cleave DNA are known (*e.g.*, S1 Nuclease; mung bean nuclease; pancreatic DNase I; micrococcal nuclease; yeast HO endonuclease; *see* also Linn *et al.* (eds.) *Nucleases*, Cold Spring Harbor Laboratory Press,1993). One or more of these enzymes (or functional fragments thereof) can be used as a source of cleavage domains and cleavage half-domains.

[0084] Similarly, a cleavage half-domain can be derived from any nuclease or portion thereof, as set forth above, that requires dimerization for cleavage activity. In general, two fusion proteins are required for cleavage if the fusion proteins comprise cleavage half-domains. Alternatively, a single protein comprising two cleavage half-domains can be used. The two cleavage half-domains can be derived from the same endonuclease (or functional fragments thereof), or each cleavage half-domain can be derived from a different endonuclease (or functional fragments thereof). In addition, the target sites for the two fusion proteins are preferably disposed, with respect to each other, such that binding of the two fusion proteins to their respective target sites places the cleavage half-domains in a spatial orientation to each other that allows the cleavage half-domains to form a functional cleavage domain, *e.g.*, by dimerizing. Thus, in certain embodiments, the near edges of the target sites are separated by 5-8 nucleotides or by 15-18 nucleotides. However any integral number of nucleotides or

nucleotide pairs can intervene between two target sites (*e.g.*, from 2 to 50 nucleotide pairs or more). In general, the site of cleavage lies between the target sites.

[0085] Restriction endonucleases (restriction enzymes) are present in many species and are capable of sequence-specific binding to DNA (at a recognition site), and cleaving DNA at or near the site of binding. Certain restriction enzymes (*e.g.*, Type IIS) cleave DNA at sites removed from the recognition site and have separable binding and cleavage domains. For example, the Type IIS enzyme *Fok* I catalyzes double-stranded cleavage of DNA, at 9 nucleotides from its recognition site on one strand and 13 nucleotides from its recognition site on the other. See, for example, US Patents 5,356,802; 5,436,150 and 5,487;994; as well as Li *et al.* (1992) *Proc. Natl. Acad. Sci. USA* **89**:4275-4279; Li *et al.* (1993) *Proc. Natl. Acad. Sci. USA* **90**:2764-2768; Kim *et al.* (1994a) *Proc. Natl. Acad. Sci. USA* **91**:883-887; Kim *et al.* (1994b) *J. Biol. Chem.* **269**:31,978-31,982. Thus, in one embodiment, fusion proteins comprise the cleavage domain (or cleavage half-domain) from at least one Type IIS restriction enzyme and one or more zinc finger binding domains, which may or may not be engineered.

[0086] An exemplary Type IIS restriction enzyme, whose cleavage domain is separable from the binding domain, is *Fok* I. This particular enzyme is active as a dimer. Bitinaite *et al.* (1998) *Proc. Natl. Acad. Sci. USA* **95:** 10,570-10,575. Accordingly, for the purposes of the present disclosure, the portion of the *Fok* I enzyme used in the disclosed fusion proteins is considered a cleavage half-domain. Thus, for targeted double-stranded cleavage and/or targeted replacement of cellular sequences using zinc finger-*Fok* I fusions, two fusion proteins, each comprising a *Fok*I cleavage half-domain, can be used to reconstitute a catalytically active cleavage domain. Alternatively, a single polypeptide molecule containing a zinc finger binding domain and two *Fok* I cleavage half-domains can also be used. Parameters for targeted cleavage and targeted sequence alteration using zinc finger-*Fok* I fusions are provided elsewhere in this disclosure.

[0087] A cleavage domain or cleavage half-domain can be any portion of a protein that retains cleavage activity, or that retains the ability to multimerize (*e.g.*, dimerize) to form a functional cleavage domain.

[0088] Exemplary Type IIS restriction enzymes are described in International Publication WO 07/014275, incorporated herein in its entirety. Additional restriction enzymes also contain separable binding and cleavage domains, and these are

contemplated by the present disclosure. See, for example, Roberts *et al.* (2003) *Nucleic Acids Res.* **31**:418-420.

[0089] In certain embodiments, the cleavage domain comprises one or more engineered cleavage half-domain (also referred to as dimerization domain mutants) that minimize or prevent homodimerization, as described, for example, in U.S. Patent Publication Nos. 20050064474; 20060188987 and 20080131962, the disclosures of all of which are incorporated by reference in their entireties herein. Amino acid residues at positions 446, 447, 479, 483, 484, 486, 487, 490, 491, 496, 498, 499, 500, 531, 534, 537, and 538 of *Fok* I are all targets for influencing dimerization of the *Fok* I cleavage half-domains.

[0090] Exemplary engineered cleavage half-domains of *Fok* I that form obligate heterodimers include a pair in which a first cleavage half-domain includes mutations at amino acid residues at positions 490 and 538 of *Fok* I and a second cleavage half-domain includes mutations at amino acid residues 486 and 499.

[0091] Thus, in one embodiment, a mutation at 490 replaces Glu (E) with Lys (K); the mutation at 538 replaces Iso (I) with Lys (K); the mutation at 486 replaced Gln (Q) with Glu (E); and the mutation at position 499 replaces Iso (I) with Lys (K). Specifically, the engineered cleavage half-domains described herein were prepared by mutating positions 490 (E→K) and 538 (I→K) in one cleavage half-domain to produce an engineered cleavage half-domain designated "E490K:I538K" and by mutating positions 486 (Q→E) and 499 (I→L) in another cleavage half-domain to produce an engineered cleavage half-domain designated "Q486E:I499L". As described in the examples a pair of ZFNs in which one ZFN comprises the "E490K:I538K" cleavage domain and other comprises "Q486E:I499L" cleavage domain is also referred to as a "EL/KK" ZFN pair. The engineered cleavage half-domains described herein are obligate heterodimer mutants in which aberrant cleavage is minimized or abolished when one or more pairs of nucleases containing these cleavage half-domains are used for cleavage. *See, e.g.,* U.S. Patent Publication No. 20080131962, the disclosure of which is incorporated by reference in its entirety for all purposes.

[0092] Engineered cleavage half-domains described herein can be prepared using any suitable method, for example, by site-directed mutagenesis of wild-type cleavage half-domains (*Fok* I) as described in U.S. Patent Publication Nos. 20050064474 (Example 5) and 20070134796 (Example 38).

C. Additional Methods for Targeted Cleavage in *GS*

[0093] Any nuclease having a target site in a *GS* gene can be used in the methods disclosed herein. For example, homing endonucleases and meganucleases have very long recognition sequences, some of which are likely to be present, on a statistical basis, once in a human-sized genome. Any such nuclease having a unique target site in a *GS* gene can be used instead of, or in addition to, a zinc finger nuclease, for targeted cleavage in a *GS* gene.

[0094] Exemplary homing endonucleases include I-*Sce*I, I-*Ceu*I, PI-*Psp*I, PI-*Sce*, I-*Sce*IV, I-*Csm*I, I-*Pan*I, I-*Sce*II, I-*Ppo*I, I-*Sce*III, I-*Cre*I, I-*Tev*I, I-*Tev*II and I-*Tev*III. Their recognition sequences are known. *See* also U.S. Patent No. 5,420,032; U.S. Patent No. 6,833,252; Belfort *et al.* (1997) *Nucleic Acids Res.* **25**:3379–3388; Dujon *et al.* (1989) *Gene* **82**:115–118; Perler *et al.* (1994) Nucleic Acids Res. 22, 1125–1127; Jasin (1996) *Trends Genet.* **12**:224–228; Gimble *et al.* (1996) *J. Mol. Biol.* **263**:163–180; Argast *et al.* (1998) *J. Mol. Biol.* **280**:345–353 and the New England Biolabs catalogue.

[0095] Although the cleavage specificity of most homing endonucleases is not absolute with respect to their recognition sites, the sites are of sufficient length that a single cleavage event per mammalian-sized genome can be obtained by expressing a homing endonuclease in a cell containing a single copy of its recognition site. It has also been reported that the specificity of homing endonucleases and meganucleases can be engineered to bind non-natural target sites. *See*, for example, Chevalier *et al.* (2002) *Molec. Cell* **10**:895-905; Epinat *et al.* (2003) *Nucleic Acids Res.* **31**:2952-2962; Ashworth *et al.* (2006) *Nature* **441**:656-659; Paques *et al.* (2007) *Current Gene Therapy* **7**:49-66. Thus, engineered homing endonucleases and/or meganucelases which are designed to specifically bind a desired target locus, such as *GS*, may also be used.

Delivery

[0096] The ZFNs described herein may be delivered to a target cell by any suitable means. Suitable cells include but not limited to eukaryotic and prokaryotic cells and/or cell lines. Non-limiting examples of such cells or cell lines include COS, CHO (*e.g.*, CHO-S, CHO-K1, CHO-DG44, CHO-DUXB11, CHO-DUKX, CHOK1SV), VERO, MDCK, WI38, V79, B14AF28-G3, BHK, HaK, NS0, SP2/0-

Ag14, HeLa, HEK293 (*e.g.*, HEK293-F, HEK293-H, HEK293-T), and perC6 cells as well as insect cells such as *Spodoptera fugiperda* (Sf), or fungal cells such as *Saccharomyces*, *Pichia* and *Schizosaccharomyces*.

[0097] Methods of delivering proteins comprising zinc fingers are described, for example, in U.S. Patent Nos. 6,453,242; 6,503,717; 6,534,261; 6,599,692; 6,607,882; 6,689,558; 6,824,978; 6,933,113; 6,979,539; 7,013,219; and 7,163,824, the disclosures of all of which are incorporated by reference herein in their entireties.

[0098] ZFNs as described herein may also be delivered using vectors containing sequences encoding one or more of the ZFNs. Any vector systems may be used including, but not limited to, plasmid vectors, retroviral vectors, lentiviral vectors, adenovirus vectors, poxvirus vectors; herpesvirus vectors and adeno-associated virus vectors, etc. *See, also,* U.S. Patent Nos. 6,534,261; 6,607,882; 6,824,978; 6,933,113; 6,979,539; 7,013,219; and 7,163,824, incorporated by reference herein in their entireties. Furthermore, it will be apparent that any of these vectors may comprise one or more ZFN encoding sequences. Thus, when one or more pairs of ZFNs are introduced into the cell, the ZFNs may be carried on the same vector or on different vectors. When multiple vectors are used, each vector may comprise a sequence encoding one or multiple ZFNs.

[0099] Conventional viral and non-viral based gene transfer methods can be used to introduce nucleic acids encoding engineered ZFPs in cells (*e.g.*, mammalian cells) and target tissues. Such methods can also be used to administer nucleic acids encoding ZFPs to cells *in vitro*. In certain embodiments, nucleic acids encoding ZFPs are administered for *in vivo* or *ex vivo* gene therapy uses. Non-viral vector delivery systems include DNA plasmids, naked nucleic acid, and nucleic acid complexed with a delivery vehicle such as a liposome or poloxamer. Viral vector delivery systems include DNA and RNA viruses, which have either episomal or integrated genomes after delivery to the cell. For a review of gene therapy procedures, see Anderson, *Science* 256:808-813 (1992); Nabel & Felgner, *TIBTECH* 11:211-217 (1993); Mitani & Caskey, *TIBTECH* 11:162-166 (1993); Dillon, *TIBTECH* 11:167-175 (1993); Miller, *Nature* 357:455-460 (1992); Van Brunt, *Biotechnology* 6(10):1149-1154 (1988); Vigne, *Restorative Neurology and Neuroscience* 8:35-36 (1995); Kremer & Perricaudet, *British Medical Bulletin* 51(1):31-44 (1995); Haddada *et al.*, in *Current Topics in Microbiology and Immunology* Doerfler and Böhm (eds.) (1995); and Yu *et al., Gene Therapy* 1:13-26 (1994).

[0100] Methods of non-viral delivery of nucleic acids encoding engineered ZFPs include electroporation, lipofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA. Sonoporation using, *e.g.*, the Sonitron 2000 system (Rich-Mar) can also be used for delivery of nucleic acids.

[0101] Additional exemplary nucleic acid delivery systems include those provided by Amaxa Biosystems (Cologne, Germany), Maxcyte, Inc. (Rockville, Maryland) and BTX Molecular Delivery Systems (Holliston, MA) and Copernicus Therapeutics Inc., (see for example U.S. Patent No. 6,008,336).

[0102] Lipofection is described in *e.g.*, US 5,049,386, US 4,946,787; and US 4,897,355) and lipofection reagents are sold commercially (*e.g.*, Transfectam™ and Lipofectin™). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Felgner, WO 91/17424, WO 91/16024. Delivery can be to cells (*ex vivo* administration) or target tissues (*in vivo* administration).

[0103] The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (*see, e.g.*, Crystal, *Science* 270:404-410 (1995); Blaese *et al., Cancer Gene Ther.* 2:291-297 (1995); Behr *et al., Bioconjugate Chem.* 5:382-389 (1994); Remy *et al., Bioconjugate Chem.* 5:647-654 (1994); Gao *et al., Gene Therapy* 2:710-722 (1995); Ahmad *et al., Cancer Res.* 52:4817-4820 (1992); U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

[0104] The use of RNA or DNA viral based systems for the delivery of nucleic acids encoding engineered ZFPs take advantage of highly evolved processes for targeting a virus to specific cells in the body and trafficking the viral payload to the nucleus. Viral vectors can be administered directly to patients (*in vivo*) or they can be used to treat cells *in vitro* and the modified cells are administered to patients (*ex vivo*). Conventional viral based systems for the delivery of ZFPs include, but are not limited to, retroviral, lentivirus, adenoviral, adeno-associated, vaccinia and herpes simplex virus vectors for gene transfer. Integration in the host genome is possible with the retrovirus, lentivirus, and adeno-associated virus gene transfer methods, often resulting in long term expression of the inserted transgene. Additionally, high

transduction efficiencies have been observed in many different cell types and target tissues.

[0105] The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors that are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system depends on the target tissue. Retroviral vectors are comprised of *cis*-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum *cis*-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immunodeficiency virus (SIV), human immunodeficiency virus (HIV), and combinations thereof (*see, e.g.,* Buchscher *et al., J. Virol.* 66:2731-2739 (1992); Johann *et al., J. Virol.* 66:1635-1640 (1992); Sommerfelt *et al., Virol.* 176:58-59 (1990); Wilson *et al., J. Virol.* 63:2374-2378 (1989); Miller *et al., J. Virol.* 65:2220-2224 (1991); PCT/US94/05700).

[0106] In applications in which transient expression of a ZFP fusion protein is preferred, adenoviral based systems can be used. Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division. With such vectors, high titer and high levels of expression have been obtained. This vector can be produced in large quantities in a relatively simple system. Adeno-associated virus ("AAV") vectors are also used to transduce cells with target nucleic acids, e.g., in the *in vitro* production of nucleic acids and peptides, and for *in vivo* and *ex vivo* gene therapy procedures (*see, e.g.,* West *et al., Virology* 160:38-47 (1987); U.S. Patent No. 4,797,368; WO 93/24641; Kotin, *Human Gene Therapy* 5:793-801 (1994); Muzyczka, *J. Clin. Invest.* 94:1351 (1994). Construction of recombinant AAV vectors are described in a number of publications, including U.S. Pat. No. 5,173,414; Tratschin *et al., Mol. Cell. Biol.* 5:3251-3260 (1985); Tratschin, *et al., Mol. Cell. Biol.* 4:2072-2081 (1984); Hermonat & Muzyczka, *PNAS* 81:6466-6470 (1984); and Samulski *et al., J. Virol.* 63:03822-3828 (1989).

[0107] At least six viral vector approaches are currently available for gene transfer in clinical trials, which utilize approaches that involve complementation of

defective vectors by genes inserted into helper cell lines to generate the transducing agent.

[0108] pLASN and MFG-S are examples of retroviral vectors that have been used in clinical trials (Dunbar *et al., Blood* 85:3048-305 (1995); Kohn *et al., Nat. Med.* 1:1017-102 (1995); Malech *et al., PNAS* 94:22 12133-12138 (1997)). PA317/pLASN was the first therapeutic vector used in a gene therapy trial. (Blaese *et al., Science* 270:475-480 (1995)). Transduction efficiencies of 50% or greater have been observed for MFG-S packaged vectors. (Ellem *et al., Immunol Immunother.* 44(1):10-20 (1997); Dranoff *et al., Hum. Gene Ther.* 1:111-2 (1997).

[0109] Recombinant adeno-associated virus vectors (rAAV) are a promising alternative gene delivery systems based on the defective and nonpathogenic parvovirus adeno-associated type 2 virus. All vectors are derived from a plasmid that retains only the AAV 145 bp inverted terminal repeats flanking the transgene expression cassette. Efficient gene transfer and stable transgene delivery due to integration into the genomes of the transduced cell are key features for this vector system. (Wagner *et al., Lancet* 351:9117 1702-3 (1998), Kearns *et al., Gene Ther.* 9:748-55 (1996)).

[0110] Replication-deficient recombinant adenoviral vectors (Ad) can be produced at high titer and readily infect a number of different cell types. Most adenovirus vectors are engineered such that a transgene replaces the Ad E1a, E1b, and/or E3 genes; subsequently the replication defective vector is propagated in human 293 cells that supply deleted gene function in *trans*. Ad vectors can transduce multiple types of tissues *in vivo*, including nondividing, differentiated cells such as those found in liver, kidney and muscle. Conventional Ad vectors have a large carrying capacity. An example of the use of an Ad vector in a clinical trial involved polynucleotide therapy for antitumor immunization with intramuscular injection (Sterman *et al., Hum. Gene Ther.* 7:1083-9 (1998)). Additional examples of the use of adenovirus vectors for gene transfer in clinical trials include Rosenecker *et al., Infection* 24:1 5-10 (1996); Sterman *et al., Hum. Gene Ther.* 9:7 1083-1089 (1998); Welsh *et al., Hum. Gene Ther.* 2:205-18 (1995); Alvarez *et al., Hum. Gene Ther.* 5:597-613 (1997); Topf *et al., Gene Ther.* 5:507-513 (1998); Sterman *et al., Hum. Gene Ther.* 7:1083-1089 (1998).

[0111] Packaging cells are used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, and ψ2 cells or PA317 cells, which package retrovirus. Viral vectors used in gene therapy are

usually generated by a producer cell line that packages a nucleic acid vector into a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host (if applicable), other viral sequences being replaced by an expression cassette encoding the protein to be expressed. The missing viral functions are supplied in *trans* by the packaging cell line. For example, AAV vectors used in gene therapy typically only possess inverted terminal repeat (ITR) sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes, namely *rep* and *cap*, but lacking ITR sequences. The cell line is also infected with adenovirus as a helper. The helper virus promotes replication of the AAV vector and expression of AAV genes from the helper plasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, e.g., heat treatment to which adenovirus is more sensitive than AAV.

[0112] In many gene therapy applications, it is desirable that the gene therapy vector be delivered with a high degree of specificity to a particular tissue type. Accordingly, a viral vector can be modified to have specificity for a given cell type by expressing a ligand as a fusion protein with a viral coat protein on the outer surface of the virus. The ligand is chosen to have affinity for a receptor known to be present on the cell type of interest. For example, Han *et al.*, *Proc. Natl. Acad. Sci. USA* 92:9747-9751 (1995), reported that Moloney murine leukemia virus can be modified to express human heregulin fused to gp70, and the recombinant virus infects certain human breast cancer cells expressing human epidermal growth factor receptor. This principle can be extended to other virus-target cell pairs, in which the target cell expresses a receptor and the virus expresses a fusion protein comprising a ligand for the cell-surface receptor. For example, filamentous phage can be engineered to display antibody fragments (*e.g.*, FAB or Fv) having specific binding affinity for virtually any chosen cellular receptor. Although the above description applies primarily to viral vectors, the same principles can be applied to nonviral vectors. Such vectors can be engineered to contain specific uptake sequences which favor uptake by specific target cells.

[0113] Gene therapy vectors can be delivered *in vivo* by administration to an individual patient, typically by systemic administration (*e.g.*, intravenous, intraperitoneal, intramuscular, subdermal, or intracranial infusion) or topical

application, as described below. Alternatively, vectors can be delivered to cells *ex vivo*, such as cells explanted from an individual patient (*e.g.*, lymphocytes, bone marrow aspirates, tissue biopsy) or universal donor hematopoietic stem cells, followed by reimplantation of the cells into a patient, usually after selection for cells which have incorporated the vector.

[0114] *Ex vivo* cell transfection for diagnostics, research, or for gene therapy (*e.g.*, via re-infusion of the transfected cells into the host organism) is well known to those of skill in the art. In a preferred embodiment, cells are isolated from the subject organism, transfected with a ZFP nucleic acid (gene or cDNA), and re-infused back into the subject organism (*e.g.*, patient). Various cell types suitable for *ex vivo* transfection are well known to those of skill in the art (*see, e.g.*, Freshney *et al., Culture of Animal Cells, A Manual of Basic Technique* (3rd ed. 1994)) and the references cited therein for a discussion of how to isolate and culture cells from patients).

[0115] In one embodiment, stem cells are used in *ex vivo* procedures for cell transfection and gene therapy. The advantage to using stem cells is that they can be differentiated into other cell types *in vitro*, or can be introduced into a mammal (such as the donor of the cells) where they will engraft in the bone marrow. Methods for differentiating CD34+ cells *in vitro* into clinically important immune cell types using cytokines such a GM-CSF, IFN-γ and TNF-α are known (*see* Inaba *et al., J. Exp. Med.* 176:1693-1702 (1992)).

[0116] Stem cells are isolated for transduction and differentiation using known methods. For example, stem cells are isolated from bone marrow cells by panning the bone marrow cells with antibodies which bind unwanted cells, such as CD4+ and CD8+ (T cells), CD45+ (panB cells), GR-1 (granulocytes), and Iad (differentiated antigen presenting cells) (*see* Inaba *et al., J. Exp. Med.* 176:1693-1702 (1992)).

[0117] Vectors (*e.g.*, retroviruses, adenoviruses, liposomes, etc.) containing therapeutic ZFP nucleic acids can also be administered directly to an organism for transduction of cells *in vivo*. Alternatively, naked DNA can be administered. Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells including, but not limited to, injection, infusion, topical application and electroporation. Suitable methods of administering such nucleic acids are available and well known to those of skill in the art, and,

although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route.

[0118] Methods for introduction of DNA into hematopoietic stem cells are disclosed, for example, in U.S. Patent No. 5,928,638. Vectors useful for introduction of transgenes into hematopoietic stem cells, *e.g.*, $CD34^+$ cells, include adenovirus Type 35.

[0119] Vectors suitable for introduction of transgenes into immune cells (*e.g.*, T-cells) include non-integrating lentivirus vectors. *See*, for example, Ory *et al.* (1996) *Proc. Natl. Acad. Sci. USA* **93**:11382-11388; Dull *et al.* (1998) *J. Virol.* **72**:8463-8471; Zuffery *et al.* (1998) *J. Virol.* **72**:9873-9880; Follenzi *et al.* (2000) *Nature Genetics* **25**:217-222.

[0120] Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions available, as described below (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed., 1989).

[0121] As noted above, the disclosed methods and compositions can be used in any type of cell including, but not limited to, prokaryotic cells, fungal cells, Archaeal cells, plant cells, insect cells, animal cells, vertebrate cells, mammalian cells and human cells. Suitable cell lines for protein expression are known to those of skill in the art and include, but are not limited to COS, CHO (*e.g.*, CHO-S, CHO-K1, CHO-DG44, CHO-DUXB11), VERO, MDCK, WI38, V79, B14AF28-G3, BHK, HaK, NS0, SP2/0-Ag14, HeLa, HEK293 (*e.g.*, HEK293-F, HEK293-H, HEK293-T), perC6, insect cells such as *Spodoptera fugiperda* (Sf), and fungal cells such as *Saccharomyces*, *Pichia* and *Schizosaccharomyces*. Progeny, variants and derivatives of these cell lines can also be used.

Applications

[0122] The disclosed methods and compositions can be used for inactivation of a *GS* genomic sequence. As noted above, inactivation includes partial or complete repression of *GS* gene expression in a cell. Inactivation of a *GS* gene can be achieved, for example, by a single cleavage event, by cleavage followed by non-homologous end joining, by cleavage at two sites followed by joining so as to delete the sequence

between the two cleavage sites, by targeted recombination of a missense or nonsense codon into the coding region, by targeted recombination of an irrelevant sequence (*i.e.*, a "stuffer" sequence) into the gene or its regulatory region, so as to disrupt the gene or regulatory region, or by targeting recombination of a splice acceptor sequence into an intron to cause mis-splicing of the transcript.

[0123] Thus, the methods and compositions described herein allow for the generation of *GS*-deficient cell lines for use in recombinant protein production, for example α1-antitrypsin and/or monoclonal antibody production. Additional genes, such as *FUT8* may also be inactivated as cells in which *FUT8* is inactivated produce antibodies that exhibit greater effector function, particularly in the induction of ADCC.

EXAMPLES

Example 1: Design and Construction of ZFNs

A. Glutamine Synthetase (*GS*) ZFNs

[0124] As the full sequence of the CHO genome is not available, the CHO *GS* gene was cloned and sequenced to generate the target DNA sequences for ZFN designs. The complete CHO *GS* sequence is shown in FIG. 13, which also designates introns and exons.

[0125] ZFN target sites in exon 6 of the CHO *GS* gene were selected because this region encodes amino acids critical for the catalytic function of the *GS* protein based on available crystal structures (see, *e.g.*, Almassy *et al.* (1986) *Nature* 323:304-309; Gill *et al.* (2002) *Biochem.* 41:9863-9872; Liaw *et al.* (1994) *Biochem.* 33:675-681) and, as such, ZFN-mediated mutation of this site was expected to result in loss of functional *GS* activity. Partial sequence for CHO *GS* exon 6 is shown below. Capital letters indicate exon sequence; small letters indicate intron sequence; and ZFN target sites 9372/9075 (Table 1, Fig. 1A and Fig. 4A) are underlined:

5'-
atggcactattctgttcctttcctcccctctgaagacttggcacatggggactttggttaacaagggtgatgacttaaaagtgg
ttcagggtagaggtaagtagaacaagctaggagcttgagttggcctgaacagttagttggccttattctaaaggtcaacatgt
tctttctagTGGGAATTCCAAATAGGACCCTGTGAAGGAATCCGCATGGGAGAT
CATCTCTGGGTGGCCCGTTTCATCTTGCATCGAGTATGTGAAGACTTTGGG
GTAATAGCAACCTTTGACCCCAAGCCCATTCCTGGGAACTGGAATGGTGC
AGGCTGCCATACCAACTTTAGCACCAAGGCCATGCGGGAGGAGAATGGTC
TGAAgtaagtagcttcctctggagccatctttattctcatggggtggaagggctttgtgttagggttgggaaagttggactt
ctcacaaactacatgccatgctcttcgtgtttgtcataagcctatcgttttgtacccgttggagaagtgacagtactctaggaat
agaattacagctgtgatatgggaaagttgtcacgtaggttcaagcatttaaaggtctttagtaagaactaaatacacatacaag

caagtgggtgacttaattcttactgatgggaagaggccagtgatgggggtcttcccatccaaaagataattggtattacatgtt
gaggactggtctgaagcacttgagacataggtcacaaggcagacacagcctgcatcaagtatttattggtttcttatggaact
catgcctgctcctgcccttgaaggacag-3' (SEQ ID NO:30)

[0126] Binding sites for ZFN9372 and ZFN9075 are shown in Figure 4B, while Figure 4C depicts the target and finger designs of these ZFNs.

[0127] In addition, ZFNs targeted to sites in exon 2 were also designed. Partial sequence for CHO exon 2 is shown below. Capital letters indicate exon sequence; small letters indicate intron sequence; and ZFN target sites 8365/8361 (Table 1, and Fig. 1A) are underlined.

5'-
ggctggcagatctccgagttcgaggctgacctggtctgaatagcaaggaaattaaggggtgaggcgtatgtctgttaaagc
aagaataaaaggcaaaggaacactccacagtcaattattcaagtcttgatggcagtaatgtagttgtattgggtggattaaga
cattctaataatgaatttttttgtctttttgttccctcttttcagctttctcaaaattaatggatattaaaaatccccttagccgggcgtt
ggtggcacacacctttaatcccagcactcgggaggcagaggcaggcagatctctgtgagttcgaggccagcctggtctcc
agattgagtgccaggataggctccaaagctacacagaaaccgtgtctcgaaaaacaaaacaaaaaaataaaaaaaaaaat
cccttaactagcccaacctacaagggatgatctttgtctaactatgaactttaaacctcttgaaagcagagtgaataatgcactt
caataatgttgacttccaaaggagagaccaccacaccgttccctgtgcctcttacgcaattcctgcaggggacccccttcag
agtagatgttaatgaaatgacttttgtctctcCAGAGCACCTTCCACCATGGCCACCTCAGCAA
GTTCCCACTTGAACAAAAACATCAAGCAAATGTACTTGTGCCTGCCCCAG
GGTGAGAAAGTCCAAGCCATGTATATCTGGGTTGATGGTACTGGAGAAGG
ACTGCGCTGCAAAACCCGCACCCTGGACTGTGAGCCCAAGTGTGTAGAAG
gtgagcatgggcaggagcaggacatgtgcctggaagtgggcaagcagcctgagatttgaccttccttctgttttgtttgcaa
agtctttcaaaagcaggtctcttcaggcctcagtcagtcacccgtaagctgccgagtagtctggaggcatagaaaacaatgg
aggcctttatttagatggaatcttgtgtgtgctggtacactgaagaaaaatattgggtcatatttgtagggggtgggaggttgg
agtattgctaacctagccaaccccaggaacctagtttgaaagacctgtaactagaatatgctatcaagtttatagagcagtggt
tctcaacctttcaaatgctttacacttgaatacaactcctcatgttctggtgattacccccatcccaaccattgctaacttcttaact
gaaatttcactactgctacgaatcataatgtatctgtgtttttggatggtcttaggtgacccctgtgaaagggttgtgagaccatc
ctcaaaggggttgtgacctacaggttgagacccttttgagtgctgtgtttattagtatttatacagtggaattctgggtgcaaag
cacatgctccaaagtagtttctctgggactggccatttgttttcgatggggatcttttaaaacttgcaaaggaaccaaaaaaaa
aaaaatgcagaaaaaaggaggtgggggagtgcacgcctttaatcccagtacttgggaggcagaggcaggcggatctctg
tgagtttgagaccagcctggtctacaagagctagttccaggacagcctccaaagccacagagaaaccctgtctcaaaacaa
acaaacaaacaaaaaaattaaaaaaaaaaaaaactttcaaaggagacctgttttatttagttgtggcctttgttttggtaggaa
gggcagctagtttaggatgagtttttattattctaagatgttgccgtttg-3' (SEQ ID NO:31)

[0128] ZFNs targeting the CHO *GS* sequence (for example as shown in Table 1), were assembled into mammalian expression vectors as described in U.S. Patent Application No. 12/218,035 and tested by transient transfection into CHO cells.

B. DHFR ZFNs

[0129] ZFNs targeted to *DHFR* were designed and produced as described in U.S. Patent Publication No2008/0015164. For experiments described herein, *DHFR*

ZFN pairs designated 9461/7844 and 9476/9477 (individual ZFNs shown in Table 2) were used.

Table 2: Exemplary zinc finger nucleases targeted to *DHFR*

ZFN name Target sequence	F1	F2	F3	F4
ZFN 7844 ccAATGCTCAGGTAct (SEQ ID NO:32)	QSGALAR (SEQ ID NO:14)	RSDNLRE (SEQ ID NO:3)	QSSDLSR (SEQ ID NO:2)	TSSNRKT (SEQ ID NO:25)
ZFN 9461 agGGAAGGTCTCCGtt (SEQ ID NO:33)	RSDTLSE (SEQ ID NO:34)	NNRDRTK (SEQ ID NO:35)	RSDHLSA (SEQ ID NO:36)	QSGHLSR (SEQ ID NO:37)
ZFN 9476 caTGGGTAGCCGCTga (SEQ ID NO:38)	QSSDLSR (SEQ ID NO:2)	DRSDLSR (SEQ ID NO:39)	QSGALAR (SEQ ID NO:14)	RSDHLTT (SEQ ID NO:40)
ZFN 9477 agTCCGGGGGGTGGtg (SEQ ID NO:41)	RSDHLST (SEQ ID NO:7)	RSAHLSR (SEQ ID NO:17)	RSDHLSR (SEQ ID NO:42)	DSSDRKK (SEQ ID NO:43)

C. FUT8 ZFNs

[0130] ZFNs targeted to *FUT8* were designed and produced as described in U.S. Serial No. 12/218,035. For experiments described herein, *FUT8* ZFNs designated 12176 and 12172 and shown in Table 3 were used.

Table 3: Exemplary zinc finger nucleases targeted to *FUT8*

ZFN name Target sequence	F1	F2	F3	F4	F5	F6
ZFN 12172 AAGGAGGCAAAGA CAAAG (SEQ ID NO:44)	RSDNLSV (SEQ ID NO:45)	QNATRIN (SEQ ID NO:46)	RSDHLSQ (SEQ ID NO:9)	QSATRTK (SEQ ID NO:47)	RSDNLSR (SEQ ID NO:48)	RNDNRKT (SEQ ID NO:49)
ZFN 12176 AAGAAGGGTCATC AG (SEQ ID NO:50)	RSDNLRE (SEQ ID NO:3)	NNTQLIE (SEQ ID NO:51)	TSSILSR (SEQ ID NO:52)	RSDNLSA (SEQ ID NO:53)	RKDTRIT (SEQ ID NO:54)	N/A
ZFN 12170 taAAGGAGGCAAAG ACAAAGt (SEQ ID NO:56)	RSDNLSV (SEQ ID NO:45)	QNATRIN (SEQ ID NO:46)	RSDNLST (SEQ ID NO:57)	QSATRTK (SEQ ID NO:47)	RSDNLSR (SEQ ID NO:48)	RNDNRKT (SEQ ID NO:49)

[0131] Plasmids comprising sequences encoding the above ZFNs were constructed essentially as described in Urnov *et al.* (2005) *Nature* 435(7042):646-651 via fusion to wild-type *Fok*I cleavage domains or obligate heterodimer *Fok*I cleavage domains described in U.S. Patent Publication No. 2008/0131962 and Miller *et al.* (2007) *Nature Biotech.* 25:778-785.

Example 2: *GS*-ZFN Modification of Endogenous *GS*

[0132] To determine whether *GS*-targeted ZFNs modified the endogenous *GS* locus as expected, CEL-1 mismatch assays were performed essentially as per the manufacturer's instructions (Trangenomic SURVEYOR™). Briefly, the appropriate ZFN plasmid pairs were transfected into CHO K-I cells growing adherently in serum-containing medium or CHO-S cells growing in suspension in serum-free chemically defined medium.

[0133] CHO K-I cells were obtained from the American Type Culture Collection and grown as recommended in F-12 medium (Invitrogen) supplemented with 10% qualified fetal calf serum (FCS, Hyclone). CHO-S cells were purchased from Invitrogen (Carlsbad, CA) and were grown and maintained as suspension cultures in chemically-defined protein-free and animal component-free CD-CHO medium supplemented with 8mM L-glutamine and HT supplement as necessary (100μM sodium hypoxanthine and 16μM thymidine) (all from Invitrogen, Carlsbad, CA) in a humidity-controlled shaker incubator (ATR, inc., Laurel, Maryland) at 125 rpm with 5% CO_2 at 37°C.

[0134] Adherent cells were disassociated from plasticware using TrypLE Select™ protease (Invitrogen). For transfection, one million CHO K-I cells were mixed with 1μg each zinc finger nuclease and 100μL Amaxa Solution T. Cells were transfected in an Amaxa Nucleofector II™ using program U-23 and recovered into 1.4mL warm F-12 medium + 10% FCS.

[0135] Genomic DNA was extracted from the ZFN-treated cells using the Qiagen DNeasy™ kit (Qiagen, Inc.), the target locus amplified by PCR using the appropriate primers for the region of the *GS* locus targeted by the ZFNs, the PCR products were subjected to a melting/annealing step resulting in the formation of distorted duplex DNA through random re-annealing of mutant and wild-type DNA. CEL-I enzyme (Surveyor™ mutation detection kit, Transgenomic, Inc.) was then added to specifically cleave the DNA duplexes at the sites of mismatches. The CEL-I cleaved samples were resolved on a 10% TBE polyacrylamide gel, stained with ethidium bromide, and the DNA bands were quantified using densitometry. The frequency of NHEJ was calculated as described essentially in Miller *et al.* (2007), *supra*.

[0136] As shown in FIG. 1A and 1B, *GS* ZFNs modified the endogenous *GS* locus. In particular, the ZFN pair including ZFN 9372 and ZFN 9075 resulted in modification of 26% (with wild-type cleavage domains) and 24% (with engineered obligate heterodimer forming cleavage domains) of chromosomes in CHO-KI cells and 25% of chromosomes in CHO-S cells (FIG. 1B). Similarly, ZFN pair including ZFN 8361 and 8365 (targeted to exon 2) resulted in modification of 7% of chromosomes.

[0137] In agreement with the results of the Surveyor™ Nuclease Assay (Fig. 1A), direct sequencing confirmed 34% (91/266) of the alleles harbored mutations at the ZFN target site typical of NHEJ-mediated DNA repair (see, *e.g.*, Weterings *et al.* (2004) *DNA repair (Amst)* 3:1425-1435). Importantly, 81% of the sequenced mutations resulted in a reading frame shift (Fig. 5).

Example 3: Generation of *GS*-negative cell lines

[0138] To generate CHO cell lines lacking *GS*, single-cell derived lines were isolated by limiting dilution from both the CHO-K1 and CHO-S transfected pools described in Example 2. Sequencing of the ZFN target region revealed that 17 of 54 CHO-S derived cell lines (31%) had at least one disrupted *GS* gene, 8 of 54 (15%) were homozygous for a mutant allele, 2 were compound heterozygous, and the remaining 7 were heterozygous (with one wild-type allele). For CHO-K1-derived cell lines, sequencing analysis identified 18 of 50 (36%) had at least one disrupted *GS* allele, with 5 (10%) homozygous for a given mutation. See, also, Fig. 1C showing the genotypes of the homozygous mutant lines.

[0139] All homozygous mutant lines harbor *GS* mutations that result in a shift in the open reading frame or an in-frame deletion of critical amino acids (*e.g.* lines B4, KA2, and KA4), and were therefore expected to produce no active *GS* enzyme. As predicted, none of the homozygous mutant cell lines grew in the absence of exogenous L-glutamine, in contrast to wild-type CHO cells (Fig. 1C).

[0140] Western blot analysis using an anti-GS monoclonal antibody (BD Biosciences) confirmed that all cell lines with frame shifts or large deletions expressed no detectable GS protein (for example, clone B3, Fig. 1D). Lines harboring small in-frame deletions (B4 and KA2) did express GS proteins that were detectable by Western blot but, consistent with the elimination of amino acids critical for GS catalytic activity, did not support the growth of the cells in the absence of L-glutamine

(Fig. 1C). Growth of cell line B3 was also shown to be dependent on glutamine supplementation (see Figure 6).

[0141] To further validate their *GS*$^{-/-}$ phenotype, three of the CHO-K1-derived clones were adapted for growth in suspension in a chemically-defined serum-free medium over a 3 month period. Growth and viability of the cells was then monitored intensively for a further 4 weeks (Fig. 1E).

[0142] The ZFN-generated *GS*$^{-/-}$ lines grew normally in serum-free suspension cultures in the presence of L-glutamine (24-27 hour doubling time similar to the industry standard CHOK1SV grown under similar conditions). Subsequent removal of L-glutamine resulted in immediate cessation of cell growth and a rapid loss of viability (see arrows in Fig. 1E). Transient transfection of a human IgG antibody expression construct confirmed all three *GS*$^{-/-}$ lines supported comparable transgene expression levels to those obtained with the CHOK1SV line.

[0143] Taken together, these data confirm the successful generation of genetically and phenotypically validated *GS* knockout CHO cell lines.

Example 4: Generation of *GS-DHFR* double knockout cell lines

[0144] To create a double-knockout cell line, ZFNs targeted to the *DHFR* gene were used on the background of the CHO-S *GS*$^{-/-}$ cell line B3. ZFN-mediated knockout of *DHFR* using the strategy described for *GS* above is described in U.S. Patent Publication No. 2008/0015164.

[0145] In this Example, two pairs of ZFNs targeting two distinct regions of the *DHFR* gene were delivered simultaneously with the goal of eliminating the intervening genomic fragment through the repair of the cleaved chromosomal ends via NHEJ. Deletion of a ZFN-specified intergenic sequence was expected to result in a larger and better defined mutation that eliminates the potential for a smaller in-frame mutation to recover protein expression *e.g.* Fig.1D (Left Panel labeled "B4").

[0146] In addition to the previously described ZFN pair 9461/7844 that target exon 1 of the CHO *DHFR* gene (U.S. Patent Publication No. 2008/0015164), a second ZFN pair was generated which targets a site ~240 bp away in the intron immediately following exon 1 (Fig. 2A and Fig. 7A).

[0147] Transient transfection was performed as described in Example 3 and transfection with either the ZFN9461/ZFN7844 pair targeting exon 1, or the ZFN9476/ZFN9477 (See Figure 7B and 7C) pair targeting the intronic site alone

resulted in allelic mutation frequencies at the endogenous *DHFR* locus of 15% and 18%, respectively in the *GS*$^{-/-}$ cell line B3 (Fig.2B). Co-transfection of both ZFN pairs into the *GS*$^{-/-}$ cell line B3 resulted in the appearance of a shorter PCR amplification product consistent with the expected ~240 bp deletion of the sequence between the ZFN binding sites (Fig. 2C). The frequency of this deletion event was estimated at ~8% of all alleles and was observed only when both pairs of ZFNs were introduced into the cells (Fig. 2C).

[0148] Cloning and sequencing of the presumptive deletion PCR fragment revealed the expected excision of the sequence between the ZFN target sites (Fig. 8). The observed minor variations in the sequence at the junction of the rejoined chromosomal ends are consistent with the expected small insertions and deletions characteristic of the NHEJ repair process.

[0149] Single-cell derived lines were isolated from the ZFN-treated pool in Fig. 2C Lane 7 by limiting dilution. PCR-amplification and sequencing revealed 9% (18 of 200) of the cell lines possessed the expected ~240-bp deletion. Four of these cell lines (2% of all lines screened, 22% of all lines containing the deletion) were found to harbor a biallelic mutation in the *DHFR* gene (Fig. 2D). Cell line 2B12.8 is homozygous for a 244-bp deletion of the intervening region between the exon1 and intron 1 ZFN cleavage sites. The remainder of the lines had just one allele with the 240-bp deletion while the other presented classical smaller NHEJ driven mutations at the exonic and/or intronic ZFN target sites. For example, cell line 1F1.6 contained a ~240-bp deletion in one allele (consistent with a dual ZFN cleavage and deletion event), but the other allele contained a 4-bp deletion in exon 1 resulting in a frame shift.

[0150] Cell lines 1F1.6 and 2B12.8 had genotypes consistent with complete gene knockout and thus were selected for further characterization. Western blot analysis revealed no full-length DHFR or GS protein in either of these single-cell derived lines (Fig. 2E). Furthermore, neither line was stainable with fluorescein-labeled methotrexate which binds to the active site of the DHFR protein, in contrast to the parental *GS*$^{-/-}$ line B3 or wild-type CHO cells. Most importantly, growth of the 1F1.6 and 2B12.8 cell lines was dependent upon the addition of exogenous hypoxanthine and thymidine (HT) and L-glutamine to the culture medium. In contrast, the parental *GS*$^{-/-}$ line B3 required L-glutamine but not HT, while the *DHFR*-

negative CHO cell line DG44 (GS^{WT}) required only HT but not L-glutamine and the wild-type CHO-S required neither supplement for growth (Fig. 2F).

[0151] The dependence on exogenous HT and L-glutamine confirms the functional loss of both GS and DHFR activity in cell lines 1F1.6 and 2B12.8.

[0152] Thus, taken together these data demonstrate the successful generation of genetically and phenotypically validated *GS*$^{-/-}$*/DHFR*$^{-/-}$ double knockout CHO cell lines.

Example 5: Generation of *GS-DHFR-FUT8* triple knockout cell lines

[0153] A triple knockout of *GS*, *DHFR* and *FUT8* was also generated using the *GS*$^{-/-}$*DHFR*$^{-/-}$CHO cell line IF1.6. As described in U.S. Serial No. 12/218.035, aberrant glycosylation resulting from the use of non-human cells *e.g.* CHO in the expression of protein therapeutics can alter the potency, half-life and even the immunogenicity of the protein product. Thus methods for humanizing the glycosylation of proteins in non-human expression systems are highly desirable. The CHO *FUT8* gene is such a target encoding an α1,6-fucosyltransferase that catalyzes the transfer of fucose from GDP-fucose to the core GlcNAc of N-linked oligosaccharides. Point mutations of amino acid residues in the highly conserved Fut motif II encoded in exon 10 result in the inactivation of the FUT8 enzyme.

[0154] Thus, we cloned and sequenced the region spanning *FUT8* exon 10 and flanking introns from CHO-K1 genome, and designed ZFNs to target exon 10 (U.S. Patent Application No. 12/218,035; Fig. 3A and Fig. 9). Transient delivery of ZFN12172/ZFN12176 into cell line 1F1.6 resulted in modification of 7.5% of the *FUT8* alleles (Fig. 3B), and single-cell derived lines were obtained by limiting dilution from this pool.

[0155] *C. griseus* FUT8 was not detectable using commercially available antibodies, so we further assayed α1,6-fucosyltransferase activity using a FACS-based fluorescent Lens culinaris agglutin (F-LCA) binding assay, as described in Yamane-Ohnuki *et al.* (2004) *Biotechnol Bioeng* 87:614-622. LCA selectively binds to cells that present core fucosylated oligosaccharides on their cell surface. Cells lacking core fucosylation due to a complete loss of FUT8 activity do not bind to LCA. Screening of the ZFN-generated cell lines for their ability to bind F-LCA showed no F-LCA binding in 2% of the line (4 of 200) indicating a complete absence of FUT8 enzymatic activity (Fig. 3C).

[0156] Sequencing of PCR amplicons of genomic DNA confirmed that both clones possess biallelic compound heterozygous mutations at the *FUT8* target locus (Fig. 3D), which encode a shift in reading frame in this functionally critical region. Thus the genotype of both cell lines is consistent with the lack of F-LCA binding observed (Fig. 3C) and demonstrates the ZFN-driven genetic and functional knockout of *FUT8* in cell lines 35F2 and 14C1. Both of the *FUT8*$^{-/-}$ clones also stably maintained their *GS*$^{-/-}$ and *DHFR*$^{-/-}$ genotypes and phenotypes, throughout the multiple rounds of ZFN transfection and single-cell cloning. Indeed, the generation of a triple knockout cell line was well-tolerated as measured by growth rate studies in serum-containing medium supplemented with HT and L-glutamine which gave mean population doubling times of 21.8 and 21.6 hours for clones 35F2 and 14C1, respectively. Taken together these data demonstrate the successful generation of single, double and triple gene knockouts in CHO cells using engineered ZFNs.

Example 6: Generation of *GR-CCR5-PPP1R12C* triple knockout cell lines

[0157] A triple knockout cell line was also generated by concurrent administration of inactivating ZFNs. In particular, K562 cell lines in which *CCR5*, glucocorticoid receptor (*GR*) and *PPP1R12C* (also known as the adeno-associated virus integration site or "*AAVS1*") were inactivated were also generated by simultaneous application of ZFNs targeted to these loci.

[0158] ZFNs targeted to *CCR5, GR* and *AAVS1* were generated as described in U.S. Patent Publication Nos. 20080159996 (*CCR5*); 20080188000 (*GR*) and U.S. Application No. 12/150,103 (*PPP1R12C/AAVS1*). Schematics showing the ZFN binding sites in portions of these genes are shown in FIG. 10A. The *CCR5* gene contains 3 exons, the coding sequence (CDS) is located within exon 3, and the *CCR5* ZFN target sequence is located in the CDS as indicated. The GR gene contains 9 exons, and the GR ZFN target sequence is located in Exon3. The *AAVS1* ZFN target sequence is located in the middle of the *AAVS1* region.

[0159] Plasmids encoding pairs of ZFNs linked to either the wild-type, ZFN-*Fok* I(wt) or an obligate heterodimer EL/KK variant, ZFN-*Fok* I(EL/KK) of the catalytic domain of *Fok* I were transiently co-transfected into K562 cells, and the modification frequency at *CCR5* (left), *GR* (middle), *AAVS1* (right) loci was determined by the Surveyor™ Nuclease Assay 10 days after transfection,

respectively. As shown in FIG. 10B, the target genes were subject to NHEJ following ZFN treatment.

[0160] Single-cell derived cell lines of these triple-knockout cells were also evaluated by PCR and sequencing of genomic DNA described above. In particular, the lane 8 samples in FIG. 10B, treated with *CCR5* ZFN-*Fok* I(EL/KK) + *GR* ZFN-*Fok* I(EL/KK) + *AAVS1* ZFN-*Fok* I(EL/KK) were examined. The PCR primers were designed to specifically amplify unmodified wild-type (wt) sequences but not sequences with deletions.

[0161] Results are shown below in the following Table 4. All clones containing wt sequences (wt or heterozygous) had visible PCR bands at predicted sizes, whereas knock-out (KO) clones had no visible PCR bands. Among 144 single cell clones screened by *CCR5* PCR, 5 clones contain *CCR5* KO. Nine clones were identified as *GR* KO by *GR* PCR. Two of the clones contain both *CCR5* KO and *GR* KO. All 12 clones, which are KO clones based on either *CCR5* PCR or *GR* PCR, were screened by *AAVS1* PCR. Among the 144 clones screened, one *CCR5* single KO clone was identified, seven *GR* single KO clones were identified, whereas no attempt was tried to identify *AAVS1* single KO clones. One *CCR5/GR* dual KO clone was identified. Two *CCR5/AAVS1* dual KO clones were identified. No *GR/AAVS1* dual KO clone was identified among the 144 clones, though it is very likely that a *GR/AAVS1* dual KO clone might have been identified if more clones were screened. One *CCR5/GR/AAVS1* triple KO clone (B17) was identified.

Table 4: Evaluation of single cell clones of putative triple knockout cells

	CCR5	*GR*	*AAVS1*
Total Clones screened	144	144	12*
Total KO clones	5	9	3
Single KO clone	1	7	N/A
***CCR5/GR* dual KO clone**	1	1	N/A
***CCR5/AAVS1* dual KO clone**	2	N/A	2
***GR/AAVS1* dual KO clone**	N/A	0	0
***CCR5/GR/AAVS1* triple KO clone**	1	1	1

* 12 clones that were identified as *CCR5* or *GR* KO clones

[0162] Exemplary sequencing data of cells from triple knockout clone B17 is shown in FIG. 10C. The ZFN target sequences are underlined. '-' indicate deletions, bold letters indicate insertions.

Example 7: *GS*-targeted ZFNs are active in multiple species and cell types

[0163] *GS*-specific ZFNs as described herein (designed to human CHO cell *GS* sequence) were also evaluated in mouse cells. As shown in FIG. 11A and 11B, ZFN target sites in *GS* were well conserved across species.

[0164] ZFN pairs 8361/8365 (targeted to exon 2) and 9075/9372 (targeted to exon 6) were evaluated for their ability to cleave *GS* in human K562 and mouse Neuro2a cells as described in Example 2 above.

[0165] As shown in FIG. 12, ZFNs designed to CHO *GS* sequences were functional in other human cell types and in other species.

[0166] *GS*-specific ZFNs (ZFN 9075 and ZFN 9372) were also tested in human embryonic kidney HEK293 cells as describe in Example 2. As shown in Figure 14A, the CEL-I enzyme (Surveyor™ mutation detection kit, Transgenomic, Inc.) indicated an NHEJ occurance rate of 21%.

[0167] GS knockout cell lines were made in a HEK293 cell background using the same approach as in CHO cells using the same *GS* ZFNs (see Example 3). Two knockout clones, clone g17 and g52, were further characterized. Clone g52 is homozygous for an 11 bp-deletion at the *GS* locus. Clone 17 has a 169 bp-deletion at one *GS* allele, and a 4 bp-insertion at the other allele. As shown in Figure 14B, neither clone expresses GS protein as determined by western blotting. Importantly, both clones required exogenously supplemented L-glutamine for growth (see Figure 14C).

[0168] Thus, ZFNs can be employed to rapidly knock out multiple genes in a single mammalian cell line by sequential or simultaneous inactivation of the target genes. The results presented here are not dependent on the cell line or the choice of ZFNs. The frequency of ZFN-driven biallelic knockout events at each individual gene (>1%), combined with the lack of dependence on selection markers results in the ability to rapidly "stack" such genetic lesions and generate complex multi-gene knockout cell lines previously considered impractical. The high efficiency of gene knock out following only transient ZFN expression and the ability to stack multiple

traits in eukaryotic cells makes it feasible to perform custom genetic engineering of essentially any cell type.

[0169] All patents, patent applications and publications mentioned herein are hereby incorporated by reference in their entirety.

[0170] Although disclosure has been provided in some detail by way of illustration and example for the purposes of clarity of understanding, it will be apparent to those skilled in the art that various changes and modifications can be practiced without departing from the spirit or scope of the disclosure. Accordingly, the foregoing descriptions and examples should not be construed as limiting.

CLAIMS

What is claimed is:

1. A zinc finger DNA-binding domain comprising four, five or six zinc finger recognition regions as shown in a single row of the following table:

ZFN name Target sequence	F1	F2	F3	F4	F5	F6
ZFN 9075 gaATGGTGCAGGCTgc (SEQ ID NO:1)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSDTLSN (SEQ ID NO:4)	RKDVRIT (SEQ ID NO:5)	N/A	N/A
ZFN 9372 gtTCCCAGGAATGGG CTTGGgg (SEQ ID NO:6)	RSDHLST (SEQ ID NO:7)	QSSDLRR (SEQ ID NO:8)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)
ZFN 8361 ctGGGTTGATGGTActg gagaaggactg (SEQ ID NO:13)	QSGALAR (SEQ ID NO:14)	RSDALTQ (SEQ ID NO:15)	RSDSLSA (SEQ ID NO:16)	RSAHLSR (SEQ ID NO:17)	N/A	N/A
ZFN 8365 taTACATGGCTTGGact ttctcaccctg (SEQ ID NO:18)	RSDHLST (SEQ ID NO:7)	QSSDLRR (SEQ ID NO:8)	RSDSLSV (SEQ ID NO:19)	DNANRTK (SEQ ID NO:20)	N/A	N/A
ZFN 9076 gaATGGTGCAGGCTgc cataccaacttt (SEQ ID NO:21)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSSALTR (SEQ ID NO:22)	RSDALTQ (SEQ ID NO:15)	N/A	N/A
ZFN 9179 ggAATGGTgCAGGCTg ccataccaactt (SEQ ID NO:23)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	QSSHLTR (SEQ ID NO:24)	TSSNRKT (SEQ ID NO:25)	N/A	N/A
ZFN 7858 gaATGGTGCAGGCTgc (SEQ ID NO:1)	QSSDLSR (SEQ ID NO:2)	RSDNLRE (SEQ ID NO:3)	RSDSLLR (SEQ ID NO:26)	RSDALTQ (SEQ ID NO:15)	N/A	N/A
ZFN 7889 gtTCCCAGGAATGGgc (SEQ ID NO:27)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)	N/A	N/A
ZFN 9373 gtTCCCAGGAATGGgC TTGGGgtcaaag (SEQ ID NO:28)	RSDHLSQ (SEQ ID NO:9)	RNADRIT (SEQ ID NO:29)	RSDHLSQ (SEQ ID NO:9)	QSANRTT (SEQ ID NO:10)	RSDNLSQ (SEQ ID NO:11)	ASNDRKK (SEQ ID NO:12)

2. A fusion protein comprising a zinc finger DNA-binding domain according to claim 1 and at least one cleavage domain or at least one cleavage half-domain.

3. The fusion protein of claim 2, wherein the cleavage half-domain is a wild-type or engineered *FokI* cleavage half-domain.

4. A polynucleotide encoding the zinc finger DNA-binding domain or fusion protein according to any of claims 1 to 3.

5. An isolated cell comprising a protein according to any of claims 1 to 3 or a polynucleotide according to claim 4.

6. A cell line in which glutamine synthetase (GS) is partially or fully inactivated by a fusion protein according to claim 2 or 3 or a polynucleotide encoding the fusion protein.

7. A method of inactivating an endogenous cellular *GS* gene in a cell, the method comprising:

(a) introducing, into a cell, a first nucleic acid encoding a first polypeptide, wherein the first polypeptide comprises:

(i) a zinc finger DNA-binding domain according to claim 2 or 3 that binds to a first target site in an endogenous *GS* gene; and

(ii) a cleavage domain; such that the polypeptide is expressed in the cell, whereby the polypeptide binds to the target site and cleaves the *GS* gene.

8. The method of claim 7, further comprising introducing a nucleic acid encoding a second polypeptide, wherein the second polypeptide comprises:

(i) a zinc finger DNA-binding domain that is engineered to bind to a second target site in the *GS* gene; and

(ii) a cleavage domain; such that the second polypeptide is expressed in the cell, whereby the first and second polypeptides bind to their respective target sites and cleave the *GS* gene.

9. The method of claim 8, wherein the first and second polypeptides are encoded by the same nucleic acid or by different nucleic acids.

10. The method of any of claims 7 to 9, further comprising inactivating a *DHFR* gene in the cell.

11. The method of any of claims 7 to 10, further comprising inactivating a *FUT8* gene in the cell.

12. A method of producing a recombinant protein of interest in a host cell, the method comprising the steps of:

(a) providing a host cell comprising an endogenous *GS* gene;

(b) inactivating the endogenous *GS* gene of the host cell by the method of any of claims 7 to 10; and

(c) introducing an expression vector comprising a transgene, the transgene comprising a sequence encoding a protein of interest into the host cell, thereby producing the recombinant protein.

13. The method of claim 12, wherein the protein of interest comprises α1-antitrypsin or a monoclonal antibody.

14. A cell line in which a *GS* gene is partially or fully inactivated, wherein the cell line is produced by

(a) inactivating the *GS* gene in a cell according to the method of any of claims 7 to 10; and

(b) culturing the cell under conditions suitable for generating a cell line in which the *GS* gene is partially or fully inactivated.

15. The cell line of claim 14, wherein the cell is a mammalian cell selected from the group consisting of a COS cell, a CHO cell, a VERO cell, a MDCK cell, a WI38 cell, a V79 cell, a B14AF28-G3 cell, a BHK cell, a HaK cell, a NS0 cell, a SP2/0-Ag14 cell, a HeLa cell, an HEK293 cell, and a perC6 cell.

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cgcccctctg ccaattgtga ccccctttgca gtgacagaag ccatcgtccg cacatgcctt 6840

ctcaatgaga ctggcgacca gcccttccaa tacaaaaact aa 6882

<210> 56
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic zinc finger target sequence: ZFN 12170

<400> 56
taaaggaggc aaagacaaag t 21

<210> 57
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically synthesized zinc finger binding domain

<400> 57

Arg Ser Asp Asn Leu Ser Thr
1 5

<210> 58
<211> 102
<212> DNA
<213> Cricetulus longicaudatus

<400> 58
gcaacctttg accccaagcc cattcctggg aactggaatg gtgcaggctg ccataccaac 60

tttagcacca aggccatgcg ggaggagaat ggtctgaagt aa 102

<210> 59
<211> 32
<212> PRT
<213> Cricetulus longicaudatus

<400> 59

Ala Thr Phe Asp Pro Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly
1 5 10 15

Cys Leu Thr Asn Phe Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu
20 25 30

<210> 60
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 60
gcaacctttg accccaagcc cattcctggg cttgctgcca taccaacttt agcaccaagg 60

ccatgcggga ggagaatggt ctgaagtaa 89

<210> 61
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 61
gcaacctttg accccaagcc ggtgcaggct gccataccaa ctttagcacc aaggccatgc 60

gggaggagaa tggtctgaag taa 83

<210> 62
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 62
gcaacctttg accccaagcc cattccaact ttagcaccaa ggccatgcgg gaggagaatg 60

gtctgaagta a 71

<210> 63
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 63
gcaacctttg accccaagct gccataccaa ctttagcacc aaggccatgc gggaggagaa 60

tggtctgaag taa 73

<210> 64
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 64
gcaacctttg accccaagcc cattcctgta cccgttggag aa 42

<210> 65
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 65
gcaacctttg accccaagcc cattcctggg ctttgtgtta gggttgggaa agttg 55

<210> 66
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 66
gcaaccagga atggtgcagg ctgccatacc aactttagca ccaaggccat gcgggaggag 60

aatggtctga agtaa 75

<210> 67
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-S clone

<400> 67
gcaacctttg accccaagcc cattccagga atggtgcagg ctgccatacc aactttagca 60

ccaaggccat gcgggaggag aatggtctga agtaa 95

<210> 68
<211> 102
<212> DNA
<213> Cricetulus longicaudatus

<400> 68
gcaacctttg accccaagcc cattcctggg aactggaatg gtgcaggctg ccataccaac 60

tttagcacca aggccatgcg ggaggagaat ggtctgaagt aa 102

<210> 69
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-K1 clone

<400> 69
gcaacctttg accccaagcc cattcctggg aatggtgcag gctgccatac caactttagc 60

accaaggcca tgcgggagga gaatggtctg aagtaa 96

<210> 70
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-K1 clone

<400> 70
gcaacctttg accccaaggc catgcgggag gagaatggtc tgaagtaa 48

<210> 71
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-K1 clone

<400> 71
gcaacctttg accccaagcc cattccagaa tggtgcaggc tgccatacca actttagcac 60

caaggccatg cgggaggaga atggtctgaa gtaa 94

<210> 72
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-K1 clone

<400> 72
gcaacctttg accccaagcc cattcctggg aactggctgg aatggtgcag gctgccatac 60

caactttagc accaaggcca tgcgggagga gaatggtctg aagtaa 106

<210> 73
<211> 97
<212> DNA

<213> Artificial Sequence

<220>
<223> Chemically synthesized CHO-K1 clone

<400> 73
gcaacctttg accccaagcc cattcctggg aaatggtgca ggctgccata ccaactttag 60

caccaaggcc atgcgggagg agaatggtct gaagtaa 97

<210> 74
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 74
aacggagacc ttccctggcc aatgctcagg tactggctgc agcaccaccc cccggacttg 60

catgggtagc cgctgag 77

<210> 75
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 75
aacggagacc ttccctggct gggtagccgc tgag 34

<210> 76
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 76
aacggagacc ttccccaatg ctcaggtact ggctgcagca ccacccccg gacttgcatg 60

ggtagccgct gag 73

<210> 77
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 77
aacggagacc ttccctggct ccccgctgag 30

<210> 78
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 78
aacggagacc ttccctggct gcatgggtag ccgctgag 38

<210> 79
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 79
aacggagacc ttccctggct ggccaatgct caggtactgg ctagcaccac cccccggact 60

tgcggtagcc gctgag 76

<210> 80
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 80
aacggagacc ttccctggca tgggtagccg ctgag 35

<210> 81
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in DHFR genotyping analysis

<400> 81
aacggagacc ttccctggcc aatgctcagg tactggctgc agcaccaccc cccggacttg 60

ccctgt 66

<210> 82
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in FUT8 gene analysis

<400> 82
aaaagagtgt atctggccac tgatgaccct tctttgttaa aggaggcaaa gacaaagtaa 60

gtt 63

<210> 83
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide used in FUT8 gene analysis

<400> 83

Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu Ala
1 5 10 15

Lys Thr

<210> 84
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in FUT8 gene analysis

<400> 84
aaaagagtgt atctggccac tgatgaccct tcttaaagga ggcaaagaca aagtaagtt 59

<210> 85
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in FUT8 gene analysis

<400> 85
aaaagagtgt atctggccac tgatgaccct tttaaaggag gcaaagacaa agtaagtt 58

<210> 86
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in FUT8 gene analysis

<400> 86
aaaagagtgt atctggccac tgatgaccct tctttggtta aaggaggcaa agacaaagta 60

agtt 64

<210> 87
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide used in FUT8 gene analysis

<400> 87
aaaagagtgt atctggccac tgatgaccct tctttgtttg ttaaaggagg caaagacaaa 60

gtaagtt 67

<210> 88
<211> 518
<212> DNA
<213> Cricetulus longicaudatus

<400> 88
agggtgatga cttaaaagtg gttcagggta gaggtaagta gaacaagcta ggagcttgag 60

ttggcctgaa cagttagttg gccttattct aaaggtcaac atgttctttc tagtgggaat 120

tccaaatagg accctgtgaa ggaatccgca tgggagatca tctctgggtg gcccgtttca 180

tcttgcatcg agtatgtgaa gactttgggg taatagcaac ctttgacccc aagcccattc 240

ctgggaactg gaatggtgca ggctgccata ccaactttag caccaaggcc atgcgggagg 300

agaatggtct gaagtaagta gcttcctctg gagccatctt tattctcatg gggtggaagg 360

gctttgtgtt agggttggga aagttggact tctcacaaac tacatgccat gctcttcgtg 420

tttgtcataa gcctatcgtt ttgtacccgt tggagaagtg acagtactct aggaatagaa 480

ttacagctgt gatatgggaa agttgtcacg taggttca 518

<210> 89
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN9075

<400> 89
ggtaatagca acctttgacc ccaagcccat tcctgggaac tggaatggtg caggctgcca 60

taccaacttt 70

<210> 90
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN9372

<400> 90
aaagttggta tggcagcctg caccattcca gttcccagga atgggcttgg ggtcaaaggt 60

tgctattacc 70

<210> 91
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 91
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggaatggtgc aggctgccat 60

accaacttta gcaccaaggc catgcgggag 90

<210> 92
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 92
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggtggtgcag gctgccatac 60

caactttagc accaaggcca tgcgggag 88

<210> 93
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 93
gtaatagcaa cctttgaccc caagcccatt cctgggatgg aatggtgcag gctgccatac 60

caactttagc accaaggcca tgcgggac 88

<210> 94
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 94
gtaatagcaa cctttgaccc caagcccatt cctgggaaca atggtgcagg ctgccatacc 60

aactttagca ccaaggccat gcgggag 87

<210> 95
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 95
gtaatagcaa cctttgaccc caagcccatt cctgggaata atggtgcagg ctgccatacc 60

aactttagca ccaaggccat gcgggag 87

<210> 96
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 96
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggggtgcagg ctgccatacc 60

aactttagca ccaaggccat gcgggac 87

<210> 97
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 97
gtaatagcaa cctttgaccc caagcccatt cctgggaact gggtgcaggc tgccatacca 60

actttagcac caaggccatg cgggag 86

<210> 98
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 98
gtaatagcaa cctttgaccc caagcccatt cctgctggaa tggtgcaggc tgccatacca 60

actttagcac caaggccatg cgggag 86

<210> 99
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 99
gtaatagcaa cctttgaccc caagcccatt cctgggaatt tggtgcaggc tgccatacca 60

actttagcac caaggccatg cgggag 86

<210> 100
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 100
gtaatagcaa cctttgaccc caagcccatt cctgggaaaa tggtgcaggc tgccatacca 60

actttagcac caaggccatg cgggag 86

<210> 101
<211> 85
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 101
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggtgcaggct gccataccaa 60

ctttagcacc aaggccatgc gggag 85

<210> 102
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 102
gtaatagcaa cctttgaccc caagcccatt cctgggaaat ggtgcaggct gccataccaa 60

ctttagcacc aaggccatgc gggag 85

<210> 103
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 103
gtaatagcaa cctttgaccc caagcccatt cctgggaatg gtgcaggctg ccataccaac 60

tttagcacca aggccatgcg ggag 84

<210> 104
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 104
gtaatagcaa cctttgaccc caagcccatt cctgggatgg tgcaggctgc cataccaact 60

ttagcaccaa ggccatgcgg gag 83

<210> 105
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 105
gtaatagcaa cctttgaccc caagcccatt cctggaatgg tgcaggctgc cataccaact 60

ttagcaccaa ggccatgcgg gag 83

<210> 106
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 106
gtaatagcaa cctttgaccc caagcccatt ctggaatggt gcaggctgcc ataccaactt 60

tagcaccaag gccatgcggg ag 82

<210> 107
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 107
gtaatagcaa cctttgaccc caagcccatt cctgggtggt gcaggctgcc ataccaactt 60

tagcaccaag gccatgcggg ag 82

<210> 108
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 108
gtaatagcaa cctttgaccc caagcccatt cctggtggtg caggctgcca taccaacttt 60

agcaccaagg ccatgcggga g 81

<210> 109
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 109
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggggctgcca taccaacttt 60

agcaccaagg ccatgcggga g 81

<210> 110
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus

from ZFN transfected cells

<400> 110
gtaatagcaa cctttgaccc caagcccatt cctgggaacc aggctgccat accaacttta 60

gcaccaaggc catgcgggag 80

<210> 111
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 111
gtaatagcaa cctttgaccc caagcccatt cctggtgcag gctgccatac caactttagc 60

accaaggcca tgcgggag 78

<210> 112
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 112
gtaatagcaa cctttgaccc caagcccaaa atggtgcagg ctgccatacc aactttagca 60

ccaaggccat gcgggag 77

<210> 113
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 113
gtaatagcaa cctttgaccc caagcccaat ggtgcaggct gccataccaa ctttagcacc 60

aaggccatgc gggag 75

<210> 114
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 114
gtaatagcaa cctttgaccc caagcccatt cctgggctgc cataccaact ttagcaccaa 60

ggccatgcgg gag 73

<210> 115
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 115
gtaatagcaa cctttgaccc ctggaatggt gcaggctgcc ataccaactt tagcaccaag 60

gccatgcggg ag 72

<210> 116
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 116
gtaatagcaa cctttgaccc caagcccatt aggctgccat accaacttta gcaccaaggc 60

catgcgggag 70

<210> 117
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 117
gtaatagcaa cctttgaccc caagcccgca ggctgccata ccaactttag caccaaggcc 60

atgcgggag 69

<210> 118
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 118
gtaatagcaa cctttgaccc caagcccatt cctggccata ccaactttag caccaaggcc 60

atgcgggag 69

<210> 119
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 119
gtaatagcaa cctttgaccc caagcccatt ccaactttag caccaaggcc atgcgggag 59

<210> 120
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 120
gtaatagcaa cctttgaccc caagcccatt cctgctttag caccaaggcc atgcgggag 59

<210> 121
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 121
gtaatagcaa cctttgaccc caagccatac caactttagc accaaggcca tgcgggag 58

<210> 122
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 122
gtaatagcaa cctttgaccc caagccaagg ccatgcggga g 41

<210> 123
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 123
gtaatagcaa cctttgaccc caagcccatt cctgggaacg tggaatggtg caggctgcca 60

taccaacttt agcaccaagg ccatgcggga 90

<210> 124
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 124
gtaatagcaa cctttgaccc caagcccatt cctgggaact gggaatggtg caggctgcca 60

taccaacttt agcaccaagg ccatgcggga 90

<210> 125
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 125
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggtaatggtg caggctgcca 60

taccaacttt agcaccaagg ccatgcggga 90

<210> 126
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 126
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggaaatggtg caggctgcca 60

taccaacttt agcaccaagg ccatgcggga 90

<210> 127
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 127
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggtggaatgg tgcaggctgc 60

cataccaact ttagcaccaa ggccatgcgg gag 93

<210> 128
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 128
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggctggaatg gtgcaggctg 60

ccataccaac tttagcacca aggccatgcg ggag 94

<210> 129
<211> 94

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 129
gtaatagcaa cctttgaccc caagcccatt cctgggaact ggactggaat ggtgcaggct 60

gccataccaa ctttagcacc aaggccatgc ggga 94

<210> 130
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 130
gtaatagcaa cctttgaccc caagcccatt cctgggaatg ggatgggaat ggtgcaggct 60

gccataccaa ctttagcacc aaggccatgc ggga 94

<210> 131
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 131
gtaatagcaa cctttgaccc caagcccatt cctgggcttt cactggtgag ccatggtgca 60

ggctgccata ccaactttag caccaaggcc atgc 94

<210> 132
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic GS locus from ZFN transfected cells

<400> 132
gtaatagcaa cctttgaccc caagcccatt cctgggaact gggggcccca taagccctgt 60

ctcatggtgc aggctgccat accaacttta gcac 94

<210> 133
<211> 572
<212> DNA
<213> Cricetulus longicaudatus

<400> 133
gggaagcagc gccgggcgac tgcaatttcg cgccaaactt gggggaagca cagcgtacag 60

gctgcctagg tgatcgctgc tgctgccatg gttcgaccgc tgaactgcat cgtcgccgtg 120

tcccagaata tgggcatcgg caagaacgga gaccttccct ggccaatgct caggtactgg 180

ctggattggg ttagggaaac cgaggcggtt cgctgaatcg ggtcgagcac ttggcggaga 240

cgcgcgggcc aactacttag ggacagtcat gaggggtagg cccgccggct gcagcccttg 300

cccatgcccg cggtgatccc catgctgtgc cagcctttgc ccagaggcgc tctagctggg 360

agcaaagtcc ggtcactggg cagcaccacc ccccggactt gcatgggtag ccgctgagat 420

ggagcctgag cacacgtgac agggtccctg ttaacgcagt gtttctctaa ctttcaggaa 480

cgaattcaag tacttccaaa gaatgaccac cacctcctca gtggaaggta atttggggtt 540

aagatgagga ttctagggtt tgtatgaagc aa 572

<210> 134
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN7844

<400> 134
gtcgccgtgt cccagaatat gggcatcggc aagaacggag accttccctg gccaatgctc 60

aggtactggc tggattgggt ta 82

<210> 135
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN9461

<400> 135
taacccaatc cagccagtac ctgagcattg gccagggaag gtctccgttc ttgccgatgc 60

ccatattctg ggacacggcg ac 82

<210> 136
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN9476

<400> 136
gcaaagtccg gtcactgggc agcaccaccc cccggacttg catgggtagc cgctgagatg 60

gagcctgagc acacgtgaca g 81

<210> 137
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN9477

<400> 137

ctgtcacgtg tgctcaggct ccatctgagc ggctacccat gcaagtccgg ggggtggtgc 60

tgcccagtga ccggactttg c 81

<210> 138
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 138
atcggcaaga acggagacct tccctggcca atgctcaggt actggctgga ttgggcactg 60

ggcagcacca ccccccggac ttgcatgggt agccgctgag atggagcctg agca 114

<210> 139
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 139
atcggcaaga acggagacct tccctggcct tgcatgggta gccgctgaga tggagcctga 60

gca 63

<210> 140
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 140
atcggcaaga acggagacct tccctggctt gcatgggtag ccgctgagat ggagcctgag 60

ca 62

<210> 141
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 141
atcggcaaga acggagacct tccctggctt gcatgggtag ccgctgagat ggagcctgag 60

ca 62

<210> 142
<211> 58
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 142
atcggcaaga acggagacct tccctggcat gggtagccgc tgagatggag cctgagca 58

<210> 143
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 143
atcggcaaga acggagacct tccctggcgg gtagccgctg agatggagcc tgagca 56

<210> 144
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 144
atcggcaaga acggagacct tcccttgcgg gtagccgctg agatggagcc tgagca 56

<210> 145
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 145
atcggcaaga acggagacct tccctggcgt agccgctgag atggagcctg agca 54

<210> 146
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 146
atcggcaaga acggagacct tccctgagcc gctgagatgg agcctgagca 50

<210> 147
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 147
atcggcaaga acggagacct tccccgctga gatggagcct gagca 45

<210> 148
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 148
atcggcaaga acggagacct tcttgcatgg gtagccgctg agatggagcc tgagca 56

<210> 149
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 149
atcggcaaga acggagacct tgcatgggta gccgctgaga tggagcctga gca 53

<210> 150
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from sequencing of genomic DHFR locus from ZFN transfected cells

<400> 150
atcggcaaga acggagacct tatggggcct gagca 35

<210> 151
<211> 484
<212> DNA
<213> Cricetulus longicaudatus

<400> 151
aacattcagc tatgttaaag tatttgtgaa gtgttttgaa atgattttat attttctaag 60

gtgagaataa atgagaaaat gttttaatat gtctccagtg cccccatgac tagggatact 120

aattgagtac cagtacatta tcagtgtgct ctccacttct ccccagagtc catgtcagac 180

gcactgacaa agtgggaaca gaagcagcct tccatcccat tgaggaatac atggtacacg 240

ttgaagaaca ttttcagctt ctcgaacgca gaatgaaagt ggataaaaaa agagtgtatc 300

tggccactga tgacccttct ttgttaaagg aggcaaagac aaagtaagtt agaccaacaa 360

gtggttctgt atgggattat ctcttagttg aagaaaatcc ttaattctgg gaacttgtgg 420

ttcttgttgc taactaatag gttccaaaat caaagactac atgtgcaaat attaatctaa 480

tcaa 484

<210> 152
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN12172

<400> 152
ataaaaaaag agtgtatctg gccactgatg acccttcttt gttaaaggag gcaaagacaa 60

agtaagtt 68

<210> 153
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing ZFN12176

<400> 153
aacttacttt gtctttgcct cctttaacaa agaagggtca tcagtggcca gatacactct 60

tttttttat 68

<210> 154
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic zinc finger target sequence: ZFN 12176

<400> 154
caaagaaggg tcatcagtg 19

<210> 155
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic zinc finger target sequence: ZFN 12172

<400> 155
taaaggaggc aaagacaaag ta 22

<210> 156
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 156
ctttggtttt gtgggcaaca tgctggtcat cctcatcctg ataaactgca aaaggctgaa 60

gagcatgact gacatctacc 80

<210> 157
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 157
ctttggtttt gtgggcaaca tgctggtcat cctcctgata aactgcaaaa ggctgaagag 60

catgactgac atctacc 77

<210> 158
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 158
ctttggtttt gtgggcaaca tgctggtcat cctcatcaaa aggctgaaga gcatgactga 60

catctacc 68

<210> 159
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 159
ctttggtttt gtgggcaaca tgctggtcat cctcatcctg atctgataaa ctgcaaaagg 60

ctgaagagca tgactgacat 80

<210> 160
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 160
gaccagatgt aagctctcct ccatccagct cctcaacagc aacaacagga ccacctccca 60

aactctgcct ggtgtgctct 80

<210> 161
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 161
gaccagatgt aagctctcct ccatccagct cctcaagcaa caacaggacc acctcccaaa 60

ctctgcctgg tgtgctct 78

<210> 162
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 162
gaccagatgt aagctctcct ccatccagct cctcaacagg accacctccc aaactctgcc 60

tggtgtgctc t 71

<210> 163
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 163
gaccagatgt aagctctcct ccatccagct cctcaggacc acctcccaaa ctctgcctgg 60

tgtgctct 68

<210> 164
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 164
ctgggtactt ttatctgtcc cctccacccc acagtggggc cactagggac aggattggtg 60

acagaaaagc cccatcctta 80

<210> 165
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence resulting from knockout clone analysis

<400> 165
ctgggtactt ttatctgtcc cctccacccc acagattggt gacagaaaag ccccatcctt 60

a 61

<210> 166
<211> 70
<212> DNA
<213> Cricetulus longicaudatus

<400> 166
tttgcagcgc agtccttctc cagtaccatc aacccagata tacatggctt ggactttctc 60

accctggggc 70

<210> 167
<211> 70
<212> DNA
<213> Homo sapiens

<400> 167
cttgcagcgc agtccttctc cagtaccatc gatccagata tacatggcct ggactttctc 60

accctgaggc 70

<210> 168
<211> 70
<212> DNA
<213> Mus musculus

<400> 168
cttgcagcgc agtccttctc cggtaccatc aacccagata tacatggctt ggactttctc 60

accctggggc 70

<210> 169
<211> 69
<212> DNA
<213> Rattus sp.

<400> 169
attgcagcat agtccttctc cagcaccatt gacctagata tacatggctt ggatttctca 60

ccctaagcc 69

<210> 170
<211> 70
<212> DNA
<213> Canine sp.

<400> 170
cttgcaacgt aatccttctc cagtcccgtc aatccaaata tacatagctt gcactttctc 60

gccctgaggc 70

<210> 171
<211> 70
<212> DNA
<213> Didelphis sp.

<400> 171
tttacagcgc agaccctcat cagtgccatc aatccagata tacatagcct ggactttgtt 60

gccttgaggc 70

<210> 172
<211> 70
<212> DNA
<213> Gallus sp.

<400> 172
tttgcagcgg aggtgctccc cagtcccgtc gatccagatg tacatggctt ggaccttctc 60

cccctgcggc 70

<210> 173
<211> 70
<212> DNA
<213> X. tropicalis

<400> 173
cttgcagcga agaccctccc cggtcccatc aacccagatg tacatagcct gcaccttatc 60

tccctgtggc 70

<210> 174
<211> 70
<212> DNA
<213> Tetraodon sp.

<400> 174
tttgcagcgt agtccttctc ctgttccatc aatccaaata tacatggcct gaactttatc 60

cccctgtggg 70

<210> 175
<211> 70
<212> DNA
<213> Cricetulus longicaudatus

<400> 175
gctaaagttg gtatggcagc ctgcaccatt ccagttccca ggaatgggct tggggtcaaa 60

ggttgctatt 70

<210> 176
<211> 70
<212> DNA
<213> Homo sapiens

<400> 176
gctgaagttg gtatggcagc ctgcaccatt ccagttccca ggaatgggct taggatcaaa 60

ggttgctatc 70

<210> 177
<211> 70
<212> DNA
<213> Mus musculus

<400> 177
gctgaagttg gtatggcagc ctgcaccatt ccagttccct ggaatgggct tggggtcaaa 60

ggttgctatc 70

<210> 178
<211> 70
<212> DNA
<213> Rattus sp.

<400> 178
gctaaaattg atttatcagc ctgcactatc accattctca agactcagtc ttggatcaaa 60

ggtcactatt 70

<210> 179
<211> 70

<212> DNA
<213> Canine sp.

<400> 179
gctgaagttg gtgtggcagc ctgcaccatt ccagtttccg ggaatgggct taggatcaaa 60

ggttgctatc 70

<210> 180
<211> 70
<212> DNA
<213> Didelphis sp.

<400> 180
actgaagtta gtgtggcaac cagctccatt ccagttccca gggattggct tgggatcaaa 60

tgatacaatc 70

<210> 181
<211> 70
<212> DNA
<213> Gallus sp.

<400> 181
gctgaagttg gtgtgacagc cagcaccgtt ccagttccca gggatgggtt tgggatcgaa 60

ggacacaatg 70

<210> 182
<211> 70
<212> DNA
<213> X. tropicalis

<400> 182
actgtagttg gtatggcaac cagcgccgtt ccagtttccg gtcatgggct tggggtccag 60

cgtggccacc 70

<210> 183
<211> 70
<212> DNA
<213> Tetraodon sp.

<400> 183
gctgaagttt gtatggcagc cagcaccgtt ccagttccct gggattggct tggggtcaaa 60

tgaggcaatg 70

<210> 184
<211> 70
<212> DNA
<213> Fugu rubripes

<400> 184
gctgaagttg gtatggcagc cggcgccgtt ccagttcccg gagatcggtt tggggtcgaa 60

ggaggcgacg 70

<210> 185
<211> 70
<212> DNA
<213> Danio rerio

<400> 185
gttgaagtta gtgtggcaac cagcaccatt ccagttgcct gggatcggct taggatcaaa 60

tgaagctacc 70