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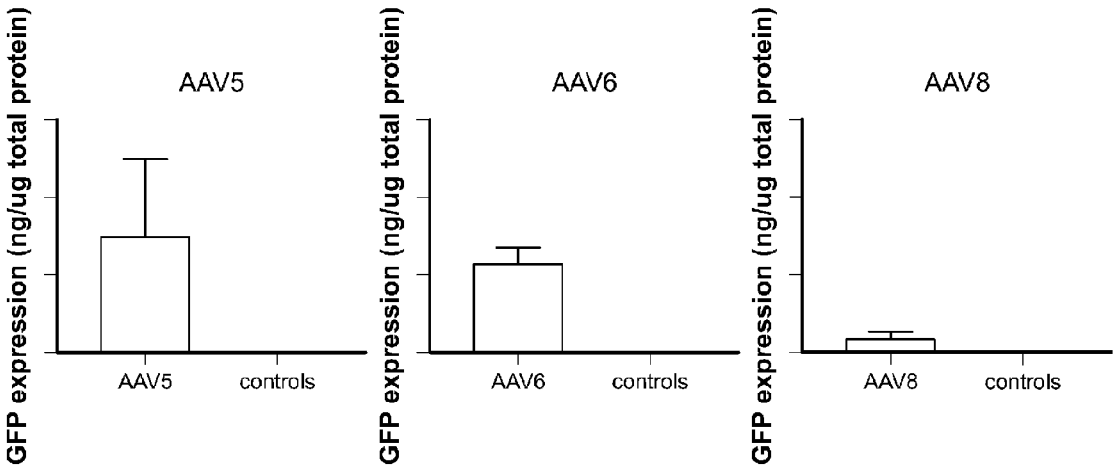


FIG. 9

(57) Abstract: Provided herein are methods for selectively delivering therapeutics to the eye using AAV vectors. For example, the cornea can be specifically targeted using the methods described. Also provided herein are compositions comprising AAV vectors packaged with CRISPR complexes, which can be delivered directly to the eye, for example the cornea, and in particular the cornea endothelium. Diseases and conditions comprising abnormalities or deterioration of tissues in the eye, such as the cornea endothelium (e.g. FECD), can be treated using the methods and compositions described herein.

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ADENO-ASSOCIATED VIRUS VECTORS FOR THE DELIVERY OF THERAPEUTICS

CROSS REFERENCE TO RELATED APPLICATIONS

[001] This application claims priority to U.S. Provisional Application Nos. 62/812,017 filed February 28, 2019; 62/831,838 filed April 10, 2019; and 62/878,865 filed July 26, 2019, each of which is hereby incorporated in its entirety.

SEQUENCE LISTING

[001.1] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on June 3, 2020, is named 67000-1023_WO_SL.txt and is 357,652 bytes in size.

FIELD OF THE INVENTION

[002] The present invention is generally directed to using adeno-associated virus (AAV) vectors to deliver therapeutics to the eye, for example to the corneal endothelium. The present invention is also directed to compositions comprising the AAV vectors. Corneal dystrophies can be treated with the methods and compositions of the present invention.

BACKGROUND

Adeno-associated virus (AAV) is a small, replication-deficient parvovirus. AAV is about 20-24 nm long, with a density of about 1.40-1.41 g/cc. AAV contains a single-stranded linear genomic DNA molecule approximately 4.7 kb in length. The single-stranded AAV genomic DNA can be either a plus strand, or a minus strand. AAV contains two open reading frames, Rep and Cap, flanked by two 145 base inverted terminal repeats (ITRs). AAVs contain a single intron. Cis-acting sequences directing viral DNA replication (Rep), encapsidation/packaging and host cell chromosome integration are contained within the ITRs. Three AAV promoters, p5, p19, and p40 (named for their relative map locations) drive the expression of the two AAV internal open reading frames encoding rep and cap genes. The p5 and p19 are the rep promoters. When coupled with the differential splicing of the single AAV intron, the two rep promoters result in the production of four rep proteins (rep 78, rep 68, rep 52, and rep 40) from the rep gene. The rep proteins have multiple enzymatic properties that are responsible for replicating the viral genome. The cap gene is expressed from the p40 promoter, and encodes the three capsid proteins VP1, VP2, and VP3. Alternative splicing and non-consensus translational start sites are responsible for the production of the three related capsid proteins. A single polyadenylationn site is located at map position 95 of the AAV genome. Muzyczka reviews the life cycle and genetics of AAV (Muzyczka, *Current Topics in Microbiology and Immunology*, 158:97-129 (1992)).

[004] AAV infection is non-cytopathic in cultured cells. Natural infection of humans and other animals is silent and asymptomatic (does not cause disease). Because AAV infects many mammalian cells, there is the possibility of targeting many different tissues *in vivo*. In addition to dividing cells, AAV transduces slowly dividing and non-dividing cells, and can persist essentially for the lifetime of those cells as a transcriptionally active nuclear episome (i.e. extrachromosomal element). The AAV proviral genome is infective as cloned DNA in plasmids, which makes construction of recombinant genomes possible. Moreover, because the signals directing AAV replication, genome encapsidation, and integration are all contained with the ITRs of the AAV genome, some or all of the approximately 4.3 kb of the genome, encoding replication and structural capsid proteins (rep-cap) are contained within the ITRs of the AAV genome, and can be replaced with heterologous DNA, such as a gene cassette containing a promoter, a DNA of interest, and a polyadenylation signal. The rep and cap proteins may be provided in trans. AAV is a very stable and robust virus, and easily withstands conditions used to inactivate adenovirus (56°C to 65°C for several hours), therefore cold preservation of AAV less critical. And, AAV-infected cells are not resistant to super-infection. These unique properties of AAV make it useful as a vector for delivering foreign DNA to cells or subjects, for example, in gene therapy.

[005] Corneal dystrophy is a term for the heterogenous group of non-inflammatory bilateral diseases restricted to the cornea. They are grouped by the anatomical location within the cornea of the pathology. Most do not have any manifestations outside of the cornea and they result with corneal opacities and affect visual acuity (see https://www.cornealdystrophyfoundation.org/what-is-corneal-dystrophy).

[006] The cornea has three major regions that are affected by corneal dystrophies: corneal epithelium, stroma, endothelium. Anterior corneal dystrophies affect the corneal epithelium and its basement membrane and the superficial corneal stroma. Stromal corneal dystrophies affect the corneal stroma. Posterior corneal dystrophies affect Descemet membrane and the corneal endothelium. The most common posterior corneal dystrophy is Fuchs' corneal endothelial dystrophy.

[007] Recently, it has been found that certain pathological conditions or diseases are associated with mutations in the *TCF4* gene, coding for transcription factor 4 protein (TCF4). Diseases associated with mutations in the *TCF4* gene include Fuchs endothelial corneal dystrophy (FECD), posterior polymorphous corneal dystrophy (PPCD), primary sclerosing cholangitis (PSC), Pitt-Hopkins syndrome, distal 18q deletion, and schizophrenia.

[008] FECD is a condition that causes vision problems. It affects the cornea of the eye, in particular the endothelium. The cornea is located on the front surface of the eye, and corneal tissue contains five basic layers. The epithelium is the cornea's outermost layer. The epithelium functions to block the passage of foreign material (e.g. dust, water, bacteria) into the eye and other layers of the cornea, and provides a smooth surface to absorb oxygen and cell nutrients from tears, distributing these nutrients to the rest of the cornea. The epithelial cells anchor and organize themselves on the basement membrane of the epithelium. Lying directly below the basement membrane of the epithelium is the Bowman's layer, which is a transparent sheet of tissue composed of collagen fibers. Beneath Bowman's layer is the stroma. The stroma comprises about 90% of the cornea's thickness, and consists primarily of water and collagen. A thin, strong sheet of tissue, Descemet's membrane is beneath the stroma. Descemet's membrane is composed of collagen fibers, and is made by the endothelial cells that lie beneath it. The endothelium is the layer below Descemet's layer.

[009] The endothelium is the extremely thin innermost layer of the cornea and is vital to keeping the cornea clear. The corneal endothelium is a monolayer of amitotic cells that form a barrier between the corneal stroma and the aqueous humor. The corneal endothelial cells function by pumping fluid from the cornea to maintain the cornea at the correct thickness to preserve clarity. In some posterior corneal dystrophies, such as FECD, the corneal endothelium is diseased and cells die over the course of this progressive disease. As these cells die, the remaining cells expand to fill the space, and the layer loses the ability to properly function. This results in corneal edema and increased opacity, leading to a reduction in visual acuity. In advanced stages of the disease, blindness may ensue. Loss of vision due to FECD is the leading cause of corneal transplants in the USA.

[0010] Because the corneal endothelium is affected in these diseases, targeting them to deliver therapeutics could aid in stopping the progression of disease. One such methodology is adeno-associated viruses (AAVs), which can be packaged to deliver the therapeutic, and

delivered via intracameral or intrastromal injection to come into contact with the cornea endothelium. Proteins or nucleotide sequences are commonly packaged into AAV vectors.

[0011] It has been suggested that genetic factors are associated with the occurrence of FECD. Genetic loci known to be associated with FECD include *FCD1* to *FCD4*, *ZEB1/TCF8*, *SLC4A11*, *LOXHD1*, and *COL8A2*. One such genetic factor is trinucleotide repeat (TNR) expansions in the *transcription factor 4* (*TCF4*) gene. Most of the genetic predisposition for FECD is associated with a TNR in the third intron of the *TCF4* gene. A repeat length of greater than 50 repeats is generally associated with a clinical diagnosis of FECD (Wieben et al., *PLOS One*, 7:11, e49083 (2012)). Recently, it has been suggested that this TNR expansion causes aggregation of the affected *TCF4* RNA, and sequestration of key RNA splicing factors (Mootha, et al., *Invest. Ophthalmol. Vis. Sci.*, 55(1):33-42 (2014); Mootha, et al., *Invest. Ophthalmol. Vis. Sci.*, 56(3):2003-11 (2015); Vasanth, et al., *Invest. Ophthalmol. Vis. Sci.*, 56(8):4531-6 (2015); Soliman et al., *JAMA Ophthalmol.*, 133(12):1386-91 (2015)). Sequestration of RNA splicing factors can lead to global changes in gene expression, resulting in significant changes in cellular function, and cell death (Du et al., *J. Biol. Chem.*, 290:10, 5979-5990 (2015)).

[0012] Another genetic mutation that is associated with FECD occurs in the *COL8A2* gene (Vedana et al., *Clinical Opththalmology*, 10, 321-330 (2016)). Collagen VIII, or COL8 (comprising COL8A1 and COL8A2) is regularly distributed in the Descemet's membrane of the cornea. It has been shown that corneas from patients with mutations in *COL8A2* have an irregular mosaic deposition of different amounts of COL8A1 and COL8A2, in a non-coordinated manner. Three point mutations of the COL8A2 lead to intracellular accumulation of mutant COL8 peptides. These point mutations are Gln455Lys, Gln455Val, and Leu450Trp. The intracellular accumulation of mutant COL8 peptides can cause early-onset FECD, as well as the related corneal disorder PPCD (which is characterized by changes in the Descemet's membrane and endothelial layer of the cornea).

[0013] Although AAV vectors have been used to deliver gene editing therapeutics directly to the eye, this has generally only been shown for posterior portions of eye, such as the retina. Delivery of gene editing therapeutics to the anterior portions of the eye, such as the cornea, is far less well researched and documented. There remains a need to develop delivery

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techniques that can preferentially deliver therapeutics only to specific areas of the eye and to specific tissues or cells, particularly the anterior portions such as the cornea.

[013a] Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each of the appended claims.

[013b] Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

SUMMARY OF THE INVENTION

[0014] The present invention provides a method of delivering a therapeutic to the corneal endothelium, to treat diseases such as corneal dystrophies, for example, FECD. The methods of the invention utilize AAVs to deliver therapeutics directly to the eye, particularly the corneal endothelium. In certain embodiments, the AAVs are packaged with proteins, or nucleotides encoding the proteins, to be expressed in certain cells of the eyes. In other embodiments, the AAVs are packed with a CRISPR RNP complex (i.e. a complex with a Cas protein) to elicit directed gene editing in the eye, and in specific areas or cells of the eye. In some embodiments, the AAVs are packaged with a CRISPR gRNA complexed with a nucleotide sequence encoding a Cas protein. The present invention also provides compositions comprising the AAVs.

[0015] In a particular aspect, the present invention provides a composition comprising:

a) a nucleotide sequence, or portion thereof, of an AAV vector; and

b) a nucleic acid editing system comprising at least one nucleotide sequence that is complementary to at least one mutant allele on a target gene associated with diseases or conditions in the cornea; a nucleic acid capable of down-regulating gene expression of at least one mutant allele on a target gene associated with diseases

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or conditions in the cornea; and/or at least one nucleotide sequence, or portion thereof, that codes for a protein to be expressed in the eye.

[015a] In another aspect, there is provided a composition comprising:

a) a nucleotide sequence, or portion thereof, of an AAV vector, wherein the AAV vector serotype is AAV6; and

b) a nucleic acid editing system comprising at least one nucleotide sequence that is complementary to at least one mutant allele on a target gene associated with diseases or conditions in the cornea; a nucleic acid capable of down-regulating gene expression of at least one mutant allele on a target gene associated with diseases or conditions in the cornea; and/or at least one nucleotide sequence, or portion thereof, that encodes for a protein to be expressed in the eye.

[015b] In another aspect, there is provided use of a composition described herein in the preparation of a medicament for targeting a gene associated with diseases or conditions in a cornea.

[015c] In another aspect, there is provided a method of targeting a gene associated with diseases or conditions in a cornea in a subject in need thereof comprising administering a composition described herein to the subject.

[015d] In another aspect, there is provided use of one or more adeno-associated virus (AAV) vectors comprising a nucleotide sequence that encodes a protein in the preparation of a medicament for expressing the protein in an eye of a subject, wherein at least one AAV vector serotype is AAV6.

[015e] In another aspect, there is provided a method of expressing a protein in an eye of a subject in need thereof comprising administering one or more adeno-associated virus (AAV) vectors comprising a nucleotide sequence that encodes the protein to the subject, wherein at least one AAV vector serotype is AAV6.

[0016] In another aspect, the present invention provides a method of expressing a protein in an eye of a subject in need thereof comprising:

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a) providing one or more adeno-associated (AAV) vectors comprising a nucleotide sequence that encodes said protein; and

b) administering the AAV vector to the eye.

[0017] In another aspect, the present invention provides a method for repairing a gene expressed in the cornea in a subject in need thereof, the method comprising:

a) providing a delivery system comprising a nucleic acid editing system comprising at least one nucleotide sequence that is complementary to at least one mutant allele on a target gene associated with diseases or conditions in the cornea; and

b) administering the delivery system to the cornea of the subject.

When the term "repairing" is used, it is also meant to include inducing repair.

[0018] In yet another aspect, the present invention provides a method of treating a disease or condition of the cornea caused by a mutant allele of a gene that comprises trinucleotide repeats (TNRs) and/or a point mutation in a subject in need thereof, said method comprising:

a) excising at least a portion of the trinucleotide repeats (TNRs) within the gene, comprising:
    i) providing an AAV5, AAV6, or AAV8 vector which comprises one or more nucleotide sequences coding for one or more guide RNAs targeting a sequence within the TNRs, 5' of the TNRs, 3' of the TNRs, or combination thereof; and
    ii) administering the vector to the cornea; and/or
b) correcting the point mutation of the gene or gene product comprising:
    i) providing an AAV5, AAV6, or AAV8 vector comprising one or more nucleotide sequences coding one or more guide RNAs targeting a sequence in the gene associated with a point mutation in the gene product; and
    ii) administering the vector to the cornea;

wherein said one or more nucleotide sequences are preferentially expressed in the cornea after intracameral injection.

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[0019] In another aspect, the present invention provides a method of treating a disease or condition of the cornea caused by a mutant allele of a gene that comprises trinucleotide repeats (TNRs) and/or a point mutation in a subject in need thereof, said method comprising:

a) excising at least a portion of the trinucleotide repeats (TNRs) within the gene, comprising:
   i) providing an AAV5, AAV6, or AAV8 vector which comprises one or more nucleotide sequences coding for one or more guide RNAs targeting a sequence within the TNRs, 5' of the TNRs, 3' of the TNRs, or combination thereof; and
   ii) administering the vector to the cornea; and/or

b) Correcting the point mutation of the gene or gene product comprising:
   i) providing an AAV5, AAV6, or AAV8 vector comprising one or more nucleotide sequences coding one or more guide RNAs targeting a sequence in the gene associated with a point mutation in the gene product; and
   ii) administering the vector to the cornea.

[0020] In another aspect, the present invention provides a method for down-regulating expression of a cornea gene in a subject in need thereof, the method comprising administering to the subject a delivery system comprising:

a) a nucleotide sequence, or portion thereof, of an AAV vector;

b) a nucleic acid capable of down-regulating gene expression of at least one mutant allele on a target gene associated with diseases or conditions in the cornea; and

c) administering the delivery system to the cornea.

[0021] In another aspect, the present invention provides a method of preferentially expressing a protein in endothelial cells of the cornea in a subject in need thereof, comprising:

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a) providing one or more adeno-associated (AAV) vectors comprising a nucleotide sequence, or portion thereof, that encodes said protein; and
b) administering the AAV vector to the cornea.

[0022] These and other aspects, advantages, and features of the invention will become apparent to those persons skilled in the art upon reading the details of the compositions and methods as more fully described below.

BRIEF DESCRIPTION OF THE DRAWINGS

[0023] Figure 1: Figure 1 is an illustration of the layers of the cornea (see https://discoveryeye.org/treatment-corneal-scratches-and-abrasions/).

[0024] Figure 2: Figure 2 is an illustration of the structure of the mouse eye, and a depiction of intracameral and intravitreal injection into the eye.

[0025] Figure 3: Figure 3 depicts the in vivo images of a mouse eye after intracameral delivery of AAV5-eGFP. Panels A-D show images from the OD eye ("OD" refers to Oculus Dexter which is latin for the right eye). Panels E-H show images from the OS eye ("OS" refers to Oculus Sinister which is latin for the left eye). Panel A provides a reference for panel B. Panel E provides a reference for panel F. Panels B & F show the image which demonstrates fluorescence in the cornea from the AAV5-eGFP. Panels C & G shows the fundus image and panels D & H show the image which demonstrates no fluorescence in the retina. Two dots of fluorescence are detected in the OS retina shown by arrows in panel H.

[0026] Figure 4: Figure 4 depicts the immunohistochemistry of the same eyes shown in Fig. 3. AAV5-eGFP was delivered by intracameral injection. The OS eye was separated into a cornea flat mount (panel A, magnified insert shown in panel B) and a retina flat mount (panel C, magnified insert shown in panel D). Staining shows eGFP localized to the cornea endothelium and a few cells staining in the retina. The OD eye was collected whole and processed for cross-sections shown in panel E. Staining shows eGFP localized to the cornea endothelium and not in the retina. Magnified inserts are shown in panels F-G. Panel F shows the cornea endothelium layer. Panel G shows the retina, where the exposure time had to be increased to capture a positive signal not seen in panel E. (green=endogenous eGFP, red=secondary staining using primary antibody to eGFP).

[0027] Figure 5: Figure 5 depicts the in vivo images of a mouse eye after intracameral delivery of AAV6-eGFP. Panel A provides a reference for panel B. Panel B shows the image which demonstrates fluorescence in the cornea from the AAV6-eGFP. Panel C shows the fundus image and panel D shows the image which demonstrates fluorescence in the retina.

[0028] Figure 6: Figure 6 depicts the immunohistochemistry of the same mouse eye shown in Fig. 5. Staining demonstrates that AAV6-eGFP is present in the corneal endothelium, stroma, and ciliary body (green=endogenous eGFP, red=secondary staining using primary antibody to eGFP, blue= DAPI stained nuclei). The white rectangle in panel A indicates the zoomed-in area shown in panel B. The left arrow in panel B indicates the positive corneal stroma layer. The right arrow in panel B indicates the positive corneal endothelium layer.

[0029] Figure 7: Figure 7 depicts the in vivo images of a mouse eye after intracameral delivery of AAV8-eGFP. Panel A provides a reference for panel B. Panel B shows the image which demonstrates fluorescence in the cornea from the AAV8-eGFP. Panel C shows the fundus image and panel D shows the image which demonstrates fluorescence in the retina.

[0030] Figure 8: Figure 8 depicts the immunohistochemistry of the same mouse eye shown in Fig. 7. Staining demonstrates that AAV8-eGFP is present in the corneal endothelium, stroma, and ciliary body (green=endogenous eGFP, red=secondary staining using primary antibody to eGFP, blue= DAPI stained nuclei). The white rectangle in panel A indicates the zoomed-in area shown in panel B. The left arrow in panel B indicates the positive corneal stroma layer. The right arrow in panel B indicates the positive corneal endothelium layer.

[0031] Figure 9: Figure 9 depicts the ELISA results of eGFP protein levels from 4 mice (whole eyes) for each of the AAV serotypes, such as AAV5-eGFP, AAV6-eGFP, AAV8-eGFP, delivered by intracameral route. Two mice that received PBS+0.001% pluronic acid were included as controls for each of the AAV serotypes tested. Means with SEM are shown.

[0032] Figure 10: Figure 10 is a composite figure that depicts the *in vivo* fluorescence images and immunochemistry results of AAV2-eGFP, AAV5-eGFP, AAV6-eGFP, AAV8-eGFP, and AAV9-eGFP after IC delivery into the mouse eye.

DETAILED DESCRIPTION

[0033] It is to be understood that the foregoing general description and the following detailed description are exemplary and explanatory only, and are not restrictive of any subject matter claimed.

[0034] Headings are used solely for organizational purposes, and are not intended to limit the invention in any way.

[0035] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the inventions belong. All patents, patent applications, published applications and publications, websites and other

published materials referred to throughout the entire disclosure herein, unless noted otherwise, are incorporated by reference in their entirety for any purpose. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods are described.

[0036] Corneal dystrophy is a term for the heterogenous group of non-inflammatory bilateral diseases restricted to the cornea. They are grouped by the anatomical location of the pathology within the cornea. Most do not have any manifestations outside of the cornea and they result with corneal opacities and affect visual acuity (see https://www.cornealdystrophyfoundation.org/what-is-corneal-dystrophy).

[0037] Anterior corneal dystrophies affect the corneal epithelium and its basement membrane and the superficial corneal stroma. Stromal corneal dystrophies affect the corneal stroma. Posterior corneal dystrophies affect Descemet membrane and the corneal endothelium. The most common posterior corneal dystrophy is Fuchs' corneal endothelial dystrophy.

[0038] The cornea has three major regions that are affected by corneal dystrophies: corneal epithelium, stroma and endothelium. AAV5 targets the corneal endothelium after IC delivery and could be utilized to deliver gene therapy for posterior corneal dystrophies. Both AAV6 and AAV8 can target the corneal stroma, endothelium, and ciliary body after IC delivery and could be utilized to deliver gene therapy for corneal stromal dystrophies and posterior corneal dystrophies. As some anterior corneal dystrophies affect both the epithelium and the superficial corneal stroma, AAV6 and AAV8 could deliver gene therapy to the stroma.

[0039] Table D1 shows corneal dystrophies and certain genes associated therewith ((Klintworth, 2009. Corneal dystrophies. Orphanet J. Rare Dis., 4, 7. doi:10.1186/1750-1172-4-7).

Table D1. Summary of the corneal dystrophies: modes of inheritance, gene loci, genes and the categories of the International Committee for the Classification of Corneal Dystrophies (IC3D) categories.

	Mode of inheritance	Gene locus	Gene	IC3D Category *
SUPERFICIAL CORNEAL DYSTROPHIES				
Meesmann dystrophy	AD	12q13	*KRT3*	1
Meesmann dystrophy	AD	17q12	*KRT12*	1
Stocker-Holt dystrophy	AD	17q12	*KRT12*	1
Granular corneal dystrophy type III (Reis-Bücklers dystrophy)	AD	5q31	*TGFB1*	1
Thiel-Behnke dystrophy	AD	5q31	*TGFB1*	1
Thiel-Behnke dystrophy	AD	10q23-q24	Unknown	2
Gelatinous droplike corneal dystrophy (familial subepithelial corneal amyloidosis)	AR	1p32	*TACSTD2 (MISI)*	1
Subepithelial mucinous corneal dystrophy	AD	Unknown	Unknown	4
Lisch epithelial dystrophy	XR	Xp22.3	Unknown	2
Epithelial recurrent erosion dystrophy	AD	Unknown	Unknown	3
CORNEAL STROMAL DYSTROPHIES				
Macular corneal dystrophy	AR	16q22	*CHST6*	1
Granular corneal dystrophy type I	AD	5q31	*TGFB1*	1
Granular corneal dystrophy type II (Avellino dystrophy, combined lattice-granular dystrophy)	AD	5q31	*TGFB1*	1
Lattice corneal dystrophy type I and variants	AD	5q31	*TGFB1*	1
Lattice corneal dystrophy type II	AD	9q34	*GSN*	1
Fleck dystrophy	AD	2q35	*PIP5K3*	1
Schnyder corneal dystrophy	AD	1p34.1-p35	*UBIAD1*	1
Posterior amorphous corneal dystrophy	AD	Unknown	Unknown	3
Congenital stromal dystrophy	AD	12q13.2	*DCN*	1
POSTERIOR DYSTROPHIES				
Fuchs dystrophy (early onset)	AD	1p34.3	*COL8A*	1
Fuchs dystrophy (late onset)	AD	13pTel-13q12.13	Unknown	2
Fuchs dystrophy (late onset)	AD	18q21.2-q21.32	Unknown	2
Fuchs dystrophy (late onset)	?	20p13-p12	*SLC4A11*	1
Fuchs dystrophy (late onset)	?	10p11.2	*TCF8*	1

	Mode of inheritance	Gene locus	Gene	IC3D Category *
Posterior polymorphous dystrophy type 1	AD	20p11.2	Unknown	2
Posterior polymorphous dystrophy type 2	AD	1p34.3-p32.3	*COL8A2* #	1
Posterior polymorphous dystrophy type 3	AD	10p11.2	*TCF8*	1
Congenital endothelial dystrophy type 1	AD	20p11.2-q11.2	Unknown	2
Congenital endothelial dystrophy type 2	AR	20p13-p12	*SLC4A11*	1
X-linked endothelial corneal dystrophy	XR	Unknown	Unknown	2

*Category 1: A well-defined corneal dystrophy in which the gene has been mapped and identified and specific mutations are known.

Category 2: A well-defined corneal dystrophy that has been mapped to 1 or more specific chromosomal loci, but the gene(s) remains to be identified.

Category 3: A well-defined corneal dystrophy in which the disorder has not yet been mapped to a chromosomal locus.

Category 4: A suspected new, or previously documented corneal dystrophy, although the evidence for it, being a distinct entity, is not yet convincing.

[0040] Table D2 is from Moore, C. B. T., Christie, K. A., Marshall, J., & Nesbit, M. A. (2018). Personalised genome editing - The future for corneal dystrophies. *Prog Retin Eye Res, 65*, 147-165. doi:10.1016/j.preteyeres.2018.01.004.

Table D2. List of known corneal dystrophies, including associated inheritance pattern, gene locus and causative genes.

		Inheritance Pattern	Genetic Locus	Gene known	Gene(s) Affected	IC3D Category
Epithelial and Sub-Epithelial Dystrophies	EBMD	Minority of cases, mostly sporadic	5q13	Some cases	*TGFB1*	Some C1
	ERED	Autosomal Dominant	Unknown	Unknown	N/A	C3
	SMCD	Likely Autosomal Dominant	Unknown	Unknown	Unknown	C4

		Inheritance Pattern	Genetic Locus	Gene known	Gene(s) Affected	IC3D Category
	MECD	Autosomal Dominant	12q13 and 17q12	Yes	*KRT3* and *KRT12* (Stocker-Holt variant)	C1
	LECD	X-chromosomal dominant	Xq22.3	Unknown	Unknown	C2
	GDCD	Autosomal Recessive	1q32	Yes	*TACSTD2*, previously *M1S1*	C1
Epithelial Stromal Dystrophies	RBCD	Autosomal Dominant	5q13	Yes	*TGFB1*	C1
	TBCD	Autosomal Dominant	5q13	Yes	*TGFB1*	C1
	LCD1	Autosomal Dominant	5q13	Yes	*TGFB1*	C1
	GCD1	Autosomal Dominant	5q13	Yes	*TGFB1*	C1
	GCD2	Autosomal Dominant	5q13	Unknown	*TGFB1*	C1
Stromal Dystrophies	MCD	Autosomal Recessive	16q22	Yes	*CHST6*	C1
	SCD	Autosomal Dominant	1q36	Yes	*UBIAD1*	C1
	CSCD	Autosomal Dominant	12q21.33	Yes	*DCN*	C1
	FCD	Autosomal Dominant	2q34	Yes	*PIKFYVE*, previously *PIP5K3*	C1
	PACD	Autosomal Dominant	12q21.33	Yes	*KERA*, *LUM*, *DCN*, *EPYC*	C1
	CCDF	Unknown	Unknown	Unknown	Unknown	C4
	PDCD	Reported AD, similar deposits seen with X-linked ichthyosis	X-linked ichthyosis = Xp22.31	Unknown	*STS*	C4

		Inheritance Pattern	Genetic Locus	Gene known	Gene(s) Affected	IC3D Category
Descemet's Membrane and Endothelial Dystrophies	FECD	Unknown, reported autosomal dominant	Early onset = 1q34.3-p32 (FECD1) Late onset = 13pt34-q12.3 (FECD2), 18q21.2-q21.3 (FECD3), 20p13-q12 (FECD4), 5q33.1-q35.2 (FECD 5), 10p11.2 (FECD 6), 9p24.1-p22.1 (FECD 7), 15q25 (FECD 8)	Some cases	Unknown, *TCF4*, *SLC4A11*, Unknown, *ZEB1*, Unknown, *AGBL1*	C2 = identified genetic loci, C3 = without known inheritance
	PPCD	Autosomal Dominant	PPCD 1 = 20p11.2-q11.2 PPCD 2 = 1p34.3-p32.3 PPCD 3 = 10p11.2	Unknown Yes Yes	Unknown *COL8A2* *ZEB1*	C2 C1 C1
	CHED	Autosomal recessive	20p13	Yes	*SLC4A11*	C1 (some cases C3)
	XECD	X-chromosomal dominant	Xq25	Unknown	Unknown	C2
Total:	22	Known = 17	Known = 18	Known = 12 Partially known = 4 Unknown = 5		

[0041] Delivering AAVs directly to the eye, for example by intracameral injection, can result in a viral targeting tropism to the cornea. Delivering AAV5 via intracameral injection results in a viral targeting tropism to the cornea endothelium, and not to other ocular structures. This targeted tropism could deliver the therapeutic to the affected structure, while sparing other ocular structures, decreasing the risk of off-target effects. Intracameral delivery of AAV6 or AAV8 also demonstrates targeting to the corneal endothelium. However, both AAV6 and

AAV8 also display tropism to other corneal and anterior structures, as well as the retina, when delivering a gene using the ubiquitous CAG promoter.

[0042] AAV is a small virus consisting of two open reading frames, Rep and Cap, flanked by two 145 base inverted terminal repeats (ITRs). When used for gene therapy, the Rep and Cap open reading frames are removed, and the desired gene, together with a promoter to drive transcription of the desired gene, is inserted between the ITRs.

[0043] CRISPR nucleotides (e.g. gRNA and/or nucleotides coding for Cas proteins) can be packaged between the ITRs, creating a viral vector for targeted delivery of therapeutics. In some embodiments, the CRISPR nucleotide gRNA is packaged with a Cas protein (e.g. Cas9 nuclease) to form a ribonucleoprotein (RNP) complex. However, the AAVs can also be packaged with nucleotides encoding other proteins. AAVs are preferred viral vectors because they can infect both dividing and non-dividing cells, and are associated with a lack of pathogenicity.

[0044] AAV vectors can thus be used to preferentially target certain layers of the cornea. AAV5, for example, specifically targets cornea endothelium. The specificity of AAV vectors reduces the risk for off-target effects of therapeutics that are delivered via the AAV vectors.

[0045] In certain embodiments, the AAV vectors can comprise one or more nucleotide sequences that are complementary to at least one target sequence on a target gene.

[0046] In some embodiments, the AAV vectors can comprise one or more nucleotide acid editing systems. Nucleotide editing systems include, but are not limited to a CRISPR system, an siRNA, an shRNA, an miRNA, an antisense RNA, or an antagomir RNA.

[0047] In certain embodiments, AAV vectors can be used for targeted gene editing or therapy in the eye, preferably the cornea or other affected anterior structures, by delivering one or more nucleotide editing systems directly to the eye.

[0048] In certain embodiments, the AAV vectors can be used for targeted gene therapy in the cornea, by delivering CRISPR complexes targeting genes involved in corneal dystrophies,

such as Fuchs endothelial corneal dystrophy (FECD). FECD is associated with trinucleotide repeat (TNR) expansions in the *transcription factor 4* (*TCF4*) gene. Most of the genetic predisposition for FECD is associated with a TNR in the third intron of the *TCF4* gene. FECD is a condition that affects the cornea of the eye, in particular the endothelium. Corneal dystrophies are also associated with mutations in the *COL8A* gene. Mutations of the *COL8A* gene lead to a Gln455Lys, Gln455Val, or Leu450Trp mutation in the gene product.

[0049] By delivering CRISPR complexes (gRNA plus a Cas protein, or a nucleotide encoding a Cas protein) to the cornea endothelium, the TNRs, or a portion thereof, can be excised from the *TCF4* gene in the corneal endothelium, without affecting the *TCF4* gene in other parts of the eye.

[0050] In certain embodiments, CRISPR complexes are packaged into one or more AAV vectors. The CRISPR complexes may target either the TNRs of the *TCF4* gene, or the mutant alleles of the *COL8A2* gene.

[0051] In certain embodiments, the AAV vectors may be delivered by themselves. In other embodiments, the AAV vectors may be enclosed in a lipid nanoparticle, liposome, non-lipid nanoparticle, or viral capsid for delivery.

Definitions

[0052] In this application, the use of the singular includes the plural unless specifically stated otherwise. As used herein, the singular forms "a," "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise.

[0053] In this application, the use of "or" means "and/or" unless stated otherwise.

[0054] As used herein, the terms "comprises" and/or "comprising" specify the presence of the stated features, integers, steps, operations, elements, and/or components, but do not preclude the presence or addition of one or more other features, integers, steps, operations, elements, components, and/or groups thereof. Furthermore, to the extent that the terms "includes," "having," "has," "with," "composed," "comprised" or variants thereof are used in

either the detailed description or the claims, such terms are intended to be inclusive in a manner similar to the term "comprising."

[0055] As used herein, ranges and amounts can be expressed as "about" a particular value or range. "About" is intended to also include the exact amount. Hence "about 5 percent" means "about 5 percent" and also "5 percent." "About" means within typical experimental error for the application or purpose intended.

[0056] As used herein, "treatment" refers to any delivery, administration, or application of a therapeutic for a disease or condition. Treatment may include curing the disease, inhibiting the disease, slowing or stopping the development of the disease, ameliorating one or more symptoms of the disease, or preventing the recurrence of one or more symptoms of the disease.

[0057] As used herein, "FECD" refers to Fuchs endothelial corneal dystrophy. FECD includes patients who have the condition, as well as individuals who do not have symptoms, but have a genetic disposition to FECD.

[0058] As used herein, "AAV" refers to an adeno-associated virus. AAV is a non-enveloped virus that is icosahedral, is about 20 to 24 nm long with a density of about 1.40-1.41 g/cc, and contains a single stranded linear genomic DNA molecule approximately 4.7 kb in length. The single stranded AAV genomic DNA can be either a plus strand, or a minus strand. In certain embodiments, the term "AAV" or "AAV vector" refers to an AAV that has been modified so that a therapeutic, such as for example, a CRISPR complex, replaces the Rep and Cap open reading frames between the inverted terminal repeats (ITRs) of the AAV genome.

[0059] As used herein, "AAV serotype" means a sub-division of AAV that is identifiable by serologic or DNA sequencing methods and can be distinguished by its antigenic character.

[0060] As used herein, a "vector" is a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Vectors include, but are not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. The term "vector" includes an

autonomously replicating plasmid or a virus. "Vector" may also include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, polylysine compounds liposomes, lipid nanoparticles, non-lipid nanoparticles, and the like. Examples of viral vectors include, but are not limited to, adenoviral vectors, adeno-associated virus (AAV) vectors, retroviral vectors, lentiviral vectors, and the like. Preferably, the vector is an AAV vector.

[0061] As used herein, "RNA" refers to a molecule comprising one or more ribonucleotide residues. A "ribonucleotide" is a nucleotide with a hydroxyl group at the 2' position of the beta-D-ribofuranose moiety. The term "RNA" includes double-stranded RNA, single-stranded RNA, isolated RNA (e.g. partially purified RNA), essentially pure RNA, synthetic RNA, and recombinantly produced RNA. The term "RNA" also refers to modified RNA that differs from naturally-occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides.

[0062] As used herein "inhibitory RNA" means a nucleic acid molecule that contains a sequence that is complementary to a target nucleic acid that mediates a decrease in the level or activity of the target nucleic acid. Inhibitory RNA includes, but is not limited to, interfering RNA (iRNA), short hairpin RNA (shRNA), small interfering RNA (siRNA), ribozymes, antagomirs, and antisense oligonucleotides.

[0063] As used herein, "shRNA" refers to an RNA molecule comprising an antisense region, a loop portion, and a sense region, wherein the sense region has complementary nucleotides that base pair with the antisense region to form a duplex stem. Following post-transcriptional processing, the shRNA is converted to siRNA by a cleavage mediated by the enzyme Dicer, which is a member of the RNase III family.

[0064] As used herein, "siRNA" refers to any small RNA molecule capable of inhibiting or down-regulating gene expression by mediating RNA interference in a sequence specific manner.

[0065] As used herein, "antisense RNA" or "antisense oligonucleotides" are short, synthetic pieces of nucleic acid whose sequence is complementary to the mRNA that codes for a protein. Antisense RNA binds to the mRNA and blocks transcription.

[0066] As used herein, an "antagomir" or "antagomir RNA" refers to small synthetic RNA that are complementary to a specific microRNA (miRNA) target, optionally with either mispairing at the cleavage site or one or more base modifications to inhibit cleavage.

[0067] As used herein, "micro RNA" or "miRNA" refers to a single-stranded RNA molecule of about 21-23 nucleotides in length, which regulates gene expression. miRNA molecules are partially complementary to one or more mRNA, and their main function is to down-regulate gene expression.

[0068] As used herein, "TNRs" refers to trinucleotide repeats (i.e. multiple repetitions of three base pairs). The term "TNR expansion" refers to a higher than normal number of TNRs. For example, about 50 or more TNRs in intron 3 of *TCF4* would be considered a TNR expansion.

[0069] As used herein "CRISPR" means a bacterial adaptive immune system known as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeat) sequences.

[0070] As used herein, "guide RNA" and "gRNA" are used interchangeably, and refer to RNA sequences that are directed to a target DNA sequence. The gRNA contains a CRISPR RNA (crRNA) and transactivating crRNA (trRNA or tracrRNA). The crRNA and the trRNA may be associated on a single RNA molecule, referred to as a single guide RNA (sgRNA). Alternatively, the crRNA and trRNA may be disassociated on separate RNA molecules, and form a dual guide RNA (dgRNA). In some embodiments, the gRNA is chemically modified, and comprises one or more modified nucleosides or nucleotides. Modification of nucleosides and nucleotides can include one or more of: i) alteration, e.g. replacement, of one or both of the non-linking phosphate oxygens and/or of one or more of the linking phosphate oxygens in the phosphodiester backbone; ii) alteration, e.g. replacement, of a constituent of the ribose sugar, such as, for example, the 2'-hydroxyl on the ribose sugar; iii) complete replacement of the phosphate moiety with "dephospho" linkers; iv) modification or replacement of a

naturally occurring nucleobase, including with a non-canonical nucleobase; v) replacement or modification of the ribose-phosphate backbone; vi) modification of the 3' end or 5' end of the oligonucleotide, e.g. removal, modification, or replacement of a terminal phosphate group, or conjugation of a moiety, cap, or linker; and vii) modification or replacement of the sugar.

[0071] As used herein, the "guide sequence" refers to an about 20 base-pair sequence within the crRNA or trRNA that is complementary to a target sequence. The guide sequence directs the gRNA to a target sequence for cleavage by a nuclease.

[0072] As used herein, "target sequence" refers to a sequence of nucleic acids, within the genomic DNA of the subject, to which a gRNA directs a nuclease for cleavage of the target sequence. For example, a Cas protein may be directed by a gRNA to a target sequence, where the gRNA hybridizes with the target sequence, and the nuclease cleaves the target sequence. Target sequences include both the positive and negative strands of DNA (i.e. the sequence, and the reverse complement of the sequence). In some embodiments, when the guide sequence is the reverse complement of the target sequence, the guide sequence may be identical to the first 20 nucleotides of the target sequence. As used herein, "target sequence" or "target site" also refers to a genomic nucleic acid sequence that defines a portion of a nucleic acid to which a binding molecule may specifically bind under conditions sufficient for binding to occur.

[0073] As used herein, the term "CRISPR complex" refers to a combination of a gRNA and an endonucleotide encoding for a Cas protein (gRNA:Cas endonucleotide), or a combination of a gRNA and a Cas protein (gRNA:Cas protein). As used herein, a "ribonucleoprotein" (RNP) refers to a gRNA:Cas protein complex. The CRISPR complexes of the present invention may be directed to and cleave a target sequence either within the TNRs, or flanking the TNRs (5' or 3') of the *TCF4* gene. The CRISPR complexes may also be directed to cleave a target sequence in the *COL8A* gene.As used herein, a "protospacer adjacent motif" or "PAM" refers to a nucleotide sequence that must be adjacent to a target nucleotide sequence. The required PAM depends on the specific CRISPR system used. For example, in the CRISPR/Cas system derived from *Streptococcus pyogenes*, the target DNA must immediately precede a 5'-NGG PAM (where "N" is any nucleobase followed by two guanine nucleobases) for optimal cutting. Although *Streptococcus pyogenes* Cas9 also recognizes the

5'-NAG PAM, it appears to cut less efficiently at these PAM sites. Other Cas9 orthologs (e.g. derived from *Staphylococcus aureus*) require different PAM sequences.

[0074] As used herein, "indels" means insertion/deletion mutations that consist of a number of nucleotides that are either inserted or deleted at the site of double-stranded breaks (DSBs) in the nucleic acid of the DNA.

[0075] As used herein, "excision fragment" or "excision fragments" refers to deletions of a consecutive number of nucleotides (such as TNRs) that may occur when two or more gRNA are used together with a Cas mRNA or Cas protein.

[0076] As used herein, "promoter" means a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate specific transcription of a polynucleotide sequence. Preferred are promoters that are operable for AAV vectors, preferably AAV5, AAV6, and/or AAV8, and tissue specific promoters, preferably specific for the eye, more preferably specific for the cornea, and most preferably specific for the endothelium of the cornea. AAV promoters include, for example, an AAV p5 promoter. Promoters include, but are not limited to, CAG, SYN1, CMV, NSE, CBA, PDGF, SV40, RSV, LTR, SV40, dihydrofolate reductase promoter, beta-actin promoter, PGK, EF1alpha, GRK, MT, MMTV, TY, RU486, RHO, RHOK, CBA, chimeric CMV-CBA, MLP, RSV, ubiquitin promoters, actin promoters, tubulin promoters, immunoglobulin promoters, functional fragments thereof, etc. In AAV packaged with heterologous DNA, a promoter normally associated with heterologous nucleic acid can be used, or a promoter normally associated with the AAV vector, or a promoter not normally associated with either, can be used.

[0077] As used herein, "constitutive promoter" is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell under most or all physiological conditions of the cell. Examples of constitutive promoters include, but are not limited to, cytomegalovirus immediate early promoter (CMV), simian virus (SV40) promoter, adenovirus major late (MLP) promoter, Rous sarcoma virus (RSV) promoter, elongation factor-alpha (EF1a)

promoter, ubiquitin promoters, actin promoters, tubulin promoters, immunoglobulin promoters, functional fragments thereof, or combinations thereof.

[0078] As used herein, "inducible promoter" is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell substantially only when an inducer which corresponds to the promoter is present in the cell. Examples of inducible promoters include, but are not limited to, those inducible by heat shock, light, chemicals, peptides, metals, steroids, antibiotics, or alcohol. In some embodiments the promoter may be tissue specific, such as a promoter specific for expression in the cornea, e.g. the corneal edothelium.

[0079] As used herein, a "tissue specific promoter" is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a cell substantially only if the cell is a cell of the tissue type corresponding to the promoter. Tissue specific promoters include, but are not limited to, CMV, CBA, RHO, and RHOK.

[0080] As used herein, a "promoter/regulatory sequence" means a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. This sequence may be the core promoter sequence, or it may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product.

[0081] As used herein, "under transcriptional control" or "operably linked" means that the promoter is in the correct location and orientation in relation to a polynucleotide to control initiation of transcription by RNA polymerase and expression of the polynucleotide. These include promoters, a 3' UTR, or a 5' UTR. The promoter may be recognized by RNA polymerase III (Pol III), such as, but limited to, U6 and H1 Pol III promoters. The Pol III promoters may be, for example, mouse or human.

[0082] As used herein, "gene editing" or "nucleic acid editing" refers to modification of the nucleic acid sequence of a target gene.

[0083] As used herein, "nucleic acid editing system" or "gene editing system" refers to a method that can be used for performing gene editing or nucleic acid editing. Nucleic acid editing systems and gene editing systems include CRISPR systems, and interfering RNAs.

[0084] As used herein, "delivery system" refers to materials used to deliver nucleic acids to target cells. Such materials may include viral vectors such as AAV vectors and pharmaceutically acceptable ingredients.

[0085] As used herein, "modulation" or "modification" includes decreasing or inhibiting expression or function, of for example, a gene or protein, as well as increasing expression or function, of for example, a gene or protein. As used herein, "modulation" or "modification" also includes complete restoration of gene function, which includes replacing mutated part(s) of a gene or replacing the mutant gene with a wild-type version.

[0086] As used herein, "down-regulating" or "down-regulation" means a reduction in expression or transcription of a target nucleotide sequence. Down-regulation may be partial or temporary reduction in the expression or transcription of a target nucleotide sequence. Down-regulation may be a complete elimination of the expression or transcription of a target nucleotide sequence.

[0087] As used herein, "knockdown" refers to a partial or temporary reduction in expression or transcription of a target nucleotide sequence. This may be accomplished by administering a complementary nucleotide sequence that binds to the target sequence. Knockdown can be elicited by antisense oligonucleotides, siRNA, and the like.

[0088] As used herein, "knockout" refers to complete elimination of the expression or transcription of a target nucleotide sequence. Knockout may be elicited, for example, by use of a CRISPR system to cleave the target nucleotide sequence out of the target gene.

[0089] As used herein, non-homologous end joining (NHEJ) is a DNA repair mechanism which is a re-ligation of break ends after cleavage of a target nucleotide sequence.

[0090] As used herein, "homologous repair/homology directed repair (HR/HDR)" refers to DNA repair which is a process of homologous recombination where a DNA template is used to provide the homology necessary for precise repair of a double-strand break. The repair may consist of insertions of desired sequences, or modification of the target sequence.

[0091] As used herein, "repair template" refers to the DNA template used in HR/HDR.

[0092] As used herein, "subject" means a living organism. Preferably, a subject is a mammal, such as a human, non-human primate, rodent, or companion animal such as a dog, cat, cow, pig, etc.

Modulation of gene expression

[0093] Gene expression can be modulated by administering to a subject in need thereof a composition comprising a nucleotide editing system.

[0094] In one embodiment, modulating expression of a target gene comprises administering to the subject a composition, wherein the composition comprises a nucleic acid editing system comprising at least one nucleotide sequence that is complementary to at least one allele on a target gene associated with corneal dystrophies. In certain embodiments, the at least one nucleotide sequence that is complementary to at least one allele on a target gene is selected from an siRNA, an shRNA, an miRNA, an antisense RNA, or an antagomir RNA.

Administration of the composition

[0095] In certain embodiments, the composition is administered by itself.

[0096] In preferred embodiments, the composition comprises an adeno-associated virus (AAV) vector, or a nucleotide sequence or portion thereof encoding an AAV vector.

AAV

[0097] Adeno-associated virus (AAV) is a small, replication-deficient parvovirus. AAV is about 20-24 nm long, with a density of about 1.40-1.41 g/cc. AAV contains a single-stranded linear genomic DNA molecule approximately 4.7 kb in length. The single-stranded AAV genomic DNA can be either a plus strand, or a minus strand. AAV contains two open

reading frames, Rep and Cap, flanked by two 145 base inverted terminal repeats (ITRs). AAVs contain a single intron. Cis-acting sequences directing viral DNA replication (Rep), encapsidation/packaging and host cell chromosome integration are contained within the ITRs. Three AAV promoters, p5, p19, and p40 (named for their relative map locations) drive the expression of the two AAV internal open reading frames encoding rep and cap genes. The p5 and p19 are the rep promoters. When coupled with the differential splicing of the single AAV intron, the two rep promoters result in the production of four rep proteins (rep 78, rep 68, rep 52, and rep 40) from the rep gene. The rep proteins have multiple enzymatic properties that are responsible for replicating the viral genome. The cap gene is expressed from the p40 promoter, and encodes the three capsid proteins VP1, VP2, and VP3. Alternative splicing and non-consensus translational start sites are responsible for the production of the three related capsid proteins. A single polyadenylation site is located at map position 95 of the AAV genome. Muzyczka reviews the life cycle and genetics of AAV (Muzyczka, *Current Topics in Microbiology and Immunology*, 158:97-129 (1992)).

[0098] AAV infection is non-cytopathic in cultured cells. Natural infection of humans and other animals is silent and asymptomatic (does not cause disease). Because AAV infects many mammalian cells, there is the possibility of targeting many different tissues *in vivo*. In addition to dividing cells, AAV transduces slowly dividing and non-dividing cells, and can persist essentially for the lifetime of those cells as a transcriptionally active nuclear episome (i.e. extrachromosomal element). The AAV proviral genome is infective as cloned DNA in plasmids, which makes construction of recombinant genomes possible. Moreover, because the signals directing AAV replication, genome encapsidation, and integration are all contained with the ITRs of the AAV genome, some or all of the approximately 4.3 kb of the genome, encoding replication and structural capsid proteins (rep-cap) are contained within the ITRs of the AAV genome, and can be replaced with heterologous DNA, such as a gene cassette containing a promoter, a DNA of interest, and a polyadenylation signal. The rep and cap proteins may be provided in trans.

[0099] Several AAV serotypes have been identified, differing in their tropism (type of cell that they infect). Serotype AAV1 shows tropism to the following tissues: CNS; heart; retinal pigment epithelium (RPE); and skeletal muscle. Serotype AAV2 shows tropism to the following tissues: CNS; kidney; photoreceptor cells; and RPE. Serotype AAV3 shows

tropism mainly to the heart and liver. Serotype AAV4 shows tropism to the following tissues: CNS; lung; and RPE. Serotype AAV5 shows tropism to the following tissues: CNS; lung; photoreceptor cells; and RPE. Serotype AAV6 shows tropism to the following tissues: lung; and skeletal muscle. Serotype AAV7 shows tropism to the following tissues: liver; and skeletal muscle. Serotype AAV8 shows tropism to the following tissues: CNS; heart; liver; pancreas; photoreceptor cells; RPE; and skeletal muscle. Serotype AAV9 shows tropism for the following tissues: CNS; heart; liver; lung; and skeletal muscle. The tropism of AAV viruses may be related to the variability of the amino acid sequences of the capsid protein, which may bind to different functional receptors present on different types of cells.

[00100] Depending on the promoter included in the heterologous DNA cassette, it may be possible to target specific tissues in the eye. Modifying the capsid proteins may also enable specific infectivity of certain tissues or cells. In one embodiment, an AAV containing an Anc80 or Anc80L65 capsid protein is used for delivery of therapeutics directly to specific tissues in the eye. In some embodiments, the AAV viral particle comprises an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6 (e.g., a wild-type AAV6 capsid, or a variant AAV6 capsid such as ShH10, as described in U.S. PG Pub. 2012/0164106), AAV7, AAV8, AAVrh8, AAVrh8R, AAV9 (e.g., a wild-type AAV9 capsid, or a modified AAV9 capsid as described in U.S. PG Pub. 2013/0323226), AAV10, AAVrh10, AAV11, AAV12, a tyrosine capsid mutant, a heparin binding capsid mutant, an AAV2R471A capsid, an AAVAAV2/2-7m8 capsid, an AAV DJ capsid (e.g., an AAV-DJ/8 capsid, an AAV-DJ/9 capsid, or any other of the capsids described in U.S. PG Pub. 2012/0066783), AAV2 N587A capsid, AAV2 E548A capsid, AAV2 N708A capsid, AAV V708K capsid, goat AAV capsid, AAV1/AAV2 chimeric capsid, bovine AAV capsid, mouse AAV capsid, rAAV2/HBoV1 capsid, or an AAV capsid described in U.S. Pat. No. 8,283,151 or International Publication No. WO/2003/042397. In some embodiments, the AAV viral particle comprises an AAV capsid comprising an amino acid substitution at one or more of positions R484, R487, K527, K532, R585 or R588, numbering based on VP1 of AAV2. In further embodiments, a AAV particle comprises capsid proteins of an AAV serotype from Classes A-F. In some embodiments, the rAAV viral particle comprises an AAV serotype 2 capsid. In further embodiments, the AAV serotype 2 capsid comprises AAV2 capsid protein comprising a R471A amino acid substitution, numbering relative to AAV2 VP1. In some embodiments, the vector comprises AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh8, AAVrh8R, AAV9,

AAV10, AAVrh10, AAV11, AAV12, AAV2R471A, AAV DJ, a goat AAV, bovine AAV, or mouse AAV serotype inverted terminal repeats (ITRs). In some embodiments, the vector comprises AAV serotype 2 ITRs. In some embodiments, the AAV viral particle comprises one or more ITRs and capsid derived from the same AAV serotype. In other embodiments, the AAV viral particle comprises one or more ITRs derived from a different AAV serotype than the capsid of the rAAV viral particles. In some embodiments, the rAAV viral particle comprises an AAV2 capsid, and wherein the vector comprises AAV2 ITRs. In further embodiments, the AAV2 capsid comprises AAV2 capsid protein comprising a R471A amino acid substitution, numbering relative to AAV2 VP1 (see US Patent Publication 2017/0304465).

[00101] It has recently been shown that including a human rhodopsin kinase (hGRK1) promoter in an AAV5 vector results in rod- and cone-specific expression in the primate retina (Boye, et al., *Human Gene Therapy*, 23:1101-1115 (October 2012) (DOI: 10.1089/hum.2012.125)).

[00102] It has also recently been shown that AAV virions with altered capsid proteins may impart greater tissue specific infectivity. For example, AAV6 with a variant capsid protein shows increased infectivity of retinal cells, compared to wild-type AAV capsid protein (US 8,663,624). A variant capsid protein comprising a peptide insertion between two adjacent amino acids corresponding to amino acids 570 ad 611 of VP1 of AAV2, or the corresponding position in a capsid protein of another AAV serotype, confers increased infectivity of retinal cells, compared to wild-type AAV (US 9,193,956).

Expression of protein in a cornea

[00103] To express specific proteins in a cornea, AAV vectors packaged with either an endonucleotide encoding the desired protein, or AAV vectors packaged with the desired protein may be delivered or administered directly to the eye. Proteins can include, for example, CRISPR associated (Cas) proteins, or marker proteins (e.g. green fluorescent protein (GFP or eGFP).

[00104] In certain embodiments, the AAV vectors may be delivered without being enclosed in any particle or lipid vessels. In other embodiments, the AAV vectors may be enclosed in a lipid nanoparticle, liposome, non-lipid nanoparticle, or viral capsid for delivery.

[00105] In some embodiments, the compositions and/or the AAV vectors can be delivered directly to the eye. The composition and/or AAV vector may be administered to the anterior chamber of the eye, the posterior chamber of the eye, the cornea, or the vitreous chamber of the eye. In preferred embodiments, the AAV vectors are administered directly to the aqueous humor of the anterior chamber, which is in contact with the cornea. More than one AAV vector such as a dual AAV vector system may be used for the purpose of modulating gene expression as defined in the present invention.

[00106] As explained above, there are several AAV serotypes, each exhibiting tropism for certain types of tissue. Although the AAV serotype used is not particularly limited, the AAV5, AAV6, and AAV8 serotypes are preferred AAV vectors for targeting corneal and anterior tissues in the eye.

[00107] To test the viral tropism of different AAV serotypes in the present invention, several serotypes were packaged with a nucleotide sequence encoding green fluorescent protein (GFP or eGFP). These AAV-eGFP complexes were delivered intracamerally into the eye. The fluorescence of the GFP could be measured in vivo, showing the localization of the AAV-GFP. The localization of the GFP could also be assessed by performing immunohistochemistry on sections of the eye. The viral tropism of AAV5, as indicated by immunohistochemical staining, was localized to the corneal endothelium. The viral tropism of AAV6 was localized to the cornea endothelium, stroma and endothelium, and ciliary body, with some targeting to retinal cells. The viral tropism of AAV8 was localized to cornea endothelium and stroma, and ciliary body, with some targeting to retinal cells. The viral tropism of AAV2 and AAV9 was localized to both the posterior and anterior segments of the eye after IC administration, with greater expression in the posterior segment than the anterior segment.

[00108] The results show that AAV5, AAV6, and AAV8 show selective tropism for corneal tissues. When selective targeting to the cornea endothelium is desired, use of AAV5 is

preferred. Use of other AAV serotypes (e.g. AAV2), which are less tissue selective, may lead to unwanted off-target effects.

[00109] In certain embodiments, the AAV vectors may be delivered by themselves. In other embodiments, the AAV vectors may be enclosed in a lipid nanoparticle, liposome, non-lipid nanoparticle, or viral capsid for delivery.

[00110] In some embodiments, the AAV vectors can be delivered directly to the eye. The AAV vector may be administered to the anterior chamber of the eye, the posterior chamber of the eye, the cornea, or the vitreous chamber of the eye. In certain embodiments, the AAV vectors can be administered to the corneal stroma, corneal limbus, onto the epithelial surface of the cornea, or onto the endothelial membrane of the cornea. In preferred embodiments, the AAV vectors are administered directly to the aqueous humor of the anterior chamber which is in direct contact with the corneal endothelium.

Gene targeting using CRISPR complexes

[00111] In certain embodiments, a CRISPR complex is used to modify a specific nucleotide sequence of the DNA of a gene. The specific nucleotide sequence of the DNA of the gene is the "target sequence."

[00112] A CRISPR complex is a combination of a gRNA and an endonucleotide encoding for a Cas protein (gRNA:Cas endonucleotide), or a combination of a gRNA and a Cas protein (gRNA:Cas protein).

[00113] The gRNA comprises RNA sequences that are directed to a target DNA sequence. The gRNA contains a CRISPR RNA (crRNA) and transactivating crRNA (trRNA or tracrRNA). The crRNA and the trRNA may be associated on a single RNA molecule, referred to as a single guide RNA (sgRNA). Alternatively, the crRNA and trRNA may be disassociated on separate RNA molecules, and form a dual guide RNA (dgRNA). The gRNA can be targeted to either the positive or negative strand of the DNA.

[00114] The gRNA guides the Cas component (i.e. endonucleotide encoding a Cas protein, or a Cas protein) to the target sequence. The gRNA is complementary to, and hybridizes with,

the target sequence, or the reverse complement of the target sequence. In some embodiments, the gRNA sequence is 100% complementary or identical to the target sequence. Preferably, the degree of complementarity or identity between a guide sequence of a gRNA and its corresponding target sequence is at least about 50% or greater. For example, the degree of complementarity or identity may be about 50%, 55%, 60%, 65%, 70%, 80%, 85%, 90%, 95%, 96%, 97% 98%, 99%, or 100%.

[00115] In some embodiments, the gRNA is chemically modified, and comprises one or more modified nucleosides or nucleotides. Modification of nucleosides and nucleotides can include one or more of: i) alteration, e.g. replacement, of one or both of the non-linking phosphate oxygens and/or of one or more of the linking phosphate oxygens in the phosphodiester backbone (e.g. phosphorothioate or boranosphosphate linkages); ii) alteration, e.g. replacement, of a constituent of the ribose sugar, such as, for example, 2'-O-methyl and/or 2'-fluoro and/or 4-thio modifications; iii) complete replacement of the phosphate moiety with "dephospho" linkers; iv) modification or replacement of a naturally occurring nucleobase, including with a non-canonical nucleobase; v) replacement or modification of the ribose-phosphate backbone; vi) modification of the 3' end or 5' end of the oligonucleotide, e.g. removal, modification, or replacement of a terminal phosphate group, or conjugation of a moiety, cap, or linker; vii) modification or replacement of the sugar; and viii) locked or unlocked nucleic acids. Other modifications include pseudouridine, 2-thiouridine, 4-thiouridine, 5-azauridine, 5-hydroxyuridine, 5-aminouridine 5-methyluridine, 2-thiopseudouridine, 4-thiopseudouridine, 5-hydroxypseudouridine, 5-methylpseudouridine, 5-aminopseduridine, pseudoisocytidine 5-methylcytidine N-4-methyctidine, 2-thiocytidine, 5-azacytidine 5-hydroxycytidine, 5-aminocytidine, N-4-methylpseudoisocytidine, 2-thiopseudoisocytidine, 5-hydroxypseudoisocytidine, 5-aminopseudisocytidine, 5-methylpseudoisocytidie, N-6-methyladenosine, 7-deazaadenosine, 6-thioguanosine, 7-deazaguanosine, 8-azaguanosine, 6-thio-7-deazaguanosine, 6-thio-8-azaguanosine, 7-deaza-8-azaguanosine, and 6-thio-7-deaza-8-azaguanosine.

[00116] In some embodiments the Cas component comprises Type-I, Type-II, or Type-III components. In certain embodiments, the Cas component is a nuclease. In some embodiments the Cas nuclease is Cas9 or Cpf1. Preferably the Cas nuclease is Cas9. In some embodiments, the gene-editing molecule is a Cas protein (e.g, Cpf1, CasX , CasY,

C2C2, Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas5e (CasD), Cas6, Cas6e, Cas6f, Cas7, Cas8a1 , Cas8a2, Cas8b, Cas8c, Cas9 (Csn1 or Csx12), Cas10, Casl0d, CasF, CasG, CasH, Csy1, Csy2, Csy3, Cse1 (CasA), Cse2 (CasB), Cse3 (CasE), Cse4 (CasC), Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1 , Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, Cu1966, or homologs or modified versions thereof). In some embodiments, the Cas protein is a Cas9 protein (e.g., wild-type Cas9, a Cas9 nickase, a dead Cas9 (dCas9), or a split Cas9). In some embodiments, the Cas9 protein is a *Streptococcus pyogenes* Cas9 protein or *Staphylococcus aureus* Cas9 protein.

[00117] Once guided to the target sequence, the Cas nuclease cleaves the target sequence. This leads to double-stranded breaks in the DNA, or single-strand breaks if a nickase enzyme is used. Double-stranded breaks in the DNA can be repaired via non-homologous end joining (NHEJ), which is re-ligation of the break ends. NHEJ can produce indel mutations. Alternatively, the DNA may be repaired via homologous repair (HR) or homology-directed repair (HDR). HR and HDR generate precise, defined modifications at the target locus in the presence of an exogenously introduced repair template. In certain embodiments, the repair template contains a nucleotide sequence encoding a desirable mutation on a target gene, and the nucleotide sequence is inserted at the target locus of the gene.

[00118] Some of the sequences disclosed herein include the following lists (*see* WO 2017/185054). SEQ ID NOs: 1-93 are target sequences 5' of the TNRs in intron 3 of the *TCF4* gene. SEQ ID NOs: 94-190 are target sequences 3' of the TNRs in intron 3 of the *TCF4* gene. SEQ ID NOs: 191-1063 are target sequences for the wild type *COL8A2* gene. SEQ ID NOs: 1064-1069 are target sequences for the *COL8A2* Gln455Lys mutation. SEQ ID NOs: 1070-1075 are target sequences for the *COL8A2* Gln455al mutation. SEQ ID NOs: 1076-1084 are target sequences for the *COL8A2* Leu450Trp mutation.

[00119] Table A shows the sequences for SEQ ID NOs: 1085-1088 (*see* Exemplary sequences from WO 2017/185054).

[00120] The guide RNA and Cas components (i.e. the CRISPR complexes) are packaged into AAV vectors for delivery to a subject. In certain embodiments, the AAV vectors may be delivered by themselves. In other embodiments, the AAV vectors may be enclosed in a lipid nanoparticle, liposome, non-lipid nanoparticle, or viral capsid for delivery.

[00121] In some embodiments, the AAV vectors can be delivered directly to the eye. The AAV vector may be administered to the anterior chamber of the eye, the posterior chamber of the eye, the cornea, or the vitreous chamber of the eye. In certain embodiments, the AAV vectors can be administered to the corneal stroma, corneal limbus, onto the epithelial surface of the cornea, or onto the endothelial membrane of the cornea. In preferred embodiments, the AAV vectors are administered directly to the aqueous humor of the anterior chamber which is in direct contact with the corneal endothelium.

TCF4 gene targeting

[00122] The *TCF4* gene is located on chromosome 18. The cytogenic location is 18q21.2 (the long arm of chromosome 18 at position 21.2). The molecular location is on base pairs 55,222,311 to 55,635,993 on chromosome 18 (Homo sapiens Annotation Release 109, GRCh38.p12 (NCBI)).

[00123] The target sequence may be within or flanking the TNRs in the *TCF4* gene. A Cas nuclease is guided to the target sequence. In some embodiments, the Cas nuclease may be guided to a target sequence within the TNRs of the *TCF4* gene. In other embodiments, the Cas nuclease may be guided to a target sequence flanking the TNR. For example, the Cas nuclease may be directed to a target sequence 5' of the TNRs. Or the Cas nuclease may be directed to a target sequence 3' of the TNRs. In some embodiments, the Cas protein may be directed by two or more gRNAs to two target sequences flanking the TNRs. In some embodiments, the Cas nuclease may be directed by two or more gRNAs to two target sequences, wherein one is within the TNRs of the *TCF4* gene, and the other flanks the TNRs of the *TCF4* gene. Target sequences for the *TCF4* gene are chosen from SEQ ID NOs: 1-190. SEQ ID NOs: 1-93 are target sequences 5' of the TNRs in intron 3 of the *TCF4* gene. SEQ ID NOs: 94-190 are target sequences 3' of the TNRs in intron 3 of the *TCF4* gene. Guide sequences for the *TCF4* gene are chosen from SEQ ID NOs: 1089-1278. (see Sequence Listing)

[00124] The one or more gRNA comprise a guide sequence that is complementary to a target sequence in the *TCF4* gene, or the reverse complement of a target sequence in the *TCF4* gene. In some embodiments, the gRNA sequence is 100% complementary or identical to the target sequence. Preferably, the degree of complementarity or identity between a guide sequence of a gRNA and its corresponding target sequence is at least about 50% or greater. For example, the degree of complementarity or identity may be about 50%, 55%, 60%, 65%, 70%, 80%, 85%, 90%, 95%, 96%, 97% 98%, 99%, or 100%.

[00125] In some embodiments, one gRNA is used. In other embodiments, a combination of two or more gRNA are used. In certain embodiments, a gRNA targeting a sequence 5' of the TNRs is used in combination with a gRNA that targets a sequence 3' to the TNRs, in order to excise the TNRs of the *TCF4* gene. In some embodiments, a gRNA complementary to a target sequence chosen from SEQ ID NOs: 1-93 is used together with a gRNA complementary to a target sequence chosen from SEQ ID NOs: 94-190. Table 1 shows target sequences and corresponding guide sequences (*from* Ex. 1 of WO 2017/185054). Table 2 shows combinations of guide sequences (From Ex. 1 of WO 2017/185054). (*see* Exemplary sequences from WO 2017/185054)

[00126] In embodiments wherein the CRISPR complex includes an endonucleotide encoding the protein, the endonucleotide may be operably linked to one or more transcriptional or translational control sequences. In certain embodiments, the endonucleotide is operably linked to one or more promoters. The promoter may be constitutive, inducible, or tissue-specific. Examples of constitutive promoters include, but are not limited to, cytomegalovirus immediate early promoter (CMV), simian virus (SV40) promoter, adenovirus major late (MLP) promoter, Rous sarcoma virus (RSV) promoter, elongation factor-alpha (EF1a) promoter, ubiquitin promoters, actin promoters, tubulin promoters, immunoglobulin promoters, functional fragments thereof, or combinations thereof. Examples of inducible promoters include, but are not limited to, those inducible by heat shock, light, chemicals, peptides, metals, steroids, antibiotics, or alcohol. In some embodiments the promoter may be tissue specific, such as a promoter specific for expression in the cornea, e.g. the corneal edothelium.

[00127] In some embodiments, the nucleotide sequence encoding the gRNA may be operably linked to at least one transcriptional or translational control sequences. These include promoters, a 3' UTR, or a 5' UTR. The promoter may be recognized by RNA polymerase III (Pol III), such as, but limited to, U6 and H1 Pol III promoters. The Pol III promoters may be, for example, mouse or human.

[00128] In certain embodiments, one or more gRNA are packaged in AAV vectors, in combination with either an endonucleotide sequence encoding a Cas protein, or a Cas protein (e.g. Cas9) (i.e. CRISPR complexes). The AAV serotype used is not particularly limited. Preferably, the AAV vectors are of the AAV5, AAV6, or AAV8 serotype.

[00129] The AAV-CRISPR complexes can be delivered directly into the eye via intracameral or intrastromal injection. In certain embodiments, the AAV vectors may be delivered by themselves. In other embodiments, the AAV vectors may be enclosed in a lipid nanoparticle, liposome, non-lipid nanoparticle, or viral capsid for delivery.

[00130] In some embodiments, the AAV vectors can be delivered directly to the eye. The AAV vector may be administered to the anterior chamber of the eye, the posterior chamber of the eye, the cornea, or to the vitreous chamber of the eye. In certain embodiments, the AAV vectors can be administered to the corneal stroma, corneal limbus, onto the epithelial surface of the cornea, or onto the endothelial membrane of the cornea. In preferred embodiments, the AAV vectors are administered directly to the aqueous humor of the anterior chamber which is in direct contact with the corneal endothelium.

COL8A2 gene targeting

[00131] Mutations in the *COL8A2* gene, and thus the mutations in the gene products, can also be treated with the methods and compositions described herein. This can be done by developing CRISPR complexes that target specific sequences in the *COL8A2* gene that lead to the mutations.

[00132] In some embodiments, a CRISPR complex can be used to excise a target mutant nucleotide sequence on the *COL8A2* gene, and excise a nucleotide sequence of the DNA encoding a mutated gene product. The DNA may then be repaired with the process of NHEJ,

leading to the generation of indels and the loss of the mutant allele. In other embodiments, use of the CRISPR complexes can be done together with either an exogenous template for HR/HDR, or using the endogenous normal allele as a template for HR/HDR, resulting in correction of the nucleic acid mutation that leads to the amino acid mutation in the alpha 2 subunit of COL8. Mutations that can be corrected include: the Gln455Lys mutation, caused by the c.1364C>A nucleotide change; the Gln455Val mutation caused by the c.1363-1364CA>GT nucleotide changes; or the Leu450Trp mutation caused by the c.1349T>G nucleotide change.

[00133] Target sequences for the *COL8A2* gene can be selected using the NCBI Reference Sequence NM_005202.3 of transcript variant 1 of the *COL8A2* gene. This sequence does not contain mutations at positions 455 and 450 in the amino acid sequence of the COL8 gene product, and may be considered the "wild type" *COL8A2* gene sequence. Target sequences can be selected between Chr1:36097532-36100270 (hg38). Target sequences for the *COL8A2* gene are selected from SEQ ID NOs: 191-1063. Target sequences for the wild type *COL8A2* gene are shown in Table 3. Guide sequences complementary to these target sequences can be developed to target the *COL8A2* gene.

[00134] Target sequences to the mutant alleles can also be developed, based on the differences in the nucleotide sequences for the mutant alleles. Table 4 shows target sequences specific for the Gln155Lys mutation, caused by the c.1364C>A nucleotide change (SEQ ID NOs: 1064-1069). Table 5 shows target sequences specific for the Gln455Val mutation, caused by the c.1363-1364CA>GT nucleotide changes (SEQ ID NOs: 1070-1075). Table 6 shows target sequences specific for Leu450Trp mutation, caused by the c.1349T>G nucleotide change (SEQ ID NOs: 1076-1084). The mutant alleles could be targeted using gRNA comprising guide sequences complementary to the target sequences, or comprising guide sequences complementary to the reverse complement of the target sequences.

[00135] In certain embodiments, one or more gRNA are packaged in AAV vectors, in combination with either an endonucleotide sequence encoding a Cas protein, or a Cas protein (e.g. Cas9) (i.e. CRISPR complexes). The AAV serotype used is not particularly limited. Preferably, the AAV vectors are of the AAV5, AAV6, or AAV8 serotype.

[00136] The AAV-CRISPR complexes can be delivered directly into the eye via intracameral or intrastromal injection. In certain embodiments, the AAV vectors may be delivered by themselves. In other embodiments, the AAV vectors may be enclosed in a lipid nanoparticle, liposome, non-lipid nanoparticle, or viral capsid for delivery.

[00137] In some embodiments, the AAV vectors can be delivered directly to the eye. The AAV vector may be administered to the anterior chamber of the eye, the posterior chamber of the eye, or the cornea. In certain embodiments, the AAV vectors can be administered to the corneal stroma, corneal limbus, onto the epithelial surface of the cornea, or onto the endothelial membrane of the cornea. In preferred embodiments, the AAV vectors are administered directly to the aqueous humor of the anterior chamber which is in direct contact with the corneal endothelium.

Exemplary embodiments

[00138] In certain embodiments, the mutant allele is encoded by a target sequence on the target gene.

[00139] In some embodiments, at least one nucleotide sequence that is complementary to at least one mutant allele on a target gene hybridizes to a target sequence on the target gene in a cell in the subject.

[00140] In certain embodiments the target gene is *TCF4* or *COL8A2*.

[00141] In some embodiments, at least one target sequence is selected from the group consisting of SEQ ID NOs: 1-1084.

[00142] In some embodiments, at least one target sequence is specific to the *TCF4* gene, and the target sequence is selected from SEQ ID NOs: 1-190.

[00143] In some embodiments, the target sequence is specific to the *COL8A2* gene and the target sequence is selected from SEQ ID NOs: 191-1084

[00144] In some embodiments, the nucleic acid editing system is a CRISPR system, an siRNA, an shRNA, an miRNA, an antisense RNA, or an antagomir RNA.

[00145] In some embodiments, the nucleic acid editing system is a CRISPR system.

[00146] In some embodiments, the nucleic acid editing system is a CRISPR-Cas system.

[00147] In some embodiments, the CRISPR-Cas system comprises a nucleotide sequence encoding a CRISPR-associated (Cas) gene and a nucleotide sequence encoding a guide RNA (gRNA).

[00148] In some embodiments, the Cas gene encodes a Cas protein.

[00149] In some embodiments, the Cas protein encoded by the Cas gene is a Cas nuclease.

[00150] In some embodiments, the Cas nuclease is Cas9.

[00151] In some embodiments, the guide RNA comprises a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA or trRNA).

[00152] In some embodiments, the guide RNA is a single guide RNA (sgRNA), and both the crRNA and the tracrRNA are combined on one guide RNA molecule.

[00153] In some embodiments, the guide RNA is a double guide RNA (dgRNA), and the crRNA and the tracrRNA are on separate RNA molecules, used at the same time, but not combined.

[00154] In some embodiments, the CRISPR-Cas system is a CRISPR-Cas9 system.

[00155] In some embodiments, the crRNA and tracrRNA form a complex with the nucleotide sequence encoding Cas9 nuclease.

[00156] In some embodiments, the nucleotide sequence that is complementary to at least one mutant allele is a gRNA.

[00157] In some embodiments, at least one guide RNA comprises a crRNA sequence that is complementary to at least one target sequence selected from SEQ ID NOs: 1-1084.

[00158] In some embodiments, at least one guide RNA comprises a guide sequence selected from the group consisting of SEQ ID NOs: 1089-1278.

[00159] In some embodiments, the delivery system, vector, gene editing system, or composition further comprises a repair template.

[00160] In some embodiments, the repair template is selected from the group consisting of a DNA repair template, an mRNA repair template, an siRNA repair template, an miRNA repair template, and an antisense oligonucleotide repair template.

[00161] In some embodiments, the AAV vector serotype is selected from the group consisting of AAV1, AAV2, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAVrh10.

[00162] In some embodiments, the AAV vector serotype is AAV5, AAV6, or AAV8.

[00163] In some embodiments, the AAV vector serotype is AAV5.

[00164] In some embodiments, the AAV vector serotype is AAV6.

[00165] In some embodiments, the AAV vector serotype is AAV8.

[00166] In some embodiments, the delivery system, vector, nucleotide or gene editing system, or composition further comprises a promoter.

[00167] In some embodiments, the promoter is optimized for use with an AAV5, AAV6 or AAV8 vector.

[00168] In some embodiments, the promoter is tissue specific, and when operably linked with the AAV vector or the nucleotide that is a sequence that is complementary to at least one mutant allele on a target gene is active in the eye.

[00169] In some embodiments, the tissue specific promoter is active in the cornea or other anterior ocular tissues.

[00170] In some embodiments, the tissue specific promoter is active in the endothelium of the cornea.

[00171] In some embodiments, the target gene is preferentially expressed in the anterior portion of the eye. Preferably, the target gene is preferentially expressed in the cornea, and most preferably, preferentially expressed in the endothelium of the cornea.

[00172] In some embodiments, the delivery system, vector, nucleotide or gene editing system, or composition is preferentially expressed in the anterior portion of the eye after IC injection. Preferably, the delivery system, vector, nucleotide or gene editing system, or composition is preferentially expressed in the cornea, and most preferably, preferentially expressed in the endothelium of the cornea, after IC injection.

[00173] In some embodiments, the delivery system, vector, nucleotide or gene editing system, or composition is suitable for treating a disease or condition in the eye.

[00174] In some embodiments, the disease or condition in the eye is a disease or condition of the cornea.

[00175] In some embodiments, the disease or condition of the cornea is a superficial corneal dystrophy, anterior corneal dystrophy, corneal stromal dystrophy, or posterior cornea dystrophy.

[00176] In some embodiments, the disease or condition of the cornea is a posterior corneal dystrophy.

[00177] In some embodiments, the posterior corneal dystrophy is Fuchs endothelial corneal dystrophy (FECD; both early and late onset), posterior polymorphous dystrophy (PPCD; types 1, 2, and 3), congenital endothelial dystrophy (types 1 and 2), and X-linked endothelial corneal dystrophy.

[00178] In some embodiments, the corneal dystrophy is FECD.

EXAMPLES

Example 1. Methods of preparing and administering AAV vectors

AAV vectors

[00179] Wildtype AAV2, AAV5, AAV6, AAV8, and AAV9 vectors were produced by methods known in the art. Each AAV encoded for eGFP under the ubiquitous CAG promoter. Each AAV was supplied at 1e13vg/mL in a PBS + 0.001% pluronic acid formulation.

Intracameral (IC) injections

[00180] Adult male C57BL/6J mice (10-11 weeks old) were purchased from Jackson Laboratories. All animal procedures and handling were conducted according to the ARVO Statement for the use of Animals and the Regeneron Pharmaceuticals IACUC reviewed protocol. Mice were anesthetized with ketamine/xylazine mixture by intraperitoneal injection. The eyes were rinsed with sterile saline followed by a drop of tropicamide (to dilate the pupil) with a drop of proparacaine (to numb the cornea). Using a Drummond Scientific Nanoject II microinjection device fitted with a pulled glass needle (sandpaper beveled), AAV solution was filled into the needle and used to inject AAV solution into each anterior chamber. The glass needle was injected through the cornea, parallel to the iris, into the aqueous humor of the anterior chamber. A small amount of aqueous humor was allowed to leak out. Bubbles were pushed into cornea followed by 1.5 µL of AAV solution, containing 1.5e10 vg. The needle was held still after the injection for 30 sec and then pulled out in a quick smooth motion. Both OD (right eye) and OS (left eye) of each animal were injected. Control animals received injections of PBS+0.001% pluronic acid instead of AAV solution. Genteal ointment was applied to each eye to prevent corneal drying and abrasion while the mouse was placed on its ventral side (to prevent leakage and pooling) to recover from anesthesia.

Intravitreal injections

[00181] Adult male C57BL/6J mice (10-11 weeks old) were purchased from Jackson Laboratories. All animal procedures and handling were conducted according to the ARVO Statement for the use of Animals and the Regeneron Pharmaceuticals IACUC reviewed protocol. Mice were anesthetized with ketamine/xylazine mixture by intraperitoneal injection. The eyes were rinsed with sterile saline followed by a drop of tropicamide (to dilate the pupil) with a drop of proparacaine (to numb the cornea). Using a Drummond Scientific Nanoject II microinjection device fitted with a pulled glass needle (sandpaper beveled), AAV solution was filled into the needle and used to inject AAV solution into the vitreous humor of the vitreous chamber. The glass needle was injected through the sclera at the limbus of the eye into the vitreous chamber. 1.5 µL of AAV solution, containing 1.5e10 vg, was injected into the vitreous chamber using the microinjection device. The needle was pulled out in a quick smooth motion. Both OD (right eye) and OS (left eye) of each animal were injected. Control animals received injections of PBS+0.001% pluronic acid instead of AAV solution. Genteal ointment was applied to each eye to prevent corneal drying and abrasion while the mouse was placed on its ventral side (to prevent leakage and pooling) to recover from anesthesia.

Example 2. Assessment of specificity of protein targeting to different tissues in the eye.

In Vivo imaging

[00182] In vivo imaging was performed at baseline prior to injections and at timepoints post injections using the Heidelberg Spectralis HRA+OCT (Heidelberg Engineering, Inc, Germany). Mice were anesthetized and a drop of tropicamide was applied to each eye to dilate the pupil, followed by a drop of proparacaine to numb the cornea. At each time point, infrared images and fluorescence images to detect AAV-eGFP fluorescence were taken of the posterior retinal fundus (+25 diopter small animal imaging lens) and the anterior cornea (anterior segment module). The FA modality on the Heidelberg Spectralis HRA+OCT was used to detect fluorescence of eGFP protein resulting from the AAV-eGFP injections.

Immunohistochemistry

[00183] Mice that received AAV-eGFP injections, such as AAV5-eGFP, AAV6-eGFP, and AAV8-eGFP, by intraocular injection were euthanized for enucleation of their eyes. Control

mice that received PBS+0.001% pluronic acid intraocular injections were euthanized for enucleation of their eyes. Each eye was enucleated and fixed in 4% PFA overnight at 4°C. The eyes were washed in PBS followed by incubation in 30% sucrose at 4°C for a minimum of 3 days. Eyes were then embedded in OCT embedding compound and a subset of the samples were sent for cross-sectioning by Histoserv Inc (Maryland). In order to amplify regions of AAV-eGFP localization, a primary antibody for eGFP was incubated on the slides containing cross-sectioned mouse eye tissues at 4°C overnight. The secondary antibody was conjugated to Alexa-Fluor 594 (red) to differentiate from the green endogenous eGFP unamplified signal. DAPI (blue) was added to the slides to label nuclei and aid in the identification of cellular types and regions.

[00184] The slides were imaged using the Keyence microscope (Keyence Corporation of America, Illinois, USA). Regions of green and/or red fluorescence were assessed for both anatomical ocular regions and cellular localization.

eGFP protein measurement

[00185] Four mice (whole eyes) for each of the AAV serotypes, such as AAV5-eGFP, AAV6-eGFP, AAV8-eGFP, delivered by intraocular injections were euthanized for enucleation of their eyes. Two mice that received PBS+0.001% pluronic acid were included as controls for each of the AAV serotypes tested and were euthanized for enucleation of their eyes. Each eye was kept separate and processed as an individual sample. The eyes were immersed in 1X cell extraction buffer PTR (provided in the ELISA kit) and were homogenized using a tissuelyzer with stainless steel beads. The samples were centrifuged and the protein containing lysate was collected. Total protein measurements were measured using the BCA kit (Pierce BCA Protein Assay kit, ThermoFisher). Samples were assayed in triplicates for eGFP protein expression using the GFP SimpleStep ELISA kit (Abcam). eGFP expression per eye was calculated as ng/μg of total protein isolated from the eye.

[00186] Transduction efficiency and tropism varied depending on the AAV serotype used. Using Heidelberg Spectralis in vivo imaging, regions of AAV transduction after IC administration were determined. AAV2, AAV6, AAV8, and AAV9were found to target both the posterior and anterior segments of the eye after IC administration with AAV2, AAV6, and AAV9 showing the strongest eGFP expression in the anterior segment, whereas AAV5

targets only anterior ocular tissues. The data also indicate that that AAV5, AAV6, and AAV8 have a strong tropism for anterior regions after IC injections. Additionally, IC injections are also capable of delivering AAVs to the posterior tissues, as shown by the strong tropism of AAV2 and AAV9 to the posterior regions after IC injections.

Example 3. Correction of a gene mutation in the endothelial cells of the cornea

[00187] Corrections of target gene mutations such as mutations in *TCF4* or *COL8A2* in the endothelial cells of the cornea are done by administering a composition comprising a nucleic acid editing system comprising a CRISPR/Cas complex.

[00188] The CRISPR/Cas complex comprises a guide sequence that is complementary to a portion of the target gene containing the mutation and is directed to the target DNA sequence, and an endonucleotide encoding for a Cas nuclease.

[00189] The CRISPR/Cas complex is guided to the target sequence, and the Cas nuclease cleaves the target sequence. A gene insertion mutation is corrected by cleaving the target sequence, and repairing the break in the DNA. A gene mutation that is a change in a nucleotide is corrected by cleaving the mutated sequence nucleotide sequence, and repairing the DNA with a repair template comprising the nucleotide sequence of the wild-type gene.

[00190] The CRISPR/Cas complex is preferably packaged in an AAV vector, such as AAV5, AAV6 or AAV8. AAV vectors are produced by methods known in the art. Each AAV encodes for a target sequence under the ubiquitous CAG promoter. Each AAV is supplied at 1e13g/mL in a PBS + 0.001% pluronic acid formulation.

[00191] The AAV vector packaged with the CRISPR/Cas complex is administered directly to the anterior chamber of the eye via intracameral injection. Mice carrying such mutations are anesthetized with ketamine/xylazine mixture by intraperitoneal injection. The eyes are rinsed with sterile saline followed by a drop of tropicamide (to dilate the pupil) with a drop of proparacaine (to numb the cornea). Using a Drummond Scientific Nanoject II microinjection device fitted with a pulled glass needle (sandpaper beveled), AAV solution is filled into the needle and used to inject AAV solution into each anterior chamber. The glass needle is injected through the cornea, parallel to the iris, into the aqueous humor of the anterior

chamber. A small amount of aqueous humor is allowed to leak out. Bubbles are pushed into cornea followed by 1.5 µL of AAV solution, containing 1.5e10 vg. The needle is held still after the injection for 30 sec and then pulled out in a quick smooth motion. Both OD (right eye) and OS (left eye) of each animal are injected. Control animals receive injections of PBS+0.001% pluronic acid instead of AAV solution. Genteal ointment is applied to each eye to prevent corneal drying and abrasion while the mouse is placed on its ventral side (to prevent leakage and pooling) to recover from anesthesia.

[00192] Corrections of gene expression is confirmed by dissecting corneas (as well as isolating endothelial cells from said corneas) from the eyes of treated and control mice, and doing DNA and/or RNA nucleic acid sequencing.

Example 4 - Downregulation of gene expression in the endothelial cells of the cornea.

[00193] Gene expression is downregulated by administering a composition comprising at least one inhibitory nucleotide sequence that is complementary to at least one allele on a target gene, selected from an siRNA, an shRNA, an miRNA, an antisense RNA, or an antagomir RNA. The target gene is any cornea mutated gene such as *TCF4* or *COL8A2*. The inhibitory RNA is present in the composition by itself, or as part of a CRISPR/Cas complex.

[00194] The inhibitory RNA is packaged in an AAV vector similarly to Example 3. The inhibitory RNA is preferably packaged in an AAV vector, such as AAV5, AAV6 or AAV8. AAV vectors are produced by methods known in the art. Each AAV encodes for a target sequence under the ubiquitous CAG promoter. Each AAV is supplied at 1e13g/mL in a PBS + 0.001% pluronic acid formulation.

[00195] Similarly to Example 3, the AAV vector packaged with the inhibitory RNA is administered directly to the anterior chamber of the eye via intracameral injection. Mice are anesthetized with ketamine/xylazine mixture by intraperitoneal injection. The eyes are rinsed with sterile saline followed by a drop of tropicamide (to dilate the pupil) with a drop of proparacaine (to numb the cornea). Using a Drummond Scientific Nanoject II microinjection device fitted with a pulled glass needle (sandpaper beveled), AAV solution is filled into the needle and used to inject AAV solution into each anterior chamber. The glass needle is

injected through the cornea, parallel to the iris, into the aqueous humor of the anterior chamber. A small amount of aqueous humor is allowed to leak out. Bubbles are pushed into the cornea followed by 1.5 μL of AAV solution, containing 1.5e10 vg. The needle is held still after the injection for 30 sec and then pulled out in a quick smooth motion. Both OD (right eye) and OS (left eye) of each animal are injected. Control animals receive injections of PBS+0.001% pluronic acid instead of AAV solution. Genteal ointment is applied to each eye to prevent corneal drying and abrasion while the mouse is placed on its ventral side (to prevent leakage and pooling) to recover from anesthesia.

[00196] Downregulation of gene expression is confirmed by dissecting corneas from the eyes of treated and control mice, and measuring the amount of the protein encoded by the gene in the samples via Western blot. Successful downregulation of gene expression results in reduced levels of the encoded protein in corneal tissue from treated mice versus control mice.

[00197] The present invention has been described in detail, including the preferred embodiments thereof. However, it will be appreciated that those skilled in the art, upon consideration of the present disclosure, may make modifications and/or improvements on this invention that fall within the scope and spirit of the invention.

Exemplary sequences from WO 2017/185054

Table A. SEQ ID NOs: 1085-1088

Sequence	Description	SEQ ID NO.
GTTTGTGTGA TTTTGCTAAA ATGCATCACC AACAGCGAAT GGCTGCCTTA GGGACGGACA AAGAGCTGAG TGATTTACTG GATTTCAGTG CGgtaagaaa gaacggtgga aactaacaac agctgtgaaa aaaacaaaac aaaaacccaa acacttcagc tagaaaccag taggaatcta aaggacagta ataatttta attggctgaa tcctggtaa atatgaaggt cttttgaca agtttttaac tataattttg tggtgtgatg gaagattcag gcttttttt ttttgagt tttattactg gccttcaatt ccctacccac tgattacccc aaataatgga atctcacccc agtggaaagc aaaaatagac acccctaaaa ctaaaccacc cctaaaactt ggccatgtct gaacactgag actactaata ctttgcacac tactcttcgt tttatttatt gttttggaa atggaaaata gaaaatagga gacccagttg tctctttaaa gttttaagct aatgatgctt tggattggta ggacctgttc cttacatctt acctcctagt tacatctttt cctaggattc ttaaaactag tatggatatg ctgagcatac attctttaga acctttggga ctgttttggt aaatttcgta gtcgtaggat cagcacaaag cggaacttga cacacttgtg gagttttacg gctgtacttg gtccttctcc atcccttgc ttcctttcc taaaccaagt cccagacatg tcaggagaat gaattcattt ttaatgccag atgagtttgg tgtaagatgc atttgtaaag caaaataaaa agaatccaca aaacacacaa ataaaatcca aacgccttc caagtggggc tctttcatgc **tgctgctgct gctgctgctg ctgctgctgc tgctgctgct gctgctgctg ctgctgctgc tgctgctgct** gctcctcctc ctcctcctcc ttctcctcct cctcctcctc ttctagacct tcttttggag aaatggcttt cggaagtttt gccaggaaac gtagccctag gcaggcagct ttgcagcccc ctttctgctt gttgcacttt ctccattcgt tcctttgctt tttgcaggct ctgactcagg gaaggtgtgc attatccact agatacgtcg aagaagaggg aaaccaatta gggtcgaaat aaatgctgga gagagaggga gtgaaagaga gagtgagagt gagagagaga gagagtcttg cttcaaattg ctctcctgtt agagacgaaa tgagaatttta gtgcaggtgg cacttttatt tttatttggg ttcacatatg acaggcaaat cctatacgag atggaaatgg acattgccac gtttatggcc aaggttttca atataaaaca aaacaacttt tttcttctcc ttggtgaaac tagtgttttt ctagagaggc tgctggcctc caacctgaat cttgataaca ttatggggac tgtgtttgtt ccaaatgtag cagtagtact gcttggccat ctaatgaacc tgaggaaaaa gaaagaacag agtgataatg ggggctgggg tgggatctgt aatgttgttt ctcttttagt tttaagttgg atggtgatgt attttactaa ataaaccctt agcataaact ctaagctgtt tggtaacagt atgaaagatc tttgaggagc tctgaaggca caagtgtctt cttttcaact gtaatatttc tttgtttctt ttagATGTTT TCACCTCCTG TGAGCAGTGG GAAAAATGGA CCAACTTCTT TGGCAAGTGG ACATTTTACT GGCTCAA	*TCF4* intron 3 sequence with flanking exons, reverse strand (GRCh37/hg19). While commonly referred to as intron 3, many alternatively spliced isoforms of the gene exist, such that this intron may not fall between the 3rd and 4th exons of every transcript. Bold font indicates ctg repeats (TNRs). This region is variable in size. Capital letters indicate sequences of adjacent 5' and 3' exons.	1085
mN*mN*mN*NNNNNNNNNNNNNNNNNGUUUUAG AmGmCmUmAmGmAmAmAmUmAmGmCAAGUUAAA AUAAGGCUAGUCCGUUA UCAmAmCmUm UmGmAm AmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmC mGmGmUmGmCm U*mU*mU*mU	sgRNA modified sequence "N" may be any natural or non-natural nucleotide. * = PS linkage; "m" = 2'-O-Me nucleotide.	1086
NNNNNNNNNNNNNNNNNNNGUUUUAGAGCUAUGCUGUUUUG	crRNA	1087

Sequence	Description	SEQ ID NO.
	sequence "N" may be any natural or non-natural nucleotide.	
AACAGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAA CUUGAAAAAGUGGCACCGAGUCGGUGCUUUUUUU	trRNA sequence	1088

Table 1. *TCF4* target sequences and corresponding guide sequences

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
1	TTGGCAAGTGGAC ATTTTACTGG	Chr18:55585285-55585307	-	5' of TNRs of TCF4	-871	1089	UUGGCAAGUG GACAUUUUAC
2	TGTCCACTTGCCA AAGAAGTTGG	Chr18:55585294-55585316	+	5' of TNRs of TCF4	-862	1090	UGUCCACUUG CCAAAGAAGU
3	GGACCAACTT CTTTGCCAAGTGG	Chr18:55585297-55585319	-	5' of TNRs of TCF4	-859	1091	GGACCAACUU CUUUGGCAAG
4	GAAAAATGGA CCAACTTCTTTGG	Chr18:55585304-55585326	-	5' of TNRs of TCF4	-852	1092	GAAAAAUGGA CCAACUUCUU
5	CCATTTTTCC CACTGCTCACAGG	Chr18:55585318-55585340	+	5' of TNRs of TCF4	-838	1093	CCAUUUUUCC CACUGCUCAC
6	CCTGTGAGCA GTGGGAAAAATGG	Chr18:55585318-55585340	-	5' of TNRs of TCF4	-838	1094	CCUGUGAGCA GUGGGAAAAA
7	TTTTTCCCAC TGCTCACAGGAGG	Chr18:55585321-55585343	+	5' of TNRs of TCF4	-835	1095	UUUUUCCCAC UGCUCACAGG
8	TTTCACCTCC TGTGAGCAGTGGG	Chr18:55585326-55585348	-	5' of TNRs of TCF4	-830	1096	UUUCACCUCC UGUGAGCAGU
9	TTTTCACCTC CTGTGAGCAGTGG	Chr18:55585327-55585349	-	5' of TNRs of TCF4	-829	1097	UUUUCACCUC CUGUGAGCAG
10	AGATCTTTCA GGAGCTCTGAAGG	Chr18:55585399-55585421	-	5' of TNRs of TCF4	-757	1098	AGAUCUUUGA GGAGCUCUGA
11	AACAGTATCA AAGATCTTTGAGG	Chr18:55585410-55585432	-	5' of TNRs of TCF4	-746	1099	AACAGUAUGA AAGAUCUUUG
12	AGCATAAACT CTAAGCTGTTTGG	Chr18:55585434-55585456	-	5' of TNRs of TCF4	-722	1100	AGCAUAAACU CUAAGCUGUU

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
13	ACAGCTTAGA GTTTATGCTAAGG	Chr18:55585438-55585460	+	5' of TNRs of TCF4	-718	1101	ACAGCUUAGA GUUUAUGCUA
14	CAGCTTAGAG TTTATGCTAAGGG	Chr18:55585439-55585461	+	5' of TNRs of TCF4	-717	1102	CAGCUUAGAG UUUAUGCUAA
15	TCTTTTAGTT TTAAGTTGGATGG	Chr18:55585483-55585505	-	5' of TNRs of TCF4	-673	1103	UCUUUUAGUU UUAAGUUGGA
16	TTTCTCTTTT AGTTTTAAGTTGG	Chr18:55585487-555585509	-	5' of TNRs of TCF4	-669	1104	UUUCUCUUUU AGUUUUAAGU
17	GTGATAATGG GGGCTGGGGTGGG	Chr18:55585523-55585545	-	5' of TNRs of TCF4	-633	1105	GUGAUAAUGG GGGCUGGGGU
18	AGTGATAATG GGGGCTGGGGTGG	Chr18:55585524-55585546	-	5' of TNRs of TCF4	-632	1106	AGUGAUAAUG GGGGCUGGGG
19	CAGAGTGATA ATGGGGGCTGGGG	Chr18:55585527-55585549	-	5' of TNRs of TCF4	-629	1107	CAGAGUGAUA AUGGGGGCUG
20	ACAGAGTGAT AATGGGGGCTGGG	Chr18:55585528-55855550	-	5' of TNRs of TCF4	-628	1108	ACAGAGUGAU AAUGGGGGCU
21	AACAGAGTGA TAATGGGGGCTGG	Chr18:5585529-5585551	-	5' of TNRs of TCF4	-627	1109	AACAGAGUGA UAAUGGGGGC
22	AAAGAACAGA GTGATAATGGGGG	Chr18:55585533-55585555	-	5' of TNRs of TCF4	-623	1110	AAAGAACAGA GUGAUAAUGG
23	GAAAGAACAG AGTGATAATGGGG	Chr18:55585534-55585556	-	5' of TNRs of TCF4	-622	1111	GAAAGAACAG AGUGAUAAUG
24	AGAAAGAACA GAGTGATAATGGG	Chr18:55585535-55585557	-	5' of TNRs of TCF4	-621	1112	AGAAAGAACA GAGUGAUAAU
25	AAGAAAGAAC AGAGTGATAATGG	Chr18:55585536-55585558	-	5' of TNRs of TCF4	-620	1113	AAGAAAGAAC AGAGUGAUAA
26	TCTGTTCTTT CTTTTTCCTCAGG	Chr18:5585546-5585568	+	5' of TNRs of TCF4	-610	1114	UCUGUUCUUU CUUUUUCCUC

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
27	TTTTCCTCAG GTTCATTAGATGG	Chr18:55585558-55585580	+	5' of TNRs of TCF4	-598	1115	UUUUCCUCAG GUUCAUUAGA
28	TTGGCCATCT AATGAACCTGAGG	Chr18:55585562-55585584	-	5' of TNRs of TCF4	-594	1116	UUGGCCAUCU AAUGAACCUG
29	AATGTAGCAG TAGTACTGCTTGG	Chr18:55585581-55585603	-	5' of TNRs of TCF4	-575	1117	AAUGUAGCAG UAGUACUGCU
30	AGCAGTACTA CTGCTACATTTGG	Chr18:55585584-55585606	+	5' of TNRs of TCF4	-572	1118	AGCAGUACUA CUGCUACAUU
31	TGAATCTTGA TAACATTATGGGG	Chr18:55585619-55585641	-	5' of TNRs of TCF4	-537	1119	UGAAUCUUGA UAACAUUAUG
32	CTGAATCTTG ATAACATTATGGG	Chr18:55585620-55585642	-	5' of TNRs of TCF4	-536	1120	CUGAAUCUUG AUAACAUUAU
33	CCATAATGTT ATCAAGATTCAGG	Chr18:55585621-55585643	+	5' of TNRs of TCF4	-535	1121	CCAUAAUGUU AUCAAGAUUC
34	CCTGAATCTT GATAACATTATGG	Chr18:55585621-55585643	-	5' of TNRs of TCF4	-535	1122	CCUGAAUCUU GAUAACAUUA
35	AATGTTATCA AGATTCAGGTTGG	Chr18:55585625-55585647	+	5' of TNRs of TCF4	-531	1123	AAUGUUAUCA AGAUUCAGGU
36	GTTATCAAGA TTCAGGTTGGAGG	Chr18:55585628-55585650	+	5' of TNRs of TCF4	-528	1124	GUUAUCAAGA UUCAGGUUGG
37	TGTTTTTCTA GAGAGGCTGCTGG	Chr18:55585651-55585673	-	5' of TNRs of TCF4	-505	1125	UGUUUUUCUA GAGAGGCUGC
38	AAACTAGTGT TTTTCTAGAGAGG	Chr18:55585658-55585680	-	5' of TNRs of TCF4	-498	1126	AAACUAGUGU UUUUCUAGAG
39	GAAAAACACT AGTTTCACCAAGG	Chr18:55585666-55585688	+	5' of TNRs of TCF4	-490	1127	GAAAAACACU AGUUUCACCA
40	AACAACTTTT TTCTTCTCCTTGG	Chr18:55585683-55585705	-	5' of TNRs of TCF4	-473	1128	AACAACUUUU UUCUUCUCCU

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
41	TTGTTTTATA TTGAAAACCTTGG	Chr18:55585706-55585728	+	5' of TNRs of TCF4	-450	1129	UUGUUUUAUA UUGAAAACCU
42	GAAAACCTTG GCCATAAACGTGG	Chr18:55585718-55585740	+	5' of TNRs of TCF4	-438	1130	GAAAACCUUG GCCAUAAACG
43	CATTGCCACG TTTATGGCCAAGG	Chr18:55585723-55585745	-	5' of TNRs of TCF4	-433	1131	CAUUGCCACG UUUAUGGCCA
44	AATGGACATT GCCACGTTTATGG	Chr18:55585729-55585751	-	5' of TNRs of TCF4	-427	1132	AAUGGACAUU GCCACGUUUA
45	TGTCCATTTC CATCTCGTATAGG	Chr18:55585744-55585766	+	5' of TNRs of TCF4	-412	1133	UGUCCAUUUC CAUCUCGUAU
46	AATCCTATAC GAGATGGAAATGG	Chr18:55585747-55585769	-	5' of TNRs of TCF4	-409	1134	AAUCCUAUAC GAGAUGGAAA
47	CAGGCAAATC CTATACGAGATGG	Chr18:55585753-55585775	-	5' of TNRs of TCF4	-403	1135	CAGGCAAAUC CUAUACGAGA
48	TATTTGGGTT CACATATGACAGG	Chr18:55585772-55585794	-	5' of TNRs of TCF4	-384	1136	UAUUUGGGUU CACAUAUGAC
49	TGGCACTTTT ATTTTTATTTGGG	Chr18:55585787-55585809	-	5' of TNRs of TCF4	-369	1137	UGGCACUUUU AUUUUUAUUU
50	GTGGCACTTT TATTTTTATTTGG	Chr18:55585788-55585810	-	5' of TNRs of TCF4	-368	1138	GUGGCACUUU UAUUUUUAUU
51	AAATGAGAAT TTAGTGCAGGTGG	Chr18:55585807-55585829	-	5' of TNRs of TCF4	-349	1139	AAAUGAGAAU UUAGUGCAGG
52	ACGAAATGAG AATTTAGTGCAGG	Chr18:55585810-55585832	-	5' of TNRs of TCF4	-346	1140	ACGAAAUGAG AAUUUAGUGC
53	ATTCTCATTT CGTCTCTAACAGG	Chr18:55585820-55585842	+	5' of TNRs of TCF4	-336	1141	AUUCUCAUUU CGUCUCUAAC
54	AAATAAATGC TGGAGAGAGAGGG	Chr18:55585898-55585920	-	5' of TNRs of TCF4	-258	1142	AAAUAAAUGC UGGAGAGAGA

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
55	GAAATAAATG CTGGAGAGAGAGG	Chr18:55585899-55585921	-	5' of TNRs of TCF4	-257	1143	GAAAUAAAUG CUGGAGAGAG
56	ATTAGGGTCG AAATAAATGCTGG	Chr18:55585908-55585930	-	5' of TNRs of TCF4	-248	1144	AUUAGGGUCG AAAUAAAUGC
57	GCATTTATTT CGACCCTAATTGG	Chr18:55585911-55585933	+	5' of TNRs of TCF4	-245	1145	GCAUUUAUUU CGACCCUAAU
58	AAGAAGAGGG AAACCAATTAGGG	Chr18:55585924-55585946	-	5' of TNRs of TCF4	-232	1146	AAGAAGAGGG AAACCAAUUA
59	GAAGAAGAGG GAAACCAATTAGG	Chr18:5585925-5585947	-	5' of TNRs of TCF4	-231	1147	GAAGAAGAGG GAAACCAAUU
60	ACTAGATACG TCGAAGAAGAGGG	Chr18:55585937-55585959	-	5' of TNRs of TCF4	-219	1148	ACUAGAUACG UCGAAGAAGA
61	CACTAGATAC GTCGAAGAAGAGG	Chr18:55585938-55585960	-	5' of TNRs of TCF4	-218	1149	CACUAGAUAC GUCGAAGAAG
62	CTCTTCTTCG ACGTATCTAGTGG	Chr18:5585939-5585961	+	5' of TNRs of TCF4	-217	1150	CUCUUCUUCG ACGUAUCUAG
63	TGCAGGCTCT GACTCAGGGAAGG	Chr18:55585972-55585994	-	5' of TNRs of TCF4	-184	1151	UGCAGGCUCU GACUCAGGGA
64	TTTTTGCAGG CTCTGACTCAGGG	Chr18:55585976-55585998	-	5' of TNRs of TCF4	-180	1152	UUUUUGCAGG CUCUGACUCA
65	CTTTTTGCAG GCTCTGACTCAGG	Chr18:55585977-55585999	-	5' of TNRs of TCF4	-179	1153	CUUUUUGCAG GCUCUGACUC
66	TCAGAGCCTG CAAAAAGCAAAGG	Chr18:55585983-55586005	+	5' of TNRs of TCF4	-173	1154	UCAGAGCCUG CAAAAAGCAA
67	TTCGTTCCTT TGCTTTTTGCAGG	Chr18:55585989-55586011	-	5' of TNRs of TCF4	-167	1155	UUCGUUCCUU UGCUUUUUGC
68	GCAAAAAGCA AAGGAACGAATGG	Chr18:55585992-55586014	+	5' of TNRs of TCF4	-164	1156	GCAAAAAGCA AAGGAACGAA

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
69	AGAAAGTGCA ACAAGCAGAAAGG	Chr18:55586015-55586037	+	5' of TNRs of TCF4	-141	1157	AGAAAGUGCA ACAAGCAGAA
70	GAAAGTGCAA CAAGCAGAAAGGG	Chr18:55586016-55586038	+	5' of TNRs of TCF4	-140	1158	GAAAGUGCAA CAAGCAGAAA
71	AAAGTGCAAC AAGCAGAAAGGGG	Chr18:55586017-55586039	+	5' of TNRs of TCF4	-139	1159	AAAGUGCAAC AAGCAGAAAG
72	AAGTGCAACA AGCAGAAAGGGGG	Chr18:55586018-55586040	+	5' of TNRs of TCF4	-138	1160	AAGUGCAACA AGCAGAAAGG
73	GGCTGCAAAG CTGCCTGCCTAGG	Chr18:55586039-55586061	+	5' of TNRs of TCF4	-117	1161	GGCUGCAAAG CUGCCUGCCU
74	GCTGCAAAGC TGCCTGCCTAGGG	Chr18:55586040-55586062	+	5' of TNRs of TCF4	-116	1162	GCUGCAAAGC UGCCUGCCUA
75	CAGGAACCT AGCCCTAGGCAGG	Chr18:55586052-55586074	-	5' of TNRs of TCF4	-104	1163	CAGGAAACGU AGCCCUAGGC
76	CTGCCTAGGG CTACGTTTCCTGG	Chr18:55586053-55586075	+	5' of TNRs of TCF4	-103	1164	CUGCCUAGGG CUACGUUUCC
77	TTGCCAGGAA ACGTAGCCCTAGG	Chr18:55586056-55586078	-	5' of TNRs of TCF4	-100	1165	UUGCCAGGAA ACGUAGCCCU
78	TGGCTTTCGG AAGTTTTGCCAGG	Chr18:55586071-55586093	-	5' of TNRs of TCF4	-85	1166	UGGCUUUCGG AAGUUUUGCC
79	TCTTTTGGAG AAATGCCTTTCGG	Chr18:55586084-55586106	-	5' of TNRs of TCF4	-72	1167	UCUUUUGGAG AAAUGGCUUU
80	AAAGCCATTT CTCCAAAAGAAGG	Chr18:55586087-55586109	+	5' of TNRs of TCF4	-69	1168	AAAGCCAUUU CUCCAAAAGA
81	TAGACCTTCT TTTGGAGAAATGG	Chr18:55586091-55586113	-	5' of TNRs of TCF4	-65	1169	UAGACCUUCU UUUGGAGAAA
82	TCCAAAAGAA GGTCTAGAAGAGG	Chr18:55586098-55586120	+	5' of TNRs of TCF4	-58	1170	UCCAAAAGAA GGUCUAGAAG

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
83	TCCTCTTCTA GACCTTCTTTTGG	Chr18:55586099-55586121	-	5' of TNRs of TCF4	-57	1171	UCCUCUUCUA GACCUUCUUUU
84	AAAAGAAGGT CTAGAAGAGGAGG	Chr18:55586101-55586123	+	5' of TNRs of TCF4	-55	1172	AAAAGAAGGU CUAGAAGAGG
85	AGAAGGTCTA GAAGAGGAGGAGG	Chr18:55586104-55586126	+	5' of TNRs of TCF4	-52	1173	AGAAGGUCUA GAAGAGGAGG
86	AGGTCTAGAA GAGGAGGAGGAGG	Chr18:55586107-55586129	+	5' of TNRs of TCF4	-49	1174	AGGUCUAGAA GAGGAGGAGG
87	TCTAGAAGAG GAGGAGGAGGAGG	Chr18:55586110-55586132	+	5' of TNRs of TCF4	-46	1175	UCUAGAAGAG GAGGAGGAGG
88	AGAGGAGGAG GAGGAGGAGAAGG	Chr18:55586116-55586138	+	5' of TNRs of TCF4	-40	1176	AGAGGAGGAG GAGGAGGAGA
89	GGAGGAGGAG GAGGAGAAGGAGG	Chr18:55586119-55586141	+	5' of TNRs of TCF4	-37	1177	GGAGGAGGAG GAGGAGAAGG
90	GGAGGAGGAG GAGAAGGAGGAGG	Chr18:55586122-55586144	+	5' of TNRs of TCF4	-34	1178	GGAGGAGGAG GAGAAGGAGG
91	GGAGGAGGAG AAGGAGGAGGAGG	Chr18:55586125-55586147	+	5' of TNRs of TCF4	-31	1179	GGAGGAGGAG AAGGAGGAGG
92	GGAGGAGAAG GAGGAGGAGGAGG	Chr18:55586128-55586150	+	5' of TNRs of TCF4	-28	1180	GGAGGAGAAG GAGGAGGAGG
93	GGAGAAGGAG GAGGAGGAGGAGG	Chr18:55586131-55586153	+	5' of TNRs of TCF4	-25	1181	GGAGAAGGAG GAGGAGGAGG
94	CAGCATGAAA GAGCCCCACTTGG	Chr18:55586225-55586247	+	3' of TNRs of TCF4	69	1182	CAGCAUGAAA GAGCCCCACU
95	ATGAAAGAGC CCCACTTGGAAGG	Chr18:55586229-55586251	+	3' of TNRs of TCF4	73	1183	AUGAAAGAGC CCCACUUGGA
96	AAAGAGCCCC ACTTGGAAGGCGG	Chr18:55586232-55586254	+	3' of TNRs of TCF4	76	1184	AAAGAGCCCC ACUUGGAAGG

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
97	GCCCCACTTG GAAGGCGGTTTGG	Chr18:55586237-55586259	+	3' of TNRs of TCF4	81	1185	GCCCCACUUG GAAGGCGGUU
98	TCCAAACCGC CTTCCAAGTG GGG	Chr18:55586238-55586260	-	3' of TNRs of TCF4	82	1186	UCCAAACCGC CUUCCAAGUG
99	ATCCAAACCG CCTTCCAAGTGGG	Chr18:55586239-55586261	-	3' of TNRs of TCF4	83	1187	AUCCAAACCG CCUUCCAAGU
100	AATCCAAACC GCCTTCCAAGTGG	Chr18:55586240-55586262	-	3' of TNRs of TCF4	84	1188	AAUCCAAACC GCCUUCCAAG
101	GATTTTATTT GTGTGTTTTGTGG	Chr18:55586259-55586281	+	3' of TNRs of TCF4	103	1189	GAUUUUAUUU GUGUGUUUUG
102	CATCTTACAC CAAACTCATCTGG	Chr18:55586308-55586330	+	3' of TNRs of TCF4	152	1190	CAUCUUACAC CAAACUCAUC
103	TTTTTAATGC CAGATGAGTTTGG	Chr18:55586317-55586339	-	3' of TNRs of TCF4	161	1191	UUUUUAAUGC CAGAUGAGUU
104	ATTCATTCTC CTGACATGTCTGG	Chr18:55586343-55586365	+	3' of TNRs of TCF4	187	1192	AUUCAUUCUC CUGACAUGUC
105	TTCATTCTCC TGACATGTCTGGG	Chr18:55586344-55586366	+	3' of TNRs of TCF4	188	1193	UUCAUUCUCC UGACAUGUCU
106	CTCCTGACAT GTCTGGGACTTGG	Chr18:55586350-55586372	+	3' of TNRs of TCF4	194	1194	CUCCUGACAU GUCUGGGACU
107	AACCAAGTCC CAGACATGTCAGG	Chr18:55586352-55586374	-	3' of TNRs of TCF4	196	1195	AACCAAGUCC CAGACAUGUC
108	ACATGTCTGG GACTTGGTTTAGG	Chr18:55586356-55586378	+	3' of TNRs of TCF4	200	1196	ACAUGUCUGG GACUUGGUUU
109	CTGGGACTTG GTTTAGGAAAAGG	Chr18:55586362-55586384	+	3' of TNRs of TCF4	206	1197	CUGGGACUUG GUUUAGGAAA

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
110	GGTTTAGGAA AAGGAAGCAAAGG	Chr18:55586371-55586393	+	3' of TNRs of TCF4	215	1198	GGUUUAGGAA AAGGAAGCAA
111	GTTTAGGAAA AGGAAGCAAAGGG	Chr18:55586372-55586394	+	3' of TNRs of TCF4	216	1199	GUUUAGGAAA AGGAAGCAAA
112	AGGAAAAGGA AGCAAAGGGATGG	Chr18:55586376-55586398	+	3' of TNRs of TCF4	220	1200	AGGAAAAGGA AGCAAAGGGA
113	AGGAAGCAAA GGGATGGAGAAGG	Chr18:55586382-55586404	+	3' of TNRs of TCF4	226	1201	AGGAAGCAAA GGGAUGGAGA
114	TGGAGTTTTA CGGCTGTACTTGG	Chr18:55586406-55586428	-	3' of TNRs of TCF4	250	1202	UGGAGUUUUA CGGCUGUACU
115	GACACACTTG TGGAGTTTTACGG	Chr18:55586416-55586438	-	3' of TNRs of TCF4	260	1203	GACACACUUG UGGAGUUUUA
116	AGCGGAACTT GACACACTTGTGG	Chr18:55586426-55586448	-	3' of TNRs of TCF4	270	1204	AGCGGAACUU GACACACUUG
117	GTCGTAGGAT CAGCACAAAGCGG	Chr18:55586444-55586466	-	3' of TNRs of TCF4	288	1205	GUCGUAGGAU CAGCACAAAG
118	TTGGTAAATT TCGTAGTCGTAGG	Chr18:55586459-55586481	-	3' of TNRs of TCF4	303	1206	UUGGUAAAUU UCGUAGUCGU
119	ATTTACCAAA ACAGTCCAAAAGG	Chr18:55586473-55586495	+	3' of TNRs of TCF4	317	1207	AUUUACCAAA ACAGUCCAAA
120	TAGAACCTTT TGGACTGTTTTGG	Chr18:55586478-55586500	-	3' of TNRs of TCF4	322	1208	UAGAACCUUU UGGACUGUUU
121	ATACATTCTT TAGAACCTTTTGG	Chr18:55586488-55586510	-	3' of TNRs of TCF4	332	1209	AUACAUUCUU UAGAACCUUU
122	TAGGATTCTT AAAACTAGTATGG	Chr18:55586522-55586544	-	3' of TNRs of TCF4	366	1210	UAGGAUUCUU AAAACUAGUA
123	ATACTAGTTT TAAGAATCCTAGG	Chr18:55586524-55586546	+	3' of TNRs of TCF4	368	1211	AUACUAGUUU UAAGAAUCCU

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
124	TCCTAGGAAA AGATGTAACTAGG	Chr18:55586540-55586562	+	3' of TNRs of TCF4	384	1212	UCCUAGGAAA AGAUGUAACU
125	TCCTAGTTAC ATCTTTTCCTAGG	Chr18:55586541-55586563	-	3' of TNRs of TCF4	385	1213	UCCUAGUUAC AUCUUUUCCU
126	TAGGAAAAGA TGTAACTAGGAGG	Chr18:55586543-55586565	+	3' of TNRs of TCF4	387	1214	UAGGAAAAGA UGUAACUAGG
127	TAACTAGGAG GTAAGATGTAAGG	Chr18:55586555-55586577	+	3' of TNRs of TCF4	399	1215	UAACUAGGAG GUAAGAUGUA
128	GGAGGTAAGA TGTAAGGAACAGG	Chr18:55586561-55586583	+	3' of TNRs of TCF4	405	1216	GGAGGUAAGA UGUAAGGAAC
129	TAATGATGCT TTGGATTGGTAGG	Chr18:55586585-55586607	-	3' of TNRs of TCF4	429	1217	UAAUGAUGCU UUGGAUUGGU
130	AAGCTAATGA TGCTTTGGATTGG	Chr18:55586589-55586611	-	3' of TNRs of TCF4	433	1218	AAGCUAAUGA UGCUUUGGAU
131	GTTTTAAGCT AATGATGCTTTGG	Chr18:55586594-55586616	-	3' of TNRs of TCF4	438	1219	GUUUUAAGCU AAUGAUGCUU
132	TAAAACTTTA AAGAGACAACTGG	Chr18:55586611-55586633	+	3' of TNRs of TCF4	455	1220	UAAAACUUUA AAGAGACAAC
133	AAAACTTTAA AGAGACAACTGGG	Chr18:55586612-55586634	+	3' of TNRs of TCF4	456	1221	AAAACUUUAA AGAGACAACU
134	GGAAATGGAA AATAGAAAATAGG	Chr18:55586638-55586660	-	3' of TNRs of TCF4	482	1222	GGAAAUGGAA AAUAGAAAAU
135	TTATTTATTG TTTTTGGAAATGG	Chr18:55586653-55586675	-	3' of TNRs of TCF4	497	1223	UUAUUUAUUG UUUUUGGAAA
136	TTCGTTTTAT TTATTGTTTTTGG	Chr18:55586659-55586681	-	3' of TNRs of TCF4	503	1224	UUCGUUUUAU UUAUUGUUUU
137	GTAGTCTCAG TGTTCAGACATGG	Chr18:55586702-55586724	+	3' of TNRs of TCF4	546	1225	GUAGUCUCAG UGUUCAGACA

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
138	TTCAGACATG GCCAAGTTTTAGG	Chr18:55586714-55586736	+	3' of TNRs of TCF4	558	1226	UUCAGACAUG GCCAAGUUUU
139	TCAGACATGG CCAAGTTTTAGGG	Chr18:55586715-55586737	+	3' of TNRs of TCF4	559	1227	UCAGACAUGG CCAAGUUUUA
140	CAGACATGGC CAAGTTTTAGGGG	Chr18:55586716-55586738	+	3' of TNRs of TCF4	560	1228	CAGACAUGGC CAAGUUUUAG
141	ACATGGCCAA GTTTTAGGGGTGG	Chr18:55586719-55586741	+	3' of TNRs of TCF4	563	1229	ACAUGGCCAA GUUUUAGGGG
142	ACTAAACCAC CCCTAAAACTTGG	Chr18:55586725-55586747	-	3' of TNRs of TCF4	569	1230	ACUAAACCAC CCCUAAAACU
143	TTTAGGGGTG GTTTAGTTTTAGG	Chr18:55586731-55586753	+	3' of TNRs of TCF4	575	1231	UUUAGGGGUG GUUUAGUUUU
144	TTAGGGGTGG TTTAGTTTTAGGG	Chr18:55586732-55586754	+	3' of TNRs of TCF4	576	1232	UUAGGGGUGG UUUAGUUUUA
145	TAGGGGTGGT TTAGTTTTAGGGG	Chr18:55586733-55586755	+	3' of TNRs of TCF4	577	1233	UAGGGGUGGU UUAGUUUUAG
146	TGTCTATTTT TGCTTTCCACTGG	Chr18:55586756-55586778	+	3' of TNRs of TCF4	600	1234	UGUCUAUUUU UGCUUUCCAC
147	GTCTATTTTT GCTTTCCACTGGG	Chr18:55586757-55586779	+	3' of TNRs of TCF4	601	1235	GUCUAUUUUU GCUUUCCACU
148	TCTATTTTTG CTTTCCACTGGGG	Chr18:55586758-55586780	+	3' of TNRs of TCF4	602	1236	UCUAUUUUUG CUUUCCACUG
149	ATAATGGAAT CTCACCCCAGTGG	Chr18:55586772-55586794	-	3' of TNRs of TCF4	616	1237	AUAAUGGAAU CUCACCCCAG
150	TGGGGTGAGA TTCCATTATTTGG	Chr18:55586776-55586798	+	3' of TNRs of TCF4	620	1238	UGGGGUGAGA UUCCAUUAUU
151	GGGGTGAGAT TCCATTATTTGGG	Chr18:55586777-55586799	+	3' of TNRs of TCF4	621	1239	GGGGUGAGAU UCCAUUAUUU

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
152	GGGTGAGATT CCATTATTTGGGG	Chr18:55586778-55586800	+	3' of TNRs of TCF4	622	1240	GGGUGAGAUU CCAUUAUUUG
153	CCATTATTTG GGGTAATCAGTGG	Chr18:55586788-55586810	+	3' of TNRs of TCF4	632	1241	CCAUUAUUUG GGGUAAUCAG
154	CCACTGATTA CCCCAAATAATGG	Chr18:55586788-55586810	-	3' of TNRs of TCF4	632	1242	CCACUGAUUA CCCCAAAUAA
155	CATTATTTGG GGTAATCAGTGGG	Chr18:55586789-55586811	+	3' of TNRs of TCF4	633	1243	CAUUAUUUGG GGUAAUCAGU
156	ATTTGGGGTA ATCAGTGGGTAGG	Chr18:55586793-55586815	+	3' of TNRs of TCF4	637	1244	AUUUGGGGUA AUCAGUGGGU
157	TTTGGGGTAA TCAGTGGGTAGGG	Chr18:55586794-55586816	+	3' of TNRs of TCF4	638	1245	UUUGGGGUAA UCAGUGGGUA
158	ATCAGTGGGT AGGGAATTGAAGG	Chr18:55586803-55586825	+	3' of TNRs of TCF4	647	1246	AUCAGUGGGU AGGGAAUUGA
159	TTTTTTTTGA GTTTTATTACTGG	Chr18:55586826-55586848	-	3' of TNRs of TCF4	670	1247	UUUUUUUUGA GUUUUAUUAC
160	TGTGGTGTGA TGGAAGATTCAGG	Chr18:55586856-55586878	-	3' of TNRs of TCF4	700	1248	UGUGGUGUGA UGGAAGAUUC
161	ACTATAATTT TGTGGTGTGATGG	Chr18:55586866-55586888	-	3' of TNRs of TCF4	710	1249	ACUAUAAUUU UGUGGUGUGA
162	AGTTTTTAAC TATAATTTTGTGG	Chr18:55586874-55586896	-	3' of TNRs of TCF4	718	1250	AGUUUUUAAC UAUAAUUUUG
163	AAAGACCTTC ATATTTACCAAGG	Chr18:55586903-55586925	+	3' of TNRs of TCF4	747	1251	AAAGACCUUC AUAUUUACCA
164	TGAATCCTTG GTAAATATGAAGG	Chr18:55586908-55586930	-	3' of TNRs of TCF4	752	1252	UGAAUCCUUG GUAAAUAUGA
165	TTTTTAATTG GCTGAATCCTTGG	Chr18:55586920-55586942	-	3' of TNRs of TCF4	764	1253	UUUUUAAUUG GCUGAAUCCU

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
166	GGACAGTAAT AATTTTTAATTGG	Chr18:55586932-55586954	-	3' of TNRs of TCF4	776	1254	GGACAGUAAU AAUUUUUAAU
167	ACTGTCCTTT AGATTCCTACTGG	Chr18:55586948-55586970	+	3' of TNRs of TCF4	792	1255	ACUGUCCUUU AGAUUCCUAC
168	AGAAACCAGT AGGAATCTAAAGG	Chr18:55586953-55586975	-	3' of TNRs of TCF4	797	1256	AGAAACCAGU AGGAAUCUAA
169	CACTTCAGCT AGAAACCAGTAGG	Chr18:55586963-55586985	-	3' of TNRs of TCF4	807	1257	CACUUCAGCU AGAAACCAGU
170	TGGTTTCTAG CTGAAGTGTTTGG	Chr18:55586968-55586990	+	3' of TNRs of TCF4	812	1258	UGGUUUCUAG CUGAAGUGUU
171	GGTTTCTAGC TGAAGTGTTTGGG	Chr18:55586969-55586991	+	3' of TNRs of TCF4	813	1259	GGUUUCUAGC UGAAGUGUUU
172	AGTGCGGTAA GAAAGAACGGTGG	Chr18:55587028-55587050	-	3' of TNRs of TCF4	872	1260	AGUGCGGUAA GAAAGAACGG
173	TTCAGTGCGG TAAGAAAGAACGG	Chr18:55587031-55587053	-	3' of TNRs of TCF4	875	1261	UUCAGUGCGG UAAGAAAGAA
174	TGATTTACTG GATTTCAGTGCGG	Chr18:55587044-55587066	-	3' of TNRs of TCF4	888	1262	UGAUUUACUG GAUUUCAGUG
175	CAAAGAGCTG AGTGATTTACTGG	Chr18:55587056-55587078	-	3' of TNRs of TCF4	900	1263	CAAAGAGCUG AGUGAUUUAC
176	CAGCTCTTTG TCCGTCCCTAAGG	Chr18:55587069-55587091	+	3' of TNRs of TCF4	913	1264	CAGCUCUUUG UCCGUCCCUA
177	GCGAATGGCT GCCTTAGGGACGG	Chr18:55587080-55587102	-	3' of TNRs of TCF4	924	1265	GCGAAUGGCU GCCUUAGGGA
178	AACAGCGAAT GGCTGCCTTAGGG	Chr18:55587084-55587106	-	3' of TNRs of TCF4	928	1266	AACAGCGAAU GGCUGCCUUA
179	CAACAGCGAA TGGCTGCCTTAGG	Chr18:55587085-55587107	-	3' of TNRs of TCF4	929	1267	CAACAGCGAA UGGCUGCCUU

SEQ ID NO	Target sequence (including PAM)	Chromosomal location	Strand	Orientation	Distance to start of TNR	SEQ ID NO	Guide sequence
180	CTAAGGCAGC CATTCGCTGTTGG	Chr18:55587086-55587108	+	3' of TNRs of TCF4	930	1268	CUAAGGCAGC CAUUCGCUGU
181	AATGCATCAC CAACAGCGAATGG	Chr18:55587095-55587117	-	3' of TNRs of TCF4	939	1269	AAUGCAUCAC CAACAGCGAA
182	ATCACACAAA CCTAGAAACATGG	Chr18:55587126-55587148	+	3' of TNRs of TCF4	970	1270	AUCACACAAA CCUAGAAACA
183	GCGGTTATTT CCATGTTTCTAGG	Chr18:55587136-55587158	-	3' of TNRs of TCF4	980	1271	GCGGUUAUUU CCAUGUUUCU
184	GGGACTGGAT TTTCTGATTGCGG	Chr18:55587155-55587177	-	3' of TNRs of TCF4	999	1272	GGGACUGGAU UUUCUGAUUG
185	GAAAATCCAG TCCCAATCCTTGG	Chr18:55587164-55587186	+	3' of TNRs of TCF4	1008	1273	GAAAAUCCAG UCCCAAUCCU
186	TTTTCTCCAA GGATTGGGACTGG	Chr18:55587170-55587192	-	3' of TNRs of TCF4	1014	1274	UUUUCUCCAA GGAUUGGGAC
187	TTGTGTTTTC TCCAAGGATTGGG	Chr18:55587175-55587197	-	3' of TNRs of TCF4	1019	1275	UUGUGUUUUC UCCAAGGAUU
188	ATTGTGTTTT CTCCAAGGATTGG	Chr18:55587176-55587198	-	3' of TNRs of TCF4	1020	1276	AUUGUGUUUU CUCCAAGGAU
189	ATCCTTGGAG AAAACACAATCGG	Chr18:55587179-55587201	+	3' of TNRs of TCF4	1023	1277	AUCCUUGGAG AAAACACAAU
190	ATCCGATTGT GTTTTCTCCAAGG	Chr18:55587181-55587203	-	3' of TNRs of TCF4	1025	1278	AUCCGAUUGU GUUUUCUCCA

Table 2. Combinations of *TCF4* guide sequences

SEQ ID NOs (5' Target Sequence)	SEQ ID NOs (3' Target Sequence)
83	109
85	109
86	112
85	125
86	109
85	107
83	125
86	125
86	107
64	106
85	114
86	114
83	114
53	114
83	112
74	114
85	108
83	107
85	115
58	109
86	108
83	96
74	109
77	115
53	96
83	108
74	125
85	94
86	96
53	107
83	94
71	115
77	96
58	112
77	109
85	95
53	94
77	95
86	115
85	96

SEQ ID NOs (5' Target Sequence)	SEQ ID NOs (3' Target Sequence)
58	94
58	115
71	96
58	107
83	95
58	96
77	94
56	94
77	108
77	112
86	94
77	107
86	95
56	96
54	94
71	94
77	114
71	114
56	95
58	95
53	112
71	109
74	112
54	96
58	114
74	108
53	108
74	107
74	94
71	107
71	95
71	112
74	96
74	95
74	115
54	95
53	95
77	125
54	112
56	114
73	101
54	109
54	114

SEQ ID NOs (5' Target Sequence)	SEQ ID NOs (3' Target Sequence)
54	107
54	108
54	115
56	109
56	107
56	108
56	112
56	115
56	125
53	125

Table 3. Target sequences for wild-type *COL8A2* gene

SEQ ID No	Chromosomal location	Strand	Target sequence
191	Chr1:36097532-36097554	+	GGGGAGGAGGCCAGGGCAGCAGG
192	Chr1:36097545-36097567	+	GGGCAGCAGGACCCCCCCCGCGG
193	Chr1:36097546-36097568	+	GGCAGCAGGACCCCCCCCGCGGG
194	Chr1:36097554-36097576	+	GACCCCCCCCGCGGGTTATGTGG
195	Chr1:36097555-36097577	+	ACCCCCCCCGCGGGTTATGTGGG
196	Chr1:36097556-36097578	+	CCCCCCCCGCGGGTTATGTGGGG
197	Chr1:36097556-36097578	−	CCCCACATAACCCGCGGGGGGGG
198	Chr1:36097557-36097579	−	GCCCCACATAACCCGCGGGGGGG
199	Chr1:36097558-36097580	−	TGCCCCACATAACCCGCGGGGGG
200	Chr1:36097559-36097581	−	CTGCCCCACATAACCCGCGGGGG
201	Chr1:36097560-36097582	−	TCTGCCCCACATAACCCGCGGGG
202	Chr1:36097561-36097583	−	CTCTGCCCCACATAACCCGCGGG
203	Chr1:36097562-36097584	−	GCTCTGCCCCACATAACCCGCGG
204	Chr1:36097578-36097600	+	GCAGAGCAAGAATCCTGAAAAGG
205	Chr1:36097581-36097603	+	GAGCAAGAATCCTGAAAAGGAGG
206	Chr1:36097586-36097608	+	AGAATCCTGAAAAGGAGGAGTGG
207	Chr1:36097591-36097613	−	TACATCCACTCCTCCTTTTCAGG
208	Chr1:36097599-36097621	+	GGAGGAGTGGATGTACTCCGTGG
209	Chr1:36097607-36097629	+	GGATGTACTCCGTGGAGTAGAGG
210	Chr1:36097614-36097636	+	CTCCGTGGAGTAGAGGCCGTTGG
211	Chr1:36097616-36097638	−	GGCCAACGGCCTCTACTCCACGG
212	Chr1:36097619-36097641	+	TGGAGTAGAGGCCGTTGGCCTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
213	Chr1:36097627-36097649	+	AGGCCGTTGGCCTGGTCCGACGG
214	Chr1:36097630-36097652	-	ATGCCGTCGGACCAGGCCAACGG
215	Chr1:36097637-36097659	-	GGTGCAGATGCCGTCGGACCAGG
216	Chr1:36097643-36097665	-	GGTCTGGGTGCAGATGCCGTCGG
217	Chr1:36097646-36097668	+	ACGGCATCTGCACCCAGACCTGG
218	Chr1:36097653-36097675	+	CTGCACCCAGACCTGGTCGTTGG
219	Chr1:36097654-36097676	+	TGCACCCAGACCTGGTCGTTGGG
220	Chr1:36097658-36097680	-	GCGGCCCAACGACCAGGTCTGGG
221	Chr1:36097659-36097681	-	TGCGGCCCAACGACCAGGTCTGG
222	Chr1:36097664-36097686	+	CCTGGTCGTTGGGCCGCAGCTGG
223	Chr1:36097664-36097686	-	CCAGCTGCGGCCCAACGACCAGG
224	Chr1:36097671-36097693	+	GTTGGGCCGCAGCTGGAGCACGG
225	Chr1:36097677-36097699	-	GTGGGGCCGTGCTCCAGCTGCGG
226	Chr1:36097688-36097710	+	GCACGGCCCCACCAGATGCCTGG
227	Chr1:36097694-36097716	+	CCCCACCAGATGCCTGGTCCAGG
228	Chr1:36097694-36097716	-	CCTGGACCAGGCATCTGGTGGGG
229	Chr1:36097695-36097717	-	ACCTGGACCAGGCATCTGGTGGG
230	Chr1:36097696-36097718	-	TACCTGGACCAGGCATCTGGTGG
231	Chr1:36097699-36097721	-	GGCTACCTGGACCAGGCATCTGG
232	Chr1:36097706-36097728	-	CAAGAAGGGCTACCTGGACCAGG
233	Chr1:36097712-36097734	-	TGAGTACAAGAAGGGCTACCTGG
234	Chr1:36097719-36097741	+	GCCCTTCTTGTACTCATCGTAGG
235	Chr1:36097720-36097742	-	ACCTACGATGAGTACAAGAAGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
236	Chr1:36097721-36097743	-	TACCTACGATGAGTACAAGAAGG
237	Chr1:36097725-36097747	+	CTTGTACTCATCGTAGGTATAGG
238	Chr1:36097728-36097750	+	GTACTCATCGTAGGTATAGGTGG
239	Chr1:36097732-36097754	+	TCATCGTAGGTATAGGTGGCCGG
240	Chr1:36097751-36097773	+	CCGGCACGTTGTTCTTGTACAGG
241	Chr1:36097751-36097773	-	CCTGTACAAGAACAACGTGCCGG
242	Chr1:36097752-36097774	+	CGGCACGTTGTTCTTGTACAGGG
243	Chr1:36097767-36097789	+	GTACAGGGCCACCCACACGTTGG
244	Chr1:36097775-36097797	-	CAAGGGCACCAACGTGTGGGTGG
245	Chr1:36097778-36097800	-	CGTCAAGGGCACCAACGTGTGGG
246	Chr1:36097779-36097801	-	ACGTCAAGGGCACCAACGTGTGG
247	Chr1:36097787-36097809	+	TGGTGCCCTTGACGTGCACATGG
248	Chr1:36097792-36097814	-	GCTTACCATGTGCACGTCAAGGG
249	Chr1:36097793-36097815	-	TGCTTACCATGTGCACGTCAAGG
250	Chr1:36097816-36097838	+	AAGTAGTAGACGCCGCCCACAGG
251	Chr1:36097817-36097839	+	AGTAGTAGACGCCGCCCACAGGG
252	Chr1:36097821-36097843	+	GTAGACGCCGCCCACAGGGCAGG
253	Chr1:36097828-36097850	-	ATCTTCACCTGCCCTGTGGGCGG
254	Chr1:36097831-36097853	-	GGCATCTTCACCTGCCCTGTGGG
255	Chr1:36097832-36097854	-	TGGCATCTTCACCTGCCCTGTGG
256	Chr1:36097836-36097858	+	AGGGCAGGTGAAGATGCCAGTGG
257	Chr1:36097840-36097862	+	CAGGTGAAGATGCCAGTGGCTGG
258	Chr1:36097841-36097863	+	AGGTGAAGATGCCAGTGGCTGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
259	Chr1:36097852-36097874	-	AGCGGCTACAACCCAGCCACTGG
260	Chr1:36097856-36097878	+	TGGCTGGGTTGTAGCCGCTGTGG
261	Chr1:36097870-36097892	-	ACTCTCTACAATGGCCACAGCGG
262	Chr1:36097874-36097896	+	TGTGGCCATTGTAGAGAGTCCGG
263	Chr1:36097879-36097901	-	TTTGACCGGACTCTCTACAATGG
264	Chr1:36097887-36097909	+	GAGAGTCCGGTCAAATTTCACGG
265	Chr1:36097888-36097910	+	AGAGTCCGGTCAAATTTCACGGG
266	Chr1:36097893-36097915	-	GCATGCCCGTGAAATTTGACCGG
267	Chr1:36097899-36097921	+	AAATTTCACGGGCATGCCCGAGG
268	Chr1:36097902-36097924	+	TTTCACGGGCATGCCCGAGGCGG
269	Chr1:36097903-36097925	+	TTCACGGGCATGCCCGAGGCGGG
270	Chr1:36097904-36097926	+	TCACGGGCATGCCCGAGGCGGGG
271	Chr1:36097908-36097930	+	GGGCATGCCCGAGGCGGGGAAGG
272	Chr1:36097909-36097931	+	GGCATGCCCGAGGCGGGGAAGGG
273	Chr1:36097914-36097936	+	GCCCGAGGCGGGGAAGGGCGAGG
274	Chr1:36097915-36097937	-	ACCTCGCCCTTCCCCGCCTCGGG
275	Chr1:36097916-36097938	-	CACCTCGCCCTTCCCCGCCTCGG
276	Chr1:36097932-36097954	+	CGAGGTGAGCACCGCAGTGAAGG
277	Chr1:36097936-36097958	+	GTGAGCACCGCAGTGAAGGCCGG
278	Chr1:36097941-36097963	+	CACCGCAGTGAAGGCCGGTGTGG
279	Chr1:36097943-36097965	-	TGCCACACCGGCCTTCACTGCGG
280	Chr1:36097946-36097968	+	CAGTGAAGGCCGGTGTGGCATGG
281	Chr1:36097947-36097969	+	AGTGAAGGCCGGTGTGGCATGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
282	Chr1:36097955-36097977	-	GCTGTCTGCCCATGCCACACCGG
283	Chr1:36097975-36097997	+	AGCTCGCCCAGCCCAAACTGTGG
284	Chr1:36097981-36098003	-	GGCAAGCCACAGTTTGGGCTGGG
285	Chr1:36097982-36098004	-	GGGCAAGCCACAGTTTGGGCTGG
286	Chr1:36097986-36098008	-	AGGGGGGCAAGCCACAGTTTGGG
287	Chr1:36097987-36098009	-	AAGGGGGGCAAGCCACAGTTTGG
288	Chr1:36097998-36098020	+	CTTGCCCCCCTTGCCCAGCACGG
289	Chr1:36098002-36098024	-	GGTGCCGTGCTGGGCAAGGGGGG
290	Chr1:36098003-36098025	-	GGGTGCCGTGCTGGGCAAGGGGG
291	Chr1:36098004-36098026	-	AGGGTGCCGTGCTGGGCAAGGGG
292	Chr1:36098005-36098027	-	GAGGGTGCCGTGCTGGGCAAGGG
293	Chr1:36098006-36098028	-	GGAGGGTGCCGTGCTGGGCAAGG
294	Chr1:36098011-36098033	-	GGTGTGGAGGGTGCCGTGCTGGG
295	Chr1:36098012-36098034	-	CGGTGTGGAGGGTGCCGTGCTGG
296	Chr1:36098019-36098041	+	GGCACCCTCCACACCGCCGTTGG
297	Chr1:36098020-36098042	+	GCACCCTCCACACCGCCGTTGGG
298	Chr1:36098023-36098045	-	CTGCCCAACGGCGGTGTGGAGGG
299	Chr1:36098024-36098046	+	CCTCCACACCGCCGTTGGGCAGG
300	Chr1:36098024-36098046	-	CCTGCCCAACGGCGGTGTGGAGG
301	Chr1:36098027-36098049	-	GCACCTGCCCAACGGCGGTGTGG
302	Chr1:36098032-36098054	-	GGCTTGCACCTGCCCAACGGCGG
303	Chr1:36098035-36098057	-	GCAGGCTTGCACCTGCCCAACGG
304	Chr1:36098053-36098075	-	TTCGATGAGACTGGCATCGCAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
305	Chr1:36098055-36098077	+	TGCGATGCCAGTCTCATCGAAGG
306	Chr1:36098062-36098084	+	CCAGTCTCATCGAAGGCCCCAGG
307	Chr1:36098062-36098084	-	CCTGGGGCCTTCGATGAGACTGG
308	Chr1:36098063-36098085	+	CAGTCTCATCGAAGGCCCCAGGG
309	Chr1:36098064-36098086	+	AGTCTCATCGAAGGCCCCAGGGG
310	Chr1:36098071-36098093	+	TCGAAGGCCCCAGGGGCACCAGG
311	Chr1:36098072-36098094	+	CGAAGGCCCCAGGGGCACCAGGG
312	Chr1:36098073-36098095	+	GAAGGCCCCAGGGGCACCAGGGG
313	Chr1:36098074-36098096	+	AAGGCCCCAGGGGCACCAGGGGG
314	Chr1:36098078-36098100	-	GGGACCCCCTGGTGCCCCTGGGG
315	Chr1:36098079-36098101	-	CGGGACCCCCTGGTGCCCCTGGG
316	Chr1:36098080-36098102	+	CCAGGGGCACCAGGGGGTCCCGG
317	Chr1:36098080-36098102	-	CCGGGACCCCCTGGTGCCCCTGG
318	Chr1:36098081-36098103	+	CAGGGGCACCAGGGGGTCCCGGG
319	Chr1:36098082-36098104	+	AGGGGCACCAGGGGGTCCCGGGG
320	Chr1:36098083-36098105	+	GGGGCACCAGGGGGTCCCGGGGG
321	Chr1:36098088-36098110	+	ACCAGGGGGTCCCGGGGGCCCGG
322	Chr1:36098089-36098111	+	CCAGGGGGTCCCGGGGGCCCGGG
323	Chr1:36098089-36098111	-	CCCGGGCCCCCGGGACCCCCTGG
324	Chr1:36098092-36098114	+	GGGGGTCCCGGGGGCCCGGGAGG
325	Chr1:36098098-36098120	+	CCCGGGGGCCCGGGAGGCCCCGG
326	Chr1:36098098-36098120	-	CCGGGGCCTCCCGGGCCCCCGGG
327	Chr1:36098099-36098121	-	TCCGGGGCCTCCCGGGCCCCCGG

SEQ ID No	Chromosomal location	Strand	Target sequence
328	Chr1:36098101-36098123	+	GGGGGCCCGGGAGGCCCCGGAGG
329	Chr1:36098102-36098124	+	GGGGCCCGGGAGGCCCCGGAGGG
330	Chr1:36098106-36098128	-	CGGGCCCTCCGGGGCCTCCCGGG
331	Chr1:36098107-36098129	-	ACGGGCCCTCCGGGGCCTCCCGG
332	Chr1:36098115-36098137	-	CTGGAATCACGGGCCCTCCGGGG
333	Chr1:36098116-36098138	+	CCCGGAGGGCCCGTGATTCCAGG
334	Chr1:36098116-36098138	-	CCTGGAATCACGGGCCCTCCGGG
335	Chr1:36098117-36098139	+	CCGGAGGGCCCGTGATTCCAGGG
336	Chr1:36098117-36098139	-	CCCTGGAATCACGGGCCCTCCGG
337	Chr1:36098118-36098140	+	CGGAGGGCCCGTGATTCCAGGGG
338	Chr1:36098125-36098147	+	CCCGTGATTCCAGGGGAGCCAGG
339	Chr1:36098125-36098147	-	CCTGGCTCCCCTGGAATCACGGG
340	Chr1:36098126-36098148	+	CCGTGATTCCAGGGGAGCCAGGG
341	Chr1:36098126-36098148	-	CCCTGGCTCCCCTGGAATCACGG
342	Chr1:36098134-36098156	+	CCAGGGGAGCCAGGGACCCCTGG
343	Chr1:36098134-36098156	-	CCAGGGGTCCCTGGCTCCCCTGG
344	Chr1:36098135-36098157	+	CAGGGGAGCCAGGGACCCCTGGG
345	Chr1:36098136-36098158	+	AGGGGAGCCAGGGACCCCTGGGG
346	Chr1:36098137-36098159	+	GGGGAGCCAGGGACCCCTGGGGG
347	Chr1:36098143-36098165	-	ACGGGGCCCCCAGGGGTCCCTGG
348	Chr1:36098145-36098167	+	AGGGACCCCTGGGGGCCCCGTGG
349	Chr1:36098146-36098168	+	GGGACCCCTGGGGGCCCCGTGGG
350	Chr1:36098150-36098172	-	TGGGCCCACGGGGCCCCCAGGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
351	Chr1:36098151-36098173	-	CTGGGCCCACGGGGCCCCCAGGG
352	Chr1:36098152-36098174	-	GCTGGGCCCACGGGGCCCCCAGG
353	Chr1:36098160-36098182	-	CTGGCACGGCTGGGCCCACGGGG
354	Chr1:36098161-36098183	+	CCCGTGGGCCCAGCCGTGCCAGG
355	Chr1:36098161-36098183	-	CCTGGCACGGCTGGGCCCACGGG
356	Chr1:36098162-36098184	-	ACCTGGCACGGCTGGGCCCACGG
357	Chr1:36098169-36098191	-	CAGGGGAACCTGGCACGGCTGGG
358	Chr1:36098170-36098192	-	GCAGGGGAACCTGGCACGGCTGG
359	Chr1:36098174-36098196	-	GAGAGCAGGGGAACCTGGCACGG
360	Chr1:36098179-36098201	-	GAGGGGAGAGCAGGGGAACCTGG
361	Chr1:36098185-36098207	+	TCCCCTGCTCTCCCCTCTCCAGG
362	Chr1:36098186-36098208	+	CCCCTGCTCTCCCCTCTCCAGGG
363	Chr1:36098186-36098208	-	CCCTGGAGAGGGGAGAGCAGGGG
364	Chr1:36098187-36098209	+	CCCTGCTCTCCCCTCTCCAGGGG
365	Chr1:36098187-36098209	-	CCCCTGGAGAGGGGAGAGCAGGG
366	Chr1:36098188-36098210	+	CCTGCTCTCCCCTCTCCAGGGGG
367	Chr1:36098188-36098210	-	CCCCCTGGAGAGGGGAGAGCAGG
368	Chr1:36098194-36098216	+	CTCCCCTCTCCAGGGGGCCCTGG
369	Chr1:36098196-36098218	-	TGCCAGGGCCCCCTGGAGAGGGG
370	Chr1:36098197-36098219	-	CTGCCAGGGCCCCCTGGAGAGGG
371	Chr1:36098198-36098220	+	CCTCTCCAGGGGGCCCTGGCAGG
372	Chr1:36098198-36098220	-	CCTGCCAGGGCCCCCTGGAGAGG
373	Chr1:36098203-36098225	+	CCAGGGGGCCCTGGCAGGCCTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
374	Chr1:36098203-36098225	-	CCAGGCCTGCCAGGGCCCCCTGG
375	Chr1:36098211-36098233	-	AGGGGGAACCAGGCCTGCCAGGG
376	Chr1:36098212-36098234	-	AAGGGGGAACCAGGCCTGCCAGG
377	Chr1:36098216-36098238	+	GCAGGCCTGGTTCCCCCTTCAGG
378	Chr1:36098221-36098243	+	CCTGGTTCCCCCTTCAGGCCCGG
379	Chr1:36098221-36098243	-	CCGGGCCTGAAGGGGGAACCAGG
380	Chr1:36098225-36098247	+	GTTCCCCCTTCAGGCCCGGCAGG
381	Chr1:36098228-36098250	-	AGGCCTGCCGGGCCTGAAGGGGG
382	Chr1:36098229-36098251	-	AAGGCCTGCCGGGCCTGAAGGGG
383	Chr1:36098230-36098252	-	CAAGGCCTGCCGGGCCTGAAGGG
384	Chr1:36098231-36098253	+	CCTTCAGGCCCGGCAGGCCTTGG
385	Chr1:36098231-36098253	-	CCAAGGCCTGCCGGGCCTGAAGG
386	Chr1:36098232-36098254	+	CTTCAGGCCCGGCAGGCCTTGGG
387	Chr1:36098233-36098255	+	TTCAGGCCCGGCAGGCCTTGGGG
388	Chr1:36098239-36098261	-	ATTGGGCCCCAAGGCCTGCCGGG
389	Chr1:36098240-36098262	-	TATTGGGCCCCAAGGCCTGCCGG
390	Chr1:36098242-36098264	+	GGCAGGCCTTGGGGCCCAATAGG
391	Chr1:36098243-36098265	+	GCAGGCCTTGGGGCCCAATAGGG
392	Chr1:36098248-36098270	-	GCTGGCCCTATTGGGCCCCAAGG
393	Chr1:36098251-36098273	+	TGGGGCCCAATAGGGCCAGCTGG
394	Chr1:36098256-36098278	-	AGGGTCCAGCTGGCCCTATTGGG
395	Chr1:36098257-36098279	-	CAGGGTCCAGCTGGCCCTATTGG
396	Chr1:36098258-36098280	+	CAATAGGGCCAGCTGGACCCTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
397	Chr1:36098266-36098288	+	CCAGCTGGACCCTGGAGTCCTGG
398	Chr1:36098266-36098288	-	CCAGGACTCCAGGGTCCAGCTGG
399	Chr1:36098267-36098289	+	CAGCTGGACCCTGGAGTCCTGGG
400	Chr1:36098275-36098297	-	TCAGGAATCCCAGGACTCCAGGG
401	Chr1:36098276-36098298	-	CTCAGGAATCCCAGGACTCCAGG
402	Chr1:36098277-36098299	+	CTGGAGTCCTGGGATTCCTGAGG
403	Chr1:36098278-36098300	+	TGGAGTCCTGGGATTCCTGAGGG
404	Chr1:36098284-36098306	-	AGGGGTCCCTCAGGAATCCCAGG
405	Chr1:36098288-36098310	+	GGATTCCTGAGGGACCCCTCAGG
406	Chr1:36098293-36098315	+	CCTGAGGGACCCCTCAGGCCAGG
407	Chr1:36098293-36098315	-	CCTGGCCTGAGGGGTCCCTCAGG
408	Chr1:36098302-36098324	+	CCCCTCAGGCCAGGCTGCCCAGG
409	Chr1:36098302-36098324	-	CCTGGGCAGCCTGGCCTGAGGGG
410	Chr1:36098303-36098325	+	CCCTCAGGCCAGGCTGCCCAGGG
411	Chr1:36098303-36098325	-	CCCTGGGCAGCCTGGCCTGAGGG
412	Chr1:36098304-36098326	-	TCCCTGGGCAGCCTGGCCTGAGG
413	Chr1:36098311-36098333	-	TTGGGGCTCCCTGGGCAGCCTGG
414	Chr1:36098319-36098341	-	AAGGTGACTTGGGGCTCCCTGGG
415	Chr1:36098320-36098342	-	AAAGGTGACTTGGGGCTCCCTGG
416	Chr1:36098328-36098350	-	TGGGGCAGAAAGGTGACTTGGGG
417	Chr1:36098329-36098351	-	CTGGGGCAGAAAGGTGACTTGGG
418	Chr1:36098330-36098352	+	CCAAGTCACCTTTCTGCCCCAGG
419	Chr1:36098330-36098352	-	CCTGGGGCAGAAAGGTGACTTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
420	Chr1:36098331-36098353	+	CAAGTCACCTTTCTGCCCCAGGG
421	Chr1:36098338-36098360	-	GCAGGAGCCCTGGGGCAGAAAGG
422	Chr1:36098346-36098368	-	CAGGGGTGGCAGGAGCCCTGGGG
423	Chr1:36098347-36098369	+	CCCAGGGCTCCTGCCACCCCTGG
424	Chr1:36098347-36098369	-	CCAGGGGTGGCAGGAGCCCTGGG
425	Chr1:36098348-36098370	-	ACCAGGGGTGGCAGGAGCCCTGG
426	Chr1:36098356-36098378	+	CCTGCCACCCCTGGTCCTCCAGG
427	Chr1:36098356-36098378	-	CCTGGAGGACCAGGGGTGGCAGG
428	Chr1:36098357-36098379	+	CTGCCACCCCTGGTCCTCCAGGG
429	Chr1:36098360-36098382	-	TCGCCCTGGAGGACCAGGGGTGG
430	Chr1:36098363-36098385	-	GGGTCGCCCTGGAGGACCAGGGG
431	Chr1:36098364-36098386	-	CGGGTCGCCCTGGAGGACCAGGG
432	Chr1:36098365-36098387	-	ACGGGTCGCCCTGGAGGACCAGG
433	Chr1:36098371-36098393	-	GGTTTCACGGGTCGCCCTGGAGG
434	Chr1:36098374-36098396	+	CCAGGGCGACCCGTGAAACCCGG
435	Chr1:36098374-36098396	-	CCGGGTTTCACGGGTCGCCCTGG
436	Chr1:36098383-36098405	-	AAGGGTGAGCCGGGTTTCACGGG
437	Chr1:36098384-36098406	-	CAAGGGTGAGCCGGGTTTCACGG
438	Chr1:36098385-36098407	+	CGTGAAACCCGGCTCACCCTTGG
439	Chr1:36098386-36098408	+	GTGAAACCCGGCTCACCCTTGGG
440	Chr1:36098392-36098414	-	ACTGGGCCCAAGGGTGAGCCGGG
441	Chr1:36098393-36098415	-	AACTGGGCCCAAGGGTGAGCCGG
442	Chr1:36098395-36098417	+	GGCTCACCCTTGGGCCCAGTTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
443	Chr1:36098401-36098423	+	CCCTTGGGCCCAGTTGGTCCAGG
444	Chr1:36098401-36098423	-	CCTGGACCAACTGGGCCCAAGGG
445	Chr1:36098402-36098424	+	CCTTGGGCCCAGTTGGTCCAGGG
446	Chr1:36098402-36098424	-	CCCTGGACCAACTGGGCCCAAGG
447	Chr1:36098403-36098425	+	CTTGGGCCCAGTTGGTCCAGGGG
448	Chr1:36098404-36098426	+	TTGGGCCCAGTTGGTCCAGGGGG
449	Chr1:36098409-36098431	-	ATGGACCCCCTGGACCAACTGGG
450	Chr1:36098410-36098432	-	CATGGACCCCCTGGACCAACTGG
451	Chr1:36098411-36098433	+	CAGTTGGTCCAGGGGGTCCATGG
452	Chr1:36098412-36098434	+	AGTTGGTCCAGGGGGTCCATGGG
453	Chr1:36098419-36098441	+	CCAGGGGGTCCATGGGCCCCAGG
454	Chr1:36098419-36098441	-	CCTGGGGCCCATGGACCCCCTGG
455	Chr1:36098428-36098450	-	AGGGGACTTCCTGGGGCCCATGG
456	Chr1:36098435-36098457	-	AGGTGAGAGGGGACTTCCTGGGG
457	Chr1:36098436-36098458	-	CAGGTGAGAGGGGACTTCCTGGG
458	Chr1:36098437-36098459	+	CCAGGAAGTCCCCTCTCACCTGG
459	Chr1:36098437-36098459	-	CCAGGTGAGAGGGGACTTCCTGG
460	Chr1:36098438-36098460	+	CAGGAAGTCCCCTCTCACCTGGG
461	Chr1:36098446-36098468	+	CCCCTCTCACCTGGGACCCCTGG
462	Chr1:36098446-36098468	-	CCAGGGGTCCCAGGTGAGAGGGG
463	Chr1:36098447-36098469	-	ACCAGGGGTCCCAGGTGAGAGGG
464	Chr1:36098448-36098470	-	AACCAGGGGTCCCAGGTGAGAGG
465	Chr1:36098455-36098477	-	GCTGGGAAACCAGGGGTCCCAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
466	Chr1:36098459-36098481	+	GGACCCCTGGTTTCCCAGCCAGG
467	Chr1:36098462-36098484	-	TGGCCTGGCTGGGAAACCAGGGG
468	Chr1:36098463-36098485	-	GTGGCCTGGCTGGGAAACCAGGG
469	Chr1:36098464-36098486	-	AGTGGCCTGGCTGGGAAACCAGG
470	Chr1:36098467-36098489	+	GGTTTCCCAGCCAGGCCACTAGG
471	Chr1:36098472-36098494	-	AGGGGCCTAGTGGCCTGGCTGGG
472	Chr1:36098473-36098495	-	CAGGGGCCTAGTGGCCTGGCTGG
473	Chr1:36098474-36098496	+	CAGCCAGGCCACTAGGCCCCTGG
474	Chr1:36098477-36098499	-	TGACCAGGGGCCTAGTGGCCTGG
475	Chr1:36098482-36098504	-	CGAGGTGACCAGGGGCCTAGTGG
476	Chr1:36098490-36098512	-	CTGGCATTCGAGGTGACCAGGGG
477	Chr1:36098491-36098513	+	CCCTGGTCACCTCGAATGCCAGG
478	Chr1:36098491-36098513	-	CCTGGCATTCGAGGTGACCAGGG
479	Chr1:36098492-36098514	-	GCCTGGCATTCGAGGTGACCAGG
480	Chr1:36098500-36098522	+	CCTCGAATGCCAGGCACTCCTGG
481	Chr1:36098500-36098522	-	CCAGGAGTGCCTGGCATTCGAGG
482	Chr1:36098501-36098523	+	CTCGAATGCCAGGCACTCCTGGG
483	Chr1:36098502-36098524	+	TCGAATGCCAGGCACTCCTGGGG
484	Chr1:36098503-36098525	+	CGAATGCCAGGCACTCCTGGGGG
485	Chr1:36098509-36098531	-	GGAGGACCCCCAGGAGTGCCTGG
486	Chr1:36098512-36098534	+	GGCACTCCTGGGGGTCCTCCAGG
487	Chr1:36098518-36098540	-	GCAGGGCCTGGAGGACCCCCAGG
488	Chr1:36098527-36098549	-	AAGGGTGAGGCAGGGCCTGGAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
489	Chr1:36098530-36098552	+	CCAGGCCCTGCCTCACCCTTAGG
490	Chr1:36098530-36098552	-	CCTAAGGGTGAGGCAGGGCCTGG
491	Chr1:36098535-36098557	-	CTGGGCCTAAGGGTGAGGCAGGG
492	Chr1:36098536-36098558	+	CCTGCCTCACCCTTAGGCCCAGG
493	Chr1:36098536-36098558	-	CCTGGGCCTAAGGGTGAGGCAGG
494	Chr1:36098537-36098559	+	CTGCCTCACCCTTAGGCCCAGGG
495	Chr1:36098538-36098560	+	TGCCTCACCCTTAGGCCCAGGGG
496	Chr1:36098539-36098561	+	GCCTCACCCTTAGGCCCAGGGGG
497	Chr1:36098540-36098562	-	GCCCCCTGGGCCTAAGGGTGAGG
498	Chr1:36098545-36098567	-	CGTGGGCCCCCTGGGCCTAAGGG
499	Chr1:36098546-36098568	-	ACGTGGGCCCCCTGGGCCTAAGG
500	Chr1:36098553-36098575	-	CTGGCAGACGTGGGCCCCCTGGG
501	Chr1:36098554-36098576	+	CCAGGGGGCCCACGTCTGCCAGG
502	Chr1:36098554-36098576	-	CCTGGCAGACGTGGGCCCCCTGG
503	Chr1:36098562-36098584	-	CAGGGCTTCCTGGCAGACGTGGG
504	Chr1:36098563-36098585	-	GCAGGGCTTCCTGGCAGACGTGG
505	Chr1:36098572-36098594	+	CCAGGAAGCCCTGCAGACCCAGG
506	Chr1:36098572-36098594	-	CCTGGGTCTGCAGGGCTTCCTGG
507	Chr1:36098580-36098602	-	CTGGACTTCCTGGGTCTGCAGGG
508	Chr1:36098581-36098603	+	CCTGCAGACCCAGGAAGTCCAGG
509	Chr1:36098581-36098603	-	CCTGGACTTCCTGGGTCTGCAGG
510	Chr1:36098582-36098604	+	CTGCAGACCCAGGAAGTCCAGGG
511	Chr1:36098583-36098605	+	TGCAGACCCAGGAAGTCCAGGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
512	Chr1:36098584-36098606	+	GCAGACCCAGGAAGTCCAGGGGG
513	Chr1:36098589-36098611	-	GGGGTCCCCCTGGACTTCCTGGG
514	Chr1:36098590-36098612	-	GGGGGTCCCCCTGGACTTCCTGG
515	Chr1:36098599-36098621	-	CAGGGTCTTGGGGGTCCCCCTGG
516	Chr1:36098602-36098624	+	GGGGGACCCCCAAGACCCTGTGG
517	Chr1:36098603-36098625	+	GGGGACCCCCAAGACCCTGTGGG
518	Chr1:36098608-36098630	-	CAGGGCCCACAGGGTCTTGGGGG
519	Chr1:36098609-36098631	-	GCAGGGCCCACAGGGTCTTGGGG
520	Chr1:36098610-36098632	-	AGCAGGGCCCACAGGGTCTTGGG
521	Chr1:36098611-36098633	-	GAGCAGGGCCCACAGGGTCTTGG
522	Chr1:36098617-36098639	+	CCCTGTGGGCCCTGCTCCCCTGG
523	Chr1:36098617-36098639	-	CCAGGGGAGCAGGGCCCACAGGG
524	Chr1:36098618-36098640	-	GCCAGGGGAGCAGGGCCCACAGG
525	Chr1:36098626-36098648	-	GATGGGGAGCCAGGGGAGCAGGG
526	Chr1:36098627-36098649	-	GGATGGGGAGCCAGGGGAGCAGG
527	Chr1:36098633-36098655	-	AGGGGAGGATGGGGAGCCAGGGG
528	Chr1:36098634-36098656	-	CAGGGGAGGATGGGGAGCCAGGG
529	Chr1:36098635-36098657	+	CCTGGCTCCCCATCCTCCCCTGG
530	Chr1:36098635-36098657	-	CCAGGGGAGGATGGGGAGCCAGG
531	Chr1:36098642-36098664	-	GGGTGAGCCAGGGGAGGATGGGG
532	Chr1:36098643-36098665	-	GGGGTGAGCCAGGGGAGGATGGG
533	Chr1:36098644-36098666	-	AGGGGTGAGCCAGGGGAGGATGG
534	Chr1:36098648-36098670	-	GGACAGGGGTGAGCCAGGGGAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
535	Chr1:36098651-36098673	-	GGGGGACAGGGGTGAGCCAGGGG
536	Chr1:36098652-36098674	-	TGGGGGACAGGGGTGAGCCAGGG
537	Chr1:36098653-36098675	-	TTGGGGGACAGGGGTGAGCCAGG
538	Chr1:36098662-36098684	+	CCCCTGTCCCCCAAGAGTCCTGG
539	Chr1:36098662-36098684	-	CCAGGACTCTTGGGGGACAGGGG
540	Chr1:36098663-36098685	+	CCCTGTCCCCCAAGAGTCCTGGG
541	Chr1:36098663-36098685	-	CCCAGGACTCTTGGGGGACAGGG
542	Chr1:36098664-36098686	-	TCCCAGGACTCTTGGGGGACAGG
543	Chr1:36098669-36098691	-	TGGGGTCCCAGGACTCTTGGGGG
544	Chr1:36098670-36098692	-	CTGGGGTCCCAGGACTCTTGGGG
545	Chr1:36098671-36098693	-	GCTGGGGTCCCAGGACTCTTGGG
546	Chr1:36098672-36098694	-	AGCTGGGGTCCCAGGACTCTTGG
547	Chr1:36098674-36098696	+	AAGAGTCCTGGGACCCCAGCTGG
548	Chr1:36098675-36098697	+	AGAGTCCTGGGACCCCAGCTGGG
549	Chr1:36098680-36098702	-	AGGGGCCCAGCTGGGGTCCCAGG
550	Chr1:36098687-36098709	-	GGGGGACAGGGGCCCAGCTGGGG
551	Chr1:36098688-36098710	-	AGGGGGACAGGGGCCCAGCTGGG
552	Chr1:36098689-36098711	-	AAGGGGGACAGGGGCCCAGCTGG
553	Chr1:36098691-36098713	+	AGCTGGGCCCCTGTCCCCCTTGG
554	Chr1:36098692-36098714	+	GCTGGGCCCCTGTCCCCCTTGGG
555	Chr1:36098693-36098715	+	CTGGGCCCCTGTCCCCCTTGGGG
556	Chr1:36098698-36098720	+	CCCCTGTCCCCCTTGGGGCCTGG
557	Chr1:36098698-36098720	-	CCAGGCCCCAAGGGGGACAGGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
558	Chr1:36098699-36098721	-	GCCAGGCCCCAAGGGGGACAGGG
559	Chr1:36098700-36098722	-	TGCCAGGCCCCAAGGGGGACAGG
560	Chr1:36098705-36098727	-	AGGACTGCCAGGCCCCAAGGGGG
561	Chr1:36098706-36098728	-	CAGGACTGCCAGGCCCCAAGGGG
562	Chr1:36098707-36098729	+	CCCTTGGGGCCTGGCAGTCCTGG
563	Chr1:36098707-36098729	-	CCAGGACTGCCAGGCCCCAAGGG
564	Chr1:36098708-36098730	-	GCCAGGACTGCCAGGCCCCAAGG
565	Chr1:36098716-36098738	-	TATGGGATGCCAGGACTGCCAGG
566	Chr1:36098724-36098746	+	TCCTGGCATCCCATAGCCAGTGG
567	Chr1:36098725-36098747	+	CCTGGCATCCCATAGCCAGTGGG
568	Chr1:36098725-36098747	-	CCCACTGGCTATGGGATGCCAGG
569	Chr1:36098726-36098748	+	CTGGCATCCCATAGCCAGTGGGG
570	Chr1:36098733-36098755	-	TGATAGGCCCCACTGGCTATGGG
571	Chr1:36098734-36098756	-	CTGATAGGCCCCACTGGCTATGG
572	Chr1:36098740-36098762	+	CCAGTGGGGCCTATCAGCCCAGG
573	Chr1:36098740-36098762	-	CCTGGGCTGATAGGCCCCACTGG
574	Chr1:36098741-36098763	+	CAGTGGGGCCTATCAGCCCAGGG
575	Chr1:36098742-36098764	+	AGTGGGGCCTATCAGCCCAGGGG
576	Chr1:36098743-36098765	+	GTGGGGCCTATCAGCCCAGGGGG
577	Chr1:36098744-36098766	+	TGGGGCCTATCAGCCCAGGGGGG
578	Chr1:36098749-36098771	-	CGGGGCCCCCCTGGGCTGATAGG
579	Chr1:36098750-36098772	+	CTATCAGCCCAGGGGGGCCCCGG
580	Chr1:36098751-36098773	+	TATCAGCCCAGGGGGGCCCCGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
581	Chr1:36098757-36098779	-	CAGGGACCCGGGGCCCCCCTGGG
582	Chr1:36098758-36098780	+	CCAGGGGGGCCCCGGGTCCCTGG
583	Chr1:36098758-36098780	-	CCAGGGACCCGGGGCCCCCCTGG
584	Chr1:36098767-36098789	-	AAAGGGGAGCCAGGGACCCGGGG
585	Chr1:36098768-36098790	-	CAAAGGGGAGCCAGGGACCCGGG
586	Chr1:36098769-36098791	+	CCGGGTCCCTGGCTCCCCTTTGG
587	Chr1:36098769-36098791	-	CCAAAGGGGAGCCAGGGACCCGG
588	Chr1:36098775-36098797	-	CAGGGGCCAAAGGGGAGCCAGGG
589	Chr1:36098776-36098798	-	TCAGGGGCCAAAGGGGAGCCAGG
590	Chr1:36098779-36098801	+	GGCTCCCCTTTGGCCCCTGATGG
591	Chr1:36098780-36098802	+	GCTCCCCTTTGGCCCCTGATGGG
592	Chr1:36098783-36098805	-	GGGCCCATCAGGGGCCAAAGGGG
593	Chr1:36098784-36098806	-	AGGGCCCATCAGGGGCCAAAGGG
594	Chr1:36098785-36098807	-	CAGGGCCCATCAGGGGCCAAAGG
595	Chr1:36098788-36098810	+	TTGGCCCCTGATGGGCCCTGTGG
596	Chr1:36098792-36098814	-	AGGACCACAGGGCCCATCAGGGG
597	Chr1:36098793-36098815	-	CAGGACCACAGGGCCCATCAGGG
598	Chr1:36098794-36098816	+	CCTGATGGGCCCTGTGGTCCTGG
599	Chr1:36098794-36098816	-	CCAGGACCACAGGGCCCATCAGG
600	Chr1:36098803-36098825	-	GCAGGGTTGCCAGGACCACAGGG
601	Chr1:36098804-36098826	-	AGCAGGGTTGCCAGGACCACAGG
602	Chr1:36098812-36098834	+	CCTGGCAACCCTGCTGCCCCTGG
603	Chr1:36098812-36098834	-	CCAGGGGCAGCAGGGTTGCCAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
604	Chr1:36098813-36098835	+	CTGGCAACCCTGCTGCCCCTGGG
605	Chr1:36098820-36098842	-	TGGGAGTCCCAGGGGCAGCAGGG
606	Chr1:36098821-36098843	-	GTGGGAGTCCCAGGGGCAGCAGG
607	Chr1:36098828-36098850	-	AGACGGTGTGGGAGTCCCAGGGG
608	Chr1:36098829-36098851	-	TAGACGGTGTGGGAGTCCCAGGG
609	Chr1:36098830-36098852	-	GTAGACGGTGTGGGAGTCCCAGG
610	Chr1:36098836-36098858	+	ACTCCCACACCGTCTACTCCAGG
611	Chr1:36098839-36098861	+	CCCACACCGTCTACTCCAGGAGG
612	Chr1:36098839-36098861	-	CCTCCTGGAGTAGACGGTGTGGG
613	Chr1:36098840-36098862	-	ACCTCCTGGAGTAGACGGTGTGG
614	Chr1:36098845-36098867	-	AAAGGACCTCCTGGAGTAGACGG
615	Chr1:36098848-36098870	+	TCTACTCCAGGAGGTCCTTTTGG
616	Chr1:36098849-36098871	+	CTACTCCAGGAGGTCCTTTTGGG
617	Chr1:36098854-36098876	-	GTGGGCCCAAAAGGACCTCCTGG
618	Chr1:36098863-36098885	+	CCTTTTGGGCCCACAGCTCCTGG
619	Chr1:36098863-36098885	-	CCAGGAGCTGTGGGCCCAAAAGG
620	Chr1:36098872-36098894	-	AGGGGGGAGCCAGGAGCTGTGGG
621	Chr1:36098873-36098895	-	CAGGGGGGAGCCAGGAGCTGTGG
622	Chr1:36098874-36098896	+	CACAGCTCCTGGCTCCCCCCTGG
623	Chr1:36098875-36098897	+	ACAGCTCCTGGCTCCCCCCTGGG
624	Chr1:36098876-36098898	+	CAGCTCCTGGCTCCCCCCTGGGG
625	Chr1:36098881-36098903	+	CCTGGCTCCCCCCTGGGGCCTGG
626	Chr1:36098881-36098903	-	CCAGGCCCCAGGGGGGAGCCAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
627	Chr1:36098888-36098910	–	TGGAGTTCCAGGCCCCAGGGGGG
628	Chr1:36098889-36098911	–	CTGGAGTTCCAGGCCCCAGGGGG
629	Chr1:36098890-36098912	+	CCCCTGGGGCCTGGAACTCCAGG
630	Chr1:36098890-36098912	–	CCTGGAGTTCCAGGCCCCAGGGG
631	Chr1:36098891-36098913	–	TCCTGGAGTTCCAGGCCCCAGGG
632	Chr1:36098892-36098914	–	CTCCTGGAGTTCCAGGCCCCAGG
633	Chr1:36098893-36098915	+	CTGGGGCCTGGAACTCCAGGAGG
634	Chr1:36098899-36098921	–	TCTGGGCCTCCTGGAGTTCCAGG
635	Chr1:36098908-36098930	–	AAGGGTGAGTCTGGGCCTCCTGG
636	Chr1:36098916-36098938	–	CAGGAGACAAGGGTGAGTCTGGG
637	Chr1:36098917-36098939	+	CCAGACTCACCCTTGTCTCCTGG
638	Chr1:36098917-36098939	–	CCAGGAGACAAGGGTGAGTCTGG
639	Chr1:36098918-36098940	+	CAGACTCACCCTTGTCTCCTGGG
640	Chr1:36098919-36098941	+	AGACTCACCCTTGTCTCCTGGGG
641	Chr1:36098926-36098948	+	CCCTTGTCTCCTGGGGCCCCAGG
642	Chr1:36098926-36098948	–	CCTGGGGCCCCAGGAGACAAGGG
643	Chr1:36098927-36098949	–	TCCTGGGGCCCCAGGAGACAAGG
644	Chr1:36098935-36098957	–	GATGGGCTTCCTGGGGCCCCAGG
645	Chr1:36098942-36098964	–	TGGTTTGGATGGGCTTCCTGGGG
646	Chr1:36098943-36098965	–	CTGGTTTGGATGGGCTTCCTGGG
647	Chr1:36098944-36098966	+	CCAGGAAGCCCATCCAAACCAGG
648	Chr1:36098944-36098966	–	CCTGGTTTGGATGGGCTTCCTGG
649	Chr1:36098952-36098974	–	TAGGCAAACCTGGTTTGGATGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
650	Chr1:36098953-36098975	-	TTAGGCAAACCTGGTTTGGATGG
651	Chr1:36098957-36098979	-	TGGCTTAGGCAAACCTGGTTTGG
652	Chr1:36098962-36098984	+	CCAGGTTTGCCTAAGCCAGCTGG
653	Chr1:36098962-36098984	-	CCAGCTGGCTTAGGCAAACCTGG
654	Chr1:36098968-36098990	+	TTGCCTAAGCCAGCTGGACCAGG
655	Chr1:36098969-36098991	+	TGCCTAAGCCAGCTGGACCAGGG
656	Chr1:36098971-36098993	-	CTCCCTGGTCCAGCTGGCTTAGG
657	Chr1:36098972-36098994	+	CTAAGCCAGCTGGACCAGGGAGG
658	Chr1:36098976-36098998	+	GCCAGCTGGACCAGGGAGGCCGG
659	Chr1:36098977-36098999	+	CCAGCTGGACCAGGGAGGCCGGG
660	Chr1:36098977-36098999	-	CCCGGCCTCCCTGGTCCAGCTGG
661	Chr1:36098978-36099000	+	CAGCTGGACCAGGGAGGCCGGGG
662	Chr1:36098979-36099001	+	AGCTGGACCAGGGAGGCCGGGGG
663	Chr1:36098980-36099002	+	GCTGGACCAGGGAGGCCGGGGGG
664	Chr1:36098981-36099003	+	CTGGACCAGGGAGGCCGGGGGGG
665	Chr1:36098985-36099007	+	ACCAGGGAGGCCGGGGGGGCCGG
666	Chr1:36098986-36099008	+	CCAGGGAGGCCGGGGGGGCCGGG
667	Chr1:36098986-36099008	-	CCCGGCCCCCCCGGCCTCCCTGG
668	Chr1:36098987-36099009	+	CAGGGAGGCCGGGGGGGCCGGGG
669	Chr1:36098988-36099010	+	AGGGAGGCCGGGGGGGCCGGGGG
670	Chr1:36098995-36099017	-	GGGGGTGCCCCCGGCCCCCCCGG
671	Chr1:36099004-36099026	+	CCGGGGGCACCCCCCTGCCCTGG
672	Chr1:36099004-36099026	-	CCAGGGCAGGGGGGTGCCCCCGG

SEQ ID No	Chromosomal location	Strand	Target sequence
673	Chr1:36099005-36099027	+	CGGGGGCACCCCCCTGCCCTGGG
674	Chr1:36099006-36099028	+	GGGGGCACCCCCCTGCCCTGGGG
675	Chr1:36099013-36099035	+	CCCCCCTGCCCTGGGGCCCCAGG
676	Chr1:36099013-36099035	-	CCTGGGGCCCCAGGGCAGGGGGG
677	Chr1:36099014-36099036	-	GCCTGGGGCCCCAGGGCAGGGGG
678	Chr1:36099015-36099037	-	TGCCTGGGGCCCCAGGGCAGGGG
679	Chr1:36099016-36099038	-	CTGCCTGGGGCCCCAGGGCAGGG
680	Chr1:36099017-36099039	-	GCTGCCTGGGGCCCCAGGGCAGG
681	Chr1:36099021-36099043	+	CCCTGGGGCCCCAGGCAGCCCGG
682	Chr1:36099021-36099043	-	CCGGGCTGCCTGGGGCCCCAGGG
683	Chr1:36099022-36099044	+	CCTGGGGCCCCAGGCAGCCCGGG
684	Chr1:36099022-36099044	-	CCCGGGCTGCCTGGGGCCCCAGG
685	Chr1:36099026-36099048	+	GGGCCCCAGGCAGCCCGGGCTGG
686	Chr1:36099029-36099051	-	GGGCCAGCCCGGGCTGCCTGGGG
687	Chr1:36099030-36099052	-	TGGGCCAGCCCGGGCTGCCTGGG
688	Chr1:36099031-36099053	-	GTGGGCCAGCCCGGGCTGCCTGG
689	Chr1:36099039-36099061	-	ATAATGGAGTGGGCCAGCCCGGG
690	Chr1:36099040-36099062	-	GATAATGGAGTGGGCCAGCCCGG
691	Chr1:36099049-36099071	-	CTCAAGGGGGATAATGGAGTGGG
692	Chr1:36099050-36099072	+	CCACTCCATTATCCCCCTTGAGG
693	Chr1:36099050-36099072	-	CCTCAAGGGGGATAATGGAGTGG
694	Chr1:36099055-36099077	-	CGAGGCCTCAAGGGGGATAATGG
695	Chr1:36099062-36099084	-	AGGTGATCGAGGCCTCAAGGGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
696	Chr1:36099063-36099085	-	CAGGTGATCGAGGCCTCAAGGGG
697	Chr1:36099064-36099086	+	CCCTTGAGGCCTCGATCACCTGG
698	Chr1:36099064-36099086	-	CCAGGTGATCGAGGCCTCAAGGG
699	Chr1:36099065-36099087	+	CCTTGAGGCCTCGATCACCTGGG
700	Chr1:36099065-36099087	-	CCCAGGTGATCGAGGCCTCAAGG
701	Chr1:36099066-36099088	+	CTTGAGGCCTCGATCACCTGGGG
702	Chr1:36099067-36099089	+	TTGAGGCCTCGATCACCTGGGGG
703	Chr1:36099073-36099095	+	CCTCGATCACCTGGGGGCCCAGG
704	Chr1:36099073-36099095	-	CCTGGGCCCCCAGGTGATCGAGG
705	Chr1:36099082-36099104	-	CAGGGGGAGCCTGGGCCCCCAGG
706	Chr1:36099083-36099105	+	CTGGGGGCCCAGGCTCCCCCTGG
707	Chr1:36099084-36099106	+	TGGGGGCCCAGGCTCCCCCTGGG
708	Chr1:36099085-36099107	+	GGGGGCCCAGGCTCCCCCTGGGG
709	Chr1:36099090-36099112	-	CAGGGCCCCAGGGGGAGCCTGGG
710	Chr1:36099091-36099113	+	CCAGGCTCCCCCTGGGGCCCTGG
711	Chr1:36099091-36099113	-	CCAGGGCCCCAGGGGGAGCCTGG
712	Chr1:36099098-36099120	-	GGGGGAACCAGGGCCCCAGGGGG
713	Chr1:36099099-36099121	-	AGGGGGAACCAGGGCCCCAGGGG
714	Chr1:36099100-36099122	-	CAGGGGGAACCAGGGCCCCAGGG
715	Chr1:36099101-36099123	+	CCTGGGGCCCTGGTTCCCCCTGG
716	Chr1:36099101-36099123	-	CCAGGGGGAACCAGGGCCCCAGG
717	Chr1:36099108-36099130	-	CAGGATTCCAGGGGGAACCAGGG
718	Chr1:36099109-36099131	+	CCTGGTTCCCCCTGGAATCCTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
719	Chr1:36099109-36099131	-	CCAGGATTCCAGGGGGAACCAGG
720	Chr1:36099110-36099132	+	CTGGTTCCCCCTGGAATCCTGGG
721	Chr1:36099111-36099133	+	TGGTTCCCCCTGGAATCCTGGGG
722	Chr1:36099112-36099134	+	GGTTCCCCCTGGAATCCTGGGG
723	Chr1:36099116-36099138	-	AGGGCCCCCAGGATTCCAGGGGG
724	Chr1:36099117-36099139	-	CAGGGCCCCCAGGATTCCAGGGG
725	Chr1:36099118-36099140	+	CCCTGGAATCCTGGGGGCCCTG
726	Chr1:36099118-36099140	-	CCAGGGCCCCCAGGATTCCAGG
727	Chr1:36099119-36099141	-	GCCAGGGCCCCCAGGATTCCAG
728	Chr1:36099127-36099149	-	CAAGGGGTGCCAGGGCCCCCAGG
729	Chr1:36099128-36099150	+	CTGGGGGCCCTGGCACCCCTTGG
730	Chr1:36099129-36099151	+	TGGGGGCCCTGGCACCCCTTGGG
731	Chr1:36099135-36099157	-	CAGGTGCCCAAGGGGTGCCAGGG
732	Chr1:36099136-36099158	+	CCTGGCACCCCTTGGGCACCTGG
733	Chr1:36099136-36099158	-	CCAGGTGCCCAAGGGGTGCCAGG
734	Chr1:36099143-36099165	-	TGGAAAACCAGGTGCCCAAGGGG
735	Chr1:36099144-36099166	-	CTGGAAAACCAGGTGCCCAAGGG
736	Chr1:36099145-36099167	+	CCTTGGGCACCTGGTTTTCCAGG
737	Chr1:36099145-36099167	-	CCTGGAAAACCAGGTGCCCAAG
738	Chr1:36099146-36099168	+	CTTGGGCACCTGGTTTTCCAGGG
739	Chr1:36099154-36099176	-	ATTACTATCCCTGGAAAACCAGG
740	Chr1:36099162-36099184	+	TCCAGGGATAGTAATGCCTGAG
741	Chr1:36099163-36099185	+	CCAGGGATAGTAATGCCTGAGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
742	Chr1:36099163-36099185	-	CCCTCAGGCATTACTATCCCTGG
743	Chr1:36099164-36099186	+	CAGGGATAGTAATGCCTGAGGGG
744	Chr1:36099169-36099191	+	ATAGTAATGCCTGAGGGGCCCGG
745	Chr1:36099170-36099192	+	TAGTAATGCCTGAGGGGCCCGGG
746	Chr1:36099173-36099195	+	TAATGCCTGAGGGGCCCGGGAGG
747	Chr1:36099178-36099200	+	CCTGAGGGGCCCGGGAGGCCAGG
748	Chr1:36099178-36099200	-	CCTGGCCTCCCGGGCCCCTCAGG
749	Chr1:36099179-36099201	+	CTGAGGGGCCCGGGAGGCCAGGG
750	Chr1:36099180-36099202	+	TGAGGGGCCCGGGAGGCCAGGGG
751	Chr1:36099181-36099203	+	GAGGGGCCCGGGAGGCCAGGGGG
752	Chr1:36099187-36099209	+	CCCGGGAGGCCAGGGGGTCCTGG
753	Chr1:36099187-36099209	-	CCAGGACCCCCTGGCCTCCCGGG
754	Chr1:36099188-36099210	+	CCGGGAGGCCAGGGGGTCCTGGG
755	Chr1:36099188-36099210	-	CCCAGGACCCCCTGGCCTCCCGG
756	Chr1:36099189-36099211	+	CGGGAGGCCAGGGGGTCCTGGGG
757	Chr1:36099190-36099212	+	GGGAGGCCAGGGGGTCCTGGGGG
758	Chr1:36099196-36099218	-	CGGGGACCCCCAGGACCCCCTG
759	Chr1:36099197-36099219	+	CAGGGGGTCCTGGGGGTCCCCGG
760	Chr1:36099200-36099222	+	GGGGTCCTGGGGGTCCCCGGAGG
761	Chr1:36099205-36099227	-	CAGGGCCTCCGGGGACCCCCAGG
762	Chr1:36099206-36099228	+	CTGGGGGTCCCCGGAGGCCCTGG
763	Chr1:36099214-36099236	-	CGAGGGGACCAGGGCCTCCGGGG
764	Chr1:36099215-36099237	-	ACGAGGGGACCAGGGCCTCCGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
765	Chr1:36099216-36099238	-	TACGAGGGGACCAGGGCCTCCGG
766	Chr1:36099223-36099245	+	CCCTGGTCCCCTCGTATTCCTGG
767	Chr1:36099223-36099245	-	CCAGGAATACGAGGGGACCAGGG
768	Chr1:36099224-36099246	-	GCCAGGAATACGAGGGGACCAGG
769	Chr1:36099230-36099252	-	GGGGGAGCCAGGAATACGAGGGG
770	Chr1:36099231-36099253	-	GGGGGGAGCCAGGAATACGAGGG
771	Chr1:36099232-36099254	-	CGGGGGGAGCCAGGAATACGAGG
772	Chr1:36099241-36099263	+	CCTGGCTCCCCCCGAAGCCCCGG
773	Chr1:36099241-36099263	-	CCGGGGCTTCGGGGGGAGCCAGG
774	Chr1:36099248-36099270	-	AGGGCAGCCGGGGCTTCGGGGGG
775	Chr1:36099249-36099271	-	CAGGGCAGCCGGGGCTTCGGGGG
776	Chr1:36099250-36099272	+	CCCCGAAGCCCCGGCTGCCCTGG
777	Chr1:36099250-36099272	-	CCAGGGCAGCCGGGGCTTCGGGG
778	Chr1:36099251-36099273	-	ACCAGGGCAGCCGGGGCTTCGGG
779	Chr1:36099252-36099274	-	CACCAGGGCAGCCGGGGCTTCGG
780	Chr1:36099253-36099275	+	CGAAGCCCCGGCTGCCCTGGTGG
781	Chr1:36099258-36099280	-	TCGGGCCACCAGGGCAGCCGGGG
782	Chr1:36099259-36099281	-	GTCGGGCCACCAGGGCAGCCGGG
783	Chr1:36099260-36099282	-	GGTCGGGCCACCAGGGCAGCCGG
784	Chr1:36099267-36099289	-	CTGGCAAGGTCGGGCCACCAGGG
785	Chr1:36099268-36099290	+	CCTGGTGGCCCGACCTTGCCAGG
786	Chr1:36099268-36099290	-	CCTGGCAAGGTCGGGCCACCAGG
787	Chr1:36099269-36099291	+	CTGGTGGCCCGACCTTGCCAGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
788	Chr1:36099276-36099298	-	CAGGGCTCCCTGGCAAGGTCGGG
789	Chr1:36099277-36099299	+	CCGACCTTGCCAGGGAGCCCTGG
790	Chr1:36099277-36099299	-	CCAGGGCTCCCTGGCAAGGTCGG
791	Chr1:36099278-36099300	+	CGACCTTGCCAGGGAGCCCTGGG
792	Chr1:36099279-36099301	+	GACCTTGCCAGGGAGCCCTGGGG
793	Chr1:36099280-36099302	+	ACCTTGCCAGGGAGCCCTGGGGG
794	Chr1:36099281-36099303	-	TCCCCCAGGGCTCCCTGGCAAGG
795	Chr1:36099286-36099308	-	GCTGGTCCCCCAGGGCTCCCTGG
796	Chr1:36099294-36099316	-	TGGGCAAGGCTGGTCCCCCAGGG
797	Chr1:36099295-36099317	-	ATGGGCAAGGCTGGTCCCCCAGG
798	Chr1:36099299-36099321	+	GGGGACCAGCCTTGCCCATCCGG
799	Chr1:36099300-36099322	+	GGGACCAGCCTTGCCCATCCGGG
800	Chr1:36099304-36099326	-	TTCTCCCGGATGGGCAAGGCTGG
801	Chr1:36099308-36099330	-	TGGCTTCTCCCGGATGGGCAAGG
802	Chr1:36099310-36099332	+	TTGCCCATCCGGGAGAAGCCAGG
803	Chr1:36099311-36099333	+	TGCCCATCCGGGAGAAGCCAGGG
804	Chr1:36099312-36099334	+	GCCCATCCGGGAGAAGCCAGGGG
805	Chr1:36099313-36099335	+	CCCATCCGGGAGAAGCCAGGGGG
806	Chr1:36099313-36099335	-	CCCCCTGGCTTCTCCCGGATGGG
807	Chr1:36099314-36099336	-	GCCCCCTGGCTTCTCCCGGATGG
808	Chr1:36099318-36099340	-	CTGGGCCCCCTGGCTTCTCCCGG
809	Chr1:36099322-36099344	+	GAGAAGCCAGGGGGCCCAGCAGG
810	Chr1:36099323-36099345	+	AGAAGCCAGGGGGCCCAGCAGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
811	Chr1:36099328-36099350	+	CCAGGGGGCCCAGCAGGGCCAGG
812	Chr1:36099328-36099350	-	CCTGGCCCTGCTGGGCCCCCTGG
813	Chr1:36099336-36099358	-	ATGGGCAGCCTGGCCCTGCTGGG
814	Chr1:36099337-36099359	-	CATGGGCAGCCTGGCCCTGCTGG
815	Chr1:36099338-36099360	+	CAGCAGGGCCAGGCTGCCCATGG
816	Chr1:36099346-36099368	+	CCAGGCTGCCCATGGAGTCCTGG
817	Chr1:36099346-36099368	-	CCAGGACTCCATGGGCAGCCTGG
818	Chr1:36099354-36099376	-	TGGGAAAGCCAGGACTCCATGGG
819	Chr1:36099355-36099377	-	ATGGGAAAGCCAGGACTCCATGG
820	Chr1:36099361-36099383	+	AGTCCTGGCTTTCCCATGCCTGG
821	Chr1:36099364-36099386	-	AAACCAGGCATGGGAAAGCCAGG
822	Chr1:36099370-36099392	+	TTTCCCATGCCTGGTTTTCCTGG
823	Chr1:36099371-36099393	+	TTCCCATGCCTGGTTTTCCTGGG
824	Chr1:36099373-36099395	-	TTCCCAGGAAAACCAGGCATGGG
825	Chr1:36099374-36099396	-	CTTCCCAGGAAAACCAGGCATGG
826	Chr1:36099379-36099401	+	CCTGGTTTTCCTGGGAAGCCAGG
827	Chr1:36099379-36099401	-	CCTGGCTTCCCAGGAAAACCAGG
828	Chr1:36099380-36099402	+	CTGGTTTTCCTGGGAAGCCAGGG
829	Chr1:36099381-36099403	+	TGGTTTTCCTGGGAAGCCAGGGG
830	Chr1:36099382-36099404	+	GGTTTTCCTGGGAAGCCAGGGGG
831	Chr1:36099383-36099405	+	GTTTTCCTGGGAAGCCAGGGGGG
832	Chr1:36099388-36099410	+	CCTGGGAAGCCAGGGGGGCCAGG
833	Chr1:36099388-36099410	-	CCTGGCCCCCCTGGCTTCCCAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
834	Chr1:36099389-36099411	+	CTGGGAAGCCAGGGGGGCCAGGG
835	Chr1:36099390-36099412	+	TGGGAAGCCAGGGGGGCCAGGGG
836	Chr1:36099391-36099413	+	GGGAAGCCAGGGGGGCCAGGGGG
837	Chr1:36099397-36099419	-	CGGGGTCCCCCTGGCCCCCCTGG
838	Chr1:36099400-36099422	+	GGGGGGCCAGGGGGACCCCGAGG
839	Chr1:36099405-36099427	+	GCCAGGGGGACCCCGAGGCCCGG
840	Chr1:36099406-36099428	+	CCAGGGGGACCCCGAGGCCCGGG
841	Chr1:36099406-36099428	-	CCCGGGCCTCGGGGTCCCCCTGG
842	Chr1:36099415-36099437	+	CCCCGAGGCCCGGGCTTCCCAGG
843	Chr1:36099415-36099437	-	CCTGGGAAGCCCGGGCCTCGGGG
844	Chr1:36099416-36099438	+	CCCGAGGCCCGGGCTTCCCAGGG
845	Chr1:36099416-36099438	-	CCCTGGGAAGCCCGGGCCTCGGG
846	Chr1:36099417-36099439	+	CCGAGGCCCGGGCTTCCCAGGGG
847	Chr1:36099417-36099439	-	CCCCTGGGAAGCCCGGGCCTCGG
848	Chr1:36099418-36099440	+	CGAGGCCCGGGCTTCCCAGGGGG
849	Chr1:36099419-36099441	+	GAGGCCCGGGCTTCCCAGGGGGG
850	Chr1:36099423-36099445	+	CCCGGGCTTCCCAGGGGGGCCGG
851	Chr1:36099423-36099445	-	CCGGCCCCCCTGGGAAGCCCGGG
852	Chr1:36099424-36099446	+	CCGGGCTTCCCAGGGGGGCCGGG
853	Chr1:36099424-36099446	-	CCCGGCCCCCCTGGGAAGCCCGG
854	Chr1:36099432-36099454	-	AGGGAGAGCCCGGCCCCCCTGGG
855	Chr1:36099433-36099455	-	AAGGGAGAGCCCGGCCCCCCTGG
856	Chr1:36099437-36099459	+	GGGGGCCGGGCTCTCCCTTCAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
857	Chr1:36099442-36099464	-	ATGGACCTGAAGGGAGAGCCCGG
858	Chr1:36099445-36099467	+	GGCTCTCCCTTCAGGTCCATCGG
859	Chr1:36099451-36099473	-	CTGCTGCCGATGGACCTGAAGGG
860	Chr1:36099452-36099474	-	GCTGCTGCCGATGGACCTGAAGG
861	Chr1:36099454-36099476	+	TTCAGGTCCATCGGCAGCAGCGG
862	Chr1:36099460-36099482	+	TCCATCGGCAGCAGCGGTAGAGG
863	Chr1:36099461-36099483	-	GCCTCTACCGCTGCTGCCGATGG
864	Chr1:36099485-36099507	+	TTTCTGAGAAAGAAAGAGAAAGG
865	Chr1:36099486-36099508	+	TTCTGAGAAAGAAAGAGAAAGGG
866	Chr1:36099487-36099509	+	TCTGAGAAAGAAAGAGAAAGGGG
867	Chr1:36099495-36099517	+	AGAAAGAGAAAGGGGCAGTCAGG
868	Chr1:36099496-36099518	+	GAAAGAGAAAGGGGCAGTCAGGG
869	Chr1:36099497-36099519	+	AAAGAGAAAGGGGCAGTCAGGGG
870	Chr1:36099509-36099531	+	GCAGTCAGGGGCCTGAACTGTGG
871	Chr1:36099510-36099532	+	CAGTCAGGGGCCTGAACTGTGGG
872	Chr1:36099511-36099533	+	AGTCAGGGGCCTGAACTGTGGGG
873	Chr1:36099516-36099538	+	GGGGCCTGAACTGTGGGGACAGG
874	Chr1:36099517-36099539	+	GGGCCTGAACTGTGGGGACAGGG
875	Chr1:36099518-36099540	+	GGCCTGAACTGTGGGGACAGGGG
876	Chr1:36099520-36099542	-	GTCCCCTGTCCCCACAGTTCAGG
877	Chr1:36099542-36099564	-	AATGGGGGAATGGGTAGATGGGG
878	Chr1:36099543-36099565	-	GAATGGGGGAATGGGTAGATGGG
879	Chr1:36099544-36099566	-	GGAATGGGGGAATGGGTAGATGG

SEQ ID No	Chromosomal location	Strand	Target sequence
880	Chr1:36099551-36099573	-	TCATACTGGAATGGGGGAATGGG
881	Chr1:36099552-36099574	-	CTCATACTGGAATGGGGGAATGG
882	Chr1:36099553-36099575	+	CATTCCCCCATTCCAGTATGAGG
883	Chr1:36099557-36099579	-	TGTACCTCATACTGGAATGGGGG
884	Chr1:36099558-36099580	-	GTGTACCTCATACTGGAATGGGG
885	Chr1:36099559-36099581	-	CGTGTACCTCATACTGGAATGGG
886	Chr1:36099560-36099582	+	CCATTCCAGTATGAGGTACACGG
887	Chr1:36099560-36099582	-	CCGTGTACCTCATACTGGAATGG
888	Chr1:36099561-36099583	+	CATTCCAGTATGAGGTACACGGG
889	Chr1:36099565-36099587	-	CTCTCCCGTGTACCTCATACTGG
890	Chr1:36099566-36099588	+	CAGTATGAGGTACACGGGAGAGG
891	Chr1:36099574-36099596	+	GGTACACGGGAGAGGAAGAATGG
892	Chr1:36099575-36099597	+	GTACACGGGAGAGGAAGAATGGG
893	Chr1:36099576-36099598	+	TACACGGGAGAGGAAGAATGGGG
894	Chr1:36099598-36099620	+	GCTGCCCCTTCCTGCTCTCATGG
895	Chr1:36099602-36099624	-	TCTTCCATGAGAGCAGGAAGGGG
896	Chr1:36099603-36099625	-	ATCTTCCATGAGAGCAGGAAGGG
897	Chr1:36099604-36099626	-	CATCTTCCATGAGAGCAGGAAGG
898	Chr1:36099605-36099627	+	CTTCCTGCTCTCATGGAAGATGG
899	Chr1:36099606-36099628	+	TTCCTGCTCTCATGGAAGATGGG
900	Chr1:36099607-36099629	+	TCCTGCTCTCATGGAAGATGGGG
901	Chr1:36099608-36099630	-	ACCCCATCTTCCATGAGAGCAGG
902	Chr1:36099612-36099634	+	CTCTCATGGAAGATGGGCTTTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
903	Chr1:36099613-36099635	+	TCTCATGGAAGATGGGGTTTGGG
904	Chr1:36099614-36099636	+	CTCATGGAAGATGGGGTTTGGGG
905	Chr1:36099615-36099637	+	TCATGGAAGATGGGGTTTGGGGG
906	Chr1:36099618-36099640	+	TGGAAGATGGGGTTTGGGGGTGG
907	Chr1:36099624-36099646	+	ATGGGGTTTGGGGGTGGCCCAGG
908	Chr1:36099625-36099647	+	TGGGGTTTGGGGGTGGCCCAGGG
909	Chr1:36099626-36099648	+	GGGGTTTGGGGGTGGCCCAGGGG
910	Chr1:36099635-36099657	+	GGGTGGCCCAGGGGACATCTTGG
911	Chr1:36099636-36099658	+	GGTGGCCCAGGGGACATCTTGGG
912	Chr1:36099637-36099659	+	GTGGCCCAGGGGACATCTTGGGG
913	Chr1:36099638-36099660	+	TGGCCCAGGGGACATCTTGGGGG
914	Chr1:36099641-36099663	-	TTGCCCCCAAGATGTCCCCTGGG
915	Chr1:36099642-36099664	-	GTTGCCCCCAAGATGTCCCCTGG
916	Chr1:36099645-36099667	+	GGGGACATCTTGGGGGCAACAGG
917	Chr1:36099646-36099668	+	GGGACATCTTGGGGGCAACAGGG
918	Chr1:36099660-36099682	+	GCAACAGGGTGTCCTCCTTAAGG
919	Chr1:36099661-36099683	+	CAACAGGGTGTCCTCCTTAAGGG
920	Chr1:36099672-36099694	-	GGTGTTAGGAGCCCTTAAGGAGG
921	Chr1:36099675-36099697	-	TTGGGTGTTAGGAGCCCTTAAGG
922	Chr1:36099685-36099707	+	TCCTAACACCCAACCTACCTAGG
923	Chr1:36099686-36099708	-	GCCTAGGTAGGTTGGGTGTTAGG
924	Chr1:36099689-36099711	+	AACACCCAACCTACCTAGGCTGG
925	Chr1:36099690-36099712	+	ACACCCAACCTACCTAGGCTGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
926	Chr1:36099693-36099715	-	AGGCCCAGCCTAGGTAGGTTGGG
927	Chr1:36099694-36099716	-	GAGGCCCAGCCTAGGTAGGTTGG
928	Chr1:36099698-36099720	-	GGAGGAGGCCCAGCCTAGGTAGG
929	Chr1:36099702-36099724	-	TCATGGAGGAGGCCCAGCCTAGG
930	Chr1:36099708-36099730	+	CTGGGCCTCCTCCATGAGCCTGG
931	Chr1:36099713-36099735	-	ATCAGCCAGGCTCATGGAGGAGG
932	Chr1:36099716-36099738	-	AGAATCAGCCAGGCTCATGGAGG
933	Chr1:36099719-36099741	-	GTGAGAATCAGCCAGGCTCATGG
934	Chr1:36099726-36099748	-	ATGAGAGGTGAGAATCAGCCAGG
935	Chr1:36099741-36099763	-	TCAGGTCATGCAGGGATGAGAGG
936	Chr1:36099744-36099766	+	CTCATCCCTGCATGACCTGAAGG
937	Chr1:36099747-36099769	+	ATCCCTGCATGACCTGAAGGTGG
938	Chr1:36099749-36099771	-	CTCCACCTTCAGGTCATGCAGGG
939	Chr1:36099750-36099772	-	ACTCCACCTTCAGGTCATGCAGG
940	Chr1:36099752-36099774	+	TGCATGACCTGAAGGTGGAGTGG
941	Chr1:36099759-36099781	-	CTGGTGGCCACTCCACCTTCAGG
942	Chr1:36099760-36099782	+	CTGAAGGTGGAGTGGCCACCAGG
943	Chr1:36099763-36099785	+	AAGGTGGAGTGGCCACCAGGTGG
944	Chr1:36099775-36099797	-	GGGCTGCTGGTGCCACCTGGTGG
945	Chr1:36099778-36099800	-	GGTGGGCTGCTGGTGCCACCTGG
946	Chr1:36099788-36099810	-	CGGGCTCTAAGGTGGGCTGCTGG
947	Chr1:36099791-36099813	+	GCAGCCCACCTTAGAGCCCGTGG
948	Chr1:36099792-36099814	+	CAGCCCACCTTAGAGCCCGTGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
949	Chr1:36099795-36099817	–	GCTCCCACGGGCTCTAAGGTGGG
950	Chr1:36099796-36099818	–	TGCTCCCACGGGCTCTAAGGTGG
951	Chr1:36099799-36099821	–	CTCTGCTCCCACGGGCTCTAAGG
952	Chr1:36099807-36099829	–	AGGTGGGGCTCTGCTCCCACGGG
953	Chr1:36099808-36099830	–	GAGGTGGGGCTCTGCTCCCACGG
954	Chr1:36099822-36099844	–	AACTGGGAAGTTGGGAGGTGGGG
955	Chr1:36099823-36099845	–	GAACTGGGAAGTTGGGAGGTGGG
956	Chr1:36099824-36099846	–	TGAACTGGGAAGTTGGGAGGTGG
957	Chr1:36099827-36099849	–	AGATGAACTGGGAAGTTGGGAGG
958	Chr1:36099830-36099852	–	GGGAGATGAACTGGGAAGTTGGG
959	Chr1:36099831-36099853	–	GGGGAGATGAACTGGGAAGTTGG
960	Chr1:36099836-36099858	+	TTCCCAGTTCATCTCCCCCTTGG
961	Chr1:36099838-36099860	–	TTCCAAGGGGGAGATGAACTGGG
962	Chr1:36099839-36099861	–	CTTCCAAGGGGGAGATGAACTGG
963	Chr1:36099850-36099872	–	GCACAGGTGGTCTTCCAAGGGGG
964	Chr1:36099851-36099873	–	GGCACAGGTGGTCTTCCAAGGGG
965	Chr1:36099852-36099874	–	TGGCACAGGTGGTCTTCCAAGGG
966	Chr1:36099853-36099875	–	CTGGCACAGGTGGTCTTCCAAGG
967	Chr1:36099863-36099885	–	GTGCAGTTAGCTGGCACAGGTGG
968	Chr1:36099866-36099888	–	ACGGTGCAGTTAGCTGGCACAGG
969	Chr1:36099872-36099894	–	CTGGAAACGGTGCAGTTAGCTGG
970	Chr1:36099873-36099895	+	CAGCTAACTGCACCGTTTCCAGG
971	Chr1:36099881-36099903	+	TGCACCGTTTCCAGGCCCTCTGG

SEQ ID No	Chromosomal location	Strand	Target sequence
972	Chr1:36099882-36099904	+	GCACCGTTTCCAGGCCCTCTGGG
973	Chr1:36099883-36099905	+	CACCGTTTCCAGGCCCTCTGGGG
974	Chr1:36099885-36099907	-	TACCCCAGAGGGCCTGGAAACGG
975	Chr1:36099890-36099912	+	TCCAGGCCCTCTGGGGTATTAGG
976	Chr1:36099891-36099913	-	TCCTAATACCCCAGAGGGCCTGG
977	Chr1:36099896-36099918	-	GTTTTTCCTAATACCCCAGAGGG
978	Chr1:36099897-36099919	-	TGTTTTTCCTAATACCCCAGAGG
979	Chr1:36099904-36099926	+	GGTATTAGGAAAAACACTGAAGG
980	Chr1:36099908-36099930	+	TTAGGAAAAACACTGAAGGTAGG
981	Chr1:36099916-36099938	+	AACACTGAAGGTAGGAAAATTGG
982	Chr1:36099919-36099941	+	ACTGAAGGTAGGAAAATTGGTGG
983	Chr1:36099920-36099942	+	CTGAAGGTAGGAAAATTGGTGGG
984	Chr1:36099921-36099943	+	TGAAGGTAGGAAAATTGGTGGGG
985	Chr1:36099928-36099950	+	AGGAAAATTGGTGGGGAATGAGG
986	Chr1:36099936-36099958	+	TGGTGGGGAATGAGGAGCTGTGG
987	Chr1:36099939-36099961	+	TGGGGAATGAGGAGCTGTGGAGG
988	Chr1:36099940-36099962	+	GGGGAATGAGGAGCTGTGGAGGG
989	Chr1:36099949-36099971	+	GGAGCTGTGGAGGGCGCCTGAGG
990	Chr1:36099958-36099980	+	GAGGGCGCCTGAGGATCTGATGG
991	Chr1:36099965-36099987	-	CTGAGAGCCATCAGATCCTCAGG
992	Chr1:36099966-36099988	+	CTGAGGATCTGATGGCTCTCAGG
993	Chr1:36099967-36099989	+	TGAGGATCTGATGGCTCTCAGGG
994	Chr1:36099970-36099992	+	GGATCTGATGGCTCTCAGGGAGG

SEQ ID No	Chromosomal location	Strand	Target sequence
995	Chr1:36099974-36099996	+	CTGATGGCTCTCAGGGAGGCAGG
996	Chr1:36099975-36099997	+	TGATGGCTCTCAGGGAGGCAGGG
997	Chr1:36099976-36099998	+	GATGGCTCTCAGGGAGGCAGGGG
998	Chr1:36099982-36100004	+	TCTCAGGGAGGCAGGGGATTTGG
999	Chr1:36099983-36100005	+	CTCAGGGAGGCAGGGGATTTGGG
1000	Chr1:36099984-36100006	+	TCAGGGAGGCAGGGGATTTGGGG
1001	Chr1:36099985-36100007	+	CAGGGAGGCAGGGGATTTGGGGG
1002	Chr1:36099989-36100011	+	GAGGCAGGGGATTTGGGGGCTGG
1003	Chr1:36099990-36100012	+	AGGCAGGGGATTTGGGGGCTGGG
1004	Chr1:36100002-36100024	+	TGGGGGCTGGGAGCGATTTGAGG
1005	Chr1:36100010-36100032	+	GGGAGCGATTTGAGGCACTGTGG
1006	Chr1:36100011-36100033	+	GGAGCGATTTGAGGCACTGTGGG
1007	Chr1:36100012-36100034	+	GAGCGATTTGAGGCACTGTGGGG
1008	Chr1:36100017-36100039	+	ATTTGAGGCACTGTGGGGTGAGG
1009	Chr1:36100020-36100042	+	TGAGGCACTGTGGGGTGAGGAGG
1010	Chr1:36100032-36100054	+	GGGTGAGGAGGCTCTCACCCAGG
1011	Chr1:36100038-36100060	+	GGAGGCTCTCACCCAGGTACTGG
1012	Chr1:36100049-36100071	-	GAGGGCAAAGGCCAGTACCTGGG
1013	Chr1:36100050-36100072	-	TGAGGGCAAAGGCCAGTACCTGG
1014	Chr1:36100053-36100075	+	GGTACTGGCCTTTGCCCTCACGG
1015	Chr1:36100057-36100079	+	CTGGCCTTTGCCCTCACGGAAGG
1016	Chr1:36100058-36100080	+	TGGCCTTTGCCCTCACGGAAGGG
1017	Chr1:36100061-36100083	+	CCTTTGCCCTCACGGAAGGGCGG

SEQ ID No	Chromosomal location	Strand	Target sequence
1018	Chr1:36100061-36100083	-	CCGCCCTTCCGTGAGGGCAAAGG
1019	Chr1:36100067-36100089	-	GTGGGACCGCCCTTCCGTGAGGG
1020	Chr1:36100068-36100090	-	TGTGGGACCGCCCTTCCGTGAGG
1021	Chr1:36100070-36100092	+	TCACGGAAGGGCGGTCCCACAGG
1022	Chr1:36100084-36100106	+	TCCCACAGGTCCTTTCTGCATGG
1023	Chr1:36100085-36100107	+	CCCACAGGTCCTTTCTGCATGGG
1024	Chr1:36100085-36100107	-	CCCATGCAGAAAGGACCTGTGGG
1025	Chr1:36100086-36100108	-	GCCCATGCAGAAAGGACCTGTGG
1026	Chr1:36100089-36100111	+	CAGGTCCTTTCTGCATGGGCTGG
1027	Chr1:36100094-36100116	-	TACATCCAGCCCATGCAGAAAGG
1028	Chr1:36100103-36100125	+	ATGGGCTGGATGTACTTCACTGG
1029	Chr1:36100104-36100126	+	TGGGCTGGATGTACTTCACTGGG
1030	Chr1:36100105-36100127	+	GGGCTGGATGTACTTCACTGGGG
1031	Chr1:36100126-36100148	+	GGCATAGCCCGCCGCCCCACCGG
1032	Chr1:36100133-36100155	-	GGCGGGGCCGGTGGGGCGGCGGG
1033	Chr1:36100134-36100156	-	TGGCGGGGCCGGTGGGGCGGCGG
1034	Chr1:36100137-36100159	-	TGGTGGCGGGGCCGGTGGGGCGG
1035	Chr1:36100140-36100162	-	CTCTGGTGGCGGGGCCGGTGGGG
1036	Chr1:36100141-36100163	+	CCCACCGGCCCCGCCACCAGAGG
1037	Chr1:36100141-36100163	-	CCTCTGGTGGCGGGGCCGGTGGG
1038	Chr1:36100142-36100164	-	TCCTCTGGTGGCGGGGCCGGTGG
1039	Chr1:36100145-36100167	-	GCGTCCTCTGGTGGCGGGGCCGG
1040	Chr1:36100149-36100171	-	GCGGGCGTCCTCTGGTGGCGGGG

SEQ ID No	Chromosomal location	Strand	Target sequence
1041	Chr1:36100150-36100172	-	CGCGGGCGTCCTCTGGTGGCGGG
1042	Chr1:36100151-36100173	+	CCGCCACCAGAGGACGCCCGCGG
1043	Chr1:36100151-36100173	-	CCGCGGGCGTCCTCTGGTGGCGG
1044	Chr1:36100154-36100176	-	GGGCCGCGGGCGTCCTCTGGTGG
1045	Chr1:36100157-36100179	-	TGTGGGCCGCGGGCGTCCTCTGG
1046	Chr1:36100167-36100189	-	GGTGCTGGGGTGTGGGCCGCGGG
1047	Chr1:36100168-36100190	-	TGGTGCTGGGGTGTGGGCCGCGG
1048	Chr1:36100174-36100196	-	TGGTGCTGGTGCTGGGGTGTGGG
1049	Chr1:36100175-36100197	-	CTGGTGCTGGTGCTGGGGTGTGG
1050	Chr1:36100180-36100202	-	TGCTACTGGTGCTGGTGCTGGGG
1051	Chr1:36100181-36100203	-	CTGCTACTGGTGCTGGTGCTGGG
1052	Chr1:36100182-36100204	-	GCTGCTACTGCTACTGGTGCTGG
1053	Chr1:36100188-36100210	-	GCTGCTGCTGCTACTGGTGCTGG
1054	Chr1:36100194-36100216	-	TTCGCTGCTGCTGCTGCTACTGG
1055	Chr1:36100200-36100222	+	GCAGCAGCAGCAGCGAAGACAGG
1056	Chr1:36100201-36100223	+	CAGCAGCAGCAGCGAAGACAGGG
1057	Chr1:36100202-36100224	+	AGCAGCAGCAGCGAAGACAGGGG
1058	Chr1:36100222-36100244	+	GGGTGTCAGAGTCCCCAGCATGG
1059	Chr1:36100231-36100253	+	AGTCCCCAGCATGGCGTCCGTGG
1060	Chr1:36100234-36100256	-	CGTCCACGGACGCCATGCTGGGG
1061	Chr1:36100235-36100257	-	ACGTCCACGGACGCCATGCTGGG
1062	Chr1:36100236-36100258	-	CACGTCCACGGACGCCATGCTGG
1063	Chr1:36100248-36100270	-	TCTTCTTTGCAGCACGTCCACGG

Table 4. Target sequences for *COL8A2* with Gln455Lys mutation

SEQ ID No	Target location	Target strand	Target sequence
1064	Chr1:36098302 -36098324	+	CCCCTCAGGCCAGGCTTCCCAGG
1065	Chr1:36098302 -36098324	-	CCTGGGAAGCCTGGCCTGAGGGG
1066	Chr1:36098303 -36098325	+	CCCTCAGGCCAGGTTGCCCAGGG
1067	Chr1:36098303 -36098325	-	CCCTGGGAAGCCTGGCCTGAGGG
1068	Chr1:36098304 -36098326	-	TCCCTGGGAAGCCTGGCCTGAGG
1069	Chr1:36098311 -36098333	-	TTGGGGCTCCCTGGGAAGCCTGG

Table 5. Target sequences for *COL8A2* with Gln455Val mutation

SEQ ID No	Target location	Target strand	Target sequence
1070	Chr1:36098302-36098324	+	CCCCTCAGGCCAGGCACCCCAGG
1071	Chr1:36098302-36098324	-	CCTGGGGTGCCTGGCCTGAGGGG
1072	Chr1:36098303-36098325	+	CCCTCAGGCCAGGCACCCCAGGG
1073	Chr1:36098303-36098325	-	CCCTGGGGTGCCTGGCCTGAGGG
1074	Chr1:36098304-36098326	-	TCCCTGGGGTGCCTGGCCTGAGG
1075	Chr1:36098311-36098333	-	TTGGGGCTCCCTGGGGTGCCTGG

Table 6. Target sequences for *COL8A2* with Leu450Trp mutation

SEQ ID No	Target location	Target strand	Target sequence
1076	Chr1:36098311-36098333	-	TGGGGGCTCCCTGGGCAGCCTGG
1077	Chr1:36098319-36098341	-	AAGGTGACTGGGGGCTCCCTGGG
1078	Chr1:36098320-36098342	-	AAAGGTGACTGGGGGCTCCCTGG

SEQ ID No	Target location	Target strand	Target sequence
1079	Chr1:36098328-36098350	-	TGGGGCAGAAAGGTGACTGGGGG
1080	Chr1:36098329-36098351	-	CTGGGGCAGAAAGGTGACTGGGG
1081	Chr1:36098330-36098352	+	CCCAGTCACCTTTCTGCCCCAGG
1082	Chr1:36098330-36098352	-	CCTGGGGCAGAAAGGTGACTGGG
1083	Chr1:36098331-36098353	+	CCAGTCACCTTTCTGCCCCAGGG
1084	Chr1:36098331-36098353	-	CCCTGGGGCAGAAAGGTGACTGG

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CLAIMS

1. A composition comprising:

a) a nucleotide sequence, or portion thereof, of an AAV vector, wherein the AAV vector serotype is AAV6; and

b) a nucleic acid editing system comprising at least one nucleotide sequence that is complementary to at least one mutant allele on a target gene associated with diseases or conditions in the cornea; a nucleic acid capable of down-regulating gene expression of at least one mutant allele on a target gene associated with diseases or conditions in the cornea; and/or at least one nucleotide sequence, or portion thereof, that encodes for a protein to be expressed in the eye.

2. The composition of claim 1, wherein said protein is preferentially expressed in the cornea as compared with other ocular tissues or cells.

3. The composition of claim 2, wherein the protein is a transcription factor, a collagen, a nuclease, or a fluorescent protein.

4. The composition of claim 3, wherein the protein is transcription factor 4 (TCF4).

5. The composition of claim 1, wherein the nucleic acid editing system is a CRISPR-Cas system.

6. The composition of claim 1, wherein the target gene is *TCF4* or *COL8A2*.

7. The composition of any one of claims 1 to 6, wherein the target gene is preferentially expressed in the anterior portion of the eye after intracameral (IC) injection.

8. The composition of any one of claims 1 to 7, wherein the disease or condition of the cornea is a superficial corneal dystrophy, anterior corneal dystrophy, corneal stromal dystrophy, or posterior cornea dystrophy; and, wherein the posterior corneal dystrophy is selected from the group consisting of: Fuchs endothelial corneal dystrophy (FECD; both early and late onset),

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posterior polymorphous dystrophy (PPCD; types 1, 2, and 3), congenital endothelial dystrophy (types 1 and 2), and X-linked endothelial corneal dystrophy.

9. Use of the composition of any one of claims 1 to 8 in the preparation of a medicament for targeting a gene associated with diseases or conditions in a cornea.

10. A method of targeting a gene associated with diseases or conditions in a cornea in a subject in need thereof comprising administering the composition of any one of claims 1 to 8 to the subject.

11. The use according to claim 9, or the method according to claim 10, wherein the disease or condition in the cornea is selected from a superficial corneal dystrophy, anterior corneal dystrophy, corneal stromal dystrophy, or posterior corneal dystrophy; and wherein the posterior corneal dystrophy is selected from the group consisting of: Fuchs endothelial corneal dystrophy (FECD; both early and late onset), posterior polymorphous dystrophy (PPCD; types 1, 2, and 3), congenital endothelial dystrophy (types 1 and 2), and X-linked endothelial corneal dystrophy.

12. Use of one or more adeno-associated virus (AAV) vectors comprising a nucleotide sequence that encodes a protein in the preparation of a medicament for expressing the protein in an eye of a subject, wherein at least one AAV vector serotype is AAV6.

13. A method of expressing a protein in an eye of a subject in need thereof comprising administering one or more adeno-associated virus (AAV) vectors comprising a nucleotide sequence that encodes the protein to the subject, wherein at least one AAV vector serotype is AAV6.

14. The use according to claim 12, or the method according to claim 13, wherein the protein is as defined in any one of claims 2 to 4, or the nucleotide sequence is a target gene is as defined in claims 6 or 7.

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15. The method according to claim 13 or the use according to claim 14, wherein said protein is preferentially expressed in the cornea or in the corneal endothelial cells as compared with other ocular tissues or cells.

16. The use according to any one of claims 9, 11, 12 or 14 of the method according to any one of claims 10, 11 or 13 to 15, wherein the AAV vector serotype is selected from the group consisting of AAV5, AAV6, and AAV8, provided that at least one AAV vector is serotype AAV6.

17. The method or the use according to claim 16, wherein the AAV vector serotype is AAV6.

18. The method according to any one of claims 13 to 17, or the use according to any one of 12 or 14 to 17, wherein the protein is preferentially expressed in the anterior portion of the eye after intracameral (IC) injection.

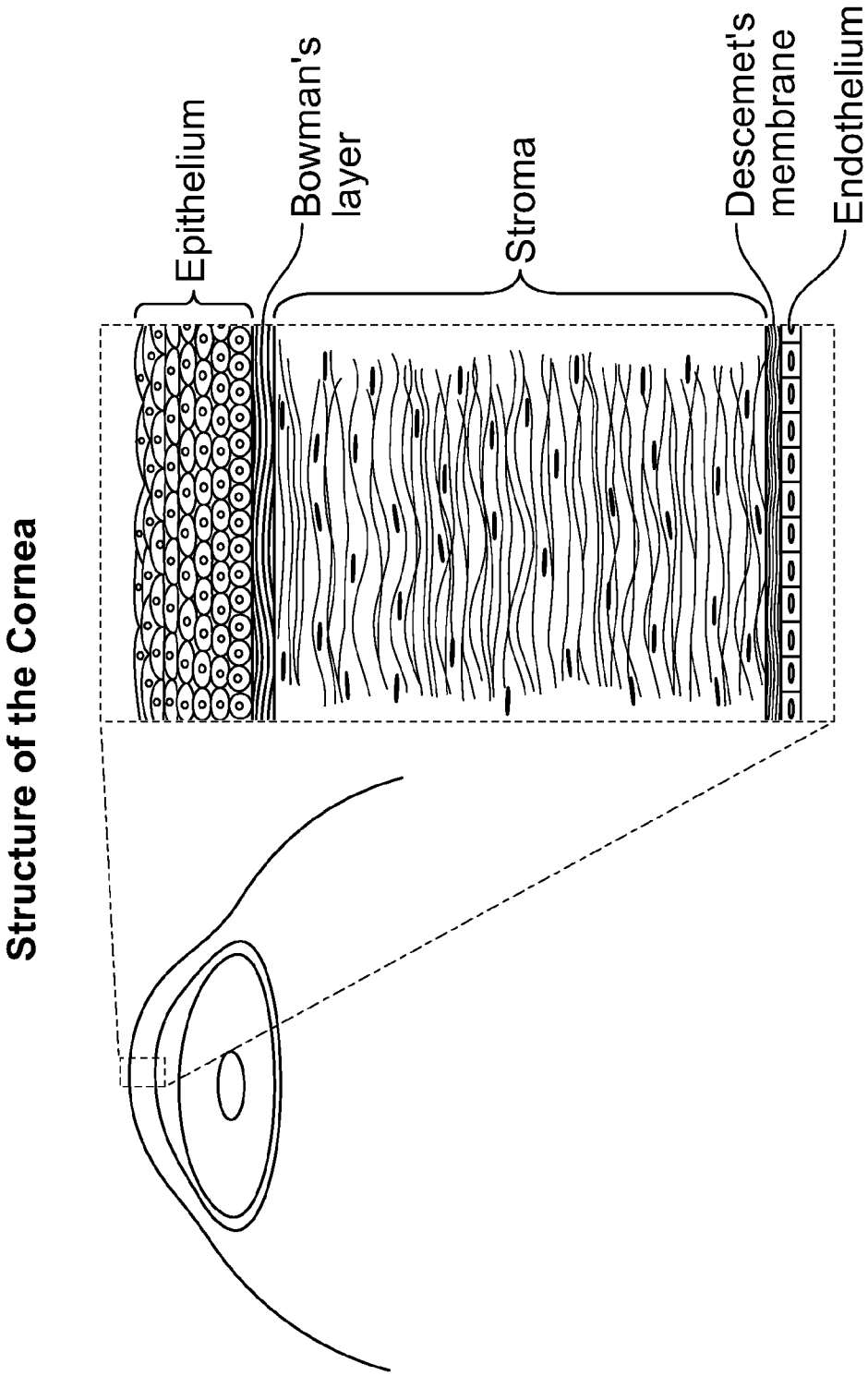

Structure of the Cornea
Epithelium
Bowman's layer
Stroma
Descemet's membrane
Endothelium

FIG. 1

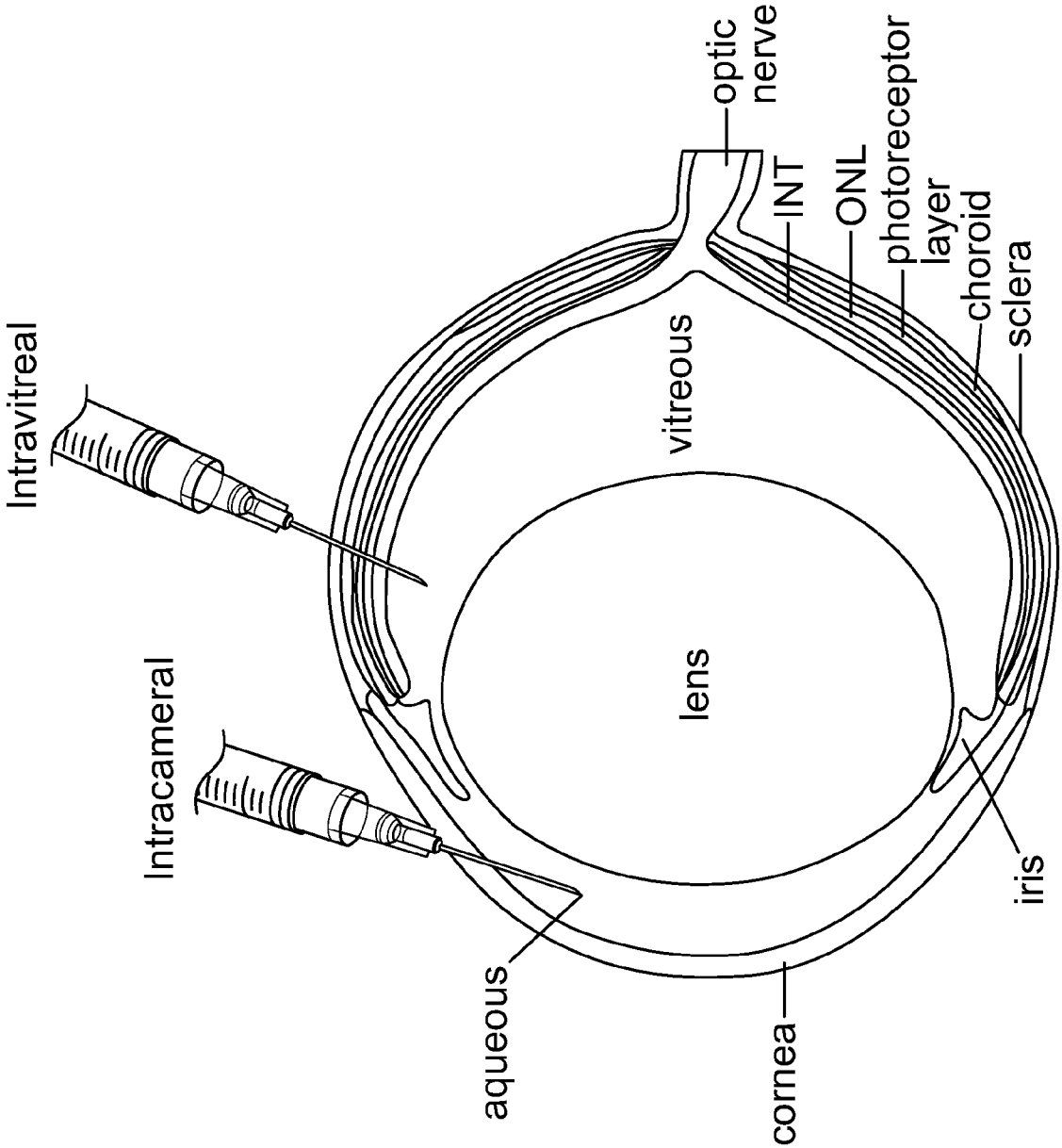

optic nerve
INT
ONL
photoreceptor layer
choroid
sclera
vitreous
Intravitreal
lens
Intracameral
iris
aqueous
cornea

FIG. 2

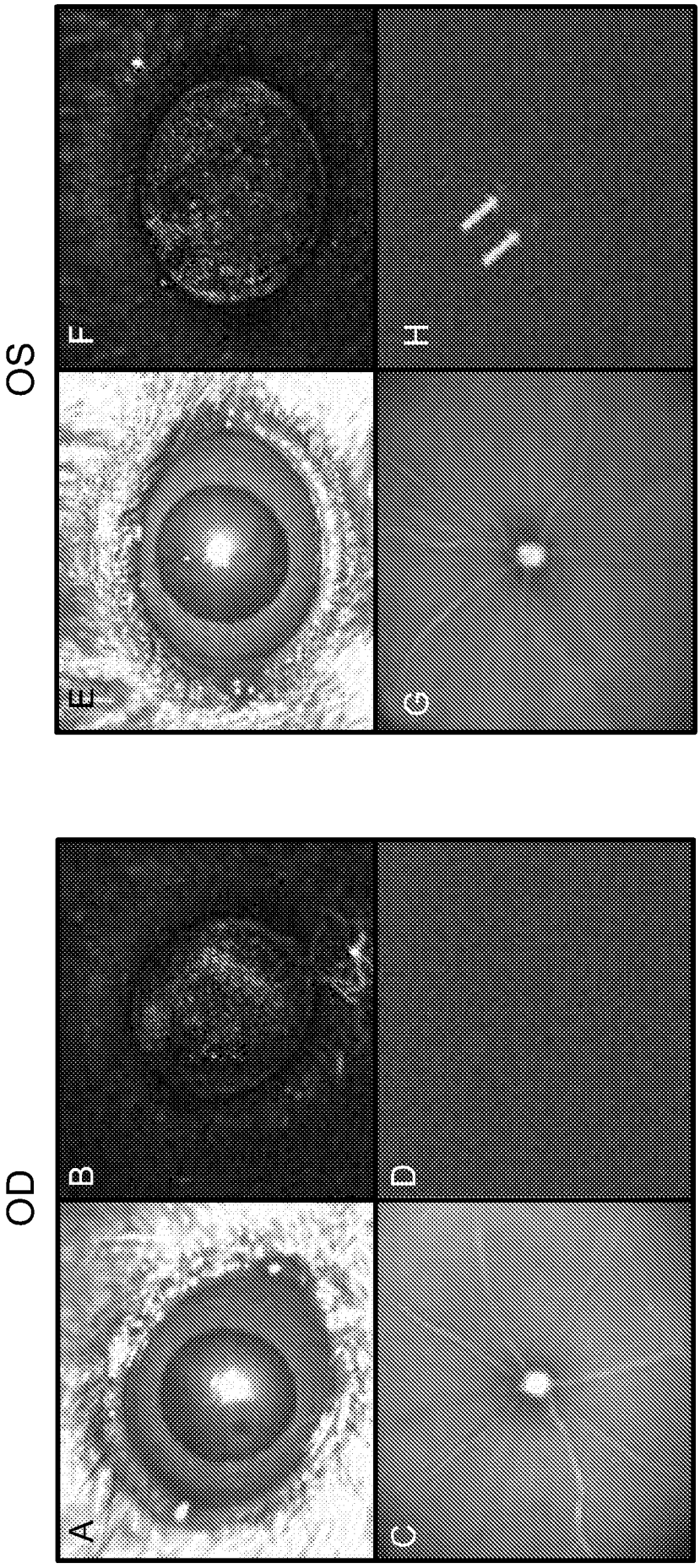


FIG. 3

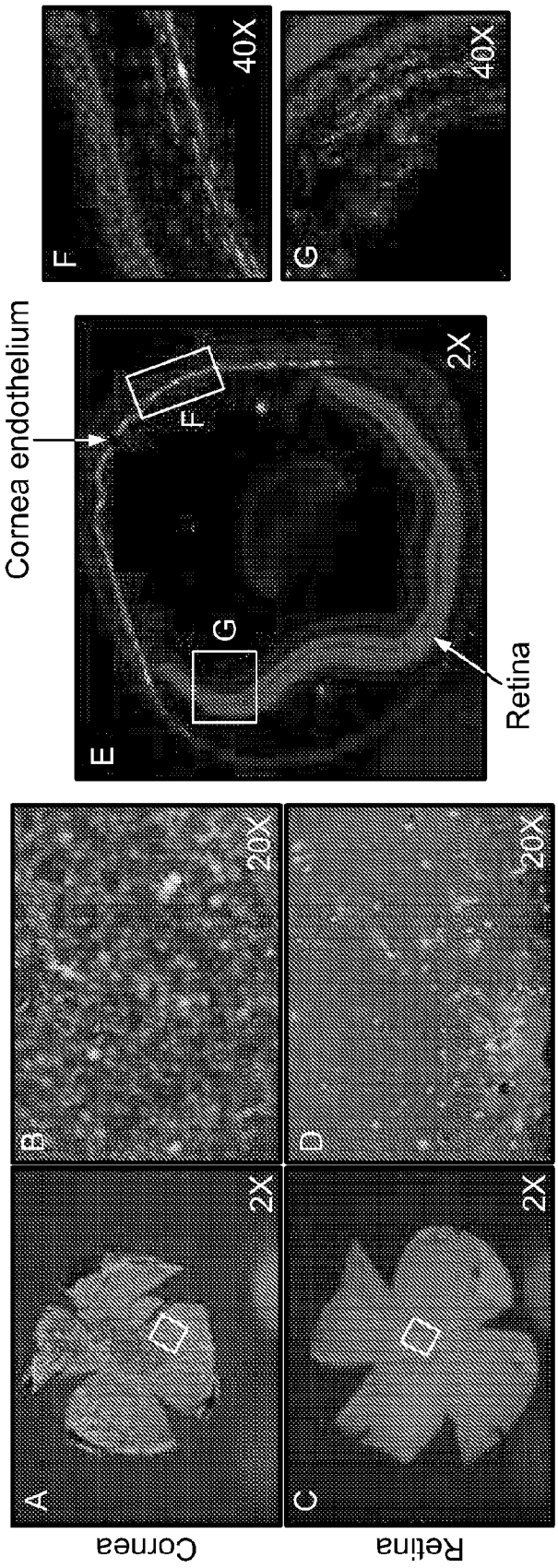

Cornea endothelium
Retina
Cornea
Retina
A
B
C
D
E
F
G
2X
20X
40X

FIG. 4

FIG. 5

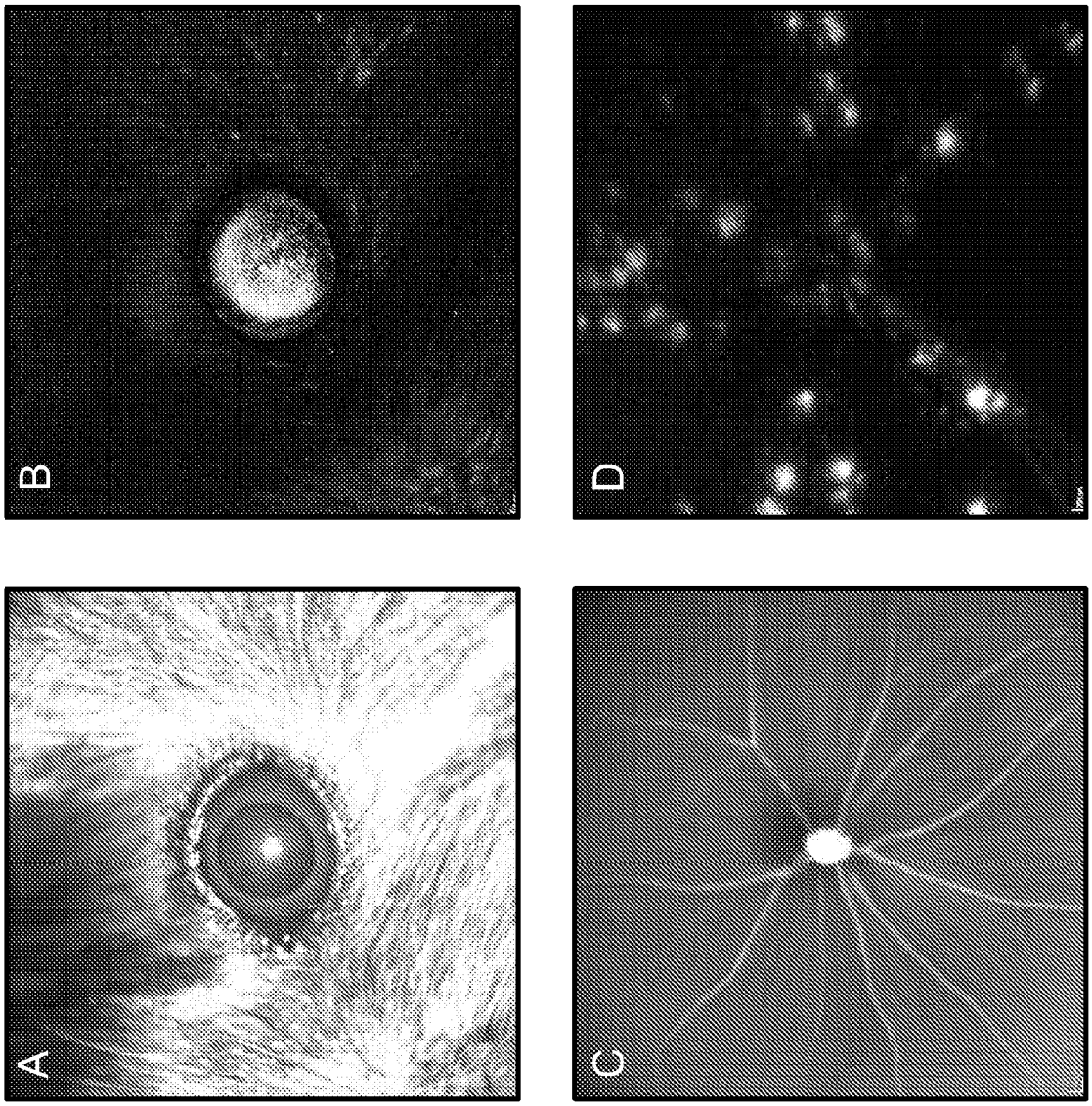


FIG. 6

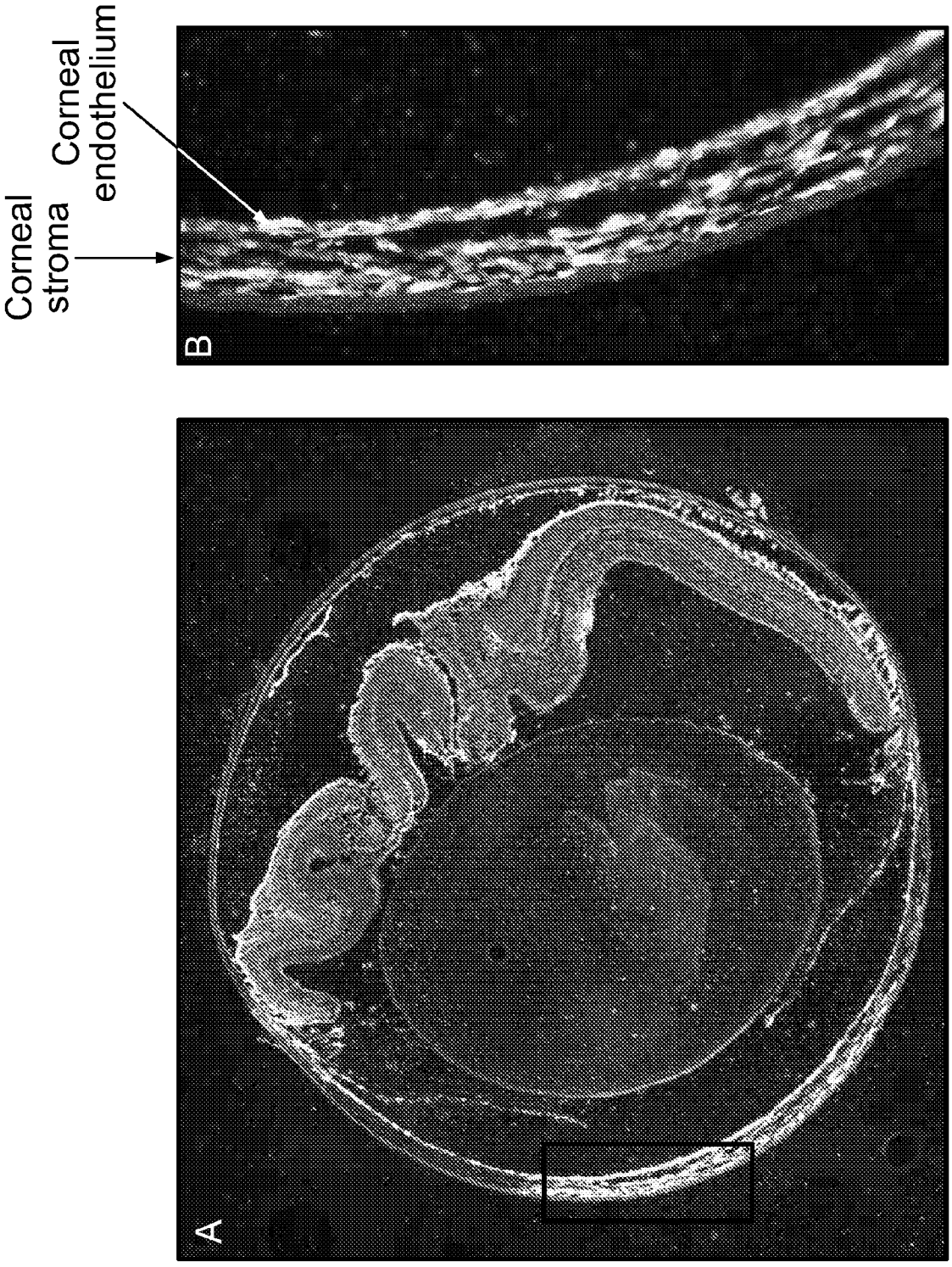
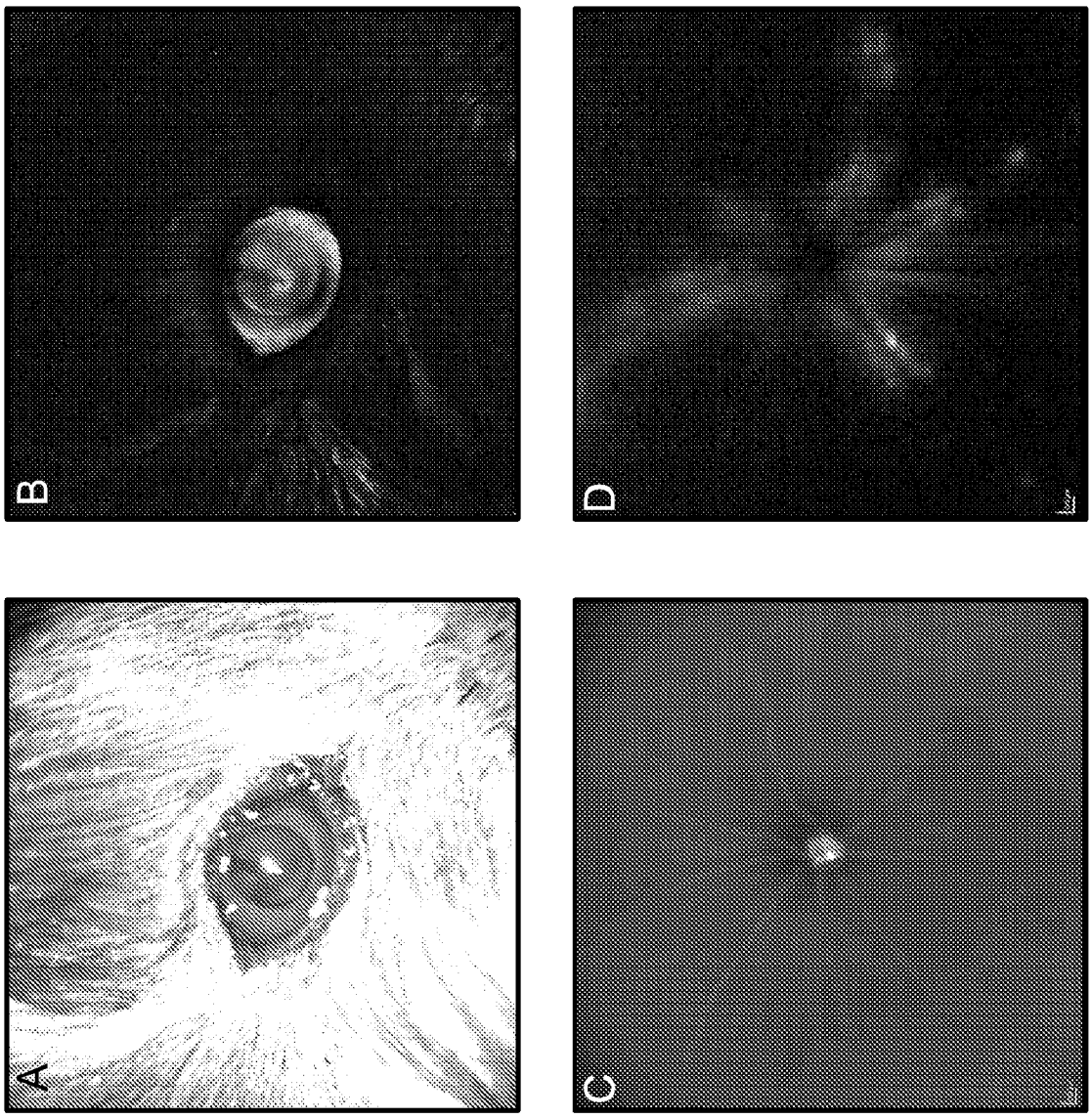


FIG. 7



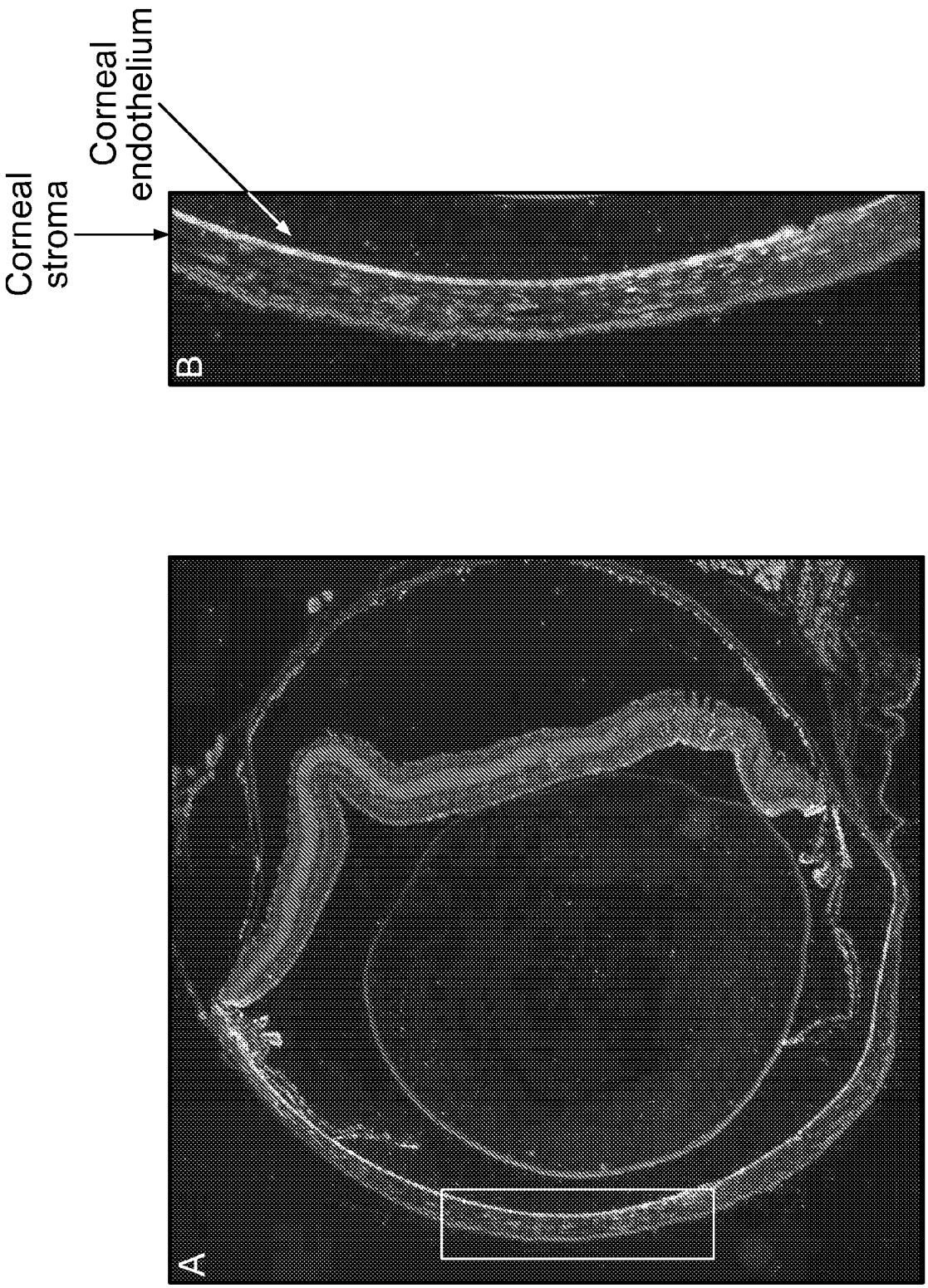


FIG. 8

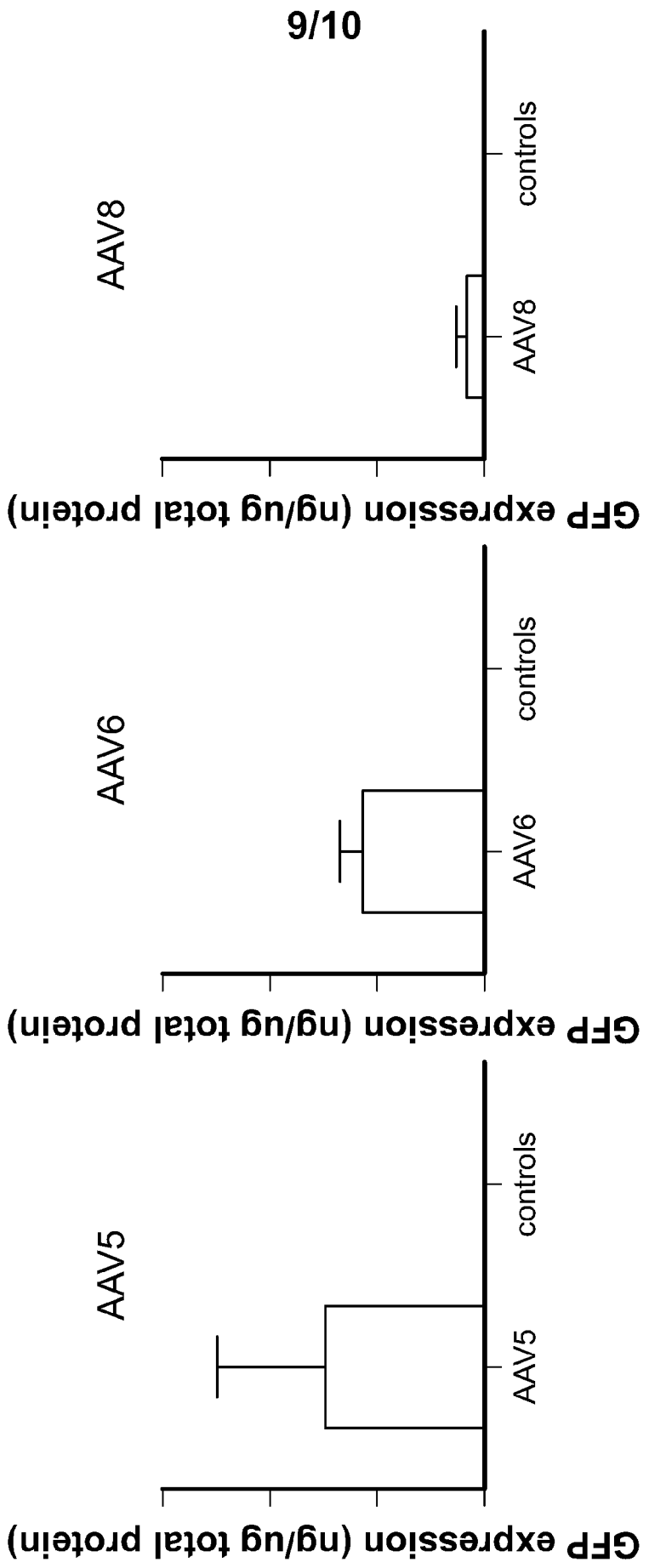

AAV5
AAV5
controls
GFP expression (ng/ug total protein)
AAV6
AAV6
controls
GFP expression (ng/ug total protein)
AAV8
AAV8
controls
GFP expression (ng/ug total protein)

FIG. 9

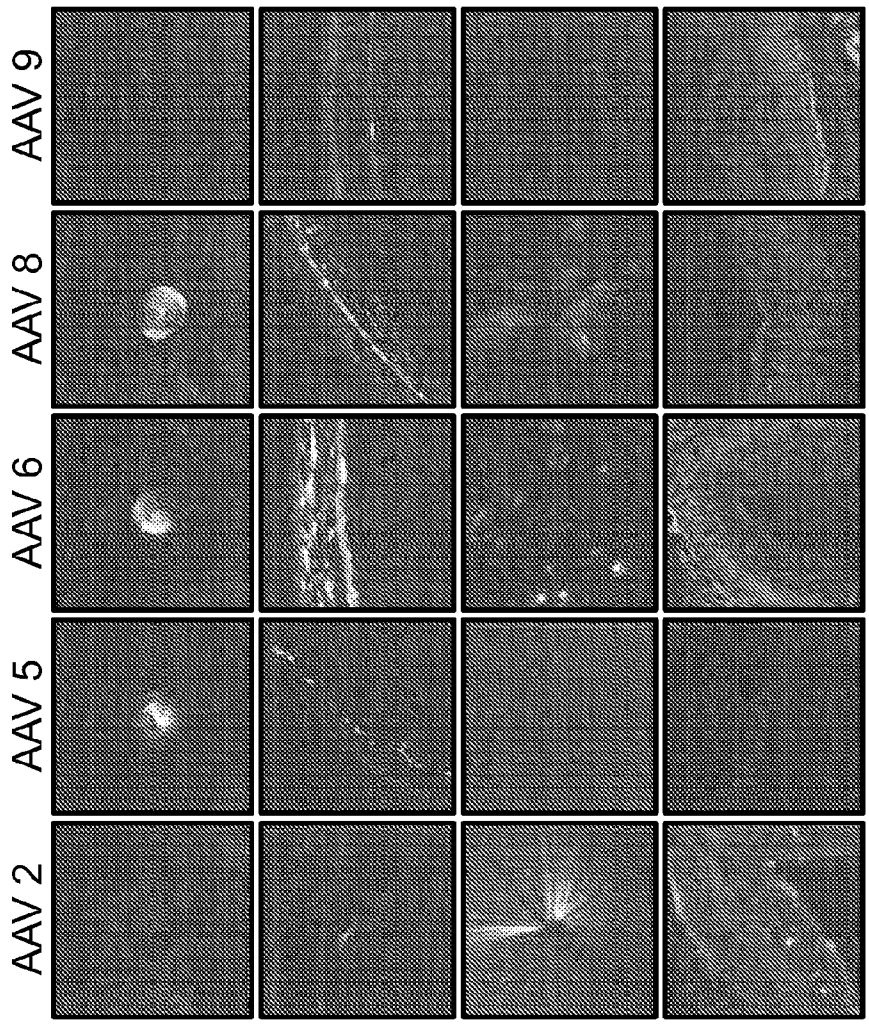

AAV 2
AAV 5
AAV 6
AAV 8
AAV 9
Anterior Segment: In Vivo Fluorescence Images of the Cornea
Cornea: Immunohistochemistry Images of the Cross-sectioned Cornea
Posterior Segment: In Vivo Fluorescence Images of the Retinal Fundus
Retina: Immunohistochemistry images of the cross-sectioned retina

FIG. 10

SEQUENCE LISTING

SEQUENCE LISTING

<110> Regeneron Pharmaceuticals Inc.

<120> ADENO-ASSOCIATED VIRUS VECTORS FOR THE DELIVERY OF THERAPEUTICS

<130> 67000-1023 WO

<160> 1278

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<400> SEQUENCE: 31
tgaatcttga taacattatg ggg 23

<210> SEQ ID NO 32
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 32
ctgaatcttg ataacattat ggg 23

<210> SEQ ID NO 33
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 33
ccataatgtt atcaagattc agg 23

<210> SEQ ID NO 34
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 34
cctgaatctt gataacatta tgg 23

<210> SEQ ID NO 35
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 35
aatgttatca agattcaggt tgg 23

<210> SEQ ID NO 36
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 36
gttatcaaga ttcaggttgg agg 23

<210> SEQ ID NO 37
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 37
tgtttttcta gagaggctgc tgg 23

<210> SEQ ID NO 38
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 38
aaactagtgt ttttctagag agg 23

<210> SEQ ID NO 39
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 39
gaaaaacact agtttcacca agg 23

<210> SEQ ID NO 40
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 40
aacaactttt ttcttctcct tgg 23

<210> SEQ ID NO 41
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 41
ttgttttata ttgaaaacct tgg 23

<210> SEQ ID NO 42
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 42
gaaaaccttg gccataaacg tgg 23

<210> SEQ ID NO 43
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 43
cattgccacg tttatggcca agg 23

<210> SEQ ID NO 44
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 44
aatggacatt gccacgttta tgg 23

<210> SEQ ID NO 45
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 45
tgtccatttc catctcgtat agg 23

<210> SEQ ID NO 46
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 46
aatcctatac gagatggaaa tgg 23

<210> SEQ ID NO 47
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 47
caggcaaatc ctatacgaga tgg 23

<210> SEQ ID NO 48
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 48
tatttgggtt cacatatgac agg 23

<210> SEQ ID NO 49
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 49
tggcactttt atttttattt ggg 23

<210> SEQ ID NO 50
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 50
gtggcacttt tatttttatt tgg 23

<210> SEQ ID NO 51
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 51
aaatgagaat ttagtgcagg tgg 23

<210> SEQ ID NO 52
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 52
acgaaatgag aatttagtgc agg 23

<210> SEQ ID NO 53
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 53
attctcattt cgtctctaac agg 23

<210> SEQ ID NO 54
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 54
aaataaatgc tggagagaga ggg 23

<210> SEQ ID NO 55
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 55
gaaataaatg ctggagagag agg 23

<210> SEQ ID NO 56
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 56
attagggtcg aaataaatgc tgg 23

<210> SEQ ID NO 57
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 57
gcatttattt cgaccctaat tgg 23

<210> SEQ ID NO 58
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 58
aagaagaggg aaaccaatta ggg 23

<210> SEQ ID NO 59
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 59
gaagaagagg gaaaccaatt agg 23

<210> SEQ ID NO 60
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 60
actagatacg tcgaagaaga ggg 23

<210> SEQ ID NO 61
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 61
cactagatac gtcgaagaag agg 23

<210> SEQ ID NO 62
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 62
ctcttcttcg acgtatctag tgg 23

<210> SEQ ID NO 63
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 63
tgcaggctct gactcaggga agg 23

<210> SEQ ID NO 64
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 64
tttttgcagg ctctgactca ggg 23

<210> SEQ ID NO 65
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 65
ctttttgcag gctctgactc agg 23

<210> SEQ ID NO 66
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 66
tcagagcctg caaaaagcaa agg 23

<210> SEQ ID NO 67
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 67
ttcgttcctt tgctttttgc agg 23

<210> SEQ ID NO 68
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 68
gcaaaaagca aaggaacgaa tgg 23

<210> SEQ ID NO 69
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 69
agaaagtgca acaagcagaa agg 23

<210> SEQ ID NO 70
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 70
gaaagtgcaa caagcagaaa ggg 23

<210> SEQ ID NO 71
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 71
aaagtgcaac aagcagaaag ggg 23

<210> SEQ ID NO 72
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 72
aagtgcaaca agcagaaagg ggg 23

<210> SEQ ID NO 73
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 73
ggctgcaaag ctgcctgcct agg 23

<210> SEQ ID NO 74
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 74
gctgcaaagc tgcctgccta ggg 23

<210> SEQ ID NO 75
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 75
caggaaacgt agccctaggc agg 23

<210> SEQ ID NO 76
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 76
ctgcctaggg ctacgtttcc tgg 23

<210> SEQ ID NO 77
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 77
ttgccaggaa acgtagccct agg 23

<210> SEQ ID NO 78
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 78
tggctttcgg aagttttgcc agg 23

<210> SEQ ID NO 79
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 79
tcttttggag aaatggcttt cgg 23

<210> SEQ ID NO 80
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 80
aaagccattt ctccaaaaga agg 23

<210> SEQ ID NO 81
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 81
tagaccttct tttggagaaa tgg 23

<210> SEQ ID NO 82
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 82
tccaaaagaa ggtctagaag agg 23

<210> SEQ ID NO 83
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 83
tcctcttcta gaccttcttt tgg 23

<210> SEQ ID NO 84
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 84
aaaagaaggt ctagaagagg agg 23

<210> SEQ ID NO 85
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 85
agaaggtcta gaagaggagg agg 23

<210> SEQ ID NO 86
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 86
aggtctagaa gaggaggagg agg 23

<210> SEQ ID NO 87
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 87
tctagaagag gaggaggagg agg 23

<210> SEQ ID NO 88
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 88
agaggaggag gaggaggaga agg 23

<210> SEQ ID NO 89
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 89
ggaggaggag gaggagaagg agg 23

<210> SEQ ID NO 90
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 90
ggaggaggag gagaaggagg agg 23

<210> SEQ ID NO 91
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 91
ggaggaggag aaggaggagg agg 23

<210> SEQ ID NO 92
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 92
ggaggagaag gaggaggagg agg 23

<210> SEQ ID NO 93

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 93
ggagaaggag gaggaggagg agg 23

<210> SEQ ID NO 94
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 94
cagcatgaaa gagccccact tgg 23

<210> SEQ ID NO 95
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 95
atgaaagagc cccacttgga agg 23

<210> SEQ ID NO 96
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 96
aaagagcccc acttggaagg cgg 23

<210> SEQ ID NO 97
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 97
gccccacttg gaaggcggtt tgg 23

<210> SEQ ID NO 98
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 98
tccaaaccgc cttccaagtg ggg 23

<210> SEQ ID NO 99
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 99
atccaaaccg ccttccaagt ggg 23

<210> SEQ ID NO 100
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 100
aatccaaacc gccttccaag tgg 23

<210> SEQ ID NO 101
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 101
gattttattt gtgtgttttg tgg 23

<210> SEQ ID NO 102
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 102
catcttacac caaactcatc tgg 23

<210> SEQ ID NO 103
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 103
tttttaatgc cagatgagtt tgg 23

<210> SEQ ID NO 104

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 104
attcattctc ctgacatgtc tgg 23

<210> SEQ ID NO 105
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 105
ttcattctcc tgacatgtct ggg 23

<210> SEQ ID NO 106
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 106
ctcctgacat gtctgggact tgg 23

<210> SEQ ID NO 107
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 107
aaccaagtcc cagacatgtc agg 23

<210> SEQ ID NO 108
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 108
acatgtctgg gacttggttt agg 23

<210> SEQ ID NO 109
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 109
ctgggacttg gtttaggaaa agg 23

<210> SEQ ID NO 110
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 110
ggtttaggaa aaggaagcaa agg 23

<210> SEQ ID NO 111
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 111
gtttaggaaa aggaagcaaa ggg 23

<210> SEQ ID NO 112
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 112
aggaaaagga agcaaaggga tgg 23

<210> SEQ ID NO 113
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 113
aggaagcaaa gggatggaga agg 23

<210> SEQ ID NO 114
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 114
tggagtttta cggctgtact tgg 23

<210> SEQ ID NO 115

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 115
gacacacttg tggagtttta cgg 23

<210> SEQ ID NO 116
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 116
agcggaactt gacacacttg tgg 23

<210> SEQ ID NO 117
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 117
gtcgtaggat cagcacaaag cgg 23

<210> SEQ ID NO 118
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 118
ttggtaaatt tcgtagtcgt agg 23

<210> SEQ ID NO 119
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 119
atttaccaaa acagtccaaa agg 23

<210> SEQ ID NO 120
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 120
tagaaccttt tggactgttt tgg 23

<210> SEQ ID NO 121
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 121
atacattctt tagaaccttt tgg 23

<210> SEQ ID NO 122
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 122
taggattctt aaaactagta tgg 23

<210> SEQ ID NO 123
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 123
atactagttt taagaatcct agg 23

<210> SEQ ID NO 124
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 124
tcctaggaaa agatgtaact agg 23

<210> SEQ ID NO 125
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 125
tcctagttac atcttttcct agg 23
<210> SEQ ID NO 126
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 126
taggaaaaga tgtaactagg agg 23

<210> SEQ ID NO 127
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 127
taactaggag gtaagatgta agg 23

<210> SEQ ID NO 128
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 128
ggaggtaaga tgtaaggaac agg 23

<210> SEQ ID NO 129
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 129
taatgatgct ttggattggt agg 23

<210> SEQ ID NO 130
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 130
aagctaatga tgctttggat tgg 23

<210> SEQ ID NO 131
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 131
gttttaagct aatgatgctt tgg 23

<210> SEQ ID NO 132
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 132
taaaacttta aagagacaac tgg 23

<210> SEQ ID NO 133
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 133
aaaactttaa agagacaact ggg 23

<210> SEQ ID NO 134
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 134
ggaaatggaa aatagaaaat agg 23

<210> SEQ ID NO 135
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 135
ttatttattg tttttggaaa tgg 23

<210> SEQ ID NO 136
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 136
ttcgttttat ttattgtttt tgg 23

<210> SEQ ID NO 137

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 137
gtagtctcag tgttcagaca tgg 23

<210> SEQ ID NO 138
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 138
ttcagacatg gccaagtttt agg 23

<210> SEQ ID NO 139
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 139
tcagacatgg ccaagtttta ggg 23

<210> SEQ ID NO 140
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 140
cagacatggc caagttttag ggg 23

<210> SEQ ID NO 141
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 141
acatggccaa gttttagggg tgg 23

<210> SEQ ID NO 142
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 142
actaaaccac ccctaaaact tgg 23

<210> SEQ ID NO 143
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 143
tttaggggtg gtttagtttt agg 23

<210> SEQ ID NO 144
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 144
ttaggggtgg tttagtttta ggg 23

<210> SEQ ID NO 145
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 145
taggggtggt ttagttttag ggg 23

<210> SEQ ID NO 146
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)
<400> SEQUENCE: 146
tgtctatttt tgctttccac tgg 23

<210> SEQ ID NO 147
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 147
gtctattttt gctttccact ggg 23

<210> SEQ ID NO 148
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 148
tctatttttg ctttccactg ggg 23

<210> SEQ ID NO 149
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 149
ataatggaat ctcaccccag tgg 23

<210> SEQ ID NO 150
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 150
tggggtgaga ttccattatt tgg 23

<210> SEQ ID NO 151
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 151
ggggtgagat tccattattt ggg 23

<210> SEQ ID NO 152
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 152
gggtgagatt ccattatttg ggg 23

<210> SEQ ID NO 153
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 153
ccattatttg gggtaatcag tgg 23

<210> SEQ ID NO 154
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 154
ccactgatta ccccaaataa tgg 23

<210> SEQ ID NO 155
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 155
cattatttgg ggtaatcagt ggg 23

<210> SEQ ID NO 156
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 156
atttggggta atcagtgggt agg 23

<210> SEQ ID NO 157
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 157
tttggggtaa tcagtgggta ggg 23

<210> SEQ ID NO 158
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 158
atcagtgggt agggaattga agg 23

<210> SEQ ID NO 159
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 159
tttttttga gttttattac tgg 23

<210> SEQ ID NO 160
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 160
tgtggtgtga tggaagattc agg 23

<210> SEQ ID NO 161
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 161
actataattt tgtggtgtga tgg 23

<210> SEQ ID NO 162
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 162
agtttttaac tataattttg tgg 23

<210> SEQ ID NO 163
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 163
aaagaccttc atatttacca agg 23

<210> SEQ ID NO 164
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 164
tgaatccttg gtaaatatga agg 23

<210> SEQ ID NO 165
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 165
tttttaattg gctgaatcct tgg 23

<210> SEQ ID NO 166
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 166
ggacagtaat aatttttaat tgg 23

<210> SEQ ID NO 167
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 167
actgtccttt agattcctac tgg 23

<210> SEQ ID NO 168
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 168
agaaaccagt aggaatctaa agg 23

<210> SEQ ID NO 169
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 169
cacttcagct agaaaccagt agg 23

<210> SEQ ID NO 170
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 170
tggtttctag ctgaagtgtt tgg 23

<210> SEQ ID NO 171
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 171
ggtttctagc tgaagtgttt ggg 23

<210> SEQ ID NO 172
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 172
agtgcggtaa gaaagaacgg tgg 23

<210> SEQ ID NO 173
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 173
ttcagtgcgg taagaaagaa cgg 23

<210> SEQ ID NO 174
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 174
tgatttactg gatttcagtg cgg 23

<210> SEQ ID NO 175
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 175
caaagagctg agtgatttac tgg 23

<210> SEQ ID NO 176
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 176
cagctctttg tccgtcccta agg 23

<210> SEQ ID NO 177
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 177
gcgaatggct gccttaggga cgg 23

<210> SEQ ID NO 178
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 178
aacagcgaat ggctgcctta ggg 23

<210> SEQ ID NO 179
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 179
caacagcgaa tggctgcctt agg 23

<210> SEQ ID NO 180
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 180
ctaaggcagc cattcgctgt tgg 23

<210> SEQ ID NO 181
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 181
aatgcatcac caacagcgaa tgg 23

<210> SEQ ID NO 182
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 182
atcacacaaa cctagaaaca tgg 23

<210> SEQ ID NO 183
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 183
gcggttattt ccatgtttct agg 23

<210> SEQ ID NO 184
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 184
gggactggat tttctgattg cgg 23

<210> SEQ ID NO 185
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 185
gaaaatccag tcccaatcct tgg 23

<210> SEQ ID NO 186
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 186
ttttctccaa ggattgggac tgg 23

<210> SEQ ID NO 187
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 187
ttgtgttttc tccaaggatt ggg 23

<210> SEQ ID NO 188
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 188
attgtgtttt ctccaaggat tgg 23

<210> SEQ ID NO 189
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 189
atccttggag aaaacacaat cgg 23

<210> SEQ ID NO 190
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence (including PAM)

<400> SEQUENCE: 190
atccgattgt gttttctcca agg 23

<210> SEQ ID NO 191
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 191
ggggaggagg ccagggcagc agg 23

<210> SEQ ID NO 192

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 192
gggcagcagg acccccccg cgg 23

<210> SEQ ID NO 193
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 193
ggcagcagga ccccccccgc ggg 23

<210> SEQ ID NO 194
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 194
gacccccccc gcgggttatg tgg 23

<210> SEQ ID NO 195
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 195
accccccccg cgggttatgt ggg 23

<210> SEQ ID NO 196
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 196
ccccccccgc gggttatgtg ggg 23

<210> SEQ ID NO 197

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 197
ccccacataa cccgcggggg ggg 23

<210> SEQ ID NO 198
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 198
gccccacata acccgcgggg ggg 23

<210> SEQ ID NO 199
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 199
tgccccacat aacccgcggg ggg 23

<210> SEQ ID NO 200
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 200
ctgccccaca taacccgcgg ggg 23

<210> SEQ ID NO 201
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 201
tctgccccac ataacccgcg ggg 23

<210> SEQ ID NO 202

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 202
ctctgcccca cataacccgc ggg 23

<210> SEQ ID NO 203
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 203
gctctgcccc acataacccg cgg 23

<210> SEQ ID NO 204
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 204
gcagagcaag aatcctgaaa agg 23

<210> SEQ ID NO 205
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 205
gagcaagaat cctgaaaagg agg 23

<210> SEQ ID NO 206
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 206
agaatcctga aaaggaggag tgg 23

<210> SEQ ID NO 207

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 207
tacatccact cctccttttc agg 23

<210> SEQ ID NO 208
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 208
ggaggagtgg atgtactccg tgg 23

<210> SEQ ID NO 209
<211> LENGTH: 23
<212> TYPE: DNA
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 209
ggatgtactc cgtggagtag agg 23

<210> SEQ ID NO 210
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 210
ctccgtggag tagaggccgt tgg 23

<210> SEQ ID NO 211
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 211
ggccaacggc ctctactcca cgg 23

<210> SEQ ID NO 212

<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 212
tggagtagag gccgttggcc tgg 23

<210> SEQ ID NO 213
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 213
aggccgttgg cctggtccga cgg 23

<210> SEQ ID NO 214
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 214
atgccgtcgg accaggccaa cgg 23

<210> SEQ ID NO 215
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<400> SEQUENCE: 215
ggtgcagatg ccgtcggacc agg 23

<210> SEQ ID NO 216
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<400> SEQUENCE: 216
ggtctgggtg cagatgccgt cgg 23

<210> SEQ ID NO 217
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<400> SEQUENCE: 217
acggcatctg cacccagacc tgg 23

<210> SEQ ID NO 218
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 218
ctgcacccag acctggtcgt tgg 23

<210> SEQ ID NO 219
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 219
tgcacccaga cctggtcgtt ggg 23

<210> SEQ ID NO 220
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<220> FEATURE:
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<400> SEQUENCE: 220
gcggcccaac gaccaggtct ggg 23

<210> SEQ ID NO 221
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<400> SEQUENCE: 221
tgcggcccaa cgaccaggtc tgg 23

<210> SEQ ID NO 222
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<400> SEQUENCE: 222
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<400> SEQUENCE: 223
ccagctgcgg cccaacgacc agg 23

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<400> SEQUENCE: 224
gttgggccgc agctggagca cgg 23

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<400> SEQUENCE: 225
gtggggccgt gctccagctg cgg 23

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<400> SEQUENCE: 226
gcacggcccc accagatgcc tgg 23

<210> SEQ ID NO 227
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<400> SEQUENCE: 227
ccccaccaga tgcctggtcc agg 23

<210> SEQ ID NO 228
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 228
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<210> SEQ ID NO 229
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 229
acctggacca ggcatctggt ggg 23

<210> SEQ ID NO 230
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 230
tacctggacc aggcatctgg tgg 23

<210> SEQ ID NO 231
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 231
ggctacctgg accaggcatc tgg 23

<210> SEQ ID NO 232
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 232
caagaagggc tacctggacc agg 23

<210> SEQ ID NO 233
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 233
tgagtacaag aagggctacc tgg 23

<210> SEQ ID NO 234
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 234
gcccttcttg tactcatcgt agg 23

<210> SEQ ID NO 235
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 235
acctacgatg agtacaagaa ggg 23

<210> SEQ ID NO 236
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 236
tacctacgat gagtacaaga agg 23

<210> SEQ ID NO 237
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 237
cttgtactca tcgtaggtat agg 23

<210> SEQ ID NO 238
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 238
gtactcatcg taggtatagg tgg 23

<210> SEQ ID NO 239
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 239
tcatcgtagg tataggtggc cgg 23

<210> SEQ ID NO 240
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 240
ccggcacgtt gttcttgtac agg 23

<210> SEQ ID NO 241
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 241
cctgtacaag aacaacgtgc cgg 23

<210> SEQ ID NO 242
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 242
cggcacgttg ttcttgtaca ggg 23

<210> SEQ ID NO 243
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 243
gtacagggcc acccacacgt tgg 23

<210> SEQ ID NO 244
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 244
caagggcacc aacgtgtggg tgg 23

<210> SEQ ID NO 245
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 245
cgtcaagggc accaacgtgt ggg 23

<210> SEQ ID NO 246
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 246
acgtcaaggg caccaacgtg tgg 23

<210> SEQ ID NO 247
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 247
tggtgccctt gacgtgcaca tgg 23

<210> SEQ ID NO 248
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 248
gcttaccatg tgcacgtcaa ggg 23

<210> SEQ ID NO 249
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 249
tgcttaccat gtgcacgtca agg 23

<210> SEQ ID NO 250
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 250
aagtagtaga cgccgcccac agg 23

<210> SEQ ID NO 251
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 251
agtagtagac gccgcccaca ggg 23

<210> SEQ ID NO 252
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 252
gtagacgccg cccacagggc agg 23

<210> SEQ ID NO 253
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 253
atcttcacct gccctgtggg cgg 23

<210> SEQ ID NO 254
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 254
ggcatcttca cctgccctgt ggg 23

<210> SEQ ID NO 255
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 255
tggcatcttc acctgccctg tgg 23

<210> SEQ ID NO 256
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 256
agggcaggtg aagatgccag tgg 23

<210> SEQ ID NO 257
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 257
caggtgaaga tgccagtggc tgg 23

<210> SEQ ID NO 258
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 258
aggtgaagat gccagtggct ggg 23

<210> SEQ ID NO 259
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 259
agcggctaca acccagccac tgg 23

<210> SEQ ID NO 260
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 260
tggctgggtt gtagccgctg tgg 23

<210> SEQ ID NO 261
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 261
actctctaca atggccacag cgg 23

<210> SEQ ID NO 262
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 262
tgtggccatt gtagagagtc cgg 23

<210> SEQ ID NO 263
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 263
tttgaccgga ctctctacaa tgg 23

<210> SEQ ID NO 264
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 264
gagagtccgg tcaaatttca cgg 23

<210> SEQ ID NO 265
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 265
agagtccggt caaatttcac ggg 23

<210> SEQ ID NO 266
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 266
gcatgcccgt gaaatttgac cgg 23

<210> SEQ ID NO 267
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 267
aaatttcacg ggcatgcccg agg 23

<210> SEQ ID NO 268
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 268
tttcacgggc atgcccgagg cgg 23

<210> SEQ ID NO 269
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 269
ttcacgggca tgcccgaggc ggg 23

<210> SEQ ID NO 270
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 270
tcacgggcat gcccgaggcg ggg 23

<210> SEQ ID NO 271
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 271
gggcatgccc gaggcgggga agg 23

<210> SEQ ID NO 272
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 272
ggcatgcccg aggcggggaa ggg 23

<210> SEQ ID NO 273
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 273
gcccgaggcg gggaagggcg agg 23

<210> SEQ ID NO 274
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 274
acctcgccct tccccgcctc ggg 23

<210> SEQ ID NO 275
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 275
cacctcgccc ttccccgcct cgg 23

<210> SEQ ID NO 276
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 276
cgaggtgagc accgcagtga agg 23

<210> SEQ ID NO 277
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 277
gtgagcaccg cagtgaaggc cgg 23

<210> SEQ ID NO 278
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 278
caccgcagtg aaggccggtg tgg 23

<210> SEQ ID NO 279
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 279
tgccacaccg gccttcactg cgg 23

<210> SEQ ID NO 280
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 280
cagtgaaggc cggtgtggca tgg 23

<210> SEQ ID NO 281
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 281
agtgaaggcc ggtgtggcat ggg 23

<210> SEQ ID NO 282
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 282
gctgtctgcc catgccacac cgg 23

<210> SEQ ID NO 283
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 283
agctcgccca gcccaaactg tgg 23

<210> SEQ ID NO 284
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 284
ggcaagccac agtttgggct ggg 23

<210> SEQ ID NO 285
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 285
gggcaagcca cagtttgggc tgg 23

<210> SEQ ID NO 286
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 286
aggggggcaa gccacagttt ggg 23

<210> SEQ ID NO 287
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 287
aaggggggca agccacagtt tgg 23

<210> SEQ ID NO 288
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 288
cttgcccccc ttgcccagca cgg 23

<210> SEQ ID NO 289
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 289
ggtgccgtgc tgggcaaggg ggg 23

<210> SEQ ID NO 290
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 290
gggtgccgtg ctgggcaagg ggg 23

<210> SEQ ID NO 291
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 291
agggtgccgt gctgggcaag ggg 23

<210> SEQ ID NO 292
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 292
gagggtgccg tgctgggcaa ggg 23

<210> SEQ ID NO 293
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<400> SEQUENCE: 293
ggagggtgcc gtgctgggca agg 23

<210> SEQ ID NO 294
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 294
ggtgtggagg gtgccgtgct ggg 23

<210> SEQ ID NO 295
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 295
cggtgtggag ggtgccgtgc tgg 23

<210> SEQ ID NO 296
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<400> SEQUENCE: 296
ggcaccctcc acaccgccgt tgg 23

<210> SEQ ID NO 297
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 297
gcaccctcca caccgccgtt ggg 23

<210> SEQ ID NO 298
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<212> TYPE: DNA
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<400> SEQUENCE: 298
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<400> SEQUENCE: 299
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<400> SEQUENCE: 300
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<210> SEQ ID NO 301
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<400> SEQUENCE: 301
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<210> SEQ ID NO 302
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 303
gcaggcttgc acctgcccaa cgg 23

<210> SEQ ID NO 304
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<400> SEQUENCE: 304
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<210> SEQ ID NO 305
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<400> SEQUENCE: 305
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<400> SEQUENCE: 306
ccagtctcat cgaaggcccc agg 23

<210> SEQ ID NO 307
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 307
cctggggcct tcgatgagac tgg 23

<210> SEQ ID NO 308
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 308
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<210> SEQ ID NO 309
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 309
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<400> SEQUENCE: 310
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 311
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<210> SEQ ID NO 312
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 312
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<210> SEQ ID NO 313
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 313
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<210> SEQ ID NO 314
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<400> SEQUENCE: 314
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<210> SEQ ID NO 315
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<400> SEQUENCE: 315
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<210> SEQ ID NO 316
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 316
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<210> SEQ ID NO 317
<211> LENGTH: 23
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 317
ccgggacccc ctggtgcccc tgg 23

<210> SEQ ID NO 318
<211> LENGTH: 23
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 318
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<210> SEQ ID NO 319
<211> LENGTH: 23
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 319
aggggcacca gggggtcccg ggg 23

<210> SEQ ID NO 320
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 320
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<210> SEQ ID NO 321
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 321
accagggggt cccgggggcc cgg 23

<210> SEQ ID NO 322
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 322
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<210> SEQ ID NO 323
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 323
cccgggcccc cgggaccccc tgg 23

<210> SEQ ID NO 324
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 324
gggggtcccg ggggcccggg agg 23

<210> SEQ ID NO 325
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 325
cccgggggcc cgggaggccc cgg 23

<210> SEQ ID NO 326
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 326
ccggggcctc ccgggccccc ggg 23

<210> SEQ ID NO 327
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 327
tccggggcct cccgggcccc cgg 23

<210> SEQ ID NO 328
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 328
gggggcccgg gaggccccgg agg 23

<210> SEQ ID NO 329
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 329
ggggcccggg aggccccgga ggg 23

<210> SEQ ID NO 330
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 330
cgggccctcc ggggcctccc ggg 23

<210> SEQ ID NO 331
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 331
acgggccctc cggggcctcc cgg 23

<210> SEQ ID NO 332
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 332
ctggaatcac gggccctccg ggg 23

<210> SEQ ID NO 333
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 333
cccggagggc ccgtgattcc agg 23

<210> SEQ ID NO 334
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 334
cctggaatca cgggccctcc ggg 23

<210> SEQ ID NO 335
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 335
ccggagggcc cgtgattcca ggg 23

<210> SEQ ID NO 336
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 336

ccctggaatc acgggccctc cgg 23

<210> SEQ ID NO 337
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 337
cggagggccc gtgattccag ggg 23

<210> SEQ ID NO 338
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 338
cccgtgattc caggggagcc agg 23

<210> SEQ ID NO 339
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 339
cctggctccc ctggaatcac ggg 23

<210> SEQ ID NO 340
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 340
ccgtgattcc aggggagcca ggg 23

<210> SEQ ID NO 341
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 341

ccctggctcc cctggaatca cgg 23

<210> SEQ ID NO 342
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 342
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<210> SEQ ID NO 343
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 343
ccaggggtcc ctggctcccc tgg 23

<210> SEQ ID NO 344
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 344
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<210> SEQ ID NO 345
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 345
aggggagcca gggacccctg ggg 23

<210> SEQ ID NO 346
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 346

ggggagccag ggacccctgg ggg 23

<210> SEQ ID NO 347
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 347
acggggcccc caggggtccc tgg 23

<210> SEQ ID NO 348
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 348
agggaccccct gggggccccg tgg 23

<210> SEQ ID NO 349
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 349
gggacccctg ggggccccgt ggg 23

<210> SEQ ID NO 350
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 350
tgggcccacg gggcccccag ggg 23

<210> SEQ ID NO 351
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 351

ctgggcccac ggggcccccа ggg 23

<210> SEQ ID NO 352
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 352
gctgggccca cggggcccccc agg 23

<210> SEQ ID NO 353
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 353
ctggcacggc tgggcccacg ggg 23

<210> SEQ ID NO 354
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 354
cccgtgggcc cagccgtgcc agg 23

<210> SEQ ID NO 355
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 355
cctggcacgg ctgggcccac ggg 23

<210> SEQ ID NO 356
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 356

acctggcacg gctgggccca cgg 23

<210> SEQ ID NO 357
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 357
caggggaacc tggcacggct ggg 23

<210> SEQ ID NO 358
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 358
gcaggggaac ctggcacggc tgg 23

<210> SEQ ID NO 359
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 359
gagagcaggg gaacctggca cgg 23

<210> SEQ ID NO 360
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 360
gaggggagag caggggaacc tgg 23

<210> SEQ ID NO 361
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 361

tcccctgctc tcccctctcc agg 23

<210> SEQ ID NO 362
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 362
cccctgctct cccctctcca ggg 23

<210> SEQ ID NO 363
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 363
ccctggagag gggagagcag ggg 23

<210> SEQ ID NO 364
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 364
ccctgctctc ccctctccag ggg 23

<210> SEQ ID NO 365
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 365
cccctggaga ggggagagca ggg 23

<210> SEQ ID NO 366
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 366

cctgctctcc cctctccagg ggg 23

<210> SEQ ID NO 367
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 367
ccccctggag aggggagagc agg 23

<210> SEQ ID NO 368
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 368
ctcccctctc caggggggccc tgg 23

<210> SEQ ID NO 369
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 369
tgccagggcc ccctggagag ggg 23

<210> SEQ ID NO 370
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 370
ctgccagggc cccctggaga ggg 23

<210> SEQ ID NO 371
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 371

cctctccagg gggccctggc agg 23

<210> SEQ ID NO 372
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 372
cctgccaggg ccccctggag agg 23

<210> SEQ ID NO 373
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 373
ccaggggcc ctggcaggcc tgg 23

<210> SEQ ID NO 374
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 374
ccaggcctgc cagggccccc tgg 23

<210> SEQ ID NO 375
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 375
aggggaacc aggcctgcca ggg 23

<210> SEQ ID NO 376
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 376

aaggggaac caggcctgcc agg 23

<210> SEQ ID NO 377
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 377
gcaggcctgg ttccccttc agg 23

<210> SEQ ID NO 378
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 378
cctggttccc ccttcaggcc cgg 23

<210> SEQ ID NO 379
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 379
ccgggcctga agggggaacc agg 23

<210> SEQ ID NO 380
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 380
gttccccctt caggcccggc agg 23

<210> SEQ ID NO 381
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 381

aggcctgccg ggcctgaagg ggg 23

<210> SEQ ID NO 382
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 382
aaggcctgcc gggcctgaag ggg 23

<210> SEQ ID NO 383
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<220> FEATURE:
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<400> SEQUENCE: 383
caaggcctgc cgggcctgaa ggg 23

<210> SEQ ID NO 384
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<400> SEQUENCE: 384
ccttcaggcc cggcaggcct tgg 23

<210> SEQ ID NO 385
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<400> SEQUENCE: 385
ccaaggcctg ccgggcctga agg 23

<210> SEQ ID NO 386
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<400> SEQUENCE: 386

cttcaggccc ggcaggcctt ggg 23

<210> SEQ ID NO 387
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<400> SEQUENCE: 387
ttcaggcccg gcaggccttg ggg 23

<210> SEQ ID NO 388
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<400> SEQUENCE: 388
attgggcccc aaggcctgcc ggg 23

<210> SEQ ID NO 389
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<400> SEQUENCE: 389
tattgggccc caaggcctgc cgg 23

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<400> SEQUENCE: 390
ggcaggcctt ggggcccaat agg 23

<210> SEQ ID NO 391
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<400> SEQUENCE: 391

gcaggccttg gggcccaata ggg 23

<210> SEQ ID NO 392
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<400> SEQUENCE: 392
gctggcccta ttgggcccca agg 23

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<400> SEQUENCE: 393
tggggcccaa tagggccagc tgg 23

<210> SEQ ID NO 394
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<400> SEQUENCE: 394
agggtccagc tggccctatt ggg 23

<210> SEQ ID NO 395
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<400> SEQUENCE: 395
cagggtccag ctggccctat tgg 23

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<400> SEQUENCE: 396

caatagggcc agctggaccc tgg 23

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<400> SEQUENCE: 397
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<400> SEQUENCE: 398
ccaggactcc agggtccagc tgg 23

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tcaggaatcc caggactcca ggg 23

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<400> SEQUENCE: 401

ctcaggaatc ccaggactcc agg 23

<210> SEQ ID NO 402
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<220> FEATURE:
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<400> SEQUENCE: 402
ctggagtcct gggattcctg agg 23
<210> SEQ ID NO 403
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 403
tggagtcctg ggattcctga ggg 23

<210> SEQ ID NO 404
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 404
aggggtccct caggaatccc agg 23

<210> SEQ ID NO 405
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 405
ggattcctga gggacccctc agg 23

<210> SEQ ID NO 406
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 406
cctgagggac ccctcaggcc agg 23

<210> SEQ ID NO 407
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 407
cctggcctga ggggtccctc agg 23

<210> SEQ ID NO 408
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 408
cccctcaggc caggctgccc agg 23

<210> SEQ ID NO 409
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 409
cctgggcagc ctggcctgag ggg 23

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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 410
ccctcaggcc aggctgccca ggg 23

<210> SEQ ID NO 411
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 411
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<210> SEQ ID NO 412
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<220> FEATURE:
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<400> SEQUENCE: 412
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<210> SEQ ID NO 413
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 413
ttggggctcc ctgggcagcc tgg 23

<210> SEQ ID NO 414
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 414
aaggtgactt ggggctccct ggg 23

<210> SEQ ID NO 415
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<400> SEQUENCE: 415
aaaggtgact tggggctccc tgg 23

<210> SEQ ID NO 416
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<400> SEQUENCE: 416
tggggcagaa aggtgacttg ggg 23

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<400> SEQUENCE: 417
ctggggcaga aaggtgactt ggg 23

<210> SEQ ID NO 418
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<400> SEQUENCE: 418
ccaagtcacc tttctgcccc agg 23

<210> SEQ ID NO 419
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 419
cctggggcag aaaggtgact tgg 23

<210> SEQ ID NO 420
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 420
caagtcacct ttctgcccca ggg 23

<210> SEQ ID NO 421
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 421
gcaggagccc tggggcagaa agg 23

<210> SEQ ID NO 422
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 422
caggggtggc aggagccctg ggg 23

<210> SEQ ID NO 423
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 423
cccagggctc ctgccacccc tgg 23

<210> SEQ ID NO 424
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 424
ccaggggtgg caggagccct ggg 23

<210> SEQ ID NO 425
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 425
accaggggtg gcaggagccc tgg 23

<210> SEQ ID NO 426
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 426
cctgccaccc ctggtcctcc agg 23

<210> SEQ ID NO 427
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 427
cctggaggac caggggtggc agg 23

<210> SEQ ID NO 428
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 428
ctgccacccc tggtcctcca ggg 23

<210> SEQ ID NO 429
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 429
tcgccctgga ggaccagggg tgg 23

<210> SEQ ID NO 430
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 430
gggtcgccct ggaggaccag ggg 23

<210> SEQ ID NO 431
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 431
cgggtcgccc tggaggacca ggg 23

<210> SEQ ID NO 432
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 432
acgggtcgcc ctggaggacc agg 23

<210> SEQ ID NO 433
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 433
ggtttcacgg gtcgccctgg agg 23

<210> SEQ ID NO 434
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 434
ccagggcgac ccgtgaaacc cgg 23

<210> SEQ ID NO 435
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 435
ccgggtttca cgggtcgccc tgg 23

<210> SEQ ID NO 436
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 436
aagggtgagc cgggtttcac ggg 23

<210> SEQ ID NO 437
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 437
caagggtgag ccgggtttca cgg 23

<210> SEQ ID NO 438
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 438
cgtgaaaccc ggctcaccct tgg 23

<210> SEQ ID NO 439
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 439
gtgaaacccg gctcaccctt ggg 23

<210> SEQ ID NO 440
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<400> SEQUENCE: 440
actgggccca agggtgagcc ggg 23

<210> SEQ ID NO 441
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 441
aactgggccc aagggtgagc cgg 23

<210> SEQ ID NO 442
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<220> FEATURE:
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<400> SEQUENCE: 442
ggctcaccct tgggcccagt tgg 23

<210> SEQ ID NO 443
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 443
cccttgggcc cagttggtcc agg 23

<210> SEQ ID NO 444
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 444
cctggaccaa ctgggcccaa ggg 23

<210> SEQ ID NO 445
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 445
ccttgggccc agttggtcca ggg 23

<210> SEQ ID NO 446
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 446
ccctggacca actgggccca agg 23

<210> SEQ ID NO 447
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 447
cttgggccca gttggtccag ggg 23

<210> SEQ ID NO 448
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 448
ttgggcccag ttggtccagg ggg 23

<210> SEQ ID NO 449
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 449
atggaccccc tggaccaact ggg 23

<210> SEQ ID NO 450
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 450
catggacccc ctggaccaac tgg 23

<210> SEQ ID NO 451
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 451
cagttggtcc aggggtccca tgg 23

<210> SEQ ID NO 452
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 452
agttggtcca gggggtccat ggg 23

<210> SEQ ID NO 453
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 453
ccaggggtc catgggcccc agg 23

<210> SEQ ID NO 454
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 454
cctggggccc atggaccccc tgg 23

<210> SEQ ID NO 455
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 455
aggggacttc ctggggccca tgg 23

<210> SEQ ID NO 456
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 456
aggtgagagg ggacttcctg ggg 23

<210> SEQ ID NO 457
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 457
caggtgagag gggacttcct ggg 23

<210> SEQ ID NO 458
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 458
ccaggaagtc ccctctcacc tgg 23

<210> SEQ ID NO 459
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 459
ccaggtgaga ggggacttcc tgg 23

<210> SEQ ID NO 460
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 460
caggaagtcc cctctcacct ggg 23

<210> SEQ ID NO 461
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 461
cccctctcac ctgggacccc tgg 23

<210> SEQ ID NO 462
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 462
ccaggggtcc caggtgagag ggg 23

<210> SEQ ID NO 463
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 463
accaggggtc ccaggtgaga ggg 23

<210> SEQ ID NO 464
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 464
aaccaggggt cccaggtgag agg 23

<210> SEQ ID NO 465
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 465
gctgggaaac caggggtccc agg 23

<210> SEQ ID NO 466
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 466
ggacccctgg tttcccagcc agg 23

<210> SEQ ID NO 467
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 467
tggcctggct gggaaaccag ggg 23

<210> SEQ ID NO 468
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 468
gtggcctggc tgggaaacca ggg 23

<210> SEQ ID NO 469
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<210> SEQ ID NO 470
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<400> SEQUENCE: 470
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<210> SEQ ID NO 471
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<400> SEQUENCE: 482
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<210> SEQ ID NO 497
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<210> SEQ ID NO 499
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<400> SEQUENCE: 501
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<400> SEQUENCE: 502
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<210> SEQ ID NO 503
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<210> SEQ ID NO 504
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 504
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<210> SEQ ID NO 505
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<210> SEQ ID NO 506
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<210> SEQ ID NO 507
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<400> SEQUENCE: 507
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<210> SEQ ID NO 508
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<210> SEQ ID NO 513
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<210> SEQ ID NO 515
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<210> SEQ ID NO 516
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<210> SEQ ID NO 517
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<400> SEQUENCE: 517
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<210> SEQ ID NO 519
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<210> SEQ ID NO 520
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<400> SEQUENCE: 521
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<400> SEQUENCE: 522
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<210> SEQ ID NO 523
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<400> SEQUENCE: 523
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<400> SEQUENCE: 529
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<400> SEQUENCE: 534
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<400> SEQUENCE: 538
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<400> SEQUENCE: 540
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<210> SEQ ID NO 541
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<400> SEQUENCE: 541
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<210> SEQ ID NO 542
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<400> SEQUENCE: 542
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<210> SEQ ID NO 543
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 556
cccctgtccc ccttggggcc tgg 23

<210> SEQ ID NO 557
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 557
ccaggcccca agggggacag ggg 23

<210> SEQ ID NO 558
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 558
gccaggcccc aagggggaca ggg 23

<210> SEQ ID NO 559
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 559
tgccaggccc caagggggac agg 23

<210> SEQ ID NO 560
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 560
aggactgcca ggccccaagg ggg 23

<210> SEQ ID NO 561
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 561
caggactgcc aggccccaag ggg 23

<210> SEQ ID NO 562
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 562
cccttggggc ctggcagtcc tgg 23

<210> SEQ ID NO 563
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 563
ccaggactgc caggccccaa ggg 23

<210> SEQ ID NO 564
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 564
gccaggactg ccaggcccca agg 23

<210> SEQ ID NO 565
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 565
tatgggatgc caggactgcc agg 23

<210> SEQ ID NO 566
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 566
tcctggcatc ccatagccag tgg 23

<210> SEQ ID NO 567
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 567
cctggcatcc catagccagt ggg 23

<210> SEQ ID NO 568
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 568
cccactggct atgggatgcc agg 23

<210> SEQ ID NO 569
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 569
ctggcatccc atagccagtg ggg 23

<210> SEQ ID NO 570
<211> LENGTH: 23
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<400> SEQUENCE: 570
tgataggccc cactggctat ggg 23

<210> SEQ ID NO 571
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 571
ctgataggcc ccactggcta tgg 23

<210> SEQ ID NO 572
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 572
ccagtggggc ctatcagccc agg 23

<210> SEQ ID NO 573
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 573
cctgggctga taggccccac tgg 23

<210> SEQ ID NO 574
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 574
cagtggggcc tatcagccca ggg 23

<210> SEQ ID NO 575
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 575
agtggggcct atcagcccag ggg 23

<210> SEQ ID NO 576
<211> LENGTH: 23
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<400> SEQUENCE: 576
gtggggccta tcagcccagg ggg 23

<210> SEQ ID NO 577
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<400> SEQUENCE: 577
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<210> SEQ ID NO 578
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<212> TYPE: DNA
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<400> SEQUENCE: 578
cggggccccc ctgggctgat agg 23

<210> SEQ ID NO 579
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 579
ctatcagccc agggggggccc cgg 23

<210> SEQ ID NO 580
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 580
tatcagccca ggggggcccc ggg 23

<210> SEQ ID NO 581
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 581
cagggacccg gggccccccct ggg 23

<210> SEQ ID NO 582
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 582
ccaggggggc cccgggtccc tgg 23

<210> SEQ ID NO 583
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 583
ccagggaccc ggggcccccc tgg 23

<210> SEQ ID NO 584
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 584
aaaggggagc cagggacccg ggg 23

<210> SEQ ID NO 585
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 585
caaaggggag ccagggaccc ggg 23

<210> SEQ ID NO 586
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 586
ccgggtccct ggctcccctt tgg 23

<210> SEQ ID NO 587
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 587
ccaaagggga gccagggacc cgg 23

<210> SEQ ID NO 588
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 588
caggggccaa aggggagcca ggg 23

<210> SEQ ID NO 589
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 589
tcaggggcca aaggggagcc agg 23

<210> SEQ ID NO 590
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 590
ggctcccctt tggcccctga tgg 23

<210> SEQ ID NO 591
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 591
gctccccttt ggcccctgat ggg 23

<210> SEQ ID NO 592
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 592
gggcccatca ggggccaaag ggg 23

<210> SEQ ID NO 593
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 593
agggcccatc aggggccaaa ggg 23

<210> SEQ ID NO 594
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 594
cagggcccat caggggccaa agg 23

<210> SEQ ID NO 595
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 595
ttggcccctg atgggccctg tgg 23

<210> SEQ ID NO 596
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 596
aggaccacag ggcccatcag ggg 23

<210> SEQ ID NO 597
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 597
caggaccaca gggcccatca ggg 23

<210> SEQ ID NO 598
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 598
cctgatgggc cctgtggtcc tgg 23

<210> SEQ ID NO 599
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 599
ccaggaccac agggcccatc agg 23

<210> SEQ ID NO 600
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 600
gcagggttgc caggaccaca ggg 23

<210> SEQ ID NO 601
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 601
agcagggttg ccaggaccac agg 23

<210> SEQ ID NO 602
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 602
cctggcaacc ctgctgcccc tgg 23

<210> SEQ ID NO 603
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 603
ccaggggcag cagggttgcc agg 23

<210> SEQ ID NO 604
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 604
ctggcaaccc tgctgcccct ggg 23

<210> SEQ ID NO 605
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 605
tgggagtccc aggggcagca ggg 23

<210> SEQ ID NO 606
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 606
gtgggagtcc caggggcagc agg 23

<210> SEQ ID NO 607
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 607
agacggtgtg ggagtcccag ggg 23

<210> SEQ ID NO 608
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 608
tagacggtgt gggagtccca ggg 23

<210> SEQ ID NO 609
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 609
gtagacggtg tgggagtccc agg 23

<210> SEQ ID NO 610
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 610
actcccacac cgtctactcc agg 23

<210> SEQ ID NO 611
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 611
cccacaccgt ctactccagg agg 23

<210> SEQ ID NO 612
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 612
cctcctggag tagacggtgt ggg 23

<210> SEQ ID NO 613
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 613
acctcctgga gtagacggtg tgg 23

<210> SEQ ID NO 614
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 614
aaaggacctc ctggagtaga cgg 23

<210> SEQ ID NO 615
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 615
tctactccag gaggtccttt tgg 23

<210> SEQ ID NO 616
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 616
ctactccagg aggtcctttt ggg 23

<210> SEQ ID NO 617
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 617
gtgggcccaa aaggacctcc tgg 23

<210> SEQ ID NO 618
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 618
ccttttgggc ccacagctcc tgg 23

<210> SEQ ID NO 619
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 619
ccaggagctg tgggcccaaa agg 23

<210> SEQ ID NO 620
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 620
agggggggagc caggagctgt ggg 23

<210> SEQ ID NO 621
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 621
cagggggggag ccaggagctg tgg 23

<210> SEQ ID NO 622
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 622
cacagctcct ggctcccccc tgg 23

<210> SEQ ID NO 623
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 623
acagctcctg gctccccccct ggg 23

<210> SEQ ID NO 624
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 624
cagctcctgg ctccccccctg ggg 23

<210> SEQ ID NO 625
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 625
cctggctccc ccctggggcc tgg 23

<210> SEQ ID NO 626
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 626
ccaggcccca ggggggagcc agg 23

<210> SEQ ID NO 627
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 627
tggagttcca ggccccaggg ggg 23

<210> SEQ ID NO 628
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 628
ctggagttcc aggccccagg ggg 23

<210> SEQ ID NO 629
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 629
cccctggggc ctggaactcc agg 23

<210> SEQ ID NO 630
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 630
cctggagttc caggccccag ggg 23

<210> SEQ ID NO 631
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 631
tcctggagtt ccaggcccca ggg 23

<210> SEQ ID NO 632
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 632
ctcctggagt tccaggcccc agg 23

<210> SEQ ID NO 633
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 633
ctggggcctg gaactccagg agg 23

<210> SEQ ID NO 634
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 634
tctgggcctc ctggagttcc agg 23

<210> SEQ ID NO 635
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 635
aagggtgagt ctgggcctcc tgg 23

<210> SEQ ID NO 636
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 636
caggagacaa gggtgagtct ggg 23

<210> SEQ ID NO 637
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 637
ccagactcac ccttgtctcc tgg 23

<210> SEQ ID NO 638
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 638
ccaggagaca agggtgagtc tgg 23

<210> SEQ ID NO 639
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 639
cagactcacc cttgtctcct ggg 23

<210> SEQ ID NO 640
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 640
agactcaccc ttgtctcctg ggg 23

<210> SEQ ID NO 641
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 641
cccttgtctc ctggggcccc agg 23

<210> SEQ ID NO 642
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 642
cctggggccc caggagacaa ggg 23

<210> SEQ ID NO 643
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<400> SEQUENCE: 643
tcctggggcc ccaggagaca agg 23

<210> SEQ ID NO 644
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 644
gatgggcttc ctggggcccc agg 23

<210> SEQ ID NO 645
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 645
tggtttggat gggcttcctg ggg 23

<210> SEQ ID NO 646
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 646
ctggtttgga tgggcttcct ggg 23

<210> SEQ ID NO 647
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 647
ccaggaagcc catccaaacc agg 23

<210> SEQ ID NO 648
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 648
cctggtttgg atgggcttcc tgg 23

<210> SEQ ID NO 649
<211> LENGTH: 23
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<400> SEQUENCE: 649
taggcaaacc tggtttggat ggg 23

<210> SEQ ID NO 650
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 650
ttaggcaaac ctggtttgga tgg 23

<210> SEQ ID NO 651
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 651
tggcttaggc aaacctggtt tgg 23

<210> SEQ ID NO 652
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 652
ccaggtttgc ctaagccagc tgg 23

<210> SEQ ID NO 653
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<400> SEQUENCE: 653
ccagctggct taggcaaacc tgg 23

<210> SEQ ID NO 654
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 654
ttgcctaagc cagctggacc agg 23

<210> SEQ ID NO 655
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 655
tgcctaagcc agctggacca ggg 23

<210> SEQ ID NO 656
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<400> SEQUENCE: 656
ctccctggtc cagctggctt agg 23

<210> SEQ ID NO 657
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<400> SEQUENCE: 657
ctaagccagc tggaccaggg agg 23

<210> SEQ ID NO 658
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 658
gccagctgga ccagggaggc cgg 23

<210> SEQ ID NO 659
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 659
ccagctggac cagggaggcc ggg 23

<210> SEQ ID NO 660
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 660
cccggcctcc ctggtccagc tgg 23

<210> SEQ ID NO 661
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 661
cagctggacc agggaggccg ggg 23

<210> SEQ ID NO 662
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 662
agctggacca gggaggccgg ggg 23

<210> SEQ ID NO 663
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 663
gctggaccag ggaggccggg ggg 23

<210> SEQ ID NO 664
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 664
ctggaccagg gaggccgggg ggg 23

<210> SEQ ID NO 665
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 665
accagggagg ccgggggggc cgg 23

<210> SEQ ID NO 666
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 666
ccagggaggc cgggggggcc ggg 23

<210> SEQ ID NO 667
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 667
cccggccccc ccggcctccc tgg 23

<210> SEQ ID NO 668
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 668
cagggaggcc gggggggccg ggg 23

<210> SEQ ID NO 669
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 669
agggaggccg gggggccgg ggg 23

<210> SEQ ID NO 670
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 670
gggggtgccc ccggcccccc cgg 23

<210> SEQ ID NO 671
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 671
ccgggggcac ccccctgccc tgg 23

<210> SEQ ID NO 672
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 672
ccagggcagg ggggtgcccc cgg 23

<210> SEQ ID NO 673
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 673
cgggggcacc cccctgccct ggg 23

<210> SEQ ID NO 674
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 674
gggggcaccc ccctgccctg ggg 23

<210> SEQ ID NO 675
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 675
ccccccctgcc ctggggcccc agg 23

<210> SEQ ID NO 676
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 676
cctggggccc cagggcaggg ggg 23

<210> SEQ ID NO 677
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 677
gcctggggcc ccagggcagg ggg 23

<210> SEQ ID NO 678
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 678
tgcctggggc cccagggcag ggg 23

<210> SEQ ID NO 679
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 679
ctgcctgggg ccccagggca ggg 23

<210> SEQ ID NO 680
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 680
gctgcctggg gccccagggc agg 23

<210> SEQ ID NO 681
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 681
ccctggggcc ccaggcagcc cgg 23

<210> SEQ ID NO 682
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 682
ccgggctgcc tggggcccca ggg 23

<210> SEQ ID NO 683
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 683
cctggggccc caggcagccc ggg 23

<210> SEQ ID NO 684
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 684
cccgggctgc ctggggcccc agg 23

<210> SEQ ID NO 685
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 685
gggccccagg cagcccgggc tgg 23

<210> SEQ ID NO 686
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 686
gggccagccc gggctgcctg ggg 23

<210> SEQ ID NO 687
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 687
tgggccagcc cgggctgcct ggg 23

<210> SEQ ID NO 688
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 688
gtgggccagc ccgggctgcc tgg 23

<210> SEQ ID NO 689
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 689
ataatggagt gggccagccc ggg 23

<210> SEQ ID NO 690
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 690
gataatggag tgggccagcc cgg 23

<210> SEQ ID NO 691
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 691
ctcaaggggg ataatggagt ggg 23

<210> SEQ ID NO 692
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 692
ccactccatt atccccttg agg 23

<210> SEQ ID NO 693
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 693
cctcaagggg gataatggag tgg 23

<210> SEQ ID NO 694
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 694
cgaggcctca agggggataa tgg 23

<210> SEQ ID NO 695
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 695
aggtgatcga ggcctcaagg ggg 23

<210> SEQ ID NO 696
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 696
caggtgatcg aggcctcaag ggg 23

<210> SEQ ID NO 697
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 697
cccttgaggc ctcgatcacc tgg 23

<210> SEQ ID NO 698
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 698
ccaggtgatc gaggcctcaa ggg 23

<210> SEQ ID NO 699
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 699
ccttgaggcc tcgatcacct ggg 23

<210> SEQ ID NO 700
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 700
cccaggtgat cgaggcctca agg 23

<210> SEQ ID NO 701
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 701
cttgaggcct cgatcacctg ggg 23

<210> SEQ ID NO 702
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 702
ttgaggcctc gatcacctgg ggg 23

<210> SEQ ID NO 703
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 703
cctcgatcac ctgggggccc agg 23

<210> SEQ ID NO 704
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 704
cctgggcccc caggtgatcg agg 23

<210> SEQ ID NO 705
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 705
caggggagc ctgggccccc agg 23

<210> SEQ ID NO 706
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 706
ctgggggccc aggctccccc tgg 23

<210> SEQ ID NO 707
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 707
tgggggccca ggctcccct ggg 23

<210> SEQ ID NO 708
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 708
gggggcccag gctccccctg ggg 23

<210> SEQ ID NO 709
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 709
cagggcccca gggggagcct ggg 23

<210> SEQ ID NO 710
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 710
ccaggctccc cctggggccc tgg 23

<210> SEQ ID NO 711
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 711
ccagggcccc agggggagcc tgg 23

<210> SEQ ID NO 712
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 712
gggggaacca gggccccagg ggg 23

<210> SEQ ID NO 713
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 713
aggggaacc agggccccag ggg 23

<210> SEQ ID NO 714
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 714
caggggaac cagggcccca ggg 23

<210> SEQ ID NO 715
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 715
cctggggccc tggttccccc tgg 23

<210> SEQ ID NO 716
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 716
ccaggggaa ccagggcccc agg 23

<210> SEQ ID NO 717
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 717
caggattcca gggggaacca ggg 23

<210> SEQ ID NO 718
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 718
cctggttccc cctggaatcc tgg 23

<210> SEQ ID NO 719
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 719
ccaggattcc agggggaacc agg 23

<210> SEQ ID NO 720
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 720
ctggttcccc ctggaatcct ggg 23

<210> SEQ ID NO 721
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 721
tggttccccc tggaatcctg ggg 23

<210> SEQ ID NO 722
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 722
ggttcccccct ggaatcctgg ggg 23

<210> SEQ ID NO 723
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 723
agggcccccca ggattccagg ggg 23

<210> SEQ ID NO 724
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 724
cagggccccc aggattccag ggg 23

<210> SEQ ID NO 725
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 725
ccctggaatc ctgggggccc tgg 23

<210> SEQ ID NO 726
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 726
ccagggcccc caggattcca ggg 23

<210> SEQ ID NO 727
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 727
gccagggccc ccaggattcc agg 23

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<400> SEQUENCE: 728
caaggggtgc cagggccccc agg 23

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<400> SEQUENCE: 729
ctgggggccc tggcacccct tgg 23

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<400> SEQUENCE: 730
tgggggccct ggcacccctt ggg 23

<210> SEQ ID NO 731
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<220> FEATURE:
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<400> SEQUENCE: 731
caggtgccca aggggtgcca ggg 23

<210> SEQ ID NO 732
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<400> SEQUENCE: 732
cctggcaccc cttgggcacc tgg 23

<210> SEQ ID NO 733
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<400> SEQUENCE: 733
ccaggtgccc aaggggtgcc agg 23

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<400> SEQUENCE: 734
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<400> SEQUENCE: 735
ctggaaaacc aggtgcccaa ggg 23

<210> SEQ ID NO 736
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<400> SEQUENCE: 736
ccttgggcac ctggttttcc agg 23

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<400> SEQUENCE: 737
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<210> SEQ ID NO 738
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<400> SEQUENCE: 738
cttgggcacc tggttttcca ggg 23

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<400> SEQUENCE: 739
attactatcc ctggaaaacc agg 23

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<400> SEQUENCE: 740
tccagggata gtaatgcctg agg 23

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ccagggatag taatgcctga ggg 23

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<400> SEQUENCE: 742
ccctcaggca ttactatccc tgg 23

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<400> SEQUENCE: 743
cagggatagt aatgcctgag ggg 23

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atagtaatgc ctgaggggcc cgg 23

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<400> SEQUENCE: 745
tagtaatgcc tgaggggccc ggg 23

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<400> SEQUENCE: 746
taatgcctga ggggcccggg agg 23

<210> SEQ ID NO 747
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<220> FEATURE:
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<400> SEQUENCE: 747
cctgaggggc ccgggaggcc agg 23

<210> SEQ ID NO 748
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<212> TYPE: DNA
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<400> SEQUENCE: 748
cctggcctcc cgggcccctc agg 23

<210> SEQ ID NO 749
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<400> SEQUENCE: 749
ctgaggggcc cgggaggcca ggg 23

<210> SEQ ID NO 750
<211> LENGTH: 23
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<400> SEQUENCE: 750
tgaggggccc gggaggccag ggg 23

<210> SEQ ID NO 751
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 751
gaggggcccg ggaggccagg ggg 23

<210> SEQ ID NO 752
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 752
cccgggaggc caggggtcc tgg 23

<210> SEQ ID NO 753
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 753
ccaggacccc ctggcctccc ggg 23

<210> SEQ ID NO 754
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 754
ccgggaggcc agggggtcct ggg 23

<210> SEQ ID NO 755
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 755
cccaggaccc cctggcctcc cgg 23

<210> SEQ ID NO 756
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 756
cgggaggcca gggggtcctg ggg 23

<210> SEQ ID NO 757
<211> LENGTH: 23
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 757
gggaggccag ggggtcctgg ggg 23

<210> SEQ ID NO 758
<211> LENGTH: 23
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<400> SEQUENCE: 758
cggggacccc caggaccccc tgg 23

<210> SEQ ID NO 759
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 759
caggggtcc tgggggtccc cgg 23

<210> SEQ ID NO 760
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 760
ggggtcctgg gggtccccgg agg 23

<210> SEQ ID NO 761
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 761
cagggcctcc ggggacccccc agg 23

<210> SEQ ID NO 762
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 762
ctgggggtcc ccggaggccc tgg 23

<210> SEQ ID NO 763
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 763
cgaggggacc agggcctccg ggg 23

<210> SEQ ID NO 764
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 764
acgaggggac cagggcctcc ggg 23

<210> SEQ ID NO 765
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 765
tacgagggga ccagggcctc cgg 23

<210> SEQ ID NO 766
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 766
ccctggtccc ctcgtattcc tgg 23

<210> SEQ ID NO 767
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 767
ccaggaatac gaggggacca ggg 23

<210> SEQ ID NO 768
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 768
gccaggaata cgaggggacc agg 23

<210> SEQ ID NO 769
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 769
gggggagcca ggaatacgag ggg 23

<210> SEQ ID NO 770
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 770
gggggggagcc aggaatacga ggg 23

<210> SEQ ID NO 771
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 771
cgggggggagc caggaatacg agg 23

<210> SEQ ID NO 772
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 772
cctggctccc cccgaagccc cgg 23

<210> SEQ ID NO 773
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 773
ccggggcttc gggggggagcc agg 23

<210> SEQ ID NO 774
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 774
agggcagccg gggcttcggg ggg 23

<210> SEQ ID NO 775
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 775
cagggcagcc ggggcttcgg ggg 23

<210> SEQ ID NO 776
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 776
ccccgaagcc ccggctgccc tgg 23

<210> SEQ ID NO 777
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 777
ccagggcagc cggggcttcg ggg 23

<210> SEQ ID NO 778
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 778
accagggcag ccggggcttc ggg 23

<210> SEQ ID NO 779
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 779
caccagggca gccggggctt cgg 23

<210> SEQ ID NO 780
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 780
cgaagccccg gctgccctgg tgg 23

<210> SEQ ID NO 781
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 781
tcgggccacc agggcagccg ggg 23

<210> SEQ ID NO 782
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 782
gtcgggccac cagggcagcc ggg 23

<210> SEQ ID NO 783
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 783
ggtcgggcca ccagggcagc cgg 23

<210> SEQ ID NO 784
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 784
ctggcaaggt cgggccacca ggg 23

<210> SEQ ID NO 785
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 785
cctggtggcc cgaccttgcc agg 23

<210> SEQ ID NO 786
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 786
cctggcaagg tcgggccacc agg 23

<210> SEQ ID NO 787
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 787
ctggtggccc gaccttgcca ggg 23

<210> SEQ ID NO 788
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 788
cagggctccc tggcaaggtc ggg 23

<210> SEQ ID NO 789
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 789
ccgaccttgc cagggagccc tgg 23

<210> SEQ ID NO 790
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 790
ccagggctcc ctggcaaggt cgg 23

<210> SEQ ID NO 791
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 791
cgaccttgcc agggagccct ggg 23

<210> SEQ ID NO 792
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 792
gaccttgcca gggagccctg ggg 23

<210> SEQ ID NO 793
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 793
accttgccag ggagccctgg ggg 23

<210> SEQ ID NO 794
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 794
tcccccaggg ctccctggca agg 23

<210> SEQ ID NO 795
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 795
gctggtcccc cagggctccc tgg 23

<210> SEQ ID NO 796
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 796
tgggcaaggc tggtccccca ggg 23

<210> SEQ ID NO 797
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 797
atgggcaagg ctggtccccc agg 23

<210> SEQ ID NO 798
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 798
ggggaccagc cttgcccatc cgg 23

<210> SEQ ID NO 799
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 799
gggaccagcc ttgcccatcc ggg 23

<210> SEQ ID NO 800
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 800
ttctcccgga tgggcaaggc tgg 23

<210> SEQ ID NO 801
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 801
tggcttctcc cggatgggca agg 23

<210> SEQ ID NO 802
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 802
ttgcccatcc gggagaagcc agg 23

<210> SEQ ID NO 803
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 803
tgcccatccg ggagaagcca ggg 23

<210> SEQ ID NO 804
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 804
gcccatccgg gagaagccag ggg 23

<210> SEQ ID NO 805
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 805
cccatccggg agaagccagg ggg 23

<210> SEQ ID NO 806
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 806
ccccctggct tctcccggat ggg 23

<210> SEQ ID NO 807
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 807
gccccctggc ttctcccgga tgg 23

<210> SEQ ID NO 808
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 808
ctgggccccc tggcttctcc cgg 23

<210> SEQ ID NO 809
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 809
gagaagccag ggggcccagc agg 23

<210> SEQ ID NO 810
<211> LENGTH: 23

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 810
agaagccagg gggcccagca ggg 23

<210> SEQ ID NO 811
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 811
ccaggggcc cagcagggcc agg 23

<210> SEQ ID NO 812
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 812
cctggccctg ctgggccccc tgg 23

<210> SEQ ID NO 813
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<400> SEQUENCE: 813
atgggcagcc tggccctgct ggg 23

<210> SEQ ID NO 814
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 814
catgggcagc ctggccctgc tgg 23

<210> SEQ ID NO 815
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 815
cagcagggcc aggctgccca tgg 23

<210> SEQ ID NO 816
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<400> SEQUENCE: 816
ccaggctgcc catggagtcc tgg 23

<210> SEQ ID NO 817
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<400> SEQUENCE: 817
ccaggactcc atgggcagcc tgg 23

<210> SEQ ID NO 818
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tgggaaagcc aggactccat ggg 23

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<400> SEQUENCE: 819
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<400> SEQUENCE: 820
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<210> SEQ ID NO 821
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<400> SEQUENCE: 821
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<210> SEQ ID NO 822
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<220> FEATURE:
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<400> SEQUENCE: 822
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<400> SEQUENCE: 823
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<400> SEQUENCE: 824
ttcccaggaa aaccaggcat ggg 23

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<220> FEATURE:
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<400> SEQUENCE: 825
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<400> SEQUENCE: 826
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<400> SEQUENCE: 827
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<400> SEQUENCE: 828
ctggttttcc tgggaagcca ggg 23

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<400> SEQUENCE: 831
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<400> SEQUENCE: 832
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<210> SEQ ID NO 833
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<400> SEQUENCE: 833
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<210> SEQ ID NO 834
<211> LENGTH: 23
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<400> SEQUENCE: 834
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<210> SEQ ID NO 835
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 835
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<210> SEQ ID NO 836
<211> LENGTH: 23
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<220> FEATURE:
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<400> SEQUENCE: 836
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<210> SEQ ID NO 837
<211> LENGTH: 23
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<220> FEATURE:
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<400> SEQUENCE: 837
cggggtcccc ctggcccccc tgg 23

<210> SEQ ID NO 838
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 838
ggggggccag ggggaccccg agg 23

<210> SEQ ID NO 839
<211> LENGTH: 23
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<400> SEQUENCE: 839
gccaggggga ccccgaggcc cgg 23

<210> SEQ ID NO 840
<211> LENGTH: 23
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 840
ccagggggac cccgaggccc ggg 23

<210> SEQ ID NO 841
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 841
cccgggcctc ggggtccccc tgg 23

<210> SEQ ID NO 842
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 842
ccccgaggcc cgggcttccc agg 23

<210> SEQ ID NO 843
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 843
cctgggaagc ccgggcctcg ggg 23

<210> SEQ ID NO 844
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 844
cccgaggccc gggcttccca ggg 23

<210> SEQ ID NO 845
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 845
ccctgggaag cccgggcctc ggg 23

<210> SEQ ID NO 846
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 846
ccgaggcccg ggcttcccag ggg 23

<210> SEQ ID NO 847
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 847
cccctgggaa gcccgggcct cgg 23

<210> SEQ ID NO 848
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 848
cgaggcccgg gcttcccagg ggg 23

<210> SEQ ID NO 849
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 849
gaggcccggg cttcccaggg ggg 23

<210> SEQ ID NO 850
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 850
cccgggcttc ccaggggggc cgg 23

<210> SEQ ID NO 851
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 851
ccggcccccc tgggaagccc ggg 23

<210> SEQ ID NO 852
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 852
ccgggcttcc cagggggcc ggg 23

<210> SEQ ID NO 853
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 853
cccggccccc ctgggaagcc cgg 23

<210> SEQ ID NO 854
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 854
agggagagcc cggccccct ggg 23

<210> SEQ ID NO 855
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 855
aagggagagc ccggcccccc tgg 23

<210> SEQ ID NO 856
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 856
gggggccggg ctctcccttc agg 23

<210> SEQ ID NO 857
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 857
atggacctga agggagagcc cgg 23

<210> SEQ ID NO 858
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 858
ggctctccct tcaggtccat cgg 23
<210> SEQ ID NO 859
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 859
ctgctgccga tggacctgaa ggg 23

<210> SEQ ID NO 860
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 860
gctgctgccg atggacctga agg 23

<210> SEQ ID NO 861
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 861
ttcaggtcca tcggcagcag cgg 23

<210> SEQ ID NO 862
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 862
tccatcggca gcagcggtag agg 23

<210> SEQ ID NO 863
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 863
gcctctaccg ctgctgccga tgg 23

<210> SEQ ID NO 864
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 864
tttctgagaa agaaagagaa agg 23

<210> SEQ ID NO 865
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 865
ttctgagaaa gaaagagaaa ggg 23

<210> SEQ ID NO 866
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 866
tctgagaaag aaagagaaag ggg 23

<210> SEQ ID NO 867
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 867
agaaagagaa aggggcagtc agg 23

<210> SEQ ID NO 868
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 868
gaaagagaaa ggggcagtca ggg 23

<210> SEQ ID NO 869
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 869
aaagagaaag gggcagtcag ggg 23

<210> SEQ ID NO 870
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 870
gcagtcaggg gcctgaactg tgg 23

<210> SEQ ID NO 871
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 871
cagtcagggg cctgaactgt ggg 23

<210> SEQ ID NO 872
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 872
agtcaggggc ctgaactgtg ggg 23

<210> SEQ ID NO 873
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 873
ggggcctgaa ctgtggggac agg 23

<210> SEQ ID NO 874
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 874
gggcctgaac tgtggggaca ggg 23

<210> SEQ ID NO 875
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 875
ggcctgaact gtggggacag ggg 23

<210> SEQ ID NO 876
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 876
gtcccctgtc cccacagttc agg 23

<210> SEQ ID NO 877
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 877
aatgggggaa tgggtagatg ggg 23

<210> SEQ ID NO 878
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 878
gaatggggga atgggtagat ggg 23

<210> SEQ ID NO 879
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 879
ggaatggggg aatgggtaga tgg 23

<210> SEQ ID NO 880
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 880
tcatactgga atgggggaat ggg 23

<210> SEQ ID NO 881
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 881
ctcatactgg aatgggggaa tgg 23

<210> SEQ ID NO 882
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 882
cattccccca ttccagtatg agg 23

<210> SEQ ID NO 883
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 883
tgtacctcat actggaatgg ggg 23

<210> SEQ ID NO 884
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 884
gtgtacctca tactggaatg ggg 23

<210> SEQ ID NO 885
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 885
cgtgtacctc atactggaat ggg 23

<210> SEQ ID NO 886
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 886
ccattccagt atgaggtaca cgg 23

<210> SEQ ID NO 887
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 887
ccgtgtacct catactggaa tgg 23

<210> SEQ ID NO 888
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 888
cattccagta tgaggtacac ggg 23

<210> SEQ ID NO 889
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 889
ctctcccgtg tacctcatac tgg 23

<210> SEQ ID NO 890
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 890
cagtatgagg tacacgggag agg 23

<210> SEQ ID NO 891
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 891
ggtacacggg agaggaagaa tgg 23

<210> SEQ ID NO 892
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 892
gtacacggga gaggaagaat ggg 23

<210> SEQ ID NO 893
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 893
tacacgggag aggaagaatg ggg 23

<210> SEQ ID NO 894
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 894
gctgcccctt cctgctctca tgg 23

<210> SEQ ID NO 895
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 895
tcttccatga gagcaggaag ggg 23

<210> SEQ ID NO 896
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 896
atcttccatg agagcaggaa ggg 23

<210> SEQ ID NO 897
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 897
catcttccat gagagcagga agg 23

<210> SEQ ID NO 898
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<400> SEQUENCE: 898
cttcctgctc tcatggaaga tgg 23

<210> SEQ ID NO 899
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<220> FEATURE:
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<400> SEQUENCE: 899
ttcctgctct catggaagat ggg 23

<210> SEQ ID NO 900
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<400> SEQUENCE: 900
tcctgctctc atggaagatg ggg 23

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<400> SEQUENCE: 901
accccatctt ccatgagagc agg 23

<210> SEQ ID NO 902
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<400> SEQUENCE: 902
ctctcatgga agatggggtt tgg 23

<210> SEQ ID NO 903
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<400> SEQUENCE: 904
ctcatggaag atggggtttg ggg 23

<210> SEQ ID NO 905
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 905
tcatggaaga tggggtttgg ggg 23

<210> SEQ ID NO 906
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<400> SEQUENCE: 906
tggaagatgg ggtttggggg tgg 23

<210> SEQ ID NO 907
<211> LENGTH: 23
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atggggtttg ggggtggccc agg 23

<210> SEQ ID NO 908
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<400> SEQUENCE: 908
tggggtttgg gggtggccca ggg 23

<210> SEQ ID NO 909
<211> LENGTH: 23
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<400> SEQUENCE: 909
ggggtttggg ggtggcccag ggg 23

<210> SEQ ID NO 910
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<400> SEQUENCE: 910
gggtggccca ggggacatct tgg 23

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<400> SEQUENCE: 911
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<400> SEQUENCE: 912
gtggcccagg ggacatcttg ggg 23

<210> SEQ ID NO 913
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<220> FEATURE:
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<400> SEQUENCE: 913
tggcccaggg gacatcttgg ggg 23

<210> SEQ ID NO 914
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<220> FEATURE:
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<400> SEQUENCE: 914
ttgcccccaa gatgtcccct ggg 23

<210> SEQ ID NO 915
<211> LENGTH: 23
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<400> SEQUENCE: 915
gttgccccca agatgtcccc tgg 23

<210> SEQ ID NO 916
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<400> SEQUENCE: 916
ggggacatct tgggggcaac agg 23

<210> SEQ ID NO 917
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<220> FEATURE:
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<400> SEQUENCE: 917
gggacatctt gggggcaaca ggg 23

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<400> SEQUENCE: 918
gcaacagggt gtcctcctta agg 23

<210> SEQ ID NO 919
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<400> SEQUENCE: 919
caacagggtg tcctccttaa ggg 23

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<400> SEQUENCE: 920
ggtgttagga gcccttaagg agg 23

<210> SEQ ID NO 921
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 921
ttgggtgtta ggagccctta agg 23

<210> SEQ ID NO 922
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 922
tcctaacacc caacctacct agg 23

<210> SEQ ID NO 923
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 923
gcctaggtag gttgggtgtt agg 23

<210> SEQ ID NO 924
<211> LENGTH: 23
<212> TYPE: DNA
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<400> SEQUENCE: 924
aacacccaac ctacctaggc tgg 23

<210> SEQ ID NO 925
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 925
acacccaacc tacctaggct ggg 23

<210> SEQ ID NO 926
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 926
aggcccagcc taggtaggtt ggg 23

<210> SEQ ID NO 927
<211> LENGTH: 23
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<400> SEQUENCE: 927
gaggcccagc ctaggtaggt tgg 23

<210> SEQ ID NO 928
<211> LENGTH: 23
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<400> SEQUENCE: 928
ggaggaggcc cagcctaggt agg 23

<210> SEQ ID NO 929
<211> LENGTH: 23
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<400> SEQUENCE: 929
tcatggagga ggcccagcct agg 23

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<400> SEQUENCE: 930
ctgggcctcc tccatgagcc tgg 23

<210> SEQ ID NO 931
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<400> SEQUENCE: 931
atcagccagg ctcatggagg agg 23

<210> SEQ ID NO 932
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 932
agaatcagcc aggctcatgg agg 23

<210> SEQ ID NO 933
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 933
gtgagaatca gccaggctca tgg 23

<210> SEQ ID NO 934
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 934
atgagaggtg agaatcagcc agg 23

<210> SEQ ID NO 935
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 935
tcaggtcatg cagggatgag agg 23

<210> SEQ ID NO 936
<211> LENGTH: 23
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<400> SEQUENCE: 936
ctcatccctg catgacctga agg 23

<210> SEQ ID NO 937
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 937
atccctgcat gacctgaagg tgg 23

<210> SEQ ID NO 938
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 938
ctccaccttc aggtcatgca ggg 23

<210> SEQ ID NO 939
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 939
actccacctt caggtcatgc agg 23

<210> SEQ ID NO 940
<211> LENGTH: 23
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<400> SEQUENCE: 940
tgcatgacct gaaggtggag tgg 23

<210> SEQ ID NO 941
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 941
ctggtggcca ctccaccttc agg 23

<210> SEQ ID NO 942
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 942
ctgaaggtgg agtggccacc agg 23

<210> SEQ ID NO 943
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 943
aaggtggagt ggccaccagg tgg 23

<210> SEQ ID NO 944
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 944
gggctgctgg tgccacctgg tgg 23

<210> SEQ ID NO 945
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 945
ggtgggctgc tggtgccacc tgg 23

<210> SEQ ID NO 946
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 946
cgggctctaa ggtgggctgc tgg 23

<210> SEQ ID NO 947
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 947
gcagcccacc ttagagcccg tgg 23

<210> SEQ ID NO 948
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 948
cagcccacct tagagcccgt ggg 23

<210> SEQ ID NO 949
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 949
gctcccacgg gctctaaggt ggg 23

<210> SEQ ID NO 950
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 950
tgctcccacg ggctctaagg tgg 23

<210> SEQ ID NO 951
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 951
ctctgctccc acgggctcta agg 23

<210> SEQ ID NO 952
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 952
aggtggggct ctgctcccac ggg 23

<210> SEQ ID NO 953
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 953
gaggtggggc tctgctccca cgg 23

<210> SEQ ID NO 954
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 954
aactgggaag ttgggaggtg ggg 23

<210> SEQ ID NO 955
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 955
gaactgggaa gttgggaggt ggg 23

<210> SEQ ID NO 956
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 956
tgaactggga agttgggagg tgg 23

<210> SEQ ID NO 957
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 957
agatgaactg ggaagttggg agg 23

<210> SEQ ID NO 958
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 958
gggagatgaa ctgggaagtt ggg 23

<210> SEQ ID NO 959
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 959
ggggagatga actgggaagt tgg 23

<210> SEQ ID NO 960
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 960
ttcccagttc atctcccct tgg 23

<210> SEQ ID NO 961
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 961
ttccaagggg gagatgaact ggg 23

<210> SEQ ID NO 962
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 962
cttccaaggg ggagatgaac tgg 23

<210> SEQ ID NO 963
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 963
gcacaggtgg tcttccaagg ggg 23

<210> SEQ ID NO 964
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 964
ggcacaggtg gtcttccaag ggg 23

<210> SEQ ID NO 965
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 965
tggcacaggt ggtcttccaa ggg 23

<210> SEQ ID NO 966
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 966
ctggcacagg tggtcttcca agg 23

<210> SEQ ID NO 967
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 967
gtgcagttag ctggcacagg tgg 23

<210> SEQ ID NO 968
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 968
acggtgcagt tagctggcac agg 23

<210> SEQ ID NO 969
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 969
ctggaaacgg tgcagttagc tgg 23

<210> SEQ ID NO 970
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 970
cagctaactg caccgtttcc agg 23

<210> SEQ ID NO 971
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 971
tgcaccgttt ccaggccctc tgg 23

<210> SEQ ID NO 972
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 972
gcaccgtttc caggccctct ggg 23

<210> SEQ ID NO 973
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 973
caccgtttcc aggccctctg ggg 23

<210> SEQ ID NO 974
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 974
taccccagag ggcctggaaa cgg 23

<210> SEQ ID NO 975
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 975
tccaggccct ctggggtatt agg 23

<210> SEQ ID NO 976
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 976
tcctaatacc ccagagggcc tgg 23

<210> SEQ ID NO 977
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 977
gtttttccta ataccccaga ggg 23

<210> SEQ ID NO 978
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 978
tgtttttcct aataccccag agg 23

<210> SEQ ID NO 979
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 979
ggtattagga aaaacactga agg 23

<210> SEQ ID NO 980
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 980
ttaggaaaaa cactgaaggt agg 23

<210> SEQ ID NO 981
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 981
aacactgaag gtaggaaaat tgg 23

<210> SEQ ID NO 982
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 982
actgaaggta ggaaaattgg tgg 23

<210> SEQ ID NO 983
<211> LENGTH: 23
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<220> FEATURE:
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<400> SEQUENCE: 983
ctgaaggtag gaaaattggt ggg 23

<210> SEQ ID NO 984
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 984
tgaaggtagg aaaattggtg ggg 23

<210> SEQ ID NO 985
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 985
aggaaaattg gtggggaatg agg 23

<210> SEQ ID NO 986
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 986
tggtggggaa tgaggagctg tgg 23

<210> SEQ ID NO 987
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 987
tggggaatga ggagctgtgg agg 23

<210> SEQ ID NO 988
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 988
ggggaatgag gagctgtgga ggg 23

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<220> FEATURE:
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<400> SEQUENCE: 989
ggagctgtgg agggcgcctg agg 23

<210> SEQ ID NO 990
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 990
gagggcgcct gaggatctga tgg 23

<210> SEQ ID NO 991
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<220> FEATURE:
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<400> SEQUENCE: 991
ctgagagcca tcagatcctc agg 23

<210> SEQ ID NO 992
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 992
ctgaggatct gatggctctc agg 23

<210> SEQ ID NO 993
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 993
tgaggatctg atggctctca ggg 23

<210> SEQ ID NO 994
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 994
ggatctgatg gctctcaggg agg 23

<210> SEQ ID NO 995
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<220> FEATURE:
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<400> SEQUENCE: 995
ctgatggctc tcagggaggc agg 23

<210> SEQ ID NO 996
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 996
tgatggctct cagggaggca ggg 23

<210> SEQ ID NO 997
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 997
gatggctctc agggaggcag ggg 23

<210> SEQ ID NO 998
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 998
tctcagggag gcaggggatt tgg 23

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 999
ctcagggagg caggggattt ggg 23

<210> SEQ ID NO 1000
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<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 1000
tcagggaggc aggggatttg ggg 23

<210> SEQ ID NO 1001
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1001
cagggaggca ggggatttgg ggg 23

<210> SEQ ID NO 1002
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1002
gaggcagggg atttgggggc tgg 23

<210> SEQ ID NO 1003
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1003
aggcagggga tttgggggct ggg 23

<210> SEQ ID NO 1004
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1004
tgggggctgg gagcgatttg agg 23

<210> SEQ ID NO 1005
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1005
gggagcgatt tgaggcactg tgg 23

<210> SEQ ID NO 1006
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1006
ggagcgattt gaggcactgt ggg 23

<210> SEQ ID NO 1007
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1007
gagcgatttg aggcactgtg ggg 23

<210> SEQ ID NO 1008
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1008
atttgaggca ctgtggggtg agg 23

<210> SEQ ID NO 1009
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1009
tgaggcactg tggggtgagg agg 23

<210> SEQ ID NO 1010
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1010
gggtgaggag gctctcaccc agg 23

<210> SEQ ID NO 1011
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1011
ggaggctctc acccaggtac tgg 23

<210> SEQ ID NO 1012
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1012
gagggcaaag gccagtacct ggg 23

<210> SEQ ID NO 1013
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1013
tgagggcaaa ggccagtacc tgg 23
<210> SEQ ID NO 1014
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1014
ggtactggcc tttgccctca cgg 23

<210> SEQ ID NO 1015
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1015
ctggcctttg ccctcacgga agg 23

<210> SEQ ID NO 1016
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1016
tggcctttgc cctcacggaa ggg 23

<210> SEQ ID NO 1017

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1017
cctttgccct cacggaaggg cgg 23

<210> SEQ ID NO 1018
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1018
ccgcccttcc gtgagggcaa agg 23

<210> SEQ ID NO 1019
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1019
gtgggaccgc ccttccgtga ggg 23

<210> SEQ ID NO 1020
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1020
tgtgggaccg cccttccgtg agg 23

<210> SEQ ID NO 1021
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1021
tcacggaagg gcggtcccac agg 23

<210> SEQ ID NO 1022

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1022
tcccacaggt cctttctgca tgg 23

<210> SEQ ID NO 1023
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1023
cccacaggtc ctttctgcat ggg 23

<210> SEQ ID NO 1024
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1024
cccatgcaga aaggacctgt ggg 23

<210> SEQ ID NO 1025
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1025
gcccatgcag aaaggacctg tgg 23

<210> SEQ ID NO 1026
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1026
caggtccttt ctgcatgggc tgg 23

<210> SEQ ID NO 1027

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1027
tacatccagc ccatgcagaa agg 23

<210> SEQ ID NO 1028
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1028
atgggctgga tgtacttcac tgg 23

<210> SEQ ID NO 1029
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1029
tgggctggat gtacttcact ggg 23

<210> SEQ ID NO 1030
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1030
gggctggatg tacttcactg ggg 23

<210> SEQ ID NO 1031
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1031
ggcatagccc gccgccccac cgg 23

<210> SEQ ID NO 1032

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1032
ggcggggccg gtggggcggc ggg 23

<210> SEQ ID NO 1033
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1033
tggcggggcc ggtggggcgg cgg 23

<210> SEQ ID NO 1034
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1034
tggtggcggg gccggtgggg cgg 23

<210> SEQ ID NO 1035
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1035
ctctggtggc ggggccggtg ggg 23

<210> SEQ ID NO 1036
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1036
cccaccggcc ccgccaccag agg 23

<210> SEQ ID NO 1037

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1037
cctctggtgg cggggccggt ggg 23

<210> SEQ ID NO 1038
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1038
tcctctggtg gcggggccgg tgg 23

<210> SEQ ID NO 1039
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1039
gcgtcctctg gtggcggggc cgg 23

<210> SEQ ID NO 1040
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1040
gcgggcgtcc tctggtggcg ggg 23

<210> SEQ ID NO 1041
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1041
cgcgggcgtc ctctggtggc ggg 23

<210> SEQ ID NO 1042

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1042
ccgccaccag aggacgcccg cgg 23

<210> SEQ ID NO 1043
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1043
ccgcgggcgt cctctggtgg cgg 23

<210> SEQ ID NO 1044
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1044
gggccgcggg cgtcctctgg tgg 23

<210> SEQ ID NO 1045
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1045
tgtgggccgc gggcgtcctc tgg 23

<210> SEQ ID NO 1046
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1046
ggtgctgggg tgtgggccgc ggg 23

<210> SEQ ID NO 1047

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1047
tggtgctggg gtgtgggccg cgg 23

<210> SEQ ID NO 1048
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1048
tggtgctggt gctggggtgt ggg 23

<210> SEQ ID NO 1049
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1049
ctggtgctgg tgctggggtg tgg 23

<210> SEQ ID NO 1050
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1050
tgctactggt gctggtgctg ggg 23

<210> SEQ ID NO 1051
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1051
ctgctactgg tgctggtgct ggg 23

<210> SEQ ID NO 1052

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1052
gctgctactg gtgctggtgc tgg 23

<210> SEQ ID NO 1053
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1053
gctgctgctg ctactggtgc tgg 23

<210> SEQ ID NO 1054
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1054
ttcgctgctg ctgctgctac tgg 23

<210> SEQ ID NO 1055
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1055
gcagcagcag cagcgaagac agg 23

<210> SEQ ID NO 1056
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1056
cagcagcagc agcgaagaca ggg 23

<210> SEQ ID NO 1057

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1057
agcagcagca gcgaagacag ggg 23

<210> SEQ ID NO 1058
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1058
gggtgtcaga gtccccagca tgg 23

<210> SEQ ID NO 1059
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1059
agtccccagc atggcgtccg tgg 23

<210> SEQ ID NO 1060
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1060
cgtccacgga cgccatgctg ggg 23

<210> SEQ ID NO 1061
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1061
acgtccacgg acgccatgct ggg 23

<210> SEQ ID NO 1062

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1062
cacgtccacg gacgccatgc tgg 23

<210> SEQ ID NO 1063
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for wild type COL8A2

<400> SEQUENCE: 1063
tcttctttgc agcacgtcca cgg 23

<210> SEQ ID NO 1064
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Lys Mutation

<400> SEQUENCE: 1064
cccctcaggc caggcttccc agg 23

<210> SEQ ID NO 1065
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Lys Mutation

<400> SEQUENCE: 1065
cctgggaagc ctggcctgag ggg 23

<210> SEQ ID NO 1066
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Lys Mutation

<400> SEQUENCE: 1066
ccctcaggcc aggttgccca ggg 23

<210> SEQ ID NO 1067

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Lys Mutation

<400> SEQUENCE: 1067
ccctgggaag cctggcctga ggg 23

<210> SEQ ID NO 1068
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Lys Mutation

<400> SEQUENCE: 1068
tccctgggaa gcctggcctg agg 23

<210> SEQ ID NO 1069
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Lys Mutation

<400> SEQUENCE: 1069
ttggggctcc ctgggaagcc tgg 23

<210> SEQ ID NO 1070
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Val Mutation

<400> SEQUENCE: 1070
cccctcaggc caggcacccc agg 23

<210> SEQ ID NO 1071
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Val Mutation

<400> SEQUENCE: 1071
cctggggtgc ctggcctgag ggg 23

<210> SEQ ID NO 1072

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Val Mutation

<400> SEQUENCE: 1072
ccctcaggcc aggcacccca ggg 23

<210> SEQ ID NO 1073
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Val Mutation

<400> SEQUENCE: 1073
ccctggggtg cctggcctga ggg 23

<210> SEQ ID NO 1074
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Val Mutation

<400> SEQUENCE: 1074
tccctggggt gcctggcctg agg 23

<210> SEQ ID NO 1075
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequence for COL8A2 Gln455Val Mutation

<400> SEQUENCE: 1075
ttggggctcc ctggggtgcc tgg 23

<210> SEQ ID NO 1076
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1076
tgggggctcc ctgggcagcc tgg 23

<210> SEQ ID NO 1077

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1077
aaggtgactg ggggctccct ggg 23

<210> SEQ ID NO 1078
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1078
aaaggtgact gggggctccc tgg 23

<210> SEQ ID NO 1079
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1079
tggggcagaa aggtgactgg ggg 23

<210> SEQ ID NO 1080
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1080
ctggggcaga aaggtgactg ggg 23

<210> SEQ ID NO 1081
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1081
cccagtcacc tttctgcccc agg 23

<210> SEQ ID NO 1082

<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1082
cctggggcag aaaggtgact ggg 23

<210> SEQ ID NO 1083
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1083
ccagtcacct ttctgcccca ggg 23

<210> SEQ ID NO 1084
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Target sequences for COL8A2 Leu450Trp Mutation

<400> SEQUENCE: 1084
ccctggggca gaaaggtgac tgg 23

<210> SEQ ID NO 1085
<211> LENGTH: 1857
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: TCF4 intron 3 sequence with flanking exons, reverse strand (GRCh37/hg19)

<400> SEQUENCE: 1085
gtttgtgtga ttttgctaaa atgcatcacc aacagcgaat ggctgcctta gggacggaca 60
aagagctgag tgatttactg gatttcagtg cggtaagaaa gaacggtgga aactaacaac 120
agctgtgaaa aaaacaaaac aaaaacccaa acacttcagc tagaaaccag taggaatcta 180
aaggacagta ataattttta attggctgaa tccttggtaa atatgaaggt ctttttgaca 240
agtttttaac tataattttg tggtgtgatg gaagattcag gctttttttt ttttttgagt 300
tttattactg gccttcaatt ccctacccac tgattacccc aaataatgga atctcacccc 360
agtggaaagc aaaaatagac acccctaaaa ctaaaccacc cctaaaactt ggccatgtct 420

gaacactgag actactaata ctttgcacac tactcttcgt tttatttatt gtttttggaa
480
atggaaaata gaaaatagga gacccagttg tctctttaaa gttttaagct aatgatgctt
540
tggattggta ggacctgttc cttacatctt acctcctagt tacatctttt cctaggattc
600
ttaaaactag tatggatatg ctgagcatac attctttaga acctttttgga ctgttttggt
660
aaatttcgta gtcgtaggat cagcacaaag cggaacttga cacacttgtg gagttttacg
720
gctgtacttg gtccttctcc atccctttgc ttccttttcc taaaccaagt cccagacatg
780
tcaggagaat gaattcattt ttaatgccag atgagtttgg tgtaagatgc atttgtaaag
840
caaaataaaa agaatccaca aaacacacaa ataaaatcca aaccgccttc caagtggggc
900
tctttcatgc tgctgctgct gctgctgctg ctgctgctgc tgctgctgct gctgctgctg
960
ctgctgctgc tgctgctgct gctcctcctc ctcctcctcc ttctcctcct cctcctcctc
1020
ttctagacct tcttttggag aaatggcttt cggaagtttt gccaggaaac gtagccctag
1080
gcaggcagct ttgcagcccc ctttctgctt gttgcacttt ctccattcgt tcctttgctt
1140
tttgcaggct ctgactcagg gaaggtgtgc attatccact agatacgtcg aagaagaggg
1200
aaaccaatta gggtcgaaat aaatgctgga gagagaggga gtgaaagaga gagtgagagt
1260
gagagagaga gagagtcttg cttcaaattg ctctcctgtt agagacgaaa tgagaatttа
1320
gtgcaggtgg cacttttatt tttatttggg ttcacatatg acaggcaaat cctatacgag
1380
atggaaatgg acattgccac gtttatggcc aaggttttca atataaaaca aaacaacttt
1440
tttcttctcc ttggtgaaac tagtgttttt ctagagaggc tgctggcctc caacctgaat
1500
cttgataaca ttatggggac tgtgtttgtt ccaaatgtag cagtagtact gcttggccat
1560
ctaatgaacc tgaggaaaaa gaaagaacag agtgataatg ggggctgggg tgggatctgt
1620
aatgttgttt ctcttttagt tttaagttgg atggtgatgt attttactaa ataaaccctt
1680
agcataaact ctaagctgtt tggtaacagt atgaaagatc tttgaggagc tctgaaggca
1740
caagtgtctt cttttcaact gtaatatttc tttgtttctt ttagatgttt tcacctcctg
1800
tgagcagtgg gaaaaatgga ccaacttctt tggcaagtgg acattttact ggctcaa
1857

<210> SEQ ID NO 1086
<211> LENGTH: 147
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: sgRNA modified sequence

<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: n is 2'-0-Me nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: n may be any natural or non-natural
nucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: n is 2'-0-Me nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: n may be any natural or non-natural
nucleotide; site of PS linkage
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: n is 2'-0-Me nucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: site of PS linkage
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(23)
<223> OTHER INFORMATION: n may be any natural or non-natural
nucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (32)..(147)
<223> OTHER INFORMATION: any n is 2'-0-Me nucleotide
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (141)..(141)
<223> OTHER INFORMATION: site of PS linkage
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (143)..(143)
<223> OTHER INFORMATION: site of PS linkage
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (145)..(145)
<223> OTHER INFORMATION: site of PS linkage

<400> SEQUENCE: 1086
nnnnnnnnnn nnnnnnnnnn nnnguuuuag angncnunan gnanananun angncaaguu
60
aaaauaaggc uaguccguua ucanancnun ungnananan anangnungn gncnancncn
120
gnangnuncn gngnungncn unununu
147

<210> SEQ ID NO 1087
<211> LENGTH: 42
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: crRNA sequence
<220> FEATURE:
<221> NAME/KEY: misc feature
<222> LOCATION: (1)..(42)
<223> OTHER INFORMATION: any n may be any natural or non-natural nucleotide

<400> SEQUENCE: 1087
nnnnnnnnnn nnnnnnnnnn guuuuagagc uaugcuguuu ug
42

<210> SEQ ID NO 1088
<211> LENGTH: 74
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: trRNA sequence

<400> SEQUENCE: 1088
aacagcauag caaguuaaaa uaaggcuagu ccguuaucaa cuugaaaaag uggcaccgag
60
ucggugcuuu uuuu
74

<210> SEQ ID NO 1089
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1089
uuggcaagug gacauuuuac 20

<210> SEQ ID NO 1090
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1090
uguccacuug ccaaagaagu 20

<210> SEQ ID NO 1091
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1091
ggaccaacuu cuuuggcaag 20

<210> SEQ ID NO 1092
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1092
gaaaaaugga ccaacuucuu 20

<210> SEQ ID NO 1093
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1093
ccauuuuucc cacugcucac 20

<210> SEQ ID NO 1094
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1094
ccugugagca gugggaaaaa 20

<210> SEQ ID NO 1095
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1095
uuuuucccac ugcucacagg 20

<210> SEQ ID NO 1096
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1096
uuucaccucc ugugagcagu 20

<210> SEQ ID NO 1097
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1097
uuuucaccuc cugugagcag 20

<210> SEQ ID NO 1098
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1098
agaucuuuga ggagcucuga 20

<210> SEQ ID NO 1099
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1099
aacaguauga aagaucuuug 20

<210> SEQ ID NO 1100
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1100
agcauaaacu cuaagcuguu 20

<210> SEQ ID NO 1101
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1101
acagcuuaga guuuaugcua 20

<210> SEQ ID NO 1102
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1102
cagcuuagag uuuaugcuaa 20

<210> SEQ ID NO 1103
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1103
ucuuuuaguu uuaaguugga 20

<210> SEQ ID NO 1104
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1104
uuucucuuuu aguuuuaagu 20

<210> SEQ ID NO 1105
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1105
gugauaaugg gggcuggggu 20

<210> SEQ ID NO 1106
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1106
agugauaaug ggggcugggg 20

<210> SEQ ID NO 1107
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1107
cagagugaua auggggcug 20

<210> SEQ ID NO 1108
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1108
acagagugau aaugggggcu 20

<210> SEQ ID NO 1109
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1109
aacagaguga uaaugggggc 20

<210> SEQ ID NO 1110
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1110
aaagaacaga gugauaaugg 20

<210> SEQ ID NO 1111
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1111
gaaagaacag agugauaaug 20

<210> SEQ ID NO 1112
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1112
agaaagaaca gagugauaau 20

<210> SEQ ID NO 1113
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1113
aagaaagaac agagugauaa 20

<210> SEQ ID NO 1114
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1114
ucuguucuuu cuuuuuccuc 20

<210> SEQ ID NO 1115
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1115
uuuuccucag guucauuaga 20

<210> SEQ ID NO 1116
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1116
uuggccaucu aaugaaccug 20

<210> SEQ ID NO 1117 <211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1117
aauguagcag uaguacugcu 20

<210> SEQ ID NO 1118
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1118
agcaguacua cugcuacauu 20

<210> SEQ ID NO 1119

<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1119
ugaaucuuga uaacauuaug 20

<210> SEQ ID NO 1120
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1120
cugaaucuug auaacauuau 20

<210> SEQ ID NO 1121
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1121
ccauaauguu aucaagauuc 20

<210> SEQ ID NO 1122
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1122
ccugaaucuu gauaacauua 20

<210> SEQ ID NO 1123
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1123
aauguuauca agauucaggu 20

<210> SEQ ID NO 1124
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1124
guuaucaaga uucagguugg 20

<210> SEQ ID NO 1125
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1125
uguuuuucua gagaggcugc 20

<210> SEQ ID NO 1126
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1126
aaacuagugu uuuucuagag 20

<210> SEQ ID NO 1127
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1127
gaaaaacacu aguuucacca 20

<210> SEQ ID NO 1128
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1128
aacaacuuuu uucuucuccu 20

<210> SEQ ID NO 1129
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1129
uuguuuuaua uugaaaaccu 20

<210> SEQ ID NO 1130

<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1130
gaaaaccuug gccauaaacg 20

<210> SEQ ID NO 1131
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1131
cauugccacg uuuauggcca 20

<210> SEQ ID NO 1132
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1132
aauggacauu gccacguuua 20

<210> SEQ ID NO 1133
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1133
uguccauuuc caucucguau 20

<210> SEQ ID NO 1134
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1134
aauccuauac gagauggaaa 20

<210> SEQ ID NO 1135
<211> LENGTH: 20
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Guide Sequence

<400> SEQUENCE: 1135
caggcaaauc cuauacgaga 20

<210> SEQ ID NO 1136 <211> LENGTH: 20
<212> TYPE: RNA
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<400> SEQUENCE: 1184
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<400> SEQUENCE: 1187
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<400> SEQUENCE: 1189
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<400> SEQUENCE: 1192
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<400> SEQUENCE: 1193
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<400> SEQUENCE: 1195
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<400> SEQUENCE: 1196
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<210> SEQ ID NO 1197
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<400> SEQUENCE: 1197
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<211> LENGTH: 20
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<400> SEQUENCE: 1202
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<212> TYPE: RNA
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<210> SEQ ID NO 1216
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<212> TYPE: RNA
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<212> TYPE: RNA
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<210> SEQ ID NO 1218
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<400> SEQUENCE: 1219
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<210> SEQ ID NO 1228
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<210> SEQ ID NO 1229
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<400> SEQUENCE: 1237

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<400> SEQUENCE: 1238
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<400> SEQUENCE: 1246
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<400> SEQUENCE: 1247
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<400> SEQUENCE: 1254
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<210> SEQ ID NO 1255
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<400> SEQUENCE: 1255
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<210> SEQ ID NO 1256
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<400> SEQUENCE: 1256
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<210> SEQ ID NO 1257
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1257
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<400> SEQUENCE: 1259
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<210> SEQ ID NO 1268
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<400> SEQUENCE: 1268
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<400> SEQUENCE: 1269
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<210> SEQ ID NO 1270
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<400> SEQUENCE: 1270
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<210> SEQ ID NO 1271
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<400> SEQUENCE: 1271
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<210> SEQ ID NO 1272
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<400> SEQUENCE: 1272
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<210> SEQ ID NO 1273
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<210> SEQ ID NO 1274
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<400> SEQUENCE: 1274
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<400> SEQUENCE: 1275
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<400> SEQUENCE: 1277
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<210> SEQ ID NO 1278
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<400> SEQUENCE: 1278
auccgauugu guuuucucca 20