

CELLULAR MODELS OF AND THERAPIES FOR OCULAR DISEASES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. § 119(e) to U.S. Application No. 62/539,473 titled “CELLULAR MODELS OF AND THERAPIES FOR OCULAR DISEASES” filed on July 31, 2017. The entire contents of the foregoing are hereby incorporated by reference.

BACKGROUND

Bietti's Crystalline Dystrophy (BCD)

Bietti's Crystalline Dystrophy (BCD, a/k/a Bietti Crystalline Corneoretinal Dystrophy, Bietti Crystalline Retinopathy, Bietti's Retinal Dystrophy (OMIM 210370)) is a rare, autosomal recessive and blinding retinal dystrophy characterized by numerous tiny glistening yellow-white crystal-like deposits at the posterior pole of the retina, associated with atrophy of the retinal pigment epithelium (RPE), pigment clumps, and choroidal sclerosis. It was first identified by Dr. G.B. Bietti in 1937. The fundus photographs and SD-OCT images of BCD patients showed that the crystalline deposits were mainly located on the retinal side of the retinal pigment epithelium (RPE). (H. Kojima, A. Otani, K. Ogino et al., “Outer retinal circular structures in patients with Bietti crystalline retinopathy,” *British Journal of Ophthalmology*, vol. 96, pp. 390–393, 2012.). Crystalline deposits in the corneal limbus have been estimated to occur in one quarter to one third of persons with BCD (Kaiser-Kupfer et al. Clinical biochemical and pathologic correlations in Bietti's crystalline dystrophy, *Am J Ophthalmol.*, 1994, 118:569–82). In some cases, crystal deposits in the lens are also observed (Chung *et al.*, *J Ophthalmol.* 57:447-450, 2013). In advanced stage, BCD patients have advanced choroidal sclerosis, decrease or absence of crystalline deposits, and attenuation of retinal vessels (Wada et al. *Am J Ophthalmol* 2005; 139:894-9). Abnormal ERG and retinal thinning are also present in BCD.

Clinically, BCD is progressive and associated with dystrophy and degeneration of RPE. Marked asymmetry between eyes of the same patient is common. Disease onset age and progression vary among BCD patients, even within the same family. Most patients develop night blindness, constricted visual field, poor color vision, macular degeneration and decreased visual

acuity between the 2nd and 4th decade of life, and progress to legal blindness between the 3rd and 6th decade of life.

Located between vessels of the choriocapillaris and light-sensitive outer segments of the photoreceptors, the RPE is a monolayer of pigmented cells that closely interacts with photoreceptors (cones and rods) in the maintenance of visual function. A key function of RPE is to nurture, and remove waste products from the photoreceptors which is the neurosensory retina. Other functions of RPE include without limitation: light absorption, epithelial transport, spatial ion buffering, visual cycle, phagocytosis, secretion and immune modulation (Strauss, 2005, The retinal pigment epithelium in visual function. *Physiol Rev* 85:845-81). Therefore, dysfunction and degeneration of RPE cause photoreceptor dysfunction and degeneration which results in loss of vision. Given BCD is associated with progressive dystrophy and degeneration of RPE, the RPE is critical for purposes of both studying and treating BCD.

BCD is a rare disease. One source estimated BCD incidence rate to be 1:67,000 (ghr.nlm.nih.gov/condition/bietti-crystalline-dystrophy#statistics on the World Wide Web). Another source estimated that BCD prevalence is 2.5% of all RP patients (3 BCD index patients out of 121 RP index patients, see Mataftsi *et al.*, *Retina*, 24:416-426, 2004). Based on this estimation and given RP incidence rate is estimated to be 1:4000 (Hartong *et al.*, *Lancet*, 368:1795-1809, 2006), BCD incidence rate is estimated to be 1:160,000. Because BCD symptoms are similar to those of other eye disorders that progressively damage the retina, it is sometimes diagnosed generally as retinitis pigmentosa (RP) (Mataftsi A et al. Bietti's crystalline corneoretinal dystrophy: a cross-sectional study. *Retina*. 2004; 24: 416-426). Although patients with BCD have been reported throughout different regions of the world, including Asia, Africa, Europe, the Middle East, North and South America, BCD has been reported to be more common in people with East Asia descent, especially in Chinese and Japanese populations (Hu 1983, Ophthalmic genetics in China. *Ophthal Paed Genet* 2:39-45; Li et al., *Am J Hum Genet*. 2004 May; 74(5): 817-826).

Currently there is no approved treatment for BCD, and patients eventually become blind. There is a strong unmet medical need to develop life-changing treatment options for patients suffering from this rare disease.

CYP4V2

CYP4V2 (Cytochrome P450, Family 4, Subfamily V, Polypeptide 2, (OMIM 608614), synonym: CYP4AH1) is one of the proteins in the cytochrome P450 superfamily and a member of the heme thiolate cytochrome P450 subfamily 4 (CYP4). Cytochrome P450s (CYPs) are important heme-containing proteins, known for their monooxygenase reaction. They are involved in the metabolism of xenobiotics and endogenous compounds, such as steroids and fatty acids. Human CYPs are primarily membrane-associated proteins located either in the inner membrane of mitochondria or in the endoplasmic reticulum of cells. P450 proteins can be identified by their signature sequence element FxxGxxxCxG (SEQ ID NO:30), where the underlined cysteine serves as an axial ligand to the heme iron. Another signature sequence element for P450 proteins is ExxR (SEQ ID NO: 31). The Human Genome Project has set the number of human P450 genes at 57. For reference, there are 103 mouse P450 genes and 89 rat P450 genes. (Guengerich & Cheng, Pharmacological Reviews, September 2011, 63 (3) 684-699).

Human CYP4 family consists of 12 genes and 10 pseudo genes. The human CYP4V2 gene (HGNC: 23198) is located at 4q35 and has 11 exons. Mutations in the CYP4V2 gene cause BCD (Li *et al.*, *Am J Hum Genet.* 74:817-826, 2004). While CYP4V2 is expressed in almost all tissues, it is expressed at high levels in the retina and RPE and at somewhat lower levels in the cornea, tissues which show the major clinical findings of BCD (Li *et al.*, *Am J Hum Genet.* 74:817-826, 2004; Nakano M, Kelly EJ, Rettie AE: Expression and Characterization of CYP4V2 as a Fatty Acid omega-Hydroxylase. *Drug Metab Dispos* 2009; Nakano M, Kelly EJ, Wiek C, Hanenberg H, Rettie AE: CYP4V2 in Bietti's crystalline dystrophy: ocular localization, metabolism of omega-3-polyunsaturated fatty acids, and functional deficit of the p.H331P variant. *Mol Pharmacol* 2012; 82: 679-686).

Since CYP4V2 is a relatively new member of the P450 family and BCD is a rare disease, the function of CYP4V2 has not been extensively studied. Prior studies showed that CYP4V2 protein is predominantly active in fatty acid metabolism. Abnormalities in fatty acids and their metabolism have been demonstrated in serum, lymphocytes and skin fibroblasts of patients with BCD (Lee J, Jiao X, Hejtmancik JF *et al*: The metabolism of fatty acids in human Bietti

crystalline dystrophy. Invest Ophthalmol Vis Sci 2001; 42: 1707-1714; Lai T, Chu KO, Chan KP et al: Alterations in serum fatty acid concentrations and desaturase activities in Bietti crystalline dystrophy unaffected by CYP4V2 genotypes. Invest Ophthalmol Vis Sci 2010; 51: 1092-1097). Another study showed that CYP4V2 is a omega-3-polyunsaturated fatty acids (PUFA) hydroxylase and a highly expressed P450 in the transformed human RPE cell line ARPE-19 (Nakano M, Kelly EJ, Wiek C, Hanenberg H, Rettie AE: CYP4V2 in Bietti's crystalline dystrophy: ocular localization, metabolism of omega-3-polyunsaturated fatty acids, and functional deficit of the p.H331P variant. Molecular pharmacology 2012; 82: 679-686).

Numerous mutations have been identified in the CYP4V2 gene and causing BCD, with at least one mutation in each of the gene's 11 exons. The most common CYP4V2 mutation among BCD patients is c.802-8_810del17insGC (referring to a 17 base deletion with two bases (GC) inserted in the place starting 8 bases from the end of intron 6 of CYP4V2 gene, also referred to as IVS6-8 del/insGC, See SEQ ID NO: 46 showing sequence of the human CYP4V2 genomic DNA region comprising the c.802-8_810del17insGC mutation and SEQ ID NO: 47 showing the corresponding wild-type sequence. The c.802-8_810del17insGC mutation is illustrated in the following sequence which shows human CYP4V2 intron 6-exon 7 junction. Intron6 sequence is shown in lower case and exon 7 sequence in CAP letters. The 17 bps deletion and the insertion of GC are in brackets): caa aca gaa gca tgt gat tat cat tca aa (tca tac agG TCA TCG CT) (GC) GAA CGG GCC AAT GAA ATG AAC GCC AAT GA (SEQ ID NO:46)) resulting in the skipping of exon 7. (Xiao et al., Biochem Biophys Res Commun. 409:181-6, 2011; Meng et al., 2014, Mol. Vis., 20:1806-14; Wada et al., Am J Ophthalmol. 139:894-9, 2005; Jiao et al., European Journal of Human Genetics (2017) 25, 461-471). A recent study estimated that the age of the c.802-8_810del17insGC mutation was to be 1,040-8,200 generations in the Chinese and 300-1100 generations in the Japanese populations. See Jiao et al., European Journal of Human Genetics (2017) 25, 461-471.

Various types of CYP4V2 mutations were found associated with BCD, including but not limited to, missense, duplicate, splice site, frameshift, deletion, insertion, indel, nonsense, polymorphisms (e.g., single nucleotide polymorphisms) and premature termination, as well as entire deletion of the CYP4V2 gene. A summary of select CYP4V2 mutations among human

BCD patients is provided in Table 1 herein and can be found in various publications and online databases, e.g., LOVD (databases.lovd.nl/shared/genes/CYP4V2 on the World Wide Web), OMIM (omim.org/allelicVariant/608614 on the World Wide Web), and ClinVar ([ncbi.nlm.nih.gov/clinvar?term=608614\[MIM\]](http://ncbi.nlm.nih.gov/clinvar?term=608614[MIM]) on the World Wide Web).

Table 1: Select CYP4V2 Mutations among BCD Patients

Exon	Nucleotide Change	Predicted Protein Change
1	c.31C >T	p.Q11X
1	c.64C >G	p.L22V
1	c.71T >C	p.L24P
1	c.77G >A	p.G26D
1	c.130T>A	p.W44R
1	c.134A>C	p.Q45P
1	c.181G>A	p.G61S
1	c.197T>G	p.M66R
IVS1	c.214+1G>A	Exon1del
IVS1	c.214+25delT	Not available
IVS1	c.215-2A>G	Exon2del
IVS1	c.215-1G>A	Exon2del
2	c.219T>A	p.F73L
2	c.237G>T	p.E79D
2	c.253C>T	p.R85C
2	c.277T>C	p.W93R
2	c.283G>A	p.G95R
2	c.327G>A	Not available
IVS2	c.327+1G>A	p.E72Gfs*5
IVS2	c.327+11G > C	Not available
3	c.332T>C	p.I111T
3	c.335T>G	p.L112*
3	c.367A>G	p.M123V
3	c.400G>T	p.G134*

3	c.413+2T>G	Splicing acceptor
4	c.518T>G	p.L173W
5	c.637_641delAGTAA	p.S213*
5	c.655T>C	p.Y219H
6	c.677T>A	p.M226K
6	c.694C>T	p.R232*
6	c.724delG	p.D242Ifs*35
6	c.732G>A	p.W244*
6	c.761A>G	p.H254R
6	c.772C>T	p.L258F
6	c.791delT	Deletion
7	c.802-8_806del13	Exon7del
7	c.802-8_810del17insGC	Exon7del
7	c.810delT	p.(Glu271Argfs*34)
7	c.838G>T	p.E280*
7	c.958C>T	p.R320*
7	c.971A>T	p.D324V
7	c.974C>T	p.T325I
IVS7	c.985+3A>G	Not available
8	c.992A>C	p.H331P
8	c.998C>A	p.T333K
8	c.1020G>A	p.W340*
8	c.1021T>C	p.S341P
8	c.1027 T>G	p.Y343D
8	c.1062dupA	p.V355Sfs*4
IVS8	c.1091-2A>G	Exon9del
9	c.1157A>C	p.K386T
9	c.1168C>T	p.R390C
9	c.1169G>A	p.R390H
9	c.1178C>T	p.P393L
9	c.1187C>T	p.P396L

9	c.1198C>T	p.R400C
9	c.1199G>A	p.R400H
9	c.1219G>T	p.E407*
9	c.1225+1 G>A	p.(G364_V408del)
10	c.1226-6_1235del16	Exon10del
10	c.1328G>A	p.R443Q
10	c.1348C>T	p.Q450*
10	c.1355G>A	p.R452H
10	c.1372G>A	p.V458M
10	c.1393A>G	p.R465G
10	c.1396 A >G	p.N466D
10	c.1399T>C	p.C467R
10	c.1441delT	p.(Ser481Argfs*4)
10	c.1445C>T	p.S482*
11	c.1523G>A	p.R508H
11	c.1526C>T	p.P509L
	c.604G>A	p.(Glu202Lys)
	c.242C>G	p.(Thr81Arg)
	c.604+4A>G	p.(?)
	c.1249dup	p.(Thr417Asnfs*2)
Entire CYP4V2		*
deletion		

This is a select list only and may not contain all pathologic CYP4V2 mutations/variants among BCD patients identified and reported to date. The mutations are relative to reference sequences (NM_207352.3) and (NP_997235.3). New CYP4V2 pathologic mutations among BCD patients are continuously being identified. All identified and future identified pathologic CYP4V2 mutations/variants associated with BCD are incorporated herein by reference.

Inherited Retinal Degenerations (IRDs)

Inherited Retinal Degenerations (IRDs) is a major cause of blindness. Currently more than 200 genes are known to be involved in IRDs and related disorders. Retinitis pigmentosa

(RP) is the leading form of IRDs in humans. There are three general modes of inheritance for RP (autosomal dominant, autosomal recessive, and X-linked). Worldwide incidence rate of RP was estimated to be one in 4000, with autosomal recessive RP accounting for 50%-60% of RP (Hartong DT, Berson EL, Dryja TP. Retinitis pigmentosa. *Lancet*. 2006;368:1795–809). A study in Europe has estimated that BCD prevalence is 2.5% of all RP patients and approximately 10% of persons with nonsyndromic autosomal recessive RP (Mataftsi A, Zografos L, Millá E, Secrétan M, Munier FL. Bietti's crystalline corneoretinal dystrophy: a cross-sectional study. *Retina*. 2004;24:416–26). The same study also noted that BCD is often diagnosed generally as RP. Therefore, BCD may have been under-diagnosed. BCD is a worldwide disease but it is most common in East Asia especially in the Chinese and Japanese populations (Li et al., *Am J Hum Genet*. 2004 May; 74(5): 817–826).

References for Table 1 mutations:

Li A, Jiao X, Munier FL, Schorderet DF, Yao W, et al. (2004) Bietti crystalline corneoretinal dystrophy is caused by mutations in the novel gene CYP4V2. *Am J Hum Genet* 74: 817-826.

Xiao X, Mai G, Li S, Guo X, Zhang Q (2011) Identification of CYP4V2 mutation in 21 families and overview of mutation spectrum in Bietti crystalline corneoretinal dystrophy. *Biochem Biophys Res Commun* 409: 181-186.

Shan M, Dong B, Zhao X, Wang J, Li G, et al. (2005) Novel mutations in the CYP4V2 gene associated with Bietti crystalline corneoretinal dystrophy. *Mol Vis* 11: 738-743.

Rossi S, Testa F, Li A, Yaylacioglu F, Gesualdo C, et al. (2013) Clinical and genetic features in Italian Bietti crystalline dystrophy patients. *Br J Ophthalmol* 97: 174-179.

Lin J, Nishiguchi KM, Nakamura M, Dryja TP, Berson EL, et al. (2005) Recessive mutations in the CYP4V2 gene in East Asian and Middle Eastern patients with Bietti crystalline corneoretinal dystrophy. *J Med Genet* 42: e38.

Manzouri B, Sergouniotis PI, Robson AG, Webster AR, Moore A (2012) Bietti crystalline retinopathy: report of retinal crystal deposition in male adolescent siblings. *ARCH OPHTHALMOL* 130: 1470-1473.

Lai TY, Ng TK, Tam PO, Yam GH, Ngai JW, et al. (2007) Genotype phenotype analysis of Bietti's crystalline dystrophy in patients with CYP4V2 mutations. *Invest Ophthalmol Vis Sci* 48: 5212-5220.

Parravano M, Sciamanna M, Giorno P, Boninfante A, Varano M (2012) Bietti crystalline dystrophy: a morpho-functional evaluation. *Doc Ophthalmol* 124: 73-77.

Wada Y, Itabashi T, Sato H, Kawamura M, Tada A, et al. (2005) Screening for mutations in CYP4V2 gene in Japanese patients with Bietti's crystalline corneoretinal dystrophy. *Am J Ophthalmol* 139: 894-899.

Zenteno JC, Ayala-Ramirez R, Graue-Wiechers F (2008) Novel CYP4V2 gene mutation in a Mexican patient with Bietti's crystalline corneoretinal dystrophy. *Curr Eye Res* 33: 313-318.

Lee KY, Koh AH, Aung T, Yong VH, Yeung K, et al. (2005) Characterization of Bietti crystalline dystrophy patients with CYP4V2 mutations. *Invest Ophthalmol Vis Sci* 46: 3812-3816.

Yokoi Y, Sato K, Aoyagi H, Takahashi Y, Yamagami M, et al. (2011) A Novel Compound Heterozygous Mutation in the CYP4V2 Gene in a Japanese Patient with Bietti's Crystalline Corneoretinal Dystrophy. *Case Rep Ophthalmol* 2: 296-301.

Haddad NM, Waked N, Bejjani R, Khoueir Z, Chouery E, et al. (2012) Clinical and molecular findings in three Lebanese families with Bietti crystalline dystrophy: report on a novel mutation. *Mol Vis* 18: 1182-1188.

Fu Q, Wang F, Wang H, Xu F, Zaneveld JE, et al. (2013) Next-generation sequencing-based molecular diagnosis of a Chinese patient cohort with autosomal recessive retinitis pigmentosa. *Invest Ophthalmol Vis Sci* 54: 4158-4166.

Song Y, Mo G, Yin G (2013) A novel mutation in the CYP4V2 gene in a Chinese patient with Bietti's crystalline dystrophy. *Int Ophthalmol* 33: 269-276.

Jin ZB, Ito S, Saito Y, Inoue Y, Yanagi Y, et al. (2006) Clinical and molecular findings in three Japanese patients with crystalline retinopathy. *Jpn J Ophthalmol* 50: 426-431.

Halford S, Liew G, Mackay DS, Sergouniotis PI, Holt R, Broadgate S, Volpi EV, Ocaka L, Robson AG, Holder GE, Moore AT, Michaelides M, Webster AR. Detailed phenotypic and genotypic characterization of bietti crystalline dystrophy. *Ophthalmology*. 2014; 121:1174-84

Houfa Yin, Chongfei Jin, Xiaoyun Fang, Qi Miao, Yingying Zhao, Zhiqing Chen, Zhaoan Su, Panpan Ye, Yao Wang and Jinfu Yin, Molecular Analysis and Phenotypic Study in 14 Chinese Families With Bietti Crystalline Dystrophy. PLoS One 9 (4), e94960. 2014 Apr 16.

Xiao Hong Meng, Hong Guo, Hai Wei Xu, Qi You Li, Xin Jin, Yun Bai, Shi Ying Li, Zheng Qin Yin, Identification of novel CYP4V2 gene mutations in 92 Chinese families with Bietti's crystalline corneoretinal dystrophy, Molecular Vision (2014); 20:1806-1814

Galuh D N Astuti, Vincent Sun, Miriam Bauwens, Ditta Zobor, Bart P Leroy, Amer Omar, Bernhard Jurklies, Irma Lopez, Huanan Ren, Volkan Yazar, Christian Hamel, Ulrich Kellner, Bernd Wissinger, Susanne Kohl, Elfride De Baere, Rob W J Collin, and Robert K Koeneke, Novel insights into the molecular pathogenesis of CYP4V2-associated Bietti's retinal dystrophy, Mol Genet Genomic Med. 2015 January; 3(1): 14-29.

Xiaodong Jiao, Anren Li, Zi-Bing Jin, Xinjing Wang, Alessandro Iannaccone, Elias I Traboulsi, Michael B Gorin, Francesca Simonelli and J Fielding Hejtmancik, Identification and Population History of CYP4V2 mutations in Patients with Bietti Crystalline Corneoretinal Dystrophy, European Journal of Human Genetics (2017) 25, 461-471.

SUMMARY

Cell Line Claims

Cell Line and Disease Model Claims

Cell Line Composition

In one aspect, a cellular disease model including a cell line is provided. Such a disease model includes (a) a stem cell provided from a subject or reprogrammed from a cell provided from a subject, or (2) a cell derived from a stem cell provided from a subject or reprogrammed from a cell provided from a subject, comprising one or more mutations in a target gene.

In some embodiments, the stem cell is an induced pluripotent stem (iPS) cell. In some embodiments, the stem cell is an embryonic stem (ES) cell, somatic (or adult) stem cell, or mesenchymal stem cell (MSC). In some embodiments, the cell provided from a subject is of any cell type and/or from any tissue of the subject. In some embodiments, the cell provided from a subject is a skin cell, a fibroblast or a blood cell. In some embodiments, wherein the cell

provided from a subject is a skin fibroblast or a peripheral blood mononuclear cell (PBMC). In some embodiments, the cell provided from a subject is a urinary cell, a renal epithelial cell, a hair follicle, or a dermal papilla cell.

In some embodiments, the cell derived from a stem cell is an ocular cell. In some embodiments, the ocular cell is a retinal pigment epithelium (RPE) cell, photoreceptor cell (PRC, including rod cell, cone cell and photoreceptor progenitor cell), retinal cell, corneal cell, corneal epithelial cell (CEC), optic nerve cell, lens cell, choroidal endothelial (CE) cell, optic nerve cell or choroidal cell. In some embodiments, the cell derived from a stem cell is a neuron cell.

In some embodiments, the mutation is endogenous to the subject. In some embodiments, the mutation is exogenous to the subject. In some embodiments, the mutation is introduced artificially via genetic editing or genetic manipulation. In some embodiments, the cell line comprises a plurality of mutations that are endogenous and/or exogenous to the subject.

In some embodiments, the subject is a mammal. In some embodiments, the subject is a human.

In some embodiments, the target gene comprises a gene set forth in Table 4. In some embodiments, the target gene comprises a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene or a CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22,

CYP4X1, CYP4Z1 or CYP46A gene that encodes a protein having defective or partial function or activity. In some embodiments, the target gene is CYP4V2.

In some embodiments, the cell line comprises an iPS cell. In some embodiments, the cell line comprises an iPS-RPE cell. In some embodiments, the cell line comprises an iPS-photoreceptor (iPS-PRC) cell, an iPS-corneal epithelial cell (iPS-CEC), an iPS-choroidal endothelial (CE) cell, an iPS-corneal cell, an iPS-choroidal cell, an iPS-optic nerve cell, an iPS-ocular cell or an iPS-neuron cell. In some embodiments, the CYP4V2 mutation in the cell line is endogenous to the subject. In some embodiments, the subject has a pathologic mutation in the CYP4V2 gene or in an ortholog of the CYP4V2 gene.

In some embodiments, the subject has at least one mutation set forth in Table 1. In some embodiments, the subject has inherited retinal degeneration (IRD) or retinitis pigmentosa (RP). In some embodiments, the subject has Bietti's Crystalline Dystrophy (BCD, a/k/a Bietti Crystalline Corneoretinal Dystrophy, Bietti Crystalline Retinopathy, Bietti's Retinal Dystrophy) or is at risk of developing BCD.

In some embodiments, the cell line comprises a CYP4V2 mutation that is exogenous to the subject and is introduced artificially via genetic editing or genetic manipulation.

In some embodiments, the cell line comprises an iPS cell, ES cell, MSC, or adult stem cell, or a RPE cell, photoreceptor cell, corneal epithelial cell, choroidal endothelial (CE) cell or choroidal cell derived from an iPS cell, ES cell, MSC, or adult stem cell. In some embodiments, the iPS cell or other type of stem cell is characterized by one or more of the following: a. the unique morphology of iPS, ES or MSC; b. one or more pluripotency markers, such as Oct-4, Sox-2, SSEA4, TRA-1-60, TRA-1-81, NANOG and AP; c. the ability to differentiate into the desired cell type (e.g., RPE), and/or d. a teratoma assay.

In some embodiments, the iPS-RPE cell or the RPE cell derived from other types of stem cell is characterized by: a. morphology: pigment and hexagonal shape, and/or b. one or more of the following biomarkers, retinaldehyde-binding protein 1 (RLBP1, alias: CRALBP), RPE65, BESTROPHIN-1, MITF, LRAT, RDH5, PAX6, MERTK, TYR, ZO-1 and/or VINCULIN.

In another aspect, a BCD human cellular model or a CYP4V2 function cellular model is provided. Such a model includes comprising an iPS cell or iPS cell line, or an iPS-RPE cell or

iPS-RPE cell line derived from a cell or a cell line of a BCD patient, or derived from a cell or a cell line with artificially created CYP4V2 mutations.

In some embodiments, the cell line has an abnormal biochemical profile in one or more compounds of the following compound groups: (i) fatty acids, (ii) ceramides, (iii) sphingomyelins, (iv) sphingosine, (v) sphinganine, or (vi) hydroxy-fatty acids. as compared to a corresponding cell line of a healthy control. In some embodiments, the cell line has an abnormal biochemical profile in one or more compounds set forth in Table 2 as compared to the corresponding cell line of a healthy control.

Method of Making the Cellular Disease Model:

In another aspect, a method of making an iPS-derived BCD disease model is provided. Such a method includes obtaining cells from a subject having endogenous mutations in the CYP4V2 gene or cells with no endogenous mutations in the CYP4V2 gene but exogenous CYP4V2 mutation is introduced artificially via gene editing or gene manipulation at this stage or any of the following stages; inducing pluripotency in the cells or reprogramming the cells to produce iPSCs; culturing the iPSCs under conditions that result in differentiation of the iPSCs into desired ocular cells, thereby producing an iPS-derived ocular cell line.

In some embodiments, the cells obtained from the subject are somatic cells. In some embodiments, the cells obtained from the subject are skin cells, fibroblasts, blood cells, peripheral blood mononuclear cells (PBMC), or ocular cells. In some embodiments, the cells obtained from the subject are urinary cells, renal epithelial cells, a hair follicles, or dermal papilla cells. In some embodiments, the ocular cells are retinal pigment epithelial (RPE) cells, corneal epithelial cells (CECs), photoreceptor cells (PRCs), choroidal endothelial (CE) cells, optic nerve cells, retinal cells, corneal cells, or choroidal cells. In some embodiments, the pluripotency is induced or the cells are reprogrammed using one or more of the OCT4, SOX2, KLF4, and c-MYC transcription factors.

In some embodiments, the mutation is pathologic. In some embodiments, the cell line comprises one or more mutation among the mutations set forth in Table 1. In some embodiments, the cell line is heterozygous for the mutation. In some embodiments, the cell line is homozygous for the mutation.

In some embodiments, the cellular disease model exhibits abnormal levels in one or more compounds from the following compound groups as compared to that in a relevant cell line of a healthy control: (i) fatty acids, (ii) ceramides, (iii) sphingomyelins, (iv) sphingosine, (v) sphinganine, or (vi) hydroxy-fatty acids. In some embodiments, the cellular disease model exhibits abnormal levels as compared to that in a relevant cell line of a healthy control in one or more compounds set forth in Table 2.

Biochemical Assay Method:

In one aspect, a method of discovering abnormalities or phenotype in a disease cellular model is provided. Such a method typically includes evaluating and comparing the levels of one or more compounds between the cell line of a patient (or an genetically edited or manipulated cell line comprising an exogenous mutation in the gene causing such disease) and a healthy control, wherein the one or more compound is selected from the following groups: (i) fatty acids, (ii) ceramides, (iii) sphingomyelins, (iv) sphingosine, (v) sphinganine, and/or (vi) hydroxy-fatty acids.

In some embodiments, one or more of the compounds evaluated is set forth in Table 2. In some embodiments, the identification and/or evaluation of compound levels is performed using LC-MS, LC-MS/MS, GC-MS, GC-MS/MS, and/or FIA-MS/MS. In some embodiments, the disease cellular model comprises a mutated or defective gene set forth in Table 4. In some embodiments, the disease cellular model comprises a mutated or defective gene among the CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene.

Method of Use of the BCD Cellular Model (Drug, Dosage and Device Screening)

In another aspect, a method of screening a test agent for therapeutic efficacy against BCD is provided. Such a method typically includes contacting cells from an iPS-RPE cell line derived

from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with a test agent; and evaluating the cells for normalization in levels of one or more compounds set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; and/or improved cell structure, morphology or function, as compared to before contacting by such test agent; wherein normalization in levels of one or more compound set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; and/or improved cell structure, morphology or function, as compared to before treatment by such test agent, is indicative of a test agent that exhibits therapeutic efficacy against BCD.

In some embodiments, the test agents are selected from the group consisting of nucleic acids or analogs thereof, vectors containing nucleic acid sequence or encoding polypeptides, polypeptides or analogs thereof, antibodies, chemicals, small molecules, and/or any combination thereof. In some embodiments, the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, function assay, microscopy or combination thereof.

In another aspect, a method of screening efficacy or efficiency of a formulation, vector or construct comprising a test agent for BCD is provided. Such a method typically includes contacting multiple cell samples from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with a test agent formulated or packaged in various formulations, vectors or constructs; and evaluating the cell samples for normalization in levels of one or more compound set forth in table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; improved cell structure, morphology or function; and/or cell tolerance or death, as compared to before treatment by such test agent and/or to cell samples treated by the same test agent but formulated or packaged in a different formulation, vector or construct, to determine and compare the efficiency or efficacy of such formulation, vector or construct; wherein the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, cell viability assay, microscopy or combination thereof.

In one aspect, a method of screening effective and safe dosage range of a test agent for BCD is provided. Such a method typically includes contacting multiple cell samples from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with a test agent in a different dose for each cell sample; evaluating the cell samples for normalization in levels of one or more compound set forth in table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; improved cell structure, morphology or function, and/or cell tolerance or death, as compared to before treatment by such test agent and/or to cell samples treated by the same test agent but with a different dose, to determine and compare the effective and safety of different doses thereby determining a proper dosage range; wherein the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, cell viability assay, function assay, microscopy or combination thereof.

In another aspect, a method of screening or evaluating efficacy or efficiency of a delivery device or method for delivering a therapeutic agent to the retina or retinal cells is provided. Such a method typically includes (i) contacting a cell sample from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with a test agent without employing the delivery device or method; (ii) contacting another cell sample from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with the test agent of the same dosage as in (i), employing the delivery device or method; (iii) evaluating and comparing the cell samples from (i) and (ii) for normalization in levels of one or more compound set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; improved cell structure, morphology or function; cell tolerance or death; and/or the levels of the test agent in the cells, as compared to before treatment by such test agent and/or treatment by the same test agent of the same dose but without employing the delivery device or method, to determine the efficacy or efficiency of such delivery

device or technique; wherein the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, function assay, microscopy or combination thereof.

In some embodiments, the retinal cells are RPE cells.

CRISPR Gene Editing Therapy

In one aspect, a composition is provided that includes: (a) a CRISPR guide RNA targeting a nucleic acid sequence (the "target sequence") of or within 100 bps to the CYP4V2 gene, and (b) a functional CRISPR-associated protein (Cas). In some embodiments, such a composition can further include (c) a donor nucleic acid sequence comprising all or a portion of a wild-type sequence or a functional sequence of the CYP4V2 gene for correction, disruption or replacement of CYP4V2 gene or a portion thereof.

In some embodiments, one or more components thereof is provided in the form of a DNA molecule encoding such component, an mRNA molecule encoding such component, a RNA molecule, a polypeptide, and/or a ribonucleoprotein (RNP) or protein-RNA complex. In some embodiments, two or more components thereof are in separate molecule or combined in one molecule or in one complex, are in separate vectors or combined in one vector, are in one or more nucleic acid complex, are in one or more RNP complex. In some embodiments, the donor nucleic acid sequence is provided in a single-stranded donor oligonucleotide (ssODN) or a vector. In some embodiments, the vector is a plasmid, a recombinant AAV vector, a recombinant lentivirus vector, and/or a combination thereof.

In some aspects, a composition including a cell with a pathologic CYP4V2 mutation that contains any of the compositions described herein is provided. In some embodiments, (a) the CRISPR guide RNA comprising (i) a CRISPR RNA (crRNA) which comprises a protospacer element sequence that is complementary to the target sequence of or within 100 bps to a target gene (the "target gene") and a sequence that corresponds to a complementary region of the trans-activating crRNA (tracrRNA), and (ii) a tracrRNA which comprises a region that is complementary to corresponding region of the crRNA and a sequence which interacts with a CRISPR-associated protein 9 (Cas9), and (b) the functional CRISPR-associated protein comprises Cas9.

In some embodiments, the protospacer element is about 20 bases, about 19 bases, about 21 bases, about 19-21 bases, about 18-22 bases, or about 16-24 bases. In some embodiments, the crRNA and the tracrRNA are in separate molecules. In some embodiments, the crRNA and the tracrRNA are combined into a single guide RNA (sgRNA). In some embodiments, the sgRNA is about 88-150 bps.

In some embodiments, the Cas9 comprises a Cas9 ortholog or a mutant Cas9 selected from: *Streptococcus pyogenes* (SpCas9), SpCas9 nickase (Cas9n D10A), SpCas9 (D1135E), eSpCas9, SpCas9-HF1, SpCas9 VRER, SpCas9 VQR, SpCas9EQR, *Staphylococcus aureus* (SaCas9), *Neisseria Meningitidis*, *Streptococcus thermophilus*, *Streptococcus pneumoniae*, *Campylobacter coli*, *Campylobacter jejuni*, *Streptococcus mutans*, *Pasteurella multocida*, *Bifidobacterium longum*, *Bacillus smithii*, *Treponema denticola*, *Mycoplasma canis* and *enterococcus faecalis*. In some embodiments, the CRISPR-associated protein, Cas9, or Cpf1, further includes one, two, three or more nuclear localization sequences (NLS) at the N-terminal and/or C-terminal, and/or a selection marker, including without limitation, GFP or EGFP.

In some embodiments, (a) the CRISPR guide RNA comprises a crRNA which comprises a protospacer element sequence that is complementary to the target sequence of or within 100 bps to a target gene, and (b) the functional CRISPR-associated protein comprises Cpf1. In some embodiments, the protospacer element is about 20 bases, about 21 bases, about 22 bases, about 23 bases, about 24 bases, about 19-25 bases, about 18-26 bases, or about 16-28 bases.

In some embodiments, the protospacer element sequence is selected from the group consisting of SEQ ID NOs: 48 to 52, or shares at least 85% sequence identity with one of SEQ ID NO: 48 to 52 for use with a Cas protein that has NGG as protospacer adjacent motif (PAM) to target the c.802-8_810del17insGC mutation of the CYP4V2 gene. In some embodiments, the donor nucleic acid sequence is selected from SEQ ID NOs: 56 and 57, (this is the two donor template sequence) or shares at least 90% sequence identity with one of SEQ ID NO: 56 and 57, or a sequence that is complementary thereof, for use to correct, disrupt or replace the c.802-8_810del17insGC mutation of the CYP4V2 gene.

CRISPR Gene Therapy method claims

In another aspect, a method of treating or preventing BCD in a subject or a cell with a mutated CYP4V2 gene is provided. Such a method includes (i) identify the pathologic mutation in the subject or the cell through sequencing; (ii) finding Cas related PAM sites within the region spanning from about 100 bps upstream from the first nucleotide involved in the mutation to about 100 bps downstream from the last nucleotide involved in the mutation; (iii) identify various protospacer element sequences targeting the CYP4V2 sequence relevant to each PAM site identified in (ii); (iv) assess activity level of each CRISPR guide RNA comprising a protospacer element sequence identified in (iii) and off-target editing profile based on the protospacer element sequence and PAM; (v) select one or more CRISPR guide RNA design based on (iv); (vi) design one or more donor nucleic acid sequence based on homology-based repair (HDR) for correcting, disrupting or replacing the targeted CYP4V2 mutation; (vii) construct the CRISPR guide RNA, Cas and donor nucleic acid sequence as provided in composition claims 1 to 18; (viii) optionally validating and further selecting the components of (vii) in a cell isolated from the subject; or an iPS cell derived from the subject or a cell differentiated from a stem cell derived from the subject, or the genomic DNA isolated from the subject or a cell isolated or derived thereof to assess the activity level and/or off-target editing profile; and (ix) administering the components in (viii) to the subject or the cell via a delivery system selected from the group consisting of a ribonucleoprotein or protein-RNA complex, a vector, a protein, a nucleic acid molecule, a nanoparticle, a liposome, a micelle, a virosome, a nucleic acid complex, and/or a combination thereof, wherein the delivery is performed by electroporation or via lipid-mediated transfection, or nucleofection, or viral transduction or injection, or a combination thereof; (x) wherein for treatment in cells *in vitro*, a selection marker including without limitation GFP, EGFP or puromycin resistance is optionally added or incorporated into the components in (viii).

In one aspect, a gene editing composition is provided for correcting or replacing the c.802-8_810del17insGC mutation in a CYP4V2 gene in a subject *in vivo* or in a cell *in vitro*. Such a composition typically includes: (i) a CRISPR guide RNA comprising a protospacer element sequence selected from one of SEQ ID NO: 48 to 52 or sharing at least 80% sequence

identity with one of the sequences in SEQ ID 48 to 52; (ii) a donor nucleic acid sequence selected from one of SEQ ID NOs: 56 and 57, or shares at least 90% sequence identity with one of SEQ ID NO: 56 and 57, or a sequence that is complementary thereof; and (iii) a Cas9 protein (exemplary sequence shown in SEQ ID NO: 58), optionally containing 1, 2, 3 or more NLS, and/or a selection marker including without limitation GFP or EGFP.

In some embodiments, an optional nucleotide G is added before the protospacer element sequence. In some embodiments, the CRISPR guide RNA includes a crRNA (exemplary sequence (excluding the 5' protospacer element sequence) shown in SEQ ID NO: 53) and a tracrRNA (exemplary sequence shown in SEQ ID NO: 54); and the protospacer element sequence is contained in the crRNA. In some embodiments, the CRISPR guide RNA includes a single guide RNA (sgRNA) comprising the protospacer element sequence (exemplary sgRNA sequence (excluding the 5' protospacer element sequence) shown in SEQ ID NO: 55).

In some embodiments, one or more components of (i), (ii) and (iii) is provided in the form of a DNA molecule encoding such component, an mRNA molecule encoding such component, a nucleic acid molecule, a vector, a RNA molecule, a polypeptide, a ribonucleoprotein (RNP) or protein-RNA complex, and/or a combination thereof.

BCD Cell Therapy Ocular Disease Autologous Cell Therapy and Combination Treatment claims
BCD Cell Therapy

Allogenic Cell Therapy or Autologous Cell Therapy without genetic repair for BCD

In some aspects, a method of treating or preventing a disease of the eye in a subject is provided, wherein the disease is associated with a pathologic genetic or epigenetic alteration in the CYP4V2 gene. Such a method typically includes administering a cellular composition to the subject, wherein the cellular composition includes: retinal pigment epithelium (RPE) cells, photoreceptors or photoreceptor progenitors (PRCs), corneal epithelial cells (CECs), choroidal endothelial (CE) cells and/or other ocular cells derived from a stem cell.

In some embodiments, the stem cell is an embryonic stem (ES) cell, an iPC cell, an MSC, an adult stem cell or a tissue-specific stem cell. In some embodiments, the stem cell is from or derived from one or more subjects not having BCD or not having a pathologic CYP4V2 gene. In

some embodiments, the stem cell is from or derived from one or more subjects with pathologic mutations in the CYP4V2 gene. In some embodiments, the subject is a human subject.

Genetically-repaired autologous cell therapy for BCD

In another aspect, a cellular composition is provided that includes (a) a stem cell reprogrammed from a cell isolated from or a stem cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene, or (b) a cell differentiated from a stem cell isolated from a subject or reprogrammed from a cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene.

In some embodiments, the stem cell reprogrammed from a cell isolated from the subject is an iPC cell. In some embodiments, the iPS cell is reprogrammed from any cell of any tissue from the subject. In some embodiments, the iPS cell is reprogrammed from a skin cell, a blood cell, a urinary cell, a hair cell, a fibroblast, a peripheral blood mononuclear cell (PBMC), a renal epithelial cell, a hair follicle, or a dermal papilla cell. In some embodiments, the stem cell isolated from the subject is an MSC, an adult stem cell or a tissue-specific stem cell. In some embodiments, the cell differentiated from a stem cell is an ocular cell. In some embodiments, the cell differentiated from a stem cell is an RPE cell, a PRC, a retinal cell, a corneal cell, a choroidal cell, a CEC or a CE cell. In some embodiments, the cell differentiated from a stem cell is an iPS-RPE, iPS-PRC, iPS-CEC or iPS-CE cell.

In some embodiments, (i) the cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene for use to reprogram into an iPSC, (ii) the stem cell isolated from a subject or iPS cell reprogrammed from a cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene, or (iii) the cell differentiated from a stem cell isolated from a subject or an iPS cell reprogrammed from a cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene, is genetically repaired to ameliorate the effect of the mutated CYP4V2 gene. In some embodiments, genetic repair is performed before reprogramming into an IPS cell. In some embodiments, genetic repair is performed after reprogramming to an iPS cell. In some embodiments, genetic repair is performed before differentiation of the stem cell or iPS cell. In some embodiments, genetic repair is performed after differentiation of the stem cell or iPS cell. In some embodiments, genetic repair

is via gene transfer therapy. In some embodiments, genetic repair is via gene transfer therapy by using any composition or method of any one of the gene therapy claims. In some embodiments, genetic repair is via gene editing. In some embodiments, genetic repair is via gene editing by using any composition or method of any one of CRiSPR gene therapy claims.

In another aspect, a method of treating or preventing a disease of the eye in a subject affected by BCD or having pathologic genetic or epigenetic alterations in the CYP4V2 gene is provided. Such a method typically includes administering any of the CYP4V2 autologous cellular compositions described herein to the subject, wherein the cellular composition includes: retinal pigment epithelium (RPE) cells, photoreceptors or photoreceptor progenitors (PRCs), corneal epithelial cells (CECs), choroidal endothelial (CE) cells, and/or other ocular cells derived from a stem cell of the subject.

In some embodiments, the stem cell is an iPC cell, an MSC, an adult stem cell or a tissue-specific stem cell. In some embodiments, the iPS cell is reprogrammed using one or more of the OCT4, SOX2, KLF4, and c-MYC transcription factors. In some embodiments, the genetically repaired cells demonstrate one or more of the following: normalization in levels of one or more compound set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of functional CYP4V2 polypeptides in the cells; and/or improved cell structure, morphology or function, as compared to before genetic repair is performed.

In some embodiments, the amount of cells administered is about 1,000 to about 100 million cells in a single administration. In some embodiments, the administration is via injection. In some embodiments, the administration is via sub-retinal injection. In some embodiments, the administration is via intravitreal injection. In some embodiments, the administration is via direct retinal injection. In some embodiments, the administration is via corneal injection. In some embodiments, the administration is by any other administration method that effectively delivers the cells to the sub-retinal place, the posterior segment, or the cornea of the eye of the subject. In some embodiments, the cells are administered via injection of cell suspension. In some embodiments, the cells are administered as part of a sheet, a matrix, a scaffold, or a tissue.

In some embodiments, the RPE cells are administered using natural and/or synthetic scaffolds to generate a functional RPE monolayer. In some embodiments, the subject is a human subject.

Genetically-repaired autologous cell therapy for ocular diseases

In another aspect, a cellular composition is provided that includes (a) a stem cell reprogrammed from a cell isolated from or a stem cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity, or (b) a cell differentiated from a stem cell isolated from a subject or reprogrammed from a cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity.

In some embodiments, the stem cell reprogrammed from a cell isolated from the subject is an iPS cell. In some embodiments, the iPS cell is reprogrammed from any cell of any tissue from the subject. In some embodiments, the iPS cell is reprogrammed from a skin cell, a blood cell, a urinary cell, a hair cell, a fibroblast, a peripheral blood mononuclear cell (PBMC), a renal epithelial cell, a hair follicle, or a dermal papilla cell. In some embodiments, the stem cell isolated from the subject is an MSC, an adult stem cell or a tissue-specific stem cell.

In some embodiments, the gene is involved in ocular development or function and/or mutation of which causes or is a risk factor to cause an ocular disease. In some embodiments, the gene is involved in neuronal development or function and/or mutation of which causes or is a risk factor to cause a neurodegenerative disease. In some embodiments, the gene is a cytochrome P450 gene. In some embodiments, the gene is one set forth in Table 4.

In some embodiments, the gene includes a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene or a CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1,

ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 or CYP46A gene that encodes a protein having defective or partial function or activity.

In some embodiments, the cell differentiated from a stem cell is any type of cell. In some embodiments, the cell differentiated from a stem cell is an ocular cell. In some embodiments, the cell differentiated from a stem cell is an RPE cell, a PRC, a retinal cell, a corneal cell, a choroidal cell, a CEC, a CE cell or an optic nerve cell. In some embodiments, the cell differentiated from a stem cell is an iPS-RPE, iPS-PRC, iPS-CEC or iPS-CE cell. In some embodiments, the cell differentiated from a stem cell is a neuron.

In some embodiments, (i) the cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity for use to reprogram into an iPSC, (ii) the stem cell isolated from a subject or iPS cell reprogrammed from a cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity, or (iii) the cell differentiated from a stem cell isolated from a subject or an iPS cell reprogrammed from a cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity, is genetically repaired to ameliorate the effect of the mutated or defective gene.

In some embodiments, genetic repair is performed before reprogramming into an IPS cell. In some embodiments, genetic repair is performed after reprogramming to an iPS cell. In some embodiments, genetic repair is performed before differentiation of the stem cell or iPS cell. In some embodiments, genetic repair is performed after differentiation of the stem cell or iPS cell. In some embodiments, genetic repair is via gene transfer therapy. In some embodiments, genetic repair is via gene transfer therapy by using any composition or method of any one of the claims related to gene therapy. In some embodiments, genetic repair is via gene editing therapy.

In some embodiments, genetic repair is via gene editing therapy by using any composition or method of any one of the claims related to CRISPR gene therapy.

In another aspect, a method of treating or preventing a disease in a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity set forth in Table 4 is provided. Such a method typically includes administering an autologous cellular composition as described herein to the subject, wherein the cellular composition includes: retinal pigment epithelium (RPE) cells, photoreceptors or photoreceptor progenitors (PRCs), corneal epithelial cells (CECs), neurons, choroidal endothelial (CE) cells and/or other ocular cells derived from a stem cell of the subject, and wherein the mutated or defective gene in the cellular composition has been genetically repaired.

In still another aspect, a method of autologously treating a subject is provided. Such a method typically includes (i) providing cells from a subject having a disease of the eye; (ii) inducing pluripotency in the cells from the subject to produce iPSCs; (iii) genetically repairing one or more mutations in a mutated or defective gene set forth in Table 4 in the iPSCs derived from the subject; (iv) differentiating the iPSCs into ocular cells; (v) alternative to step (iii), genetically repair the iPS-ocular cells via gene transfer therapy; and (vi) introducing the iPS-ocular cells into the subject, thereby autologously treating the subject having the disease of the eye.

In some embodiments, the stem cell is an iPC cell, an MSC, an adult stem cell or a tissue-specific stem cell. In some embodiments, the iPS cell is reprogrammed using one or more of the OCT4, SOX2, KLF4, and c-MYC transcription factors. In some embodiments, the genetically repaired cells demonstrate one or more of the following: an increase in non-defective target gene nucleic acid sequence in the cells; an increase in the amount of functional polypeptides encoded by the target gene in the cells; ; improved cell structure, morphology or function, and/or improved or normalized biochemical functions in the cells, as compared to before genetic repair is performed. In some embodiments, the amount of cells administered is about 1,000 to about 100 million cells in a single administration.

In some embodiments, the administration is via injection. In some embodiments, the administration is by sub-retinal injection. In some embodiments, the administration is by

intravitreal injection. In some embodiments, the administration is by direct retinal injection. In some embodiments, the administration is by corneal injection. In some embodiments, the administration is by any other administration method that effectively delivers the cells to the sub-retinal place, the posterior segment, or the cornea of the eye of the subject. In some embodiments, the cells are administered via injection of cell suspension. In some embodiments, the cells are administered as part of a sheet, a matrix, a scaffold or a tissue. In some embodiments, the RPE cells are administered using natural and/or synthetic scaffolds to generate a functional RPE monolayer. In some embodiments, the subject is a human subject.

In some embodiments, the disease is associated with a genetic or epigenetic alteration or risk factor in the subject. In some embodiments, the disease is photoreceptor degeneration, retinal pigment epithelium cell degeneration, retinal degeneration, cornea degeneration, and/or choroidal disorders. In some embodiments, the disease is an inherited retinal degeneration (IRD). In some embodiments, the disease is retinitis pigmentosa (RP). In some embodiments, the disease is Bietti Crystalline Dystrophy (also known as Bietti Crystalline Corneoretinal Dystrophy; BCD). In some embodiments, the disease is related to neurological degeneration. In some embodiments, the disease is corneal dystrophy. In some embodiments, the subject has BCD or is at risk of developing BCD.

In some embodiments, the cells are fibroblasts, blood cells, or ocular cells. In some embodiments, the cells are obtained from urine or from hair or hair follicles. In some embodiments, the ocular cells are retinal pigment epithelial (RPE) cells, corneal epithelial cells (CECs), choroidal endothelial (CE) cells, or photoreceptor cells (PRCs).

In some embodiments, the genetic or epigenetic alteration is selected from the group consisting of a mutation, an insertion, a single nucleotide polymorphism, improper methylation, improper demethylation, and combinations thereof. In some embodiments, the genetic or epigenetic alteration is a mutation. In some embodiments, the genetic or epigenetic alteration in the iPS-ocular cells from the subject has been genetically repaired using gene editing. In some embodiments, the gene editing method utilizes a zinc-finger nuclease, TALEN technology, or CRISPR technology. In some embodiments, the genetic or epigenetic alteration in the iPSC-ocular cells from the subject has been genetically repaired using gene transfer. In some

embodiments, the gene transfer method utilizes a recombinant AAV vector or another viral vector or non-viral vector to deliver a healthy copy of the target gene (e.g., cDNA) to the cells to be transplanted.

In some embodiments, the administering step takes place before the onset of disease symptoms or after the onset of disease symptoms. In some embodiments, the administration is to the eye or to another organ or tissue comprising neurons. In some embodiments, the administration is by injection. In some embodiments, the administration is by sub-retinal or intravitreal injection. In some embodiments, the administration is by direct retinal injection. In some embodiments, the administration is by corneal injection. In some embodiments, the administration is by any other administration method that effectively delivers the cells to the sub-retinal place, the posterior segment, or the cornea of the eye of the subject.

In some embodiments, the method further includes, prior to administering or transplanting, performing genotypic analysis on the cells to identify the presence or absence of the genetic or epigenetic alteration in one or more genes set forth in Table 4. In some embodiments, the genetic or epigenetic alteration is a mutation. In some embodiments, the mutation is in the CYP4V2 nucleic acid molecule. In some embodiments, the method further includes, prior to administering, evaluating the eye of the subject to identify the area(s) and extent of damaged or retained photoreceptors, retinal cells, or corneal cells.

In some embodiments, the method further includes, following administering, monitoring the subject. In some embodiments, the monitoring comprises performing non-invasive retinal imaging, corneal tests, perimetry, ERG, OCT, visual acuity tests, and/or functional studies. In some embodiments, the monitoring comprises evaluating the subject for an immune response. In some embodiments, the method further includes, following administering, evaluating the eye of the subject to identify the area(s) and extent of damaged or retained photoreceptors, retinal cells, or corneal cells.

Cell Therapy - RNP Claims

RNP Claims

In another aspect, a composition is provided that includes: (a) a CRISPR guide RNA targeting a nucleic acid sequence (the "target sequence") of or within 100 bps to a target gene

(the "target gene"), and (b) a functional CRISPR-associated protein, in a ribonucleoprotein (RNP) or protein-RNA complex.

In some embodiments, the composition further includes (c) a donor nucleic acid sequence including all or a portion of a wild-type sequence or a functional sequence of the target gene for correction or replacement of such target gene or a portion thereof. In some embodiments, the target gene is involved in ocular development or function and/or mutation of which causes or is a risk factor to cause an ocular disease. In some embodiments, the target gene is involved in neuronal development or function and/or mutation of which causes or is a risk factor to cause a neurodegenerative disease.

In some embodiments, the target gene is a cytochrome P450 gene. In some embodiments, the target gene includes a gene set forth in Table 4 that is mutated or defective, or encodes a protein having defective or partial function or activity. In some embodiments, the donor nucleic acid sequence is provided in a single-stranded donor oligonucleotide (ssODN) or a vector.

In some embodiments, (a) the CRISPR guide RNA including (i) a CRISPR RNA (crRNA) which includes a protospacer element sequence that is complementary to the target sequence of or within 100 bps to a target gene and a sequence that corresponds to a complementary region of the trans-activating crRNA (tracrRNA), and (ii) a tracrRNA which includes a region that is complementary to corresponding region of the crRNA and a sequence which interacts with a CRISPR-associated protein 9 (Cas9), and (b) the functional CRISPR-associated protein comprises Cas9.

In some embodiments, the protospacer element is about 20 bases, about 19 bases, about 21 bases, about 19-21 bases, about 18-22 bases, or about 16-24 bases. In some embodiments, the crRNA and the tracrRNA are in different nucleic acid molecules. In some embodiments, the crRNA and the tracrRNA are combined into a single guide RNA (sgRNA). In some embodiments, the sgRNA is about 88-150 bps.

In some embodiments, the Cas9 comprises a Cas9 ortholog or a mutant Cas9 selected from: *Streptococcus pyogenes* (SpCas9), SpCas9 nickase (Cas9n D10A), SpCas9 (D1135E), eSpCas9, SpCas9-HF1, SpCas9 VRER, SpCas9 VQR, SpCas9EQR, *Staphylococcus aureus* (SaCas9), *Neisseria Meningitidis*, *Streptococcus thermophilus*, *Streptococcus pneumoniae*,

Campylobacter coli, *Campylobacter jejuni*, *Streptococcus mutans*, *Pasteurella multocida*, *Bifidobacterium longum*, *Bacillus smithii*, *Treponema denticola*, *Mycoplasma canis* and *Enterococcus faecalis*.

In some embodiments, (a) the CRISPR guide RNA comprises a crRNA which comprises a protospacer element sequence that is complementary to the target sequence of or within 100 bps to a target gene, and (b) the functional CRISPR-associated protein comprises Cpf1. In some embodiments, the protospacer element is about 20 bases, about 21 bases, about 22 bases, about 23 bases, about 24 bases, about 19-25 bases, about 18-26 bases, or about 16-28 bases. In some embodiments, the CRISPR-associated protein, Cas9, or Cpf1, further comprises one, two, three or more nuclear localization sequences (NLS) at the N-terminal and/or C-terminal, and/or a selection marker, including without limitation, GFP or EGFP.

In some embodiments, the protospacer element is 100% complementary to the target sequence or contains 1, 2, 3, 4, or 5 nucleotide mismatches corresponding to the target sequence. In some embodiments, the crRNA sequence further comprises a G nucleotide optionally added to the crRNA sequence immediately before the protospacer element. In some embodiments, the CRISPR guide RNA, crRNA and/or the tracrRNA, or the sgRNA, is chemically modified.

In some embodiments, the donor nucleic acid sequence is no more than about 1kb, 800bp, 600bp, 500bp, 400bp, 300bp, 280bp, 260bp, 240bp, 220bp, or 200bp for a donor nucleic acid sequence provided in a ssODN and no more than about 30kb, 25kb, 20kb, 15kb, 10kb, 9kb, 8kb, 7kb, 6kb, 5kb, 4.5kb, 4kb, 3.5kb, 3kb, 2.5kb, 2kb, 1.5kb, 1kb, 0.5kb, 0.2kb, or 0.1kb for a donor nucleic acid sequence provided in a vector. In some embodiments, the wild-type version of the target gene encodes an enzyme.

In some embodiments, the target gene includes a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or

CYP46A gene or a CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 or CYP46A gene that encodes a protein having defective or partial function or activity.

In some embodiments, any one or more components thereof including the CRISPR guide RNA, CRISPR-associated protein, and/or the donor nucleic acid sequence, is provided separately and/or additionally in a vector, a DNA and/or an mRNA which can transcribe and/or translate into such component. In one aspect, a pharmaceutical formulation including any of the compositions described herein are provided.

In another aspect, a method of treating a disease of a subject caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity is provided. Such a method includes disrupting, correcting or replacing such gene by administering to the subject any of the compositions described herein.

In another aspect, a method of treating an ocular disease or ameliorating a risk factor related thereto of a subject caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity is provided. Such a method includes disrupting, correcting or replacing such gene by administering to the subject any of the compositions described herein.

In another aspect, a method of treating a neurodegenerative disease or ameliorating a risk factor related thereto of a subject caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity is provided. Such a method includes disrupting, correcting or replacing such gene by administering to the subject any of the compositions described herein.

In another aspect, a method of treating a disease or ameliorating a risk factor related thereto of a subject caused by a mutated or defective cytochrome P450 gene, or a cytochrome

P450 gene encoding a protein having defective or partial function or activity is provided. Such a method includes disrupting, correcting or replacing such gene by administering to the subject any of the compositions described herein.

In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, disrupted, corrected or replaced is a mutated or defective version of a gene set forth in Table 4, or a version of a gene set forth in Table 4 that encodes a protein having defective or partial function or activity. In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is present in fibroblasts, blood, RPE, photoreceptor, retinal, corneal, choroidal, ocular, optic nerve, neuron, or stem cells, or any type of cells derived from a stem cell.

In some embodiments, the composition therein is delivered to fibroblasts, blood, RPE, photoreceptor, retinal, corneal, choroidal, ocular, optic nerve, neuron, or stem cells, or any type of cells derived from a stem cell. In some embodiments, delivery is performed by electroporation or via lipid-mediated transfection, or nucleofection, or viral transduction, or injection or a combination thereof. In some embodiments, any one or more components thereof including the CRISPR guide RNA, CRISPR-associated protein, and/or the donor nucleic acid sequence is administered to the subject or to the cells via a delivery system selected from the group consisting of a ribonucleoprotein or protein-RNA complex, a nanoparticle, a liposome, a micelle, a virosome, a nucleic acid complex, and/or a combination thereof.

In some embodiments, the treatment is performed to a subject *in vivo*. In some embodiments, the treatment is performed *in vitro* in fibroblasts, blood, RPE, photoreceptor, retinal, corneal, choroidal, ocular, optic nerve, neuron, or stem cells, or any type of cells derived from a stem cell. In some embodiments, the treated cells are transplanted to a subject *in vivo*, or if the treated cell is a stem cell, such stem cell is differentiated into the desired type of cells for transplantation and then the differentiated cells are transplanted into a subject *in vivo*.

In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is replaced. In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, has

one or more mutations corrected or replaced. In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted.

In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, has 1-20, 21-40, 41-60, 61-80, 81-100, 101-1000, 1001-10000 base pairs of nucleotides or mutations disrupted, corrected or replaced. In some embodiments, a region of the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced. In some embodiments, a region of less than about 10, 8, 6, 4, 2 or 1 kb of the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced.

In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced via insertion and/or deletion of nucleotides. In some embodiments, the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced in one allele or both alleles. In some embodiments, two or more different CRISPR guide RNAs, CRISPR-associated proteins and/or donor nucleic acid sequences are used to disrupt, correct or replace one or more mutations or defects in the mutated or defective gene, or gene encoding a protein having defective or partial function.

In some embodiments, the subject is a mammal. In some embodiments, the subject is a human. In some embodiments, the method improves ocular development or function, or prevents ocular, retinal or corneal degeneration. In some embodiments, the method improves neurological development or function, or prevents neural degeneration. In some embodiments, the method improves expression or function of a P450 enzyme.

In some embodiments, a homology directed repair based on the donor nucleic acid sequence resulted in an intron and/or an exon of the target gene. In some embodiments, a homology directed repair based on the donor nucleic acid sequence resulted in a splice acceptor of the target gene. Such a method can further include (c) a donor nucleic acid sequence comprising all or a portion of a target gene set forth in Table 4 with a mutation or alteration for generation of a mutated or altered target gene or a portion thereof.

In some aspects, a method of generating a cellular disease model of a disease caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity, by generating a mutation in such gene is provided. Such a method includes delivery to the cells of a healthy version of such gene via any of the compositions described herein. In some embodiments, delivery is performed by electroporation or via lipid-mediated transfection, or nucleofection, or viral transduction, or microinjection, or a combination thereof. In some embodiments, the cells are fibroblasts, blood, RPE, photoreceptor, retinal, corneal, choroidal, ocular, optic nerve, neuron, or stem cells, or any type of cells derived from a stem cell.

In still another aspect, a composition is provided that includes a cell with a mutated or defective gene set forth in Table 4.

In another aspect, a composition is provided that includes a cell with a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene comprising a composition of any one of the claims herein

In some embodiments, the vector is an AAV vector. In some embodiments, the protospacer element sequence is selected from the group consisting of SEQ ID NOs: 48 to 52, or shares at least 80% sequence identity with one of SEQ ID NO: 48 to 52 for use with a Cas protein that has NGG as protospacer adjacent motif (PAM) to target the c.802-8_810del17insGC mutation of the CYP4V2 gene. In some embodiments, the donor nucleic acid sequence is selected from SEQ ID NOs: 56 and 57, or shares at least 90% sequence identity with one of SEQ ID NO: 56 and 57, or a sequence that is complementary thereof, for use to correct, disrupt or replace the c.802-8_810del17insGC mutation of the CYP4V2 gene.

Gene Therapy Claims

Codon-optimized sequence related claims:

In one aspect, a nucleic acid molecule including the nucleic acid sequence of SEQ ID NO: 2 encoding a human CYP4V2 protein or a nucleic acid sequence sharing at least 90% sequence identity with the nucleic acid sequence of SEQ ID NO: 2 is provided.

In another aspect, an expression cassette including a nucleic acid molecule as described herein and one or more regulatory sequence operably linked to the nucleic acid sequence is provided. In still another aspect, a vector including a nucleic acid molecule as described herein or an expression cassette as described herein is provided.

In some embodiments, the vector is a viral vector. In some embodiments, the viral vector is selected from the group consisting of a recombinant adenovirus vector, a recombinant lentivirus vector, a recombinant herpes simplex virus vector, a recombinant sendai virus vector, and a recombinant retrovirus vector. In some embodiments, the vector is a recombinant adeno-associated virus (rAAV) vector or a plasmid. In some embodiments, the vector is a plasmid or a non-viral vector. In some embodiments, the non-viral vector is selected from the group consisting of naked nucleic acids, liposomes, dendrimers, and nanoparticles.

In some embodiments, a host cell including any of the nucleic acid molecules described herein and/or any of the compositions described herein. In some embodiments, the host cell is a bacteria cell, an E. Coli cell, a plant cell, an insect cell or a mammalian cell. In some embodiments, the host cell is a HEK293, HeLa, Vero, V27, A549, K562, B50, WI38, Hep G2 or BHK cell.

In another aspect, the use of any of the nucleic acid molecule described herein, of any of the expression cassettes described herein, or of any of the vectors described herein, to express the product encoded by such nucleic acid molecule, in a bacteria cell, an insect cell, a plant cell, a mammalian cell, an RPE cell, a photoreceptor or photoreceptor progenitor (PRC), a retinal cell, a corneal cell, an ocular cell, a neuron, a neuronal cell, a blood cell, an epithelial cell, a somatic cell, an iPS cell, a ES cell, an MSC, an adult stem cell, a stem cell, or any cell derived from a stem cell.

EFS and/or SPA related Claims

In another aspect, a self-complementary adeno-associated virus (scAAV) vector including an elongation factor 1 α short (EFS) promoter and/or a small polyadenylation (polyA) signal (SPA) operably linked to a nucleic acid molecule encoding a polypeptide, an interfering RNA molecule or an oligonucleotide is provided. In some embodiments, the EFS promoter consists of a nucleic acid sequence having at least 80% sequence identity of SEQ ID NO: 35 and the SPA consists of a nucleic acid sequence having at least 80% sequence identity of SEQ ID NO: 36.

In some embodiments, the scAAV vector is delivered to a cell such that the product encoded by the nucleic acid molecule is expressed in the cell. In some embodiments, the cell is a mammalian cell. In some embodiments, the cell is a retinal cell, a corneal cell, a choroidal cell, an ocular cell, a brain cell, a neuron, a neuronal cell, an iPS cell, a ES cell, an MSC, a stem cell, or any cell derived from a stem cell.

In one aspect, a method to reduce immune responses to viral vectors and preserve transduction efficiency in gene therapy and/or to maximize therapeutic effect to different patients of the same genetic disease is provided. Such a method includes (a) establishing a pool of more than one recombinant viral vectors (e.g., rAAVs) with sufficient transduction efficiency in the target cell type for the gene therapy. The viral vector pool can be expanded by creating variants with antigenic region mutations or other mutations or variants on the capsids of said viral vectors and such mutations or variants confirmed with sufficient transduction efficiency in target cells relevant to the disease (e.g., in iPS-RPE cell lines for CYP4V2 gene therapy for BCD); (b) detecting pre-existing neutralizing anti-viral vector antibodies (NAbs) against different viral vector serotypes and/or capsid mutations or variants in the subject in need of the gene therapy, and/or testing and comparing different viral vectors in patient-specific cells (e.g., iPS-RPE cells) derived from such subject; (c) selecting a viral vector from the pool of viral vectors with sufficient transduction efficiency with lowest of cross-reactivity with the pre-existing NAbs in the subject and/or one viral vector with the best phenotype rescue result in the subject's patient-specific cells, such viral vector pool comprising different serotypes and capsid-modified viral vectors (e.g., including without limitation, capsid-mutant AAVs and/or capsid protein variant

AAVs); (d) use the viral vector selected from (c) for administration to the subject; and (e) repeat (b) through (d) (only the part relating to pre-existing NAb) above each time the subject requires a gene therapy administration, including without limitation, a follow-up administration to the same eye or an administration to the contralateral eye, or to another organ.

In another aspect, a composition for treating or preventing a disease in a subject is provided, including an effective amount of a vector and a pharmaceutically acceptable carrier. Typically, the vector includes a nucleic acid molecule or a non-pathogenic variant thereof encoding a non-mutant or functional CYP4V2 protein operably linked to a regulatory sequence.

In some embodiments, the disease is Bietti Crystalline Dystrophy (also known as Bietti Crystalline Corneoretinal Dystrophy; BCD). In some embodiments, the disease is associated with a genetic or epigenetic alteration in the subject. In some embodiments, the disease is photoreceptor degeneration, retinal pigment epithelium cell degeneration, retinal degeneration, cornea degeneration, or choroidal degeneration. In some embodiments, the retinal degeneration is retinitis pigmentosa (RP). In some embodiments, the retinal degeneration is an inherited retinal degeneration (IRD). In some embodiments, the disease is BCD. In some embodiments, the disease is corneal dystrophy. In some embodiments, the subject has BCD or is at risk of developing BCD.

In one aspect, a vector including a nucleic acid molecule or a non-pathogenic variant thereof encoding a non-mutant or functional CYP4V2 protein operably linked to a regulatory sequence is provided.

In some embodiments, the vector is a viral vector. In some embodiments, the viral vector is selected from the group consisting of an adeno-associated virus (AAV) vector, an adenovirus vector, a lentivirus vector, a herpes simplex virus vector, a sendai virus vector, and a retrovirus vector. In some embodiments, the AAV is a recombinant AAV (rAAV). In some embodiments, the rAAV comprises an AAV genome or a derivative thereof, and/or an AAV capsid protein or a derivative thereof. In some embodiments, the rAAV is a chimeric AAV, a shuffled AAV, or a capsid-modified AAV.

In some embodiments, the AAV genome or AAV capsid protein is from any one of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12,

or another naturally derived serotype or isolate or Glade of AAV, or any derivative or hybrid thereof. In some embodiments, the rAAV is a pseudotyped AAV (e.g., AAV2/5, AAV2/8, AAV2/1, AAV2/4, AAV2/6, AAV2/7, AAV2/12, AAV2/10 and AAV2/9). In some embodiments, the rAAV is a hybrid AAV (e.g., AAV-DJ, AAV-DJ/8, or AAV-DJ/9). In some embodiments, the rAAV is developed through directed evolution and/or rational design (e.g., AAV 7m8 or AAV-PHP.B).

In some embodiments, the rAAV comprises one or more capsid mutations (e.g., Y-F, K-R, T-A, S-A and/or T-V mutations, (e.g., AAV2 with one or more capsid mutations among Y444F, Y500F, Y730F, Y252F, Y272F, Y700F, Y704F and T491V, or the corresponding mutation for a different AAV serotype, (e.g., AAV2/8 (Y733F), AAV2 (Y444F+Y500F+Y730F) and AAV2 (quadY-F+T-V))). In some embodiments, the serotype of the rAAV is selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, Anc80, rh10 and ShH10. In some embodiments, the rAAV vector is selected from the group consisting of AAV2/5, AAV2/8, AAV2/8(Y733F), AAV2 (Y444F+Y500F+Y730F), AAV2/1, AAV2/4, AAV2/9, AAV2/6, AAV2/7, AAV1, AAV2, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV12, Anc80, AAV 7m8, AAV-DJ, ShH10, AAV-PHP.B or a hybrid, a derivative or variant thereof.

In some embodiments, the rAAV vector is a single-stranded AAV vector or a self-complementary AAV (scAAV) vector. In some embodiments, the vector is a plasmid, or a non-viral vector (e.g., naked nucleic acids, liposomes, dendrimers, and nanoparticles).

In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises: (i) the human CYP4V2 protein (SEQ ID NO: 4); (ii) a variant of (e.g., changing of the amino acids and/or a splice variant) of the human CYP4V2 protein or a functional CYP4V2 protein (e.g., SEQ ID NO: 5); (iii) one or more fragments of a functional CYP4V2 protein (e.g., SEQ ID NO: 6); (iv) all or part of sequences from one or more of the CYP4V2 ortholog of other species, (v) all or part of sequences from one or more other P450 proteins, including but not limited to, other CYP4 proteins and CYP46A1, (vi) a polypeptide which can ameliorate, treat, or arrest one or more biochemical abnormalities in one or more of

the genes listed in Table 4 in a patient cell (e.g., the iPS-RPE cell of a BCD patient), and/or (vii) a combination of the above.

In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises all or part of the amino acid sequence shown in SEQ ID NO: 4, 5 or 6. In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises all or part of an amino acid sequence selected from the group consisting of CYP4V2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 and CYP46A1 (SEQ ID NOs: 4-18), and derivatives, hybrids, variants and/or fragments thereof. In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises all or part of the amino acid sequence selected from the group consisting of CYP4V2 (or orthologs of CYP4V2) of chimpanzee, Rhesus monkey, dog, cow, mouse, rat, chicken, frog, horse, rabbit and fruit fly (SEQ ID NOs: 19-29), and derivatives, hybrids, variants and/or fragments thereof.

In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises a polypeptide having at least 80% amino acid sequence identity (e.g., at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity) to any of the sequences selected from the group consisting of SEQ ID NOs: 4-29. In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises sequence elements of FxxGxxxCxG and ExxR (SEQ ID NOs: 30 and 31). In some embodiments, the non-mutant or functional CYP4V2 protein is a compound or agent which can ameliorate, treat, or arrest one or more biochemical abnormalities in one or more of the genes listed in Table 4 in a patient cell (e.g., the iPS-RPE cell of a BCD patient).

In some embodiments, the nucleic acid molecule encodes a non-mutant or functional CYP4V2 protein of any one of claims 43-50. In some embodiments, the nucleic acid molecule encodes a non-mutant or functional CYP4V2 protein comprising an amino acid sequence shown in SEQ ID NO: 4, 5 or 6 or having at least 80% sequence identity with any one of SEQ ID NO: 4, 5, or 6. In some embodiments, the nucleic acid molecule has at least 60% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3. In some embodiments, the nucleic acid molecule

has at least 70% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3. In some embodiments, the nucleic acid molecule has at least 75% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3. In some embodiments, the nucleic acid molecule has at least 76% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3. In some embodiments, the nucleic acid molecule comprises a sequence shown in SEQ ID NO: 1, 2, or 3.

In some embodiments, the regulatory sequence comprises a promoter. In some embodiments, the promoter is an RPE cell-specific promoter, a retinal cell-specific promoter, a corneal cell-specific promoter, an ocular-cell specific promoter or a constitutive promoter. In some embodiments, the promoter is a mammalian beta actin promoter or a viral promoter.

In some embodiments, the promoter is selected from the group consisting of a CAG promoter (hybrid CMV early enhancer/Chicken beta actin promoter, also known as CAGGS promoter, CB promoter or CBA promoter), a chicken beta actin promoter, a small CBA (smCBA) promoter, a CB^{SB} promoter, or a CBh promoter, another beta-actin promoter such as the human beta actin promoter, a elongation factor 1 alpha short (EFS) promoter, a elongation factor 1 alpha short (EF-1 alpha) promoter, a CMV promoter, a PGK promoter, a UBC promoter, a GUSB promoter, a UCOE promoter, a VMD2 (vitelliform macular dystrophy 2; also known as BEST1) promoter, a RPE65 promoter, or a hybrid or a derivative thereof.

In some embodiments, the promoter is a CAG promoter (hybrid CMV early enhancer/Chicken beta actin promoter, also known as CAGGS promoter, CB promoter or CBA promoter), a elongation factor 1 alpha short (EFS) promoter, a elongation factor 1 alpha short (EF-1 alpha) promoter or a CMV promoter, or a derivative or a hybrid thereof. In some embodiments, the regulatory sequence comprises an enhancer.

In some embodiments, the enhancer is a viral enhancer, including without limitation, a WPRE enhancer, an HPRE enhancer, a CTE enhancer or a derivative or hybrid thereof. In some embodiments, the regulatory sequence comprises a polyadenylation (polyA) signal. In some embodiments, the polyA signal is a bovine growth hormone polyadenylation signal (bGH polyA), a small polyA signal (SPA), a human growth hormone polyadenylation signal (hGH polyA), a SV40 polyA signal, a SV40 late polyA signal, or a derivative or hybrid thereof. In some embodiments, the regulatory sequence comprises a Kozak sequence (SEQ ID NO: 37 or 38)

In some embodiments, the composition is formulated with a carrier and additional components suitable for the specific route of administration.

In another aspect, a host cell including any of the vectors described herein are provided.

In another aspect, a method of treating or preventing a disease of the eye in a subject is provided, the method including administering a vector to the subject, wherein the vector comprises a nucleic acid molecule or a non-pathogenic variant thereof encoding a human CYP4V2 protein or a functional CYP4V2 protein operably linked to a regulatory sequence.

In one aspect, a method of preventing, arresting or slowing progression of, or ameliorating the dysfunction, dystrophy, disorder, degeneration and/or death of an ocular cell is provided, the method including delivering a vector to the ocular cell, wherein the vector comprises a nucleic acid molecule or a non-pathogenic variant thereof encoding a human CYP4V2 protein or a functional CYP4V2 protein operably linked to a regulatory sequence.

In some embodiments, the disease is Bietti Crystalline Dystrophy (also known as Bietti Crystalline Corneoretinal Dystrophy; Bietti Crystalline Retinopathy; Bietti's Retinal Dystrophy; BCD). In some embodiments, the subject is affected by other ophthalmological clinically-defined conditions (e.g., inherited retinal degeneration (IRD), retinitis pigmentosa (RP) or corneal dystrophy) caused by mutations in the CYP4V2 gene. In some embodiments, the disease of the eye is photoreceptor degeneration, retinal pigment epithelium cell degeneration, retinal degeneration, corneal dystrophy, or BCD.

In some embodiments, the vector is a viral vector. In some embodiments, the viral vector is selected from the group consisting of a recombinant adeno-associated virus (rAAV) vector, a recombinant adenovirus vector, a recombinant lentivirus vector, a recombinant herpes simplex virus vector, a recombinant sendai virus vector, and a recombinant retrovirus vector. In some embodiments, the viral vector is a rAAV vector. In some embodiments, the rAAV vector comprises a VP1, VP2, or VP3 capsid protein selected from any serotype of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or another naturally derived serotype or isolate or Glade of AAV, or hybrids, variants or derivatives thereof.

In some embodiments, the rAAV vector 5' AAV ITR is selected from any one of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12,

or another naturally derived serotype or isolate or Glade of AAV, or mutations, chimeras, variants or fusions thereof. In some embodiments, the rAAV vector 3' AAV ITR is selected from any one of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or another naturally derived serotype or isolate or Glade of AAV, or mutations, chimeras, variants or fusions thereof. In some embodiments, the rAAV is a chimeric AAV, a shuffled AAV, or a capsid-modified AAV. In some embodiments, the rAAV is a pseudotyped AAV (e.g., AAV2/5, AAV2/8, AAV2/1, AAV2/4, AAV2/6, AAV2/7, AAV2/12, AAV2/10 and AAV2/9). In some embodiments, the rAAV is a hybrid AAV (e.g., AAV-DJ, AAV-DJ/8, or AAV-DJ/9). In some embodiments, the rAAV is developed through directed evolution and/or rational design (e.g., AAV 7m8 or AAV-PHP.B).

In some embodiments, the rAAV comprises one or more capsid mutations (e.g., Y-F, K-R, T-A, S-A and/or T-V mutations (e.g., AAV2 with one or more capsid mutations among Y444F, Y500F, Y730F, Y252F, Y272F, Y700F, Y704F and T491V, or the corresponding mutation for a different AAV serotype, (e.g., AAV2/8 (Y733F), AAV2 (Y444F +Y500F+Y730F) and AAV2 (quadY-F+T-V))). In some embodiments, the serotype of the rAAV is selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, Anc80, rh10 and ShH10. In some embodiments, the rAAV vector is selected from the group consisting of AAV2/5, AAV2/8, AAV2/8(Y733F), AAV2 (Y444F+Y500F+Y730F), AAV2/1, AAV2/4, AAV2/9, AAV2/6, AAV2/7, AAV1, AAV2, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV12, Anc80, AAV 7m8, AAV-DJ, ShH10, AAV-PHP.B or a hybrid, a derivative or variant thereof.

In some embodiments, the rAAV vector is a single-stranded AAV vector or a self-complementary AAV (scAAV) vector. In some embodiments, the vector is a plasmid or a non-viral vector. In some embodiments, the non-viral vector is selected from the group consisting of naked nucleic acids, liposomes, dendrimers, and nanoparticles.

In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises: (i) the human CYP4V2 protein (SEQ ID NO: 4); (ii) a variant of (e.g., changing of the amino acids and/or a splice variant) of the human CYP4V2 protein or a functional CYP4V2 protein (e.g., SEQ ID NO: 5); (iii) one or more fragments of a functional

CYP4V2 protein (e.g., SEQ ID NO: 6); (iv) all or part of sequences from one or more of the CYP4V2 ortholog of other species; (v) all or part of sequences from one or more other P450 proteins, including but not limited to, other CYP4 proteins and CYP46A1; (vi) a polypeptide which can ameliorate, treat, or arrest one or more biochemical abnormalities in one or more genes listed in Table 4 in a patient cell (e.g., the iPS-RPE cell of a BCD patient), and/or (vii) a combination of the above.

In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises all or part of the amino acid sequence shown in SEQ ID NO: 4, 5 or 6. In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises all or part of an amino acid sequence selected from the group consisting of CYP4V2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 and CYP46A1 (SEQ ID NOs: 4-18), and derivatives, hybrids, variants and/or fragments thereof.

In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises all or part of the amino acid sequence selected from the group consisting of CYP4V2 (or orthologs of CYP4V2) of chimpanzee, Rhesus monkey, dog, cow, mouse, rat, chicken, frog, horse, rabbit and fruit fly (SEQ ID NOs: 19-29), and derivatives, hybrids, variants and/or fragments thereof. In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises a polypeptide having at least 80% amino acid sequence identity (e.g., at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity) to any of the sequences selected from the group consisting of SEQ ID NOs: 4-29.

In some embodiments, the non-mutant or functional CYP4V2 protein encoded by the nucleic acid sequence comprises sequence elements of FxxGxxxCxG and ExxR (SEQ ID NOs: 30 and 31). In some embodiments, the non-mutant or functional CYP4V2 protein is a compound or agent which can ameliorate, treat, or arrest one or more biochemical abnormalities in one or more of the genes listed in Table 4 in a patient cell (e.g., the iPS-RPE cell of a BCD patient). In some embodiments, the nucleic acid molecule encodes a non-mutant or functional CYP4V2 protein of any one of claims 91-97. In some embodiments, the nucleic acid molecule encodes a

non-mutant or functional CYP4V2 protein comprising an amino acid sequence shown in SEQ ID NO: 4, 5 or 6 or having at least 80% sequence identity with any one of SEQ ID NO: 4, 5, or 6. In some embodiments, the nucleic acid molecule encoding a functional CYP4V2 protein has a nucleic acid sequence shown in SEQ ID NO: 1, 2 or 3. In some embodiments, the nucleic acid molecule encoding a functional CYP4V2 protein has a sequence identity of at least 60% to any of SEQ ID NOs 1, 2 or 3.

In some embodiments, the regulatory sequence comprises a promoter. In some embodiments, the promoter is an RPE cell-specific promoter, a retinal cell-specific promoter, a corneal cell-specific promoter, or an ocular-cell specific promoter. In some embodiments, the promoter is a constitutive promoter. In some embodiments, the promoter is a mammalian beta actin promoter or a viral promoter.

In some embodiments, the promoter is selected from the group consisting of a CAG promoter (hybrid CMV early enhancer/Chicken beta actin promoter, also known as CAGGS promoter, CB promoter or CBA promoter), a chicken beta actin promoter, a small CBA (smCBA) promoter, a CB^{SB} promoter, or a CBh promoter, another beta-actin promoter such as the human beta actin promoter, a elongation factor 1 alpha short (EFS) promoter, a elongation factor 1 alpha short (EF-1 alpha) promoter, a CMV promoter, a PGK promoter, a UBC promoter, a GUSB promoter, a UCOE promoter, a VMD2 (vitelliform macular dystrophy 2; also known as BEST1) promoter, a RPE65 promoter, or a hybrid or a derivative thereof. In some embodiments, the promoter is a CAG promoter (hybrid CMV early enhancer/Chicken beta actin promoter, also known as CAGGS promoter, CB promoter or CBA promoter), a elongation factor 1 alpha short (EFS) promoter, a elongation factor 1 alpha short (EF-1 alpha) promoter or a CMV promoter, or a derivative or a hybrid thereof.

In some embodiments, the regulatory sequence comprises an enhancer. In some embodiments, the enhancer is viral enhancer, including without limitation, a WPRE enhancer, an HPRE enhancer, a CTE enhancer or a derivative or hybrid thereof. In some embodiments, the regulatory sequence comprises a polyadenylation (polyA) signal. In some embodiments, the polyA signal is a bovine growth hormone polyadenylation signal (bGH polyA), a small polyA signal (SPA), a SV40 polyA signal, a human growth hormone polyadenylation signal (hGH

polyA), a SV40 late polyA signal, or a derivative or hybrid thereof. In some embodiments, the regulatory sequence comprises a Kozak sequence (SEQ ID NO: 37 or 38)

In some embodiments, for in vitro treatment, the target cell is infected at a dose (MOI) of about 1×10^3 GC to about 1×10^6 GC per cell (GC: genomic copies, measuring genome containing AAV particles (a/k/a vector genome (vg) or genome particles (gp)). In some embodiments, for in vivo administration to a subject's eye, a single administration can be on the order of from about 1×10^6 to 2×10^{13} GC (e.g., a high dose range of about 1×10^{11} GC to about 1×10^{12} GC, a medium dose range of about 1×10^{10} GC to about 1×10^{11} GC, a low dose range of about 1×10^9 GC to about 1×10^{10} GC, a very low dose range of about 1×10^6 GC to about 1×10^9 GC, and a very high dose range of about 1×10^{12} GC to about 2×10^{13} GC), or any dose within these ranges that is sufficient to provide the desired effect.

In some embodiments, the administering step takes place before the onset of disease symptoms or after the onset of disease symptoms. In some embodiments, the administration is to the eye. In some embodiments, the administration is by sub-retinal injection. In some embodiments, the administration is by intravitreal injection. In some embodiments, the administration is by direct retinal injection. In some embodiments, the administration is by any other administration method that effectively delivers the vectors to the sub-retinal place, the posterior segment of the eye, the cornea or the RPE cells, the photoreceptor cells or corneal epithelial cells of the subject.

In some embodiments, the administration is by corneal delivery. In some embodiments, the administration to the eye is achieved by delivery through the bloodstream. In some embodiments, the administration is via eye drops. In some embodiments, the administration is by delivery to the lens. In some embodiments, the administration is into the subretinal space, the cornea, the lens, or into the vitreus. In some embodiments, the ocular cells are selected from the group consisting of retinal pigment epithelium (RPE) cells, photoreceptor cells (PRCs), corneal epithelial cells (CECs), choroidal endothelial (CE) cells, retinal cells, corneal cells, lens cells, ganglion cells, optic nerve cells, and/or choroidal cells, as well as the said types of cells derived from a stem cell (including without limitation, an iPSC, a ES cell, an MSC, an adult stem cell and/or a tissue-specific stem cell), .

In some embodiments, the methods described herein can further include identifying a subject having BCD or at risk of developing BCD.

Use of EFS and/or SPA in an rAAV vector comprising a nucleic acid sequence encoding Cas related Claims

In one aspect, a composition including a recombinant adeno-associated virus (rAAV) vector comprising an elongation factor 1 α short (EFS) promoter and/or a small polyadenylation (polyA) signal (SPA) operably linked to a nucleic acid molecule encoding a CRISPR associated protein (Cas) is provided.

In some embodiments, the EFS promoter consists of a nucleic acid sequence having at least 80% sequence identity of SEQ ID NO: 35 and the SPA consists of a nucleic acid sequence having at least 80% sequence identity of SEQ ID NO: 36. In some embodiments, the Cas encoded by the nucleic acid sequence operably linked to the EFS promoter and/or the SPA is a Cas9 or a Cpf1.

Host cells including a rAAV as described herein is provided. In some embodiments, the host cell is a bacteria cell, an E. Coli cell, a plant cell, an insect cell, or a mammalian cell. In some embodiments, the cell is a somatic cell or a stem cell. In some embodiments, the host cell is a retinal cell, a corneal cell, a choroidal cell, an ocular cell, a brain cell, a neuron, a neuronal cell, an iPS cell, a ES cell, an MSC, an adult stem cell, a tissue-specific cell, a stem cell, or any cell derived from a stem cell. In some embodiments, the rAAV vector is delivered to a host cell such that the Cas encoded by the nucleic acid molecule is expressed in the cell. In some embodiments, the host cell comprising any cell of any one of claims 131 to 134.

Other features and advantages of the inventions will be apparent from the Detailed Description, Description of Drawings, and Examples, and also from the claims. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety.

DESCRIPTION OF DRAWINGS

The inventions are further illustrated in the following figures and drawings, which do not limit the scope of the inventions described in the claims.

Cell Line Patent:

Figure 1: iPS cell lines derived from BCD patients

(a) iPS cells generated from fibroblasts of skin biopsy samples of BCD patients:

- (i) Patient 1 (P1) iPS cells
- (ii) Patient 2 (P2) iPS cells
- (iii) characterization of P1 and P2 iPS cell lines by Oct-4, Sox-2 and SSEA-4

markers

(iv) characterization of P1 and P2 iPS cell lines by Nanog and Tra-1-60 markers

(b) iPS cells generated from a BCD patient and a healthy control from peripheral blood mononuclear cells (PBMC) of blood samples:

- (i) phase contrast images of iPS cell lines
- (ii) AP staining results of iPS cell lines

(c) BCD patient-derived iPS cell karyotype images showing apparently normal human karyotype.

Figure 2: iPS-RPE cell lines derived from BCD patients:

(a) light-field pictures of iPS-RPE cell lines derived from BCD patients showing RPE unique morphology - hexagonal shape, pigmentation and monolayer:

- (i) P1 iPS-RPE cells
- (ii) P2 iPS-RPE cells

(b) RPE markers results of BCD patients' iPS-RPE cells, showing the presence of RPE-specific markers, RPE65, CRALBP and MITF.

Figure 3: qRT-PCR results of CYP4V2 expression in iPS-RPE samples. WT (controls). WT AVE (average of controls). P1 (BCD Patient 1). P1-AAV8 (P1 sample treated by AAV8.CYP4V2fv, MOI=1.5x10⁴ GC/cell).

Figure 4: qRT-PCR results of CYP4V2op expression in iPS-RPE samples. WT (controls). WT AVE (average of controls). P1 and P2 (BCD Patient 1 and Patient 2). P1-AAV2 (P1 sample

treated by AAV2.CYP4V2op at MOI of 2×10^4 GC/cell). P2-AAV2 (P2 sample treated by AAV2.CYP4V2op at MOI of 2×10^4 GC/cell). P2-scAAV1 (P2 sample treated by scAAV1.CYP4V2op at MOI of 2×10^4 GC/cell).

Figure 5: Cell viability images of iPS-RPE samples without exposure to blue light. WT (controls). P1 and P2 (BCD Patient 1 and Patient 2). Red (dead/sick cells); Green (live/healthy cells). Figure 5(a): Red only. Figure 5(b): Red and green.

Figure 6: Cell viability images of iPS-RPE samples after 1 hour exposure to blue light. WT (controls). P1 and P2 (BCD Patient 1 and Patient 2). Red (dead/sick cells); Green (live/healthy cells). Figure 6(a): Red only. Figure 6(b): Red and green.

Gene Therapy:

Figure 7: Schematics of and annotations to exemplary CYP4V2 expression cassettes and recombinant AAV (rAAV) vectors

(a) CYP4V2 expression cassette (with an enhancer) packaged in single-stranded AAV (ssAAV) vectors

(b) CYP4V2 expression cassette (without an enhancer) packaged in single-stranded AAV (ssAAV) vectors

(c) CYP4V2 expression cassette packaged in self-complementary AAV (scAAV) or ssAAV vectors.

Annotations: An CYP4V2 expression cassette (as shown flanked by AAV ITRs) can be packaged in an rAAV vector with capsid from any AAV serotype or a hybrid or variant thereof. ITRs: Inverted terminal repeats (can be AAV2 ITRs or ITRs from other AAV serotypes). Exemplary AAV2 ITRs sequences shown in SEQ ID NOs: 42 and 43. CYP4V2: a cDNA encoding the human CYP4V2 protein or a functional variant thereof, e.g., CYP4V2st (SEQ ID NO: 1) or CYP4V2op (SEQ ID NO: 2) encoding the human CYP4V2 protein (SEQ ID NO: 4), or CYP4V2fv (SEQ ID NO: 3) encoding a functional CYP4V2 protein (SEQ ID NO: 5). A Kozak sequence (sequence shown in SEQ ID NO: 37 or 38) is inserted immediately before the CYP4V2 cDNA sequence. CAG: hybrid CAG promoter (exemplary sequence shown in SEQ ID NO: 32). Other promoters discussed herein can also be used, including without limitation, a

CMV promoter (exemplary sequence shown in SEQ ID NO: 40) or a EF-1 α promoter (exemplary sequence shown in SEQ ID NO: 41). WPRE: woodchuck hepatitis virus posttranscriptional regulatory element (exemplary sequence shown in SEQ ID NO: 33). bGH polyA: bovine growth hormone polyadenylation signal (exemplary sequence shown in SEQ ID NO: 34). Alternative polyA signals can be used, e.g., an SV40 late poly A signal (exemplary sequence shown in SEQ ID NO: 39). EFS: elongation factor 1 α short (EFS) core promoter. Exemplary sequence shown in SEQ ID NO: 35. SPA: a small polyA signal. Exemplary sequence shown in SEQ ID NO: 36. Mutant/truncated ITR: One of the two ITRs used in an scAAV vector is a mutant/truncated ITR (shown as ITR*). Exemplary sequence shown in SEQ ID NO: 44. An enhancer is optional in CYP4V2 expression cassettes.

Figure 8: Cell viability images of BCD patient-derived iPS-RPE samples after 1 hour exposure to blue light (without AAV.CYP4V2 treatment vs. treated by AAV2.CYP4V2op or scAAV1.CYP4V2op at MOI of 1x10⁵ GC/cell). P1 and P2 (BCD Patient 1 and Patient 2). Red (dead/sick cells); Green (live/healthy cells). Figure 8(a): Red only. Figure 8(b): Red and green.

Figure 9: Cell viability images of BCD patient-derived iPS-RPE samples after 1 hour exposure to blue light (without AAV.CYP4V2 treatment vs. treated by AAV5.CYP4V2op, AAV5.CYP4V2st, or AAV8.CYP4V2fv at MOI of 1x10⁵ GC/cell). P1 (BCD Patient 1). Red (dead/sick cells); Green (live/healthy cells). Figure 9(a): Red only. Figure 9(b): Red and green.

Figure 10: Cell viability images of BCD patient-derived iPS-RPE samples after 1 hour exposure to blue light (without AAV.CYP4V2 treatment vs. treated by AAV5.CYP4V2op, scAAV1.CYP4V2op, or scAAV5.CYP4V2op at MOI of 1x10⁴ GC/cell). P2 (BCD Patient 2). Red (dead/sick cells); Green (live/healthy cells). Figure 10(a): Red only. Figure 10(b): Red and green.

Figure 11: Cell viability images of BCD patient-derived iPS-RPE samples after 1 hour exposure to blue light (without AAV.CYP4V2 treatment vs. treated by scAAV9.CYP4V2op at MOI of 1x10⁵ GC/cell). P1 (BCD Patient 1). Red (dead/sick cells); Green (live/healthy cells). Figure 11(a): Red only. Figure 11(b): Red and green.

Cell Therapy:

Figure 12 shows a region of the CYP4V2 sequence and the position of the guide RNAs (gRNAs) designed relative to the c.802-8_810del17insGC mutation and primers (orange arrows) for gRNA activity assay

Figure 13 shows an *in vitro* surveyor assay. Lanes 1: amplicon+Cas9; 2: amplicon + g1 + Cas9; 3: amplicon + g2 + Cas9; 4: amplicon + g3 + Cas9; 5: amplicon + g4 + Cas9; 6: amplicon + g5 + Cas9; 7: amplicon only; M: 1kb DNA marker.

Figure 14 is a sequence comparison confirming the DNA origin used in the surveyor assay. Top: untreated amplicon; Middle: fragment from g2 treated amplicon; Lower: CYP4V2 locus indicating mutation site.

Figure 15 is an illustration of gRNA vector construction.

Figure 16 is a vector map of gRNA (using g1 as example), Cas9 and PuroR co-expression plasmid pX459-hSpCas9-2A-Puro.

Figure 17 shows the position of the gRNA (using g1 as an example) relative to the U6 promoter in the pX459-hSpCas9-2A-Puro plasmid. The "G" nucleotide in between the U6 promoter and the gRNA is to enhance transcription efficiency driven by the U6 promoter. It is optional and not necessary when a different promoter is used or when the gRNA starts with a "G" nucleotide.

DEFINITIONS

It is to be understood that as used in the specification and in the claims, "a" or "an" can mean one or more, depending upon the context in which it is used. Thus, for example, reference to "a cell" can mean "at least one cell" or "more than one cell".

The term "about" or "approximately" or the symbol "~" refers to within plus or minus 10% (inclusive) range of a given value or state. Unless otherwise clear from context, all numerical values provided herein can be modified by the term about.

The term "AAV.CYP4V2" refers to a recombinant adeno-associated virus (AAV) vector comprising a polynucleotide encoding a functional CYP4V2 protein.

The term "CYP4V2 gene therapy" refers to the introduction of a functional CYP4V2 protein or a polynucleotide encoding a functional CYP4V2 protein into a cell and/or a subject. See detailed discussion in the disclosure.

The term "effective amount" or "effective dosage" or "therapeutically effective dosage" refers to an amount of a compound (e.g., a vector) and/or cells sufficient and/or suitable to effect treatment when administered to a subject in need of such treatment. The effective amount will vary depending upon the specific activity of the therapeutic agent being used, the severity of the patient's disease state, and the age, physical condition, existence of other disease states, and nutritional status of the subject. Additionally, other medication and/or treatment the patient may be receiving will affect the determination of the effective amount of the therapeutic agent to administer. See description herein for more detailed discussion.

The term "treatment" or "treating" refers to administration of a composition as disclosed herein (e.g., an AAV comprising a transgene and/or cells) to a subject for purposes including 1) preventing or protecting against the disease or condition, that is, causing the clinical symptoms not to develop; 2) inhibiting the disease or condition, that is, arresting, slowing down, ameliorating or suppressing the development of clinical symptoms; 3) relieving the disease or condition, that is, causing the regression of clinical symptoms; and/or 4) replacing and/or restoring the function loss of the diseased cells, tissue and/or organ. In some embodiments, the term "treatment" or "treating" refers to relieving the disease or condition; that is, causing the regression of clinical symptoms. In some embodiments, the term "treatment" or "treating" alternately or additionally refers to the prophylactic treatment of a subject in need thereof. The prophylactic treatment can be accomplished by providing an appropriate dose of a therapeutic agent to a subject at risk of suffering from an ailment, thereby substantially averting onset of the ailment. It will be understood by those skilled in the art that it is not always possible to distinguish between "preventing" and "suppressing", since the ultimate inductive event or events may be unknown or latent, or the patient may not be ascertained until well after the occurrence of the event or events. Therefore, as used herein, the term "prophylaxis" is intended as an element of "treatment" to encompass both "preventing" and "suppressing" as defined herein.

The term “subject” refers to an animal, such as a mammal, e.g., a human. The methods described herein can be useful in human therapeutics, pre-clinical, and veterinary applications. In some embodiments, the subject is a mammal, and in some embodiments, the subject is human.

A “variant” is a protein with sequence homology to a reference biologically active protein that retains at least a portion of the therapeutic and/or biological activity of the biologically active protein. For example, a variant protein can have at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% amino acid sequence identity compared with the reference biologically active protein. The term “biologically active protein” includes proteins modified deliberately, as for example, by site directed mutagenesis, insertions, or accidentally through mutations. A “variant” includes a “fragment”, which is a truncated form of a native or non-native biologically active protein that retains at least a portion of the therapeutic and/or biological activity.

The term “nucleic acid” is used herein to refer to all forms of nucleic acid, polynucleotides and oligonucleotides, including deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). Nucleic acids include genomic DNA, cDNA and RNA. Polynucleotides include naturally occurring, synthetic, and intentionally modified or altered polynucleotides. Polynucleotides can be single, double, or triplex, linear or circular, and can be of any length. A sequence or structure of a particular polynucleotide may be described herein according to the convention of providing the sequence in the 5' to 3' direction.

The term “sequence variant” means genes or polypeptides that have been modified compared to their native or original sequence by one or more nucleotide or amino acid insertions, deletions, and/or substitutions. Insertions can be located at either or both termini of the gene or protein, and/or can be positioned within internal regions of the nucleotide sequence or amino acid sequence. In deletion variants, one or more nucleotide or amino acid residues in a gene or polypeptide as described herein are removed. In substitution variants, one or more nucleotide or amino acid residues of a gene or polypeptide are removed and replaced with alternative residues. In one aspect, the substitutions are conservative in nature and conservative substitutions of this type are well known in the art.

As used herein, the term "therapy" or "treatment" can be applied either *in vivo* to a subject or *in vitro* in a cell.

As used herein, a plasmid is a type of a vector.

As used herein, the term "genetically repaired" or "genetic repair" refers to a cell which originally harbors a genetic defect (e.g., a mutation or a pathologic alteration) in a gene, its genetic defect having been repaired either through gene correction or disruption in the cell's genomic DNA or mRNA (herein defined as "gene editing", "gene editing therapy" or "gene correction"), or via gene transfer or supplementation of an exogenous nucleic acid molecule to the cell which expresses a functional protein corresponds the defective gene (herein defined as "gene transfer therapy" or "gene therapy").

As used herein, the term "percent sequence identity" or "sequence identity" shall be determined and calculated as follows. In calculating (percent) sequence identity, two sequences are aligned and the number of identical matches of nucleotides or amino acid residues between the two sequences is determined. The number of identical matches is divided by the length of the aligned region (i.e., the number of aligned nucleotides or amino acid residues) and multiplied by 100 to arrive at a percent sequence identity value (and rounded up to the next higher whole number (e.g., 65.01% shall be rounded up to 66% and deemed as 66% for purposes herein)). It will be appreciated that the length of the aligned region can be a portion of one or both sequences up to the full net length (without applying gap) size of the shorter sequence. To determine identical matches and calculate sequence identity between two protein encoding nucleotide sequences, any non-coding nucleotide sequence (e.g., without limitation, intron, UTR, Kozak sequence, promoter, enhancer or other regulatory sequences) shall be removed before submitting the two sequences for alignment and calculating the sequence identity. The alignment of two sequences to determine the number of identical matches of nucleotides or amino acid residues between the two sequences can be performed by using the Pairwise Sequence Alignment EMBOSS Needle which creates an optimal global alignment of two sequences using the Needleman-Wunsch algorithm (available at The European Bioinformatics Institute (EMBL-EBI) and on the World Wide Web: ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html for nucleotide alignment and ebi.ac.uk/Tools/psa/emboss_needle/ for protein alignment) and using default

parameters (For nucleotide sequence use: Matrix: EDNAFULL. Gap Open Penalty: 10. Gap Extend Penalty: 0.5. Output format: pair. End Gap Penalty: false. End Gap Open Penalty: 10. End Gap Extend Penalty: 0.5. For protein sequence use: Matrix: EBLOSUM62. Gap Open Penalty: 10. Gap Extend Penalty: 0.5. Output format: pair. End Gap Penalty: false. End Gap Open Penalty: 10. End Gap Extend Penalty: 0.5).

The term “adeno-associated virus vector” refers to a nucleic acid derived from any AAV serotype, e.g. AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12 serotype, or any other virus or serotype that shares homologous in its capsid protein sequence to the capsid protein of an AAV serotype. The term “recombinant adeno-associated virus” or “rAAV” refers to an infectious, replication-defective virus composed of an AAV protein shell encapsulating a nucleic acid molecule of interest, which is flanked on one or both sides by AAV ITRs. As used herein, the reference to a particular AAV serotype means an AAV having at least one capsid protein of that AAV serotype. For example, the term “AAV2” refers to an AAV having at least one AAV serotype 2 capsid protein.

The term “CYP4V2,” refers to Cytochrome P450 4V2 or Cytochrome P450, family 4, subfamily V, polypeptide 2 (sometimes referred to as CYP4AH1), and its orthologues in other species. Mutations in CYP4V2 have been associated with BCD (see, for example, Li *et al.*, *Am J Hum Genet.* 74:817-826, 2004) and retinitis pigmentosa (see, for example, Wang *et al.*, *PLOS ONE* 7:e33673, 2012). The full-length genomic human CYP4V2 gene is about 22,053 bp in length and can be found at, e.g., genecards.org/cgi-bin/carddisp.pl?gene=CYP4V2&keywords=CYP4V2 on the World Wide Web. As used herein, the term “hCYP4V2” refers to a human CYP4V2 gene or protein. It would be understood that hCYP4V2 and CYP4V2 can refer to a gene or protein that contains a genetic or epigenetic alteration or a gene or protein that does not contain a genetic or epigenetic alteration.

As used herein, the term “functional CYP4V2” refers to a protein, or a nucleotide molecule that, when expressed, produces a protein that is effective to provide therapeutic benefits (e.g., to ameliorate or rescue abnormal fatty acid levels (e.g., DHA level) in target cells) to an individual (e.g., an individual with a genetic or epigenetic alteration in a CYP4V2 molecule). A functional CYP4V2 molecule can correspond to a wild-type hCYP4V2 sequence,

or a naturally occurring variant thereof (e.g., a polymorphic variant; e.g., a variant that does not contain a pathologic alteration), or an optimized sequence. In some embodiments, a functional CYP4V2 molecule is a CYP4V2 molecule from another species (e.g., another mammal, such as a rodent, rabbit, dog, pig or a non-human primate) that shares a similar orthology as human CYP4V2. For example, an ortholog of a human CYP4V2 sequence is the murine mCyp4v3 sequence. In some embodiments, a functional CYP4V2 molecule is another P450 molecule (e.g., a CYP4 protein).

The term “ocular cell” refers to any cell in, or associated with the function of, the eye, including without limitation, a retina cell, a retina bipolar cell, a photoreceptor cell or a photoreceptor progenitor cell (including rod and/or cone, altogether “PRCs”), a ganglion cell, a retinal pigment epithelium (RPE) cell, a choroidal epithelial (CE) cell, a corneal epithelium cell (CEC), a choroidal cell, or a corneal cell, or an optic-nerve cell.

The term “function loss” or “dysfunction” refers to a decrease in, or loss of, cellular function (e.g., photoreceptor function, photoreceptor cell function, retinal pigment epithelium cell function, lens function, choroid function or cornea function) as compared to a normal, non-diseased cell, or compared to the other eye or the same eye at an earlier time point. As used herein, “degeneration,” “atrophy,” “disorder,” “disease,” and/or “dystrophy” can be used synonymously with loss of function. The term “increased function” means to improve the function (e.g., the function of the photoreceptors, photoreceptors cells, retinal pigment epithelium cells, choroidal cells or corneal cells), or increase the number or percentage of functional photoreceptors or cells (e.g., photoreceptors cells, retinal pigment epithelium cells, choroidal cells or corneal cells) as compared to a diseased eye (having the same ocular disease), the same eye at an earlier time point, a non-treated portion of the same eye, or the contralateral eye of the same patient.

The term “transgene” refers to a donor nucleic acid that is intended or has been introduced into a cell or organism. Transgenes include any gene, such as a gene or cDNA set forth in Table 4.

The term “pharmaceutically acceptable formulation” and “physiologically acceptable formulation” and “pharmaceutically acceptable carrier” mean a biologically acceptable

formulation, gaseous, liquid or solid, or mixture thereof, which is suitable for one or more routes of administration, in vivo delivery, in vitro delivery or contact, and can include a formulation or carrier used in therapies for other diseases (for example, gene therapy or cell therapy for other ocular diseases). A "pharmaceutically acceptable" or "physiologically acceptable" composition is a material that is not biologically or otherwise undesirable, e.g., the material may be administered to a subject without causing substantial undesirable biological effects. Thus, such a pharmaceutical composition may be used, for example in administering a protein, a polynucleotide, a plasmid, a viral vector or a nano-particle to a cell or a subject. Such compositions include, without limitation, solvents (aqueous or non-aqueous), solutions (aqueous or non-aqueous), emulsions (e.g., oil-in-water or water-in-oil), suspensions, syrups, elixirs, dispersion and suspension media, coatings, isotonic and absorption promoting or delaying agents, compatible with pharmaceutical administration or in vivo or in vitro contact or delivery. Aqueous and non-aqueous solvents, solutions and suspensions may include suspending agents, lubricating agent and thickening agents. Such pharmaceutically acceptable carriers include tablets (coated or uncoated), capsules (hard or soft), microbeads, powder, granules and crystals. Supplementary active compounds (e.g., preservatives, antibacterial, antiviral and antifungal agents, and immunosuppressant) can also be incorporated into the compositions. Pharmaceutical compositions can be formulated to be compatible with a particular route of administration or delivery, as set forth herein or known to one of skill in the art. Thus, pharmaceutical compositions include carriers, diluents, or excipients suitable for administration by various routes.

The term "crRNA" refers to CRISPR RNA, which contains both the protospacer element and additional nucleotides which are complementary to the tracrRNA.

The term "tracrRNA" refers to transactivating crRNA, which hybridizes to the crRNA and binds to a Cas9 protein activating the complex to creating double-stranded breaks at specific sites within genomic sequence.

The term "sgRNA" refers to single-guide RNA, which combines the crRNA and tracrRNA, which are separate molecules in the native CRISPR/Cas9 system in *S. pyogenes*, into a single RNA construct.

The term "PAM" refers to "protospacer adjacent motif" which is a short sequence in either strand of the genome recognized by CRISPR nucleases as a cutting site. PAM varies with the nuclease (e.g., Cas9, Cpf1, etc.). The protospacer element sequence is usually directly upstream of the PAM site.

The term "protospacer element" (also referred to as "guide RNA" or "CRISPR gRNA" or "gRNA" or g1, g2, g3, g4, g5, etc.) refers to the portion of the crRNA (or sgRNA) that is complementary to the genomic DNA target sequence.

DHA: Docosahexaenoic Acid, a polyunsaturated omega-3 fatty acid, also known as 22:6 (ω-3) or C22:6 n3.

AA: Arachidonic Acid, a polyunsaturated omega-6 fatty acid, also known as 20:4(ω-6) or C20:4 n6, or ARA.

PBS(+): phosphate buffered saline (PBS) with Calcium and Magnesium.

PBS(-): phosphate buffered saline (PBS) without Calcium or Magnesium.

DETAILED DESCRIPTION

Methods and Compositions for BCD Cellular Disease Models

Developing a proper BCD disease model and ascertaining the molecular level phenotype for BCD is critical BCD related research, development and testing of drugs and treatment options for BCD. It is also important for the study of CYP4V2 function. As outlined in the Background section herein, the clinical phenotype of BCD has been characterized, established and studied since 80 years ago, the genetic mutations causing BCD has been identified over a decade. However, there is still a gap between the clinical phenotype (e.g., crystal-like deposits in BCD patients' retina) and the underlying CYP4V2 mutations.

Prior studies on BCD have found abnormal fatty acid levels in BCD patients, including in fibroblasts, lymphocytes and serum. For example, in Lee et al., The Metabolism of Fatty Acids in Human Bietti Crystalline Dystrophy, Invest Ophthalmol Vis Sci. 2001 Jul;42(8):1707-14, the researchers used a pulse-chase method to study abnormalities in BCD patients' fibroblast and lymphocytes. BCD patient and normal control's fibroblast and lymphocytes were incubated with [(14)C]18:3n-3 or [(14)C]18:2n-6. Fibroblasts from patients with BCD showed lower conversion

of 18:3n-3, but not of 18:2n-6, into polyunsaturated fatty acids (PUFAs) than those of normal subjects. In another study (Lai et al., Alterations in Serum Fatty Acid Concentrations and Desaturase Activities in Bietti Crystalline Dystrophy Unaffected by CYP4V2 Genotypes, *Invest Ophthalmol Vis Sci* 2010;51:1092–7), the researchers used GC-MS to analyze serum fatty acid concentrations in serum samples of BCD patients and control. The study found a higher concentration of octadecanoic acid (18:0) in BCD patients' serum than that in control subjects, as well as a lower concentration of octadecadienoic acid (18:1n-9) than that in control subjects. In addition, the total monounsaturated fatty acid concentration was significantly lower in BCD than in the control. Yet in another study (Nakano et al., CYP4V2 in Bietti's Crystalline Dystrophy: Ocular Localization, Metabolism of omega-3-Polyunsaturated Fatty Acids, and Functional Deficit of the p.H331P Variant, *Mol Pharmacol* 82:679–686, 2012) which did not use BCD patient samples as study subject, the results suggested that the CYP4V2 enzyme possesses omega-hydroxylase activity toward omega-3-PUFAs.

It is important to confirm whether the abnormal fatty acid levels found in BCD patients' fibroblast and serum actually exist in BCD patients' RPE cells, which are the disease causing cells for BCD. Therefore, a BCD disease model allowing the direct investigation in BCD patients' RPE cells is desired to gain more understanding of BCD disease pathology and CYP4V2 functions, as well as to assess efficacy of potential treatment options. However, given RPE's location and rarity of BCD, it is not practical to obtain native RPE cells from BCD patients.

The present disclosure provides BCD cellular models and methods to generate BCD cellular models. BCD cellular models consist of BCD patient-specific stem cells (including without limitation, induced pluripotent stem cells (iPSCs), embryonic stem (ES) cells, somatic (or adult) stem cells, mesenchymal stem cells (MSC)) and ocular cells (including without limitation, RPE cells, photoreceptor (rod or cone) cells, photoreceptor progenitor cells, corneal epithelial cells, lens cells and/or choroid cells) derived from any stem cell of a BCD patient. In addition to patient-specific stem cells, BCD cellular model can also be generated by creating artificial CYP4V2 mutations in cells of individuals not having BCD and such cells can be ES

cells, iPS cells or other stem cells, or any cells that can be reprogrammed into stem cells, or any ocular cells (whether derived from a stem cell or not).

Induced pluripotent stem cell technology provides an alternative for disease modeling to animal models. However, not all diseases have been successfully modeled using iPSC. (Urbach, A., Bar-Nur, O., Daley, G. Q. & Benvenisty, N. Differential Modeling of Fragile X Syndrome by Human Embryonic Stem Cells and Induced Pluripotent Stem Cells. *Cell Stem Cell* 6, 407-411 (2010)). In addition, given the reported fatty acid anabolism associated with BCD, it was unclear whether BCD patient-specific iPS or patient-specific iPS-RPE cells can be generated by iPS technology.

A. Inducing Pluripotency

Methods of making induced pluripotent stem cells (iPSCs) are known in the art. Virtually all types of somatic cells can be used as the source cell for iPSC reprogramming. Briefly, iPSCs can be made by introducing a particular set of proteins (e.g., nucleic acids encoding a particular set of proteins or by direct delivery of proteins) into cells. It would be understood by the skilled artisan that one exemplary, non-limiting method is by introducing one or more transgenes encoding one or more of OCT4, SOX2, KLF4, and/or c-MYC (e.g., the “Yamanaka factors”). In some embodiment, the reprogramming uses all four transcription factors. In some embodiment, one, two or three transcription factors can be used. Li et al., *Stem Cells*, 2009;27:2992–3000. Zhu et al., *Cell Stem Cell* 2010;7: 651–655. In some embodiments, iPSCs can be generated by direct delivery of the reprogramming proteins. Kim et al., *Cell Stem Cell*. 2009;4(6):472–6. The Examples section provides methods for producing iPSCs using non-integrating methods, e.g., by Sendai virus (Example 1), or by episomal methods (Example 2). Any method of producing iPSCs, however, is contemplated within the scope of this disclosure.

Various methods (e.g., Sendai virus, episomal method, with or without small molecules) can be used to generate iPSCs, see Examples section, see also, for example, Hubbard et al., *J. Vis. Exp.*, 2014, 92:52009. In addition, methods of making iPSCs from a number of different cell types are known in the art. See, for example, Hayashi et al., 2012, *PLoS One*, 7(9): e45435; Poon et al. 2015, *PLoS One*, 10(7): e0131288; Lamba et al. 2010, *PLoS One*, 5(1): e8763.

Typically, iPSCs express detectable levels of at least one marker including, without limitation, Oct-4, Sox-2, SSEA4, TRA-1-60, TRA-1-81, AP and/or NANOG.

Any type of stem cells can be used in generating the BCD cellular model described herein including without limitation, induced pluripotent stem cells (iPSCs), hematopoietic stem cells (HSCs), embryonic stem (ES) cells, mesenchymal stem cells, adult stem cells, or tissue-specific stem cells. Stem cells for use in the methods described herein can be pluripotent, multipotent, or totipotent stem cells.

As used herein, the term “pluripotent” refers to a cell capable of at least developing into one of ectodermal, endodermal and mesodermal cells. In one embodiment, the term “pluripotent” refers to cells that are totipotent and multipotent. As used herein, the term “totipotent” cell refers to a cell capable of developing into all lineages of cells. As used herein, the term “multipotent” refers to a cell that is not terminally differentiated. The pluripotent cells of the disclosure herein can be any stem cells or produced from non-pluripotent cells, such as fibroblasts, using induction, de-differentiation and nuclear transfer methods known in the art. The pluripotent cells described herein, whether stem cells or produced from non-pluripotent cells, can be from a subject having BCD or having CYP4V2 mutations, or from a healthy individual not having BCD for use as control or for use to create artificial CYP4V2 mutations.

Virtually any type of cells can be reprogrammed into iPS cells. See discussion in the sub-section entitled “Origination of Cells” herein.

B. Differentiation of iPSCs

BCD patient iPS cells were differentiated into iPS-RPE cells (or another type of ocular cells (e.g., iPS-CEC, iPS-CE cells or iPS-PRC). Methods for differentiating iPSCs into RPE cells or another type of ocular cell (e.g., CEC and PRC) are known. See, for example, the Examples section; Hayashi et al., 2012, PLoS One, 7(9):e45435; Songstad, et al., Investigative Ophthalmology & Visual Science December 2015, Vol.56, 8258-8267; and Lamba et al., PLoS One. 2010 Jan 20;5(1):e8763. For example, induced pluripotent stem cells (iPSCs) reprogrammed from cells can be produced and further differentiated into, for example, RPE cells (referred to herein as “iPS-RPE”), corneal epithelial cells (referred to herein as “iPS-CEC”),

photoreceptor cells (or photoreceptor progenitors; referred to herein as "iPS-PRC") or iPS-choroidal endothelial (CE) cells (referred to as "iPS-CE")

Differentiated cells, e.g., iPS-RPE cells, were tested for biochemical functions (as described herein and in the Examples section) to assess its biochemical defects/abnormalities as compared to iPS-RPE cells of healthy controls.

The iPS-RPE cell lines produced as described herein exhibit the morphology (e.g., pigmentation and hexagonal shape) and/or expresses one or more biomarkers that are indicative of RPE cells. Biomarkers for RPE cells (and iPS-RPE cells) are known and include, without limitation, one or more of RLBP1 (a/k/a CRALBP), RPE65, BESTROPHIN-1, MITF, VINCULIN, LRAT, RDH5, PAX6, MERTK, TYR, and/or ZO-1, and can be used to determine or confirm that RPE differentiation has taken place. Similarly, biomarkers for CECs (and iPS-CECs) and PRCs (and iPS-PRCs) are known and include, for example, cytokeratin 12 and cytokeratin 3 for corneal epithelial cells; and Crx for photoreceptors, recoverin for rods and cones, and Nrl for rods.

Through iPS reprogramming and RPE differentiation methods as described in Examples section, BCD patient-specific iPS and iPS-RPE cells were successfully generated.

C A Biochemical Assay to Identify Biochemical Defects/Abnormalities and Cell Viability Assay to Assess RPE Atrophy in BCD Patients' iPS-RPE Cells

A set of biochemical assays were developed and used to assess and determine the phenotype in the BCD patient-specific iPS-RPE cells.

First, a more complete list of fatty acids was included in our biochemical assay. In a prior study has identified abnormal serum fatty acid levels in BCD patients, the samples were tested for the following fatty acids, 16:0, 16:1, 18:0, 18:1n-9, 18:2n-6, 18:3n-3, 20:3n-6, 20:4n-6, 22:5n-3, 22:6n-3, 24:0 and 24:1. The study found a higher concentration of octadecanoic acid (18:0) in BCD patients' serum than that in control subjects, as well as a lower concentration of octadecadienoic acid (18:1n-9) than that in control subjects. To determine whether the same fatty acids abnormalities exist in BCD patient-specific iPS-RPE cells and whether there are more abnormalities in other fatty acids, a biochemical assay encompassing more fatty acids was developed (See Table 2) using LC-MS.

Furthermore, to determine whether the BCD patient-specific iPS-RPE cells harbor other abnormalities in addition to fatty acids, other lipid species were included in the assay, including, ceramides (Cer), sphingomyelins (SM), and sphingosine and sphinganine (SOSA), to analyze the phenotype in BCD disease model and to determine the biochemical functions of the CYP4V2 protein. See Table 2 for a list of different species and compounds included in the biochemical assay used to test the BCD patient-specific iPS-RPE cells.

Surprisingly, the testing results (see Examples section) showed that BCD patient-specific iPS-RPE cells have a different fatty acids abnormality profile from those found in BCD patients' serum.

The eye is the light sensing organ of the human body. BCD begins with RPE atrophy, which in turn causes photoreceptor death and vision loss. A key function of the RPE is light absorption (Strauss, 2005, The retinal pigment epithelium in visual function. *Physiol Rev* 85:845-81). Environmental light exposure may affect the development and progression of human retinal degenerations such as age-related macular degeneration (AMD) and retinitis pigmentosa (RP). The use of light exposure in ocular disease models is a suitable model system to study retinal degenerations. Light exposure including blue light exposure have been widely used in retinal research (Dual roles of polyunsaturated fatty acids in retinal physiology and pathophysiology associated with retinal degeneration, Masaki Tanito & Robert Anderson (2009) *Clinical Lipidology*, 4:6, 821-827. Seko, et al., *Graefes Arch Clin Exp Ophthalmol*. 2001 Jan; 239 (1): 47-52. Blue light-induced apoptosis in cultured retinal pigment epithelium cells of the rat. Narimatsu, et al., *Exp Eye Res*. 2015 Mar;132:48-51. Blue light-induced inflammatory marker expression in the retinal pigment epithelium-choroid of mice and the protective effect of a yellow intraocular lens material in vivo). Blue light exists in environmental light such as sunlight and artificial lighting (e.g., office lighting), as well as from electronic display devices such as TVs, monitors, smartphones, notebooks and tablets (Moon, et al., Blue light effect on retinal pigment epithelial cells by display devices, *Integr Biol (Camb)*. 2017, 22;9(5):436-443. doi: 10.1039/c7ib00032d).

In this study, cell viability assay discovered RPE atrophy in BCD cellular model. Exposure to (blue) light caused significantly higher cell death in BCD patients' iPS-RPE samples

than in controls' samples. Clinical phenotype of BCD (i.e., RPE atrophy) is evident in BCD cellular model. AAV.CYP4V2 demonstrated efficacy in rescuing RPE atrophy in BCD cellular model.

D. Applications of BCD Cellular Model

In addition to assessing cellular level phenotype associated with BCD, the BCD Cellular Model can be used for other applications of a disease model, including without limitation, drug screening, developing therapeutic agents or devices, determining dosage ranges, safety and toxicity testing, testing different formulations for BCD or other conditions related to CYP4V2, or the study of CYP4V2 functions and uses, including without limitation, developing and screening drugs comprising or expressing CYP4V2 protein, e.g., CYP4V2 gene therapy. Further, the BCD patient-specific iPSC-RPE (and other BCD patient-specific stem cell derived ocular cells, including without limitation, iPSC-photoreceptor cells, iPSC-corneal cells) can be used as cell therapy, either in unmodified form or after genetic repair (e.g., by gene transfer or gene editing as described herein). The Examples section provides examples of non-limiting examples of applications of BCD Cellular Model.

E. Methods of Screening Compounds

Significantly, the iPSC-RPE cell lines described herein can provide human cellular disease models (e.g., BCD, retinitis pigmentosa, IRD). Such iPSC-RPE cells, iPSC-CEC cells or iPSC-PRC cells, which can be collectively referred to as "iPSC-ocular cells," can be used for diagnosing, prognosing, predicting the disease onset, severity and progression rate of a BCD patient or of a retinitis pigmentosa patient or of a patient having another type of inherited retinal disease. For example, such iPSC-ocular cell lines also can be used to screen test compounds for those that might have therapeutic efficacy for treating or preventing diseases associated with genetic or epigenetic alterations in a CYP4V2 nucleic acid (e.g., BCD).

The pluripotent cells described herein, particularly those produced from a subject having a genetic or epigenetic alteration in CYP4V2 or a subject that has an eye disease (e.g., BCD), can be used as a research tool in methods to identify compounds that are therapeutic candidates for treatment, diagnosis, prognosis or prevention of the eye disease (e.g., BCD). It would be understood that the test compounds can be any type of compounds. They may be of natural

origin or may have been produced by chemical synthesis. They may be a library of structurally defined chemical compounds, of non-characterized compounds or substances, or a mixture of compounds. It would be appreciated by a skilled artisan that test compounds can be, without limitation, nucleic acids or analogs thereof, polypeptides or analogs thereof, antibodies, chemicals, and small molecules.

The cells described herein, in the presence or absence of a test compound, can be evaluated for their ability to grow and function in an animal model (e.g., in the eye of an animal model) and for their propensity, or lack of propensity, to form tumors. A number of methods can be used to evaluate the cells including, without limitation, PCR techniques, immunoassays, and/or lipid / fatty acid metabolism analyses.

Methods and Compositions for Cell Therapies

As discussed herein, CYP4V2 gene therapy demonstrated efficacy in correcting the biochemical abnormalities in BCD patient-specific iPS-RPE cells. However, a prerequisite for gene therapy to work in vivo is that the subject still has some RPE and photoreceptor cells remaining in the eye being treated. For late-stage BCD patients who have few or no RPE cells or photoreceptor cells left in the eye, cell therapy can be used as an alternative or in combination with gene therapy as a treatment option.

Cell therapy involves transplanting new cells to replace the dead or degenerated cells. For BCD, the new cells can be RPE cells, photoreceptor cells (cone and/or rod), photoreceptor progenitor cells, choroid cells, corneal epithelial cells, lens cells or other types of ocular cells, depending on which type of cells have shown degeneration and need a replacement in the subject. The following description and Examples herein used iPS-RPE cells to illustrate the methods and processes. They can be applied to other type of ocular cells.

Cell therapy for BCD and other types of ocular diseases including without limitation, inherited retinal diseases (IRD), retinitis pigmentosa (RP), macular degeneration (including age-related macular degeneration (AMD)), can be categorized as follows.

(1) Allogenic transplantation:

In one embodiment, RPE cells, PRCs, CECs, CE cells and other ocular cells derived from embryonic stem cells (ESC) or iPSCs from a healthy donor can be used in allogenic transplantation as cell therapy for BCD. It involves differentiating a healthy ESC or iPSC from a healthy individual (i.e., one without CYP4V2 mutations) into RPE cells and transplanting such ESC-RPE cell to a BCD patient's eye. Methods to reprogram iPSC and differentiate ESC or iPSC to RPE are provided herein the Examples section. In a prior study, embryonic stem cell (ESC) derived RPE cells have been used to treat age-related macular degeneration (AMD), see, Schwartz et al., Investigative Ophthalmology & Visual Science April 2016, Vol.57, ORSFC1-ORSFC9. The pros of an allo-graft or allogenic transplantation is that it is less expensive than autologous transplantation because one common source can be used to treat multiple patients. However, it has significant downside such as immune rejection by the host subject may significantly affect its efficacy and duration. In addition, it requires long-term immunosuppressant which may lead to severe systemic side effects. Finally, the use of ESC can give rise to ethical concerns.

(2) Autologous transplantation without genetic repair:

In one embodiment, autologous cells can be used in cell therapy for BCD. One such autologous source is iPS cells and iPS-RPE cells derived from a BCD patient, which can be transplanted to such BCD patient's eye. BCD is a relatively late onset disease. Symptom in BCD patients are usually developed in the 2nd, 3rd or even 4th decade of life. In addition, iPS reprogramming process have some degree of "reset the clock" effect on the iPS cells and cells derived from the iPS cells. Therefore, the iPS-RPE cells and other iPS-ocular cells derived a BCD patient can be used as a cell therapy for transplantation to the BCD patient even without any genetic repair of the CYP4V2 mutations in the iPS-RPE cells. iPS reprogramming and RPE differentiation methods are provided in the Examples section herein. As a precaution, whole genome sequencing can be performed to compare the genomic DNA in the iPS or iPS-RPE cells and the genomic DNA in the source cell (e.g., fibroblast or blood cell) whether there is any disease causing mutations was created during the iPS reprogramming and RPE differentiation process.

(3) Genetically Repaired Patient Autologous Cells for Cell Therapy for BCD and other types of IRDs and RPs

The disclosure herein provides methods and compositions for generating genetically repaired autologous cells for cell therapy. As used herein, "genetically repaired" or "genetic repair" refers to correction of the CYP4V2 mutations through either gene editing of the patient's genome (e.g., directly on the chromosome using, e.g., CRISPR/Cas9, CRISPR/Cpf1, Zinc Finger, TALEN), or through gene transfer of a healthy copy of the CYP4V2 gene (cDNA, RNA or other form) into the patient cell, which typically does not integrate into the genome (e.g., the CYP4V2 gene therapy as described here) or correcting or compensating for the defective mRNA in the patient's cell.

As a disease caused by genetic mutations, the autologous cells for use in cell therapy for BCD or another IRD or RP ideally should have its genetic defects (i.e., the CYP4V2 mutations) and/or its dysfunctional CYP4V2 protein repaired before transplantation. In one embodiment, such genetic repair can be achieved by gene transfer therapy as discussed herein, including without limitation, an AAV-mediated gene therapy transfer of a nucleic acid sequencing encoding and expressing a functional CYP4V2 protein. Compositions and methods of CYP4V2 gene transfer therapy are provided here in, see detailed description herein and the Examples section. BCD patient-specific source cell, iPS or iPS-RPE cells can be treated by AAV.CYP4V2 (as provided herein), followed by iPS reprogramming and/or RPE differentiation (if applicable) and verification of improved biochemical functions (as provided herein), and then be transplanted to the same patient's eye. In another embodiment, such genetic repair can be achieved by gene editing, e.g., correcting the CYP4V2 mutation(s) in the genome or RNA in the cells of the BCD patient. In addition to being applied in vitro as a part of a cell therapy, such gene editing can also be applied directly in vivo as a gene therapy. Such gene editing can be performed on the patient's source cell (e.g., fibroblast or blood cell), iPS, iPS-RPE or other types of iPS-ocular cells. iPS reprogramming and RPE differentiation to generate the patient-specific iPS and iPS-RPE can be performed either before or after the genetic repair (e.g., gene transfer therapy or gene editing).

The disclosure herein provides compositions and methods to correct a CYP4V2 mutation through gene editing. The description in the Examples section herein illustrates the compositions and methods using a CRISPR/Cas9 construct to correct the c.802-8_810del17insGC mutation, the most common mutation among BCD patients. It can also apply to other gene editing methods (e.g., CRISPR/Crp1, TALEN, Zinc finger) and other IRD mutations (e.g. without limitation, other CYP4V2 mutations in Table 1) in combination with methods known in the art.

The most common CYP4V2 mutation among BCD patients is c.802-8_810del17insGC (referring to a 17 base deletion with two bases (GC) inserted in the place starting 8 bases from the end of intron 6 of CYP4V2 gene, also referred to as IVS6-8 del/insGC, See SEQ ID NO: 46 showing sequence of the human CYP4V2 genomic DNA region comprising the c.802-8_810del17insGC mutation and SEQ ID NO: 47 showing the corresponding wild-type sequence. The c.802-8_810del17insGC mutation is illustrated in the following sequence which shows human CYP4V2 intron 6-exon 7 junction. Intron 6 sequence is shown in lower case and exon 7 sequence in CAP letters. The 17 bps deletion and the insertion of GC are in brackets): caa aca gaa gca tgt gat tat cat tca aa (tca tac agG TCA TCG CT) (GC) GAA CGG GCC AAT GAA ATG AAC GCC AAT GA) (SEQ ID NO: 46) resulting in the predicted skipping of exon 7. (Xiao et al., Biochem Biophys Res Commun. 409:181-6, 2011; Meng et al., 2014, Mol. Vis., 20:1806-14; Wada et al., Am J Ophthalmol. 139:894-9, 2005; Jiao et al., European Journal of Human Genetics (2017) 25, 461-471). A recent study estimated that the age of the c.802-8_810del17insGC mutation was to be 1,040-8,200 generations in the Chinese and 300-1100 generations in the Japanese populations. See Jiao et al., European Journal of Human Genetics (2017) 25, 461-471.

Cell therapy (also known as cellular therapy or cytototherapy) can be used as described herein to treat or prevent an eye disease in a subject. As described herein, BCD, certain RP, IRD and other eye diseases referred to herein are associated with a genetic or epigenetic alteration in a CYP4V2 nucleic acid sequence.

Cell therapy generally involves injecting, implanting, transplanting, or otherwise delivering a composition that includes cells to a subject (e.g., into a tissue or organ of a patient

(e.g., an eye)). The methods described herein are unique because they allow genetically repaired autologous cell therapy of a subject having an eye disease.

Methods are described herein that include obtaining cells from a subject having an eye disease (e.g., associated with a genetic or epigenetic alteration in a CYP4V2 nucleic acid sequence) and repairing the mutation(s) within the CYP4V2 nucleic acid (e.g., DNA or RNA) using, for example, gene editing, or repairing via delivering a nucleic acid sequence encoding a functional CYP4V2 protein (e.g., gene transfer). The cells can be made pluripotent (e.g., by inducing pluripotency, e.g., to make iPSCs) and be differentiated into one or more ocular cells (e.g., iPS-RPE, iPS-CECs, iPS-PRCs) prior to administration back into the subject (e.g., into the eye of the subject). It would be appreciated that the cells can be genetically repaired prior to or after being made pluripotent, or after being differentiated into the ocular cells.

A. Origination of Cells

In some instances, autologous cells (e.g., subject (e.g., patient) -specific cells) can be used in the cell therapy methods described herein. For example, cells such as fibroblasts or peripheral blood mononuclear cells (PBMCs) can be obtained from a subject and used to produce iPSCs as described in the Examples section. Virtually all types of cells can be used to generate iPSCs and therefore can be used as source cells. In some instances, cells obtained from urine (see, e.g., Zhou et al., 2012, Nat. Protoc., 7:2080-9) or hair follicles or dermal papilla cells (see, e.g., Muchkaeva et al., 2014, Acta Naturae, 6:45-53) can be used to produce iPSCs.

B. Inducing Pluripotency

Methods of making induced pluripotent stem cells (iPSCs) are known in the art. Briefly, iPSCs can be made by introducing a particular set of proteins (e.g., nucleic acids encoding a particular set of proteins) into cells. It would be understood by the skilled artisan that one exemplary, non-limiting method is by introducing one or more transgenes encoding OCT4, SOX2, KLF4, c-MYC (e.g., the “Yamanaka factors”). In some embodiment, the reprogramming uses all four transcription factors. In some embodiment, one, two or three transcription factors can be used. Li et al., Stem Cells, 2009;27:2992–3000. Zhu et al., Cell Stem Cell 2010;7: 651–655. In some embodiments, iPSCs can be generated by direct delivery of the reprogramming proteins. Kim et al., Cell Stem Cell. 2009;4(6):472–6. The Examples section provides method

for producing iPSCs using non-integrating methods, e.g., by Sendai virus (Example 1), or by episomal methods (Example 2). Any method of producing iPSCs, however, is contemplated within the scope of this disclosure.

Various methods (e.g., Sendai virus, episomal method, with or without small molecules) can be used to generate iPSCs, see Examples section, see also, for example, Hubbard et al., J. Vis. Exp., 2014, 92:52009. In addition, methods of making iPSCs from a number of different cell types are known in the art. See, for example, Hayashi et al., 2012, PLoS One, 7(9): e45435; Poon et al. 2015, PLoS One, 10(7): e0131288; Lamba et al. 2010, PLoS One, 5(1): e8763. Typically, iPSCs express detectable levels of at least one marker including, without limitation, Oct-4, Sox-2, SSEA4, TRA-1-60, TRA-1-81, AP and/or NANOG.

Any type of stem cells can be used in the cell therapy methods described herein including without limitation, induced pluripotent stem cells (iPSCs), hematopoietic stem cells (HSCs), embryonic stem (ES) cells, mesenchymal stem cells, adult stem cells, or tissue-specific stem cells. Stem cells for use in the methods described herein can be pluripotent, multipotent, or totipotent stem cells.

As used herein, the term “pluripotent” refers to a cell capable of at least developing into one of ectodermal, endodermal and mesodermal cells. In one embodiment, the term “pluripotent” refers to cells that are totipotent and multipotent. As used herein, the term “totipotent” cell refers to a cell capable of developing into all lineages of cells. As used herein, the term “multipotent” refers to a cell that is not terminally differentiated. The pluripotent cells of the present invention can be any stem cells or produced from non-pluripotent cells, such as fibroblasts, using induction, de-differentiation and nuclear transfer methods known in the art. The pluripotent cells described herein, whether stem cells or produced from non-pluripotent cells, can be from a subject having BCD or having CYP4V2 mutations or a healthy individual.

iPSCs can be characterized by one or more of the following: a. the unique morphology of iPSC; b. one or more pluripotency markers, such as Oct-4, Sox-2, SSEA-4, TRA-1-60, TRA-1-81, Nanog and AP; c. the ability to differentiate into the desired cell type (e.g., RPE cells), and/or d. a teratoma assay. Not all of the above are necessary for characterizing iPSCs and validating pluripotency (e.g., teratoma; see, e.g., Buta et al., 2013, Stem Cell Res., 11(1):552–562).

C. Gene Editing

A number of gene editing technologies can be used in the methods described herein to repair a genetic or epigenetic alteration present in the CYP4V2 nucleic acid of a subject. Gene editing can be performed using any number of technologies including clustered regularly interspaced short palindromic repeats (CRISPR) technology (see, for example, US Patent Nos. 8,697,359; 8,889,418; 8,999,641; and US 2014/0068797), transcription activator-like effector nucleases (TALEN) technology (see, for example, Li et al., 2011, *Nucleic Acids Res.*, 39(14):6315-25) or zinc-finger nuclease technology (see, for example, Wright et al., 2005, *The Plant J.*, 44:693-705).

To accomplish gene editing using CRISPR technology, nucleic acids encoding a nuclease (e.g., oftentimes a Cas9 nuclease but other nucleases (e.g., other Cas nucleases, e.g., Cpf1, or non-Cas nucleases) also can be used) can be incorporated into one or more vectors and administered to a subject as described herein. Simply by way of example, the cells described herein (e.g., subject cells prior to reprogramming to iPSCs, subject iPSCs prior to differentiation into RPE, corneal epithelial cells or photoreceptor cells, or after differentiation into RPE, corneal epithelial cells or photoreceptor cells (referred to herein as “iPSCs-RPE,” “iPSC-CEC,” or “iPSC-PRC”)) can be transduced or transfected with one or more constructs (e.g., vectors, RNP, mRNAs) containing and/or encoding at least one guide RNA (gRNA), at least one CRISPR-associated protein (e.g., Cas9 or Cpf1), and at least one donor template nucleic acid. In some embodiments, the donor template nucleic acid is not required, e.g., when the genetic repair is achieved through knock out.

Similarly, to accomplish gene editing using TALEN technology, a nucleic acid encoding a TALEN (e.g., dimeric transcription factor / nuclease) can be incorporated into a vector and administered to a subject as described herein. Likewise, to accomplish gene editing using zinc-finger nuclease technology, a nucleic acid encoding a custom DNA endonuclease (e.g., a heterodimer in which each subunit contains a zinc finger domain and a FokI endonuclease domain) can be incorporated into one or more vectors and administered to a subject as described herein.

The components necessary to perform each of these technologies are available commercially and are customizable to the particular target sequence(s). See, for example, Caribou Biosciences; GenScript, CRISPR Therapeutics; Editas Medicine; Collectis BioResearch; Life Technologies; Sangamo BioSciences; or Sigma Aldrich Chemical Co.

Under the appropriate circumstances, gene editing can occur such that the genetic or epigenetic alteration in a subject's CYP4V2 nucleic acid is repaired and as a result a functional CYP4V2 protein is expressed. A CYP4V2 nucleic acid sequence has been repaired when the presence of the CYP4V2 nucleic acid (e.g., the CYP4V2 mRNA) is restored, the presence of the CYP4V2 protein is restored, or the function of the CYP4V2 protein is restored. Similarly, "repaired," or "corrected," can refer to a restoration of the affected sequence (e.g., the genetic or epigenetic alteration) to the wild type sequence or to another non-mutant sequence as described herein.

There may be some instances when it is desirable to introduce, using gene editing, one or more mutations into a cell (e.g., in the CYP4V2 nucleic acid). This is a way in which a cellular model of disease (e.g., BCD) can be created. For example, gene editing can be performed on embryonic stem cells (ES cells) to create cell lines with artificial CYP4V2 mutations, which then can be differentiated into RPE cells. Alternatively, gene editing can be performed on iPS cell lines from a healthy subject (e.g., a non-BCD subject) or on an RPE cell line (e.g., ARPE-19 cell line) to create CYP4V2 mutant iPS or RPE cell lines.

In some instances, it is desirable to screen the cells (e.g., using whole genome sequencing) after the gene editing steps are complete to confirm that the targeted mutation has been repaired and that no significant off-target editing occurred.

CRISPR and the CRISPR-associated protein 9 (Cas9), known as CRISPR-Cas9, consisting of an RNA-guided nuclease (Cas9) and a guide RNA, generates site-specific DNA breaks, which are repaired by endogenous cellular mechanisms. Possible outcomes of the approach include mutating a specific site through mutagenic non-homologous end-joining (NHEJ), creating insertions or deletions (indels) at the site of the break, and precise change of a genomic sequence through homologous recombination (HR) using an exogenously introduced donor template. The CRISPR guide RNA is composed of two RNAs termed CRISPR targeting

RNA (crRNA, also referred to herein as CRISPR RNA) and trans-activating crRNA (tracrRNA). The crRNAs are typically about 20 nucleotides (nt) long. It hybridize to a target DNA sequence by Watson-Crick base pairing and guide the Cas endonuclease to cleave the target genomic DNA.

To genetically repair the most common CYP4V2 mutation via gene editing, various CYP4V2 mutation CRISPR correction constructs were developed (See the Example section). CRISPR was used because it is simpler to implement and edits at higher efficiency than other forms of gene editing, such as TALENs and zinc finger nucleases. The CRISPR constructs contain optimized and in vitro validated gRNA sequences and different construct options that can be readily used to correct the c.802-8_810del17insGC mutation in BCD patient cell lines, resulting in genetically repaired cells that can be used in cell therapy, including without limitation, autologous cell therapy, for BCD.

CRISPR gene editing therapy involves the use of a CRISPR associated protein (Cas) which is a nuclease and a CRISPR guide RNA. The role of the CRISPR guide RNA is to guide Cas to the sequence that is targeted by the CRISPR guide RNA via a protospacer element contained in the CRISPR guide RNA that is complementary (or specific to) the target sequence. For Cas (e.g., Cas9 or Cpf1) to bind to and cleaves at or close to the target sequence, a protospacer adjacent motif (PAM) sequence also needs to be present. A PAM sequence is a short stretch of DNA (typically 2-6 nucleotides) that serves as a binding signal for Cas. Different Cas can have different PAM and cleavage pattern. For example, for *Streptococcus pyogenes* Cas9 (SpCas9), the canonical PAM sequence is NGG. For *Staphylococcus aureus* (SaCas9), PAM sequence is NGRRT or NGRRN. For *Neisseria meningitidis* (NM) and *Treponema denticola* (Td), the PAM sequence is NNNNGATT and NAAAAC, respectively. Engineered or mutated Cas can also result in altered PAM sequence. For example, SpCas9 VQR variant (D1135V, R1335Q and T1337R)'s PAM sequence is NGAN or NGNG. SpCas9 EQR variant (D1135E, R1335Q and T1337R)'s PAM sequence is NGAG. SpCas9 VRER variant (D1135V, G1218R, R1335E and T1337R)'s PAM sequence is NGCG. For Cpf1, the PAM sequence is TTTN. Typically Cas generates a double-stranded break (DSB) but altered Cas can result in a single-stranded break (e.g., SpCas9 Nickase (Cas9n D10A)) or no break (dCas9).

Whereas Cas9 generates blunt ends 3 nt upstream of the PAM site, Cpf1 cleaves in a staggered fashion, creating a 5 nucleotide 5' overhang 18-23 bases away from the PAM.

The CRISPR guide RNA for Cas9 typically comprises a CRISPR RNA (crRNA) and a trans-activating crRNA (tracrRNA). The crRNA comprises a protospacer element sequence that is designed to be complementary (or specific) to a targeted sequence within or close to the gene targeted for correction, disruption or replacement, and a sequence that corresponds to a complementary region of the tracrRNA. The tracrRNA which comprises a region that is complementary to corresponding region of the crRNA and a sequence which interacts with the CRISPR-associated protein 9 (Cas9). No tracrRNA is required for Cpf1.

The length of protospacer element is typically about 20 nucleotides. Longer or shorter protospacer element sequence (about 16-24 nt) can also be used. The protospacer element can be 100% complementary to the target sequence or can contain mismatches to the target sequence. In some embodiments, a "G" nucleotide can be optionally added at the start of the protospacer element sequence.

After a DNA molecule is cleaved by Cas, it can be repaired by one of two ways. An error-prone non-homologous end joining (NHEJ) repair can result in an indel mutation that can disrupt protein function encoded by the gene. NHEJ can be used to create artificial mutations in a cell line. In some embodiments, it can be used to create mutations in the CYP4V2 gene (e.g., an indel in an exon or a splice acceptor region) of a cell line (e.g., an ES cell, an iPS cell or an ARPE-19 cell line) with no endogenous CYP4V2 mutations and thereby generating a disease cellular model (e.g., a BCD cellular model). In addition, two more CRISPR guide RNAs can be used together to knock out a targeted region of a target gene or the entire target gene thereby generating a knockout model. In some embodiments, CRISPR based gene silencing is used to disrupt (or silence) or defective gene, e.g., in treating a dominant genetic disease. During gene silencing, the cell attempts to repair the broken DNA, but NHEJ often does so with errors that disrupt the gene hence effectively silencing it. In some embodiments, NHEJ may also result in correction of a mutation, e.g., especially when the mutation is a single nucleotide variation or of no more than about 10 nucleotides. Alternatively, if a donor nucleic acid sequence is available, the DNA break can be repaired by homology-directed repair (HDR) for correction or

replacement of the target gene. A donor nucleic acid sequence can be provided in the form of a single-stranded DNA (ssDNA), or a single-stranded oligo DNA nucleotide (ssODN) or a vector. In some embodiments, the donor nucleic acid sequence is no more than about 1kb, 800bp, 600bp, 500bp, 400bp, 300bp, 280bp, 260bp, 240bp, 220bp, or 200bp for a donor nucleic acid sequence provided in a ssODN. In some embodiments, the donor nucleic acid sequence is no more than about 25kb, 20kb, 15kb, 10kb, 9kb, 8kb, 7kb, 6kb, 5kb, 4.5kb, 4kb, 3.5kb, or 3kb for a donor nucleic acid sequence provided in a vector. In some embodiments, a donor nucleic acid sequence is symmetrical. In some embodiments, a donor nucleic acid sequence is asymmetrical. In some embodiments, the length of a donor nucleic acid sequence can be adjusted for higher HDR rate. In some embodiments, if the PAM targeted by the Cas used in the CRISPR gene editing is also present in the donor nucleic acid sequence, it can be mutated (change to a different nucleotide) so that the PAM no longer exists in the donor nucleic acid sequence to avoid the donor template or the DNA sequence repaired by the donor template being cleaved and destroyed by Cas. In addition to correcting or replacing a mutated or defective gene or a portion thereof, HDR can also be used to create artificial mutation(s) in the CYP4V2 gene (e.g., inserting mutation in an exon or a splice acceptor region) of a cell line (e.g., an ES cell, an iPS cell or an ARPE-19 cell line) with no endogenous CYP4V2 mutations and thereby generating a disease cellular model (e.g., BCD cellular model).

The CRISPR guide RNA and Cas used in CRISPR gene editing therapy can be provided in a vector (e.g., a plasmid (e.g., pX330, pX458, pX459), a recombinant AAV vector or a recombinant lentivirus vector) or an mRNA encoding such component(s) and/or RNA and protein form.

The donor template can be provided in a ssDNA (e.g., ssODN) or cloned in a plasmid or other type of vectors (e.g., an AAV vector (e.g., AAV2 or AAV6) for use in HDR.

Various compositions and methods can be used to improve the on-target editing or repair efficiencies and/or to lower the potential off-target. For example, different Cas (e.g., Cas9 or Cpf1) or Cas of different species (e.g., SpCas9, SaCas9, NMCas9) or variants (SpCas9, SpCas9 VQR) can be used to broaden the PAM selections available for a target sequence thereby enhancing specificity. If a target sequence region lacks the NGG PAM site for SpCas9 but is

AT-rich, Cpf1 can be considered instead. Cas9 nickase (e.g., Cas9 D10A) only generates a single-strand break in the target DNA and therefore requires two pairing CRISPR guide RNAs to generate a double-strand break. This requirement dramatically increases target specificity, since it is unlikely that two off-target nicks will be generated within close enough proximity to cause a DSB. Furthermore, asymmetrical donor template may enhance HDR rate. Catalytically inactive dCas9 does not cut target DNA but can still attain a sequence replacement without any of the error-prone repair that normally accompanies Cas9 cutting. See, Richardson et al., *Nature Biotechnology* 34, 339–344 (2016).

Achieving targeted gene correction and in the meantime avoiding or minimizing off-target editing are the two objectives of gene editing. Prior research has revealed the off-target mutations caused by gene editing technologies, including without limitation, CRISPR and TALEN, see, e.g., Tsai et al, *Nature Biotechnology* 33, 187–197 (2015); Wang et al., *Nature Biotechnology* 33, 175–178 (2015); Wu, W.H. et al. CRISPR repair reveals causative mutation in a preclinical model of retinitis pigmentosa. *Mol. Ther.* 24, 1388–1394 (2016). For gene editing used in vivo, or in cell therapy (e.g., in vitro in cells first and then transplanting the cells in vivo), the second objective, avoiding or minimizing off-target editing is as important as achieving targeted gene correction because off-target editing may cause disease or induce tumor formation. It should be noted not all off-target editing can be predicted by computer software or algorithm.

Therefore, a careful design, validation and improvements were employed in developing and validating the CYP4V2 mutation CRISPR gene correction constructs:

(1) Multiple gRNA candidates were generated based on the mutant CYP4V2 nucleic acid sequence which contains the c.802-8_810del17insGC mutation

(2) Top 5 gRNAs were selected using the following criteria (See SEQ ID NOs: 48-52, Table 5 and Figure 12):

- a. The proximity of the gRNA cleavage site to the modification site, and
- b. The off-target profile of the gRNA;

(3) The activity of the top 5 gRNAs were validated in the genomic DNA of a BCD patient with homozygous c.802-8_810del17insGC mutations (See Figure 13);

(4) Based on (2) and (3), three gRNAs were selected. Each of the 3 gRNAs was cloned into a pX459 plasmid together with nucleic acid sequences encoding Cas9 and puromycin resistance gene (Puro) for transfected cell selection using puromycin (See Figure 15 and 18).

(5) Two donor templates (both forward and reverse complementary) providing HDR donor nucleic acid sequence were generated. The ssODNs containing the donor template sequences were synthesized by IDT (See SEQ ID NO: 56 and 57).

(6) In addition to plasmid constructs, a CRISPR RNP construct was developed. A RNP construct offers certain advantages over other constructs. A detailed discussion is provided below and in the Examples section.

(7) The CYP4V2 CRISPR correction constructs are validated in iPS cells derived from a BCD patient with homozygous c.802-8_810del17insGC mutations.

(8) Whole genome sequencing is performed in unmodified cells and iPS cells genetically repaired by the CYP4V2 mutation CRISPR correction constructs to confirm the correction of the c.802-8_810del17insGC mutation and to assess off-target edits.

Methods to determine the optimal conditions for transfection in iPSCs and to select for transfected cells are provided. See the Examples section for detailed description. It is contemplated that these constructs can be used in treating not only BCD patient-specific iPS cells *in vitro*, but also the source cells (e.g., fibroblasts or PBMCs) or iPS-RPE, iPS-PRC, iPS-CE cells or iPS-CEC cells or other ocular cells derived from BCD patient-specific iPS cells *in vitro*, as well as *in vivo* in patients with the c.802-8_810del17insGC mutation. In one embodiment, the components of the constructs can be used directly. In some embodiments, the components in the construct can be modified, or cloned into a different vector to achieve higher transduction efficiency *in vivo* or higher specificity to the target cell type or to achieve other purposes. For example, Cas9 can be modified to Cas9 nickase (Cas9n D10A), which contains a mutation allowing the endonuclease to create single-strand nicks, as opposed to double-stranded breaks. Pairing two opposite facing gRNA sequences with SpCas9 nickase is an efficient method of gene editing that prevents unwanted indels from forming. In addition to plasmids, other common vectors used to package CRISPR components include lentivirus vectors and adeno-associated virus (AAV) vectors. When using AAV vectors, the *Staphylococcus aureus* Cas9 orthologue

(SaCas9) may be used as the endonuclease because SaCas9 is approximately 1 kb shorter than SpCas9, and offers additional flexibility around AAV packaging constraints.

Various improvements were made to the CRISPR RNP construct. Instead of IVT sgRNA or a crRNA:tracrRNA duplex, a synthetic sgRNA was used. Synthetic gRNAs have higher purity than IVT sgRNAs and therefore lower the risk of off-target editing caused by impurities in sgRNA. In addition, chemical modification is applied to the sgRNA to protect the sgRNA from intracellular degradation, which can increase editing efficiency. See Examples section for more details.

It is contemplated that, in addition to the plasmid constructs and CRISPR RNP constructs described herein, a mRNA construct comprising a Cas9-encoding mRNA and a guide RNA oligonucleotide also can be used.

After BCD patient-specific iPS cells are transfected with the CYP4V2 mutation CRISPR correction constructs the transfected cells are selected using puromycin. It should be understood that other markers, such as GFP, can be incorporated into the constructs and used as a marker in lieu of or in addition to puromycin. Following selection, single cell cloning is carried out, after which some cells from the single cell clone are harvested for sequencing. After sequencing results confirm successful on-target gene editing and no disease-causing gene edits are found, the remaining cells of the same clone are used for differentiation into the desired ocular cell type, e.g., iPS-RPE cells.

D. Differentiation of iPSCs

The genetically repaired BCD patient iPS cells are differentiated into iPS-RPE cells (or another type of ocular cells (e.g., iPS-CEC, iPS-CE cells or iPS-PRC)). Methods for differentiating iPSCs into RPE cells or another type of ocular cell (e.g., CEC and PRC) are known. See, for example, Hayashi et al., 2012, PLoS One, 7(9):e45435; Songstad, et al., Investigative Ophthalmology & Visual Science December 2015, Vol.56, 8258-8267; and Lamba et al., PLoS One. 2010 Jan 20;5(1):e8763. For example, induced pluripotent stem cells (iPSCs) reprogrammed from cells can be produced and further differentiated into, for example, RPE cells (referred to herein as “iPS-RPE”), corneal epithelial cells (referred to herein as “iPS-CEC”),

photoreceptor cells (or photoreceptor progenitors; referred to herein as "iPS-PRC"), or iPS-choroidal endothelial (CE) cells (referred to as "iPS-CE").

Differentiated cells, e.g., iPS-RPE cells, is tested for its biochemical functions (as described in the Examples section) to confirm it has improved biochemical functions as compared to iPS-RPE cells of the patient without genetic repair.

The iPS-RPE cell lines produced as described herein exhibit the morphology (e.g., pigmentation and hexagonal shape) and/or expresses one or more biomarkers that are indicative of RPE cells. Biomarkers for RPE cells (and iPS-RPE cells) are known and include, without limitation, one or more of RLBP1 (a/k/a CRALBP), RPE65, BESTROPHIN-1, MITF, VINCULIN, LRAT, RDH5, PAX6, MERTK, TYR, and/or ZO-1, and can be used to determine or confirm that RPE differentiation has taken place. Similarly, biomarkers for CECs (and iPS-CECs) and PRCs (and iPS-PRCs) are known and include, for example, cytokeratin 12 and cytokeratin 3 for corneal epithelial cells; and Crx for photoreceptors, recoverin for rods and cones, and Nrl for rods.

E. Administration / Delivery

The genetically repaired iPS-RPE cells can be used in autologous transplantation to the patient from whom the iPS-RPE cells are derived. Patients with BCD or another ophthalmological condition due to CYP4V2 mutations can be treated by the cell therapy methods provided herein. Similarly, the method can be used to provide a genetically repaired autologous cell therapy for other ocular diseases caused by one or more genetic mutations.

Methods of administering or delivering cells are known, and methods of administering or delivering cells to the eye are known. see, e.g., Wert et al., J Vis Exp. 2012; (69): 4286; WO 2016/179496; Schwartz et al., Investigative Ophthalmology & Visual Science April 2016, Vol.57, ORSFC1-ORSFC9. In one embodiment, the ocular cell can be transplanted via injection of cell suspension, e.g., suspension of RPE cells. In another embodiment, the cells can be transplanted as part of a sheet or scaffold, e.g., an in vitro tissue using natural and/or synthetic scaffolds to generate a polarized functional RPE monolayer.

The therapeutically effective amount of cells administered to the eye is known to those of skill in the art and will vary with the type of cells being transplanted, the maturity of the cells

being transplanted and whether it is expected to divide post transplantation, the size of the area or number of cells targeted for replacement, and the subject being treated (e.g., the age, sex, weight, development stage of the disease and condition of the subject to be treated); the route of administration; and the required regimen. The therapeutically effective amount of cells used in ocular cell therapy can range from about 1×10^3 to about 1×10^8 cells in a single administration.

While iPSC cell lines can be generated for individual subjects, a cell bank of iPSCs having common HLA haplotypes (or in which the HLA haplotype has been genetically manipulated) can be generated, which would be designed to achieve immunologic matching with a large portion of the patient population. See, for example, Turner et al., *Cell Stem Cell*, 13:382–384, 2013. In addition, an iPSC cell line can be generated that is immunologically silent irrespective of the subject's genotype (see, for example, Riolobos et al., *Mol. Ther.*, 21:1232–41, 2013). When combined with these methods, the patient-specific iPS cells and iPS-ocular cells can be used not only in a strict autologous sense, but can also be used for transplantation to other patients.

Typically cell therapy administering step takes place after the onset of disease symptoms or after the subject has shown signs of retinal degeneration or corneal dystrophy, as applicable. In one embodiment, ocular cell therapy provided herein can be used independently in treating an ocular disease (e.g., BCD). In another embodiment, ocular cell therapy provided herein can be used in combination with one or more other treatment options, including without limitation, the CYP4V2 gene transfer therapy and/or CYP4V2 CRISPR gene editing therapy provided herein.

Similarly, administration can occur once, or a plurality of times (e.g., over several weeks, months, or years) and can be applied to the same eye or to the contralateral eye. Further, one or more types of cells can be administered in a single or separate administrations.

Post-treatment assessment can use methods described in the CYP4V2 Gene Therapy section herein, including without limitation, through eye exams such as visual function, e.g., as measured by visual acuity, visual field, dark adaptation, visual function and/or Optical Coherence Tomography (OCT, e.g., Spectral Domain-OCT (SD-OCT)) and ERG.

Methods of Using CRISPR RNP in Ocular Cell Therapy and Gene Therapy

CRISPR RNP is a gene-editing ribonucleoprotein (RNP) complex that includes a guide RNA complexed with a Cas protein (e.g., Cas9 protein). The guide RNA is made up of two RNAs termed CRISPR RNA (crRNA) and trans-activating crRNA (tracrRNA). In one embodiment, the crRNA and the tracrRNA are provided as two separate nucleic acid molecules. In another embodiment, the crRNA and tracrRNA can be combined in a chimeric single guide RNA (sgRNA). The sgRNAs can be about 100 nucleotides (nt) in length, or shorter or longer as desired or necessary. Twenty nt at the 5' end (crRNA) hybridize to a target DNA sequence by Watson-Crick base pairing and guide the Cas endonuclease to cleave the target genomic DNA, with the remaining double-stranded structure at the 3' side for Cas9 recognition.

CRISPR RNPs have pros and cons as compared to traditional Cas9/gRNA constructs (e.g., plasmid constructs which incorporate nucleic acid sequences the CRISPR guide RNA and Cas9 protein). For example, the guide RNA (crRNA and tracrRNA) and Cas9 protein can be delivered into target cells as intact complexes, overcoming the need for the cell's own transcription machinery to express the CRISPR components. As a result, CRISPR RNPs can edit quickly after transfection. In addition, the CRISPR components deplete quicker from cells, which can reduce the chance of off-target editing. Furthermore, it may reduce the chance of integrational mutagenesis caused by plasmids. Given these advantages, RNP can also be advantageous in *in vivo* gene editing. On the other hand, however, as RNP clears quickly from cells through protein degradation, it may have lower on-target editing efficiency than the plasmid constructs whose expression last longer in cells.

To evaluate the above hypothesis and to prove whether CRISPR RNP constructs can achieve both objectives of the gene editing desired in ocular cell therapy and gene therapy, two sets of constructs were designed. One construct is a plasmid construct and the other is a RNP construct. Both constructs use the same BCD patient's iPS cells for transfection, which are subsequently sequenced to analyze on-target genetic repair and off-target editing of each construct. Off-target editing are determined by comparing against genomic DNA from unmodified fibroblasts of the same patient. Results from both plasmid construct and RNP construct can be compared.

Detailed description of RNP, methods to form RNP and to use the RNP construct to generate genetically repaired cells (iPS and iPS-RPE cells) for a BCD patient, is provided in the Examples section.

It should be noted that a similar CRISPR RNP construct can be used to correct or inactivate other mutations of BCD and mutations of other RP and IRDs. In one aspect, the crRNA sequence used herein is changed to another crRNA sequence specifically targeting a different target mutation sequence. In another aspect, a guide RNA or a sgRNA in a RNP construct can be modified to enhance gene editing efficiency. See, Hendel et al, Nat Biotechnol. 2015 Sep; 33(9): 985–989. In some embodiments, the CRISPR RNP constructs can be transfected using electroporation. In some embodiments, the CRISPR RNP construct can be transfected using lipofection or nucleofection. In some embodiments, the CRISPR RNP construct can be delivered via microinjection.

In addition to genetically repairing and treating patients' cells *in vitro*, CRISPR RNP constructs can also be used to treat an ocular disease caused by genetic mutations *in vivo* and have advantages over other types of CRISPR constructs (e.g., plasmids and/or mRNAs encoding the CRISPR components) for *in vivo* applications. For example, CRISPR RNP constructs have higher potency, lower off-target risk, and/or lower toxicity or innate immune response activation as compared to *in vitro* transcribed Cas9 mRNA and sgRNAs. In one embodiment, CRISPR RNP constructs comprised of a Cas9 protein complexed with a guide RNA targeting the region of the mutant DNA sequence can be injected directly into the subject's eye (e.g., sub-retinal injection, intravitreal injection or to the cornea). In another embodiment, engineered variants of Cas9 with multiple SV40 nuclear localization sequences (NLS) which have shown increased editing efficiency in brain cells *in vivo* (Staahl et al., Nat Biotechnol. 2017 May;35(5):431-434) can be used to achieve higher editing efficiency in ocular cells. Cas9 protein with one or multiple NLSs (at N-terminal and/or C-terminal) are commercially available at various CROs, such as IDT and Feldan. In some embodiments, the CRISPR RNP construct is delivered “as is.” In some embodiments, the CRISPR RNP construct is formulated with a pharmaceutically acceptable carrier when delivered. In some embodiments, the CRISPR RNP construct is delivered in a packaged form, e.g., in a nanoparticle.

It would be understood that the ratio between the CRISPR RNP components, e.g., the guide RNA and Cas9 protein can be adjusted and optimized by testing different ratios in patient cell lines *in vitro* (e.g., BCD patient-specific iPS cells or iPS-RPE cells) before treatment *in vitro* or *in vivo*. The CRISPR RNP construct can be used independently or in combination with another CRISPR construct, including without limitation, a plasmid or vector encoding a CRISPR guide RNA or crRNA, or a Cas protein or a combination thereof; a Cas9-encoding mRNA; a guide RNA oligonucleotide; another CRISPR RNP construct; or a combination or hybrid thereof. In addition, the CRISPR RNP constructs can be used to correct or inactivate one or more than one mutations related to one or more than one ocular diseases.

Gene Therapy and Cell Therapy Combination Treatment

The disclosure herein provides multiple treatment options for BCD and other ocular diseases caused by CYP4V2 mutations, including without limitation, CYP4V2 gene transfer therapy and CYP4V2 CRISPR gene editing therapy. Both CYP4V2 gene transfer therapy and CYP4V2 gene editing therapy can be used either *in vivo* or *in vitro* or both *in vivo* and *in vitro*. When applied *in vivo*, CYP4V2 gene transfer therapy and/or CYP4V2 CRISPR gene editing therapy can treat remaining ocular cells affected by BCD as gene therapy. When applied *in vitro* in patient cells or patient derived cells, the cells treated by CYP4V2 gene transfer therapy and/or by CYP4V2 CRISPR gene editing therapy can be transplanted to the patient to replace died or degenerated ocular cells as cell therapy. Significantly, gene therapy and cell therapy compositions and methods provided herein can be combined to provide additional benefits to patients which cannot be achieved by using gene therapy or cell therapy alone. The “combination treatment” can also broaden the eligible patient base. For example, for late-stage patients who have no or little photoreceptor or RPE cells left, gene therapy is not as effective as for early-stage patients. In this case, cell therapy can benefit by providing new cells (e.g., RPE or photoreceptor cells), whereas gene therapy can improve the effect of cell therapy by rescuing the remaining RPE or photoreceptor cells and/or by improving the conditions of choroid cells whose healthy affects the conditions of ocular cells. The combination of the “rescue” and “replacement” effect of gene therapy and cell therapy, respectively, makes the combination

treatment an improvement from either gene therapy or cell therapy. This combination treatment method can be applied to other ocular diseases caused by one or more genetic mutations.

Methods and Compositions for CYP4V2 Gene Therapy

The present disclosure relates to various compositions comprising a nucleic acid molecule encoding a functional CYP4V2 protein and various methods utilizing the same for treating an ocular cell and/or ocular disease. In one embodiment, a functional CYP4V2 protein can be used directly for treatment purpose. In some embodiments, a nucleic acid molecule encoding a functional CYP4V2 protein is used. In some embodiments, an expression cassette comprising such nucleic acid molecule encoding a functional CYP4V2 protein operably linked with one or more regulatory sequences is used to direct and control expression of the product of the nucleic acid molecule. In some embodiments, a vector is used to package such CYP4V2 expression cassette comprising a nucleic acid molecule encoding a functional CYP4V2 protein and one or more regulatory sequences for enhanced delivery to the target cell and to achieve the desired expression of the product of such CYP4V2 encoding nucleic acid molecule and expression cassette.

In some embodiments, the vector is a recombinant adeno-associated virus (rAAV) vector. In some embodiments, the vector is a plasmid. In some embodiments, the vector is another type of viral or non-viral vector. The treatment methods comprise administering or delivering an effective amount (or an effective concentration) of said vectors to the subject's eye and/or the target cells. In one embodiment, the treatment is directly applied in vivo. In another embodiment, the treatment comprises treatment ex vivo in target cells (e.g., an ocular cell) and transplanting the treated target cells into the subject (e.g., to the subject's eye). The treatment methods are directed to ocular diseases and other conditions associated with CYP4V2 mutations. In one embodiment, the ocular disease is Bietti's Crystalline Dystrophy (BCD).

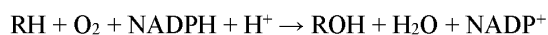
A. Functional CYP4V2 Protein and Nucleic Acids encoding a Functional CYP4V2 Protein

CYP4V2 (Cytochrome P450, Family 4, Subfamily V, Polypeptide 2, (MIM 608614), synonym: CYP4AH1) is one of the proteins in the cytochrome P450 superfamily (P450) and a

member of the cytochrome P450 subfamily 4 (CYP4). Cytochrome P450s (CYPs) are important heme-containing proteins, known for their roles as oxidase enzymes. The term P450 is derived from the spectrophotometric peak at the wavelength of the absorption maximum of the enzyme (450 nm) when it is in the reduced state and complexed with carbon monoxide. They are involved in the metabolism of xenobiotics and endogenous compounds, such as steroids and fatty acids. CYP enzymes have been identified in all kingdoms of life: animals, plants, fungi, protists, bacteria, archaea, and even in viruses. However, they are not omnipresent; for example, they have not been found in *Escherichia coli*.

P450 proteins share key elements in structure. For example, P450 proteins can be identified by their signature sequence element FXXGXXXCXG (SEQ ID NO: 30), where the cysteine serves as an axial ligand to the heme iron. Sequence identity is relatively low among P450 proteins but their general topography and structural fold are highly conserved. The conserved core is composed of a coil termed the 'meander', a four-helix bundle, helices J and K, and two sets of beta-sheets. These constitute the haem-binding loop (with an absolutely conserved cysteine that serves as the 5th ligand for the haem iron), the proton-transfer groove and the conserved EXXR motif (SEQ ID NO: 31) in helix K. P450 proteins are primarily membrane-associated proteins located either in the inner membrane of mitochondria or in the endoplasmic reticulum of cells.

In addition to structural similarities, P450 proteins also share functional similarities. The most common reaction catalyzed by P450 enzymes is a monooxygenase reaction, e.g., insertion of one atom of oxygen into the aliphatic position of an organic substrate (RH) while the other oxygen atom is reduced to water:



Many hydroxylation reactions (insertion of hydroxyl groups) use P450 enzymes. Many P450 enzymes have steroids and/or fatty acids as substrates.

The human CYP4V2 protein (NCBI RefSeq: NP_997235.3) has 525 amino acids (amino acid sequence shown in SEQ ID NO: 4). There are variants of human CYP4V2 protein, including pathologic variants (i.e., mutations) (See Table 1 herein for a select list of CYP4V2 mutations among BCD patients) and non-pathologic (i.e., functional) variants.

In one aspect, a functional CYP4V2 protein is the human CYP4V2 protein (SEQ ID NO: 4). In other aspects, a functional CYP4V2 protein is a functional variant or fragment of the human CYP4V2 protein, including without limitation, one with an amino acid sequence as shown in SEQ ID NO: 5).

A functional CYP4V2 protein can also be a variant of another functional CYP4V2 protein. The following is a discussion based upon changing of the amino acids of a polypeptide described herein to create an equivalent, or even an improved, second-generation molecule. For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, binding sites on substrate molecules. e.g., binding site for fatty acids. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid substitutions can be made in a protein sequence, and in its underlying DNA or RNA coding sequence, and nevertheless produce a protein with like properties. It is thus contemplated that various changes can be made in the amino acid sequence of a functional CYP4V2 protein or the DNA or RNA sequences of genes or coding regions thereof without appreciable loss of their biological utility or activity, as discussed herein. For example, SEQ ID NO: 5 is the amino acid sequence of a CYP4V2 protein variant which has one amino acid change from the human CYP4V2 protein sequence shown in SEQ ID NO: 4.

Various techniques, algorithms, software and tools can be used to design or engineer functional derivatives, variants and/or fragments of a functional CYP4V2 protein, e.g., the human CYP4V2 protein. For example, the structure and functions of the various polypeptides or changes can be modeled, resolved or predicted by NMR, x-ray crystallography, or computer modeling, e.g., ClustalW, SWISS-MODEL server, Swiss-Pdb Viewer, Polyphen-2, PROVEAN, SIFT, Condel, MutationAssessor and FatHMM.

A functional CYP4V2 protein can also be a fragment or derived from a fragment of a functional CYP4V2 protein. For example, the human CYP4V2 protein (SEQ ID NO: 4) and its variant (SEQ ID NO: 5) both have a transmembrane domain between about the 13th amino acid residue and about the 35th residue from the N-terminus. The backbone of human CYP4V2 protein (SEQ ID NO: 4) is located between about 36-525aa. Thus, a functional CYP4V2 can be

derived from deletion of the first about 35 amino acids from the human CYP4V2 protein (SEQ ID NO: 6) and replacing it with an alternative transmembrane domain sequence. Another source of a functional CYP4V2 protein is a splice variant of a functional CYP4V2 protein.

The predicted transmembrane segment of CYP4V2 resides near the N terminus, followed by a globular structural domain typical of the CYP450 family. The globular domain of CYP4V2 includes 18 helices and beta structural segments. The heme group is located close to the surface of the protein, coordinated by the I helix toward the protein interior and the L helix superficially. Li et al., *Am J Hum Genet.* 74:817-826, 2004. CYP4V2 protein is predominantly active in fatty acid metabolism. Many other P450 enzymes are also involved in fatty acid metabolism. CYP4V2 is ubiquitously expressed in almost all tissues and organs. Expression of CYP4V2 was found in heart, brain, placenta, lung, liver, skeletal muscle, kidney, pancreas, retina, retinal pigment epithelium, cornea and lymphocytes (Li et al., *Am J Hum Genet.* 74:817-826, 2004). However, most other P450 enzymes are not present in ocular cells. For example, CYP4V2 and CYP1B1 were the only P450 enzymes expressed at high levels in ARPE-19 cell line; CYP2E1, CYP2J2, and CYP3A4 were transcribed at only low levels (5% of CYP4V2 mRNA expression), and transcripts for CYP4A11, CYP4B1, CYP4F2, CYP4F3, and CYP4F12 were not detectable (Nakano, et al., *Mol Pharmacol* 2012; 82: 679-686). The fact that symptoms of CYP4V2 mutations is restricted to the eye, where CYP4V2 is the only major P450 enzymes expressed besides CYP1B1 and the only P450 sub-family 4 (CYP4) enzymes expressed, but not shown in organs where CYP4V2 is present with other P450 enzymes, suggest that other P450 enzymes, particularly CYP4 enzymes, can be used to substitute all or part of the functions of CYP4V2. Indeed, the CYP4 sub-family has been found to share common roles in fatty acid metabolism, including without limitation, as hydroxylase for PUFAs. See, Hardwick, *Biochem. Pharmacol.*, 75(12):2263–75; Fer et al., *J. Lipid Res.*, 49(11):2379-89 ; Nakano et al., *Mol. Pharmacol.*, 2012, 82:679-686). Protein sequences of human CYP4 proteins are shown in SEQ ID NOs: 8-18.

In addition to shared substrates and functions with the other proteins of the CYP4 sub-family, computational analysis revealed that CYP4V2 was formed from the duplication of the ancestors of CYP46A (SEQ ID NO: 7), which was then duplicated to generate the whole CYP4 family. Pan et al., *Int. J. Mol. Sci.*, 2016, 17(7) pii: E1020. doi: 10.3390/ijms17071020.

Furthermore, the CYP4V2 gene (or orthologs of the CYP4V2 gene, e.g., Cyp4v3 for mouse) is conserved in many species, including without limitation, human, chimpanzee, Rhesus monkey, dog, cow, mouse, rat, chicken, frog, horse, rabbit and fruit fly (SEQ ID NOs: 19-29). Orthologs with human gene CYP4V2 have been found in 196 organisms.

A functional CYP4V2 protein can comprise or be designed, engineered, or derived from, including without limitation, the following:

- (i) the human CYP4V2 protein (SEQ ID NO: 4)
- (ii) a variant of (e.g., changing of the amino acids and/or a splice variant) of the human CYP4V2 protein or a functional CYP4V2 protein (e.g., SEQ ID NO: 5),
- (iii) one or more fragments of a functional CYP4V2 protein (e.g., SEQ ID NO: 6),
- (iv) a CYP4V2 (or ortholog) protein of other species,
- (v) another CYP4 protein or CYP46A1,
- (vi) a polypeptide which can ameliorate, treat, or arrest one or more biochemical abnormalities in one or more compounds listed in Table 2 in a patient cell (e.g., the iPS-RPE cell of a BCD patient), and/or
- (vii) a derivative, hybrid or variant of any one or more of (i) to (vi) above.

It is contemplated that the compositions and methods disclosed herein may be utilized to express any functional CYP4V2 protein as described above. In one embodiment, a functional CYP4V2 protein is a polypeptide comprising all or part of the amino acid sequence shown in SEQ ID NO: 4, 5 or 6. In some embodiments, a functional CYP4V2 protein is a polypeptide comprising all or part of an amino acid sequence selected from the group consisting of CYP4V2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 and CYP46A (SEQ ID NOs: 4-18), and CYP4V2 of chimpanzee, Rhesus monkey, dog, cow, mouse, rat, chicken, frog, horse, rabbit and fruit fly (SEQ ID NOs: 19-29), and derivatives, hybrids, variants and/or fragments thereof. In some embodiments, a functional CYP4V2 protein can have at least 80% amino acid sequence identity (e.g., at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity) to any of the sequences selected from the group consisting of

SEQ ID NOs: 4-29. In one embodiment, a functional CYP4V2 protein is a polypeptide comprising sequence elements of FxxGxxxCxG and ExxR (SEQ ID NOs: 30 and 31).

In some embodiments, a functional CYP4V2 protein is a compound or agent which can ameliorate, treat, or arrest one or more biochemical abnormalities in a patient cell (e.g., the iPS-RPE cell of a BCD patient).

In one embodiment, a functional CYP4V2 protein can be used directly to treat BCD, similar to protein-based drugs for other diseases. In another embodiment, a nucleic acid molecule encoding a functional CYP4V2 protein is used to express the functional CYP4V2 protein in the targeted cells. In one embodiment, the nucleic acid molecule is a RNA. In another embodiment, the nucleic acid molecule is a DNA, including without limitation, a complementary DNA (cDNA), for long-term expression. The cDNA can be positive- or negative-sense, single- or double-stranded. In some embodiments, the nucleic acid encoding a functional CYP4V2 protein is operably linked with one or more regulatory sequences to form a CYP4V2 expression cassette. In some embodiments, such an expression cassette is packaged in a vector for enhanced delivery and/or expression efficiency.

A codon consists of a set of three nucleotides and encodes a specific amino acid or results in the termination of translation (i.e. stop codons). The vast majority of amino acids (usually everything but methionine) are encoded by multiple codons. Therefore, different nucleic acid sequences can be used to express the same protein. The sequence identity between two nucleic acid molecules encoding the same protein sequence can range from 0% to over 99%. For example, a nucleic acid sequence (SEQ ID NO: 1) and another nucleic acid sequence (SEQ ID NO: 2), both encoding the human CYP4V2 protein (SEQ ID NO: 4), only share a sequence identity of 77%.

Codon-optimization of nucleic acid sequences may improve and/or stabilize protein expression without changing the encoded amino acid sequence. Codon optimization replaces codons present in a nucleic acid sequence with preferred codons encoding the same amino acid, for example, codons preferred for mammalian expression. Various strategies and parameters can be used in codon-optimization, including without limitation, codon usage bias, GC content, CpG dinucleotides content, mRNA secondary structure, cryptic splicing sites, premature PolyA sites,

internal chi sites and ribosomal binding sites, negative CpG islands, RNA instability motif (ARE), repeat sequences (direct repeat, reverse repeat, and Dyad repeat) and restriction sites that may interfere with cloning. Methods of codon optimization are known in the art, e.g., U.S. Patent No. 6,114,148 and US 20110081708. A codon optimized nucleic acid sequence of a given amino acid sequence or a nucleic acid sequence encoding a polypeptide can be generated by the methods described herein and/or by using various codon optimization software, including through online software.

It would be appreciated that, depending on the codon-optimization methods, configuration, algorithms or software being used, different codon-optimized nucleic acid sequences encoding the same protein can be generated. However, codon optimization does not always lead to improved expression compared to a wild-type, unmodified nucleic acid sequence. See Alexeyev MF, Winkler HH: Gene synthesis, bacterial expression and purification of the *Rickettsia prowazekii* ATP/ADP translocase. *Biochim Biophys Acta*. 1999, 1419: 299-306. 10.1016/S0005-2736(99)00078-4; Curran KA, Leavitt JM, Karim AS, Alper HS: Metabolic engineering of muconic acid production in *Saccharomyces cerevisiae*. *Metab Eng*. 2013, 15: 55-66; Agashe D, Martinez-Gomez NC, Drummond DA, Marx CJ: Good codons, Bad transcript: large reductions in gene expression and fitness arising from synonymous mutations in a Key enzyme. *Mol Biol Evol*. 2013, 30 (3): 549-560. 10.1093/molbev/mss273. doi:10.1093/molbev/mss273.

A codon optimized nucleic acid sequence (SEQ ID NO: 2) encoding the human CYP4V2 protein (SEQ ID NO: 4) is provided herein. Both SEQ ID NO: 1 and SEQ ID NO: 2 encode the same human CYP4V2 protein (SEQ ID NO: 4). The codon-optimized nucleic acid sequence (SEQ ID NO: 2) has an improved codon adaptation index (CAI) of 0.95 over a CAI of 0.94 for the nucleic acid sequence shown in SEQ ID NO: 1. A CAI of 1.0 is considered to be perfect in the desired expression organism. It would be understood that the present disclosure covers all forms and types of the codon-optimized nucleic acid sequence as represented by the cDNA sequence shown in SEQ ID NO: 2, including any RNA sequence or DNA sequence or other nucleic acid sequence corresponding to such cDNA sequence or derived therefrom, and it can be

in single-stranded or double-stranded form of, and/or positive-, negative-, anti-, or complementary-sense to the sequence provided herein.

In addition to codon-optimization, other methods can be used to improve translational performance. For example, Kozak sequence or Shine-Dalgarno Sequence can be used to increase the efficiency of translational initiation. A different stop codon (e.g., TGA) can be used to increase the efficiency of translational termination. In addition to ORF sequence, a nucleic acid sequence encoding a functional CYP4V2 protein may also include one or more non-coding sequences such as UTR(s) and/or one or more introns to improve protein expression. A Kozak sequence (exemplary sequence shown in SEQ ID NO: 36) can be inserted immediately before a CYP4V2 encoding cDNA to enhance expression.

As discussed herein, it is contemplated that functional variants and/or fragments of the human CYP4V2 protein can be utilized. A nucleic acid sequence encoding a functional variant (SEQ ID NO: 5) of the human CYP4V2 protein (SEQ ID NO: 4) is provided in SEQ ID NO: 3.

In some embodiments, a CYP4V2 nucleic acid molecule is a polynucleotide molecule that encodes any functional CYP4V2 protein, including without limitation, SEQ ID NOs: 4-30 or encoding a polypeptide with at least 80% amino acid sequence identity to any of the sequences shown in SEQ ID NOs: 4-30. In some embodiments, a CYP4V2 nucleic acid molecule is a polynucleotide sharing at least 60% sequence identity to any of SEQ ID NO: 1, 2 or 3.

A vector (e.g., a viral or non-viral vector) and a CYP4V2 expression cassette as described herein typically contains one or more CYP4V2 nucleic acid molecules or a fragment thereof. It would be understood that a nucleic acid molecule can take many forms including, without limitation, DNA or RNA, single-stranded nucleic acids (e.g., ssDNA, ssRNA), double-stranded nucleic acids (e.g., dsDNA, dsRNA), plus-strand or minus-strand nucleic acids, complementary DNAs (cDNAs), genomic DNA, messenger RNA (mRNA), small interfering RNA (siRNA), and/or DNA directed RNA interference (ddRNAi)). Nucleic acid molecules also can include one or more nucleotide analogs or backbone modifications. In addition, it would be understood that a cDNA can be synthesized from an mRNA template in a reaction catalyzed by a reverse transcriptase enzyme, or can be designed and synthesized based on the protein it intends to encode, including without limitation, a codon-optimized cDNA, or can be synthesized from

another nucleic acid molecule through mutagenesis. It also would be understood that a cDNA can contain only exons, or can contain exons plus other sequences, e.g., untranslated regions (UTR) and/or introns. In some instances, a vector and a CYP4V2 expression cassette described herein can include a nucleic acid molecule that has a sequence encoding the human CYP4V2 protein, or a functional variant or a fragment thereof.

A suitable nucleic acid sequence can be any nucleic acid sequence that encodes a functional CYP4V2 protein. Such nucleic acid sequence may or may not contain non-coding elements, such as UTRs, introns or a Kozak sequence. It may include a wild type sequence or a synthetic or modified sequence (e.g., a codon-optimized sequence). A nucleic acid sequence encoding a functional CYP4V2 protein can be generated as described herein or by other methods known in the art.

A nucleic acid molecule with the sequence as shown in SEQ ID NO: 1 encoding the human CYP4V2 protein is herein referred to as “CYP4V2st.” A nucleic acid molecule with a codon-optimized sequence as shown in SEQ ID NO: 2 encoding the human CYP4V2 protein is herein referred to as “CYP4V2op.” A nucleic acid molecule with the sequence shown in SEQ ID NO: 3 encoding a functional variant of the human CYP4V2 protein is herein referred to as “CYP4V2fv.” In some embodiments, a nucleic acid sequence encoding a functional CYP4V2 protein has a sequence identity of at least 60% with one of SEQ ID NOs 1, 2 or 3.

A functional CYP4V2 protein and a nucleic acid molecule encoding such functional CYP4V2 protein can be synthesized or isolated, purified and detected by methods known in the art. In addition, protein synthesis or isolation, purification and detection are also commercially available through CROs including Wuxi Apptec (Shanghai, China) and GenScript (Piscataway, New Jersey). Nucleic acid molecule synthesis or isolation, purification cloning, and detection are commercially available through CROs including GenScript (Piscataway, New Jersey) and Integrated DNA Technologies (Coralville, Iowa).

A polypeptide can be synthesized (e.g., through recombinant protein expression or chemical synthesis) or isolated. As used herein, a “purified” polypeptide is a polypeptide that has been separated or purified from cellular components that naturally accompany it. Typically, a polypeptide is considered “purified” when it is at least 70% (e.g., at least 75%, 80%, 85%, 90%,

95%, or 99%), by dry weight, free from the polypeptides and naturally occurring molecules with which it is naturally associated. Since a polypeptide that is chemically synthesized is, by nature, separated from the components that naturally accompany it, a synthetic polypeptide is “purified.”

Polypeptides can be purified from natural sources (e.g., a biological sample) by known methods such as DEAE ion exchange, gel filtration, and hydroxyapatite chromatography. A polypeptide also can be purified, for example, by expressing a nucleic acid in an expression vector. In addition, a purified polypeptide can be obtained by chemical synthesis. The extent of purity of a polypeptide can be measured using any appropriate method, e.g., column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

Polypeptides typically are detected using antibodies. Techniques for detecting polypeptides using antibodies include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. An antibody can be polyclonal or monoclonal. An antibody having specific binding affinity for a polypeptide or a portion of a polypeptide can be generated using methods well known in the art. The antibody can be attached to a solid support such as a microtiter plate using methods known in the art. In the presence of a polypeptide, an antibody-polypeptide complex is formed.

An “isolated” nucleic acid molecule typically refers to a nucleic acid molecule that is free of sequences that naturally flank one or both ends of the nucleic acid in the genome of the organism from which the isolated nucleic acid molecule is derived (e.g., a cDNA or genomic DNA fragment produced by PCR or restriction endonuclease digestion). Such an isolated nucleic acid molecule is generally introduced into a construct (e.g., a cloning construct, or an expression construct for use in gene therapy), usually for convenience of manipulation, to express a protein, to generate a fusion protein, or for other purposes, including without limitation, for packaging into a vector (e.g., a viral or non-viral vector).

Nucleic acids can be isolated using techniques routine in the art. For example, nucleic acids can be isolated using any method including, without limitation, recombinant nucleic acid technology, site-specific mutagenesis, the polymerase chain reaction (PCR) and/or other genetic engineering methods. General PCR techniques are described, for example, in *PCR Primer: A Laboratory Manual*, Dieffenbach & Dveksler, Eds., Cold Spring Harbor Laboratory Press, 1995.

Recombinant nucleic acid techniques include, for example, restriction enzyme digestion and ligation, which can be used to isolate a nucleic acid. Mutagenesis protocols are described, for example, in *In Vitro Mutagenesis Protocols*, Braman, ed., Humana Press, 2002.

Isolated nucleic acids also can be chemically synthesized, either as a single nucleic acid molecule or as a series of oligonucleotides.

Constructs containing a nucleic acid are known in the art. Constructs, including cloning constructs and expression constructs, can be custom made commercially or can be produced by recombinant DNA techniques routine in the art. A construct can have regulatory sequences operably linked to a nucleic acid to be expressed, and further can include sequences such as those encoding a selectable marker (e.g., an antibiotic resistance gene). Regulatory sequences are discussed herein. A construct containing a nucleic acid can encode a chimeric or fusion polypeptide (i.e., a polypeptide operatively linked to a heterologous polypeptide, which can be at either the N-terminus or C-terminus of the polypeptide). Representative heterologous polypeptides are those that can be used in purification or detection of the encoded polypeptide (e.g., 6xHis tag, glutathione S-transferase (GST), CFP, Fc, FLAG, HA, Myc, RFP, Strep, VSV, GFP, and YFP).

Constructs carrying a nucleic acid sequence can be introduced into a host cell. As used herein, "host cell" refers to the particular cell into which the nucleic acid is introduced and also includes the progeny of such a cell that carry the construct. A host cell can be any prokaryotic or eukaryotic cell. For example, host cells can be bacterial cells such as *E. coli*, or in insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO), COS cells, HEK293 cells, HeLa, Vero, V27, A549, K562, B50, WI38 and BHK cells). Other host cells include without limitation iPS cells, ES cells, RPE cells, iPS-RPE cells, iPS-photoreceptor cells, ES-RPE cells, ARPE-19 cells, cornea cells, photoreceptor cells, choroid cells, optic nerve cells, any other type of ocular cells discussed herein, neuronal cells, epithelial cells, blood cells, fibroblasts, lymphocytes, and stem cell derived cells. Many methods for introducing nucleic acids or a vector or an expression cassette carrying a nucleic acid transgene into host cells, both in vivo and in vitro, are well known to those skilled in the art and include, without limitation,

electroporation, sonoporation, calcium phosphate precipitation, polyethylene glycol (PEG) transformation, heat shock, lipofection, microinjection, and viral-mediated nucleic acid transfer.

Nucleic acids can be detected using any number of amplification techniques (see, e.g., PCR Primer: A Laboratory Manual, 1995, Dieffenbach & Dveksler, Eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; and U.S. Patent Nos. 4,683,195; 4,683,202; 4,800,159; and 4,965,188) with an appropriate pair of oligonucleotides (e.g., primers). A number of modifications to the original PCR have been developed and can be used to detect a nucleic acid. Nucleic acids also can be detected using hybridization. Hybridization between nucleic acids is discussed in detail in Sambrook et al. (1989, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Sections 7.37-7.57, 9.47-9.57, 11.7-11.8, and 11.45-11.57). Sambrook et al. discloses suitable Southern blot conditions for oligonucleotide probes less than about 100 nucleotides (Sections 11.45-11.46) and Southern blot conditions for oligonucleotide probes greater than about 100 nucleotides (see Sections 9.47-9.54).

B. Vectors

In some embodiments, the nucleic acid molecule encoding a functional CYP4V2 protein or fragment thereof is delivered to the ocular cells in need of treatment by means of a vector. For delivery to the ocular cells, the therapeutic vector is desirably non-toxic and efficient in delivering a nucleic acid molecule (e.g., DNA, RNA) into the target cells. Gene therapy vectors are known in the art and can be viral vectors or non-viral vectors.

One approach for in vivo introduction of nucleic acid into a cell is by use of a viral vector containing nucleic acid molecule, e.g., a cDNA. Infection of cells with a viral vector has the advantage that a large proportion of the targeted cells can receive the nucleic acid molecule. Additionally, molecules encoded within the viral vector, e.g., by a cDNA contained in the viral vector, are expressed efficiently in cells that have taken up viral vectors containing the nucleic acid molecule.

Examples of viral vectors that can be used include, without limitation, adenovirus vectors, adeno-associated virus vectors (AAV), lentivirus vectors, herpes virus (HV) vectors such as herpes simplex virus (HSV) vectors, papillomavirus vectors, poxvirus vectors, human

foamy virus (HFV) vectors, Epstein Barr virus (EBV) vectors, vaccinia virus vectors, Sendai virus vectors and retrovirus vectors. Plasmids can also be used to deliver a nucleic acid molecule into the target cell. In some instances, the viral vector is a recombinant viral vector such as a recombinant AAV (rAAV) vector. It would be understood by a skilled artisan that certain vectors will integrate, or are more prone to integrate, into the genome of the host cell (e.g., the subject's cells), while other vectors will not integrate, or are less prone to integrate, into the genome of the host cell (e.g., extrachromosomal expression).

Recombinant AAV (rAAV) vectors are commonly used in gene therapy approaches. AAVs belong to the parvovirus family and each contains a single strand DNA. rAAV vectors are currently considered to be the safest and most efficient platform for gene transfer in mammalian cells (Salganik et al, 2015, *Microbiol. Spectr.*, 3(4): doi:10.1128 / microbiolspec.MDNA3-0052-2014). To date, 12 AAV serotypes (AAV1 to AAV12) and more than 100 variants have been isolated from human and nonhuman primate tissue samples (see, e.g., Gao et al., 2005, *Curr. Gene Ther.*, 5:285–97) and from other species. Both naturally occurring and modified AAV types can be used in the methods described herein.

Wild-type AAVs contain a linear single-stranded DNA genome enclosed within a capsid composed of three proteins VP1, VP2, and VP3. In recombinant AAVs (rAAVs), the rep and cap genes from the wild-type AAV genome are typically replaced by a transgene expression cassette, flanked by the AAV inverted terminal repeats (ITRs) required for packaging. As used herein, “rAAV vector” refers to a recombinant AAV vector containing one or more capsid elements of or derived from one or more AAV virus.

Despite the advantages of AAV and other viral vector-mediated gene therapy, not all viral vectors and not all AAV types are suitable for treating a particular disease. Two major challenges faced by gene therapy using viral vectors (e.g., AAV vectors). First, sufficient transduction efficiency by the AAV vector in the cell type targeted for treatment is desirable. Second, potential immune reactions triggered by the viral vector need to be considered. See Madsen et al., Adeno-associated virus serotype 2 induces cell-mediated immune responses directed against multiple epitopes of the capsid protein VP1. *J Gen Virol* 90, 2622–2633 (2009); Mingozzi et al., CD8(+) T-cell responses to adeno-associated virus capsid in humans. *Nat Med*

13, 419–422 (2007). Although as compared to most other organs and tissues, the eye is considered as an immune-privileged organ relative to many other organs and immune responses in AAV-mediated gene therapy in the eye can be controlled by the use of immunosuppressant, the role of immune responses such as neutralizing antibodies (NABs) in AAV transduction of the eye, is unclear in large animals. In addition, intravitreal AAV administration is more susceptible to interactions with the immune system than subretinal administration. Therefore, the viral vector used in ocular gene therapy will trigger minimal or no immune response, so to avoid potential side effects and ensure the transduction/expression efficiency of the viral vectors are not substantially reduced by immune reactions, e.g., pre-existing NABs in the subject, and/or to lower the dose of rAAV vectors.

Various compositions and methods relating to AAV vector design and selection can be used to address these challenges. For use of CYP4V2 gene therapy to treat BCD, a vector with sufficient transduction efficiency in RPE cells is desired when the cells targeted for treatment are primarily RPE cells. When treating the corneal cells of a BCD patient, a vector with sufficient transduction efficiency in corneal cells is desired. In some embodiments, a vector with sufficient transduction efficiency in RPE cells is used. In some embodiments, a vector with sufficient transduction efficiency in corneal cells is used. In some embodiments, a vector with sufficient transduction efficiency in RPE and photoreceptor cells is used. In some embodiments, a vector with sufficient transduction efficiency in RPE, photoreceptor and choroid cells is used. In some embodiments, a vector with sufficient transduction efficiency in retinal cells is used. In some embodiments, a vector with sufficient transduction efficiency in ocular cells is used. In some embodiments, a vector with sufficient transduction efficiency in ocular cells and/or blood cells is used. To address the potential immune response (e.g., NABs and cell-based immune responses against the gene therapy vectors), different AAV serotypes and variants, modified AAV vectors and/or immuno-suppression protocols can be used.

An rAAV vector used herein can be based on or derived from either a wild type AAV (e.g., from one of AAV1 to AAV12 or other wild-type AAV variants isolated from human or other species, including without limitation, AAV1, AAV2, AAV4, AAV5, AAV6, AAV8, AAV9, AAV10, AAV11 and AAV12) or a modified AAV. A modified AAV can be generated

in many different ways, including without limitation, a pseudotyped AAV (e.g., AAV2/5, AAV2/8, AAV2/1, AAV2/4, AAV2/6, AAV2/7, AAV2/9, AAV2/12, AAV8/2), a chimeric AAV (e.g., AAV-DJ), a capsid modified AAV (e.g., a capsid mutant AAV (e.g., AAV with Y-F, K-R, T-A, S-A and/or T-V mutations, and AAV-DJ/8 or AAV-DJ/9 which are capsid mutant AAVs from AAV-DJ), a capsid variant AAV (e.g., AAV 7m8 and derivatives), an ancestral AAV (e.g., Anc80), a recombinant AAV involving any change to the genome and/or capsid of a naturally occurring AAV or variant, and any combination thereof. It would be understood that there are different ways to refer to a modified AAV, including without limitation, artificial, modified, synthesized, reconstructed, engineered, evolved, designed, derived or enhanced AAV, or AAV generated through rational designed and/or directed evolution and/or DNA shuffling, or an AAV variant. The use of a modified AAV can have certain advantages over an unmodified AAV, including without limitation, higher transduction efficiency, higher tissue- or cell- specificity, less immune reactions, and/or more suitable for certain type of administration (e.g., intravitreal injection, or delivery through the blood stream).

In some embodiments, a modified AAV vector used herein is a pseudotyped AAV. AAV pseudotyping refers to the mixing of a capsid and genome from different viral serotypes. These serotypes are denoted using a slash, so that AAV2/5 indicates a virus containing the genome (e.g., ITRs) of serotype 2 packaged in the capsid from serotype 5. In some embodiments, an AAV vector is an AAV2/1, AAV2/2, AAV2/5, AAV2/8, AAV2/6, AAV2/9, AAV2/4, AAV2/7, AAV2/10 or AAV2/12 vector.

In some embodiments, a modified AAV vector used herein is a chimeric (sometimes also referred to as hybrid or shuffled) AAV which is derived from different AAV serotypes, including from different AAV serotypes isolated from different species. In some embodiments, an AAV vector is AAV-DJ, AAV-DJ/8 or AAV-DJ/9. AAV-DJ is an AAV variant generated from the libraries of AAV hybrids of eight serotypes by DNA shuffling method. Grimm, D. et al. (2008). *J. Virol.* 82: 5887-5911. It is able to efficiently transduce a broad range of cell types including ocular cells. Moreover, chimeric AAVs possess more ability to evade immune neutralization than naturally occurring AAVs and thus can efficiently deliver higher quantities of therapeutic transgene. A hybrid AAV can be further modified. For example, AAV-DJ/8 and AAV-DJ/9 were

created by making point mutations in the heparin binding domain (HBD) of AAV-DJ. Grimm, D. et al. (2008). *J. Virol.* 82: 5887-5911.

In some embodiments, a modified AAV used herein is a capsid mutant AAV. It involves creating one or more mutations (e.g., point mutations) in AAV capsid protein. Capsid mutant AAVs can have advantages over unmodified AAVs. For example, point mutation of surface exposed tyrosine (Y) residues of AAV capsid protein was reported as a simple and effective method for evading phosphorylation and subsequent ubiquitination, leading to higher transduction efficiency both in vitro and in vivo (Zhong et al., *Proc Natl Acad Sci U S A.* 2008;105(22): 7827–32; Markusic et al., *Mol Ther.* 2010;18(12):2048–56; Li et al., *Hum Gene Ther.* 2010 Nov; 21(11): 1527–1543). For example, site-directed mutagenesis of each of the seven AAV2 capsid tyrosine residues (Y252, Y272, Y444, Y500, Y700, Y704, and Y730) by phenylalanine residue substitution leads to increased vector transduction and transgene expression by circumventing EGFR-PTK phosphorylation and the ubiquitin-proteasome pathway in human cells in vitro and murine hepatocytes in vivo (Zhong et al., *Virology.* 2008 Nov 25; 381(2):194-202). It has also been reported that point mutations on the AAV capsid at specific tyrosine (Y), serine (S), threonine (T) and lysine (K) residues could lead to significant transduction improvement both in vitro and in vivo (Gabriel et al., *Hum Gene Ther Methods.* 2013;24(2):80–93; Sen et al., *Hum Gene Ther Methods.* 2013;24(2):104–16; Sen et al., *Sci Rep.* 2013;3:1832; Wu et al., *J Virol.* 2006;80(22):11393–7). Capsid mutations can also be made to a modified AAV to generate another modified AAV. For example, AAV-DJ/8 and AAV-DJ/9 were created by making point mutations in the heparin binding domain (HBD) of AAV-DJ, a hybrid AAV. Grimm, D. et al. (2008). *J. Virol.* 82: 5887-5911. Capsid mutations can also make an AAV evade NABs and generate less immune response. Furthermore, certain capsid mutations can make an AAV more suitable for intravitreal delivery. Kay et al., *PLoS One*, 8:e62097, 2013. In some embodiments, an AAV vector used herein is a modified AAV with one or more capsid mutations, include without limitation, Tyrosine to Phenylalanine (Y-F), Threonine to Valine (T-V), Lysine to Arginine (K-R), Threonine to Alanine (T-A), Serine to Alanine (S-A) and/or affecting the AAV's heparin binding domain (HBD), and/or in its antigenic regions, including without limitations at positions 459, 493 and 551. In some embodiments, an

AAV vector is an AAV2 with one or more capsid mutations among Y444F, Y500F, Y730F, Y252F, Y272F, Y700F, Y704F and T491V, wherein the number (e.g., 444) indicates the location of a point mutation of the AAV capsid. In some embodiments, an AAV vector is an AAV5 with one or more capsid mutations among Y263F and Y719F. In some embodiments, an AAV vector is an AAV8 with one or more capsid mutations among Y447F, Y733F, and T494V. In some embodiments, an AAV vector is an AAV1 with a capsid mutant of Y731F. In some embodiments, an AAV vector is an AAV6 with one or more capsid mutations among Y445F and Y731F. In some embodiments, an AAV vector is an AAV9 with a capsid mutation of Y731F. In some embodiments, an AAV vector is an AAV-DJ, AAV-DJ/8 or AAV-DJ/9 with one or more capsid mutations among K137R, T251A and S503A.

In some embodiments, a modified AAV vector is an AAV with variant AAV capsid proteins. Variant AAV capsid proteins are known in the art. In some embodiments, a non-naturally occurring capsid protein can include a selected AAV sequence (e.g., a fragment of a vp1 capsid protein) in combination with heterologous sequences (e.g., sequences obtained from a different selected AAV serotype, non-contiguous portions of the same AAV serotype, from a non-AAV viral source, or from a non-viral source). In some embodiments, a modified AAV vector includes one or more insertions of amino acids (e.g., from about 5 amino acids to about 11 amino acids) in the capsid protein GH loop. Variant AAV capsid proteins can confer increased infectivity of a retinal cell compared to the infectivity of the retinal cell by a non-variant AAV (e.g., wild type AAVs). In some embodiments, a modified AAV is one that can deliver the transgene across the blood-ocular barrier (BOB) which makes it suitable for delivery through the bloodstream, offering an alternative route of administration/delivery from the conventional administrations (e.g., sub-retinal injection or intravitreal injection) used in ocular gene therapy. In some embodiments, an AAV with variant AAV capsid proteins is an AAV 7m8, or its derivatives or variants (Dalkara et al., Science Translation Medicine, 5:189ra76, 2013; PCT Application No. PCT/US2012/034413, PCT Application No. PCT/US2014/039015, US Application No. 14/214,011 and US Application No. 13/899,481). In some embodiments, an AAV with variant AAV capsid proteins is an AAV-PHP.B.

In some embodiments, an AAV vector can be reconstructed or synthesized through reconstruction of the viral evolutionary lineage. Such reconstruction can yield ancestral, ancient or parental AAVs. In one embodiment, an AAV vector is an Anc80 (an ancestor of AAV1, 2, 8 and 9) or its derivative. Zinn et al., *Cell Rep.* 2015 Aug 11;12(6):1056-68.

In some embodiments, one or more AAVs and/or other viral vectors can be modified (e.g., optimized for intravitreal delivery, for enhanced transduction in target cell type (e.g., RPE cells), or for delivery through the bloodstream) by means of techniques known in the art including, e.g., “directed evolution” and/or “rational design”. See, e.g., Asuri et al., *Mol Ther.* 20:329-338, 2012 and Yang et al., *Methods Mol Biol.* 709:127-139, 2011. Modified AAVs or other viral vectors can be described as, e.g., “engineered”, “hybrid”, “evolved”, “enhanced” or “designed” vectors. Such modifications can, e.g., improve vector targeting (e.g., improving suitability for intravitreal delivery or for delivery through the bloodstream), transduction efficiency and/or lower immune reaction, resulting in, e.g., a lower dose being required. In some embodiments, an rAAV vector is an AAV serotype rh10 (EP 20100178940) or ShH10. In some embodiments, an rAAV vector is an AAV-PHP.B (US 20150079038).

In some embodiments, an AAV vector can be generated and/or selected from a combination of more than one strategies stated herein. For example, AAV-DJ/8 and AAV-DJ/9 were created by making point mutations in the heparin binding domain (HBD) of AAV-DJ, a hybrid AAV.

It is known in the art that certain AAVs can be more suitable for intravitreal delivery than some other AAVs. Many such AAVs for intravitreal delivery involve modifying the AAV capsid protein via mutations (e.g., AAV2 (quadY-F+T-V) (Kay et al., *PLoS One.* 2013 Apr 26;8(4)). or variant AAV capsid proteins (e.g., AAV 7m8). In addition, there are AAVs suitable for delivery through the bloodstream, e.g., AAV-PHP.B. Their use, however, are not limited to intravitreal delivery or delivery through the bloodstream, e.g., they can also be used as AAV vectors for sub-retinal and other routes of administration.

In some embodiments, a self-complementary AAV vector (scAAV) is used. Wild type AAVs have a single-stranded DNA genome. One downside of AAV is its single-stranded DNA genome. Because the single-stranded AAV genome depends on the cell’s DNA replication

machinery to synthesize the complementary strand, transgene expression is delayed and is not as robust as double-stranded DNA. For CYP4V2 gene therapy, we developed an scAAV design (see Figure 7) to circumvent rate-limiting second-strand synthesis in conventional single-stranded AAV vectors and to facilitate robust transgene expression. The scAAV.CYP4V2 comprises an intra-molecular self-complementary CYP4V2 DNA structure which eliminates the requirement for host cell DNA synthesis and results in faster and more robust expression upon transduction. The self-complementary structure of an scAAV, however, reduces the scAAV vector's packaging limit from about 4.7-5.0 kb for ssAAV to about 2.4-2.5 kb for scAAV. Therefore, shorter length regulatory sequences (e.g., promoter, enhancer and/or polyA signal) are required in an scAAV design. To ensure the expression cassette does not exceed the vector packaging limit and depending on the length of the cDNA and other regulatory sequences used, certain optional regulatory sequence may need to be excluded from the scAAV construct, such as an enhancer. One of the two ITRs in an scAAV design is a truncated ITR and has a mutation in the terminal resolution site (TRS). For a detailed discussion on scAAV structure, purification and production, see McCarthy, *Molecular Therapy*, Volume 16, Issue 10, p1648–1656, October 2008.

A number of other vector designs can be utilized. For example, a dual vector system (e.g., an AAV-based dual vector system, e.g., trans-splicing or hybrid dual AAV vectors) can be used to express a nucleic acid sequence (e.g., a CYP4V2 nucleic acid sequence). See, e.g., Colella, et al., *Gene Ther.* 21, 450–456, 2014. For example, a dual vector system can include (i) a first AAV vector polynucleotide having an inverted terminal repeat at each end (5' and 3' end) of the polynucleotide, and between the inverted terminal repeats, a suitable promoter operably linked to a partial coding sequence that encodes an N-terminal part of the protein encoded by the nucleic acid sequence of interest; and ii) a second AAV vector polynucleotide having an inverted terminal repeat at each end (5' and 3' end) of the polynucleotide, and between the inverted terminal repeats, a partial coding sequence that encodes a C-terminal part of the protein encoded by the nucleic acid sequence of interest, followed by a polyadenylation (pA) signal sequence.

Various rAAVs vectors were designed and generated for our study, including scAAV2/1, AAV2/2, AAV2/5, scAAV2/5, AAV2/8, scAAV2/9 and AAV2/2 (Y444F+Y500F+Y730F) (see

schematic drawings and annotations in Figure 7 herein). They demonstrate that rAAV vectors of various vector designs can be used in CYP4V2 gene therapy. In addition, inclusion of multiple rAAV vectors as options can help to reduce potential immune response in CYP4V2 gene therapy given the pre-existing neutralizing antibodies and other individual immune response against certain AAV types among the patient population. It would also provide more options if a subsequent administration to the same eye or an administration to the contralateral eye of the same subject is desired.

Methods to produce viral delivery vectors, including production using helper-free system, are known in the art. See, e.g., PCT/US2007/010055; Patent No: 6458587, Patent No: US 6428988 B1). Production of various vectors used in gene therapy, including without limitation, AAV, adenovirus, lentivirus and retrovirus vectors, is also commercially available through contract research organizations (CROs) and contract manufacturing organizations (CMOs), e.g., Vector Biolabs (Malvern, PA) and Cell Biolabs, Inc., (San Diego, CA).

In some embodiments, a recombinant AAV vector useful in the methods described herein can be generated by culturing a host cell (e.g., a HEK293 cell) which contains a nucleic acid molecule encoding an AAV serotype capsid protein, or fragment thereof; a rep gene; a minigene comprising, at a minimum, AAV inverted terminal repeats (ITRs) and a nucleic acid molecule of interest (e.g., having a CYP4V2 nucleic acid sequence); and sufficient helper functions to permit packaging of the nucleic acid of interest into the AAV capsid protein. The components required to be cultured in the host cell to package a nucleic acid in an AAV capsid can be provided to the host cell in cis or trans. Alternatively, any one or more of the required components (e.g., nucleic acid molecule of interest, rep sequences, cap sequences, and/or helper functions) can be provided by a stable host cell which has been engineered to contain one or more of the required components. Any of these components can be selected from among any suitable serotype. For example, rAAV vectors are generated by co-transfecting producer cells (e.g., HEK 293 cells) with (a) a plasmid (AAV cis-plasmid) containing a cloned recombinant AAV genome composed of the gene of interest (e.g., a cDNA encoding CYP4V2) and other desired regulatory sequences flanked by the two AAV ITRs, (b) a separate construct expressing in trans the AAV viral Rep and Cap genes. (c) the adenovirus helper factors, which are provided by either adenovirus

infection or transfecting into producer cells a third plasmid that provides these adenovirus helper factors. In addition to HEK293 cells, other cell lines can be used in the production of rAAV vectors, including without limitation, HeLa, Vero, A549, B50, WI38 and BHK cells.

In some embodiments, the viral delivery vector is a rAAV2 virus, a rAAV2/5 virus, a rAAV2/8 virus, a rAAV2/1 virus, a rAAV2/4 virus, a rAAV2/6 virus, a rAAV2/9 virus, a rAAV2/12 virus or a rAAV virus with capsid elements from one or more of AAV1, AAV2, AAV5, AAV8, AAV9 and/or AAV12 virus. In one embodiment, the viral delivery vector is a rAAV virus with one or more Y-F mutations, including without limitation, AAV2 (Y444F+Y500F+Y730F), or AAV8 (Y733F).

In some embodiments, the viral delivery vector is a single-stranded rAAV (ssAAV) virus. In some embodiments, the viral delivery vector is a self-complementary rAAV (scAAV) virus.

In addition to AAV vectors, other viral vectors can be used in CYP4V2 gene therapy. For example, adenoviral vectors have also been demonstrated to be useful for gene delivery. For example, Mori et al., 2002. IOVS, 43:1610-1615 discloses the use of an adenoviral vector that is an E-1 deleted, partially E-3 deleted type 5 Ad in which the transgene (green fluorescent protein) is driven by a CMV promoter. Peak expression levels were demonstrated upon injection of 10^7 to 10^8 viral particles, with subretinal injection providing higher levels of expression than intravitreal injection.

In some embodiments, the delivery vector is a plasmid containing a nucleic acid molecule encoding the human CYP4V2 protein or a functional variant or fragment thereof.

Non-viral vectors also can be used in CYP4V2 gene therapy. Examples of non-viral vectors include, without limitation, naked nucleic acids, dendrimers, liposomes (e.g., cationic or anionic liposomes), polymers (e.g., polyplexes), lipid-polymer systems, and nanoparticles (e.g., inorganic or synthesized nanoparticles). For example, efficient non-viral ocular gene transfer was demonstrated by Farjo et al., 2006, PLoS 1:e38, who used compacted DNA nanoparticles as a system for non-viral gene transfer to ocular tissues. As a proof of concept, the pZEGFP5.1 (5,147 bp) expression construct that encodes the enhanced green fluorescent protein (GFP) cDNA transcriptionally-controlled by the CMV immediate-early promoter and enhancer was used. DNA nanoparticles were formulated by mixing plasmid DNA with CK3OPEG10K, a 30-

mer lysine peptide with an N-terminal cysteine that is conjugated via a maleimide linkage to 10 kDa polyethylene glycol using known methods. Nanoparticles were concentrated up to 4 mg/ml of DNA in saline. The compacted DNA was delivered at a 0.6 µg dose to the vitreal cavity. GFP expression was observed in the lens, retina, and pigment epithelium/choroid/sclera by PCR and microscopy.

Further, a number of patents have been issued for methods of ocular gene transfer including, but not limited to, U.S. Pat. No. 7,144,870 which provides methods of hyaluronic acid mediated adenoviral transduction; U.S. Pat. Nos. 7,122,181 and 6,555,107 which provide lentiviral vectors and their use to mediate ocular gene delivery; U.S. Pat. No. 6,106,826 which provides herpes simplex viral vectors and their use to mediate ocular gene delivery; and U.S. Pat. No. 5,770,580 which provides DNA expression vectors and their use to mediate ocular gene delivery.

A method of screening and selecting suitable vectors for use in CYP4V2 gene therapy from different vectors is provided in the Examples section herein. The Examples used different AAV vectors to illustrate the method. It would be understood that such method can also be used by the skilled in the art to compare and select among different types of vectors, e.g., viral- vs. non-viral vectors, adenovirus vs. AAV, lentivirus vs. AAV, HSV vs. AAV, etc.

C. CYP4V2 Expression Cassettes and Regulatory Sequences

The disclosure also provides an expression cassette comprising a nucleic acid sequence encoding a functional CYP4V2 protein (e.g., a nucleic acid sequence of SEQ ID NO: 1, 2 or 3) and an expression control sequence operably linked to the CYP4V2 encoding nucleic acid sequence. In addition to the nucleic acid molecule encoding a functional CYP4V2 protein, the other key elements of an expression cassette used in CYP4V2 gene therapy include one or more regulatory sequences to control the expression of said nucleic acid molecule. In some embodiments, the expression cassette is packaged in a delivery vector (e.g., in a rAAV vector flanked by the AAV ITRs) for enhanced delivery, transduction and/or expression efficiency. Any AAV ITRs can be used in the methods described herein. The ssAAV vectors described in the Examples herein contain two AAV2 ITRs of about 141 bp each (exemplary sequences shown in SEQ ID NO 40). The scAAV vector described in the Examples contains two AAV2 ITRs, one of

which is truncated (exemplary sequences shown in SEQ ID NO 41). An AAV2 ITR usually has a length of about 132 to about 167 bp depending on the parental vector being used.

As used herein, the term "regulatory sequence" refers to any genetic element (e.g., polynucleotide sequence) that can exert a regulatory effect on the replication or expression (transcription or translation) of the nucleic acid sequence, or otherwise direct, influence and/or regulate expression of the nucleic acid sequence. Common expression control sequences include promoters, polyadenylation (polyA) signals, enhancers, upstream regulatory domains, introns, UTRs, response elements, or inducible elements, origins of replication, internal ribosome entry sites (IRES), transcription initiation sequences, termination sequences, RNA processing sequences such as splicing and polyadenylation (polyA) sequences, sequences that stabilize cytoplasmic mRNA, sequences that enhance translation efficiency (i.e., Kozak consensus sequence), sequences that enhance protein stability, or sequences that enhance secretion of the encoded protein. Regulatory sequences can be of bacterial, yeast, insect, mammalian, or viral origin or can be derivatives, hybrids or variants thereof, or can be synthetic, and vectors can contain a combination of regulatory sequences from different origins. For example, regulatory sequences can be heterologous (e.g., of a different origin or from a different gene; e.g., from a non-CYP4V2 gene) or homologous (e.g., from the same gene; e.g., from a CYP4V2 gene) relative to the coding sequence whose expression they are regulating (e.g., a CYP4V2 gene). As used herein, "operably linked" means that a promoter and/or other regulatory sequence(s) are positioned relative to a nucleic acid coding sequence in such a way as to direct, influence or regulate expression of the nucleic acid coding sequence. A regulatory sequence can be "operably linked" with a nucleic acid coding sequencing in the same vector or in a different vector. One or more regulatory sequences operably linked to a nucleic acid coding sequence can be contiguous and/or can act in trans or at a distance to direct, influence or regulate expression of the nucleic acid coding sequence. Among the regulatory sequences, a promoter is essential, while other regulatory sequences such enhancers, introns and terminators can be beneficial but are optional.

Various promoter sequences can be used to drive expression of a nucleic acid coding sequence. Some promoters are constitutive promoters, which direct expression in virtually all tissues and most cell types. while other promoters are more controlled. Regulated promoters

might act only in certain tissues or cells (i.e., tissue- or cell-specific promoters) or at certain times in development (i.e., development-stage specific promoters) and/or may be conditioned to environmental conditions or external stimuli such as a chemical, oxygen levels, heat, or light (i.e., inducible promoters).

In some instances, it may be desirable to use a constitutive (or ubiquitous) promoter. Exemplary constitutive promoters include without limitation, the cytomegalovirus (CMV) promoter (Gray et al., Hum Gene Ther. 2011 Sep; 22(9): 1143–1153; Norman et al., PLoS ONE 5(8): e12413, Aug 2010), the chicken β -actin promoter, the hybrid CAG (a/k/a CAGGS, CBA or CB) promoter derived from CMV/Chicken beta actin/rabbit beta-globin (Miyazaki J, Takaki S, Araki K, Tashiro F, Tominaga A, Takatsu K, Yamamura K. 1989. Expression vector system based on the chicken β -actin promoter directs efficient production of interleukin-5. Gene 79: 269–277; Acland, G. M. et al. Mol Ther, 2005, 12:1072-1082), the small CBA (smCBA) promoter (~953 bps, see, Mah, et al. 2003, Hum. Gene Ther. 14:143-152; Haire, et al. 2006 IOVS, 2006, 47:3745-3753), the CBh promoter (~800 bps, see, Gray et al., Hum Gene Ther. 2011 Sep; 22(9): 1143–1153), the human β -actin promoter (ACTB) (Norman et al., PLoS ONE 5(8): e12413, Aug 2010), the elongation factor 1 alpha (EF-1 alpha) promoter (see, Gill et al., Gene Ther. 2001;8(20):1539–1546; Norman et al., PLoS ONE 5(8): e12413, Aug 2010), the phosphoglycerate kinase (PGK, human or mouse) promoter (Norman et al., PLoS ONE 5(8): e12413, Aug 2010), the Ubiquitin C (UBC) promoter (Norman et al., PLoS ONE 5(8): e12413, Aug 2010), the GUSB (Glucuronidase Beta) promoter, the GUSB minimal promoter (hGBp) (Husain, Gene Therapy (2009) 16, 927–932), the UCOE promoter, the elongation factor 1 α short (EFS) promoter, the Simian virus 40 (SV40) promoter, the Rous sarcoma virus (RSV) promoter, See, e.g., Powell, Discov Med. 2015 Jan; 19(102): 49–57, for a general comparison and discussion of various promoters. It should be understood that in some cases "constitutive" or "ubiquitous" promoters can be prone to silencing or promote differential expression strength in selected cell types, see, e.g., McCown et al., Brain Res. 1996;713(1–2):99–107; Gray et al., Hum Gene Ther. 2011;22:1143–1153.

In some instances, it is desirable to use a cell-specific or tissue-specific promoter, which directs expression of a nucleic acid coding sequence in a particular type of cell or tissue. Based

on the disclosure herein, it would be appreciated that a cell-specific or a tissue-specific promoter can be specific for an ocular cell or tissue, or for lymphocytes. Ocular cell types include, without limitation, retina cells, retina bipolar cells, photoreceptor cells, rod cells and cone cells, ganglion cells, retinal pigment epithelium (RPE) cells, choroid cells or corneal epithelium cells. Thus, a cell-specific promoter as described herein can be a retina-specific promoter (e.g., RPE-specific, photoreceptor-specific (e.g., cone-specific and/or rod-specific) and/or choroid-specific) or a cornea-specific promoter. Exemplary ocular cell-specific promoters include, without limitation, the human G-protein-coupled receptor protein kinase 1 a/k/a rhodopsin kinase 1 (GRK1) promoter (Genbank Accession number AY327580), a 292 nt fragment (positions 1793-2087) of the GRK1 promoter (see, Beltran et al., *Gene Therapy* 17:1162-74, 2010), the human interphotoreceptor retinoid-binding protein proximal (IRBP) promoter, a 235 nt fragment of the hIRBP promoter, the RPGR proximal promoter, the red opsin promoter, the red-green opsin promoter, the blue opsin promoter, the mouse opsin promoter (both long and short versions, Le et al., *Molecular Vision* 2006; 12:389-398; Beltran et al., *Gene Therapy* 17: 1162-74, 2010), the rhodopsin (Rho) promoter (Mussolino et al., *Gene Therapy*, 18:637-45, 2011); the alpha-subunit of cone transducin (Morrissey et al., *BMC Dev. Biol.* 11:3, 2011); beta phosphodiesterase (PDE) promoter; the retinitis pigmentosa (RP1) promoter (Nicord et al., *J. Gene Med.* 9: 1015-23, 2007), the NXNL2/NXNL1 promoter (Lambard et al., *PLoS One*, 5:e13025, 2010), the RPE65 promoter (Li et al., *Investigative Ophthalmology & Visual Science*, December 2002, Vol.43, 3640); the retinal degeneration slow/peripherin 2 (Rds/perphZ) promoter (Cai et al., *Exp Eye Res*, 91: 186-94, 2010), the VMD2 promoter (vitelliform macular dystrophy 2; a/k/a BEST1, Kachi et al., *Human Gene Therapy*, 20:31-9, 2009), the IRBP/GNAT2 promoter (hIRBP enhancer fused to cone transducin alpha promoter), the Rds (retinal degeneration slow) promoter, the hPDE6b promoter, or the VEcad promoter (VE-cadherin/Cadherin 5 (CDH5)/CD144 promoter). It would be appreciated that other promoters are known in the art can be used in lieu of, or in addition to, any of the exemplary promoters provided herein based on the rationale and discussions provided herein.

Exemplary inducible promoters include without limitation, a calcium-sensitive promoter (e.g., the NFAT promoter, see, *Gene Ther.* 2013 Mar;20(3):248-54), the zinc-inducible sheep

metalioihionine (MX) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7 polymerase promoter system; the ecdysone insect promoter, the tetracycline-repressible system, the tetracycline-inducible system, the RU486-inducible system, the rapamycin-inducible system, a number of commercial available inducible promoters, and inducible promoters regulated by a specific physiological state, e.g., temperature, acute phase, a particular differentiation state of the cell, or in replicating cells only. In some embodiments, the inducible promoter is one that is tightly regulated and specific for a particular ocular cell type.

A promoter can be a hybrid of, or truncated/shortened or modified version of or otherwise derived from another promoter and/or another regulatory sequence, e.g., the CAG promoter is a hybrid of CMV immediate early enhancer, chicken beta actin promoter and rabbit beta-globin gene, the smCBA promoter is a truncated version of the CBA promoter. A promoter can contain other elements, e.g., an intron, exon and/or an enhancer, e.g., the CAG promoter. More than one promoters can be used together in an expression cassette.

In some instances, it may be desirable to use an enhancer sequence in order to increase and/or stabilize expression above that which occurs due to the promoter. Representative enhancer sequences include, without limitation, a post-transcriptional regulatory element (e.g., a woodchuck hepatitis virus post-transcriptional regulatory element (a/k/a WPRE), or a Hepatitis B Virus post-transcriptional regulatory element (a/k/a HPRE or HBVPRE, Donello et al., J Virol. 1998 Jun; 72(6):5085-92; Sun et al., DNA Cell Biol. 2009 May; 28(5): 233-240), or various shortened, mutant or modified WPREs, e.g., a ~247 bps shortened WPRE containing minimal gamma and alpha elements of the WPRE (Choi et al., Mol Brain. 2014; 7: 17; Donello et al., J Virol. 1998 Jun; 72(6): 5085-5092; Zanta-Boussif et al., Gene Therapy (2009) 16, 605-619), or the 1RBP enhancer (Nicord et al., J. Gene Vied. 9: 1015-23, 2007), a constitutive transport element (CTE) enhancer (e.g., the Mason-Pfizer Monkey Virus CTE or Avian Leukemia Virus CTE), the cytomegalovirus (CMV) immediate early enhancer, one derived from an immunoglobulin gene or SV40 enhancer, or the cis-acting element identified in the mouse proximal promoter, an intron regulatory sequence, e.g., a mini-intron splice donor/splice acceptor referred to as SD-SA derived from SV-40, an internal ribosome entry site (IRES), which can be used to produce more than one polypeptide from a single gene transcript, e.g., a protein that

contains more than one polypeptide chain, or two different proteins, can be a poliovirus internal ribosome entry sequence, which supports transgene expression in RPE, photoreceptors and ganglion cells.

The polyadenylation of a transcript is important for nuclear export, translation, and mRNA stability. Therefore, the efficiency of transcript polyadenylation is important for transgene expression. Representative PolyA signal sequences include, without limitation, an SV40 polyA signal, an SV40 late polyA signal, an SV40 early polyA signal, a bovine growth hormone polyadenylation (bGH polyA) signal, a small polyA, or a human growth hormone polyadenylation signal (hGH polyA). In some instances, an upstream enhancer (USE) sequence can be used to increase the efficiency of a polyA signal, e.g., SV40 late 2xUSE, HIV-1 USE (Human immunodeficiency virus 1), GHV USE (Ground squirrel hepatitis virus), Adenovirus (L3) USE (Adenovirus), hTHGB USE (Human prothrombin), or hC2 USE (Human C2 complement gene) (Schambach A, Galla M, Maetzig T, Loew R, Baum C. Improving transcriptional termination of self-inactivating gamma-retroviral and lentiviral vectors. *Mol Ther*. 2007;15(6):1167–1173).

Like promoter sequences, the other regulatory sequences used in an expression cassette can be a hybrid of, shortened/truncated, modified or otherwise derived versions of a regulatory sequence. For example, the shortened WPRE, the SV40 late 2 x USE, the SV40 late polyA. In addition to the elements described herein, an expression cassette can also contain other regulatory sequences, e.g., introns, UTRs, and linker sequences. The inclusion of a splice site (i.e., exon flanked by two introns) has been demonstrated to be useful to increase gene expression of proteins from expression cassettes.

It is known in the art that it is common for a regulatory sequence or a hybrid regulatory sequences to have multiple versions and have more than one names.. For example, various promoters, enhancers and polyA signals have multiple versions, including without limitation, the CMV promoter, EF1 α promoter, the WPRE enhancer, and the SV40 polyA signal. The CAG promoter has multiple alternative names including without limitation, the CBA promoter, CB promoter or CAGGS promoter. In addition, it is also known the in art that a regulatory sequence can be shortened, modified or combined with other sequences to generate a derivative or variant,

e.g., the CAG (a/k/a CBA, CB or CAGGS) promoter is a hybrid of CMV immediate early enhancer, chicken beta actin promoter and rabbit beta-globin gene, the smCBA promoter is a truncated CAG promoter, the CB^{SB} promoter is a shortened CAG promoter, differing by about 152 bp at the 5' end of the CMV immediate early enhancer. Furthermore, a regulatory sequence can be termed differently, e.g., a post-transcriptional regulatory element such as HPRE or WPRE can also be referred to as an enhancer. Any regulatory sequences described herein contemplate all variations, derivatives and/or hybrids of such regulatory sequence. Any exemplary sequence provided herein relating to a regulatory sequence is exemplary in nature and does not limit the definition or scope of such regulatory sequence to the one shown in the exemplary sequence.

In some embodiments, microRNA (miRNA) technique can be used in the expression cassette design to achieve targeted expression specificity, e.g., via repress off-target transgene expression. Simply by way of example and without limitation, a target sequence for miR181 (an miRNA shown to be expressed exclusively in ganglion cells and inner retina) can be added immediately downstream of CYP4V2 cDNA to inhibit synthesis of expression cassette-mediated CYP4V2 protein in ganglion cells and inner retinal cells. Similarly, a target sequence for an miRNA that is exclusively expressed in certain cell types can be used to repress expression cassette-mediated CYP4V2 protein expression in these types of cells to achieve targeted tissue- or cell-specific expression.

D. Designing Efficient Expression Cassettes and Delivery Vectors for CYP4V2 Gene Therapy

A detailed discussion on the CYP4V2 expression cassette and delivery vector design method and various designs for these studies are provided in the Examples section herein.

Use of EFS promoter and/or small PolyA Signal (SPA) in treating an ocular disease

As discussed herein, a gene delivery vector has a packaging size limit. For example, single-stranded AAV vectors have a packaging limit of about 4.7-5.0 kb, exceeding which the transduction and expression efficiency would drop significantly. For self-complementary AAVs (scAAVs), the packaging limit is halved to about 2.4-2.5 kb. Therefore, size does matter for vector-mediated gene delivery and gene therapy. For double stranded self-complementary vectors, it is desirable and sometimes critical to use small size regulatory sequences to make

enough room for the transgene (e.g., cDNA). Because of this size limitation, large promoters also are not suitable for use with scAAV. For CYP4V2 gene therapy, given the size of the cDNA is about 1578 bp and the AAV ITRs (with mutation) are about 258 bp, there is only about 500-600 bp left for the regulatory sequences. Because CYP4V2 is almost ubiquitously expressed, in some embodiments, it is desirable to use a constitutive promoter to drive the CYP4V2 transgene expression. However, there is no room for the constitutive CAG promoter we used in the single-stranded AAV design which is about 1.7 kb, or for a shortened CBA promoter (smCBA) which is about 953 bp or for CBh promoter which is about 800 bp, nor for many other constitutive promoters such as the CMV promoter which is about 600 bp. Instead, a short length EFS promoter can be used (exemplary sequence shown in SEQ ID NO: 34) for the scAAV design. The same size limitation applies other regulatory sequences, e.g., polyA signal. A bGH Poly A is about 225 bp, an SV40 polyA is about 240 bp and an SV40 late polyA is about 120 bp. Any one of them would take up a large portion of the ~500 bp length left for regulatory sequences including the promoter. Therefore, a small polyA signal (SPA) was used, which is only about 54 bp (exemplary sequence shown in SEQ ID NO: 35) for the scAAV design.

The design using a EFS promoter and a SPA only occupy about 300 bps and together with the AAV ITRs occupy a total of about 600 bps, thus leaving about 1.8-1.9 kb remaining packaging space for the nucleic acid sequencing encoding the desired protein and any other sequences in an expression cassette designed for a scAAV, and leaving about 4.1-4.4 kb remaining packaging space for the nucleic acid sequencing encoding the desired protein and any other sequences in an expression cassette designed for a ssAAV. As a result, larger size cDNAs and/or other sequences can be packaged in a rAAV vector with the EFS promoter and the SPA, as compared to the use of larger promoters and polyA signal sequences, including without limitation, CMV promoter, CAG promoter, smCBA promoter, CBh promoter, EF1 alpha promoter, bGH polyA, SV40 polyA and SV40 late polyA.

A schematic of the expression cassette comprising the EFS promoter and the SPA are provided in Figure 4b. The construct shown in Figure 7b includes a CYP4V2 cDNA. The CYP4V2 cDNA can be replaced by another gene of interest for the expression cassette to be used for other transgene expression.

The use of the EFS promoter and the SPA in an expression cassette and a delivery vector to drive a nucleic acid coding sequence to treat an ocular disease was tested in this study. An scAAV2/1 vector containing the EFS promoter, a CYP4V2 cDNA and the SPA, termed the scAAV1.EFS.CYP4V2op.SPA, was generated. The scAAV1-EFS-CYP4V2op-SPA was applied in the iPS-RPE cells of BCD patient. The scAAV1-EFS-CYP4V2op-SPA showed fast and robust action in iPS-RPE cells of BCD patient in just 4 days despite the short lengths of the EFS promoter and the SPA (See Table 3). It demonstrates that the EFS promoter and/or SPA are small size regulatory sequences that are very useful in an scAAV system for ocular gene therapy. In addition, the robust expression of scAAV vectors make the scAAV design also suitable for other routes of administration (e.g., intravitreal delivery) in addition to sub-retinal delivery.

The use of the EFS promoter and/or SPA is not limited to CYP4V2 gene therapy or in a scAAV construct. They can be used for gene therapy involving other genes, where the transgene size and/or an scAAV design requires the use of short length promoter and polyA signal to drive fast and sufficient protein expression.

E. Treatment Options, Subject Selection and Administration

CYP4V2 gene therapy can be applied in multiple ways. In some instances, the treatment can be applied in vivo to a subject (e.g., a BCD patient) through an effective delivery of the delivery vectors containing the CYP4V2 expression cassette to the cells, tissue or organ targeted for treatment, e.g., RPE, photoreceptors, choroid, cornea, lymphocytes, the retina or the eye, of the subject. In some instances, the treatment can be applied in vitro in the targeted cells (e.g., patient iPS-RPE cells, patient iPS-photoreceptor cells, iPS-photoreceptor progenitor cells, iPS-CEC, lymphocytes). Then the treated cells can be transplanted to a subject in need (e.g., a BCD patient). In some instances, the treatment can be applied through combining both the in vivo and in vitro approaches. In some instances, CYP4V2 gene therapy can be used independently. In some instances, CYP4V2 gene therapy can be used with another treatment option.

Subjects who are candidates for the present methods of treatment include those who are diagnosed of BCD. Subjects suffering from other ophthalmological clinically-defined conditions (e.g., inherited retinal degeneration (IRD), retinitis pigmentosa (RP) or corneal dystrophy) caused by mutations in the CYP4V2 gene can also be treated using the methods described herein.

A diagnosis of BCD, IRD, RP, corneal dystrophy or another ophthalmological condition caused by mutations in the CYP4V2 gene can be made using methods known in the art. The methods described herein can include identifying a subject, e.g., a child, adolescent, or adult subject, who has BCD or another ophthalmological condition caused by mutations in the CYP4V2 gene, or who is suspected of having BCD or another ophthalmological condition caused by mutations in the CYP4V2 gene (e.g., based on the presence of symptoms of the condition and no other obvious cause), and obtaining a sample comprising genomic DNA from the subject, detecting the presence of mutations in the CYP4V2 gene using known molecular biological methods.

Numerous mutations have been identified in the CYP4V2 gene and causing BCD, with at least one mutation in each of the gene's 11 exons. Genotype analysis has shown that the most common CYP4V2 mutation among BCD patients is c.802-8_810del17insGC (referring to a 17 base deletion with two bases (GC) inserted in the place starting 8 bases from the end of intron 6 of CYP4V2 gene, also referred to as IVS6-8 del/insGC; this insertion-deletion mutation is at intron 6-exon 7 junction and the 17 bp deletion includes the exon 7 splice-acceptor site, leading to an in-frame deletion of 62 amino acid-encoding exon 7) resulting in the skipping of exon 7. (Xiao et al., *Biochem Biophys Res Commun.* 409:181-6, 2011; Meng et al., 2014, *Mol. Vis.*, 20:1806-14; Wada et al., *Am J Ophthalmol.* 139:894-9, 2005; Jiao et al., *European Journal of Human Genetics* (2017) 25, 461-471). Various types of mutations were found in CYP4V2 mutations associated with BCD, including but not limited to, missense, splice site, frameshift, deletion, insertion, indel, nonsense, polymorphisms (e.g., single nucleotide polymorphisms) and premature termination. A summary of select CYP4V2 mutations among human BCD patients is provided in Table 1 and can be found in various publications and online databases, e.g., LOVD (databases.lovd.nl/shared/genes/CYP4V2 on the World Wide Web), OMIM (omim.org/allelicVariant/608614 on the World Wide Web), and ClinVar ([ncbi.nlm.nih.gov/clinvar/?term=608614\[MIM\]](http://ncbi.nlm.nih.gov/clinvar/?term=608614[MIM]) on the World Wide Web).

It should be noted that the human CYP4V2 mutations in Table 1 are not exhaustive. More CYP4V2 mutations may be identified in the future. It would be understood that not all variations to the reference sequence are mutations. Some variations are non-pathologic. Methods to confirm whether a genetic variation is pathologic, i.e., a mutation, is known in the art, including but not

limited to, comparing the variation to previously clinically identified known mutations, and/or determining whether a corresponding alteration in function exists. For example, one method to ascertain whether a genetic variation is a pathologic variation (i.e., a mutation) is to test the biochemical functions of the iPS-RPE cell line derived from the subject as described herein and assess whether any abnormalities exist as compared to those of healthy control's iPS-RPE cell line.

Patients with BCD or another ophthalmological condition due to CYP4V2 mutations that can be treated using a method described herein preferably retain some photoreceptors and visual function, e.g., as measured by visual acuity, visual field, visual function and/or Optical Coherence Tomography (OCT, e.g., Spectral Domain-OCT (SD-OCT)).

Before administration, the final product will undergo a series of steps (e.g., ultrapurification) to meet clinical grade criteria. Clinical grade productions are commercially available through various GMP facilities, including without limitation, the facilities in the NIH Gene Therapy Resource Program (GTRP) and contract manufacturing organizations (CMOs).

Prior to administration, the subject can test for pre-existing neutralizing antibodies (NAb) against the type of AAV vector which the subject is going to receive administration of. In one embodiment, if the subject has pre-existing NAb against such AAV type, an alternate AAV vector with low cross-reactivity to the subject's pre-existing NAb or an AAV vector with modified capsid structure can be used for administration to such subject to lower immune reactions and retain sufficient transduction efficiency by AAV vector. Other methods to minimize immune response are known in the art, including without limitation, applying immunosuppression agents and protocols before, during and/or post-treatment.

Viral or non-viral vectors, or combinations thereof (e.g., hybrid vectors), can be delivered into ocular cells of a subject using one or more physical means. Ocular cells as used herein refers to, without limitation, retinal pigment epithelium (RPE) cells, photoreceptor cells, corneal epithelial cells, retina cells, retina bipolar cells, rod cells, cone cells, ganglion cells, choroid cells and/or lens cells. In addition to, or alternatively, vectors can be delivered into nearby or neighboring cells or cells which can in contact with the targeted cells, including, without limitation, cells in the brain or cells in the optic nerve or blood cells.

Treatment *in vitro* can use any method or a combination of methods and/or agents that effectively delivers a vector to the cell targeted for treatment (e.g., an iPS-RPE cell from a BCD patient). Treatment *in vitro* can be done through one or more than one rounds of infections. In some instances, the vectors are applied in cultured cells directly to transfect or transduce the cells. In some instances, other methods of delivery and/or enhancing transfection/transduction efficiency in cells can be used, including without limitation, multiple transfections/transductions, electroporation, magnetofection, or sonoporation. Methods and agents used in infecting/transfecting a cell with a vector or an expression cassette is known in the art, including without limitation, as described in the Examples section herein.

The cells treated *in vitro* can then be transplanted to the eye of the subject. For example, the genetically repaired iPS-RPE cells from a BCD patient can be transplanted to the patient via sub-retinal injection. Methods, agents and devices used in cell transplantation to the eye are known in the art, see, e.g., Wert et al., J Vis Exp. 2012; (69): 4286; WO 2016/179496; Schwartz et al., Investigative Ophthalmology & Visual Science April 2016, Vol.57, ORSFc1-ORSFc9.

For *in vivo* treatment, the vector and/or expression cassette can be delivered to the cells targeted for treatment *in vivo* (e.g., through administration to the eye of a subject in need of treatment for delivery to the cells targeted for treatment). Delivery methods of a nucleic acid molecule, an expression cassette, a vector to a target ocular cell *in vivo* is known in the art. For example, administration to the eye can use any method (or a combination of methods and/or agents) that effectively delivers a vector to the retina, the sub-retinal space, the choroid, or generally to the posterior segment of the eye, the cornea, the lens, or the vitreous, depending on the cells targeted for treatment. Administration can be via any suitable means including, without limitation, injection (e.g., sub-retinal injection, intravitreal injection, direct retinal injection, direct injection into the eye's posterior suprachoroidal space), eye drops, and can be applied in combination with other delivery techniques (e.g., electrically assisted delivery to the corneal epithelium). A CYP4V2 nucleic acid, expression cassette and/or delivery vector can also be introduced into cells using, for example, DNA particle bombardment (e.g., by a gene gun), hydrodynamic gene transfer, eye drops, electroporation, magnetofection, or sonoporation. Administration and delivery methods and techniques to the eye are known in the art. Simply by

way of example, see, without limitation, Wert et al., J Vis Exp. 2012; (69): 4286; WO 2016/179496; Mohan et al., Prog Retin Eye Res. 2012 Jan; 31(1): 43–64.

In addition to conventional delivery to RPE cells using sub-retinal injection, one aspect of the methods discussed herein is intravitreal delivery of the nucleic acid molecule (e.g., having a non-mutant CYP4V2 nucleic acid sequence) for treatment or prevention of an eye disease. Some vectors (e.g., AAV2 (quadY-F+T-V) and AAV 7m8) show particular promise for efficient transduction in the retina through intravitreal administration. In addition, AAVs or other viral vectors can be modified by means of techniques known in the art including, e.g., “directed evolution” and “rational design” to improve or optimize their suitability as vectors for gene delivery to one or more types of cells or tissues (e.g., intravitreal injection) other than through the conventional sub-retinal injection. scAAV vectors can also be used in intravitreal delivery in addition to sub-retinal delivery because of its prompt and robust expression profile. Because CYP4V2 is almost ubiquitously distributed with particularly high expression in the retina, genetic and epigenetic alterations of CYP4V2 are particularly suitable for repair via intravitreal administration of one or more vectors. Current gene therapy methods generally require sub-retinal administration of the vector. Therefore, one of the technical advances achieved by the materials and methods disclosed herein is the intravitreal delivery of a nucleic acid sequence (e.g., a wild type or non-mutant nucleic acid sequence, or a nucleic acid sequences encoding gene editing polypeptides) and/or a polypeptide for treating and preventing diseases of the eye associated with genetic or epigenetic alterations in the nucleic acid sequence of CYP4V2.

Certain techniques and agents may be used to facilitate the administration or delivery process. Non-limiting examples including the use of a lubricating agent such that adherence of the vector to the delivery vehicle (e.g., a needle) is avoided. In addition, the use of immunosuppressive drugs before, during and/or after the administration or delivery process can increase the infection or transduction efficiency.

A vector can be formulated for delivery into ocular cells of a subject using various pharmaceutically and/or physiologically acceptable vehicle excipients, diluents, and/or carriers. Examples of vehicle excipients, diluents, and/or carriers suitable for administration to the eye, which can be referred to as pharmaceutically acceptable carriers, include sterile, pyrogen-free

water and sterile, pyrogen-free, buffered saline (e.g., saline buffered using phosphate or other buffers such as HEPES to maintain pH at appropriate physiological levels), isotonic sodium chloride solution, balanced salt solution, emulsions (e.g., oil/water emulsions), and various types of wetting agents. In some instances, the formulation can include other medicinal agents, pharmaceutical agents, stabilizing agents, buffers, carriers, adjuvants, and diluents. In some instances, the formulation can include DBPS, glycerol or Tween20 for long-term storage.

Methods of determining the most effective means of administration and therapeutically effective dosages are known to those of skill in the art and will vary with the vector, its capsid structure, the vector design (e.g., ssAAV vs. scAAV), the composition of the expression cassette, the expression levels of the vector, the promoter, other regulatory sequences or the nucleic acid molecule, the vector titer, the target cell type, the target expression levels, the size of the area or number of cells targeted, and the subject being treated (e.g., the age, sex, weight, development stage of the disease and condition of the subject to be treated, and potential immune reactions); the route of administration; the location of the cells targeted for treatment (e.g., retina vs. cornea); the nature and expression level of the relevant gene in wild-type cells and/or tissue; and the required regimen. Therapeutically effective doses can be determined and evaluated in disease models (e.g., BCD cellular model (e.g., iPS-RPE cell line from BCD patients) or an animal model, and confirmed or refined by clinical trials. For treatment of cells *in vitro*, the dose is usually expressed as MOI and then multiple the MOI by the number of cells being treated. The MOI generally ranges between about 1×10^3 GC to about 1×10^6 GC per cell or an infectious MOI of about 100 to about 10,000 GC per cell (GC: genomic copies, measuring genome containing AAV particles (a/k/a vector genome (vg) or genome particles (gp)). For *in vivo* treatment, in addition to the factors described above, the actual dose administered may also be affected by individual situations specific to each patient during the administration, e.g., a reduced dose during the sub-retinal administration for patient 6 in the Choroideremia case described below. Therefore, the therapeutically effective dose for a single administration *in vivo* can be on the order of from about 1×10^6 to 2×10^{13} GC, inclusive (e.g., a high dose range of about 1×10^{11} GC to about 1×10^{12} GC, a medium dose range of about 1×10^{10} GC to about 1×10^{11} GC, a low dose range of about 1×10^9 GC to about 1×10^{10} GC, a very low dose range

of about 1×10^6 GC to about 1×10^9 GC, and a very high dose range of about 1×10^{12} GC to about 2×10^{13} GC), or any dose within these ranges that is sufficient to provide the desired effect. In one embodiment, the composition is administered at a dose of about 1×10^6 to 2×10^{13} GC. In another embodiment, the in vivo administered dose is determined by multiplying the number of cells targeted for treatment by the target MOI (e.g., 1×10^3 GC to about 1×10^6 GC per cell). The volume of the agent containing the rAAV vectors in any single administration to the eye can range from about 1 uL (0.001 mL) to about 1000 uL (1 mL).

The compositions as described herein can be formulated as a single dose or a plurality of doses. Similarly, administration can occur once, or a plurality of times (e.g., over several weeks, months, or years) and can be applied to the same eye or to the contralateral eye. Under circumstances of multiple administrations, the same or different AAV serotypes and/or route(s) of administration can be considered. Administration can also be applied to treat different tissues and cells, e.g., one administration targeting the RPE and another administration targeting the cornea.

Methods of viral vector generation, GMP production, purification, formulation and doses for use in gene therapy (including ocular gene therapy) are known to those of skill in the art, and methods of preparation of viral vectors can be performed by any of a number of companies and methods as demonstrated in various groups' gene therapy studies for LCA-2 below. Expression cassettes provided herein can be inserted into any of the exemplary viral vectors listed below. Alternatively, viral vectors can be generated based on the examples provided below. See, Bainbridge et al., 2008. *N Engl J Med.* 358:2231-9; Maguire et al., 2008. *N Engl J Med.* 358:2240-8;; Hauswirth et al., *Hum Gene Ther.* 2008 Oct; 19(10): 979–990.

For example, in the Bainbridge study, the tgAAG76 vector, a recombinant adeno-associated virus vector of serotype 2 was used for gene delivery. The vector contains the human RPE65 coding sequence driven by a human RPE65 promoter and terminated by the bovine growth hormone polyadenylation site, as described elsewhere. The vector was produced by Targeted Genetics Corporation according to Good Manufacturing Practice guidelines with the use of a B50 packaging cell line, an adenovirus-adeno-associated virus hybrid shuttle vector containing the tgAAG76 vector genome, and an adenovirus 5 helper virus. The vector was filled

in a buffered saline solution at a titer of 1×10^{11} vector particles per milliliter and frozen in 1-ml aliquots at -70°C .

Maguire used the recombinant AAV2.hRPE65v2 viral vector which is a replication-deficient AAV vector containing RPE65 cDNA that has been documented to provide long-term, sustained (>7.5 years, with ongoing observation) restoration of visual function in a canine model of LCA2 after a single sub-retinal injection of AAV2.RPE65. The cis plasmid used to generate AAV2.RPE65 contains the kanamycin-resistance gene. The virus was manufactured by The Center for Cellular and Molecular Therapeutics after triple transfection of HEK293 cells and was isolated and purified by microfluidization, filtration, cation exchange chromatography (POROS 50HS; GE Healthcare, Piscataway, N.J.), density gradient ultracentrifugation and diafiltration in PBS. This combination provides optimal purity of the AAV vector product, including efficient removal of empty capsids and residual cesium chloride. A portion of the product was supplemented with PF68 NF Prill Poloxamer 188 (PF68; BASF, Ludwigshafen, Germany) to prevent subsequent losses of vector to product contact surfaces. The purified virus, with or without PF68, was then passed through a $0.22\text{-}\mu\text{m}$ filter using a sterile 60-ml syringe and syringe filter, and stored frozen (-80°C) in sterile tubes until use. An injection of 1.5×10^{10} vector genome of AAV2.hRPE65v2 in a volume of $150\text{ }\mu\text{l}$ of phosphate-buffered saline supplemented with Pluronic F-68 NF Prill Poloxamer 188 was administered into the subretinal space.

The viral vector used by Hauswirth was a recombinant adeno-associated virus serotype 2 (rAAV2) vector, altered to carry the human RPE65 gene (rAAV2- CB^{SB}-hRPE65), that had been previously demonstrated to restore vision in animal models with RPE65 deficiency. The RPE65-LCA viral vector was delivered by subretinal injection (5.96×10^{10} vector genomes in $150\text{ }\mu\text{l}$).

Methods and protocols of administration of therapeutic agents (e.g., protein, nucleic acid molecule, expression cassettes, gene therapy vectors, cells), including without limitation, to the eye, and other procedures and protocols (including without limitation, immunology tests, eye examinations and immunosuppressant) are known in the art. For example, the following is an example of sub-retinal injection of AAV vectors used by MacLaren in treating choroideremia. Surgery was first undertaken to detach the retina through a 41G Teflon cannula (DORC International BV, Zuidland, Netherlands) using balanced salt solution (Alcon Laboratories, Fort

Worth, TX, USA). Once the retinal target area had been detached from the underlying retinal pigment epithelium, a fixed volume (0.1 mL) containing 1×10^{10} genome particles of AAV2.REP1 was injected through a fresh syringe into the sub-retinal space that had been created in the first five patients. In patient 6, a reduced dose of up to 6×10^9 genome particles was injected. The vector was injected slowly through the same retinotomy, causing the detachment to extend further. Surgery was uncomplicated in the first five patients, but in patient 6, difficulty in detachment of the retina from the peripheral macula necessitated the induction of detachment from a point close to the fovea, which caused visible stretching of the papillomacular bundle. Because of concerns about stretch-related damage of this vital structure in a patient with 6/7.5 vision, a smaller volume of vector (maximum 0.06 mL) was injected in the second step. In all patients, the surplus vector remaining in the syringe was expelled through the cannula into a polypropylene vial and then frozen. This surplus vector was later tested for potency with Western blot after transduction of the human-derived HT1080 cell line. Patients were treated with a 10-day oral course of prednisolone, starting 2 days before surgery at 1 mg/kg (70–100 mg) for 7 days and then reduced to 40 mg for 1 day, 20 mg for 1 day, and 10 mg for 1 day. Blood samples were taken for immunological tests before, and 1 week and 5–6 weeks after surgery. See MacLaren et al., *Lancet*. 2014 March 29; 383(9923): 1129–1137.

In the Hauswirth study, administration was performed as follows. After mild intravenous sedation, the surgical eye received retrobulbar anesthesia and was then prepped and draped in a standard sterile fashion. A standard three-port 23-gauge core and peripheral vitrectomy was performed. The conjunctiva over the right-sided sclerotomy was dissected with Westcott scissors and 0.3 forceps. Hemostasis was maintained by eraser-tipped cautery. The sclerotomy was enlarged with a 20-gauge MVR blade so that the sub-retinal cannula could easily be inserted into the eye. The vector was drawn into a 39-gauge injection cannula (Synergetics, O'Fallon, MO) and was introduced into the sub-retinal space. At the end of the procedure, the sclerotomy sites were secured with 7.0 Vicryl sutures and the conjunctiva was closed with interrupted sutures. Sub-conjunctival antibiotics and steroids were administered. Topical antibiotics and steroids were used for 20 days after surgery. See, Hauswirth et al., *Hum Gene Ther*. 2008 Oct; 19(10): 979–990.

For CYP4V2 gene therapy treatment *in vitro*, post-treatment assessment can compare cell morphology and/or biochemical dysfunctions of patient's cells, e.g., comparing the levels of the compounds showed abnormalities in BCD patient's iPS-RPE cells (or iPS-PRC or iPS-CEC cells, if applicable) before and post-treatment, to assess whether the morphology and/or the biochemical function of the cells has improved post treatment.

For CYP4V2 gene therapy treatment *in vivo*, post-treatment assessment can use eye and retinal (and corneal tests, if applicable) examinations known in the art for retinal and corneal diseases, including without limitation, dark adaptation, contrast sensitivity, visual field test, visual acuity test, color vision test, ERG, OCT, fundus imaging, cornea examination, functional tests such as mobility, etc. Efficacy can be verified by one of the following: improved vision, stop of disease progression, or slower than expected rate of retinal degeneration or loss of vision.

One challenge of viral vector-mediated gene therapy is immune responses from the subject receiving the gene therapy. In addition to conventionally associated risks to the subject, the immune responses can significantly reduce the transduction efficiency of the viral vectors and/or result in a failure to establish long-term transgene expression. Mingozi F, Meulenberg JJ, Hui DJ, Basner-Tschakarjan E, Hasbrouck NC, Edmonson SA, Hutnick NA, Betts MR, Kastelein JJ, Stroes ES, High KA, AAV-1-mediated gene transfer to skeletal muscle in humans results in dose-dependent activation of capsid-specific T cells. *Blood*. 2009 Sep 3; 114(10):2077-86.

Perhaps, in part because of the unique immunological environment of the eye, the immunological effects of various recombinant viral vectors (e.g., AAV, lentivirus, adenovirus) in ocular gene therapy appear to be fairly benign. Nevertheless, a significant cell-mediated immune response can develop after intraocular administration of adenovirus. Neither AAV nor lentivirus, however, elicit a cell-mediated response and are thus promising vectors for treatment of chronic ocular (retinal) diseases. J Bennett, Immune response following intraocular delivery of recombinant viral vectors, *Gene Therapy* (2003) 10, 977–982. doi:10.1038/sj.gt.3302030. On the other hand, however, previous study showed that intravitreal administration of AAV vectors resulted in an increase in anti-AAV antibodies levels in both vitreal fluid as well as serum of non-human primates. Moreover, the presence of pre-existing neutralizing antibody titers in the

serum of monkeys correlated strongly with weak, decaying, or no transgene expression following intravitreal administration of AAV. Kotterman et al., Antibody Neutralization Poses a Barrier to Intravitreal Adeno-Associated Viral Vector Gene Delivery to Non-Human Primates, *Gene Ther.* 2015 February; 22(2): 116–126. Therefore, it is desirable to reduce immune responses in ocular gene therapy, especially those of neutralizing antibodies (NAbs), to preserve desired transduction efficiency and/or long-term transgene expression.

Historically a common practice for companies in the gene therapy field has been using AAV vector of one serotype. It typically uses a vector type with good transduction efficiency and large amount of safety data in animal studies and/or clinical trials of other gene therapy. For example, AAV2 is the most commonly used AAV serotype for ocular gene therapy in clinical trials. However, the best serotype for one patient is not always the best for another patient due to the individual differences in the immune system, e.g., pre-existing anti-AAV antibodies. For example, prevalence of pre-existing anti-AAV neutralizing antibodies against specific AAV serotypes are different among countries and populations. In addition, immune reactions can significantly reduce the transduction efficiency which can reduce efficacy of the gene therapy being applied and/or require a higher dose being administered.

A method is provided herein to reduce immune responses to viral vectors, preserve transduction efficiency, to lower viral vector and/or immunosuppressant dose, and/or to maximize therapeutic effect to different patients of the same genetic disease, in viral vector mediated gene therapy, comprising:

(a) establishing a pool of more than one recombinant viral vectors (e.g., rAAVs) with sufficient transduction efficiency in the target cell type for the gene therapy. The viral vector pool can be expanded by creating variants with antigenic region mutations or other mutations or variants on the capsids of said viral vectors after such mutations or variants are confirmed with sufficient transduction efficiency in target cells relevant to the disease (e.g., in iPS-RPE or RPE cell lines for CYP4V2 gene therapy for BCD).

(b) detecting pre-existing neutralizing anti-viral vector antibodies (NAbs) against different viral vector serotypes and/or capsid mutations or variants in the subject in need of the

gene therapy, and/or testing and comparing different viral vectors in patient-specific disease target cells (e.g., iPS-RPE cells) derived from such subject.

(c) selecting a viral vector from said pool of viral vectors with (i) sufficient transduction efficiency in the disease target cells and (ii) low cross-reactivity with the pre-existing NABs in the subject, and/or (iii) good phenotype rescue result in the subject's patient-specific disease target cells (e.g., patient-specific iPS-RPE or RPE cell lines for CYP4V2 gene therapy for BCD), wherein such viral vector pool comprising different serotypes and/or capsid-modified viral vectors (e.g., including without limitation, capsid-mutant AAVs and/or capsid protein variant AAVs).

(d) use the viral vector selected from (c) for administration to the subject.

(e) repeat (b) through (d) (only the part relating to pre-existing NABs) above each time the subject requires a gene therapy administration, including without limitation, a follow-up administration to the same organ (e.g., an eye or a contralateral eye), or to another organ.

Potential benefits of this method include reduced use of immunosuppressants, lower dose of rAAV vectors, higher transduction efficiency and longer-term transgene expression, and/or higher percentage of patients eligible for the gene therapy.

It would be appreciated that this method can be used in connection with other viral vectors. In addition, this method can be used in all types of ocular gene therapy and non-ocular gene therapy, whether it relates to the CYP4V2 gene or another gene(s).

Methods of detecting pre-existing anti-AAV antibodies are known in the art. It is worth noting that the anti-AAV antibodies include both neutralizing antibodies and non-neutralizing antibodies. Methods to detect pre-existing anti-AAV neutralizing antibodies and other immune response to AAVs are known in the art. Melvin Y Rincon et al., *JMIR Res Protoc*. 2016 Apr-Jun; 5(2): e102; Hauswirth et al., *Hum Gene Ther*. 2008 Oct; 19(10): 979–990. Although the effect is most significant with neutralizing antibodies, even non-neutralizing antibodies can trigger vector clearance by the immune system. The non-neutralizing antibodies can be detected by ELISA. Boutin S, Monteilhet V, Veron P, Leborgne C, Benveniste O, Montus MF, Masurier C, Prevalence of serum IgG and neutralizing factors against adeno-associated virus (AAV) types 1,

2, 5, 6, 8, and 9 in the healthy population: implications for gene therapy using AAV vectors. Hum Gene Ther. 2010 Jun; 21(6):704-12.

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 the methods and compositions of matter belong. In addition to the definitions of terms provided herein, definitions of common terms in molecular biology may also be found in *Glossary of Genetics: Classical and Molecular*, Rieger et al., 1991, 5th Ed, Springer-Verlag; in *Current Protocols in Molecular Biology*, Ausubel et al., Eds., 1998 Supplement, Greene Publishing Associates, Inc. and John Wiley & Sons, Inc.; in *Current Protocols in Cell Biology*, Bonifacino et al., Eds., 1999 Supplement, John Wiley & Sons, Inc.; and in *Current Protocols in Neuroscience*, Crawley et al., Eds., 1999 Supplement, John Wiley & Sons, Inc.

Representative methods and materials are described herein; other suitable methods and materials known in the art also can be used. The methods and materials are illustrative only and not intended to be limiting.

EXAMPLES

The inventions are further described in the following examples, which do not limit the scope of the inventions nor the claims.

The studies were initiated, designed, organized and sponsored by Reflection Biotechnologies Limited (“ReflectionBio”), a biotechnology company founded and driven by a patient and family living with a rare retinal disease. Rare disease patients shoulder the inevitable odds of genetic mutations for mankind, but are often ignored by society and under-supported by public resources. As a patient-driven biotechnology company, ReflectionBio applies a ‘*By Patients, For Patients*’ approach for the patients to join forces and to play a more active role in driving scientific and medical R&D on rare diseases and other challenging diseases.

Patients diagnosed with BCD and having different bi-allelic CYP4V2 mutations (including homozygous CYP4V2 mutation or compound heterozygous CYP4V2 mutations) were included in this study. Particularly, one patient (herein referred to as Patient 1, P1 or RB001) has

homozygous c.802-8_810del17insGC mutation. The c.802-8_810del17insGC mutation results in an in-frame deletion of 62 amino acid-encoding exon 7. The c.802-8_810del17insGC mutation is the most common mutation among BCD patients. Patient 2 (P2 or RB002) has compound heterozygous CYP4V2 mutations, each of the mutations is a single nucleotide change that results in only one amino acid change in the 525-amino acid long CYP4V2 protein.

Informed consents were obtained. Procedures followed the Declaration of Helsinki guidelines and were approved by an Institutional Review Board.

BCD Human Cellular Disease Model Examples

Clinically, BCD is associated with RPE atrophy, which in turn causes photoreceptor death and vision loss. Therefore, it is critical to create and use a human RPE model to study BCD and to develop treatment for BCD.

Example 1—Generation and Characterization of Induced Pluripotent Stem Cells (iPSCs) Derived from BCD Patients

In the study, integration-free methods were used to generate iPSCs from BCD patients. Traditional technologies used for iPSC reprogramming (e.g., lentivirus, retrovirus) integrate into the genome of the target cells. The resulting iPSCs and cells differentiated from those iPSCs will contain foreign DNA and could be unsafe and problematic for use in cell therapy and drug discovery applications. Furthermore, the integration could occur in a critical region of the genome, causing problems with unrelated developmental processes. Comparing to traditional reprogramming methods, integration-free reprogramming methods generate iPSCs that do not contain detectable vectors or transgenes, thus making them more suitable for cell therapy and drug discovery applications.

In the study, two different integration-free reprogramming methods were used to generate iPSCs from BCD patients, one employing Sendai virus, the other employing episomal vectors. Two different types of samples were used, one is skin sample (skin fibroblasts) and the other is blood sample (peripheral blood mononuclear cells (PBMCs)). Either method can be used to

generate BCD patient-specific iPSCs from skin, blood or other samples, such as urine and hair samples.

A. iPSC reprogramming from skin sample

Skin biopsy was performed on BCD patients, and human fibroblast cells were obtained from the biopsy. BCD patient-specific fibroblast cells were then reprogrammed into iPS cell lines using Sendai virus, a footprint-free RNA virus that carries no risk of altering the host genome. Other vectors, including without limitation, lentivirus, also can be used in iPS reprogramming, but with a risk of integrating into the genome of the host cell. See Figure 1 for photos of iPS cells derived from BCD patients. Fibroblast cells from healthy individuals also were reprogrammed in the same way to generate wild-type (or control) iPS cell lines.

To generate iPSCs, 5×10^4 fibroblasts were plated and cultured in 12-well plate until the cells became adherent (for about 12 hours) and were around 70%-80% confluent. The culture medium was removed, and the cells were transfected with a Sendai virus expressing Oct3/4, Sox2, Klf4 and c-Myc (CytoTune™-iPS 2.0 Sendai Reprogramming Kit, A16517, Life Technologies) at a MOI of 5:5:3:5 in 500 μ l of fibroblast culture medium. The cells were incubated at 37°C and 5% CO₂ overnight, after which the virus-containing medium was removed and replaced with KO-DMEM medium (KnockOut DMEM, 15 % KnockOut serum replacement, 1 L-glutamine, 1 nonessential amino acids, 1 penicillin-streptomycin, 0.1 mM β -Mercaptoethanol, basic fibroblast growth factor (bFGF) 10 ng/ml.). The transfected cells were incubated for about 7 days, with the medium changed every day.

The transfected cells were washed in PBS, exposed to trypsin (e.g., TrypLE Express at 37°C for 4 mins) and resuspended in 2 ml KO-DMEM medium containing 10 μ M ROCK inhibitor. The cells were then plated on a mitomycin-C-treated MEF feeder layer and returned to 37°C and 5% CO₂. After 24 hours and every day following, the medium was removed and replaced with KO-DMEM medium (without ROCK inhibitor). Colonies were visible 7-14 days after passage. Each iPS colony was microdissected into chunks of about 100-150 cells, following a brief treatment with KO-DMEM medium with 10 μ M ROCK inhibitor, and then cultured again in KO-DMEM medium at 37°C and 5% CO₂ for another week.

iPSC characterization was performed using primary antibodies of pluripotent markers: OCT4 Santa Cruz sc-9081 Rabbit poly, SOX2 R&D Systems 245610 Mouse IgG, TRA-1-60 Millipore (Chemicon) MAB4381, Mouse, IgM, SSEA4 Millipore (Chemicon) MAB4304 Mouse IgG, Nanog R&D Systems AF1997 Goat poly. Typically for characterization using markers, cells were washed, blocked (e.g., with 3% serum and 0.1% Triton X), exposed to a primary antibody (1:200) and incubated at room temperature for 2-3 hours. The cells were washed again, exposed to a secondary antibody and incubated at room temperature for 60 mins. Cells were then nuclear counterstained (e.g., using 1:10000 Dapi in PBST).

See Figure 1(a) for iPSCs generated from fibroblasts of BCD patients, and characterization by Oct-4, Sox-2, SSEA-4, Nanog and Tra-1-60 markers,

B. iPSC reprogramming from blood sample

In addition to skin biopsy samples, iPSCs also were generated from blood samples of BCD patient and healthy control. The iPSCs were generated from peripheral blood mononuclear cells (PBMCs) using an episomal method. The protocol is described as below.

T cells activation:

- a) Frozen PBMCs were thawed and about 0.5 million viable cells were subjected to T cell activation using Dynabeads (Human T activator, CD3/CD28, Thermo Fisher, Cat#11132D) according to the manufacturer's protocol.
- b) Activated T cells were then expanded in blood cell culture medium for 10-14 days.

Reprogramming:

- a) To generate iPSC lines, activated T cells were dissociated from dynabeads and electroporated with Episomal iPSC Reprogramming Vectors (Cat. No. A14703, Invitrogen, Carlsbad, CA, USA) using the Neon Transfection System (Cat. No. MPK10096, Invitrogen) according to the manufacturer's instructions.
- b) The two sets of electroporated cells were plated on two sets of 35 mm dishes pre-cultured with CF1 MEF feeders (Cat #: ASF-1213, Applied StemCell, Milpitas, CA, USA). The cells were fed daily with human iPSC growth medium.
- c) After 2-3 weeks, human ESC-like iPSC colonies were picked and transferred to matri-gel coated 24-well plates for expansion.

- d) Patient-specific human iPSC lines were then grown and passaged on Matrigel (Corning Cat# 354277) in Human iPSC Feeder-Free Growth Medium (mTeSR™1, Catalog # 05850, StemCell Technologies Inc., Vancouver, Canada) for 2-3 more passages until enough cell number obtained before cryopreservation.

Alkaline phosphatase:

- a) For alkaline phosphatase (AP) staining, iPSCs were fixed and then stained with alkaline phosphatase staining solution (Naphthol/fast red violet, Sigma).
- b) Cell images are captured using an Olympus microscope (IX51, Olympus, Tokyo, Japan).

See Figure 1(b) for phase contrast Images of iPSCs generated from peripheral blood mononuclear cells (PBMC) of blood samples of a BCD patient and a healthy control, and AP staining results.

See Figure 1(c) for BCD patient-derived iPSC karyotype images showing apparently normal human karyotype.

Example 2—Differentiation of iPSCs of BCD Patients Into Retinal Pigment Epithelium (RPE) Cells

iPSC differentiation started at passage 3 to 6 for all iPSC lines of BCD patients and healthy controls. For differentiation, iPS colonies were cultured to confluence in 6-well culture dishes (Costar, Corning, Corning, NY) pre-treated with 1:50 diluted Matrigel (CORNING, 356230) in differentiation medium consisting of Knock-Out (KO) DMEM (Thermo Fisher Scientific, 10829018), 15% KO serum replacement (Thermo Fisher Scientific, 10829028), 1% non-essential amino acids (Thermo Fisher Scientific, 11140050), 2 mmol/L glutamine (Thermo Fisher Scientific, 35050061), 50 U/ml penicillin-streptomycin (Thermo Fisher Scientific, 10378016), and 10 mmol/L nicotinamide (Sigma-Aldrich, N0636) for the first 14 days. During the 15th to 28th days of differentiation, differentiation medium was supplemented with 100 ng/ml human Activin-A (PeproTech, 120-14). From day 29, Activin-A was removed until differentiation was completed. After 8–10 weeks, pigmented clusters formed and were manually picked and plated on Matrigel-coated dishes. Those cells were maintained in MEM (alpha

modification, Sigma-Aldrich, M-4526)-based RPE medium, which contains N1 supplement (5 ml per 500 ml medium), Taurine (125 mg per 500 ml medium), Hydrocortisone (10 µg per 500 ml medium), Triiodo-thyronin (0.0065 µg per 500 ml medium) (all from Sigma-Aldrich), 2 mmol/L glutamine, 50 U/ml penicillin-streptomycin, 1% non-essential amino acids and 5% fetal bovine serum (all from GIBCO-BRL). Cells were cultured for another 6-8 weeks to allow them to form a functional monolayer for functional assays.

The RPE cells differentiated from BCD patients' iPSCs were observed under light microscopy and distinct RPE pigment and hexagonal cell shapes were seen (See Figure 2). In addition to morphological distinctions, iPS-derived RPE cells from BCD patients were also validated by the presence of RPE-specific markers, RPE65, CRALBP and MITF. See Figure 2(b) for RPE markers results of BCD patients' iPS-RPE cells, showing the presence of RPE-specific markers, RPE65, CRALBP and MITF.

Multiple protocols can be used to differentiate iPSCs into RPE cells. The RPE differentiation protocol described herein is an extended protocol which usually takes more than 3 months. Other protocols take less time, e.g., less than 2 months. While both shorter and extended protocols can differentiate iPSCs into RPE cells, there can be differences in terms of the risk of tumorigenesis among iPSC-RPE cells generated by different protocols. The risk of tumorigenesis associated with iPSC differentiation is attributed to a portion of the iPS cells remaining undifferentiated or not fully differentiated at the end of the protocol, and the extended protocol likely contributes to the lack of tumor formation because the iPSCs are fully differentiated into mature RPE cells. The longer-term protocol was used to ensure the purity of the iPS-RPE cell lines generated for biochemical and other assays and functional studies, and to support the safety of iPSC-RPE cells for cell therapy, including without limitation, autologous transplantation.

Example 3—Biochemical, Cell Viability and other Assays for BCD Cellular Model and CYP4V2 Functional Studies

Lipid Assays:

Previous studies on BCD and function of the CYP4V2 enzyme have focused on fatty acids. In this study, more lipid assays including not only fatty acids but also ceramides (Cer), sphingomyelins (SM), and sphingosine and sphinganine (SOSA), were used to analyze the biochemical abnormalities/phenotype in BCD disease model and to analyze the biochemical functions of the CYP4V2 protein.

Biochemical assays in free fatty acids (FFA), ceramides (Cer), sphingomyelins (SM), and sphingosine and sphinganine (SOSA) were conducted at the Biomarkers Core Laboratory of Columbia University (New York, NY, USA) based on its relevant assays and protocols.

Free fatty acids (FFA), ceramide, sphingosine and sphinganine were extracted by using chloroform:methanol. Briefly, about 1 million of iPS-RPE cells were homogenized in 150 μ L water. 100 μ L of homogenate was mixed with 3 mL of chloroform:methanol (v:v=2:1) containing internal standards (Palmitic acid-D31, C12 ceramide, C25 ceramide, C17 sphingosine, C17 sphinganine). The sample was vortexed well and 0.5 mL of water was added to allow for phase separation. The mixture was vortexed again and centrifuged at 3,000 g for 10 minutes at 4°C. The lower organic phase was transferred to a second clean glass tube using a Pasteur pipette. Two mL of chloroform was added to the residual aqueous phase, followed by vortex mixing and centrifugation again to extract any remaining lipids. The lower organic phases were pooled and evaporated under nitrogen at 37°C. The extracted lipids were reconstituted in 50 μ L of methanol:acetonitrile (v:v=1:1) and transferred to LC autosampler vials for injection. Sphingomyelin was also extracted by chloroform:methanol like other lipids, but only 2 μ L cell homogenate was placed for sample preparation for sphingomyelin. All assays were performed on a Waters Xevo TQ MS ACQUITY UPLC system (Waters, Milford, MA, USA). FFA was eluted by a 100 mm Waters ACQUITY UPLC HSS C18 column. Ceramide, sphingosine, sphinganine, sphingomyelin were separated on a 100 mm Waters ACQUITY UPLC BEH Phenyl column. FFA was monitored by using negative SIR method and others by positive MRM acquisition.

A list of compounds tested in the biochemical assays is provided in Table 2 below. Certain chemical compounds were purchased for use as standards in this study (as annotated in Table 2. Nu-Chek: Nu-Chek Prep, Inc., Elysian, MN, USA; Cayman: Cayman Chemical Company, Ann Arbor, MI, USA). Other compounds used existing standards available at the Biomarkers Core Laboratory of the Columbia University (New York, NY, USA). All FFAs were detected by single MS, whereas other types of compounds were detected by MS/MS.

TABLE 2: TEST COMPOUND LIST						
	Description	Vendor	Cat #		Ceramides (Cer)	Description
Fatty Acids (FFA)						
C12	C12:0 (LAURIC ACID)	Nu-Chek	N-12-A		C14	C14 Ceramide (d18:1/14:0)
C13	C13:0 (TRIDECANOIC ACID)	Nu-Chek	N-13-A		C16:1	C16:1 Ceramide (d18:1/16:1)
C14:1 Isomer 1					C16	C16 Ceramide (d18:1/16:0)
C14:1 Isomer 2					C18:1	C18:1 Ceramide (d18:1/18:1)
C14 Myristic Acid	C14:0 (MYRISTIC ACID)				C18	C18 Ceramide (d18:1/18:0)
C15	C15:0 (PENTADECANOIC ACID)	Nu-Chek	N-15-A		C20:5	C20:5 Ceramide (d18:1/20:5)
C16:1 n7 cis	Δ 9 cis (PALMITOLEIC ACID)	Nu-Chek	U-40-A		C20:4	C20:4 Ceramide (d18:1/20:4)
C16:1 n9 cis	cis-7-Hexadecenoic Acid	Cayman	1000729 0		C20:1	C20:1 Ceramide (d18:1/20:1)
C16:1 n7 trans	Δ 9 trans (PALMITELAIDIC ACID)	Nu-Chek	U-41-A		C20	C20 Ceramide (d18:1/20:0)
C16 Palmitic Acid	C16:0 (PALMITIC ACID)				C22:6	C22:6 Ceramide (d18:1/22:6)
C17	C17:0 (MARGARIC ACID)	Nu-Chek	N-17-A		C22:5	C22:5 Ceramide (d18:1/22:5)
C18:3 n3 Alpha	C18:3n-3 (ALPHA LINOLENIC ACID)	Nu-Chek	U-62-A		C22:1	C22:1 Ceramide (d18:1/22:1)
C18:3 n6 Gamma	C18:3n-6 (GAMMA LINOLENIC ACID)	Nu-Chek	U-63-A		C22	C22 Ceramide (d18:1/22:0)
C18:2 n6 9,12 cis	Δ 9 cis,12 cis (LINOLEIC ACID)	Nu-Chek	U-59-A		C24:1	C24:1 Ceramide (d18:1/24:1)
C18:2 n6 9,12 trans	Δ 9 trans 12 trans (LINOELAIDIC ACID)	Nu-Chek	U-60-A		C24	C24 Ceramide (d18:1/24:0)
C18:1 Oleic Acid	C18:1n-9 (OLEIC ACID)				C26:1	C26:1 Ceramide (d18:1/26:1)
C18 Stearic Acid	C18:0 (STEARIC ACID)				C26	C26 Ceramide (d18:1/26:0)
C19	C19:0 (NONADECANOIC ACID)	Nu-Chek	N-19-A		C28:1	C28:1 Ceramide (d18:1/28:1)
C20:5 n3 EPA	EICOSAPENTAENOIC ACID (EPA)	Nu-Chek	U-99-A		C28	C28 Ceramide (d18:1/28:0)
C20:4 n6 AA	ARACHIDONIC ACID (AA)	Nu-Chek	U-71-A			
C20:4 Isomer					Sphingomyelins (SM)	
C20:3 n6	HOMO GAMMA LINOLENIC ACID	Nu-Chek	U-69-A		C14:1	C14:1 Sphingomyelin (d18:1/14:1)
C20:3 Isomer 1					C14	C14 Sphingomyelin (d18:1/14:0)
C20:3 Isomer 2					C16:1	C16:1 Sphingomyelin (d18:1/16:1)
C20:2 n6	11-14 EICOSADIENOIC ACID	Nu-Chek	U-68-A		C16	C16 Sphingomyelin (d18:1/16:0)
C20:2 Isomer					C18:1	C18:1 Sphingomyelin (d18:1/18:1)
C20:1 n9	11-EICOSENOIC ACID	Nu-Chek	U-66-A		C18	C18 Sphingomyelin (d18:1/18:0)
C20 Arachidic Acid	C20:0 (ARACHIDIC ACID)				C20:5	C20:5 Sphingomyelin (d18:1/20:5)
C21	HENEICOSANOIC ACID	Nu-Chek	N-21-A		C20:4	C20:4 Sphingomyelin (d18:1/20:4)
C22:6 n3 DHA	DOCOSAHEXAENOIC ACID (DHA)	Nu-Chek	U-84-A		C20:1	C20:1 Sphingomyelin (d18:1/20:1)
C22:5 n3 DPA	7-10-13-16-19 DOCOSAPENTAENOIC ACID	Nu-Chek	U-101-A		C20	C20 Sphingomyelin (d18:1/20:0)

C22:5 n6	4-7-10-13-16	DOCOSAPENTAENOIC ACID	Nu-Chek	U-102-A	C22:6	C22:6 Sphingomyelin (d18:1/22:6)
C22:4 n6	7-10-13-16	DOCOSATETRAENOIC	Nu-Chek	U-83-A	C22:5	C22:5 Sphingomyelin (d18:1/22:5)
C22:1 n9	13-DOCOSENOIC (ERUCIC)				C22:1	C22:1 Sphingomyelin (d18:1/22:1)
C22	BEHENIC ACID		Nu-Chek	N-22-A	C22	C22 Sphingomyelin (d18:1/22:0)
C23	TRICOSANOIC ACID		Nu-Chek	N-23-A	C24:1	C24:1 Sphingomyelin (d18:1/24:1)
C24:1 n9	NERVONIC ACID		Nu-Chek	U-88-A	C24	C24 Sphingomyelin (d18:1/24:0)
C24	LIGNOCERIC ACID		Nu-Chek	N-24-A	C26:1	C26:1 Sphingomyelin (d18:1/26:1)
C25	PANTACOSANOIC ACID		Cayman	15197	C26	C26 Sphingomyelin (d18:1/26:0)
C26:1	C26:1 n9 (Hexacosanoic acid)				C28:1	C28:1 Sphingomyelin (d18:1/28:1)
C26	HEXACOSANOIC ACID		Cayman	13354	C28	C28 Sphingomyelin (d18:1/28:0)
SOSA						
SO	Sphingosine (d18:1)					
SA	Sphinganine (d18:0)					
SO-1P	Sphingosine-1-Phosphate (d18:1)					
SA-1P	Sphinganine-1-Phosphate (d18:0)					

Hydroxy-fatty acid Assays:

In addition, LC-MS/MS was used to detect hydroxy-fatty acids in iPS-RPE cells, including 16-HEPE, 17-HEPE, 18-HEPE, 19-HEPE, 20-HEPE, 17-HDHA, 18-HDHA, 19-HDHA, 20-HDHA, 21-HDHA, 22-HDHA, 19(20)-EpDPA (formal name: ($\pm$)19,20-epoxy-4Z,7Z,10Z,13Z,16Z-docosapentaenoic acid, a/k/a ($\pm$)19,20 EDP, ($\pm$)19,20-epoxy Docosapentaenoic Acid, ($\pm$)19,20-epoxy DPA, ($\pm$)19,20-EpDPE), and 19(20)-DiHDPA (formal name: ($\pm$)19,20-dihydroxy-4Z,7Z,10Z,13Z,16Z-docosapentaenoic acid, a/k/a: ($\pm$)19,20-DiHDoPE). The HDHA compounds are hydroxy-metabolites of DHA and the HEPE compounds are hydroxy-metabolites of EPA, respectively. 19(20)-EpDPA is a DHA epoxigenase metabolite, derived via epoxidation of the ω -3 double bond of DHA. 19(20)-DiHDPA is also a metabolite of DHA. DHA is an important fatty acids and the most abundant ω -3 fatty acid for the brain and retina. A previous research indicated that CYP4V2 is a hydroxylase for ω -3 fatty acids, particularly DHA.

Materials: Hydroxy-fatty acid standards ($\pm$)18-HEPE (Item No. 32840), ($\pm$)20-HDHA (Item No. 33750), ($\pm$)19(20)-EpDPA (Item No. 10175) and ($\pm$)19(20)-DiHDPA (Item No. 10007001) were purchased from Cayman Chemical Company (Ann Arbor, MI, USA). Internal standard deuterated palmitic acid (C16-D31 fatty acid) was purchased from C/D/N Isotopes Inc. (#D-2002, Quebec, Canada).

It should be understood that in addition to LC-MS or LC-MS/MS methods described above, the chemical species and compounds tested in the study can also be detected and/or quantified by using other methods. For example, there are GC-MS or GC-MS/MS methods for FFA with methylation pre-treatment. For Cer and SM, FIA-MS/MS or GC-MS/MS can be used.

Cell Viability Assay:

Blue light exposure: iPS-RPE cells were seeded in 3.5cm dishes and 4-well chamber dishes. After 2 months, they were exposed to 430 ± 20 nm (blue) light at $1.5\text{mW}/\text{cm}^2$ for 1 hour in PBS(+) containing $10\text{ }\mu\text{g}/\text{ml}$ glucose. The same seeding density was used for all cell lines. After blue light exposure, treated cells were fed with fresh RPE medium and recovered in incubator of 5% CO_2 and 37°C overnight.

In addition to 1 hour, shorter or longer light exposure durations can be used, e.g., no exposure, 30 minutes, 45 minutes, 75 minutes, 90 minutes or 120 minutes, etc. Similarly, exposure to light of a different wavelength or a broader spectrum can also be used. Moreover, iPS-RPE samples of different culture days (e.g., 2 months, 3 months, 4 months, 5 months or 6 months in RPE culture) can be used, e.g., to study the effect of aging.

Cell viability assay: Live/healthy cells were labeled by cell-permeant dye Calcein AM (Thermo Fisher Scientific, catalog no.: C3099, USA) at a final concentration of 3 $\mu\text{mol/ml}$ PBS(+) (1 ml for each 3.5cm dish or 200 μl for each chamber) and dead/sick cells were labeled by Propidium Iodide (PI) (Thermo Fisher Scientific, catalog no.: P3566, USA) at a final concentration of 2 $\mu\text{g/ml}$ PBS(+) (1 ml for each 3.5cm dish or 200 μl for each chamber) at room temperature for 1 hour. Since PI is DNA-binding and is not permeant to live cells, it is commonly used to detect dead cells in a population. Then after washing with PBS(-), cellular fluorescent levels were observed and photos were taken by inverted fluorescent microscope (Nikon Eclipse Ts2R) at 20 times magnification. Dead/live cell ratios were calculated after photos were processed by ImageJ (Fiji).

In addition to biochemical assays and cell viability test, RPE function tests can be performed in BCD patient iPS-RPE cells such as phagocytic activity, transepithelial resistance.

CYP4V2 Expression:

Experiments were performed to detect and compare CYP4V2 expression levels in control and BCD patient-specific iPS-RPE cells. CYP4V2 expression in cell lines can be assessed by either anti-CYP4V2 antibody (Western Blot) or by quantitative PCR.

CYP4V2 Western Blot: 45 μg whole cell protein from each iPS-RPE sample was run on a 7.5% SDS page gel, then wet transfer to a membrane. The membrane was blocked with 5% BSA in PBST for 1 hour at room temperature then incubated with primary antibody (Anti-CYP4V2 produced in rabbit, Sigma Aldrich catalog #: SAB 1410565, USA) at a concentration of 1: 1000 in 5% BSA overnight at 4°C. Wash was done for 3 x 10 minutes with PBST. The membrane then was incubated with secondary antibody goat anti-rabbit IgG HRP (Santa Cruz

catalog #: sc-2004, USA) at a concentration of 1:3000 in 5% BSA for 4 hours at 4°C. Final wash was done for 3x10 minutes with PBST. GAPDH was used as loading control.

CYP4V2 western blot detected CYP4V2 protein expression in controls' iPS-RPE samples but not in BCD patient iPS-RPE sample. After treatment by AAV.CYP4V2, CYP4V2 protein was detected in BCD patient-specific iPS-RPE samples.

Real-time PCR and relative mRNA quantification: Healthy controls' (WT), BCD patient's, BCD patient's AAV.CYP4V2 treated iPS-RPE samples were harvested and lysed with TRIZOL reagent (Invitrogen). Total RNA was isolated according to the manufacturer's instructions. DNase I (Invitrogen) treatment was then performed to prevent genomic DNA contamination. The reverse transcription reaction was conducted by Superscript III Reverse Transcription kit, and a random hexamer (Invitrogen) was used to generate cDNA. Real-time PCR method was performed using Maxima SYBR Green/ROX qPCR Master Mix (Fisher Scientific) with StepOne Real-time PCR System (Invitrogen) to quantify gene expression levels (38 cycles). Primers specific to CYP4V2 exon 7 region and CYP4V2op, respectively, were used. Actin was used as the housekeeping gene.

Results: Quantitative PCR was performed to test the expression of CYP4V2 and CYP4V2op in iPS-RPE cell samples. The transcript levels of CYP4V2 and CYP4V2op were normalized by a patient sample and a control sample, respectively. For CYP4V2, all non-patient control samples expressed similar levels of CYP4V2, several hundred folds higher than the CYP4V2 expression level in the patient sample. After AAV.CYP4V2 treatment, the patient sample CYP4V2 expression level increased more than a hundred folds to a level comparable to the non-patient control samples (Figure 3). For CYP4V2op, all the AAV-treated samples expressed much higher levels compared with non-treated samples (Figure 4). These results demonstrated that AAV vectors were able to deliver the CYP4V2 cDNA into BCD patients' iPS-RPE cells and the expression cassettes were able to express the gene.

Example 4—Phenotype in BCD Cellular Model and Findings on CYP4V2 Functions*Lipid Testing results:*

To determine whether and which biochemical defects / abnormalities (i.e., phenotype) exist in the BCD cellular model (e.g., BCD patient iPS-RPE cells), the biochemical assays described in Example 3 was used to detect and quantify fatty acids, ceramides, sphingomyelins, sphingosina, sphinganine, and hydroxy-fatty acids in the iPS-RPE cells derived from BCD patients as compared to those of the iPS-RPE cells derived from healthy controls.

Before testing, the cells were harvested as follows. Approximately 1 million iPS-RPE cells derived from a BCD patient were washed twice with PBS, then detached from dish by a plastic cell lifter and transferred to a 1.5 ml Eppendorf tube using a 1 ml pipette. The Eppendorf tube was placed in a -80°C freezer before testing. Health control iPS-RPE cells were harvested in the same way. Biochemical assay results are shown in Table 3 below:

Table 3 Fatty Acid Test Results									
mol % of total fatty acids	WT	P1	P1 AAV2.op	P2	P2 AAV2tri.op	P2 AAV2.op	P2 AAV8.fv	P2 scAAV1.op	
C12	0.2%	0.1%	0.1%	0.1%	0.1%	0.0%	0.0%	0.1%	
C13	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
C14:1 Isomer 1	0.1%	0.1%	0.1%	0.0%	0.0%	0.0%	0.1%	0.1%	
C14:1 Isomer 2	0.0%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%	0.1%	
C14 Myristic Acid	1.0%	0.6%	0.6%	0.7%	0.8%	0.8%	0.8%	1.1%	
C15	1.3%	0.5%	0.7%	0.5%	0.5%	0.6%	0.6%	0.7%	
C16:1 n7 cis	2.7%	2.4%	1.7%	2.3%	2.9%	2.9%	2.8%	3.8%	
C16:1 n9 cis	0.9%	0.9%	0.8%	1.0%	1.0%	1.1%	1.2%	1.6%	
C16:1 n7 trans	0.4%	0.5%	0.4%	0.5%	0.5%	0.4%	0.5%	0.4%	
C16 Palmitic Acid	20.3%	14.2%	12.7%	14.8%	17.0%	17.2%	17.9%	17.4%	
C17	1.1%	0.5%	0.8%	0.5%	0.4%	0.5%	0.5%	0.4%	
C18:3 n3 Alpha	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
C18:3 n6 Gamma	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	
C18:2 n6 9,12 cis	1.6%	1.1%	0.9%	0.9%	0.9%	1.0%	1.0%	1.3%	
C18:2 n6 9,12 trans	0.1%	0.1%	0.1%	0.1%	0.1%	0.0%	0.1%	0.1%	
C18:1 n9 Oleic Acid	22.2%	20.9%	19.0%	18.5%	19.4%	20.8%	19.7%	28.6%	
C18 Stearic Acid	26.3%	17.9%	24.2%	19.4%	16.5%	16.6%	17.7%	14.4%	
C19	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	
C20:5 n3 EPA	0.8%	1.9%	1.3%	1.9%	1.6%	1.7%	1.4%	1.6%	
C20:4 n6 AA	5.4%	15.2%	13.3%	14.7%	14.2%	13.2%	13.0%	7.9%	
C20:4 Isomer	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
C20:3 n6	0.6%	0.8%	0.8%	0.9%	0.8%	0.9%	0.8%	0.6%	
C20:3 Isomer 1	0.1%	0.3%	0.3%	0.4%	0.3%	0.3%	0.3%	0.1%	
C20:3 Isomer 2	3.8%	6.0%	5.5%	5.1%	5.5%	4.1%	4.2%	3.0%	
C20:2 n6	0.4%	0.4%	0.5%	0.3%	0.4%	0.3%	0.4%	0.6%	
C20:2 Isomer	0.6%	0.6%	0.8%	0.7%	0.8%	0.7%	0.7%	0.9%	
C20:1 n9	3.7%	2.9%	2.7%	2.7%	3.6%	3.4%	3.3%	6.1%	
C20 Arachidic Acid	0.8%	0.5%	0.5%	0.5%	0.6%	0.6%	0.5%	0.5%	
C21	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	
C22:6 n3 DHA	2.2%	6.1%	5.6%	7.2%	6.2%	6.5%	6.5%	4.1%	
C22:5 n3 DPA	1.0%	2.0%	2.4%	2.8%	2.1%	2.6%	2.1%	1.7%	

C22:5 n6		0.1%	0.4%	0.5%	0.4%	0.3%	0.3%	0.4%	0.2%
C22:4 n6		0.7%	1.3%	1.7%	1.4%	1.4%	1.3%	1.3%	1.0%
C22:1 n9		0.5%	0.6%	0.6%	0.6%	0.7%	0.7%	0.7%	0.9%
C22		0.2%	0.2%	0.2%	0.1%	0.2%	0.2%	0.2%	0.1%
C23		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
C24:1 n9		0.3%	0.4%	0.4%	0.4%	0.4%	0.4%	0.5%	0.3%
C24		0.1%	0.2%	0.2%	0.2%	0.2%	0.2%	0.2%	0.1%
C25		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
C26:1		0.0%	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%	0.0%
C26		0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
Sum		100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
Total of n-3 Fatty acids		4.0%	10.0%	9.4%	11.9%	9.9%	10.8%	10.1%	7.4%

Footnote to Table 3:

WT: Wild-type control iPS-RPE. P1: Patient 1 iPS-RPE. P2: Patient 2 iPS-RPE.
Patient untreated and AAV treated samples were culture day and clone line matched.
P1 AAV2.op and P2 AAV2.op samples were treated by AAV2.CYP4V2op (1 day. MOI: 5×10^4 GC/cell) and harvested 10 days post treatment. P2 AAV2trip.op sample was treated by AAV2tri(Y-F).CYP4V2op (1 day. MOI: 5×10^4 GC/cell) and harvested 10 days post treatment. P2 AAV8.fv sample was treated by AAV8.CYP4V2fv (1 day. MOI: 2×10^5 GC/cell) and harvested 10 days post treatment. P2 scAAV1.op sample was treated by scAAV1.CYP4V2op (1 day. MOI: 2×10^5 GC/cell) and harvested 4 days post treatment.

The results showed that BCD patient iPS-RPE cell samples have a different fatty acid profile from that of the control. In particular, BCD patient samples have much higher levels of DHA (22:6 n3) and total of omega-3 (ω -3, or n3) fatty acids (sum of C18:3 n3 Alpha, C20:5 n3 EPA, C22:6 n3 DHA and C22:5 n3 DPA) than those of control. This confirmed suggestions from a previous study that CYP4V2 affects omega-3 fatty acid metabolism.

Surprisingly, in addition to abnormalities in n3 fatty acid levels, BCD patient iPS-RPE cells also showed higher level of C20:4 n6 (Arachidonic Acid, or AA). Abnormal level of AA has not been reported in prior studies relating to BCD.

Interestingly, abnormalities in n3 fatty acids (including DHA) and n6 fatty acids (including AA) was not found in a prior research which tested fatty acid levels in BCD patients' serum. The different fatty acid profiles of BCD patient iPS-RPE cells and serum supports the hypothesis that the function of CYP4V2 is substituted by other CYP4 enzymes in non-retinal or non-RPE cells, many of which are expressed in other organs and tissues together with CYP4V2 except that CYP4V2 is the only CYP4 enzyme with relatively high expression level in RPE cells.

In addition to fatty acids, BCD patient iPS-RPE cells may have phenotype in other compounds or compound classes. Experiments are conducted to screen for phenotype in other compound classes, including without limitation, corticosteroid, sphingolipids and phospholipids including sphingomyelin, ceramide, sphingosine and sphinganine, and in lipid signaling. Furthermore, isotopic tracing experiment and proteomic analysis (e.g., mass spectrometry-based proteomic analysis) is performed in BCD patients' iPS-RPE cells.

Further, a prior research found that CYP4V2 is a ω -3 fatty acid (DHA and EPA) hydroxylase. Interestingly, hydroxy-DHAs or hydroxy-EPAs described in Example 3 were not detected in either healthy control or BCD patient's iPS-RPE cells using LC-MS/MS. It is possible that the CYP4V2 enzymatic functions are different in live cells vs. in a chemical reaction outside live cells which was conducted in the prior research, or the hydroxy-fatty acids are intermediates that are fast converted into other compounds or forms in live cells, or the hydroxy-fatty acids are at trace level which can be detected only when a sample contains a very large amount of cells.

Cell Viability Assay results:

Clinically, BCD is associated with RPE atrophy, which in turn causes photoreceptor death and vision loss. Cell viability assay (as described in Example 3 above) revealed RPE

atrophy in BCD patients' iPS-RPE cell samples. See Figures 5 and 6 for cell viability comparison between iPS-RPE samples of controls and BCD patients (Figure 5 – without exposure to blue light; Figure 6 – after 1 hour exposure to blue light).

Significantly, these images revealed that:

- 5 (1) After exposure to light, significant levels of cell death were shown in iPS-RPE samples derived from BCD patients (P1 and P2), much higher than those of controls (WT1 and WT2) (See Figure 6). For example, the dead/live cell ratio of P1 iPS-RPE was 20.87%, as compared to 3.0% for WT2 iPS-RPE. The clinical phenotype of BCD, RPE atrophy, was evident in the BCD Cellular Model.
- 10 (2) Different levels of RPE atrophy was observed between BCD P1 and P2 iPS-RPE samples. P1 iPS-RPE showed a higher cell death level than P2 iPS-RPE.
- (3) Even without blue light exposure, BCD patient iPS-RPE sample (P1) showed RPE atrophy (Figure 5).

BCD patients differ widely in disease onset age and progression. BCD onset ranges from
15 early teenage to the 3rd decade of life or even beyond the 3rd decade; leading to legal blindness during the 3rd decade to 6th decade of life. In addition, BCD sibling patients with the same CYP4V2 mutation can have material difference in disease onset age and progression. Previously there was no explanation to these differences. The difference in RPE atrophy levels between different BCD patient's iPS-RPE samples provides a guidance at the cellular level as to the
20 difference in disease onset and progression among BCD patients.

Multiple phenotypes (both molecule-level phenotype such as biochemical (e.g., lipid) abnormalities and cellular-level phenotype such as cell viability) have been found in the BCD Cellular Model in this study, including the clinical phenotype of BCD (i.e., RPE atrophy).

25 Example 5—Use of iPS and iPS-RPE Cells from a BCD Subject to Screen Drug Candidates and Dosage Range, Study BCD and CYP4V2 Function and in Cell Therapy, and to Assess Patient-specific Responses

As the BCD disease human cellular model, iPS and iPS-RPE cells from BCD patients have a broad range of applications, including without limitation, to study BCD and CYP4V2

function (see Examples 3 and 4 above, for example); to screen drug candidates and dosage range for BCD and related diseases (see the Examples herein).

Methods and examples to use the BCD cellular model (e.g., BCD patient-specific iPS-RPE cell line or iPS-RPE cell lines with artificially generated CYP4V2 mutations) is described in detail in the Examples herein, which are related to the use of the BCD cellular model in gene therapy and cell therapy. In addition to testing gene therapy and as cellular base for cell therapy, such BCD cellular model can be used to screen and test efficacy and/or safety of other therapeutic agents (e.g., drug candidates) and dosage, formulation and vector (viral or non-viral vectors) thereof or devices or delivery mechanisms for treating BCD, IRD or RP, in the same or similar way as described in detail in the Examples herein.

In using the BCD cellular model, the efficacy of a therapeutic agent can be assessed by comparing the levels of compounds in the various species and RPE atrophy described in Examples 3 and 4 above and other Examples herein before treatment and post treatment by such therapeutic agent and assess whether the abnormalities in the levels of these compounds and whether RPE atrophy in the BCD cellular model improve post treatment. Similarly, different doses, formulations (e.g., formulation for chemical compounds, active pharmaceutical ingredients, or vector type and/or capsid for gene therapy, or vector type for gene editing) or key constructs (e.g., a promoter or other regulatory sequence in a gene therapy expression cassette) of a therapeutic agent can be compared using the BCD cellular model. In addition, BCD cellular model can be used to test the efficacy of a medical device or method, including without limitation, in delivering therapeutic agents to the ocular cells or in improving transduction or transfection efficiency. It would be understood that the treated cells can be compared to untreated cells or to the same cells prior to exposure to the compound. Different dosages can be used to determine the effective dosage range (measured by per cell, per 1 million cells or per 0.5 million cells, etc.). Data relating to the levels of different compounds of fatty acids and other compounds and RPE atrophy stated in Examples 3 and 4 above, in BCD patient's iPS-RPE cells (post treatment vs. without treatment) as compared to those in RPE or iPS-RPE cells of healthy control can be used to assess therapeutic effect and effective dosage range.

Furthermore, BCD patient-specific iPS cell lines, iPS-RPE cell lines and other iPS-derived cell lines can be used to assess such patient's individual responses to a therapeutic agent,

dose, or device. The patient-specific iPS cells, iPS-RPE cells and other iPS-derived cells possess traits specific to each patient, including without limitation, immune response (e.g., intracellular immunity, RPE immunity), genotype (e.g., different mutations between patients which may result in a different response). Such application can be used to develop and screen individualized therapeutic agent (e.g., different AAV vector serotypes or capsid mutations) or personalized optimal dosage for different patients of the same disease. This approach can be used for other diseases, including without limitation, other ocular diseases.

Since BCD patient-specific iPS-RPE revealed individual differences in BCD patients, it can be used to assess individualized optimal dosage and develop personalized medicine. For example, as seen in the gene therapy Examples below, at the same dosage of 1×10^5 MOI, AAV2.CYP4V2op achieved different rescue levels (i.e., different efficacy levels) of RPE atrophy between P1 and P2's iPS-RPE. This is an advantage BCD cellular model has over animal models.

BCD patient-specific iPS-RPE cells (i.e., BCD cellular model) can be used to assess and suggest therapeutic effective dosage for treatment *in vivo* by multiply the optimal dose level (e.g., indicated as MOI for gene therapy *in vitro*) determined in BCD cellular model *in vitro* by the estimated number of ocular cells (e.g., RPE cells) targeted for treatment *in vivo* to arrive the dose level of gene therapy vectors for use *in vivo* (e.g., GC or gp). Such vector dose level is adjusted by a multiplier (e.g., 1 to 10 (e.g., 1 to 5 for sub-retinal injection or 5 to 10 for intravitreal injection); the other factors affecting the multiplier to be applied include the size of the area targeted, and the subject being treated (e.g., the age, weight, development stage of the disease and condition of the subject to be treated, and potential immune reactions (i.e., pre-existing NAbs); the location and density of the cells targeted for treatment) to suggest the therapeutic effective dose range for treatment *in vivo*, which can be confirmed or further refined by clinical trials. This method can also be used to assess or suggest personalized optimal dose for treatment *in vivo* for individual patient.

Example 6—BCD Cellular Model with Artificially Created CYP4V2 Mutations

Because BCD is a rare disease, patient samples can be difficult to obtain. To overcome this difficulty, a BCD cellular model can be generated by using gene editing technologies such as

CRISPR to create artificial mutations in the CYP4V2 gene in non-BCD patient cells such as embryonic stem (ES) cell lines or iPS cells from a subject without BCD.

For example, as demonstrated in the Examples herein, sgRNA 1, sgRNA 2, sgRNA 3, sgRNA 4 or sgRNA 5 (See SEQ ID NOs: 48 to 52 for the protospacer element sequence in each of sgRNA1, sgRNA2, sgRNA3, sgRNA4 and sgRNA5, respectively; See SEQ ID NO: 55 and 59 for additional sequence for the IVT sgRNAs) were used in combination with SpCas9 protein to create cleavage in a region of the CYP4V2 gene in a BCD patient's genomic DNA containing the c.802-8_810del17insGC mutation, the most common CYP4V2 mutation among BCD patient. Amongst them, sgRNA 3, sgRNA 4, and sgRNA 5 are not specific to the c.802-8_810del17insGC mutation sequence and therefore can create double stranded DNA break (DSB) in the CYP4V2 gene of a healthy cell (e.g., an ES or iPSC without a CYP4V2 mutation). In particular, after transfection, sgRNA 4 and Cas9 can create a DSB in exon 7 of CYP4V2 gene, which can result in a mutation in exon 7 (in one or both alleles) when the DNA is repaired through non-homologous end joining (NHEJ) in cells, e.g., an indel error created by NHEJ can result in a frameshift mutation. As a result, some cells can have artificially created CYP4V2 mutations and can be used as a BCD cellular disease model or used to generate BCD cellular model (e.g, differentiate the ES or iPS cells into RPE cells to generate CYP4V2 mutation containing ES-RPE or iPS-RPE cells). Similarly, two sets of gRNAs designed to create DSB at different regions of the CYP4V2 gene can be used to generate a large deletion or a knockout mutation within the CYP4V2 gene or to knockout the entire CYP4V2 gene in cells, thereby generating a BCD cellular model containing a CYP4V2 mutation(s). More detailed discussion on how to use CRISPR system to cut and/or correct a target sequence, and how to validate the results are provided in the Examples and disclosure herein.

These BCD cellular model with artificially created CYP4V2 mutations can be used to mimic BCD patient-specific cellular model in studying BCD and CYP4V2 functions, as well as in related applications as discussed herein, including but not limited to, testing and comparing drug candidates, determining dosage range and testing medical device or delivery method.

The same method can be used to generate cellular disease models with artificially created mutations for an ocular or other disease, including the ones associated with the a mutation or genetic defect in one or more gene(s) set forth in Table 4.

Example 7—Generation and Use of Isogenic Control for Ocular Diseases

A mutation-corrected isogenic patient-specific iPS cell line and/or other cell lines derived from thereof (e.g., iPS-RPE cells, iPS-RPCs, iPS-CECs, iPS-CE cells or other iPS-ocular cells) can be used as an isogenic control in studying a disease and/or the implications of the specific mutation or defective gene. A conventional control (e.g., a cell line, e.g., an ES-RPR or iPS-RPE cell line) derived from ES or another individual possesses individual differences including genetic differences from a patient in addition to differences in the disease related gene. This Example provides a method to eliminate individual differences between controls and the "background noise" resulted therefrom. It comprises generating and using a mutation-corrected isogenic control from a patient to compare to the same patient's cell line harboring the mutation. Since a patient-specific disease model and an mutation-corrected isogenic control derived from the same patient do not have any individual differences, they can be analyzed and compared to precisely identify the phenotype, biochemical abnormalities, and other structural and functional defects associated with the mutation or defective gene of the patient. A mutation-corrected isogenic control can be generated by using gene-editing technologies including without limitation CRISPR, ZFN and TALEN. A specific example on how to use CRISPR gene editing to correct the c.802-8_810del17insGC mutation, the most common mutation among BCD patients, thereby generating an isogenic control from a BCD patient is provided in the Examples herein. The same approach can be used to create isogenic control for other ocular diseases. Isogenic controls have significant advantages over conventional controls and can be indispensable in studying ocular diseases with a subtle phenotype (e.g., age-related macular degeneration (AMD)). In addition, isogenic controls can be used to compare and identity the impact differences of multiple genetic risk factors, mutations and/or multiple genes in an ocular disease by creating isogenic control with each one of the genetic risk factor, mutation or gene corrected and compare such isogenic control to the disease model to determine the impact of related risk factor, mutation or gene in the ocular and other disease, including the ones associated with the a mutation or genetic defect in one or more gene(s) set forth in Table 4.

An isogenic control can be compared to a patient-specific cellular disease model to identify phenotype, biochemical abnormalities, and other structural and functional defects

associated with the genetic mutation and/or the related defective protein, A specific non-limiting Example and discussions on how to use bio-assays to identity biochemical abnormalities/phenotype between patient cell lines and controls are provided herein in Examples 3 and 4 above, including without limitation, lipidomics, proteomics and isotopic tracing.

5 Discussion on BCD Human Cellular Disease Model

Given that BCD is a rare disease, it is impracticable to obtain the disease manifesting human RPE cells from BCD patients through biopsy. The lack of a viable BCD human disease model has limited prior research on BCD to using non-BCD disease causing cells (e.g., fibroblasts and lymphocytes, which are not part of the eye) and serum from BCD patients as
10 study subjects. The results from these studies were centered around fatty acid anabolism.

In the study described herein, iPS cell lines derived from BCD patients were successfully generated and utilized to generate patient-specific BCD disease RPE cells, which carry BCD disease phenotype *in vitro*. The BCD phenotype was directly identified in BCD patient-specific iPS-RPE cells, the primary cell type affected in BCD. Before the present study, it was not
15 known whether iPS cell lines and iPS-RPE cell lines could be successfully generated due, in part, to the fatty acid anabolism associated with BCD.

Biochemical testing showed that iPS-RPE cells from BCD patients have abnormal levels of fatty acids as compared to those of healthy control's iPS-RPE cells, including ones which have not been reported in prior BCD studies. The *in vitro* phenotype of BCD disease-specific
20 iPS-RPE cells provide more insights to the pathways regulated by CYP4V2 and pathogenesis of BCD, and provided invaluable insights into the pathogenesis of BCD and function of CYP4V2 protein, and further supports the use of iPS-RPE cell lines from BCD patients as a viable and robust BCD human disease model.

The iPS cell lines, iPS-RPE cell lines and other iPS-ocular cell lines from BCD patients
25 have further applications, such as use for drug screening, developing novel therapeutic agents or determining dosage ranges, as well as use in cell therapy.

In addition to BCD patient-specific iPS, iPS-RPE and other iPS-ocular cell lines, a BCD human disease cellular model can be developed via gene editing to create pathologic CYP4V2 mutations artificially in other cell lines derived from ES cells or iPS cells of non-BCD
30 individuals, including without limitation, ES cell lines, iPS cell lines and RPE cell lines.

Furthermore, methods to generate isogenic controls for ocular diseases are provided. Isogenic controls do not possess individual differences from a patient-specific disease model. Hence an isogenic control has its advantages in studying ocular diseases over conventional controls.

5

CYP4V2 Gene Therapy

Example 8—cDNAs Encoding the human CYP4V2 Protein and a Functional CYP4V2 Protein

Three cDNAs were used in the study. The cDNA with sequence shown in SEQ ID NO: 1 (herein referred to as CYP4V2st) and the cDNA with sequence shown in SEQ ID NO: 2 (herein referred to as CYP4V2op) both encode the human CYP4V2 protein (amino acid sequence shown in SEQ ID NO: 4. NP_997235.3). The cDNA with sequence shown in SEQ ID NO: 3 (herein referred to as CYP4V2fv) encodes a functional variant of the human CYP4V2 protein (amino acid sequence shown in SEQ ID NO: 5).

SEQ ID NO: 5 is the amino acid sequence of a functional variant of the human CYP4V2 protein (SEQ ID NO: 4). Both proteins (SEQ ID NO: 4 and SEQ ID NO: 5) are functional CYP4V2 proteins as defined herein. The functional CYP4V2 protein shown in SEQ ID NO: 5 has one amino acid change from the human CYP4V2 protein shown in SEQ ID NO: 4. The cDNA shown in SEQ ID NO: 3 encoding the functional CYP4V2 protein (SEQ ID NO: 5) has two nucleotide differences from the cDNA shown in SEQ ID NO: 1 which encodes the human CYP4V2 protein (SEQ ID NO: 4). Both of the codon-optimized cDNA shown in SEQ ID NO: 2 and cDNA shown in SEQ ID NO: 1 encode the human CYP4V2 protein (SEQ ID NO: 4) and share a sequence identity of 77%.

A codon-optimized cDNA (CYP4V2fv-op) encoding the functional CYP4V2 protein of SEQ ID NO: 5 is provided herein which comprises the cDNA sequence of CYP4V2op (SEQ ID NO: 2), except that the CYP4V2 fv-op sequence retains the one or two nucleotide differences between SEQ ID NO: 1 and 3.

In addition to CYP4V2op and CYP4V2fv-op, other codon-optimized cDNAs or nucleic acid sequences encoding the human CYP4V2 protein or a functional CYP4V2 protein (e.g., any of SEQ ID NOs: 4 to 29) can be generated by methods described in the disclosure herein. A codon-optimized nucleic acid molecule encoding the human CYP4V2 protein (SEQ ID NO: 4) or a

30

functional CYP4V2 protein (SEQ ID NO: 5 or any of SEQ ID Nos: 6 to 29) can be tested in BCD patient-specific iPS-RPE cells lines (or RPE cells with artificially created CYP4V2 mutations) to determine and/or confirm its expression efficiency and rescue function for treating BCD. Such tests includes without limitation, protein expression (e.g., western blot specific to the functional CYP4V2 protein it encodes), PCR to detect the related gene expression, and/or efficacy in rescuing the biochemical abnormalities and RPE atrophy in BCD patient-specific iPS-RPE cell lines by compositions (e.g., in an expression cassette and/or a vector) and methods provided herein.

10 SEQ ID NO: 1 (CYP4V2st cDNA, 1578 bp)
 ATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCGCGGCGAGTGCCCT
 TTCCCTGGCCGGCGCCAGTCTGGTCTGAGCCTGCTGCAGAGGGTGGCGAGCTACGCGCGGAAAT
 GGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTGGGCCACGCGCTGCTG
 ATGAAGCCGGACGGGCGAGAATTTTTTTCAGCAGATCATTGAGTACACAGAGGAATACCGCCACAT
 15 GCCGCTGCTGAAGCTCTGGGTGGGGCCAGTGGCCATGGTGGCCCTTTATAATGCAGAAAATGTGG
 AGGTAATTTTAACTAGTTCAAAGCAAATTGACAAATCCTCTATGTACAAGTTTTTAGAACCATGG
 CTTGGCCTAGGACTTCTTACAAGTACTGAAACAAATGGCGCTCCAGGAGAAAGATGTTAACACC
 CACTTTCATTTTACCATTCTGGAAGATTTCTTAGATATCATGAATGAACAAGCAAATATATTGG
 TTAAGAACTTGAAAAACACATTAACCAAGAAGCATTTAACTGCTTTTTTTTACATCACTCTTTGT
 20 GCCTTAGATATCATCTGTGAAACAGCTATGGGGAAGAATATTGGTGCTCAAAGTAATGATGATTC
 CGAGTATGTCCGTGCAGTTTATAGAATGAGTGAGATGATATTTTCAAGAATAAAGATGCCCTGGC
 TTTGGCTTGATCTCTGGTACCTTATGTTTAAAGAAGGATGGGAACACAAAAAGAGCCTTCAGATC
 CTACATACTTTTACCAACAGTGTTCATCGCTGAACGGGGCCAATGAAATGAACGCCAATGAAGACTG
 TAGAGGTGATGGCAGGGGCTCTGCCCCCTCCAAAAATAAACGCAGGGCCTTTCTTGACTTGCTTT
 25 TAAGTGTGACTGATGACGAAGGGAACAGGCTAAGTCATGAAGATATTCGAGAAGAAGTTGACACC
 TTCATGTTTGAGGGGCACGATACAACCTGCAGCTGCAATAAACTGGTCCTTATACCTGTTGGGTTC
 TAACCCAGAAGTCCAGAAAAAAGTGGATCATGAATTGGATGACGTGTTTGGGAAGTCTGACCGTC
 CCGCTACAGTAGAAGACCTGAAGAACTTCGGTATCTGGAATGTGTTATTAAGGAGACCCTTCGC
 CTTTTTCCTTCTGTTCCCTTTATTTGCCCCGTAGTGTTAGTGAAGATTGTGAAGTGGCAGGTTACAG
 30 AGTTCTAAAAGGCACTGAAGCCGTCATCATTCCTATGCATTGCACAGAGATCCGAGATACTTCC
 CCAACCCCGAGGAGTTCCAGCCTGAGCGGTCTTCCCCGAGAATGCACAAGGGCGCCATCCATAT
 GCCTACGTGCCCTTCTCTGCTGGCCCCAGGAACTGTATAGGTCAAAGTTTGCTGTGATGGAAGA
 AAAGACCATTCTTTCTGTCATCCTGAGGCACCTTTGGATAGAATCCAACCAGAAAAGAGAAGAGC
 TTGGTCTAGAAGGACAGTTGATTCTTCGTCCAAGTAATGGCATCTGGATCAAGTTGAAGAGGAGA
 35 AATGCAGATGAACGCTAA

SEQ ID NO: 2 (CYP4V2op cDNA, 1578 bp)
 ATGGCTGGACTGTGGCTGGGACTGGTGTGGCAGAACTGCTGCTGTGGGGGGCCGCTTCCGCACT
 GTCAGTGGCTGGGGCTTCACTGGTGTGAGCCTGCTGCAGAGGGTGGCCTCCTACGCCAGAAAGT
 40 GGCAGCAGATGAGGCCCATCCCTACCGTGGCCAGAGCCTATCCACTGGTGGGACACGCACTGCTG
 ATGAAGCCTGACGGCAGAGAGTTCTTTCAGCAGATCATCGAGTACACAGAGGAGTATAGGCACAT

GCCACTGCTGAAGCTGTGGGTGGGACCCGTGCCTATGGTGGCCCTGTACAACGCCGAGAATGTGG
AAGTGATCCTGACCAGCAGCAAGCAGATCGATAAGTCTAGCATGTATAAGTTCTTGAGCCTTGG
CTGGGCCTGGGCCTGCTGACCTCTACAGGCAACAAGTGGAGGAGCCGGAGAAAGATGCTGACCCC
AACATTCCACTTTTACAATCCTGGAGGACTTCCTGGACATCATGAACGAGCAGGCCAATATCCTGG
5 TGAAGAAGCTGGAGAAGCACATCAACCAGGAGGCCCTTTAATTGCTTCTTTTACATCACCTGTGC
GCCCTGGACATCATCTGTGAGACAGCTATGGGCAAGAACATCGGCGCCCAGTCTAATGACGATAG
CGAGTACGTGCGGGCCGTGTATAGAATGAGCGAGATGATCTTTAGGCGCATCAAGATGCCCTGGC
TGTGGCTGGATCTGTGGTATCTGATGTTCAAGGAGGGCTGGGAGCACAAGAAGTCCCTGCAGATC
CTGCACACCTTTACAACTCTGTGATCGCCGAGAGAGCCAATGAGATGAACGCCAATGAGGACTG
10 TAGGGGCGATGGAAGGGGCAGCGCCCCCTTCCAAGAACAAAGCGGAGAGCCTTCCTGGACCTGCTGC
TGAGCGTGACCGACGATGAGGGCAATCGCCTGTCCCACGAGGACATCCGGGAGGAGGTGGATACA
TTCATGTTTGAGGGACACGACACCACAGCCCGCCCATCAACTGGTCCCTGTACCTGCTGGGCTC
TAATCCAGAGGTGCAGAAGAAGGTGGATCACGAGCTGGACGACGTGTTCCGCAAGTCCGACAGGC
CAGCAACCGTGGAGGATCTGAAGAAGCTGAGATACCTGGAGTGCCTGATCAAGGAGACACTGCGC
15 CTGTTCCCTCTGTGCCTCTGTTTGCCCGGTCCGTGTCTGAGGACTGTGAGGTGGCCGGCTATCG
CGTGCTGAAGGGCACCGAGGCCGTGATCATCCCTTACGCCCTGCACCGGGACCCCAGGTATTTCC
CTAACCAGAGAGTTTTCAGCCAGAGAGATTCTTTCCCGAGAATGCCAGGGCAGGCACCCCTTAC
GCCTATGTGCCATTCTCCGCCGACCAAGGAACCTGCATCGGACAGAAGTTTGCCGTGATGGAGGA
GAAAACCATCCTGTCTTGTATCCTGAGACACTTCTGGATCGAGAGCAATCAGAAGAGGAGGAGC
20 TGGGCCTGGAGGGACAGCTGATCCTGCGGCCAAGCAACGGCATCTGGATCAAACCTGAAAAGAAGG
AACGCTGACGAGAGGTAA

SEQ ID NO: 3 (CYP4V2fv cDNA, 1578 bp)
ATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCGCGGCGAGTGCCCT
25 TTCCCTGGCCGGCGCCAGTCTGGTCTGAGCCTGCTGCAGAGGGTGGCGAGCTACGCGCGGAAAT
GGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTGGGCCACGCGCTGCTG
ATGAAGCCGGACGGGCGAGAATTTTTTTCAGCAGATCATTGAGTACACAGAGGAATACCGCCACAT
GCCGCTGCTGAAGCTCTGGGTGCGGCCAGTGCCCATGGTGGCCCTTTATAATGCAGAAAATGTGG
AGGTAATTTTAACTAGTTCAAAGCAAATTGACAAATCCTCTATGTACAAGTTTTTAGAACCATGG
30 CTTGGCCTAGGACTTCTTACAAGTACTGAAACAAATGGCGCTCCAGGAGAAAGATGTAAACACC
CACTTTCCATTTTACCATTCTGGAAGATTTCTTAGATATCATGAATGAACAAGCAAATATATTGG
TTAAGAACTTGA AAAACACATTAACCAAGAAGCATTTAACTGCTTTTTTTTACATCACTCTTTGT
GCCTTAGATATCATCTGTGAAACAGCTATGGGGAAGAATATTGGTGTCAAAGTAATGATGATTC
CGAGTATGTCCGTGCAGTTTATAGAATGAGTGAGATGATATTTCAAGAATAAAGATGCCCTGGC
35 TTTGGCTTGATCTCTGGTACCTTATGTTTAAAGAAGGATGGGAACACAAAAAGAGCCTTAAGATC
CTACATACTTTTACCAACAGTGTATCGCGGAACGGGCCAATGAAATGAACGCCAATGAAGACTG
TAGAGGTGATGGCAGGGGCTCTGCCCCCTCCAAAAATAAACGCAGGGCCTTTCTTGACTTGCTTT
TAAGTGTGACTGATGACGAAGGGAACAGGCTAAGTCATGAAGATATTCGAGAAGAAGTTGACACC
TTCATGTTTGAGGGGCACGATACAACTGCAGCTGCAATAAACTGGTCCTTATACCTGTTGGGTTC
40 TAACCCAGAAGTCCAGAAAAAAGTGGATCATGAATTGGATGACGTGTTTGGGAAGTCTGACCGTC
CCGCTACAGTAGAAGACCTGAAGAACTTCGGTATCTGGAATGTGTTATTAAGGAGACCCCTTCGC
CTTTTTCTTCTGTTCCCTTTATTTGCCCGTAGTGTTAGTGAAGATTGTGAAGTGGCAGGTTACAG
AGTTCTAAAAGGCACTGAAGCCGTATCATTTCCCTATGCATTGCACAGAGATCCGAGATACTTCC
CCAACCCCGAGGAGTTCCAGCCTGAGCGGTCTTCCCCGAGAATGCACAAGGGCGCCATCCATAT
45 GCCTACGTGCCCTTCTCTGCTGGCCCCAGGAACTGTATAGGTCAAAGTTTGCTGTGATGGAAGA
AAAGACCATTCTTTCTGTGCATCCTGAGGCACCTTTGGATAGAATCCAACCAGAAAAAGAGAAGAGC

TTGGTCTAGAAGGACAGTTGATTCTTCGTCCAAGTAATGGCATCTGGATCAAGTTGAAGAGGAGA
AATGCAGATGAACGCTAA

SEQ ID NO: 4 (human CYP4V2 protein, NP_997235.3, 525 aa)

5 MAGLWLGLVWQKLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLVGHALL
MKPDGREFFQQIIIEYTEEYRHMPLLLKLWVGVPVMVALYNAENVEVILTSSKQIDKSSMYKFLEPW
LGLGLLTSTGNKWSRRKMLTPTFHFTILEDFLDIMNEQANILVKKLEKHINQEAFCFFYITLC
ALDIICETAMGKNIGASNDSEYVRAVYRMSEMI FRRIKMPWLWLDLWYLMFKEGWEHKKSLQI
LHTFTNSVIAERANEMNANEDCRGDGRGSAPSKNKRRFLDLLSVTDDEGNRLSHEDIREEVD
10 FMFEGHDTTAAAINWSLYLLGSNPEVQKKVDHELDVFGKSDRPATVEDLKKLRYLECVIKETLR
LFPSVPLFARSVSEDCEVAGYRVLKGTEAVIIPYALHRDPRYFPNPEEFQPERFFPENAQGRHPY
AYVPFSAGPRNCIGQKFAVMEEKTILSCILRHFWIESNQKREELGLEGLILRPSNGIWIKLRR
NADER

15 SEQ ID NO: 5 (functional variant of human CYP4V2 protein; 525 aa)

MAGLWLGLVWQKLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLVGHALL
MKPDGREFFQQIIIEYTEEYRHMPLLLKLWVGVPVMVALYNAENVEVILTSSKQIDKSSMYKFLEPW
LGLGLLTSTGNKWSRRKMLTPTFHFTILEDFLDIMNEQANILVKKLEKHINQEAFCFFYITLC
ALDIICETAMGKNIGASNDSEYVRAVYRMSEMI FRRIKMPWLWLDLWYLMFKEGWEHKKSLKI
LHTFTNSVIAERANEMNANEDCRGDGRGSAPSKNKRRFLDLLSVTDDEGNRLSHEDIREEVD
20 FMFEGHDTTAAAINWSLYLLGSNPEVQKKVDHELDVFGKSDRPATVEDLKKLRYLECVIKETLR
LFPSVPLFARSVSEDCEVAGYRVLKGTEAVIIPYALHRDPRYFPNPEEFQPERFFPENAQGRHPY
AYVPFSAGPRNCIGQKFAVMEEKTILSCILRHFWIESNQKREELGLEGLILRPSNGIWIKLRR
NADER

25 SEQ ID NO: 6 (fragment of CYP4V2 without transmembrane domain;
490 aa)

RVASYARKWQQMRPIPTVARAYPLVGHALLMKPDGREFFQQIIIEYTEEYRHMPLLLKLWVGVPVMV
ALYNAENVEVILTSSKQIDKSSMYKFLEPWLGLGLLTSTGNKWSRRKMLTPTFHFTILEDFLDI
30 MNEQANILVKKLEKHINQEAFCFFYITLCALDIICETAMGKNIGASNDSEYVRAVYRMSEMI
FRRIKMPWLWLDLWYLMFKEGWEHKKSLQILHTFTNSVIAERANEMNANEDCRGDGRGSAPSKNK
RRAFLDLLSVTDDEGNRLSHEDIREEVDTFMFEGHDTTAAAINWSLYLLGSNPEVQKKVDHELD
DVFGKSDRPATVEDLKKLRYLECVIKETLR LFPSVPLFARSVSEDCEVAGYRVLKGTEAVIIPYA
LHRDPRYFPNPEEFQPERFFPENAQGRHPYAYVPFSAGPRNCIGQKFAVMEEKTILSCILRHFWI
35 ESNQKREELGLEGLILRPSNGIWIKLRRNADER

Example 9—Designing Efficient Expression Cassettes and Delivery Vectors for CYP4V2 Gene Therapy

As described herein, an expression cassette and a delivery vector comprise various
40 elements. Results can vary significantly based on different designs. Given the large amount of
options in each of the important elements including but not limited to the ones listed below and
numerous combinations thereof, a thoughtful design of efficient expression cassettes and

delivery vectors is required for the success of CYP4V2 gene therapy. In addition, the design process need to take into consideration the disease phenotype and characteristics (e.g., types of cells/tissues targeted for treatment) and safety (e.g., toxicity, immune response). Finally, a design needs to be tested and verified in a sound disease model.

- 5 (a) Type of delivery vector;
- (b) Vector serotype and capsid design/selection;
- (c) Additional vector design, e.g., ssAAV vs. scAAV;
- (d) cDNA design;
- (e) promoter design/selection;
- 10 (f) polyA signal design/selection; and
- (g) any other regulatory sequences, e.g., an enhancer, or junction/linker sequence.

For (a), a viral vector was chosen to achieve high transduction efficiency in target cells (e.g., human RPE). Among various types of viral vectors, AAV vectors were chosen because of its safety profile and the size of the CYP4V2 encoding nucleic acid (e.g., a CYP4V2 cDNA) fits
15 in the packaging limit of AAV vectors. Vectors with larger packaging limit, e.g., a HSV vector, a lentivirus vector, a Baculovirus or adenovirus vectors, can also be used for CYP4V2 gene therapy. In addition to viral vectors, non-viral vectors, e.g., nanoparticles, including but not limited to, liposome nanoparticles, solid lipid nanoparticles, liposome protamine/DNA lipoplex (LPD), can also be used for CYP4V2 gene therapy.

20 For (b), because RPE cells are the primary cell type targeted for treatment in CYP4V2 gene therapy for BCD, an AAV serotypes with sufficient transduction efficiency in RPE cells is preferred. In addition, the following factors were considered. Because expression of CYP4V2 was observed broadly in various human tissues and organs, e.g., heart, brain, placenta, lung, liver, skeletal muscle, kidney, pancreas, retina, RPE, cornea and lymphocytes, and in addition to RPE,
25 BCD also affects choroid, photoreceptors and, in some patients, the cornea, and that abnormalities have been previously reported in BCD patients' skin fibroblast, lymphocytes and serum, AAV serotypes and capsid structures that do not restrict AAV transduction only in RPE cells, but also can transduce other cells/tissues, e.g., photoreceptors, choroid, and/or cornea, can be designed and/or selected, in addition to AAV serotypes and capsid structures with good
30 transduction efficiency in RPE cells. As a result, a wide range of AAV serotypes and capsid

structures are suitable and can be used. AAV2, AAV5, AAV8, AAV1, AAV9 and a capsid mutant AAV vector (AAV2 (Y444F+Y500F+Y730F)) were selected for the study. In addition to transduction efficiency, another factor that was considered is the pre-existing NABs against different AAV serotypes in the general population and other potential individual differences among patients (including without limitation other types of immune responses (e.g., intracellular immunity or RPE immunity) or due to difference in genotype (e.g., different mutations)). In this design, multiple AAV types were used and tested including ones sharing low cross-reactivity to NABs to lower potential immune responses and to maximize therapeutic effect to different patients.

For (c), because the full-length CYP4V2 cDNA is 1578 bp (including start and stop codons), both ssAAV and scAAV designs can be used in CYP4V2 gene therapy. ssAAV and scAAV designs each has its own pros and cons as described herein. Compared to ssAAV, a scAAV design offers rapid expression and higher DNA stability. However, its packaging limit (about 2.4-2.5 kb) restricts the use of larger size and potentially more active regulatory sequences (e.g., promoter, PolyA signal). In addition, depending on the size of the promoter used, a scAAV design may need to shorten or go without some optional regulatory sequences (e.g., an enhancer). Both ssAAV and scAAV vectors were designed and generated for use in CYP4V2 gene therapy. Various pseudotyped AAVs containing AAV2 genome (e.g., the AAV2 ITRs (SEQ ID NOs: 42 and 43)) and a capsid from each of the AAV types described in (b) above were generated. For the scAAV, one of the two AAV2 ITRs was truncated/mutated (SEQ ID NO: 44).

For (d), as discussed herein, there are multiple functional CYP4V2 proteins. Further, numerous nucleic acid sequences can encode the same protein. Three (3) cDNAs were generated in the study; the first one (SEQ ID NO: 1, referred to as CYP4V2st) encoding the human CYP4V2 protein (SEQ ID NO: 4), the second one is a codon-optimized cDNA (SEQ ID NO: 2, referred to as CYP4V2op) encoding the human CYP4V2 protein (SEQ ID NO: 4), and the third one (SEQ ID NO: 3, referred to as CYP4V2fv) encoding a functional variant of the human CYP4V2 protein (SEQ ID NO: 5). A Kozak sequence (exemplary sequences shown in SEQ ID NO: 37 or 38) was inserted before the cDNA start codon.

For (e), similar to the rationale in (b), the promoter needs to work well to drive expression in target cells (e.g., RPE cells when the target cell type for treatment is RPE, cornea

cells when the target cell type is cornea cells). The promoter is a major element in the expression cassette of gene therapy vectors. Optimal promoter selection can enhance target specificity and gene expression. Depending on the cell or tissue type(s) targeted for treatment, the promoter used in CYP4V2 gene therapy can be either a constitutive promoter or a cell-specific promoter (e.g., a promoter specific to RPE cells, a promoter specific to both RPE and photoreceptors, a promoter specific to RPE cells and choroid cells, a promoter specific to RPE, photoreceptor and choroid cells, a promoter specific to cornea cells, a promoter specific to RPE, photoreceptor, choroid, and cornea cells, or a promoter specific to ocular cells). Because CYP4V2 is almost ubiquitously expressed and multiple cell types are affected in BCD (the primary one being RPE, other cell types include, e.g., cornea, retina, lymphocytes), constitutive promoters were chosen in this design to broaden the effect of the expression cassette and delivery vector in multiple tissue and cell types. For the expression cassette used in ssAAV vectors, a strong constitutive promoter was used, the CAG promoter which is ~1.7kb in length (exemplary sequence shown in SEQ ID NO: 32). The CAG promoter (also known as CBA, CAGGS or CB promoter) is a strong synthetic promoter. The CAG promoter is composed of the following regulatory elements: (C) cytomegalovirus (CMV) early enhancer element; (A) the promoter region and the first exon of the chicken beta-Actin gene, and a chimeric intron from chicken beta-actin gene and the rabbit beta-globin gene, and (G) the splice acceptor of the rabbit beta-Globin gene. The CAG promoter was used because it has both stronger and longer-lasting activity than the CMV promoter (exemplary sequence shown in SEQ ID NO: 40), which is the most commonly used constitutive promoter to drive expression in mammalian cells. For the expression cassette used in scAAV vectors, due to the packaging size limitation of scAAV, a much shorter constitutive promoter was used, the elongation factor 1 alpha short (EFS) promoter (exemplary sequence shown in SEQ ID NO: 35). The EFS promoter is the miniaturized version of the EF-1 alpha promoter (~1.2 Kb, exemplary sequence shown in SEQ ID NO: 41). The EF-1 alpha promoter is a constitutive promoter derived from human elongation factor-1 alpha (EF-1 α). The EFS promoter also can be used in the expression cassette design for ssAAVs. In addition to the CAG promoter, CMV promoter, EF1 alpha promoter and EFS promoter, other constitutive promoters can be used, including without limitation, another viral promoter such as the CMV promoter, a derivative or variant of the CAG (a/k/a CBA, CAGGS or CB promoter) such as the smCBA promoter, CB^{SB}

promoter, or the CBh promoter, another beta-actin promoter such as the human beta actin promoter, a derivative or variant of the EF-1 alpha promoter, PGK promoter, the UBC promoter, the GUSB promoter, the UCOE promoter or other promoters described herein. Further, a cell-specific promoter can be used, including without limitation, the ocular cell-specific promoters described herein, e.g., a VMD2 (a/k/a BEST1) promoter or a RPE65 promoter to drive
5 expression in RPE.

For (f), a bGH polyA was used (exemplary sequence shown in SEQ ID NO: 34) for the expression cassette design used in ssAAVs and a shorter polyA signal, a small polyA (SPA) (exemplary sequence shown in SEQ ID NO: 36) for the expression cassette design used in
10 scAAVs. The SPA also can be used in expression cassette for ssAAVs. Other polyA signals (including derivatives or variants) also can be used instead, including without limitation, a SV40 polyA signal, a SV40 late polyA signal (exemplary sequence shown in SEQ ID NO: 39) or other polyA signals as described herein, including without limitation, a polyA signal used in combination with an upstream enhancer (USE).

For (g), a WPRE enhancer was used (exemplary sequence shown in SEQ ID NO: 33) for the expression cassette used in ssAAVs. For expression cassette design used in scAAVs, given the size limit, an enhancer was not included. It should be noted that an enhancer is optional in both ssAAV and scAAV CYP4V2 expression cassettes. It should also be noted, however, that it is possible to include short-length enhancer sequences, e.g., a shortened WPRE containing
20 minimal gamma and alpha elements of the WPRE, in combination with small-sized promoter and polyA signal in the scAAV CYP4V2 expression cassette. Besides WPRE, other enhancers as described herein, such as an HPRE enhancer or a CTE enhancer can be used.

In some instances, the CYP4V2 expression cassette includes a promoter (e.g., a CAG (a/k/a CBA, CAGGS, CB) promoter, a EF-1 alpha promoter, a smCBA promoter, a CBh
25 promoter, a EFS promoter, a human beta-actin promoter, a CMV promoter, a VMD2 promoter, or a RPE65 promoter), a nucleic acid sequence encoding a functional CYP4V2 protein (e.g., a cDNA encoding the human CYP4V2 protein or a functional variant or fragment thereof), optionally linked with an enhancer sequence (e.g., a WPRE enhancer, a HPRE enhancer or a shortened WPRE or HPRE enhancer), and a polyA signal (e.g., a bGH polyA, a SPA, or an

SV40 PolyA, or a fragment or derivative thereof, e.g., an SV40 late polyA), and other regulatory sequences (e.g., a Kozak sequence). See SEQ ID NOs: 1-41 for exemplary sequences.

It would be understood that (i) the exemplary sequences of various regulatory sequences provided in the SEQ section are exemplary in nature and there are different versions of these regulatory sequences that can achieve the same or similar function, and (ii) there are different variants, fragments and/or derivatives of these sequences that can also be used, e.g., a truncated CAG promoter, a shortened WPRE enhancer, a SV40 late polyA.

Based on the design approach described above, multiple CYP4V2 cDNAs, CYP4V2 expression cassettes and rAAV vectors for use in CYP4V2 gene therapy were generated, including:

(1) Three CYP4V2 cDNAs as shown in SEQ ID NO: 1, 2 and 3, respectively. CYP4V2st (SEQ ID NO: 1) and CYP4V2op (SEQ ID NOs 2) both encode the human CYP4V2 protein (SEQ ID NO: 4). CYP4V2fv (SEQ ID NO: 3) encodes a functional variant of the human CYP4V2 protein (SEQ ID NO: 5);

(2) Two CYP4V2 expression cassettes (CYP4V2 denotes a nucleic acid sequence encoding the human CYP4V2 protein or a functional CYP4V2 protein. See Figure 7 for a schematic drawing):

- (i) CAG-CYP4V2-WPRE-bGH polyA
- (ii) EFS-CYP4V2-SPA

(3) The above mentioned CYP4V2 cDNAs and CYP4V2 expression cassettes were packaged in six different AAV vectors (AAV2, AAV5, AAV8, AAV1, AAV2(Y444F+Y500F+Y730F) and AAV9) to create the following rAAV vectors containing a CYP4V2 cDNA and expression cassette, including both ssAAV and scAAV vector constructs:

- (i) recombinant AAV2/2-CAG-CYP4V2op-WPRE-bGH polyA (herein referred to as AAV2.CYP4V2op),
- (ii) recombinant AAV2/2 (Y444F+Y500F+Y730F)-CAG-CYP4V2op-WPRE-bGH PolyA (herein referred to as AAV2tri(Y-F).CYP4V2op or AAV2tri.CYP4V2op),
- (iii) recombinant AAV2/5-CAG-CYP4V2op-WPRE-bGH PolyA (herein referred to as AAV5.CYP4V2op).

(iv) recombinant AAV2/5-CAG-CYP4V2st-WPRE-bGH polyA (herein referred to as AAV5.CYP4V2st),

(v) recombinant AAV2/8-CAG-CYP4V2fv-WPRE-bGH polyA (herein referred to as AAV8.CYP4V2fv),

5 (vi) recombinant self-complementary AAV2/1-EFS-CYP4V2op-SPA (herein referred to as scAAV1.CYP4V2op),

(vii) recombinant self-complementary AAV2/5-EFS-CYP4V2op-SPA (herein referred to as scAAV5.CYP4V2op), and

10 (viii) recombinant self-complementary AAV2/9-EFS-CYP4V2op-SPA (herein referred to as scAAV9.CYP4V2op).

When packaged in an rAAV vector, the expression cassette was flanked by two AAV2 ITRs (SEQ ID NOs: 42 and 43). For scAAV, one of the AAV2 ITRs was truncated/mutated (SEQ ID NO: 44). It would be understood that non-AAV2 genome, including non-AAV2 ITRs can also be used to package the expression cassette. A Kozak sequence (SEQ ID NO: 37 or 38) was inserted immediately before the CYP4V2 cDNAs. See Figure 7 for schematic drawings showing the design of these expression cassettes. It would be appreciated that a CYP4V2 cDNA can be packaged in different expression cassettes and that a CYP4V2 expression cassette can be packaged in different AAV vectors. For example, the CYP4V2op cDNA can be used in both CAG-CYP4V2-WPRE-bGH PolyA expression cassette and EFS-CYP4V2-SPA expression cassette. Either CAG-CYP4V2-WPRE-bGH PolyA expression cassette or EFS-CYP4V2-SPA expression cassette can be packaged in any suitable AAV vector, including but not limited to, AAV1, AAV2, AAV2(Y444F+Y500F+Y730F), AAV5, AAV8, AAV8 (Y733F), AAV9, AAV6, AAV7, AAV4, AAV12, AAV-PHP.B and other vectors. An scAAV design can be used in any suitable AAV vector to create a recombinant scAAV vector, e.g., scAAV1, scAAV2, scAAV2(Y444F+Y500F+Y730F), scAAV5, scAAV8, scAAV8 (Y733F), scAAV3, scAAV4, scAAV6, scAAV7, scAAV9, scAAV12, etc.

It would be understood that similar design process can be used in designing other vectors (e.g., a lentivirus vector or a plasmid) for the CYP4V2 gene therapy. Depending on the type of the vector, certain elements described above may not be necessary or may need to be adjusted accordingly, e.g., a promoter sequence.

In addition to the cDNAs, regulatory sequences and AAV types and designs specified herein, other design options for each key element of the CYP4V2 expression cassette and delivery vector can also be used. An example on how to compare transduction efficiency of various AAV types and the strength of different promoters in a targeted cell type is provided herein in the Examples section. Similar methods can be used to assess and compare the design options for other key elements of the expression cassette and delivery vector, e.g., cDNA, enhancer, polyA signal, ssAAV vs. scAAV, AAV vs. HSV etc. Further, as provided herein, the efficiency of a CYP4V2 expression cassette and delivery vector can be assessed and compared through testing in BCD cellular model, e.g., iPS-RPE cells of BCD patients, with methods described herein and/or other methods to assess biochemical abnormalities, RPE function or atrophy.

The CYP4V2 cDNAs, expression cassettes and delivery vectors described above were tested in BCD patient-specific human iPS-RPE cell lines, and the results are shown and discussed in the following Examples.

In addition, the junction/linker sequences between various regulator sequences (including without limitation, between ITR and a promoter, between an enhancer and a polyA signal, or between a polyA signal and ITR), or between a regulatory sequence and a cDNA (including without limitation, between a promoter and a cDNA, between a cDNA and an enhancer, or between a cDNA and a polyA signal) may also play a role in regulating the expression of the target gene (e.g., CYP4V2). Sequences of different CYP4V2 expression cassettes (inclusive of ITRs and junction/linker sequences) used in the study are listed in Example 11 below.

Exemplary sequences of certain regulatory sequences and ITR sequences discussed in this Example are provided as follows:

SEQ ID NO: 32 (CAG promoter, 1715 bp)

GACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCC
CATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGAC
CCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTG
ACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGC
CAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATG
ACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGGTGC
AGGTGAGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCCTCCCCACCCCCAATTTTGTAT
TTATTTATTTTTTAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGGGGGGCGCGCCAGGCG

GGGCGGGGCGGGGCGAGGGGCGGGGCGGGGCGAGGCGGAGAGGTGCGGCGGCAGCCAATCAGAGC
GGCGCGCTCCGAAAGTTTCTTTTATGGCGAGGCGGCGGCGGCGGCCCTATAAAAAGCGAAG
CGCGCGGCGGGGCGGGAGTCGCTGCGTTGCCCTCGCCCCGTGCCCCGCTCCGCGCCGCTCGCGCC
GCCCCGCCCGGCTCTGACTGACCGCGTTACTCCCACAGGTGAGCGGGCGGGACGGCCCTTCTCCT
5 CCGGGCTGTAATTAGCGCTTGGTTTAATGACGGCTCGTTTCTTTTCTGTGGCTGCGTGAAAGCCT
TAAAGGGCTCCGGGAGGGCCCTTTGTGCGGGGGGAGCGGCTCGGGGGGTGCGTGCGTGTTGTG
TGCGTGGGGAGCGCCGCGTGCGGCCCCGCGTGCCCGGCGGCTGTGAGCGCTGCGGGCGCGGCGCG
GGGCTTTGTGCGCTCCGCGTGTCGCGAGGGGAGCGCGGCCGGGGGCGGTGCCCCGCGGTGCGGG
GGGGCTGCGAGGGGAACAAAGGCTGCGTGCGGGGTGTGTGCGTGGGGGGGTGAGCAGGGGGTGTG
10 GGCGCGGCGGTGCGGCTGTAACCCCCCTGCACCCCCCTCCCCAGTTGCTGAGCACGGCCCCG
CTTCGGGTGCGGGGCTCCGTGCGGGGCGTGCGCGGGGCTCGCCGTGCGGGGCGGGGGTGCGCG
CAGGTGGGGGTGCCGGGCGGGGCGGGGCCCTCGGGCCGGGAGGGCTCGGGGAGGGGCGCGG
CGCCCCGAGCGCCGGCGGCTGTGAGGCGCGGCGAGCCGAGCCATTGCCTTTTATGGTAATC
GTGCGAGAGGGCGCAGGGACTTCCTTTGTCCCAAATCTGGCGGAGCCGAAATCTGGGAGGCGCCG
15 CCGCACCCCTCTAGCGGGCGCGGGCGAAGCGGTGCGGCGCCGGCAGGAAGGAAATGGGCGGGGA
GGGCTTCGTGCGTCGCCGCGCCGCGCTCCCTTCTCCATCTCCAGCCTCGGGGCTGCCGAGGG
GGACGGCTGCCCTTCGGGGGGACGGGGCAGGGCGGGGTTCGGCTTCTGGCGTGACCGGCGGCT
CTAGAGCCTCTGCTAACCATGTTTCATGCCTTCTTCTTTTCTACAGCTCCTGGGCAACGTGCTG
GTTATTGTGCTGTCTCATCATTTTGGCAAA

20
SEQ ID NO: 33 (WPRE enhancer, 589 bp)

AATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCT
CCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGC
TTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTG
25 TCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGTGACGCAACCCCCACTGGTTGGGGCATTGCC
ACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCAT
CGCCGCCTGCCTTGCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGT
TGTCGGGGAAATCATCGTCCTTTCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGG
ACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCC
30 GGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCG
CCTCCCCG

SEQ ID NO: 34 (bGH polyA, 225 bp)

CTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCCGTGCCCTTCCTTGACCC
35 TGGAAGGTGCCACTCCCACTGTCTTTTCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGT
AGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAA
TAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGG

SEQ ID NO: 35 (EFS promoter, 235 bp)

40 g attggctccg gtgcccgtca gtgggcagag cgcacatcgc ccacagtccc
cgagaagttg gggggagggg tccgcaattg aaccggtgcc tagagaaggt ggcgcggggg
aaactgggaa agtgatgtcg tgtactggct ccgccttttt cccgaggggtg ggggagaacc
gtatataagt gcagtagtcg ccgtgaacgt tctttttcgc aacggggttg ccgccagaac
acag

45

- SEQ ID NO: 36 (SPA, 54 bp)
GATCCAATAAAAGATCTTTATTTTCATTAGATCTGTGTGTTGGTTTTTTGTGTG
- 5 SEQ ID NO: 37 (Kozak sequence, 6 bp)
GCCACC
- SEQ ID NO: 38 (Kozak sequence, 5 bp)
CCACC
- 10 SEQ ID NO: 39 (SV40 late PolyA, 120 bp)
TTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAAT
AAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAACTCATCAATGTATCTTAT
- 15 SEQ ID NO: 40 (CMV promoter, 576 bp)
TAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGAC
GTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
AAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAAT
GACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTACTTGGCA
20 GTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGC
GTGGATAGCGTTTTGACTCACGGGGATTTCCTCAAGTCTCCACCCATTGACGTCAATGGGAGTTTG
TTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTGACGCAAT
GGGCGGTAGGCGGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAG
- 25 SEQ ID NO: 41 (EF-1 alpha promoter, 1184 bp)
cgtgaggctccggtgcccgtcagtgggcagagcgcacatcgcccacagtccccgagaagt
tggggggaggggtcggaattgaaccggtgcctagagaaggtggcgcggggttaaactgggaaagt
gatgtcgtgtactggctccgcctttttcccgagggtgggggagaaccgtatataagtgcagtagt
cgccgtgaacgttctttttcgcaacgggtttgcccgcagaacacaggtaagtgcggtgtgtggtt
30 cccgcgggcctggcctctttacgggttatggcccttgctgccttgaattacttccacctggctg
cagtacgtgattcttgatcccgagcttccgggttggaagtgggtgggagagttcgaggccttgcgc
ttaaggagcccccttcgcctcgtgcttgagttgaggcctggcctgggcgctggggcgccgcgctgc
gaatctggtggcaccttcgcgcctgtctcgtgcttttcgataagtctctagccatttaaaat
tgatgacctgctgcgacgctttttttctggcaagatagctcttgtaaatgcggggccaagatctgca
35 cactggtatttcggtttttggggccgcggggcgccgacggggcccgctgcgtcccgagcgcacatggt
cggcgaggcggggcctgcgagcgcggccaccgagaatcggacgggggtagctctcaagctggccgg
cctgctctggtgcctggcctcgcgcgcgcgtgtatcgccccgcctggggcggaaggctggcccg
gtcggcaccagttgctgagcggaaagatggccgcttcccggccctgctgcaggagctcaaaat
ggaggacgcggcgctcgggagagcgggcgggtgagtcacccacacaaaggaaaaggccctttccg
40 tcctcagccgtcgttcatgtgactccacggagtaccgggcgcgctccaggcacctcgattagtt
ctcgagcttttggagtacgtcgtcttttaggttggggggaggggttttatgcatgaggtttcccc
aactgagtgggtggagactgaagttaggccagcttggcacttgatgtaattctccttgggaattt
gccctttttgagtttggatcttgggttcattctcaagcctcagacagtggttcaaagtttttttct
tccatttcagggtgctcgtga
- 45

SEQ ID NO: 42 (AAV2 5' Left-ITR, 141 bp)

cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag
cccgggcgtc gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc gcgagagag
ggagtggcca actccatcac taggggttcc t

5

SEQ ID NO: 43 (AAV2 3' Right-ITR, 141 bp)

ag gaacccttag tgatggagtt ggccactccc tctctgcgcg ctgcgtcgct
cactgaggcc gggcgaccaa aggtcgcccg acgcccgggc tttgcccggg cggcctcagt
gagcgagcga gcgcgagct gcctgcagg

10

SEQ ID NO: 44 (mutant AAV2 5' ITR in scAAV construct, 117 bp)

cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag
cccgggcgtc gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc gcgagagag
ggagtgg

15

SEQ ID NO: 45 (AAV2 3' ITR in scAAV construct, 141 bp)

aggaacc ctagtgatgg agttggccac tccctctctg cgcgctcgct
cgctcactga ggccgggcga ccaaaggtcg cccgacgcc gggctttgcc cgggcggcct
cagtgcgcga gcgagcgcg agctgcctgc agg

20

Example 10—Methods of Using BCD Cellular Model to Test, Compare and Screen AAV Serotypes and Capsid Structure, Promoter and Other Regulatory Sequence Activity and cDNA Expression Levels, as well as a Vector's Overall Efficacy and Dosage Levels in CYP4V2 Gene Therapy and to Assess Personalized Optimal Vector and Dosage for Different Patients

25 The BCD cellular model (e.g., BCD patient-specific iPS-RPE cell lines, or ES-RPE, iPS-RPE or RPE cell lines with artificially generated CYP4V2 mutations) can be used in drug and dosage screening. BCD patient-specific iPS-RPE samples were used to test, compare and screen various components and dosage for CYP4V2 gene therapy, including vector type (e.g., AAV serotypes and capsid structure), promoter, enhancer, polyA signal and other sequences in the
30 CYP4V2 expression cassette and CYP4V2 cDNA, as well as a vector's overall efficacy and dosage levels. Phenotype rescue was used to test and compare efficacy.

Vectors of different serotype (e.g., AAV1, AAV2, AAV5, AAV8, AAV9) or capsid (e.g., AAV with capsid mutation(s), e.g., AAV2 vs AAV2tri(Y-F)) or structure (e.g., scAAV vs. ssAAV) can be tested, compared by using different vectors with the same expression cassette.

35 For example, AAV2.CYP4V2op, AAV2tri(Y-F).CYP4V2op and AAV5.CYP4V2op all have the same expression cassette but are different in AAV serotype/capsid. scAAV1.CYP4V2op, scAAV5.CYP4V2op and scAAV9.CYP4V2op all share the same expression cassette but are

different in AAV serotype. Results from phenotype rescue can be used to test and compare AAV serotype/capsid (e.g., AAV2 vs AAV2tri(Y-F) vs AAV5) and structure (e.g., scAAV5 vs ssAAV5) efficiency difference in transducing and delivering the CYP4V2 cDNA to BCD patient RPE cells.

5 The same method can be used to test and compare activity level of different expression cassette, cDNA, or regulatory sequences or other sequences (e.g., junction/linker sequences) by testing phenotype rescue efficacy of rAAV vectors of the same construct (except for the element being tested and compared).

10 Furthermore, as described in the Examples herein, different dosages (e.g., 1×10^4 and 1×10^5) of the same vector (e.g., rAAV vector, e.g., scAAV1.CYP4V2op) can be applied to iPS-RPE samples of the same patient to assess therapeutic effective dosage range (measured by MOI per cell).

15 In addition, given BCD cellular model exhibited individual differences, it can also be used to assess and discover the personalized optimal dosage and vector construct for each patient individually.

See related Examples and disclosure herein for more related discussion.

Example 11— Generation of Various Recombinant Adeno-Associated Virus (rAAV) Vectors Carrying a Functional CYP4V2-encoding Nucleic Acid Sequence and Expression Cassette

20 Various AAV.CYP4V2 vectors designed for this study (See Examples herein), including AAV2.CYP4V2op, AAV2tri(Y-F).CYP4V2op, AAV5.CYP4V2st, AAV5.CYP4V2op, AAV8.CYP4V2fv and scAAV1.CYP4V2op, were custom made by Vector BioLabs (Malvern, PA, USA). Recombinant AAV vectors from Vector BioLabs are helper-free. The production process involves: (1) cloning a pAAV cis-plasmid, which is an AAV2 ITR-containing plasmid that includes the relevant CYP4V2 cDNA (i.e., CYP4V2st, CYP4V2op or CYP4V2fv) and regulatory sequences of a CYP4V2 expression cassette, (2) large-scale preparation of pAAV cis-plasmid and complimentary plasmids (a plasmid that carries the relevant AAV Rep-Cap genes and a plasmid that provides the helper genes isolated from adenovirus) by using Qiagen Endo-free Mega Prep kit, (3) large-scale co-transfection of the three plasmids described above into
30 plates of HEK293 cells. (4) Two days after transfections, cell pellets were harvested, and viruses

were released using three cycles of freeze/thaw. AAV viruses were purified using CsCl-gradient ultra-centrifugation, followed by desalting, and (5) viral titer (genome copies (GC)/ml) were determined using real-time PCR. The purified rAAV vectors were stored at -80°C until use.

Sequences of different CYP4V2 expression cassettes (inclusive of ITRs and
5 junction/linker sequences) packaged in various AAV.CYP4V2 vectors for the study are listed as follows.

SEQ ID NO: 60 - Sequence of CYP4V2 expression cassette in AAV2.CYP4V2op,
AAV2tri(Y-F).CYP4V2op, and AAV5.CYP4V2op.:
10 Left-ITR: 1-141
CAG promoter: 237-1951
CYP4V2op cDNA: 2002-3579
WPRE enhancer: 3736-4324
bGH polyA: 4350-4574
15 Right-ITR 4659-4799

```

1   CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG
5   CCCGGGCGTC GGGCGACCTT TGGTCGCCCC GCCTCAGTGA GCGAGCGAGC
10  101 GCGCAGAGAG GGAGTGGCCA ACTCCATCAC TAGGGGTTCC TGCGGCCAAT
15  151 TCAGTCGATA ACTATAACGG TCCTAAGGTA GCGATTTAAA TACGCGCTCT
20  201 CTTAAGGTAG CCCC GGACG CGTCAATTGA GATCTCGACA TTGATTATTG
25  251 ACTAGTTATT AATAGTAATC AATTACGGGG TCATTAGTTC ATAGCCATA
30  301 TATGGAGTTC CGCGTTACAT AACTTACGGT AAATGGCCCC CCTGGCTGAC
35  351 CGCCCAACGA CCCC GGCCA TTGACGTCAA TAATGACGTA TGTTCCCAT
40  401 GTAACGCCAA TAGGGACTTT CCATTGACGT CAATGGGTGG ACTATTACG
45  451 GTAAACTGCC CACTTGGCAG TACATCAAGT GTATCATATG CCAAGTACGC
50  501 CCCCTATTGA CGTCAATGAC GGTAATGGC CCGCCTGGCA TTATGCCAG
55  551 TACATGACCT TATGGGACTT TCCTACTTGG CAGTACATCT ACGTATTAGT
60  601 CATCGCTATT ACCATGGGTC GAGGTGAGCC CCACGTTCTG CTTCACTCTC
65  651 CCCATCTCCC CCCCTCCCC ACCCCCAATT TTGTATTTAT TTATTTTTTA
70  701 ATTATTTTGT GCAGCGATGG GGGCGGGGGG GGGGGGGGCG CGCGCCAGGC
75  751 GGGGCGGGGC GGGGCGAGGG GCGGGGCGGG GCGAGGCGGA GAGGTGCGGC
80  801 GGCAGCCAAT CAGAGCGGCG CGCTCCGAAA GTTTCCTTTT ATGGCGAGGC
85  851 GGC GGCGC GCGGCCCTAT AAAAAGCGAA GCGCGCGGCG GCGGGGAGTC
90  901 GCTGCGTTGC CTTGCCCCCG TGCCCCGCTC CGCGCCGCCCT CGCGCCGCC
95  951 GCGCGGCTC TGA CTGACCG CGTTACTCCC ACAGGTGAGC GGGCGGGACG
100 1001 GCCCTTCTCC TCCGGGCTGT AATTAGCGCT TGGTTTAATG ACGGCTCGTT
105 1051 TCTTTTCTGT GGCTGCGTGA AAGCCTTAAA GGGCTCCGGG AGGGCCCTTT
110 1101 GTGCGGGGGG GAGCGGCTCG GGGGGTGCGT GCGTGTGTGT GTGCGTGGGG
115 1151 AGCGCCGCGT GCGGCCGCG CTGCCC GCGTGTGAGCG CTGCGGGCGC
120 1201 GCGCGGGGGC TTTGTGCGCT CCGCGTGTGC GCGAGGGGAG CGCGGCCGGG
125 1251 GCGGTTGCC CGCGGTGCGG GGGGGTGCG AGGGGAACAA AGGCTGCGTG
130 1301 CGGGGTGTGT GCGTGGGGGG GTGAGCAGGG GGTGTGGGCG CGGCGGTCGG
135 1351 GCTGTAACCC CCCCTGCAC CCCCTCCCC GAGTTGCTGA GCACGGCCCG
140 1401 GCTTCGGGTG CGGGGCTCCG TGCGGGGCGT GGC CGGGGCG TCGCCGTGCC
145 1451 GGGCGGGGGG TGGCGGCAGG TGGGGGTGCC GGGCGGGGCG GGGCCGCCCTC
150 1501 GGGCGGGGGA GGGCTCGGGG GAGGGGCGCG GCGGCCCGG AGCGCCGGCG
155 1551 GCTGTCTGAG CGCGGCGAGC CGCAGCCATT GCCTTTTATG GTAATCGTGC
160 1601 GAGAGGGCGC AGGGACTTCC TTTGTCCCAA ATCTGGCGGA GCCGAAATCT

```

1651 GGGAGGCGCC GCCGCACCCC CTCTAGCGGG CGCGGGCGAA GCGGTGCGGC
 1701 GCCGGCAGGA AGGAAATGGG CGGGGAGGGC CTTCGTGCGT CGCCGCGCCG
 1751 CCGTCCCCTT CTCCATCTCC AGCCTCGGGG CTGCCGCAGG GGGACGGCTG
 1801 CCTTCGGGGG GGACGGGGCA GGGCGGGGTT CGGCTTCTGG CGTGTGACCG
 5 1851 GCGGCTCTAG AGCCTCTGCT AACCATGTTC ATGCCTTCTT CTTTTTCCTA
 1901 CAGCTCCTGG GCAACGTGCT GGTATATGTG CTGTCTCATC ATTTTGGCAA
 1951 AGAATTCTAA TACGACTCAC TATAGGGAGA CCCAAGCTGG CTAGAGCCAC
 2001 CATGGCTGGA CTGTGGCTGG GACTGGTGTG GCAGAACTG CTGCTGTGGG
 2051 GGGCCGCTTC CGCACTGTCA CTGGCTGGGG CTTCACTGGT GCTGAGCCTG
 10 2101 CTGCAGAGGG TGGCCTCCTA CGCCAGAAAG TGGCAGCAGA TGAGGCCCAT
 2151 CCCTACCGTG GCCAGAGCCT ATCCACTGGT GGGACACGCA CTGCTGATGA
 2201 AGCCTGACGG CAGAGAGTTC TTTCAGCAGA TCATCGAGTA CACAGAGGAG
 2251 TATAGGCACA TGCCACTGCT GAAGCTGTGG GTGGGACCCG TGCCTATGGT
 2301 GGCCCTGTAC AACGCCGAGA ATGTGGAAGT GATCCTGACC AGCAGCAAGC
 15 2351 AGATCGATAA GTCTAGCATG TATAAGTTCC TGGAGCCTTG GCTGGGCCTG
 2401 GGCCTGTGTA CCTCTACAGG CAACAAGTGG AGGAGCCGGA GAAAGATGCT
 2451 GACCCCAACA TTCCACTTTA CAATCCTGGA GGACTTCCTG GACATCATGA
 2501 ACGAGCAGGC CAATATCCTG GTGAAGAAGC TGGAGAAGCA CATCAACCAG
 2551 GAGGCCTTTA ATTGCTTCTT TTACATCACC CTGTGCGCCC TGGACATCAT
 20 2601 CTGTGAGACA GCTATGGGCA AGAACATCGG CGCCCAGTCT AATGACGATA
 2651 GCGAGTACGT GCGGGCCGTG TATAGAAATGA GCGAGATGAT CTTTAGGCGC
 2701 ATCAAGATGC CCTGGCTGTG GCTGGATCTG TGGTATCTGA TGTTCAAGGA
 2751 GGGCTGGGAG CACAAGAAGT CCCTGCAGAT CCTGCACACC TTTACAAACT
 2801 CTGTGATCGC CGAGAGAGCC AATGAGATGA ACGCCAATGA GGAAGTAGG
 25 2851 GGCGATGGAA GGGGCAGCGC CCCTTCCAAG AACAAGCGGA GAGCCTTCCT
 2901 GGACCTGCTG CTGAGCGTGA CCGACGATGA GGGCAATCGC CTGTCCCACG
 2951 AGGACATCCG GGAGGAGGTG GATACATTCA TGTTCGAGG ACACGACACC
 3001 ACAGCCGCCG CCATCAACTG GTCCTGTAC CTGCTGGGCT CTAATCCAGA
 3051 GGTGCAGAAG AAGGTGGATC ACGAGCTGGA CGACGTGTTT GGCAAGTCCG
 30 3101 ACAGGCCAGC AACCGTGGAG GATCTGAAGA AGCTGAGATA CCTGGAGTGC
 3151 GTGATCAAGG AGACACTGCG CCTGTTCCCC TCTGTGCCTC TGTTTGCCCG
 3201 GTCCGTGTCT GAGGACTGTG AGGTGGCCGG CTATCGCGTG CTGAAGGGCA
 3251 CCGAGGCCGT GATCATCCCT TACGCCCTGC ACCGGGACCC CAGGTATTTT
 3301 CCTAACCAGG AGGAGTTTCA GCCAGAGAGA TTCTTTCCCG AGAATGCCCA
 35 3351 GGGCAGGCAC CCTTACGCCT ATGTGCCATT CTCCGCGGGA CCAAGGAACT
 3401 GCATCGGACA GAAGTTTGCC GTGATGGAGG AGAAAACCAT CCTGTCTTGT
 3451 ATCCTGAGAC ACTTCTGGAT CGAGAGCAAT CAGAAGAGGG AGGAGCTGGG
 3501 CCTGGAGGGA CAGCTGATCC TGCGGCCAAG CAACGGCATC TGGATCAAAC
 3551 TGAAAAGAAG GAACGCTGAC GAGAGGTAAA AGCTTGGTAC CGATATCGCG
 40 3601 GCCGCCCTAG GGAGCTCCTC GAGGCGGCCC GCTCGAGTCT AGAGGGCCCT
 3651 TCGAAGGTAA GCCTATCCCT AACCCTCTCC TCGGTCTCGA TTCTACGCGT
 3701 ACCGGTCATC ATCACCATCA CCATTGAGTT TCGATAATCA ACCTCTGGAT
 3751 TACAAAATTT GTGAAAGATT GACTGGTATT CTTAACTATG TTGCTCCTTT
 45 3801 TACGCTATGT GGATACGCTG CTTTAATGCC TTTGTATCAT GCTATTGCTT
 3851 CCCGTATGGC TTTCATTTTC TCCTCCTTGT ATAAATCCTG GTTGCTGTCT
 3901 CTTTATGAGG AGTTGTGGCC CGTTGTCAGG CAACGTGGCG TGGTGTGCAC
 3951 TGTGTTTGTCT GACGCAACCC CCACTGGTTG GGGCATTGCC ACCACCTGTC
 4001 AGCTCCTTTC CGGGACTTTC GCTTTCCTCC TCCCTATTGC CACGGCGGAA
 4051 CTCATCGCCG CTGCTTGTG CCGCTGCTGG ACAGGGGCTC GGCTGTTGGG
 50 4101 CACTGACAAT TCCGTGGTGT TGTGCGGGAA ATCATCGTCC TTTCTTGGC
 4151 TGCTCGCCTG TGTTGCCACC TGGATTCTGC GCGGGACGTC CTTCTGCTAC
 4201 GTCCCTTCGG CCCTCAATCC AGCGGACCTT CCTTCCCGCG GCCTGCTGCC
 4251 GGCTCTGCGG CCTCTTCCGC GTCTTCGCTT TCGCCCTCAG ACGAGTCGGA
 4301 TCTCCCTTTG GGCCGCCTCC CCGCATCGAA ACCCGCTGAT CAGCCTCGAC
 55 4351 TGTGCCCTCT AGTTGCCAGC CATCTGTTGT TTGCCCCCTC CCCGTGCCTT

4401 CCTTGACCCT GGAAGGTGCC ACTCCCCTG TCCTTTCCTA ATAAAATGAG
 4451 GAAATTGCAT CGCATTGTCT GAGTAGGTGT CATTCTATTC TGGGGGGTGG
 4501 GGTGGGGCAG GACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG
 4551 CTGGGGATGC GGTGGGCTCT ATGGCTTCTG AGGCGGAAAG AACCAGATCC
 5 4601 TCTCTTAAAG TAGCATCGAG ATTTAAATTA GGGATAACAG GGTAATGGCG
 4651 CGGGCCGCAG GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG
 4701 CTCGCTCGCT CACTGAGGCC GGGCGACCAA AGGTCGCCCC ACGCCCGGGC
 4751 TTTGCCCGGG CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG

10 SEQ ID NO: 61 - Sequence of CYP4V2 expression cassette in AAV5.CYP4V2st.
 AAV5.CYP4V2st has the same promoter (CAG), enhancer (WPRE) and polyA (bGH-
 polyA) as AAV2.CYP4V2op, AAV2tri(Y-F).CYP4V2op and AAV5.CYP4V2op (SEQ ID NO:
 60) but different CYP4V2 cDNA and junction/linker sequences:
 Left-ITR: 1-141
 15 CAG promoter: 166-1880
 CYP4V2st cDNA: 1938-3515
 WPRE enhancer: 3551-4139
 bGH polyA: 4163-4387
 Right-ITR: 4399-4539

20 1 CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG
 51 CCCGGGCGTC GGGCGACCTT TGGTCGCCCC GCCTCAGTGA GCGAGCGAGC
 101 GCGCAGAGAG GGAGTGGCCA ACTCCATCAC TAGGGGTTCC TGCGGCCTAA
 151 GGCAATTGAG ATCTCGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA
 25 201 ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
 251 ACTTACGGTA AATGGCCCCG CTGGCTGACC GCCCAACGAC CCCCGCCCAT
 301 TGACGTC AATGACGTAT GTTCCCATAG TAACGCCAAT AGGGACTTTC
 351 CATTGACGTC AATGGGTGGA CTATTTACGG TAAACTGCCC ACTTGCGAGT
 401 ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC GTCAATGACG
 30 451 GTAAATGGCC CGCCTGGCAT TATGCCAGT ACATGACCTT ATGGGACTTT
 501 CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGGTCG
 551 AGGTGAGCCC CACGTTCTGC TTCACTCTCC CCATCTCCCC CCCCTCCCCA
 601 CCCCCAATTT TGTATTTATT TATTTTTTAA TTATTTTGTG CAGCGATGGG
 651 GCGGGGGGGG GGGGGGGCGC GCGCCAGGCG GGGCGGGGCG GGGCGAGGGG
 35 701 CGGGGGCGGG CGAGGCGGAG AGGTGCGGCG GCAGCCAATC AGAGCGGCGC
 751 GCTCCGAAAG TTTCCTTTTA TGGCGAGGCG GCGGCGGCGG CGGCCCTATA
 801 AAAAGCGAAG CGCGCGGCGG GCGGGAGTCG CTGCGTTGCC TTCGCCCGGT
 851 GCCCCGCTCC GCGCCGCTC GCGCCGCCCC CCCCGGCTCT GACTGACCGC
 901 GTTACTCCCA CAGGTGAGCG GCGGGGACGG CCCTTCTCCT CCGGGCTGTA
 40 951 ATTAGCGCTT GGTTAATGA CGGCTCGTTT CTTTCTGTG GCTGCGTGAA
 1001 AGCCTTAAAG GGCTCCGGA GGGCCCTTTG TCGGGGGGGG AGCGGCTCGG
 1051 GGGGTGCGTG CGTGTGTGTG TCGTGGGGA GCGCCGCGTG CGGCCGCGC
 1101 TGCCCGGCGG CTGTGAGCGC TGCGGGCGCG GCGCGGGGCT TTGTGCGCTC
 1151 CGCGTGTGCG CGAGGGGAGC GCGGCCGGGG GCGGTGCCCC GCGGTGCGGG
 45 1201 GGGGCTGCGA GGGGAACAAA GGCTGCGTGC GGGGTGTGTG CGTGGGGGGG
 1251 TGAGCAGGGG GTGTGGGCGC GCGGTGCGGG CTGTAACCCC CCCCTGCACC
 1301 CCCCTCCCCG AGTTGCTGAG CACGGCCCGG CTTGCGGTGC GGGGCTCCGT
 1351 GCGGGGCGTG GCGCGGGGCT CGCCGTGCCG GCGGGGGGGT GCGGCGAGGT
 1401 GGGGTGCCC GCGGGGGCGG GGCCGCTCG GCGGGGGGAG GGCTCGGGGG
 50 1451 AGGGGCGCGG CGGCCCGGA GCGCCGCGCG CTGTCGAGGC GCGGCGAGCC
 1501 GCAGCCATTG CTTTTATGG TAATCGTGCG AGAGGGCGCA GGGACTTCCT
 1551 TTGTCCAAA TCTGGCGGAG CCGAAATCTG GGAGGCGCCG CCGCACCCCC
 1601 TCTAGCGGGC GCGGGCGAAG CCGTGCGGCG CCGGCAGGAA GGAAATGGGC
 1651 GGGGAGGGCC TTCGTGCGTC GCGCGCCGCG CGTCCCCTTC TCCATCTCCA
 55 1701 GCCTCGGGGC TGCCGACGGG GGACGGCTGC CTTGCGGGGG GACGGGGCAG

5 1751 GCGGGGGTTC GGCTTCTGGC GTGTGACCGG CGGCTCTAGA GCCTCTGCTA
1801 ACCATGTTCA TGCCTTCTTC TTTTTCCTAC AGCTCCTGGG CAACGTGCTG
1851 GTTATTGTGC TGTCTCATCA TTTTGGCAAA GAATTCCTAAT ACGACTCACT
1901 ATAGGGAGAC CCAAGCTGGC TAGCCAAAGC TTCCACCATG GCGGGGCTCT
1951 GGCTGGGGCT CGTGTGGCAG AAGCTGCTGC TGTGGGGCGC GCGAGTGCC
2001 CTTTCCCTGG CCGGCGCCAG TCTGGTCTTG AGCCTGCTGC AGAGGGTGGC
2051 GAGCTACGCG CGGAAATGGC AGCAGATGCG GCCCATCCCC ACGGTGGCCC
2101 GCGCCTACCC ACTGGTGGGC CACGCGCTGC TGATGAAGCC GGACGGGCGA
10 2151 GAATTTTTC AGCAGATCAT TGAGTACACA GAGGAATACC GCCACATGCC
2201 GCTGCTGAAG CTCTGGGTCG GGCCAGTGCC CATGGTGGCC CTTTATAATG
2251 CAGAAAATGT GGAGGTAATT TTAAC TAGTT CAAAGCAAAT TGACAAATCC
2301 TCTATGTACA AGTTTTTAGA ACCATGGCTT GGCCTAGGAC TTCTTACAAG
2351 TACTGGAAAC AAATGGCGCT CCAGGAGAAA GATGTTAACA CCCACTTTCC
2401 ATTTTACCAT TCTGGAAGAT TTCTTAGATA TCATGAATGA ACAAGCAAAT
15 2451 ATATTGGTTA AGAACTTGA AAAACACATT AACCAAGAAG CATTTAACTG
2501 CTTTTTTTAC ATCACTCTTT GTGCCCTAGA TATCATCTGT GAAACAGCTA
2551 TGGGGAAGAA TATTGGTGCT CAAAGTAATG ATGATTCCGA GTATGTCCGT
2601 GCAGTTTATA GAATGAGTGA GATGATATTT CGAAGAATAA AGATGCCCTG
2651 GCTTTGGCTT GATCTCTGGT ACCTTATGTT TAAAGAAGGA TGGGAACACA
20 2701 AAAAGAGCCT TCAGATCCTA CATACTTTTA CCAACAGTGT CATCGCTGAA
2751 CGGGCCAATG AAATGAACGC CAATGAAGAC TG TAGAGGTG ATGGCAGGGG
2801 CTCTGCCCCC TCCAAAAATA AACGCAGGGC CTTTCTTGAC TTGCTTTTAA
2851 GTGTGACTGA TGACGAAGGG AACAGGCTAA GTCATGAAGA TATTCGAGAA
2901 GAAGTTGACA CCTTCATGTT TGAGGGGCAC GATACAAC TG CAGCTGCAAT
25 2951 AAAGTGGTCC TTATACCTGT TGGGTTCTAA CCCAGAAAGT CAGAAAAAAG
3001 TGGATCATGA ATTGGATGAC GTGTTTGGGA AGTCTGACCG TCCCGCTACA
3051 GTAGAAGACC TGAAGAAACT TCGGTATCTG GAATGTGTTA TTAAGGAGAC
3101 CCTTCGCTT TTTCTTCTG TTTCTTTATT TGCCCGTAGT GTTAGTGAAG
3151 ATTGTGAAGT GGCAGGTTAC AGAGTTCTAA AAGGCACTGA AGCCGTATC
30 3201 ATTCCCTATG CATTGCACAG AGATCCGAGA TACTTCCCCA ACCCGAGGA
3251 GTTCCAGCCT GAGCGGTTCT TCCCCGAGAA TGCACAAGGG CGCCATCCAT
3301 ATGCCTACGT GCCCTTCTCT GCTGGCCCCA GGAAGTGTAT AGGTCAAAAG
3351 TTTGCTGTGA TGGGAAGAAA GACCATTCTT TCGTGCATCC TGAGGCACTT
3401 TTGGATAGAA TCCAACCAGA AAAGAGAAGA GCTTGGTCTA GAAGGACAGT
35 3451 TGATTCTTCG TCCAAGTAAT GGCATCTGGA TCAAGTTGAA GAGGAGAAAT
3501 GCAGATGAAC GCTAAGCGGC CGCAACTCGA GACTCTAGAG GTTAATCGAT
3551 AATCAACCTC TGGATTACAA AATTTGTGAA AGATTGACTG GTATTCTTAA
3601 CTATGTTGCT CCTTTTACGC TATGTGGATA CGCTGCTTTA ATGCCTTTGT
3651 ATCATGCTAT TGCTTCCCGT ATGGCTTTCA TTTTCTCCTC CTTGTATAAA
40 3701 TCCTGGTTGC TGTCTCTTTA TGAGGAGTTG TGGCCCGTTG TCAGGCAACG
3751 TGGCGTGGTG TGCACTGTGT TTGCTGACGC AACCCCCACT GGTTGGGGCA
3801 TTGCCACCAC CTGTGAGCTC CTTTCCGGGA CTTTCGCTTT CCCCTCCCT
3851 ATTGCCACGG CGGAATCAT CGCCGCTGCT CTTGCCCGCT GCTGGACAGG
3901 GGCTCGGCTG TTGGGCACTG ACAATTCCGT GGTGTTGTCG GGGAAATCAT
45 3951 CGTCCTTTCC TTGGCTGCTC GCCTGTGTTG CCACCTGGAT TCTGCGCGGG
4001 ACGTCCCTCT GCTACGTCCC TTCGGCCCTC AATCCAGCGG ACCTTCCTTC
4051 CCGCGGCTG CTGCGGCTC TGCGGCTCT TCCGCTCTT CGCCTTCGCC
4101 CTCAGACGAG TCGGATCTCC CTTTGGGCGG CCTCCCCGCA TCGAAACCCG
4151 CTGACTAGAC GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC
50 4201 TCCCCCTGCT CTTCTTTGAC CTTGGAAGGT GCCACTCCCA CTGCTCTTC
4251 CTAATAAAAT GAGGAAATTG CATCGCATTG TCTGAGTAGG TGTCATTCTA
4301 TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA TTGGGAAGAC
4351 AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCCG CGGGCCGAG
4401 GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG CTCGCTCGCT
55 4451 CACTGAGGCC GGGCGACCAA AGGTCGCCCC ACGCCCGGGC TTTGCCCGGG

4501 CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG

- 5 SEQ ID NO: 62 - Sequence of CYP4V2 expression cassette in AAV8.CYP4V2fv. AAV8.CYP4V2fv has the same promoter (CAG), enhancer (WPRE) and polyA (bGH-polyA) and junction/linker sequences as AAV5.CYP4V2st (SEQ ID NO: 61) and differs only in CYP4V2 cDNA sequence:

- 10 Left-ITR: 1-141
CAG promoter: 166-1880
CYP4V2fv cDNA: 1938-3515
WPRE enhancer: 3551-4139
bGH polyA: 4163-4387
15 Right-ITR: 4399-4539

- 1 CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG
51 CCCGGGCGTC GGGCGACCTT TGGTCGCCCC GCCTCAGTGA GCGAGCGAGC
101 GCGCAGAGAG GGAGTGGCCA ACTCCATCAC TAGGGGTTCC TGCGGCCTAA
20 151 GGCAATTGAG ATCTCGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA
201 ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
251 ACTTACGGTA AATGGCCCCG CTGGCTGACC GCCCAACGAC CCCCGCCCAT
301 TGACGTCAAT AATGACGTAT GTTCCCATAG TAACGCCAAT AGGGACTTTC
351 CATTGACGTC AATGGGTGGA CTATTTACGG TAAACTGCCC ACTTGGCAGT
25 401 ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC GTCAATGACG
451 GTAAATGGCC CGCCTGGCAT TATGCCCAGT ACATGACCTT ATGGGACTTT
501 CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGGTCG
551 AGGTGAGCCC CACGTTCTGC TTCACTCTCC CCATCTCCCC CCCCTCCCCA
601 CCCCCAATT TGTATTTATT TATTTTTTAA TTATTTTGTG CAGCGATGGG
30 651 GCGGGGGGGG GGGGGGGCGC GCGCCAGGCG GGGCGGGGCG GGGCGAGGGG
701 GCGGGCGGGG CGAGGCGGAG AGGTGCGGCG GCAGCCAATC AGAGCGGCGC
751 GCTCCGAAAG TTTCTTTTAA TGGCGAGGCG GCGGCGGCGG CGGCCCTATA
801 AAAAGCGAAG CGCGCGGCGG GCGGGAGTCG CTGCGTTGCC TTCGCCCCGT
851 GCGCCGCTCC CGCGCGCCTC GCGCCGCCCG CCCCGGCTCT GACTGACCGC
35 901 GTTACTCCCA CAGGTGAGCG GCGGGGACGG CCCTTCTCCT CCGGGCTGTA
951 ATTAGCGCTT GGTTTAATGA CGGCTCGTTT CTTTTCTGTG GCTGCGTGAA
1001 AGCCTTAAAG GGCTCCGGGA GGGCCCTTTG TCGGGGGGGG AGCGGCTCGG
1051 GGGGTGCGTG CGTGTGTGTG TCGTGGGGA GCGCCGCGTG CGGCCCGCGC
1101 TGCCCCGGCG CTGTGAGCGC TGCGGGCGCG GCGCGGGGCT TTGTGCGCTC
40 1151 CGCGTGTGCG CGAGGGGAGC GCGGCCGGGG GCGGTGCCCC GCGGTGCGGG
1201 GGGGCTGCGA GGGGAACAAA GGCTGCGTGC GGGGTGTGTG CGTGGGGGGG
1251 TGAGCAGGGG GTGTGGGCGC GCGGTCGGG CTGTAACCCC CCCCTGCACC
1301 CCCCTCCCCG AGTTGCTGAG CACGGCCCGG CTTGCGGTGC GGGGCTCCGT
1351 GCGGGGCGTG GCGCGGGGCT CGCCGTGCCG GCGGGGGGGT GCGGCGAGGT
45 1401 GGGGGTGCCG GCGGGGCGG GGC CGCCTCG GCGCGGGGAG GGCTCGGGGG
1451 AGGGGCGCGG CGGCCCGGGA GCGCGGCGG CTGTGAGGC GCGGCGAGCC
1501 GCAGCCATTG CCTTTTATGG TAATCGTGCG AGAGGGCGCA GGGACTTCCT
1551 TTGTCCCAAA TCTGGCGGAG CCGAAATCTG GGAGGCGCCG CCGCACCCCC
1601 TCTAGCGGGC GCGGGCGAAG CGGTGC GGCG CCGGCAGGAA GGAAATGGGC
50 1651 GGGGAGGGCC TTCGTGCGTC GCGCGCGCGC CGTCCCCTTC TCCATCTCCA
1701 GCCTCGGGGC TGCCGAGGGG GGACGGCTGC CTTGCGGGGG GACGGGGCAG
1751 GCGGGGGTTC GGCTTCTGGC GTGTGACCGG CGGCTCTAGA GCCTCTGCTA
1801 ACCATGTTCA TGCTTCTTC TTTTTCCTAC AGTCCTGGG CAACGTGCTG
1851 GTTATTGTGC TGTCTCATCA TTTTGCCAAA GAATTCCTAAT ACGACTCACT
55 1901 ATAGGGAGAC CCAAGCTGGC TAGCCAAAGC TTCCACCATG GCGGGGCTCT

1951 GGCTGGGGCT CGTGTGGCAG AAGCTGCTGC TGTGGGGCGC GGCGAGTGCC
 2001 CTTTCCCTGG CCGGCGCCAG TCTGGTCCTG AGCCTGCTGC AGAGGGTGGC
 2051 GAGCTACGCG CGGAAATGGC AGCAGATGCG GCCCATCCCC ACGGTGGCCC
 2101 GCGCCTACCC ACTGGTGGGC CACGCGCTGC TGATGAAGCC GGACGGGCGA
 5 2151 GAATTTTTTC AGCAGATCAT TGAGTACACA GAGGAATACC GCCACATGCC
 2201 GCTGCTGAAG CTCTGGGTCG GGCCAGTGCC CATGGTGGCC CTTTATAATG
 2251 CAGAAAATGT GGAGGTAATT TTAACAGTTC CAAAGCAAAT TGACAAATCC
 2301 TCTATGTACA AGTTTTTAGA ACCATGGCTT GGCCTAGGAC TTCTTACAAG
 2351 TACTGGAAAC AAATGGCGCT CCAGGAGAAA GATGTTAACA CCCACTTTCC
 10 2401 ATTTTACCAT TCTGGAAGAT TTCTTAGATA TCATGAATGA ACAAGCAAAT
 2451 ATATTGGTTA AGAACTTGA AAAACACATT AACCAGAAG CATTTAACATG
 2501 CTTTTTTTAC ATCACTCTTT GTGCCTTAGA TATCATCTGT GAAACAGCTA
 2551 TGGGGAAGAA TATTGGTGCCT CAAAGTAATG ATGATTCCGA GTATGTCCGT
 2601 GCAGTTTATA GAATGAGTGA GATGATATTT CGAAGAATAA AGATGCCCTG
 15 2651 GCTTTGGCTT GATCTCTGGT ACCTTATGTT TAAAGAAGGA TGGGAACACA
 2701 AAAAGAGCCT TAAGATCCTA CATACTTTTA CCAACAGTGT CATCGCGGAA
 2751 CGGGCCCAATG AAATGAACGC CAATGAAGAC TGTAGAGGTG ATGGCAGGGG
 2801 CTCTGCCCCC TCCAAAAATA AACGCAGGGC CTTTCTTGAC TTGCTTTTAA
 2851 GTGTGACTGA TGACGAAGGG AACAGGCTAA GTCATGAAGA TATTGAGAA
 20 2901 GAAGTTGACA CCTTCATGTT TGAGGGGCAC GATACAACTG CAGCTGCAAT
 2951 AAAGTGGTCC TTATACCTGT TGGGTTCTAA CCCAGAAGTC CAGAAAAAAG
 3001 TGGATCATGA ATTGGATGAC GTGTTTGGGA AGTCTGACCG TCCCGGTACA
 3051 GTAGAAGACC TGAAGAACT TCGGTATCTG GAATGTGTTA TTAAGGAGAC
 3101 CCTTCGCCTT TTTCTTCTG TTCCTTTATT TGCCCGTAGT GTTAGTGAAG
 25 3151 ATTGTGAAGT GGCAGGTTAC AGAGTTCTAA AAGGCACTGA AGCCGTCATC
 3201 ATTCCCTATG CATTGCACAG AGATCCGAGA TACTTCCCCA ACCCGAGGA
 3251 GTTCCAGCCT GAGCGGTTCT TCCCGGAGAA TGACACAAGG CGCCATCCAT
 3301 ATGCCCTACGT GCCCTTCTCT GCTGGCCCCA GGAAGTGTAT AGGTCAAAAG
 3351 TTTGCTGTGA TGGAAGAAAA GACCATTCTT TCGTGCATCC TGAGGCACTT
 30 3401 TTGGATGAAA TCCAACCAGA AAAGAGAAGA GCTTGGTCTA GAAGGACAGT
 3451 TGATTCTTCG TCCAAGTAAT GGCATCTGGA TCAAGTTGAA GAGGAGAAAT
 3501 GCAGATGAAC GCTAAGCGGC CGCAACTCGA GACTCTAGAG GTTAATCGAT
 3551 AATCAACCTC TGGAATTACAA AATTTGTGAA AGATTGACTG GTATTCTTAA
 3601 CTATGTTGCT CCTTTTACGC TATGTGGATA CGCTGCTTTA ATGCCTTTGT
 35 3651 ATCATGCTAT TGCTTCCCGT ATGGCTTTCA TTTTCTCCTC CTTGTATAAA
 3701 TCCTGGTTGC TGTCTCTTTA TGAGGAGTTG TGGCCCGTTG TCAGGCAACG
 3751 TGGCGTGGTG TGCACTGTGT TTGCTGACGC AACCCCCACT GGTGGGGCA
 3801 TTGCCACCAC CTGTCAGCTC CTTTCCGGGA CTTTCGCTTT CCCCTCCCT
 3851 ATTGCCACGG CGGAATCAT CGCCGCCTGC CTTGCCCGCT GCTGGACAGG
 40 3901 GGCTCGGCTG TTGGGCACTG ACAATTCCGT GGTGTTGTCG GGGAAATCAT
 3951 CGTCCTTTCC TTGGCTGCTC GCCTGTGTTG CCACCTGGAT TCTGCGCGGG
 4001 ACGTCCTTCT GCTACGTCCC TTCGGCCCTC AATCCAGCGG ACCTTCCTTC
 4051 CCGCGGCTG CTGCGGCTC TGCGGCTCT TCCGCGTCT CGCCTTCGCC
 4101 CTCAGACGAG TCGGATCTCC CTTTGGGCCG CCTCCCCGCA TCGAAACCCG
 45 4151 CTGACTAGAC GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC
 4201 TCCCCGTGCT CTTCTTGAC CCTGGAAGGT GCCACTCCCA CTGTCTTTTC
 4251 CTAATAAAAT GAGGAAATTG CATCGCATTG TCTGAGTAGG TGTCATTCTA
 4301 TTCTGGGGGG TGGGTGGGG CAGGACAGCA AGGGGAGGA TTGGGAAGAC
 4351 AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCCG CGGGCCGCG
 50 4401 GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG CTCGCTCGCT
 4451 CACTGAGGCC GGGCGACCAA AGGTCGCCCC ACGCCGGGC TTTGCCCGGG
 4501 CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG

55 SEQ ID NO: 63 - Sequence of CYP4V2 expression cassette in AAV5.CYP4V2op (new).
 AAV5.CYP4V2op (new) has the same promoter (CAG), enhancer (WPRe) and polyA

(bGH-polyA) and the same junction/linker sequences as AAV5.CYP4V2st (SEQ ID NO: 61) and AAV8.CYP4V2fv (SEQ ID NO: 62) but different CYP4V2 cDNA sequences:
Left-ITR: 1-141

CAG promoter: 166-1880

5 CYP4V2op cDNA: 1938-3515

WPRES enhancer: 3551-4139

bGH polyA: 4163-4387

Right-ITR: 4399-4539

10 CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG
CCCGGGCGTC GGGCGACCTT TGGTCGCCCG GCCTCAGTGA GCGAGCGAGC
GCGCAGAGAG GGAGTGGCCA ACTCCATCAC TAGGGGTTC TGCGGCCATA
GGCAATTGAG ATCTCGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA
ATTACGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
15 ACTTACGGTA AATGGCCCGC CTGGCTGACC GCCCAACGAC CCCCAGCCAT
TGACGTCAAT AATGACGTAT GTTCCCATAG TAACGCCAAT AGGGACTTTC
CATTGACGTC AATGGGTGGA CTATTTACGG TAAACTGCCC ACTTGGCAGT
ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC GTCAATGACG
GTAAATGGCC CGCCTGGCAT TATGCCAGT ACATGACCTT ATGGGACTTT
20 CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGGTCG
AGGTGAGCCC CACGTTCTGC TTCACTCTCC CCATCTCCCC CCCCTCCCCA
CCCCCAATTT TGATTTTATT TATTTTAA TTTATTTGTG CAGCGATGGG
GGCGGGGGGG GGGGGGGCGC GCGCCAGGCG GGGCGGGGCG GGGCGAGGGG
CGGGGCGGGG CGAGGCGGAG AGGTGCGGCG GCAGCCAATC AGAGCGGCGC
25 GCTCCGAAAG TTTCCTTTTA TGGCGAGGCG GCGGCGGCGG CGGCCCTATA
AAAAGCGAAG CGCGCGGCGG GCGGGAGTCG CTGCGTTGCC TTCGCCCGT
GCCCCGCTCC GCGCGGCCCTC GCGCCGCCCG CCCCGGCTCT GACTGACCGC
GTTACTCCCA CAGGTGAGCG GCGGGACGCG CCCTTCTCCT CCGGGCTGTA
ATTAGCGCTT GGTTAATGA CGGCTCGTTT CTTTCTGTG GCTGCGTGAA
30 AGCCTTAAAG GGCTCCGGGA GGGCCCTTTG TCGGGGGGG AGCGGCTCGG
GGGGTGCGTG CGTGTGTGTG TCGTGGGGA GCGCCGCGTG GGGCCGCGC
TGCCCGCGCG CTGTGAGCGC TCGGGGCGCG GCGCGGGGCT TTGTGCGCTC
CGCGTGTGCG CGAGGGGAGC GCGCCCGGGG GCGGTGCCCC GCGGTGCGGG
GGGGTGCGCA GGGGAACAAA GGCTGCGTGC GGGGTGTGTG CGTGGGGGGG
35 TGAGCAGGGG GTGTGGGCGC GCGGTCGGG CTGTAACCC CCCCTGCACC
CCCCTCCCCG AGTTGCTGAG CACGGCCCGG CTTGCGGTGC GGGGCTCCGT
GCGGGGCGTG GCGCGGGGCT CGCCGTGCCG GCGGGGGGGT GCGGCGAGGT
GGGGGTGCCG GCGGGGGCGG GCGCGCCTCG GCGCGGGGAG GGCTCGGGGG
AGGGGCGCGG CGGCCCGGA GCGCGGCGG CTGTCGAGG GCGGCGAGCC
40 GCAGCCATTG CCTTTTATGG TAATCGTGCG AGAGGGCGCA GGGACTTCCT
TTGTCCCAA TCTGGCGGAG CCGAAATCTG GGAGGCGCCG CCGCACCCCC
TCTAGCGGGC GCGGGCGAAG CCGTGCGGCG CCGGCAGGAA GGAAATGGGC
GGGGAGGGCC TCTGTGCGTC GCGCGCGCGC CGTCCCTTC TCCATCTCCA
GCCTCGGGG TGCCGAGGG GGACGGCTGC CTTGCGGGG GACGGGCGAG
45 GCGGGGGTTC GGCTTCTGGC GTGTGACCG CGGCTCTAGA GCCTCTGCTA
ACCATGTTCA TGCTTCTTC TTTTCTCTAC AGCTCCTGGG CAACGTGCTG
GTTATTGTGC TGTCTCATCA TTTTGGCAA GAATTCTAAT ACGACTCACT
ATAGGGAGAC CCAAGCTGGC TAGCCAAAGC TTCCACC
ATGGCTGGACTGTGGCTGGGACTGGTGTGGCAGAACTGCTGCTGTGGGGGGCGCTTCCGCACTGTCACTGGCTGGG
50 GCTTCACTGGTGCTGAGCCTGCTGCAGAGGGTGGCCTCCTACGCCAGAAAGTGGCAGCAGATGAGGCCCATCCCTACC
GTGGCCAGAGCCTATCCACTGGTGGGACACGCACTGCTGATGAAGCCTGACGGCAGAGAGTTCTTTCAGCAGATCATC
GAGTACACAGAGGAGTATAGGCACATGCCACTGCTGAAGCTGTGGGTGGGACCCGTGCCTATGGTGGCCCTGTACAAC
GCCGAGAAATGTGGAAGTGATCTGACCAGCAGCAAGCAGATCGATAAGTCTAGCATGTATAAGTTCCTGGAGCCTTGG
CTGGGCCTGGGCTGCTGACCTCTACAGGCAACAAGTGGAGGAGCCGGAGAAAGATGCTGACCCCAACATTCCACTTT
55 ACAATCCTGGAGGACTTCCTGGACATCATGAACGAGCAGGCCAATATCCTGGTGAAGAAGCTGGAGAAGCACATCAAC

CAGGAGGCCTTTAATTGCTTCTTTTACATCACCCGTGTGCGCCCTGGACATCATCTGTGAGACAGCTATGGGCAAGAAC
 ATCGGGCGCCAGTCTAATGACGATAGCGAGTACGTGCGGGCCGTGTATAGAATGAGCGAGATGATCTTTAGGCGCATC
 AAGATGCCCTGGCTGTGGCTGGATCTGTGGTATCTGATGTTCAAGGAGGGCTGGGAGCACAAGAAGTCCCTGCAGATC
 CTGCACACCTTTTACAAACTCTGTGATCGCCGAGAGAGCCAATGAGATGAACGCCAATGAGGACTGTAGGGGCCGATGGA
 5 AGGGGACAGCGCCCTTCCAAGAACAAGCGGAGAGCCTTCTGGACCTGCTGCTGAGCGTGACCGACGATGAGGGCAAT
 CGCCTGTCCACGAGGACATCCGGGAGGAGGTGGATACATTGTTTGTAGGGACACGACACCACAGCCGCCGCCATC
 AACTGGTCCCTGTACCTGCTGGGCTCTAATCCAGAGGTGCAGAAGAAGGTGGATCACGAGCTGGACGACGTGTTCCGGC
 AAGTCCGACAGGCCAGCAACCGTGGAGGATCTGAAGAAGCTGAGATACCTGGAGTGCGTGATCAAGGAGACACTGCGC
 CTGTTCCCTCTGTGCTCTCTGTTTGGCCGTCCTGTCTGAGGACTGTGAGGTGGCCGGCTATCGCGTGCTGAAGGGC
 10 ACCGAGGCCGTGATCATCCCTTACGCCCTGCACCGGACCCAGGTATTTCCCTAACCCAGAGGAGTTTCAGCCAGAG
 AGATTCTTTCCCGAGAATGCCAGGGCAGGCACCCCTACGCCCTATGTGCCATTCTCCGCCGACCAAGGAAGTGCATC
 GGACAGAAGTTTGGCGTGATGGAGGAGAAAACCATCTGTCTTGTATCCTGAGACACTTCTGGATCGAGAGCAATCAG
 AAGAGGGAGGAGCTGGGCCCTGGAGGGACAGCTGATCCTGCGGCCAAGCAACGGCATCTGGATCAAACCTGAAAAGAAGG
 AACGCTGACGAGAGGTAAGCGGC CGCAACTCGA GACTCTAGAG GTTAATCGAT
 15 AATCAACCTC TGGATTACAA AATTTGTGAA AGATTGACTG GTATTCTTAA
 CTATGTTGCT CTTTTTACGC TATGTGGATA CGCTGCTTTA ATGCCTTTGT
 ATCATGCTAT TGCTTCCCGT ATGGCTTTCA TTTTCTCCTC CTTGTATAAA
 TCCTGGTTGC TGTCTCTTTA TGAGGAGTTG TGGCCCGTTG TCAGGCAACG
 TGGCGTGGTG TGCACGTGTG TTGCTGACGC AACCCCACT GGTGGGGCA
 20 TTGCCACCAC CTGTCAGCTC CTTTCCGGGA CTTTCGCTTT CCCCCTCCCT
 ATTGCCACGG CGGAATCAT CGCCGCTGC CTTGCCCGCT GCTGGACAGG
 GGCTCGGCTG TTGGGCACTG ACAATTCCTG GGTGTTGTCG GGGAAATCAT
 CGTCCTTTTC TTGGCTGCTC GCCTGTGTTG CCACCTGGAT TCTGCGCGGG
 ACGTCCCTTCT GCTACGTCCC TTCGGCCCTC AATCCAGCG ACCTTCCTTC
 25 CCGCGGCTG CTGCGGCTC TGCGGCCTCT TCCGCGTCTT CGCCTTCGCC
 CTCAGACGAG TCGGATCTCC CTTTGGGCCG CCTCCCCGCA TCGAAACCCG
 CTGACTAGAC GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC
 TCCCCGTGC CTTCCTTGAC CCTGGAAGGT GCCACTCCCA CTGTCTTTTC
 CTAATAAAAT GAGGAAATTG CATCGATTG TCTGAGTAGG TGTCATTCTA
 30 TTCTGGGGG TGGGTGGGG CAGGACAGCA AGGGGAGGA TTGGGAAGAC
 AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCCG CGGGCCGCAG
 GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG CTCGCTCGCT
 CACTGAGGCC GGGCGACCAA AGGTGCGCCG ACGCCCGGGC TTTGCCCGGG
 CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG
 35

SEQ ID NO: 64 - Sequence of CYP4V2 expression cassette in scAAV1.CYP4V2op,
 scAAV5.CYP4V2op, and scAAV9.CYP4V2op.
 Left-ITR (truncated): 1-117
 EFS promoter: 130-364
 CYP4V2op cDNA: 520-2097
 SPA: 2116-2169
 Right-ITR: 2263-2403

1 cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag cccgggcgctc
 61 gggcgacctt tggctcgccg gcctcagtga gcgagcgagc gcgcagagag ggagtggacg
 45 121 cgtaggcctg attggctccg gtgcccgtca gtgggcagag cgcacatcgc ccacagtccc
 181 cgagaagttg gggggagggg tcggcaattg aaccggtgcc tagagaaggt ggcgcggggt
 241 aaactgggaa agtgatgtcg tgtactggct ccgccttttt cccgaggggtg ggggagaacc
 301 gtatataagt gcagtagtcg ccgtgaacgt tcttttttcgc aacgggtttg ccgccagaac
 361 acaggtgtcg tgacgcgacc aggtatgcat ctgcagctct aaggtaaata taaaattttt
 50 421 aagtgtataa tgtgttaaac tactgattct aattgtttct ctcttttaga ttccaacctt
 481 tggaaactgac tgcagggatc caagctttct agagccacca tggctggact gtggctggga
 541 ctggtgtggc agaaactgct gctgtggggg gccgcttccg cactgtcact ggctggggct
 601 tcaactggtg tgagcctgct gcagagggtg gcctcctacg ccagaaagtg gcagcagatg
 661 aggcccatcc ctaccgtggc cagagcctat ccactggtgg gacacgcact gctgatgaag
 55 721 cctgacggca gagagttctt tcagcagatc atcgagtaca cagaggagta taggcacatg

5 781 ccaactgctga agctgtgggt gggacccgtg cctatggtgg cctgtacaa cggcgagaat
 841 gtggaagtga tcctgaccag cagcaagcag atcgataagt ctagcatgta taagttcctg
 901 gagccttgge tgggcctggg cctgctgacc tctacaggca acaagtggag gagccggaga
 961 aagatgctga ccccaacatt ccactttaca atcctggagg acttcctgga catcatgaac
 10 1021 gagcaggcca atatcctggt gaagaagctg gagaagcaca tcaaccagga ggcttttaat
 1081 tgctttctttt acatcacccct gtgcgccttg gacatcatct gtgagacagc tatgggcaag
 1141 aacatcgccg ccaggtctaa tgacgatagc gagtacgtgc gggccgtgta tagaatgagc
 1201 gagatgatct ttaggcgcat caagatgccc tggctgtggc tggatctgtg gtatctgatg
 1261 ttcaaggagg gctgggagca caagaagtcc ctgcagatcc tgcacacctt tacaactct
 1321 gtgatcgccg agagagccaa tgagatgaac gccaatgagg actgtagggg cgaagggaag
 1381 ggcagcgccc cttccaagaa caagcggaga gccttcctgg acctgctgct gacgtgacc
 1441 gacgatgagg gcaatcgccct gtcccaagag gacatccggg agggagtgga tacattcatg
 1501 tttgagggac acgacaccac agccgcccgc atcaactggt ccctgtacct gctgggctct
 1561 aatccagagg tgcaagaaga ggtggatcac gagctggacg acgtgttcgg caagtccgac
 1621 aggccagcaa ccgtggagga tctgaagaag ctgagatacc tggagtgctg gatcaaggag
 1681 aactgcccag tgttcccctc tgtgcctctg tttgcccggg ccgtgtctga ggactgtgag
 1741 gtggccggtc atcgcggtgct gaagggcacc gaggccgtga tcatccctta cgccctgcac
 1801 cgggacccca ggtatttccc taaccagag gagtttcagc cagagagatt ctttcccag
 1861 aatgcccagg gcaggcaccc ttacgcctat gtgccattct ccgcccggac aaggaactgc
 1921 atcgacagca agtttgccgt gatggaggag aaaaccatcc tgtcttgat cctgagacac
 1981 ttctggatcg agagcaatca gaagaggag gagctgggcc tggagggaca gctgatcctg
 2041 cggccaagca acggcatctg gatcaaaactg aaaagaagga acgctgacga gaggtaaaag
 2101 cttgaattcc tcgaggatcc aataaaaagat ctttattttc attagatctg tgtgttggtt
 2161 ttttgtgtgt ctagtgtgcca gccatctgtt gtttgccctt ccccgtgcc ttccctgacc
 2221 ctggaaggtg ccactcccag tttaaactta attaggggcc gcaggaaccc ctagtgtatg
 2281 agttggccac tccctctctg cgcgctcgt cgctcactga ggccgggcca ccaagggtcg
 2341 cccgacgccc gggctttgcc cgggcggcct cagttagcga gcgagcgccg agctgcctgc
 2401 agg

30 To assess the difference in efficacy between CYP4V2st and CYP4V2op cDNAs in
 CYP4V2 gene therapy, two AAV5 vectors with the same promoter (CAG), enhancer (WPRES)
 and polyA (bGH-polyA) and the same junction/linker sequences, one carrying the CYP4V2st
 cDNA (AAV5.CYP4V2st (SEQ ID NO: 61)) and the other carrying the CYP4V2op cDNA
 (AAV5.CYP4V2op (new) (SEQ ID NO: 63)) are compared for efficacy in rescuing RPE atrophy
 35 in BCD patient-derived iPS-RPE using cell viability assay described herein.

To assess whether different junction/linker sequences used in SEQ ID NO: 60 and SEQ
 ID NO: 63 affect the expression of CYP4V2 cDNA or expression cassette, two AAV5 vectors
 (AAV5.CYP4V2op (SEQ ID NO: 60) and AAV5.CYP4V2op(new) (SEQ ID NO: 63)) with the
 same promoter (CAG), enhancer (WPRES) and polyA (bGH-polyA) and the same CYP4V2
 40 cDNA (CYP4V2op (SEQ ID NO: 2)) but different junction/linker sequences are compared for
 efficacy in rescuing RPE atrophy in BCD patient-derived iPS-RPE using cell viability assay
 described herein.

It should be understood that different CYP4V2 cDNAs (SEQ ID Nos: 1, 2, 3, or others) can be used in any CYP4V2 expression cassette described herein in lieu of the CYP4V2 cDNA contained in the expression cassette sequences provided herein for use in CYP4V2 gene therapy. It should also be understood that each CYP4V2 expression cassette described herein can be

5 packaged in rAAV vectors of various serotypes/capsids for use in CYP4V2 gene therapy, including those different from the ones used in this study (e.g., AAV1, AAV2, AAV2(Y444F+Y500F+Y730F), AAV5, AAV8 and AAV9). In addition, the CYP4V2 expression cassette packaged in scAAV vectors used in this study can also be packaged in ssAAV vectors for use in CYP4V2 gene therapy, after changing the mutant AAV ITR used in

10 scAAV construct to non-mutant AAV ITR used in ssAAV construct. Moreover, the CYP4V2 cDNAs or expression cassettes (with or without the AAV ITRs) described herein can be packaged in other viral vectors (i.e., non-AAV vectors, such as retroviruses, lentiviruses, adenoviruses and herpes simplex viruses or other viral vectors) or non-viral vectors (e.g., plasmids, nanoparticles, or lipid-based nanoparticles (e.g., liposome-protamine-DNA complex

15 (LPD)) for use in CYP4V2 gene therapy.

Example 12—Treating BCD Patient-derived iPS-RPE Cells by AAV.CYP4V2

iPS-RPE cells derived from BCD patients were infected with various AAV.CYP4V2 vectors described above in serum-free RPE medium. After 1 day, the virus-containing medium

20 was replaced with fresh serum-containing RPE medium to continue RPE culture. To assess therapeutic effects of different dosage, different multiplicity of infection (MOI, genomic copies (GC)/cell) was tested.

Example 13— Assaysto Assess the Effect of AAV.CYP4V2 Gene Therapy

25 After AAV.CYP4V2 infection, the iPS-RPE cells of BCD patients were cultured in RPE medium for at least 4 days for scAAV or at least 10 days for ssAAV before the cells were harvested for testing. Cell harvesting protocols and sample preparation protocols were followed as previously described.

The biochemical tests described in the Examples herein for detecting fatty acids,

30 ceramides (Cer), sphingomyelins (SM), and sphingosine and sphinganine (SOSA), were

performed on AAV.CYP4V2-treated BCD patient iPS-RPE cells and the same biochemical testing protocol using LC-MS was followed. Table 3 above shows the results in healthy control iPS-RPE cells, BCD patient iPS-RPE cells without AAV.CYP4V2 treatment and post-AAV.CYP4V2 treatment.

5 The results demonstrated that phenotype in BCD patient iPS-RPE cells (e.g., abnormal fatty acids levels (e.g., DHA, AA and total of n3 fatty acids) as compared to control) were ameliorated or corrected by AAV.CYP4V2 gene therapy. This established the efficacy of AAV.CYP4V2 gene therapy in BCD patient-derived iPS-RPE cell lines. Because BCD is primarily caused by RPE degeneration, the efficacy of AAV.CYP4V2 gene therapy in BCD
10 patient-specific iPS-RPE cell lines established the efficacy of AAV.CYP4V2 gene therapy for BCD patients.

 Significantly, the scAAV1.CYP4V2op treatment achieved most significant improvement in a very short time (just 4 days post treatment). This proved that scAAV is fast acting because it does not require the cell machinery to synthesize a complementary DNA strand. For the same
15 reason, it is expected that longer time window between AAV.CYP4V2 treatment and cell harvesting for testing can generate more significant improvements in results, particularly for CYP4V2 gene therapy packaged in ssAAV vectors.

 The fast and robust results achieved by scAAV vector in human RPE cells established that scAAV vectors can be particularly useful in rescuing early onset diseases and/or late stage
20 human patient of RPE or retinal degenerations. In addition, the robust expression profile of scAAV vectors make it also suitable for intravitreal administration for delivery to the retina.

Rescue of RPE atrophy by AAV.CYP4V2

BCD patient-derived iPS-RPE samples were exposed to blue light for 1 hour, then cell viability assay was performed on the samples the next day as previously described herein.

25 Cell viability images comparing patient iPS-RPE samples without vs. with AAV.CYP4V2 treatment are shown in Figures herein.

 Each of AAV2.CYP4V2op and scAAV1.CYP4V2op treatment showed rescue of RPE atrophy in BCD patient-derived iPS-RPE samples as compared to untreated patient samples (Figure 8. MOI=1x10⁵ GC/cell). Interestingly, rescue efficacy by AAV2.CYP4V2op and
30 scAAV1.CYP4V2op at 1x10⁵ MOI is higher in P2 iPS-RPE than in P1 iPS-RPE. This suggests

that the optimal dosage for use of AAV.CYP4V2 gene therapy to treat BCD can vary based on individual differences among patients and that BCD patient-specific iPS-RPE is a useful tool in assessing personalized optimal dose for different patients.

Each of AAV5.CYP4V2op, AAV5.CYP4V2st and AAV8.CYP4V2fv treatment rescued
5 RPE atrophy in BCD patient-derived iPS-RPE sample as compared to untreated patient sample (Figure 9. MOI=1x10e5).

Each of AAV5.CYP4V2op, scAAV1.CYP4V2op and scAAV5.CYP4V2op treatment rescued RPE atrophy in BCD patient-derived iPS-RPE sample as compared to untreated patient sample (Figure 10. MOI=1x10e4).

10 scAAV9.CYP4V2op treatment rescued RPE atrophy in BCD patient-derived iPS-RPE sample as compared to untreated patient sample (Figure 11. MOI=1x10e5. 2 weeks post treatment).

Significantly, AAV.CYP4V2 treatment at a lower dose (MOI=1x10e4) in P2 samples achieved similar or better results than a higher dose (MOI=1x10e5 GC/cell) of treatment by the
15 same vector in P1 samples. This demonstrated at the cellular level that to achieve the same or similar efficacy in rescuing RPE atrophy, different patients may need different dosage. In other words, one vector and one similar dose level for all patients of the same disease may not be the most medically or economically efficient approaching for gene therapy. BCD cellular model and similar cellular models for other ocular diseases can provide a guidance on personalized optimal
20 dose.

Other AAV.CYP4V2 vectors are also tested and show improved RPE atrophy in BCD patient iPS-RPE sample, including AAV2tri(Y-F).CYP4V2op treatment (MOI of 1x10e4) and AAV5.CYP4V2op(new) (SEQ ID NO: 63) at different MOI levels (1x10e4 and 1x10e5 GC/cell). Additionally, the cell viability images were processed by ImageJ(Fiji) to count the number of
25 dead and live cells in the iPS-RPE samples. Four different areas/images from each sample were used to count and the dead/live cell ratios from multiple images of the same sample were averaged. Dead/live cell ratios demonstrated AAV.CYP4V2 treatment rescued RPE cell atrophy in BCD patient-derived iPS-RPE. For example, the dead/live cell ratio of WT2 is 3.0%, P1 (no AAV.CYP4V2 treatment) is 20.87%, and P1 treated by AAV5.CYP4V2st is 9.69%. Treatment

by other AAV.CYP42 vectors also reduced the dead/live cell ratio in BCD patient iPS-RPE samples.

These results demonstrated that:

- (1) various AAV.CYP4V2 vectors, expression cassettes and CYP4V2 cDNAs rescued RPE atrophy in BCD;
- (2) Self-complementary AAV vector (scAAV) is fast in achieving rescue efficacy;
- (3) Efficacy can be achieved at different dosage levels.

Example 14—Safety of AAV.CYP4V2 Vectors and GMP manufacturing for Clinical Use

Prior studies demonstrated that CYP4V2 is almost ubiquitously expressed in human organs and expression level within the eye is high in retina. In addition, the safety of AAV vectors have been established in gene therapy studies and clinical trials for other diseases. Therefore, it is reasonable to expect that AAV.CYP4V2 vectors are safe to use in gene therapy.

In this study, various AAV.CYP4V2 vectors were used to treat human iPS-RPE samples at a high dose (e.g., 1×10^5 MOI). No material difference in cell death between untreated and AAV.CYP4V2 treated samples was observed, except that AAV.CYP4V2 rescued RPE atrophy in BCD patient-derived iPS-RPE samples as described in the Example above. This established the safety of AAV.CYP4V2 vectors and demonstrates that high levels of expression of the transduced CYP4V2-encoding gene can be achieved without significant evidence of toxicity.

In addition to testing in cell lines, the safety of AAV.CYP4V2 gene therapy can also be tested in animals, e.g., in mice, rats or non-human primates, and/or via human clinical trials. Various manufacturing methods and platforms are available to produce recombinant AAV vectors for human clinical use. For example, and without limitation, GMP manufacturing of rAAV vectors can use a 2-plasmid transfection method or a 3-plasmid transfection method, can use mammalian cell lines such as HEK293, A459 or 293T, or insect cell line such as the baculovirus/Sf9 cell platform, can use adherent or suspension cell culture. Further, various methods, processes and/or platforms, including without limitation, herpes simplex virus (HSV)-based production system, single-use bioreactors (e.g., iCELLis), HYPERStacks, roller bottles, and column chromatography, can be used to increase yield or titer, or improve purity, and/or to avoid potential contamination. These rAAV vector clinical production methods, processes,

techniques and platforms are known in the art and are commercially available via contract manufacturing organizations (CMOs) or academic GMP facilities, e.g., Lonza (USA), Cobra Biologics (UK), Nationwide Children's Hospital (NCH, Ohio, USA), Children's Hospital of Philadelphia (CHOP, USA), WuXi Biologics (China and USA). AAV.CYP4V2 vectors for human clinical use can be manufactured using any one or more of the methods, processes, techniques, platforms and GMP facilities mentioned herein and/or others known in the art or to be developed in the future.

Example 15—Subject Selection and Administration of AAV.CYP4V2 *in vivo* to Treat BCD

An exemplary subject eligibility criteria for AAV.CYP4V2 human clinical trial is listed as follows:

Inclusion Criteria

Subjects are eligible for study participation if they meet all of the following inclusion criteria.

1. Are willing and able to provide informed consent for participation in the study.
2. ≥ 18 years of age.
3. Have a genetically-confirmed diagnosis of bi-allelic CYP4V2 mutation.
4. Have active disease clinically visible within the macular region in the study eye.
5. Have a best corrected visual acuity (BCVA) of 34-73 ETDRS letters (equivalent to worse than or equal to 20/40 Snellen acuity, but better than or equal to 20/200 Snellen acuity) in the study eye.

Exclusion Criteria

Subjects are not eligible for study participation if they meet any of the following exclusion criteria.

1. Have a history of amblyopia in the eligible eye.
2. Are unwilling to use barrier contraception methods, for a period of 3 months, if treated with AAV.

3. Previous intraocular surgery performed in the study eye within 3 months of first visit.

4. Have any other significant ocular or non-ocular disease/disorder which, in the opinion of the investigator, may either put the subjects at risk because of participation in the study, or may influence the results of the study, or the subject's ability to participate in the study. This includes but is not limited to, a subject:

- with a contraindication to oral corticosteroid (eg prednisolone/prednisone)

- with a clinically significant cataract

- who, in the clinical opinion of the study investigator, is not an appropriate candidate for the surgical procedure (e.g., sub-retinal surgery).

5. Have participated in another research study involving an investigational product in the past 12 weeks or received a gene/cell-based therapy at any time previously.

For use of AAV.CYP4V2 to treat BCD, the patient should have genetic or molecular confirmed diagnosis of BCD, i.e., confirmation of bi-allelic CYP4V2 mutation via genetic testing (single gene test or multi gene panel test if medically necessary). Because BCD is sometimes diagnosed as inherited retinal disorder (IRD), retinal degeneration (RD), or retinitis pigmentosa (RP), AAV.CYP4V2 can also be used to treat a patient of IRD, RD or RP with genetically confirmed bi-allelic CYP4V2 mutation.

For AAV.CYP4V2 treatment *in vivo*, the patient should have viable retinal cells as determined by optical coherence tomography (OCT) and/or ophthalmoscopy. Preferably, the patient should have some vision left (e.g., best corrected visual acuity (BCVA) better than or equal to 20/200 (Decimal 0.1 in the to-be-treated eye.

Various means/route of administration can be used to deliver AAV.CYP4V2 vectors to the target cells (e.g., retinal or corneal cells) *in vivo*, including without limitation, administration to the retina can be performed via sub-retinal injection, intravitreal injection (using AAV vectors suitable for intravitreal delivery, e.g., AAV2(Y444F+Y500+Y730F), AAV 7m8 or their derivatives), or delivery through the bloodstream (using AAV vectors that can penetrate the

blood-retinal barrier, e.g., AAV9 or AAV-PHP.B). In addition, AAV.CYP4V2 vectors can also be encapsulated in a device to be implanted intravitreally as a way of administration.

Surgical/administration methods related to gene therapy, as well as certain techniques to improve delivery/transduction efficiency (e.g., internal limiting membrane (ILM) peeling and vitrectomy (VIT)), are known in the art. Immunosuppressants, e.g., corticosteroids may be used before, during and/or after AAV administration to minimize immune responses.

In addition to treating patients *in vivo*, CYP4V2 gene therapy (including AAV.CYP4V2 gene therapy) can be used to treat the target cells (e.g., BCD patient's iPS derived RPE cells, retinal cells corneal epithelium cells, or corneal cells) *in vitro* and then transplant such cells to the patient as a cell therapy. Methods of using AAV.CYP4V2 vectors to treat BCD patient iPS-RPE cells are provided in the Examples and disclosure herein. Methods of cell implantation/transplantation, e.g., to the retina and cornea, are known in the art. For example, the same or similar methods and surgical techniques to transplant ES-RPE cells to the retina can be used to transplant BCD patient's iPS-RPE cells.

Therapeutically effective doses can be determined and evaluated in disease models (e.g., BCD cellular model (e.g., iPS-RPE cell line derived from BCD patients) or an animal model, and confirmed or refined by clinical trials. For treatment of cells *in vitro*, the dose is usually expressed as MOI and then multiply the MOI by the number of cells being treated. The MOI generally ranges between about 1×10^3 GC to about 1×10^6 GC per cell or an infectious MOI of about 100 to about 10,000 GC per cell (GC: genomic copies, measuring genome containing AAV particles (a/k/a vector genome (vg) or genome particles (gp)). For *in vivo* treatment, typical clinical factors should be considered to determine the dose, such as route of administration, the size of the area or number of cells targeted, and the subject being treated (e.g., the age, weight, development stage of the disease and condition of the subject to be treated, and potential immune reactions); the location of the cells targeted for treatment (e.g., retina vs. cornea). In addition, the transduction efficiency and rescue efficacy of the AAV.CYP4V2 vector being used should also be considered. Finally, if possible, individual differences in optimal dose at the cellular level among patients should also be considered, which can be assessed in the patient-specific iPS-RPE cells. Therefore, the therapeutically effective dose for a single local administration to the eye *in vivo* can be on the order of from about 1×10^6 to about 2×10^{13}

GC, inclusive (e.g., a high dose range of about 1×10^{11} GC to about 1×10^{12} GC, a medium dose range of about 1×10^{10} GC to about 1×10^{11} GC, a low dose range of about 1×10^9 GC to about 1×10^{10} GC, a very low dose range of about 1×10^6 GC to about 1×10^9 GC, and a very high dose range of about 1×10^{12} GC to about 2×10^{13} GC), or any dose within
5 these ranges that is sufficient to provide the desired effect. In one embodiment, the composition is administered at a dose of about 1×10^6 to about 2×10^{13} GC. In another embodiment, the *in vivo* administered dose is determined by multiplying the number of cells targeted for treatment by the target MOI (e.g., about 1×10^3 GC to about 1×10^6 GC per cell). The volume of the agent containing the rAAV vectors in any single local administration to the eye can range from
10 about 1 uL (0.001 mL) to about 1000 uL (1 mL). Treatment by delivery via bloodstream requires a much higher dose and can be in the range of about 1×10^6 to about 2×10^{14} GC per kg of body weight.

See “E. Treatment Options, Subject Selection and Administration” and other disclosure herein for more description.

15

Example 16—Post-treatment Evaluation

Since the clinical symptoms of BCD are similar to those of many other types of IRDs, RDs and RP, e.g., loss in visual acuity, restricted visual fields, night blindness, reduced dark adaptation, contrast sensitivity and color vision, changes in the retina (and in cornea for some
20 patients) and diminished responses on electroretinogram (ERG), related measures can be used to assess a BCD patient’s disease state and progression pre- and post-treatment, thereby evaluating treatment outcome. These measures and related examinations and tests are known in the art for retinal and corneal diseases. For example, and without limitation, best corrected visual acuity (using visual acuity chart) can be used as the primary outcome measure for BCD gene therapy,
25 with one or more of the following as secondary outcome measures: microperimetry (change in sensitivity), fundus autofluorescence (AF) (change in AF), optical coherence tomography (OCT) (ellipsoid zone and retinal thickness), contrast sensitivity (Pelli-Robson chart), color vision (Farnsworth-Munsell 100 hue test) and ERG (changes in ERG). In addition, functional tests such as mobility test can also be used as a primary or secondary outcome measure. Evaluations can be
30 performed at different time points post treatment, e.g., 2 weeks, 1 month, 2 months, 3 months, 6

months and 12 months. Results can be used to evaluate treatment outcome. Efficacy can be shown as one of the following: improvement in one or more of the primary or secondary outcome measures, stop of disease progression, or slower than expected rate of retinal degeneration or loss of vision (by using data from a natural history study if necessary).

5

Example 17: Method to Reduce Immune Responses and to Address Individual Differences in Gene Therapy

Viral vector-mediated gene therapy may trigger cellular, local or systemic immune responses, which may pose safety risks. Immune reactions also may decrease transduction efficiency and thereby diminish the treatment effect of viral vector-mediated gene therapy. Immune responses may occur in the form of the humoral response (or antibody-mediated response) recognizing antigens or pathogens that in the lymph or blood, and/or cell-mediated immunity. To minimize immune responses, immunosuppressants such as corticosteroids are often used in connection with a gene therapy administration. Immunosuppressant drugs have effects, e.g., may cause increased intraocular pressure, cataracts, and other adverse events (e.g., prolonged use of immunosuppressant may increase risk of cancer). In addition to immune response, other individual differences exist among patients, e.g., in response to different types (e.g., different serotype or different capsid mutation/structure) of vectors, or in response to the same vector at the same dose.

A method to reduce immune responses to viral vectors, preserve transduction efficiency, to lower viral vector and/or immunosuppressant dose, and/or to maximize therapeutic effect to different patients of the same genetic disease, in viral vector mediated gene therapy, comprising:

(a) establishing a pool of more than one recombinant viral vectors (e.g., rAAVs) with sufficient transduction efficiency in the target cell type for the gene therapy. The viral vector pool can be expanded by creating variants with antigenic region mutations or other mutations or variants on the capsids of said viral vectors after such mutations or variants are confirmed with sufficient transduction efficiency in target cells relevant to the disease (e.g., in iPS-RPE or RPE cell lines for CYP4V2 gene therapy for BCD).

(b) detecting pre-existing neutralizing anti-viral vector antibodies (NAbs) against different viral vector serotypes and/or capsid mutations or variants in the subject in need of the

30

gene therapy, and/or testing and comparing different viral vectors in patient-specific disease target cells (e.g., iPS-RPE cells) derived from such subject.

(c) selecting a viral vector from said pool of viral vectors with (i) sufficient transduction efficiency in the disease target cells and (ii) low cross-reactivity with the pre-existing NABs in the subject, and/or (iii) good phenotype rescue result in the subject's patient-specific disease target cells (e.g., patient-specific iPS-RPE or RPE cell lines for CYP4V2 gene therapy for BCD), wherein such viral vector pool comprising different serotypes and/or capsid-modified viral vectors (e.g., including without limitation, capsid-mutant AAVs and/or capsid protein variant AAVs).

10 (d) use the viral vector selected from (c) for administration to the subject.

(e) repeat (b) through (d) (only the part relating to pre-existing NABs) above each time the subject requires a gene therapy administration, including without limitation, a follow-up administration to the same organ (e.g., an eye or a contralateral eye), or to another organ.

Specifically, various rAAV vectors including five different AAV (AAV1, AAV2, AAV5, AAV8 and AAV9) serotypes and a capsid mutation AAV (AAV2.tri(Y-F)) were generated and tested to assess differences among different patients' cell lines in this study.

Example 18: Use of scAAV in Rapid Rescue of Retinal Diseases and Use of EFS and/or SPA in an scAAV or an AAV vector in Treating Ocular Diseases

20 As demonstrated in Example 13 above, scAAV.CYP4V2 treatment achieved robust rescue of biochemical phenotype in BCD patient iPS-RPE cells in a very short time (just 4 days). In addition, scAAV.CYP4V2 showed rescue of RPE atrophy in BCD patient iPS-RPE cell line two weeks post AAV treatment (See Figure 11). The fast and robust expression in human iPS-RPE cells driven by the EFS promoter (exemplary sequence shown in SEQ ID NO: 35) and SPA (exemplary sequence shown in SEQ ID NO: 36) in an scAAV vector demonstrated the suitability of EFS promoter and/or SPA in driving a transgene expression in human ocular cells and treating human ocular diseases. The fast rescue achieved by scAAV vectors with the EFS promoter and SPA make them particularly useful in treating fast progressing diseases or patients of advanced disease stage.

In addition, the study proved the fast and robust expression of an scAAV design in human retinal cells. The makes scAAV-mediated gene therapy particularly helpful in treating early onset retinal disease patient or in treating a late stage patient who requires a rapid rescue.

Discussion on CYP4V2 Gene Therapy

5 BCD is a rare blinding eye disease for which currently there is no approved treatment available. In a clinical research involving the use the BCD patient-specific iPS-RPE cell lines, the efficacy of various AAV.CYP4V2 vector and expression cassette designs in rescuing the phenotype in BCD patient-specific iPS-RPE cells were proved in this study as assessed through fatty acid and lipid assays. In addition, different doses (MOI) were tested which can serve as a
10 guidance for determining the dose range for treatment in vivo. Finally, there is no significant evidence of toxicity associated with AAV.CYP4V2 gene therapy.

Cell Therapy and CRISPR Gene-editing Therapy Examples

Example 19—Use of iPSCs, iPS-RPE or iPS-ocular Cells from a BCD Subject in Cell Therapy

15 BCD is a relatively late onset disease. Symptom in BCD patients are usually developed in the 2nd, 3rd or even 4th decade of life. In addition, iPS reprogramming process can have some "reset the clock" effect. Therefore, the iPS-RPE cells and other iPS-ocular cells derived a BCD patient can be used as a cell therapy for transplantation to the BCD patient even without any genetic repair of the CYP4V2 mutations in the iPS-RPE cells.

20 Alternatively, the iPSCs, iPS-RPE cells, iPS-PRCs, iPS-CE cells, iPS-CECs and/or other iPS-ocular cells derived from a BCD patient can be genetically repaired before cell therapy transplantation. Genetic repair can be achieved by either CYP4V2 gene therapy as described in Examples above or by gene editing. See the Examples herein for more detailed description on gene editing.

25

Example 20—Genetically Repaired Patient Autologous Cells for Ocular Cell Therapy

Patient-specific iPSC derived cells (e.g., iPS-RPE cells, iPS-CECs, iPS-CE cells, iPS-PRCs, or iPS-ocular cells) can be used as a source of autologous cells for transplantation in cell therapy for ocular diseases, including without limitation, retinal and corneal diseases. Compared
30 to cells generated from allogenic sources, such as ES cells (e.g., ES-RPE cells, ES-CEC or ES-

PRC, and tissues made up of such ES-derived cells) or iPS cells of another individual, such patient-specific iPS-derived autologous cells and tissues made from such cells usually requires little to no immunosuppression of the patient and do not have ethical issues related to the use of ES and ES-derived cells.

5 However, iPSCs generated from a patient source cells (e.g., fibroblasts or blood cells) and cells and tissues derived from such patient-specific iPSCs (e.g., patient-specific iPS-RPE cells, iPS-PRCs, iPS-CECs, iPS-CE cells and iPS-ocular cells) still possess disease-causing mutations and related phenotype. To generate healthy patient-derived cells and/or tissues, pathologic mutations can be genetically repaired or corrected with gene-editing technology,
10 including without limitation, the clustered regularly interspersed short palindromic repeats (CRISPR), which can be designed to correct a target mutation in a patient's cell. These genetically repaired healthy iPSCs then can be used to generate various cell types (e.g., iPS-RPE cells, iPS-CECs, iPS-CE cells, iPS-PRCs or other iPS-ocular cells) that no longer harbor the pathologic mutations of the patient.

15 Furthermore, this proof-of-concept study demonstrates these gene-corrected iPSCs and/or gene-corrected iPS-derived cells (e.g., iPS-RPE cells) no longer have the phenotype (e.g., abnormal biochemical profile as assessed by bioassays, e.g., lipidomics and/or proteomics) as seen in (uncorrected) iPS-derived cells from the patient. Therefore, these gene-corrected cells serve as a source of regenerative, genetically-repaired autologous cells that can be used as
20 replacement cells in cell therapy. Compositions and methods relating to gene-corrected patient autologous cells are described in detail herein and in Examples below.

 Another type of genetically repaired patient cells are patient iPSCs or iPS-derived cells (e.g., iPS-RPE cells, iPS-PRCs, iPS-CE cells, iPS-CECs and iPS-ocular cells, iPS-neuron cells) treated by gene supplementation therapy (e.g., CYP4V2 gene therapy) as described herein above.
25 Post gene therapy treatment, the patient-specific cells possess a healthy copy of the mutated gene (e.g., a cDNA) and/or express a functional protein encoded by the healthy transgene. Furthermore, the gene therapy treated patient-specific cells demonstrate improved or normalized biochemical profile or other phenotype seen in untreated patient cells. Therefore, they also can be used as a source of genetically repaired autologous cells for use as replacement cells in cell
30 therapy, e.g., CYP4V2 gene therapy treated BCD patient-specific iPS-RPE cells, iPS-PRCs, iPS-

CECs, iPS-CE cells and iPS-ocular cells as genetically-repaired patient autologous cells for use in cell therapy for BCD. Compositions and methods relating to CYP4V2 gene therapy treated BCD patient-specific cells are described in detail in Examples herein above. The discussion herein below focuses on the type of genetic repair by correcting the mutation in genomic DNA.

5 Autologous cell replacement for ocular and retinal degenerative diseases associated with genetic mutations depends on the ability to repair a patient's pathogenic mutation by genetically correcting the mutation via gene editing or to repair or mitigate the consequence of the mutation (e.g., via delivery of a healthy copy of a transgene relative to the disease gene, e.g., CYP4V2 gene therapy) before transplantation. Here, patient-specific iPSCs from a BCD patient with the
10 most common CYP4V2 mutation (c.802-8_810del17insGC) were generated and the CRISPR gene-editing components (CRISPR guide RNA and donor template) and various constructs (plasmid and RNP) to correct this mutation were developed. Although CRISPR/Cas9 is used herein as the means for gene editing, it is anticipated that other CRISPR system (e.g., Cpf1) and other gene editing techniques including but not limited to TALEN as well as emerging and future
15 gene editing techniques such as CRISPR/Cpf1 can be used to achieve same or similar results. It is also expected that gene editing can be applied not only to iPSCs, but also to the original source cells that will be used to generate the iPSCs, as well as to the cells generated from the iPSCs, to correct the pathogenic mutation(s) in such cells.

While the iPS-derived cell lines are generated on a patient-specific basis, its application
20 in cell therapy does not have to be. A key factor limiting the wide use of iPSC-based cell therapy is immunologic differences among human individuals. There are multiple approaches to solve this problem. For example, one approach is to develop a number of cell banks that contain a limited number of lines with common HLA haplotypes, designed to achieve immunologic matching with a large portion of the patient population. Such a cell bank can be created by
25 generating iPSCs from patients with selected haplotypes or by genetic manipulation of HLA genotypes. Another approach is to produce a cell type that would be immunologically silent regardless of the patient's genotype.

The following describes the methods on how to generate genetically repaired patient-specific autologous cells, how to assess the effect of the genetic repair in the cells, and how to
30 use them in cell therapy. The examples provided herein are related to generating genetically-

repaired patient autologous cells from a BCD patient with the c.802-8_810del17insGC mutation in the CYP4V2 gene, the most common mutation among BCD patients. The same methods can be used to generate genetically-repaired patient autologous cells from a patient with a different mutation in CYP4V2, or a patient with a mutation in another gene associated with an ocular disease, or a patient with a mutation in a gene associated with other types of diseases, including without limitation, in any gene contained in Table 4.

Table 4
Target Gene List

10	ABCA4, ABCC6, ABHD12, ADAM9, AHI1, AIPL1, ALMS1, ARL13B, ARL6, ARMS2, ATXN7, BBS1, BBS10, BBS12, BBS2, BBS4, BBS5, BBS7, BBS9, BEST1, C1QTNF5, C2, C2orf71, C3, C5orf42, C8orf37, CA4, CABP4, CACNA1F, CACNA2D4, CAPN5, CC2D2A, CDH23, CDH3, CDHR1, CEP164, CEP290, CEP41, CERKL, CFB, CFH, CHM, CHR2, CIB2, CLN3, CLN5, CLN6, CLN8, CLRN1, CNGA1, CNGA3, CNGB1, CNGB3, CNNM4,
15	COL11A1, COL2A1, COL9A1, CRB1, CRX, CYP4V2, DFNB31, DHDDS, EFEMP1, ELOVL4, ERCC6, EYS, FAM161A, FBLN5, FLVCR1, FSCN2, FZD4, GNAT1, GNAT2, GNPTG, GPR143, GPR179, GPR98, GRK1, GRM6, GRN, GUCA1A, GUCA1B, GUCY2D, HARS, HMCN1, HTRA1, IDH3B, IFT140, IFT80, IMPDH1, IMPG2, INPP5E, INVS, IQCB1, ITM2B, JAG1, KCNJ13, KCNV2, KCTD7, KIF11, KLHL7, LCA5, LRAT, LRIT3, LRP5,
20	LZTFL1, MAK, MERTK, MFN2, MFRP, MFSD8, MKKS, MKS1, MT-ND4, MTPP, MYO7A, NDP, NEK4, NEK8, NMNAT1, NPHP1, NPHP3, NPHP4, NR2E3, NRL, NUB1, NYX, OA1, OAT, OCA1, OCA2, OFD1, OPA1, OPA3, OPN1LW, OPN1MW, OPN1SW, OTX2, PANK2, PAX2, PCDH15, PDE6A, PDE6B, PDE6C, PDE6G, PDE6H, PDGF, PDZD7, PEX1, PEX10, PEX14, PEX16, PEX19, PEX2, PEX5, PEX6, PEX7, PGK1, PHYH, PITPNM3, PLA2G5,
25	PPT1, PRCD, PROM1, PRPF3, PRPF31, PRPF6, PRPF8, PRPH2, RAB28, RAX2, RBP3, RBP4, RD3, RDH12, RDH5, RDS, RGR, RGS9, RGS9BP, RHO, RIMS1, RLBP1, ROM1, RP1, RP1L1, RP2, RP9, RPE65, RPGR, RPGRIP1, RPGRIP1L, RS1, SAG, SDCCAG8, SEMA4A, SLC24A1, SLC45A2, SNRNP200, SPATA7, TEAD1, TIMM8A, TIMP3, TLR3, TLR4, TMEM126A, TMEM231, TMEM237, TMEM67, TOPORS, TPP1, TREX1, TRIM32, TRPM1,
30	TSPAN12, TTC21B, TTC8, TTPA, TULP1, TYR, TYRP1, UNC119, USH1C, USH1G, USH2A, VCAN, VPS13B, WDPCP, WDR19, WFS1, WHRN, ZNF423, ZNF513, ACO2, AFG3L2, AUH, C12orf65, CISD2, CYP1B1, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPTN, PAX6, PITX2, POLG, SPG7, TEK, TXNRD2, ATXN2, ROBO3, PHOX2A, HOXA1, SALL4, CHN1, TUBB3, KIF21A, HOXB1, FAM47E, GBA, GCH1,
35	HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, CYP46A1

Using BCD, a disease with CYP4V2 mutations, as an example, iPSCs were generated from patient-specific cells carrying the BCD patient's specific mutation. The patient-specific

iPSCs are transfected with CRISPR guide RNAs (gRNA), Cas9 endonuclease, and a donor homology template. CYP4V2 gene copies show mutation correction and conversion to the wild-type allele. The corrected iPSCs then are used to generate gene-corrected iPS-RPE cells. The gene-corrected iPS-RPE cells are then tested to confirm they no longer have phenotype (e.g., abnormal biochemical profile (e.g., fatty acids profile)). These genetically-repaired patient autologous cells can be transplanted (either directly (e.g., cell suspension) or in other forms, such as part of a layer, a sheet, a matrix, a scaffold or a tissue) to the same patient as an autologous cell therapy for BCD.

(i) Generation of BCD Patient-Specific iPSC Lines:

iPSCs were generated from patient-specific cells from a BCD patient carrying homozygous c.802-8_810del17insGC mutation in the CYP4V2 gene as described herein. See Example 1 for methods to generate patient-specific iPSCs. The BCD patient's mutation was identified by sequencing

(ii) Designing, Screening and Selection of CRISPR gene editing components and constructs targeting the mutation:

See the Examples herein on CRISPR gene editing therapy for a detailed description.

(CRISPR gRNAs were selected to minimize the off-target editing and to maximize specificity with a target sequence directly centered on the mutation site. Multiple gRNAs with high specificity to the region containing the patient-specific CYP4V2 mutation were screened.

The candidate gRNAs were separately inserted into an expression vector also containing the Cas9 endonuclease responsible for mediating target DNA cleavage and transfected into a 293 cell line. Genomic DNA from the patient was amplified by PCR using primers for the CYP4V2 region, and the PCR products were analyzed for DNA cleavage activity. A survey assay was used to assess which gRNA candidate has relatively high activity for the mutation site. The gRNA with the highest cutting efficiency is used for gene editing.)

(iii) Gene Editing in iPSCs:

See Examples below on CRISPR gene editing therapy for a detailed description.

For genetic recessive diseases like BCD, gene correction in one allele or mutation is sufficient. Multiple CRISPR constructs targeting different mutations can be used to correct multiple mutations harbored by a cell.

(iv) Generation of iPS-RPE Cells or other iPS-ocular cells from Gene Corrected iPSC:

After confirming precise correction of the pathogenic mutation with no or minimal off-target editing via sequencing, the iPSC corrected by gene editing is used to differentiate into and generate iPS-RPE cells or the other type of iPS-ocular cells (e.g., iPS-PRCs, iPS-CECs, or iPS-CE cells) affected by the relevant disease as described herein. The corrected iPS-RPE cells derived from BCD patient then go through the same RPE fate confirmation (e.g., distinct RPE morphology (e.g., pigment and/or hexagonal shape) and/or RPE-specific markers).

(v) Bioassays to confirm phenotype-free

Bioassays are used to confirm these gene-corrected iPSCs and/or gene-corrected iPS-derived cells (e.g., iPS-RPE cells) no longer have the phenotype as seen in (uncorrected) iPS-derived cells from the patient. The bioassays can be any type of biological assay which can identify and assess the cellular and/or molecular level phenotype in patient cells as it relates to a specific disease. For example, they can include without limitation, lipidomics, proteomics, protein expression and/or other biochemical tests. For BCD, the bioassay includes fatty acids and ceramides tests as described in the Examples herein. Results indicate that these gene corrected iPS-RPE cells derived from the BCD patient no longer have the relevant biochemical defect / dysfunction as seen in uncorrected iPS-RPE cells derived from BCD patients. This proves that gene-corrected, iPS-RPE cells are phenotype-free and therefore is a source of replacement cells suitable for cell therapy.

(vi) Transplantation:

These genetically-repaired patient autologous cells (e.g., iPS-RPE cells, iPS-PRCs, iPS-CE cells, iPS-CECs and other iPS-ocular cells) can be transplanted (either directly or as part of a layer, a sheet, a matrix, a scaffold or a tissue) to the same patient as a cell therapy for BCD.

Example 21—Specific Example of CRISPR Gene Editing Therapy for an Ocular Disease

CRISPR/Cas9 is highly specific when gRNAs are designed correctly, but specificity and off-target editing is still a major concern, particularly as CRISPR is being developed for clinical use. The following Example describes in detail methods to develop CRISPR gene editing therapy constructs with high on-target specificity and low off-target editing risk for use in treating on ocular disease. In addition, the c.802-8_810del17insGC mutation represents one of

the most challenging mutations to correct among all known CYP4V2 mutations and other genetic ocular diseases. Most CYP4V2 mutations are single nucleotide change, insertion or deletion (See Table 1: Select CYP4V2 Mutations among BCD Patients), whereas the c.802-8_810del17insGC mutation involves a 17 bp deletion and a 2 bp insertion, and both an intron and an exon.

Several sets of CRISPR gene editing therapy constructs to correct the most common pathologic CYP4V2 mutation (c.802-8_810del17insGC mutation) were designed and constructed. The following is a detailed description on the design, compositions and methods of use of these CRISPR CYP4V2 Gene Editing constructs to correct the mutation and treat BCD.

10 (a) Analyzing the Mutation

The c.802-8_810del17insGC mutation involves both an intron and an exon, and both a deletion and an insertion, and it affects a splice acceptor site.

The c.802-8_810del17insGC mutation refers to a 17 base deletion with two bases (GC) inserted in the place starting 8 bases from the end of intron 6 of CYP4V2 gene, also referred to as IVS6-8 del/insGC; See SEQ ID NO: 46 showing sequence of the human CYP4V2 genomic DNA region comprising the c.802-8_810del17insGC mutation and SEQ ID NO: 47 showing the corresponding wild-type sequence. The c.802-8_810del17insGC mutation is illustrated in the following sequence which shows human CYP4V2 intron 6-exon 7 junction. Intron6 sequence is shown in lower case and exon 7 sequence in CAP letters. The 17 bps deletion and the insertion of GC are in brackets): caa aca gaa gca tgt gat tat cat tca aa (tca tac agG TCA TCG CT) (GC) GAA CGG GCC AAT GAA ATG AAC GCC AAT GA) is predicted to result in the skipping of exon 7. The wild type CYP4V2 has the following sequence: CAA ACA GAA GCA TGT GAT TAT CAT TCA AA(T CAT ACA GGT CAT CGC T)GA ACG GGC CAA TGA AAT GAA CGC CAA TGA (SEQ ID NO:47), while the c.802-8_810del17insGC mutant CYP4V2 has the following sequence: CAA ACA GAA GCA TGT GAT TAT CAT TCA AA(G C)GA ACG GGC CAA TGA AAT GAA CGC CAA TGA (SEQ ID NO:46). The bracketed nucleotides in the wild type sequence are the 17 nucleotides that are deleted and the bracketed nucleotides in the mutant sequence are the 2 nucleotides that are inserted following the 17 base pair deletion.

To achieve good repair rate using CRISPR, a Cas generated cleavage as close as possible to the mutated sequence is desired. The region of the CYP4V2 genomic DNA containing the

c.802-8_810del17insGC mutation has multiple SpCas9 PAM sites (NGG). Therefore, regular SpCas9 can be used to correct this mutation. Alternatively, Cas9 of other species, a mutated Cas9 or other CRISPR nuclease (e.g., Cpf1) with a different PAM (e.g., TTTN for Cpf1 which is present in the mutated sequence) can be used to correct the c.802-8_810del17insGC mutation and/or other mutations.

(b) *CRISPR gRNA design and selection*

Based on the various PAM sites present in the c.802-8_810del17insGC mutation region of the CYP4V2 gene, multiple related protospacer element sequences (herein referred to as gRNA, typically is 20 nt in length but can be in different length, e.g., 17-22nt for use with Cas9) were screened using DeskGen software. Five (5) gRNA candidates were selected using the following criteria: a) the proximity of the gRNA/Cas9 cleavage site to the target correction site; and b) the predicted off-target profiles of the gRNA (See Table 5 and Figure 12; See SEQ ID NOs: 48 to 52 for gRNA sequences).

Table 5. Sequences of gRNA candidates

gRNA	Off-target score	Sequence
CYP4V2 g1	87	5'-TGA TTA TCA TTC AAA GCG AA CGG -3'
CYP4V2 g2	98	5'-GAT TAT CAT TCA AAG CGA AC GGG -3'
CYP4V2 g3	73	5'-GAT AAT CAC ATG CTT CTG TT TGG -3'
CYP4V2 g4	70	5'-TTC ATT GGC GTT CAT TTC AT TGG -3'
CYP4V2 g5	32	5'-CAC ATG CTT CTG TTT GGA CT TGG -3'

The PAM site corresponding to each gRNA candidate is highlighted in bold. To avoid confusion, PAM sequence is not part of the gRNA (protospacer element) sequence.

(c) *gRNA Validation using Patient Genomic DNA*

Genomic DNA of a BCD patient (P1) with homozygous c.802-8_810del17insGC mutations was used to select and validate the gRNAs. DNA amplicons flanking a region of CYP4V2 containing the mutation site and various target sites were prepared using primers (See Table 6 and Figure 12). DNA amplicons, single guide RNA (sgRNA) prepared by *in vitro* transcription (IVT) (each comprising one of the gRNA1, gRNA2, gRNA3, gRNA4, or gRNA5) and SpCas9 protein were mixed and incubated at 37°C for 1 hr. Active sgRNA mediated Cas9

protein to create double stranded breaks in the amplicons and display various fragment patterns (Table 7). The reactions were loaded and DNA fragments were resolved on 1.5% agarose gel (Figure 13).

5

Table 6. Primers used in gRNA validation

	Sequences	Amplicon (bp)
CYP4V2 1F	5'-CAG AAA TCG CAA GCA TAG AGG GTG AAT TCA-3'	1062bp
CYP4V2 1R	5'-CTG TTG GAG GGC TCT TAA CTG TCC-3'	

Table 7. Predicted DNA fragments created by active gRNAs

gRNA	DNA amplicon size (bp)	Fragment sizes (bp)	
g1	1062bp	442	620
g2		443	619
g3		416	646
g4		455	607
g5		410	652

To confirm the fragments are indeed originated from the amplicon, DNA samples of untreated amplicon (Figure 16, top panel) and the smallest fragment of g2-treated (Figure 16, middle panel) were subjected to Sanger sequencing (Figure 14). All 5 gRNAs showed predicted cleavage activities.

In addition to or in lieu of validation in patient genomic DNA harboring the mutation, gRNAs activities can also be validated in patient cells, including without limitation, somatic cells, stem cells, iPSCs, or cells derived from a stem cell.

(d) *Construction of gRNA expressing vectors*

Three gRNAs (g1, g2 and g3) with highest activities and highest off-target scores were cloned into pX-U6-CBh-Cas9-Puro gRNA expression vector by inserting a double-stranded oligo cassette of each active gRNA. Each cassette was synthesized based on one of the gRNA sequences of g1, g2 and g3. Schematic illustrations showing the construct of the expression vector and the insertion site of the gRNA is provided in Figure 15 and Figure 16. See Figure 17 for a more detailed illustration (using g1 as example) showing the entire IVT sgRNA sequence (SEQ ID NO: 55 (not including the protospacer element sequence or the optional "G"))

following the U6 promoter. The "G" nucleotide (SEQ ID NO: 59) inserted at the start of each protospacer element (gRNA) sequence is optional. It is mainly to enhance the transcription efficiency of the U6 promoter. It is not needed if the protospacer element sequence starts with a "G" residue or if a non-UT promoter is used (e.g., H1 promoter). All gRNA constructs were
5 verified by both restriction enzyme digestion and sequencing.

Three plasmids each expressing a top gRNA (g1, g2 or g3) and co-expressing hSpCas9 and Puromycin resistance genes, namely pX459-hSpCas9-2A-Puro, were developed (Figures 15 and 16) and included as one of the constructs (see Table 8 below) for gene correction of the c.802-8_810del17insGC mutation.

10 It would be understood that the guide RNA, Cas protein and/or selection marker (e.g., puromycin resistance gene and/or GFP, EGFP or RFP) can be packaged in one plasmid or in separate plasmid. Furthermore, when more than one gRNA is used (either to correct multiple mutations or to correct the same mutation, e.g., a pairing gRNAs for use with Cas9 Nickase), they can be packaged in the same vector or in separate vectors.

15 In addition to the plasmid vector described herein, various other vector(s) can be used to package CRISPR gene editing components (guide RNA and/or Cas protein), and/or selection marker, including without limitation, pX458 plasmid vector, adeno-associated virus (AAV) vectors, and/or lentivirus vectors.. In addition to DNA constructs encoding the CRISPR components, guide RNA, Cas protein and/or selection markers can be used directly or in an
20 mRNA construct or RNP construct.

(e) *Construction and validation of CRISPR RNP*

In addition to a DNA construct in a vector (e.g., a pX459 plasmid as described above), a CRISPR ribonucleoprotein (RNP) construct was developed for each of g1, g2, g3, g4 and g5 (See Tables 5 and 8). Each RNP construct comprises (i) a chimeric single guide RNA (sgRNA)
25 comprising the relevant protospacer element (See Tables 5 and 8 and detailed description herein); and (ii) a SpCas9 protein forming a ribonucleoprotein (RNP) complex. The cleavage activities of various RNP constructs (sgRNA1:Cas9, sgRNA2:Cas9, sgRNA3:Cas9, sgRNA4:Cas9, sgRNA5:Cas9) at the target site of the CYP4V2 gene were validated in patient genomic DNA (See Figure 12, 13 and 14) as described in paragraph (c) above.

A sgRNA typically is about 100nt in length but can vary in lengths comprising a 17nt-22nt protospacer element sequence. A sgRNA can be IVT derived or synthetic. IVT sgRNAs corresponding to g1, g2, g3, g4, and g5 were generated and validated as described above. Synthetic sgRNAs corresponding to g1 and g2 were custom ordered from Synthego (Silicon Valley, CA, USA) as described below.

In lieu of a sgRNA, a crRNA (exemplary sequence in SEQ ID NO: 53) and tracrRNA (exemplary sequence in SEQ ID NO: 54) duplex can be used together with a Cas protein (e.g., Cas9) to form a CRISPR RNP complex (crRNA:tracrRNA:Cas9). When using a Cpf1 protein, no tracrRNA is required.

A sgRNA or crRNA:tracrRNA can be chemically modified to protect against intracellular RNA degradation. For example, a chemically modified synthetic RNA can contain 2'-O-methyl analogs and 3' phosphorothioate internucleotide linkages at the 5' and 3' terminal three bases of the gRNA (Synthego (Silicon Valley, CA, USA)). Synthetic sgRNA or crRNA and tracrRNA based on a given protospacer element sequence (e.g., CRISPR g1, g2, g3, g4 or g5 (See SEQ ID NOs: 48 to 52) are commercially available, e.g., from Synthego Corporation (Silicon Valley, CA, USA) or IDT, with chemically modification available as an option.

(f) Construction of Donor Template

In a homology-directed repair (HDR), a donor template is used to provide the donor nucleic acid sequence required to correct the mutated sequence of the target gene. Two separate donor templates for HDR were generated in the form of single-stranded Oligo DeoxyNucleotide (ssODN). The first one, referred to as CPY4V2 donor template 1 or CYP4V2 ssODN 1 (SEQ ID NO: 56), contains the 17 bp correction and has the sequence as follows: 5'-AGA AAA ATA AAT GAA AGA AAC TAG CAT ATT TTA TAA GAA AAT GTG TTA ACT AGG GTG CAT CCA AGT CCA AAC AGA AGC ATG TGA TTA TCA TTC AAA **TCA TAC AGG TCA** **TCG CTG** AAC GGG CCA ATG AAA TGA ACG CCA ATG AAG ACT GTA GAG GTG ATG GCA GGG GCT CTG CCC CCT CCA AAA ATA AAC GCA GGG CCT TT-3'; while the second donor template, referred to as CYP4V2 donor template 2 or CYP4V2 ssODN 2 (SEQ ID NO: 57) is the reverse complement of CYP4V2.donor template 1.

Either one of the donor templates can be used with any gRNA or sgRNA (g1, g2, g3, g4 or g5) described above, and a Cas9 protein to generate homology-directed repair (HDR) to correct the target CYP4V2 (c.802-8_810del17insGC) mutation.

The donor templates provided herein are 200 nt in length. Donor templates of various lengths can be used. A donor template can be symmetrical or asymmetrical relative to the target site. A donor template can be provided by an ssDNA, ssODN or a vector (e.g., a plasmid or an AAV vector) containing or encoding the donor nucleic acid sequence. If the donor template has an intact sequence complementary to the protospacer element in the CRISPR guide RNA and the PAM sequence targeted by the Cas protein, to avoid this donor template being degraded by the Cas protein (e.g., Cas9) in cells, mutations can be made to the donor template, e.g., to mutate the Cas9 PAM "NGG" in the donor template and change it to "NGT" or another non-PAM sequence. However, if the intended PAM mutation to be introduced by the donor template is within coding region, cautions need to be made to ensure it would be a silent mutation.

Donor templates can be synthetically made and are commercially available. For example, DNA oligos of a given sequence can be custom ordered (Ultrasmer® DNA Oligonucleotides, Integrated DNA Technologies (IDT), Coralville, Iowa, USA)

(g) *Cas Protein and Selection Marker*

CRISPR-associated proteins/nucleases (Cas) (e.g., Cas9 or Cpf1) are commercially available, including without limitation, encoded by a plasmid or as recombinant protein for use in a RNP construct. A Cas protein can also include one, two or more nuclear localization sequences (NLS) (e.g., Catalog #: 1074182, Integrated DNA Technologies (IDT), Coralville, Iowa, USA; Catalog #: A034a-a-1000, Feldan (Quebec, Canada); Cpf1: Catalog #: 1076158 (IDT)) and may also be fused with a selection marker (e.g., a SpCas9 protein fused with EGFP, Catalog #: PR-137211-E (Novatein Biosciences, Woburn, MA, USA)).

When transfecting a CRISPR gene editing construct in vitro in cells, a selection marker can be used to evaluate the rate of transfection and/or to assist in picking the cells for next step processing. Various selection markers including without limitation fluorescence (e.g., GFP, EGFP, RFP) and/or puromycin can be used in the process. A selection marker can be integrated with any component of a CRISPR construct or can be provided separately in a transfection process. For example, a fluorescence labeling can be combined with the tracrRNA (IDT) or the

Cas9 protein (Novatein Biosciences, Catalogue #: PR-137211-E) for convenient imaging and manual or FACS sorting of transfected cells. A puromycin resistance gene can be provided in a vector that is co-transfected with the CRISPR construct for selection using puromycin. Selection using puromycin is illustrated in the Examples. Selection markers of various types such as antibiotics selection marker (e.g., puromycin) or fluorescence labeling are commercially available and can be integrated into a CRISPR component (e.g., the Cas9 protein or the CRISPR guide RNA) or provided separately (e.g., an expression plasmid expressing the puromycin resistance gene), including without limitation: IDT, Sigma Aldrich, Novatein Biosciences, Clontech Laboratories, and InvivoGen.

10 (h) *Constructs and recommended protocol*

The following table (Table 8) shows the CRISPR gene editing constructs (plasmid and RNP) generated for each one of the 3 gRNAs (gRNA1, gRNA2 and gRNA3). They contain three gRNA plasmid constructs or respective sgRNA, two donor templates (forward and reverse complimentary) and SpCas9 protein.

15

Table 8. Plasmid and RNP Constructs for CYP4V2 mutation (c.802-8_810del17insGC) CRISPR Gene Correction Therapy¹

Item #	Type	Name
1	DNA construct/plasmid ²	CYP4V2-g1 (See Table 5 and SEQ ID NO: 48 for sequence)
2	DNA construct/plasmid ²	CYP4V2-g2 (See Table 5 and SEQ ID NO: 49 for sequence)
3	DNA construct/plasmid ²	CYP4V2-g3 (See Table 5 and SEQ ID NO: 50 for sequence)
4	sgRNA ³	CYP4V2-g1 (See Table 5 and SEQ ID NO: 48 for sequence)
5	sgRNA ³	CYP4V2-g2 (See Table 5 and SEQ ID NO: 49 for sequence)
6	sgRNA ³	CYP4V2-g3 (See Table 5 and SEQ ID NO: 50 for sequence)
7	Donor template ⁴	CYP4V2 donor template 1 (See para (f) and SEQ ID NO: 56)
8	Donor template ⁴	CYP4V2 donor template 2 (See para (f) and SEQ ID NO: 57)
9	Protein	SpCas9 (See SEQ ID NO: 58 for exemplary sequence)

¹ The constructs for correcting the c.802-8_810del17insGC mutation, the most common CYP4V2 mutation among BCD patients. CRISPR gRNAs and constructs for correcting other CYP4V2 mutations can be designed and validated by using the methods as described herein. In addition to plasmid and RNP constructs, other constructs including without limitation, mRNA and viral vector, can also be used to provide/express one or more CRISPR components.

² A pX459 plasmid encoding the CRISPR components (sgRNA and SpCas9 protein), and puromycin (Puro) resistance gene as selection marker. See Figure 17 showing DNA construct and sequence encoding the sgRNA (using g1 as example, and Figure 15 and 16 for vector construct and map). Each sgRNA sequence contains (a) a 20 nt protospacer element (SEQ ID NO: 48, 49, or 50 for g1, g2 and g3, respectively), and (b) a 82nt sequence (SEQ ID NO: 55 (sequence shown in DNA format as included in the plasmid DNA; for RNA sequence, use "U" to replace "T" in the DNA sequence). The pX459 vector contains a "G" nucleotide (SEQ ID NO: 59 and Figure 17) immediately after the human U6 promoter sequence and before the protospacer element sequence to enhance transcription efficiency driven by the U6 promoter, which is also included in the IVT derived sgRNA. The CRISPR components (gRNA and Cas protein) can also be cloned in other vectors, including without limitation, viral vectors such as lentivirus vectors or AAV vectors. CRISPR gRNA and Cas protein (e.g., Cas9 protein) can be cloned in separate vectors or in one vector.

³ sgRNA based on various protospacer elements (CYP4V2 g1, CYP4V2 g2, or CYP4V2 g3, see Table 5 and SEQ ID NO: 48, 49 or 50, respectively). See description above for the IVT sgRNAs. In addition to IVT sgRNAs, synthetic sgRNAs with chemical modifications were ordered from Synthego Corporation (Silicon Valley, CA, USA). Instead of sgRNA, a crRNA (comprising the 20nt protospacer sequence of CYP4V2 g1, g2 or g3, and remaining sequence of the crRNA (exemplary sequence shown in SEQ ID NO: 53)) and a tracrRNA (exemplary sequence shown in SEQ ID NO: 54) duplex can be used.

⁴ A donor template for homology-directed repair (HDR). Donor templates of different lengths can also be used, and can be constructed in different forms, including without limitation, as ssODN or in a vector (e.g., in an adeno-associated virus (AAV) vector (e.g., AAV2 or AAV6). Concentration of each reagent is at about 1000 (ng/ μ L).

The following protocols are for delivering CYP4V2 mutation CRISPR gene repair constructs to the patient iPSCs via electroporation and nucleofection. Other methods, including without limitation, lipofection, viral vector transduction (e.g., lentivirus or AAV vectors (e.g., use AAV6 to deliver the donor template), or microjection can also be used. P1 iPSCs of passages 11 to 14 are used.

Protocol No. 1 (Electroporation using plasmids):

1. Following Neon® transfection system (Life Technologies) instructions, use mixture containing 2.5 µg (2.5 µl of stock) pX459.gRNA (Item # 1, or 2 or 3. Do not combine gRNAs) and 2.5 µg (2.5 µl of stock) ssODN (Either item # 7 or 8) for about 1 million cells.
2. Apply electroporation (EP) conditions: a) 1100V, 30ms, 1 pulse; or b) 1200V, 30 ms, 1 pulse.
3. After EP, evenly split cells into 3 wells of a 6-well plate with Rock inhibitor (10 µM).
4. Two days after plating, add puromycin as indicated in Table 9.
5. Two days after adding Puromycin, replace the spent media with fresh puromycin-free media.
6. Maintain the cultures for 2 weeks before picking colonies.

Table 9. Conditions and puromycin concentration level for diseased iPSCs

	Puromycin concentration (µg/ml)		
1100V 30ms 1p	0.1	0.15	0.2
1200V 30ms 1p	0.1	0.15	0.2

Protocol No. 2 (Electroporation using RNP):

1. Use ice bucket. Thaw one sgRNA (Item # 4, or 5, or 6; do not combine gRNAs), one ssODN donor template (either item # 7 or 8) and SpCas9 protein (Item # 9), as well as the Cas9-Puro expression vector on ice. The Cas9-Puro expression vector is used as a selection marker. It

is a pX459-hSpCas9-2A-Puro plasmid and has a structure shown in Figure 15 except that it did not clone in a gRNA.

2. Label 1.7 ml Eppendorf tubes and 6-well-plates clearly. For each sample, prepare one Eppendorf tube and 1 well. Add 3 ml culture medium (TeSR-E8 from StemCell Technologies (Cat# 05940)) into each well.
3. Prepare one 10 cm dish with 25 ml PBS to wash Neon® tip.
4. Prepare 6-well-plate for plating the electroporated cells. Add 3ml of culture medium into each well.
5. In each Eppendorf tube, add 4 µg (4 µl of stock) sgRNA (Item 4, 5 or 6. Do not combine sgRNAs) and 10 µg (10 µl of stock) SpCas9 protein (Item # 9), leave the tube at room temperature for at least 10 min.
6. Add 5 µg (5 µl of stock) ssODN (either item # 7 or 8) and 2.5 µg (2.5 µl of stock) Cas9-Puro expression vector in each tube.
7. Resuspend the cells in appropriate Neon® EP buffer R to final density 1×10^7 cells/ml.
8. Aliquot 105 µL cell suspension and add into each Eppendorf tube with CRISPR RNP mixture.
9. Add 3 ml Buffer E2 to Neon® pipette and sit the Neon® pipette on Neon® pipette station.
10. Use 100 µL Neon® tip. Aspirate 100 µL EP mixture from each Eppendorf tube and insert into the Neon® pipette.
11. Apply one of the EP conditions in Table 9 above and follow steps 3 to 6 of Protocol No. 1 above.

Note: If iPSCs do not grow well, condition media is recommended. Collect spent medium (without Puromycin) and filter it to get rid of cell debris. Mix at 1: 1 ratio of spent medium and fresh medium. The use of Matrigel (Corning Cat# 354277) and the media TeSR-E8 from StemCell Technologies (Cat# 05940) is recommended for culturing human iPSCs in feeder free conditions throughout the gene editing process. The addition of Rock Inhibitor (final concentration 10 µM) to the media for 48 hours when plating the cells after EP will help preserve cell viability.

Protocol No. 3 (Nucleofection using RNP):

1. Lonza 4D-nucleofector, parameter set up: Lonza program, DS-150
 2. Prepare RNP (cas9+gRNA) and ssODN separately (bring the volume to a maximum of 10 μ L), mix it before use. See Table 10.
- 5 (1) gRNA1 +CYP4V2 Forward ssODN (2) gRNA2 +CYP4V2 Forward ssODN
 (3) gRNA1 +CYP4V2 Reverse ssODN (4) gRNA2 +CYP4V2 Reverse ssODN

Table 10

Each group reaction	gRNA 30 μ M (μ L)	Cas9 20 μ M (μ L)	ssODN 30 μ M (μ L)	PBS (μ L)
P1 iPS cells	4	1	4	1

kit buffer/each group	Volume (μ L) /sample	4 sample 10 (μ L)
Solution	16.4	65.6
Supplement	3.6	14.4

- 15 3. Harvest and count cells: 5×10^5 iPS cells
4. Suspend cell with RNP+ssODN (10 μ L) by gently pipetting up and down 3-5 times
5. Add Lonza kit buffer 20 μ L into cell suspension, minimize the incubation time before nucleofection.
6. Load the mixture (30 μ L) into the Lonza kit well. Check impedance.
- 20 7. Electroporate the cells using the setting parameter (DS150).
8. Gently resuspend the electroporated cells by adding 70 μ L of mTeSR (w/ Rock inhibitor) directly into the kit well.
9. Plate cells in passage medium at one well of 6 well plate.
10. Observe cell viability 24 hours after electroporation and replace the medium with
- 25 culture medium.

Note: No selection marker is used for this protocol. Cells survived nucleofection are picked for single cell expansion. In addition to Lonza DS-150 program, other parameters such as CB-150 can also be used.

5 Example 22 - Generating Genetically-repaired Patient Cell Line and Use of RNP in Generating Genetically-repaired Patient Cell Line and in Ocular Cell Therapy

Each of expression plasmid construct containing CRISPR g1 or g2 (Item # 1 or 2) and CRISPR RNP construct containing sgRNA1 or sgRNA2 (Item #4 or 5, Synthego, Silicon Valley, CA, USA) and SpCas9 (Item #9, Catalog #: A034a-a-1000 from Feldan (Quebec, Canada), or
10 from Synthego (e.g., Cas9 nuclease 2NLS, *S. pyogenes*), alongside a CYP4V2 donor template (Item #7 or #8, ssODN, Ultramer DNA Oligonucleotides, Integrated DNA Technologies (IDT), Coralville, Iowa, USA), is used to transfect patient iPSCs harboring the c.802-8_810del17insGC mutation.

Assessing Gene Correction by Homology-directed Repair (HDR):

15 After transfection, picked cells are collected for PCR followed by targeted amplicon sequencing to assess for gene correction in the CYP4V2 region containing the c.802-8_810del17insGC mutation. Deep sequencing of transfected cells shows that the reads contained precise correction of the mutation, with insertion of the 17 bp
"TCATACAGGTCATCGCT" and deletion of "GC", resulting in correcting the mutation to the
20 wild-type sequence (SEQ ID NO: 47). Correction of mutation is not seen in any untransfected control iPSCs. The results also serve as an indication of HDR frequency among transfected cells.

Obtaining iPS clones with minimal or no off-target editing:

After assessing HDR, the transfection is performed again in patient iPSCs harboring the c.802-8_810del17insGC mutation. Transfected cells go through single-cell cloning and
25 expansion. Clonal cell lines with confirmed on-target HDR are then assessed for off-target editing through sequencing. For clinical application, whole-genome sequencing (60x coverage) is used to compare the edited and untransfected cell lines of the same patient. An edited clonal iPS cell line with no off-target editing or minimal off-target editing with no known material adverse consequence in the genome is selected.

Differentiate of genetically corrected iPS into the desired type of cells

The selected iPS clonal cell line is then differentiated into iPS-RPE cells (See the Examples herein). The selected iPS clonal cell line can be differentiated into other types of cells that are desired for use in cell therapy (e.g., iPS-RPE cells, iPS-PRCs, iPS-CE cells, iPS-CECs or
5 other iPS-ocular cells).

Bio-assay to confirm genetically-repaired iPS or iPS-derived cells no longer have phenotype

The genetically-corrected (or genetically-repaired) iPS-RPE cells are tested for biochemical function (See the Examples herein) and confirmed that they no longer have
10 phenotype as seen in untreated patient iPS-RPE cells. CYP4V2 expression is detected in genetically repaired patient iPS-RPE cells.

Unlike a plasmid or other vector constructs (e.g., AAV, lentivirus) which results in sustained expression of CRISPR components it encodes (e.g., gRNA, the Cas nuclease, and/or the donor template), a CRISPR RNP construct is fast on and fast off. Components of a RNP
15 construct are degraded relatively quickly in the transfected cells. Therefore, the use of RNP constructs lowers the risk of off-target editing as compared to plasmid and other constructs. This makes RNP construct particularly suitable for clinical application, such as in generating genetically-repaired patient cells suitable for transplantation, as well as for *in vivo* treatment (e.g., injecting the RNP constructs to a subject's eye for *in vivo* gene correction). In addition to treating
20 BCD, the CRISPR RNP constructs and methods provided herein can be used in treating other diseases, including diseases associated with a mutated or defective gene set forth in Table 4.

Example 23: Use of Genetically Repaired Cells in Ocular Cell Therapy

The genetically-repaired iPS-RPE cells, iPS-PRCs, iPS-CECs, iPS-CE cells or other iPS-
25 ocular cells can be transplanted to the patient's eye as an ocular cell therapy. For example, they can be used as autologous replacement cells for dead or degenerated RPE cells, photoreceptors or other ocular cells in a BCD patient. The genetically repaired cells can be transplanted either directly (e.g., cell suspension) or in other forms, including without limitation, as part of a layer, a sheet, a matrix, a scaffold or a tissue. The amount of genetically repaired cells used in a
30 transplanted depends on the cell type targeted for replacement, the size of the area needing

replacement cells, and the subject being treated (e.g., the age, sex, weight, development stage of the disease and condition of the subject to be treated); the route of administration; the location of the transplantation (e.g., retina vs. cornea); the form of the transplantation (e.g., cell suspension vs. as part of a layer, a sheet, a matrix, a scaffold or a tissue); and the required regimen. The amount of cells in a single transplantation to one eye of a given cell type (e.g., RPE cells, photoreceptors, CECs, or CE cells) can range from about 1,000 cells to 10 million cells.

If required, cells can be manufactured in a GMP facility for clinical use. GMP facilities for cell therapy products are commercially available via research institutes, contract manufacturing organizations (CMOs) and contract research organizations (CROs), e.g., Cellular Therapy Integrated Services at Case Western Reserve University, Center for Cell and Gene Therapy at Baylor College of Medicine, CELLforCURE, New York Stem Cell Foundation and Lonza.

Patient-specific autologous administration can use the same administration/delivery methods as used in allogenic ocular cell therapy (e.g., embryonic stem cell derived RPE (ES-RPE) transplant) for retinal degeneration diseases, including those affected by RPE degeneration, such as age-related macular degeneration (AMD). Such administration/surgical methods are known in the art.

Example 24 - Gene Therapy and Cell Therapy Combination Treatment for Ocular Diseases

The disclosures herein described compositions and methods for use in gene therapy and cell therapy for BCD. For ocular diseases, gene therapy and cell therapy each has its own pros and cons. On the one hand, gene therapy works better in early- to mid-disease stage when the patient still has plenty of retinal (or ocular) cells remaining to receive and get rescued by the gene therapy treatment. However, gene therapy does not work well or may not work at all for late-stage patients who have no the relevant ocular cells left (e.g., RPE or PRC). Cell therapy, on the other hand, provides replacement cells to replace the dead or degenerated cells in the patient's eye and has its advantages over gene therapy particularly for late-stage patients and dominantly inherited diseases. However, cell therapy cannot rescue the remaining "original" cells in the patient's eye, whose survival not only preserves the patient's remaining vision, but also benefits the integration of the replacement cells.

To overcome the limitations of gene therapy and cell therapy and bring maximum benefits to patients, a gene therapy and cell therapy combination treatment method was developed for BCD, which can also be used for other ocular diseases. Such method comprising:

- (a) apply gene therapy (e.g., AAV.CYP4V2 gene therapy or CRISPR gene correction therapy) in the patient's eye *in vivo*; and
- (b) *in vitro* generation of genetically-repaired patient-specific autologous iPS-ocular cells (e.g., iPS-RPE cells, iPS-PRCs, iPS-CE cells, iPS-CECs or other types of ocular cells which is affected by the disease) and transplant these cells into the patient's eye.

wherein (a) and (b) can be applied sequentially (first (a) then (b), or first (b) then (a)) or simultaneously (e.g., injecting gene therapy vectors and cells in one administration). Each of (a) or (b) can be applied one or more times to the same eye. Depending on the disease, disease-stage and patient's individual situation, (a) and (b) can target the same types or different types of ocular cells. For example, in the case of BCD, gene therapy vectors driven by a ubiquitous promoter can result in CYP4V2 expression in RPE cells, photoreceptors and other retinal cells, whereas cell therapy may focus on providing regenerated RPE cells and/or photoreceptors. In this case, cell therapy can benefit by providing new cells (e.g., RPE or photoreceptor cells), whereas gene therapy can improve the effect of cell therapy by rescuing the remaining RPE or photoreceptor cells and/or by improving the conditions of choroid cells whose healthy affects the conditions of ocular cells. The combination of the "rescue" and "replacement" effect of gene therapy and cell therapy, respectively, makes the combination treatment an improvement from either gene therapy or cell therapy. This combination treatment method can be applied to ocular and oither diseases caused by one or more genetic mutations, including without limitation, diseases associated with a mutated or defective gene set forth in Table 4.

It is to be understood that, while the methods and compositions of matter have been described herein in conjunction with a number of different aspects, the foregoing description of the various aspects is intended to illustrate and not limit the scope of the methods and compositions of matter. Other aspects, advantages, and modifications are within the scope of the following claims.

Disclosed are methods and compositions that can be used for, can be used in conjunction with, can be used in preparation for, or are products of the disclosed methods and compositions. These and other materials are disclosed herein, and it is understood that combinations, subsets, interactions, groups, etc. of these methods and compositions are disclosed. That is, while
5 specific reference to each various individual and collective combinations and permutations of these compositions and methods may not be explicitly disclosed, each is specifically contemplated and described herein. For example, if a particular composition of matter or a particular method is disclosed and discussed and a number of compositions or methods are discussed, each and every combination and permutation of the compositions and the methods are
10 specifically contemplated unless specifically indicated to the contrary. Likewise, any subset or combination of these is also specifically contemplated and disclosed.

WHAT IS CLAIMED IS:

1. A composition for treating or preventing an ocular disease in a human subject, comprising a vector, the vector comprising an expression cassette, the expression cassette comprising a nucleic acid molecule or a non-pathogenic variant thereof encoding a functional or non-mutant CYP4V2 protein operably linked to one or more regulatory sequence, wherein the disease is associated with the dysfunction, dystrophy, disorder, degeneration, atrophy and/or death of ocular cells
2. A composition for preventing, arresting, slowing progression of, treating or ameliorating the dysfunction, dystrophy, disorder, degeneration, atrophy and/or death of an ocular cell, comprising a vector, the vector comprising an expression cassette, the expression cassette comprising a nucleic acid molecule or a non-pathogenic variant thereof encoding a functional or non-mutant CYP4V2 protein operably linked to one or more regulatory sequence.
- Diseases:
 3. The composition of claim 1 or 2, wherein the ocular disease or ocular cell degeneration is an inherited retinal degeneration (IRD) or retinitis pigmentosa (RP) with bi-allelic mutation in the CYP4V2 gene
 4. The composition of claim 1, 2 or 3, wherein the disease is or the ocular cell degeneration is associated with Bietti Crystalline Dystrophy (also known as Bietti Crystalline Corneoretinal Dystrophy; BCD).
 5. The composition of any one of claims 1-4, wherein the vector is a viral vector, a plasmid, or a non-viral vector.
 6. The composition of claim 5, wherein the viral vector is selected from the group consisting of an adeno-associated virus (AAV) vector, an adenovirus vector, a lentivirus vector, a herpes simplex virus vector, a baculovirus vector, a sendai virus vector, and a retrovirus vector.

7. The composition of claim 5 or 6, wherein the vector is a recombinant AAV vector (rAAV).

5 8. The composition of claim 5, 6, or 7, wherein the AAV genome or AAV capsid protein in the rAAV is from any one of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or another serotype or isolate or Glade of AAV, or any derivative, variant or hybrid thereof.

10 9. The composition of any one of claims 5-8, wherein the rAAV is a pseudotyped AAV (e.g., AAV2/5, AAV2/8, AAV2/1, AAV2/9, AAV2/6, AAV2/4, AAV2/6, AAV5/2, AAV8/1, AAV8/2, AAV2/7, AAV2/12 and AAV2/10) or a hybrid AAV (e.g., AAV-DJ, AAV-DJ/8, or AAV-DJ/9).

15 10. The composition of any one of claims 5-9, wherein the rAAV comprises one or more capsid mutations (e.g., Y-F, K-R, T-A, S-A and/or T-V mutations, (e.g., AAV2 with one or more capsid mutations among Y444F, Y500F, Y730F, Y252F, Y272F, Y700F, Y704F and T491V, or the corresponding mutation for a different AAV serotype, (e.g., AAV2 (Y444F +Y500F+Y730F), AAV2 (quadY-F+T-V), or AAV2/8 (Y733F)))).

20

 11. The composition of any one of claims 5-10, wherein the serotype of the rAAV is selected or derived from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, Anc80, rh10 and/or ShH10.

25 12. The composition of any one of claims 5-11, wherein the rAAV is selected or derived from the group consisting of AAV2/5, AAV2/8, AAV2/2, AAV2 (Y444F+Y500F+Y730F), AAV2/1, AAV2/9, AAV2/8(Y733F), AAV2/6, AAV2/4, AAV2/7, AAV5, AAV2, AAV8, AAV1, AAV9, AAV6, AAV10, AAV4, AAV7, AAV12, Anc80, AAV 7m8, AAV-DJ, ShH10, AAV-PHP.B or a hybrid, a derivative or variant thereof.

30

13. The composition of any one of claims 5-12, wherein the rAAV vector is a single-stranded AAV vector or a self-complementary AAV (scAAV) vector.

14. The composition of claim 5, wherein the vector is a plasmid, a naked nucleic acid, liposomes (e.g., cationic or anionic liposomes), dendrimer, nanoparticle, polymers (e.g., polyplexes), lipid-polymer system, solid lipid nanoparticle, or liposome protamine/DNA lipoplex (LPD).

15. The composition of any of the preceding claims, wherein the functional or non-mutant CYP4V2 protein encoded by the nucleic acid sequence comprises a polypeptide having at least 80% amino acid sequence identity (e.g., at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity) to any of the sequences selected from the group consisting of SEQ ID NOs: 4-6.

16. The composition of any of the preceding claims, wherein the nucleic acid molecule has at least 75% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3.

17. The composition of any of the preceding claims, wherein the nucleic acid molecule has at least 80% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3.

18. The composition of any of the preceding claims, wherein the nucleic acid molecule comprises a sequence shown in SEQ ID NO: 1, 2, or 3.

19. The composition of any of the preceding claims, wherein the nucleic acid molecule comprises a codon-optimized sequence encoding a protein comprising an amino acid sequence selected from SEQ ID NO: 4, 5, or 6.

20. The composition of any of the preceding claims, wherein the regulatory sequence comprises a promoter.

30

21. The composition of claim 20, wherein the promoter is an RPE cell-specific promoter, a retinal cell-specific promoter, a corneal cell-specific promoter, an ocular cell-specific promoter or a constitutive promoter.

5 22. The composition of claim 20, wherein the promoter is a beta actin promoter or a viral promoter or a hybrid thereof.

23. The composition of claim 20, wherein the promoter is selected from the group consisting of a CAG promoter (hybrid CMV early enhancer/Chicken beta actin promoter, also
10 known as CAGGS promoter, CB promoter or CBA promoter), a chicken beta actin promoter, a small CBA (smCBA) promoter, a CB^{SB} promoter, or a CBh promoter, another beta-actin promoter such as the human beta actin promoter, a elongation factor 1 alpha short (EFS) promoter, a elongation factor 1 alpha (EF-1 alpha) promoter, a CMV promoter, a PGK promoter, a UBC promoter, a GUSB promoter, a UCOE promoter, a VMD2 (vitelliform macular dystrophy
15 2; also known as BEST1) promoter, a RPE65 promoter, or a hybrid, a variant or a derivative thereof.

24. The composition of any of the preceding claims, wherein the regulatory sequence is a polyA signal selected from the group consisting of a bovine growth hormone polyadenylation
20 signal (bGH polyA), a small polyA signal (SPA), a human growth hormone polyadenylation signal (hGH polyA), a SV40 polyA signal, a SV40 late polyA signal, or a derivative, a hybrid and a variant thereof.

25 25. The composition of any of the preceding claims, wherein the regulatory sequence comprises a Kozak sequence.

26. The composition of any of the preceding claims, wherein the regulatory sequence comprises an enhancer.

27. The composition of claim 26, wherein the enhancer is a viral enhancer, including without limitation, a WPRE enhancer, an HPRE enhancer, a CTE enhancer or a derivative or hybrid or variant thereof.

5 28. A composition for treating or preventing BCD or for producing a composition for treating or preventing BCD comprising a nucleic acid molecule sharing at least 80% sequence identity with any of the CYP4V2 expression cassette sequence in SEQ ID NOs: 60 to 64.

10 29. The composition of any of the preceding claims, wherein the composition is formulated with a pharmaceutically acceptable carrier and additional components suitable for the specific route of administration.

15 30. A method of treating or preventing an ocular disease in a human subject, the method comprising administering a vector to the subject, wherein the vector comprises an expression cassette, the expression cassette comprising a nucleic acid molecule or a non-pathogenic variant thereof encoding a functional or non-mutant CYP4V2 protein operably linked to one or more regulatory sequence, wherein the disease is associated with the dysfunction, dystrophy, disorder, degeneration, atrophy and/or death of ocular cells

20 31. A method of preventing, arresting, slowing progression of, treating or ameliorating the dysfunction, dystrophy, disorder, degeneration, atrophy and/or death of an ocular cell, the method comprising delivering a vector to the ocular cell, wherein the vector comprises an expression cassette, the expression cassette comprising a nucleic acid molecule or a non-pathogenic variant thereof encoding a functional or non-mutant CYP4V2 protein operably linked
25 to one or more regulatory sequence.

30 32. The method of claim 30 or 31, wherein the ocular cells are retinal cells, corneal cells, choroidal cells, retinal pigment epithelial (RPE) cells, photoreceptor cells, and/or choroidal epithelial cells.

33. The method of claim 30 or 31, wherein the ocular disease or ocular cell degeneration is an inherited retinal degeneration (IRD) or retinitis pigmentosa (RP) with bi-allelic mutation in the CYP4V2 gene.

5 34. The method of claim 30 or 31, wherein the disease is or the ocular cell degeneration is associated with Bietti Crystalline Dystrophy (also known as Bietti Crystalline Corneoretinal Dystrophy; BCD).

35. The method of any one of claims 30-34, wherein the vector is a viral vector, a
10 plasmid, or a non-viral vector.

36. The method of claim 35, wherein the viral vector is selected from the group consisting of an adeno-associated virus (AAV) vector, an adenovirus vector, a lentivirus vector, a herpes simplex virus vector, a baculovirus vector, a sendai virus vector, and a retrovirus vector.

15 37. The method of claim 36, wherein the vector is a recombinant AAV vector (rAAV).

38. The method of claim 37, wherein the rAAV comprises an AAV genome or a derivative thereof, and/or an AAV capsid protein or a derivative or variant thereof.

20 39. The method of claim 37 or 38, wherein the rAAV is a chimeric AAV, a shuffled AAV, or a capsid-modified AAV.

40. The method of claim 36, 37, 38 or 39, wherein the AAV genome or AAV capsid protein in the rAAV is from any one of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or another serotype or isolate or Glade of AAV, or any derivative, variant or hybrid thereof.

41. The method of any one of claims 37-40, wherein the rAAV is a pseudotyped AAV
30 (e.g., AAV2/5, AAV2/8, AAV2/1, AAV2/9, AAV2/6, AAV2/4, AAV2/6, AAV5/2, AAV8/1,

AAV8/2, AAV2/7, AAV2/12 and AAV2/10) or a hybrid AAV (e.g., AAV-DJ, AAV-DJ/8, or AAV-DJ/9).

42. The method of any one of claims 37-41, wherein the rAAV comprises one or more
5 capsid mutations (e.g., Y-F, K-R, T-A, S-A and/or T-V mutations, (e.g., AAV2 with one or more
capsid mutations among Y444F, Y500F, Y730F, Y252F, Y272F, Y700F, Y704F and T491V, or
the corresponding mutation for a different AAV serotype, (e.g., AAV2 (Y444F +Y500F+Y730F),
AAV2 (quadY-F+T-V), or AAV2/8 (Y733F)))).

10 43. The method of any one of claims 37-42, wherein the serotype of the rAAV is
selected or derived from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6,
AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, Anc80, rh10 and/or ShH10.

15 44. The method of any one of claims 37-43, wherein the rAAV is selected or derived
from the group consisting of AAV2/5, AAV2/8, AAV2/2, AAV2 (Y444F+Y500F+Y730F),
AAV2/1, AAV2/9, AAV2/8(Y733F), AAV2/6, AAV2/4, AAV2/7, AAV5, AAV2, AAV8,
AAV1, AAV9, AAV6, AAV10, AAV4, AAV7, AAV12, Anc80, AAV 7m8, AAV-DJ, ShH10,
AAV-PHP.B or a hybrid, a derivative or variant thereof.

20 45. The method of any one of claims 37-44, wherein the rAAV vector is a single-
stranded AAV vector or a self-complementary AAV (scAAV) vector.

25 46. The method of any one of claims 30-34, wherein the vector is a plasmid, a naked
nucleic acid, liposomes (e.g., cationic or anionic liposomes), dendrimer, nanoparticle, polymers
(e.g., polyplexes), lipid-polymer system, solid lipid nanoparticle, or liposome protamine/DNA
lipoplex (LPD).

30 47. The method of any one of claims 30-46, wherein the functional or non-mutant
CYP4V2 protein encoded by the nucleic acid sequence comprises a polypeptide having at least
80% amino acid sequence identity (e.g., at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%,

88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity) to any of the sequences selected from the group consisting of SEQ ID NOs: 4-6.

48. The method of any one of claims 30-47, wherein the nucleic acid molecule has at least 75% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3.

49. The method of any one of claims 30-48, wherein the nucleic acid molecule has at least 80% sequence identity to any of the sequences in SEQ ID NO: 1, 2 or 3.

50. The method of any one of claims 30-49, wherein the nucleic acid molecule comprises a sequence shown in SEQ ID NO: 1, 2, or 3.

51. The method of any one of claims 30-50, wherein the nucleic acid molecule comprises a codon-optimized sequence encoding a protein comprising an amino acid sequence selected from SEQ ID NO: 4, 5, or 6.

52. The method of any one of claims 30-51, wherein the regulatory sequence comprises a promoter.

53. The method of claim 52, wherein the promoter is an RPE cell-specific promoter, a retinal cell-specific promoter, a corneal cell-specific promoter, an ocular cell-specific promoter or a constitutive promoter.

54. The method of claim 52, wherein the promoter is a beta actin promoter or a viral promoter or a hybrid thereof.

55. The method of claim 52, wherein the promoter is selected from the group consisting of a CAG promoter (hybrid CMV early enhancer/Chicken beta actin promoter, also known as CAGGS promoter, CB promoter or CBA promoter), a chicken beta actin promoter, a small CBA (smCBA) promoter, a CB^{SB} promoter, or a CBh promoter, another beta-actin promoter such as

the human beta actin promoter, a elongation factor 1 alpha short (EFS) promoter, a elongation factor 1 alpha (EF-1 alpha) promoter, a CMV promoter, a PGK promoter, a UBC promoter, a GUSB promoter, a UCOE promoter, a VMD2 (vitelliform macular dystrophy 2; also known as BEST1) promoter, a RPE65 promoter, or a hybrid, a variant or a derivative thereof.

5

56. The method of any one of claims 30-55, wherein the regulatory sequence comprises a polyadenylation (polyA) signal.

57. The method of claim 56, wherein the polyA signal is a bovine growth hormone polyadenylation signal (bGH polyA), a small polyA signal (SPA), a human growth hormone polyadenylation signal (hGH polyA), a SV40 polyA signal, a SV40 late polyA signal, or a derivative, a hybrid or a variant thereof.

58. The method of any one of claims 30-57, wherein the regulatory sequence comprises a Kozak sequence.

59. The method of any one of claims 30-57, wherein the regulatory sequence comprises an enhancer.

60. The method of claim 59, wherein the enhancer is a viral enhancer, including without limitation, a WPRE enhancer, an HPRE enhancer, a CTE enhancer or a derivative or hybrid or variant thereof.

61. A method for treating or preventing BCD, the method comprising administering a vector comprising a nucleic acid molecule sharing at least 80% sequence identity with any of the CYP4V2 expression cassette sequence in SEQ ID NOs: 60 to 64.

62. The method of any one of claims 30-61, wherein the composition is formulated with a pharmaceutically acceptable carrier and additional components suitable for the specific route of administration.

30

63. A composition for use in producing a vector for treating or preventing BCD, the composition comprising a nucleic acid molecule sharing at least 80% sequence identity with any of the CYP4V2 expression cassette sequence in SEQ ID NOs: 60 to 64.

5

64. The method of any one of claims 30-63, wherein for in vitro treatment, the target cell is infected at a dose (MOI) of about 1×10^3 GC to about 1×10^6 GC per cell (GC: genomic copies, measuring genome containing AAV particles).

10

65. The method of any one of claims 30-64, wherein for in vivo administration to a subject's eye, a single administration can be on the order of from about 1×10^6 to 2×10^{13} GC (e.g., a high dose range of about 1×10^{11} GC to about 1×10^{12} GC, a medium dose range of about 1×10^{10} GC to about 1×10^{11} GC, a low dose range of about 1×10^9 GC to about 1×10^{10} GC, a very low dose range of about 1×10^6 GC to about 1×10^9 GC, and a very high dose range of about 1×10^{12} GC to about 2×10^{13} GC), or any dose within these ranges that is sufficient to provide the desired effect.

15

66. The method of any one of claims 30-65, wherein the administering step takes place before the onset of disease symptoms or after the onset of disease symptoms.

20

67. The method of any one of claims 30-66, wherein the administration and/or targeted delivery is to the eye and/or to an ocular cell.

68. The method of any one of claims 30-67, wherein the administration is by sub-retinal injection, intravitreal injection, or by implanting intravitreally a device encapsulating the vector.

25

69. The method of any one of claims 30-68, wherein the administration is by any other administration method that effectively delivers the vectors to the sub-retinal place, the posterior segment of the eye, the cornea, the retina, the choroid, the RPE cells, the photoreceptors or corneal epithelial cells, the CE cells of the subject.

30

70. The method of claim 67, wherein the administration to the eye is achieved by delivery through the bloodstream.

5 71. The method of any of the preceding claims, wherein the ocular cells are selected from the group consisting of retinal pigment epithelium (RPE) cells, photoreceptor cells (PRCs), corneal epithelial cells (CECs), choroidal endothelial (CE) cells, retinal cells, corneal cells, lens cells, ganglion cells, optic nerve cells, and/or choroidal cells, as well as the said types of cells derived from a stem cell (including without limitation, an iPSC, a ES cell, an MSC, an adult stem
10 cell and/or a tissue-specific stem cell).

72. The method of any of claims 30-71, wherein the vector is formulated with a pharmaceutically acceptable carrier and additional components suitable for the specific route of administration.

15

73. The method of any of claims 30-72, further comprising identifying a subject having BCD or at risk of developing BCD, or having bi-allelic CYP4V2 mutation.

74. A method for treating or preventing Bietti Crystalline Dystrophy (BCD) in a human
20 subject, the method comprising delivering to the subject's ocular cells a vector comprising a nucleic acid molecule comprising the nucleic acid sequence of SEQ ID NO: 2 encoding a human CYP4V2 protein or a nucleic acid sequence sharing at least 90% sequence identity to the nucleic acid sequence of SEQ ID NO: 2, operably linked to one or more regulatory sequence.

25 75. The method of claim 74, wherein the vector is an adeno-associated virus (AAV) vector.

76. The method of claim 74 and 75, wherein the regulatory sequence is a promoter.

77. A nucleic acid molecule comprising the nucleic acid sequence of SEQ ID NO: 2 encoding a human CYP4V2 protein or a nucleic acid sequence sharing at least 90% sequence identity to the nucleic acid sequence of SEQ ID NO: 2.

5 78. An expression cassette comprising the nucleic acid molecule of claim 77 and one or more regulatory sequence operably linked to such nucleic acid sequence.

79. A vector comprising the nucleic acid molecule of claim 77 or the expression cassette of claim 78.

10

80. The vector of claim 79, wherein the vector is a viral vector or is selected from the group consisting of a recombinant adeno-associated virus (rAAV) vector, a recombinant adenovirus vector, a recombinant lentivirus vector, a recombinant herpes simplex virus vector, a recombinant baculovirus vector, a recombinant sendai virus vector, and a recombinant retrovirus
15 vector.

81. The vector of claim 79, wherein the vector is a plasmid or a non-viral vector.

82. The vector of claim 81, wherein the non-viral vector is selected from a naked nucleic acid, liposomes (e.g., cationic or anionic liposomes), dendrimer, nanoparticle, polymers (e.g., polyplexes), lipid-polymer system, solid lipid nanoparticle, or liposome protamine/DNA lipoplex (LPD)..

20

83. A host cell comprising the nucleic acid molecule of claim 77 and/or the vector of any one of claims 79 to 82.

25

84. A method to reduce immune responses to viral vectors, preserve transduction efficiency, to lower viral vector and/or immunosuppressant dose, and/or to maximize therapeutic effect to different patients of the same genetic disease, in viral vector mediated gene therapy, comprising:

30

(a) establishing a pool of more than one recombinant viral vectors (e.g., rAAVs) with sufficient transduction efficiency in the target cell type for the gene therapy by creating variants with antigenic region mutations or other mutations or variants on the capsids of said viral vectors after such mutations or variants are confirmed with sufficient transduction
5 efficiency in target cells relevant to the disease (e.g., in iPS-RPE or RPE cell lines for CYP4V2 gene therapy for BCD).

(b) detecting pre-existing neutralizing anti-viral vector antibodies (NAbs) against different viral vector serotypes and/or capsid mutations or variants in the subject in need of the gene therapy, and/or testing and comparing different viral vectors in patient-specific disease
10 target cells (e.g., iPS-RPE cells) derived from such subject.

(c) selecting a viral vector from said pool of viral vectors with (i) sufficient transduction efficiency in the disease target cells and (ii) low cross-reactivity with the pre-existing NAbs in the subject, and/or (iii) good phenotype rescue result in the subject's patient-specific disease target cells (e.g., patient-specific iPS-RPE or RPE cell lines for CYP4V2 gene
15 therapy for BCD), wherein such viral vector pool comprising different serotypes and/or capsid-modified viral vectors (e.g., including without limitation, capsid-mutant AAVs and/or capsid protein variant AAVs).

(d) using the viral vector selected from (c) for administration to the subject.

(e) repeating (b) through (d) (only the part relating to pre-existing NAbs) above
20 each time the subject requires a gene therapy administration, including without limitation, a follow-up administration to the same organ (e.g., an eye or a contralateral eye), or to another organ.

85. A method of using AAV vector-mediated gene therapy in treating or preventing
25 human retinal diseases, wherein the AAV vector comprises a nucleic acid molecule comprising a EFS promoter (SEQ ID NO: 35) and/or a small polyA (SEQ ID NO: 36) operably linked to the therapeutic transgene, or a nucleic acid molecule shares at least 90% sequence identity with SEQ ID NO: 35 or at least 85% sequence identity with SEQ ID NO: 36.

30 86. The method of claim 85, wherein the AAV vector is a single-stranded AAV.

87. The method of claim 85, wherein the AAV vector is a self-complementary AAV (scAAV).

5 88. A cellular disease model comprising a cell line composition comprising (a) a stem cell provided from a subject or reprogrammed from a cell provided from a subject, or (2) a cell derived from a stem cell provided from a subject or reprogrammed from a cell provided from a subject, comprising one or more mutations in a target gene.

10 89. The composition of claim 88, wherein the stem cell is an induced pluripotent stem (iPS) cell.

 90. The composition of claim 88, wherein the stem cell is an embryonic stem (ES) cell, somatic (or adult) stem cell, tissue specific stem cell, or mesenchymal stem cell (MSC).

15 91. The composition of claim 88, wherein the cell provided from a subject is a somatic cell.

 92. The composition of claim 88, wherein the cell provided from a subject is a skin cell,
20 a fibroblast or a blood cell.

 93. The composition of claim 88 or 92, wherein the cell provided from a subject is a skin fibroblast or a peripheral blood mononuclear cell (PBMC).

25 94. The composition of claim 88, wherein the cell provided from a subject is a urinary cell, a renal epithelial cell, a hair follicle, or a dermal papilla cell.

 95. The composition of claim 88, wherein the cell derived from a stem cell is an ocular
30 cell.

96. The composition of claim 95, wherein the ocular cell is a retinal pigment epithelial (RPE) cell, photoreceptor cell (PRC, including rod cell, cone cell and photoreceptor progenitor cell), retinal cell, corneal cell, corneal epithelial cell (CEC), optic nerve cell, lens cell, choroidal endothelial (CE) cell, optic nerve cell or choroidal cell.

5

97. The composition of claim 88, wherein the cell derived from a stem cell is a neuron cell.

10

98. The composition of claim 88, wherein the mutation is endogenous to the subject.

99. The composition of claim 88 or 98, wherein the mutation is introduced artificially via genetic editing or genetic manipulation.

15

100. The composition of claim 88, wherein the cell line comprises a plurality of mutations that are endogenous and/or exogenous to the subject.

101. The composition of claim 88, wherein the subject is a mammal.

20

102. The composition of claim 88, wherein the subject is a human.

103. The composition of claim 88, wherein the target gene comprises a gene set forth in Table 4.

104. The composition of claim 88, wherein the target gene comprises a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22,

30

CYP4X1, CYP4Z1, or CYP46A gene or a CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 or CYP46A gene that encodes a protein having defective or partial function or activity.

10 105. The composition of claim 88, wherein the target gene is CYP4V2.

106. The composition of claim 105, wherein the cell line comprises an iPS cell.

107. The composition of claim 105, wherein the cell line comprises an iPS-RPE cell.

15

108. The composition of claim 105, wherein the cell line comprises an iPS-photoreceptor (iPS-PRC) cell, an iPS-corneal epithelial cell (iPS-CEC), an iPS-choroidal endothelial (CE) cell, an iPS-corneal cell, an iPS-choroidal cell, an iPS-optic nerve cell, an iPS-ocular cell or an iPS-neuron cell.

20

109. The composition of any one of claims 88 or 105-108, wherein the CYP4V2 mutation in the cell line is endogenous to the subject.

25 110. The composition of claim 88 or 109, wherein the subject has a pathologic mutation in the CYP4V2 gene or in an ortholog of the CYP4V2 gene.

111. The composition of claim 88 or 109, wherein the subject has at least one homozygous mutation or two compound heterozygous mutations set forth in Table 1.

112. The composition of claim 88, wherein the subject has inherited retinal degeneration (IRD) or retinitis pigmentosa (RP).

113. The composition of claim 88, wherein the subject has Bietti's Crystalline Dystrophy (BCD, a/k/a Bietti Crystalline Corneoretinal Dystrophy, Bietti Crystalline Retinopathy, Bietti's Retinal Dystrophy) or is at risk of developing BCD.

114. The composition of claim 88 or 105, wherein the cell line comprises at least one CYP4V2 mutation that is exogenous to the subject and is introduced artificially via genetic editing or genetic manipulation.

115. The composition of claim 88 or 114, wherein the cell line comprises an iPS cell, ES cell, MSC, tissue-specific stem cell or adult stem cell, or a RPE cell, photoreceptor cell, corneal epithelial cell, choroidal endothelial (CE) cell or choroidal cell derived from an iPS cell, ES cell, MSC, tissue specific stem cell or adult stem cell.

116. A BCD human cellular model composition or a CYP4V2 dysfunction cellular model composition comprising an iPS cell or iPS cell line, or an iPS-RPE cell or iPS-RPE cell line derived from a cell or a cell line of a BCD patient, or derived from a cell or a cell line with artificially created bi-allelic CYP4V2 mutation.

117. The composition of any one of claims 88 or 105-116, wherein the cell line has an abnormal biochemical profile in one or more compounds of the following compound groups: (i) fatty acids, (ii) ceramides, (iii) sphingomyelins, (iv) sphingosine, (v) sphinganine, (vi) hydroxy-fatty acids, (vii) corticosteroid, or (viii) proteins (other than CYP4V2) or abnormal RPE function, or higher cell atrophy, degeneration or death level as compared to a corresponding cell line of a healthy control.

118. The composition of one of claims 88 or 105-117, wherein the cell line has an abnormal biochemical profile in one or more compounds set forth in Table 2 as compared to the corresponding cell line of a healthy control.

5 119. A method of discovering abnormalities or phenotype in a disease cellular model, comprising evaluating and comparing the cell viability levels of the cell line of a patient (or an genetically edited or manipulated cell line comprising an exogenous mutation in the gene causing such disease) and a healthy control.

10 120. A method of discovering abnormalities or phenotype in a disease cellular model, comprising evaluating and comparing the RPE function levels (e.g., phagocytic activity, transepithelial resistance) of the cell line of a patient (or an genetically edited or manipulated cell line comprising an exogenous mutation in the gene causing such disease) and a healthy control, wherein the cell line is a RPE cell line (including RPE cell line derived from a stem cell).

15 121. The method of claim 119 or 120, wherein the comparison between cell lines are made without exposure to light.

 122. The method of claim 119 or 120, wherein the comparison between cell lines are
20 made after exposure to light.

 123. The method of claim 119, 120 or 122, wherein the comparison between cell lines are made after exposure to blue light.

25 124. The method of claim 119, 121, 122 or 123, wherein cell viability is measured by dead/live cell ratio, sick/healthy cell ratio or similar ratios, or percentage of dead/overall cells or live/overall cells.

 125. A method of discovering abnormalities or phenotype in a disease cellular model,
30 comprising evaluating and comparing the levels of one or more compounds between the cell line

of a patient (or an genetically edited or manipulated cell line comprising an exogenous mutation in the gene causing such disease) and a healthy control, wherein the one or more compound is selected from the following groups: (i) fatty acids, (ii) ceramides, (iii) sphingomyelins, (iv) sphingosine, (v) sphinganine, (vi) hydroxy-fatty acids, (vii) corticosteroid and/or (viii) proteins.

5

126. The method of claim 125, wherein one or more of the compounds evaluated is set forth in Table 2.

127. The method of claim 125 or 126, wherein the identification and/or evaluation of
10 compound levels is performed using LC-MS, LC-MS/MS, GC-MS, GC-MS/MS, and/or FIA-MS/MS.

128. The method of claim 119, 120 or 125, wherein the disease cellular model comprises a mutated or defective gene set forth in Table 4.

15

129. The method of claim 119, 120 or 125, wherein the disease cellular model comprises a mutated or defective gene among the CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6,
20 PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene.

25 130. A method of screening a test agent for therapeutic efficacy against BCD, comprising:

contacting cells from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with a test agent; and

evaluating the cells for normalization in levels of one or more compounds set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; and/or improved cell structure, morphology or function, or improved cell viability, as compared to before contacting by such test agent;

5 wherein normalization in levels of one or more compound set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; and/or improved cell structure, morphology, function or cell viability, as compared to before treatment by such test agent, is indicative of a test agent that exhibits therapeutic efficacy against BCD;

10 wherein the comparison among cell lines can be made after exposure to light and/or without exposure to light.

131. The method of claim 130, wherein the test agents are selected from the group consisting of nucleic acids or analogs thereof, vectors containing nucleic acid sequence or
15 encoding polypeptides, polypeptides or analogs thereof, antibodies, chemicals, small molecules, and/or any combination thereof.

132. The method of claim 130, wherein the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, function assay, cell viability assay, microscopy
20 or combination thereof.

133. A method of screening efficacy or efficiency of a formulation, vector or construct comprising a test agent for BCD, comprising:

contacting multiple cell samples from an iPS-RPE cell line derived from a BCD patient
25 or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with a test agent formulated or packaged in various formulations, vectors or constructs; and

evaluating the cell samples for normalization in levels of one or more compound set forth in table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in
30 the amount of CYP4V2 polypeptides in the cells; improved cell structure, morphology, function

or viability; and/or cell tolerance or death, as compared to before treatment by such test agent and/or to cell samples treated by the same test agent but formulated or packaged in a different formulation, vector or construct, to determine and compare the efficiency or efficacy of such formulation, vector or construct;

- 5 wherein the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, cell viability assay, microscopy or combination thereof;
 wherein the comparison among cell lines can be made after exposure to light and/or without exposure to light.

- 10 134. A method of screening effective and safe dosage range of a test agent for BCD, comprising:

 contacting multiple cell samples from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with a test agent in a different dose for each cell sample.

- 15 evaluating the cell samples for normalization in levels of one or more compound set forth in table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; improved cell structure, morphology, viability or function, and/or cell tolerance or death, as compared to before treatment by such test agent and/or to cell samples treated by the same test agent but with a different dose, to determine and
20 compare the effective and safety of different doses thereby determining a proper dosage range;
 wherein the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, function assay, cell viability assay, microscopy or combination thereof;
 wherein the comparison among cell lines can be made after exposure to light and/or without exposure to light.

- 25 135. A method of screening or evaluating efficacy or efficiency of a delivery device or method for delivering a therapeutic agent to the retina or retinal cells comprising:

 (i) contacting a cell sample from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial

genetic editing or manipulation with a test agent without employing the delivery device or method;

(ii) contacting another cell sample from an iPS-RPE cell line derived from a BCD patient or an iPS-RPE cell line comprising a mutated or defective CYP4V2 gene as a result of artificial genetic editing or manipulation with the test agent of the same dosage as in (i), employing the delivery device or method;

(iii) evaluating and comparing the cell samples from (i) and (ii) for normalization in levels of one or more compound set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of CYP4V2 polypeptides in the cells; improved cell structure, morphology or function; cell tolerance or death; and/or the levels of the test agent in the cells, as compared to before treatment by such test agent and/or treatment by the same test agent of the same dose but without employing the delivery device or method, to determine the efficacy or efficiency of such delivery device or technique;

wherein the cells are evaluated using PCR techniques, immunoassays, sequencing, biochemical assay, function assay, cell viability, microscopy or combination thereof;

wherein the comparison among cell lines can be made after exposure to light and/or without exposure to light.

136. The method of claim 135, wherein the retinal cells are RPE cells.

137. A method of generating an isogenic control comprising genetically correcting the mutation in a patient cell line by any of the claims in gene editing therapy or RNP claims herein.

138. A method of using patient-specific iPS-ocular cells to assess and suggest therapeutic effective dosage for treatment *in vivo*, the method comprising multiplying the optimal dose level (e.g., indicated as MOI for gene therapy *in vitro*) determined in patient-specific iPS-ocular cellular model *in vitro* by the estimated number of ocular cells (e.g., RPE cells, photoreceptor cells, or RPE cells and photoreceptor cells) targeted for treatment *in vivo* to arrive the dose level of gene therapy vectors for *in vivo* use (e.g., GC or gp), and such vector dose level is adjusted by a multiplier (e.g., 1 to 10 (e.g., 1 to 5 for sub-retinal injection or 5 to 10 for

intravitreal injection; the other factors affecting the multiplier to be applied include the size of the area targeted, and the subject being treated (e.g., the age, weight, development stage of the disease and condition of the subject to be treated, and potential immune reactions (i.e., pre-existing NABs); the location and density of the ocular cells targeted for treatment) to suggest the therapeutic effective dose range for treatment *in vivo*, which can be confirmed or further refined by clinical trials.

139. The method of claim 138, wherein the method is used to assess or suggest personalized optimal dose used in treatment *in vivo* for an individual patient.

10

140. The method of claim 138 or 139, wherein the disease is an inherited retinal disorder (IRD) or retinitis pigmentosa (RP).

141. The method of claim 138 or 139, wherein the disease is BCD and the iPS-ocular cells are iPS-RPE cells and the ocular cells targeted for treatment *in vivo* are RPE cells.

15

142. A composition comprising: (a) a CRISPR guide RNA targeting a nucleic acid sequence (the "target sequence") of or within 100 bps to the CYP4V2 gene, and (b) a functional CRISPR-associated protein (Cas).

20

143. The composition of claim 142, further comprising (c) a donor nucleic acid sequence comprising all or a portion of a wild-type sequence or a functional sequence of the CYP4V2 gene for correction, disruption or replacement of CYP4V2 gene or a portion thereof.

144. The composition of claim 142 or 143, wherein one or more components thereof is provided in the form of a DNA molecule encoding such component, an mRNA molecule encoding such component, a RNA molecule, a polypeptide, and/or a ribonucleoprotein (RNP) or protein-RNA complex.

25

145. The composition of claim 142 or 143, wherein two or more components thereof are in separate molecule or combined in one molecule or in one complex, are in separate vectors or combined in one vector, are in one or more nucleic acid complex, are in one or more RNP complex.

5

146. The composition of claim 143, wherein the donor nucleic acid sequence is provided in a single-stranded donor oligonucleotide (ssODN) or a vector.

147. The composition of any one of claims 142-146, wherein the vector is a plasmid, a recombinant AAV vector, a recombinant lentivirus vector, and/or a combination thereof.

10

148. A composition comprising a cell with a pathologic CYP4V2 mutation comprising a composition of any one of claims 142-147.

149. The composition of any one of claims 142-148, wherein (a) the CRISPR guide RNA comprising (i) a CRISPR RNA (crRNA) which comprises a protospacer element sequence that is complementary to the target sequence of or within 100 bps to a target gene (the "target gene") and a sequence that corresponds to a complementary region of the trans-activating crRNA (tracrRNA), and (ii) a tracrRNA which comprises a region that is complementary to corresponding region of the crRNA and a sequence which interacts with a CRISPR-associated protein 9 (Cas9), and (b) the functional CRISPR-associated protein comprises Cas9.

15

20

150. The composition of claim 149, wherein the protospacer element is about 20 bases, about 19 bases, about 21 bases, about 19-21 bases, about 18-22 bases, or about 16-24 bases.

25

151. The composition of claim 149 or 150, wherein the crRNA and the tracrRNA are in separate molecules.

152. The composition of claim 149 or 150, wherein the crRNA and the tracrRNA are combined in a single guide RNA (sgRNA).

30

153. The composition of claim 152, wherein the sgRNA is about 88-150 bps.

154. The composition of any one of claims 149-153, wherein the Cas9 comprises a Cas9
5 ortholog or a mutant Cas9 selected from: *Streptococcus pyogenes* (SpCas9), SpCas9 nickase
(Cas9n D10A), SpCas9 (D1135E), eSpCas9, SpCas9-HF1, SpCas9 VRER, SpCas9 VQR,
SpCas9EQR, *Staphylococcus aureus* (SaCas9), *Neisseria Meningitidis*, *Streptococcus*
thermophilus, *Streptococcus pneumoniae*, *Campylobacter coli*, *Campylobacter jejuni*,
Streptococcus mutans, *Pasteurella multocida*, *Bifidobacterium longum*, *Bacillus smithii*,
10 *Treponema denticola*, *mycoplasma canis* and *enterococcus faecalis*.

155. The composition of any one of claims 142-148, wherein (a) the CRISPR guide
RNA comprises a crRNA which comprises a protospacer element sequence that is
complementary to the target sequence of or within 100 bps to a target gene, and (b) the
15 functional CRISPR-associated protein comprises Cpf1.

156. The composition of any one of claims 142-155, wherein the CRISPR-associated
protein, Cas9, or Cpf1, further comprises one, two, three or more nuclear localization sequences
(NLS) at the N-terminal and/or C-terminal, and/or a selection marker, including without
20 limitation, GFP or EGFP.

157. The composition of claim 142, wherein the protospacer element sequence is
selected from the group consisting of SEQ ID NOs: 48 to 52, or shares at least 85% sequence
identity with any one of SEQ ID NO: 48 to 52 for use with a Cas protein that has NGG as
25 protospacer adjacent motif (PAM) to target the c.802-8_810del17insGC mutation of the
CYP4V2 gene.

158. The composition of claim 142, 143 or 157, wherein the donor nucleic acid sequence
is selected from SEQ ID NOs: 56 and 57, or shares at least 90% sequence identity with one of

SEQ ID NO: 56, 57, or a sequence that is complementary thereof, for use to correct, disrupt or replace the c.802-8_810del17insGC mutation of the CYP4V2 gene.

159. A method of treating or preventing BCD in a subject or a cell with a mutated
5 CYP4V2 gene, comprising:
- (i) identifying the pathologic mutation in the subject or the cell through sequencing;
 - (ii) finding Cas related PAM sites within the region spanning from about 100
10 bps upstream from the first nucleotide involved in the mutation to about 100 bps downstream from the last nucleotide involved in the mutation;
 - (iii) identifying various protospacer element sequences targeting the CYP4V2 sequence relevant to each PAM site identified in (ii);
 - (iv) assessing activity level of each CRISPR guide RNA comprising a protospacer element sequence identified in (iii) and off-target editing profile based on the
15 protospacer element sequence and PAM;
 - (v) selecting one or more CRISPR guide RNA design based on (iv);
 - (vi) designing one or more donor nucleic acid sequence based on homology-directed repair (HDR) for correcting, disrupting or replacing the targeted CYP4V2 mutation;
 - (vii) constructing the CRISPR guide RNA, Cas and donor nucleic acid sequence
20 as provided in composition claims 1 to 18;
 - (viii) optionally validating and further selecting the components of (vii) in a cell isolated from the subject; or an iPS cell derived from the subject or a cell differentiated from a stem cell derived from the subject, or the genomic DNA isolated from the subject to assess the activity level and/or off-target editing profile; and
 - (ix) administering the components in (viii) to the subject or the cell via a delivery
25 system selected from the group consisting of a ribonucleoprotein or protein-RNA complex, a vector, a protein, a nucleic acid molecule, a nanoparticle, a liposome, a micelle, a virosome, a nucleic acid complex, and/or a combination thereof, wherein the delivery is performed by electroporation or via lipid-mediated transfection, or nucleofection, or viral transduction or
30 injection, or a combination thereof.

160. A gene editing composition for correcting or replacing the c.802-8_810del17insGC mutation in a CYP4V2 gene in a subject in vivo or in a cell in vitro, comprising:

- 5 (i) a CRISPR guide RNA comprising a protospacer element sequence selected from one of SEQ ID NO: 48 to 52 or sharing at least 80% sequence identity with one of the sequences in SEQ ID 48 to 52;
- (ii) a donor nucleic acid sequence selected from one of SEQ ID NOs: 56 and 57, or shares at least 90% sequence identity with one of SEQ ID NO: 56, 57, or a sequence that is complementary thereof; and
- 10 (iii) a Cas9 protein (exemplary sequence shown in SEQ ID NO: 58), optionally containing 1, 2, 3 or more NLS, and/or a selection marker including without limitation GFP or EGFP.

161. The composition of claim 160, wherein an optional nucleotide G (SEQ ID NO: 59)
15 is added before the protospacer element sequence.

162. The composition of claim 160 or 161, wherein the CRISPR guide RNA comprises a crRNA (exemplary sequence (excluding the 5' protospacer element sequence) shown in SEQ ID NO: 53) and a tracrRNA (exemplary sequence shown in SEQ ID NO: 54); and the protospacer
20 element sequence is contained in the crRNA.

163. The composition of any of claims 160-162, wherein the CRISPR guide RNA comprises a single guide RNA (sgRNA) comprising the protospacer element sequence (exemplary sgRNA sequence (excluding the 5' protospacer element sequence) shown in SEQ ID
25 NO: 55).

164. The composition of any of claims 160-163, wherein one or more components of (i), (ii) and (iii) is provided in the form of a DNA molecule encoding such component, an mRNA molecule encoding such component, a nucleic acid molecule, a vector, a RNA molecule, a
30 polypeptide, a ribonucleoprotein (RNP) or protein-RNA complex, and/or a combination thereof.

165. A method of treating or preventing a disease of the eye in a subject, wherein the disease is associated with a pathologic genetic or epigenetic alteration in the CYP4V2 gene, the method comprising administering a cellular composition to the subject, wherein the cellular
5 composition comprises: retinal pigment epithelium (RPE) cells, photoreceptors or photoreceptor progenitors (PRCs), corneal epithelial cells (CECs), choroidal endothelial (CE) cells and/or other ocular cells or other cells derived from a stem cell.

166. The method of claim 165, wherein the stem cell is an embryonic stem (ES) cell, an
10 iPC cell, an MSC, an adult stem cell or a tissue-specific stem cell.

167. The method of claim 165, wherein the stem cell is from or derived from one or more subjects not having BCD or not having a pathologic CYP4V2 gene.

15 168. The method of claim 165, wherein the stem cell is from or derived from one or more subjects with pathologic mutations in the CYP4V2 gene.

169. The method of any of claims 165-168, wherein the subject is a human subject.

20 170. A cellular composition comprising (a) a stem cell reprogrammed from a cell isolated from or a stem cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene, or (2) a cell differentiated from a stem cell isolated from a subject or reprogrammed from a cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene.

25 171. The composition of claim 170, wherein the stem cell reprogrammed from a cell isolated from the subject is an iPC cell.

172. The composition of claim 170, wherein the iPS cell is reprogrammed from a
30 somatic cell from the subject.

173. The composition of claim 170, wherein the iPS cell is reprogrammed from a skin cell, a blood cell, a urinary cell, a hair cell, a fibroblast, a peripheral blood mononuclear cell (PBMC), a renal epithelial cell, a hair follicle, or a dermal papilla cell.

5

174. The composition of claim 170, wherein the stem cell isolated from the subject is an MSC, an adult stem cell or a tissue-specific stem cell.

175. The composition of claim 170, wherein the cell differentiated from a stem cell is an ocular cell.

10

176. The composition of claim 170 or 175, wherein the cell differentiated from a stem cell is an RPE cell, a PRC, a retinal cell, a corneal cell, a choroidal cell, a CEC or a CE cell.

177. The composition of claim 170, wherein the cell differentiated from a stem cell is an iPS-RPE, iPS-PRC, iPS-CEC or iPS-CE cell.

15

178. The composition of claim 170, wherein (i) the cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene for use to reprogram into an iPSC, (ii) the stem cell isolated from a subject or iPS cell reprogrammed from a cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene, or (iii) the cell differentiated from a stem cell isolated from a subject or an iPS cell reprogrammed from a cell isolated from a subject affected by BCD or having pathologic mutations in the CYP4V2 gene, is genetically repaired to ameliorate the effect of the mutated CYP4V2 gene.

20

25

179. The composition of claim 178, wherein genetic repair is via gene transfer therapy.

180. The composition of claim 178, wherein genetic repair is via gene transfer therapy by using any composition or method of any one of the gene therapy claims.

30

181. The composition of any of the preceding claims, wherein genetic repair is via gene editing therapy.

182. The composition of claim 181, wherein genetic repair is via gene editing therapy by
5 using any composition or method of any one of CRISPR gene therapy claims.

183. A method of treating or preventing a disease of the eye in a subject affected by BCD or have pathologic genetic or epigenetic alterations in the CYP4V2 gene, the method comprising administering a composition of any one of the claims related to CYP4V2 autologous
10 cellular compositions to the subject, wherein the cellular composition comprises: genetically repaired cells comprising retinal pigment epithelium (RPE) cells, photoreceptors or photoreceptor progenitors (PRCs), corneal epithelial cells (CECs), choroidal endothelial (CE) cells, and/or other ocular cells or other cells derived from a stem cell of the subject.

184. The method of claim 183, wherein the stem cell is an iPC cell, an MSC, an adult stem cell or a tissue-specific stem cell.

185. The method of claim 184, wherein the iPS cell is reprogrammed using one or more of the OCT4, SOX2, KLF4, and c-MYC transcription factors.
20

186. The method of any of the preceding claims, wherein the genetically repaired cells demonstrate one or more of the following: normalization in levels of one or more compound set forth in Table 2; an increase in non-defective CYP4V2 nucleic acid sequence in the cells; an increase in the amount of functional CYP4V2 polypeptides in the cells; and/or improved cell
25 structure, morphology, viability or function, as compared to before genetic repair is performed.

187. The method of any of the preceding claims, wherein the amount of cells administered is about 1,000 to about 10 million cells in a single administration.

188. The method of any of the preceding claims, wherein the administration is via injection, sub-retinal injection or intravitreal injection, .

189. The method of any of the preceding claims, wherein the administration is by any
5 other administration method that effectively delivers the cells to the sub-retinal place, the posterior segment, or the cornea of the eye of the subject.

190. The method of any of the preceding claims, wherein the cells are administered via
10 injection of cell suspension.

191. The method of any of the preceding claims, wherein the cells are administered as part of a sheet, a matrix, a scaffold, a tissue, or a 3D retinal structure.

192. The method of any of the preceding claims, whereas the RPE cells are administered
15 using natural and/or synthetic scaffolds to generate a functional RPE monolayer.

193. The method of any of the preceding claims, wherein the subject is a human subject.

194. A cellular composition comprising (a) a stem cell reprogrammed from a cell
20 isolated from or a stem cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity, or (2) a cell differentiated from a stem cell isolated from a subject or reprogrammed from a cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity.

25 195. The composition of claim 194, wherein the stem cell reprogrammed from a cell isolated from the subject is an iPS cell.

196. The composition of claim 195, wherein the iPS cell is reprogrammed from a
30 somatic cell of the subject.

197. The composition of claim 195 or 196, wherein the iPS cell is reprogrammed from a skin cell, a blood cell, a urinary cell, a hair cell, a fibroblast, a peripheral blood mononuclear cell (PBMC), a renal epithelial cell, a hair follicle, or a dermal papilla cell.

5

198. The composition of claim 194, wherein the stem cell isolated from the subject is an MSC, an adult stem cell or a tissue-specific stem cell.

199. The composition of claim 194, wherein the gene is involved in ocular development or function and/or mutation of which causes or is a risk factor to cause an ocular disease.

10

200. The composition of claim 194, wherein the gene is involved in neuronal development or function and/or mutation of which causes or is a risk factor to cause a neurodegenerative disease.

15

201. The composition of claim 194, wherein the gene is a cytochrome P450 gene.

202. The composition of claim 194, wherein the gene is one set forth in Table 4.

203. The composition of claim 194, wherein the gene comprises a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene or a CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B,

25
30

RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 or CYP46A gene that encodes a protein having defective or partial function or activity.

5

204. The composition of any of the preceding claims, wherein the cell differentiated from a stem cell is any type of cell.

205. The composition of any of the preceding claims, wherein the cell differentiated from a stem cell is an ocular cell.

10

206. The composition of any of the preceding claims, wherein the cell differentiated from a stem cell is an RPE cell, a PRC, a retinal cell, a corneal cell, a choroidal cell, a CEC, a CE cell or an optic nerve cell.

15

207. The composition of any of the preceding claims, wherein the cell differentiated from a stem cell is an iPS-RPE, iPS-PRC, iPS-CEC or iPS-CE cell.

20

208. The composition of any of the preceding claims, wherein the cell differentiated from a stem cell is a neuron.

25

209. The composition of any of the preceding claims, wherein (i) the cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity for use to reprogram into an iPSC, (ii) the stem cell isolated from a subject or iPS cell reprogrammed from a cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity, or (iii) the cell differentiated from a stem cell isolated from a subject or an iPS cell reprogrammed from a cell isolated from a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial

function or activity, is genetically repaired to ameliorate the effect of the mutated or defective gene.

210. The composition of any of the preceding claims, wherein genetic repair is via gene transfer therapy.

211. The composition of any of the preceding claims, wherein genetic repair is via gene transfer therapy by using any composition or method of any one of the claims related to gene therapy.

212. The composition of any of the preceding claims, wherein genetic repair is via gene editing therapy.

213. The composition of any of the preceding claims, wherein genetic repair is via gene editing therapy by using any composition or method of any one of the claims related to CRISPR gene editing therapy.

214. A method of treating or preventing a disease in a subject affected by a disease caused by a mutated or defective gene or a gene encoding a protein having defective or partial function or activity set forth in Table 4, the method comprising administering a cellular composition of any one of the claims related to an autologous cell composition to the subject, wherein the cellular composition comprises: genetically repaired cells comprising retinal pigment epithelium (RPE) cells, photoreceptors or photoreceptor progenitors (PRCs), corneal epithelial cells (CECs), neurons, choroidal endothelial (CE) cells and/or other ocular cells or other cells derived from a stem cell of the subject, and wherein the mutated or defective gene in the cellular composition has been genetically repaired.

215. A method of autologously treating a subject, comprising:
(i) providing cells from a subject having a disease of the eye;
(ii) inducing pluripotency in the cells from the subject to produce iPSCs;

(iii) genetically repairing one or more mutations in a mutated or defective gene set forth in Table 4 in the iPSCs derived from the subject via gene editing therapy;

(iv) differentiating the iPSCs into ocular cells or other cells as needed for replacement transplantation;

5 (v) alternative to step (iii), genetically repair the iPS-derived cells via gene transfer therapy; and

(vi) introducing the iPS-derived cells into the subject, thereby autologously treating the subject having the disease associated with a mutated or defective gene (the "target gene").

10 216. The method of claim 214 or 215, wherein the stem cell is an iPC cell, an MSC, an adult stem cell or a tissue-specific stem cell.

217. The method of claim 216, wherein the iPS cell is reprogrammed using one or more of the OCT4, SOX2, KLF4, and c-MYC transcription factors.

15

218. The method of claim 214 or 215, wherein the genetically repaired cells demonstrate one or more of the following: an increase in non-defective target gene nucleic acid sequence in the cells; an increase in the amount of functional polypeptides encoded by the target gene in the cells; ; improved cell structure, morphology, viability or function, and/or improved or
20 normalized biochemical functions in the cells, as compared to before genetic repair is performed.

219. The method of any of the preceding claims, wherein the amount of cells administered is about 1,000 to about 10 million cells in a single administration.

25 220. The method of any of the preceding claims, wherein the administration is via injection, sub-retinal injection, or intravitreal injection, .

221. The method of any of the preceding claims, wherein the administration is by any other administration method that effectively delivers the cells to the sub-retinal place, the

posterior segment, or the cornea of the eye of the subject, or the tissue or organ in need of the replacement cells.

222. The method of any of the preceding claims, wherein the cells are administered via
5 injection of cell suspension.

223. The method of any of the preceding claims, wherein the cells are administered as part of a sheet, a matrix, a scaffold, a tissue or a 3D retinal structure.

10 224. The method of any of the preceding claims, whereas the RPE cells are administered using natural and/or synthetic scaffolds to generate a functional RPE monolayer.

225. The method of any of the preceding claims, wherein the subject is a human subject.

15 226. The method of any of the preceding claims, wherein the disease is associated with a genetic or epigenetic alteration or risk factor in the subject in a gene set forth in Table 4.

227. The method of any of the preceding claims, wherein the disease is photoreceptor degeneration, retinal pigment epithelium cell degeneration, retinal degeneration, cornea
20 degeneration, and/or choroidal disorders.

228. The method of any of the preceding claims, wherein the disease is an inherited retinal degeneration (IRD).

25 229. The method of any of the preceding claims, wherein the disease is retinitis pigmentosa (RP).

230. The method of any of the preceding claims, wherein the disease is Bietti Crystalline Dystrophy (also known as Bietti Crystalline Corneoretinal Dystrophy; BCD).

30

231. The method of any of the preceding claims, wherein the disease is related to neurological degeneration.

5 232. The method of any of the preceding claims, wherein the disease is corneal dystrophy.

233. The method of any of the preceding claims, wherein the subject has BCD or is at risk of developing BCD.

10 234. The composition of any of the preceding claims, wherein the cells are fibroblasts, blood cells, or ocular cells.

235. The composition of any of the preceding claims, wherein the cells are obtained from urine or from hair or hair follicles.

15

236. The composition of any of the preceding claims, wherein the ocular cells are retinal pigment epithelial (RPE) cells, corneal epithelial cells (CECs), choroidal endothelial (CE) cells, or photoreceptor cells (PRCs).

20 237. The composition of any of the preceding claims, wherein the genetic or epigenetic alteration is selected from the group consisting of a mutation, an insertion, a single nucleotide polymorphism, improper methylation, improper demethylation, and combinations thereof.

25 238. The composition of any of the preceding claims, wherein the genetic or epigenetic alteration is a mutation.

239. The composition of any of the preceding claims, wherein the genetic or epigenetic alteration in the iPS-ocular cells from the subject has been genetically repaired using gene editing therapy.

30

240. The composition of any of the preceding claims, wherein the gene editing therapy method utilizes a zinc-finger nuclease, TALEN technology, or CRISPR technology.

241. The composition of any of the preceding claims, wherein the genetic or epigenetic alteration in the iPSC-ocular cells from the subject has been genetically repaired using gene transfer therapy.

242. The composition of any of the preceding claims, wherein the gene transfer therapy method utilizes a recombinant AAV vector or another viral vector or non-viral vector to deliver a healthy copy of the target gene (e.g., cDNA) to the cells to be transplanted.

243. The method of any of the preceding claims, wherein the administering step takes place before the onset of disease symptoms or after the onset of disease symptoms.

244. The method of any of the preceding claims, wherein the administration is to the eye or to another organ or tissue comprising neurons.

245. The method of any of the preceding claims, wherein the administration is by injection, sub-retinal or intravitreal injection, direct retinal injection, or.

246. The method of any of the preceding claims, wherein the administration is by any other administration method that effectively delivers the cells to the sub-retinal place, the posterior segment, or the cornea of the eye of the subject, or to the tissue or organ in need of replacement cells.

247. The method of any of the preceding claims, further comprising, prior to administering or transplanting, performing genotypic analysis on the cells to identify the presence or absence of the genetic or epigenetic alteration in one or more genes set forth in Table 4.

30

248. The method of any of the preceding claims, wherein the genetic or epigenetic alteration is a mutation.

249. The method of any of the preceding claims, wherein the mutation is in the CYP4V2 nucleic acid molecule.

250. The method of any of the preceding claims, further comprising, prior to administering, evaluating the eye of the subject to identify the area(s) and extent of damaged or retained photoreceptors, retinal cells, or corneal cells.

10

251. The method of any of the preceding claims, further comprising, following administering, monitoring the subject.

252. The method of any of the preceding claims, wherein the monitoring comprises performing non-invasive retinal imaging, corneal tests, dark adaptation, contrast sensitivity, perimetry, ERG, OCT, visual acuity tests, and/or functional studies.

15

253. The method of any of the preceding claims, wherein the monitoring comprises evaluating the subject for an immune response.

20

254. The method of any of the preceding claims, further comprising, following administering, evaluating the eye of the subject to identify the area(s) and extent of damaged or retained photoreceptors, retinal cells, or corneal cells.

255. A composition comprising: (a) a CRISPR guide RNA targeting a nucleic acid sequence (the "target sequence") of or within 100 bps to a target gene (the "target gene"), and (b) a functional CRISPR-associated protein, in a ribonucleoprotein (RNP) or protein-RNA complex.

25

256. The composition of claims 255, further comprising (c) a donor nucleic acid sequence comprising all or a portion of a wild-type sequence or a functional sequence of the target gene for correction or replacement of such target gene or a portion thereof.

5 257. A composition of claim 255 or 256, wherein the target gene is involved in ocular development or function and/or mutation of which causes or is a risk factor to cause an ocular disease.

10 258. A composition of claim 255 or 256, wherein the target gene is involved in neuronal development or function and/or mutation of which causes or is a risk factor to cause a neurodegenerative disease.

15 259. A composition of claim 255 or 256, wherein the target gene is a cytochrome P450 gene.

20 260. The composition of claim 255 or 256, wherein the target gene comprises a gene set forth in Table 4 that is mutated or defective, or encodes a protein having defective or partial function or activity.

25 261. The composition of claim 256, wherein the donor nucleic acid sequence is provided in a single-stranded donor oligonucleotide (ssODN) or a vector.

30 262. The composition of any one of claims 255-261, wherein (a) the CRISPR guide RNA comprising (i) a CRISPR RNA (crRNA) which comprises a protospacer element sequence that is complementary to the target sequence of or within 100 bps to a target gene and a sequence that corresponds to a complementary region of the trans-activating crRNA (tracrRNA), and (ii) a tracrRNA which comprises a region that is complementary to corresponding region of the crRNA and a sequence which interacts with a CRISPR-associated protein 9 (Cas9), and (b) the functional CRISPR-associated protein comprises Cas9.

263. The composition of claim 261 or 262, wherein the crRNA and the tracrRNA are in different nucleic acid molecules.

264. The composition of claim 261 or 262, wherein the crRNA and the tracrRNA are
5 combined in a single guide RNA (sgRNA).

265. The composition of any one of claims 261-264, wherein the Cas9 comprises a Cas9 ortholog or a mutant Cas9 selected from: *Streptococcus pyogenes* (SpCas9), SpCas9 nickase (Cas9n D10A), SpCas9 (D1135E), eSpCas9, SpCas9-HF1, SpCas9 VRER, SpCas9 VQR,
10 SpCas9EQR, *Staphylococcus aureus* (SaCas9), *Neisseria Meningitidis*, *Streptococcus thermophilus*, *Streptococcus pneumoniae*, *Campylobacter coli*, *Campylobacter jejuni*, *Streptococcus mutans*, *Pasteurella multocida*, *Bifidobacterium longum*, *Bacillus smithii*, *Treponema denticola*, *mycoplasma canis* and *enterococcus faecalis*.

15 266. The composition of any one of claims 255-265, wherein (a) the CRISPR guide RNA comprises a crRNA which comprises a protospacer element sequence that is complementary to the target sequence of or within 100 bps to a target gene, and (b) the functional CRISPR-associated protein comprises Cpf1.

20 267. The composition of any one of claims 255-266, wherein the CRISPR-associated protein, Cas9, or Cpf1, further comprises one, two, three or more nuclear localization sequences (NLS) at the N-terminal and/or C-terminal, and/or a selection marker, including without limitation, GFP or EGFP.

25 268. The composition of any one of claims 255-267, wherein the protospacer element is 100% complementary to the target sequence or contains 1, 2, 3, 4, or 5 nucleotide mismatches corresponding to the target sequence.

269. The composition of claim 255 or 256, wherein the crRNA sequence further comprises a G nucleotide optionally added to the crRNA sequence immediately before the protospacer element.

5 270. The composition of any one of claims 255-269, wherein the CRISPR guide RNA, crRNA and/or the tracrRNA, or the sgRNA, is chemically modified.

 271. The composition of any one of claims 255-270, wherein the wild-type version of the target gene encodes an enzyme.

10

 272. The composition of claim 255 or 256, wherein the target gene comprises a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene or a CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1, RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1 or CYP46A gene that encodes a protein having defective or partial function or activity.

15
20
25

 273. The composition of any one of claims 255-272, wherein any one or more components thereof including the CRISPR guide RNA, CRISPR-associated protein, and/or the donor nucleic acid sequence, is provided separately and/or additionally in a vector, a DNA and/or an mRNA which can transcribe and/or translate into such component.

30

274. A pharmaceutically acceptable formulation comprising the composition of claim 255 or 273.

5 275. A method of treating a disease of a subject caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity, comprising administering to the subject a composition of any one of claims 255-274.

10 276. A method of treating an ocular disease or ameliorating a risk factor related thereto of a subject caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity, comprising administering to the subject a composition of any one of claims 255-274.

15 277. A method of treating a neurodegenerative disease or ameliorating a risk factor related thereto of a subject caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity, comprising administering to the subject a composition of any one of claims 255, 256, or 258-276.

20 278. A method of treating a disease or ameliorating a risk factor related thereto of a subject caused by a mutated or defective cytochrome P450 gene, or a cytochrome P450 gene encoding a protein having defective or partial function or activity, comprising administering to the subject a composition of any one of claims 255-277.

25 279. The method of claim 278, wherein the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, disrupted, corrected or replaced is a mutated or defective version of a gene set forth in Table 4, or a version of a gene set forth in Table 4 that encodes a protein having defective or partial function or activity.

30 280. The method of claim 278, wherein the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is present in fibroblasts, blood, RPE,

photoreceptor, retinal, corneal, choroidal, ocular, optic nerve, neuron, or stem cells, or any type of cells derived from a stem cell.

281. The method of claim 278 or 279, wherein the composition therein is delivered to
5 fibroblasts, blood, RPE, photoreceptor, retinal, corneal, choroidal, ocular, optic nerve, neuron, or stem cells, or any type of cells derived from a stem cell.

282. The method of claim 281, wherein delivery is performed by electroporation or via
lipid-mediated transfection, or nucleofection, or viral transduction, or injection or a combination
10 thereof.

283. The method of any one of claims 278-282, wherein any one or more components
thereof including the CRISPR guide RNA, CRISPR-associated protein, and/or the donor nucleic
acid sequence is administered to the subject or to the cells via a delivery system selected from
15 the group consisting of a ribonucleoprotein or protein-RNA complex, a nanoparticle, a liposome, a micelle, a virosome, a nucleic acid complex, and/or a combination thereof.

284. The method of any one of claims 278-283, wherein the treatment is performed to a
subject *in vivo*.
20

285. The method of any one of claims 278-283, wherein the treatment is performed *in vitro* in fibroblasts, blood, RPE, photoreceptor, retinal, corneal, choroidal, ocular, optic nerve, neuron, or stem cells, or any type of cells derived from a stem cell.

286. The method of claim 285, wherein the treated cells are transplanted to a subject *in vivo*, or if the treated cell is a stem cell, such stem cell is differentiated into the desired type of cells for transplantation and then the differentiated cells are transplanted into a subject *in vivo*. .
25

287. The method of any one of claims 278-280, wherein the mutated or defective gene,
30 or gene encoding a protein having defective or partial function or activity, is replaced.

288. The method any one of claims 278-280, wherein the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, has one or more mutations corrected or replaced.

5

289. The method of any one of claims 278-280, wherein the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted.

290. The method of any one of claims 278-280, wherein the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, has 1-20, 21-40, 41-60, 61-80, 81-100, 101-1000, 1001-10000 base pairs of nucleotides or mutations disrupted, corrected or replaced.

291. The method of any one of claims 278-280, wherein a region of the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced.

292. The method of any one of claims 278-280, wherein a region of less than about 10, 8, 6, 4, 2 or 1 kb of the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced.

293. The method of any one of claims 278-280, wherein the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced via insertion and/or deletion of nucleotides.

25

294. The method of any one of claims 278-280, wherein the mutated or defective gene, or gene encoding a protein having defective or partial function or activity, is disrupted, corrected or replaced in one allele or both alleles.

295. The method of any one of claims 278-280, wherein two or more different CRISPR guide RNAs, CRISPR-associated proteins and/or donor nucleic acid sequences are used to disrupt, correct or replace one or more mutations or defects in the mutated or defective gene, or gene encoding a protein having defective or partial function.

5

296. The method of claim 278, wherein the subject is a mammal.

297. The method of claim 278, wherein the subject is a human.

10

298. The method of claim 278, wherein the method improves ocular development or function, or prevents ocular, retinal or corneal degeneration.

299. The method of claim 278, wherein the method improves neurological development or function, or prevents neural degeneration.

15

300. The method of claim 278, wherein the method improves expression or function of a P450 enzyme.

301. The composition of any one of claims 255, 257, 258 or 259, further comprising (c) a donor nucleic acid sequence comprising all or a portion of a target gene set forth in Table 4 with a mutation or alteration for generation of a mutated or altered target gene or a portion thereof.

20

302. A composition comprising a cell with a mutated or defective gene set forth in Table 4.

25

303. A composition comprising a cell with a mutated or defective CYP4V2, CYP1B1, MYO7A, DFNB31, USH1C, USH1G, CDH23, PCDH15, CLRN1, ACO2, AFG3L2, ATXN2, AUH, C12orf65, CISD2, FOXC1, FOXF2, LTBP2, MTPAP, MYOC, NDUFS1, NR2F1, OPA1, OPA3, OPTN, PAX6, PDGF, PITX2, POLG, SPG7, TEK, TXNRD2, WFS1, ABCA4, REP-1,

30

RPE65, CEP290, PDE6B, RPGR, MERTK, MT-ND4, FAM47E, GBA, GCH1, HTRA2, LRRK2, PARK2, PINK1, SNCA, SYNJ1, NPC1, NPC2, CYP4A11, CYP4A22, CYP4B1, CYP4F2, CYP4F3, CYP4F8, CYP4F11, CYP4F12, CYP4F22, CYP4X1, CYP4Z1, or CYP46A gene comprising a composition of any one of the claims herein

5

304. The composition of claim 303, wherein the vector is an AAV vector.

305. The composition of any of the preceding claims, wherein the protospacer element sequence is selected from the group consisting of SEQ ID NOs: 48 to 52, or shares at least 80% sequence identity with one of SEQ ID NO: 48 to 52 for use with a Cas protein that has NGG as protospacer adjacent motif (PAM) to target the c.802-8_810del17insGC mutation of the CYP4V2 gene.

306. The composition of any of the preceding claims, wherein the donor nucleic acid sequence is selected from SEQ ID NOs: 56 and 57, or shares at least 90% sequence identity with one of SEQ ID NO: 56 and 57, or a sequence that is complementary thereof, for use to correct, disrupt or replace the c.802-8_810del17insGC mutation of the CYP4V2 gene.

307. A method of treating a disease of a subject caused by a mutated or defective gene, or a gene encoding a protein having defective or partial function or activity, comprising administering to the subject a combination of (i) a composition targeting the existing diseased cells in the subject comprising a gene editing therapy composition or a gene transfer therapy composition, and (ii) a cellular composition comprising replacement cells.

308. The method of claim 307, wherein the subject is a human

309. The method of claim 307, wherein the disease causes degeneration in the subject's cells.

310. The method of claim 307 and 308, wherein the degeneration occurs in an RPE cells, a RPC, a CEC, a CE cell, a retinal cell, a corneal cell, a choroid cell, an optic-nerve cell, an ocular cell, a neuron, a neuronal cell, a brain cell, a liver cell, a lung cell and a cardiac cell.

5 311. The method of claim 307, wherein the disease is caused by a gene set forth in Table 4.

312. The method of claim 307, wherein the gene editing therapy composition is a composition of any of the gene editing therapy claims herein.

10

313. The method of claim 307, wherein the gene transfer therapy composition is a composition of any of the gene transfer therapy claims herein.

314. The method of claim 307, wherein the cellular composition comprises a composition of any of the cell therapy claims or the autologous cell therapy claims herein.

15

315. The method of claim 307, wherein the cellular composition is allogenic to the subject being treated.

20 316. The method of claim 307, wherein the cellular composition is autologous to the subject being treated.

317. The method of claim 307 or 314, wherein the cellular composition is genetically repaired prior to administration to the subject.

25

318. The method of claim 307 or 317, wherein the genetic repair is via gene editing therapy.

319. The method of claim 307 or 318, wherein the gene editing therapy is via any of the claims in the gene editing therapy claims herein.

30

320. The method of claim 307, 318 or 319, wherein the gene editing therapy is via any of the CRISPR RNP claims herein.

5 321. The method of claim 307 or 317, wherein the genetic repair is via gene transfer therapy.

322. The method of claim 307 or 321, wherein the gene transfer therapy is via any of gene transfer therapy or gene therapy claims herein.

10

323. The method of claim 307, wherein the compositions of (i) and (ii) are administered in a single administration.

324. The method of claim 307, wherein the compositions of (i) and (ii) are administered separately or in separate administrations.

15

325. The method of claim 307, wherein the replacement cells are derived from a stem cell.

20 326. The method of claim 307 and 325, wherein the replacement cells are derived from an iPS cell.

327. The method of claim 307 or 326, wherein the iPS cell is derived from the same subject being treated.

25

328. The method of claim 307 or 326, wherein the replacement cell is an iPS-RPE, iPS-PRC, iPS-CEC or iPS-CE cell.

329. The method of claim 307 or 326, wherein the replacement cell is an iPS-ocular cell.

30

330. The method of claim 307 or 326, wherein the replacement cell is an iPS-neuron cell.

331. The method of claim 307, wherein the method improves ocular development or function, or prevents ocular, retinal or corneal degeneration in the subject.

5

332. The method of claim 307, wherein the method improves neurological development or function, or prevents neural degeneration in the subject.

333. The method of claim 307, wherein the method improves expression or function of a
10 P450 enzyme in the subject.

334. The method of any of claims 307-332, wherein the subject has suffered from ocular, retinal, corneal, choroidal or neuronal degenerations.

SEQUENCESLIST OF SEQUENCES

* All reference numbers used in the sequences are NCBI reference numbers unless otherwise annotated.

Part I: Gene Therapy Sequences

A. cDNA and functional CYP4V2 protein sequences

- SEQ ID NO:1 - a cDNA sequence (1578 bp) encoding the human CYP4V2 protein (SEQ ID NO:4), referred to as CYP4V2st herein.
- SEQ ID NO:2 - a codon-optimized cDNA sequence (1578 bp) encoding the human CYP4V2 protein (SEQ ID NO:4), referred to as CYP4V2op herein.
- SEQ ID NO:3 - a cDNA sequence (1578 bp) encoding a functional CYP4V2 protein (SEQ ID NO:5), referred to as CYP4V2fv herein.
- SEQ ID NO:4 - amino acid sequence (525 aa) of the human CYP4V2 protein (NP_997235.3)
- SEQ ID NO:5 - amino acid sequence (525 aa) of a functional variant of the human CYP4V2 protein
- SEQ ID NO:6 - fragment of human CYP4V2 protein without transmembrane domain (490 aa)
- SEQ ID NO:7 - amino acid sequence of human CYP46A1
- SEQ ID NO:8 - amino acid sequence of human CYP4A11
- SEQ ID NO:9 - amino acid sequence of human CYP4A22
- SEQ ID NO:10 - amino acid sequence of human CYP4B1
- SEQ ID NO:11 - amino acid sequence of human CYP4F2
- SEQ ID NO:12 - amino acid sequence of human CYP4F3
- SEQ ID NO:13 - amino acid sequence of human CYP4F8
- SEQ ID NO:14 - amino acid sequence of human CYP4F11
- SEQ ID NO:15 - amino acid sequence of human CYP4F12
- SEQ ID NO:16 - amino acid sequence of human CYP4F22
- SEQ ID NO:17 - amino acid sequence of human CYP4X1
- SEQ ID NO:18 - amino acid sequence of human CYP4Z1
- SEQ ID NO:19 - amino acid sequence of CYP4V2 chimpanzee
- SEQ ID NO:20 - amino acid sequence of CYP4V2 Rhesus Monkey
- SEQ ID NO:21 - amino acid sequence of CYP4V2 dog
- SEQ ID NO:22 - amino acid sequence of CYP4V2 cattle
- SEQ ID NO:23 - amino acid sequence of CYP4V2 house mouse
- SEQ ID NO:24 - amino acid sequence of CYP4V2 Norway rat
- SEQ ID NO:25 - amino acid sequence of CYP4V2 chicken
- SEQ ID NO:26 - amino acid sequence of CYP4V2 tropical clawed frog
- SEQ ID NO:27 - amino acid sequence of CYP4V2 horse
- SEQ ID NO:28 - amino acid sequence of CYP4V2 rabbit
- SEQ ID NO:29 - amino acid sequence of CYP4V2 fruit fly
- SEQ ID NO:30 - P450 signature element sequence
- SEQ ID NO:31 - P450 signature element sequence

B. Exemplary regulatory sequences and ITR sequences

- SEQ ID NO:32 - CAG promoter sequence
- SEQ ID NO:33 - WPRE enhance sequence

- SEQ ID NO:34 - bGH PolyA sequence
 SEQ ID NO:35 - EFS promoter sequence
 SEQ ID NO:36 - small polyA (SPA) sequence
 SEQ ID NO:37 - Kozak sequence
 5 SEQ ID NO:38 - Kozak sequence
 SEQ ID NO:39 - SV40 late PolyA sequence
 SEQ ID NO:40 - CMV promoter sequence
 SEQ ID NO:41 - EF-1 alpha promoter sequence
 SEQ ID NO:42 - AAV2 5' Left-ITR sequence
 10 SEQ ID NO:43 - AAV2 3' Right-ITR sequence
 SEQ ID NO:44 - mutant AAV2 5' ITR sequence used in scAAV
 SEQ ID NO:45 - AAV2 3' ITR sequence used in scAAV
- Part II. Cell Therapy Sequences
- 15 SEQ ID NO:46 - region of human CYP4V2 gene containing c.802-8_810del17insGC mutation
 SEQ ID NO:47 - region of wild-type human CYP4V2 gene without the c.802-8_810del17insGC mutation
 SEQ ID NO:48 - gRNA 1
 20 SEQ ID NO:49 - gRNA 2
 SEQ ID NO:50 - gRNA 3
 SEQ ID NO:51 - gRNA 4
 SEQ ID NO:52 - gRNA 5
 SEQ ID NO:53 - crRNA exemplary sequence
 25 SEQ ID NO:54 - tracrRNA exemplary sequence
 SEQ ID NO:55 - sgRNA exemplary sequence
 SEQ ID NO:56 - donor template 1 sequence
 SEQ ID NO:57 - donor template 2 sequence
 SEQ ID NO:58 - SpCas9 amino acid sequence
 30 SEQ ID NO:59 - additional nucleotide inserted immediately after the U6 promoter sequence and before the protospacer element sequence in a plasmid construct and in an IVT sgRNA
- 35
- Part III: CYP4V2 Expression Cassette Sequences (inclusive of AAV ITRs and junction/linker sequences).
 SEQ ID NO: 60 - Sequence of CYP4V2 expression cassette in AAV2.CYP4V2op, AAV2tri(Y-F).CYP4V2op, and AAV5.CYP4V2op.
 40 SEQ ID NO: 61 - Sequence of CYP4V2 expression cassette in AAV5.CYP4V2st. AAV5.CYP4V2st has the same promoter (CAG), enhancer (WPRe) and polyA (bGH-polyA) as AAV2.CYP4V2op, AAV2tri(Y-F).CYP4V2op and AAV5.CYP4V2op (SEQ ID NO: 60) but different CYP4V2 cDNA and junction/linker sequences.
 45 SEQ ID NO: 62 - Sequence of CYP4V2 expression cassette in AAV8.CYP4V2fv. AAV8.CYP4V2fv has the same promoter (CAG), enhancer (WPRe) and polyA (bGH-polyA) and junction/linker sequences as AAV5.CYP4V2st (SEQ ID NO: 61) and differs only in CYP4V2 cDNA sequence.

- SEQ ID NO: 63 - Sequence of CYP4V2 expression cassette in AAV5.CYP4V2op (new). AAV5.CYP4V2op (new) has the same promoter (CAG), enhancer (WPRE) and polyA (bGH-polyA) and the same junction/linker sequences as AAV5.CYP4V2st (SEQ ID NO: 61) and AAV8.CYP4V2fv (SEQ ID NO: 62) but different CYP4V2 cDNA sequences.
- 5 SEQ ID NO: 64 - Sequence of CYP4V2 expression cassette in scAAV1.CYP4V2op, scAAV5.CYP4V2op, and scAAV9.CYP4V2op.

10 SEQUENCES

- SEQ ID NO: 1 (CYP4V2st cDNA, 1578 bp)
- 15 ATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAACTGCTGCTGTGGGGCGCGGGCAGTGCCCTTTCCC
TGGCGGGCGCCAGTCTGGTCTGAGCCTGCTGCAGAGGGTGGCGAGCTACGCGCGGAAATGGCAGCAGAT
CGGGCCCATCCCCACGGTGGCCCCGCGCCTACCCACTGGTGGGCCACGCGCTGCTGATGAAGCCGGACGGG
CGAGAATTTTTTTCAGCAGATCATTGAGTACACAGAGGAATACCGCCACATGCCGCTGCTGAAGCTCTGGG
TCGGGCCAGTGCCCATGGTGGCCCTTTATAATGCAGAAAATGTGGAGGTAATTTTAAGTACTTCAAAGCA
AATTGACAAATCCTCTATGTACAAGTTTTTAGAACCATGGCTTGGCCTAGGACTTCTTACAAGTACTGGA
AACAAATGGCGCTCCAGGAGAAAGATGTTAACACCCACTTCCATTTTACCATTCTGGAAGATTTCTTAG
20 ATATCATGAATGAACAAGCAAATATATTGGTTAAGAACTTGAAAAACACATTAACCAAGAAGCATTATA
CTGCTTTTTTTTACATCACTCTTTGTGCCTTAGATATCATCTGTGAAACAGCTATGGGGAAGAATATTGGT
GCTCAAAGTAATGATGATTCCGAGTATGTCCGTGCAGTTTATAGAATGAGTGAGATGATATTTCAAGAA
TAAAGATGCCCTGGCTTTGGCTTGATCTCTGGTACCTTATGTTTAAAGAAGGATGGGAACACAAAAAGAG
CCTTCAGATCCTACATACTTTTACCAACAGTGTTCATCGCTGAACGGGCCAATGAAATGAACGCCAATGAA
25 GACTGTAGAGGTGATGGCAGGGGCTCTGCCCCCTCCAAAAATAAACGCAGGGCCTTTCTTGACTTGCTTT
TAAGTGTGACTGATGACGAAGGGAACAGGCTAAGTCATGAAGATATTCGAGAAGAAGTTGACACCTTCAT
GTTTGAGGGGCACGATACAACTGCAGCTGCAATAAACTGGTCTTATACCTGTTGGGTCTAACCCAGAA
GTCCAGAAAAAAGTGGATCATGAATTGGATGACGTGTTGGGAAGTCTGACCGTCCCGCTACAGTAGAAG
ACCTGAAGAACTTCGGTATCTGGAATGTGTTATTAAGGAGACCCTTCGCCTTTTTCTTCTGTTCTCTTT
30 ATTTGCCCCGTAGTGTTAGTGAAGATTGTGAAGTGGCAGGTTACAGAGTTCTAAAAGGCACTGAAGCCGTC
ATCATTCCCTATGCATTGCACAGAGATCCGAGATACTTCCCCAACCCCGAGGAGTTCCAGCCTGAGCGGT
TCTTCCCCGAGAAATGCACAAGGGCGCCATCCATATGCCCTACGTGCCCTTCTCTGTGGCCCCAGGAACGT
TATAGGTCAAAAGTTTGCTGTGATGGAAGAAAAGACCATTCTTTCGTGCATCCTGAGGCACTTTTGATA
GAATCCAACCAGAAAAGAGAAGAGCTTGGTCTAGAAGGACAGTTGATTCTTCGTCCAAGTAATGGCATCT
35 GGATCAAGTTGAAGAGGAGAAATGCAGATGAACGCTAA

- SEQ ID NO: 2 (CYP4V2op cDNA, 1578 bp)
- 40 ATGGCTGGACTGTGGCTGGGACTGGTGTGGCAGAACTGCTGCTGTGGGGGGCCGCTTCCGCACTGTCAC
TGGCTGGGGCTTCACTGGTGCTGAGCCTGCTGCAGAGGGTGGCCTCCTACGCCAGAAAGTGGCAGCAGAT
GAGGCCCCATCCCTACCGTGGCCAGAGCCTATCCACTGGTGGGACACGCACTGCTGATGAAGCCTGACGGC
AGAGAGTTCTTTTCAGCAGATCATCGAGTACACAGAGGAGTATAGGCACATGCCACTGCTGAAGCTGTGGG
TGGGACCCGTGCCTATGGTGGCCCTGTACAACGCCGAGAATGTGGAAGTGATCCTGACCAGCAGCAAGCA
GATCGATAAGTCTAGCATGTATAAGTTCTTGAGCCTTGGCTGGGCCTGGGCCTGCTGACCTCTACAGGC
AACAAGTGGAGGAGCCGAGAAAGATGCTGACCCCAACATTCCACTTTACAATCCTGGAGGACTTCTTG
45 ACATCATGAACGAGCAGGCAATATCCTGGTGAAGAAGCTGGAGAAGCACATCAACCAGGAGGCCTTTAA
TTGCTTCTTTTACATCACCTGTGCGCCCTGGACATCATCTGTGAGACAGCTATGGGCAAGAACATCGGC
GCCAGTCTAATGACGATAGCGAGTACGTGCGGGCCGTGTATAGAATGAGCGAGATGATCTTTAGGCGCA
TCAAGATGCCCTGGCTGTGGCTGGATCTGTGGTATCTGATGTTCAAGGAGGGCTGGGAGCACAAGAAGTC
CCTGCAGATCCTGCACACCTTTACAACTCTGTGATCGCCGAGAGAGCAATGAGATGAACGCCAATGAG
50 GACTGTAGGGCGATGGAAGGGGCAGCGCCCTTCCAAGAACAAGCGGAGAGCCTTCTTGACCTGCTGC

TGAGCGTGACCGACGATGAGGGCAATCGCCTGTCCCACGAGGACATCCGGGAGGAGGTGGATACATTCAT
GTTTGAGGGACACGACACCACAGCCGCCGCCATCAACTGGTCCCTGTACCTGCTGGGCTCTAATCCAGAG
GTGCAGAAGAAGGTGGATCACGAGCTGGACGACGTGTTCCGGCAAGTCCGACAGGCCAGCAACCGTGGAGG
ATCTGAAGAAGCTGAGATACCTGGAGTGCCTGATCAAGGAGACACTGCGCCTGTTCCTCTGTGCCTCT
5 GTTTGCCCCGTCCGTGTCTGAGGACTGTGAGGTGGCCGGCTATCGCGTGCTGAAGGGACCCGAGGCCGTG
ATCATCCCTTACGCCCTGCACCGGGACCCAGGTATTTCCCTAACCAGAGGAGTTTCAGCCAGAGAGAT
TCTTTCCCGAGAATGCCAGGGCAGGCACCTTACGCCTATGTGCCATTCTCCGCCGACCAAGGAAGT
CATCGACAGAAGTTTGGCGTGATGGAGGAGAAAACCATCTGTCTTGTATCCTGAGACACTTCTGGATC
GAGAGCAATCAGAAGAGGGAGGAGCTGGGCCTGGAGGGACAGCTGATCCTGCGGCCAAGCAACGGCATCT
10 GGATCAAACCTGAAAAGAAGAACGCTGACGAGAGGTAA

SEQ ID NO: 3 (CYP4V2fv cDNA, 1578 bp)
ATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCGCGGCGAGTGCCCTTTCCC
TGCCCGGCGCCAGTCTGGTCTGAGCCTGCTGCAGAGGTGGCGAGCTACGCGCGGAAATGGCAGCAGAT
15 GCGGCCCATCCCCACGGTGGCCCCGCGCCTACCCACTGGTGGGCCACGCGCTGCTGATGAAGCCGGACGGG
CGAGAATTTTTTTCAGCAGATCATTGAGTACACAGAGGAATACCGCCACATGCCGCTGCTGAAGCTCTGGG
TCGGGCCAGTGCCCATGGTGGCCCTTTATAATGCAGAAAATGTGGAGGTAATTTTAACTAGTTCAAAGCA
AATTGACAAATCCTCTATGTACAAGTTTTTAGAACCATGGCTTGGCCTAGGACTTCTTACAAGTACTGGA
AACAAATGGCGCTCCAGGAGAAAGATGTTAACACCCACTTTCCATTTTACCATTCTGGAAGATTTCTTAG
20 ATATCATGAATGAACAAGCAAATATATTGGTTAAGAACTTGAAAAACACATTAACCAAGAAGCATTTAA
CTGCTTTTTTTTACATCACTCTTTGTGCCTTAGATATCATCTGTGAAACAGCTATGGGGAAGAATATTGGT
GCTCAAAGTAATGATGATTCCGAGTATGTCCGTGCAGTTTATAGAATGAGTGAGATGATATTTCAAGAA
TAAAGATGCCCTGGCTTTGGCTTGATCTCTGGTACCTTATGTTTAAAGAAGGATGGGAACACAAAAAGAG
CCTTAAGATCCTACATACTTTTACCAACAGTGTCTATCGCGGAACGGGCAATGAAATGAACGCCAATGAA
25 GACTGTAGAGGTGATGGCAGGGGCTCTGCCCCCTCCAAAAATAAACGCAGGGCCTTTCTTGACTTGCTTT
TAAGTGTGACTGATGACGAAGGGAACAGGCTAAGTCATGAAGATATTCGAGAAGAAGTTGACACCTTCAT
GTTTGAGGGGCACGATACAACTGCAGCTGCAATAAACTGGTCTTATACCTGTTGGGTCTAATCCAGAA
GTCCAGAAAAAAGTGGATCATGAATTGGATGACGTGTTTGGGAAGTCTGACCGTCCCGCTACAGTAGAAG
ACCTGAAGAACTTCGGTATCTGGAATGTGTTATTAAGGAGACCCTTCGCCTTTTTCTTCTGTTTCTTT
30 ATTTGCCCGTAGTGTTAGTGAAGATTGTGAAGTGGCAGGTTACAGAGTTCTAAAAGGCACTGAAGCCGTC
ATCATTCCCTATGCATTGCACAGAGATCCGAGATACTTCCCCAACCCCGAGGAGTTCCAGCCTGAGCGGT
TCTTCCCGGAGAATGCACAAGGGCGCCATCCATATGCCTACGTGCCCTTCTCTGTGCCCCAGGAAGT
TATAGGTCAAAAGTTTGTGTGATGGAAGAAAAGACCATTCTTTCGTGCATCCTGAGGCACTTTTGGATA
GAATCCAACCAGAAAAGAGAAGAGCTTGGTCTAGAAGGACAGTTGATTCTTCGTCCAAGTAATGGCATCT
35 GGATCAAGTTGAAGAGGAGAAATGCAGATGAACGCTAA

SEQ ID NO: 4 (human CYP4V2 protein, NP_997235.3, 525 aa)
MAGLWLGLVWQKLLLWGAASALSLAGASLVLSLLQVRVASYARKWQMRPIPTVARAYPLVGHALLMKPDG
REFFQQIIIEYTEEYRHMPLLKLWVGPPVPMVALYNAENVEVILTSSKQIDKSSMYKFLEPWGLGLLLTSTG
40 NKWRSRRKMLTPTFHFTILEDFLDIMNEQANILVKKLEKHINQEAFFNYITLCALDIICETAMGKNIG
AQSNDDSEYVRVYRMSEMIFFRIKMPWLWLDLWYLMFKEGWHEHKKSLQILHTFTNSVIAERANEMNANE
DCRGDGRGSAPSKNKRRAFLDLLSVTDDEGNRLSHEDIREEVDTFMFEGHDTTAAAINWSLYLLGSNPE
VQKKVDHELDDVFGKSDRPATVEDLKKLRYLECVIKETLRLFPSPVPLFARSVSEDCVAGYRVLKGTEAV
IIPYALHRDPRYFPNPEEFQPERFFPENAQGRHPYAYVPFSAGPRNCIGQKFAVMEETILSCILRHFWI
45 ESNQKREELGLEGLILRPSNGIWIKLKRRNADER

SEQ ID NO: 5 (functional variant of human CYP4V2 protein; 525 aa)
MAGLWLGLVWQKLLLWGAASALSLAGASLVLSLLQVRVASYARKWQMRPIPTVARAYPLVGHALLMKPDG
REFFQQIIIEYTEEYRHMPLLKLWVGPPVPMVALYNAENVEVILTSSKQIDKSSMYKFLEPWGLGLLLTSTG
50 NKWRSRRKMLTPTFHFTILEDFLDIMNEQANILVKKLEKHINQEAFFNYITLCALDIICETAMGKNIG

5 AQSND DSEYVRAYRMSEMI FRRIKMPWLWLDLWYLMFKEGWEHKKSLKILHTFTNSVIAERANEMNANE
DCRGDGRGSAPSKNKRRAFLDLLLSVTDDEGNRLSHEDIREEVDTFMFEGHDTTAAAINWSLYLLGSNPE
VQKKVDHELDDVFGKSDRPATVEDLKKLRYLECVIKETLRLFPSVPLFARSVSEDCEVAGYRVLKGTEAV
IIPYALHRDPRYFPNPEEFQPERFFPENAQGRHPYAYVPFSAGPRNCIGQKFAVMEEEKTILSCILRHF
5 BSNQKREELGLEGLILRPSNGIWIKLKRRNADER

SEQ ID NO: 6 (functional fragment of CYP4V2 (lacking transmembrane domain; 490 aa)
RVASYARKWQQMRPIPTVARAYPLVGHALLMKPDGREFFQQIIEYTEEYRHMPLKLLWVGVPVPMVALYNA
10 ENVEVILTSSKQIDKSSMYKFLEPWGLGLLLTSTGNKWSRRKMLTPTFHFTILEDFLDIMNEQANILVK
KLEKHINQEA FNCFYITLCALDIICETAMGKNIGAQSNDDSEYVRAYRMSEMI FRRIKMPWLWLDLWY
LMFKEGWEHKKSLQILHTFTNSVIAERANEMNANEDCRGDGRGSAPSKNKRRAFLDLLLSVTDDEGNRLS
HEDIREEVDTFMFEGHDTTAAAINWSLYLLGSNPEVQKKVDHELDDVFGKSDRPATVEDLKKLRYLECVI
KETLRLFPSVPLFARSVSEDCEVAGYRVLKGTEAVIIPYALHRDPRYFPNPEEFQPERFFPENAQGRHPY
15 AYVPFSAGPRNCIGQKFAVMEEEKTILSCILRHFWIESNQKREELGLEGLILRPSNGIWIKLKRRNADER

SEQ ID NO: 7 (CYP46A1, NP_006659, 500 aa)
MSPGLLLLLSAVLLAFGLCCTFVHRARSRYEHI PGPPRPSFLLGHLPCFWKKDEVGGRVLQDVFLDWAKK
YGPVVRVNVFHKTSVIVTSPESVKKFLMSTKYNKDSKMYRALQTVFGERLFGQGLVSECNYERWHKQRRV
20 IDLAFSRSSLVSLMETFNEKAEQLVEILEAKADGQTPVSMQDMLTYTAMDILAKAAF GMETSMLLGAQKP
LSQAVKLMLEGITASRNTLAKFLPGKRKQLREVRESIRFLRQVGRDWVQRRREALKRGEV PADILTQIL
KAEEGAQDDEGLLDNFVTFFIAGHETSANHLAFTVMELSRQPEIVARLQAEVDEVIGSKRYLDFEDLGR
QYLSQVLKESLRLYPPAWGTFRLLEEETLIDGVRVPGNTPLLFSTYVMGRMDTYFEDPLTFNPDRFGPGA
PKPRFTYFPFSLGHRSCIGQQFAQMEVKVVMALLQRLERLVPQGQRFGLQEATLKLPLDPLVCLTLRPRG
25 WQPAPPPPPC

SEQ ID NO: 8 (CYP4A11, NP_000769, 519 aa)
msvsvlsp sr llgdvsgilq aaslllillll likavqlylh rqwllkalqq fpcppshwlf
ghiqelqqdq elqriqkwve tfpsacphwl wggkvrqvly dpdymkvilg rsdpkshgsy
30 rflapwigyg llll ngqt wf qhrrmltpaf hydilkpyvg lmadsrvml dkweellgqd
splevfqhvs lmtldtimkc afshqgsiqv drnsqsyiq a isdl nnlv fs rvrnafhqnd
tiysltsagr wthracqlah qhtdqviqlr kaqlqkegel ekikrkrhld fldillllakm
engsil sddk lraevdtfmf eghdttasgi swilyalath pkhqercree ihslldgdgas
itwnhldqmp yttmcikeal rlyppvpig relstpvtfp dgrslpkgim vl lsiyglhh
35 npkvwpnpev fdpsrfapgs aqhshaf lpf sggsrncigk qfamnelkva taltllrfel
lpdptripip iarlvlskn gihlrlrrlp npcedkdql

SEQ ID NO: 9 (CYP4A22, NP_001010969, 519 aa)
msvsvlsp sr rlgdvsgilq vtsllillll likaaqlylh rqwllkalqq fpcppshwlf
40 ghigefqhdq elqriqervk tfpsacpywi wggkvrqvly dpdymkvilg rsdpkshgsy
kflaprigyg llll ngqt wf qhrrmltpaf hndilkpyvg lmadsrvml dkweellgqd
splevfqhvs lmtldtimks afshqgsiqv drnsqsyiq a isdl nslvfc cmrnafhend
tiysltsagr wthracqlah qhtdqviqlr kaqlqkegel ekikrkrhld fldillllakm
engsil sddk lraevdtfmf eghdttasgi swilyalath pkhqercree ihgllgdgas
45 itwnhldqmp yttmcikeal rlyppvpig relstpvtfp dgrslpkgim vl lsiyglhh
npkvwpnlev fdpsrfapgs aqhshaf lpf sggsrncigk qfamnlkva raltllrfel
lpdptripip marlvlskn gihlrlrrlp npcedkdql

SEQ ID NO: 10 (CYP4B1, NP_000770, 511 aa)

mvpsflslsf sslglwasgl ilvlglflkli hlllrrqtla kamdkfpgpp thwlfghale
 iqetgsldkv vswahqfpya hplwfgqfig flniyepdya kavysrgdpk apdvydfflq
 wigrgllvle gpkwlqhrkl ltpgfhydvl kpyvavftes trimldkwee karegksfdi
 fcdvghmaln tlmkctfgrg dtglghrdss yylavsdltl lmqgrlvsfq yhndfiywlt
 5 phgrrflrac qvahdhtdqv irerkaalqd ekvrkkiqnr rhldfldill gardeddikl
 sdadlraevd tfmfeghdtl tsgiswflyc malybehqhr creevreilg dqdffqwdl
 gkmtyltmc i kesfrlyppv pqvyrqlskp vtfvdgrslp agslismhiy alhrnsavwp
 dpevfdsrlf stenaskrhp fafmpfsagp rncigqqfam semkvvtamc llrfefslp
 srlpikmpql vlrsknghl hlkplpgsg k
 10
 SEQ ID NO: 11 (CYP4F2, NP_001073, 520 aa)
 msqslslswlg lwpvaaspwl llllvgaswl lahvlawtya fydnccrlrc fpqpprrnwf
 wghqgmvnpt eegmrvtlql vatypqgfkv wmgpispills lchpdiirsv inasaaiaipk
 dkffysflep wlgdglllsa gdkwsrhrm ltpafhfnil kpymkifnes vnimhakwql
 15 lasegsacld mfehislmtdl dslqkcvfsf dshcqekeps yiaailelsa lvskrhheil
 lhldflyylt pdgqrfracc rlvhdftdav iqerrrtlps qgvddflqak aksktldfid
 vlllskdedg kklssedira eadtfrmegh dttasglswv lyhlakhpey qercrgevqe
 llkdrpkei ewddlahlpf ltmcmkeslr lhppvpvisr hvtqdivlpd grvipkgiic
 lisvfgthhn pavwpdpevy dpfrfdpeni kersplafip fsagprncig qtfamaemkv
 20 vlaltllrfr vlpdhteprr kpelvlraeg glwlrvepls

 SEQ ID NO: 12 (CYP4F3, NP_000887, 520 aa)
 mpqlslslswlg lwpmaaspwl llllvgaswl larilawtyt fydnccrlrc fpqppkrnwf
 lghlglihs eeglytqsl actfgdmccw wvgpwhaivr ifhptyikpv lfapaaivpk
 25 dkvfysflkp wlgdglllsa gekwsrhrm ltpafhfnil kpymkifnes vnimhakwql
 lasegsarld mfehislmtdl dslqkcvfsf dshcqekeps yiaailelsa lvtkrhqqil
 lyidflyylt pdgqrfracc rlvhdftdav iqerrrtlps qgvddflqak aksktldfid
 vlllskdedg kklssedira eadtfrmegh dttasglswv lyhlakhpey qercrgevqe
 llkdrpkei ewddlaqlpf ltmckeslr lhppvpavsr cctqdivlpd grvipkgiic
 30 lisvfgthhn pavwpdpevy dpfrfdpeni kersplafip fsagprncig qafamaemkv
 vlgltllrfr vlpdhteprr kpelvlraeg glwlrvepls

 SEQ ID NO: 13 (CYP4F8, NP_009184, 520 aa)
 msllslswlg lrpvaaspwl llllvgaswl larilawtya fyhngrrlrc fpqpprkqnwf
 35 lghlgltvpt eeglrvltql vatypqgfvr wlgpitiin lchpdivrsv intsdaiddk
 divfyktlcp wlgdglllsv gdkwrhrrl ltpafhfnil kpyikifsk animhakwqr
 lamegstcld vfehislmtdl dslqkcifsf dsncqekeps yitaimelsa lvvkrnngff
 rykdfllyft pcgrrfhrac rlvhdftdav iqerrrtlts qgvddflqak aksktldfid
 vlllsedkng kelsdedira eadtfrmegh dttasglswv lynlarhpey qercrgevqe
 40 llkdrpkei ewddlaqlpf ltmclkeslr lhppiptfar gctqdvlpd srvipkgnvc
 ninifaihn psvwpdpevy dpfrfdpena qkrspmafip fsagprncig qkfamaemkv
 vlaltllrfr ilpdhreppr tpeivlraed glwlrveplg

 SEQ ID NO: 14 (CYP4F11, NP_067010, 524 aa)
 45 mpqlslswlg lgpvaaspwl llllvggswl larvlawtyt fydnccrlqc fpqppkqnwf
 wghqglvtpt eegmktltql vttypqgfk l wlgptfpili lchpdiirpi tsasaavap
 dmifygflkp wlgdglllsg gdkwsrhrm ltpafhfnil kpymkifnks vnimhdkwqr
 lasegsarld mfehislmtdl dslqkcvfsf esncqekeps yiaailelsa fvekrnngqil
 lhtdflyylt pdgqrfracc hlvhdftdav iqerrctlpt qgidflknk aksktldfid
 50 vlllskdedg kelsdedira eadtfrmegh dttasglswv lyhlakhpey qeqcrgevqe

llkdrepiei ewddlaqlpf ltmcikeslr lhppvpvisr cctqdfvlpd grvipkgivc
 liniigihyn ptvwpdpevy dpfrfdqeni kersplafip fsagprncig qafamaemkv
 vlatllhfr ilphttepr kpelilraeg glwlrveplg ansq

5 SEQ ID NO: 15 (CYP4F12, NP_076433, 524 aa)
 mslslpwl lrpvatspwl llllvvgswl larilawtya fynncrrlqc fpqppkrnwf
 wghlglitpt eeglknstqm satysqgftv wlgiipfiv lchpdtirsi tnasaaiaipk
 dnlfirflkp wlgegillsg gdwksrhrm ltpafhfnil ksyitifnks animldkwqh
 lasegssrld mfehismltl dslqkcifsf dshcqerpse yiatilelsa lvekrshil
 10 qhmdflyyls hdgrrfhrac rlvhdftdav irerrrtlpt qgiddffkdk aksktldfid
 vlllskdedg kalsdedira eadtfrmfggh dttasglswv lynlarhpey qercrqevqe
 llkdrdpkei ewddlaqlpf ltmcvkeslr lhppapfisr cctqdivlpd grvipkgitc
 lidiigvhhn ptvwpdpevy dpfrfdpens kgrsplafip fsagprncig qafamaemkv
 vlatllhfr flpdhtepr klelimraeg glwlrvepln vslq

15 SEQ ID NO: 16 (CYP4F22, NP_775754, 531 aa)
 mlpitdrllh llglektafr iyavstlllf llfflfrlll rflrlcrsfy itcrrlrcfp
 qprrnwllg hlglmylpnea glqdekkvld nmhhvllvwm gpvlplllvlv hpdvikp11g
 asaaiaipkdd lfygflkpwl gdgl1llskgd kwsrhrllt pafhfdilkp ymkifnqsad
 20 imhakwrhla egsavslmfm ehislmtlds lqkcvfsyns ncqekmsdyi saaielsals
 vrrqyrlhhy ldfiyyrsad grrfrqacdm vhhfhteveiq errralrqqg aeawlkakqg
 ktldfidvll lardedgkel sdediraeat tfmfeghdt ssgiswmlfn lakypeyqek
 creeigevmk grelelewd dltqlpfttm cikeslrqyp pvtlvsrqct ediklpdgri
 ipkgiiclvls iygthhnptv wpdskvynpy rfdpdpnpqqr splayvpfsa gprncigqsf
 25 amaelrvvva ltlrlfrlsv drtrkvrrkp elilrtengl wlkveplppr a

SEQ ID NO: 17 (CYP4X1, NP_828847, 509 aa)
 mefswletrw arpfylafvf clalgl1lqai klylrrqrll rd1rpfpapp thwflghqkf
 iqddnmekle eiiekypraf pfwigpfqaf fciydpdyak tllsrt1pks qylqkfsppl
 30 lgkglaaldg pkwfhrrll tpgfhfnilk ayievmahsv kmml1dkweki cstq1dtsvev
 yehinsmsld iimkcafske tncqtnsthd pyakaifels kiifhrlysl lyhsdiifkl
 spqgyrfqkl sr1lnqytdt i1qerks1q agvkqdn1pk rkyqd1ldiv lsakdesgss
 fsdidvhsev stfllaghd1t laasiswily clal1npehqe rcreevrgil gdgssitwdq
 lgemsyttmc iketcr1lipa vpsisrd1sk pltfpdgct1 pagitv1lsi wglh1npavw
 35 knpkvfdplr fsqensdqrh pyaylpfsag srncigqefa mielkv1tial illhfrv1tpd
 ptrpltfpnh filkpkn1gmy lhlkl1sec

SEQ ID NO: 18 (CYP4Z1, NP_835235, 505 aa)
 mepswlqelm ahpfl1l1l1 cmsl1llf1qvi rlyqrrrrwmi ralhlfpapp ahwfyghkef
 40 ypvkefevyh klmekypcav plwvgpftmf fsvhdpdyak illkrqdpks avshkilesw
 vgrglvtldg skwkkhrqiv kpgfnisilk ifitmm1sesv rmm1lnkweeh iaqnsrl1elf
 qhvs1lmtlds imkcafs1hg siql1dstlds ylkavfn1sk isnqrmn1fl hhndlvfkfs
 sqgqifskfn qelhqftek1v iqdrkes1kd klkqdt1tqkr rwdfldills aksentkdfs
 ead1lqaevkt fmfaghd1tts sa1swilycl akypehqqrc rdeirellgd gssitwehls
 45 qmpyttmcik eclrlyapvv nisr1ldkpi tfpdgrslpa gitvfiniwa lhhnpyfwd
 pqvfnplrfs renseki1hpy afipfsaglr ncigqhfaii eckvavatl1 lrfklapdhs
 rppqpvrqvv lkskngihvf akkvc

50 SEQ ID NO: 19 (cytochrome P450 4V2 isoform X1 [Pan troglodytes
 chimpanzee)], XP_001165629.1, 525 aa)

- maglwlglvw qklllwgaas avslagaslv lsllqrvaty arkwqqmrpi ptvarayplv
ghallmkpdg reffqqiiey teeyrhmp11 klwvgpvpv alynaenvev iltsskqidk
ssmykflepwl lglgl1tstg nkwsrrkml tptfhftile dfldimnega ntlvkklekh
inqeafncff yitlcaldii cetamgknig aqsnddseyv ravymsemi frrikmpwlw
5 ldlwylmfke gwehkkslki lhtftnsvia eranemnane dcrdgrgsa psknkrrafl
d111svtdde gnrlshedir eevdtfmfeg hdttaaa1nw slyllgsnpe vqkkvdheld
dvfgksdrpa tvedlkk1ry lecviketlr lfpsvplfar svsedcevag yrvlkgteav
iipyalhrdp ryfpnp1efq perffpknaq grhpyayvpf sagprncigq kfavmeekti
lscilrhfw1 esnqkreelg legqlilrps ngiwiklrr nader
- 10 SEQ ID NO: 20 (cytochrome P450 4V2 [Macaca mulatta (Rhesus Macaque,
Rhesus Monkey)], NP_001180767.1, 525 aa)
magiwlglvw qklllwgaas avslagaslv lsllqrvasy vrkwqqmrpi ptvarayplv
ghallmkrdg reffqqiiey teeyrhmp11 klwvgpvpv alynaenvev iltsskqidk
15 ssm1kflepwl lglgl1tstg nkwsrrkml tptfhftile dfldimnega nilvkklekh
vnqeafncfv yitlcaldii cetamgknig aqsnddseyv ravymsemi frrikmpwlw
ldlwylmfke gwehkkslki lhaftnnvia eranemn1vde dcrdgrdsa psknkrrafl
d111svtdde gnrlshedir eevdtfmfeg hdttaaa1nw slyllgsnpe vqkkvdheld
dvfgrsdrpa tvedlkk1ry lecviketlr lfpsvplfar svsedcevag yrvlkgteav
20 iipyalhrdp ryfpnp1efr perffpenaq grhpyayvpf sagprncigq kfavmeekti
lscilrhfw1 esnqkreelg legqlilrpt ngiwiklrr nadep
- SEQ ID NO: 21 (cytochrome P450 4V2 [Canis lupus familiaris (dog)],
XP_013975571.1, 539 aa)
25 mlkvkwkenv fregdkdsnm ldavqlpsik vesalsdaea ggspggrrpv ltvergrlaq
gsmss1lkn1 kdttrns1ki kyflpeffqg vilyseesrh lp11klwlgp ipivaiysae
nveviltssr qidksyvykf lepwlglgl1 tstgnkwsr rkmltptfhf tiledfldvm
nehanilv1k lekhvnqeaf ncf1yitlca ldiicetamg knigaqnned seyvr1iym
sdtihrrmkm pwlwldflfl mfkegrehkr nleilhnftn nviterasel krdeehgsad
30 kdcspsknr rafld111nv tddeg1klrh edvreevdtf mfeghdttaa ainwslyllg
sy1evqkqv1d seledvfgks drpatledlk klkylecvik eslrlf1psvp lfarn1nedc
vvagykv1kg sqaii1pyal hrdpryfpnp eefqperffp enlqgrhpya yipfsagprn
cigqrfaime ektvlscv1r hfwvesnqkr eelglageli lrptngiwik lkrrnades
- 35 SEQ ID NO: 22 (cytochrome P450 4V2 [Bos taurus (cattle)],
NP_001029545, 527 aa)
mlapw11svg pk111wsglc avslagatlt ln11kmvasy arkwrqmrpv ptigdpyp1v
ghalm1kpd1 rdffqqi1df teecrh1p11 klwlgvp1v alynaetvev ilssskhiekh
sym1kflepwl lglgl1tstg nkwsrrkml tptfhftile dfldvmnega nilv1klekh
40 vnqeafncff yvtlctldii cetamgknig aqrnddseyv ravym1dsi hqrmkmpwlw
ldlifymfkn grehrrs1ki vhdftnnvit eranemkrhe egtsndked fprk1kcra
fld111nvtd dqgnklshed ireevdtfmf eghdttaaai nwslyllgwy pevqqr1vde
leevfgksdr pvtledlkk1 kyldcvikes lrlf1psvpff arnl1tedcev aghkivqgcq
viivpyalhr dpkyfpd1ee fkperff1pen lkgrhtyayv pfsagprnci gqkfai1meek
45 tilscilrhf wvesnqkree lg1lagelilr psngiwikl rrntdes
- SEQ ID NO: 23 (Cyp4v3, cytochrome P450 4V2 [Mus musculus (house
mouse)], NP_598730.1, 525 aa)
50 mlwlwlglsg qklllwgaas avslagatil isifpmlvsy arkwqqmr1si psvarayplv
ghalymkpnn ae1ffq1iyy teefrh1pii klwigvp1v alykaenvev iltsskqidk

- sflykflqpwlglglststgskwrtrrkmltptfhftilenflldvmnega nilvinklekh
 vnqeafncff yitlcaldii cetamgknig aqsndseyv rtvyrmsdmi yrrmkmpwlw
 fdlwylvfke grdhkrglkc lhtftnnvia ervkerkaee dwtgagrgpi psknkrkafl
 dlllsvtdee gnrlsqedir eevdtfmfeg hdttaaaainw slyllgtntpe vqrkvqdeld
 5 evfgrshrpv tledlklky ldcviketlr vfpsvplfar slsedcevvg ykvtkgteai
 iipyalhrdp ryfpdpeefr perffpensq grhpyayvpf sagprncigq kfavmeekti
 lacilrqfwv esnqkreelg lagdlilrpn ngiwiklrr hedd
- SEQ ID NO: 24 (Cyp4v3, cytochrome P450 4V2 [Rattus norvegicus (Norway
 rat)], NP_001129072, 525 aa)
 10 mlwlglsq qklilwgaas avsvagatvl lnllqmlvsy arkwqmrpi psvarayplv
 ghalfmkpnn teffqqiiqy teefrhlpil klwigpvplv alykaenvev iltsskqidk
 sfmykflqpwlglglststgskwrarrkml tpsfhftile dflldvmnega nilvinklekh
 vnqeafncff pitlcaldii cetamgknig aqsgndseyv rtvyrmsdmi yrrmkmpwfw
 15 fdlwylmfke grdhkkgllks lhtftnnvia ervnarkaee dcigagrgpl psktkrkafl
 dlllsvtdee gnlshedir eevdtfmfeg hdttaaaainw slyllgsnpe vqrkvdkeld
 dvfgrshrpv tledlklky ldcviketlr vfpsvplfar slsedcevag ykiskgteav
 iipyalhrdp ryfpdpeefq perffpensq grhpyayvpf sagprncigq kfavmeekti
 lacilrefwi esnqkreelg lagdlilrpn ngiwiklrr hedd
- 20 SEQ ID NO: 25 (cytochrome P450 4V2 [Gallus gallus (chicken)],
 NP_001001879, 530 aa)
 mameitlgsm egtqlpwva gaitllltv tvhflpslln ywwwvwmkp ipgirpcypf
 vgnalllern gegffkqlqg yadefrkmpm fklwlgplpv tvlfhpdsve vilssskhik
 25 ksflytflhp wlggtlltst gdkwrsrrkm itptfhfail ndflevmneq ggvllekkek
 hvdkepfni tditlcaldi icetamgknl gaqdnkdsey vravyrmsdl iqqrqkspwl
 whdlmyllfk egrehernlk ilhgftdtvi aekvaalent kltkhdtvnteeesgskkr
 eafldmllna tddegkksy kdireevdtf mfeghdttaa amnwvlyllg hpeaqgkvh
 qeldevfgnt erpvtvddlk klrylecvvk ealrlfsvp mfarslqedc yisgyklpkg
 30 tnlvltyvl hrdpeifpep defrperffp enskgrhpya yvpfsagprn cigqrfaqme
 eklallilr rfwdcsqkp eelglsgeli lrpnnngiwwq lkrpktvte
- SEQ ID NO: 26 (cytochrome P450 family 4 subfamily V member 2 [Xenopus
 tropicalis (tropical clawed frog)], NP_001072667.1, 523 aa)
 35 melggevhll vwvaavvll tllalsilpa lqdyvrkrri lkpipgpgpn ypligdalfl
 knnggdfflq iceytesyrl qpllkwigt ipfivvyhad tvepvlsssk hmdkaflykf
 lhpwlkgll tstgekwrsr rkmitptfhf ailseflevm neqskilvek lqthvdgesf
 dcfmdvtlca ldiisetamg rkiqaqsnrd seyvgaiykm sdiqrrqkm pwlwldflya
 hlrdgkehdk nlkilhsftd kaileraeel kkmgeqkkeh cdsdpesdkp kkrasflmdl
 40 lmatddagnk msymdireev dtfmfeghdt taaalnswlf llgshpeaqr qvhkeldevf
 gksdrpvtmd dlklrlylea vikeslriyp svplfgtrvt edcsirgfhv pkgvnnviip
 yalhrdpeyf pepefrper ffpenasgrn pyayipfsag lncigqrfa lmeekvvlls
 ilrnyweas qkreelcllg elilrpqdgw wiklknreta pta
- 45 SEQ ID NO: 27 (cytochrome P450 4V2 [Equus caballus (horse)],
 XP_014592182.1, 469 aa)
 mfvliefkik yslsdfqql iyyteenrhl pllklwlgpv pvvifynaen veviltssrq
 idksymkfl kpwlgllt stgnkwsrr kmltptfhft nledfldvmn eqanilvnkl
 ekhvnqeafn cflyitlcal diicetamgk nigaqrnds eyvravyrms dmihrrmkmp
 50 wlwldiffml fkegrehrll lkilhnftnn viverasemk kdeersrsdd ggsapsknkr

- rafldlllnv tddegnklsh edirgevdtf mfeghdttaa ainwslyllg cypevqkkvd
 seleevfgks drpatledlk klkylecvmk etlrlfpsvp lfarnlnedc evagykivkg
 sqaiivsyal hrdsryfnp eefkperffp ensqgrhpya yvpfsagprn cigqkfavme
 ekiilscilr hfwvesnqkr eelglageli lrpsngiwik lkrntees
- 5
- SEQ ID NO: 28 (cytochrome P450 4V2 [*Oryctolagus cuniculus* (rabbit)],
 XP_002709379.1, 524 aa)
 mwlwlglvvg kllfwgaasa vslagaslfl nllqmvasya rkwqqmrpip tigrpyplvg
 halymkpsgk effqqliqyt eeyrhlpplk lwlglpiva lynaenvevi lnsskqinks
 10 smyqflepwl glglltstgy kwsrrkmlt ptfhftiled fldimneqan ilvhklekhv
 dqeafncffy itlcaldiic etamgkniga qsnedseyvr avyrmsdvif rrmkmpwlwl
 dlwylmfkeg wehkrclkil hrftnnviae rvsemktdee hrdadsncap stmkrkafl
 llltvtdeeg nklshedire evdtfmfegh dttaaaainws lyllgshpev qrkvddelde
 vfgksdrpat sedlklkyl ecviketlrl fpsvplfars lsddcevagf rvvkgqtavi
 15 vpyalhrdpk yfpnpeefrp erffpenaqq rhpyayvpfs agprncigqk faimeektil
 scilrklwve snqkmeelgl agelilrptn giwiklkrn adka
- SEQ ID: 29 (cytochrome P450-4c3 [*Drosophila melanogaster* (fruit fly)],
 NP_524598, 535 aa)
 20 msskvitslm aesillskvg qvisgyspit vlllgslif lvvynkrsr lvkyiekipg
 paampflgna iemnvhdhel fnrvigmqkl wgtriginrv wqgtaprll fepetvepil
 nsqkfvnksh dydylhpwlgl eglststdrk whsrrkilt pafhfkildd idvfneqsav
 larklavevg seafnlfpv tlctldivce tamgriyaq snseseyvka vygigsivqs
 rqakiwlsd fifsltaeyk lhqsyintl gfsnmvire kaelailqen nnnnnnapd
 25 ayddvgkkkr lafldllida skegtvlsne direevdtfm feghdttsaa iswtlflg
 hpeyqervve eldsifgddk etpatmknml dmryleccik dslrlfpsvp mmarmvgedv
 niggkivpag tqaiimtyal hrnprvfpkp eqfnpdnflp encagrhpf yipfsagprn
 cigqkfaile ekavistvrlr kykieavdr edltlilgeli lrpkdglrvk itprd
- 30
- SEQ ID NO: 30 (P450 signature element, "x" denotes any amino acid)
 FxxGxxxCxG
- SEQ ID NO: 31 (P450 signature element, "x" denotes any amino acid)
 ExxR
- 35
- SEQ ID NO: 32 (CAG promoter, 1715 bp)
 GACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGA
 GTTCCGCGTTACATAACTTACGGTAAATGGCCGCGCTGGCTGACCGCCCAACGACCCCGCCATTGACG
 TCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATT
 40 TACGGTAAACTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAA
 TGACGGTAAATGGCCGCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTTGGCAGTAC
 ATCTACGTATTAGTCATCGCTATTACCATGGGTGCGAGGTGAGCCCCACGTTCTGCTTCACTCTCCCCATC
 TCCCCCCCCCTCCCCACCCCCAATTTTGTATTTATTTTATTTTAAATTATTTTGTGCAGCGATGGGGGCGG
 GGGGGGGGGGGGCGCGCCAGGCGGGGCGGGGCGGGGCGAGGGGCGGGGCGGGGCGAGGCGGAGAGGTG
 45 CGGCGGCAGCCAATCAGAGCGGCGCGCTCCGAAAGTTTCCTTTTATGGCGAGGCGGCGGCGGCGGCC
 CTATAAAAAGCGAAGCGCGCGGCGGGGAGTCGCTGCGTTGCCTTCGCCCCGTGCCCCGCTCCGCGCC
 GCCTCGCGCGCCCGCCCGCCCGCTCTGACTGACCGCGTTACTCCACAGGTGAGCGGGCGGGACGGCCCTT
 CTCCTCCGGGCTGTAATTAGCGCTTGGTTTAAATGACGGCTCGTTTCTTTCTGTGGCTGCGTGAAAGCCT
 TAAAGGGCTCCGGGAGGGCCCTTTGTGCGGGGGGAGCGGCTCGGGGGGTGCGTGCGTGTGTGTGCGT
 50 GGGGAGCGCCGCGTGCGGCCCGCGCTGCCGGCGGCTGTGAGCGCTGCGGGCGGGCGCGGGGCTTTGTG

- TAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAA
ATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGT
AACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTA
CATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATT
5 ATGCCCAGTACATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTAC
CATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGA CTCACGGGGATTTCCAAGT
CTCCACCCCATTGACGTCAATGGGAGTTTGT TTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGG
TTTAGTGAACCGTCAG
- 10 SEQ ID NO: 41 (EF-1 alpha promoter, 1184 bp)
cgtgaggctccggtgcccgctcagtgggcagagcgcacatcgccacagtccccgagaagttggggggagg
ggtcggcaattgaaccggtgcctagagaagtggtggcggggtaaactgggaaagtgatgtcgtgtactgg
ctccgcctttttcccgagggtgggggagaaccgtatataagtgcagtagtcgccgtgaacgttcttttttc
15 gcaacggggtttgcccagaaacacaggttaagtgcctgtgtgtggttcccgcgggcctggcctctttacggg
ttatggcccttgctgccttgaattacttccacctggctgcagtagtgattcttgatcccagagcttcgg
ggttgaagtgggtgggagagttcgaggccttgcgcttaaggagcccccttcgcctcgtgcttgagttgagg
cctggcctgggctggtgggcccgcgctgcgaatctggtggcaccttcgcgcctgtctcgtgcttttcga
taagtctctagccattttaaaatttttgatgacctgctgcgacgctttttttctggcaagatagtccttgta
20 aatgcgggccaagatctgcacactggtatttcggtttttggggccgcgggcccgcacggggcccgctgct
cccagcgcacatgttcggcgaggcggggcctgcgagcgcggccaccgagaatcggacgggggtagtctca
agctggccggcctgctctggtgcctggcctcgcgcgcgctgtatcgccccgccttgggcggaaggctg
gcccggctcggcaccagttgctgtagcggaagatggccgcttcccggccctgctgcaggagagctcaaaat
ggaggacgcggcgctcgggagagcgggcggtgagtcacccacacaaaaggaaaaggcctttccgctcctc
25 agccgtcgcttcatgtgactccacggagtaccgggcccgtccaggcacctcgattagttctcgagcttt
tgagtagctcgtcttttagttggggggaggggttttatgcatggagtttccccacactgagtggtgg
agactgaagttaggccagcttggcacttgatgtaattctccttggaatttgcccttttgagtttgatc
ttggttcattctcaagcctcagacagtggttcaaagttttttcttccatttcaggtgtcgtga
- 30 SEQ ID NO: 42 (AAV2 5' Left-ITR, 141 bp)
cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag cccggggcgtc
gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc gcgcagagag ggagtggcca
actocatcac taggggttcc t
- 35 SEQ ID NO: 43 (AAV2 3' Right-ITR, 141 bp)
ag gaacccttag tgatggagtt ggccactccc tctctgcgcg ctgcctcgct cactgaggcc
gggcgaccaa aggtcgcccg acgcccgggc tttgccggg cggcctcagt gacgagcgca
gcgcgcagct gcctgcagg
- 40 SEQ ID NO: 44 (mutant AAV2 5' ITR in scAAV construct, 117 bp)
cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag cccggggcgtc
gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc gcgcagagag ggagtggg
- SEQ ID NO: 45 (AAV2 3' ITR in scAAV construct, 141 bp)
45 aggaaccc ctagtgatgg agttggccac tccctctctg cgcgctcgct cgctcactga
ggccggggcga ccaaaggctc cccgacgcc gggttttgcc cgggcggcct cagtgagcga
gcgagcgcg agctgcctgc agg
- SEQ ID NO: 46 (region of human CYP4V2 gene containing c.802-
50 8_810del17insGC mutation)

CAAACAGAAGCATGTGATTATCATTCAAAGCGAACGGGCCAATGAAATGAACGCCAATGA

SEQ ID NO: 47 (region of wild-type human CYP4V2 gene without the c.802-8_810del17insGC mutation)

5 CAAACAGAAGCATGTGATTATCATTCAAATCATAACAGGTCATCGCTGAACGGGCCAATGAAATGAACGCCAATGA

SEQ ID NO: 48 (g1 protospacer element, RNA sequence, 20 nt)
UGAUUAUCAUCAAAGCGAA

10

SEQ ID NO: 49 (g2 protospacer element, RNA sequence, 20 nt)
GAUUAUCAUCAAAGCGAAC

SEQ ID NO: 50 (g3 protospacer element, RNA sequence, 20 nt)
15 GAUAAUCACAUGCUUCUGUU

SEQ ID NO: 51 (g4 protospacer element, RNA sequence, 20 nt)
UUCAUUGGCGUUAUUUCAU

20

SEQ ID NO: 52 (g5 protospacer element, RNA sequence, 20 nt)
CACAUUCUUCUGUUUGGACU

SEQ ID NO: 53 (crRNA exemplary sequence (excluding the 5' protospacer element sequence, 16 nt)

25

GUUUUAGAGCUAUGCU

SEQ ID NO: 54 (tracrRNA exemplary sequence, 67 nt)

AGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUU

30

SEQ ID NO: 55 (sgRNA exemplary sequence, excluding 5' protospacer element sequence and the optional "G" before the protospacer element. Sequence shown in DNA format as in a plasmid construct. For sequence in RNA format, use "U" to replace "T", 82 nt)

35

gttttagagctagaaatagcaagttaaaataaggctagtcggttatcaacttgaaaaagtggcaccgagt
cggtgctttttt

SEQ ID NO: 56 (CYP4V2 donor template 1 sequence, 200 bases)

AGA AAA ATA AAT GAA AGA AAC TAG CAT ATT TTA TAA GAA AAT GTG TTA ACT
40 AGG GTG CAT CCA AGT CCA AAC AGA AGC ATG TGA TTA TCA TTC AAA TCA TAC
AGG TCA TCG CTG AAC GGG CCA ATG AAA TGA ACG CCA ATG AAG ACT GTA GAG
GTG ATG GCA GGG GCT CTG CCC CCT CCA AAA ATA AAC GCA GGG CCT TT

SEQ ID NO: 57 (CYP4V2 donor template 2 sequence, the reverse complement of CYP4V2 donor template 1 sequence, 200 bases)

45

AA AGG CCC TGC GTT TAT TTT TGG AGG GGG CAG AGC CCC TGC CAT CAC CTC TAC
AGT CTT CAT TGG CGT TCA TTT CAT TGG CCC GTT CAG CGA TGA CCT GTA TGA
TTT GAA TGA TAA TCA CAT GCT TCT GTT TGG ACT TGG ATG CAC CCT AGT TAA
CAC ATT TTC TTA TAA AAT ATG CTA GTT TCT TTC ATT TAT TTT TCT

50

SEQ ID NO: 58 (SpCas9 exemplary amino acid sequence (1368 aa))

MDKKYSIGLDIGTNSVGWAVITDEYKVPSSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARR
 RYTRRKNRICYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRK
 KLVDSTDKADLRILIYLAHMIKFRGHFLIEGDLNPDNSDVKLFQILVQTYNQLFEENPINASGVDAKA
 ILSARLSKSRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLNLLA
 5 QIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLKALVRQQLPEKYKEI
 FFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELH
 AILRRQEDFYFPLKDNREKIEKILTFRIPIYVGPLARGNSRFAWMTRKSEETITPWNFEVVVDKGASAQS
 FIERMTNFDKNLPNEKVLPHKSLLEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVT
 VKQLKEDYFKKIECFDSVEISGVEDRFNASLGYHDLKIKDKDFLDNEENEDILEDIVLTLTLFEDRE
 10 MIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFQMQLIHDD
 SLTFKEDIQKAQVSGQDSLHEHIANLAGSPAIIKKGILQTVKVVDLVKVMGRHKPENIVIEMARENQTT
 QKGQKNSRERMKRIEEGKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDH
 IVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKMKNYWRQLLNAKLITQRKFDNLTKAERGGGLSE
 LDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVRINN
 15 YHHAHDAYLNAVVGITALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEI
 TLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSPQVNIIVKKTEVQTGGFSKESILPKRNSDKLI
 ARKKDWDPPKYGGFDSPTVAYSVLVVAKEGKSKKLKSVKELLGITIMERSSEFEKNPIDFLEAKGYKEV
 KKDIIKLPKYSLEFELNGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVE
 QHKHYLDEIIIEQISEFSKRVILADANLDKVL SAYNKHDKPIREQAENIIHLFTLTNLGAPAAFKYFDTT
 20 IDRKYRTSTKEVLDTLIHQSIITGLYETRIDLSQLGGD

SEQ ID NO: 59 (additional nucleotide inserted immediately after the U6
 promoter sequence and before the protospacer element sequence in a
 plasmid construct and in an IVT sgRNA, 1 nt)

25 G

SEQ ID NO: 60 - Sequence of CYP4V2 expression cassette in
 AAV2.CYP4V2op, AAV2tri(Y-F).CYP4V2op, and AAV5.CYP4V2op.:

Left-ITR: 1-141

30 CAG promoter: 237-1951

CYP4V2op cDNA: 2002-3579

WPRES enhancer: 3736-4324

bGH polyA: 4350-4574

Right-ITR 4659-4799

35

	1	CCTGCAGGCA	GCTGCGCGCT	CGCTCGCTCA	CTGAGGCCGC	CCGGGCAAAG
	51	CCCGGGCGTC	GGGCGACCTT	TGGTCGCCCG	GCCTCAGTGA	GCGAGCGAGC
	101	GCGCAGAGAG	GGAGTGGCCA	ACTCCATCAC	TAGGGGTTCC	TGCGGCCAAT
	151	TCAGTCGATA	ACTATAACGG	TCCTAAGGTA	GCGATTTAAA	TACGCGCTCT
40	201	CTTAAGGTAG	CCCCGGGACG	CGTCAATTGA	GATCTCGACA	TTGATTATTG
	251	ACTAGTTATT	AATAGTAATC	AATTACGGGG	TCATTAGTTC	ATAGCCCAT
	301	TATGGAGTTC	CGCGTTACAT	AACTTACGGT	AAATGGCCCC	CCTGGCTGAC
	351	CGCCCAACGA	CCCCCGCCCA	TTGACGTCAA	TAATGACGTA	TGTTCCCAT
	401	GTAACGCCAA	TAGGGACTTT	CCATTGACGT	CAATGGGTGG	ACTATTTACG
45	451	GTAAACTGCC	CACTTGGCAG	TACATCAAGT	GTATCATATG	CCAAGTACGC
	501	CCCCTATTGA	CGTCAATGAC	GGTAAATGGC	CCGCCTGGCA	TTATGCCAG
	551	TACATGACCT	TATGGGACTT	TCCTACTTGG	CAGTACATCT	ACGTATTAGT
	601	CATCGCTATT	ACCATGGGTC	GAGGTGAGCC	CCACGTTCTG	CTTCACTCTC
	651	CCCATCTCCC	CCCCCTCCCC	ACCCCCAATT	TTGTATTTAT	TTATTTTTTA
50	701	ATTATTTTGT	GCAGCGATGG	GGGCGGGGGG	GGGGGGGGCG	CGCGCCAGGC

5 751 GGGGCGGGGC GGGGCGAGGG GCGGGGCGGG GCGAGGCGGA GAGGTGCGGC
801 GGCAGCCAAT CAGAGCGGCG CGCTCCGAAA GTTTCCTTTT ATGGCGAGGC
851 GGCGGCGGCG GCGGCCCTAT AAAAAGCGAA GCGCGCGGCG GCGGGGAGTC
901 GCTGCGTTGC CTTCGCCCCG TGCCCCGCTC CGCGCCGCCT CGCGCCGCCC
10 951 GCCCCGGCTC TGA CTGACCG CGTTACTCCC ACAGGTGAGC GGGCGGGACG
1001 GCCCTTCTCC TCCGGGCTGT AATTAGCGCT TGGTTTAATG ACGGCTCGTT
1051 TCTTTTCTGT GGCTGCGTGA AAGCCTTAAA GGGCTCCGGG AGGGCCCTTT
1101 GTGCGGGGGG GAGCGGCTCG GGGGGTGCGT GCGTGTGTGT GTGCTGGGG
1151 AGCGCCGCGT GCGGCCCGCG CTGCCCCGCG GCTGTGAGCG CTGCGGGCGC
10 1201 GGCGCGGGGC TTTGTGCGCT CCGCGTGTGC GCGAGGGGAG CGCGGCCGGG
1251 GGCGGTGCCC CGCGGTGCGG GGGGGCTGCG AGGGGAACAA AGGCTGCGTG
1301 CGGGGTGTGT GCGTGGGGGG GTGAGCAGGG GGTGTGGGCG CGGCGGTGCG
1351 GCTGTAACCC CCCCCTGCAC CCCCCTCCCC GAGTTGCTGA GCACGGCCCC
1401 GCTTCGGGTG CGGGGCTCCG TCGGGGCGT GCGCGGGGC TCGCCGTGCC
15 1451 GGGCGGGGGG TGGCGGCAGG TGGGGTGCC GGGCGGGGCG GGGCCGCTC
1501 GGGCCGGGGA GGGCTCGGGG GAGGGGCGCG GCGGCCCCG AGCGCCGGCG
1551 GCTGTCGAGG CGCGGCGAGC CGCAGCCATT GCCTTTTATG GTAATCGTGC
1601 GAGAGGGCGC AGGGA CTTC TTTGTCCAA ATCTGGCGGA GCCGAAATCT
1651 GGGAGGCGCC GCCGCACCCC CTCTAGCGGG CGCGGGCGAA GCGGTGCGGC
20 1701 GCCGGCAGGA AGGAAATGGG CGGGGAGGGC CTTCGTGCGT CGCCGCGCCG
1751 CCGTCCCCCT CTCCATCTCC AGCCTCGGGG CTGCCGAGG GGGACGGCTG
1801 CCTTCGGGGG GGACGGGGCA GGGCGGGGTT CGGCTTCTGG CGTGTGACCG
1851 GCGGCTCTAG AGCCTCTGCT AACCATGTTT ATGCCTTCTT CTTTTTCCTA
1901 CAGCTCCTGG GCAACGTGCT GGTTATTGTG CTGTCTCATC ATTTTGGCAA
25 1951 AGAATTCTAA TACGACTCAC TATAGGGAGA CCAAGCTGG CTAGAGCCAC
2001 CATGGCTGGA CTGTGGCTGG GACTGGTGTG GCAGAACTG CTGCTGTGGG
2051 GGGCCGCTTC CGCACTGTCA CTGGCTGGGG CTTCCTGCTG GCTGAGCCTG
2101 CTGCAGAGGG TGGCCTCCTA CGCCAGAAAG TGGCAGCAGA TGAGGCCCAT
2151 CCCTACCGTG GCCAGAGCCT ATCCACTGGT GGGACACGCA CTGCTGATGA
30 2201 AGCCTGACGG CAGAGAGTTC TTTCAGCAGA TCATCGAGTA CACAGAGGAG
2251 TATAGGCACA TGCCACTGCT GAAGCTGTGG GTGGGACCCG TGCCTATGGT
2301 GGCCCTGTAC AACGCCGAGA ATGTGGAAGT GATCCTGACC AGCAGCAAGC
2351 AGATCGATAA GTCTAGCATG TATAAGTTCC TGGAGCCTTG GCTGGCCTG
2401 GGCCTGCTGA CCTCTACAGG CAACAAGTGG AGGAGCCGGA GAAAGATGCT
35 2451 GACCCCAACA TTCCACTTTA CAATCCTGGA GGA CTTCCTG GACATCATGA
2501 ACGAGCAGGC CAATATCCTG GTGAAGAAGC TGGAGAAGCA CATCAACCAG
2551 GAGGCCTTTA ATTGCTTCTT TTACATCACC CTGTGCGCCC TGGACATCAT
2601 CTGTGAGACA GCTATGGGCA AGAACATCGG CGCCAGTCT AATGACGATA
2651 GCGAGTACGT GCGGGCCGTG TATAGAATGA GCGAGATGAT CTTTAGGCGC
40 2701 ATCAAGATGC CCTGGCTGTG GCTGGATCTG TGGTATCTGA TGTTCAGGA
2751 GGGCTGGGAG CACAAGAAGT CCCTGCAGAT CCTGCACACC TTTACAAAT
2801 CTGTGATCGC CGAGAGAGCC AATGAGATGA ACGCCAATGA GGACTGTAGG
2851 GGCGATGGAA GGGGCGAGCG CCCTTCCAAG AACAAGCGGA GAGCCTTCCT
2901 GGACCTGCTG CTGAGCGTGA CCGACGATGA GGGCAATCGC CTGTCCCACG
45 2951 AGGACATCCG GGAGGAGGTG GATACATTCA TGTTTGAGGG ACACGACACC
3001 ACAGCCGCCG CCATCAACTG GTCCCTGTAC CTGCTGGGCT CTAATCCAGA
3051 GGTGCAGAAG AAGGTGGATC ACGAGCTGGA CGACGTGTTT GGCAAGTCCG
3101 ACAGGCCAGC AACCGTGGAG GATCTGAAGA AGCTGAGATA CCTGGAGTGC
3151 GTGATCAAGG AGACACTGCG CCGTGTCCCC TCTGTGCCTC TGTTTGCCCG
50 3201 GTCCGTGTCT GAGGACTGTG AGGTGGCCGG CTATCGCGTG CTGAAGGGCA

```

5   3251 CCGAGGCCGT GATCATCCCT TACGCCCTGC ACCGGGACCC CAGGTATTTT
    3301 CCTAACCCAG AGGAGTTTCA GCCAGAGAGA TTCTTTCCCG AGAATGCCCA
    3351 GGGCAGGCAC CCTTACGCCT ATGTGCCATT CTCCGCCGGA CCAAGGAACT
    3401 GCATCGGACA GAAGTTTGCC GTGATGGAGG AGAAAACCAT CCTGTCTTGT
10  3451 ATCCTGAGAC ACTTCTGGAT CGAGAGCAAT CAGAAGAGGG AGGAGCTGGG
    3501 CCTGGAGGGA CAGCTGATCC TGC GGCC AAG CAACGGCATC TGGATCAAAC
    3551 TGAAGAAG GAACGCTGAC GAGAGGTAAA AGCTTGGTAC CGATATCGCG
    3601 GCCGCCCTAG GGAGCTCCTC GAGGCGGCCC GCTCGAGTCT AGAGGGCCCT
    3651 TCGAAGGTAA GCCTATCCCT AACCCTCTCC TCGGTCTCGA TTCTACGCGT
10  3701 ACCGGTCATC ATCACCATCA CCATTGAGTT TCGATAATCA ACCTCTGGAT
    3751 TACAAAATTT GTGAAAGATT GACTGGTATT CTTAACTATG TTGTCCTTTT
    3801 TACGCTATGT GGATACGCTG CTTTAATGCC TTTGTATCAT GCTATTGCTT
    3851 CCCGTATGGC TTTCATTTTC TCCTCCTTGT ATAAATCCTG GTTGCTGTCT
15  3901 CTTTATGAGG AGTTGTGGCC CGTTGTCAGG CAACGTGGCG TGGTGTGCAC
    3951 TGTGTTTGCT GACGCAACCC CCACTGGTTG GGGCATTGCC ACCACCTGTC
    4001 AGCTCCTTTC CGGGACTTTC GCTTTCCCCC TCCCTATTGC CACGGCGGAA
    4051 CTCATCGCCG CCTGCCTTGC CCGCTGCTGG ACAGGGGCTC GGCTGTTGGG
    4101 CACTGACAAT TCCGTGGTGT TGTGCGGGAA ATCATCGTCC TTTCCTTGGC
    4151 TGCTCGCCTG TGTTGCCACC TGGATTCTGC GCGGGACGTC CTTCTGCTAC
20  4201 GTCCCTTCGG CCCTCAATCC AGCGGACCTT CTTTCCCGCG GCCTGCTGCC
    4251 GGCTCTGCGG CCTCTTCCGC GTCTTCGCCT TCGCCCTCAG ACGAGTCGGA
    4301 TCTCCCTTTG GGCCGCCTCC CCGCATCGAA ACCCGCTGAT CAGCCTCGAC
    4351 TGTGCCCTTC AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT
    4401 CCTTGACCTT GGAAGGTGCC ACTCCCCTG TCCTTTCCTA ATAAATGAG
25  4451 GAAATTGCAT CGCATTGTCT GAGTAGGTGT CATTCTATTC TGGGGGTGG
    4501 GGTGGGGCAG GACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG
    4551 CTGGGGATGC GGTGGGCTCT ATGGCTTCTG AGGCGGAAAG AACCAGATCC
    4601 TCTCTTAAGG TAGCATCGAG ATTTAAATTA GGGATAACAG GGTAAATGCG
    4651 CGGGCCGCAG GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG
30  4701 CTCGCTCGCT CACTGAGGCC GGGCGACCAA AGGTGCGCCG ACGCCCGGGC
    4751 TTGCCCCGGG CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG

```

SEQ ID NO: 61 - Sequence of CYP4V2 expression cassette in AAV5.CYP4V2st. AAV5.CYP4V2st has the same promoter (CAG), enhancer (WPRE) and polyA (bGH-polyA) as AAV2.CYP4V2op, AAV2tri(Y-F).CYP4V2op and AAV5.CYP4V2op (SEQ ID NO: 60) but different CYP4V2 cDNA and junction/linker sequences:

```

Left-ITR: 1-141
CAG promoter: 166-1880
40 CYP4V2st cDNA: 1938-3515
    WPRE enhancer: 3551-4139
    bGH polyA: 4163-4387
    Right-ITR: 4399-4539

```

```

45   1 CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG
    51 CCCGGGCGTC GGGCGACCTT TGGTCGCCCG GCCTCAGTGA GCGAGCGAGC
    101 GCGCAGAGAG GGAGTGCCCA ACTCCATCAC TAGGGGTTCC TGCGGCCTAA
    151 GGCAATTGAG ATCTCGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA
    201 ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
50  251 ACTTACGGTA AATGGCCCGC CTGGCTGACC GCCCAACGAC CCCC GCCCAT

```

301 TGACGTCAAT AATGACGTAT GTTCCCATAG TAACGCCAAT AGGGACTTTC
351 CATTGACGTC AATGGGTGGA CTATTTACGG TAAACTGCCC ACTTGGCAGT
401 ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC GTCAATGACG
451 GTAAATGGCC CGCCTGGCAT TATGCCAGT ACATGACCTT ATGGGACTTT
5 501 CCTACTTGCC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGGTCG
551 AGGTGAGCCC CACGTTCTGC TTCACTCTCC CCATCTCCCC CCCCTCCCCA
601 CCCCCAATTT TGTATTTATT TATTTTTTAA TTATTTTGTG CAGCGATGGG
651 GCGGGGGGGG GGGGGGGGCG GCGCCAGGCG GGGCGGGGCG GGGCGAGGGG
701 CGGGGCGGGG CGAGGCGGAG AGGTGCGGCG GCAGCCAATC AGAGCGGCGC
10 751 GCTCCGAAAG TTTCCTTTTA TGGCGAGGCG GCGGCGGCGG CGGCCCTATA
801 AAAAGCGAAG CGCGCGGCGG GCGGGAGTCG CTGCGTTGCC TTCGCCCCGT
851 GCCCCGCTCC GCGCCGCGCTC GCGCCGCCCG CCCCGGCTCT GACTGACCGC
901 GTTACTCCCA CAGGTGAGCG GCGGGGACGG CCCTTCTCCT CCGGGCTGTA
951 ATTACGCTT GGTTTAATGA CGGCTCGTTT CTTTCTGTG GCTGCGTGAA
15 1001 AGCCTTAAAG GGCTCCGGGA GGGCCCTTTG TGCGGGGGGG AGCGGCTCGG
1051 GGGGTGCGTG CGTGTGTGTG TGCCTGGGGA GCGCCGCGTG CGGCCCGCGC
1101 TGCCCGGCGG CTGTGAGCGC TCGGGGCGCG GCGCGGGGCT TTGTGCGCTC
1151 CGCGTGTGCG CGAGGGGAGC GCGGCCGGGG GCGGTGCCCC GCGGTGCGGG
1201 GGGGCTGCGA GGGGAACAAA GGCTGCGTGC GGGGTGTGTG CGTGGGGGGG
20 1251 TGAGCAGGGG GTGTGGGCGC GCGGTCGGG CTGTAACCCC CCCCTGCACC
1301 CCCCTCCCCG AGTTGCTGAG CACGGCCCCG CTTGCGGTGC GGGGCTCCGT
1351 GCGGGGCGTG GCGCGGGGCT CGCCGTGCCG GCGGGGGGTT GCGGGCAGGT
1401 GGGGGTGCCG GCGGGGGCGG GGCCGCCTCG GCGCGGGGAG GGCTCGGGGG
1451 AGGGGCGCGG CGGCCCCGGA GCGCCGGCGG CTGTGAGAGC GCGGCGAGCC
25 1501 GCAGCCATTG CCTTTTATGG TAATCGTGCG AGAGGGCGCA GGGACTTCCT
1551 TTGTCCCAA TCTGGCGGAG CCGAAATCTG GGAGGCGCCG CCGCACCCCC
1601 TCTAGCGGGC GCGGGCGAAG CGGTGCGGCG CCGGCAGGAA GGAAATGGGC
1651 GGGGAGGGCC TTCGTGCGTC GCCGCGCCGC CGTCCCCTTC TCCATCTCCA
1701 GCCTCGGGGC TGCCGCGAGG GGACGGCTGC CTTGCGGGGG GACGGGGCAG
30 1751 GGCGGGGTTT GGCTTCTGGC GTGTGACCGG CGGCTCTAGA GCCTCTGCTA
1801 ACCATGTTCA TGCCCTCTTC TTTTTCCTAC AGCTCCTGGG CAACGTGCTG
1851 GTTATTGTGC TGTCTCATCA TTTTGGCAA GAATTCTAAT ACGACTCACT
1901 ATAGGGAGAC CCAAGCTGGC TAGCCAAAGC TTCCACCATG GCGGGGCTCT
1951 GGCTGGGGCT CGTGTGGCAG AAGCTGCTGC TGTGGGGCGC GGCAGTGCC
35 2001 CTTTCCCTGG CCGGCGCCAG TCTGGTCCTG AGCCTGCTGC AGAGGTGGC
2051 GAGCTACGCG CGGAAATGGC AGCAGATGCG GCCCATCCCC ACGGTGGCCC
2101 GCGCCTACCC ACTGGTGGGC CACGCGCTGC TGATGAAGCC GGACGGGCGA
2151 GAATTTTTTC AGCAGATCAT TGAGTACACA GAGGAATACC GCCACATGCC
2201 GCTGCTGAAG CTCTGGGTCG GGCCAGTGCC CATGGTGGCC CTTTATAATG
40 2251 CAGAAAATGT GGAGGTAATT TTAAGTAGTT CAAAGCAAAT TGACAAATCC
2301 TCTATGTACA AGTTTTTAGA ACCATGGCTT GGCTAGGAC TTCTTACAAG
2351 TACTGGAAC AAATGGCGCT CCAGGAGAAA GATGTTAACA CCCACTTTCC
2401 ATTTTACCAT TCTGGAAGAT TTCTTAGATA TCATGAATGA ACAAGCAAAT
2451 ATATTGGTTA AGAAACTTGA AAAACACATT Aaccaagaag CATTTAACTG
45 2501 CTTTTTTTAC ATCACTCTTT GTGCCTTAGA TATCATCTGT GAAACAGCTA
2551 TGGGGAAGAA TATTGGTGCT CAAAGTAATG ATGATTCCGA GTATGTCCGT
2601 GCAGTTTATA GAATGAGTGA GATGATATTT CGAAGAATAA AGATGCCCTG
2651 GCTTTGGCTT GATCTCTGGT ACCTTATGTT TAAAGAAGGA TGGGAACACA
2701 AAAAGAGCCT TCAGATCCTA CATACTTTTA CCAACAGTGT CATCGCTGAA
50 2751 CGGGCCAATG AAATGAACGC CAATGAAGAC TGTAGAGGTG ATGGCAGGGG

```

2801 CTCTGCCCCC TCCAAAAATA AACGCAGGGC CTTTCTTGAC TTGCTTTTAA
2851 GTGTGACTGA TGACGAAGGG AACAGGCTAA GTCATGAAGA TATTCGAGAA
2901 GAAGTTGACA CCTTCATGTT TGAGGGGCAC GATACAACCTG CAGCTGCAAT
2951 AAAGTGGTCC TTATACCTGT TGGGTTCTAA CCCAGAAGTC CAGAAAAAAG
5 3001 TGGATCATGA ATTGGATGAC GTGTTTGGA AGTCTGACCG TCCCGCTACA
3051 GTAGAAGACC TGAAGAAACT TCGGTATCTG GAATGTGTTA TTAAGGAGAC
3101 CCTTCGCCTT TTTCTTCTG TTTCTTTATT TGCCCGTAGT GTTAGTGAAG
3151 ATTGTGAAGT GGCAGGTAC AGAGTTCTAA AAGGCACTGA AGCCGTCATC
3201 ATTCCCTATG CATTGCACAG AGATCCGAGA TACTTCCCCA ACCCGAGGA
10 3251 GTTCCAGCCT GAGCGGTTCT TCCCCGAGAA TGCACAAGGG CGCCATCCAT
3301 ATGCCTACGT GCCCTTCTCT GCTGGCCCCA GGAAGTGTAT AGGTCAAAAG
3351 TTTGCTGTGA TGAAGAAAA GACCATTCTT TCGTGCATCC TGAGGCACTT
3401 TTGGATAGAA TCCAACCAGA AAAGAGAAGA GCTTGGTCTA GAAGGACAGT
3451 TGATTCTTCG TCCAAGTAAT GGCATCTGGA TCAAGTTGAA GAGGAGAAAT
15 3501 GCAGATGAAC GCTAAGCGGC CGCAACTCGA GACTCTAGAG GTTAATCGAT
3551 AATCAACCTC TGGATTACAA AATTTGTGAA AGATTGACTG GTATTCTTAA
3601 CTATGTTGCT CCTTTTACGC TATGTGGATA CGCTGCTTTA ATGCCTTTGT
3651 ATCATGCTAT TGCTTCCCGT ATGGCTTTCA TTTTCTCCTC CTTGTATAAA
3701 TCCTGGTTGC TGTCTCTTTA TGAGGAGTTG TGGCCCGTTG TCAGGCAACG
20 3751 TGGCGTGGTG TGCAGTGTGT TTGCTGACGC AACCCCCACT GGTGGGGCA
3801 TTGCCACCAC CTGTCAGCTC CTTTCCGGGA CTTTCGCTTT CCCCCTCCCT
3851 ATTGCCACGG CGGAACATCAT CGCCGCCTGC CTTGCCCGCT GCTGGACAGG
3901 GGCTCGGCTG TTGGGCACGT ACAATTCCGT GGTGTTGTCG GGGAAATCAT
3951 CGTCCTTTCC TTGGCTGCTC GCCTGTGTTG CCACCTGGAT TCTGCGCGGG
25 4001 ACGTCCTTCT GCTACGTCCC TTCGGCCCTC AATCCAGCGG ACCTTCCTTC
4051 CCGCGGCTG CTGCCGCTC TCGGCCCTCT TCCGCGTCTT CGCCTTCGCC
4101 CTCAGACGAG TCGGATCTCC CTTTGGGCCG CCTCCCCGCA TCGAAACCCG
4151 CTGACTAGAC GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC
4201 TCCCCCGTGC CTTCTTGGAC CCTGGAAGGT GCCACTCCCA CTGTCCTTTC
30 4251 CTAATAAAAT GAGGAAATTG CATCGCATTG TCTGAGTAGG TGTCATTCTA
4301 TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA TTGGGAAGAC
4351 AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCCG CGGGCCGAG
4401 GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG CTCGCTCGCT
4451 CACTGAGGCC GGGCGACCAA AGGTCGCCCG ACGCCGGGC TTTGCCCGGG
35 4501 CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG

```

40 SEQ ID NO: 62 - Sequence of CYP4V2 expression cassette in AAV8.CYP4V2fv. AAV8.CYP4V2fv has the same promoter (CAG), enhancer (WPRE) and polyA (bGH-polyA) and junction/linker sequences as AAV5.CYP4V2st (SEQ ID NO: 61) and differs only in CYP4V2 cDNA sequence:

45 Left-ITR: 1-141
CAG promoter: 166-1880
CYP4V2fv cDNA: 1938-3515
WPRE enhancer: 3551-4139
bGH polyA: 4163-4387
50 Right-ITR: 4399-4539

1 CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG
51 CCCGGGCGTC GGGCGACCTT TGGTCGCCCG GCCTCAGTGA GCGAGCGAGC
101 GCGCAGAGAG GGAGTGGCCA ACTCCATCAC TAGGGGTTCC TGCGGCCTAA
5 151 GGCAATTGAG ATCTCGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA
201 ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
251 ACTTACGGTA AATGGCCCGC CTGGCTGACC GCCCAACGAC CCCC GCCCAT
301 TGACGTCAAT AATGACGTAT GTTCCCATAG TAACGCCAAT AGGGACTTTC
351 CATTGACGTC AATGGGTGGA CTATTTACGG TAAACTGCCC ACTTGGCAGT
10 401 ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC GTCAATGACG
451 GTAAATGGCC CGCCTGGCAT TATGCCCAGT ACATGACCTT ATGGGACTTT
501 CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGGTCTG
551 AGGTGAGCCC CACGTTCTGC TTCACTCTCC CCATCTCCCC CCCCTCCCCA
601 CCCCCAATT TGTATTTATT TATTTTTTAA TTATTTTGTG CAGCGATGGG
15 651 GCGGGGGGGG GGGGGGGCGC GCGCCAGGCG GGGCGGGGCG GGGCGAGGGG
701 CGGGGCGGGG CGAGGCGGAG AGGTGCGGCG GCAGCCAATC AGAGCGGCGC
751 GCTCCGAAAG TTTCTTTTAA TGGCGAGGCG GCGGCGGCGG CGGCCCTATA
801 AAAAGCGAAG CGCGCGGCGG GCGGGAGTCG CTGCGTTGCC TTCGCCCGCT
851 GCCCCGCTCC GCGCCGCGCTC GCGCCGCCCG CCCC GGCTCT GACTGACCGC
20 901 GTTACTCCCA CAGGTGAGCG GGCGGGACGG CCCTTCTCCT CCGGGCTGTA
951 ATTAGCGCTT GGTTTAATGA CGGCTCGTTT CTTTTCTGTG GCTGCGTGAA
1001 AGCCTTAAAG GGCTCCGGGA GGGCCCTTTG TGCGGGGGGG AGCGGCTCGG
1051 GGGGTGCGTG CGTGTGTGTG TGCGTGGGGA GCGCCGCGTG CGGCCGCGC
1101 TGCCCGGCGG CTGTGAGCGC TGCGGGCGCG GCGCGGGGCT TTGTGCGCTC
25 1151 CGCGTGTGCG CGAGGGGAGC GCGGCCGGGG GCGGTGCCCC GCGGTGCGGG
1201 GGGGCTGCGA GGGGAACAAA GGCTGCGTGC GGGGTGTGTG CGTGGGGGGG
1251 TGAGCAGGGG GTGTGGGCGC GCGGGTCGGG CTGTAACCCC CCCCTGCACC
1301 CCCCTCCCCG AGTTGCTGAG CACGGCCCGG CTTCGGGTGC GGGGTCCGCT
1351 GCGGGGCGTG GCGCGGGGCT CGCCGTGCCG GGCGGGGGGT GGCGGCAGGT
30 1401 GGGGGTGCCG GGCGGGGCGG GGCCGCCCTC GGCCGGGGAG GGCTCGGGGG
1451 AGGGGCGCGG CGGCCCCGGA GCGCCGCGCG CTGTGAGGC GCGGCAGGCC
1501 GCAGCCATTG CCTTTTATGG TAATCGTGCG AGAGGGCGCA GGGACTTCCT
1551 TTGTCCCAAA TCTGGCGGAG CCGAAATCTG GGAGGCGCCG CCGCACCCCC
1601 TCTAGCGGGC GCGGGCGAAG CCGTGC GGCGC CCGGCAGGAA GGAATGGGC
35 1651 GGGGAGGGCC TTCGTGCGTC GCCGCGCCGC CGTCCCCTTC TCCATCTCCA
1701 GCCTCGGGGC TGCCGCAGGG GGACGGCTGC CTTCGGGGGG GACGGGGCAG
1751 GGCGGGGTTC GGCTTCTGGC GTGTGACCGG CGGCTCTAGA GCCTCTGCTA
1801 ACCATGTTCA TGCCTTCTTC TTTTCTCTAC AGCTCCTGGG CAACGTGCTG
1851 GTTATTGTGC TGTCTCATCA TTTTGGCAAA GAATTCTAAT ACGACTCACT
40 1901 ATAGGGAGAC CCAAGCTGGC TAGCCAAAAG TTCCACCATG GCGGGGCTCT
1951 GGCTGGGGCT CGTGTGGCAG AAGCTGCTGC TGTGGGGCGC GGCAGGTGCC
2001 CTTTCCCTGG CCGGCGCCAG TCTGGTCTG AGCCTGCTGC AGAGGGTGGC
2051 GAGCTACGCG CGGAAATGGC AGCAGATGCG GCCCATCCCC ACGGTGGCCC
2101 GCGCCTACCC ACTGGTGGGC CACGCGCTGC TGATGAAGCC GGACGGGCGA
45 2151 GAATTTTTTC AGCAGATCAT TGAGTACACA GAGGAATACC GCCACATGCC
2201 GCTGCTGAAG CTCTGGGTCTG GGCCAGTGCC CATGGTGGCC CTTTATAATG
2251 CAGAAAATGT GGAGGTAATT TTAAGTAGTT CAAAGCAAAT TGACAAAATCC
2301 TCTATGTACA AGTTTTTAGA ACCATGGCTT GGCCTAGGAC TTCTTACAAG
2351 TACTGGAAC AAATGGCGCT CCAGGAGAAA GATGTTAACA CCCACTTTC
50 2401 ATTTTACCAT TCTGGAAGAT TTCTTAGATA TCATGAATGA ACAAGCAAAT

```

2451 ATATTGGTTA AGAAACTTGA AAAACACATT AACCAAGAAG CATTTAAGTG
2501 CTTTTTTTAC ATCACTCTTT GTGCCCTAGA TATCATCTGT GAAACAGCTA
2551 TGGGGAAGAA TATTGGTGCT CAAAGTAATG ATGATTCCGA GTATGTCCGT
2601 GCAGTTTATA GAATGAGTGA GATGATATTT CGAAGAATAA AGATGCCCTG
5 2651 GCTTTGGCTT GATCTCTGGT ACCTTATGTT TAAAGAAGGA TGGGAACACA
2701 AAAAGAGCCT TAAGATCCTA CATACTTTTA CCAACAGTGT CATCGCGGAA
2751 CGGGCCAATG AAATGAACGC CAATGAAGAC TGTAGAGGTG ATGGCAGGGG
2801 CTCTGCCCCC TCCAAAAATA AACGCAGGGC CTTTCTTGAC TTGCTTTTAA
2851 GTGTGACTGA TGACGAAGGG AACAGGCTAA GTCATGAAGA TATTCGAGAA
10 2901 GAAGTTGACA CCTTCATGTT TGAGGGGCAC GATACAACTG CAGCTGCAAT
2951 AAAGTGGTCC TTATACCTGT TGGGTTCTAA CCCAGAAAGT CAGAAAAAAG
3001 TGGATCATGA ATTGGATGAC GTGTTTGGGA AGTCTGACCG TCCCCTACAC
3051 GTAGAAGACC TGAAGAAACT TCGGTATCTG GAATGTGTTA TTAAGGAGAC
3101 CCTTCGCCTT TTTCTTCTG TTTCTTTATT TGCCCGTAGT GTTAGTGAAG
15 3151 ATTGTGAAGT GGCAGGTTAC AGAGTTCTAA AAGGCACTGA AGCCGTCATC
3201 ATTCCCTATG CATTGCACAG AGATCCGAGA TACTTCCCCA ACCCCGAGGA
3251 GTTCCAGCCT GAGCGGTTCT TCCCCGAGAA TGCACAAGGG CGCCATCCAT
3301 ATGCCTACGT GCCCTTCTCT GCTGGCCCCA GGAAGTGTAT AGGTCAAAAG
3351 TTTGCTGTGA TGGGAAGAAA GACCATTCTT TCGTGCATCC TGAGGCACTT
20 3401 TTGGATAGAA TCCAACCAGA AAAGAGAAGA GCTTGGTCTA GAAGGACAGT
3451 TGATTCTTCG TCCAAGTAAT GGCATCTGGA TCAAGTTGAA GAGGAGAAAT
3501 GCAGATGAAC GCTAAGCGGC CGCAACTCGA GACTCTAGAG GTTAATCGAT
3551 AATCAACCTC TGGATTACAA AATTTGTGAA AGATTGACTG GTATTCTTAA
3601 CTATGTTGCT CTTTTTACGC TATGTGGATA CGCTGCTTTA ATGCCTTTGT
25 3651 ATCATGCTAT TGCTTCCCGT ATGGCTTTCA TTTTCTCCTC CTTGTATAAA
3701 TCCTGGTTGC TGTCTCTTTA TGAGGAGTTG TGGCCCGTTG TCAGGCAACG
3751 TGGCGTGGTG TGCATGTGT TTGCTGACGC ACCCCCCT GGTGGGGCA
3801 TTGCCACCAC CTGTCAGCTC CTTTCCGGGA CTTTCGCTTT CCCCCCCT
3851 ATTGCCACGG CGGAACTCAT CGCCGCCTGC CTTGCCCGCT GCTGGACAGG
30 3901 GGCTCGGCTG TTGGGCACTG ACAATTCCGT GGTGTTGTG GGGAAATCAT
3951 CGTCCTTTCC TTGGCTGCTC GCCTGTGTTG CCACCTGGAT TCTGCGCGGG
4001 ACGTCCTTCT GCTACGTCCT TTCGGCCCTC AATCCAGCGG ACCTTCCTTC
4051 CCGCGGCTTG CTGCCGCTC TGCGGCCTCT TCCGCGTCTT CGCCTTCGCC
4101 CTCAGACGAG TCGGATCTCC CTTTGGGCGG CCTCCCCGCA TCGAAACCCG
35 4151 CTGACTAGAC GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC
4201 TCCCCCGTGC CTTCCCTGAC CCTGGAAGGT GCCACTCCCA CTGTCCTTTC
4251 CTAATAAAAT GAGGAAATTG CATCGCATTG TCTGAGTAGG TGTCATTCTA
4301 TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA TTGGGAAGAC
4351 AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCCG CGGGCCGCAG
40 4401 GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG CTCGCTCGCT
4451 CACTGAGGCC GGGCGACCAA AGGTCGCCC GCGCCCGGGC TTTGCCCGGG
4501 CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG

```

SEQ ID NO: 63 - Sequence of CYP4V2 expression cassette in
45 AAV5.CYP4V2op (new). AAV5.CYP4V2op (new) has the same promoter (CAG),
enhancer (WPRES) and polyA (bGH-polyA) and the same junction/linker
sequences as AAV5.CYP4V2st (SEQ ID NO: 61) and AAV8.CYP4V2fv (SEQ ID
NO: 62) but different CYP4V2 cDNA sequences:
Left-ITR: 1-141
50 CAG promoter: 166-1880

CYP4V2op cDNA: 1938-3515

WPRE enhancer: 3551-4139

bGH polyA: 4163-4387

Right-ITR: 4399-4539

5
 CCTGCAGGCA GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG
 CCCGGGCGTC GGGCGACCTT TGGTCGCCCC GCCTCAGTGA GCGAGCGAGC
 GCGCAGAGAG GGAGTGGCCA ACTCCATCAC TAGGGGTTCC TGCGGCCTAA
 GGCAATTGAG ATCTCGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA
 10 ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA
 ACTTACGGTA AATGGCCCCG CTGGCTGACC GCCCAACGAC CCCCGCCCAT
 TGACGTCAAT AATGACGTAT GTTCCCATAG TAACGCCAAT AGGGACTTTC
 CATTGACGTC AATGGGTGGA CTATTTACGG TAAACTGCCC ACTTGGCAGT
 ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC GTCAATGACG
 15 GTAAATGGCC CGCCTGGCAT TATGCCAGT ACATGACCTT ATGGGACTTT
 CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGGTCG
 AGGTGAGCCC CACGTTCTGC TTCACTCTCC CCATCTCCCC CCCCTCCCCA
 CCCCCAATTT TGTATTTATT TATTTTTTAA TTATTTTGTG CAGCGATGGG
 GCGCGGGGGG GGGGGGGCGC GCGCCAGGCG GGGCGGGGCG GGGCGAGGGG
 20 CGGGGCGGGG CGAGGCGGAG AGGTGCGGCG GCAGCCAATC AGAGCGGCGC
 GCTCCGAAAG TTTCTTTTAA TGGCGAGGCG GCGGCGGCGG CGGCCCTATA
 AAAAGCGAAG CGCGCGGCGG GCGGGAGTCG CTGCGTTGCC TTCGCCCCGT
 GCGCCGCTCC GCGCCGCTTC GCGCCGCCCC CCGCGCTCT GACTGACCGC
 GTTACTCCCA CAGGTGAGCG GCGGGACG CGCTTCTCCT CCGGGCTGTA
 25 ATTAGCGCTT GGTTTAATGA CGGCTCGTTT CTTTCTGTG GCTGCGTGAA
 AGCCTTAAAG GGCTCCGGGA GGGCCCTTTG TGCGGGGGG AGCGGCTCGG
 GGGGTGCGTG CGTGTGTGTG TGCGTGGGGA GCGCCGCGTG CGGCCCCGCG
 TGCCCGGCGG CTGTGAGCGC TGCGGGCGCG GCGCGGGGCT TTGTGCGCTC
 CGCGTGTGCG CGAGGGGAGC GCGGCCGGGG GCGGTGCCCC GCGGTGCGGG
 30 GGGGCTGCGA GGGGAACAAA GGCTGCGTGC GGGGTGTGTG CGTGGGGGGG
 TGAGCAGGGG GTGTGGGCGC GCGGTCGGG CTGTAACCCC CCCCTGCACC
 CCCCTCCCCG AGTTGCTGAG CACGGCCCGG CTTGCGGTGC GGGGCTCCGT
 GCGGGGCGTG GCGCGGGGCT CGCCGTGCCG GCGGGGGGTT GCGGCAGGT
 GGGGGTGCCG GCGGGGCGG GCGCGCCTCG GCGCGGGGAG GGCTCGGGGG
 35 AGGGGCGCGG CGGCCCCGGA GCGCCGGCGG CTGTCGAGGC GCGGCGAGCC
 GCAGCCATTG CCTTTTATGG TAATCGTGCG AGAGGGCGCA GGGACTTCCT
 TTGTCCCAA TCTGGCGGAG CCGAAATCTG GGAGGCGCCG CCGCACCCCC
 TCTAGCGGGC GCGGGCGAAG CGGTGCGGCG CCGGCAGGAA GGAAATGGGC
 GGGGAGGGCC TTCGTGCGTC GCGCGCGCGC CGTCCCCTTC TCCATCTCCA
 40 GCCTCGGGGG TGCCGCAAGG GGACGGCTGC CTTGCGGGGG GACGGGGCAG
 GCGGGGGTTC GGCTTCTGGC GTGTGACCGG CGGCTCTAGA GCCTCTGCTA
 ACCATGTTCA TGCCTTCTTC TTTTTCCTAC AGCTCCTGGG CAACGTGCTG
 GTTATTGTGC TGTCTCATCA TTTTGGCAA GAATTCTAAT ACGACTCACT
 ATAGGGAGAC CCAAGCTGGC TAGCCAAAGC TTCCACC
 45 ATGGCTGGACTGTGGCTGGGACTGGTGTGGCAGAACTGCTGCTGTGGGGGGCCGCTTCCGCACTGTCAC
 TGGCTGGGGCTTCACTGGTGCTGAGCCTGCTGCAGAGGGTGGCCTCCTACGCCAGAAAGTGGCAGCAGAT
 GAGGCCCATCCCTACCGTGGCCAGAGCCTATCCACTGGTGGGACACGCACTGCTGATGAAGCCTGACGGC
 AGAGAGTTCTTTCAGCAGATCATCGAGTACACAGAGGAGTATAGGCACATGCCACTGCTGAAGCTGTGGG
 TGGGACCCGTGCCTATGGTGGCCCTGTACAACGCCGAGAATGTGGAAGTGATCCTGACCAGCAGCAAGCA
 50 GATCGATAAGTCTAGCATGTATAAGTTCTTGAGCCTTGCTGGGCCTGGGCCTGCTGACCTCTACAGGC

AACAAAGTGGAGGAGCCGGAGAAAGATGCTGACCCCAACATTCCACTTTACAATCCTGGAGGACTTCCTGG
 ACATCATGAACGAGCAGGCCAATATCCTGGTGAAGAAGCTGGAGAAGCACATCAACCAGGAGGCCTTTAA
 TTGCTTCTTTTACATCACCCTGTGCGCCCTGGACATCATCTGTGAGACAGCTATGGGCAAGAACATCGGC
 5 GCCCAGTCTAATGACGATAGCGAGTACGTGCGGGCCGTGTATAGAATGAGCGAGATGATCTTTAGGCGCA
 TCAAGATGCCCTGGCTGTGGCTGGATCTGTGGTATCTGATGTTCAAGGAGGGCTGGGAGCACAAGAAGTC
 CCTGCAGATCCTGCACACCTTTACAAACTCTGTGATCGCCGAGAGAGCCAATGAGATGAACGCCAATGAG
 GACTGTAGGGGCGATGGAAGGGGCGAGCGCCCTTCCAAGAACAAGCGGAGAGCCTTCTGGACCTGCTGC
 TGAGCGTGACCGACGATGAGGGCAATCGCCTGTCCCACGAGGACATCCGGGAGGAGGTGGATACATTTCAT
 GTTTGAGGGACACGACACCACAGCCGCCCATCAACTGGTCCCTGTACCTGCTGGGCTCTAATCCAGAG
 10 GTGCAGAAGAAGGTGGATCACGAGCTGGACGACGTGTTCCGCAAGTCCGACAGGCCAGCAACCGTGGAGG
 ATCTGAAGAAGCTGAGATACCTGGAGTGCGTGATCAAGGAGACACTGCGCCTGTTCCTCTGTGCCTCT
 GTTTGCCCGGTCCGTGTCTGAGGACTGTGAGGTGGCCGGCTATCGCGTGCTGAAGGGCACCAGGCGCGTG
 ATCATCCCTTACGCCCTGCACCGGGACCCAGGTATTTCCCTAACCCAGAGGAGTTTCAGCCAGAGAGAT
 TCTTTCCCGAGAATGCCAGGGCAGGCACCCTTACGCCTATGTGCCATTCTCCGCCGACCAAGGAATG
 15 CATCGGACAGAAGTTTGCCGTGATGGAGGAGAAAACCATCCTGTCTTGATCCTGAGACACTTCTGGATC
 GAGAGCAATCAGAAGAGGGAGGAGCTGGGCCTGGAGGGACAGCTGATCCTGCGGCCAAGCAACGGCATCT
 GGATCAAACCTGAAAAGAAGGAACGCTGACGAGAGGTAAGCGGC CGCAACTCGA GACTCTAGAG
 GTTAATCGAT
 AATCAACCTC TGGATTACAA AATTTGTGAA AGATTGACTG GTATTCTTAA
 20 CTATGTTGCT CTTTTTACGC TATGTGGATA CGTGCTTTA ATGCCTTTGT
 ATCATGCTAT TGCTTCCCGT ATGGCTTTCA TTTTCTCCTC CTTGTATAAA
 TCCTGGTTGC TGTCTCTTTA TGAGGAGTTG TGGCCCGTTG TCAGGCAACG
 TGGCGTGTTG TGCACGTGTG TTGCTGACGC AACCCCACT GGTGGGGCA
 TTGCCACCAC CTGTCAGCTC CTTTCCGGGA CTTTCGCTTT CCCCCTCCCT
 25 ATTGCCACGG CGGAACCTCAT CGCCGCCTGC CTTGCCCGCT GCTGGACAGG
 GGCTCGGCTG TTGGGCACTG ACAATTCCGT GGTGTTGTCG GGGAAATCAT
 CGTCCCTTTC TTGGCTGCTC GCCTGTGTTG CCACCTGGAT TCTGCGCGGG
 ACGTCCTTCT GCTACGTCCC TTCGGCCCTC AATCCAGCGG ACCTTCCTTC
 CCGCGGCCTG CTGCCGGCTC TGCGGCCTCT TCCGCGTCTT CGCCTTCGCC
 30 CTCAGACGAG TCGGATCTCC CTTTGGGCCG CCTCCCCGCA TCGAAACCCG
 CTGACCTAGAC GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC
 TCCCCCGTGC CTTCCCTGAC CCTGGAAGGT GCCACTCCCA CTGTCCTTTC
 CTAATAAAAT GAGGAAATTG CATCGCATTG TCTGAGTAGG TGTCATTCTA
 TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA TTGGGAAGAC
 35 AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCCG CGGGCCGCAG
 GAACCCCTAG TGATGGAGTT GGCCACTCCC TCTCTGCGCG CTCGCTCGCT
 CACTGAGGCC GGGCGACCAA AGGTCGCCCC ACGCCCGGGC TTTGCCCGGG
 CGGCCTCAGT GAGCGAGCGA GCGCGCAGCT GCCTGCAGG
 40 SEQ ID NO: 64 - Sequence of CYP4V2 expression cassette in
 scAAV1.CYP4V2op, scAAV5.CYP4V2op, and scAAV9.CYP4V2op.
 Left-ITR (truncated): 1-117
 EFS promoter: 130-364
 CYP4V2op cDNA: 520-2097
 45 SPA: 2116-2169
 Right-ITR: 2263-2403
 1 cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaa
 cccgggcgctc
 61 gggcgacctt tggtcgcccc gcctcagtga gcgagcgagc gcgagagag
 50 ggagtggacg

121 cgtaggcctg attggctccg gtgcccgtca gtgggcagag cgcacatcgc
ccacagtccc
181 cgagaagttg gggggagggg tcggcaattg aaccggtgcc tagagaaggt
ggcgcggggt
5 241 aaactgggaa agtgatgtcg tgtactggct ccgccttttt cccgaggggtg
ggggagaacc
301 gtatataagt gcagtagtcg ccgtgaacgt tctttttcgc aacgggtttg
ccgccagaac
10 361 acaggtgtcg tgacgcgacc aggtatgcat ctgcagctct aaggtaaata
taaaattttt
421 aagtgtataa tgtgttaaac tactgattct aattgtttct ctcttttaga
ttccaacctt
481 tggaactgac tgcagggatc caagctttct agagccacca tggctggact
gtggctggga
15 541 ctggtgtggc agaaactgct gctgtggggg gccgcttccg cactgtcact
ggctggggct
601 tcaactgtgc tgagcctgct gcagaggggtg gcctcctacg ccagaaagtg
gcagcagatg
20 661 agggccatcc ctaccgtggc cagagcctat ccactgggtg gacacgact
gctgatgaag
721 cctgacggca gagagttctt tcagcagatc atcgagtaca cagaggagta
taggcacatg
781 ccactgctga agctgtgggt gggaccctg cctatgggtg ccctgtacaa
cgccgagaat
25 841 gtggaagtga tcctgaccag cagcaagcag atcgataagt ctagcatgta
taagttcctg
901 gagccttggc tgggcctggg cctgctgacc tctacaggca acaagtggag
gagccggaga
30 961 aagatgctga cccaacatt ccactttaca atcctggagg acttcctgga
catcatgaac
1021 gagcaggcca atatcctggt gaagaagctg gagaagcaca tcaaccagga
ggcctttaat
1081 tgcttctttt acatcaccct gtgcgccctg gacatcatct gtgagacagc
tatgggcaag
35 1141 aacatcggcg ccaggtctaa tgacgatagc gagtacgtgc gggccgtgta
tagaatgagc
1201 gagatgatct ttaggcgcat caagatgccc tggctgtggc tggatctgtg
gtatctgatg
40 1261 ttcaaggagg gctgggagca caagaagtcc ctgcagatcc tgcacacctt
tacaaactct
1321 gtgatcgccg agagagccaa tgagatgaac gccaatgagg actgtagggg
cgatggaagg
1381 ggcagcgccc cttccaagaa caagcggaga gccttcctgg acctgctgct
gagcgtgacc
45 1441 gacgatgagg gcaatgcct gtcccacgag gacatccggg aggaggtgga
tacattcatg
1501 tttgagggac acgacaccac agccgccgcc atcaactggg ccctgtacct
gctgggctct
1561 aatccagagg tgcagaagaa ggtggatcac gagctggacg acgtgttcgg
50 caagtcggac

1621 aggccagcaa ccgtggagga tctgaagaag ctgagatacc tggagtgcgt
gatcaaggag
1681 aactgcgcc tgttcccctc tgtgcctctg tttgcccggt ccgtgtctga
ggactgtgag
5 1741 gtggccggct atcgcgtgct gaagggcacc gaggccgtga tcatccctta
cgccctgcac
1801 cgggacccca ggtatttccc taaccacagag gagtttcagc cagagagatt
ctttcccgag
1861 aatgcccagg gcaggcaccc ttacgcctat gtgccattct ccgccggacc
10 aaggaactgc
1921 atcggacaga agtttgccgt gatggaggag aaaaccatcc tgtcttgat
cctgagacac
1981 ttctggatcg agagcaatca gaagaggag gagctgggcc tggagggaca
gctgacctg
15 2041 cggccaagca acggcatctg gatcaaactg aaaagaagga acgctgacga
gaggtaaaag
2101 cttgaattcc tcgaggatcc aataaaagat ctttattttc attagatctg
tgtgttggtt
2161 ttttgtgtgt ctagttgcca gccatctggt gtttgcccct ccccgctgcc
20 ttccttgacc
2221 ctggaagggtg ccaactccag tttaaaactta attaagggcc gcaggaacco
ctagtgatgg
2281 agttggccac tccctctctg cgcgctcgt cgctcactga ggccgggcca
ccaaagggtc
25 2341 cccgacgcc gggctttgcc cgggcggcct cagtgaagca gcgagcgccg
agctgcctgc
2401 agg

30