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(71) Demandeur/Applicant:
AKOUOS, INC., US

(72) Inventeurs/Inventors:
SIMONS, EMMANUEL JOHN, US;
NG, ROBERT, US;
REISINGER, ELLEN, DE;
AL-MOYED, HANAN, DE;
KUGLER, SEBASTIAN, DE

(74) Agent: BORDEN LADNER GERVAIS LLP

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(54) Title: COMPOSITIONS AND METHODS FOR TREATING NON-AGE-ASSOCIATED HEARING IMPAIRMENT IN A HUMAN SUBJECT

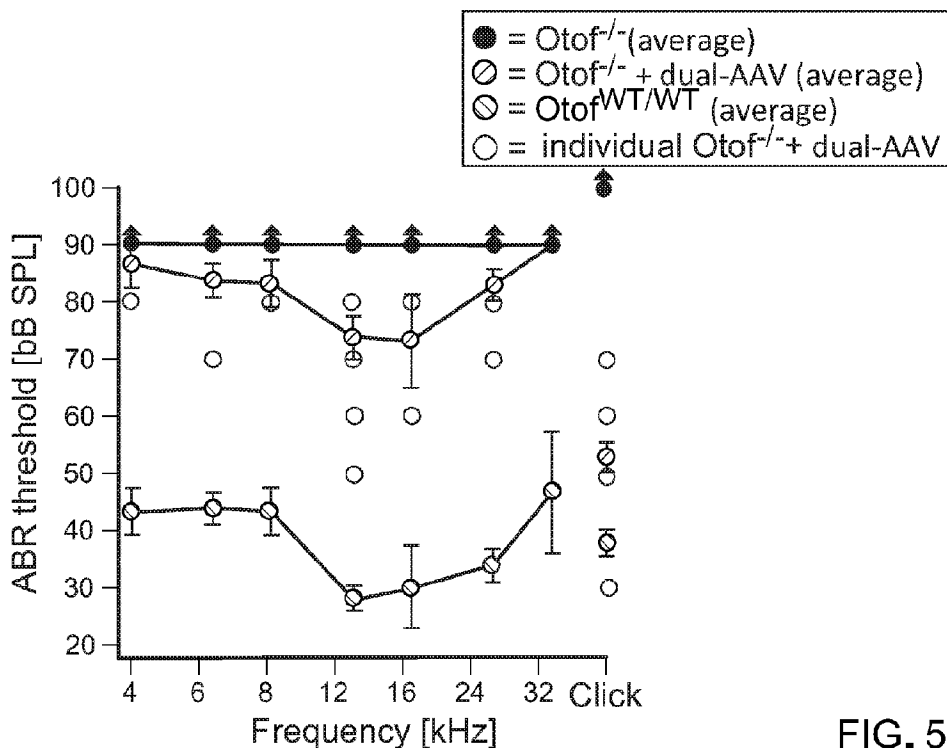


FIG. 5

(57) **Abrégé/Abstract:**

Provided herein are compositions that include at least two different nucleic acid vectors, where each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, and the use of these compositions to treat hearing loss in a subject.

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(71) Applicants: **AKOUOS, INC.** [US/US]; 7 Stetson Street, Brookline, Massachusetts 02446 (US). **GEORG-AUGUST-UNIVERSITÄT GÖTTINGEN STIFTUNG OFFENTLICHEN RECHTS, UNIVERSITÄTSMEDIZIN, REPRESENTED BY BOARD** [DE/DE]; Robert-Koch-Strasse 40, 37075 Göttingen (DE).

(72) Inventors: **SIMONS, Emmanuel John**; 7 Stetson Street, Brookline, Massachusetts 02446 (US). **NG, Robert**; 47 Lincoln Road, Unit 1, Newton, Massachusetts 02130 (US). **REISINGER, Ellen**; Gustav-Hertz-Eck 16, 37077 Göttingen (DE).

(74) Agent: **REITER, Tiffany** et al.; Fish & Richardson P.C., P.O. Box 1022, Minneapolis, Minnesota 55440-1022 (US).

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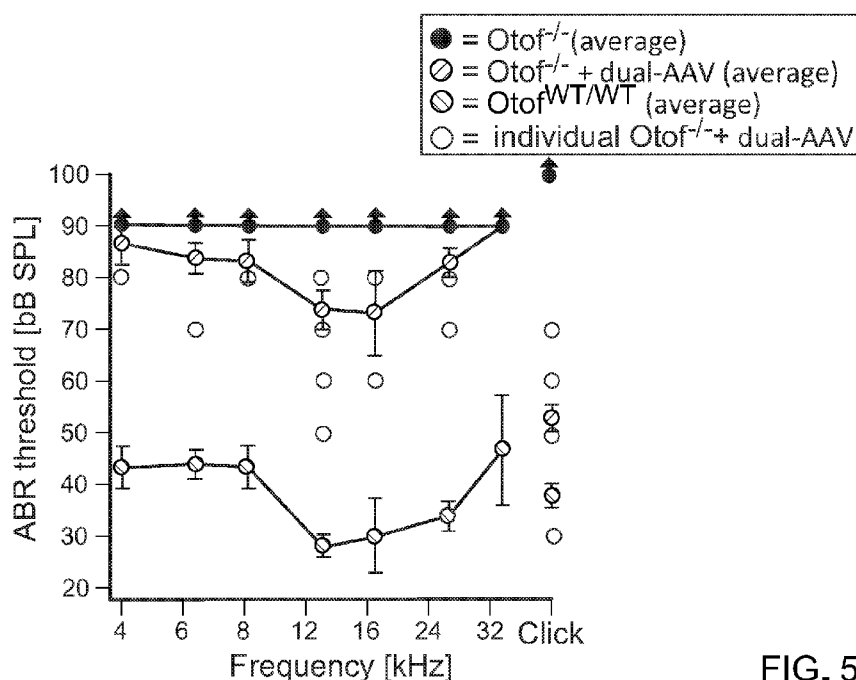


FIG. 5

(57) Abstract: Provided herein are compositions that include at least two different nucleic acid vectors, where each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, and the use of these compositions to treat hearing loss in a subject.

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COMPOSITIONS AND METHODS FOR TREATING NON-AGE-ASSOCIATED HEARING IMPAIRMENT IN A HUMAN SUBJECT

CROSS-REFERENCE TO RELATED APPLICATION

5 This application claims priority to U.S. Provisional Patent Application Serial No. 62/634,088, filed February 22, 2018; the entire contents of which are herein incorporated by reference.

SEQUENCE LISTING

10 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 February 21, 2019, is named SequenceListing.txt.

TECHNICAL FIELD

15 The present invention relates generally to the use of nucleic acids to treat hearing loss in a human subject.

BACKGROUND OF THE INVENTION

20 The ear is a complex organ, classically described as including the outer ear, the middle ear, the inner ear, the hearing (acoustic) nerve and the auditory system (which processes sound as it travels from the ear to the brain). In addition to detecting sound, the ear also helps to maintain balance. Thus, disorders of the inner ear can cause hearing loss, tinnitus, vertigo and imbalance. Vertigo is a hallucination of motion, and is the cardinal symptom of vestibular system disease. Vertigo can be caused by problems in the
25 inner ear or central nervous system. Common inner ear causes of vertigo include: vestibular neuritis (sudden, unilateral vestibular loss), Meniere's disease (episodic vertigo), benign paroxysmal positional vertigo (BPPV), and bilateral vestibular loss. Common central nervous system causes of vertigo include: post-concussion syndrome, cervical vertigo, vestibular migraine, cerebrovascular disease, and acoustic neuroma.

30 Hearing loss is one of the most common human sensory deficits, and can occur for many reasons. Some people may be born with hearing loss while others may lose

their hearing slowly over time. Presbycusis (also spelled presbyacusis) is age-related hearing loss. Approximately 36 million American adults report some degree of hearing loss, and one in three people older than 60 and half of those older than 85 experience hearing loss.

5 Hearing loss can be the result of environmental factors or a combination of genetic and environmental factors. About half of all people who have tinnitus--phantom noises in their auditory system (ringing, buzzing, chirping, humming, or beating)--also have an over-sensitivity to/reduced tolerance for certain sound frequency and volume ranges, known as hyperacusis (also spelled hyperacousis). Williams syndrome (also
10 known as Williams-Beuren Syndrome) is a multisystem disorder caused by the hemizygous deletion of a 1.6 Mb region at 7q11.23 encompassing about 26 genes, including the gene encoding LIM kinase 1 (LIMK1). Individuals with Williams Syndrome manifest hyperacusis and progressive hearing loss, and hyperacusis early onset suggests that it could be associated with one of the deleted genes.

15 Environmental causes of hearing loss include certain medications, specific infections before or after birth, and exposure to loud noise over an extended period. Hearing loss can result from noise, ototoxic agents, presbyacusis, disease, infection or cancers that affect specific parts of the ear. Ischemic damage can cause hearing loss via pathophysiological mechanisms initiated by. As another example, autoimmune inner ear
20 disease (AIED) is characterized by rapidly progressive bilateral sensorineural hearing loss, occurring when the body's immune system attacks cells in the inner ear that are mistaken for a virus or bacteria.

 Approximately 1.5 in 1,000 children are born with profound hearing loss, and another two to three per 1,000 children are born with partial hearing loss (Smith et al.,
25 2005, Lancet 365:879-890). More than half of these cases are attributed to a genetic basis (Di Domenico, et al., 2011, J. Cell. Physiol. 226:2494-2499).

 Nonsyndromic deafness is hearing loss that is not associated with other signs and symptoms. In contrast, syndromic deafness involves hearing loss that occurs with abnormalities in other parts of the body. Most cases of genetic deafness (70 percent to
30 80 percent) are nonsyndromic; the remaining cases are caused by specific genetic syndromes.

Hearing loss can be conductive (arising from the ear canal or middle ear), sensorineural (arising from the inner ear or auditory nerve), or mixed. Most forms of nonsyndromic deafness are associated with permanent hearing loss caused by damage to structures in the inner ear (sensorineural deafness). The great majority of human
5 sensorineural hearing loss is caused by abnormalities in the hair cells of the organ of Corti in the cochlea. There are also very unusual sensorineural hearing impairments that involve the eighth cranial nerve (the vestibulocochlear nerve) or the auditory portions of the brain. In the rarest of these sorts of hearing loss, only the auditory centers of the brain are affected. In this situation, cortical deafness, sounds may be heard at normal
10 thresholds, but the quality of the sound perceived is so poor that speech cannot be understood. However, most sensorineural hearing loss is due to poor hair cell function. The hair cells may be abnormal at birth, or damaged during the lifetime of an individual. There are both external causes of damage, like noise trauma and infection, and intrinsic abnormalities, like congenital mutations to genes that play an important role in cochlear
15 anatomy or physiology.

Hearing loss that results from changes in the middle ear is called conductive hearing loss. Some forms of nonsyndromic deafness involve changes in both the inner ear and the middle ear, called mixed hearing loss. Hearing loss that is present before a child learns to speak is classified as prelingual or congenital. Hearing loss that occurs
20 after the development of speech is classified as postlingual. Most autosomal recessive loci cause prelingual severe-to-profound hearing loss.

Nonsyndromic deafness can have different patterns of inheritance, and can occur at any age. Types of nonsyndromic deafness are named according to their inheritance patterns. Autosomal dominant forms are designated DFNA, autosomal recessive forms
25 are DFNB, and X-linked forms are DFN. Each type is also numbered in the order in which it was described. For example, DFNA1 was the first described autosomal dominant type of nonsyndromic deafness.

Between 75 percent and 80 percent of cases are inherited in an autosomal recessive pattern, which means both copies of the gene in each cell have mutations.
30 Usually, each parent of an individual with autosomal recessive deafness is a carrier of one copy of the mutated gene, but is not affected by this form of hearing loss.

Another 20 percent to 25 percent of nonsyndromic deafness cases are autosomal dominant, which means one copy of the altered gene in each cell is sufficient to result in hearing loss. People with autosomal dominant deafness most often inherit an altered copy of the gene from a parent who has hearing loss.

Between 1 percent and 2 percent of cases show an X-linked pattern of inheritance, which means the mutated gene responsible for the condition is located on the X chromosome (one of the two sex chromosomes). Males with X-linked nonsyndromic deafness tend to develop more severe hearing loss earlier in life than females who inherit a copy of the same gene mutation. A characteristic of X-linked inheritance is that fathers cannot pass X-linked traits to their sons.

Mitochondrial nonsyndromic deafness, which results from changes to mitochondrial DNA, occurs in less than one percent of cases in the United States. The altered mitochondrial DNA is passed from a mother to all of her sons and daughters. This type of deafness is not inherited from fathers.

Auditory neuropathy spectrum disorder (ANSD), a hearing disorder characterized by normal outer hair cells function and abnormal or absent auditory brain stem response, is one of the most common diseases leading to hearing and speech communication barriers in infants and young children. Approximately 10 percent of children with permanent hearing loss may have ANSD. The OTOF gene is the first gene identified for autosomal recessive non-syndromic ANSD, and mutations in OTOF have been found to account for approximately 5% of all cases of autosomal recessive nonsyndromic hearing loss in some populations (Rodriguez-Ballesteros et al. 2008 *Human Mut* 29(6):823-831).

The causes of nonsyndromic deafness are complex. Researchers have identified more than 30 genes that, when altered, are associated with nonsyndromic deafness; however, some of these genes have not been fully characterized. Different mutations in the same gene can be associated with different types of hearing loss, and some genes are associated with both syndromic and nonsyndromic deafness.

For example, genes associated with nonsyndromic deafness include, but are not limited to, ATP2B2, ACTG1, CDH23, CLDN14, COCH, COL11A2, DFNA5, DFNB31, DFNB59, ESPN, EYA4, GJB3, KCNQ4, LHFPL5, MYO1A, MYO15A, MYO6,

MYO7A, OTOF, PCDH15, SLC26A4, STRC, TECTA, TMC1, TMIE, TMPRSS3, TRIOBP, USH1C, and WFS1.

The most common cause of hearing loss is Nonsyndromic Hearing Loss and Deafness, DFNB1 (also called GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness; Autosomal Recessive Deafness 1; Neurosensory Nonsyndromic Recessive Deafness 1). Nonsyndromic hearing loss and deafness (DFNB1) is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment. It is caused by mutations in GJB2 (which encodes the protein connexin 26) and GJB6 (which encodes connexin 30). Diagnosis of DFNB1 depends on molecular genetic testing to identify deafness-causing mutations in GJB2 and upstream cis-regulatory elements that alter the gap junction beta-2 protein (connexin 26). Molecular genetic testing of GJB2 detects more than 99% of deafness-causing mutations in these genes. Unlike some other forms of hearing loss, DFNB1 nonsyndromic hearing loss and deafness does not affect balance or movement. The degree of hearing loss is difficult to predict based on which genetic mutation one has. Even if members of the same family are affected by DFNB1 nonsyndromic hearing loss and deafness, the degree of hearing loss may vary among them.

Mutations in genes coding for connexin26 (Cx26) and/or Cx30 are linked to approximately half of all cases of human autosomal nonsyndromic prelingual deafness. Cx26 and Cx30 are the two major Cx isoforms found in the cochlea, and they coassemble to form hybrid (heteromeric and heterotypic) gap junctions (GJs) (Ahmad, et al., Proc. Natl. Acad. Sci., 2007, 104(4):1337-1341). Nonsyndromic hearing loss and deafness, DFNA3, is caused by a dominant-negative pathogenic variant in the GJB2 or GJB6 gene, altering either the protein connexin 26 (Cx26) or connexin 30 (Cx30), respectively, and is characterized by pre- or postlingual, mild to profound, progressive high-frequency sensorineural hearing impairment.

OTOF-related deafness (DFNB9 nonsyndromic hearing loss) is characterized by two phenotypes: prelingual nonsyndromic hearing loss and, less frequently, temperature-sensitive nonsyndromic auditory neuropathy (TS-NSAN). Another form of progressive hearing impairment associated with a mutation in the otoferlin gene (e.g., a I1573T

mutation or a P1987R mutation, and/or a E1700Q mutation), or is not temperature sensitive.

Pendred syndrome/DFNB4 (deafness with goiter) is an autosomal recessive inherited disorder, and accounts for 7.5% of all cases of congenital deafness. Pendred syndrome has been linked to mutations in the PDS gene (also known as DFNB4, EVA, PDS, TDH2B and solute carrier family 26, member 4, SLC26A4) on the long arm of chromosome 7 (7q31), which encodes the pendrin protein. Mutations in this gene also cause enlarged vestibular aqueduct syndrome (EVA or EVAS), another congenital cause of deafness; specific mutations are more likely to cause EVAS, while others are more linked with Pendred syndrome. (Azaiez, et al. (December 2007), Hum. Genet. 122 (5): 451-7).

Transmembrane protease, serine 3 is an enzyme encoded by the TMPRSS3 gene (also known as DFNB10, DFNB8, ECHOS1, and TADG12). The gene was identified by its association with both congenital and childhood onset autosomal recessive deafness.

Mutations in TMPRSS3 are associated with postlingual and rapidly progressive hearing impairment. The protein encoded by the TMPRSS3 gene contains a serine protease domain, a transmembrane domain, an LDL receptor-like domain, and a scavenger receptor cysteine-rich domain. Serine proteases are known to be involved in a variety of biological processes, whose malfunction often leads to human diseases and disorders.

This gene is expressed in fetal cochlea and many other tissues, and is thought to be involved in the development and maintenance of the inner ear or the contents of the perilymph and endolymph. This gene was also identified as a tumor associated gene that is overexpressed in ovarian tumors. Four alternatively spliced variants have been described, two of which encode identical products.

DFN3 deafness is caused by mutations in the POU3F4 gene, which is located on the X chromosome. In people with this condition, one of the small bones in the middle ear (the stapes) cannot move normally, which interferes with hearing. This characteristic sign of DFN3 is called stapes fixation. At least four other regions of the X chromosome are involved in hearing loss, but the responsible genes have not been discovered.

DFNB59 (deafness, autosomal recessive 59), also known as Pejvakini or PJVK, is a 352 amino acid protein belonging to the gasdermin family in vertebrates. DFNB59 is

encoded by a gene that maps to human chromosome 2q31.2, essential for the proper function of auditory pathway neurons and outer hair cell function. Mutations in DFNB59 are believed to cause non-syndromic sensorineural deafness autosomal recessive type 59, a form of sensorineural hearing impairment characterized by absent or severely abnormal auditory brainstem response but normal otoacoustic emissions (auditory neuropathy or auditory dys-synchrony). DFNB59 shares significant similarity with DFNA5, indicating that these genes share a common origin.

Alport syndrome is caused by mutations in the COL4A3, COL4A4, and COL4A5 genes involved in collagen biosynthesis. Mutations in any of these genes prevent the proper production or assembly of the type IV collagen network, which is an important structural component of basement membranes in the kidney, inner ear, and eye. One of the criteria used in diagnosis of Alport syndrome is bilateral sensorineural hearing loss in the 2000 to 8000 Hz range. The hearing loss develops gradually, is not present in early infancy and commonly presents before the age of 30 years.

Defects in ion channels are associated with deafness: DFNA2 nonsyndromic hearing loss is inherited as an autosomal dominant mutation in the KCNQ4 gene, which encodes the potassium voltage-gated channel subfamily KQT member 4 also known as voltage-gated potassium channel subunit Kv7.4. DFNA2 nonsyndromic hearing loss is characterized by symmetric, predominantly high-frequency sensorineural hearing loss (SNHL) that is progressive across all frequencies. At younger ages, hearing loss tends to be mild in the low frequencies and moderate in the high frequencies; in older persons, the hearing loss is moderate in the low frequencies and severe to profound in the high frequencies. Although the hearing impairment is often detected during routine hearing assessment of a school-age child, it is likely that hearing is impaired from birth, especially at high frequencies. Most affected persons initially require hearing aids to assist with sound amplification between ages ten and 40 years. By age 70 years, all persons with DFNA2 hearing loss have severe-to-profound hearing impairment.

Mutations in the KCNE1 and KCNQ1 genes cause Jervell and Lange-Nielsen syndrome (JLNS), a type of long QT syndrome, associated with severe, bilateral hearing loss. This condition is an autosomal recessive disorder that affects an estimated 1.6 to 6 in 1 million children, and is responsible for less than 10 percent of all cases of long QT

syndrome. It has a markedly higher incidence in Norway and Sweden, up to 1:200,000. The proteins produced by the KCNE1 and KCNQ1 genes work together to form a potassium channel that transports positively charged potassium ions out of cells. The movement of potassium ions through these channels is critical for maintaining the normal functions of the inner ear and cardiac muscle.

EAST/SeSAME syndrome, characterized by mental retardation, ataxia, seizures, hearing loss, and renal salt waste, is believed to be caused by mutations in KCNJ10 inwardly rectifying potassium channels.

Subjects with Bartter's syndrome with sensorineural deafness type 4 (also known as Bartter syndrome IV or BSND) have defects in a Cl⁻ channel accessory subunit.

Mutations in the ATP6V1B1 gene expressed both in the kidney and in the cochlea are associated with distal renal tubular acidosis (DRTA). A significant percentage of children with autosomal recessive DRTA were also found to experience progressive bilateral sensorineural hearing loss.

Usher syndrome (also known as Hallgren syndrome, Usher-Hallgren syndrome, retinitis pigmentosa-dysacusis syndrome, and dystrophia retinae dysacusis syndrome) is a rare disorder caused by a mutation in any one of at least ten genes, resulting in a combination of hearing loss and a gradual visual impairment, and is a leading cause of deafblindness. The hearing loss is caused by a defective inner ear, whereas the vision loss results from retinitis pigmentosa (RP), a degeneration of the retinal cells. Usher syndrome has three clinical subtypes, denoted as I, II, and III. Subjects with Usher I are born profoundly deaf and begin to lose their vision in the first decade of life, learn to walk slowly as children due to problems in their vestibular system, and exhibit balance difficulties. Subjects with Usher II are not born deaf, but do have hearing loss, but do not seem to have noticeable problems with balance; they also begin to lose their vision later (in the second decade of life) and may preserve some vision even into middle age. Subjects with Usher syndrome III are not born deaf, but experience a gradual loss of their hearing and vision; they may or may not have balance difficulties.

A mouse model of congenital deafness has been generated by making a null mutation in the gene encoding the vesicular glutamate transporter-3 (VGLUT3).

Recently, hearing was restored in the VGLUT3 knockout mouse using viral-mediated gene therapy (Akil, et al., 2012, Neuron 75:283-293).

Math1 (Mouse Homolog of ATH1; also known as HATH1 or Atonal, Drosophila, Homolog of (ATOH1) is essential for hair cell development in the inner ear; Math1 was therefore proposed to act as a 'pro-hair cell gene' in the developing sensory epithelia (Bermingham et al., 1999, Science 284:1837-1841). Several studies have now demonstrated regeneration of hair cells in injured mice cochlea and improvement of both hearing and balance with virally mediated delivery of Math1 (Baker et al., 2009, Adv. Otorhinolaryngol. 66:52-63; Husseman and Raphael, 2009, Adv. Otorhinolaryngol. 66:37-51; Izumikawa et al., 2008, Hear. Res. 240:52-56; Kawamoto et al., 2003, J. Neurosci. 23:4395-4400; Praetorius et al., 2010, Acta Otolaryngol. 130:215-222; Staecker et al., 2007, Otol. Neurotol. 28:223-231).

Mutations in the WFS1 gene cause more than 90 percent of Wolfram syndrome type 1 cases; Wolfram syndrome is a condition that affects many of the body's systems, most often characterized by high blood sugar levels resulting from a shortage of the hormone insulin (diabetes mellitus) and progressive vision loss due to degeneration of the nerves that carry information from the eyes to the brain (optic atrophy). However, people with Wolfram syndrome often also have pituitary gland dysfunction that results in the excretion of excessive amounts of urine (diabetes insipidus), hearing loss caused by changes in the inner ear (sensorineural deafness), urinary tract problems, reduced amounts of the sex hormone testosterone in males (hypogonadism), or neurological or psychiatric disorders. About 65 percent of people with Wolfram syndrome have sensorineural deafness that can range in severity from deafness beginning at birth to mild hearing loss beginning in adolescence that worsens over time. Furthermore, about 60 percent of people with Wolfram syndrome develop a neurological or psychiatric disorder, most commonly problems with balance and coordination (ataxia), typically beginning in early adulthood.

The WFS1 gene encodes a protein called wolframin thought to regulate the amount of calcium in cells. When Wolfram syndrome is caused by mutations in the WFS1 gene, it is inherited in an autosomal recessive pattern, and the wolframin protein has reduced or absent function. As a result, calcium levels within cells are not regulated

and the endoplasmic reticulum does not work correctly. When the endoplasmic reticulum does not have enough functional wolframin, the cell triggers its own cell death (apoptosis). The death of cells in the pancreas, specifically cells that make insulin (beta cells), causes diabetes mellitus in people with Wolfram syndrome. The gradual loss of cells along the optic nerve eventually leads to blindness in affected individuals. The death of cells in other body systems likely causes the various signs and symptoms of Wolfram syndrome type 1.

Mutations in the mitochondrial genes MT-TS1 and MT-RNR1 have been found to increase the risk of developing nonsyndromic deafness. Nonsyndromic mitochondrial hearing loss and deafness is characterized by moderate-to-profound hearing loss. Pathogenic variants in MT-TS1 are usually associated with childhood onset of sensorineural hearing loss. Pathogenic variants in MT-RNR1 are associated with predisposition to hearing loss if they are exposed to certain antibiotic medications called aminoglycosides (ototoxicity) and/or late-onset sensorineural hearing loss; however, some people with a mutation in the MT-RNR1 gene develop hearing loss even without exposure to these antibiotics. Hearing loss associated with aminoglycoside ototoxicity is bilateral and severe to profound, occurring within a few days to weeks after administration of any amount (even a single dose) of an aminoglycoside antibiotic such as gentamycin, tobramycin, amikacin, kanamycin, or streptomycin.

Treatments for hearing loss currently consist of hearing amplification for mild to severe losses and cochlear implantation for severe to profound losses (Kral and O'Donoghue, 2010, N. Engl. J. Med. 363:1438-1450). To date, a majority of the research in this arena has focused on cochlear hair cell regeneration, applicable to the most common forms of hearing loss, including presbycusis, noise damage, infection, and ototoxicity.

In animal models for cochlear ischemia, ischemic damage may be prevented by compounds such as insulin-like growth factor (IGF-1), AM-111 (an apoptosis inhibitor), edarabone (a free radical scavenger), ginsenoside RB 1 (Kappo), glia-cell derived neurotrophic factor (GDNF), BDNF, CNTF, SOD1, SOD2, Necrostatin-1, DFNA5 and MSRB3. However, it appears that a combination of substances might be more effective than a single compound (e.g. complementary therapies to modulate oxidative stress,

exotoxicity, blood flow, calcium and stimulation overload, apoptotic pathways, neurotrophic or hormonal control mechanisms).

Inhibition of JNK-1 induced apoptosis (mitochondria-induced) may be prevented by compounds such as dominant-negative JNK-1 and d-stereoisomer JNK-1 (Mol. Pharmacol. 2007 March; 71(3):654-66; the contents of which are herein incorporated by reference in its entirety).

A long-felt need remains for agents and methods for preventing or reversing deafness.

DESCRIPTION OF DRAWINGS

Figure 1 is an exemplary schematic representation of a genetic map of the 5' and 3' vectors for dual-AAV transduction in inner hair cells (IHCs) using the trans-splicing approach. In the 5' vector, a CMV enhancer (CMVe) and a human β -actin promoter (hbA) drive the transcription of an mRNA coding for eGFP and a P2A peptide, which is cleaved during translation. The 5' vector also contains cDNA encoding an N-terminal portion of otoferlin and a splice donor site (SD). The SD DNA sequence was provided by Trapani et al. (2014) *EMBO Mol Med* 6 194–211. In the 3' vector, a splice acceptor site (SA) was subcloned after the first inverted terminal repeat (ITR) and before the 3' part of the coding sequence of otoferlin. This is followed by mRNA stabilizing sequences, woodchuck hepatitis virus posttranscriptional regulatory element (WPRE), and the poly-adenylation signal (pA).

Figure 2 is an exemplary schematic representation of a genetic map of the 5' and 3' vectors for dual-AAV transduction in IHCs, using the hybrid approach. In addition to the elements described in Figure 1, highly recombinogenic sequences from F1 phage (AK) sequences were included at the 3' end of the 5' vector and at the 5' end of the 3' vector to force correct vector assembly (Trapani et al. (2014) *EMBO Mol Med* 6 194–211).

Figure 3 is a graph showing auditory brainstem responses (ABR) amplitude over time in non-transduced *Otof*^{-/-} mice (n=25; thin black line) and *Otof*^{-/-} mice after dual-AAV mediated expression of otoferlin (n=14; grey lines represent individual animals, thick black line is the average response across all animals).

Figure 4 is a graph showing ABR amplitude over time in non-transduced *Otof*^{-/-} mice (n=25; long dashed line), *Otof*^{-/-} mice after dual-AAV mediated expression of

otoferlin (n=14; short dashed line) and wild type *Otof^{wt/wt}* mice after dual-AAV with enhanced green fluorescent protein (eGFP) transduction (n=5; thin black lines represent individual animals, thick black line is the average amplitude across all animals).

Figure 5 is an exemplary graph showing ABR threshold (in dB SPL) over frequency (in kHz) in response to pure tones or click stimuli. The minimal sound pressure level (SPL) at which waves can be detected is displayed for individual *Otof^{-/-}* animals with dual-AAV mediated expression of otoferlin (white circles represent individual animals, circle with diagonal line fill is the average threshold across all animals), for non-transduced *Otof^{-/-}* animals (black circles), and for *Otof^{wt/wt}* animals after dual-AAV with eGFP transduction (circle with checkered fill), in response to pure tones or click stimuli.

Figure 6 is a graph showing the transduction rates of IHCs along the cochlea (e.g., entire Corti, apical turn, and midbasal/basal turn), determined by immunohistochemistry using two different antibodies, one binding the N-terminal otoferlin fragment, and the other binding to the very C-terminal part of otoferlin.

Figure 7 is a set of immunohistochemical images of one organ of Corti from an *Otof^{-/-}* mouse after dual-AAV mediated expression of otoferlin. Calbindin was used as marker for inner and outer hair cells. Cells expressing eGFP indicate virus transduction of at least the 5' virus. Left and middle panels show anti-otoferlin antibody staining (Abcam) in the N-terminal half of otoferlin. Right panel shows C-terminal anti-otoferlin antibody staining (Synaptic Systems). Together, all three panels demonstrate that full-length otoferlin is expressed in IHCs. Importantly, despite the AAVs transduce several cell types in the organ of Corti (indicated by eGFP fluorescence), otoferlin expression was restricted to inner hair cells. Scale bar: 100 μ m.

Figure 8 is a graph showing Ca^{2+} currents over the depolarization stimulus for *Otof^{-/-}*IHCs (white; n=10), *Otof^{-/-}* IHC after dual-AAV mediated expression of otoferlin (diagonal line; n=8), and wild-type IHCs from background matched control animals (black; n=6).

Figure 9 is a graph showing plasma membrane capacitance (ΔC_m) over the duration of depolarization in dual-AAV transduced IHCs of *Otof^{-/-}* mice (black line, individual IHCs; diamond with diagonal line fill: mean $\pm$ s.e.m; n = 8), two individual

dual-AAV-transduced IHCs from injected *Otof*^{-/-} mice (dashed line), which displayed only minor amounts of exocytosis, and background-matched wild-type controls (black diamonds; n=6). Wild-type data from Strenzke et al. (2016) EMBO J. 35 2519–2535 is shown with black circles for comparison.

Figure 10 is a representative graph showing Q_{real} over the duration of depolarization (ms) in *Otof*^{-/-} IHCs (white diamond), dual-AAV transduced IHCs of *Otof*^{-/-} mice (black circle), and background-matched wild-type controls (black diamond).

Figure 11 is a representative plasmid map of pAAV-AK-SA-3'mOTOF-EWB.

Figure 12 is a representative plasmid map of pAAV-SA-3'mOTOF-EWB.

Figure 13 is a representative plasmid map of pAAV-HBA-eGFP-P2A-5'mOTOF-SD.

Figure 14 is a representative plasmid map of pAAV-HBA-eGFP-P2A-5'mOTOF-SD-AK.

Figure 15 is a graph showing plasma membrane capacitance (ΔC_m) over the duration of depolarization in IHCs of *Otof*^{-/-} mice transduced with the two vectors shown in Figure 2 (medium shading; thick line), IHCs in wildtype mice (dark shading; medium thickness line), and IHCs in *Otof*^{-/-} mice.

Figure 16 is a representative graph showing Q_{real} over the duration of depolarization (ms) in *Otof*^{-/-} IHCs (white diamond), IHCs of *Otof*^{-/-} mice transduced with the two vectors shown in Figure 2 (gray diamonds), and IHCs of background-matched wild-type controls (black diamond).

Figure 17 is a representative plasmid map of pAAV-AK-SA-3'mOTOF-EWB.

Figure 18 is a representative plasmid map of pAAV-HBA-eGFP-P2A-5'mOTOF-SD.

Figure 19 is a representative plasmid map of pAAV-HBA-eGFP-P2A-5'mOTOF-SD-AK.

Figure 20 is a representative plasmid map of pAAV-SA-3'mOTOF-EWB.

Figure 21 is a representative schematic of a portion of pAKOS102 (SEQ ID NO: 43).

Figure 22 is a representative schematic of a portion of pAKOS103 (SEQ ID NO: 44).

Figure 23 is a representative schematic of a portion of pAKOS103.

Figure 24 is a representative plasmid map of pAKOS104 (SEQ ID NO: 45).

Figure 25 is a representative schematic of a portion of pAKOS104-DHFR (SEQ ID NO: 46).

5 Figure 26 is a representative schematic of a portion of pAKOS104-DHFR.

Figure 27 is a representative schematic of a portion of pAKOS105 (SEQ ID NO: 47).

Figure 28 is a representative schematic of a portion of pAKOS105.

10 Figure 29 is a representative schematic of a portion of pAKOS105_GFP (SEQ ID NO: 48).

Figure 30 is a representative schematic of a portion of pAKOS106 (SEQ ID NO: 49).

Figure 31 is a representative schematic of a portion of pAKOS106.

15 Figure 32 is a representative schematic of a portion of pAKOS107 (SEQ ID NO: 50).

Figure 33 is a representative schematic of a portion of pAKOS107.

Figure 34 is a representative schematic of a portion of pAKOS108 (SEQ ID NO: 51).

Figure 35 is a representative schematic of a portion of pAKOS108.

20 Figure 36 is a representative schematic of a portion of pAKOS109 (SEQ ID NO: 52).

Figure 37 is a representative schematic a factor VIII stuffer (SEQ ID NOs. 54-57).

Figure 38 is a representative schematic of p109 (SEQ ID NO: 84).

Figure 39 is a representative schematic of p105 (SEQ ID NO: 85).

25 Figure 40 is a representative schematic of 105.WPRE.

Figure 41 is a representative schematic of p108.

Figure 42 is a representative schematic of 1OTOF18.CL1.

Figure 43 is a representative schematic of 19OTOF48.

Figure 44 is a representative schematic of 1OTOF20.CL1.

30 Figure 45 is a representative schematic of 21OTOF48.WPRE.

Figure 46 is a representative schematic of 1OTOF21.CL1.

Figure 47 is a representative schematic of 22OTOF48.WPRE.

Figure 48 is a representative schematic of 105.pA.NTF3.CMVd.

Figure 49 is an immunoblot showing the expression of full-length human otoferlin in HEK293FT cells transfected with the different pairs of plasmids indicated.

5 Figure 50 is a table showing the quantitation of expression of full-length human otoferlin from three replicates of the experiment described in Figure 49.

Figure 51 is a graph of the click ABR threshold in wildtype not treated with a vector or Otof^{-/-} mice not treated with a vector or treated with DualAAV Anc80.hOtof vectors (p105 and p109 vectors). Hearing in the Otof^{-/-} mice administered the DualAAV
10 Anc80.hOtof vectors (p105 and 109 vectors) was measured at 26-28 days and 91 days after treatment.

Figure 52 is a graph of the tone burst ABR threshold in wildtype not treated with a vector or Otof^{-/-} mice not treated with a vector or treated with DualAAV Anc80.hOtof vectors (p105 and p109 vectors). Hearing in the Otof^{-/-} mice administered the DualAAV
15 Anc80.hOtof vectors (p105 and 109 vectors) was measured at 26-28 days and 91 days after treatment.

Figure 53 is a representative schematic of a portion of pAAV-HBA-eGFP-P2A-5'mOTOF.SD (SEQ ID NO: 87).

Figure 54 is a representative schematic of a portion of pAAV-SA-
20 3'mOTOF.WPRE (SEQ ID NO: 88).

Figure 55 is a representative schematic of a portion of pAAV-HBA-eGFP-P2A-5'mOTOF.SD-AK.

Figure 56 is a representative schematic of a portion of pAAV-AK-SA-3'mOTOF.WPRE.

25 Figure 57 is a representative schematic of a portion of pAAV-CMV-5'hOTOF-SD-AK.

Figure 58 is a representative schematic of a portion of pAAV-HBA-5'hOTOF-SD-AP.

Figure 59 is a representative schematic of a portion of pAAV-HBA-5'hOTOF-
30 SD-AK.

Figure 60 is a representative schematic of a portion of pAAV-HBA-5'hOTOFcodop-SD-AK.

Figure 61 is a representative schematic of a portion of pAAV-HBA-5'hOTOFcodop-SD.

5 Figure 62 is a representative schematic of a portion of pAAV-CMV-5'hOTOFcodop-SD.

Figure 63 is a representative schematic of a portion of pAAV-CMV-5'hOTOFcodop-SD-AK.

10 Figure 64 is a representative schematic of a portion of pAAV-CBA-5'hOTOFcodop-SD-AK.

Figure 65 is a representative schematic of a portion of pAAV-CBA-5'hOTOF-SD.

Figure 66 is a representative schematic of a portion of pAAV-SA-3'OTOF.

Figure 67 is a representative schematic of a portion of pAAV-AP-SA-3'OTOF.

15 Figure 68 is a representative schematic of a portion of pAAV-AK-SA-3'OTOFcodop.

Figure 69 is a representative immunoblot showing the expression of full-length human otoferlin in HEK293FT cells transfected using DNA transfection reagent jetPRIME® (polyplus) with 600 ng of the different pairs of plasmids indicated. Lane 1 contained a prestained protein ladder. Lane 2 contained a protein sample of HEK293FT cells that were transfected with vector pAKOS104 (as shown in Figures 24 and 59) and vector pAKOS105 (as shown in Figures 27, 28 and 39). Lane 3 contained a protein sample of HEK293FT cells that were transfected with vector pAKOS108 (as shown in Figures 34, 35, 41 and 57) and vector pAKOS105 (as shown in Figures 27, 28 and 39). Lane 4 contained a protein sample of HEK293FT cells that were transfected with vector pAKOS109 (as shown in Figures 36 and 38) and vector pAKOS105 (as shown in Figures 27, 28 and 39). Lane 5 contained a protein sample of HEK293FT cells that were transfected with vector pAAV-HBA-5'hOTOFcodop-SD-AK (as shown in Figure 60) and vector pAAV-AK-SA-3'OTOFcodop (as shown in Figure 68). Lane 6 contained a protein sample of HEK293FT cells that were transfected with vector pAAV-CMV-5'hOTOFcodop-SD-AK (as shown in Figure 63) and vector pAAV-AK-SA-

3'OTOFcodop (as shown in Figure 68). Lane 7 contained a protein sample of HEK293FT cells that were transfected with vector pAAV_CBA-5'hOTOFcodop-SD-AK (as shown in Figure 64) and vector pAAV-AK-SA-3'OTOFcodop (as shown in Figure 68). Lane 8 contained a protein sample of HEK293FT cells that were transfected with vector pAKOS102 (as shown in Figure 21) and vector pAKOS103 (as shown in Figures 22, 23 and 66). Lane 9 contained a protein sample of HEK293FT cells that were transfected with a CBA.TS vector and vector pAKOS103 (as shown in Figures 22, 23 and 66). Lane 10 contained a protein sample of HEK293FT cells that were transfected with vector pAKOS106 (as shown in Figures 30, 31 and 58) and pAKOS107 (as shown in Figures 32, 33 and 67). Ninety-six hours post-transfection, cells were harvested and lysed using RIPA buffer and analyzed in 4-12% Bolt protein gel, which was then transferred onto a nitrocellulose membrane. Human otoferlin was detected using an anti-OTOF polyclonal antibody (Thermo PA5-52935). Human beta-actin was used as the primary antibody for internal loading control between lanes. The experiment was repeated in triplicate. Relative quantitative measurements for each experiment are provided under the immunoblot, along with the average measurement and standard deviation (STDEV).

Figure 70 is an immunoblot showing the expression of full-length human otoferlin in HEK293FT cells transfected with the different pairs of plasmids indicated at different multiplicity of infections (MOI). HEK293FT cells were seeded overnight at 4×10^4 cells/well on a 96-well plate. Six hours post-seeding, the dual vectors were added to each well. Ninety-six hours post-transfection, cells were harvested and lysed using RIPA buffer and analyzed in 4-12% Bolt protein gel, which was then transferred onto a nitrocellulose membrane. Human otoferlin was detected using an anti-OTOF polyclonal antibody (Thermo PA5-52935). Human beta-actin was used as the primary antibody for internal loading control between lanes. Lane 1: CBA.OTOF(AK) with MOI 503,000; lane 2: CBA.OTOF(AK) with MOI 1,510,000; lane 3: CBA.OTOF(AK) with MOI 100,000; lane 4: CBA.OTOF(AK) with MOI 303,000; lane 5: CMV.OTOF(AK) with MOI 638,000; lane 6: CMV.OTOF(AK) with MOI 1,910,000; lane 7: CMV.OTOF(AK) with MOI 127,000; lane 8: CMV.OTOF(AK) with MOI 382,000; lane 9: negative control.

Figure 71 a set of immunohistochemical images of one organ of Corti from an *Otof*^{-/-} mouse age P17 after unilateral intracochlear administration of dual-AAV vectors expressing CBA.hOTOFAK (p105 and 109 vectors). Ipsilateral cochlea was dissected and analyzed for protein expressing using immunohistochemistry at three different frequency regions (base – apex).

Figure 72 is a graph showing the percentage of N- and C- terminal otoferlin labeled inner hair cells (IHC) in dual-AAV-TS (n=10 mice) and dual-AAV-Hyb (n=9 mice) injected CD1B6F1-*Otof*^{+/+} mice (aged P18-P30). Individual animals are depicted with open symbols. Data are displayed as mean $\pm$ standard error of mean (s.e.m.), ns $P > 0.05$; * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$, Wilcoxon matched-pair signed rank test, and unpaired t-test with Welch's correction.

Figure 73 is a graph showing the average N-terminal and C-terminal otoferlin immunofluorescence levels in dual-AAV-transduced *Otof*^{+/+} and wild-type inner hair cells (IHC) from mice (aged P23-30). Otoferlin levels were normalized to immunofluorescence levels in non-transduced B6 wild-type IHCs for each antibody separately. The number of quantified IHCs is indicated inside the bars. Data are displayed as mean $\pm$ standard error of mean (s.e.m.), ns $P > 0.05$; * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$, Kruskal-Wallis test followed by Dunn's multiple comparison test.

Figure 74 is a graph showing synaptic ribbon numbers quantified from inner hair cells (IHCs) in apical cochlear turns of wild-type (B6: n= 48 IHCs, CD1B6F1: n= 108 IHCs), transduced *Otof*^{+/+} (dualAAV-TS: n= 59 IHCs, dualAAV-Hyb: n= 37 IHCs), and non-transduced *Otof*^{+/+} IHCs from injected (-AAV-injected ear, n= 65 IHCs) and contralateral non-injected (-AAV non-injected ear, n= 46 IHCs) ears (from mice aged P25-P29). Individual animals are depicted with open symbols. Data are displayed as mean $\pm$ standard error of mean (s.e.m.), ns $P > 0.05$, ** $P \leq 0.001$ (Kruskal-Wallis test followed by Dunn's multiple comparison test).

Figure 75 is a graph showing synapse numbers quantified from inner hair cells (IHCs) in apical turns (c) of B6 wild-type (P6: n= 53 IHCs; P14: n= 73 IHCs) and B6 *Otof*^{+/+} (P6: n= 62 IHCs; P14: n= 65 IHCs) mice at two different developmental stages (P6 and P14). Individual animals are depicted with open symbols. Data are displayed as

mean $\pm$ standard error of mean (s.e.m.), ns $P > 0.05$, $**P \leq 0.001$ (Kruskal-Wallis test followed by Dunn's multiple comparison test).

Figure 76 is a graph showing summed auditory brainstem response (ABR) wave I-V amplitudes at different click sound intensities in otoferlin dual-AAV-injected, non-injected *Otof*^{-/-}, and wild-type control mice aged P23-30. Number of analyzed mice: CD1B6F1 wild-type animals (+AAV.eGFP: n=12 mice, dualAAV-TS: n = 6 mice) and CD1B6F1 *Otof*^{-/-} animals (dualAAV-TS: n = 16 mice, dualAAV-Hyb: n = 8 mice, =AAV: n = 38 mice). Data are represented as mean $\pm$ standard error of mean (s.e.m.) Individual animals are depicted with open symbols.

Figure 77 is a graph showing summer auditory brainstem response (ABR) wave I-V amplitudes of individual dual-AAV-TS treated CD1B6F1 *Otof*^{-/-} animals (n= 8 animals; from Figure 76) plotted against their full-length otoferlin inner hair cell (IHC) transduction rate (from Figure 5, C-terminal otoferlin). r : correlation coefficient. = 8 mice, =AAV: n = 38 mice). Individual animals are depicted with open symbols. $r \geq 0.5$ positive correlation (70 decibel of sound pressure level (dB SPL) and 90 dB SPL: Pearson correlation test; 50 dB SPL: Spearman correlation test).

SUMMARY

The present invention is based on the discovery that a composition including at least two different nucleic acid vectors, where each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, can be used to generate a sequence encoding an active otoferlin protein (e.g., a full-length otoferlin protein) in a mammalian cell, and thereby treat non-syndromic sensorineural hearing loss in a subject in need thereof.

Provided herein are compositions that include at least two different nucleic acid vectors, wherein: each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions being at least 30 amino acid residues in length, wherein the amino acid sequence of each of the encoded portions may optionally partially overlap with the amino acid sequence of a different one of the encoded portions; no single vector of the at least two different vectors encodes a full-length otoferlin protein; at least one of the coding sequences

includes a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons; and when introduced into a mammalian cell the at least two different vectors undergo concatemerization or homologous recombination with each other, thereby forming a recombined nucleic acid that encodes a full-length otoferlin protein. In some embodiments of any of the compositions described herein, each of the at least two different vectors is a plasmid, a transposon, a cosmid, an artificial chromosome, or a viral vector. In some embodiments of any of the compositions described herein, each of the at least two different vectors is a human artificial chromosome (HAC), yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC), or a P1-derived artificial chromosome (PAC). In some embodiments of any of the compositions described herein, each of the at least two different vectors is a viral vector selected from an adeno-associated virus (AAV) vector, an adenovirus vector, a lentivirus vector, or a retrovirus vector. In some embodiments of any of the compositions described herein, each of the at least two different vectors is an AAV vector.

In some embodiments of any of the compositions described herein, the amino acid sequence of one of the encoded portions overlaps with the amino acid sequence of a different one of the encoded portions. In some embodiments of any of the compositions described herein, the amino acid sequence of each of the encoded portions partially overlaps with the amino acid sequence of a different encoded portion. In some embodiments of any of the compositions described herein, the overlapping amino acid sequence is between about 30 amino acid residues to about 1000 amino acid residues in length.

In some embodiments of any of the compositions described herein, the vectors include two different vectors, each of which includes a different segment of an intron, wherein the intron includes the nucleotide sequence of an intron that is present in otoferlin genomic DNA, and wherein the two different segments overlap in sequence by at least 100 nucleotides. In some embodiments of any of the compositions described herein, the two different segments overlap in sequence by about 100 nucleotides to about 800 nucleotides. In some embodiments of any of the compositions described herein, the nucleotide sequence of each of the at least two different vectors is between about 500

nucleotides to about 10,000 nucleotides in length. In some embodiments of any of the compositions described herein, the nucleotide sequence of each of the at least two different vectors is between 500 nucleotides to 5,000 nucleotides in length.

In some embodiments of any of the compositions described herein, the number of different vectors in the composition is two. In some embodiments of any of the compositions described herein, a first of the two different vectors includes a coding sequence that encodes an N-terminal portion of the otoferlin protein. In some embodiments of any of the compositions described herein, the N-terminal portion of the otoferlin protein is between 30 amino acids to 1600 amino acids in length. In some embodiments of any of the compositions described herein, the N-terminal portion of the otoferlin protein is between 200 amino acids to 1500 amino acids in length. In some embodiments of any of the compositions described herein, the first vector further includes one or both of a promoter and a Kozak sequence. In some embodiments of any of the compositions described herein, the first vector includes a promoter that is an inducible promoter, a constitutive promoter, or a tissue-specific promoter.

In some embodiments of any of the compositions described herein, one of the two vectors comprises SEQ ID NO: 39 (or comprises a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 39) and the second of the two vectors comprises SEQ ID NO: 40 (or comprises a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 40). In some embodiments of any of the compositions described herein, one of the two vectors comprises SEQ ID NO: 41 (or comprises a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 41) and the second of the two vectors comprises SEQ ID NO: 42 (or comprises a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 42). In some embodiments of any of the compositions described herein, one of the two vectors comprises SEQ ID NO: 84 (or comprises a sequence that is at least 80%, at least 82%, at

least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 84) and the second of the two vectors comprises SEQ ID NO: 85 (or comprises a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 85).

In some embodiments of any of the compositions described herein, wherein one of the at least two different vectors comprises a sequence encoding a NTF3 protein.

In some embodiments of any of the compositions described herein, wherein the sequence encoding a NTF3 protein is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 78.

In some embodiments of any of the compositions described herein, the first vector further includes a coding sequence encoding a destabilization domain, wherein the destabilization domain is 3' to the coding sequence that encodes the N-terminal portion of the otoferlin protein.

In some embodiments of any of the compositions described herein, the coding sequence that encodes the N-terminal portion of the otoferlin protein comprises exons 1-21 of isoform 5 of the human otoferlin gene.

In some embodiments of any of the compositions described herein, the second of the two different vectors includes a coding sequence that encodes a C-terminal portion of the otoferlin protein. In some embodiments of any of the compositions described herein, the C-terminal portion of the otoferlin protein is between 30 amino acids to 1600 amino acids in length. In some embodiments of any of the compositions described herein, the C-terminal portion of the otoferlin protein is between 200 amino acids to 1500 amino acids in length. In some embodiments of any of the compositions described herein, the second vector further includes a poly(dA) signal sequence. In some embodiments of any of the compositions described herein, the coding sequence that encodes the C-terminal portion of the otoferlin protein comprises exons 22-47 of isoform 5 of the human otoferlin gene. In some embodiments of any of the compositions described herein, the second vector further includes sequences for mRNA stabilization. Some embodiments of

any of the compositions described herein further include a pharmaceutically acceptable excipient.

Also provided herein are kits that include any of the compositions described herein. Some embodiments of any of the kits described herein further include a pre-loaded syringe containing the composition.

Also provided herein are methods that include introducing into a cochlea of a mammal a therapeutically effective amount of any of the compositions described herein. In some embodiments of any of the compositions described herein, the mammal is a human. In some embodiments of any of the compositions described herein, the mammal has been previously identified as having a defective otoferlin gene.

Also provided herein are methods of increasing expression of a full-length otoferlin protein in a mammalian cell that include introducing any of the compositions described herein into the mammalian cell. In some embodiments of any of the methods described herein, the mammalian cell is a cochlear inner hair cell. In some embodiments of any of the methods described herein, the mammalian cell is a human cell. In some embodiments of any of the methods described herein, the mammalian cell has previously been determined to have a defective otoferlin gene.

Also provided herein are methods of increasing expression of a full-length otoferlin protein in an inner hair cell in a cochlea of a mammal that include: introducing into the cochlea of the mammal a therapeutically effective amount of any of the compositions described herein. In some embodiments of any of the methods described herein, the mammal has been previously identified as having a defective otoferlin gene. In some embodiments of any of the methods described herein, the mammal is a human.

Also provided herein are methods of treating non-syndromic sensorineural hearing loss in a subject identified as having a defective otoferlin gene that include administering a therapeutically effective amount of a composition of any one of the compositions described herein into the cochlea of the subject. In some embodiments of any of the methods described herein, the subject is a human. Some embodiments of any of the methods described herein further include, prior to the administering step, determining that the subject has a defective otoferlin gene.

Also provided herein are compositions that include two different nucleic acid vectors, wherein: a first nucleic acid vector of the two different nucleic acid vectors includes a promoter, a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' of the promoter, and a splicing donor signal sequence positioned at the 3' end of the first coding sequence; and a second nucleic acid vector of the two different nucleic acid vectors includes a splicing acceptor signal sequence, a second coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence, and a polyadenylation sequence at the 3' end of the second coding sequence; wherein each of the encoded portions is at least 30 amino acid residues in length, wherein the amino acid sequences of the encoded portions do not overlap, wherein no single vector of the two different vectors encodes a full-length otoferlin protein, and, when the coding sequences are transcribed in a mammalian cell, to produce RNA transcripts, splicing occurs between the splicing donor signal sequence on one transcript and the splicing acceptor signal sequence on the other transcript, thereby forming a recombined RNA molecule that encodes a full-length otoferlin protein. In some embodiments of any of the compositions described herein, the coding sequence of at least one of the vectors includes a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons.

Also provided herein are compositions that include: a first nucleic acid vector including a promoter, a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' of the promoter, a splicing donor signal sequence positioned at the 3' end of the first coding sequence, and a first detectable marker gene positioned 3' of the splicing donor signal sequence; and a second nucleic acid vector, different from the first nucleic acid vector, including a second detectable marker gene, a splicing acceptor signal sequence positioned 3' of the second detectable marker gene, a second coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence, and a polyadenylation sequence positioned at the 3' end of the second coding sequence; wherein each of the encoded portions is at least 30 amino acid residues in length, wherein the respective amino acid sequences of the encoded portions do not overlap with each other, wherein no

single vector of the two different vectors encodes a full-length otoferlin protein, and, when the coding sequences are transcribed in a mammalian cell to produce RNA transcripts, splicing occurs between the splicing donor signal on one transcript and the splicing acceptor signal on the other transcript, thereby forming a recombined RNA molecule that encodes a full-length otoferlin protein. In some embodiments of any of the compositions described herein, the coding sequence of at least one of the vectors includes a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons. In some embodiments of any of the compositions described herein, the first or second detectable marker gene encodes alkaline phosphatase. In some embodiments of any of the compositions described herein, the first and second detectable marker genes are the same.

Also provided herein are compositions that include a first nucleic acid vector including a promoter, a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' to the promoter, a splicing donor signal sequence positioned at the 3' end of the first coding sequence, and a highly recombinogenic sequence (e.g., a F1 phage recombinogenic region, e.g., SEQ ID NO: 66) positioned 3' to the splicing donor signal sequence; and a second nucleic acid vector, different from the first nucleic acid vector, including a second highly recombinogenic sequence (e.g., a F1 phage recombinogenic region, e.g., SEQ ID NO: 67, or an alkaline phosphatase recombinogenic region, e.g., SEQ ID NO: 89), a splicing acceptor signal sequence positioned 3' of the second highly recombinogenic sequence (e.g., a F1 phage recombinogenic region or an alkaline phosphatase recombinogenic region), a second coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence, and a polyadenylation sequence positioned at the 3' end of the second coding sequence; wherein each of the encoded portions is at least 30 amino acid residues in length, wherein the respective amino acid sequences of the encoded portions do not overlap with each other, wherein no single vector of the two different vectors encodes a full-length otoferlin protein, and, when the coding sequences are transcribed in a mammalian cell to produce RNA transcripts, splicing occurs between the splicing donor signal one transcript and the splicing acceptor

signal on the other transcript, thereby forming a recombined RNA molecule that encodes a full-length otoferlin protein.

In some embodiments of any of the compositions described herein, the coding sequence of at least one of the vectors includes a nucleotide sequence spanning two
5 neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons.

Also provided herein are kits that include any of the compositions described herein. Some embodiments of any of the kits described herein further include a pre-loaded syringe containing the composition.

10 Also provided herein are methods that include introducing into a cochlea of a mammal a therapeutically effective amount of any of the compositions described herein. In some embodiments of any of the methods described herein, the mammal is a human. In some embodiments of any of the methods described herein, the mammal has been previously identified as having a defective otoferlin gene.

15 Also provided herein are methods of increasing expression of a full-length otoferlin protein in a mammalian cell that include introducing any of the compositions described herein into the mammalian cell. In some embodiments of any of the methods described herein, the mammalian cell is a cochlear inner hair cell. In some embodiments of any of the methods described herein, the mammalian cell is a human cell. In some
20 embodiments of any of the methods described herein, the mammalian cell has previously been determined to have a defective otoferlin gene.

Also provided herein are methods of increasing expression of a full-length otoferlin protein in an inner hair cell in a cochlea of a mammal that include introducing into the cochlea a therapeutically effective amount of any of the compositions described
25 herein. In some embodiments of any of the methods described herein, the mammal has been previously identified as having a defective otoferlin gene. In some embodiments of any of the methods described herein, the mammal is a human.

Also provided herein are methods of treating non-symptomatic sensorineural hearing loss in a subject identified as having a defective otoferlin gene that include
30 administering a therapeutically effective amount of any of the compositions described herein into a cochlea of the subject. In some embodiments of any of the methods

described herein, the subject is a human. Some embodiments of any of the methods described herein further include, prior to the administering step, determining that the subject has a defective otoferlin gene.

5 Provided herein are therapeutic compositions including a plurality of adeno-associated viral (AAV) vectors, wherein the plurality of AAV vectors are capable of constituting an auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

10 In some embodiments of any of the therapeutic compositions described herein, the plurality of AAV vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

Some embodiments of any of the therapeutic composition described herein further include a first AAV vector and a second AAV vector, wherein the first and second AAV vectors independently contain packaging capacity of less than about 6kb.

15 In some embodiments of any of the therapeutic compositions described herein, the auditory polypeptide messenger RNA encodes an auditory polypeptide selected from the group of otoferlin and an ortholog or homolog thereof.

20 Some embodiments of any of the therapeutic compositions described herein, can further include a nucleic acid (e.g., a vector) including a nucleic acid sequence encoding an auditory polypeptide messenger RNA encodes an auditory polypeptide selected from the group consisting of Cav1.3, a scaffold protein selected from bassoon, piccolo, ribeye, and harmonin, Vglut3, synaptotagmin, a vesicle tethering / docking protein, a vesicle priming protein, a vesicle fusion proteins, GluA2/3, and GluA4.

25 In some embodiments of any of the therapeutic compositions described herein, the first AAV vector further includes at least one promoter sequence selected from a CBA, a CMV, or a CB7 promoter.

In some embodiments of any of the therapeutic compositions described herein, the first AAV vector further includes at least one promoter sequence selected from Cochlea-specific promoters.

30 In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated for intra-cochlear administration. In some

embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a lipid nanoparticle. In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a polymeric nanoparticle. In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a mini-circle DNA. In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a CELiD DNA. In some embodiments of any of the compositions described herein, the therapeutic composition is formulated to include a synthetic perilymph solution. In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a synthetic perilymph solution including 20-200mM NaCl; 1-5 mM KCl; 0.1-10mM CaCl₂; 1-10mM glucose; and 2-50 mM HEPES; and having a pH of between about 6 and about 9.

Also provided herein are therapeutic compositions that include an auditory polypeptide messenger RNA.

Also provided herein are therapeutic compositions that include one or a plurality of adenoviral (AV) vectors, where the one or the plurality of AV vectors are capable of constituting an auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

In some embodiments of any of the therapeutic compositions described herein, the one or the plurality of AV vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

Also provided herein are therapeutic compositions including one or a plurality of lentiviral vectors, where the one or the plurality of lentiviral vectors are capable of constituting an auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

In some embodiments of any of the therapeutic compositions described herein, the one or the plurality of lentiviral vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

Also provided herein are surgical methods that include the steps of: i) introducing into a cochlea of a human subject a first incision at a first incision point; ii) administering intra-cochlearly an effective dose of a therapeutic composition (e.g., any of the therapeutic compositions described herein).

5 In some embodiments of any of the methods described herein, the therapeutic composition is administered to the subject at the first incision point. In some embodiments of any of the methods described herein, the therapeutic composition is administered to the subject into or through the first incision.

10 In some embodiments of any of the methods described herein, the therapeutic composition is administered to the subject into or through the cochlea oval window membrane. In some embodiments of any of the methods described herein, the therapeutic composition is administered to the subject into or through the cochlea round window membrane.

15 In some embodiments of any of the methods described herein, the therapeutic composition is administered using a medical device capable of creating a plurality of incisions in the round window membrane.

20 In some embodiments of any of the methods described herein, the medical device includes a plurality of micro-needles. In some embodiments of any of the methods described herein, the medical device includes a plurality of micro-needles including a generally circular first aspect, where each micro-needle has a diameter of at least about 10 microns.

25 In some embodiments of any of the methods described herein, the medical device includes a base and/or a reservoir capable of holding the therapeutic composition. In some embodiments of any of the methods described herein, the medical device includes a plurality of hollow micro-needles individually including a lumen capable of transferring the therapeutic composition.

 In some embodiments of any of the methods described herein, the medical device includes a means for generating at least a partial vacuum.

30 Also provided herein are therapeutic delivery systems, that include i) a medical device capable of creating a plurality of incisions in a round window membrane of an inner ear of a human subject in need thereof, and ii) an effective dose of a therapeutic

composition including a plurality of adeno-associated viral (AAV) vectors, wherein the plurality of AAV vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of the inner ear.

Also provided herein are means for performing a surgical method that includes the steps of: i) administering intra-cochlearly to a human subject in need thereof an effective dose of the therapeutic composition (e.g., any of the therapeutic composition described herein), where the therapeutic composition is capable of being administered by using a medical device including a) means for creating a plurality of incisions in the round window membrane and b) the effective dose of the therapeutic composition.

In some embodiments of any of the means for performing a surgical method described herein, the medical device includes a plurality of micro-needles.

Also provided herein are therapeutic compositions that include a single adeno-associated viral (AAV) vector, where the AAV vector is capable of constituting an auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

In some embodiments of any of the therapeutic compositions described herein, the single AAV vector is capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered. In some embodiments of any of the methods described herein, a single vector (e.g., any of the vectors described herein) that includes a sequence encoding an active otoferlin protein (e.g., any of the truncated active otoferlin proteins described herein) can be administered to the subject.

In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition further includes a second vector other than an AAV vector, where the single AAV vector and the second vector independently contain packaging capacity of less than about 6kb.

In some embodiments of any of the therapeutic compositions described herein, the auditory polypeptide messenger RNA encodes an auditory polypeptide selected from the group of otoferlin and an ortholog or homolog thereof.

In some embodiments of any of the therapeutic compositions described herein, the auditory polypeptide messenger RNA encodes an auditory polypeptide selected from the group of otoferlin and truncation mutant thereof.

In some embodiments of any of the therapeutic compositions described herein, the
5 otoferlin truncation mutant includes at least a single C2 domain of the following:

C2 Domain	a.a. Designation (from Pangrsic et al. 2012 <i>Trends Neurosci</i> 35(11):671-680)
C2A	1-121
C2B	256-378
C2C	419-542
C2D	962-1095
C2E	1494-1622
C2F	1734-1895

In some embodiments of any of the therapeutic compositions described herein, the
10 otoferlin truncation mutant does not include an endogenous otoferlin polypeptide C-terminal region.

In some embodiments of any of the therapeutic compositions described herein, the auditory polypeptide messenger RNA encodes an auditory polypeptide selected from the group consisting of Cav1.3, a scaffold protein selected from bassoon, piccolo, ribeye, and harmonin, Vglut3, synaptotagmin, a vesicle tethering / docking protein, a vesicle priming
15 protein, a vesicle fusion proteins, GluA2/3, and GluA4.

In some embodiments of any of the therapeutic compositions described herein, the single AAV vector further includes at least one promoter sequence selected from a CBA, a CMV, or a CB7 promoter.

In some embodiments of any of the therapeutic compositions described herein, the
20 single AAV vector further includes at least one promoter sequence selected from a Cochlea-specific promoters.

In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated for intra-cochlear administration.

In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a lipid nanoparticle.

In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a polymeric nanoparticle.

5 In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a mini-circle DNA.

In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a CELiD DNA.

10 In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a synthetic perilymph solution.

In some embodiments of any of the therapeutic compositions described herein, the therapeutic composition is formulated to include a synthetic perilymph solution including 20-200mM NaCl; 1-5 mM KCl; 0.1-10mM CaCl₂; 1-10mM glucose; 2-50 mM HEPES; having a pH of between about 6 and about 9.

15 Also provided herein are therapeutic compositions that include an auditory polypeptide messenger RNA encoding an otoferlin truncation mutant.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains.

20 The terms “a” and “an” refer to one or to more than one (i.e., at least one) of the grammatical object of the article. By way of example, “an element” encompasses one element and more than one element.

The term “about” when referring to a measurable value such as an amount, a temporal duration, and the like, is meant to encompass variations of up to $\pm 20\%$. These variations can be, for example, up to $\pm 10\%$, or in some instances $\pm 5\%$, or in some instances $\pm 1\%$, or in some instances $\pm 0.1\%$ from the specified value, as such variations are appropriate to perform the disclosed methods.

25 The term “signaling domain” refers to the functional portion of a protein which acts by transmitting information within the cell to regulate cellular activity via defined signaling pathways by generating second messengers or functioning as effectors by responding to such messengers. Otoferlin is believed to be a calcium sensor required for

exocytosis in inner hair cells, as well as neurotransmitter release in immature outer hair cells. Five of the six C2 domains of the otoferlin protein (C2B-F) bind calcium ions with moderate and low affinity constants in solution ($K_d = 25\text{-}95\ \mu\text{M}$ and $400\text{-}700\ \mu\text{M}$, respectively) (Padmanarayana et al. 2014 *Biochem* 53:5023-5033). In the presence of phosphatidylserine (PS), calcium concentrations of $10\ \mu\text{M}$ result in significant C2-liposome interaction for the C2C-C2E domains of otoferlin. Thus, otoferlin possesses domains that appear to operate using an “electrostatic switch” mechanism, as well as domains that bind regardless of calcium. PI(4,5)P₂, a major signaling molecule at the presynapse, has been shown to interact with the C2C and C2F domains of otoferlin in a calcium-independent fashion (Padmanarayana et al. 2014 *Biochem* 53:5023-5033).

The term “antibody,” as used herein, refers to a protein, or polypeptide sequence derived from an immunoglobulin molecule, which specifically binds with an antigen. Antibodies can be polyclonal or monoclonal, multiple or single chain, or intact immunoglobulins, and may be derived from natural sources or from recombinant sources. Antibodies can be tetramers of immunoglobulin molecules. The term “antibody fragment” refers to at least one portion of an intact antibody, or recombinant variants thereof, and refers to the antigen binding domain, e.g., an antigenic determining variable region of an intact antibody, that is sufficient to confer recognition and specific binding of the antibody fragment to a target, such as an antigen. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')₂, and Fv fragments, scFv antibody fragments, linear antibodies, single domain antibodies such as sdAb (either VL or VH), camelid VHH domains, and multi-specific antibodies formed from antibody fragments. The term “scFv” refers to a fusion protein including at least one antibody fragment including a variable region of a light chain and at least one antibody fragment including a variable region of a heavy chain, wherein the light and heavy chain variable regions are contiguously linked via a short flexible polypeptide linker, and capable of being expressed as a single chain polypeptide, and wherein the scFv retains the specificity of the intact antibody from which it is derived. Unless specified, as used herein an scFv may have the VL and VH variable regions in either order, e.g., with respect to the N-terminal and C-terminal ends of the polypeptide, the scFv may comprise VL-linker-VH or may comprise VH-linker-VL.

The term “recombinant polypeptide” refers to a polypeptide which is generated using recombinant DNA technology, such as, for example, a polypeptide expressed by a viral vector expression system. The term should also be construed to mean a polypeptide which has been generated by the synthesis of a DNA molecule encoding the polypeptide and which DNA molecule expresses a protein, or an amino acid sequence specifying the polypeptide, wherein the DNA or amino acid sequence has been obtained using recombinant DNA or amino acid sequence technology which is available and well known in the art.

The term “mutation in an otoferlin gene” refers to a modification in a wildtype otoferlin gene that results in the production of an otoferlin protein having one or more of: a deletion of one or more amino acids, one or more amino acid substitutions, and one or more amino acid insertions, as compared to the wildtype otoferlin protein, and/or results in a decrease in the expressed level of the encoded otoferlin protein in a mammalian cell as compared to the expressed level of the encoded otoferlin protein in a mammalian cell not having the mutation. In some embodiments, a mutation can result in the production of an otoferlin protein having a deletion of one or more amino acids (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids). In some embodiments, the mutation can result in a frameshift in the otoferlin gene. The term “frameshift” is known in the art to encompass any mutation in a coding sequence that results in a shift in the reading frame of the coding sequence. In some embodiments, a frameshift can result in a nonfunctional protein. In some embodiments, a point mutation can be a nonsense mutation (i.e., result in a premature stop codon in an exon of the gene). A nonsense mutation can result in the production of a truncated protein (as compared to a corresponding wildtype protein) that may or may not be functional. In some embodiments, the mutation can result in the loss (or a decrease in the level) of expression of otoferlin mRNA or otoferlin protein or both the mRNA and protein. In some embodiments, the mutation can result in the production of an altered otoferlin protein having a loss or decrease in one or more biological activities (functions) as compared to a wildtype otoferlin protein.

In some embodiments, the mutation is an insertion of one or more nucleotides into an otoferlin gene. In some embodiments, the mutation is in a regulatory sequence of the

otoferlin gene, i.e., a portion of the gene that is not coding sequence. In some embodiments, a mutation in a regulatory sequence may be in a promoter or enhancer region and prevent or reduce the proper transcription of the otoferlin gene.

Modifications can be introduced into a nucleotide sequence by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis.

The term “conservative sequence modifications” refers to amino acid modifications that do not significantly affect or alter the binding characteristics of the antibody or antibody fragment containing the amino acid sequence. Such conservative modifications include amino acid substitutions, additions, and deletions. Modifications can be introduced into an antibody or antibody fragment of the invention by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions are ones in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, and histidine), acidic side chains (e.g., aspartic acid and glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, and tryptophan), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, and methionine), beta-branched side chains (e.g., threonine, valine, and isoleucine), and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, and histidine).

The term “encoding” refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of a defined sequence of amino acids, in accordance with the genetic code. Thus, a gene, cDNA, or RNA encodes a protein if transcription and translation of mRNA corresponding to that gene, cDNA or RNA produces the protein. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription, can be referred to as encoding the protein product.

The term “homologous” or “identity” refers to the subunit sequence identity between two polymeric molecules, e.g., between two nucleic acid molecules, such as two DNA molecules or two RNA molecules, or between two polypeptide molecules. When a subunit position in both of the two molecules is occupied by the same monomeric subunit; e.g., if a position in each of two DNA molecules is occupied by adenine, then they are homologous or identical at that position. The homology between two sequences is a direct function of the number of matching or homologous positions; e.g., if half (e.g., five positions in a polymer ten subunits in length) of the positions in two sequences are homologous, the two sequences are 50% homologous; if 90% of the positions (e.g., 9 of 10), are matched or homologous, the two sequences are 90% homologous.

Unless otherwise specified, a “nucleotide sequence encoding an amino acid sequence” includes all nucleotide sequences that are degenerate versions of each other and thus encode the same amino acid sequence. A nucleotide sequence that encodes a protein may also include introns.

The term “endogenous” refers to any material from or produced inside an organism, cell, tissue or system.

The term “exogenous” refers to any material introduced from outside or produced outside an organism, cell, tissue or system.

The term “isolated” means altered or removed from the natural state. For example, a nucleic acid or a peptide naturally present in a living animal is not “isolated,” but the same nucleic acid or peptide partially or completely separated from the coexisting materials of its natural state is “isolated.” An isolated nucleic acid or protein can exist in substantially purified form, or can exist in a non-native environment such as, for example, a host cell.

The term “substantially purified cell” refers to a cell that is essentially free of other cell types. A substantially purified cell also refers to a cell which has been separated from other cell types with which it is normally associated in its naturally occurring state. In some instances, a population of substantially purified cells refers to a homogenous population of cells. In other instances, this term refers simply to cells that have been separated from the cells with which they are naturally associated in their

natural state. In some aspects, the cells are cultured in vitro. In other aspects, the cells are not cultured in vitro.

The term “transfected” or “transformed” or “transduced” refers to a process by which exogenous nucleic acid is transferred or introduced into the host cell. A

5 “transfected” or “transformed” or “transduced” cell is one which has been transfected, transformed or transduced with exogenous nucleic acid. The cell includes the primary subject cell and its progeny.

The term “expression” refers to the transcription and/or translation of a particular nucleotide sequence driven by a promoter.

10 As used herein, “transient” refers to expression of a non-integrated transgene for a period of hours, days or weeks, wherein the period of time of expression is less than the period of time for expression of the gene if integrated into the genome or contained within a stable plasmid replicon in the host cell.

The term “subject” is intended to include living organisms in which an immune
15 response can be elicited (e.g., mammals, human). In some embodiments, the subject is a rodent (e.g., a rat or mouse), a rabbit, a sheep, a dog, a cat, a horse, a non-human primate, or a human. In some embodiments, the subject has or is at risk of developing non-syndromic deafness. In some embodiments, the subject has been previously identified as having a mutation in an otoferlin gene. In some embodiments, the subject has been
20 identified as having a mutation in an otoferlin gene and has been diagnosed with non-symptomatic sensorineural hearing loss. In some embodiments, the subject has been identified as having non-symptomatic sensorineural hearing loss.

The term “therapeutic” as used herein means a treatment. A therapeutic effect is obtained by reduction, suppression, remission, or eradication of a disease state.

25 The term “prophylaxis” as used herein means the prevention of, or protective treatment for, a disease or disease state. “Prevention” in this context includes reducing the likelihood the subject will experience the disease.

The term “effective amount” or “therapeutically effective amount” are used interchangeably herein, and refer to an amount of a compound, formulation, material, or
30 composition as described herein effective to achieve a particular biological result.

In some embodiments, a therapeutically effective amount of a composition can result in an increase in the expression level of an active otoferlin protein (e.g., a wildtype, full-length otoferlin protein or of a variant of an otoferlin protein that has the desired activity) (e.g., as compared to the expression level prior to treatment with the composition). In some embodiments, a therapeutically effective amount of a composition can result in an increase in the expression level of an active otoferlin protein (e.g., a wildtype, full-length otoferlin protein or active variant) in a target cell (e.g., a cochlear inner hair cell). In some embodiments, a therapeutically effective amount of a composition can result in a different cellular localization of an active otoferlin protein (e.g., a wildtype, full-length otoferlin protein or an active variant) in a target cell (e.g., a cochlear inner hair cell). In some embodiments, a therapeutically effective amount of a composition can result in an increase in the expression level of an active otoferlin protein (e.g., a wildtype, full-length otoferlin protein or active variant), and/or an increase in one or more activities of an otoferlin protein in a target cell (e.g., as compared to a reference level, such as the level(s) in a subject prior to treatment, the level(s) in a subject having a mutation in an otoferlin gene, or the level(s) in a subject or a population of subjects having non-symptomatic sensorineural hearing loss).

The term “parenteral” administration of a composition includes, e.g., subcutaneous (s.c.), intravenous (i.v.), intramuscular (i.m.), or intrasternal injection, or infusion techniques.

The term “nucleic acid” or “polynucleotide” refers to deoxyribonucleic acids (DNA) or ribonucleic acids (RNA) and polymers thereof in either single- or double-stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al.,

Nucleic Acid Res. 19:5081 (1991); Ohtsuka et al., J. Biol. Chem. 260:2605-2608 (1985); and Rossolini et al., Mol. Cell. Probes 8:91-98 (1994)).

In some embodiments of any of the nucleic acids described herein, the nucleic acid is DNA. In some embodiments of any of the nucleic acids described herein, the
5 nucleic acid is RNA.

In the context of the present invention, the following abbreviations for the commonly occurring nucleic acid bases are used. "A" refers to adenosine, "C" refers to cytosine, "G" refers to guanosine, "T" refers to thymidine, and "U" refers to uridine.

As used herein, "in vitro transcribed RNA" refers to RNA, preferably mRNA, that
10 has been synthesized in vitro. Generally, the in vitro transcribed RNA is generated from an in vitro transcription vector. The in vitro transcription vector includes a template that is used to generate the in vitro transcribed RNA.

The terms "peptide," "polypeptide," and "protein" are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide
15 bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein's or peptide's sequence. Polypeptides include any peptide or protein including two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short
20 chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. "Polypeptides" include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. A polypeptide includes a natural peptide, a
25 recombinant peptide, or a combination thereof.

The term "signal transduction pathway" refers to the biochemical relationship between a variety of signal transduction molecules that play a role in the transmission of a signal from one portion of a cell to another portion of a cell. The phrase "cell surface receptor" includes molecules and complexes of molecules capable of receiving a signal
30 and transmitting signal across the membrane of a cell.

The term “active otoferlin protein” means a protein encoded by DNA that, if substituted for both wildtype alleles encoding full-length otoferlin protein in auditory hair cells (e.g., auditory inner hair cells) of what is otherwise a wildtype mammal, and if expressed in the auditory hair cells of that mammal, results in that mammal’s having a level of hearing approximating the normal level of hearing of a similar mammal that is entirely wildtype. Non-limiting examples of active otoferlin proteins are full-length otoferlin proteins (e.g., any of the full-length otoferlin proteins described herein).

For example, an active otoferlin protein can include a sequence of a wildtype, full-length otoferlin protein (e.g., a wildtype, human, full-length otoferlin protein) including 1 amino acid substitution to about 240 amino acid substitutions, 1 amino acid substitution to about 235 amino acid substitutions, 1 amino acid substitution to about 230 amino acid substitutions, 1 amino acid substitution to about 225 amino acid substitutions, 1 amino acid substitution to about 220 amino acid substitutions, 1 amino acid substitution to about 215 amino acid substitutions, 1 amino acid substitution to about 210 amino acid substitutions, 1 amino acid substitution to about 205 amino acid substitutions, 1 amino acid substitution to about 200 amino acid substitutions, 1 amino acid substitution to about 195 amino acid substitutions, 1 amino acid substitution to about 190 amino acid substitutions, 1 amino acid substitution to about 185 amino acid substitutions, 1 amino acid substitution to about 180 amino acid substitutions, 1 amino acid substitution to about 175 amino acid substitutions, 1 amino acid substitution to about 170 amino acid substitutions, 1 amino acid substitution to about 165 amino acid substitutions, 1 amino acid substitution to about 160 amino acid substitutions, 1 amino acid substitution to about 155 amino acid substitutions, 1 amino acid substitution to about 150 amino acid substitutions, 1 amino acid substitution to about 145 amino acid substitutions, 1 amino acid substitution to about 140 amino acid substitutions, 1 amino acid substitution to about 135 amino acid substitutions, 1 amino acid substitution to about 130 amino acid substitutions, 1 amino acid substitution to about 125 amino acid substitutions, 1 amino acid substitution to about 120 amino acid substitutions, 1 amino acid substitution to about 115 amino acid substitutions, 1 amino acid substitution to about 110 amino acid substitutions, 1 amino acid substitution to about 105 amino acid substitutions, 1 amino acid substitution to about 100 amino acid substitutions, 1 amino acid substitution to about

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to about 170 amino acid substitutions, about 8 amino acid substitutions to about 165 amino acid substitutions, about 8 amino acid substitutions to about 160 amino acid substitutions, about 8 amino acid substitutions to about 155 amino acid substitutions, about 8 amino acid substitutions to about 150 amino acid substitutions, about 8 amino acid substitutions to about 145 amino acid substitutions, about 8 amino acid substitutions to about 140 amino acid substitutions, about 8 amino acid substitutions to about 135 amino acid substitutions, about 8 amino acid substitutions to about 130 amino acid substitutions, about 8 amino acid substitutions to about 125 amino acid substitutions, about 8 amino acid substitutions to about 120 amino acid substitutions, about 8 amino acid substitutions to about 115 amino acid substitutions, about 8 amino acid substitutions to about 110 amino acid substitutions, about 8 amino acid substitutions to about 105 amino acid substitutions, about 8 amino acid substitutions to about 100 amino acid substitutions, about 8 amino acid substitutions to about 95 amino acid substitutions, about 8 amino acid substitutions to about 90 amino acid substitutions, about 8 amino acid substitutions to about 85 amino acid substitutions, about 8 amino acid substitutions to about 80 amino acid substitutions, about 8 amino acid substitutions to about 75 amino acid substitutions, about 8 amino acid substitutions to about 70 amino acid substitutions, about 8 amino acid substitutions to about 65 amino acid substitutions, about 8 amino acid substitutions to about 60 amino acid substitutions, about 8 amino acid substitutions to about 55 amino acid substitutions, about 8 amino acid substitutions to about 50 amino acid substitutions, about 8 amino acid substitutions to about 45 amino acid substitutions, about 8 amino acid substitutions to about 40 amino acid substitutions, about 8 amino acid substitutions to about 35 amino acid substitutions, about 8 amino acid substitutions to about 30 amino acid substitutions, about 8 amino acid substitutions to about 25 amino acid substitutions, about 8 amino acid substitutions to about 20 amino acid substitutions, about 8 amino acid substitutions to about 15 amino acid substitutions, about 8 amino acid substitutions to about 10 amino acid substitutions, between about 10 amino acid substitutions to about 240 amino acid substitutions, about 10 amino acid substitutions to about 235 amino acid substitutions, about 10 amino acid substitutions to about 230 amino acid substitutions, about 10 amino acid substitutions to about 225 amino acid substitutions, about 10 amino acid substitutions substitution to about 220 amino acid

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An active otoferlin protein can include, e.g., a sequence of a wildtype, full-length otoferlin protein (e.g., a wildtype, human, full-length otoferlin protein) that has 1 amino acid to about 200 amino acids, 1 amino acid to about 195 amino acids, 1 amino acid to about 190 amino acids, 1 amino acid to about 185 amino acids, 1 amino acid to about 180 amino acids, 1 amino acid to about 175 amino acids, 1 amino acid to about 170 amino acids, 1 amino acid to about 165 amino acids, 1 amino acid to about 160 amino acids, 1 amino acid to about 155 amino acids, 1 amino acid to about 150 amino acids, 1 amino acid to about 145 amino acids, 1 amino acid to about 140 amino acids, 1 amino acid to about 135 amino acids, 1 amino acid to about 130 amino acids, 1 amino acid to about 125 amino acids, 1 amino acid to about 120 amino acids, 1 amino acid to about 115 amino acids, 1 amino acid to about 110 amino acids, 1 amino acid to about 105 amino acids, 1 amino acid to about 100 amino acids, 1 amino acid to about 95 amino acids, 1 amino acid to about 90 amino acids, 1 amino acid to about 85 amino acids, 1 amino acid to about 80 amino acids, 1 amino acid to about 75 amino acids, 1 amino acid to about 70 amino acids, 1 amino acid to about 65 amino acids, 1 amino acid to about 60 amino acids, 1 amino acid to about 55 amino acids, 1 amino acid to about 50 amino acids, 1 amino acid to about 45 amino acids, 1 amino acid to about 40 amino acids, 1 amino acid to about 35 amino acids, 1 amino acid to about 30 amino acids, 1 amino acid to about 25 amino acids, 1 amino acid to about 20 amino acids, 1 amino acid to about 15 amino acids, 1 amino acid to about 10 amino acids, 1 amino acid to about 9 amino acids, 1 amino acid to about 8 amino acids, 1 amino acid to about 7 amino acids, 1 amino acid to about 6

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about 165 amino acids, about 140 amino acids to about 160 amino acids, about 140 amino acids to about 155 amino acids, about 140 amino acids to about 150 amino acids, about 40 amino acids to about 145 amino acids, about 145 amino acids to about 200 amino acids, about 145 amino acids to about 195 amino acids, about 145 amino acids to about 190 amino acids, about 145 amino acids to about 185 amino acids, about 145 amino acids to about 180 amino acids, about 145 amino acids to about 175 amino acids, about 145 amino acids to about 170 amino acids, about 145 amino acids to about 165 amino acids, about 145 amino acids to about 160 amino acids, about 145 amino acids to about 155 amino acids, about 145 amino acids to about 150 amino acids, about 150 amino acids to about 200 amino acids, about 150 amino acids to about 195 amino acids, about 150 amino acids to about 190 amino acids, about 150 amino acids to about 185 amino acids, about 150 amino acids to about 180 amino acids, about 150 amino acids to about 175 amino acids, about 150 amino acids to about 170 amino acids, about 150 amino acids to about 165 amino acids, about 150 amino acids to about 160 amino acids, about 150 amino acids to about 155 amino acids, about 155 amino acids to about 200 amino acids, about 155 amino acids to about 195 amino acids, about 155 amino acids to about 190 amino acids, about 155 amino acids to about 185 amino acids, about 155 amino acids to about 180 amino acids, about 155 amino acids to about 175 amino acids, about 155 amino acids to about 170 amino acids, about 155 amino acids to about 165 amino acids, about 155 amino acids to about 160 amino acids, about 160 amino acids to about 200 amino acids, about 160 amino acids to about 195 amino acids, about 160 amino acids to about 190 amino acids, about 160 amino acids to about 185 amino acids, about 160 amino acids to about 180 amino acids, about 160 amino acids to about 175 amino acids, about 160 amino acids to about 170 amino acids, about 160 amino acids to about 165 amino acids, about 165 amino acids to about 200 amino acids, about 165 amino acids to about 195 amino acids, about 165 amino acids to about 190 amino acids, about 165 amino acids to about 185 amino acids, about 165 amino acids to about 180 amino acids, about 165 amino acids to about 175 amino acids, about 165 amino acids to about 170 amino acids, about 170 amino acids to about 200 amino acids, about 170 amino acids to about 195 amino acids, about 170 amino acids to about 190 amino acids, about 170 amino acids to about 185 amino acids, about 170 amino acids to about 180

amino acids, about 170 amino acids to about 175 amino acids, about 175 amino acids to about 200 amino acids, about 175 amino acids to about 195 amino acids, about 175 amino acids to about 190 amino acids, about 175 amino acids to about 185 amino acids, about 175 amino acids to about 180 amino acids, about 180 amino acids to about 200 amino acids, about 180 amino acids to about 195 amino acids, about 180 amino acids to about 190 amino acids, about 180 amino acids to about 185 amino acids, about 185 amino acids to about 200 amino acids, about 185 amino acids to about 195 amino acids, about 185 amino acids to about 190 amino acids, about 190 amino acids to about 200 amino acids, about 190 amino acids to about 195 amino acids, about 195 amino acids to about 200 amino acids, deleted. In some embodiments where two or more amino acids are deleted from the sequence of a wildtype, full-length otoferlin protein, the two or more deleted amino acids can be contiguous in the sequence of the wildtype, full-length protein. In other examples where two or more amino acids are deleted from the sequence of a wildtype, full-length otoferlin protein, the two or more deleted amino acids are not contiguous in the sequence of the wildtype, full-length protein. One skilled in the art would appreciate that amino acids that are not conserved between wildtype, full-length otoferlin proteins from different species can be deleted without losing activity, while those amino acids that are conserved between wildtype, full-length otoferlin proteins from different species should not be deleted as they are more likely (than amino acids that are not conserved between different species) to be involved in activity.

In some examples, an active otoferlin protein can, e.g., include a sequence of a wildtype, full-length otoferlin protein that has between 1 amino acid to about 100 amino acids, 1 amino acid to about 95 amino acids, 1 amino acid to about 90 amino acids, 1 amino acid to about 85 amino acids, 1 amino acid to about 80 amino acids, 1 amino acid to about 75 amino acids, 1 amino acid to about 70 amino acids, 1 amino acid to about 65 amino acids, 1 amino acid to about 60 amino acids, 1 amino acid to about 55 amino acids, 1 amino acid to about 50 amino acids, 1 amino acid to about 45 amino acids, 1 amino acid to about 40 amino acids, 1 amino acid to about 35 amino acids, 1 amino acid to about 30 amino acids, 1 amino acid to about 25 amino acids, 1 amino acid to about 20 amino acids, 1 amino acid to about 15 amino acids, 1 amino acid to about 10 amino acids, 1 amino acid to about 9 amino acids, 1 amino acid to about 8 amino acids, 1 amino acid

to about 7 amino acids, 1 amino acid to about 6 amino acids, 1 amino acid to about 5 amino acids, 1 amino acid to about 4 amino acids, 1 amino acid to about 3 amino acids, about 2 amino acids to about 100 amino acids, about 2 amino acid to about 95 amino acids, about 2 amino acids to about 90 amino acids, about 2 amino acids to about 85 amino acids, about 2 amino acids to about 80 amino acids, about 2 amino acids to about 75 amino acids, about 2 amino acids to about 70 amino acids, about 2 amino acids to about 65 amino acids, about 2 amino acids to about 60 amino acids, about 2 amino acids to about 55 amino acids, about 2 amino acids to about 50 amino acids, about 2 amino acids to about 45 amino acids, about 2 amino acids to about 40 amino acids, about 2 amino acids to about 35 amino acids, about 2 amino acids to about 30 amino acids, about 2 amino acids to about 25 amino acids, about 2 amino acids to about 20 amino acids, about 2 amino acids to about 15 amino acids, about 2 amino acids to about 10 amino acids, about 2 amino acids to about 9 amino acids, about 2 amino acids to about 8 amino acids, about 2 amino acids to about 7 amino acids, about 2 amino acids to about 6 amino acids, about 2 amino acids to about 5 amino acids, about 2 amino acids to about 4 amino acids, about 3 amino acids to about 100 amino acids, about 3 amino acid to about 95 amino acids, about 3 amino acids to about 90 amino acids, about 3 amino acids to about 85 amino acids, about 3 amino acids to about 80 amino acids, about 3 amino acids to about 75 amino acids, about 3 amino acids to about 70 amino acids, about 3 amino acids to about 65 amino acids, about 3 amino acids to about 60 amino acids, about 3 amino acids to about 55 amino acids, about 3 amino acids to about 50 amino acids, about 3 amino acids to about 45 amino acids, about 3 amino acids to about 40 amino acids, about 3 amino acids to about 35 amino acids, about 3 amino acids to about 30 amino acids, about 3 amino acids to about 25 amino acids, about 3 amino acids to about 20 amino acids, about 3 amino acids to about 15 amino acids, about 3 amino acids to about 10 amino acids, about 3 amino acids to about 9 amino acids, about 3 amino acids to about 8 amino acids, about 3 amino acids to about 7 amino acids, about 3 amino acids to about 6 amino acids, about 3 amino acids to about 5 amino acids, about 4 amino acids to about 100 amino acids, about 4 amino acid to about 95 amino acids, about 4 amino acids to about 90 amino acids, about 4 amino acids to about 85 amino acids, about 4 amino acids to about 80 amino acids, about 4 amino acids to about 75 amino acids, about 4 amino

acids to about 70 amino acids, about 4 amino acids to about 65 amino acids, about 4 amino acids to about 60 amino acids, about 4 amino acids to about 55 amino acids, about 4 amino acids to about 50 amino acids, about 4 amino acids to about 45 amino acids, about 4 amino acids to about 40 amino acids, about 4 amino acids to about 35 amino acids, about 4 amino acids to about 30 amino acids, about 4 amino acids to about 25 amino acids, about 4 amino acids to about 20 amino acids, about 4 amino acids to about 15 amino acids, about 4 amino acids to about 10 amino acids, about 4 amino acids to about 9 amino acids, about 4 amino acids to about 8 amino acids, about 4 amino acids to about 7 amino acids, about 4 amino acids to about 6 amino acids, about 5 amino acids to about 100 amino acids, about 5 amino acid to about 95 amino acids, about 5 amino acids to about 90 amino acids, about 5 amino acids to about 85 amino acids, about 5 amino acids to about 80 amino acids, about 5 amino acids to about 75 amino acids, about 5 amino acids to about 70 amino acids, about 5 amino acids to about 65 amino acids, about 5 amino acids to about 60 amino acids, about 5 amino acids to about 55 amino acids, about 5 amino acids to about 50 amino acids, about 5 amino acids to about 45 amino acids, about 5 amino acids to about 40 amino acids, about 5 amino acids to about 35 amino acids, about 5 amino acids to about 30 amino acids, about 5 amino acids to about 25 amino acids, about 5 amino acids to about 20 amino acids, about 5 amino acids to about 15 amino acids, about 5 amino acids to about 10 amino acids, about 5 amino acids to about 9 amino acids, about 5 amino acids to about 8 amino acids, about 5 amino acids to about 7 amino acids, about 6 amino acids to about 100 amino acids, about 6 amino acid to about 95 amino acids, about 6 amino acids to about 90 amino acids, about 6 amino acids to about 85 amino acids, about 6 amino acids to about 80 amino acids, about 6 amino acids to about 75 amino acids, about 6 amino acids to about 70 amino acids, about 6 amino acids to about 65 amino acids, about 6 amino acids to about 60 amino acids, about 6 amino acids to about 55 amino acids, about 6 amino acids to about 50 amino acids, about 6 amino acids to about 45 amino acids, about 6 amino acids to about 40 amino acids, about 6 amino acids to about 35 amino acids, about 6 amino acids to about 30 amino acids, about 6 amino acids to about 25 amino acids, about 6 amino acids to about 20 amino acids, about 6 amino acids to about 15 amino acids, about 6 amino acids to about 10 amino acids, about 6 amino acids to about 9 amino acids, about 6 amino

acids to about 8 amino acids, about 7 amino acids to about 100 amino acids, about 7 amino acid to about 95 amino acids, about 7 amino acids to about 90 amino acids, about 7 amino acids to about 85 amino acids, about 7 amino acids to about 80 amino acids, about 7 amino acids to about 75 amino acids, about 7 amino acids to about 70 amino acids, about 7 amino acids to about 65 amino acids, about 7 amino acids to about 60 amino acids, about 7 amino acids to about 55 amino acids, about 7 amino acids to about 50 amino acids, about 7 amino acids to about 45 amino acids, about 7 amino acids to about 40 amino acids, about 7 amino acids to about 35 amino acids, about 7 amino acids to about 30 amino acids, about 7 amino acids to about 25 amino acids, about 7 amino acids to about 20 amino acids, about 7 amino acids to about 15 amino acids, about 7 amino acids to about 10 amino acids, about 7 amino acids to about 9 amino acids, about 8 amino acids to about 100 amino acids, about 8 amino acid to about 95 amino acids, about 8 amino acids to about 90 amino acids, about 8 amino acids to about 85 amino acids, about 8 amino acids to about 80 amino acids, about 8 amino acids to about 75 amino acids, about 8 amino acids to about 70 amino acids, about 8 amino acids to about 65 amino acids, about 8 amino acids to about 60 amino acids, about 8 amino acids to about 55 amino acids, about 8 amino acids to about 50 amino acids, about 8 amino acids to about 45 amino acids, about 8 amino acids to about 40 amino acids, about 8 amino acids to about 35 amino acids, about 8 amino acids to about 30 amino acids, about 8 amino acids to about 25 amino acids, about 8 amino acids to about 20 amino acids, about 8 amino acids to about 15 amino acids, about 8 amino acids to about 10 amino acids, about 10 amino acids to about 100 amino acids, about 10 amino acid to about 95 amino acids, about 10 amino acids to about 90 amino acids, about 10 amino acids to about 85 amino acids, about 10 amino acids to about 80 amino acids, about 10 amino acids to about 75 amino acids, about 10 amino acids to about 70 amino acids, about 10 amino acids to about 65 amino acids, about 10 amino acids to about 60 amino acids, about 10 amino acids to about 55 amino acids, about 10 amino acids to about 50 amino acids, about 10 amino acids to about 45 amino acids, about 10 amino acids to about 40 amino acids, about 10 amino acids to about 35 amino acids, about 10 amino acids to about 30 amino acids, about 10 amino acids to about 25 amino acids, about 10 amino acids to about 20 amino acids, about 10 amino acids to about 15 amino acids, about 20 amino acids to

about 100 amino acids, about 20 amino acid to about 95 amino acids, about 20 amino acids to about 90 amino acids, about 20 amino acids to about 85 amino acids, about 20 amino acids to about 80 amino acids, about 20 amino acids to about 75 amino acids, about 20 amino acids to about 70 amino acids, about 20 amino acids to about 65 amino acids, about 20 amino acids to about 60 amino acids, about 20 amino acids to about 55 amino acids, about 20 amino acids to about 50 amino acids, about 20 amino acids to about 45 amino acids, about 20 amino acids to about 40 amino acids, about 20 amino acids to about 35 amino acids, about 20 amino acids to about 30 amino acids, about 20 amino acids to about 25 amino acids, about 30 amino acids to about 100 amino acids, about 30 amino acid to about 95 amino acids, about 30 amino acids to about 90 amino acids, about 30 amino acids to about 85 amino acids, about 30 amino acids to about 80 amino acids, about 30 amino acids to about 75 amino acids, about 30 amino acids to about 70 amino acids, about 30 amino acids to about 65 amino acids, about 30 amino acids to about 60 amino acids, about 30 amino acids to about 55 amino acids, about 30 amino acids to about 50 amino acids, about 30 amino acids to about 45 amino acids, about 30 amino acids to about 40 amino acids, about 30 amino acids to about 35 amino acids, about 40 amino acids to about 100 amino acids, about 40 amino acid to about 95 amino acids, about 40 amino acids to about 90 amino acids, about 40 amino acids to about 85 amino acids, about 40 amino acids to about 80 amino acids, about 40 amino acids to about 75 amino acids, about 40 amino acids to about 70 amino acids, about 40 amino acids to about 65 amino acids, about 40 amino acids to about 60 amino acids, about 40 amino acids to about 55 amino acids, about 40 amino acids to about 50 amino acids, about 40 amino acids to about 45 amino acids, about 50 amino acids to about 100 amino acids, about 50 amino acid to about 95 amino acids, about 50 amino acids to about 90 amino acids, about 50 amino acids to about 85 amino acids, about 50 amino acids to about 80 amino acids, about 50 amino acids to about 75 amino acids, about 50 amino acids to about 70 amino acids, about 50 amino acids to about 65 amino acids, about 50 amino acids to about 60 amino acids, about 50 amino acids to about 55 amino acids, about 60 amino acids to about 100 amino acids, about 60 amino acid to about 95 amino acids, about 60 amino acids to about 90 amino acids, about 60 amino acids to about 85 amino acids, about 60 amino acids to about 80 amino acids, about 60 amino acids to

about 75 amino acids, about 60 amino acids to about 70 amino acids, about 60 amino acids to about 65 amino acids, about 70 amino acids to about 100 amino acids, about 70 amino acid to about 95 amino acids, about 70 amino acids to about 90 amino acids, about 70 amino acids to about 85 amino acids, about 70 amino acids to about 80 amino acids, about 70 amino acids to about 75 amino acids, about 80 amino acids to about 100 amino acids, about 80 amino acid to about 95 amino acids, about 80 amino acids to about 90 amino acids, about 80 amino acids to about 85 amino acids, about 90 amino acids to about 100 amino acids, about 90 amino acids to about 95 amino acids, or about 95 amino acids to about 100 amino acids, removed from its N-terminus and/or from its C-terminus.

In some embodiments, an active otoferlin protein can, e.g., include the sequence of a wildtype, full-length otoferlin protein where 1 amino acid to 50 amino acids, 1 amino acid to 45 amino acids, 1 amino acid to 40 amino acids, 1 amino acid to 35 amino acids, 1 amino acid to 30 amino acids, 1 amino acid to 25 amino acids, 1 amino acid to 20 amino acids, 1 amino acid to 15 amino acids, 1 amino acid to 10 amino acids, 1 amino acid to 9 amino acids, 1 amino acid to 8 amino acids, 1 amino acid to 7 amino acids, 1 amino acid to 6 amino acids, 1 amino acid to 5 amino acids, 1 amino acid to 4 amino acids, 1 amino acid to 3 amino acids, about 2 amino acids to 50 amino acids, about 2 amino acids to 45 amino acids, about 2 amino acids to 40 amino acids, about 2 amino acids to 35 amino acids, about 2 amino acids to 30 amino acids, about 2 amino acids to 25 amino acids, about 2 amino acids to 20 amino acids, about 2 amino acids to 15 amino acids, about 2 amino acids to 10 amino acids, about 2 amino acids to 9 amino acids, about 2 amino acids to 8 amino acids, about 2 amino acids to 7 amino acids, about 2 amino acids to 6 amino acids, about 2 amino acids to 5 amino acids, about 2 amino acids to 4 amino acids, about 3 amino acids to 50 amino acids, about 3 amino acids to 45 amino acids, about 3 amino acids to 40 amino acids, about 3 amino acids to 35 amino acids, about 3 amino acids to 30 amino acids, about 3 amino acids to 25 amino acids, about 3 amino acids to 20 amino acids, about 3 amino acids to 15 amino acids, about 3 amino acids to 10 amino acids, about 3 amino acids to 9 amino acids, about 3 amino acids to 8 amino acids, about 3 amino acids to 7 amino acids, about 3 amino acids to 6 amino acids, about 3 amino acids to 5 amino acids, about 4 amino acids to 50 amino acids, about 4 amino acids to 45 amino acids, about 4 amino acids to 40 amino acids, about 4 amino acids to 35 amino

acids, about 4 amino acids to 30 amino acids, about 4 amino acids to 25 amino acids, about 4 amino acids to 20 amino acids, about 4 amino acids to 15 amino acids, about 4 amino acids to 10 amino acids, about 4 amino acids to 9 amino acids, about 4 amino acids to 8 amino acids, about 4 amino acids to 7 amino acids, about 4 amino acids to 6 amino acids, about 5 amino acids to 50 amino acids, about 5 amino acids to 45 amino acids, about 5 amino acids to 40 amino acids, about 5 amino acids to 35 amino acids, about 5 amino acids to 30 amino acids, about 5 amino acids to 25 amino acids, about 5 amino acids to 20 amino acids, about 5 amino acids to 15 amino acids, about 5 amino acids to 10 amino acids, about 5 amino acids to 9 amino acids, about 5 amino acids to 8 amino acids, about 5 amino acids to 7 amino acids, about 6 amino acids to 50 amino acids, about 6 amino acids to 45 amino acids, about 6 amino acids to 40 amino acids, about 6 amino acids to 35 amino acids, about 6 amino acids to 30 amino acids, about 6 amino acids to 25 amino acids, about 6 amino acids to 20 amino acids, about 6 amino acids to 15 amino acids, about 6 amino acids to 10 amino acids, about 6 amino acids to 9 amino acids, about 6 amino acids to 8 amino acids, about 7 amino acids to 50 amino acids, about 7 amino acids to 45 amino acids, about 7 amino acids to 40 amino acids, about 7 amino acids to 35 amino acids, about 7 amino acids to 30 amino acids, about 7 amino acids to 25 amino acids, about 7 amino acids to 20 amino acids, about 7 amino acids to 15 amino acids, about 7 amino acids to 10 amino acids, about 7 amino acids to 9 amino acids, about 8 amino acids to 50 amino acids, about 8 amino acids to 45 amino acids, about 8 amino acids to 40 amino acids, about 8 amino acids to 35 amino acids, about 8 amino acids to 30 amino acids, about 8 amino acids to 25 amino acids, about 8 amino acids to 20 amino acids, about 8 amino acids to 15 amino acids, about 8 amino acids to 10 amino acids, about 10 amino acids to 50 amino acids, about 10 amino acids to 45 amino acids, about 10 amino acids to 40 amino acids, about 10 amino acids to 35 amino acids, about 10 amino acids to 30 amino acids, about 10 amino acids to 25 amino acids, about 10 amino acids to 20 amino acids, about 10 amino acids to 15 amino acids, about 15 amino acids to 50 amino acids, about 15 amino acids to 45 amino acids, about 15 amino acids to 40 amino acids, about 15 amino acids to 35 amino acids, about 15 amino acids to 30 amino acids, about 15 amino acids to 25 amino acids, about 15 amino acids to 20 amino acids, about 20 amino acids to 50 amino acids, about 20 amino acids to

45 amino acids, about 20 amino acids to 40 amino acids, about 20 amino acids to 35 amino acids, about 20 amino acids to 30 amino acids, about 20 amino acids to 25 amino acids, about 25 amino acids to 50 amino acids, about 25 amino acids to 45 amino acids, about 25 amino acids to 40 amino acids, about 25 amino acids to 35 amino acids, about 25 amino acids to 30 amino acids, about 30 amino acids to 50 amino acids, about 30 amino acids to 45 amino acids, about 30 amino acids to 40 amino acids, about 30 amino acids to 35 amino acids, about 35 amino acids to 50 amino acids, about 35 amino acids to 45 amino acids, about 35 amino acids to 40 amino acids, about 40 amino acids to 50 amino acids, about 40 amino acids to 45 amino acids, or about 45 amino acids to about 50 amino acids, are inserted. In some examples, the inserted amino acid(s) can be inserted as a contiguous sequence into the sequence of a wildtype, full-length protein. In some examples, the amino acid(s) are not inserted as a contiguous sequence into the sequence of a wildtype, full-length protein. As can be appreciated in the art, the amino acid(s) can be inserted into a portion of the sequence of a wildtype, full-length protein that is not well-conserved between species.

Ranges: throughout this disclosure, various aspects of the invention can be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6. As another example, a range such as 95-99% identity includes something with 95%, 96%, 97%, 98% or 99% identity, and includes subranges such as 96-99%, 96-98%, 96-97%, 97-99%, 97-98% and 98-99% identity. This applies regardless of the breadth of the range.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present

invention; other suitable methods and materials known in the art can also be used. The materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety. In case of
5 conflict, the present specification, including definitions, will control.

DETAILED DESCRIPTION

Mutations in *OTOF* lead to DFNB9, a recessively inherited, non-syndromic prelingual hearing disorder. Deficiency in otoferlin, the protein encoded by *OTOF*,
10 abolishes fast exocytosis from auditory inner hair cells (IHCs). Due the impairment of neurotransmission at the first auditory synapse, no sound signals are transmitted to the brain, explaining the profound deafness.

The presently claimed methods were discovered to result in expression of full-length otoferlin in inner auditory hair cells and to successfully restore hearing with ABR
15 thresholds of 30 dB to 70 dB for click stimuli and 50 dB to 90 dB for pure tones in otoferlin knock-out mice. In view of this discovery, provided herein are compositions and methods for treating non-symptomatic sensorineural hearing loss in a subject (e.g., a human) identified as having a defective otoferlin gene.

Provided herein are compositions that include at least two different nucleic acid
20 vectors, where: each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions being at least 30 amino acid residues in length, where the amino acid sequence of each of the encoded portions may optionally partially overlap with the amino acid sequence of a different one of the encoded portions; no single vector of the at least two different vectors
25 encodes an active otoferlin protein (e.g., a full-length otoferlin protein); at least one of the coding sequences comprises a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons; and, when introduced into a mammalian cell, the at least two different vectors undergo homologous recombination with each other, thereby forming a recombined
30 nucleic acid, where the recombined nucleic acid encodes an active otoferlin protein (e.g., a full-length otoferlin protein). In some examples, the recombined nucleic acid that

encodes an active otoferlin protein (e.g., a full-length otoferlin protein) exists as an episome in a mammalian cell (e.g., any of the types of mammalian cells described herein). Also provided are kits that include any of the compositions described herein. Also provided herein are methods that include introducing into a cochlea of a mammal a therapeutically effective amount of any of the compositions described herein.

Also provided herein are methods of increasing expression of an active otoferlin protein (e.g., a full-length otoferlin protein) in a mammalian cell that include introducing any of the compositions described herein into the mammalian cell. Also provided herein are methods of increasing expression of an active otoferlin protein (e.g., a full-length otoferlin protein) in an inner hair cell in a cochlea of a mammal that include introducing into the cochlea of the mammal a therapeutically effective amount of any of the compositions described herein. Also provided herein are methods of treating non-symptomatic sensorineural hearing loss in a subject identified as having a defective otoferlin gene that include: administering a therapeutically effective amount of any of the compositions described herein into the cochlea of the subject.

Additional non-limiting aspects of the compositions, kits, and methods are described herein and can be used in any combination without limitation.

Otoferlin

To date, several hundred mutations in the human *OTOF* gene have been identified to cause profound prelingual deafness DFNB9. Such mutations are the cause of deafness in 2-8% of people that are born with an autosomal, recessively inherited, non-syndromic deafness in different populations (Rodríguez-Ballesteros et al. (2008) Hum. Mutat. 29 823–831; Choi et al. (2009) Clinical Genetics 75 237–243; Duman et al. (2011) Genet Test Mol Biomarkers 15 29–33; Varga et al. (2006) J Med Genet 43 576–581; Iwasa et al. (2013) BMC Med. Genet. 14 95). For example, two substitutions in exon 15 at positions 490 and 515 in the conserved C2C domain of otoferlin cause DFNB9 (Mirqhomizadeh et al. (2002) Neurobiol. Dis. 10(2): 157-164). Migliosi et al. found a novel mutation Q829X in OTOF in Spanish patients with prelingual non-syndromic hearing loss (Migliosi et al. (2002) J. Med. Genet. 39(7): 502-506).

Additional exemplary mutations in a otoferlin gene detected in subjects having hearing loss and methods of sequencing a nucleic acid encoding otoferlin are described in, e.g., Rodriguez-Ballesteros et al. (2003) *Hum Mutat.* 22: 451-456; Wang et al. (2010) *BMC Med Genet.* 11:79; Yildirim-Baylan et al. (2014) *Int. J. Pediatr. Otorhinolaryngol* 78: 950-953; Choi et al. (2009) *Clin. Genet.* 75(3): 237-243; and Marlin et al. (2010) *Biochem Biophys Res Commun* 394: 737-742.

Otoacoustic emissions from DFNB9 patients are normal, at least for the first decade of life, indicating morphological integrity of the inner ear and proper function of outer hair cells. Apart from the lack of synaptic transmission and the subsequent loss of synapses, the morphology and physiology of the inner ear remains preserved in DFNB9, at least during the first decade in life in humans.

Studies in mouse models revealed that synapses are structurally normal, and IHCs preserve normal synapse numbers in mice within the first postnatal week. Between P6 and P15, about half of the synapses get lost (Roux et al. (2006) *Cell* 127 277-289).

Animal models allowed studying the effect of mutations in otoferlin on synaptic transmission by recording the change in plasma membrane capacitance after vesicle fusion and the activity in the auditory nerve. In otoferlin knock-out (*Otof*^{-/-}) mice, almost no exocytosis could be triggered in IHCs by depolarization induced Ca²⁺ influx through voltage gated Ca²⁺ channels (Roux et al. (2006) *Cell* 127 277-289). In profoundly hearing impaired pachanga (*Otof*^{Pga}/*Pga*) mice with a random point mutation in the C2F domain, short (<10ms) depolarizations of the IHCs elicited vesicle fusion of similar size as in wild type mice, however sustained stimulations uncovered a strong deficiency in replenishing vesicles to the readily releasable pool (Pangrsic et al. (2010) *Nat. Neurosci.* 13 869-876). The p.Ile515Thr mutation, found in human patients with only mildly elevated hearing thresholds but a severe reduction in speech understanding and a temperature-dependent deafening (Varga et al. (2006) *J Med Genet* 43 576-581), uncovered an intermediate phenotype when studied in a mouse model (Strenzke et al. (2016) *EMBO J.* 35:2519-2535). These *Otof*^{I515T}/*I515T* mice showed a moderate elevation of hearing thresholds when assessed by ABR with a reduction in wave I amplitude, but normal auditory thresholds in behavioral tests and recordings of single auditory nerve units. Exocytosis of the RRP is again intact, but sustained exocytosis is

reduced, although not as severe as in OtofPga/Pga. While in wild type mice at room temperature, during a sustained stimulus 750 vesicles can fuse per second at each active zone, this rate drops to 350 vesicles/s/active zone in OtofI515T/I515T mice and to 200 vesicles/s/active zone in OtofPga/Pga IHCs (Pangrsic et al. (2010) Nat. Neurosci. 13 869–876; Strenzke et al. (2016) EMBO J. 35 2519–2535). This correlated with lower otoferlin protein levels at the plasma membrane of IHCs, indicating that the amount of otoferlin scales with exocytosis and hearing (Strenzke et al. (2016) EMBO J. 35 2519–2535).

Methods of detecting mutations in a gene are well-known in the art. Non-limiting examples of such techniques include: real-time polymerase chain reaction (RT-PCR), PCR, sequencing, Southern blotting, and Northern blotting.

The OTOF gene encodes otoferlin, a protein that is involved in synaptic vesicle exocytosis in cochlear hair cells (see, e.g., Johnson and Chapman (2010) J. Cell Biol. 191(1):187-198; and Heidrych et al. (2008) Hum. Mol. Genet. 17:3814-3821).

The human OTOF gene is located on chromosome 2p23.3. It contains 48 exons encompassing ~ 132 kilobases (kb) (NCBI Accession No. NG009937.1). The mRNA encoding the long-form of otoferlin expressed in the brain includes 48 exons (Yasunaga et al., *Am. J. Hum. Genet.* 67:591-600, 2000). Forward and reverse primers that can be used to amplify each of the 48 exons in the OTOF gene are described in Table 2 of Yasunaga et al., *Am. J. Hum. Genet.* 67:591-600, 2000. In some examples, the full-length OTOF protein is a full-length wildtype OTOF protein. The full-length wildtype OTOF protein expressed from the human OTOF gene is 1997 residues in length.

An exemplary human wildtype otoferlin protein is or includes the sequence of any one of SEQ ID NOs: 1-5. Isoform e of human otoferlin protein (SEQ ID NO: 5) is encoded by an mRNA that includes exon 48 and does not include exon 47 of the otoferlin gene (Yasunaga et al., *Am. J. Hum. Genet.* 67:591-600, 2000). In some embodiments, the active otoferlin protein has the sequence of SEQ ID NO: 5, but is missing the 20 amino acids including the RXR motif identified in Strenzke et al., *EMBO J.* 35(23):2499-2615, 2016). Non-limiting examples of nucleic acids encoding a wildtype otoferlin protein are or include any one of SEQ ID NO: 7-11. As can be appreciated in the art, at least some or all of the codons in SEQ ID NO: 7-11 can be codon-optimized to allow for optimal

expression in a non-human mammal or in a human. Orthologs of human otoferlin proteins are known in the art.

Human Otoferlin Protein cDNA Sequences:

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Human canonical (long) isoform sequence (otoferlin protein) (SEQ ID NO: 1) (also called otoferlin isoform a) (NCBI Accession No. AAD26117.1)

10

Human Isoform 2 (short 1) (otoferlin protein) (SEQ ID NO: 2) (also called otoferlin isoform d) (NCBI Accession No. NP_919304.1)

Human Isoform 3 (short 2) (otoferlin protein) (SEQ ID NO: 3) (also called otoferlin isoform c) (NCBI Accession No. NP_919303.1)

15

Human Isoform 4 (short 3) (otoferlin protein) (SEQ ID NO: 4) (also called otoferlin isoform b) (NCBI Accession No. NP_004793.2)

Human Isoform 5 (short 4) (otoferlin protein) (SEQ ID NO: 5) (also called otoferlin isoform e) (NCBI Accession No. NP_001274418.1)

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Complete cds (otoferlin cDNA) (www.ncbi.nlm.nih.gov/nuccore/AF107403.1) (SEQ ID NO: 6) (encodes the protein of SEQ ID NO: 1)

Human Otoferlin Transcript Variant 1

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(www.ncbi.nlm.nih.gov/nuccore/NM_194248.2) (SEQ ID NO: 7) (encodes the protein of SEQ ID NO: 1)

Human Otoferlin Transcript Variant 2

30

(www.ncbi.nlm.nih.gov/nuccore/NM_004802.3) (SEQ ID NO: 8) (encodes the protein of SEQ ID NO: 4)

Human Otoferlin Transcript Variant 3

(www.ncbi.nlm.nih.gov/nucore/NM_194322.2) (SEQ ID NO: 9) (encodes the protein of SEQ ID NO: 3)

5 **Human Otoferlin Transcript Variant 4**

(www.ncbi.nlm.nih.gov/nucore/NM_194323.2) (SEQ ID NO: 10) (encodes the protein of SEQ ID NO: 2)

Human Otoferlin Transcript Variant 5

10 (www.ncbi.nlm.nih.gov/nucore/NM_001287489.1) (SEQ ID NO: 11) (encodes the protein of SEQ ID NO: 5)

A non-limiting example of a human wildtype otoferlin genomic DNA sequence is SEQ ID NO: 12. The exons in SEQ ID NO: 12 are: nucleotide positions 5001-5206
 15 (exon 1), nucleotide positions 25925-25983 (exon 2), nucleotide positions 35779-35867 (exon 3), nucleotide positions 44590-44689 (exon 4), nucleotide positions 47100-47281 (exon 5), nucleotide positions 59854-59927 (exon 6), nucleotide positions 61273-61399 (exon 7), nucleotide positions 61891-61945 (exon 8), nucleotide positions 68626-68757(exon 9), nucleotide positions 73959-74021 (exon 10), nucleotide positions 74404-
 20 74488 (exon 11), nucleotide positions 79066-79225 (exon 12), nucleotide positions 80051-80237 (exon 13), nucleotide positions 81107-81293 (exon 14), nucleotide positions 82690-82913 (exon 15), nucleotide positions 83388-83496 (exon 16), nucleotide positions 84046-84226 (exon 17), nucleotide positions 84315-84435 (exon 18), nucleotide positions 85950-86050 (exon 19), nucleotide positions 86193-86283
 25 (exon 20), nucleotide positions 86411-86527 (exon 21), nucleotide positions 86656-86808 (exon 22), nucleotide positions 87382-87571 (exon 23), nucleotide positions 87661-87785 (exon 24), nucleotide positions 88206-88340 (exon 25), nucleotide positions 89025-89186 (exon 26), nucleotide positions 89589-89708 (exon 27), nucleotide positions 90132-90293 (exon 28), nucleotide positions 90405-90567 (exon
 30 29), nucleotide positions 91050-91180 (exon 30), nucleotide positions 92549-92578 (exon 31), nucleotide positions 92978-93106 (exon 32), nucleotide positions 95225-

95291 (exon 33), nucleotide positions 96198-96334 (exon 34), nucleotide positions 96466-96600 (exon 35), nucleotide positions 96848-96985 (exon 36), nucleotide positions 97623-97750 (exon 37), nucleotide positions 97857-98027 (exon 38), nucleotide positions 98670-98830 (exon 39), nucleotide positions 99593-99735 (exon 40), nucleotide positions 100128-100216 (exon 41), nucleotide positions 101518-101616 (exon 42), nucleotide positions 101762-102003 (exon 43), nucleotide positions 102669-102847 (exon 44), nucleotide positions 102952-103052 (exon 45), nucleotide positions 103494-103691 (exon 46), nucleotide positions 105479-106496 (exon 47), and exon 48 (the sequence starting with CCGGCCCGAC; see also the description of this exon in Yasunaga et al., *Am. J. Hum. Genet.* 67:591-600, 2000).

The introns are located between each contiguous pair of exons in SEQ ID NO: 12, i.e., at nucleotide positions 100-5001 (intron 1), nucleotide 5207-25924 (intron 2), nucleotide positions 25984-35778 (intron 3), nucleotide positions 35868-44589 (intron 4), nucleotide positions 44690-47099 (intron 5), nucleotide positions 47282-59853 (intron 6), nucleotide positions 59928-61272 (intron 7), nucleotide positions 61400-61890 (intron 8), nucleotide positions 61946-68625 (intron 9), nucleotide positions 68758-73958 (intron 10), nucleotide positions 74022-74403 (intron 11), nucleotide positions 74489-79065 (intron 12), nucleotide positions 79226-80050 (intron 13), nucleotide positions 80238-81106 (intron 14), nucleotide positions 81294-82689 (intron 15), nucleotide positions 82914-83387 (intron 16), nucleotide positions 83497-84045 (intron 17), nucleotide positions 84227-84314 (intron 18), nucleotide positions 84436-85949 (intron 19), nucleotide positions 86051-86192 (intron 20), nucleotide positions 86284-86410 (intron 21), nucleotide positions 86528-86655 (intron 22), nucleotide positions 86809-87381 (intron 23), nucleotide positions 87572-87660 (intron 24), nucleotide positions 87786-88205 (intron 25), nucleotide positions 88341-89024 (intron 26), nucleotide positions 89187-89588 (intron 27), nucleotide positions 89709-90131 (intron 28), nucleotide positions 90294-90404 (intron 29), nucleotide positions 90568-91049 (intron 30), nucleotide positions 91181-92548 (intron 31), nucleotide positions 92579-92977 (intron 32), nucleotide positions 93107-95224 (intron 33), nucleotide positions 95292-96197 (intron 34), nucleotide positions 96335-96465 (intron 35), nucleotide positions 96601-96847 (intron 36), nucleotide positions 96986-97622 (intron 37),

nucleotide positions 97751-97856 (intron 38), nucleotide positions 98028-98669 (intron 39), nucleotide positions 98831-99592 (intron 40), nucleotide positions 99736-100127 (intron 41), nucleotide positions 100217-101517 (intron 42), nucleotide positions 101617-101761 (intron 43), nucleotide positions 102004-102668 (intron 44), nucleotide positions 102848-102951 (intron 45), nucleotide positions 103053-103494 (intron 46), nucleotide positions 103692-105478 (intron 47), and nucleotide positions 106497-108496 (intron 48).

Human Otoferlin Gene Sequence ([ncbi.nlm.nih.gov/nucore/224465243](https://www.ncbi.nlm.nih.gov/nucore/224465243)) (SEQ ID NO: 12)

Mouse Otoferlin Protein (SEQ ID NO: 13) (NCBI Accession No. NP_001300696.1)

Mouse Otoferlin cDNA (SEQ ID NO: 14) (NCBI Accession No. NM_001313767.1)

Mouse Otoferlin Gene Sequence (www.ncbi.nlm.nih.gov/gene/83762) (SEQ ID NO: 15) Accession: NC_000071 REGION: complement(30367066..30462730) GPC_000000778; NCBI Reference Sequence: NC_000071.6

Zebrafish Otoferlin A Gene Sequence (www.ncbi.nlm.nih.gov/gene/557476) (SEQ ID NO: 16) ACCESSION NC_007131 REGION: 31173357..31310109 GPC_000001574 NCBI Reference Sequence: NC_007131.7

Rhesus Monkey Otoferlin Gene Sequence (www.ncbi.nlm.nih.gov/gene/696717) (SEQ ID NO: 17) ACCESSION NC_027905 REGION: complement(26723411..26826586) GPC_000002105 NCBI Reference Sequence: NC_027905.1

Dog Otoferlin Gene Sequence (www.ncbi.nlm.nih.gov/gene/607961) (SEQ ID NO: 18) ACCESSION NC_006599 REGION: complement(20518502..20619461) GPC_000000676 NCBI Reference Sequence: NC_006599.3

Chimpanzee Otoferlin Gene Sequence (www.ncbi.nlm.nih.gov/gene/459083) (SEQ ID NO: 19) ACCESSION NC_006469 REGION: complement(27006052..27107747) GPC_000002338 NCBI Reference Sequence: NC_006469.4

Rat Otoferlin Protein (SEQ ID NO: 20)

Zebrafish Otoferlin Protein (SEQ ID NO: 21)

Cow Otoferlin Protein (SEQ ID NO: 22)

Baboon Otoferlin Protein (SEQ ID NO: 23)

5'mOTOF DNA Sequence (SEQ ID NO: 94)

ATGGCCCTGATTGTTACCTCAAGACTGTCTCAGAGCTCCGAGGCAAAGGTGACCGGATTGCCAAAGTCAC
 TTTCCGAGGGCAGTCTTTCTACTCCCGGGTCTGGGAACTGCGAGGGTGTGGCTGACTTTGATGAGACGT
 TCCGGTGGCCAGTGGCCAGCAGCATCGACCGGAATGAAGTGTTGGAGATTCAGATTTTCAACTACAGCAAA
 5 GTCTTCAGCAACAAGCTGATAGGGACCTTCTGCATGGTGTCTGCAGAAAGTGGTGGAGGAGAATCGGGTAGA
 GGTGACCGACACGCTGATGGATGACAGCAATGCTATCATCAAGACCAGCCTGAGCATGGAGGTCCGGTATC
 AGGCCACAGATGGCACTGTGGGCCCCTGGGATGATGGAGACTTCCTGGGAGATGAATCCCTCCAGGAGGAG
 AAGGACAGCCAGGAGACAGATGGGCTGCTACCTGGTTCCTCGACCCAGCACCCGGATATCTGGCGAGAAGAG
 CTTTCGCGAGAGCGGGAAGGAGTGTGTTCTCGGCCATGAAACTCGGCAAAACTCGGTCCCACAAAGAGGAGC
 10 CCCAAAGACAAGATGAGCCAGCAGTGTGGAGATGGAGGACCTGGACCACCTAGCCATTAGCTGGGGGAT
 GGGCTGGACCCTGACTCCGTGTCTCTAGCCTCGGTACCGCTCTCACCAGCAATGTCTCCAACAAACGGTC
 TAAGCCAGATATTAAGATGGAGCCAGTGTGGAAGGCCCATGGATTACCAGGTGAGCATCACAGTGATTG
 AGGCTCGGCAGCTGGTGGGCTTGAACATGGACCCTGTGGTGTGTGTGGAGGTGGGTGATGACAAGAAATAC
 ACGTCAATGAAGGAGTCCACAACTGCCCTTACTACAACGAGTACTTTGTCTTCGACTTCCATGTCTCTCC
 15 TGATGTCATGTTTGACAAGATCATCAAGATCTCGGTTATCCATTCTAAGAACCTGCTTCGGAGCGGCACCC
 TGGTGGGTTTCCTTCAAATGGATGTGGGGACTGTGTATTCCAGCCTGAACACCAGTTCATCACAAATGG
 GCCATCCTGTGACACCCCGATGACATCTCTGCTGGGTTGAAGGGTTATGTAAAGTGTGATGTGCTGTGGT
 GGGCAAGGGAGACAACATCAAGACACCCACAAGGCCAACGAGACGGATGAGGACGACATTGAAGGGAACT
 TGCTGCTCCCCGAGGGCGTGCCCCCGAACGGCAGTGGGCACGGTTCATGTGAAAATTTACCGAGCAGAG
 20 GGACTGCCCCGGATGAACACAAGCCTCATGGCCAACGTGAAGAAGGCGTTCATCGGTGAGAACAAGGACCT
 CGTCGACCCCTATGTGCAAGTCTTCTTTGCTGGACAAAAGGGCAAAACATCAGTGCAGAAGAGCAGCTATG
 AGCCGCTATGGAATGAGCAGGTCGTCTTCACAGACTTGTTCCCCCACTCTGCAAACGCATGAAGGTGCAG
 ATCCGGGACTCTGACAAGGTCAATGATGTGGCCATCGGCACCCACTTCATCGACCTGCGCAAGATTTCCAA
 CGATGGAGACAAAGGCTTCCTGCCTACCCTCGGTCCAGCCTGGGTGAACATGTACGGCTCCACGCGCAACT
 25 ACACACTGCTGGACGAGCACCAGGACTTGAATGAAGGCCTGGGGGAGGGTGTGTCTTCCGGGCCCCGCCTC
 ATGTTGGGACTAGCTGTGGAGATCCTGGACACCTCCAACCCAGAGCTCACCAGCTCCACGGAGGTGCAGGT
 GGAGCAGGCCACGCCTGTCTCGGAGAGCTGCACAGGGAGAATGGAAGAATTTTTTCTATTTGGAGCCTTCT
 TGGAAGCCTCAATGATTGACCGGAAAAATGGGGACAAGCCAATTACCTTTGAGGTGACCATAGGAACTAC
 GGCAATGAAGTCGATGGTATGTCCCGGCCCTGAGGCCTCGGCCCCGAAAGAGCCTGGGGATGAAGAAGA
 30 GGTAGACCTGATTGAGAACTCCAGTGACGATGAAGGTGACGAAGCCGGGGACCTGGCCTCGGTGTCTCCA
 CCCCACCTATGCGGCCCCAGATCACGGACAGGAATTTTCCACCTGCCCTACCTGGAGCGCAAGCCCTGC
 ATCTATATCAAGAGCTGGTGGCCTGACCAGAGGCGGCGCCTCTACAATGCCAACATCATGGATCACATTGC
 TGACAAGCTGGAAGAAGGCCTGAATGATGTACAGGAGATGATCAAAACGGAGAAGTCTTACCCGGAGCGCC
 GCCTGCGGGGTGTGCTAGAGGAACTCAGCTGTGGCTGCCACCGCTTCCTCTCCCTCTCGGACAAGGACCAG
 35 GGCCGCTCGTCCCGCACCAGGCTGGATCGAGAGCGTCTTAAGTCCTGTATGAGGGAGTTGGAGAGCATGGG
 ACAGCAGGCCAAGAGCCTGAGGGCTCAGGTGAAGCGGCACACTGTTCTGGGACAAGCTGAGGTGATGCCAGA
 ACTTTCTGCAGAAGCTACGCTTCCTGGCGGATGAG

3'mOTOF DNA Sequence (SEQ ID NO: 95)

40 CCCCAGCACAGCATTCCGGATGTGTTCAATTTGGATGATGAGCAACAACAAACGTATCGCCTATGCCCCGCT
 GCCTTCCAAAGACCTGCTCTTCTCCATCGTGGAGGAGGAACTGGGCAAGGACTGCGCCAAAGTCAAGACCC

TCTTCCTGAAGCTGCCAGGGAAGAGGGGCTTCGGCTCGGCAGGCTGGACAGTACAGGCCAAGCTGGAGCTC
 TACCTGTGGCTGGGCCTCAGCAAGCAGCGAAAGGACTTCCTGTGTGGTCTGCCCTGTGGCTTCGAGGAGGT
 CAAGGCAGCCCAAGGCCTGGGCCTGCATTCTTTCCGCCCATCAGCCTAGTCTACACCAAGAAGCAAGCCT
 TCCAGCTCCGAGCACACATGTATCAGGCCCCGAAGCCTCTTTGCTGCTGACAGCAGTGGGCTCTCTGATCCC
 5 TTTGCCCCGTGTCTTCTTCATCAACCAGAGCCAATGCACTGAGGTTCTAAACGAGACACTGTGTCCCACCTG
 GGACCAGATGCTGGTATTTGACAACCTGGAGCTGTACGGTGAAGCTCACGAGTTACGAGATGATCCCCCA
 TCATTGTCAATTGAAATCTACGACCAGGACAGCATGGGCAAAGCCGACTTCATGGGCCGGACCTTCGCCAAG
 CCCCTGGTGAAGATGGCAGATGAAGCATACTGCCCACCTCGCTTCCCGCCGCAGCTTGAGTACTACCAGAT
 CTACCGAGGCAGTGCCACTGCCGGAGACCTACTGGCTGCCTTCGAGCTGCTGCAGATTGGGCCATCAGGGA
 10 AGGCTGACCTGCCACCCATCAATGGCCCAGTGGACATGGACAGAGGGCCCATCATGCCTGTGCCCGTGGGA
 ATCCGGCCAGTGCTCAGCAAGTACCGAGTGGAGGTGCTGTTCTGGGGCCTGAGGGACCTAAAGAGGGTGAA
 CCTGGCCCAGGTGGACCGACCACGGGTGGACATCGAGTGTGCAGGAAAGGGGGTACAATCCTCCCTGATTTC
 ACAATTATAAGAAGAACCCCCAACTTCAACACGCTGGTCAAGTGGTTTGAAGTGGACCTCCCGGAGAATGAG
 CTCTGCACCCACCCTTGAACATCCGAGTGGTAGATTGCCGGGCCTTTGGACGATACACCCTGGTGGGTTC
 15 CCACGCAGTCAGCTCACTGAGGCGCTTCATCTACCGACCTCCAGACCGCTCAGCCCCCACTGGAACACCA
 CAGGGGAGGTTGTAGTAAGCATGGAGCCTGAGGAGCCAGTTAAGAAGCTGGAGACCATGGTGAACTGGAT
 GCGACTTCTGATGCTGTGGTCAAGGTGGATGTGGCTGAAGATGAGAAGGAAAGGAAGAAGAAGAAAAAGAA
 AGGCCCCGTCAGAGGAGCCAGAGGAGGAAGAGCCCGATGAGAGCATGCTGGATTGGTGGTCCAAGTACTTCG
 CCTCCATCGACACAATGAAGGAGCAACTTCGACAACATGAGACCTCTGGAAGTGAAGTGGAAAGAGAAGGAA
 20 GAGATGGAAAGCGCTGAGGGCCTGAAGGGACCAATGAAGAGCAAGGAGAAGTCCAGAGCTGCAAAGGAGGA
 GAAAAAGAAGAAAAACCAGAGCCCTGGCCCTGGCCAGGGATCGGAGGCTCCTGAGAAGAAGAAAGCCAAGA
 TCGATGAGCTTAAGGTGTACCCCAAGGAGCTGGAATCGGAGTTTGACAGCTTTGAGGACTGGCTGCACACC
 TTCAACCTGTTGAGGGGCAAGACGGGAGATGATGAGGATGGCTCCACAGAGGAGGAGCGCATAGTAGGCCG
 ATTCAAGGGCTCCCTCTGTGTGTACAAAGTGCCACTCCCAGAAGATGTATCTCGAGAAGCTGGCTATGATC
 25 CCACCTATGGAATGTTCCAGGGCATCCCAAGCAATGACCCCATCAATGTGCTGGTCCGAATCTATGTGGTC
 CGGGCCACAGACCTGCACCCGGCCGACATCAATGGCAAAGCTGACCCCTATATTGCCATCAAGTTAGGCAA
 GACCGACATCCGAGACAAGGAGAACTACATCTCCAAGCAGCTCAACCCTGTGTTTGGGAAGTCTTTGACA
 TTGAGGCCTCCTTCCCCATGGAGTCCATGTTGACAGTGGCCGTGTACGACTGGGATCTGGTGGGCACTGAT
 GACCTCATCGGAGAAACCAAGATTGACCTGGAAAACCGCTTCTACAGCAAGCATCGCGCCACCTGCGGCAT
 30 CGCACAGACCTATTCCATACATGGCTACAATATCTGGAGGGACCCCATGAAGCCCAGCCAGATCCTGACAC
 GCCTCTGTAAAGAGGGCAAAGTGGACGGCCCCCACTTTGGTCCCCATGGGAGAGTGAGGGTTGCCAACCCT
 GTCTTCACGGGGCCTTCAGAAATAGAGGATGAGAATGGTCAGAGGAAGCCACAGATGAGCACGTGGCACT
 GTCTGCTCTGAGACACTGGGAGGACATCCCCGGGTGGGCTGCCGCCTTGTGCCGGAACACGTGGAGACCA
 GGCCGCTGCTCAACCCTGACAAGCCAGGCATTGAGCAGGGCCGCCTGGAGCTGTGGGTGGACATGTTCCCC
 35 ATGGACATGCCAGCCCCTGGGACACCTCTGGATATATCCCCCAGGAAACCCAAGAAGTACGAGCTGCGGGT
 CATCGTGTGGAACACAGACGAGGTGGTCTGGAAGACGATGATTTCTTCACGGGAGAGAAGTCCAGTGACA
 TTTTTGTGAGGGGTGGCTGAAGGGCCAGCAGGAGGACAAACAGGACACAGATGTCCACTATCACTCCCTC
 ACGGGGGAGGGCAACTTCAACTGGAGATACCTCTTCCCCTTCGACTACCTAGCGGCCGAAGAGAAGATCGT
 TATGTCCAAAAGGAGTCTATGTTCTCCTGGGATGAGACGGAGTACAAGATCCCTGCGCGGCTCACCCCTGC
 40 AGATCTGGGACGCTGACCACTTCTCGGCTGACGACTTCTGGGGGCTATCGAGCTGGACCTGAACCGGTTC
 CCGAGGGGCGCTAAGACAGCCAAGCAGTGCACCATGGAGATGGCCACCGGGGAGGTGGACGTACCCCTGGT

TTCCATCTTTAAACAGAAACGTGTCAAAGGCTGGTGGCCCCCTCCTGGCCCGCAATGAGAATGATGAGTTTG
 AGCTCACAGGCAAAGTGGAGGCGGAGCTACACCTACTCACGGCAGAGGAGGCAGAGAAGAACCCTGTGGGC
 CTGGCTCGCAATGAACCTGATCCCCTAGAAAAACCCACCGGCCTGACACGGCATTCTGTCTGGTTTCTGAA
 CCCACTCAAATCTATCAAGTACCTCATCTGCACCCGGTACAAGTGGCTGATCATCAAGATCGTGCTGGCGC
 5 TGCTGGGGCTGCTCATGCTGGCCCTCTTCCTTTACAGCCTCCCAGGCTACATGGTCAAGAAGCTCCTAGGG
 GCCTGA

Some embodiments of any of the compositions described herein can include a first vector including the coding sequence of SEQ ID NO: 94 (or include a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 94). Some embodiments of any of the compositions described herein can include a first vector including the coding sequence of SEQ ID NO: 95 (or include a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, or at least 99% identical to SEQ ID NO: 95).

Vectors

Provided herein are compositions of matter and methods of use for the treatment of a disease such as nonsyndromic hearing loss, using nucleic acid therapeutics such as auditory polypeptide messenger RNAs. Preferably, the auditory polypeptide nucleic acids are present in viral vectors, such as adeno-associated viral vectors, adenoviral vectors, lentiviral vectors, and retroviral vectors.

The foregoing methods for packaging recombinant vectors in desired AAV capsids to produce the rAAVs of the invention are not meant to be limiting and other suitable methods will be apparent to the skilled artisan.

Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (polyA) signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (i.e., Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. A great number of expression control sequences,

including promoters which are native, constitutive, inducible and/or tissue-specific, are known in the art and may be utilized.

As used herein, a nucleic acid sequence (e.g., coding sequence) and regulatory sequences are said to be “operably” linked when they are covalently linked in such a way as to place the expression or transcription of the nucleic acid sequence under the influence or control of the regulatory sequences. If it is desired that the nucleic acid sequences be translated into a functional protein, two DNA sequences are said to be operably linked if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably linked to a nucleic acid sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide. Similarly two or more coding regions are operably linked when they are linked in such a way that their transcription from a common promoter results in the expression of two or more proteins having been translated in frame. In some embodiments, operably linked coding sequences yield a fusion protein. In some embodiments, operably linked coding sequences yield a functional RNA (e.g., shRNA, miRNA, miRNA inhibitor).

For nucleic acids encoding proteins, a polyadenylation sequence generally is inserted following the transgene sequences and before the 3' AAV ITR sequence. A rAAV construct useful in the present invention may also contain an intron, desirably located between the promoter/enhancer sequence and the transgene. One possible intron sequence is derived from SV-40, and is referred to as the SV-40 T intron sequence. Another vector element that may be used is an internal ribosome entry site (IRES). An IRES sequence is used to produce more than one polypeptide from a single gene transcript. An IRES sequence would be used to produce a protein that contains more than one polypeptide chain. Selection of these and other common vector elements is conventional, and many such sequences are available [see, e.g., Sambrook et al.

"Molecular Cloning. A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory, New York (1989), and references cited therein at, for example, pages 3.18 3.26 and 16.17 16.27 and Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989]. In some embodiments, a Foot and Mouth Disease Virus 2A sequence
5 is included in polyprotein; this is a small peptide (approximately 18 amino acids in length) that has been shown to mediate the cleavage of polyproteins (Ryan, M D et al., EMBO, 1994; 4: 928-933; Mattion, N M et al., J Virology, November 1996; p. 8124-8127; Furler, S et al., Gene Therapy, 2001; 8: 864-873; and Halpin, C et al., The Plant Journal, 1999; 4: 453-459). The cleavage activity of the 2A sequence has previously been
10 demonstrated in artificial systems including plasmids and gene therapy vectors (AAV and retroviruses) (Ryan, M D et al., EMBO, 1994; 4: 928-933; Mattion, N M et al., J Virology, November 1996; p. 8124-8127; Furler, S et al., Gene Therapy, 2001; 8: 864-873; and Halpin, C et al., The Plant Journal, 1999; 4: 453-459; de Felipe, P et al., Gene Therapy, 1999; 6: 198-208; de Felipe, P et al., Human Gene Therapy, 2000; 11: 1921-
15 1931; and Klump, H et al., Gene Therapy, 2001; 8: 811-817).

The precise nature of the regulatory sequences needed for gene expression in host cells may vary between species, tissues or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence,
20 CAAT sequence, enhancer elements, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region that includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design
25 of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Examples of constitutive promoters include, without limitation, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, e.g.,
30 Boshart et al. (1985) Cell, 41:521-530], the SV40 promoter, the dihydrofolate reductase

promoter, the .beta.-actin promoter, the phosphoglycerol kinase (PGK) promoter (Gilham et al., *J. Gene Med.* 12(2):129-136, 2010), and the EF1.alpha. promoter [Invitrogen].

Inducible promoters allow regulation of gene expression and can be regulated by exogenously supplied compounds, environmental factors such as temperature, or the presence of a specific physiological state, e.g., acute phase, a particular differentiation state of the cell, or in replicating cells only. Inducible promoters and inducible systems are available from a variety of commercial sources, including, without limitation, Invitrogen, Clontech and Ariad. Many other systems have been described and can be readily selected by one of skill in the art. Examples of inducible promoters regulated by exogenously supplied promoters include the zinc-inducible sheep metallothioneine (MT) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7 polymerase promoter system (WO 98/10088); the ecdysone insect promoter (No et al. (1996) *Proc. Natl. Acad. Sci. USA*, 93:3346-3351), the tetracycline-repressible system (Gossen et al. *Proc. Natl. Acad. Sci. USA*, 89:5547-5551 (1992)), the tetracycline-inducible system (Gossen et al. *Science*, 268:1766-1769 (1995), see also Harvey et al. *Curr. Opin. Chem. Biol.*, 2:512-518 (1998)), the RU486-inducible system (Wang et al. *Nat. Biotech.*, 15:239-243 (1997) and Wang et al. *Gene Ther.*, 4:432-441 (1997)) and the rapamycin-inducible system (Magari et al. *J. Clin. Invest.*, 100:2865-2872 (1997)). Still other types of inducible promoters which may be useful in this context are those which are regulated by a specific physiological state, e.g., temperature, acute phase, a particular differentiation state of the cell, or in replicating cells only.

In another embodiment, the native promoter for the transgene will be used. The native promoter may be preferred when it is desired that expression of the transgene should mimic the native expression. The native promoter may be used when expression of the transgene must be regulated temporally or developmentally, or in a tissue-specific manner, or in response to specific transcriptional stimuli. In a further embodiment, other native expression control elements, such as enhancer elements, polyadenylation sites or Kozak consensus sequences may also be used to mimic the native expression.

In some embodiments, the regulatory sequences impart tissue-specific gene expression capabilities. In some cases, the tissue-specific regulatory sequences bind tissue-specific transcription factors that induce transcription in a tissue specific manner.

Such tissue-specific regulatory sequences (e.g., promoters, enhancers, etc.) are well known in the art. Exemplary tissue-specific regulatory sequences include, but are not limited to the following tissue specific promoters: a liver-specific thyroxin binding globulin (TBG) promoter, a insulin promoter, a glucagon promoter, a somatostatin promoter, a pancreatic polypeptide (PPY) promoter, a synapsin-1 (Syn) promoter (Kugler et al., *Virology* 311:89-95, 2003; Hioki et al., *Gene Ther.* 14:872-882, 2007; Kuroda et al., *J. Gene Med.* 10:1163-1175, 2008), a creatine kinase (MCK) promoter (Wang et al., *Gene Ther.* 15:1489-1499, 2008; Talbot et al., *Mol. Ther.* 18:601-608, 2010; Katwal et al., *Gene Ther.* 20(9):930-938, 2013), a mammalian desmin (DES) promoter (Talbot et al., *Mol. Ther.* 18:601-608, 2010), a C5-12 promoter (Wang et al., *Gene Ther.* 15:1489-1499, 2008), an α -myosin heavy chain (α -MHC) promoter, a PDGF promoter (Patterna, *Gene Ther.* 7(15):1304-1311, 2000; Hioki et al., *Gene Ther.* 14:872-882, 2007), MecP2 promoter (Rastegar et al., *PLoS One* 4:e6810, 2009; Gray et al., *Human Gene Ther.* 22:1143-1153, 2011), CaMKII promoter (Hioki et al., *Gene Ther.* 14:872-882, 2007; Kuroda et al., *J. Gene Med.* 10:1163-1175, 2008), mGluR2 promoter (Brene et al., *Eur. J. Neurosci.* 12:1525-1533, 2000; Kuroda et al., *J. Gene Med.* 10:1163-1175, 2008), NFL promoter (Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001), NFH promoter (Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001), n β 2 promoter (Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001), PPE promoter (Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001), Enk promoter (Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001), EAAT2 promoter (Su et al., *Proc. Natl. Acad. Sci. U.S.A.* 100:1955-1960, 2003; Kuroda et al., *J. Gene Med.* 10:1163-1175, 2008), GFAP promoter (Brenner et al., *J. Neurosci.* 14:1030-1037, 1994; Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001; Lee et al., *Glia* 56:481-493, 2008; Dirren et al., *Human Gene Ther.* 25:109-120, 2014), MBP promoter (Chen et al., *Gene Ther.* 5(1):50-58, 1998), or a cardiac Troponin T (cTnT) promoter. Other exemplary promoters include Beta-actin promoter, hepatitis B virus core promoter, Sandig et al., *Gene Ther.*, 3:1002-9 (1996); alpha-fetoprotein (AFP) promoter, Arbuthnot et al., *Hum. Gene Ther.*, 7:1503-14 (1996)), bone osteocalcin promoter (Stein et al., *Mol. Biol. Rep.*, 24:185-96

(1997)); bone sialoprotein promoter (Chen et al., J. Bone Miner. Res., 11:654-64 (1996)), CD2 promoter (Hansal et al., J. Immunol., 161:1063-8 (1998); immunoglobulin heavy chain promoter; T cell receptor .alpha.-chain promoter, neuronal such as neuron-specific enolase (NSE) promoter (Andersen et al., Cell. Mol. Neurobiol., 13:503-15 (1993); Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001), neurofilament light-chain gene promoter (Piccioli et al., Proc. Natl. Acad. Sci. USA, 88:5611-5 (1991)), and the neuron-specific vgf gene promoter (Piccioli et al., Neuron, 15:373-84 (1995)), among others which will be apparent to the skilled artisan.

In some embodiments, one or more bindings sites for one or more miRNAs are incorporated in a transgene of a rAAV vector, to inhibit the expression of the transgene in one or more tissues of an subject harboring the transgene. The skilled artisan will appreciate that binding sites may be selected to control the expression of a transgene in a tissue specific manner. For example, binding sites for the liver-specific miR-122 may be incorporated into a transgene to inhibit expression of that transgene in the liver. The target sites in the mRNA may be in the 5' UTR, the 3' UTR or in the coding region. Typically, the target site is in the 3' UTR of the mRNA. Furthermore, the transgene may be designed such that multiple miRNAs regulate the mRNA by recognizing the same or multiple sites. The presence of multiple miRNA binding sites may result in the cooperative action of multiple RISCs and provide highly efficient inhibition of expression. The target site sequence may comprise a total of 5-100, 10-60, or more nucleotides. The target site sequence may comprise at least 5 nucleotides of the sequence of a target gene binding site.

Auditory Polypeptides and Auditory Polypeptide Transgene Coding Sequences

The composition of the auditory polypeptide transgene sequence of the rAAV vector will depend upon the use to which the resulting vector will be generated. Thus, the invention embraces the delivery of rAAV vectors encoding one or more auditory polypeptides, peptides, or proteins, which are useful for the treatment or prevention of disease states associated with hearing loss in a mammalian subject. Exemplary therapeutic proteins include one or more polypeptides selected from the group consisting of otoferlin, Cav1.3, a scaffold protein selected from bassoon, piccolo, ribeye, and

harmonin, Vglut3, synaptotagmin, a vesicle tethering / docking protein, a vesicle priming protein, a vesicle fusion protein, GluA2/3, or GluA4.

Optionally included in the AAV compositions are polypeptide reporter proteins. Reporter sequences that may be provided in a transgene include, without limitation, DNA sequences encoding .beta.-lactamase, .beta.-galactosidase (LacZ), alkaline phosphatase, thymidine kinase, green fluorescent protein (GFP), chloramphenicol acetyltransferase (CAT), luciferase, and others well known in the art. When associated with regulatory elements which drive their expression, the reporter sequences provide signals detectable by conventional means, including enzymatic, radiographic, colorimetric, fluorescence or other spectrographic assays, fluorescent activating cell sorting assays, and immunological assays, including enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and immunohistochemistry. For example, where the marker sequence is the LacZ gene, the presence of the vector carrying the signal is detected by assays for β -galactosidase activity. Where the transgene is green fluorescent protein or luciferase, the vector carrying the signal may be measured visually by color or light production in a luminometer. Such reporters can, for example, be useful in verifying the tissue-specific targeting capabilities and tissue specific promoter regulatory activity of an rAAV.

In another example, the transgene encodes a protein or functional RNA that is intended to be used to create an animal model of disease. Appropriate transgene coding sequences will be apparent to the skilled artisan.

The rAAV vectors may comprise a gene or a portion of a gene encoding an auditory polypeptide, to be transferred to a subject to treat a disease associated with reduced expression, lack of expression or dysfunction of the auditory polypeptide gene or another gene in the functional pathway of an auditory polypeptide.

In a first aspect, provided are therapeutic compositions including a plurality of adeno-associated viral (AAV) vectors, wherein the plurality of AAV vectors are capable of constituting an auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered. Preferably, the plurality of AAV vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered. The plurality of AAV vectors include a first AAV vector and a second

AAV vector, wherein the first and second AAV vectors independently contain packaging capacity of less than about 6kb. The auditory polypeptide messenger RNA encodes an auditory polypeptide selected from the group consisting of otoferlin and an ortholog or homolog thereof, for example, as provided herein. The AAV vectors contain at least one promoter sequence selected from a CBA, a CMV, or a CB7 promoter, or one or more Cochlea-specific promoters. In some embodiments, an AAV vector can include a CMV enhancer and promoter sequence, e.g., SEQ ID NO: 70. In some embodiments, an AAV vector can include a CMV enhancer and a chicken β -actin promoter, e.g., SEQ ID NO: 61. In some embodiments, an AAV vector can include a CMVd promoter sequence, e.g., SEQ ID NO: 86.

The compositions provided herein include at least two (e.g., two, three, four, five, or six) nucleic acid vectors, where: each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions being at least 30 amino acids (e.g., between about 30 amino acids to about 1950 amino acids, about 30 amino acids to about 1900 amino acids, about 30 amino acids to about 1850 amino acids, about 30 amino acids to about 1800 amino acids, about 30 amino acids to about 1750 amino acids, about 30 amino acids to about 1700 amino acids, about 30 amino acids to about 1650 amino acids, about 30 amino acids to about 1600 amino acids, about 30 amino acids to about 1550 amino acids, about 30 amino acids to about 1500 amino acids, about 30 amino acids to about 1450 amino acids, about 30 amino acids to about 1400 amino acids, about 30 amino acids to about 1350 amino acids, about 30 amino acids to about 1300 amino acids, about 30 amino acids to about 1250 amino acids, about 30 amino acids to about 1200 amino acids, about 30 amino acids to about 1150 amino acids, about 30 amino acids to about 1100 amino acids, about 30 amino acids to about 1050 amino acids, about 30 amino acids to about 1000 amino acids, about 30 amino acids to about 950 amino acids, about 30 amino acids to about 900 amino acids, about 30 amino acids to about 850 amino acids, about 30 amino acids to about 800 amino acids, about 30 amino acids to about 750 amino acids, about 30 amino acids to about 700 amino acids, about 30 amino acids to about 650 amino acids, about 30 amino acids to about 600 amino acids, about 30 amino acids to about 550 amino acids, about 30 amino acids to about 500 amino acids, about 30 amino acids to about 450

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1900 amino acids, about 1800 amino acids to about 1850 amino acids, about 1850 amino acids to about 1950 amino acids, about 1850 amino acids to about 1900 amino acids, about 1900 amino acids to about 1950 amino acids), wherein the amino acid sequence of each of the encoded portions may optionally partially overlap with the amino acid sequence of a different one of the encoded portions; no single vector of the at least two different vectors encodes an active otoferlin protein (e.g., a full-length otoferlin protein (e.g., a full-length wildtype otoferlin protein)); and, when introduced into a mammalian cell, the at least two different vectors undergo homologous recombination with each other, thereby forming a recombined nucleic acid, where the recombined nucleic acid encodes an active otoferlin protein (e.g., a full-length otoferlin protein). In some embodiments, one of the nucleic acid vectors can include a coding sequence that encodes a portion of an otoferlin protein, where the encoded portion is, e.g., about 900 amino acids to about 1950 amino acids, about 900 amino acids to about 1900 amino acids, about 900 amino acids to about 1850 amino acids, about 900 amino acids to about 1800 amino acids, about 900 amino acids to about 1750 amino acids, about 900 amino acids to about 1700 amino acids, about 900 amino acids to about 1650 amino acids, about 900 amino acids to about 1600 amino acids, about 900 amino acids to about 1550 amino acids, about 900 amino acids to about 1500 amino acids, about 900 amino acids to about 1450 amino acids, about 900 amino acids to about 1400 amino acids, about 900 amino acids to about 1350 amino acids, about 900 amino acids to about 1300 amino acids, about 900 amino acids to about 1250 amino acids, about 900 amino acids to about 1200 amino acids, about 900 amino acids to about 1150 amino acids, about 900 amino acids to about 1100 amino acids, about 900 amino acids to about 1050 amino acids, about 900 amino acids to about 1000 amino acids, about 900 amino acids to about 950 amino acids, about 950 amino acids to about 1950 amino acids, about 950 amino acids to about 1900 amino acids, about 950 amino acids to about 1850 amino acids, about 950 amino acids to about 1800 amino acids, about 950 amino acids to about 1750 amino acids, about 950 amino acids to about 1700 amino acids, about 950 amino acids to about 1650 amino acids, about 950 amino acids to about 1600 amino acids, about 950 amino acids to about 1550 amino acids, about 950 amino acids to about 1500 amino acids, about 950 amino acids to about 1450 amino acids, about 950 amino acids to about 1400 amino acids, about 950 amino acids to about

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In some embodiments of these compositions, at least one of the coding sequences includes a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks the intronic sequence that naturally occurs between the two neighboring exons.

In some embodiments, the amino acid sequence of none of the encoded portions overlaps even in part with the amino acid sequence of a different one of the encoded portions. In some embodiments, the amino acid sequence of one or more of the encoded portions partially overlaps with the amino acid sequence of a different one of the encoded portions. In some embodiments, the amino acid sequence of each of the encoded portions partially overlaps with the amino acid sequence of a different one of the encoded portions.

In some embodiments, the overlapping amino acid sequence is between about 30 amino acid residues to about 1000 amino acids (e.g., or any of the subranges of this range described herein) in length.

In some examples, the vectors include two different vectors, each of which comprises not only exon(s), but also a different segment of an intron, wherein the intron includes the nucleotide sequence of an intron that is present in an otoferlin genomic DNA (e.g., any of the exemplary introns in SEQ ID NO: 12 described herein), and wherein the two different segments overlap in sequence by at least 100 nucleotides (e.g., about 100 nucleotides to about 5,000 nucleotides, about 100 nucleotides to about 4,500 nucleotides, about 100 nucleotides to about 4,000 nucleotides, about 100 nucleotides to about 3,500 nucleotides, about 100 nucleotides to about 3,000 nucleotides, about 100 nucleotides to about 2,500 nucleotides, about 100 nucleotides to about 2,000 nucleotides, about 100 nucleotides to about 1,500 nucleotides, about 100 nucleotides to about 1,000 nucleotides, about 100 nucleotides to about 800 nucleotides, about 100 nucleotides to about 600 nucleotides, about 100 nucleotides to about 400 nucleotides, about 100 nucleotides to about 200 nucleotides, about 200 nucleotides to about 5,000 nucleotides, about 200 nucleotides to about 4,500 nucleotides, about 200 nucleotides to about 4,000 nucleotides, about 200 nucleotides to about 3,500 nucleotides, about 200 nucleotides to about 3,000 nucleotides, about 200 nucleotides to about 2,500 nucleotides, about 200 nucleotides to about 2,000 nucleotides, about 200 nucleotides to about 1,500 nucleotides, about 200 nucleotides to about 1,000 nucleotides, about 200 nucleotides to about 800 nucleotides, about 200 nucleotides to about 600 nucleotides, about 200 nucleotides to about 400 nucleotides, about 400 nucleotides to about 5,000 nucleotides, about 400 nucleotides to about 4,500 nucleotides, about 400 nucleotides to about 4,000 nucleotides, about 400

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10 about 600 nucleotides to about 1,000 nucleotides, about 600 nucleotides to about 800 nucleotides, about 800 nucleotides to about 5,000 nucleotides, about 800 nucleotides to about 4,500 nucleotides, about 800 nucleotides to about 4,000 nucleotides, about 800 nucleotides to about 3,500 nucleotides, about 800 nucleotides to about 3,000 nucleotides, about 800 nucleotides to about 2,500 nucleotides, about 800 nucleotides to about 2,000
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20 1,000 nucleotides to about 2,000 nucleotides, about 1,000 nucleotides to about 1,500 nucleotides, about 1,500 nucleotides to about 5,000 nucleotides, about 1,500 nucleotides to about 4,500 nucleotides, about 1,500 nucleotides to about 4,000 nucleotides, about 1,500 nucleotides to about 3,500 nucleotides, about 1,500 nucleotides to about 3,000 nucleotides, about 1,500 nucleotides to about 2,500 nucleotides, about 1,500 nucleotides
25 to about 2,000 nucleotides, about 2,000 nucleotides to about 5,000 nucleotides, about 2,000 nucleotides to about 4,500 nucleotides, about 2,000 nucleotides to about 4,000 nucleotides, about 2,000 nucleotides to about 3,500 nucleotides, about 2,000 nucleotides to about 3,000 nucleotides, about 2,000 nucleotides to about 2,500 nucleotides, about 2,500 nucleotides to about 5,000 nucleotides, about 2,500 nucleotides to about 4,500
30 nucleotides, about 2,500 nucleotides to about 4,000 nucleotides, about 2,500 nucleotides to about 3,500 nucleotides, about 2,500 nucleotides to about 3,000 nucleotides, about

3,000 nucleotides to about 5,000 nucleotides, about 3,000 nucleotides to about 4,500 nucleotides, about 3,000 nucleotides to about 4,000 nucleotides, about 3,000 nucleotides to about 3,500 nucleotides, about 3,500 nucleotides to about 5,000 nucleotides, about 3,500 nucleotides to about 4,500 nucleotides, about 3,500 nucleotides to about 4,000 nucleotides, about 4,000 nucleotides to about 5,000 nucleotides, about 4,000 nucleotides to about 4,500 nucleotides, about 4,500 nucleotides to about 5,000 nucleotides), in length.

The overlapping nucleotide sequence in any two of the different vectors can include part or all of one or more exons of an otoferlin gene (e.g., any one or more of the exemplary exons in SEQ ID NO: 12 described herein).

In some embodiments, the number of different vectors in the composition is two, three, four, or five. In compositions where the number of different vectors in the composition is two, the first of the two different vectors can include a coding sequence that encodes an N-terminal portion of the otoferlin protein. In some examples, the N-terminal portion of the otoferlin gene is between about 30 amino acids to about 1950 amino acids (or any of the subranges of this range described above) in length. In some examples, the first vector further includes one or both of a promoter (e.g., any of the promoters described herein or known in the art) and a Kozak sequence (e.g., any of the exemplary Kozak sequences described herein or known in the art). In some examples, the first vector includes a promoter that is an inducible promoter, a constitutive promoter, or a tissue-specific promoter. In some examples, the second of the two different vectors includes a coding sequence that encodes a C-terminal portion of the otoferlin protein. In some examples, the C-terminal portion of the otoferlin protein is between 30 amino acids to about 1950 amino acids (or any of the subranges of this range described above) in length. In some examples, the second vector further includes a poly(A) signal sequence.

In some examples where the number of different vectors in the composition is two, the N-terminal portion encoded by one of the two vectors can include a portion comprising amino acid position 1 to about amino acid position 1,950, about amino acid position 1,940, about amino acid position 1,930, about amino acid position 1,920, about amino acid position 1,910, about amino acid position 1,900, about amino acid position 1,900, about amino acid position 1,890, about amino acid position 1,880, about amino acid position 1,870, about amino acid position 1,860, about amino acid position 1,850,

about amino acid position 1,840, about amino acid position 1,830, about amino acid position 1,820, about amino acid position 1,810, about amino acid position 1,800, about amino acid position 1,790, about amino acid position 1,780, about amino acid position 1,770, about amino acid position 1,760, about amino acid position 1,750, about amino acid position 1,740, about amino acid position 1,730, about amino acid position 1,720, about amino acid position 1,710, about amino acid position 1,700, about amino acid position, about amino acid position 1,690, about amino acid position 1,680, about amino acid position 1,670, about amino acid position 1,660, about amino acid position 1,650, about amino acid position 1,640, about amino acid position 1,630, about amino acid position 1,620, about amino acid position 1,610, about amino acid position 1,600, about amino acid position 1,590, about amino acid position 1,580, about amino acid position 1,570, about amino acid position 1,560, about amino acid position 1,550, about amino acid position 1,540, about amino acid position 1,530, about amino acid position 1,520, about amino acid position 1,510, amino acid position 1 to about amino acid position 1,500, about amino acid position 1,490, about amino acid position 1,480, about amino acid position 1,470, about amino acid position 1,460, about amino acid position 1,450, about amino acid position 1,440, about amino acid position 1,430, about amino acid position 1,420, about amino acid position 1,410, about amino acid position 1,400, about amino acid position 1,390, about amino acid position 1,380, about amino acid position 1,370, about amino acid position 1,360, about amino acid position 1,350, about amino acid position 1,340, about amino acid position 1,330, about amino acid position 1,320, about amino acid position 1,310, about amino acid position 1,300, about amino acid position 1,290, about amino acid position 1,280, about amino acid position 1,270, about amino acid position 1,260, about amino acid position 1,250, about amino acid position 1,240, about amino acid position 1,230, about amino acid position 1,220, about amino acid position 1,210, about amino acid position 1,200, about amino acid position 1,190, about amino acid position 1,180, about amino acid position 1,170, about amino acid position 1,160, about amino acid position 1,150, about amino acid position 1,140, about amino acid position 1,130, about amino acid position 1,120, about amino acid position 1,110, about amino acid position 1,100, about amino acid position 1,090, about amino acid position 1,080, about amino acid position 1,070, about

amino acid position 1,060, about amino acid position 1,050, about amino acid position 1,040, about amino acid position 1,030, about amino acid position 1,020, about amino acid position 1,010, about amino acid position 1,000, about amino acid position 990, about amino acid position 980, about amino acid position 970, about amino acid position 960, about amino acid position 950, about amino acid position 940, about amino acid position 930, about amino acid position 920, about amino acid position 910, about amino acid position 900, about amino acid position 890, about amino acid position 880, about amino acid position 870, about amino acid position 860, about amino acid position 850, about amino acid position 840, about amino acid position 830, about amino acid position 820, about amino acid position 810, about amino acid position 800, about amino acid position 790, about amino acid position 780, about amino acid position 770, about amino acid position 760, about amino acid position 750, about amino acid position 740, about amino acid position 730, about amino acid position 720, about amino acid position 710, about amino acid position 700, about amino acid position 690, about amino acid position 680, about amino acid position 670, about amino acid position 660, about amino acid position 650, about amino acid position 640, about amino acid position 630, about amino acid position 620, about amino acid position 610, about amino acid position 600, about amino acid position 590, about amino acid position 580, about amino acid position 570, about amino acid position 560, about amino acid position 550, about amino acid position 540, about amino acid position 530, about amino acid position 520, about amino acid position 510, about amino acid position 500, about amino acid position 490, about amino acid position 480, about amino acid position 470, about amino acid position 460, about amino acid position 450, about amino acid position 440, about amino acid position 430, about amino acid position 420, about amino acid position 410, about amino acid position 400, about amino acid position 390, about amino acid position 380, about amino acid position 370, about amino acid position 360, about amino acid position 350, about amino acid position 340, about amino acid position 330, about amino acid position 320, about amino acid position 310, about amino acid position 300, about amino acid position 290, about amino acid position 280, about amino acid position 270, about amino acid position 260, about amino acid position 250, about amino acid position 240, about amino acid position 230, about amino acid

position 220, about amino acid position 210, about amino acid position 200, about amino acid position 190, about amino acid position 180, about amino acid position 170, about amino acid position 160, about amino acid position 150, about amino acid position 140, about amino acid position 130, about amino acid position 120, about amino acid position 110, about amino acid position 100, about amino acid position 90, about amino acid position 80, about amino acid position 70, about amino acid position 60, about amino acid position 50, or about amino acid position 40 of a wildtype otoferlin protein (e.g., SEQ ID NO: 5).

In some examples where the number of different vectors in the composition is two, the N-terminal portion of the precursor otoferlin protein can include a portion comprising amino acid position 1 to amino acid position 310, amino acid position 1 to about amino acid position 320, amino acid position 1 to about amino acid position 330, amino acid position 1 to about amino acid position 340, amino acid position 1 to about amino acid position 350, amino acid position 1 to about amino acid position 360, amino acid position 1 to about amino acid position 370, amino acid position 1 to about amino acid position 380, amino acid position 1 to about amino acid position 390, amino acid position 1 to about amino acid position 400, amino acid position 1 to about amino acid position 410, amino acid position 1 to about amino acid position 420, amino acid position 1 to about amino acid position 430, amino acid position 1 to about amino acid position 440, amino acid position 1 to about amino acid position 450, amino acid position 1 to about amino acid position 460, amino acid position 1 to about amino acid position 470, amino acid position 1 to about amino acid position 480, amino acid position 1 to about amino acid position 490, amino acid position 1 to about amino acid position 500, amino acid position 1 to about amino acid position 510, amino acid position 1 to about amino acid position 520, amino acid position 1 to about amino acid position 530, amino acid position 1 to about amino acid position 540, amino acid position 1 to about amino acid position 550, amino acid position 1 to about amino acid position 560, amino acid position 1 to about amino acid position 570, amino acid position 1 to about amino acid position 580, amino acid position 1 to about amino acid position 590, amino acid position 1 to about amino acid position 600, amino acid position 1 to about amino acid position 610, amino acid position 1 to about amino acid position 620, amino acid position 1 to about

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1,570, amino acid position 1 to about amino acid position 1,580, amino acid position 1 to about amino acid position 1,590, amino acid position 1 to about amino acid position 1,600, amino acid position 1 to about amino acid 1,610, amino acid position 1 to about amino acid 1,620, amino acid position 1 to about amino acid 1,630, amino acid position 1 to about amino acid 1,640, amino acid position 1 to about amino acid 1,650, amino acid position 1 to about amino acid 1,660, amino acid position 1 to about amino acid 1,670, amino acid position 1 to about amino acid 1,680, amino acid position 1 to about amino acid 1,690, amino acid position 1 to about amino acid 1,700, amino acid position 1 to about amino acid 1,710, amino acid position 1 to about amino acid 1,720, amino acid position 1 to about amino acid 1,730, amino acid position 1 to about amino acid 1,740, amino acid position 1 to about amino acid 1,750, amino acid position 1 to about amino acid 1,760, amino acid position 1 to about amino acid 1,770, amino acid position 1 to about amino acid 1,780, amino acid position 1 to about amino acid 1,790, amino acid position 1 to about amino acid 1,800, amino acid position 1 to about amino acid 1,810, amino acid position 1 to about amino acid 1,820, amino acid position 1 to about amino acid 1,830, amino acid position 1 to about amino acid 1,840, amino acid position 1 to about amino acid 1,850, amino acid position 1 to about amino acid 1,860, amino acid position 1 to about amino acid 1,870, amino acid position 1 to about amino acid 1,880, amino acid position 1 to about amino acid 1,890, amino acid position 1 to about amino acid 1,900, amino acid position 1 to about amino acid 1,910, amino acid position 1 to about amino acid 1,920, amino acid position 1 to about amino acid 1,930, amino acid position 1 to about amino acid 1,940, amino acid position 1 to about amino acid 1,950, amino acid position 1 to about amino acid 1,960, amino acid position 1 to about amino acid 1,970, amino acid position 1 to about amino acid 1,980 of a wildtype otoferlin protein (e.g., SEQ ID NO: 5).

In some examples, the composition includes two vectors, where a first of the two vectors includes a coding sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 62, and the second of the two vectors includes a coding sequence that is at least 80%, at least 82%, at least 84%, at least 86%,

at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 63.

As used herein, the term “vector” includes any genetic element, such as a plasmid, phage, transposon, cosmid, chromosome, artificial chromosome, virus, virion, etc., that is capable of replication when associated with the proper control elements and that can transfer gene sequences between cells. Thus, the term includes cloning and expression vehicles, as well as viral vectors. In some embodiments, useful vectors are contemplated to be those vectors in which the nucleic acid segment to be transcribed is positioned under the transcriptional control of a promoter.

In some examples, a vector can be an artificial chromosome (e.g., a human artificial chromosome (HAC), a yeast artificial chromosome (YAC), a bacterial artificial chromosome (BAC), or a P1-derived artificial chromosome (PAC)) or a viral vector (e.g., any adenoviral vectors (e.g., pSV or pCMV vectors), any retroviral vectors as described herein, and any Gateway® vectors). A vector can, e.g., include sufficient cis-acting elements for expression; other elements for expression can be supplied by the host mammalian cell or in an in vitro expression system.

A “promoter” refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a polynucleotide sequence (e.g., a gene). The phrases “operatively positioned,” “under control” or “under transcriptional control” means that the promoter is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the gene. The term “expression vector or construct” means any type of genetic construct containing a nucleic acid in which part or all of the nucleic acid coding sequence is capable of being transcribed. In some embodiments, expression includes transcription of the nucleic acid, for example, to generate a biologically-active polypeptide product or inhibitory RNA (e.g., shRNA, miRNA, miRNA inhibitor) from a transcribed gene.

Vectors include all those known in the art, including cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide. Skilled practitioners will be capable of selecting suitable vectors and

mammalian cells for making any of the nucleic acids described herein.

In some embodiments the vector is a plasmid (i.e. a circular DNA molecule that can autonomously replicate inside a cell). In some embodiments, the vector can be a cosmid (e.g., pWE and sCos series (Wahl et al. (1987) Proc. Natl. Acad. Sci. USA 84:2160-2164, Evans et al. (1989) Proc. Natl. Acad. Sci. USA 86:5030-5034).

The term “transfer vector” refers to a composition of matter which includes an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Thus, the term “transfer vector” includes an autonomously replicating plasmid or a virus. The term should also be construed to further include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, a polylysine compound, liposome, and the like. Examples of viral transfer vectors include, but are not limited to, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, lentiviral vectors, and the like.

The term “expression vector” refers to a vector including a recombinant polynucleotide including expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector includes sufficient cis-acting elements for expression; other elements for expression can be supplied by the host cell or in an in vitro expression system. Expression vectors include all those known in the art, including cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide.

In some embodiments, the vector(s) is an artificial chromosome. An artificial chromosome is a genetically engineered chromosome that can be used as a vector to carry large DNA inserts. In some embodiments, the artificial chromosome is human artificial chromosome (HAC) (see, e.g., Kouprina et al., *Expert Opin. Drug Deliv* 11(4): 517-535, 2014; Basu et al., *Pediatr. Clin. North Am.* 53: 843-853, 2006; Ren et al., *Stem. Cell Rev.* 2(1):43-50, 2006; Kazuki et al., *Mol. Ther.* 19(9):1591-1601, 2011; Kazuki et al., *Gen. Ther.* 18: 384-393, 2011; and Katoh et al., *Biochem. Biophys. Res. Commun.* 321:280-290, 2004).

In some embodiments, the vector(s) is a yeast artificial chromosome (YAC) (see, e.g., Murray et al., *Nature* 305: 189-193, 1983; Ikeno et al. (1998) *Nat. Biotech.* 16:431-439, 1998). In some embodiments, the vector(s) is a bacterial artificial chromosome (BAC) (e.g., pBeloBAC11, pECBAC1, and pBAC108L). In some embodiments, the vector(s) is a P1-derived artificial chromosome (PAC). Examples of artificial chromosome are known in the art.

In some embodiments, the vector(s) is a viral vector (e.g., adeno-associated virus, adenovirus, lentivirus, and retrovirus). Non-limiting examples of viral vectors are described herein.

Recombinant AAV Vectors

“Recombinant AAV vectors” or “rAAVs” of the invention are typically composed of, at a minimum, a transgene or a portion thereof and a regulatory sequence, and optionally 5' and 3' AAV inverted terminal repeats (ITRs). It is this recombinant AAV vector which is packaged into a capsid protein and delivered to a selected target cell. In some embodiments, the transgene is a nucleic acid sequence, heterologous to the vector sequences, which encodes a polypeptide, protein, functional RNA molecule (e.g., miRNA, miRNA inhibitor) or other gene product, of interest. The nucleic acid coding sequence is operatively linked to regulatory components in a manner which permits transgene transcription, translation, and/or expression in a cell of a target tissue.

In some embodiments, the vector(s) is an adeno-associated viral vector (AAV) (see, e.g., Asokan et al., *Mol. Ther.* 20: 699-7080, 2012). “Recombinant AAV vectors” or “rAAVs” are typically composed of, at a minimum, a transgene or a portion thereof and a regulatory sequence, and optionally 5' and 3' AAV inverted terminal repeats (ITRs). Such a recombinant AAV vector is packaged into a capsid and delivered to a selected target cell (e.g., an inner hair cell).

The AAV sequences of the vector typically comprise the cis-acting 5' and 3' inverted terminal repeat sequences (See, e.g., B. J. Carter, in "Handbook of Parvoviruses", ed., P. Tijsser, CRC Press, pp. 155 168 (1990)). The ITR sequences are about 145 nt in length. Preferably, substantially the entire sequences encoding the ITRs are used in the molecule, although some degree of minor modification of these sequences

is permissible. The ability to modify these ITR sequences is within the skill of the art. (See, e.g., texts such as Sambrook et al. "Molecular Cloning. A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory, New York (1989); and K. Fisher et al., *J Virol.*, 70:520-532 (1996)). An example of such a molecule employed in the present invention is a "cis-acting" plasmid containing the transgene, in which the selected transgene sequence and associated regulatory elements are flanked by the 5' and 3' AAV ITR sequences. The AAV ITR sequences may be obtained from any known AAV, including presently identified mammalian AAV types.

A non-limiting example of a 5' AAV ITR sequence is SEQ ID NO: 59. A non-limiting example of a 3' AAV ITR sequence is SEQ ID NO: 60.

In addition to the major elements identified above for the recombinant AAV vector, the vector also includes conventional control elements that are operably linked to the transgene in a manner which permits its transcription, translation and/or expression in a cell transfected with the plasmid vector or infected with the virus produced by the invention. As used herein, "operably linked" sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act in trans or at a distance to control the gene of interest.

AAV vectors as described herein may include any of the regulatory elements described herein (e.g., one or more of a promoter, a polyA sequence, and an IRES).

Recombinant AV and Lentiviral Vectors

Also provided are therapeutic compositions including one or more adenoviral (AV) vectors, wherein the one or the plurality of AV vectors are capable of constituting an auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered. Preferably, the one or the plurality of AV vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

In some embodiments, the vector(s) is an adenovirus (see, e.g., Dmitriev et al. (1998) *J. Virol.* 72: 9706-9713; and Poulin et al., *J. Virol* 8: 10074-10086, 2010). In some embodiments, the vector(s) is a retrovirus (see, e.g., Maier et al. (2010) *Future Microbiol* 5: 1507-23).

In some embodiments, the vector(s) is a lentivirus (see, e.g., Matrai et al. (2010) *Mol Ther.* 18: 477-490; Banasik et al. (2010) *Gene Ther.* 17:150-7; and Wanisch et al. (2009) *Mol. Ther.* 17: 1316-32). A lentiviral vector refers to a vector derived from at least a portion of a lentivirus genome, including especially a self-inactivating lentiviral vector as provided in Milone et al., *Mol. Ther.* 17(8): 1453-1464 (2009). Non-limiting lentivirus vectors that may be used in the clinic include the LENTIVECTOR® gene delivery technology from Oxford BioMedica, the LENTIMAX™ vector system from Lentigen, and the like. Other types of lentiviral vectors are also available and would be known to one skilled in the art.

The term “lentivirus” refers to a genus of the Retroviridae family. Lentiviruses are unique among the retroviruses in being able to infect non-dividing cells; they can deliver a significant amount of genetic information into the DNA of the host cell, so they are one of the most efficient methods of a gene delivery vector. HIV, SIV, and FIV are all examples of lentiviruses.

The term “lentiviral vector” refers to a vector derived from at least a portion of a lentivirus genome, including especially a self-inactivating lentiviral vector as provided in Milone et al., *Mol. Ther.* 17(8): 1453-1464 (2009). Other examples of lentivirus vectors that may be used in the clinic include but are not limited to, e.g., the LENTIVECTOR® gene delivery technology from Oxford BioMedica, the LENTIMAX™ vector system from Lentigen and the like. Nonclinical types of lentiviral vectors are also available and would be known to one skilled in the art.

For example, provided are therapeutic compositions including one or a plurality of lentiviral vectors, wherein the one or the plurality of lentiviral vectors are capable of constituting an auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered. In one embodiment, the one or the plurality of lentiviral vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of a human subject to whom the therapeutic composition is administered.

In some embodiments of any of the compositions described herein, the first vector includes an ITR (e.g., any of the exemplary ITR sequences described herein), a promoter and/or enhancer (e.g., any of the exemplary enhancers and any of the exemplary

promoters described herein), an intron sequence of a OTOF gene (e.g., a human OTOF gene, e.g., any of the exemplary intron sequences of a human OTOF gene described herein), a Kozak sequence (e.g., any of the exemplary Kozak sequences described herein), and a sequence encoding a first, N-terminal portion of a human otoferlin protein (e.g., any of the exemplary sequences encoding a first, N-terminal portion of a human otoferlin protein described herein), an AK sequence (e.g., any of the exemplary AK sequences described herein), and an ITR (e.g., any of the exemplary ITR sequences described herein). In some embodiments of any of the compositions described herein, the second vector includes an ITR sequence (e.g., any of the exemplary ITR sequences described herein), an AK sequence (e.g., any of the exemplary AK sequences described herein), a splicing acceptor sequence (e.g., any of the splicing acceptor sequences described herein), a sequence encoding a second portion of a human otoferlin protein (e.g., any of the exemplary sequences encoding a second, C-terminal portion of a human otoferlin protein described herein), a poly(A) signal sequence (e.g., any of the exemplary poly(A) signal sequences described herein), a stuffer sequence (e.g., any of the exemplary stuffer sequences described herein), and an ITR sequence (e.g., any of the exemplary ITR sequences described herein).

In some embodiments of any of the compositions described herein, the vector is pAAV-AK-SA-3'mOTOF-EWB (SEQ ID NO: 39), depicted in Figures 11, 17 and 56, or is a vector including a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 39. The pAAV-AK-SA-3'mOTOF-EWB vector is 7625 bp in length and has an AK sequence at nucleotide positions 2-78, a splicing acceptor (SA) site at nucleotide positions 79-129, a 3' mOTOF at nucleotide positions 130-3540, C2D at nucleotide positions 490-891, C2E at nucleotide positions 1996-2516, C2F at nucleotide positions 2749-3234, a WPRE at nucleotide positions 3595-4188, an ampicillin (AMP) resistance gene at nucleotide positions 5537-6537, a bovine growth hormone poly A-tail (bGH pA) at nucleotide positions 4212-4422, a phage-derived f1(+) origin of replication (ORI) at nucleotide positions 4674-5133, an origin of replication (ORI) at nucleotide positions 6787-7012.

In some embodiments of any of the compositions described herein, the vector is pAAV-SA-3'mOTOF-EWB (SEQ ID NO: 40), depicted in Figures 12, 20 and 54, or is a vector including a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 40. The pAAV-SA-3'mOTOF-EWB vector is 7548 bp in length and has a splicing acceptor (SA) site at nucleotide positions 2-52, a 3' mOTOF at nucleotide positions 53-3463, C2D at nucleotide positions 413-814, C2E at nucleotide positions 1919-2439, C2F at nucleotide positions 2672-3157, a WPRE at nucleotide positions 3518-4111, an ampicillin (AMP) resistance gene at nucleotide positions 5460-6460, a bovine growth hormone poly A-tail (bGH pA) at nucleotide positions 4135-4345, and a phage-derived fl(+) origin of replication (ORI) at nucleotide positions 4597-5056.

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-eGFP-P2A-5'mOTOF-SD (SEQ ID NO: 41), depicted in Figures 13, 18 and 53, or is a vector including a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 41. The pAAV-HBA-eGFP-P2A-5'mOTOF-SD vector is 7346 bp in length and has a Kozak sequence(*) at nucleotide positions 662-667, an enhanced green fluorescent protein (eGFP) sequence at nucleotide positions 668-1384, a P2A at nucleotide positions 1391-1456, a Kozak sequence at nucleotide positions 1463-1468, a 5' mOTOF sequence at nucleotide positions 1469-3988, a C2A at nucleotide positions 1469-1831, a C2B at nucleotide positions 2231-2599, a C2C at nucleotide positions 2720-3091, human OTOF exon 21 at nucleotide positions 3872-3988, a splicing donor (SD) site at nucleotide positions 3989-4070, an AMP resistance gene at nucleotide positions 5186-6186, a fl(+)ORI at nucleotide positions 4323-4782, an ORI at nucleotide positions 6436-6661, and a human cytomegalovirus (hCMV) enhancer at nucleotide positions 7277-272.

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-eGFP-P2A-5'mOTOF-SD-AK (SEQ ID NO: 42), depicted in Figures 14, 19 and 55, or is a vector including a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at

least 98%, at least 99%, or 100% identical to SEQ ID NO: 42. The pAAV-HBA-eGFP-P2A-5'mOTOF-SD-AK is 7423 bp in length and has a Kozak sequence(*) at nucleotide positions 662-667, an enhanced green fluorescent protein (eGFP) sequence at nucleotide positions 668-1384, a P2A at nucleotide positions 1391-1456, a Kozak sequence at

5 nucleotide positions 1463-1468, a 5' mOTOF sequence at nucleotide positions 1469-3988, a C2A at nucleotide positions 1469-1831, a C2B at nucleotide positions 2231-2599, a C2C at nucleotide positions 2720-3091, human OTOF exon 21 at nucleotide positions 3872-3988, a splicing donor (SD) site at nucleotide positions 3989-4070, an AK sequence at nucleotide positions 4071-4147, an AMP resistance gene at nucleotide

10 positions 5263-6263, a fl(+)ORI at nucleotide positions 4400-4859, an ORI at nucleotide positions 6513-6738, and a human cytomegalovirus (hCMV) enhancer at nucleotide positions 7354-272.

In some embodiments of any of the compositions described herein, the vector is pAKOS102 (SEQ ID NO: 43), or is a vector including a sequence that is at least 80%, at

15 least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 43. pAKOS102 is shown in Figure 21. The pAKOS102 vector is 7006 bp in length and has an AAV ITR sequence at nucleotide positions 1-130, a factor VIII stuffer sequence at nucleotide positions 145-1144, a human cytomegalovirus (hCMV) enhancer at nucleotide

20 positions 1145-1486, a human ACTB promoter at nucleotide positions 1487-1869, a Kozak sequence at nucleotide positions 1883-1888, a 5' hOTOF isoform 5 sequence at nucleotide positions 1889-4411, a SD intron sequence at nucleotide positions 4412-4493, an AAV2 ITR sequence at nucleotide positions 4519-4659, a fl(+)ORI at nucleotide positions 4734-5189, an KAN resistance gene at nucleotide positions 5469-6278, and an

25 ORI at nucleotide positions 6357-6945.

In some embodiments of any of the compositions described herein, the vector is pAKOS104 (SEQ ID NO: 45), or is a vector including a sequence that is at least 80%, at

least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 45.

30 pAKOS104 is shown in Figure 24. The pAKOS104 vector is 7083 bp in length and has an AAV ITR sequence at nucleotide positions 1-130, a factor VIII stuffer sequence at

nucleotide positions 145-1144, a human cytomegalovirus (hCMV) enhancer at nucleotide positions 1145-1486, a human ACTB promoter at nucleotide positions 1487-1869, a Kozak sequence at nucleotide positions 1883-1888, a 5' hOTOF isoform 5 sequence at nucleotide positions 1889-4411, a SD intron sequence at nucleotide positions 4412-4493, an AK sequence at nucleotide positions 4494-4570, an AAV2 ITR sequence at nucleotide positions 4596-4736, a fl(+)ORI at nucleotide positions 4811-5266, an KAN resistance gene at nucleotide positions 5546-6355, and an ORI at nucleotide positions 6434-7022.

In some embodiments of any of the compositions described herein, the vector is pAKOS105_GFP (SEQ ID NO: 48), depicted in Figure 29, or is a vector including a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 48. The pAKOS105_GFP vector is 7761 bp in length and has an AAV ITR sequence at nucleotide positions 1-130, an AK sequence at nucleotide positions 145-221, a SA site sequence at nucleotide positions 222-272, a 3' hOTOF isoform 5 sequence at nucleotide positions 273-3740, a T2A sequence at nucleotide positions 3750-3803, a turboGFP sequence at nucleotide positions 3804-4499, a bGH poly(A) signal at nucleotide positions 4509-4748, a factor VIII stuffer sequence at nucleotide positions 4749-5248, an AAV2 ITR sequence at nucleotide positions 5274-5414, a fl(+)ORI at nucleotide positions 5489-5944, an KAN resistance gene at nucleotide positions 6224-7033, and an ORI at nucleotide positions 7112-7700.

In some embodiments of any of the compositions described herein, the vector is pAKOS109 (SEQ ID NO: 52), or is a vector including a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 52.

pAKOS109 is shown in Figures 36. The pAKOS109 vector is 7056 bp in length and has an AAV ITR sequence at nucleotide positions 1-130, a human cytomegalovirus (hCMV) enhancer at nucleotide positions 145-524, a chicken β -actin promoter at nucleotide positions 527-802, a chimeric intron at nucleotide positions 803-1815, a Kozak sequence at nucleotide positions 1856-1861, a 5' hOTOF isoform 5 sequence at nucleotide positions 1862-4384, a SD intron sequence at nucleotide positions 4385-4466, an AK sequence at nucleotide positions 4467-4543, an AAV2 ITR sequence at nucleotide

positions 4569-4709, a fl(+)ORI at nucleotide positions 4784-5239, an KAN resistance gene at nucleotide positions 5519-6328, and an ORI at nucleotide positions 6407-6995.

In some embodiments of any of the compositions described herein, the vector is p109 (SEQ ID NO: 84) or is a vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 84. The p109 vector is 4,711 bp in length and is shown in Figure 38.

In some embodiments of any of the compositions described herein, the vector is p105 (SEQ ID NO: 85) or is a vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 85. The p105 vector is 4,664 bp in length and is shown in Figures 28 and 39.

In some embodiments of any of the compositions described herein, the vector is 105.WPRE, shown in Figure 40. The WPRE sequence present in the 105.WPRE vector is SEQ ID NO: 69.

In some embodiments of any of the compositions described herein, the vector is p108, shown in Figure 41. The p108 vector includes the FVIII stuffer sequence of SEQ ID NO: 58 and the CMV enhancer and promoter sequence of SEQ ID NO: 70.

In some embodiments of any of the compositions described herein, the vector is 10TOF18.CL1, shown in Figure 42. The 10TOF18.CL1 vector includes the CL1 degradation sequence of SEQ ID NO: 71.

In some embodiments of any of the compositions described herein, the vector is 19OTOF48, shown in Figure 43.

In some embodiments of any of the compositions described herein, the vector is 10TOF20.CL1, shown in Figure 44. The intron 21 splice donor sequence in 10TOF20,CL1 is SEQ ID NO: 72.

In some embodiments of any of the compositions described herein, the vector is 21OTOF48.WPRE, shown in Figure 45. The intron 21 splice acceptor sequence is SEQ ID NO: 73.

In some embodiments of any of the compositions described herein, the vector is 1OTOF21.CL1, shown in Figure 46. The intron 22 splice donor sequence is SEQ ID NO: 74.

In some embodiments of any of the compositions described herein, the vector is 22OTOF48.WPRE, shown in Figure 47. The intron 22 splice acceptor sequence is SEQ ID NO: 75.

In some embodiments of any of the compositions described herein, the vector is 105.pA.NTF3.CMVd, shown in Figure 48. The 105.pA.NTF3.CMVd vector includes the following sequences: SV40 polyA (SEQ ID NO: 76), HSV-TK poly(A) (SEQ ID NO: 77), sequence encoding human NTF3 (SEQ ID NO: 79), and CMVd (SEQ ID NO: 86).

In some embodiments, a vector can include a CMV enhancer and a chicken β -actin promoter, e.g., a sequence of SEQ ID NO: 61.

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-eGFP-P2A-5'mOTOF.SD (SEQ ID NO: 87), or is a vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 87. The pAAV-HBA-eGFP-P2A-5'mOTOF.SD vector is 4,472 bp in length and is shown in Figure 53. The pAAV-HBA-eGFP-P2A-5'mOTOF.SD vector includes an AAV ITR (SEQ ID NO: 59), a CMV enhancer (SEQ ID NO: 70), a sequence encoding a portion of 5'mOTOF (SEQ ID NO: 94), and a splice donor sequence (SEQ ID NO: 64).

In some embodiments of any of the compositions described herein, the vector is pAAV-SA-3'mOTOF.WPRE (SEQ ID NO: 88), or is a vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 88. The pAAV-SA-3'mOTOF.WPRE vector is 4,674 bp in length and is shown in Figure 54. The pAAV-SA-3'mOTOF.WPRE vector includes an AAV ITR (SEQ ID NO: 59), a splice acceptor sequence (SEQ ID NO: 65), a sequence encoding a portion 3'mOTOF (SEQ ID NO: 95), a WPRE sequence (SEQ ID NO: 69), a BGHpA sequence (SEQ ID NO: 68), and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-eGFP-P2A-5'mOTOF.SD-AK, shown in Figure 55, and is 4,549 bp in length. The pAAV-HBA-eGFP-P2A-5'mOTOF.SD-AK vector includes an AAV ITR (SEQ ID NO: 59), a CMV enhancer (SEQ ID NO: 70), a sequence encoding a portion
 5 5'mOTOF (SEQ ID NO: 94), a SD-intron sequence (SEQ ID NO: 72), an AK sequence (SEQ ID NO: 67), and an AAV ITR (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-AK-SA-3'mOTOF-WPRE, shown in Figure 56 and is 4,751 bp in length. The pAAV-AK-SA-3'mOTOF-WPRE vector includes an AAV ITR (SEQ ID NO: 59), an
 10 AK sequence (SEQ ID NO: 66), a sequence encoding a portion of 3' mOTOF (SEQ ID NO: 95), a WPRE sequence (SEQ ID NO: 69), a BGHpA sequence (SEQ ID NO: 68), and an AAV ITR (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-CMV-5'hOTOF-SD-AK (p108 plasmid), shown in Figure 57 and is 4,567 bp in
 15 length. The pAAV-CMV-5'hOTOF-SD-AK vector includes an AAV ITR (SEQ ID NO: 59), a FVII stuffer (SEQ ID NO: 90), a FVII stuffer (SEQ ID NO: 91), a CMV enhancer and promoter (SEQ ID NO: 70), a portion of a sequence encoding 5'hOTOF (SEQ ID NO: 62), a SD intron sequence (SEQ ID NO: 72), an AK sequence (SEQ ID NO: 67), and an AAV ITR sequence (SEQ ID NO: 60). In some embodiments, the vector that includes
 20 a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 90. In some embodiments, the vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to
 25 SEQ ID NO: 91.

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-5'hOTOF-SD-AP, shown in Figure 58, and is 4,540 bp in length. The pAAV-HBA-5'hOTOF-SD-AP includes an AAV ITR sequence (SEQ ID NO: 59), a CMV enhancer (SEQ ID NO: 70), a sequence encoding a portion 5'hOTOF (SEQ ID
 30 NO: 62), an AP rec sequence (SEQ ID NO: 89), and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-5'hOTOF-SD-AK, shown in Figure 59, and is 4,745 bp in length. The pAAV-HBA-5'hOTOF-SD-AK includes an AAV ITR sequence (SEQ ID NO: 59), a FVIII stuffer (4677-5173) sequence (SEQ ID NO: 90), a FVIII stuffer (3679-4177) sequence (SEQ ID: 91), a CMV enhancer (SEQ ID NO: 70), a sequence encoding a portion 5'hOTOF (SEQ ID NO: 62), and an AAV ITR sequence (SEQ ID NO: 60). In some embodiments, the vector includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 90, or a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 91.

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-5'hOTOFcodop-SD-AK, shown in Figure 60, and is 4,745 bp in length. The pAAV- CMV-5'hOTOF-SD-AK vector includes an AAV ITR sequence (SEQ ID NO: 59), a FVIII stuffer (4677-5173) sequence (SEQ ID NO: 90), a FVIII stuffer (3679-4177) sequence (SEQ ID: 91), a CMV enhancer (SEQ ID NO: 70), a sequence encoding a portion a 5'OTOF codop sequence (SEQ ID NO: 92), an AK sequence (SEQ ID NO: 67), and an AAV ITR sequence (SEQ ID NO: 60). In some embodiments, the vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 90. In some embodiments, the vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 91.

In some embodiments of any of the compositions described herein, the vector is pAAV-HBA-5'hOTOFcodop-SD, shown in Figure 61, and is 4,668 bp in length. The pAAV- HBA-5'hOTOFcodop-SD vector includes an AAV ITR sequence (SEQ ID NO: 59), a FVIII stuffer (4677-5173) sequence (SEQ ID NO: 90), a FVIII stuffer (3679-4177) sequence (SEQ ID: 91), a CMV enhancer (SEQ ID NO: 70), a sequence encoding a portion 5'OTOF codop sequence (SEQ ID NO: 92), and an AAV ITR sequence (SEQ ID

NO: 60). In some embodiments, the vector that includes a sequence that is at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 90. In some embodiments, the vector that includes a sequence that is at least 80%, at least 82%,
 5 at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100% identical to SEQ ID NO: 91.

In some embodiments of any of the compositions described herein, the vector is pAAV-CMV-5'hOTOF-SD, shown in Figure 62, and is 4,490 bp in length. The pAAV-CMV-5'hOTOF-SD vector includes an AAV ITR sequence (SEQ ID NO: 59), two FVIII
 10 stuffer sequences, a CMV enhancer and promoter (SEQ ID NO: 70), a sequence encoding a portion of a 5'OTOF codop sequence (SEQ ID NO: 92), a SD-intron sequence (SEQ ID NO: 64), and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-CMV-5'hOTOF-SD-AK, shown in Figure 63, and is 4,567 bp in length. The
 15 pAAV-CMV-5'hOTOF-SD-AK vector includes an AAV ITR sequence (SEQ ID NO: 59), two FVIII stuffer sequences, a CMV enhancer and promoter (SEQ ID NO: 70), a sequence encoding a portion of a 5'OTOF codop sequence (SEQ ID NO: 92), a splice donor (SD) intron sequence (SEQ ID NO: 64), an AK sequence (SEQ ID NO: 67), and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-CBA-5'hOTOF-SD-AK, shown in Figure 64, and is 4,711 bp in length. The
 20 pAAV-CBA-5'hOTOF-SD-AK vector includes an AAV ITR sequence (SEQ ID NO: 59), a CMV enhancer and chicken beta-actin promoter (SEQ ID NO: 61), a chimeric intronic sequence, a sequence encoding a portion of a 5'hOTOF codop sequence (SEQ ID
 25 NO: 92), an intronic sequence, an AK sequence (SEQ ID NO: 67), and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-CBA-5'hOTOF-SD, shown in Figure 65, and is 4,634 bp in length. The pAAV-CBA-5'hOTOF-SD vector includes an AAV ITR sequence (SEQ ID NO: 59), a CMV
 30 enhancer and beta-actin promoter (SEQ ID NO: 61), a chimeric intronic sequence, a

sequence encoding a portion of a 5'OTOF codop sequence (SEQ ID NO: 92), an intronic sequence, and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-SA-3'OTOF, shown in Figure 66, and is 4,587 bp in length. The pAAV-CBA-5'hOTOF-SD vector includes an AAV ITR sequence (SEQ ID NO: 59), a splice acceptor sequence (SEQ ID NO: 65), a sequence encoding a portion 3'OTOF sequence (SEQ ID NO: 63), a bGHpA sequence (SEQ ID NO: 68), a FVIII stuffer 9 sequence (SEQ ID NO: 57), and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-AP-SA-3'OTOF, shown in Figure 67, and is 4,959 bp in length. The pAAV-AP-SA-3'OTOF vector includes an AAV ITR sequence (SEQ ID NO: 59), an AP rec sequence (SEQ ID NO: 89), a splice acceptor sequence (SEQ ID NO: 65), a sequence encoding a portion of a 3'OTOF sequence (SEQ ID NO: 63), a bGHpolyA sequence (SEQ ID NO: 68), and an AAV ITR sequence (SEQ ID NO: 60).

In some embodiments of any of the compositions described herein, the vector is pAAV-AK-SA-3'OTOFcodop, shown in Figure 68, and is 4,664 bp in length. The pAAV-AK-SA-3'OTOFcodop vector includes an AAV ITR (SEQ ID NO: 59), an AK sequence (SEQ ID NO: 66), a sequence encoding a portion of a 3'OTOF codop sequence (SEQ ID NO: 93), a bGH polyA sequence (SEQ ID NO: 68), and an AAV ITR sequence (SEQ ID NO: 60).

The vectors provided herein can be of different sizes. The choice of vector that is used in any of the compositions, kits, and methods described herein may depend on the size of the vector.

In some embodiments, the vector(s) is a plasmid and can include a total length of up to about 1 kb, up to about 2 kb, up to about 3 kb, up to about 4 kb, up to about 5 kb, up to about 6 kb, up to about 7 kb, up to about 8kb, up to about 9 kb, up to about 10 kb, up to about 11 kb, up to about 12 kb, up to about 13 kb, up to about 14 kb, or up to about 15 kb. In some embodiments, the vector(s) is a plasmid and can have a total length in a range of about 1 kb to about 2 kb, about 1 kb to about 3 kb, about 1 kb to about 4 kb, about 1 kb to about 5 kb, about 1 kb to about 6 kb, about 1 kb to about 7 kb, about 1 kb to about 8 kb, about 1 kb to about 9 kb, about 1 kb to about 10 kb, about 1 kb to about 11

kb, about 1 kb to about 12 kb, about 1 kb to about 13 kb, about 1 kb to about 14 kb, about 1 kb to about 15 kb, about 2 kb to about 3 kb, about 2 kb to about 4 kb, about 2 kb to about 5 kb, about 2 kb to about 6 kb, about 2 kb to about 7 kb, about 2 kb to about 8 kb, about 2 kb to about 9 kb, about 2 kb to about 10 kb, about 2 kb to about 11 kb, about 2 kb to about 12 kb, about 2 kb to about 13 kb, about 2 kb to about 14 kb, about 2 kb to about 15 kb, about 3 kb to about 4 kb, about 3 kb to about 5 kb, about 3 kb to about 6 kb, about 3 kb to about 7 kb, about 3 kb to about 8 kb, about 3 kb to about 9 kb, about 3 kb to about 10 kb, about 3 kb to about 11 kb, about 3 kb to about 12 kb, about 3 kb to about 13 kb, about 3 kb to about 14 kb, about 3 kb to about 15 kb, about 4 kb to about 5 kb, about 4 kb to about 6 kb, about 4 kb to about 7 kb, about 4 kb to about 8 kb, about 4 kb to about 9 kb, about 4 kb to about 10 kb, about 4 kb to about 11 kb, about 4 kb to about 12 kb, about 4 kb to about 13 kb, about 4 kb to about 14 kb, about 4 kb to about 15 kb, about 5 kb to about 6 kb, about 5 kb to about 7 kb, about 5 kb to about 8 kb, about 5 kb to about 9 kb, about 5 kb to about 10 kb, about 5 kb to about 11 kb, about 5 kb to about 12 kb, about 5 kb to about 13 kb, about 5 kb to about 14 kb, or about 5 kb to about 15 kb.

In some embodiments, the vector(s) is a transposon (e.g., PiggyBac transposon) and can include greater than 200 kb. In some examples, the vector(s) is a transposon having a total length in the range of about 1 kb to about 10 kb, about 1 kb to about 20 kb, about 1 kb to about 30 kb, about 1 kb to about 40 kb, about 1 kb to about 50 kb, about 1 kb to about 60 kb, about 1 kb to about 70 kb, about 1 kb to about 80 kb, about 1 kb to about 90 kb, about 10 kb to about 20 kb, about 10 kb to about 30 kb, about 10 kb to about 40 kb, about 10 kb to about 50 kb, about 10 kb to about 60 kb, about 10 kb to about 70 kb, about 10 kb to about 90 kb, about 10 kb to about 100 kb, about 20 kb to about 30 kb, about 20 kb to about 40 kb, about 20 kb to about 50 kb, about 20 kb to about 60 kb, about 20 kb to about 70 kb, about 20 kb to about 80 kb, about 20 kb to about 90 kb, about 20 kb to about 100 kb, about 30 kb to about 40 kb, about 30 kb to about 50 kb, about 30 kb to about 60 kb, about 30 kb to about 70 kb, about 30 kb to about 80 kb, about 30 kb to about 90 kb, about 30 kb to about 100 kb, about 40 kb to about 50 kb, about 40 kb to about 60 kb, about 40 kb to about 70 kb, about 40 kb to about 80 kb, about 40 kb to about 90 kb, about 40 kb to about 100 kb, about 50 kb to about 60 kb, about 50 kb to about 70 kb, about 50 kb to about 80 kb, about 50 kb to about

90 kb, about 50 kb to about 100 kb, about 60 kb to about 70 kb, about 60 kb to about 80 kb, about 60 kb to about 90 kb, about 60 kb to about 100 kb, about 70 kb to about 80 kb, about 70 kb to about 90 kb, about 70 kb to about 100 kb, about 80 kb to about 90 kb, about 80 kb to about 100 kb, about 90 kb to about 100 kb, about 1 kb to about 100 kb, about 100 kb to about 200 kb, about 100 kb to about 300 kb, about 100 kb to about 400 kb, or about 100 kb to about 500 kb.

In some embodiments, the vector is a cosmid and can have a total length of up to 55 kb. In some examples, the vector is a cosmid and has a total number of nucleotides of about 1 kb to about 10 kb, about 1 kb to about 20 kb, about 1 kb to about 30 kb, about 1 kb to about 40 kb, about 1 kb to about 50 kb, about 1 kb to about 55 kb, about 10 kb to about 20 kb, about 10 kb to about 30 kb, about 10 kb to about 40 kb, about 10 kb to about 50 kb, about 10 kb to about 55 kb, about 15 kb to about 55 kb, about 15 kb to about 50 kb, about 15 kb to about 40 kb, about 15 kb to about 30 kb, about 15 kb to about 20 kb, about 20 kb to about 55 kb, about 20 kb to about 50 kb, about 20 kb to about 40 kb, about 20 kb to about 30 kb, about 25 kb to about 55 kb, about 25 kb to about 50 kb, about 25 kb to about 40 kb, about 25 kb to about 30 kb, about 30 kb to about 55 kb, about 30 kb to about 50 kb, about 30 kb to about 40 kb, about 35 kb to about 55 kb, about 40 kb to about 55 kb, about 40 kb to about 50 kb, or about 45 kb to about 55 kb.

In some embodiments, the vector(s) is an artificial chromosome and can have a total number of nucleotides of about 100 kb to about 2000 kb. In some embodiments, the artificial chromosome(s) is a human artificial chromosome (HAC) and can have a total number of nucleotides in the range of about 1 kb to about 10 kb, 1 kb to about 20 kb, about 1 kb to about 30 kb, about 1 kb to about 40 kb, about 1 kb to about 50 kb, about 1 kb to about 60 kb, about 10 kb to about 20 kb, about 10 kb to about 30 kb, about 10 kb to about 40 kb, about 10 kb to about 50 kb, about 10 kb to about 60 kb, about 20 kb to about 30 kb, about 20 kb to about 40 kb, about 20 kb to about 50 kb, about 20 kb to about 60 kb, about 30 kb to about 40 kb, about 30 kb to about 50 kb, about 30 kb to about 60 kb, about 40 kb to about 50 kb, about 40 kb to about 60 kb, or about 50 kb to about 60 kb.

In some embodiments, the artificial chromosome(s) is a yeast artificial chromosome (YAC) and can have a total number of nucleotides up to 1000 kb. In some embodiments, the artificial chromosome(s) is a YAC having a total number of nucleotides in the range of about 100 kb to about 1,000 kb, about 100 kb to about 900 kb, about 100 kb to about 800 kb, about 100 kb to about 700 kb, about 100 kb to about 600 kb, about 100 kb to about 500 kb, about 100 kb to about 400 kb, about 100 kb to about 300 kb, about 100 kb to about 200 kb, about 200 kb to about 1,000 kb, about 200 kb to about 900 kb, about 200 kb to about 800 kb, about 200 kb to about 700 kb, about 200 kb to about 600 kb, about 200 kb to about 500 kb, about 200 kb to about 400 kb, about 200 kb to about 300 kb, about 300 kb to about 1,000 kb, about 300 kb to about 900 kb, about 300 kb to about 800 kb, about 300 kb to about 700 kb, about 300 kb to about 600 kb, about 300 kb to about 500 kb, about 300 kb to about 400 kb, about 400 kb to about 1,000 kb, about 400 kb to about 900 kb, about 400 kb to about 800 kb, about 400 kb to about 700 kb, about 400 kb to about 600 kb, about 400 kb to about 500 kb, about 500 kb to about 1,000 kb, about 500 kb to about 900 kb, about 500 kb to about 800 kb, about 500 kb to about 700 kb, about 500 kb to about 600 kb, about 600 kb to about 1,000 kb, about 600 kb to about 900 kb, about 600 kb to about 800 kb, about 600 kb to about 700 kb, about 700 kb to about 1,000 kb, about 700 kb to about 900 kb, about 700 kb to about 800 kb, about 800 kb to about 1,000 kb, about 800 kb to about 900 kb, or about 900 kb to about 1,000 kb.

In some embodiments, the artificial chromosome(s) is a bacterial artificial chromosome (BAC) and can have a total number of nucleotides of up to 750 kb. In some embodiments, the artificial chromosome(s) is a BAC and can have a total number of nucleotides in the range of about 100 kb to about 750 kb, about 100 kb to about 700 kb, about 100 kb to about 600 kb, about 100 kb to about 500 kb, about 100 kb to about 400 kb, about 100 kb to about 300 kb, about 100 kb to about 200 kb, about 150 kb to about 750 kb, about 150 kb to about 700 kb, about 150 kb to about 600 kb, about 150 kb to about 500 kb, about 150 kb to about 400 kb, about 150 kb to about 300 kb, about 150 kb to about 200 kb, about 200 kb to about 750 kb, about 200 kb to about 700 kb, about 200 kb to about 600 kb, about 200 kb to about 500 kb, about 200 kb to about 400 kb, about 200 kb to about 300 kb, about 250 kb to about 750 kb, about 250 kb to

about 700 kb, about 250 kb to about 600 kb, about 250 kb to about 500 kb, about 250 kb to about 400 kb, about 250 kb to about 300 kb, about 300 kb to about 750 kb, about 300 kb to about 700 kb, about 300 kb to about 600 kb, about 300 kb to about 500 kb, about 300 kb to about 400 kb, about 350 kb to about 750 kb, about 350 kb to about 700 kb, about 350 kb to about 600 kb, about 350 kb to about 500 kb, about 350 kb to about 400 kb, about 400 kb to about 750 kb, about 400 kb to about 700 kb, about 450 kb to about 600 kb, about 450 kb to about 500 kb, about 500 kb to about 750 kb, about 500 kb to about 700 kb, about 500 kb to about 600 kb, about 550 kb to about 750 kb, about 550 kb to about 700 kb, about 550 kb to about 600 kb, about 600 kb to about 750 kb, about 600 kb to about 700 kb, or about 650 kb to about 750 kb.

In some embodiments, the artificial chromosome(s) is a P1-derived artificial chromosome (PAC) and can have a total number of nucleotides of up to 300 kb. In some embodiments, the P1-derived artificial chromosome(s) can have a total number of nucleotides in the range of about 100 kb to about 300 kb, about 100 kb to about 200 kb, or about 200 kb to about 300 kb.

In some embodiments, the vector(s) is a viral vector and can have a total number of nucleotides of up to 10 kb. In some embodiments, the viral vector(s) can have a total number of nucleotides in the range of about 1 kb to about 2 kb, 1 kb to about 3 kb, about 1 kb to about 4 kb, about 1 kb to about 5 kb, about 1 kb to about 6 kb, about 1 kb to about 7 kb, about 1 kb to about 8 kb, about 1 kb to about 9 kb, about 1 kb to about 10 kb, about 2 kb to about 3 kb, about 2 kb to about 4 kb, about 2 kb to about 5 kb, about 2 kb to about 6 kb, about 2 kb to about 7 kb, about 2 kb to about 8 kb, about 2 kb to about 9 kb, about 2 kb to about 10 kb, about 3 kb to about 4 kb, about 3 kb to about 5 kb, about 3 kb to about 6 kb, about 3 kb to about 7 kb, about 3 kb to about 8 kb, about 3 kb to about 9 kb, about 3 kb to about 10 kb, about 4 kb to about 5 kb, about 4 kb to about 6 kb, about 4 kb to about 7 kb, about 4 kb to about 8 kb, about 4 kb to about 9 kb, about 4 kb to about 10 kb, about 5 kb to about 6 kb, about 5 kb to about 7 kb, about 5 kb to about 8 kb, about 5 kb to about 9 kb, about 5 kb to about 10 kb, about 6 kb to about 7 kb, about 6 kb to about 8 kb, about 6 kb to about 9 kb, about 6 kb to about 10 kb, about 7 kb to about 8 kb, about 7 kb to about 9 kb, about 7 kb to about 10 kb, about 8 kb to about 9 kb, about 8 kb to about 10 kb, or about 9 kb to about 10 kb.

In some embodiments, the vector(s) is a lentivirus and can have a total number of nucleotides of up to 8 kb. In some examples, the lentivirus(es) can have a total number of nucleotides of about 1 kb to about 2 kb, about 1 kb to about 3 kb, about 1 kb to about 4 kb, about 1 kb to about 5 kb, about 1 kb to about 6 kb, about 1 kb to about 7 kb, about 1 kb to about 8 kb, about 2 kb to about 3 kb, about 2 kb to about 4 kb, about 2 kb to about 5 kb, about 2 kb to about 6 kb, about 2 kb to about 7 kb, about 2 kb to about 8 kb, about 3 kb to about 4 kb, about 3 kb to about 5 kb, about 3 kb to about 6 kb, about 3 kb to about 7 kb, about 3 kb to about 8 kb, about 4 kb to about 5 kb, about 4 kb to about 6 kb, about 4 kb to about 7 kb, about 4 kb to about 8 kb, about 5 kb to about 6 kb, about 5 kb to about 7 kb, about 5 kb to about 8 kb, about 6 kb to about 8 kb, about 6 kb to about 7 kb, or about 7 kb to about 8 kb.

In some embodiments, the vector(s) is an adenovirus and can have a total number of nucleotides of up to 8 kb. In some embodiments, the adenovirus(es) can have a total number of nucleotides in the range of about 1 kb to about 2 kb, about 1 kb to about 3 kb, about 1 kb to about 4 kb, about 1 kb to about 5 kb, about 1 kb to about 6 kb, about 1 kb to about 7 kb, about 1 kb to about 8 kb, about 2 kb to about 3 kb, about 2 kb to about 4 kb, about 2 kb to about 5 kb, about 2 kb to about 6 kb, about 2 kb to about 7 kb, about 2 kb to about 8 kb, about 3 kb to about 4 kb, about 3 kb to about 5 kb, about 3 kb to about 6 kb, about 3 kb to about 7 kb, about 3 kb to about 8 kb, about 4 kb to about 5 kb, about 4 kb to about 6 kb, about 4 kb to about 7 kb, about 4 kb to about 8 kb, about 5 kb to about 6 kb, about 5 kb to about 7 kb, about 5 kb to about 8 kb, about 6 kb to about 7 kb, about 6 kb to about 8 kb, or about 7 kb to about 8 kb.

In some embodiments, the vector(s) is an adeno-associated virus (AAV vector) and can include a total number of nucleotides of up to 5 kb. In some embodiments, the AAV vector(s) can include a total number of nucleotides in the range of about 1 kb to about 2 kb, about 1 kb to about 3 kb, about 1 kb to about 4 kb, about 1 kb to about 5 kb, about 2 kb to about 3 kb, about 2 kb to about 4 kb, about 2 kb to about 5 kb, about 3 kb to about 4 kb, about 3 kb to about 5 kb, or about 4 kb to about 5 kb.

In some embodiments, the vector(s) is a Gateway® vector and can include a total number of nucleotides of up to 5 kb. In some embodiments, each Gateway® vector(s) includes a total number of nucleotides in the range of about 1 kb to about 2 kb, about 1 kb

to about 3 kb, about 1 kb to about 4 kb, about 1 kb to about 5 kb, about 2 kb to about 3 kb, about 2 kb to about 4 kb, about 2 kb to about 5 kb, about 3 kb to about 4 kb, about 3 kb to about 5 kb, or about 4 kb to about 5 kb.

In some embodiments of any of the compositions, kits, and methods provided
5 herein, the at least two different vectors can be substantially the same type of vector and may differ in size. In some embodiments, the at least two different vectors can be different types of vector, and may have substantially the same size or have different sizes.

In some embodiments, any of the at least two vectors can have a total number of
nucleotides in the range of about 500 nucleotides to about 10,000 nucleotides, about 500
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A variety of different methods known in the art can be used to introduce any of the vectors disclosed herein into a mammalian cell (e.g., a cochlear inner hair cell). Non-limiting examples of methods for introducing nucleic acid into a mammalian cell include: lipofection, transfection (e.g., calcium phosphate transfection, transfection using highly branched organic compounds, transfection using cationic polymers, dendrimer-based transfection, optical transfection, particle-based transfection (e.g., nanoparticle transfection), or transfection using liposomes (e.g., cationic liposomes)), microinjection, electroporation, cell squeezing, sonoporation, protoplast fusion, impalefection, hydrodynamic delivery, gene gun, magnetofection, viral transfection, and nucleofection.

Skilled practitioners will appreciate that any of the vectors described herein can be introduced into a mammalian cell by, for example, lipofection.

Various molecular biology techniques that can be used to introduce a mutation(s) and/or a deletion(s) into an endogenous gene are also known in the art. Non-limiting examples of such techniques include site-directed mutagenesis, CRISPR (e.g., CRISPR/Cas9-induced knock-in mutations and CRISPR/Cas9-induced knock-out mutations), and TALENs. These methods can be used to correct the sequence of a defective endogenous gene present in a chromosome of a target cell.

Any of the vectors described herein can further include a control sequence, e.g., a control sequence selected from the group of a transcription initiation sequence, a transcription termination sequence, a promoter sequence, an enhancer sequence, an RNA splicing sequence, a polyadenylation (polyA) sequence, and a Kozak consensus sequence. Non-limiting examples of these control sequences are described herein. In some embodiments, a promoter can be a native promoter, a constitutive promoter, an inducible promoter, and/or a tissue-specific promoter.

Promoters

Non-limiting examples of promoters are described herein. Additional examples of promoters are known in the art.

In some embodiments, a vector encoding an N-terminal portion of an otoferlin protein (e.g., a human otoferlin protein) can include a promoter and/or an enhancer. The vector encoding the N-terminal portion of the otoferlin protein can include any of the promoters and/or enhancers described herein or known in the art.

In some embodiments, the promoter is an inducible promoter, a constitutive promoter, a mammalian cell promoter, a viral promoter, a chimeric promoter, an engineered promoter, a tissue-specific promoter, or any other type of promoter known in the art. In some embodiments, the promoter is a RNA polymerase II promoter, such as a mammalian RNA polymerase II promoter. In some embodiments, the promoter is a RNA polymerase III promoter, including, but not limited to, a H1 promoter, a human U6 promoter, a mouse U6 promoter, or a swine U6 promoter. The promoter will generally be one that is able to promote transcription in cochlear cells such as hair cells. In some examples, the promoter is a cochlea-specific promoter or a cochlea-oriented promoter.

A variety of promoters are known in the art that can be used herein. Non-limiting examples of promoters that can be used herein include: human elongation factor 1 α -subunit (EF1a) (Liu et al. (2007) Exp. Mol. Med. 39(2): 170-175; Accession No. J04617.1; Gill et al., *Gene Ther.* 8(20):1539-1546, 2001; Xu et al., Human Gene Ther. 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332; Ikeda et al., *Gene Ther.* 9:932-938, 2002; Gilham et al., *J. Gene Med.* 12(2):129-136, 2010), cytomegalovirus (Xu et al., Human Gene Ther. 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332; Gray et al.,

Human Gene Ther. 22:1143-1153, 2011), human immediate-early cytomegalovirus (CMV) (US Patent No. 5,168,062, Liu et al. (2007) *Exp. Mol. Med.* 39(2): 170-175; Accession No. X17403.1 or KY490085.1), human ubiquitin C (UBC) (Gill et al., *Gene Ther.* 8(20):1539-1546, 2001; Qin et al., *PLoS One* 5(5):e10611, 2010), mouse

5 phosphoglycerate kinase 1, polyoma adenovirus, simian virus 40 (SV40), β -globin, β -actin, α -fetoprotein, γ -globin, β -interferon, γ -glutamyl transferase, mouse mammary tumor virus (MMTV), Rous sarcoma virus, rat insulin, glyceraldehyde-3-phosphate dehydrogenase, metallothionein II (MT II), amylase, cathepsin, MI muscarinic receptor, retroviral LTR (e.g. human T-cell leukemia virus HTLV), AAV ITR, interleukin-2,

10 collagenase, platelet-derived growth factor, adenovirus 5 E2, stromelysin, murine MX gene, glucose regulated proteins (GRP78 and GRP94), α -2-macroglobulin, vimentin, MHC class I gene H-2 κ b, HSP70, proliferin, tumor necrosis factor, thyroid stimulating hormone α gene, immunoglobulin light chain, T-cell receptor, HLA DQ α and DQ β , interleukin-2 receptor, MHC class II, MHC class II HLA-DR α , muscle creatine kinase,

15 prealbumin (transthyretin), elastase I, albumin gene, c-fos, c-HA-ras, neural cell adhesion molecule (NCAM), H2B (TH2B) histone, rat growth hormone, human serum amyloid (SAA), troponin I (TN I), duchenne muscular dystrophy, human immunodeficiency virus, Gibbon Ape Leukemia Virus (GALV) promoters, promoter of HNRPA2B1-CBX1 (UCOE) (Powell and Gray (2015) *Discov. Med.* 19(102): 49-57; Antoniou et al., *Human*

20 *Gene Ther.* 24(4):363-374, 2013), β -glucuronidase (GUSB) (Husain et al., *Gene Ther.* 16:927-932, 2009), chicken β -actin (CBA) (Liu et al. (2007) *Exp. Mol. Med.* 39(2): 170-175; Stone et al. (2005) *Mol. Ther.* 11(6): 843-848; Klein et al., *Exp. Neurol.* 176(1):66-74, 2002; Ohlfest et al., *Blood* 105:2691-2698, 2005; Gray et al., *Human Gene Ther.* 22:1143-1153, 2011), a human β -actin promoter (HBA) (Accession No. Y00474.1),

25 murine myosin VIIA (musMyo7) (Boeda et al. (2001) *Hum. Mol. Genet.* 10(15): 1581-1589; Accession No. AF384559.1), human myosin VIIA (hsMyo7) (Boeda et al. (2001) *Hum. Mol. Genet.* 10(15): 1581-1589; Accession No. NG_009086.1), murine poly(ADP-ribose) polymerase 2 (musPARP2) (Ame et al. (2001) *J. Biol. Chem.* 276(14): 11092-11099; Accession No. AF191547.1), human poly(ADP-ribose) polymerase 2 (hsPARP2)

30 (Ame et al. (2001) *J. Biol. Chem.* 276(14): 11092-11099; Accession No. X16612.1 or AF479321.1), acetylcholine receptor epsilon-subunit (ACh ϵ) (Duclert et al. (1993) *PNAS*

90(7): 3043-3047; Accession No. S58221.1 or CR933736.12), Rous sarcoma virus (RSV) (Liu et al. (2007) *Exp. Mol. Med.* 39(2): 170-175; Accession No. M77786.1), (GFAP) (Liu et al. (2007) *Exp. Mol. Med.* 39(2): 170-175; Stone et al. (2005) *Mol. Ther.* 11(6): 843-848; Accession No. NG_008401.1 or M67446.1), hAAT (Van Linthout et al.,
 5 *Human Gene Ther.* 13(7):829-840, 2002; Cunningham et al., *Mol. Ther.* 16(6):1081-1088, 2008), and a CBA hybrid (CBh) (Gray et al. (2011) *Hum. Gen. Therapy* 22: 1143-1153; Accession No. KF926476.1 or KC152483.1). Additional examples of promoters are known in the art. See, e.g., Lodish, *Molecular Cell Biology*, Freeman and Company, New York 2007. In some embodiments, the promoter is the CMV immediate early
 10 promoter. In some embodiments, the promoter is a CAG promoter or a CAG/CBA promoter.

The term “operably linked” or “transcriptional control” refers to functional linkage between a regulatory sequence and a heterologous nucleic acid sequence resulting in expression of the latter. For example, a first nucleic acid sequence is operably
 15 linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences can be contiguous with each other and, e.g., where necessary to join two protein coding regions, are in the
 20 same reading frame.

The term “constitutive” promoter refers to a nucleotide sequence that, when operably linked with a nucleic acid encoding a protein (e.g., an otoferlin protein), causes RNA to be transcribed from the nucleic acid in a mammalian cell under most or all physiological conditions.

25 The term “constitutive” promoter refers to 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, without limitation, the retroviral
 30 Rous sarcoma virus (RSV) LTR promoter, the cytomegalovirus (CMV) promoter (see, e.g., Boshart et al. *Cell* 41:521-530, 1985), the SV40 promoter, the dihydrofolate

reductase promoter, the beta-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1-alpha promoter (Invitrogen).

The term "inducible" promoter refers to 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.

Inducible promoters allow regulation of gene expression and can be regulated by exogenously supplied compounds, environmental factors such as temperature, or the presence of a specific physiological state, e.g., acute phase, a particular differentiation state of the cell, or in replicating cells only. Inducible promoters and inducible systems are available from a variety of commercial sources, including, without limitation, Invitrogen, Clontech, and Ariad. Additional examples of inducible promoters are known in the art.

Examples of inducible promoters regulated by exogenously supplied compounds include the zinc-inducible sheep metallothioneine (MT) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7 polymerase promoter system (WO 98/10088); the ecdysone insect promoter (No et al. *Proc. Natl. Acad. Sci. U.S.A.* 93:3346-3351, 1996), the tetracycline-repressible system (Gossen et al. *Proc. Natl. Acad. Sci. U.S.A.* 89:5547-5551, 1992), the tetracycline-inducible system (Gossen et al. *Science* 268:1766-1769, 1995, see also Harvey et al. *Curr. Opin. Chem. Biol.* 2:512-518, 1998), the RU486-inducible system (Wang et al. *Nat. Biotech.* 15:239-243, 1997) and Wang et al. *Gene Ther.* 4:432-441, 1997), and the rapamycin-inducible system (Magari et al. *J. Clin. Invest.* 100:2865-2872, 1997).

The term "tissue-specific" promoter refers to a promoter that is active only in certain specific cell types and/or tissues (e.g., transcription of a specific gene occurs only within cells expressing transcription regulatory proteins that bind to the tissue-specific promoter).

The term "tissue-specific" promoter refers to a nucleotide sequence which, when operably linked with a polynucleotide encodes or specified by a gene, 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.

The term “regulatory sequence” refers to a nucleic acid sequence which is regulates expression of a gene product operably linked to the regulatory sequence. In some instances, this sequence may be an enhancer sequence and other regulatory elements which regulate expression of the gene product.

5 In some embodiments, the regulatory sequences impart tissue-specific gene expression capabilities. In some cases, the tissue-specific regulatory sequences bind tissue-specific transcription factors that induce transcription in a tissue-specific manner.

In some embodiments, the tissue-specific promoter is a cochlea-specific promoter. In some embodiments, the tissue-specific promoter is a cochlear hair cell-specific
10 promoter. Non-limiting examples of cochlear hair cell-specific promoters include but are not limited to: a ATOH1 promoter, a POU4F3 promoter, a LHX3 promoter, a MYO7A promoter, a MYO6 promoter, a α 9ACHR promoter, and a α 10ACHR promoter.

Enhancers and 5' Cap

15 In some instances, a vector can include a promoter sequence and/or an enhancer sequence. The term “enhancer” refers to a nucleotide sequence that can increase the level of transcription of a nucleic acid encoding a protein of interest (e.g., an otoferlin protein). Enhancer sequences (50-1500 basepairs in length) generally increase the level of transcription by providing additional binding sites for transcription-associated proteins
20 (e.g., transcription factors). In some embodiments, an enhancer sequence is found within an intronic sequence. Unlike promoter sequences, enhancer sequences can act at much larger distance away from the transcription start site (e.g., as compared to a promoter). Non-limiting examples of enhancers include a RSV enhancer, a CMV enhancer, and a SV40 enhancer. An example of a CMV enhancer is described in, e.g., Boshart et al., Cell
25 41(2):521-530, 1985.

As used herein, a 5' cap (also termed an RNA cap, an RNA 7-methylguanosine cap or an RNA m.sup.7G cap) is a modified guanine nucleotide that has been added to the “front” or 5' end of a eukaryotic messenger RNA shortly after the start of transcription. The 5' cap consists of a terminal group which is linked to the first
30 transcribed nucleotide. Its presence is critical for recognition by the ribosome and protection from RNases. Cap addition is coupled to transcription, and occurs co-

transcriptionally, such that each influences the other. Shortly after the start of transcription, the 5' end of the mRNA being synthesized is bound by a cap-synthesizing complex associated with RNA polymerase. This enzymatic complex catalyzes the chemical reactions that are required for mRNA capping. Synthesis proceeds as a multi-
5 step biochemical reaction. The capping moiety can be modified to modulate functionality of mRNA such as its stability or efficiency of translation.

Poly(A) Sequences

In some embodiments, any of the vectors provided herein can include a poly(A)
10 sequence. Most nascent eukaryotic mRNAs possess a poly(A) tail at their 3' end which is added during a complex process that includes cleavage of the primary transcript and a coupled polyadenylation reaction (see, e.g., Proudfoot et al., *Cell* 108:501-512, 2002). The poly(A) tail confers mRNA stability and transferability (Molecular Biology of the Cell, Third Edition by B. Alberts et al., Garland Publishing, 1994). In some
15 embodiments, the poly(A) sequence is positioned 3' to the nucleic acid sequence encoding the C-terminus of the otoferlin protein.

As used herein, "polyadenylation" refers to the covalent linkage of a polyadenylyl moiety, or its modified variant, to a messenger RNA molecule. In eukaryotic organisms, most messenger RNA (mRNA) molecules are polyadenylated at the 3' end. The 3'
20 poly(A) tail is a long sequence of adenine nucleotides (often several hundred) added to the pre-mRNA through the action of an enzyme, polyadenylate polymerase. In higher eukaryotes, the poly(A) tail is added onto transcripts that contain a specific sequence, the polyadenylation signal. The poly(A) tail and the protein bound to it aid in protecting mRNA from degradation by exonucleases. Polyadenylation is also important for
25 transcription termination, export of the mRNA from the nucleus, and translation. Polyadenylation occurs in the nucleus immediately after transcription of DNA into RNA, but additionally can also occur later in the cytoplasm. After transcription has been terminated, the mRNA chain is cleaved through the action of an endonuclease complex associated with RNA polymerase. The cleavage site is usually characterized by the
30 presence of the base sequence AAUAAA near the cleavage site. After the mRNA has been cleaved, adenosine residues are added to the free 3' end at the cleavage site.

As used herein, a “poly(A) signal sequence” is a sequence that triggers the endonuclease cleavage of an mRNA and the additional of a series of adenosines to the 3' end of the cleaved mRNA.

As used herein, a “poly(A)” is a series of adenosines attached by polyadenylation to the mRNA. In the preferred embodiment of a construct for transient expression, the polyA is between 50 and 5000, preferably greater than 64, more preferably greater than 100, most preferably greater than 300 or 400. Poly(A) sequences can be modified chemically or enzymatically to modulate mRNA functionality such as localization, stability or efficiency of translation.

There are several poly(A) signal sequences that can be used, including those derived from bovine growth hormone (bgh) (Woychik et al., *Proc. Natl. Acad. Sci. U.S.A.* 81(13):3944-3948, 1984; U.S. Patent No. 5,122,458; Yew et al., *Human Gene Ther.* 8(5):575-584, 1997; Xu et al., *Human Gene Ther.* 12(5):563-573, 2001; Xu et al., *Gene Ther.* 8:1323-1332, 2001; Wu et al., *Mol. Ther.* 16(2):280-289, 2008; Gray et al., *Human Gene Ther.* 22:1143-1153, 2011; Choi et al., *Mol. Brain* 7:17, 2014), mouse- β -globin, mouse- α -globin (Orkin et al., *EMBO J.* 4(2):453-456, 1985; Thein et al., *Blood* 71(2):313-319, 1988), human collagen, polyoma virus (Batt et al., *Mol. Cell Biol.* 15(9):4783-4790, 1995), the Herpes simplex virus thymidine kinase gene (HSV TK), IgG heavy-chain gene polyadenylation signal (US 2006/0040354), human growth hormone (hGH) (Szymanski et al., *Mol. Therapy* 15(7):1340-1347, 2007; Ostegaard et al., *Proc. Natl. Acad. Sci. U.S.A.* 102(8):2952-2957, 2005), synthetic polyA (Levitt et al., *Genes Dev.* 3(7):1019-1025, 1989; Yew et al., *Human Gene Ther.* 8(5):575-584, 1997; Ostegaard et al., *Proc. Natl. Acad. Sci. U.S.A.* 102(8):2952-2957, 2005; Choi et al., *Mol. Brain* 7:17, 2014), HIV-1 upstream poly(A) enhancer (Schambach et al., *Mol. Ther.* 15(6):1167-1173, 2007), adenovirus (L3) upstream poly(A) enhancer (Schambach et al., *Mol. Ther.* 15(6):1167-1173, 2007), hTHGB upstream poly(A) enhancer (Schambach et al., *Mol. Ther.* 15(6):1167-1173, 2007), hC2 upstream poly(A) enhancer (Schambach et al., *Mol. Ther.* 15(6):1167-1173, 2007), the group consisting of SV40 poly(A) signal sequence, such as the SV40 late and early poly(A) signal sequence (Schek et al., *Mol. Cell Biol.* 12(12):5386-5393, 1992; Choi et al., *Mol. Brain* 7:17, 2014; Schambach et al.,

Mol. Ther. 15(6):1167-1173, 2007). A non-limiting example of a poly(A) signal sequence is SEQ ID NO: 68, 76, or 77.

The poly(A) signal sequence can be the sequence AATAAA. The AATAAA sequence may be substituted with other hexanucleotide sequences with homology to AATAAA which are capable of signaling polyadenylation, including ATTAAA, AGTAAA, CATAAA, TATAAA, GATAAA, ACTAAA, AATATA, AAGAAA, AATAAT, AAAAAA, AATGAA, AATCAA, AACAAA, AATCAA, AATAAC, AATAGA, AATTAA, or AATAAG (see, e.g., WO 06/12414).

In some embodiments, the poly(A) signal sequence can be a synthetic polyadenylation site (see, e.g., the pCI-neo expression vector of Promega which is based on Levitt et al, *Genes Dev.* 3(7):1019-1025, 1989). In some embodiments, the poly(A) signal sequence is the polyadenylation signal of soluble neuropilin-1 (sNRP) (AAATAAAATACGAAATG) (see, e.g., WO 05/073384). Additional examples of poly(A) signal sequences are known in the art.

In some embodiments, any of the vectors provided herein can include a woodchuck hepatitis virus posttranscriptional regulatory element (WPRE), e.g., SEQ ID NO: 69.

Internal Ribosome Entry Site (IRES)

In some embodiments, a vector encoding the C-terminus of the otoferlin protein can include a polynucleotide internal ribosome entry site (IRES). An IRES sequence is used to produce more than one polypeptide from a single gene transcript. An IRES forms a complex secondary structure that allows translation initiation to occur from any position with an mRNA immediately downstream from where the IRES is located (see, e.g., Pelletier and Sonenberg, *Mol. Cell. Biol.* 8(3):1103-1112, 1988).

There are several IRES sequences known to those skilled in the art, including those from, e.g., foot and mouth disease virus (FMDV), encephalomyocarditis virus (EMCV), human rhinovirus (HRV), cricket paralysis virus, human immunodeficiency virus (HIV), hepatitis A virus (HAV), hepatitis C virus (HCV), and poliovirus (PV). See e.g., Alberts, *Molecular Biology of the Cell*, Garland Science, 2002; and Hellen et al., *Genes Dev.* 15(13):1593-612, 2001.

In some embodiments, the IRES sequence that is incorporated into the vector that encodes the C-terminus of an otoferlin protein is the foot and mouth disease virus (FMDV). The Foot and Mouth Disease Virus 2A sequence is a small peptide (approximately 18 amino acids in length) that has been shown to mediate the cleavage of polyproteins (Ryan, M D et al., *EMBO* 4:928-933, 1994; Mattion et al., *J. Virology* 70:8124-8127, 1996; Furler et al., *Gene Therapy* 8:864-873, 2001; and Halpin et al., *Plant Journal* 4:453-459, 1999). The cleavage activity of the 2A sequence has previously been demonstrated in artificial systems including plasmids and gene therapy vectors (AAV and retroviruses) (Ryan et al., *EMBO* 4:928-933, 1994; Mattion et al., *J. Virology* 70:8124-8127, 1996; Furler et al., *Gene Therapy* 8:864-873, 2001; and Halpin et al., *Plant Journal* 4:453-459, 1999; de Felipe et al., *Gene Therapy* 6:198-208, 1999; de Felipe et al., *Human Gene Therapy* 11:1921-1931, 2000; and Klump et al., *Gene Therapy* 8:811-817, 2001).

15 **Reporter Sequences**

Any of the vectors provided herein can optionally include a sequence encoding a reporter protein ("a reporter sequence"). Non-limiting examples of reporter sequences are described herein. Additional examples of reporter sequences are known in the art. In some embodiments, the reporter sequence can be used to verify the tissue-specific targeting capabilities and tissue-specific promoter regulatory activity of any of the vectors described herein.

NTF3

Any of the vectors provided herein can optionally include a sequence encoding a neurotrophin-3 (NTF3) protein. In some embodiments, a NTF3 protein can have a sequence that is at least 70% identical, at least 72% identical, at least 74% identical, at least 76% identical, at least 78% identical, at least 80% identical, at least 82% identical, at least 84% identical, at least 86% identical, at least 88% identical, at least 90% identical, at least 92% identical, at least 94% identical, at least 96% identical, at least 98% identical, at least 99% identical, or 100% identical to SEQ ID NO: 78. In some embodiments, a NTF3 protein can include a sequence that is identical to SEQ ID NO: 78,

except that it includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions and/or deletions.

In some embodiments, a NTF3 protein can be encoded by a sequence that is at least 70% identical, at least 72% identical, at least 74% identical, at least 76% identical, at least 78% identical, at least 80% identical, at least 82% identical, at least 84% identical, at least 86% identical, at least 88% identical, at least 90% identical, at least 92% identical, at least 94% identical, at least 96% identical, at least 98% identical, at least 99% identical, or 100% identical to SEQ ID NO: 79 or 80.

One skilled in the art would appreciate that mutation of amino acids that are not conserved between the same protein from different species is less likely to have an effect on the function of a protein and therefore, these amino acids should be selected for mutation. Amino acids that are conserved between the same protein from different species should not be mutated, as these mutations are more likely to result in a change in the function of the protein. Non-limiting examples of neutrophin-3 from other mammalian species are shown below.

Cow Neurotrophin-3 (SEQ ID NO: 81)

Rat Neurotrophin-3 (SEQ ID NO: 82)

Pig Neurotrophin-3 (SEQ ID NO: 83)

Flanking Regions Untranslated Regions (UTRs)

In some embodiments, any of the vectors described herein (e.g., any of the at least two different vectors) can include an untranslated region. In some embodiments, a vector can include a 5' UTR or a 3' UTR.

Untranslated regions (UTRs) of a gene are transcribed but not translated. The 5' UTR starts at the transcription start site and continues to the start codon but does not include the start codon. The 3' UTR starts immediately following the stop codon and continues until the transcriptional termination signal. There is growing body of evidence about the regulatory roles played by the UTRs in terms of stability of the nucleic acid

molecule and translation. The regulatory features of a UTR can be incorporated into any of the vectors, compositions, kits, or methods as described herein to enhance the stability of an otoferlin protein.

Natural 5' UTRs include a sequence that plays a role in translation initiation. They harbor signatures like Kozak sequences, which are commonly known to be involved in the process by which the ribosome initiates translation of many genes. Kozak sequences have the consensus sequence CCR(A/G)CCAUGG, where R is a purine (A or G) three bases upstream of the start codon (AUG), which is followed by another "G". The 5' UTRs have also been known, e.g., to form secondary structures that are involved in elongation factor binding.

For example, in some embodiments, a 5' UTR is included in any of the vectors described herein. Non-limiting examples of 5' UTRs including those from the following genes: albumin, serum amyloid A, Apolipoprotein A/B/E, transferrin, alpha fetoprotein, erythropoietin, and Factor VIII, can be used to enhance expression of a nucleic acid molecule, such as a mRNA.

In some embodiments, a 5' UTR from a mRNA that is transcribed by a cell in the cochlea can be included in any of the vectors, compositions, kits, and methods described herein.

3' UTRs are known to have stretches of adenosines and uridines embedded in them. These AU-rich signatures are particularly prevalent in genes with high rates of turnover. Based on their sequence features and functional properties, the AU-rich elements (AREs) can be separated into three classes (Chen et al., *Mol. Cell. Biol.* 15:5777-5788, 1995; Chen et al., *Mol. Cell Biol.* 15:2010-2018, 1995): Class I AREs contain several dispersed copies of an AUUUA motif within U-rich regions. For example, c-Myc and MyoD mRNAs contain class I AREs. Class II AREs possess two or more overlapping UUAUUUA(U/A) (U/A) nonamers. GM-CSF and TNF-alpha mRNAs are examples that contain class II AREs. Class III AREs are less well defined. These U-rich regions do not contain an AUUUA motif. Two well-studied examples of this class are c-Jun and myogenin mRNAs.

Most proteins binding to the AREs are known to destabilize the messenger, whereas members of the ELAV family, most notably HuR, have been documented to

increase the stability of mRNA. HuR binds to AREs of all the three classes. Engineering the HuR specific binding sites into the 3' UTR of nucleic acid molecules will lead to HuR binding and thus, stabilization of the message *in vivo*.

In some embodiments, the introduction, removal, or modification of 3' UTR AREs can be used to modulate the stability of an mRNA encoding an otoferlin protein. In other embodiments, AREs can be removed or mutated to increase the intracellular stability and thus increase translation and production of an otoferlin protein.

In other embodiments, non-UTR sequences may be incorporated into the 5' or 3' UTRs. In some embodiments, introns or portions of intron sequences may be incorporated into the flanking regions of the polynucleotides in any of the vectors, compositions, kits, and methods provided herein. Incorporation of intronic sequences may increase protein production as well as mRNA levels. An intron can be an intron from an otoferlin gene or can be an intron from a heterologous gene, e.g., a hybrid adenovirus/mouse immunoglobulin intron (Yew et al., *Human Gene Ther.* 8(5):575-584, 1997), an SV40 intron (Ostedgaard et al., *Proc. Natl. Acad. Sci. U.S.A.* 102(8):2952-2957, 2005), an MVM intron (Wu et al., *Mol. Ther.* 16(2):280-289, 2008), a factor IX truncated intron 1 (Wu et al., *Mol. Ther.* 16(2):280-289, 2008; Kurachi et al., *J. Biol. Chem.* 270(10):5276-5281, 1995), a chimeric β -globulin splice donor/immunoglobulin heavy chain splice acceptor intron (Wu et al., *Mol. Ther.* 16(2):280-289, 2008; Choi et al., *Mol. Brain* 7:17, 2014), SV40 late splice donor/splice acceptor intron (19S/16S) (Yew et al., *Human Gene Ther.* 8(5):575-584, 1997), hybrid adenovirus splice donor / IgG splice acceptor (Choi et al., *Mol. Brain* 7:17, 1991; Huang and Gorman, *Mol. Cell Biol.* 10(4):1805-1810, 1990).

Non-limiting examples of a splice donor and splice acceptor sequences are SEQ ID NOs: 64 and 65, respectively; SEQ ID NOs: 72 and 73, respectively; and SEQ ID NOs: 74 and 75, respectively.

Destabilization Domains

Any of the vectors provided herein can optionally include a sequence encoding a destabilization domain (“a destabilization domain sequence”). A destabilization domain is an amino acid sequence that decreases the *in vivo* or *in vitro* half-life of a protein that

includes the destabilization domain, e.g., as compared to the same protein lacking the stabilization domain. For example, a destabilization domain may result in the targeting of a protein that includes the destabilization domain for proteosomal degradation. Non-limiting examples of destabilization domains include the destabilizing domain of the *E. coli* dihydrofolate reductase (DHFR) (Iwamoto et al. (2010) Chem. Biol. 17(9): 981-998) and FK-506 binding protein (FKBP) (Wenlin et al. (2015) PLoS One 10(12): e0145783). SEQ ID NO: 53 is an exemplary amino acid sequence of a DHFR destabilization domain. Additional examples of destabilization domains are known in the art.

In some embodiments, any of the vectors provided herein can optionally include a degradation sequence, e.g., a CL1 degradation sequence of SEQ ID NO: 71.

Additional Sequences

Any of the vectors provided herein can optionally include additional nucleotide sequences (“a stuffer sequence”) in order to optimize the total number of basepairs in the vector. For example, in order to optimize packaging, each vector can be designed to contain a total of about 4,000 base pairs to about 4,700 base pairs, e.g., about 4,000 base pairs to about 4,650 base pairs, about 4,000 base pairs to about 4,600 base pairs, about 4,000 base pairs to about 4,550 base pairs, about 4,000 base pairs to about 4,500 base pairs, about 4,000 base pairs to about 4,450 base pairs, about 4,000 base pairs to about 4,400 base pairs, about 4,000 base pairs to about 4,350 base pairs, about 4,000 base pairs to about 4,300 base pairs, about 4,000 base pairs to about 4,250 base pairs, about 4,000 base pairs to about 4,200 base pairs, about 4,000 base pairs to about 4,150 base pairs, about 4,000 base pairs to about 4,100 base pairs, about 4,000 base pairs to about 4,050 base pairs, about 4,050 base pairs to about 4,700 base pairs, about 4,050 base pairs to about 4,650 base pairs, about 4,050 base pairs to about 4,600 base pairs, about 4,050 base pairs to about 4,550 base pairs, about 4,050 base pairs to about 4,500 base pairs, about 4,050 base pairs to about 4,450 base pairs, about 4,050 base pairs to about 4,400 base pairs, about 4,050 base pairs to about 4,350 base pairs, about 4,050 base pairs to about 4,300 base pairs, about 4,050 base pairs to about 4,250 base pairs, about 4,050 base pairs to about 4,200 base pairs, about 4,050 base pairs to about 4,150 base pairs, about 4,050 base pairs to about 4,100 base pairs, about 4,100 base pairs to about 4,700 base pairs,

about 4,100 base pairs to about 4,650 base pairs, about 4,100 base pairs to about 4,600
base pairs, about 4,100 base pairs to about 4,550 base pairs, about 4,100 base pairs to
about 4,500 base pairs, about 4,100 base pairs to about 4,450 base pairs, about 4,100 base
pairs to about 4,400 base pairs, about 4,100 base pairs to about 4,350 base pairs, about
5 4,100 base pairs to about 4,300 base pairs, about 4,100 base pairs to about 4,250 base
pairs, about 4,100 base pairs to about 4,200 base pairs, about 4,100 base pairs to about
4,150 base pairs, about 4,150 base pairs to about 4,700 base pairs, about 4,150 base pairs
to about 4,650 base pairs, about 4,150 base pairs to about 4,600 base pairs, about 4,150
base pairs to about 4,550 base pairs, about 4,150 base pairs to about 4,500 base pairs,
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20 base pairs, about 4,250 base pairs to about 4,600 base pairs, about 4,250 base pairs to
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4,350 base pairs to about 4,400 base pairs, about 4,400 base pairs to about 4,700 base pairs, about 4,400 base pairs to about 4,650 base pairs, about 4,400 base pairs to about 4,600 base pairs, about 4,400 base pairs to about 4,550 base pairs, about 4,400 base pairs to about 4,500 base pairs, about 4,400 base pairs to about 4,450 base pairs, about 4,450 base pairs to about 4,700 base pairs, about 4,450 base pairs to about 4,650 base pairs, about 4,450 base pairs to about 4,600 base pairs, about 4,450 base pairs to about 4,550 base pairs, about 4,450 base pairs to about 4,500 base pairs, about 4,500 base pairs to about 4,700 base pairs, about 4,500 base pairs to about 4,650 base pairs, about 4,500 base pairs to about 4,600 base pairs, about 4,500 base pairs to about 4,550 base pairs, about 4,550 base pairs to about 4,700 base pairs, about 4,550 base pairs to about 4,650 base pairs, about 4,550 base pairs to about 4,600 base pairs, about 4,600 base pairs to about 4,700 base pairs, about 4,600 base pairs to about 4,650 base pairs, or about 4,650 base pairs to about 4,700 base pairs (inclusive).

A stuffer sequence can be any nucleotide sequence, e.g., up to 1000 bp, that can be included in any of the vectors described herein that is not transcribed and that does not serve a regulatory function in order to achieve a desirable vector size (e.g., a vector size of about 4 kb to about 5 kb, or any of the vector sizes provided herein). For example, a stuffer sequence can be any nucleotide sequence of about 100 bp to about 1000 bp (e.g., about 100 bp to about 900 bp, about 100 bp to about 800 bp, about 100 bp to about 700 bp, about 100 bp to about 600 bp, about 100 bp to about 500 bp, about 100 bp to about 400 bp, about 100 bp to about 300 bp, about 100 bp to about 100 bp, about 200 bp to about 1000 bp, about 200 bp to about 900 bp, about 200 bp to about 800 bp, about 200 bp to about 700 bp, about 200 bp to about 600 bp, about 200 bp to about 500 bp, about 200 bp to about 400 bp, about 200 bp to about 300 bp, about 300 bp to about 1000 bp, about 300 bp to about 900 bp, about 300 bp to about 800 bp, about 300 bp to about 700 bp, about 300 bp to about 600 bp, about 300 bp to about 500 bp, about 300 bp to about 400 bp, about 400 bp to about 1000 bp, about 400 bp to about 900 bp, about 400 bp to about 800 bp, about 400 bp to about 700 bp, about 400 bp to about 600 bp, about 400 bp to about 500 bp, about 500 bp to about 1000 bp, about 500 bp to about 900 bp, about 500 bp to about 800 bp, about 500 bp to about 700 bp, about 500 bp to about 600 bp, about 600 bp to about 1000 bp, about 600 bp to about 900 bp, about 600 bp to about 800 bp, about

600 bp to about 700 bp, about 700 bp to about 1000 bp, about 700 bp to about 900 bp, about 700 bp to about 800 bp, about 800 bp to about 1000 bp, about 800 bp to about 900 bp, about 900 bp to about 1000 bp, about 100 bp, about 150 bp, about 200 bp, about 250 bp, about 300 bp, about 350 bp, about 400 bp, about 450 bp, about 500 bp, about 550 bp, about 600 bp, about 650 bp, about 700 bp, about 750 bp, about 800 bp, about 850 bp, about 900 bp, about 950 bp, or about 1000 bp. SEQ ID NOs. 54-58, 90 and 91 are exemplary human factor VIII stuffer sequences that can be used in any of the vectors described herein. Additional stuffer sequences are known in the art. Exemplary vectors that include stuffer sequences are shown in Figures 21-31, 36,37, 59-63 and 66.

Mammalian Cells

Also provided herein is a cell (e.g., a mammalian cell) that includes any of the nucleic acids, vectors (e.g., at least two different vectors described herein), or compositions described herein. Skilled practitioners will appreciate that the nucleic acids and vectors described herein can be introduced into any mammalian cell. Non-limiting examples of vectors and methods for introducing vectors into mammalian cells are described herein.

In some embodiments, the cell is a human cell, a mouse cell, a porcine cell, a rabbit cell, a dog cell, a cat cell, a rat cell, a sheep cell, a cat cell, a horse cell, or a non-human primate cell. In some embodiments, the cell is a specialized cell of the cochlea. In some embodiments, the cell is a cochlear inner hair cell or a cochlear outer hair cell. In some embodiments, the cell is a cochlear inner hair cell. In some embodiments, the cell is a cochlear inner hair cell.

In some embodiments, the mammalian cell is *in vitro*. In some embodiments, the mammalian cell is present in a mammal. In some embodiments, the mammalian cell is autologous cell obtained from a subject and cultured *ex vivo*.

Methods

Also provided herein is a method of introducing into a cochlea of a mammal (e.g., a human) a therapeutically effective amount of any of the compositions described herein. Also provided are methods of increasing expression of an active otoferlin protein (e.g., a

full-length otoferlin protein) in an inner hair cell in a cochlea of a mammal (e.g., a human) that include introducing into the cochlea of the mammal a therapeutically effective amount of any of the compositions described herein. Also provided are methods of treating non-symptomatic sensorineural hearing loss in a subject (e.g., a human) identified as having a defective otoferlin gene, where the methods include administering a therapeutically effective amount of any of the compositions described herein into the cochlea of a subject. In some examples, the methods described herein can further include administering a neurotrophic factor to the cochlea of the subject (e.g., at substantially the same time as any of the compositions described herein are administered to the subject). In some examples, the methods described herein can further include administering a cochlear implant to the subject (e.g., at substantially the same time as any of the compositions described herein are administered to the subject).

In some embodiments of any of these methods, the mammal has been previously identified as having a defective otoferlin gene (e.g., an otoferlin gene having a mutation that results in a decrease in the expression and/or activity of an otoferlin protein encoded by the gene). Some embodiments of any of these methods further include, prior to the introducing or administering step, determining that the subject has a defective otoferlin gene. Some embodiments of any of these methods can further include detecting a mutation in an otoferlin gene in a subject. Some embodiments of any of the methods can further include identifying or diagnosing a subject as having non-symptomatic sensorineural hearing loss.

In some embodiments of any of these methods, two or more doses of any of the compositions described herein are introduced or administered into the cochlea of the mammal or subject. Some embodiments of any of these methods can include introducing or administering a first dose of the composition into the cochlea of the mammal or subject, assessing hearing function of the mammal or subject following the introducing or the administering of the first dose, and administering an additional dose of the composition into the cochlea of the mammal or subject found not to have a hearing function within a normal range (e.g., as determined using any test for hearing known in the art).

In some embodiments of any of the methods described herein, the composition can be formulated for intra-cochlear administration. In some embodiments of any of the methods described herein, the compositions described herein can be administered via intra-cochlear administration or local administration. In some embodiments of any of the methods described herein, the compositions are administered through the use of a medical device (e.g., any of the exemplary medical devices described herein).

In some embodiments, intra-cochlear administration can be performed using any of the methods described herein or known in the art. For example, a composition can be administered or introduced into the cochlea using the following surgical technique: first using visualization with a 0 degree, 2.5-mm rigid endoscope, the external auditory canal is cleared and a round knife is used to sharply delineate an approximately 5-mm tympanomeatal flap. The tympanomeatal flap is then elevated and the middle ear is entered posteriorly. The chorda tympani nerve is identified and divided, and a curette is used to remove the scutal bone, exposing the round window membrane. To enhance apical distribution of the administered or introduced composition, a surgical laser may be used to make a small 2-mm fenestration in the oval window to allow for perilymph displacement during trans-round window membrane infusion of the composition. The microinfusion device is then primed and brought into the surgical field. The device is maneuvered to the round window, and the tip is seated within the bony round window overhang to allow for penetration of the membrane by the microneedle(s). The footpedal is engaged to allow for a measured, steady infusion of the composition. The device is then withdrawn and the round window and stapes foot plate are sealed with a gelfoam patch.

In some embodiments of any of the methods described herein, the subject or mammal is a rodent, a non-human primate, or a human. In some embodiments of any of the methods described herein, the subject or mammal is an adult, a teenager, a juvenile, a child, a toddler, an infant, or a newborn. In some embodiments of any of the methods described herein, the subject or mammal is 1-5, 1-10, 1-20, 1-30, 1-40, 1-50, 1-60, 1-70, 1-80, 1-90, 1-100, 1-110, 2-5, 2-10, 10-20, 20-30, 30-40, 40-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-110, 10-30, 10-40, 10-50, 10-60, 10-70, 10-80, 10-90, 10-100, 10-110, 20-40, 20-50, 20-60, 20-70, 20-80, 20-90, 20-100, 20-110, 30-50, 30-60, 30-70, 30-80,

30-90, 30-100, 40-60, 40-70, 40-80, 40-90, 40-100, 50-70, 50-80, 50-90, 50-100, 60-80, 60-90, 60-100, 70-90, 70-100, 70-110, 80-100, 80-110, or 90-110 years of age. In some embodiments of any of the methods described herein, the subject or mammal is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 months of age.

5 In some embodiments of any of the methods described herein, the methods result in improvement in hearing (e.g., any of the metrics for determining improvement in hearing described herein) in a subject in need thereof for at least 10 days, at least 15 days, at least 20 days, at least 25 days, at least 30 days, at least 35 days, at least 40 days, at least 45 days, at least 50 days, at least 55 days, at least 60 days, at least 65 days, at least 70
10 days, at least 75 days, at least 80 days, at least 85 days, at least 100 days, at least 105 days, at least 110 days, at least 115 days, at least 120 days, at least 5 months, at least 6 months, at least 7 months, at least 8 months, at least 9 months, at least 10 months, at least 11 months, or at least 12 months.

In some embodiments of any of the methods described herein, the subject or
15 mammal has or is at risk of developing non-syndromic sensorineural hearing loss. In some embodiments of any of the methods described herein, the subject or mammal has been previously identified as having a mutation in an otoferlin gene. In some embodiments of any of the methods described herein, the subject or mammal has any of the mutations in an otoferlin gene that are described herein or are known in the art to be
20 associated with non-symptomatic sensorineural hearing loss.

In some embodiments of any of the methods described herein, the subject or mammal has been identified as being a carrier of a mutation in an otoferlin gene (e.g., via genetic testing). In some embodiments of any of the methods described herein, the subject or human has been identified as having a mutation in an otoferlin gene and has
25 been diagnosed with non-symptomatic sensorineural hearing loss. In some embodiments of any of the methods described herein, the subject or human has been identified as having non-symptomatic sensorineural hearing loss.

In some embodiments, successful treatment of non-symptomatic sensorineural hearing loss can be determined in a subject using any of the conventional functional
30 hearing tests known in the art. Non-limiting examples of functional hearing tests are various types of audiometric assays (e.g., pure-tone testing, speech testing, test of the

middle ear, auditory brainstem response, and otoacoustic emissions).

Also provided herein are methods of increasing expression of an active otoferlin protein (e.g., a full-length otoferlin protein) in a mammalian cell that include introducing any of the compositions described herein into the mammalian cell. In some embodiments of these methods, the mammalian cell is a cochlear inner hair cell. In some embodiments of these methods, the mammalian cell is a human cell (e.g., a human cochlear inner hair cell). In some embodiments of these methods, the mammalian cell is *in vitro*. In some embodiments of these methods, the mammalian cell is in a mammal. In some embodiments of these methods, the mammalian cell is originally obtained from a mammal and is cultured *ex vivo*. In some embodiments, the mammalian cell has previously been determined to have a defective otoferlin gene.

Methods for introducing any of the compositions described herein into a mammalian cell are known in the art (e.g., via lipofection or through the use of a viral vector, e.g., any of the viral vectors described herein).

An increase in expression of an active otoferlin protein (e.g., a full-length otoferlin protein) as described herein is, e.g., as compared to a control or to the level of expression of an active otoferlin protein (e.g., a full-length otoferlin protein) prior to the introduction of the vector(s).

Methods of detecting expression and/or activity of otoferlin are known in the art. In some embodiments, the level of expression of an otoferlin protein can be detected directly (e.g., detecting otoferlin protein or detecting otoferlin mRNA). Non-limiting examples of techniques that can be used to detect expression and/or activity of otoferlin directly include: real-time PCR, Western blotting, immunoprecipitation, immunohistochemistry, or immunofluorescence. In some embodiments, expression of an otoferlin protein can be detected indirectly (e.g., through functional hearing tests).

Pharmaceutical Compositions and Kits

Pharmaceutical compositions of the present invention may comprise a nucleic acid, e.g., one or a plurality of AAV vectors, as described herein, in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients. Such compositions may comprise buffers such as neutral buffered saline,

phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose, or dextrans; mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. Compositions of the present invention are in one aspect
5 formulated for intra-cochlear administration. Compositions of the present invention are in one aspect formulated for intravenous administration.

Preferably, the therapeutic compositions are formulated for intra-cochlear administration. Optionally, the therapeutic compositions are formulated to comprise a lipid nanoparticle. Optionally, the therapeutic compositions are formulated to comprise a
10 polymeric nanoparticle. Optionally, the therapeutic compositions are formulated to comprise a mini-circle DNA. Optionally, the therapeutic compositions are formulated to comprise a CELiD DNA. Optionally, the therapeutic compositions are formulated to comprise a synthetic perilymph solution. An exemplary synthetic perilymph solution includes 20-200mM NaCl; 1-5 mM KCl; 0.1-10mM CaCl₂; 1-10mM glucose; and 2-50
15 mM HEPES, with a pH between about 6 and about 9.

In some embodiments, any of the compositions described herein can further include one or more agents that promote the entry of a nucleic acid or any of the vectors described herein into a mammalian cell (e.g., a liposome or cationic lipid).

In some embodiments, any of the vectors described herein can be formulated using
20 natural and/or synthetic polymers. Non-limiting examples of polymers that may be included in any of the compositions described herein can include, but are not limited to, DYNAMIC POLYCONJUGATE® (Arrowhead Research Corp., Pasadena, Calif.), formulations from Mirus Bio (Madison, Wis.) and Roche Madison (Madison, Wis.), PhaseRX polymer formulations such as, without limitation, SMARTT POLYMER
25 TECHNOLOGY® (PhaseRX, Seattle, Wash.), DMRI/DOPE, poloxamer, VAXFECTIN® adjuvant from Vical (San Diego, Calif.), chitosan, cyclodextrin from Calando Pharmaceuticals (Pasadena, Calif.), dendrimers and poly (lactic-co-glycolic acid) (PLGA) polymers, RONDEL™ (RNAi/Oligonucleotide Nanoparticle Delivery) polymers (Arrowhead Research Corporation, Pasadena, Calif.), and pH responsive co-
30 block polymers, such as, but not limited to, those produced by PhaseRX (Seattle, Wash.). Many of these polymers have demonstrated efficacy in delivering oligonucleotides *in*

vivo into a mammalian cell (see, e.g., deFougerolles, *Human Gene Ther.* 19:125-132, 2008; Rozema et al., *Proc. Natl. Acad. Sci. U.S.A.* 104:12982-12887, 2007; Rozema et al., *Proc. Natl. Acad. Sci. U.S.A.* 104:12982-12887, 2007; Hu-Lieskovan et al., *Cancer Res.* 65:8984-8982, 2005; Heidel et al., *Proc. Natl. Acad. Sci. U.S.A.* 104:5715-5721, 2007). Any of the compositions described herein can be, e.g., a pharmaceutical composition.

In some embodiments, the composition includes a pharmaceutically acceptable carrier (e.g., phosphate buffered saline, saline, or bacteriostatic water). Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, injectable gels, drug-release capsules, and the like.

As used herein, the term “pharmaceutically acceptable carrier” includes solvents, dispersion media, coatings, antibacterial agents, antifungal agents, and the like that are compatible with pharmaceutical administration. Supplementary active compounds can also be incorporated into any of the compositions described herein.

In some embodiments, a single dose of any of the compositions described herein can include a total sum amount of the at least two different vectors of at least 1 ng, at least 2 ng, at least 4 ng, about 6 ng, about 8 ng, at least 10 ng, at least 20 ng, at least 30 ng, at least 40 ng, at least 50 ng, at least 60 ng, at least 70 ng, at least 80 ng, at least 90 ng, at least 100 ng, at least 200 ng, at least 300 ng, at least 400 ng, at least 500 ng, at least 1 µg, at least 2 µg, at least 4 µg, at least 6 µg, at least 8 µg, at least 10 µg, at least 12 µg, at least 14 µg, at least 16 µg, at least 18 µg, at least 20 µg, at least 22 µg, at least 24 µg, at least 26 µg, at least 28 µg, at least 30 µg, at least 32 µg, at least 34 µg, at least 36 µg, at least 38 µg, at least 40 µg, at least 42 µg, at least 44 µg, at least 46 µg, at least 48 µg, at least 50 µg, at least 52 µg, at least 54 µg, at least 56 µg, at least 58 µg, at least 60 µg, at least 62 µg, at least 64 µg, at least 66 µg, at least 68 µg, at least 70 µg, at least 72 µg, at least 74 µg, at least 76 µg, at least 78 µg, at least 80 µg, at least 82 µg, at least 84 µg, at least 86 µg, at least 88 µg, at least 90 µg, at least 92 µg, at least 94 µg, at least 96 µg, at least 98 µg, at least 100 µg, at least 102 µg, at least 104 µg, at least 106 µg, at least 108 µg, at least 110 µg, at least 112 µg, at least 114 µg, at least 116 µg, at least

118 µg, at least 120 µg, at least 122 µg, at least 124 µg, at least 126 µg, at least 128 µg, at least 130 µg, at least 132 µg, at least 134 µg, at least 136 µg, at least 138 µg, at least 140 µg, at least 142 µg, at least 144 µg, at least 146 µg, at least 148 µg, at least 150 µg, at least 152 µg, at least 154 µg, at least 156 µg, at least 158 µg, at least 160 µg, at least 162 µg, at least 164 µg, at least 166 µg, at least 168 µg, at least 170 µg, at least 172 µg, at least 174 µg, at least 176 µg, at least 178 µg, at least 180 µg, at least 182 µg, at least 184 µg, at least 186 µg, at least 188 µg, at least 190 µg, at least 192 µg, at least 194 µg, at least 196 µg, at least 198 µg, or at least 200 µg, e.g., in a buffered solution.

The compositions provided herein can be, e.g., formulated to be compatible with their intended route of administration. A non-limiting example of an intended route of administration is local administration (e.g., intra-cochlear administration).

In some embodiments, the therapeutic compositions are formulated to include a lipid nanoparticle. In some embodiments, the therapeutic compositions are formulated to include a polymeric nanoparticle. In some embodiments, the therapeutic compositions are formulated to comprise a mini-circle DNA. In some embodiments, the therapeutic compositions are formulated to comprise a CELiD DNA. In some embodiments, the therapeutic compositions are formulated to comprise a synthetic perilymph solution. An exemplary synthetic perilymph solution includes 20-200 mM NaCl; 1-5 mM KCl; 0.1-10 mM CaCl₂; 1-10 mM glucose; 2-50 mM HEPES, having a pH of between about 6 and about 9.

Also provided are kits including any of the compositions described herein. In some embodiments, a kit can include a solid composition (e.g., a lyophilized composition including the at least two different vectors described herein) and a liquid for solubilizing the lyophilized composition. In some embodiments, a kit can include a pre-loaded syringe including any of the compositions described herein.

In some embodiments, the kit includes a vial comprising any of the compositions described herein (e.g., formulated as an aqueous composition, e.g., an aqueous pharmaceutical composition).

In some embodiments, the kits can include instructions for performing any of the methods described herein.

Routes of Administration

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms. In many cases the form is sterile and fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

For administration of an injectable aqueous solution, for example, the solution may be suitably buffered, if necessary, and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the host. The person responsible for administration will, in any event, determine the appropriate dose for the individual host.

Sterile injectable solutions are prepared by incorporating the active rAAV in the required amount in the appropriate solvent with various of the other ingredients enumerated herein, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

The rAAV compositions disclosed herein may also be formulated in a neutral or salt form. Pharmaceutically-acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug-release capsules, and the like.

As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art.

Supplementary active ingredients can also be incorporated into the compositions. The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a host.

Delivery vehicles such as liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, may be used for the introduction of the compositions of the present invention into suitable host cells. In particular, the rAAV vector delivered transgenes may be formulated for delivery either encapsulated in a lipid particle, a

liposome, a vesicle, a nanosphere, or a nanoparticle or the like.

Such formulations may be preferred for the introduction of pharmaceutically acceptable formulations of the nucleic acids or the rAAV constructs disclosed herein. The formation and use of liposomes is generally known to those of skill in the art. Recently, liposomes were developed with improved serum stability and circulation half-times (U.S. Pat. No. 5,741,516). Further, various methods of liposome and liposome like preparations as potential drug carriers have been described (U.S. Pat. Nos. 5,567,434; 5,552,157; 5,565,213; 5,738,868 and 5,795,587).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures. In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs, radiotherapeutic agents, viruses, transcription factors and allosteric effectors into a variety of cultured cell lines and animals. In addition, several successful clinical trials examining the effectiveness of liposome-mediated drug delivery have been completed.

Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)). MLVs generally have diameters of from 25 nm to 4 μ m. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 $\text{\AA}$, containing an aqueous solution in the core.

Alternatively, nanocapsule formulations of the rAAV may be used. Nanocapsules can generally entrap substances in a stable and reproducible way. To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μ m) should be designed using polymers able to be degraded in vivo. Biodegradable polyalkylcyanoacrylate nanoparticles that meet these requirements are contemplated for use.

In addition to the methods of delivery described above, the following techniques are also contemplated as alternative methods of delivering the rAAV compositions to a host. Sonophoresis (ie., ultrasound) has been used and described in U.S. Pat. No. 5,656,016 as a device for enhancing the rate and efficacy of drug permeation into and through the circulatory system. Other drug delivery alternatives contemplated are intraosseous injection (U.S. Pat. No. 5,779,708), microchip devices (U.S. Pat.

No. 5,797,898), ophthalmic formulations (Bourlais et al., 1998), transdermal matrices (U.S. Pat. Nos. 5,770,219 and 5,783,208) and feedback-controlled delivery (U.S. Pat. No. 5,697,899).

The administration of the subject compositions may be carried out in any
5 convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The compositions described herein may be administered to a patient trans arterially, subcutaneously, intradermally, intranodally, intramedullary, intramuscularly, by intravenous (i.v.) injection, or intraperitoneally. In one aspect, the nucleic acid compositions of the present invention are administered to a patient by
10 intradermal or subcutaneous injection. In one aspect, the nucleic compositions of the present invention are administered by i.v. injection.

Devices and Surgical Methods

Provided herein are therapeutic delivery systems for treating deafness and other
15 hearing-associated diseases, disorders and conditions. In one aspect, provided are therapeutic delivery systems that include i) a medical device capable of creating a one or a plurality of incisions in a round window membrane of an inner ear of a human subject in need thereof, and ii) an effective dose of a therapeutic composition including one or a plurality of adeno-associated viral (AAV) vectors, wherein the one or the plurality of
20 AAV vectors are capable of constituting a full-length auditory polypeptide messenger RNA in a target cell of the inner ear.

A means for performing a surgical method, the method including the steps of: administering intra-cochlearly to a human subject in need thereof an effective dose of the therapeutic composition of claim 1, wherein the therapeutic composition is capable of
25 being administered by using a medical device including a) means for creating a one or a plurality of incisions in the round window membrane and b) the effective dose of the therapeutic composition.

Provided herein are surgical methods for treatment of hearing loss. In one aspect, the methods include the steps of: introducing into a cochlea of a human subject a first
30 incision at a first incision point; and administering intra-cochlearly an effective dose of a therapeutic composition (e.g., any of the compositions described herein) as provided

herein. In one embodiment, the therapeutic composition (e.g., any of the compositions described herein) is administered to the subject at the first incision point. In one embodiment, the therapeutic composition is administered to the subject into or through the first incision. In one embodiment, the therapeutic composition is administered to the subject into or through the cochlea oval window membrane. In one embodiment, the therapeutic composition is administered using a medical device capable of creating a plurality of incisions in the round window membrane. In one embodiment, the medical device includes a plurality of micro-needles. In one embodiment, the medical device includes a plurality of micro-needles including a generally circular first aspect, wherein each micro-needle has a diameter of at least about 10 microns. In one embodiment, the medical device includes a base and/or a reservoir capable of holding the therapeutic composition. In one embodiment, the medical device includes a plurality of hollow micro-needles individually including a lumen capable of transferring the therapeutic composition. In one embodiment, the medical device includes a means for generating at least a partial vacuum.

The invention is further described in detail by reference to the following experimental examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified. Thus, the invention should in no way be construed as being limited to the following examples, but rather should be construed to encompass any and all variations that become evident as a result of the teaching provided herein.

Other assays, including those described in the Example section herein as well as those that are known in the art, can also be used to evaluate the auditory polypeptide nucleic acids and nucleic acid constructs of the invention.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples specifically point out various aspects of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1: Characterization of human Otoferlin Gene, Homologs, Orthologs.

The otoferlin gene and the corresponding mRNA are provided below.

5

Example 2: Construction of Viral Vectors

Recombinant AAV is generated by transfection with an adenovirus-free method as used by Xiao et al. *J Virol* 1999, 73(5):3994-4003. The cis plasmids with AAV ITRs, the trans plasmid with AAV Rep and Cap genes, and a helper plasmid with an essential region from an adenovirus genome are co-transfected in 293 cells in a ratio of 1:1:2. The AAV vectors used here express human otoferlin or mouse otoferlin under multiple dual vector strategies using the constructs described below. AAV serotypes 1, 2, 3, 4, 5, 6, 7, 8, 9, rh8, rh10, rh39, rh43, and Anc80 are each prepared to encapsulate three sets of otoferlin constructs to test (i) a concatemerization-trans-splicing strategy, (ii) a hybrid intronic-homologous recombination-trans-splicing strategy, and (iii) an exonic homologous recombination strategy, as summarized by Pryadkina et al. *Meth Clin Devel* 2015, 2:15009.

Example 3: Cloning OTOF Components

Oligo-dT and random-primed cDNA libraries are constructed from poly(A)+ mRNA of human total fetus, adult brain, heart, kidney, and murine fetal heart as described by Yasunaga et al. *Am J Genet* 2000, 67:591-600. RACE-PCR experiments are performed on these libraries using linker primers and a series of primers selected from the otoferlin cDNA sequence. The PCR products are directly cloned into pGEM-T Easy vector and sequenced. To isolate the human cDNA long form (7 kb), a reverse primer (5'-TTCACCTGGGCCCGCA-GCATCCT-3' (SEQ ID NO: 29)) is designed from the sequence encoding aa 63-70 of the initially reported short form of otoferlin (Yasunaga et al., 1999) (GenBank 107403).

Total RNAs are extracted from mouse cochlea using the methods described in Strenzke et al., *EMBO J.* 35(23):2519-2535, 2016. RT-PCR experiments are performed in various murine and human RNA sources, according to the GeneAmp RNA PCR kit.

Two primer pairs are used to reconstitute the murine cDNAs derived from the brain and the cochlea, one from the exon 1 5'-UTR (5'-AGGCGTGTGAGCCACACTCCACCA-3' (SEQ ID NO: 30)) and exon 22 (5'-CATAACCTCAGCTTGTCCCGAACA-3' (SEQ ID NO: 31)), and the other from the exon 18-19 junction (5'-

5 GGCCCCAGATCACGGACAGGAAC-3' (SEQ ID NO: 32)) and exon 48 3'-UTR (5'-GGCCAGTACACCTGATTCACACT-3' (SEQ ID NO: 33)). To reconstitute the entire 5' part of the human brain cDNA long form, primers derived from the 5'-UTR exon 1 (5'-GGAGGAGGCAGCGGCAGAGAAGA-3' (SEQ ID NO: 34)) and exon 22 (5'-TTCACCTGGGCCCCGCAGCATCCT-3' (SEQ ID NO: 35)) are used.

10 For the concatemerization-trans-splicing strategy, two cassettes are composed such that the 5' cassette includes a synthetic hair cell-oriented promoter, a chimeric intron (β -globin), a consensus Kozak sequence, the exons 1 to 26 of otoferlin and the half intron 26 of otoferlin (representing 3,836 bp, or the 3,494 bp of otoferlin cDNA corresponding to exons 1 through 26, plus the first 342 bp of intron 26), and the 3' cassette includes the
15 second half of intron 26 (342 bp), exons 27 to 48 (3,843 bp) of otoferlin, and a polyadenylation signal sequence. In some examples, the a hair cell-oriented promoter is not required for expression of an otoferlin protein in an auditory inner hair cell. For the intronic-homologous recombination-splicing strategy, the cassettes from the concatemerization-splicing strategy described above are modified such that the full length
20 intron 26 of otoferlin is added in the place of the half intron 26 in both plasmids.

For the exonic homologous recombination strategy, the two cassettes are composed such that the 5' cassette includes a hair cell-oriented promoter, a chimeric intron, a consensus Kozak sequence and the exons 1 to 28 (the first 3,776 bp of the otoferlin cDNA), and the 3' cassette includes the exons 23 to 48 (the final 4,446 bp of the
25 otoferlin cDNA) and a polyadenylation signal sequence. The region of homology between the two cassettes is 885 bp.

Example 4: Generating and Purifying Viral Particles

Recombinant AAV-1 is produced using a triple transfection protocol and purified
30 by two sequential cesium chloride (CsCl) density gradients, as described by Pryadkina et al. *Mol Ther* 2015, 2:15009. At the end of second centrifugation, 11 fractions of 500 μ l

are recovered from the CsCl Density Gradient tube and purified through dialysis in 1× PBS. The fractions are analyzed by dot blot to determine those containing rAAV genomes. The viral genome number (vg) of each preparation is determined by quantitative real-time PCR-based titration method using primers and probe corresponding to the ITR region of the AAV vector genome (Bartoli et al. Gene Ther 2006, 13:20-28).

Example 5: Formulation of Viral Particles

AAV produced at a titer of 1e14 vg / mL is prepared at dilutions of 3.2e13, 1.0e13, 3.2e12, 1.0e12 vg / mL in artificial perilymph. Artificial perilymph is prepared by combining the following reagents, in mM: NaCl, 120; KCl, 3.5; CaCl₂, 1.5; glucose, 5.5; HEPES, 20. The artificial perilymph is titrated with NaOH to adjust its pH to 7.5 (total Na⁺ concentration of 130 mM) (Chen et al. J Controlled Rel 2005, 110:1-19).

Example 6: In Vitro Demonstration of OTOF mRNA and Protein Production (anti-OTOF antibody)

To confirm the AAV-OTOF vectors are capable of successfully transducing mammalian cells *in vitro*, human retinal epithelial cells and neonate mouse cochlear explants are incubated with AAV-OTOF at titers of 3.2e13, 1.0e13, 3.2e12, 1.0e12 viral genome-containing particles (vg / mL) and assayed for levels of otoferlin DNA, mRNA and protein as described previously (Duncker et al., 2013 *J Neurosci* 33(22):9508-9519. Antibodies against mouse otoferlin are obtained from Abcam and used as described by Engel et al., 2006 *Neurosci* 143:837-849.

Example 7: Device Description

The AAV-OTOF formulation is delivered to the cochlea using a specialized microcatheter designed for consistent and safe penetration of the RWM. The microcatheter is shaped such that the surgeon performing the delivery procedure can enter the middle ear cavity via the external auditory canal and contact the end of the microcatheter with the RWM. The distal end of the microcatheter is comprised of at least one microneedle with diameter of between 10 and 1,000 microns, which produce

perforations in the RWM that are sufficient to allow AAV-OTOF to enter the cochlear perilymph of the scala tympani at a rate of approximately 1 uL/min, but heal without surgical repair. The remaining portion of the microcatheter, proximal to the microneedle(s), is loaded with the AAV-OTOF/artificial perilymph formulation at a titer of approximately 1×10^{13} vg/mL. The proximal end of the microcatheter is connected to a micromanipulator that allows for precise, low volume infusions of approximately 1 μ L / min.

Example 8: Animal Model 1: Aged Mice

Otoferlin rescue with cochlear delivery of AAV-OTOF is assessed in three OTOF knockout mouse models (mouse models as described in Longo-Guess et al. *Hearing Res* 2007, 234(1-2):21-28; Roux et al. *Cell* 2006, 127:277-289; and Reisinger et al., *J. Neurosci.* 31(13):4886-4895, 2011). Rescue experiments are tested in neonate (P1), juvenile (P6 or P12) and adult (P42) mice, in order to evaluate the postnatal treatment window relative to stage of cochlear development.

Baseline auditory brainstem response (ABR) and distortion product otoacoustic emissions (DPOAEs) are measured in the juvenile and adult mice (n=32), bilaterally, to assess pre-treatment inner hair cell (IHC) and outer hair cell (OHC) function. All animals are expected to display the characteristic audiometric profile of otoferlin dysfunction – i.e., abnormal ABRs across tested sound frequencies but normal DPOAEs, indicative of dysfunctional IHC signal transduction and normal OHC function (Yasunaga et al. 2000, *Am J Hum Genet* 67:591-600).

Following baseline ABR and DPOAE measurements, 0.3 uL of AAV1-OTOF at titers of 1.0×10^{13} , 3.2×10^{12} , and 1.0×10^{12} vg/mL is injected into the left scala tympani of the juvenile and adult mice (n=32), as described below. Equivalent titers are injected in the left scala tympani of the neonatal mice, but at a volume of 0.2 uL (n=16) (surgical procedure described below). Each animals' right ear is left as an untreated control. ABR and DPOAE measurements are taken again bilaterally in the juvenile and adult animals 1, 5 and 10 days following the surgical procedure. At 4 weeks (n=24) and 12 weeks (n=24) post-procedure, additional bilateral ABR and DPOAE measurements are taken from all

animals in the neonate, juvenile and adult groups (total n=48), and the animals are subsequently sacrificed and their cochleae removed.

In half of the sacrificed animals (n=4 from each of the 4 week and 12 week post-treatment groups), immunostaining is performed to identify hair cell structures and to assess OTOF protein expression along the cochlear sensory epithelium. Antibodies against markers for hair cells (Myo7a), supporting cells (Sox2) and otoferlin are used as described previously (Duncker et al. 2013, *J Neurosci* 33(22):9508-9519. At the basal, middle and apical turns of the organ of corti, total numbers of hair cells and those hair cells expressing OTOF were counted within 200 um regions; the entire length of the organ of corti was divided into three pieces of equal length, designated the basal, middle and apical regions.

In the remaining half of the sacrificed animals (remaining 4 animals from each of the 4 week and 12 week post-treatment groups), cochlear tissue samples are collected from the same basal, middle and apical regions as described above, and assayed for otoferlin mRNA transcript as described previously (Duncker et al. 2013, *J Neurosci* 33(22):9508-9519, Heidrych et al. 2008, *Hum Mol Genet* 17:3814-3821, Heidrych et al., 2009, *Hum Mol Genet* 18:2779-2790).

Example 9: Animal Model 1A: Surgical Method in Aged Mice

AAV-OTOF prepared in artificial perilymph is administered to the scala tympani in mice as described by Shu et al. 2016 (Shu Yilai, Tao Yong, Wang Zhengmin, Tang Yong, Li Huawei, Dai Pu, Gao Guanping, and Chen Zheng-Yi. Human Gene Therapy. June 2016, ahead of print. doi:10.1089/hum.2016.053). Six-week-old male mice are anesthetized using an intraperitoneal injection of xylazine (20 mg/kg) and ketamine (100 mg/kg). Body temperature is maintained at 37 °C using an electric heating pad. An incision is made from the right post-auricular region and the tympanic bulla is exposed. The bulla is perforated with a surgical needle and the small hole is expanded to provide access to the cochlea. The bone of the cochlear lateral wall of the scala tympani is thinned with a dental drill so that the membranous lateral wall is left intact. A Nanoliter Microinjection System in conjunction with glass micropipette is used to deliver a total of approximately 300 nL of AAV-OTOF in artificial perilymph to the scala tympani at a

rate of 2 nL/second. The glass micropipette is left in place for 5 minutes post-injection. Following cochleostomy and injection, the opening in the tympanic bulla is sealed with dental cement, and the muscle and skin are sutured. The mice are allowed to awaken from anesthesia and their pain is controlled with 0.15 mg/kg buprenorphine hydrochloride for 3 days.

Example 10: Animal Model 2: Reciprocating Micropump in Guinea Pig

Surgical Procedure

AAV-OTOF prepared in artificial perilymph is administered to guinea pigs to assess distribution and toxicity following intracochlear delivery with a reciprocating micropump as described by Tandon et al. *Lab Chip* 2015 (DOI: 10.1039/c5lc01396h). Male guinea pigs weighing approximately 350 g each (n=16) are anesthetized with a combination of pentobarbital sodium (Nembutal; 25 mg kg⁻¹, injected intraperitoneally), fentanyl (0.2 mg kg⁻¹, intramuscularly), and haloperidol (10 mg kg⁻¹, intramuscularly). Lidocaine with epinephrine is given subcutaneously at the incision site as a topical anesthetic. Using a dorsal approach, a 5 mm diameter hole is made in the bulla and a cochleostomy is created approximately 0.5 mm distal to the round window membrane. The cannula of the micropump (described below) is inserted into the cochleostomy, threaded into the cochlea 3 mm apically, and glued to the bulla with a common cyanoacrylate glue. For compound action potential (CAP) measurements, a perfluoroalkoxy-alkane-insulated silver wire electrode (203 µm uncoated diameter) is inserted near the round window niche and glued to the bulla.

Procedures for measurement of distortion product otoacoustic emissions (DPOAEs) and CAPs are performed as previously described in Tandon et al. *Biomed Microdevices* 2015, 17:3-21. DPOAEs are measured before and after the cochleostomy procedure at the characteristic frequencies: 32, 24, 16, 12, 8, 5.6, 4, and 2.78 kHz in order to monitor any damage that occurs as a result of the surgery.

Micropump description

AAV-OTOF at a maximum titer of 1e14 vg/mL is administered to the guinea pig using a micropump as described by Tandon et al. *Lab Chip* 2015 (DOI:

10.1039/c5lc01396h). The micropump system has 4 selectable ports. These ports are connected to: (i) a large fluidic capacitor used for artificial perilymph storage; (ii) an outlet that connects to the cochlea; (iii) the outlet from an integrated AAV-OTOF reservoir; (iv) the inlet to the integrated AAV-OTOF reservoir. Each port is fluidically
 5 connected to a central pump chamber, and each is individually addressed with a valve. The sequence of events for reciprocating AAV-OTOF delivery is as follows: (i) an internal AAV-OTOF-refresh loop is run, transferring AAV-OTOF from the AAV-OTOF reservoir into the main infuse-withdraw line; (ii) AAV-OTOF is infused into the cochlea and some artificial perilymph is drained from the artificial perilymph storage capacitor;
 10 (iii) the first two steps can be repeated several times for additional doses; (iv) after the AAV-OTOF has been allowed to diffuse for some time, a volume of perilymph is withdrawn from the cochlea that is equal to the volume infused in steps (i)–(iii), refilling the artificial perilymph storage capacitor. This process results in net delivery of drug with zero net fluid volume added to the cochlea.

15 The fluidic capacitors in the micropump are cylindrical chambers whose ceilings are a thin (25.4 μm), flexible, polyimide membrane. The pump chamber has a diameter of 3.5 mm, the fluidic storage capacitor has a diameter of 14 mm, and all of the remaining capacitors have diameters of 4 mm. The same membrane is deflected to block flow at each of the valves. The valve chambers have diameters of 3.1 mm. The serpentine
 20 channel that comprises the drug reservoir has a square cross section of width 762 μm and a length of 410 mm for a total volume of 238 μL . All of the other microchannels in the pump have a width of 400 μm and a height of 254 μm .

Acute drug delivery in guinea pigs

25 The micropump is loaded with AAV-OTOF and artificial perilymph, and the cannula inserted into a cochleostomy made in the region of the cochlea between the locations with characteristic frequency sensitivity of 24 and 32 kHz, and threaded apically 3 mm, terminating in the 12–16 kHz region. Baseline DPOAE and CAP hearing tests are performed prior to the start of AAV-OTOF/artificial perilymph infusion. The
 30 pump is then activated and approximately 1 μL of artificial perilymph is infused every 5 min until a total of approximately 10 μL of artificial perilymph is delivered to the

cochlea. After a 20 min wait time, approximately 10 μ L of perilymph is withdrawn from the cochlea. AAV-OTOF delivery is then initiated at a rate of approximately 1 μ L every 5 min until a total of approximately 10 μ L of fluid is delivered.

Animals are sacrificed at 1 week, 1 month, 3 months, and 6 months post-treatment (n=4 per group) and their cochleae extracted. Extent of AAV transduction and OTOF expression along the organ of Corti is assessed via immunostaining with anti-OTOF antibodies. Antibodies against markers for hair cells (Myo7a) and supporting cells (Sox2) are used to quantify IHCs, OHCs, supporting cells and stereocilia morphology. Annexin V staining is used to assess evidence of apoptosis in cells along the cochlear sensory epithelium.

Example 11: Animal Model 3: Large Animal Tox in Sheep

AAV-OTOF prepared in artificial perilymph is administered to juvenile sheep to assess distribution and toxicity following delivery to the cochlea via trans-RWM infusion. Baseline auditory brainstem response (ABR) and distortion product otoacoustic emissions (DPOAEs) are measured in female sheep at 3 months of age (n=40), bilaterally, to assess pre-treatment inner hair cell (IHC) and outer hair cell (OHC) function. Following baseline ABR and DPOAE measurements, 20 μ L of AAV1-OTOF at titers of 1.0×10^{14} , 3.2×10^{13} , 1.0×10^{13} and 3.2×10^{12} vg/mL is injected into the left scala tympani of the sheep (n=10 per group). Each animal's right ear is left as an untreated control. ABR and DPOAE measurements are taken again bilaterally 1, 5 and 10 days following the surgical procedure. At 6 months post-procedure, additional bilateral ABR and DPOAE measurements are taken from all animals, and the animals are subsequently sacrificed and their cochleae removed.

In half of the sacrificed animals (n=5 from each of the dose cohorts), immunostaining is performed to identify hair cell structures and to assess OTOF protein expression along the cochlear sensory epithelium. Antibodies against markers for hair cells (Myo7a), supporting cells (Sox2) and otoferlin are used as described previously (Duncker et al. 2013, *J Neurosci* 33(22):9508-9519). At the basal, middle and apical turns of the organ of corti, total numbers of hair cells and those hair cells expressing OTOF are counted within 200 μ m regions.

In the remaining half of the sacrificed animals (remaining 5 animals from each dose cohort), cochlear tissue samples are collected from the same basal, middle and apical regions as described above, and assayed for otoferlin mRNA transcript as described previously (Duncker et al. 2013, *J Neurosci* 33(22):9508-9519, Heidrych et al. 2008, *Hum Mol Genet* 17:3814-3821, Heidrych et al., 2009, *Hum Mol Genet* 18:2779-2790).

Example 12: Animal Model 3A: CRISPR Generated Transgenic Large Animal Model (Sheep)

10 Generation of plasmid co-expressing Cas9 and sgRNA

The pX330-U6-Chimeric_BB-CBh-hSpCas9 plasmid (Addgene plasmid #42230) is digested with BsbI, dephosphorylated using Antarctic Phosphatase, and the linearized vector is gel purified. To generate the bicistronic vector (pX330-cas9-OTOF) expressing Cas9 and sgRNA against OTOF, a pair of oligos for targeting otoferlin exon 1 is annealed, phosphorylated and ligated to a linearized vector (Cong et al. 2013 *Science* 339(6121):819-23).

Genome editing assay in cells

The A15 astroglial sheep cell line (Vilette et al., 2000 *In Vitro Cell Dev Biol Anim* 36(1):45-9) is maintained in DMEM in 10% Fetal Bovine Serum, 2mM glutamine, 1% sodium pyruvate and 1% penicillin/streptomycin. Cells are transfected in 24-well plates with 2 µg of pX330-cas9-OTOF co-expressing Cas9 and sgRNA against otoferlin using lipofectamine LTX reagent. Three days later, genomic DNA from transfected cells is extracted and quantified using a NanoDrop2000 spectrophotometer, measuring

25 A260/A280 and A260/A230 ratios to account for sample purity

Gene mutation activity of sgRNA sequence at the target locus of OTOF exon 1 is quantified using the T7EI mismatch detection assay. DNA sequence of interest is PCR-amplified with a high-fidelity polymerase (Herculase II fusion polymerase) using specific primers. The resultant PCR product is then denatured and slowly re-annealed (95°C, 2 min; 95°C to 85°C, -2°C/sec; 85°C to 25°C, -1°C/sec) to produce homoduplex/heteroduplex mix. This is then digested by 5U of T7EI restriction enzyme

at 37°C for 30 minutes. Digestion products are separated by 2% agarose gel electrophoresis. The ratio of cleaved to uncleaved products is used to calculate NHEJ frequency as previously described using Image J software (Menoret et al. 2011 *Advanced protocols for Animal Transgenesis. An ISTT Manual*. Heidelberg: Springer. p117-36).

- 5 NHEJ frequency is calculated as % gene modification = $100 \times (1 - (1 - \text{fraction cleaved})^{1/2})$.

Production of sgRNA and Cas9 mRNA

As described previously (Bellec et al. 2015, Current Gene Ther), T7 promoter is added to sgRNA template by PCR amplification of pX330-cas9-OTOF plasmid. The PCR product is purified using NucleoSpin Gel and PCR Clean-up. It is used as the template for in vitro transcription using MEGAshortscript T7 kit according to the manufacturer's manual. Following completion of transcription, DNase I treatment is performed.

- 15 The Cas9 mRNA is transcribed using PmeI-digested Cas9 expression JDS246 plasmid (Addgene plasmid # 43861) and the mMACHINE T7 ULTRA Transcription Kit according to the manufacturer's manual. Following completion of transcription, the poly(A) tailing reaction and DNase I treatment are performed. Both the Cas9 mRNA and the sgRNAs are purified using MEGAclear kit and eluted in elution buffer.

In vitro production of embryos

- The embryos are produced by *in vitro* fertilization according to routine procedure as described previously (Crispo et al. 2014 *Transgenic Res*, 24(1):31-41). Briefly, ovaries from slaughterhouse are transported to the laboratory and cumulus oocyte complexes (COCs) are aspirated in recovery medium. The selected COCs are placed in maturation medium for 24 h in 5% CO₂ in humidified air atmosphere at 39°C. Then, expanded COCs are inseminated in 100 µl drops with 1 x 10⁶ dose of frozen-thawed semen selected by ascendant migration on a swim up method. Fertilization is carried out in 5% CO₂ with humidified atmosphere at 39°C for 22 h.

Microinjection into zygotes

Soon after fertilization, 572 presumptive zygotes are randomly assigned to three experimental groups to be microinjected (CRISPR group, n = 200; and Buffer group, n = 200) or not (Control group, n = 200). Microinjection of CRISPR group is performed into the cytoplasm with 5 ng/μl of sgRNA and 20ng/μl of Cas9 mRNA diluted in injection buffer (10mM Tris pH 7.5, 0.1mM EDTA), while Buffer group is injected with the same procedure but with buffer alone. Lastly, injected and non-injected embryos are transferred to culture medium under mineral oil, in 5% CO₂, 5% O₂ and 90% N₂ in humidified atmosphere at 39°C. Cleavage rate on Day 2 (cleaved zygotes per total oocytes) and development rate on Day 6 (morulae and blastocysts per total oocytes) are recorded for all experimental groups. After Day 6, DNA from 20 CRISPR group embryos are analyzed by Sanger sequencing to detect the mutation at the OTOF gene level.

To determine the *in vivo* efficiency of the system, 53 blastocysts produced by CRISPR/Cas9 zygote microinjection are transferred to 29 recipient females. Only early blastocysts, blastocysts and expanded blastocysts classified as excellent or good (i.e. Grade 1 as defined in Stringfellow et al. 2010, *Manual of the International Embryo Transfer Society*) are transferred on Day 6 after fertilization. Embryo transfer is performed by minimally invasive surgery assisted by laparoscopy to place the embryos into the cranial side of the ipsilateral uterine horn to the corpus luteum. Recipient ewes are previously synchronized to be on Day 6 of the estrous cycle using a standard protocol to control ovulation described previously, as described by Menchaca et al. 2004, *Reprod Fertil Dev.* 16(4):403-413.

Monitoring of fetuses and lambs

Pregnancy diagnosis and fetal development are performed on Day 30 and 105, respectively, by using B-mode ultrasonography equipped with a 5 and 3.5 MHz probe. Day 0 of the experiment is defined as the moment of embryo fertilization. Several parameters are measured to study the development of fetuses at Day 105 of gestation: thoracic diameter, biparietal diameter, occipitonasal length and heart rate. At delivery, length of gestation, gender, rectal temperature, heart and respiratory rates, body weight, thoracic perimeter, biparietal diameter, crown-rump and occipitonasal length, height at

withers, height at hips, width at hips and width at chest were recorded. Body weight and morphometric variables are determined at birth, and 15, 30 and 60 days later.

Identification and genotyping of transgenic animals

5 Samples from skin and limb muscle of the lambs are taken seven days after birth and T7EI assay, western blot test and histology examinations are performed in order to identify and characterize KO founders and off-target sites. Total DNA is isolated from skin biopsies for all animals and from muscle for some animals. Samples are analyzed using capillary electrophoresis. Genotyping of OTOF exon 1 is performed by direct
10 sequencing of PCR amplicons and in muscle biopsies by additional sequencing of isolated bacterial clones with individual amplicon sequences.

Analysis of otoferlin expression

 Western blotting is performed to determine the presence of myostatin in the
15 muscle fiber. Equal amounts of total proteins are run on 12% (v/v) gel electrophoresis and electrophoretically transferred to a PVDF membrane. Monoclonal mouse anti-otoferlin antibody is used in the western blotting. The washed membranes are incubated with 1:50000 dilution of secondary antibody linked to horseradish peroxidase (HPR). HPR activity is detected using western blot chemiluminescence.

20

AAV-OTOF rescue therapy in transgenic sheep model

 AAV-OTOF prepared in artificial perilymph is administered to OTOF knockout transgenic sheep to assess the ability to restore normal hearing function following delivery to the cochlea via trans-RWM infusion. Baseline auditory brainstem response
25 (ABR) and distortion product otoacoustic emissions (DPOAEs) are measured in female sheep at 3 months of age (n=30), bilaterally, to assess pre-treatment inner hair cell (IHC) and outer hair cell (OHC) function. Following baseline ABR and DPOAE measurements, 20 uL of AAV1-OTOF at titers of 1.0e14, 3.2e13 and 1.0e13 vg/mL is injected into the left scala tympani of the sheep (n=10 per group). Each animal's right
30 ear is left as an untreated control. ABR and DPOAE measurements are taken again bilaterally 1, 5 and 10 days following the surgical procedure. At 6 months post-

procedure, additional bilateral ABR and DPOAE measurements are taken from all animals, and the animals are subsequently sacrificed and their cochleae removed.

In half of the sacrificed animals (n=5 from each of the dose cohorts), immunostaining is performed to identify hair cell structures and to assess OTOF protein expression along the cochlear sensory epithelium. Antibodies against markers for hair cells (Myo7a), supporting cells (Sox2) and otoferlin are used as described previously (Duncker et al. 2013, *J Neurosci* 33(22):9508-9519). At the basal, middle and apical turns of the organ of corti, total numbers of hair cells and those hair cells expressing OTOF are counted within 200 um regions.

In the remaining half of the sacrificed animals (remaining 5 animals from each dose cohort), cochlear tissue samples are collected from the same basal, middle and apical regions as described above, and assayed for otoferlin mRNA transcript as described previously (Duncker et al. 2013, *J Neurosci* 33(22):9508-9519, Heidrych et al. 2008, *Hum Mol Genet* 17:3814-3821, Heidrych et al., 2009, *Hum Mol Genet* 18:2779-2790).

Example 13: Human Clinical Example (Pediatric Treatment)

The patient is put under general anesthesia. The surgeon approaches the tympanic membrane from external auditory canal, makes a small incision at the inferior edge of the external auditory canal where it meets the tympani membrane, and lifts the tympanic membrane as a flap to expose the middle ear space. A surgical laser is used to make a small opening (approximately 2 mm) in the stapes footplate. The surgeon then penetrates the round window membrane with a microcatheter loaded with a solution of AAV-OTOF prepared in artificial perilymph at a titer of 1×10^{13} vg/mL. The microcatheter is connected to a micromanipulator that infuses approximately 20 uL of the AAV-OTOF solution at a rate of approximately 1 uL / min. At the conclusion of the AAV-OTOF infusion, the surgeon withdraws the microcatheter and patches the holes in the stapes foot plate and RWM with a gel foam patch. The procedure concludes with replacement of the tympanic membrane flap.

Example 14: Non-Invasive Prenatal Testing of Maternal Blood to Detect OTOF Mutation

Maternal blood samples (20-40 mL) are collected into Cell-free DNA tubes. At least 7 mL of plasma is isolated from each sample via a double centrifugation protocol of 2,000 g for 20 minutes, followed by 3,220 g for 30 minutes, with supernatant transfer following the first spin. cfDNA is isolated from 7-20 mL plasma using a QIAGEN QIAmp Circulating Nuclei Acid kit and eluted in 45 μ L TE buffer. Pure maternal genomic DNA is isolated from the buffy coat obtained following the first centrifugation.

By combining thermodynamic modeling of the assays to select probes with minimized likelihood of probe-probe interaction with amplification approaches described previously (Stiller et al. 2009 *Genome Res* 19(10):1843-1848), multiplexing of 11,000 assays can be achieved. Maternal cfDNA and maternal genomic DNA samples are pre-amplified for 15 cycles using 11,000 target-specific assays and an aliquot is transferred to a second PCR reaction of 15 cycles using nested primers. Samples are prepared for sequencing by adding barcoded tags in a third 12-cycle round of PCR. The targets include SNPs corresponding to the 100 mutations in chromosome 2 known to lead to otoferlin loss-of-function (Zhang et al. 2016 *Clin Genetics* Jan 27). The amplicons are then sequenced using an Illumina HiSeq sequencer. Genome sequence alignment is performed using commercially available software.

Example 15: Alternative Examples (mRNA, Single Viral Vector, Non-Viral Vectors)

Single viral vector preparation

Mouse otoferlin lacking the N-terminal domains can rescue the knockdown phenotype in otoferlin knockout zebrafish (Chatterjee et al. *Mol Cell Biol* 2015, 35(6):1043-1054). However, in mammals, missense mutations in the C2B and C2C domains have been linked to hearing loss (Longo-Guess et al., 2007 *Hear Res*, 234:21-28; Mirghomizadeh et al., 2002 *Neurobiol Dis* 10:157-164), suggesting that these domains are essential to the normal hearing-related function of otoferlin in higher species. The C2A domain of mammalian otoferlin does not bind Ca^{2+} , whereas all other C2 domains bind Ca^{2+} with moderate (20-50 μ M) or low (400-700 μ M) affinity in the

absence of acidic lipids. The C2D and C2E domains bind Ca^{2+} as well as phosphatidylserine (PS) in a Ca^{2+} -dependent manner. A cDNA is produced that encodes a truncated form of otoferlin lacking the C2A, C2D and C2E domains. This cDNA is suitable for packaging in an AAV vector.

5 The truncated otoferlin construct (OTOF Δ C2ADE) is derived and cloned from an original wildtype otoferlin plasmid encoding the full OTOF gene, as described by Padmanarayana et al. 2014 *Biochem* 53:5023-5033. Deletion of the coding region of the C2 domains is performed by PCR mutagenesis using domain-spanning oligonucleotides and a QuikChange site-directed mutagenesis kit applying the double mutagenic primer
10 approach. Briefly, the PCR is performed as follows: 95°C for 3 minutes; 18 cycles at 95°C for 15 seconds, 65°C for 1 minute, and 68°C for 12 minutes; and 68°C for 7 minutes. The PCR product is digested with DpnI, cloned into the DSC-B vector, and transformed into DH5alpha or XL10-Gold bacterial cells. Plasmid DNA is isolated by mini preparations and subsequently sequenced.

15 A plasmid containing a CBA promoter, a chimeric intron (β -globin), a consensus Kozak sequence, the OTOF Δ C2ADE cDNA and a polyadenylation signal sequence is used for the AAV construct. Recombinant AAV is generated by transfection with an adenovirus-free method as used by Xiao et al. *J Virol* 1999, 73(5):3994-4003. The cis plasmids with AAV ITRs, the trans plasmid with AAV Rep and Cap genes, and a helper
20 plasmid with an essential region from an adenovirus genome are co-transfected in 293 cells in a ratio of 1:1:2. AAV serotypes 1, 2, 3, 4, 5, 6, 7, 8, 9, rh8, rh10, rh39, rh43, and Anc80 are each prepared to encapsulate the OTOF Δ C2ADE cDNA construct.

CELiD preparation

25 The otoferlin gene is prepare for non-viral gene transfer as described by Li et al. 2013, *PLoS ONE* 8(8):e69879. First, *Spodoptera frugiperda* Sf9 cells are grown in suspension in serum-free media. The blasticidin-S deaminase (bs) gene is PCR-amplified from pIB/V5-His/CAT using the following primer pair:

5'-ATAAGCTTACGCTCAGTGGAACGAAAAC-3' (SEQ ID NO: 36) and

30 5'-ATAAGCTTGACGTGTCAGTGTCAGTCCTGCTCCT-3' (SEQ ID NO: 37).

The 865 bp PCR product is digested with HindIII and ligated into HindIII-digested

pFBGR. Sf9 cells are transfected with pFBGR-bsd using Cellfectin Transfection Reagent. At three days post-transfection, antibiotic-resistant cells are selected by the addition of blasticidin-S HCl (50 µg/mL) to the growth medium. After two weeks in selective medium, blasticidin-resistant (bsd^r) clones are derived by single-cell dilution or
5 direct colony transfer techniques. The bsd^r clones are expanded in insect cell culture medium supplemented with 10% FBS and blasticidin-S HCl (10 µg/mL) for 2 to 3 additional passages, then returned to serum-free medium with 10 µg/mL blasticidin-S HCl. After an additional 12 passages, blasticidin-S HCl is omitted from the medium and the cell lines are expanded for analysis. For functional screening, clonal Sf9/ITR-OTOF
10 cell lines are infection (MOI=5) with a recombinant baculovirus, Bac-Rep, expressing the AAV type 2 Rep78 and Rep52 proteins and analyzed for induced OTOF expression. Clonal Sf9/ITR-OTOF cells with the highest levels of OTOF expression are expanded for CELiD-OTOF DNA preparation.

Clonal Sf9/ITR-OTOF cells are seeded at 2e6 cells/mL and infected with Bac-
15 Rep (MOI = 1 to 3). Cell viability and diameter are monitored daily until the cell diameter increased to 18-20 µm (uninfected cell diameter 14-15 µm), indicating that the cells are in the late stages of the viral infection. Extrachromosomal DNA is extracted from the Bac-Rep-infected, Sf9/ITR-GFP cells using a commercially available plasmid isolation kit. CELiD production is monitored by agarose gel electrophoresis and
20 ethidium bromide staining of extrachromosomal DNA. CELiD DNA is produced in parental Sf9 cells by co-infection with two separate baculovirus expression vectors (BEV): Bac-Rep and a second BEV bearing an ITR-flanked transgene, such as Bac-OTOF. Infected Sf9 cells are harvested once the mean cell diameter increases by 4-5 µm and the percent viability decreases to 80-90%. CELiD DNA is isolated using a
25 comemercially available plasmid purification kit.

Clonal Sf9/ITR-OTOF cells are inoculated with various amounts of Bac-Rep stock. Cells are periodically harvested and extrachromosomal DNA is recovered using a commercially available DNA isolation kit. Extracted DNA is examined by either agarose gel electrophoresis or by PCR with OTOF-specific primer pairs for quantitative
30 determination of CELiD DNA amounts. For western blotting, cell proteins are fractionated by SDS-polyacrylamide gel electrophoresis and transferred to nitrocellulose

membranes. The membranes are incubated in blocking buffer (BB) composed of 5% non-fat dry milk (w:v) in phosphate-buffered saline plus 0.05% Tween-20 (PBST) for 1 hr at ambient temperature with orbital agitation. After washing the membranes in wash buffer (WB) composed of 3% non-fat dry milk in PBST, membranes are incubated with the appropriate primary antibody solution (diluted in BB) either at ambient temperature (1 hr) or 4°C (overnight) with continuous orbital agitation. The following primary antibodies and dilution ratios are used: anti-AAV Rep mouse monoclonal antibody (mAb); 2. anti-baculovirus envelope glycoprotein gp64 mouse mAb; anti-OTOF mouse mAb. After incubation, primary antibody solutions are removed and membranes are washed in WB (3×5 mins). Non-conjugated mAbs are incubated with secondary antibody solution (goat, anti-mouse horseradish peroxidase (HRP)-conjugate for 1 hr, and then washed with WB as above. HRP activity is detected by enhanced chemiluminescence (ECL).

Lipid nanoparticles

Otoferlin cDNA or mRNA is encapsulated in poly(lactic-co-glycolic acid) nanoparticles by the double-emulsion solvent evaporation method described previously (O'Donnell and McGinity 1997 *Adv Drug Delivery Rev* 28(1):25-42), and in lipid nanoparticles (Pezzoli et al. 2013 *Methods Mol Biol* 1025:269-279). Briefly, solid lipid nanoparticles can be generated from a microemulsion using Precirol ATO-5 and stearylamine as the cationic lipid. 500 mg of Precirol ATO-5 is heated to 10°C above its melting point, and 10 mL of a hot aqueous solution of poloxamer and stearylamine in different proportions (1/1.25; 1/1.87; 1/3.12; 1/4.37 and 1/5) is added. The sample is stirred for 30 minutes at 14,000 rpm. The nanoparticles are generated by dispersing the hot microemulsion in cold water (2-5°C) in an emulsion:water ratio of 1:5. To recover nanoparticles, the resultant suspension is centrifuged for three times at 3,000 rpm for 20 minutes at a temperature of 20°C, reconstituting the precipitate after centrifugation. Cationic solid lipid nanoparticles are lyophilized by being added an aqueous solution of cryoprotectant (5% mannitol) in a 1:2 (SLN:mannitol) ratio. The freezing temperature is set at -40°C in the lyophilizer and samples are kept at this temperature for 2 hours. Lyophilization temperature is then set to 25°C at a pressure of 0.2-0.4 mBa for 48 hours. A solution of the OTOF cDNA plasmid is prepared to a concentration of 2µg/µL. A 25 µL aliquot of the plasmid DNA solution is then added to different volumes of the

cationic SLN suspension to obtain ratios of between 15:1 and 1:1 (SLN:OTOF) by stirring.

Modified RNA

5 Polynucleotides, primary constructs mRNA (or modified mRNA, or “mmRNA”) for use in accordance with the invention may be prepared according to any available technique including, but not limited to chemical synthesis, enzymatic synthesis, which is generally termed in vitro transcription (IVT), or enzymatic or chemical cleavage of a longer precursor, etc. Methods of synthesizing RNAs are known in the art (see, e.g., Gait,
10 M. J. (ed.) Oligonucleotide synthesis: a practical approach, Oxford [Oxfordshire], Washington, D.C.: IRL Press, 1984; and Herdewijn, P. (ed.) Oligonucleotide synthesis: methods and applications, Methods in Molecular Biology, v. 288 (Clifton, N.J.) Totowa, N.J.: Humana Press, 2005; both of which are incorporated herein by reference).

The process of design and synthesis of the primary constructs of the invention
15 generally includes the steps of gene construction, mRNA production (either with or without modifications) and purification. In the enzymatic synthesis method, a target polynucleotide sequence encoding the polypeptide of interest is first selected for incorporation into a vector, which will be amplified to produce a cDNA template. Optionally, the target polynucleotide sequence and/or any flanking sequences may be
20 codon optimized. The cDNA template is then used to produce mRNA through in vitro transcription (IVT). After production, the mRNA may undergo purification and clean-up processes. The steps of which are provided in more detail below.

Gene Construction

25 The step of gene construction may include, but is not limited to gene synthesis, vector amplification, plasmid purification, plasmid linearization and clean-up, and cDNA template synthesis and clean-up.

Gene Synthesis

30 Once a polypeptide of interest, or target, is selected for production, a primary construct is designed. Within the primary construct, a first region of linked nucleosides

encoding the polypeptide of interest may be constructed using an open reading frame (ORF) of a selected nucleic acid (DNA or RNA) transcript. The ORF may comprise the wild type ORF, an isoform, variant or a fragment thereof. As used herein, an "open reading frame" or "ORF" is meant to refer to a nucleic acid sequence (DNA or RNA) that encodes a polypeptide of interest. ORFs often begin with the start codon, ATG, and end with a nonsense or termination codon or signal. Further, the nucleotide sequence of the first region may be codon optimized. Codon optimization methods are known in the art and may be useful in efforts to achieve one or more of several goals. These goals include to match codon frequencies in target and host organisms to ensure proper folding, bias GC content to increase mRNA stability or reduce secondary structures, minimize tandem repeat codons or base runs that may impair gene construction or expression, customize transcriptional and translational control regions, insert or remove protein trafficking sequences, remove/add post translation modification sites in encoded protein (e.g. glycosylation sites), add, remove or shuffle protein domains, insert or delete restriction sites, modify ribosome binding sites and mRNA degradation sites, adjust translational rates to allow the various domains of the protein to fold properly, or reduce or eliminate problematic secondary structures within the mRNA. Codon optimization tools, algorithms and services are known in the art. Non-limiting examples include services from GeneArt (Life Technologies) and DNA2.0 (Menlo Park Calif.) and/or proprietary methods. In one embodiment, the ORF sequence is optimized using optimization algorithms. Codon options for each amino acid are known in the art.

Stop Codons

In one embodiment, the primary constructs of the present invention may include at least two stop codons before the 3' untranslated region (UTR). The stop codon may be selected from TGA, TAA and TAG. In one embodiment, the primary constructs of the present invention include the stop codon TGA and one additional stop codon. In a further embodiment, the additional stop codon may be TAA. In another embodiment, the primary constructs of the present invention include three stop codons.

Vector Amplification

The vector containing the primary construct is then amplified and the plasmid isolated and purified using methods known in the art such as, but not limited to, a maxi prep using the Invitrogen PURELINK.TM. HiPure Maxiprep Kit (Carlsbad, Calif.).

5

Plasmid Linearization

The plasmid may then be linearized using methods known in the art such as, but not limited to, the use of restriction enzymes and buffers. The linearization reaction may be purified using methods including, for example Invitrogen's PURELINK® PCR Micro Kit (Carlsbad, Calif.), and HPLC based purification methods such as, but not limited to, strong anion exchange HPLC, weak anion exchange HPLC, reverse phase HPLC (RP-HPLC), and hydrophobic interaction HPLC (HIC-HPLC) and Invitrogen's standard PURELINK.TM. PCR Kit (Carlsbad, Calif.). The purification method may be modified depending on the size of the linearization reaction conducted. The linearized plasmid is then used to generate cDNA for in vitro transcription (IVT) reactions.

10

15

cDNA Template Synthesis

A cDNA template may be synthesized by having a linearized plasmid undergo polymerase chain reaction (PCR). Primer-probe design for any amplification is within the skill of those in the art. Probes may also contain chemically modified bases to increase base-pairing fidelity to the target molecule and base-pairing strength. Such modifications may include 5-methyl-Cytidine, 2,6-di-amino-purine, 2'-fluoro, phosphoro-thioate, or locked nucleic acids.

20

25

mRNA Production

The process of mRNA or mmRNA production may include, but is not limited to, in vitro transcription, cDNA template removal and RNA clean-up, and mRNA capping and/or tailing reactions.

30

In Vitro Transcription

The cDNA produced above may be transcribed using an in vitro transcription (IVT) system. The system typically comprises a transcription buffer, nucleotide triphosphates (NTPs), an RNase inhibitor and a polymerase. The NTPs may be manufactured in house, may be selected from a supplier, or may be synthesized as described herein. The NTPs may be selected from, but are not limited to, those described herein including natural and unnatural (modified) NTPs. The polymerase may be selected from, but is not limited to, T7 RNA polymerase, T3 RNA polymerase and mutant polymerases such as, but not limited to, polymerases able to incorporate modified nucleic acids.

5' Capping

The 5' cap structure of an mRNA is involved in nuclear export, increasing mRNA stability. It binds the mRNA Cap Binding Protein (CBP), which is responsible for mRNA stability in the cell and translation competency through the association of CBP with poly(A) binding protein to form the mature cyclic mRNA species. The cap further assists the removal of 5' proximal introns during mRNA splicing. Endogenous mRNA molecules may be 5'-end capped generating a 5'-ppp-5'-triphosphate linkage between a terminal guanosine cap residue and the 5'-terminal transcribed sense nucleotide of the mRNA molecule. This 5'-guanylate cap may then be methylated to generate an N7-methyl-guanylate residue. The ribose sugars of the terminal and/or antiterminal transcribed nucleotides of the 5' end of the mRNA may optionally also be 2'-O-methylated. 5'-decapping through hydrolysis and cleavage of the guanylate cap structure may target a nucleic acid molecule, such as an mRNA molecule, for degradation. Modifications to the polynucleotides, primary constructs, and mmRNA of the present invention may generate a non-hydrolyzable cap structure preventing decapping and thus increasing mRNA half-life. Because cap structure hydrolysis requires cleavage of 5'-ppp-5' phosphodiester linkages, modified nucleotides may be used during the capping reaction. For example, a Vaccinia Capping Enzyme from New England Biolabs (Ipswich, Mass.) may be used with .alpha.-thio-guanosine nucleotides according to the manufacturer's instructions to create a phosphorothioate linkage in the 5'-ppp-5' cap.

Additional modified guanosine nucleotides may be used such as .alpha.-methyl-phosphonate and seleno-phosphate nucleotides. Additional modifications include, but are not limited to, 2'-O-methylation of the ribose sugars of 5'-terminal and/or 5'-antiterminal nucleotides of the mRNA (as mentioned above) on the 2'-hydroxyl group of the sugar
 5 ring. Multiple distinct 5'-cap structures can be used to generate the 5'-cap of a nucleic acid molecule, such as an mRNA molecule.

Flanking Regions Untranslated Regions (UTRs)

Untranslated regions (UTRs) of a gene are transcribed but not translated. The
 10 5'UTR starts at the transcription start site and continues to the start codon but does not include the start codon, whereas the 3'UTR starts immediately following the stop codon and continues until the transcriptional termination signal. UTRs can be incorporated into the polynucleotides, primary constructs and/or mRNA of the present invention to enhance the stability of the molecule. UTRs also be incorporated to ensure controlled down-
 15 regulation of the transcript in case they are misdirected to undesired organs sites.

5' UTR and Translation Initiation

By engineering the features typically found in abundantly expressed genes of specific target organs, one can enhance the stability and protein production of the polynucleotides, primary constructs or mmRNA of the invention. For example, introns
 20 or portions of introns sequences may be incorporated into the flanking regions of the polynucleotides, primary constructs or mmRNA of the invention.

AU Rich Elements

AU rich elements (AREs) can be separated into three classes (Chen et al., Mol.
 25 Cell. Biol. 15:5777-5788, 1995; Chen et al., Mol. Cell Biol. 15:2010-2018, 1995): Class I AREs contain several dispersed copies of an AUUUA motif within U-rich regions. C-Myc and MyoD contain class I AREs. Class II AREs possess two or more overlapping UUAUUUA(U/A)(U/A) (SEQ ID NO: 38)nonamers. Molecules containing this type of AREs include GM-CSF and TNF-a. Class III AREs are less well defined. These U rich
 30 regions do not contain an AUUUA motif. c-Jun and Myogenin are two well-studied examples of this class. Most proteins binding to the AREs are known to destabilize the

messenger, whereas members of the ELAV family, most notably HuR, have been documented to increase the stability of mRNA. HuR binds to AREs of all the three classes. Engineering the HuR specific binding sites into the 3' UTR of nucleic acid molecules will lead to HuR binding and thus, stabilization of the message in vivo.

5 Introduction, removal or modification of 3' UTR AU rich elements (AREs) can be used to modulate the stability of polynucleotides, primary constructs or mmRNA of the invention. When engineering specific polynucleotides, primary constructs or mmRNA, one or more copies of an ARE can be introduced to make polynucleotides, primary constructs or mmRNA of the invention less stable and thereby curtail translation and
10 decrease production of the resultant protein. Likewise, AREs can be identified and removed or mutated to increase the intracellular stability and thus increase translation and production of the resultant protein. Transfection experiments can be conducted in relevant cell lines, using polynucleotides, primary constructs or mmRNA of the invention and protein production can be assayed at various time points post-transfection. For
15 example, cells can be transfected with different ARE-engineering molecules and by using an ELISA kit to the relevant protein and assaying protein produced at 6 hour, 12 hour, 24 hour, 48 hour, and 7 days post-transfection. The polynucleotide, primary construct, and mRNA of the invention can be formulated using natural and/or synthetic polymers. Non-limiting examples of polymers which may be used for delivery include, but are not
20 limited to, DYNAMIC POLYCONJUGATE® (Arrowhead Research Corp., Pasadena, Calif.) formulations from MIRUS® Bio (Madison, Wis.) and Roche Madison (Madison, Wis.), PHASERX™ polymer formulations such as, without limitation, SMARTT POLYMER TECHNOLOGY™ (PHASERX.RTM., Seattle, Wash.), DMRI/DOPE, poloxamer, VAXFECTIN® adjuvant from Vical (San Diego, Calif.), chitosan,
25 cyclodextrin from Calando Pharmaceuticals (Pasadena, Calif.), dendrimers and poly(lactic-co-glycolic acid) (PLGA) polymers. RONDEL™ (RNAi/Oligonucleotide Nanoparticle Delivery) polymers (Arrowhead Research Corporation, Pasadena, Calif.) and pH responsive co-block polymers such as, but not limited to, PHASERX® (Seattle, Wash.). Many of these polymer approaches have demonstrated efficacy in delivering
30 oligonucleotides in vivo into the cell cytoplasm (reviewed in deFougerolles Hum Gene Ther. 2008 19:125-132; herein incorporated by reference in its entirety). Two polymer

approaches that have yielded robust in vivo delivery of nucleic acids, in this case with small interfering RNA (siRNA), are dynamic polyconjugates and cyclodextrin-based nanoparticles. The first of these delivery approaches uses dynamic polyconjugates and has been shown in vivo in mice to effectively deliver siRNA and silence endogenous target mRNA in hepatocytes (Rozema et al., Proc Natl Acad Sci USA. 2007 104:12982-12887; herein incorporated by reference in its entirety). This particular approach is a multicomponent polymer system whose key features include a membrane-active polymer to which nucleic acid, in this case siRNA, is covalently coupled via a disulfide bond and where both PEG (for charge masking) and N-acetylgalactosamine (for hepatocyte targeting) groups are linked via pH-sensitive bonds (Rozema et al., Proc Natl Acad Sci USA. 2007 104:12982-12887; herein incorporated by reference in its entirety). On binding to the hepatocyte and entry into the endosome, the polymer complex disassembles in the low-pH environment, with the polymer exposing its positive charge, leading to endosomal escape and cytoplasmic release of the siRNA from the polymer. Through replacement of the N-acetylgalactosamine group with a mannose group, it was shown one could alter targeting from asialoglycoprotein receptor-expressing hepatocytes to sinusoidal endothelium and Kupffer cells. Another polymer approach involves using transferrin-targeted cyclodextrin-containing polycation nanoparticles. These nanoparticles have demonstrated targeted silencing of the EWS-FLI1 gene product in transferrin receptor-expressing Ewing's sarcoma tumor cells (Hu-Lieskovan et al., Cancer Res. 2005 65: 8984-8982; herein incorporated by reference in its entirety) and siRNA formulated in these nanoparticles was well tolerated in non-human primates (Heidel et al., Proc Natl Acad Sci USA 2007 104:5715-21; herein incorporated by reference in its entirety). Both of these delivery strategies incorporate rational approaches using both targeted delivery and endosomal escape mechanisms.

Example 16 – Restoration of Hearing in *Otof*^{-/-} Mice by the Trans-Splicing

Approach

An experiment was performed to determine whether hearing could be restored in *Otof*^{-/-} mice using a combination of two different vectors using the methods described herein.

Materials and Methods

Cloning

Mouse otoferlin cDNA transcript variant 4 (KX060996; coding DNA sequence (CDS) identical to reference sequence NM_001313767) that had been subcloned from cochlear cDNA (Strenzke et al. (2016) EMBO J. 35 2519–2535) was subcloned into the backbone for AAV production using standard cloning strategies including restriction digests and ligation. Both vectors contain ITRs of serotype 2. A CMV enhancer and human β -actin promoter were subcloned into the 5' vector, which contains eGFP cDNA and a P2A signal (Figure 1). The otoferlin CDS was split at the exon21-exon22 junction into two halves of about similar size. The 5' vector encodes the N-terminal part of otoferlin from amino acid 1 to 844, the 3' vector contains the coding sequence for amino acids 845 to 1977 and woodchuck hepatitis virus posttranscriptional regulatory element (WPRE) and poly-adenylation signals.

For the trans-splicing approach, a splice donor site (Trapani *et al.* (2014) *EMBO Mol. Med.* 6(2):194-211, 2014) follows the coding sequence in the 5' vector. In the 3' vector, a splice acceptor site was subcloned just before the coding sequence for otoferlin. Within the coding sequence, a silent mutation was introduced, generating an additional site for restriction digestion.

For the hybrid approach, an F1 phage recombinogenic region for homologous recombination was subcloned right after the splice donor site in the 5' vector and before the splice acceptor site of the 3' vector (Figure 2). The plasmid identities were verified by Sanger sequencing.

Virus production and purification

Dual AAV vectors were produced by transient transfection of HEK293 cells grown in multi-level cell factories. The cells were co-transduced with helper plasmids for virus production encoding serotype 6 capsid proteins. Purification of cell lysates was performed by iodixanol density-gradient ultracentrifugation, followed by a second purification and concentration step by FPLC affinity-chromatography (Asai et al. (2015) *Nat. Neurosci.* 18 1584–1593; Tereshchenko et al. (2014) *Neurobiol. Dis.* 65 35–42). For

the trans-splicing approach, the 5' vector achieved a concentration of $\sim 2.8 \times 10^8$ transducing units/ μL . The 3' vector reached $\sim 1.4 \times 10^8$ transducing units/ μL . For the hybrid approach, both viruses were purified simultaneously in the same solutions, reaching slightly higher virus titers.

5

Mouse strains

Otoferlin knock-out (*Otof*^{-/-}) mice were generated as described (Reisinger et al. (2011) J. Neurosci. 31 4886–4895) and backcrossed for at least 5 generations to either C57/Bl6N or to CD1 strains. For virus injection, F1 offspring from *Otof*^{-/-} CD1 females and *Otof*^{-/-} C57/Bl6N males were used. For wild type controls, *Otof*^{+/+} mice from *Otof*^{+/+} C57/Bl6N breeding were crossed with CD1 wild type mice (Charles River).

10

Virus injection

Mice at postnatal day 6 to 7 (P6-7) were anesthetized using 2.5% - 5% isoflurane. The skin behind the left bulla was opened and the round window niche was exposed. Virus solution in a glass capillary was injected through the round window membrane using a PLI-100A BASIC PICOLITER microinjector (Harvard Apparatus GmbH, Germany) as pressure source, thereby injecting about 0.2-0.5 μL solution per inner ear (Jung *et al.* (2015) EMBO J. 34 2686–2702). The skin was closed and the pups were raised by their mothers.

15
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Immunohistochemistry

Immunostaining was performed as previously described (Strenzke et al. (2016) EMBO J. 35 2519–2535). Temporal bones were isolated after decapitation and a part of the cochlear bony shelf was opened and the round window was perforated. The temporal bones were fixed in 4% formaldehyde in PBS for 45 min at 4 °C. Cochleas of mice older than P20 were decalcified either for 5 min in Morse's solution or 2 days in 0.12M EDTA solution. Blocking was performed with 17% normal goat serum, 0.3% Triton X-100, 0.45mM NaCl, and 20mM phosphate buffer, pH 7.4. Antibodies were diluted in blocking solution and applied to the organ of Corti situated in the temporal bones before apical and basal turns were excised. The following antibodies were used: goat IgG1 anti-Ctbp2

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mouse anti-otoferlin (RRID:AB_881807, Abcam, Cambridge, UK, 1:300), rabbit anti-otoferlin (Synaptic Systems, Göttingen, Germany, 1:100), goat anti-calbindin D28k and secondary Alexa Fluor®405, Alexa Fluor®488-, Alexa Fluor®568-, Alexa Fluor®594-, and AlexaFluor647-labeled antibodies (Invitrogen, 1:200). Confocal microscopy images were acquired as stacks of 2D images with a step size of 0.6 μm using a laser scanning confocal microscope (Leica TCS SP5, Leica Microsystems CMS GmbH, Mannheim, Germany) with a 63x glycerol immersion objective (NA = 1.456). The number of synapses in 14-16 day old inner hair cells (IHCs) were counted using the cell counter plugin in ImageJ software as number of Ctbp2 spots. Image analysis to determine fractional levels of membrane bound otoferlin is described in Strenzke et al. (2016a) EMBO J. 35 2519–2535).

Electrophysiology

Ca^{2+} currents and plasma membrane capacitance from IHCs were measured by patch-clamp of IHCs from the apical coils of freshly dissected organs of Corti in the perforated-patch configuration at room temperature (20 – 25 °C) as described (Moser & Beutner (2000) Proc Natl Acad Sci U S A 97 883–888). The pipette solution contained 130 mM Cs-gluconate, 10 mM tetraethylammonium-chloride (TEA-Cl), 10 mM 4-aminopyridine (Merck, Darmstadt, Germany), 1 mM MgCl_2 , 10 mM Cs-HEPES (pH 7.17, osmolarity approx. 290 mOsm), 300 $\mu\text{g/mL}$ amphotericin B (Calbiochem, La Jolla, CA). The extracellular solution contained 110 mM NaCl, 35 mM TEA-Cl, 2.8 mM KCl, 2 mM CaCl_2 , 1 mM MgCl_2 , 10 mM Na-HEPES, 1 mM CsCl, 11.1 mM D-glucose (pH 7.2, osmolarity approx. 300 mOsm). Unless stated otherwise, all chemicals were obtained from Sigma-Aldrich (Taufkirchen, Germany). An EPC-9 amplifier (HEKA Electronics, Lambrecht, Germany) controlled by *Pulse* software was used to sample and filter currents at 20 kHz and at 5 kHz, respectively. Potentials were corrected for liquid junction potentials (-14mV). ΔCm was measured using depolarizations of different durations to peak Ca^{2+} current potential, with 30-60 sec inter-stimulus intervals, as previously described (Beutner & Moser (2000) Proc Natl Acad Sci U S A 97 883–888). All currents were leak-corrected using a P/6-protocol. The vesicle replenishment rate was calculated as ΔCm during 100 ms depolarization minus ΔCm at 20 ms

depolarization, divided by 45 aF per vesicle (Neef et al. (2007) The Journal of Neuroscience 27 12933–12944) to get the number of vesicles. The number of active zones per cell was determined with immunohistochemistry (10 synapses for transduced *Otof*^{-/-} IHCs, 14 synapses for *Otof*^{+/+} IHCs).

5

ABR Recordings

Auditory brainstem responses were recorded as described (Jing *et al.* (2013) J Neurosci 33 4456–4467).

10 *RNA Isolation, Reverse Transcription, PCR and Sequencing*

Total RNA was isolated from acutely dissected organs of Corti with Invitrogen™ TRIzol™ Plus RNA Purification Kit (Thermo Fisher Scientific, 12183555) according to the manufacturer's instructions and used as a template for cDNA synthesis using SuperScript® IV First-Strand Synthesis System (ThermoFisher Scientific, 18091050) with Oligo(dT)₂₀ and Random Hexamer primers. The cDNA was further used in PCR amplification reactions using DreamTaq® Polymerase (Thermo Fisher Scientific, EP0702), using the following primers:

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N-terminal fragment 3'-CCCACAAGGCCAACGAGACGGATGAGGAC-5' (SEQ ID NO: 24) and 3'-AAGAGGCTTCGGGCCTGATACATGTGTGCT-5' (SEQ ID NO: 25);

20

Assembly fragment 3'-ACGGCAATGAAGTCGATGGTATGTCCCGGC-5' (SEQ ID NO: 26);

C-terminal fragment 3'-CTGACCTGCCACCCATCAATGGCCCAGTGG-5' (SEQ ID NO: 27) and 3'-CTATGCGCTCCTCCTCTGTGGAGCCATCCT-5' (SEQ ID NO: 28).

25

All bands were excised, cloned into a pCR2.1™-TOPO® vector using the TOPO® TA® Cloning Kit (Thermo Fisher Scientific, 450641), and shot into One Shot™ TOP10 Electrocomp™ *E. coli* cells (Thermo Fisher Scientific, C404050). All clones were screened for the correct insert and verified by Sanger sequencing.

30

Results

To test the trans-splicing approach, dual-AAV vectors were generated, each comprising one half of the otoferlin CDS. In the first vector, a human β -actin promoter and a CMV enhancer were used to drive the expression of eGFP and the 5' otoferlin fragment, separated by a P2A sequence (Figure 1). The second vector contained the 3' otoferlin CDS and mRNA stabilizing elements. AAV vectors underwent head-to-tail multimerization in the nuclei of target cells by non-homologous end joining of the inverted terminal repeats (ITRs), thereby promoting the assembly of the two vector genomes. A splice donor site in the 5' vector and a splice acceptor site in the 3' vector were included to force the processing of a correct full-length otoferlin mRNA (Figure 1).

Otoferlin knock-out *Otof*^{-/-} animals on postnatal day 6-7 (P6-7) were co-injected with both AAVs ($\sim 1.4 - 2.8 \times 10^8$ transducing units/ μ L) through the round window membrane of the left ear (Figure 3). Non-injected *Otof*^{-/-} littermates and wild-type animals, some of which were injected with eGFP-encoding AAVs, served as controls. At P23-28, hearing was tested using auditory brainstem recordings (ABRs), and the inner hair cell (IHC) transduction rate and otoferlin expression levels were tested using immunohistochemistry. As shown in Figure 3, in non-transduced *Otof*^{-/-} mice, ABR recordings elicited a prominent summing potential (SP) due to the depolarization of IHCs, but these signals were not transmitted to the brainstem, resulting in a flat line. After dual-AAV transduction, mice displayed typical ABR waves, indicating that auditory information was processed to the brain stem.

In response to click stimuli, thresholds in successfully transduced ears were at 54 ± 3 dB (range: 30-70dB). In control experiments, non-transduced *Otof*^{-/-} littermate animals showed no ABR waves except the summing potential, even at 100 dB sound stimulus. Pure tone stimuli elicited ABR responses in most transduced ears, but not in non-transduced *Otof*^{-/-} littermate controls (Figures 3-6). Pure tone ABRs were detectable for low (6kHz), mid (12kHz), and high frequencies (24kHz). The *Otof*^{+/+} controls showed normal ABR wave forms with a threshold of 39 ± 1 dB (range: 30-40dB) (Figures 4 and 5). As shown in Figure 4, the amplitudes of ABR waves in transduced *Otof*^{-/-} mice are smaller than in wild type *Otof*^{wt/wt} mice transduced with dual-AAV with enhanced green fluorescent protein (eGFP).

To test for correct concatemerization and reassembly of the full-length otoferlin mRNA in the right orientation, mRNA was extracted from transduced and non-transduced P14 *Otof*^{-/-} organs of Corti. After reverse transcription into cDNA, three fragments from otoferlin mRNA were amplified: one encoded by the 5' virus, one
 5 encoded by the 3' virus, and one fragment covering the site of assembly of the two vectors. Sanger sequencing of the PCR amplicons revealed the correct otoferlin transcripts containing the silent mutation of virally transduced otoferlin, indicating correct assembly of dual-AAV transduced otoferlin mRNA.

To study the inner hair cell (IHC) transduction rate and otoferlin expression
 10 levels, organs of Corti were dissected at P18-28 and analyzed by immunohistochemistry using two anti-otoferlin antibodies, one binding to the N-terminal part and the other binding to the very C-terminal part of otoferlin (Figure 6 and Figure 7). As shown in Figure 7, calbindin was used as marker for inner and outer hair cells. Cells expressing eGFP indicated virus transduction of at least the 5' virus. Anti-otoferlin antibody
 15 staining (Abcam) in the N-terminal half of otoferlin indicated expression of the N-terminal part of otoferlin. C-terminal anti-otoferlin antibody staining (Synaptic Systems) indicated expression of the C-terminal part of otoferlin. Taken together, all three panels in Figure 7 demonstrated that full-length otoferlin was expressed in IHCs. Twelve to
 20 fifty-one percent (on average $32 \pm 4\%$, s.e.m.) of IHCs showed full-length otoferlin expression with higher IHC transduction rates in the apex of the cochlea (low frequency region, $35 \pm 5\%$ transduction rate; range: 19-52%) than in the basal turn ($24 \pm 6\%$, range: 0-51%). About 10% of all IHCs showed N-terminal otoferlin signal, but no C-terminal otoferlin expression, presumably indicating transduction of the 5' vector only. No signal was observed in the *Otof*^{-/-} control littermates. Remarkably, both N-terminal and C-
 25 terminal otoferlin signal was found only in IHCs, whereas eGFP fluorescence could additionally be found in outer hair cells (OHCs) as well as in other cell types that did not express otoferlin in parallel. Thus, despite AAV transduced in several cell types in the organ of Corti, expression of otoferlin was restricted to IHCs. To quantify otoferlin expression levels, immunofluorescence using the N-terminal anti-otoferlin antibody in
 30 confocal stacks of immunostained IHCs was measured (as in Strenzke et al. (2016)

EMBO J. 35 2519–2535). In dual-AAV transduced *Otof*^{-/-} IHCs, otoferlin levels were found to be ~30% of wild-type controls.

Since synapses in *Otof*^{-/-} mice are partially lost during the second postnatal week, an experiment was conducted to determine whether expression of otoferlin in these IHCs affected synapse numbers. Synaptic ribbons were immunolabelled; 9 ± 0.3 synapses were found in 26 day old non-transduced *Otof*^{-/-} IHCs ($n = 42$ cells, $N = 3$ animals). In dual-AAV transduced *Otof*^{-/-}, 10 ± 0.2 synapses were identified by eGFP fluorescence ($n = 59$ cells; $N = 3$ animals). In contrast, wild-type IHCs displayed 13-16 synapses per IHC (Strenzke et al. (2016) EMBO J. 35 2519–2535). Thus, the expression of otoferlin after dual-AAV injection at P6 partially prevented the loss of synapses from P26 *Otof*^{-/-} IHCs.

The data in Figures 15 and 16 also show that the hybrid approach (administration of the vectors shown in Figure 2) also restores otoferlin activity in the IHCs of *Otof*^{-/-} mice.

These data indicate that the presently claimed methods can restore hearing in mammals having an inactivating mutation in an otoferlin gene.

Example 17 – Restoration of Exocytosis in Response to Short Depolarization Stimuli Restored by Trans-Splicing Dual-AAV Mediated Expression of Otoferlin in IHCs of *Otof*^{-/-} Mice

An experiment was performed to determine whether the presently claimed methods would restore fusion of synaptic vesicles with inner auditory hair cells in *Otof*^{-/-} mice.

Since the fusion of synaptic vesicles increases the plasma membrane surface of the cell, this fusion can be measured as an increase in plasma membrane capacitance (ΔC_m). In order to quantify exocytosis of the readily releasable pool of vesicles and sustained exocytosis, the change of plasma membrane capacitance (ΔC_m) was measured in perforated patch-clamp configuration (Figures 8-10). Exocytosis was recorded as the change in membrane capacitance after depolarizing the IHC to -14 mV for the indicated duration.

IHCs from acutely explanted organs of Corti of mice were depolarized at postnatal days 14 to 18 (P14-P18) to the voltage where maximum Ca^{2+} currents were elicited, typically -14 mV. Ca^{2+} currents and ΔC_m from *Otof*^{-/-} IHCs with and without viral transduction were recorded, with virally transduced IHCs being identified by their eGFP fluorescence during the experiment. Consistent with the synapse numbers in untreated and transduced *Otof*^{-/-} IHCs, Ca^{2+} currents were found to be comparable in size to those of *Otof*^{+/+} age- and background matched controls (Figures 8 and 10). As shown in Figure 8, Ca^{2+} currents did not differ in amplitude or gating properties between non-transduced *Otof*^{-/-} IHCs, dual-AAV transduced IHCs, or wild-type IHCs from background-matched control animals. In response to depolarization pulses of 5 or 10 ms, exocytosis in transduced *Otof*^{-/-} IHCs was found to be of similar size as in *Otof*^{+/+} IHCs, while almost no change in C_m could be detected in non-transduced *Otof*^{-/-} IHCs (Figure 9). Indeed, for short depolarization stimuli up to 20 ms, exocytosis was wild-type like in dual-AAV transduced IHCs of *Otof*^{-/-} mice, indicating an intact, readily-releasable pool of vesicles. During sustained depolarization, vesicles of the readily-releasable pool need to be replenished; otoferlin is known to be required for this process (Pangrsic et al. (2010) Nat. Neurosci. 13 869–876; Strenzke et al. (2016) EMBO J. 35 2519–2535). For longer depolarization stimuli, exocytosis was in the range of the mildly hearing impaired *Otof*^{I515T/I515T} mice (Strenzke et al. (2016) EMBO J. 35 2519–2535). As shown in Figure 9, for 50 - 100 ms depolarizations, exocytosis in transduced *Otof*^{-/-} IHCs was found to be ~60% of *Otof*^{+/+} IHCs, while non-transduced *Otof*^{-/-} IHCs showed hardly any vesicle fusion, as previously described (Roux et al. (2006) Cell 127 277–289). The rates of vesicle replenishment were calculated in individual transduced cells. Approximately three hundred and eighty vesicles/sec/active zone were found to undergo exocytosis, compared to 750 vesicles/sec/active zone in *Otof*^{+/+} IHCs (Strenzke et al. (2016) EMBO J. 35 2519–2535). Thus, in transduced *Otof*^{-/-} IHCs, the rate of vesicle replenishment to the RRP could be partially recovered and was between that of wild type controls and mildly hearing impaired *Otof*^{I515T/I515T} mice (Strenzke et al. (2016) EMBO J. 35 2519–2535). As shown in Figure 10, Ca^{2+} integrals during the depolarization step indicate that a similar charge of Ca^{2+} entered IHCs in transduced and non-transduced *Otof*^{-/-} IHCs and in wild-type control cells.

The AAV serotype 6 was chosen, which resulted in IHC transduction rates of up to 51%. The artificial serotype Anc80L65 might, as recently has been shown (Landegger et al. (2017) Nat. Biotechnol. 35 280–284), increase the IHC transduction rate further, especially when applied to more mature ears (Suzuki et al. (2017) Scientific Reports 7 45524).

In sum, these data show that hearing was restored in nine injected *Otof*^{-/-} animals, using the methods described herein. These data also indicate that hearing thresholds get better the more IHCs express otoferlin.

10 **Example 18: Adeno-Associated Virus (AAV) Trans-Splicing Strategy**

At least two different nucleic acid vectors (e.g., AAV vectors) can be used to reconstitute an active otoferlin gene (e.g., a full-length otoferlin gene) within a cell following intermolecular concatamerization and trans-splicing. See, e.g., Yan et al., *Proc. Natl. Acad. Sci. U.S.A.* 97:12; 6716-6721, 2000, incorporated in its entirety herein.

15 In some examples, two different nucleic acid vectors will be used. A first nucleic acid vector can include a promoter (e.g., any of the promoters described herein), a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' of the promoter (e.g., any of the sizes of a portion of an otoferlin protein described herein and/or any of the N-terminal portions of an otoferlin protein described herein), and a
20 splicing donor signal sequence positioned at the 3' end of the first coding sequence. A second nucleic acid vector can include a splicing acceptor signal sequence, a second coding sequence that encodes a C-terminal portion of an otoferlin protein (i.e., the entire portion of the otoferlin protein that is not included in the N-terminal portion) positioned at the 3' end of the splicing acceptor signal sequence (e.g., any of the sizes of a portion of
25 an otoferlin protein described herein and/or any of the C-terminal portions of an otoferlin protein described herein), and a polyadenylation sequence at the 3' end of the second coding sequence (e.g., any of the polyadenylation sequences described herein). In some embodiments, each of the encoded portions is at least 30 amino acid residues in length (e.g., at least 50 amino acids, at least 75 amino acids, or at least 100 amino acids in
30 length), the amino acid sequence of each of the encoded portions does not overlap with the sequence of the other encoded portion, and no single vector of the two different

vectors encodes an active otoferlin protein (e.g., a full-length otoferlin protein). When the two coding sequences of the two vectors are expressed in a mammalian cell (e.g., any of the mammalian cells described herein), splicing occurs between the splicing donor signal sequence and the splicing acceptor signal sequence, thereby forming a recombined mRNA that encodes an active otoferlin protein (e.g., a full-length otoferlin protein).

In another example, three different nucleic acid vectors can be used. A first nucleic acid vector can include a portion of a promoter sequence (e.g., any of the promoter sequences described herein), a first coding sequence of an otoferlin gene that encodes a first portion of an otoferlin protein (e.g., any of the otoferlin coding sequences described herein) positioned 3' of the promoter, and a first splicing donor signal sequence positioned at the 3' end of the first coding sequence. A second nucleic acid vector can include a first splicing acceptor signal sequence, a second coding sequence of an otoferlin gene that encodes a second portion of an otoferlin protein positioned at the 3' end of the first splicing acceptor signal sequence, and a second splicing donor signal sequence positioned at the 3' end of the second coding sequence (e.g., any of the splicing donor signals described herein). A feature of the second nucleic acid vector will be that self-splicing cannot occur (i.e., splicing will not occur between the second splicing donor signal sequence and the first splicing acceptor signal sequence of the second nucleic acid vector). In some embodiments, the splicing donor signal sequence of the first nucleic acid vector and the second splicing donor signal of the second nucleic acid vector are the same (e.g., any of the splicing donor signals described herein or known in the art). In some embodiments, the first splicing donor signal sequence of the first nucleic acid vector and the second splicing donor signal sequence of the second nucleic acid vector are different (e.g., any of the splicing donor signal sequences described herein or known in the art). A third nucleic acid vector will include a second splicing acceptor signal sequence, a third coding sequence of an otoferlin gene that encodes a third portion of an otoferlin protein positioned at the 3' end of the second splicing acceptor signal sequence, and a polyadenylation sequence positioned at the 3' end of the third coding sequence (e.g., any of the polyadenylation sequences described herein). In such methods where three nucleic acid vectors are used, the first splicing donor sequence and the first splicing acceptor sequence can assemble together and the second splicing donor sequence and the

second slicing acceptor sequence can assemble together (recombine), and the portions of otoferlin protein respectively encoded by the first, second, and third coding sequences do not overlap, and when introduced into a mammalian cell (e.g., any of the mammalian cells described herein), splicing occurs between the first splicing donor sequence and the first splicing acceptor sequence, and between the second splicing donor sequence and the second splicing acceptor sequence, to form a spliced nucleic acid that encodes an active otoferlin protein (e.g., a full-length otoferlin protein). Based on the strategies provided above, one skilled in the art would understand how to develop a strategy using four, five, or six different nucleic acid vectors.

In any of the examples of these methods, the amino acid sequence of each of the encoded portions does not overlap with the sequence any of the other encoded portions, and no single vector encodes an active otoferlin protein (e.g., a full-length otoferlin protein).

Each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions can be at least 30 amino acids (e.g., between about 30 amino acids to about 1600 amino acids, or any of the other subranges of this range described herein).

In some embodiments, each of the coding sequences can include at least one exon and at least one intron of SEQ ID NO: 12 (e.g., at least two exons and at least one intron, at least two exons and at least two introns, at least three exons and at least one intron, at least three exons and at least two introns, or at least three exons and at least three introns). In some embodiments, each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions can encode up to 80% of the amino acid sequence of SEQ ID NO: 5 (e.g., up to 10%, up to 20%, up to 30%, up to 40%, up to 50%, up to 60%, or up to 70% of SEQ ID NO: 5) such that each of the encoded portions is non-overlapping. In some embodiments, each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions encoding up to 80% of the amino acid sequence of SEQ ID NO: 5 (e.g., up to 10%, up to 20%, up to 30%, up to 40%, up to 50%, up to 60%, or up to 70% of SEQ ID NO: 5), such that each of the encoded portions is non-overlapping.

Each of the at least two nucleic acid vectors may further include an inverted terminal repeat (ITR) to allow head-to-tail recombination. The ITR will be subsequently removed via splicing. For example, the ITR could be a palindromic double-D ITR as described in Yan et al., *Proc. Natl. Acad. Sci. U.S.A.* 97(12):6716-6721, 2000, incorporated in its entirety herein. For example, the ITR could be a AAV serotype-2 ITR as described in Gosh et al., *Mol. Ther.* 16:124-130, 2008, and Gosh et al., *Human Gene Ther.* 22: 77-83, 2011. Non-limiting examples of splicing acceptor and/or donor signal sequences are known in the art. See, e.g., Reich et al., *Human Gene Ther.* 14(1):37-44, 2003, and Lai et al. (2005) *Nat. Biotechnol.* 23(11):1435-1439, 2005, 2005. The splicing donor and acceptor signal sequences can be any endogenous intron splicing signal of a gene (e.g., an otoferlin gene).

For example, the splicing donor signal sequence can be:

5'-GTAAGTATCAAGGTTACAAGACAGGTTTAAGGAGACCAATAGA
AACTGGGCTTGTCGAGACAGAGAAGACTCTTGCGTTTCT-3' (SEQ ID NO: 6)

and the splicing acceptor signal can be:

5'-ATAGGCACCTATTGGTCTTACTGACATCCACTTTGCCTTTCTCTC
CACAG-3' (SEQ ID NO: 7) (see, e.g., Trapani et al., *EMBO Mol. Med.* 6(2):194-211, 2014).

Methods of evaluating splicing and splicing efficiency are known in the art (see, e.g., Lai et al., *Nat. Biotechnol.* 23(11): 1435-1439, 2005).

Example 19: Hybrid Vector Trans-Splicing Strategy using an alkaline phosphatase (AP) highly recombinogenic exogenous gene region

At least two (e.g., two, three, four, five, or six) different nucleic acid vectors (e.g., AAV vectors) can also be used in any of the methods described herein to reconstitute an active otoferlin gene (e.g., a full-length otoferlin gene) within a cell following intermolecular concatamerization, marker gene-mediated recombination, and trans-splicing. This strategy is a hybrid strategy as it will include homologous recombination and/or trans-splicing. See, e.g., Gosh et al., *Mol. Ther.* 16: 124-130, 2008; Gosh et al., *Human Gene Ther.* 22: 77-83, 2011; and Duan et al., *Mol. Ther.* 4: 383-391, 2001, each incorporated in its entirety herein. As used herein, a detectable marker gene can be a

highly recombinogenic DNA sequence that will allow for coding sequence-independent recombination. An non-limiting example of a detectable marker gene is an alkaline phosphatase (AP) gene. For example, the detectable marker gene can be the middle one-third of the human placental AP complementary DNA, which is 872 bp in length (see, 5 e.g., Gosh et al., 2008). At least two different nucleic acid vectors will contain a detectable marker gene (e.g., any of the detectable marker genes described herein). Since the hybrid vector will be constructed based on a trans-splicing vector as described in Example 18, an active otoferlin gene (e.g., a full-length otoferlin gene) may be reconstituted using either ITR-mediated recombination and trans-splicing or detectable 10 marker gene-mediated (e.g., AP-gene mediated) recombination and trans-splicing. After trans-splicing, an active otoferlin gene (e.g., a full-length otoferlin gene) will be reconstituted in the genomic DNA of a mammalian cell (e.g., any mammalian cell described herein).

In one example, two different nucleic acid vectors will be used. A first nucleic 15 acid vector can include a promoter (e.g., any of the promoters described herein), a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' of the promoter (e.g., any of the sizes of a portion of an otoferlin protein described herein and/or any of the N-terminal portions of an otoferlin protein described herein), a splicing donor signal sequence positioned at the 3' end of the first coding sequence, and a first 20 detectable marker gene positioned 3' of the splicing donor signal sequence. A second nucleic acid vector can include a second detectable marker gene, a splicing acceptor signal sequence positioned 3' of the second detectable marker gene, a second coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence (e.g., any of the sizes of a portion of an otoferlin 25 protein described herein and/or any of the C-terminal portions of an otoferlin protein described herein), and a polyadenylation sequence at the 3' end of the second coding sequence (e.g., any of the polyadenylation sequences described herein). In some embodiments, each of the encoded portions is at least 30 amino acid residues in length (e.g., at least 50 amino acids, at least 75 amino acids, or at least 100 amino acids in 30 length), the amino acid sequence of each of the encoded portions do not overlap, and no single vector of the two different vectors encodes an active otoferlin protein (e.g., a full-

length otoferlin protein). When introduced into a mammalian cell (e.g., any of the mammalian cells described herein) splicing occurs between the splicing donor signal sequence and the splicing acceptor signal sequence, thereby forming an RNA acid that encodes an active otoferlin protein (e.g., a full-length otoferlin protein).

5 In another example, three different nucleic acid vectors can be used. A first nucleic acid vector can include a portion of promoter sequence (e.g., any of the promoter sequences described herein), a first coding sequence of an otoferlin gene that encodes a first portion of an otoferlin protein (e.g., any of the otoferlin coding sequences described herein) positioned 3' of the promoter, a first splicing donor signal sequence positioned at
10 the 3' end of the first coding sequence, and a first detectable marker gene. A second nucleic acid vector can include a second detectable marker gene, a first splicing acceptor signal sequence positioned 3' of the second detectable marker gene, a second coding sequence of an otoferlin gene that encodes a second portion of an otoferlin protein positioned at the 3' end of the first splicing acceptor signal sequence, a second splicing
15 donor signal sequence positioned at the 3' end of the second coding sequence (e.g., any of the splicing donor signals described herein), and a third detectable marker gene. A feature of the second nucleic acid vector will be that self-splicing cannot occur (i.e., splicing will not occur between the second splicing donor signal sequence and the first splicing acceptor signal sequence of the second nucleic acid vector). In some
20 embodiments, the splicing donor signal sequence of the first nucleic acid vector and the second splicing donor signal of the second nucleic acid vector are the same (e.g., any of the splicing donor signals described herein or known in the art). In some embodiments, the first splicing donor signal sequence of the first nucleic acid vector and the second splicing donor signal sequence of the second nucleic acid vector are different (e.g., any of
25 the splicing donor signal sequences described herein or known in the art). A third nucleic acid vector can include a fourth detectable marker gene, a second splicing acceptor signal sequence positioned 3' of the fourth detectable marker gene, a third coding sequence of an otoferlin gene that encodes a third portion of an otoferlin protein positioned at the 3' end of the second splicing acceptor signal sequence, and a polyadenylation sequence
30 positioned at the 3' end of the third coding sequence (e.g., any of the polyadenylation sequences described herein). In such methods where three nucleic acid vectors are used,

the first splicing donor sequence and the first splicing acceptor sequence can assemble together (recombine) and the second splicing donor sequence and the second splicing acceptor sequence can assemble together (recombine), and the portion of otoferlin protein encoded by the first, second, and third coding sequences do not overlap, and when
5 introduced into a mammalian cell (e.g., any of the mammalian cells described herein), splicing occurs between the first splicing donor sequence and the first splicing acceptor sequence, and between the second splicing donor sequence and the second splicing acceptor sequence, to form a recombined nucleic acid that encodes an active otoferlin protein (e.g., a full-length otoferlin protein). As can be appreciated in the art, when three
10 nucleic acid vectors are used, two of the at least two different nucleic acid vectors can include a detectable marker gene (e.g., an AP marker gene), and one of the at least two different nucleic acid vectors may include a splicing acceptor signal sequence that is complementary to a splicing donor signal sequence in a nucleic acid vector that includes a detectable marker gene. For example, in some embodiments, the first and second
15 nucleic acid vectors can include a detectable marker gene (e.g., an AP marker gene), and the third nucleic acid vector will include a splicing acceptor signal sequence that is complementary to the splicing donor signal sequence in the second nucleic acid vector, and the third nucleic acid vector will not include a detectable marker gene (e.g., an AP marker gene). In other examples, the second and third nucleic acid vector can include a
20 detectable marker gene (e.g., an AP marker gene), and the first nucleic acid vector will include a splicing donor signal sequence that is complementary to the splicing acceptor signal sequence in the second nucleic acid vector and the first nucleic acid vector will not include a detectable marker gene (e.g., an AP marker gene).

Based on the strategies provided above, one skilled in the art would understand
25 how to develop a strategy using four, five, or six vectors.

The coding sequences provided in the at least two nucleic acid vectors (e.g., two, three, four, five or six) will not be overlapping. Each of the at least two different vectors can include a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions being, e.g., at least 30 amino acids (e.g., about 30 amino
30 acids to about 1600 amino acids, or any of the other subranges of this range described herein).

In some embodiments, each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions encoding at least one exon and at least one intron of SEQ ID NO: 12 (e.g., at least two exons and at least one intron, at least two exons and at least two introns, at least three exons at least one intron, at least three exons and at least two introns, or at least three exons and at least three introns). In some embodiments, each of the at least two different vectors include a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions encoding up to 80% of SEQ ID NO: 5 (e.g., up to 10%, up to 20%, up to 30%, up to 40%, up to 50%, up to 60%, up to 70% of SEQ ID NO: 5) such that each of the encoded portions is non-overlapping. In some embodiments, each of the at least two different vectors include a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions encoding up to 80% of SEQ ID NO: 5 (e.g., up to 10%, up to 20%, up to 30%, up to 40%, up to 50%, up to 60%, or up to 70% of SEQ ID NO: 5), such that each of the encoded portions is non-overlapping.

As described in Example 18, each of the at least two nucleic acid vectors may further include an inverted terminal repeat (ITR) to allow head-to-tail recombination. The ITR will be subsequently removed via splicing. Examples of ITRs and splicing acceptor and/or donor signal sequences are known in the art and have been described in Example 18.

Example 20: Hybrid Vector Trans-Splicing Strategy using a F1 phage highly recombinogenic exogenous gene region (AK)

At least two (e.g., two, three, four, five, or six) different nucleic acid vectors (e.g., AAV vectors) can also be used in any of the methods described herein to reconstitute an active otoferlin gene (e.g., a full-length otoferlin gene) within a cell following intermolecular concatamerization, marker gene-mediated recombination, and trans-splicing. See, e.g., the vectors shown in Figure 2. This strategy is a hybrid strategy as it will include homologous recombination and/or trans-splicing. See, e.g., Trapani et al., *EMBO Mol. Med.* 6(2):194-211, 2014, incorporated in its entirety herein. As used herein, an F1 phage recombinogenic region (AK) will be used to allow coding sequence-

independent recombination. The F1 phage recombinogenic region may be a 77 bp recombinogenic region from the F1 phage genome as described in Trapani et al. (2014) EMBO Mol. Med. 6(2):194-211, 2014. At least two different nucleic acid vectors will contain an F1 phage recombinogenic region. Since the hybrid vector will be constructed
5 based on a trans-splicing vector as described in Example 18, a nucleic acid encoding an active otoferlin protein (e.g., a full-length stereocilin protein) may be generated using either ITR-mediated recombination and trans-splicing or F1 phage recombinogenic region-induced recombination and trans-splicing. After trans-splicing, a nucleic acid encoding an active otoferlin protein (e.g., a full-length otoferlin protein) will be generated
10 in a mammalian cell (e.g., any of the mammalian cells described herein).

In one example, two different nucleic acid vectors will be used. A first nucleic acid vector can include a promoter (e.g., any of the promoters described herein), a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' of the promoter (e.g., any of the sizes of a portion of an otoferlin protein described herein
15 and/or any of the N-terminal portions of an otoferlin protein described herein), a splicing donor signal sequence positioned at the 3' end of the first coding sequence, and an F1 phage recombinogenic region positioned 3' of the splicing donor signal sequence. A second nucleic acid vector can include an F1 phage recombinogenic region, a splicing acceptor signal sequence positioned 3' of the F1 phage recombinogenic region, a second
20 coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence (e.g., any of the sizes of a portion of an otoferlin protein described herein and/or any of the C-terminal portions of an otoferlin protein described herein), and a polyadenylation sequence at the 3' end of the second
25 coding sequence (e.g., any of the polyadenylation sequences described herein). In some embodiments, each of the encoded portions is at least 30 amino acid residues in length (e.g., at least 50 amino acids, at least 75 amino acids, or at least 100 amino acids in length), the amino acid sequence of each of the encoded portions do not overlap, and no single vector of the two different vectors encodes an active otoferlin protein (e.g., a full-length otoferlin protein). When the vectors are introduced into a mammalian cell (e.g.,
30 any of the mammalian cells described herein), splicing occurs between the splicing donor

signal sequence and the splicing acceptor signal sequence, thereby forming a recombined nucleic acid that encodes an active otoferlin protein (e.g., a full-length otoferlin protein).

In another example, three different nucleic acid vectors will be used. A first nucleic acid vector can include a portion of promoter sequence (e.g., any of the promoter sequences described herein), a first coding sequence of an otoferlin gene that encodes a first portion of an otoferlin protein (e.g., any of the otoferlin coding sequences described herein) positioned 5' of the promoter, a first splicing donor signal sequence positioned at the 3' end of the first coding sequence, and an F1 phage recombinogenic region. A second nucleic acid vector can include an F1 phage recombinogenic region, a first splicing acceptor signal sequence positioned 3' of the F1 phage recombinogenic region, a second coding sequence of an otoferlin gene that encodes a second portion of an otoferlin protein positioned at the 3' end of the first splicing acceptor signal sequence, a second splicing donor signal sequence positioned at the 3' end of the second coding sequence (e.g., any of the splicing donor signals described herein), and an F1 phage recombinogenic region. A feature of the second nucleic acid vector will be that self-splicing cannot occur (i.e., splicing will not occur between the second splicing donor signal sequence and the first splicing acceptor signal sequence of the second nucleic acid vector). In some embodiments, the splicing donor signal sequence of the first nucleic acid vector and the second splicing donor signal of the second nucleic acid vector are the same (e.g., any of the splicing donor signals described herein or known in the art). In some embodiments, the first splicing donor signal sequence of the first nucleic acid vector and the second splicing donor signal sequence of the second nucleic acid vector are different (e.g., any of the splicing donor signal sequences described herein or known in the art). A third nucleic acid vector can include an F1 phage recombinogenic region, a second splicing acceptor signal sequence positioned 3' of the F1 phage recombinogenic region, a third coding sequence of an otoferlin gene that encodes a third portion of an otoferlin protein positioned at the 3' end of the second splicing acceptor signal sequence, and a polyadenylation sequence positioned at the 3' end of the third coding sequence (e.g., any of the polyadenylation sequences described herein). In such methods where three nucleic acid vectors are used, the first splicing donor sequence and the first splicing acceptor sequence can assemble together (recombine) and the second splicing donor

sequence and the second slicing acceptor sequence can assemble together (recombine), and the portion of otoferlin protein encoded by the first, second, and third coding sequences do not overlap, and when introduced into a mammalian cell (e.g., any of the mammalian cells described herein), splicing occurs between the first splicing donor sequence and the first splicing acceptor sequence, and between the second splicing donor sequence and the second splicing acceptor sequence, to form a recombined nucleic acid that encodes an active otoferlin protein (e.g., a full-length otoferlin protein). As can be appreciated in the art when three nucleic acid vectors are used, two of the different nucleic acid vectors can include an F1 phage recombinogenic region and one of the different nucleic acid vectors may include a splicing acceptor signal sequence that is complementary to a splicing donor signal sequence in a nucleic acid vector that includes an F1 phage recombinogenic region. For example, in some embodiments, the first and second nucleic acid vectors can include an F1 phage recombinogenic region, and the third nucleic acid vector will include a splicing acceptor signal that is complementary to the splicing donor signal sequence in the second nucleic acid vector, and the third nucleic acid vector will not include an F1 phage recombinogenic region (e.g., an AP marker gene). In other examples, the second and third nucleic acid vector can include an F1 phage recombinogenic region and the first nucleic acid vector will include a splicing donor signal sequence that is complementary to the splicing acceptor signal sequence in the second nucleic acid vector and the first nucleic acid vector will not include an F1 phage recombinogenic region. Based on the strategies provided above, one skilled in the art would understand how to develop a strategy using four, five, or six vectors.

The coding sequences provided in each of the at least two nucleic acid vectors (e.g., two, three, four, five or six) will not be overlapping. Each of the at least two different vectors include a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions being at least 30 amino acids (e.g., about 30 amino acids to about 1600 amino acids, or any of the subranges of this range described herein).

In some embodiments, each of the at least two different vectors include a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions encoding at least one exon and at least one intron of SEQ ID NO: 12 (e.g., at

least two exons and at least one intron, at least two exons and at least two introns, at least three exons at least one intron, at least three exons and at least two introns, or at least three exons and at least three introns). In some embodiments, each of the at least two different vectors includes a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions encoding up to 80% of SEQ ID NO: 5 (e.g., up to 10%, up to 20%, up to 30%, up to 40%, up to 50%, up to 60%, or up to 70% of SEQ ID NO: 5) such that each of the encoded portions is non-overlapping. In some embodiments, each of the at least two different vectors include a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions encoding up to 80% of SEQ ID NO: 5 (e.g., up to 10%, up to 20%, up to 30%, up to 40%, up to 50%, up to 60%, or up to 70% of SEQ ID NO: 5), such that each of the encoded portions is non-overlapping.

As described in Example 18 each of the at least two nucleic acid vectors may further include an inverted terminal repeat (ITR) to allow head-to-tail recombination. The ITR will be subsequently removed via splicing. Examples of ITRs and splicing acceptor and/or donor signals are known in the art and have been described in Example 18.

These methods have been used to improve hearing in five animals. The data in Figures 15 and 16 show that the *Otof*^{-/-} mice administered the vectors shown in Figure 2 restores otoferlin function in the IHCs of *Otof*^{-/-} mice.

Example 21. In Vitro Expression of Full-Length Human Otoferlin Using Two Vectors

A variety of different vectors were generated which each include a nucleic acid sequence that encodes a portion of otoferlin: p109 (SEQ ID NO: 84), which is shown in Figure 38; p105 (SEQ ID NO: 85), which is shown in Figure 39; 105.WPRE, which is shown in Figure 40; p108, which is shown in Figure 41; 1OTOF18.CL1, which is shown in Figure 42; 19OTOF48, which is shown in Figure 43; 1OTOF20.CL1, which is shown in Figure 44; 21OTOF48.WPRE, which is shown in Figure 45; 1OTOF21.CL1, which is shown in Figure 46; and 22OTOF48.WPRE, which is shown in Figure 47; 105.pA.NTF3.CMVd, which is shown in Figure 48.

Pairs of these vectors were used to transfect HEK293FT cells. In these experiments, 1.2×10^5 cells/well were seeded in a 24-well plate overnight at 37 °C with 5% CO₂. On the next day, pairs of linearized ITR containing plasmids (the pairs shown in Figure 49) were transfected into the HEK293FT cells using JetPrime reagent (Polyplus). Seventy-two hours post-transfection, the cells were harvested and lysed using RIPA buffer and analyzed in 4-12% Bolt protein gel. The gel was transferred onto nitrocellulose membrane and blotted with anti-OTOF polyclonal antibody (Thermo PA5-52935). Anti-human beta-actin monoclonal antibody was used as the primary antibody for internal-loading control between the lanes. Three independent in vitro experiments were performed to analyze and compare the expression of full-length protein using various recombination strategies relative to single plasmid CMV.fl-OTOF transfection (lane 10).

Compared to the negative control, expression of full-length otoferlin protein (approximately 226 kD) were observed in every lane except lane number 6 (Figures 50 and 51).

Example 22. In Vivo Recovery of Hearing Function in OTOF^{-/-} Mice Using Two Vectors

A set of experiments were performed to determine whether hearing function could be recovered in Otof^{-/-} mice that have two vectors (p109 and p105; SEQ ID NOs: 84 and 85, respectively) introduced into their cochlea. Briefly, a virus preparation (e.g., $1-2 \times 10^{10}$ vg/ μ L) was injected through the auditory bulla covering the round window membrane (RWM) into the scala tympani of the left cochlea at approximately postnatal day 6-7 (P6-7). See, e.g., Jung et al. (2015) *EMBO J* 34: 2686-2702, and Al-Moyed et al. (2019) *EMBO Molecular Medicine* 11(1). pii: e9396. Prior to injection, all mice were anesthetized via isoflurane and were locally anesthetized, e.g., with xylocaine pumpspray, before retroauricular incision.

Auditory brainstem responses (ABRs) were recorded from approximately 3- to 4-week old anesthetized mice subjected to 4, 6, 8, 12, 16, 24, or 32 kHz tone burst (e.g., 10 ms plateau, 1 ms cos² rise/fall or 0.03 ms broadband click sound stimuli presented at 20 Hz. See, e.g., Jing et al. (2013) *J Neurosci* 33: 4456-4467. Ears that were injected were

clogged with an electrode gel while ABRs were recorded from contralateral non-injected ears.

ABR click sound thresholds were determined as the lowest sound pressure levels necessary to evoke reproducible ABR wave response and were measured in 10 decibel
5 sound pressure levels (dB SPL) steps from 30 dB SPL to 100 dB SPL. Tone burst thresholds were recorded in 10 dB SPL steps from 10 dB SPL below the lowest reproducible ABR and up to 90 dB SPL. ABR wave I was defined as the first distinguishable peak between the summing receptor potential (SP) and the prominent ABR wave II peak. The amplitude of each ABR wave was calculated as the difference
10 between the highest point of a wave and the subsequent local minimum. The summed ABR wave I-V amplitude was calculated by adding up the individual amplitude values of ABR waves I-V.

The click ABR threshold and the tone burst ABR threshold were determined in wildtype mice that were not treated, *Otof*^{-/-} that were not treated, and *Otof*^{-/-} mice that
15 were treated with the two vectors (p109 and p105). Hearing function was tested in the treated *Otof*^{-/-} at days 26-28 and day 91 after administration. The data show that *Otof*^{-/-} mice demonstrated significant improvements in hearing function after treatment with the two vectors, as compared to untreated *Otof*^{-/-} mice (Figures 51 and 52).

20 **Example 23. In Vivo Recovery of Hearing Function in Human Subjects Using Two Vectors**

A set of experiments are performed to determine whether hearing function could be recovered in human subjects that have two vectors (p109 and p105; SEQ ID NOS: 84 and 85, respectively) introduced into their cochlea. Hearing function is tested in the
25 human subject at days 15, 30, 45, 60 and 90 after administration, and is compared to the functional hearing of human subject that did not receive treatment.

OTHER EMBODIMENTS

It is to be understood that the words which have been used are words of
30 description rather than limitation, and that changes may be made within the purview of the appended claims without departing from the true scope and spirit of the invention in

its broader aspects.

While the present invention has been described at some length and with some particularity with respect to the several described embodiments, it is not intended that it should be limited to any such particulars or embodiments or any particular embodiment, but it is to be construed with references to the appended claims so as to provide the broadest possible interpretation of such claims in view of the prior art and, therefore, to effectively encompass the intended scope of the invention.

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, section headings, the materials, methods, and examples are illustrative only and not intended to be limiting.

What is claimed is:

1. A composition comprising at least two different nucleic acid vectors, wherein:
each of the at least two different vectors comprises a coding sequence that encodes a different portion of an otoferlin protein, each of the encoded portions being at least 30 amino acid residues in length, wherein the amino acid sequence of each of the encoded portions may optionally partially overlap with the amino acid sequence of a different one of the encoded portions;
no single vector of the at least two different vectors encodes a full-length otoferlin protein;
at least one of the coding sequences comprises a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons; and
when introduced into a mammalian cell the at least two different vectors undergo concatamerization or homologous recombination with each other, thereby forming a recombined nucleic acid that encodes a full-length otoferlin protein.
2. The composition of claim 1, wherein each of the at least two different vectors is a plasmid, a transposon, a cosmid, an artificial chromosome, or a viral vector.
3. The composition of claim 1, wherein each of the at least two different vectors is a human artificial chromosome (HAC), yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC), or a P1-derived artificial chromosome (PAC).
4. The composition of claim 1, wherein each of the at least two different vectors is a viral vector selected from an adeno-associated virus (AAV) vector, an adenovirus vector, a lentivirus vector, or a retrovirus vector.
5. The composition of claim 1, wherein each of the at least two different vectors is an AAV vector.

6. The composition of any one of claims 1-5, wherein the amino acid sequence of one of the encoded portions overlaps with the amino acid sequence of a different one of the encoded portions.

7. The composition of claim 6, wherein the amino acid sequence of each of the encoded portions partially overlaps with the amino acid sequence of a different encoded portion.

8. The composition of claim 7, wherein the overlapping amino acid sequence is between about 30 amino acid residues to about 1000 amino acid residues in length.

9. The composition of any one of claims 1-5, wherein the vectors include two different vectors, each of which comprises a different segment of an intron, wherein the intron comprises the nucleotide sequence of an intron that is present in otoferlin genomic DNA, and wherein the two different segments overlap in sequence by at least 100 nucleotides.

10. The composition of claim 9, wherein the two different segments overlap in sequence by about 100 nucleotides to about 800 nucleotides.

11. The composition of any one of claims 1-10, wherein the nucleotide sequence of each of the at least two different vectors is between about 500 nucleotides to about 10,000 nucleotides in length.

12. The composition of claim 11, wherein the nucleotide sequence of each of the at least two different vectors is between 500 nucleotides to 5,000 nucleotides in length.

13. The composition of any one of claims 1-12, wherein the number of different vectors in the composition is two.

14. The composition of claim 13, wherein a first of the two different vectors comprises a coding sequence that encodes an N-terminal portion of the otoferlin protein.

15. The composition of claim 14, wherein the N-terminal portion of the otoferlin protein is between 30 amino acids to 1600 amino acids in length.

16. The composition of claim 15, wherein the N-terminal portion of the otoferlin protein is between 200 amino acids to 1500 amino acids in length.

17. The composition of any one of claims 14-16, wherein the first vector further comprises one or both of a promoter and a Kozak sequence.

18. The composition of claim 17, wherein the first vector comprises a promoter that is an inducible promoter, a constitutive promoter, or a tissue-specific promoter.

19. The composition of any one of claims 14-18, wherein the first vector further comprises a coding sequence encoding a destabilization domain, wherein the destabilization domain is 3' to the coding sequence that encodes the N-terminal portion of the otoferlin protein.

20. The composition of claim 19, wherein the coding sequence that encodes the N-terminal portion of the otoferlin protein comprises exons 1-21 of isoform 5 of the human otoferlin gene.

21. The composition of any one of claims 14-20, wherein the second of the two different vectors comprises a coding sequence that encodes a C-terminal portion of the otoferlin protein.

22. The composition of claim 21, wherein the C-terminal portion of the otoferlin protein is between 30 amino acids to 1600 amino acids in length.

23. The composition of claim 22, wherein the C-terminal portion of the otoferlin protein is between 200 amino acids to 1500 amino acids in length.

24. The composition of any one of claims 21-23, wherein the second vector further comprises a poly(dA) sequence.

25. The composition of claim 21, wherein the coding sequence that encodes the C-terminal portion of the otoferlin protein comprises exons 22-47 of isoform 5 of the human otoferlin gene.

26. The composition of any one of claims 1-25, further comprising a pharmaceutically acceptable excipient.

27. A kit comprising a composition of any one of claims 1-26.

28. A kit of claim 27, further comprising a pre-loaded syringe comprising the composition.

29. A method comprising:
introducing into a cochlea of a mammal a therapeutically effective amount of the composition of any one of claims 1-26.

30. The method of claim 29, wherein the mammal is a human.

31. The method of claim 29 or 30, wherein the mammal has been previously identified as having a defective otoferlin gene.

32. A method of increasing expression of a full-length otoferlin protein in a mammalian cell, the method comprising introducing the composition of any one of claims 1-26 into the mammalian cell.

33. The method of claim 32, wherein the mammalian cell is an inner hair cell.

34. The method of claim 32 or 33, wherein the mammalian cell is a human cell.

35. The method of any one of claims 32-34, wherein the mammalian cell has previously been determined to have a defective otoferlin gene.

36. A method of increasing expression of a full-length otoferlin protein in an inner hair cell in a cochlea of a mammal, the method comprising:

introducing into the cochlea of the mammal a therapeutically effective amount of the composition of any one of claims 1-26.

37. The method of claim 36, wherein the mammal has been previously identified as having a defective otoferlin gene.

38. The method of claim 36 or 37, wherein the mammal is a human.

39. A method of treating non-symptomatic sensorineural hearing loss in a subject identified as having a defective otoferlin gene, the method comprising:

administering a therapeutically effective amount of a composition of any one of claims 1-26 into the cochlea of the subject.

40. The method of claim 39, wherein the subject is a human.

41. The method of claim 39 or 40, further comprising, prior to the administering step, determining that the subject has a defective otoferlin gene.

42. A composition comprising two different nucleic acid vectors, wherein:

a first nucleic acid vector of the two different nucleic acid vectors comprises a promoter, a first coding sequence that encodes an N-terminal portion of an otoferlin

protein positioned 3' of the promoter, and a splicing donor signal sequence positioned at the 3' end of the first coding sequence; and

a second nucleic acid vector of the two different nucleic acid vectors comprises a splicing acceptor signal sequence, a second coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence, and a polyadenylation sequence at the 3' end of the second coding sequence;

wherein each of the encoded portions is at least 30 amino acid residues in length, wherein the amino acid sequences of the encoded portions do not overlap, wherein no single vector of the two different vectors encodes a full-length otoferlin protein, and, when the coding sequences are transcribed in a mammalian cell, to produce RNA transcripts, splicing occurs between the splicing donor signal sequence on one transcript and the splicing acceptor signal sequence on the other transcript, thereby forming a recombined RNA molecule that encodes a full-length otoferlin protein.

43. The composition of claim 42, wherein the coding sequence of at least one of the vectors comprises a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons.

44. A composition comprising:

a first nucleic acid vector comprising a promoter, a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' of the promoter, a splicing donor signal sequence positioned at the 3' end of the first coding sequence, and a first detectable marker gene positioned 3' of the splicing donor signal sequence; and

a second nucleic acid vector, different from the first nucleic acid vector, comprising a second detectable marker gene, a splicing acceptor signal sequence positioned 3' of the second detectable marker gene, a second coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence, and a polyadenylation sequence positioned at the 3' end of the second coding sequence;

wherein each of the encoded portions is at least 30 amino acid residues in length, wherein the respective amino acid sequences of the encoded portions do not overlap with

each other, wherein no single vector of the two different vectors encodes a full-length otoferlin protein, and, when the coding sequences are transcribed in a mammalian cell to produce RNA transcripts, splicing occurs between the splicing donor signal on one transcript and the splicing acceptor signal on the other transcript, thereby forming a recombined RNA molecule that encodes a full-length otoferlin protein.

45. The composition of claim 44, wherein the coding sequence of at least one of the vectors comprises a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons.

46. The composition of claim 44, wherein the first or second detectable marker gene encodes alkaline phosphatase.

47. The composition of claim 44 or 46, wherein the first and second detectable marker genes are the same.

48. A composition comprising:

a first nucleic acid vector comprising a promoter, a first coding sequence that encodes an N-terminal portion of an otoferlin protein positioned 3' to the promoter, a splicing donor signal sequence positioned at the 3' end of the first coding sequence, and a F1 phage recombinogenic region positioned 3' to the splicing donor signal sequence; and

a second nucleic acid vector, different from the first nucleic acid vector, comprising a second F1 phage recombinogenic region, a splicing acceptor signal sequence positioned 3' of the second F1 phage recombinogenic region, a second coding sequence that encodes a C-terminal portion of an otoferlin protein positioned at the 3' end of the splicing acceptor signal sequence, and a polyadenylation sequence positioned at the 3' end of the second coding sequence;

wherein each of the encoded portions is at least 30 amino acid residues in length, wherein the respective amino acid sequences of the encoded portions do not overlap with each other, wherein no single vector of the two different vectors encodes a full-length otoferlin protein, and, when the coding sequences are transcribed in a mammalian cell to

produce RNA transcripts, splicing occurs between the splicing donor signal on one transcript and the splicing acceptor signal on the other transcript, thereby forming a recombined RNA molecule that encodes a full-length otoferlin protein.

49. The composition of claim 48, wherein the coding sequence of at least one of the vectors comprises a nucleotide sequence spanning two neighboring exons of otoferlin genomic DNA, and lacks an intronic sequence between the two neighboring exons.

50. A kit comprising a composition of any one of claims 42-49.

51. A kit of claim 50, wherein the composition is pre-loaded in a syringe.

52. A method comprising introducing into a cochlea of a mammal a therapeutically effective amount of the composition of any one of claims 42-49.

53. The method of claim 52, wherein the mammal is a human.

54. The method of claim 52 or 53, wherein the mammal has been previously identified as having a defective otoferlin gene.

55. A method of increasing expression of a full-length otoferlin protein in a mammalian cell, the method comprising introducing the composition of any one of claims 42-49 into the mammalian cell.

56. The method of claim 55, wherein the mammalian cell is a cochlear inner hair cell.

57. The method of claim 55 or 56, wherein the mammalian cell is a human cell.

58. The method of any one of claims 55-57, wherein the mammalian cell has previously been determined to have a defective otoferlin gene.

59. A method of increasing expression of a full-length otoferlin protein in an inner hair cell in a cochlea of a mammal, the method comprising introducing into the cochlea a therapeutically effective amount of the composition of any one of claims 39-46.

60. The method of claim 59, wherein the mammal has been previously identified as having a defective otoferlin gene.

61. The method of claim 59 or 60, wherein the mammal is a human.

62. A method of treating non-symptomatic sensorineural hearing loss in a subject identified as having a defective otoferlin gene, the method comprising administering a therapeutically effective amount of a composition of any one of claims 42-49 into a cochlea of the subject.

63. The method of claim 62, wherein the subject is a human.

64. The method of claim 62 or 63, further comprising, prior to the administering step, determining that the subject has a defective otoferlin gene.

65. The composition of claim 13, wherein the one of the two vectors comprises SEQ ID NO: 39 and the second of the two vectors comprises SEQ ID NO: 40.

66. The composition of claim 13, wherein the one of the two vectors comprises SEQ ID NO: 41 and the second of the two vectors comprises SEQ ID NO: 42.

67. The composition of claim 13, wherein one of the two vectors comprises SEQ ID NO: 84 and the second of the two vectors comprises SEQ ID NO: 85.

68. The composition of claim 1, wherein one of the at least two different vectors comprises a sequence encoding a NTF3 protein.

69. The composition of claim 68, wherein the sequence encoding a NTF3 protein is at least 90% identical to SEQ ID NO: 78.

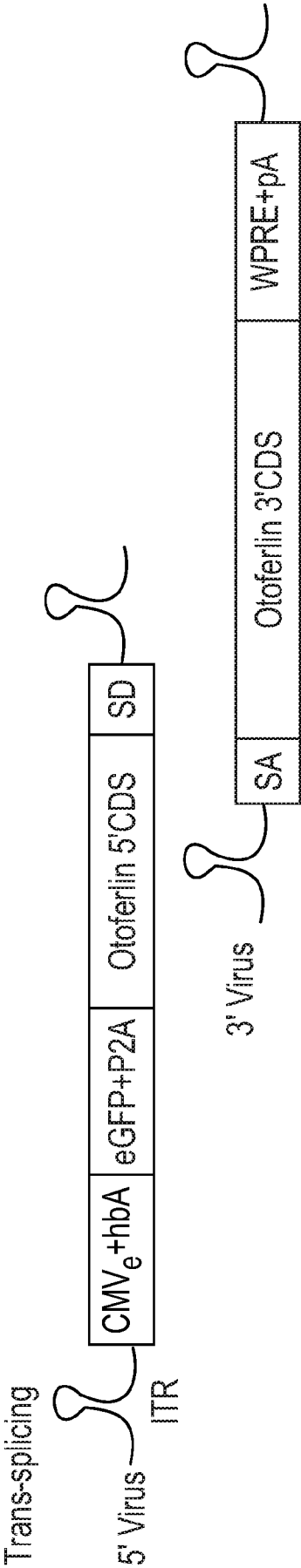


FIG. 1 1/43

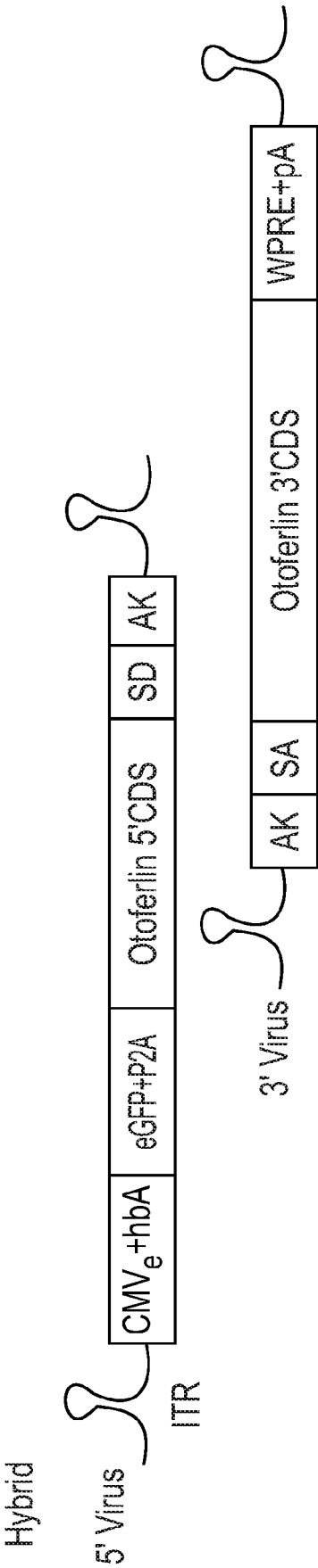


FIG. 2

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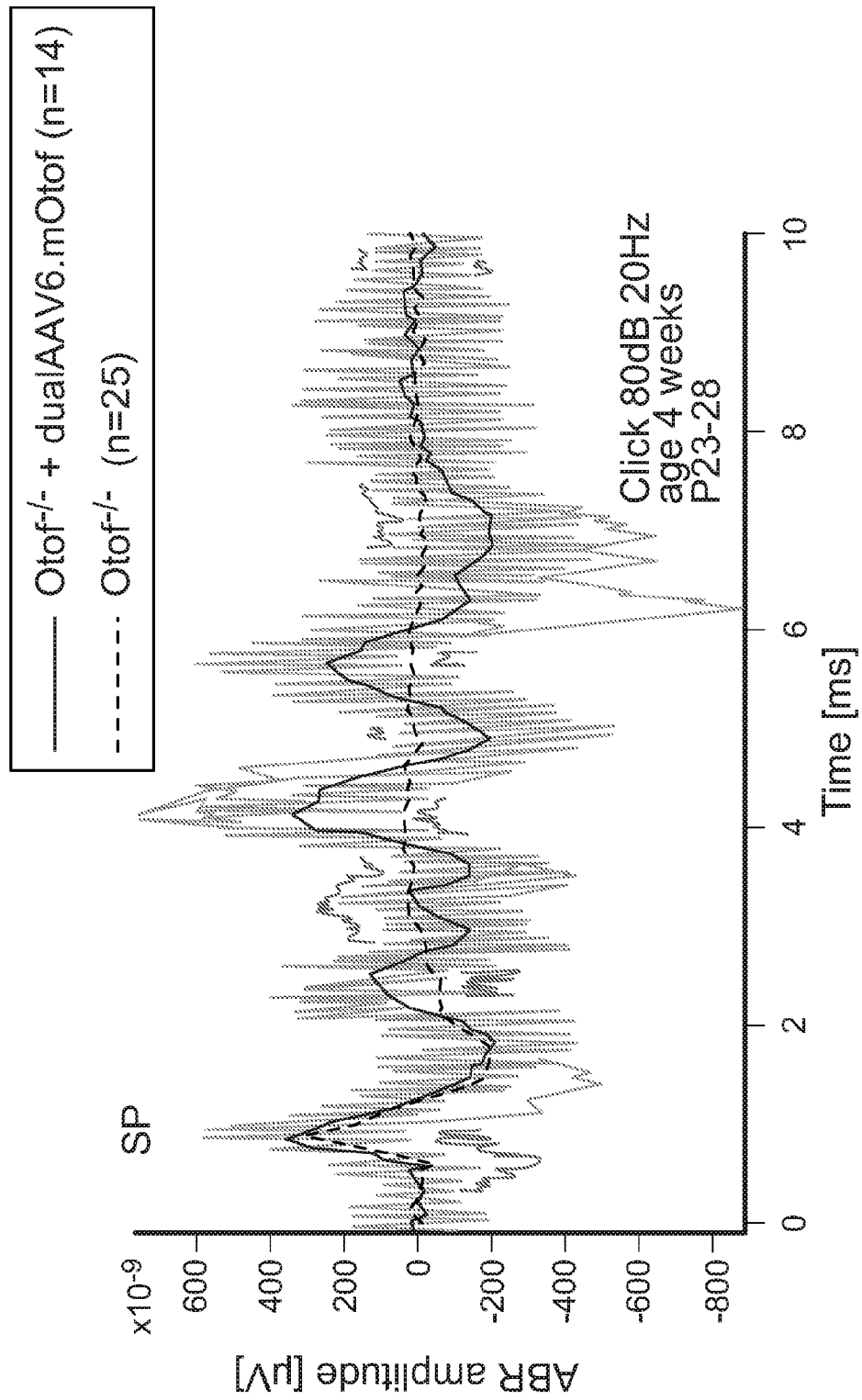


FIG. 3

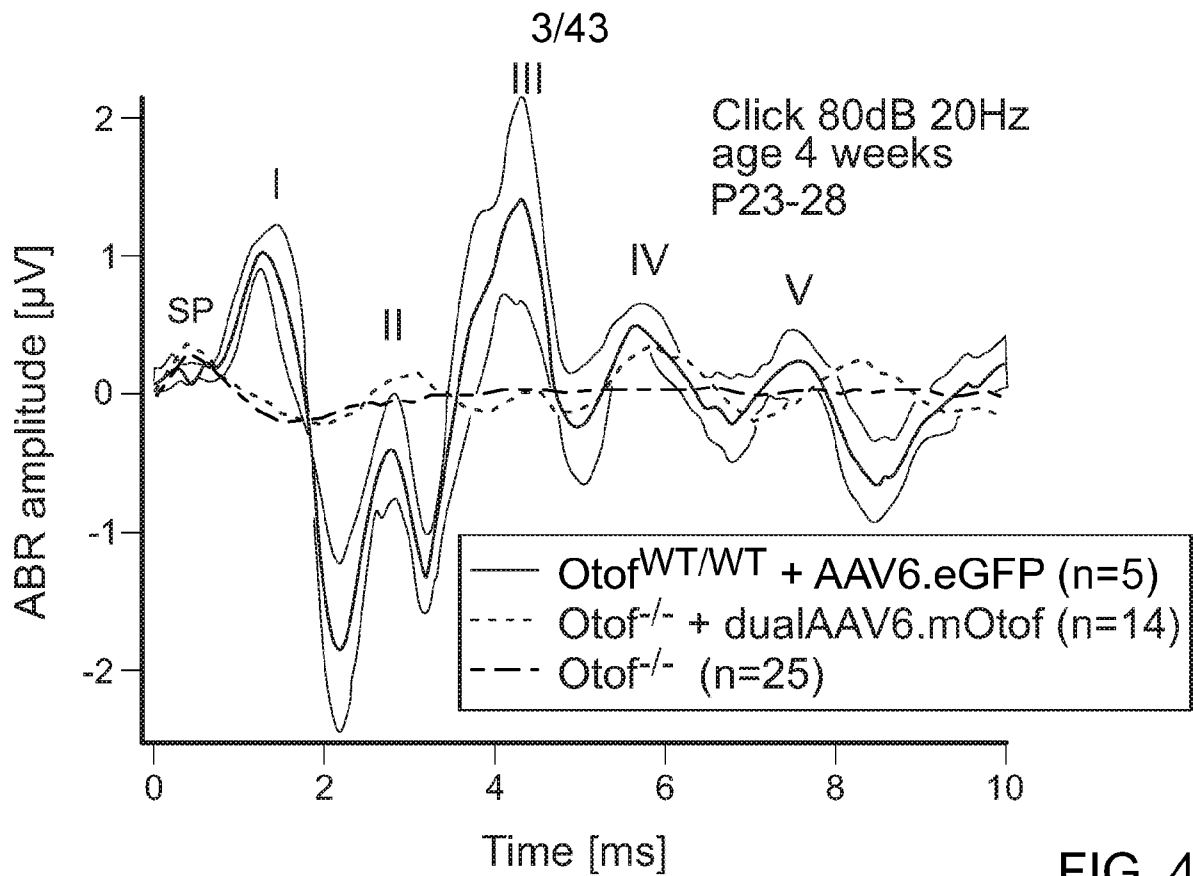


FIG. 4

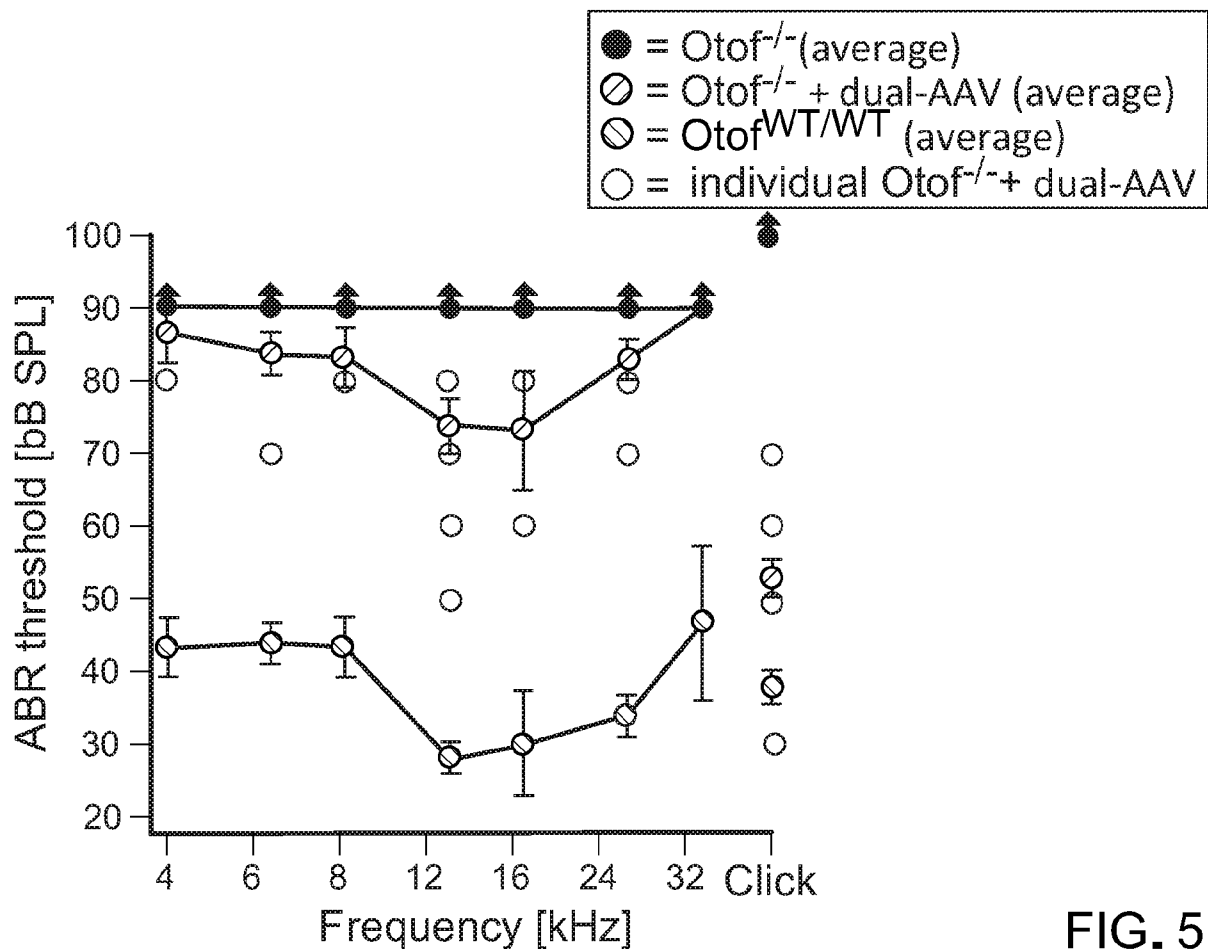


FIG. 5

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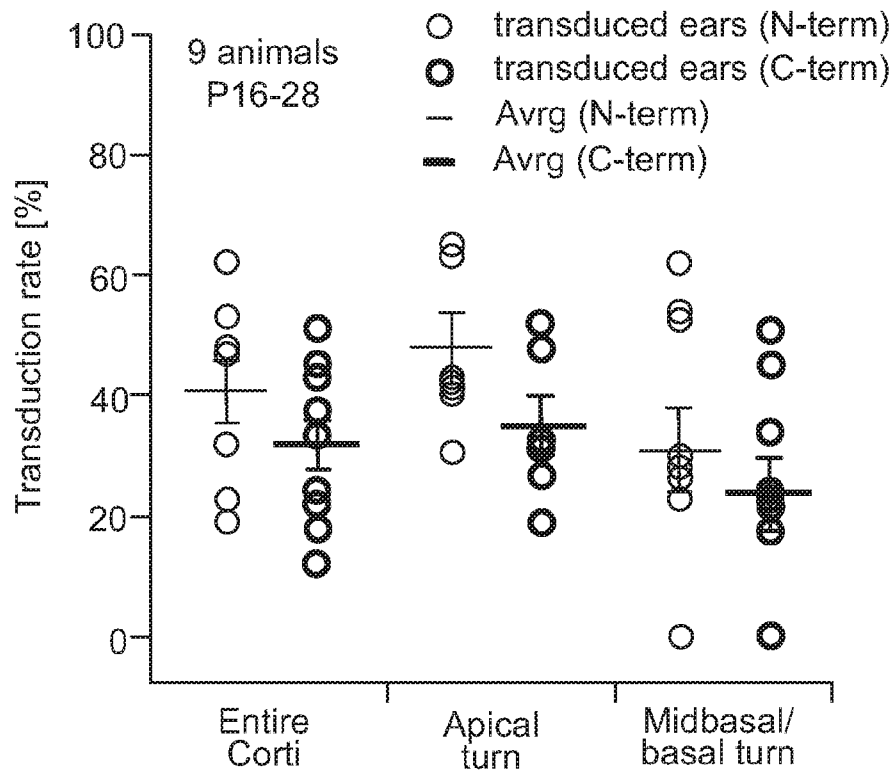


FIG. 6

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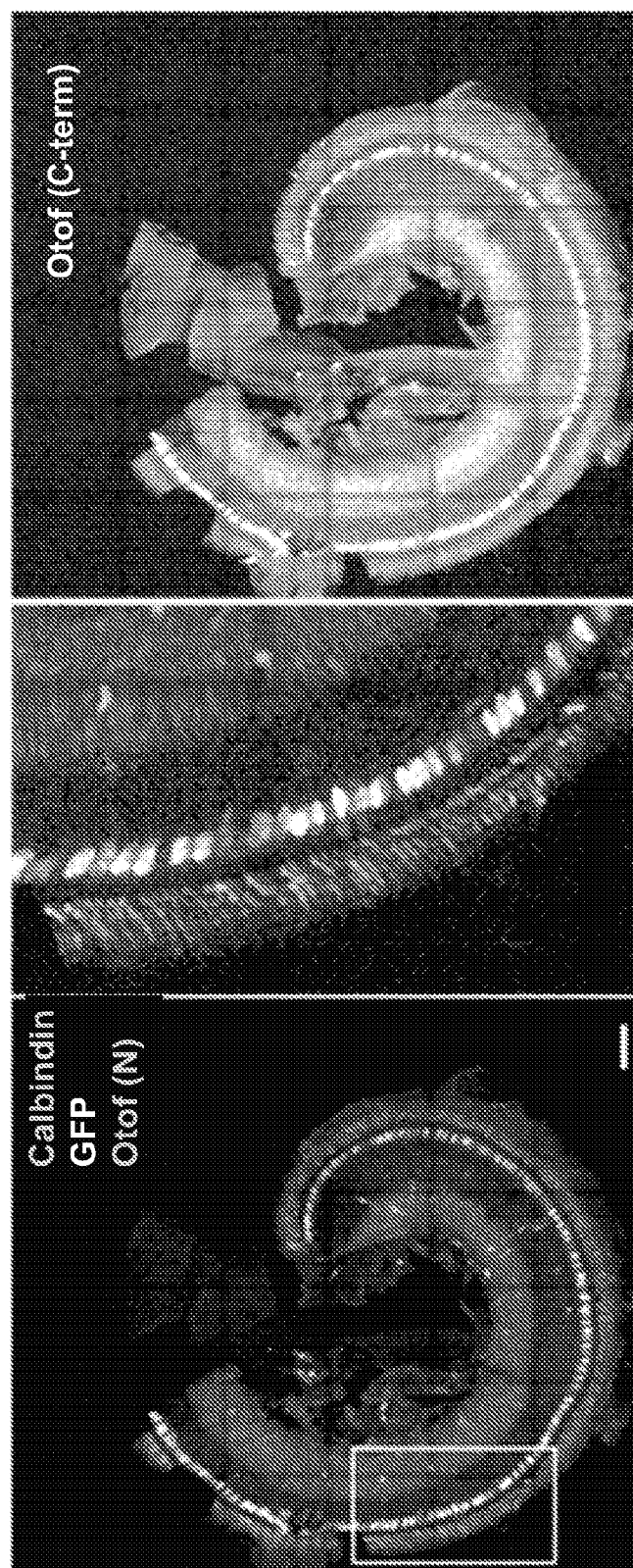


FIG. 7

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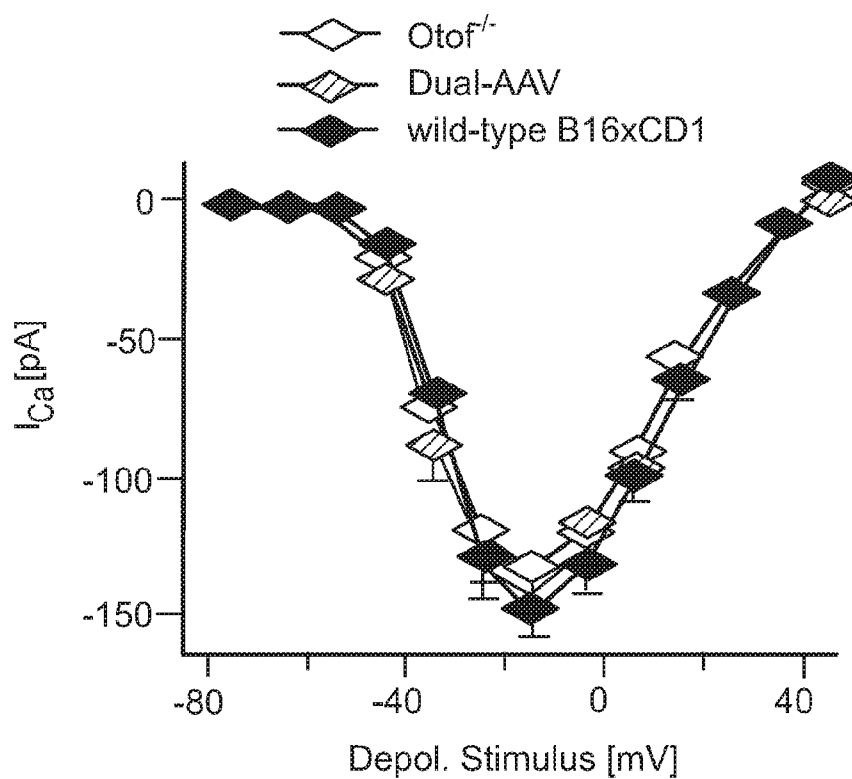


FIG. 8

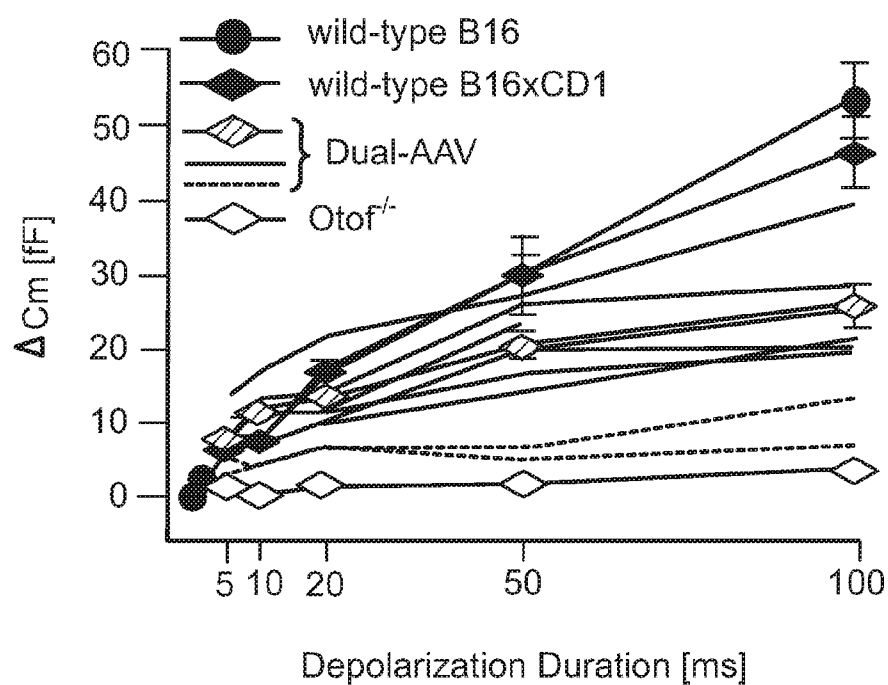


FIG. 9

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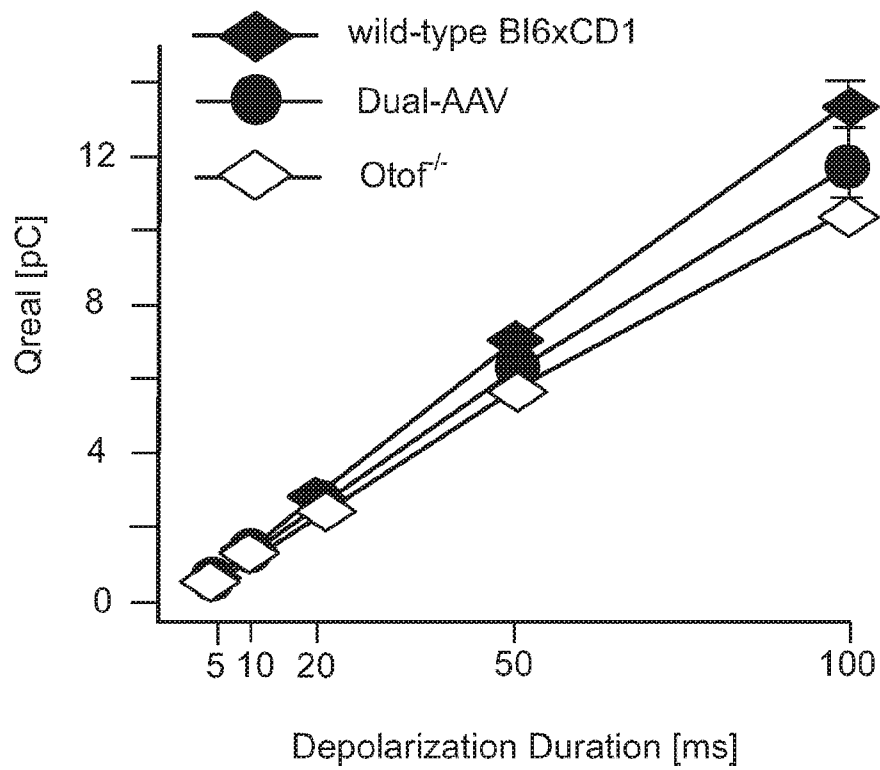


FIG. 10

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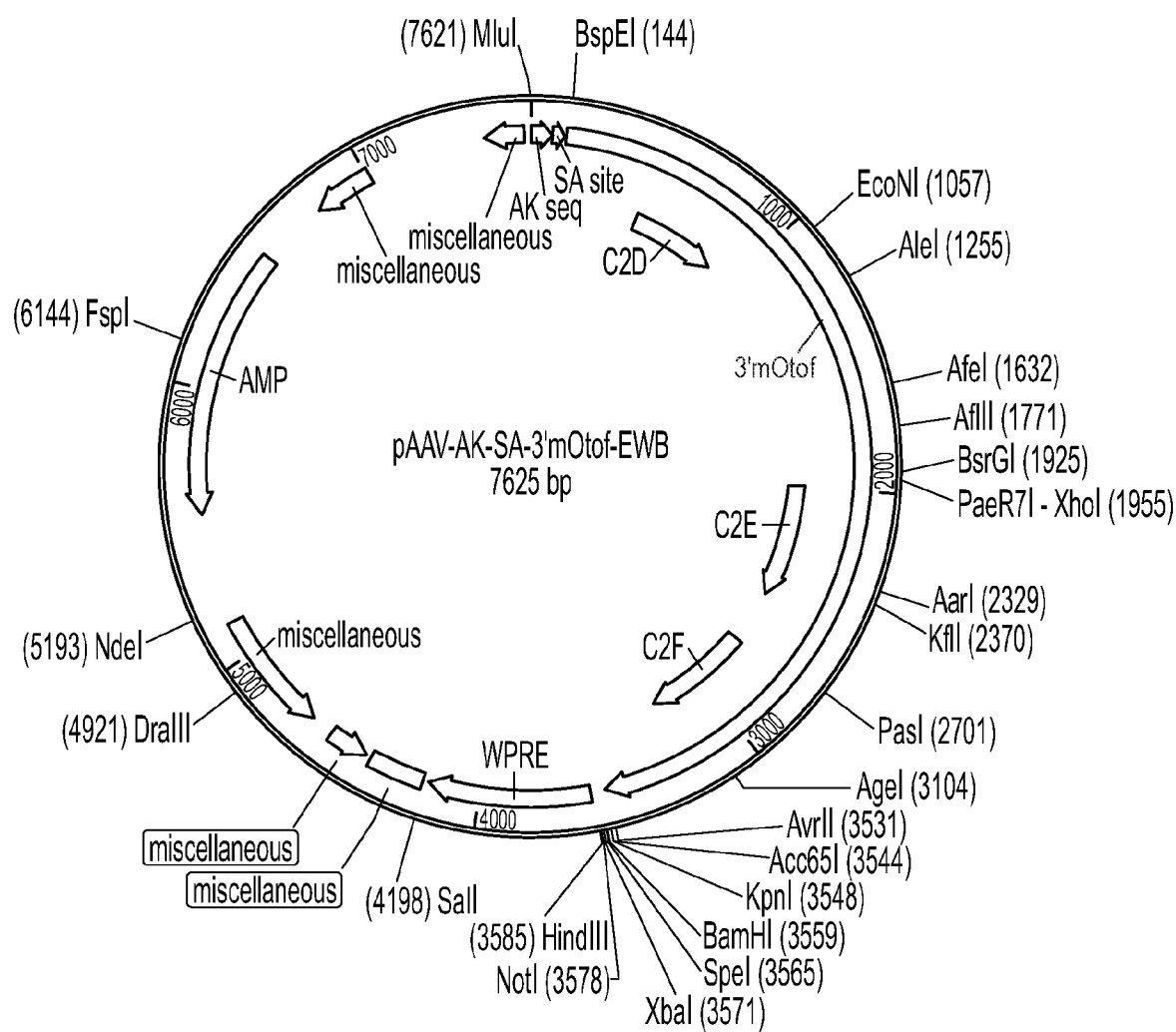


FIG. 11

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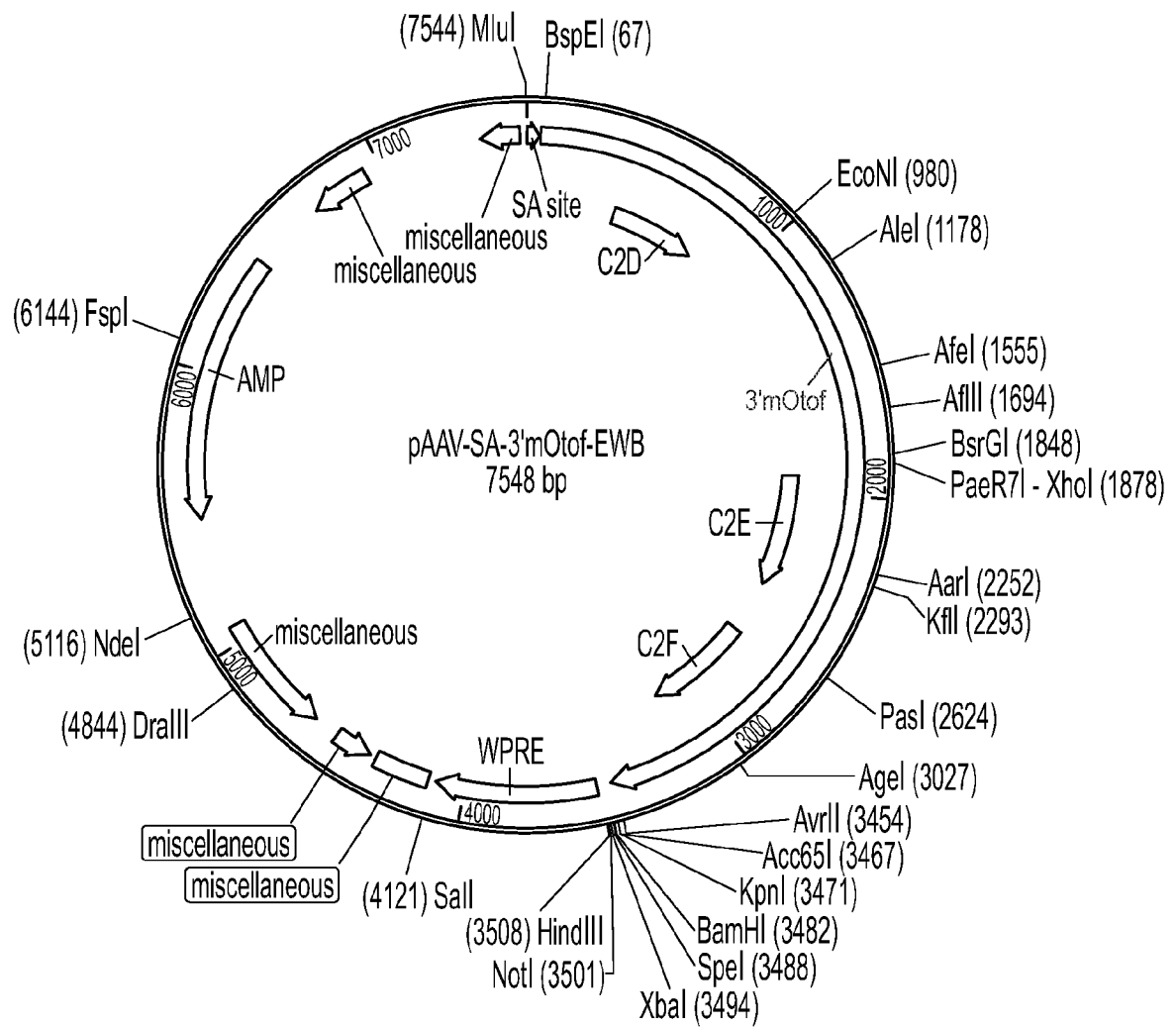


FIG. 12

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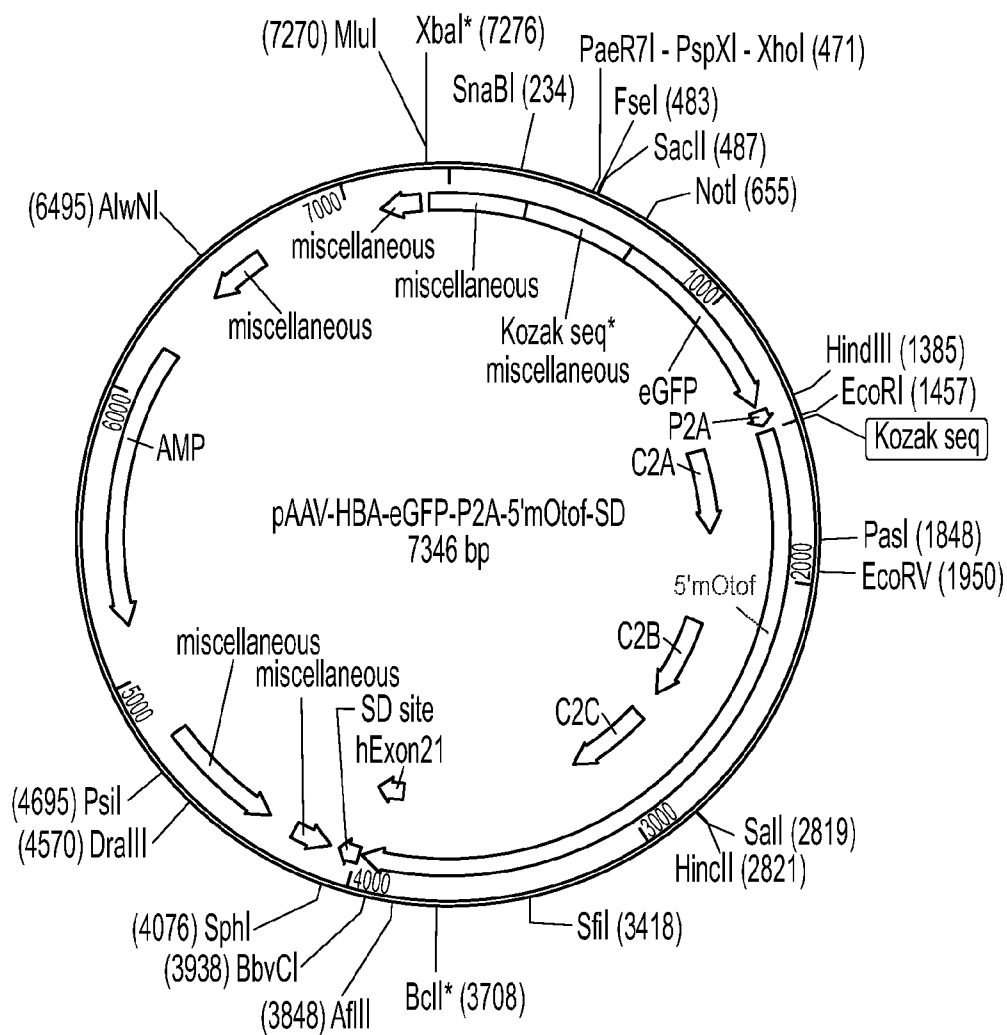


FIG. 13

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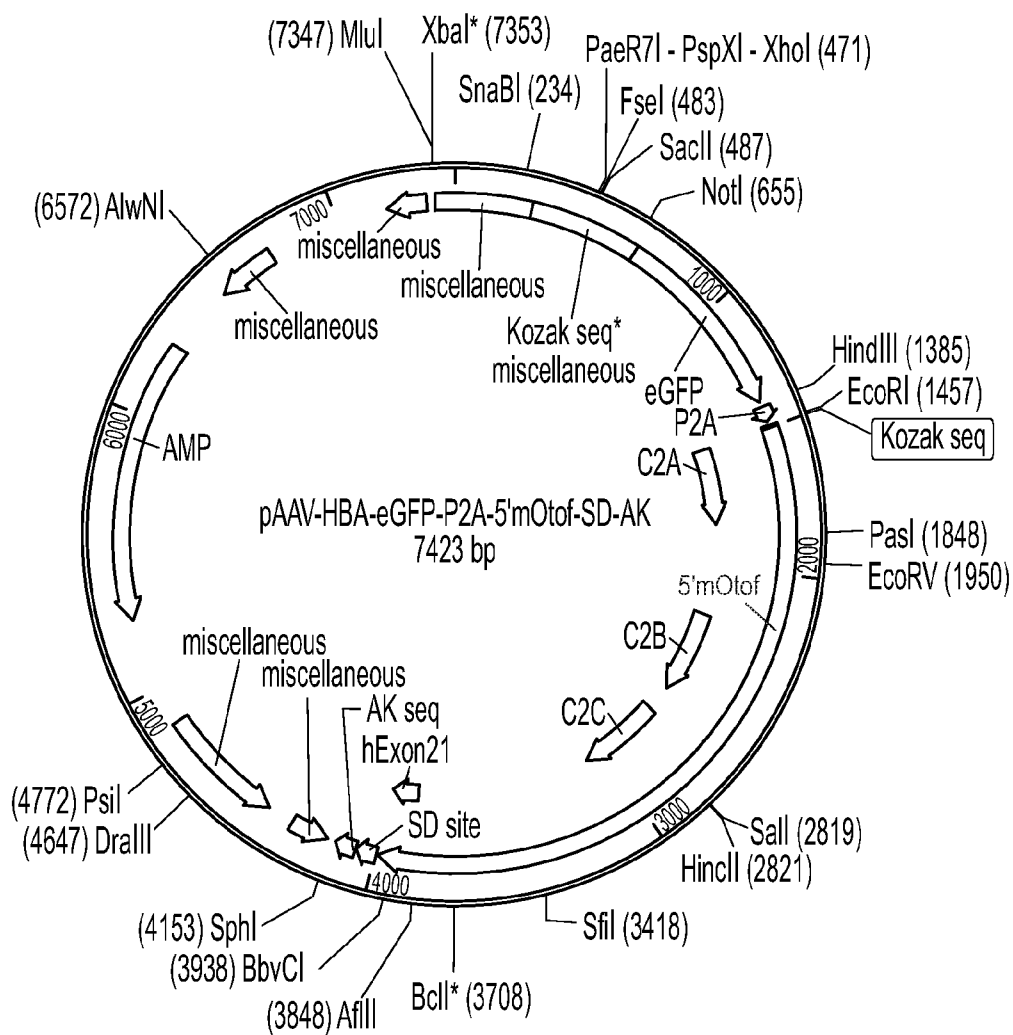


FIG. 14

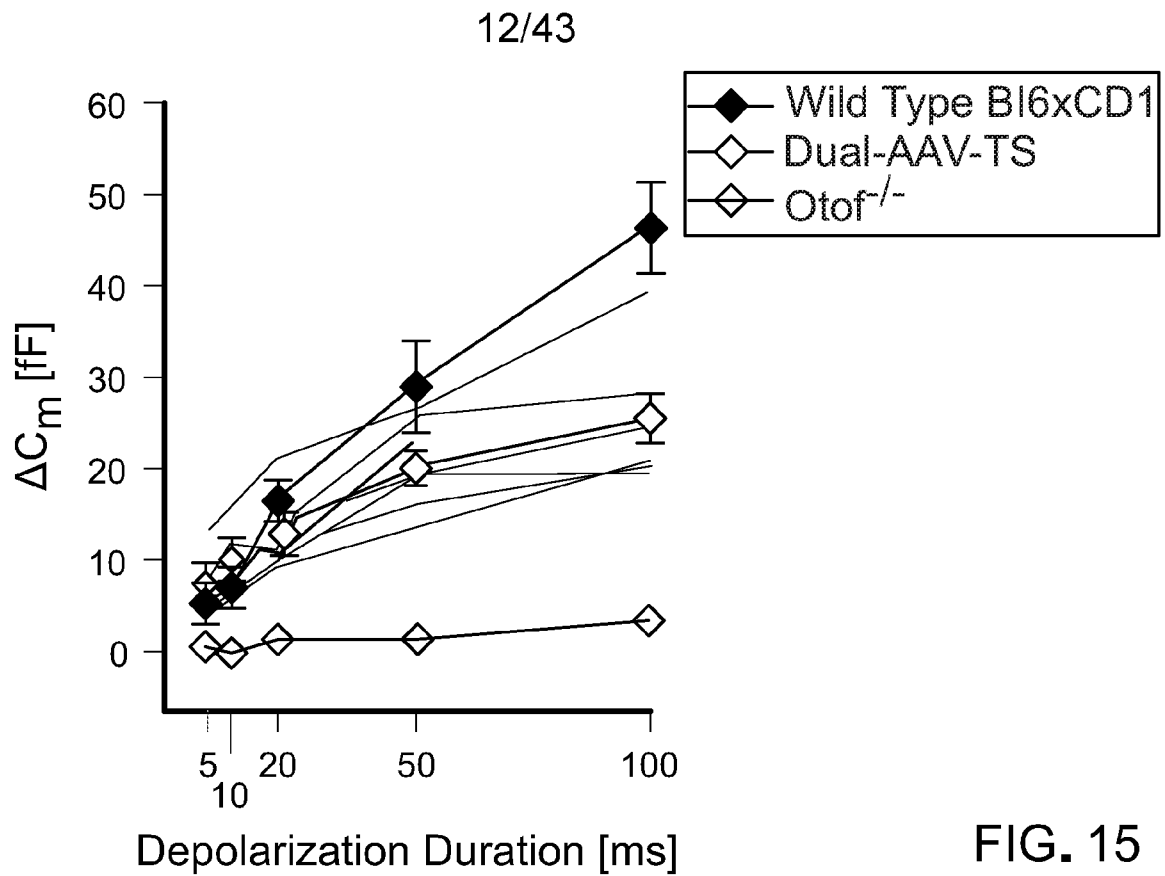


FIG. 15

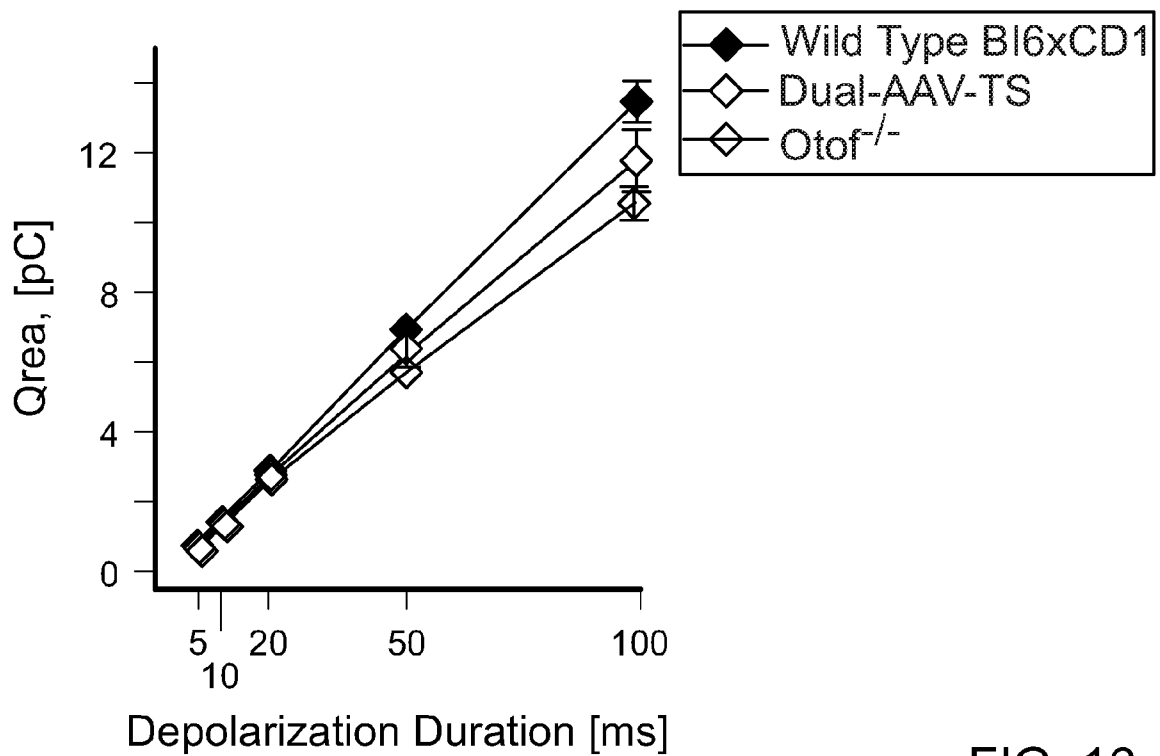


FIG. 16

A circular map of the pAAV-AK-SA-3'mOtof-EWB plasmid, which is 7625 bp in size. The map shows the following elements in clockwise order starting from the top: AK seq, SA site, ITR, C2D, 3'mOtof, C2E, C2F, WPRE, BGH polyA, ITR, f1 ori, AMP, and ori. The plasmid is labeled pAAV-AK-SA-3'mOtof-EWB 7625 bp.

FIG. 17

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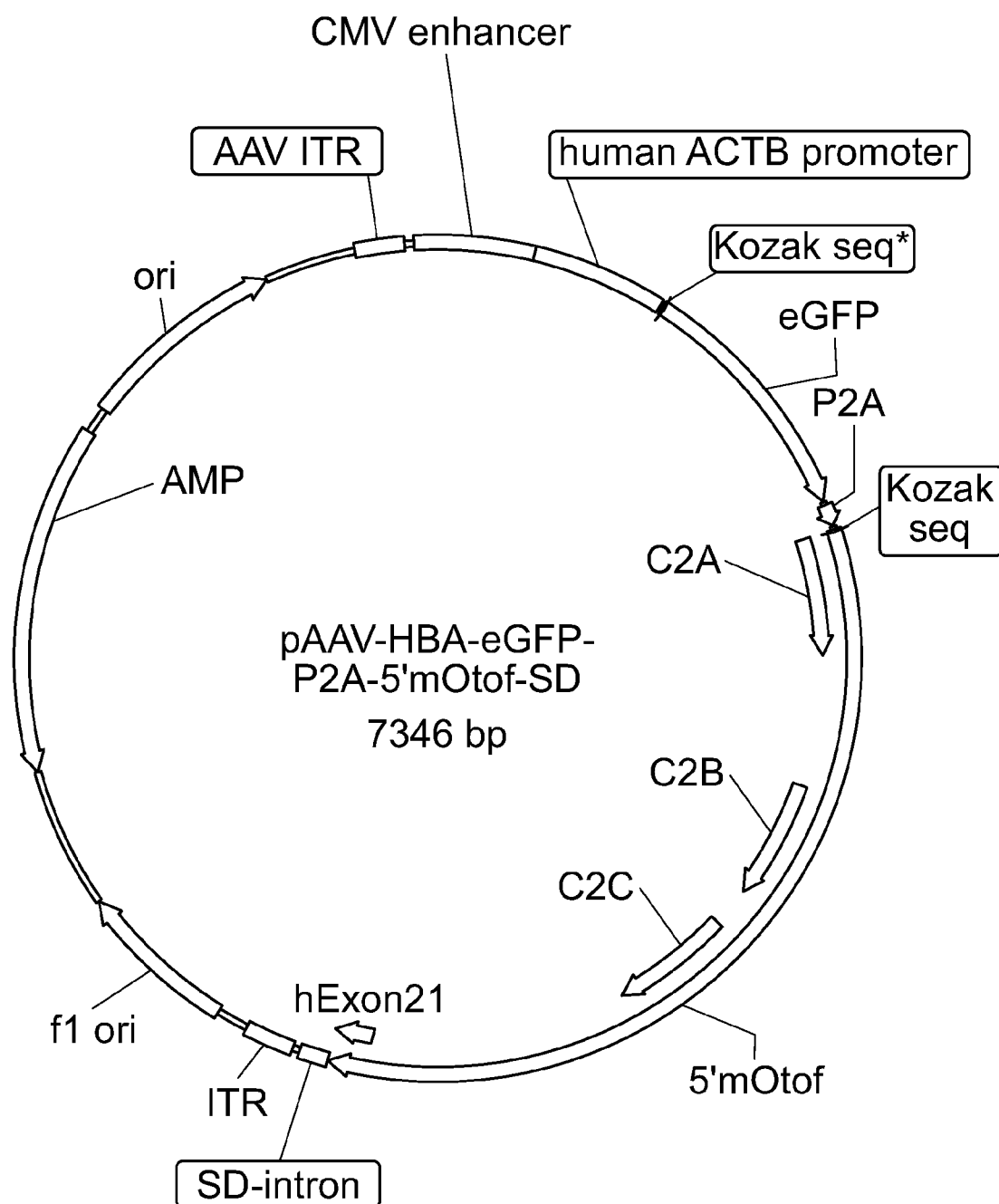


FIG. 18

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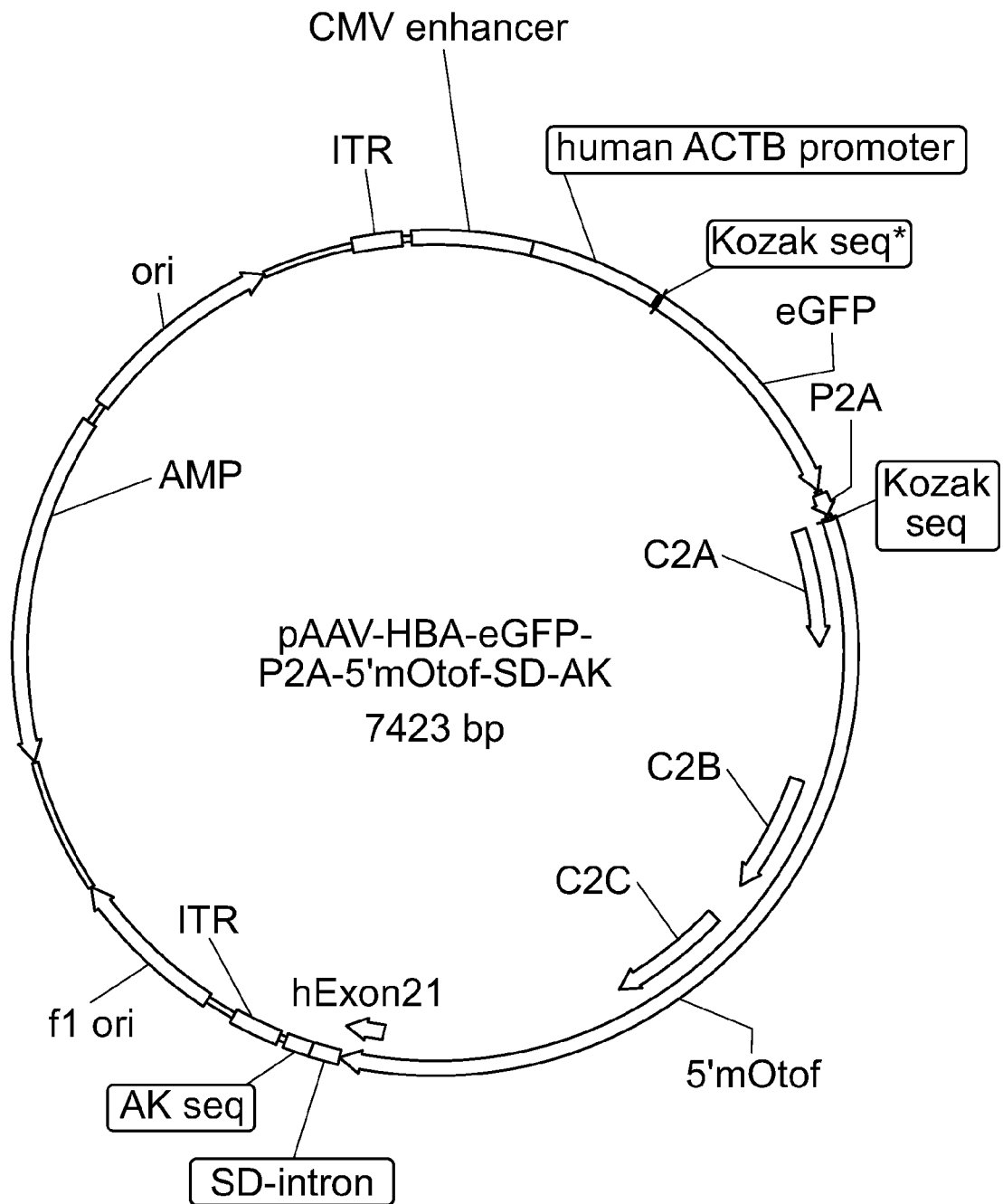


FIG. 19

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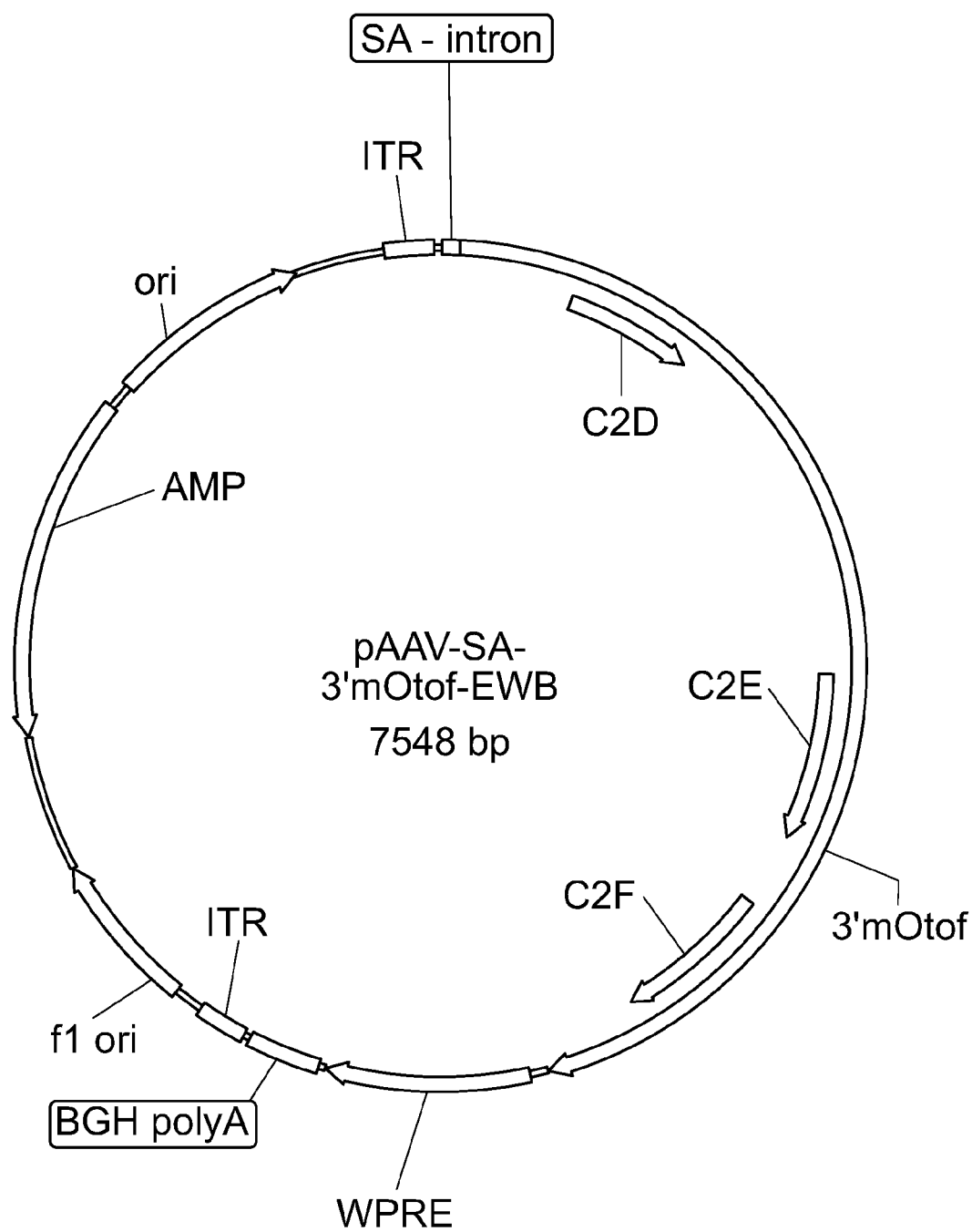


FIG. 20

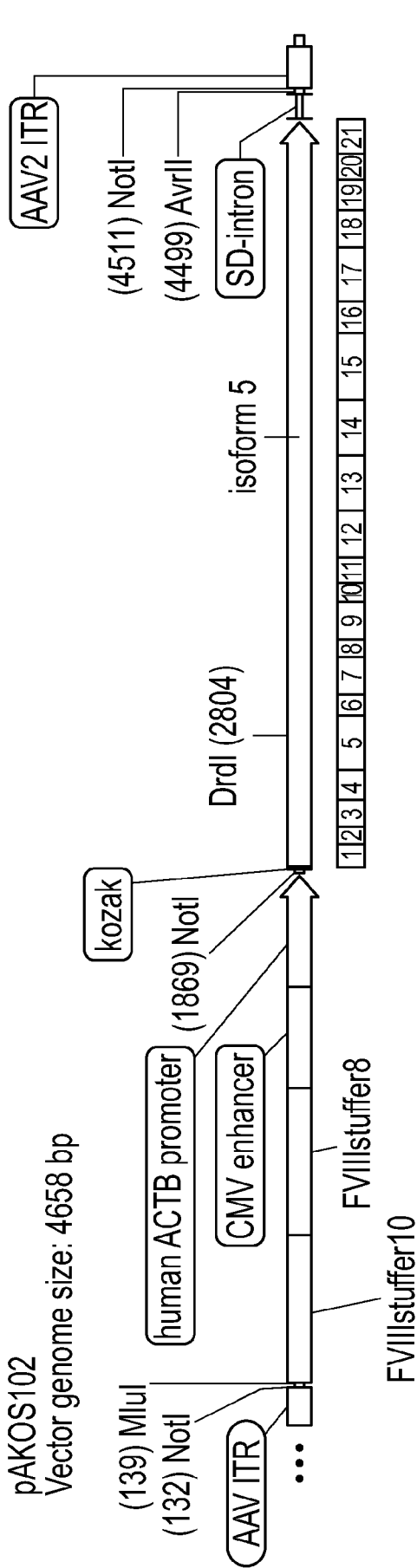


FIG. 21

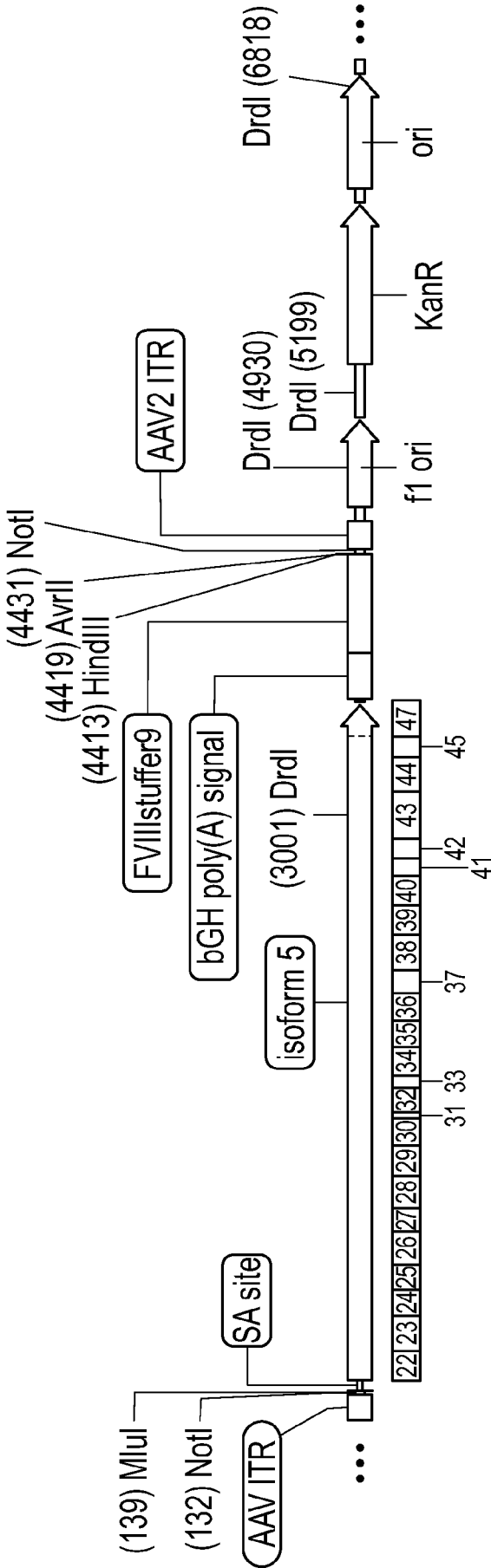


FIG. 22

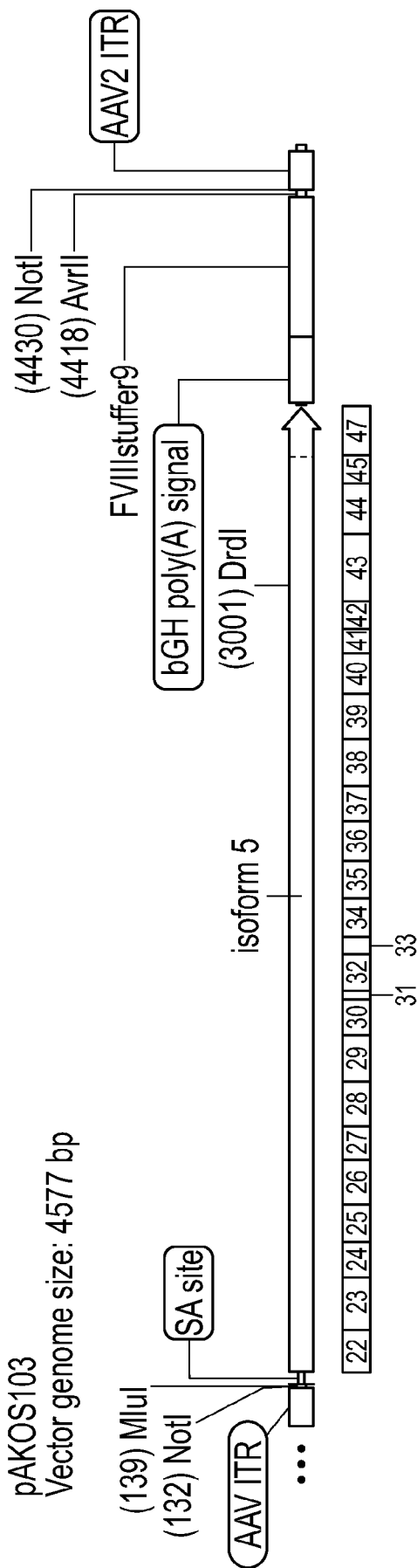


FIG. 23

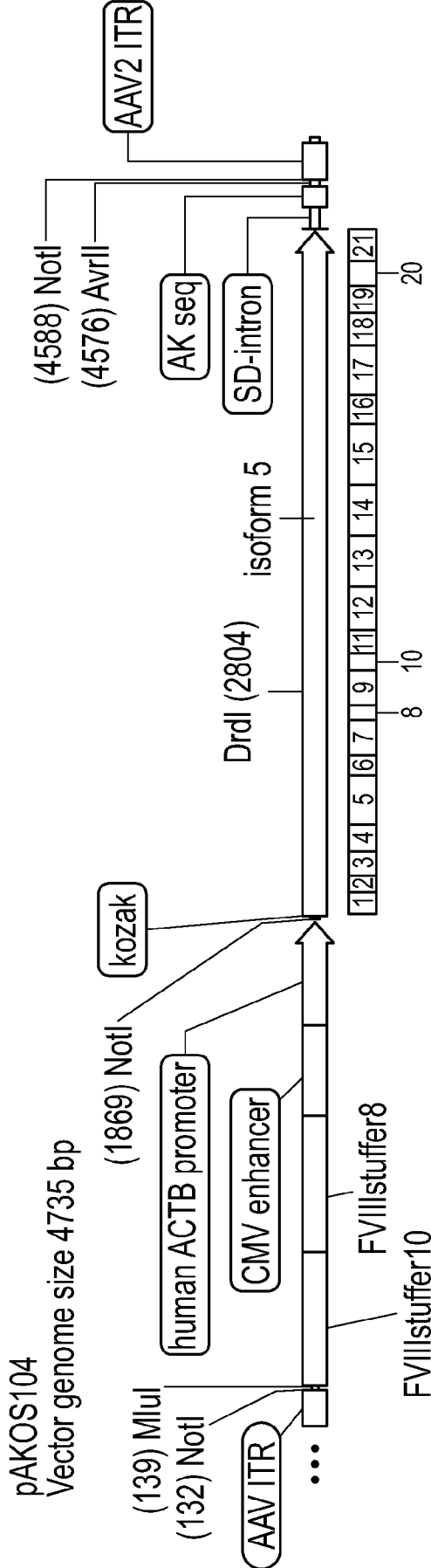


FIG. 24

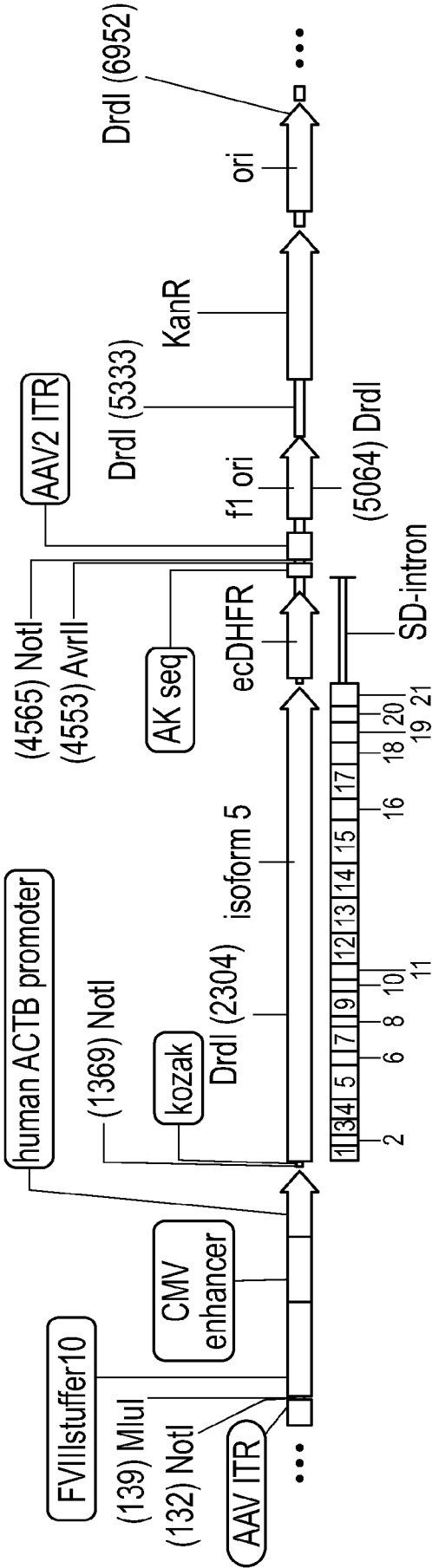


FIG. 25

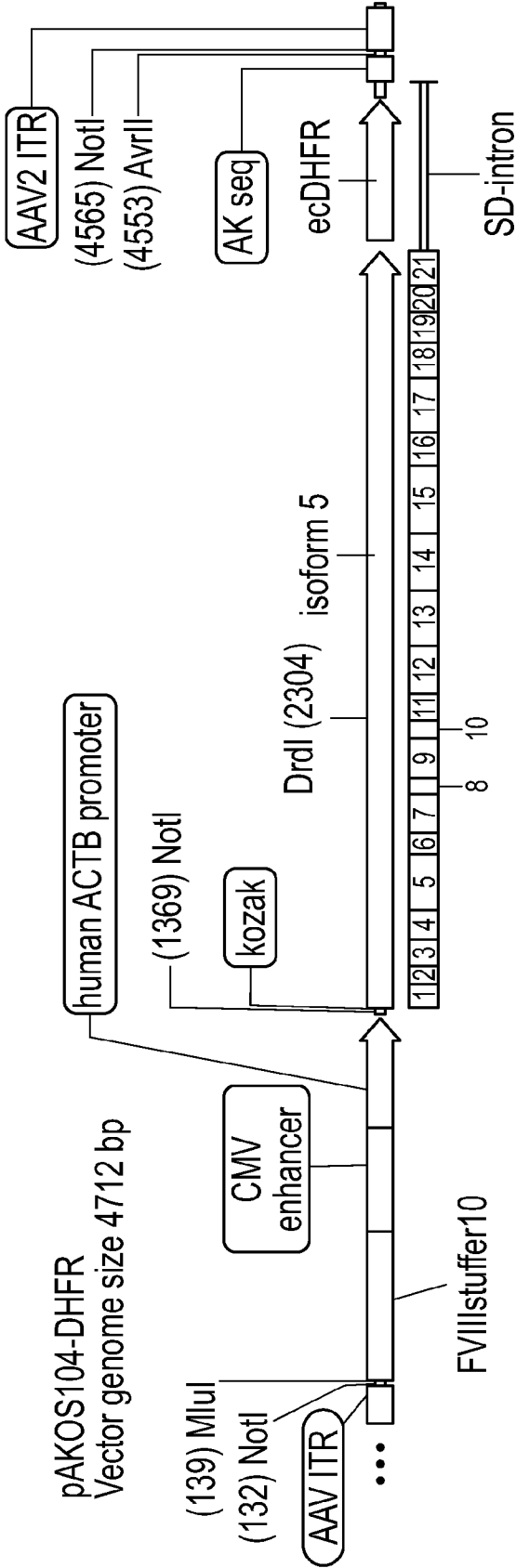


FIG. 26

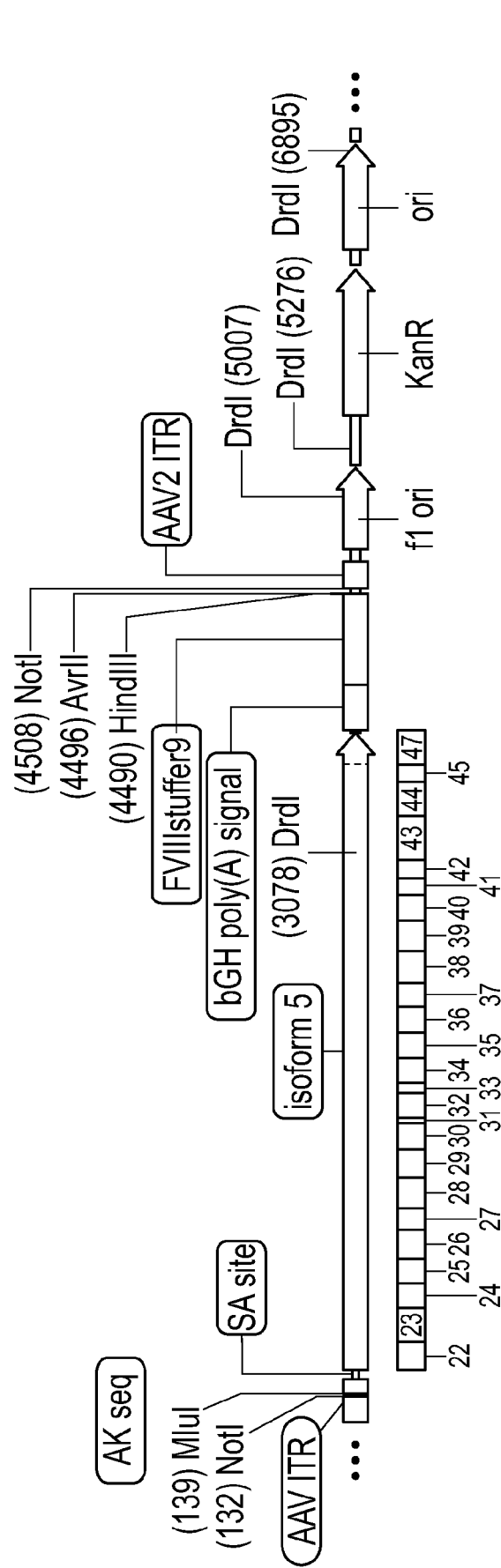


FIG. 27

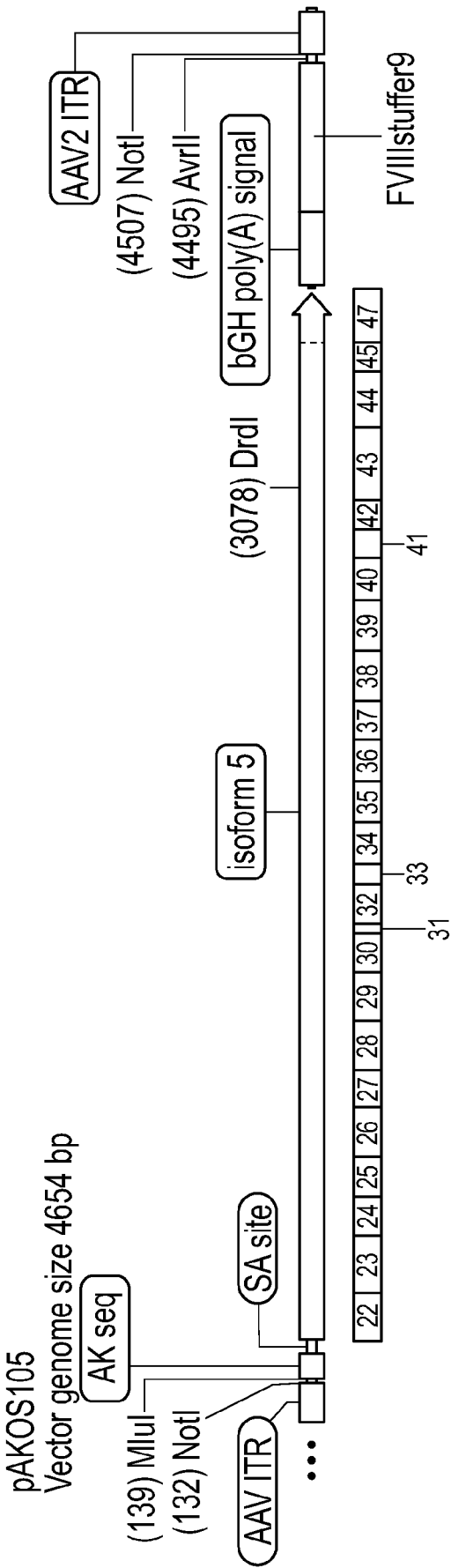


FIG. 28

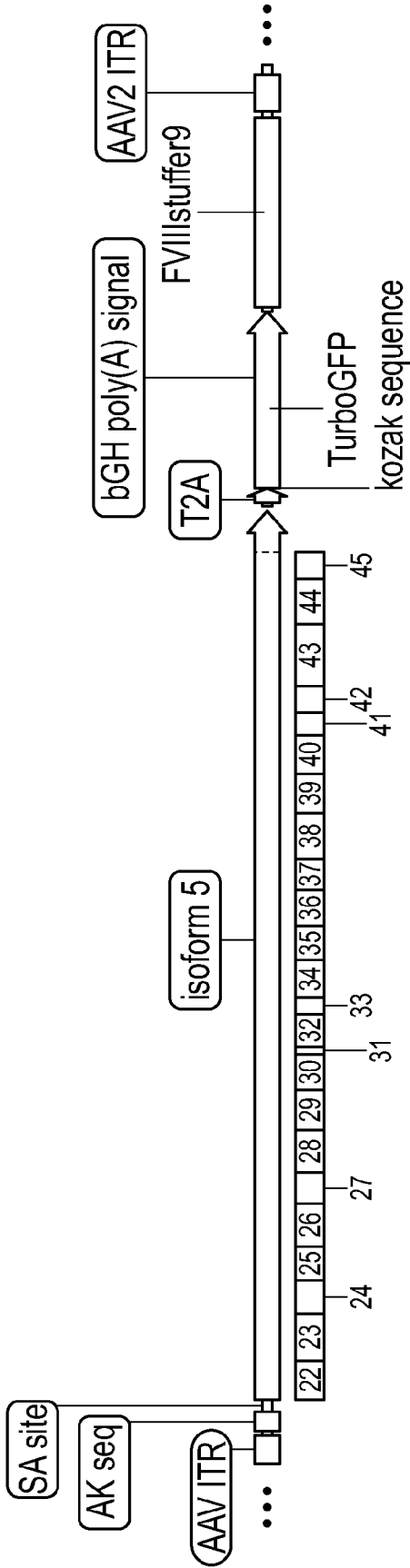


FIG. 29

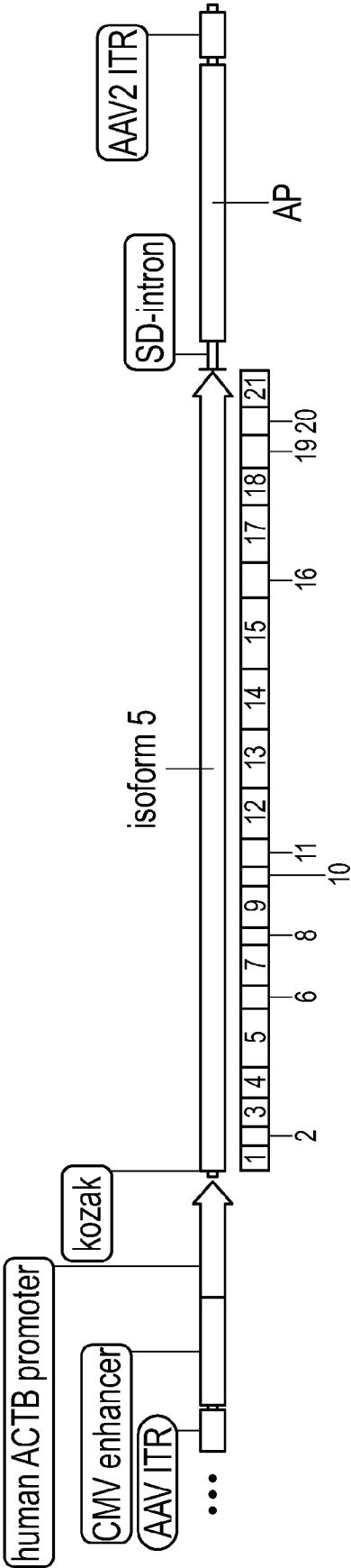


FIG. 30

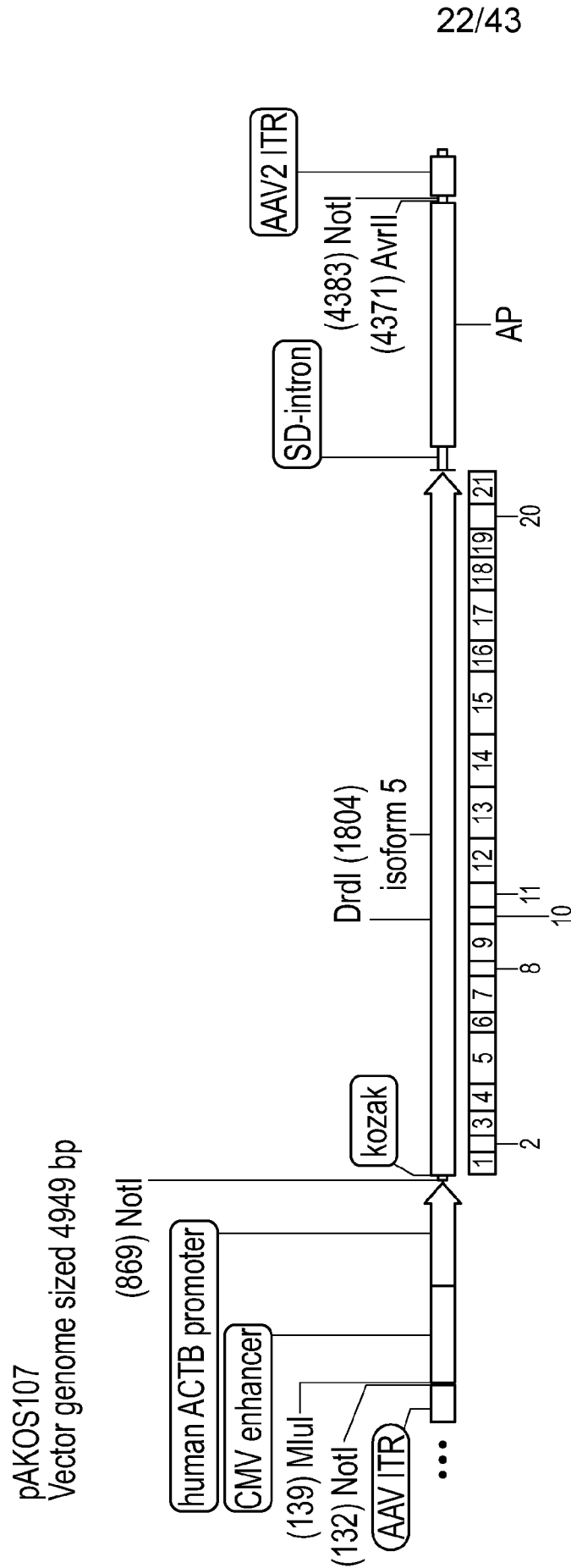


FIG. 31

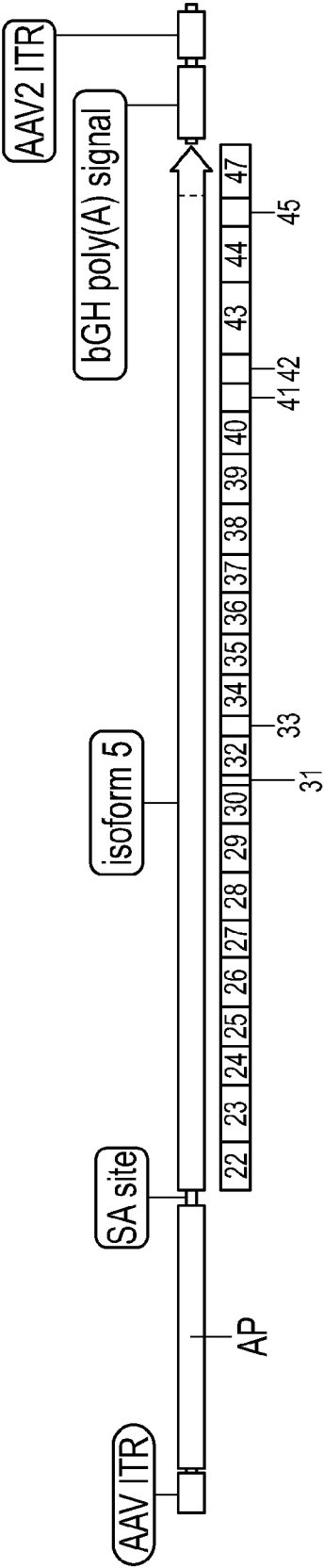


FIG. 32

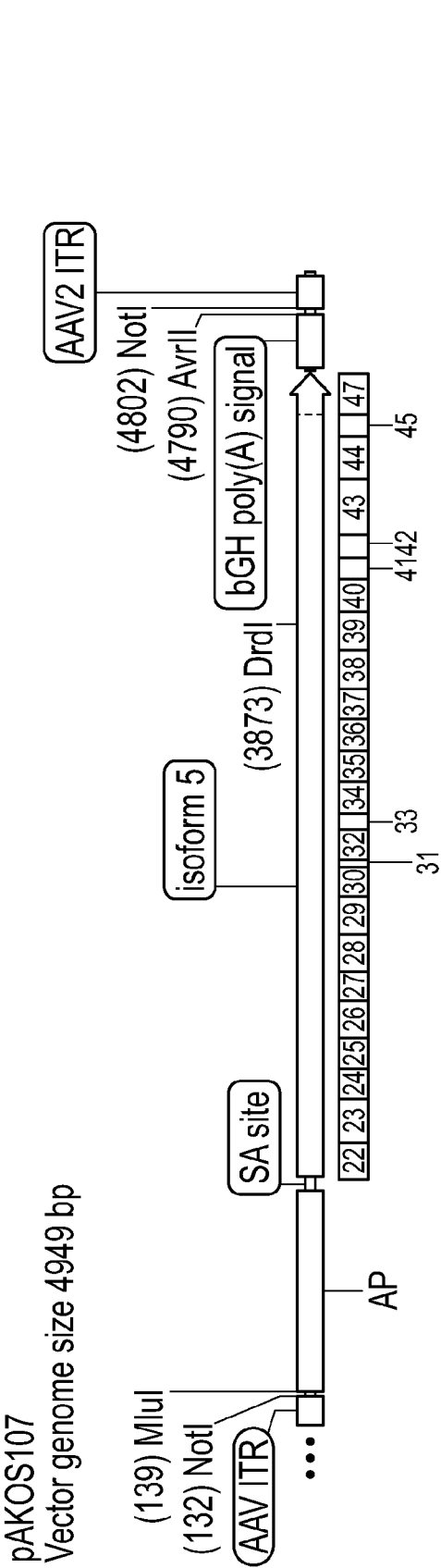


FIG. 33

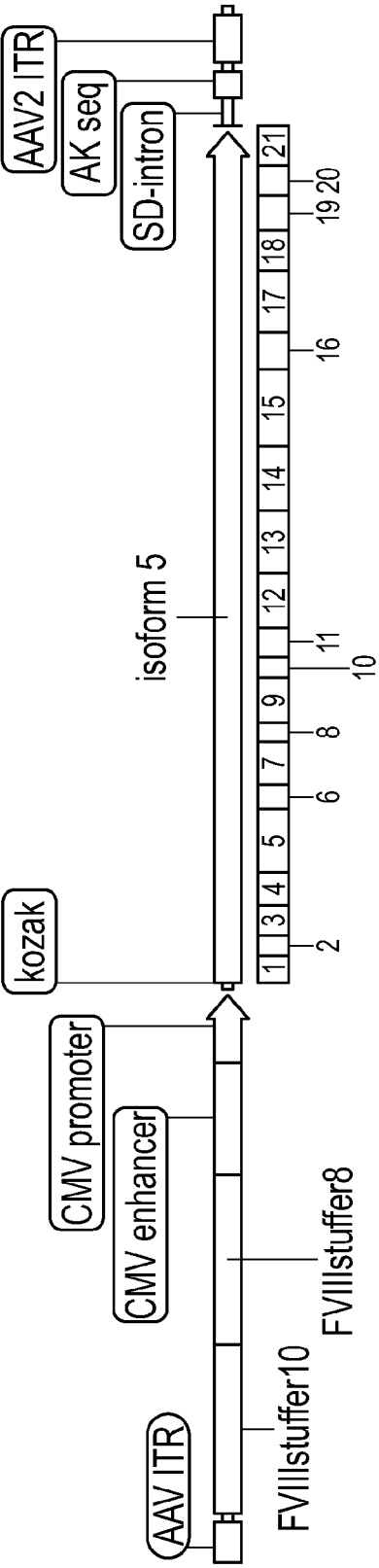
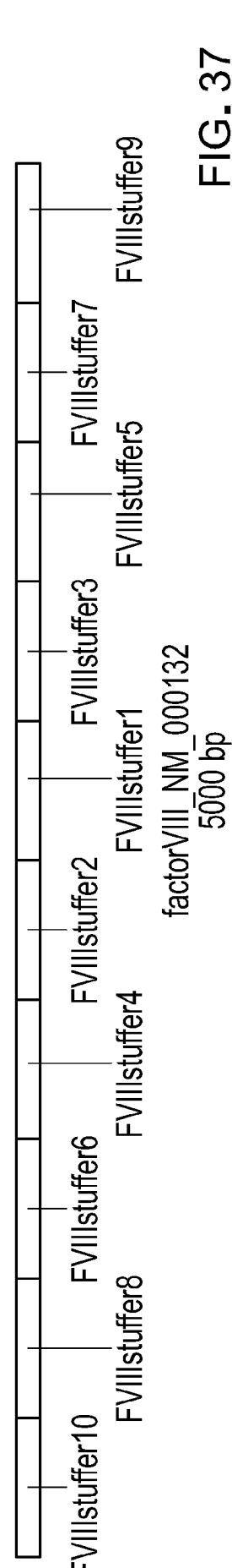
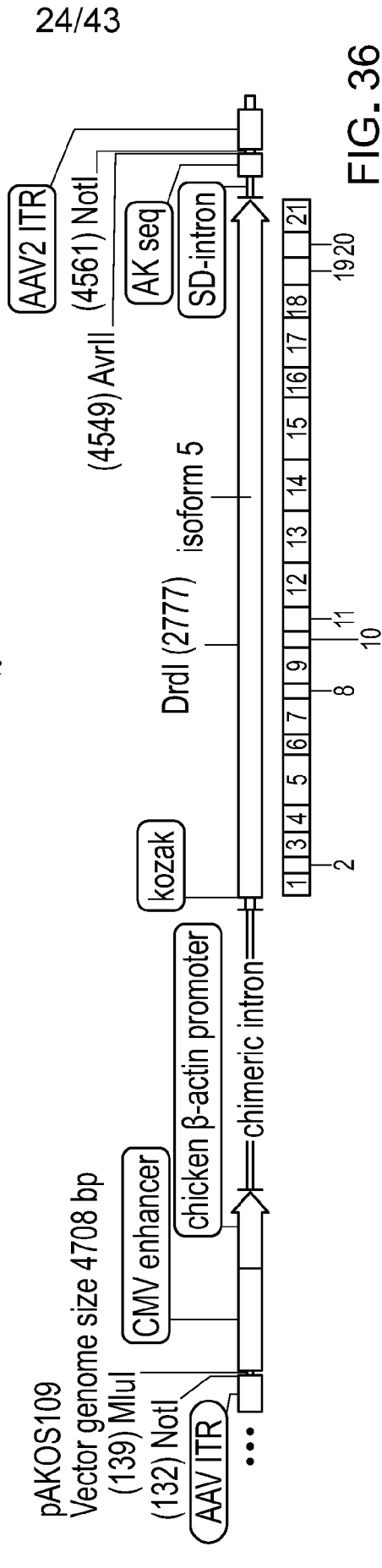
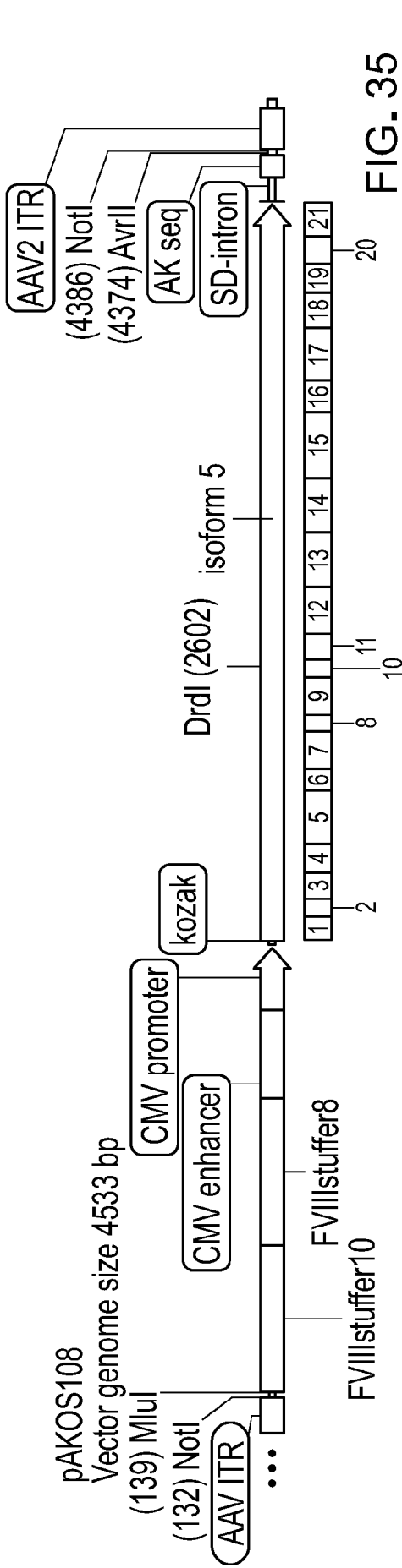


FIG. 34







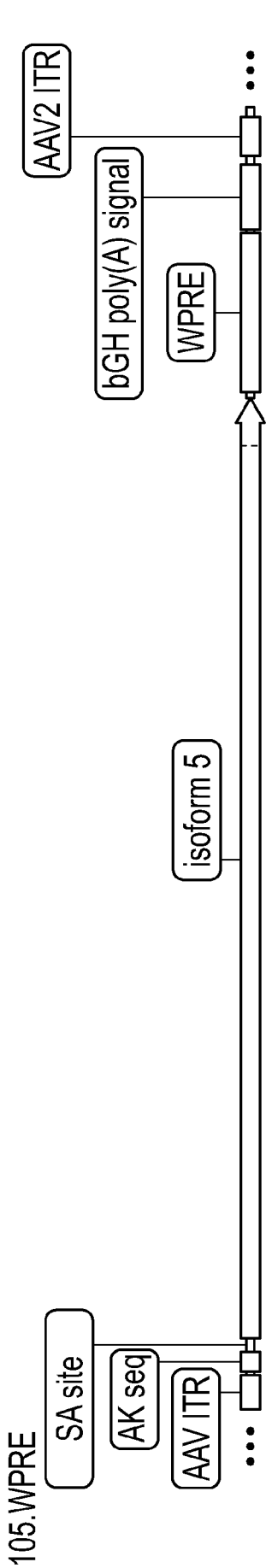


FIG. 40

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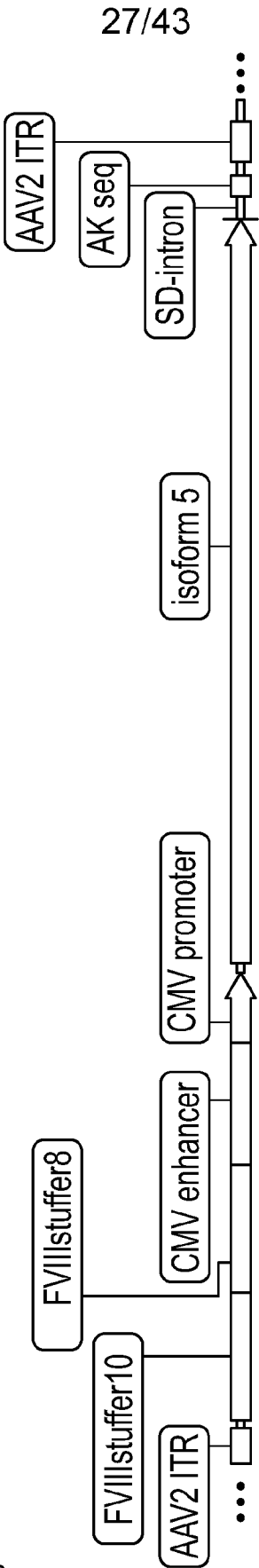


FIG. 41

10TOF18.CL1

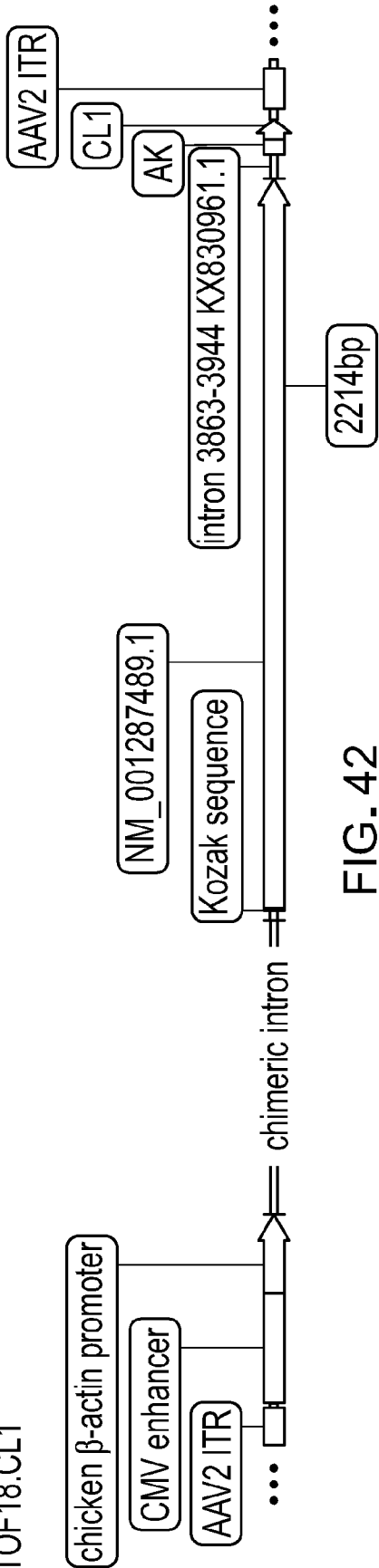


FIG. 42

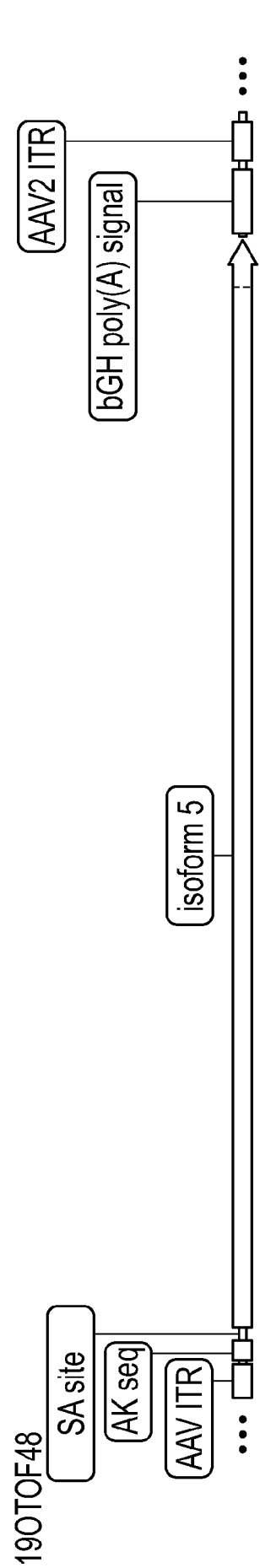


FIG. 43

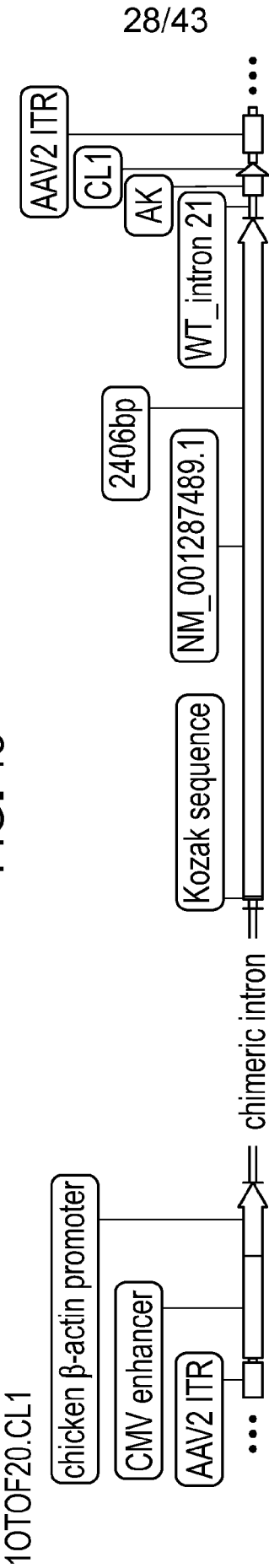


FIG. 44

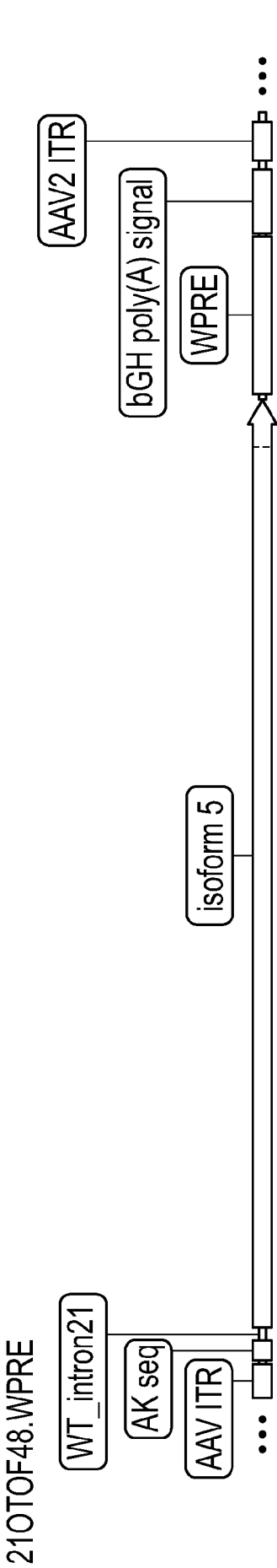


FIG. 45

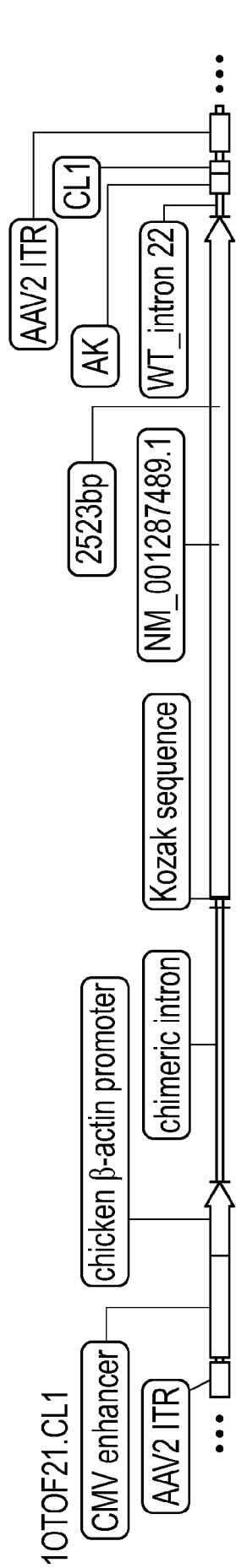


FIG. 46

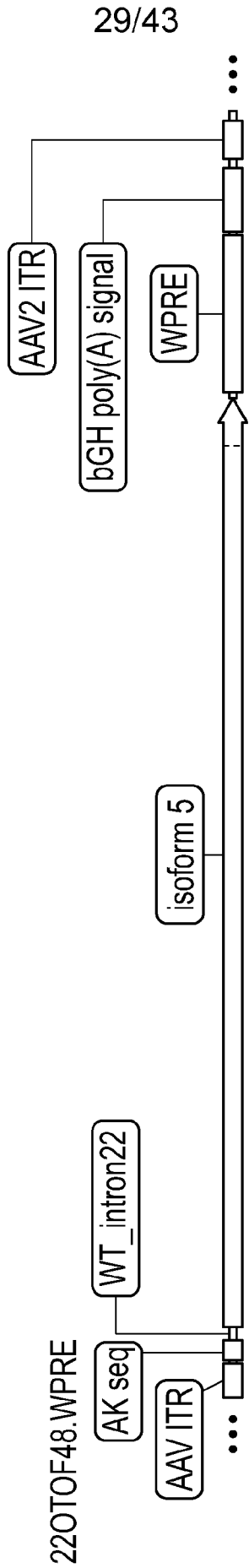


FIG. 47

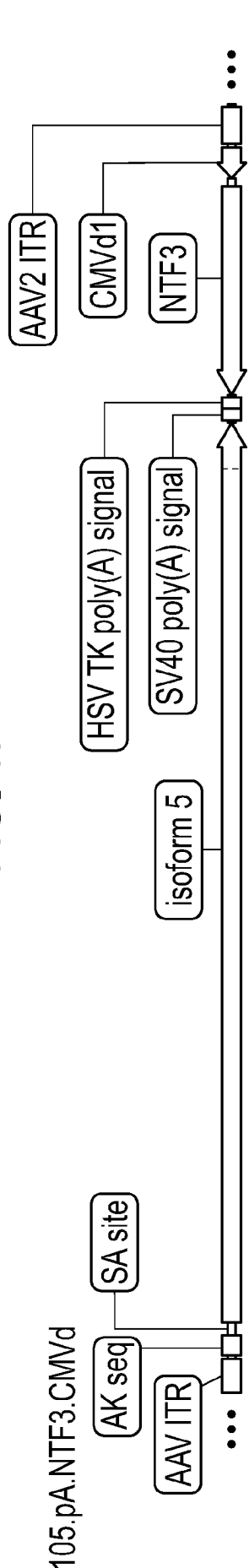


FIG. 48

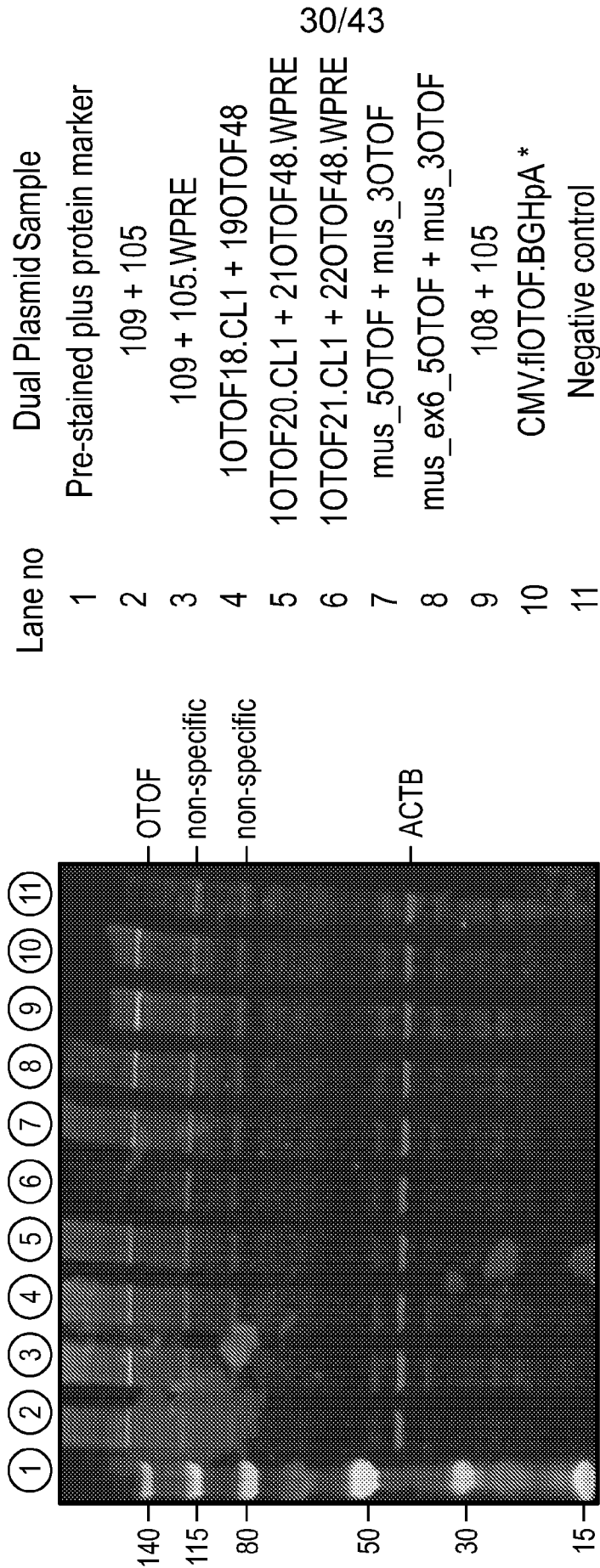


FIG. 49

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400ng	400ng	Experiment 1			Experiment 2			Experiment 3			Final		
		I.I. ACTB	I.I. OTOF	Ratio	I.I. ACTB	I.I. OTOF	Ratio	I.I. ACTB	I.I. OTOF	Ratio	Average	STDEV	%CV
Plasmid 1	Plasmid 2												
	105	22.29	0.12	0.005	18.57	0.39	0.021	13.41	0.13	0.010	0.012	0.01	67.07
109	105WPRE	18.46	0.23	0.012	19.32	0.82	0.042	16.37	0.28	0.017	0.024	0.02	67.24
10TOF18.CL1	190TOF48	18.15	0.17	0.009	17.11	0.36	0.021	18.84	0.28	0.015	0.015	0.01	38.70
10TOF20.CL1	210TOF48.WPRE	19.47	0.30	0.015	16.52	0.22	0.013	16.97	0.15	0.009	0.013	0.00	26.80
10TOF21.CL1	220TOF48.WPRE	18.31	0.04	0.002	17.07	0.03	0.002	18.32	0.00	0.000	0.001	0.00	N/A
mus_50TOF	mus_30TOF	17.37	1.00	0.058	17.97	0.36	0.020	18.77	0.32	0.017	0.032	0.02	71.58
mus_ex6_50TOF	mus_30TOF	16.06	0.71	0.044	16.11	0.53	0.033	16.08	0.13	0.008	0.028	0.02	65.07
108	105	15.49	1.06	0.068	15.77	0.91	0.058	18.38	0.27	0.015	0.047	0.03	60.59
CMV.fl.OTOF	CMV.fl.OTOF	18.17	0.48	0.026	16.29	0.50	0.031	14.54	0.62	0.043	0.033	0.01	25.29
N/A	N/A	19.10	0.01	0.001	16.94	-0.01	-0.001	14.73	-0.01	-0.001	0.000	0.00	N/A

FIG. 50

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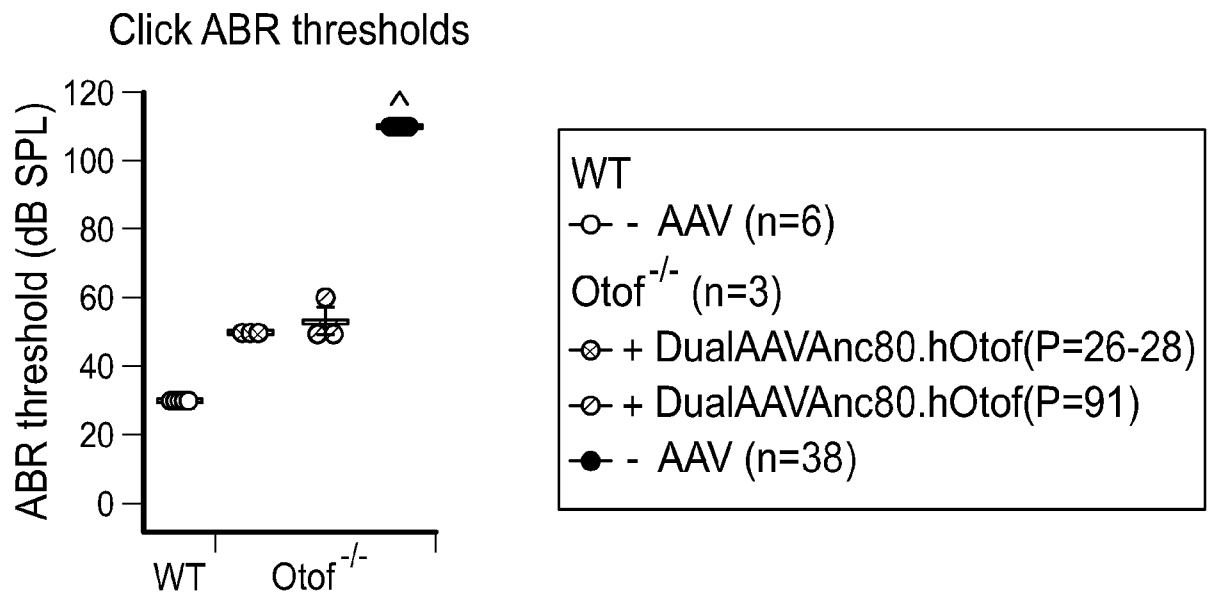


FIG. 51

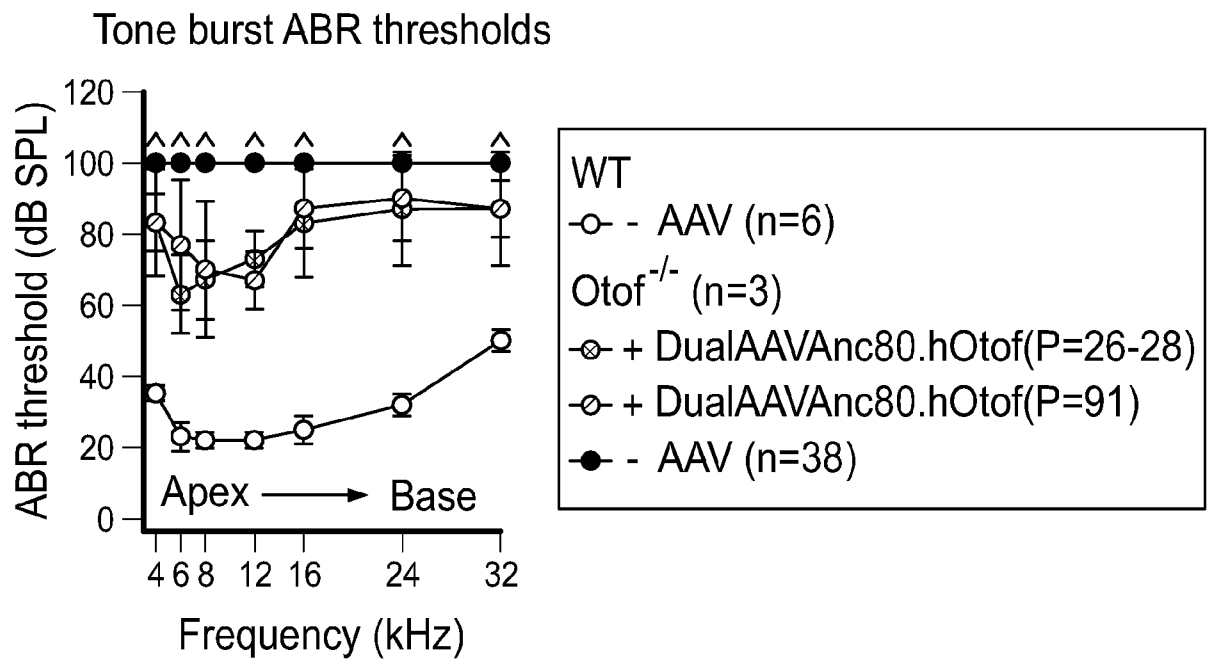
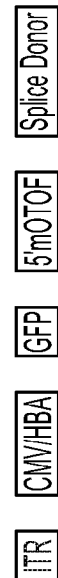


FIG. 52



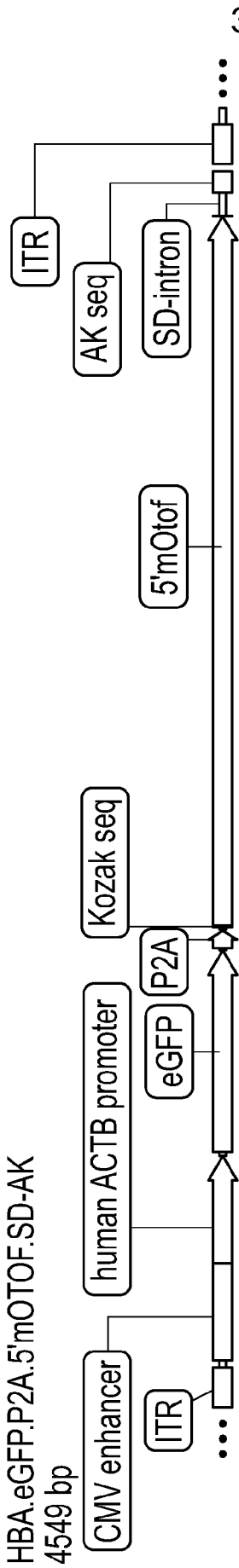


FIG. 55

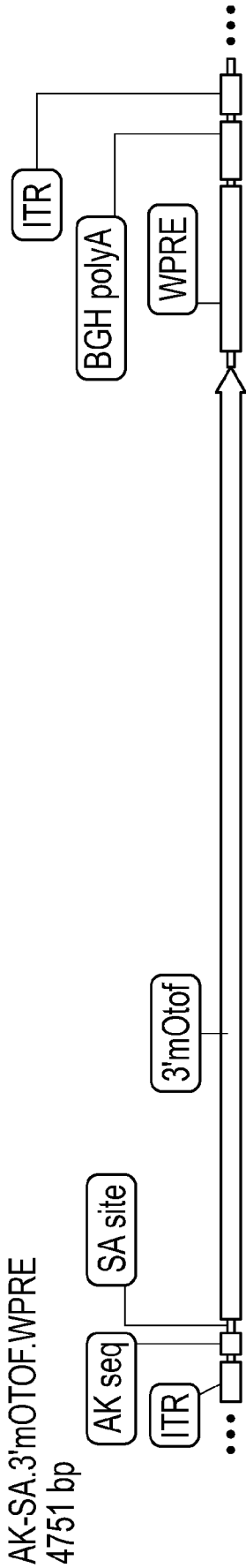


FIG. 56

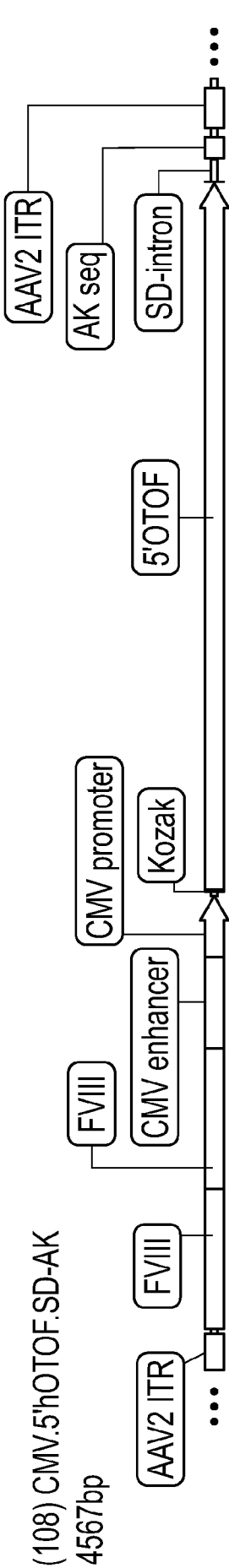


FIG. 57

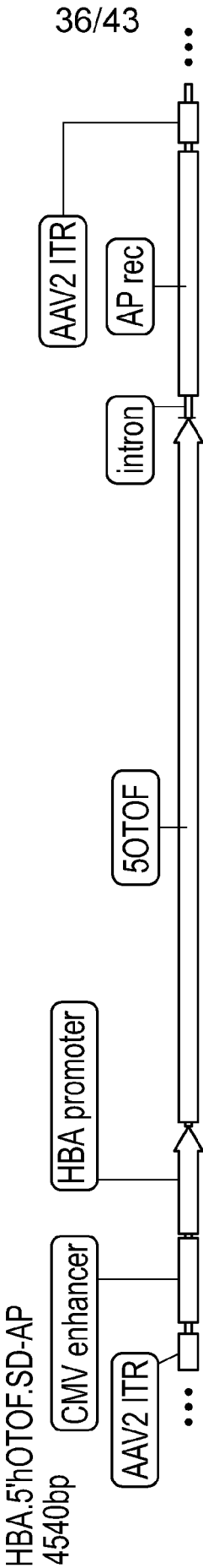


FIG. 58

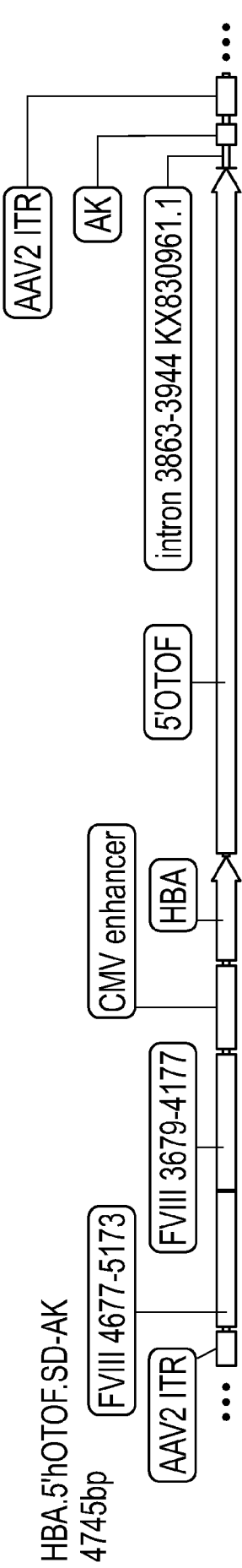


FIG. 59

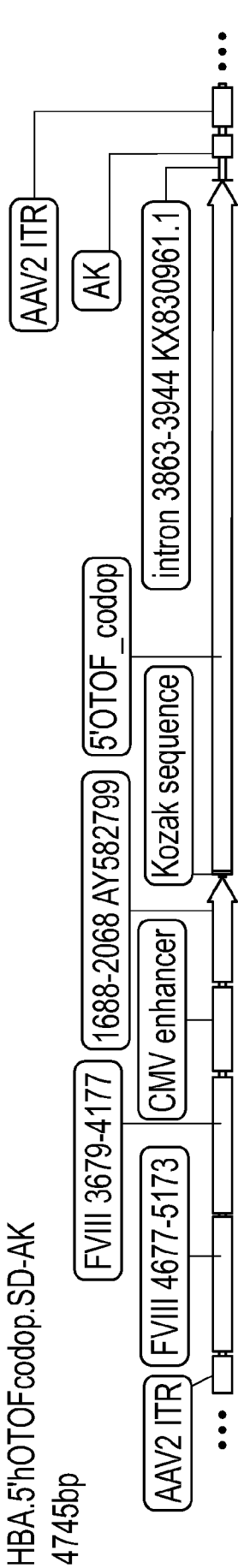


FIG. 60

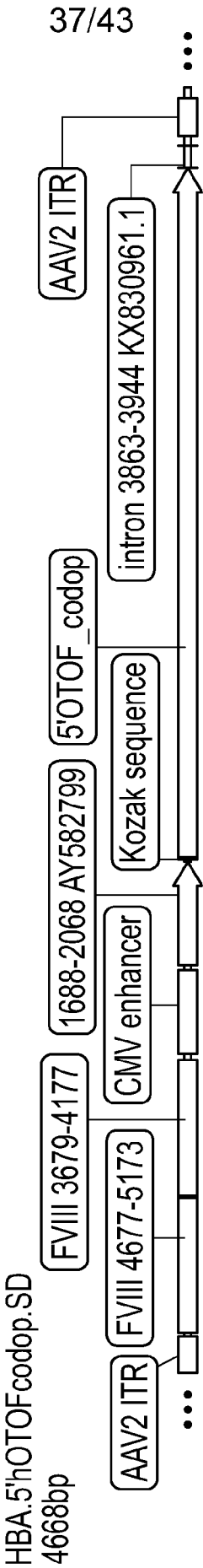


FIG. 61

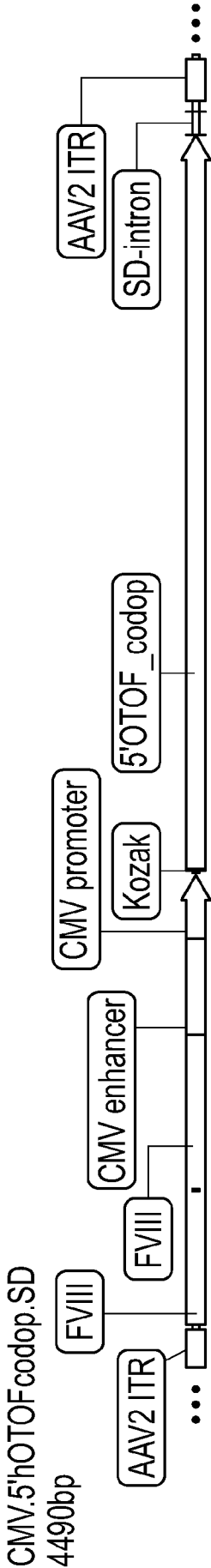


FIG. 62

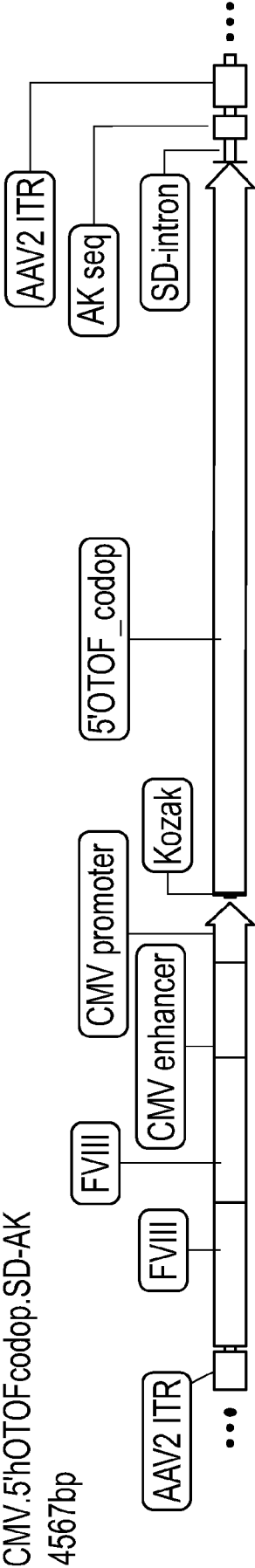


FIG. 63

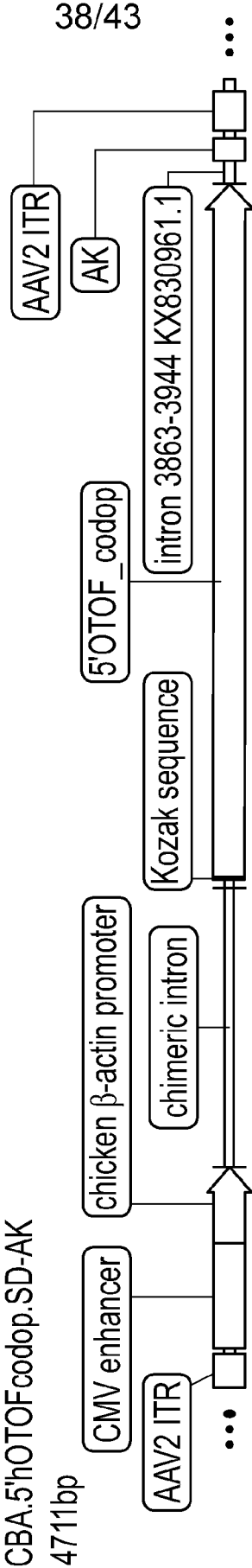


FIG. 64

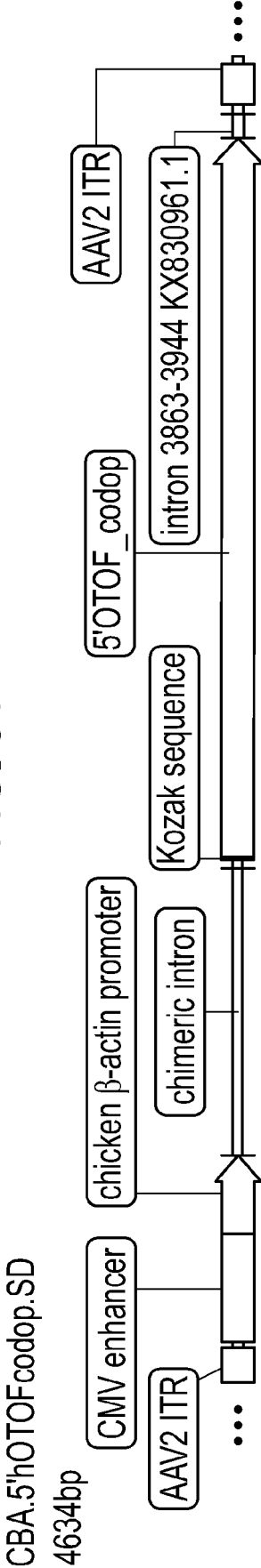


FIG. 65

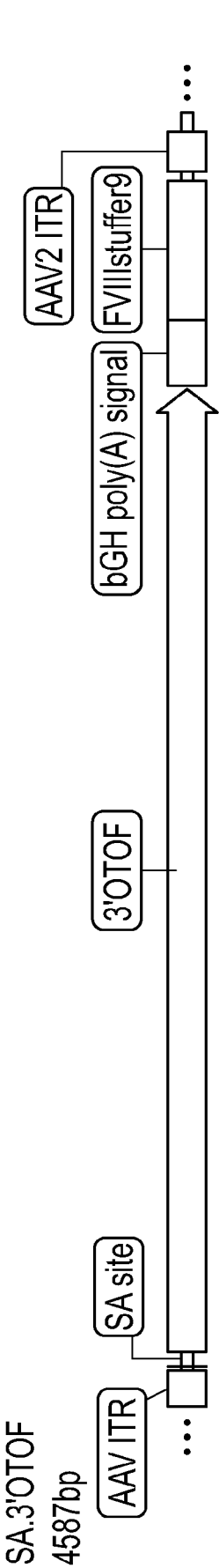


FIG. 66

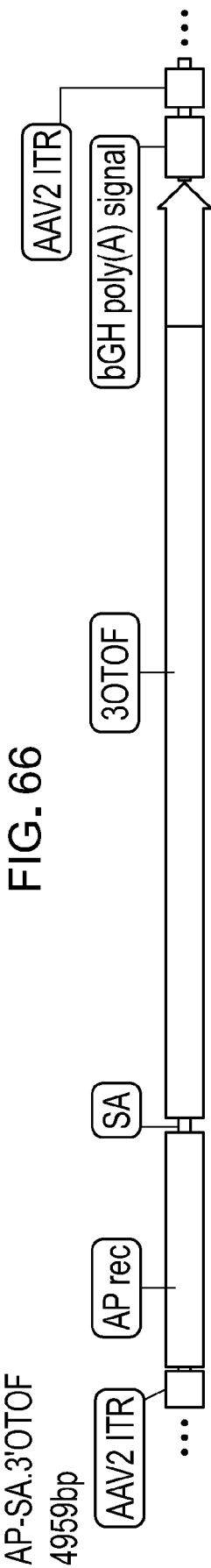


FIG. 67

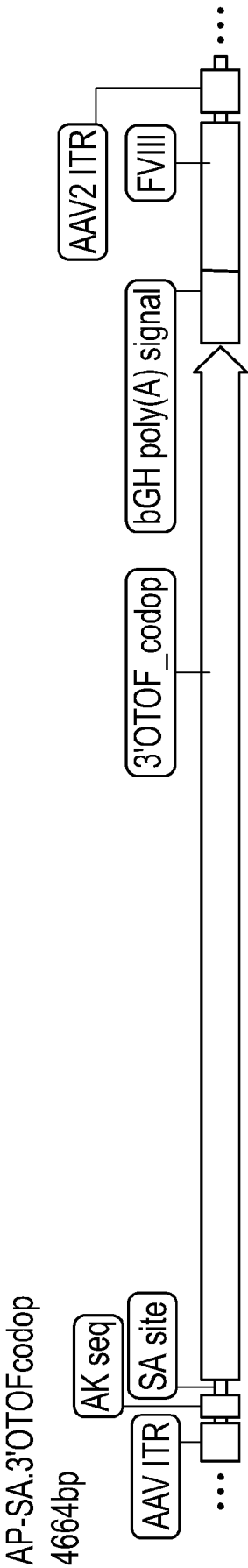
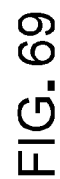
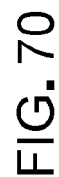
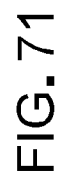


FIG. 68



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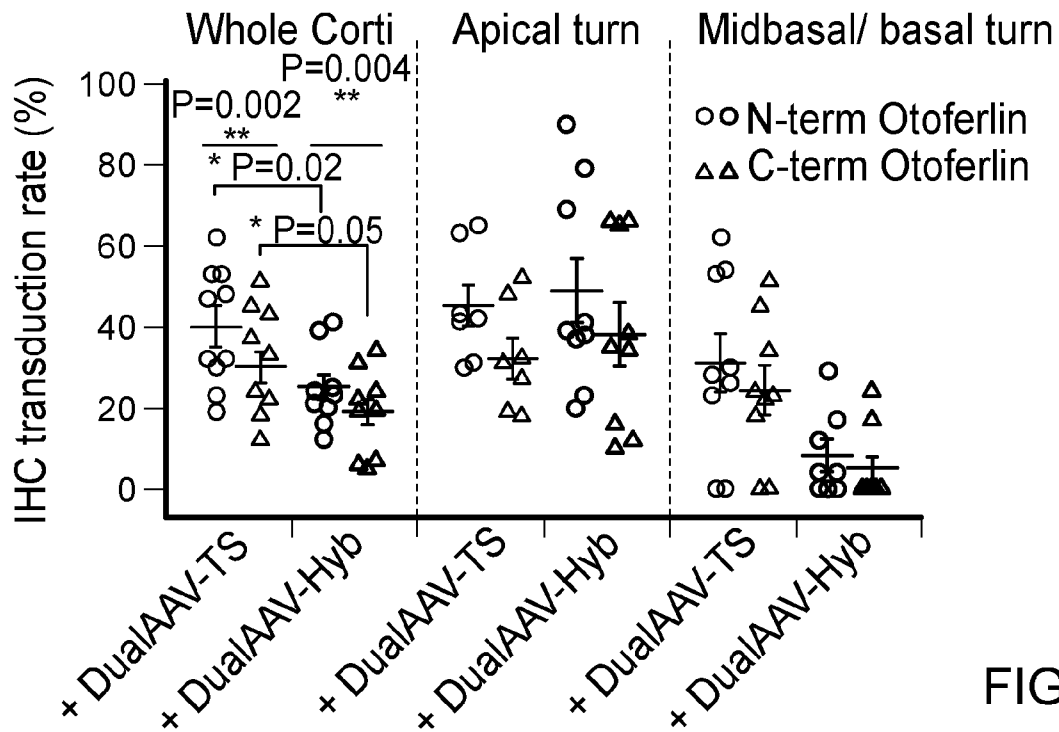


FIG. 72

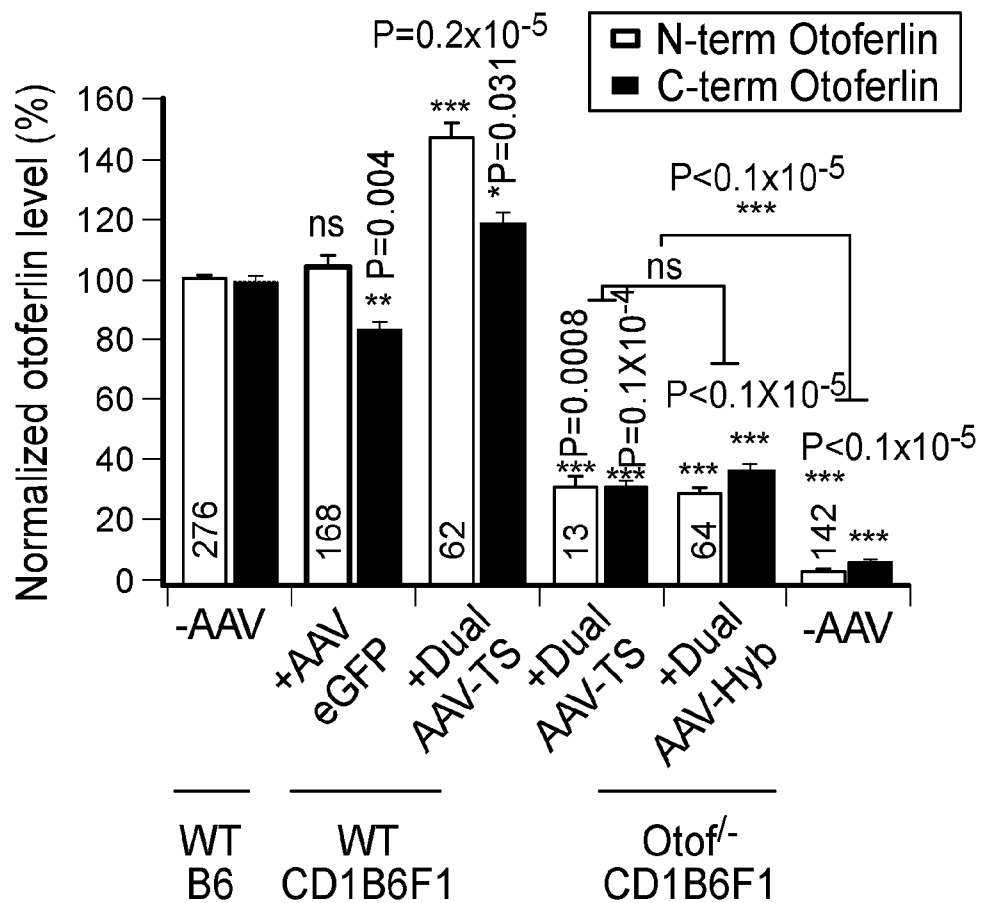


FIG. 73

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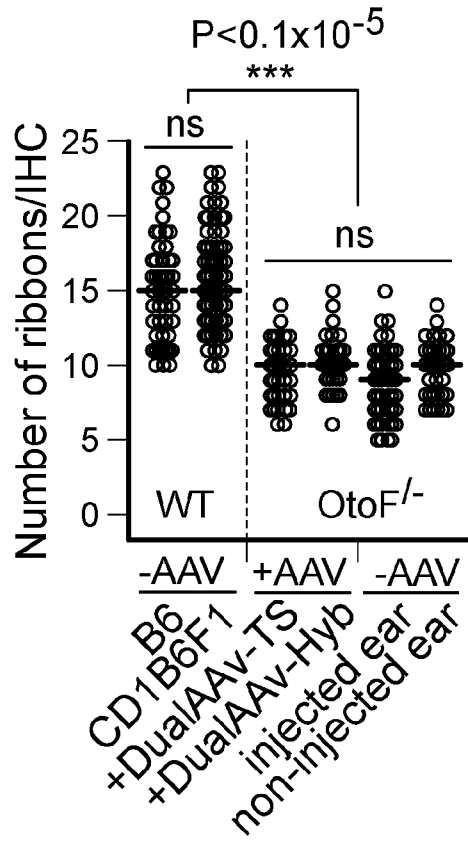


FIG. 74

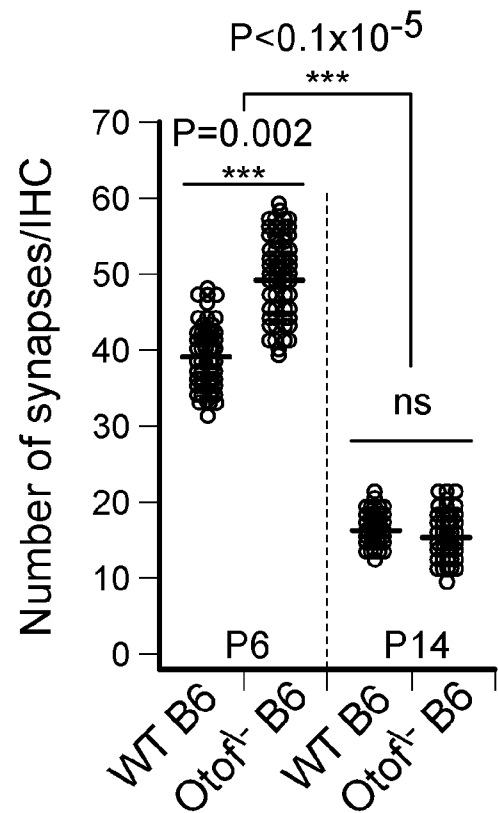


FIG. 75

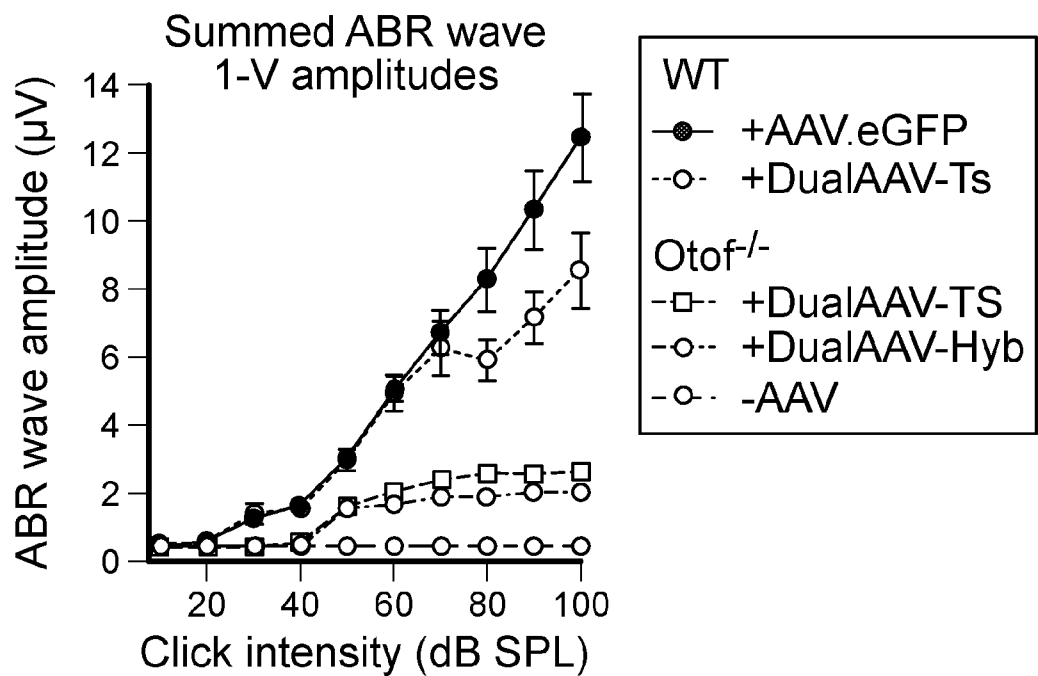


FIG. 76

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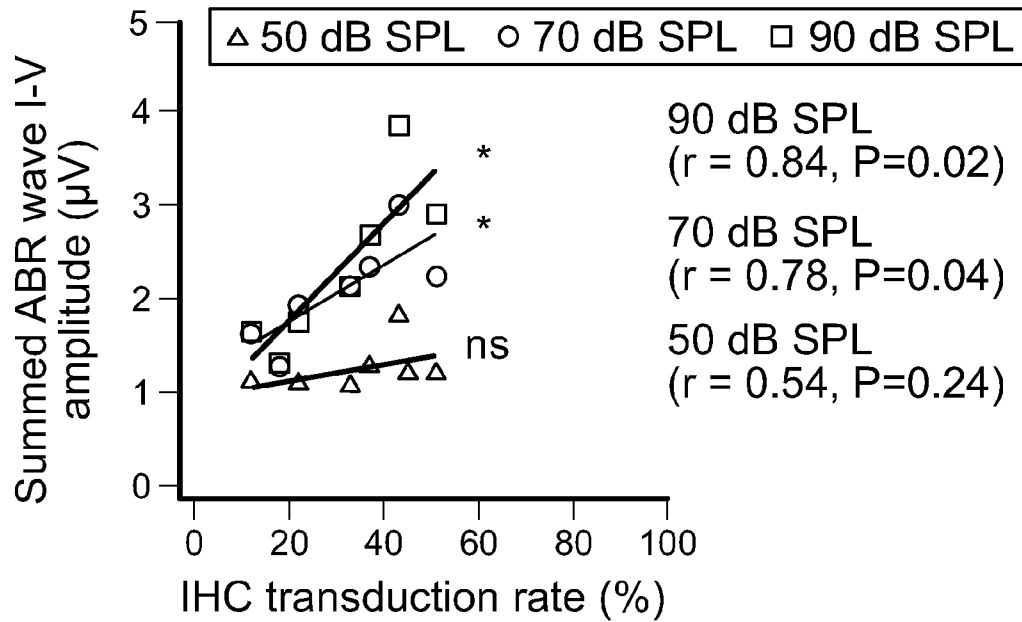
Otof^{-/-}+ DualAAV-TS

FIG. 77

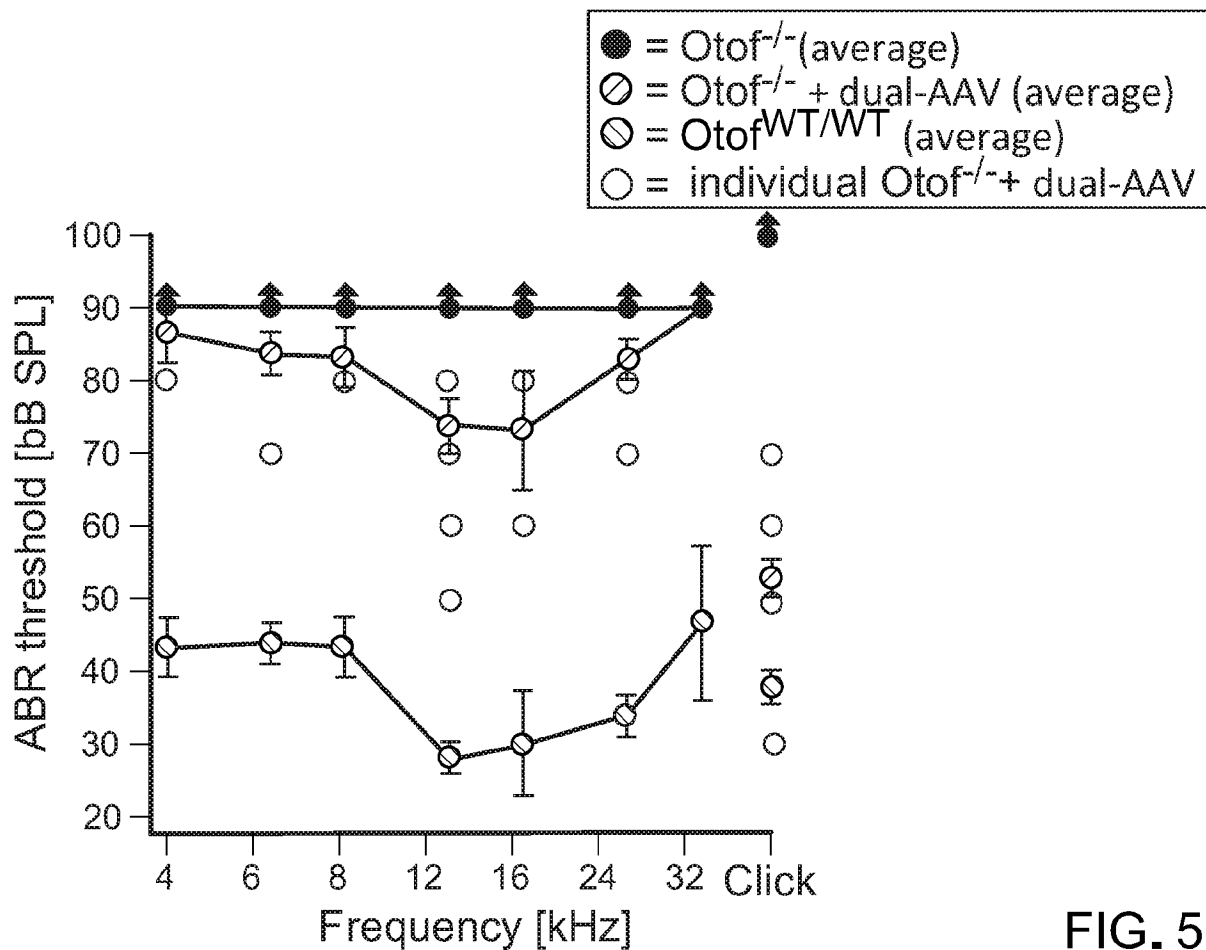


FIG. 5