Spliceosome-Mediated Pre-mRNA trans-Splicing Can Repair CEP290 mRNA

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Ocular gene therapy with recombinant adeno-associated virus (AAV) has shown vector-mediated gene augmentation to be safe and efficacious in the retina in one set of diseases (retinitis pigmentosa and Leber congenital amaurosis (LCA) caused by RPE65 deficiency), with excellent safety profiles to date and potential for efficacy in several additional diseases. However, size constraints imposed by the packaging capacity of the AAV genome restrict application to diseases with coding sequence lengths that are less than 5,000 nt. The most prevalent retinal diseases with monogenic inheritance are caused by mutations in genes that exceed this capacity. Here, we designed a spliceosome mediated pre-mRNA trans-splicing strategy to rescue expression of CEP290, which is associated with Leber congenital amaurosis type 10 (LCA10) and several syndromic diseases including Joubert syndrome. We used this reagent to demonstrate editing of CEP290 in cell lines in vitro and in vivo in a mini-gene mouse model. This study is the first to show broad editing of CEP290 transcripts and in vivo proof of concept for editing of CEP290 transcripts in photoreceptors and paves the way for future studies evaluating therapeutic effects.

INTRODUCTION

Leber congenital amaurosis (LCA) is the most severe subset of the set of diseases classified as retinitis pigmentosa, affecting 1 in 100,000 people with nearly 20 identified disease-associated genes. LCA is typically diagnosed in infants with severely abnormal vision through finding of non-recordable electroretinograms. Children with LCA have trouble seeing in dim light (nyctalopia), have reduced visual resolution (visual acuity) and peripheral vision (visual fields), and often have abnormal rotatory eye movements (nystagmus). Whatever poor vision they have early in life gradually disappears due to the degenerative component of the disease.° Amelioration of one form of early-onset retinal degeneration caused by the gene RPE65 has been demonstrated following sub-retinal administration of recombinant adeno-associated virus (AAV) encoding the complete RPE65 coding DNA sequence.2° Other forms of inherited retinal degeneration may be amenable to rescue following this strategy; however, the genes associated with the most prevalent forms of retinal disease exceed the DNA coding capacity of AAV.° Mutations in CEP290 are designated as LCA type 10 (LCA10), and the complete coding DNA sequence is 7,440 nt (GeneBank: NM_025114.3). Therefore, it is necessary to develop a gene therapy strategy that can correct a broad range of mutations in large genes such as CEP290 with AAV.

Most LCA10 patients harbor two mutations in CEP290, which are typically compound heterozygous. The most common mutation in LCA10 is a single nucleotide polymorphism of A to G within the intron between exons 26 and 27. The mutation is annotated as IVS26.c.2991+1655A>G, hereafter IVS26, and generates a cryptic splice site leading to inclusion of a cryptic exon, known as exon X, which encodes an immediate stop codon (Figure 1A). Though fully differentiated, light-responsive photoreceptors generated from induced pluripotent stem cells have yet to be generated, optic cups generated from IVS26 homozygous patients show reduced CEP290 protein, shorter cilia, and other deficits compared to wild-type cell lines.5 Additionally, other cell types, including primary fibroblasts, show similar phenotypes.5

Based on the prevalence of IVS26 within LCA10 patients and likely disease pathogenesis through haploinsufficiency, several strategies have been developed to specifically prevent inclusion of cryptic exon X. Several groups have targeted the RNA-directed endonuclease Cas9 to the cryptic splice site to either alter the sequence or specifically use homology-directed repair to correct the mutation.6° Anti-sense oligonucleotides have also been evaluated in several settings with IVS26 homozygous patient-derived cells and shown to reduce inclusion of exon X and restore CEP290 protein levels.6° One concern is that the utility of the Cas9 or anti-sense oligonucleotide methods directed at exon X may not be as high in compound heterozygous patients or in patients lacking the IVS26 mutation since the second allele would not benefit from therapy. Lastly, efforts have been made to break the coding DNA sequence of a large gene into fragments across multiple viral genomes.7° When applied to LCA10, two AAV genomes are designed with either the 5' or 3' half of CEP290 along with elements required to reconstitute the open DNA sequence.2

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Figure 1. Strategy to Rescue CEP290 through 5' Pre-mRNA trans-Splicing

(A) Diagram of the most prevalent mutation in Leber congenital amaurosis type 10. This intron variant sequence (IVS) is an A-to-G transition that creates a canonical 5' splice site (5' SS). The novel splice site leads to inclusion of a cryptic exon, exon X. This cryptic exon encodes a premature stop codon leading to a truncated protein. (B) Left, computational analysis of required elements for a trans-splicing molecule and the size limitations of adeno-associated virus. Right, analysis of CEP290 exon and intron boundaries reveals the size of a 5' PCDS when using a 5' trans-splicing approach to target various introns. When exon X is included in the transcript, intron 26-27 is split into intron 26-X and intron X-27. A complete table for CEP290 is included in Table 1. (C) Schematic of an approach to utilize a 5' pre-mRNA trans-splicing molecule (PTM) to rescue mutations in CEP290 that are located 5' to intron X-27. The PTM transcript is bound via Watson-Crick base pairing to the pre-mRNA of a target via a sequence known as the binding domain, located at the 3' end of the PTM, and that is reverse complementary to the target sequence. (D) Three potential splicing outcomes with CEP290 IVS26 following introduction of a 5' PTM: (1) joining of exon 26 to exon 27 from cis-splicing for the wild-type junction; (2) inclusion of exon X from cis-splicing (predominant mRNA...
The limitations of this approach concern (1) efficiency—vectors of each genome must transduce the same cell and further, the genomes must recombine or undergo concatamerization in the proper orientation, and (2) potential immunogenicity—both fragments have the potential to produce partial gene products, which may trigger an immune response.

Delivery of AAV genomes encoding partial coding DNA sequences designed to trans-splice to endogenous pre-mRNA is also an attractive strategy. This strategy is akin to the multiple vectors strategy but differs in that a single viral genome is used that targets endogenous pre-mRNA transcripts to yield a hybrid exogenous-endogenous mRNA. Additionally, this strategy takes advantage of endogenous expression levels, which is a safety consideration since CEP290 over-expression may cause toxicity.27

Trans-splicing was first shown to occur in vitro.14,15 Since then, trans-splicing molecules have been demonstrated with 5', 3', or internal exon replacement.20-24 Pre-mRNA trans-splicing molecules have been demonstrated to edit genes across many disease models including cystic fibrosis,19-22 muscular dystrophy,23-25 hypertrophic cardiomyopathy,24,26 and retinitis pigmentosa.1,17 Some efforts have also been made to apply trans-splicing to the treatment of cancer cells, including functional repair of p53 in colorectal cancer cells and hepatocellular carcinoma cells.27,28 Here, we evaluated the potential of pre-mRNA trans-splicing to edit CEP290 and demonstrated that this approach can be effective in yielding hybrid RNA both in vitro and in vivo.

RESULTS

Design of a trans-Splicing Strategy for CEP290

A strategy to rescue CEP290 should cover as many disease-associated mutations as possible. Therefore, we wanted the maximum length of possible partial coding DNA sequence. We initially designed a hypothetical pre-mRNA trans-splicing molecule consisting of flanking inverted terminal repeats, the cytomegalovirus immediate-early enhancer and promoter, the partial coding DNA sequence whose maximum size we were to determine, a canonical 5' splice site, 20 nt of intron spacer sequence, a putative binding domain, and a bovine growth hormone polyadenylation signal sequence. After subtracting these elements from the maximum 4,700 nt of AAV, the maximum partial coding DNA sequence (PCDS) size for a trans-splicing AAV genome can be estimated to be between 3,000 and 3,500 nt (Figure 1B, left).

For a 5' pre-mRNA trans-splicing molecule (PTM), the PCDS must end at the 3' end of an exon to allow for a 5' splice site. Therefore, PCDS size increases by the size of the exon proximal to a target intron. When plotted as a table, the PCDS size is the sum of all coding nucleotides upstream to the target intron. The first methionine of the open reading frame (ORF) for CEP290 is encoded in the second exon. Therefore, the PCDS begins within exon 2 and continues to the stop codon in exon 54. We generated a table consisting of CEP290 exon numbers, nucleotide length of exons and introns, and a tally of the coding nucleotides at each boundary (Table 1).

To rescue the most common mutations that cause LCA10, at minimum, a 5' PTM must be targeted to a region downstream of exon X. By definition, exon X breaks intron 26-27 into the novel introns 26-X and X-27. We determined that intron X-27 would be 4,188 nt and would require a 5' PCDS consisting of 2,991 nt (Figure 1B, right). We selected intron X-27 as the region to target and screen for putative binding domains (Figure 1C). Treatment of cells containing the IVS26 mutation with a trans-splicing AAV genome targeting intron X-27 would result in three predicted outcomes: (1) a fraction of transcripts splicing normally to generate a wild-type allele, (2) inclusion of exon X via cis-splicing leading to expected nonsense mediated decay, and (3) the trans-spliced hybrid of 5' PCDS and endogenous exons 27-54 with the potential to generate wild-type protein (Figure 1D).

We then designed an AAV genome encoding the cytomegalovirus (CMV) promoter driving expression of a 5' PTM containing coding nucleotides 1 through 2,991, which encodes Met1 through Glu997 p.(M1-E997) and added a cloning site for addition of a binding domain (Figure 1E).

Screening of Binding Domains in CEP290 Intron 26

The specificity of a PTM is conferred by the binding domain annealing to a target pre-mRNA through Watson-Crick base pairing. To identify a functional binding domain in intron X-27, we adapted a previously described fluorescence reconstitution assay.29,30 In brief, the complete coding DNA sequence of the Aequorea coeruleascens-derived GFP mammalian enhanced (codon-optimized) sequence was split between Glu112 and Val113 (GAG/GTG).31 To screen binding domains for a 5' trans-splicing strategy, the 5' GFP PCDS (Met1 through Glu112) was cloned into a 5' PTM reporter, while the 3' GFP PCDS (Val113 through Stop240) was cloned downstream of the complete CEP290 target intron 26-27 in a novel mini-gene plasmid. A trans-splicing event between the pre-mRNAs of the two plasmids would thus reconstitute the GFP ORF and result in GFP-positive cells (Figure 2A).

We evaluated the sequence of intron X-27 for frequently cutting blunt restriction enzymes with consensus sites in the target region.32 This analysis revealed that a combination of Rsal and Dral was predicted to yield fragments between 50 and 300 nt, which has been described as the optimal size for binding domains33 (Figure 2B). We then amplified intron X-27 from genomic DNA of a healthy donor and

species with IVS26 present); (3) joining of the 5’ PCDS to exon 27 from trans-splicing. Both outcomes 1 and 3 would result in full-length CEP290 peptide. (E) Illustration of an adeno-associated virus genome encompassing the therapeutically relevant CEP290 5’ trans-splicing molecule. Inverted terminal repeats (ITR) flank an expression cassette consisting of the cytomegalovirus promoter (CMV), a PCDS encoding the first 2,991 nt of the coding DNA sequence, a 5’ splice site (5’ SS), a spacer region, a binding domain that is reverse complementary to a region of intron X-27, and a polyadenylation signal sequence (pA).
confirmed the presence of expected fragments after restriction enzyme digestion (Figure 2C). The fragment pool was then cloned into the reporter to generate a plasmid library.

The library and the mini-gene target were transfected alone or co-transfected at an equimolar ratio into HEK293T cells (ATCC, Manassas, Virginia). GFP-positive wells were visualized with fluorescence microscopy and assayed at 48 hr after transfection by flow cytometry to quantify the percentage of GFP-positive cells in each population. Co-transfection of target with reporter PTMs encoding fragments 02 or 07 resulted in the highest expression of GFP, while transfection with the reporter PTMs alone resulted in less than 1% GFP-positive cells (Figure 2D). Interestingly, the reporter with no binding domain (NBD) generated a small fraction of GFP-positive cells when co-transfected with the target. Reporters with a binding domain sequence in forward orientation, demarcated “f,” were predicted to not improve trans-splicing efficiency, and samples 09f and 13f were not above the level of NBD, while 05f was slightly increased (Figure 2D; BD_05f/09f/13f). Sequence comparisons between the target and test molecules using ClustalOmega and BLASTn did not reveal regions of homology that would be predicted to facilitate targeted trans-splicing by canonical mechanisms.

We next validated that GFP signal was resulting from reconstitution of the GFP ORF and not from a post-translational event. We used primers specific to the junction between the 5' and 3' portions of GFP to probe cDNA generated from treated cells. A band of expected size was amplified in all samples co-transfected with both the target mini-gene and the reporter molecules, but not when individually transfected (Figure 2E). As CEP290 is a ubiquitously expressed gene, the test molecules were predicted to also trans-splice to endogenous pre-mRNA. To investigate this, we used the same 5' GFP primer and paired it with a primer binding to CEP290 exon 27. A band was exclusively detected in cDNA from cells that were transfected with BD_07, and co-transfection reduced the intensity of this band (Figure 2F).

| Exon No. | Exon Size | 5' PCDS | 3' PCDS | Intron Size | Intron Name |
|----------|-----------|---------|---------|-------------|-------------|
| 1        | 317       | 7,440   | 565     | 1-2         |
| 2        | 129       | 7,338   | 172     | 2-3         |
| 3        | 78        | 7,260   | 1,391   | 3-4         |
| 4        | 70        | 7,190   | 303     | 4-5         |
| 5        | 47        | 7,143   | 2,358   | 5-6         |
| 6        | 144       | 6,999   | 5,424   | 6-7         |
| 7        | 54        | 6,945   | 599     | 7-8         |
| 8        | 21        | 6,924   | 124     | 8-9         |
| 9        | 153       | 6,771   | 391     | 9-10        |
| 10       | 183       | 6,588   | 658     | 10-11       |
| 11       | 90        | 6,498   | 2,507   | 11-12       |
| 12       | 123       | 6,375   | 946     | 12-13       |
| 13       | 124       | 6,251   | 4,079   | 13-14       |
| 14       | 170       | 6,081   | 720     | 14-15       |
| 15       | 163       | 5,818   | 1,370   | 15-16       |
| 16       | 101       | 5,817   | 72      | 16-17       |
| 17       | 88        | 5,729   | 1,337   | 17-18       |
| 18       | 113       | 5,616   | 1,850   | 18-19       |
| 19       | 85        | 5,531   | 535     | 19-20       |
| 20       | 143       | 5,388   | 2,561   | 20-21       |
| 21       | 165       | 5,223   | 342     | 21-22       |
| 22       | 150       | 5,073   | 2,020   | 22-23       |
| 23       | 116       | 4,957   | 1,967   | 23-24       |
| 24       | 103       | 4,854   | 99      | 24-25       |
| 25       | 231       | 4,623   | 3,663   | 25-26       |
| 26       | 274       | 4,449   | 5,838   | 26-27       |
| 27       | 112       | 4,337   | 2,912   | 27-28       |
| 28       | 306       | 4,131   | 937     | 28-29       |
| 29       | 346       | 3,979   | 1,841   | 29-30       |
| 30       | 112       | 3,867   | 1,240   | 30-31       |
| 31       | 456       | 3,411   | 1,087   | 31-32       |
| 32       | 165       | 3,246   | 1,281   | 32-33       |
| 33       | 108       | 3,138   | 217     | 33-34       |
| 34       | 135       | 3,003   | 1,186   | 34-35       |
| 35       | 267       | 2,736   | 631     | 35-36       |
| 36       | 108       | 2,628   | 616     | 36-37       |
| 37       | 200       | 2,428   | 2,635   | 37-38       |
| 38       | 214       | 2,214   | 952     | 38-39       |
| 39       | 138       | 2,076   | 1,173   | 39-40       |
| 40       | 222       | 1,854   | 352     | 40-41       |
| 41       | 123       | 1,731   | 5,295   | 41-42       |
| 42       | 146       | 1,585   | 331     | 42-43       |
| 43       | 156       | 1,429   | 2,648   | 43-44       |

Table 1. CEP290 Exon and Intron Boundaries with Corresponding Partial Coding DNA Sequence

Table 1. Continued

| Exon No. | Exon Size | 5' PCDS | 3' PCDS | Intron Size | Intron Name |
|----------|-----------|---------|---------|-------------|-------------|
| 44       | 124       | 6,135   | 1,305   | 4,406       | 44-45       |
| 45       | 135       | 6,270   | 1,170   | 1,202       | 45-46       |
| 46       | 87        | 6,357   | 1,083   | 1,697       | 46-47       |
| 47       | 165       | 6,522   | 918     | 809         | 47-48       |
| 48       | 123       | 6,645   | 795     | 877         | 48-49       |
| 49       | 173       | 6,818   | 622     | 3,130       | 49-50       |
| 50       | 142       | 6,960   | 480     | 1,162       | 50-51       |
| 51       | 74        | 7,034   | 406     | 593         | 51-52       |
| 52       | 95        | 7,129   | 311     | 3,218       | 52-53       |
| 53       | 80        | 7,209   | 231     | 939         | 53-54       |
| 54       | 395       | 7,440   | 1       | 1           |

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Editing of Endogenous CEP290 Transcripts in HEK293T by trans-Splicing

Since transfection of HEK293T with the screening plasmid resulted in detectable trans-splicing of 5′ GFP to endogenous CEP290, we then cloned the BD_07 sequence into a PTM encoding the 5′ PCDS of CEP290. The presence of a transcriptional terminator on a PTM has been demonstrated to have mixed results, which may be context dependent. Lack of a terminator is expected to retain a pre-mRNA in the nucleus, which could facilitate the trans-splicing reaction. To assess this effect in our system, we generated constructs with a bovine growth hormone poly-adenylation signal sequence (PTM_07 PA) or no poly-adenylation sequence (PTM_07 NPA) (Figure 3A).

To elucidate nuanced differences between treatments, we performed qPCR with TaqMan probes on cDNA from HEK293T cells transfected with the 5′ PTMs or a GFP plasmid and isolated RNA at 72 hr post-treatment. Cells treated with PTM_07 PA showed a slight but insignificant reduction of the CEP290 exon 26-27 junction...
We also designed a probe internal to the 5' codon-optimized sequence that detects overall expression of the 5' PCDS regardless of trans-splicing to endogenous pre-mRNA or of RNA maturation of the PTM transcript without trans-splicing. This probe showed a trend toward a 2.5-fold increase in PTM expression for PTM_07 PA when compared to PTM_07 NPA, though it was also
not statistically significant across biological replicates (Figure 3B, center). Similarly, we observed amplification of trans-spliced products with treatment by both NPA and PA PTMs with an insignificant 3-fold trend for higher trans-splicing in the samples with a poly-adenylation signal (Figure 3B, right). Additionally, we generated similar PTMs lacking a binding domain. We did not detect trans-splicing in cells treated with NBD (data not shown). We also validated the trans-spliced product by visualizing the PCR product of the trans-splicing detection reaction and confirmed a band of the expected size in PTM_07 PA and GFP-treated reactions (Figure 3C). Additionally, the band of PTM_07 PA had a slightly higher density than PTM_07 NPA (Figure 3D).

Finally, we further validated the novel splice junction with Sanger sequencing of both the qPCR band and a second PCR amplicon derived from end-point PCR with another primer pair. Analysis of these sequencing reads confirmed the novel junction of codon-optimized exon 26 to endogenous exon 27 with asterisks (*) indicating nucleotide changes designed by codon-optimization (Figure 3E).

**Maturation of the PTM Is Detected at High Levels**

After observing higher cycle threshold (Ct) values of codon-optimized sequence expression than trans-splicing following transfection, we suspected that PTM genomes could be transcribing and generating mature mRNA without trans-splicing. We added an amino-terminal HA-tag to PTM_NBD PA and PTM_07 PA to assess peptide production from the PTMs and added the CMV enhancer to further increase expression. In silico sequence analysis of the 5' PTM revealed an ORF that could generate a predicted peptide of 118.7 kDa if the pre-mRNA matures without trans-splicing. (Figure 4A). To assess if this peptide was indeed present, we performed western blot analysis of protein extracts from HEK293T transfected with the HA-tagged PTMs. This revealed an HA-tagged protein between 110 kDa and 160 kDa with a minor band between 80 and 110 kDa, while no HA-tagged protein was detected above 260 kDa (Figure 4B). A 290 kDa band would be expected for trans-splicing to endogenous CEP290. There was neither significant change to the levels of CEP290 protein following transfection nor a statistically significant difference in levels of the 118.7 kDa peptide between PTM_NBD and PTM_07 (Figure 4C).

The addition of a downstream intronic splice enhancer (DISE) derived from rat FGFR2 has been demonstrated to promote inclusion of exons and PTMs. We inserted the corresponding sequence into the spacer region of PTM_07 and performed transfections in HEK293T. We observed no significant differences in RNA or protein levels between treatment with PTM_07 or PTM_07 FGFR2 DISE (data not shown).
Figure 5. Editing of Mini-CEP290 Transcripts Occurs In Vivo following Sub-retinal Injection of 7m8AAV-5' PTMs

(A) Diagram of the CEP290 intron 26 mini-gene. The mini-gene is driven by the murine Rhodopsin promoter (mRho). CEP290 exons 25 and 26 are joined and followed by the complete intron 26-27 and exon 27. An A > G mutation corresponding to c.2991+1655 was included to assess exon X splicing in the model. An amino-terminal Myc and a carboxy-terminal FLAG tag were added to flank the mini-gene. Additionally, an internal ribosomal entry site (IRES) was added to drive expression of EGFP and is terminated by a bovine growth hormone poly-adenylation signal sequence (pA).

(B) Immunofluorescence staining of a retinal cross-section from a mini-CEP290 mouse. OS, outer segment. ONL, outer nuclear layer. INL, inner nuclear layer. Scale bar is 50 μm.

(C) Illustration of potential splicing outcomes within the mini-CEP290 mouse. Canonical cis-splicing would result in a predicted 24.3-kDa peptide. Alternative cis-splicing with exon X would yield a predicted non-sense mediated decay transcript encoding a truncated peptide with Myc at 17.1 kDa and no FLAG translation. Trans-splicing with a 5' PTM would replace the amino-terminal Myc and generate a 124.1-kDa peptide with a FLAG tag. Arrow pairs indicate locations of PCR primers used to detect specific splicing events.

(D) Representative western blot images of Myc and FLAG at 24.3 kDa showing OD and OS lanes per animal for each contralateral treatment cohort.

(E) Densitometry quantification showing the mean log10 values of each contralateral treatment cohort. Samples were standardized to α-tubulin. Error bars are SEM. Sample sizes as indicated. Individual animal data is available in Figure S1A.

(F) qPCR from cDNA generated by RNA extracts (legend continued on next page)
Evaluating trans-Splicing in a Murine Mini-gene Model of hCEP290 Intron 26-27

To demonstrate in vivo proof-of-concept pre-mRNA editing of this region of CEP290, we utilized an engineered mouse model. This model contains an LCA10 mini-gene driven by the murine sequence immediately upstream to the Rhodopsin gene and encoding the genomic region of Homo sapiens CEP290 exons 25, 26, intron 26 carrying the IVS26 mutation, and exon 27. The promoter selection limits expression of the mini-gene to rod photoreceptor cells. A detected trans-splicing event can thus be presumed to be the product of activity in photoreceptors, even in samples that may contain material from other cell types. Additionally, a 5′ Myc tag and a 3′ 3×FLAG tag are in-frame with the CEP290 coding sequences. The cassette is followed by an internal ribosomal entry site and enhanced GFP coding sequence (Figure 5A). Expression of GFP was confirmed to be restricted to photoreceptors in the outer nuclear layer and the transition zone between the outer nuclear layer and outer segments (Figure S1B). In this model (which was not designed to manifest disease), normal cis-spliced products are expected to generate a 24.3-kDa peptide, while a trans-spliced product would generate a novel 124.1 kDa FLAG band (Figure 5C). Additionally, trans-splicing would be predicted to reduce the amount of 24.3 kDa Myc and FLAG protein.

To investigate these changes, we packaged the proviral PTM genomes in the AAV7m8 capsid, which has been shown to be effective for efficient transduction in vivo in mouse and primate retinas as well as in vitro for several cell lines. We then performed sub-retinal injections of control and experimental AAVs at post-natal day 15 and harvested whole eyes for either RNA or protein analysis 30 days post-injection. Treatment with the control AAV7m8-PTM_NBD and the experimental AAV7m8-PTM_07 trended toward reduction of Myc- and FLAG-tagged proteins at 24 kDa, though only Myc was statistically significant (Figures 5D, 5E, and S1A). FLAG detection of a novel 124.1 kDa band, an indicator of trans-splicing activity, was not observed in any sample (data not shown). However, we also observed baseline variability between the untreated eyes of animals for Myc and FLAG protein levels in several untreated mice (Figure S1A, cohort A).

To assess if we were observing an effect of RNA editing and not exclusively an artifact of AAV injection, we generated cDNA from additional mice and evaluated transcript levels using TaqMan probes specific to (1) the Homo sapiens exon 27-FLAG junction to gauge expression of all mini-gene transcripts including cis-spliced or trans-spliced, (2) an internal sequence of the codon-optimized PCDS to gauge expression of all PTM-generated transcripts including cis-spliced or trans-spliced, or (3) the novel junction specifically indicating trans-splicing of the codon-optimized PCDS to Homo sapiens exon 27. Analysis of samples by biological groups revealed that injection of either PTM_NBD or PTM_07 reduced overall expression of the mini-gene by approximately 75% (Figure 5F, left). Total levels of PTM_07 were detected as 4-fold higher than PTM_NBD, while no detection was observed in untreated samples (Figure 5F, center).

Despite the higher overall levels of PCDS expression observed following treatment with PTM_07, trans-splicing of the codon-optimized 3′ PCDS was detected with either treatment, but, importantly, levels were 25-fold higher with PTM_07 (Figure 5F, right). Individual data grouped by contralateral eye treatments demonstrate variability between mice but show consistently that trans-spliced products are detected at higher levels after treatment with PTM_07 relative to PTM_NBD, and in 5 out of 27 untreated eyes, some level of trans-splicing was detected but at amounts resembling PTM_NBD (Figure S1B, bottom). One animal that was injected with PTM_07 had no visible bleb after injection. Interestingly, in this sample, the level of codon-optimized PCDS was reduced, and trans-splicing was not detected (Figure S1B, animal 26). This sample provided evidence that successful sub-retinal injection of AAV7m8 PTM vectors is required to mediate trans-splicing activity to a photoreceptor-specific target.

DISCUSSION

Gene augmentation and editing strategies for targets with a coding sequence greater than 4,000 nt face many challenges. The size of delivery vectors imposes a restriction on which targets can be utilized in canonical gene augmentation. In this study, we have shown that splicing-mediated pre-mRNA trans-splicing can be utilized to edit transcripts of CEP290, which causes severe early-onset blindness (LCA10), which can also be accompanied by systemic disease. We created an analysis paradigm that can be applied to any gene target to maximize potential benefit. Further refinements to the components of the PTMs will allow for optimization of the analysis parameters. With regards to CEP290, we could target a PTM downstream of cryptic exon X. This approach could ultimately correct at least one allele in nearly 70% of LCA10 patients and approximately 50% of all reported loci with mutations within CEP290.

Many studies have also shown that 3′ PTMs can replace the 3′ region of genes. By applying our analysis paradigm in the reverse direction, one can also calculate a maximal 3′ PCDS size (Table 1). Through the two approaches, nearly 90% of reported CEP290 mutation loci can hypothetically be targeted.

Our high-throughput screen identified two candidate binding domains that could reconstitute GFP. High-throughput screens have been utilized in a variety of other studies by applying techniques including sonication to generate robust libraries. Regardless of

from whole eyes of mini-CEP290 mice. TaqMan probes were designed to the junctions of Homo sapiens exon 27 and FLAG to detect total expression of the mini-gene (left) to a region within the PCDS to detect total expression of the PTM (center) or to the novel junction of codon-optimized CEP290 PCDS and Homo sapiens CEP290 exon 27 (right). Values from treatment-matched samples were averaged as biological groups, standardized to murine β-2-microglobin and normalized to PTM_NBD. p < 0.05 was considered significant. Error bars are relative quantity minimum and maximum 95% confidence intervals. Sample sizes as indicated. Individual animal data is available in Figure S1B.
screening method, efficiency of trans-splicing continues to be the rate-limiting step for efficacy. Indeed, in another study, repair of Rho showed in vivo trans-splicing and protein production after sub-retinal injection but did not demonstrate phenotypic rescue.\(^1\) The ideal binding domain length, nucleotide composition, and other parameters have yet to be ascertained. Ongoing studies will identify what properties influence binding-domain characteristics and trans-splicing efficiency. There may be additional features that affect efficiency of trans-splicing, such as the efficiency of splicing in the native molecule.\(^3\)

Our negative control of the untargeted PTM with NBD unexpectedly did reconstitute the ORF in our GFP screen. Additionally, three of the GFP-positive library clones had binding-domain fragments in forward orientation, which were expected to not confer specificity of the PTM (05f, 09f, 13f). Since the levels of the forward binding-domain clones were not significantly higher than the no-binding-domain sample, the observation may be the result of non-specific, random trans-splicing resulting from an abundance of transcription template following transfection. Transcripts resulting from expression of transfected plasmids may be compartmentalized such that there is an increase in the local concentrations of the two molecules sufficient for stochastic trans-splicing. Further studies including in situ hybridization will help identify the cause of this untargeted trans-splicing.

Regarding the transcriptional terminator, our findings suggest that the poly-adenylation signal sequence increased PTM expression, and this correlated with higher trans-splicing, albeit not statistically significant. The basis for removal of the transcriptional terminator was to prevent maturation of the pre-mRNA and promote nuclear retention since the molecule would lack the elements required for nuclear export. Increasing heterogeneous nuclear ribonucleoprotein (hnRNP) binding sites may be another option for preventing export from nucleus. However, we cannot rule out other variables such as RNA structure that may be independent of the poly-adenylation tail and a result of changes to the overall PTM genome. Indeed, PTMs targeting murine dystrophin were improved with an intron splice enhancer sequence.\(^3\)\(^6\) Addition of this particular enhancer did not improve trans-splicing in our system, but there may be alternative sequences that can improve spliceosome recruitment in this context. A thorough analysis of additional transcriptional terminators and other intron binding elements on trans-splicing molecules may help reveal copy number, RNA structure, and other context-dependent effects that can contribute to future optimizations.

Specificity of the trans-splicing reaction to endogenous transcript conferred by the binding domain was confirmed by comparing transfection of BD_07 alone or BD_07 co-transfected with the mini-gene. Reduction in the trans-spliced 5’ GFP—exon 27 product when co-transfected reflects specificity of the binding domain since overexpression of the target mini-gene would create additional target sites for the PTM transcripts. By probing for the HA-tag on our 5’ codon-optimized CEP290 PTM, we discovered that translation of the PTM occurred with a peptide at the size predicted by an ORF present in the PTM. This ORF is only present if the 5’ splice site does not prevent maturation of the pre-mRNA. With BD_07 present, in silico analysis revealed multiple putative stop codons for the ORF. Mutation of the PTM to remove these putative stop codons would require changes to not only the spacer but also within the binding domain, which may reduce specificity and binding efficiency. Alternative transcriptional terminators and additional nuclear retention elements may be required to reduce this cis-splicing and increase the retention of PTM pre-mRNA, which, per the earlier poly-adenylation signal work, could increase trans-splicing availability.

Mini-gene systems have been used to dissect alternative splicing in a variety of models.\(^4\)\(^5\) When the Homo sapiens CEP290 exon 26, intron 26 with IVS26, and exon 27 region was targeted for specific insertion into the homologous region in a mouse, an mRNA species was identified that retained a second cryptic exon, dubbed exon Y, which is not observed in any human cDNA samples.\(^4\)\(^6\) This finding suggested that splicing in the mouse may not accurately recapitulate human splicing as a model of IVS26.

We thus investigated the utility of a tagged mini-gene containing only the region of interest when expressed in mouse photoreceptors. Variability in both baseline levels of mini-gene and in expression of transduced 5’ PTMs was observed between mice and is potentially due to biological and/or injection variability resulting in dose variations. However, dose variation alone would not account for the 25-fold overall difference seen for PTM_07 trans-splicing as a group or the consistently higher levels of trans-splicing in individual animals treated with PTM_07 compared to the contralateral eye treated with PTM_NBD. With Ct values after 35 cycles, the PTM_NBD signal is likely the result of rare un-targeted trans-splicing events. These same events were observed in the initial screen when using the 5’ GFP with NBD. Additionally, five untreated samples from cohort C had slight amplification with a mean value significantly less than that of PTM_NBD, which may indicate that the primer-probe set may not be perfectly specific.

We validated the PCR products to ensure the observed signal was not a result of secondary sources such as primer dimers or non-specific amplification within the sample. Non-specific trans-splicing may be resolved by improved engineering of the trans-splicing molecules and will be important to consider in future safety studies of trans-splicing.

Efficiency of trans-splicing molecules may also be context specific. Our mouse model maintained a higher genomic copy number of the mini-gene, which may be contributing to increased pre-mRNA expression and trans-splicing. It will be important to evaluate trans-splicing in additional models including patient-derived samples. Regarding LCA10, patient-derived induced pluripotent stem cells have been shown to have lower levels of CEP290 transcripts.\(^4\)\(^5\)
Evaluating trans-splicing in these models, including nuclear fractionation to detect pre-mRNA, will help reveal if pre-mRNA is present in sufficient quantities to facilitate trans-splicing.

Collectively, we have demonstrated that 5′ pre-mRNA trans-splicing can be targeted to edit CEP290 transcripts. This establishes an approach that can be further optimized to correct a broad range of patient mutations in the region 5′ to and including IVS26. Contrary to other methods of treatment, this approach creates the opportunity to correct both alleles. The approach can ultimately be expanded to other monogenic ocular and extra-ocular disease-associated genes that are too large to fit in AAV.

**MATERIALS AND METHODS**

**In Silico Analysis**

Nucleic acid sequences were analyzed, and Sanger sequencing alignments were performed with SnapGene software (GSL Biotech, Chicago, IL). Analysis of real-time PCR results was performed with Expression Suite Software v1.1 (Applied Biosystems). Graphs and statistical calculations were generated with GraphPad Prism v7 (GraphPad Software, La Jolla, CA). Densitometry analysis of immunoblot images was performed with ImageJ software (https://fiji.sc). Computation of densitometry values was performed using Microsoft Excel.

**Statistics**

Densitometry measurements of western blots were standardized to sample-matched α-tubulin values. For HA-tagged PTM experiments (Figure 4), six independent transfections were performed, and protein lysates were evaluated by immunoblotting. Densitometry values were normalized to PTM_NBD-treated lanes. Adjusted densitometry values of peptides of interest were compared in Graphpad Prism software using one-way ANOVA followed by Tukey’s multiple comparison test. A p value less than 0.05 was considered statistically significant.

Ct values of TaqMan PCR were standardized to the β-2-microglobulin control gene. Samples with matching treatments were considered biological groups, and mean ΔCt values were computed per group. All reactions were performed in technical triplicates for each biological replicate and processed with the ΔΔCt method. Values were normalized to PTM_NPA (Figure 3) or PTM_NBD (Figure 5). The means of biological groups were compared via Student’s t test with confidence intervals calculated at 95%. A p value less than 0.05 was considered statistically significant.

A post-hoc power analysis was conducted for the trans-splicing Ct values of the in vivo studies with a two-sample one-sided test. With an alpha of 0.05, the power was greater than 0.999 when comparing cohorts and the study included more than the minimal number of samples for significance.

**Culture Conditions and Transfection of HEK293T**

HEK293Ts were maintained in DMEM with GlutaMax (Thermo Fisher Scientific, Waltham, MA) supplemented with 10% (v/v) fetal bovine serum (GE Healthcare, Little Chalfont, UK) and 100 U/mL Pen Strep (Thermo Fisher Scientific). Dissociation of cells was achieved by washing with Dulbecco’s PBS (DPBS; Corning, Corning, NY) and incubation with Trypsin-EDTA 0.05% (v/v) (Thermo Fisher Scientific).

All transfections were performed with Lipofectamine LTX (Thermo Fisher Scientific) per manufacturer’s instructions at a 3:1 ratio of reagent to plasmid. For binding domain screening, 5 × 10⁴ cells were plated in 24-well cluster plates. 1 μg of library clone plasmid was transfected either alone or with equimolar target plasmid along with an equal volume per weight of PLUS reagent. For protein extracts, 3 × 10⁵ cells were plated in 6-well cluster plates and transfected with 2.5 μg plasmid with an equal volume per weight of PLUS reagent. At harvest, 10% of dissociated cells were separated for RNA and 90% for protein.

**cDNA Preparation and RT-qPCR**

RNA was isolated from whole mouse eyes following euthanasia and enucleation. Eyes were stored in 500 μL of RNAlater (Thermo Fisher Scientific) and homogenized by electric pestle in 350 μL Buffer RLT Plus. RNA was isolated from cell pellets or homogenized eyes with the RNeasy Plus Kit (QIAGEN, Germantown, MD) per manufacturer’s instructions following homogenization through QiAshredder columns (QIAGEN). Total RNA concentration was quantified on NanoDrop 8000 spectrophotometer (Thermo Fisher Scientific).

Reverse transcription was performed with Superscript III 1st Strand Synthesis (Thermo Fisher Scientific). qPCR was performed with TaqMan Fast Universal PCR Master Mix (Applied Biosystems, Foster City, CA) with cycling performed in an Applied Biosystems 7500 Fast Real-Time PCR system. Stock primer probes included human and murine beta-2-microglobulin (Thermo Fisher Scientific). Custom primer-probes were ordered from Thermo Fisher Scientific for codon-optimized PCDS internal FW 5′-ACC AAG GAA ATC AAT AAG CTC GGA CT-3′, RV 5′-GAT CAT TGT TG- GGC TTC CAG TCC TA-3′, probe 5′-CAG GGC TTC GTT CTC ATC G-3′; or CEP290 exon 27-FLAG FW 5′-ACT ATT GAA CAA GCC TGG GAA CAG-3′, RV 5′-TCA TCC TTG TAA TGG ATG TGC TGA TCT TT-3′, probe 5′-TGT GGC TCC CCA TAA TTT AG-3′. The codon-optimized exon 26 to endogenous exon 27 for detection of trans-splicing was ordered from Integrated DNA Technologies: FW 5′-CTT GGT CCT GCA GAG AAC TTC ATT CGG TAA AA-3′, RV 5′-TAT TGA ACA AGC CTG GGA ACA-3′, probe 5′-TCT TGA GCA CTT GGA GTG TGA AA-3′.

**Protein Extraction**

Protein extracts were isolated from either cell pellets or whole eyes by lysis buffer consisting of Radioimmunoprecipitation assay (RIPA) Buffer (Cell Signaling Technologies, Danvers, MA) supplemented with cComplete proteasome inhibitor (Roche, Basel, Switzerland). Following euthanasia and enucleation, whole eyes were homogenized in 250 μL of RIPA Buffer by electric pestle. Cell pellets were re-suspended in RIPA at a 1:1 volume to the cell pellet. Cell or eye lysis solutions were vortexed for 30 s, rotated end-over-end for 30 min at
4°C, vortexed for 30 s, centrifuged at 21,000 × g for 20 min at 4°C, and protein-containing supernatant was harvested. Quantification of protein concentration was performed with Micro BCA Protein Assay Kit (Thermo Fisher Scientific).

**Western Blotting**
Protein samples were separated via the NuPage Electrophoresis System (Thermo Fisher Scientific) per manufacturer’s instructions. Samples were heated at 70°C for 10 min and loaded to NuPAGE 3%–8% Tris-Acetate (Figure 4) or NuPage 4%–12% Bis-Tris (Figures 5 and S1) Protein Gels (Thermo Fisher Scientific). Novex Sharp Pre-stained Protein Standards (Thermo Fisher Scientific) was used to mark protein band sizes. Separated proteins were then transferred in an XCell II Blot Module (Thermo Fisher Scientific) to Immuno-Blot polyvinylidene difluoride membranes for Protein Blotting (Bio-Rad, Hercules, CA) at 30 V for 1 hr. After transfer, membranes were incubated in Tris-buffered saline with 0.1% v/v Tween 20 (Bio-Rad) supplemented with 5% (w/v) non-fat dry milk (LabScientific, Highlands, NJ) for 1 hr at room temperature. Primary antibodies and respective dilutions included: rabbit polyclonal anti-CEP290 (Abcam, Cambridge, MA) 1:1,000; mouse monoclonal antibody (mAb) anti-tubulin DM1A (Cell Signaling Technologies) 1:1,000; mouse mAb β-actin 8H10D10 (Cell Signaling Technologies) 1:2,000; rabbit mAb HA-Tag C29F4 (Cell Signaling Technologies) 1:500; mouse mAb Myc-Tag 9B11 (Cell Signaling Technologies) 1:500; mouse mAb FLAG M2 (Sigma-Aldrich, St. Louis, MO). Primary antibodies were diluted in Tris-buffered saline with 0.1% v/v Tween-20 (TBST)-5% milk and incubated with respective membrane portions at 4°C overnight. Membranes were washed 3 × 15 min in TBST. Secondary antibodies anti-mouse horseradish peroxidase (HRP) enhanced chemiluminescence (ECL) (GE Healthcare) 1:10,000 or anti-rabbit HRP ECL (GE Healthcare) 1:10,000 were diluted in TBST-5% milk and incubated with membranes for 1 hr at room temperature. Membranes were washed then incubated with ECL2 (Thermo Fisher Scientific) per manufacturer’s instructions for 5 min. Membranes were imaged with an Amersham Imager 600 (GE Healthcare) with chemiluminescence settings.

**Generation of PTM Binding Domain Reporter Library**
*Acquarea coerulescens* GFP (AcGFP) 5′ binding domain reporter plasmid was a gift from Lloyd Mitchell (Retrotherapy, Bethesda, MD). The 5′ GFP reporter consists of a 5′ GFP portion encoding Met1 through Glu112 and is followed by a canonical GTAAG 5′ splice site, a 20-nt spacer sequence, and a multiple cloning site. The reporter vector was digested with the blunt cutting endonuclease EcoRV and dephosphorylated with recombinant Shrimp Alkaline Phosphatase (New England Biolabs, Ipswich, MA). The treated reporter was separated by size-exclusion on Tris-borate-EDTA (TBE)-agarose gel electrophoresis and a band of expected size was excised from the gel and column purified with NucleoSpin Gel and PCR Cleanup Kit (Macherey-Nagel, Bethlehem, PA).

A 4,000-nt target region of CEP290 intron X-27 was amplified from genomic DNA of a healthy donor by PCR using Q5 Hot Start High-Fidelity 2× Master Mix (New England Biolabs). Primers were designed to be offset from the splice sites of exon X and exon 27: I26 FW 4kb 5′-CCA GGA TGG TGT CGA TCT CC-3′ and I26 RV 4kb 5′-TCT TCT AAT TCC GGC CAC CA-3′. Reactions were separated by size exclusion on TBE-agarose gel by electrophoresis and a band of expected size was excised from the gel. Gel pieces were then column purified using NucleoSpin. The purified fragment was digested with the blunt-end-generating restriction enzymes DraI and RsaI in CutSmart Buffer (New England Biolabs) at 37°C for 2 hr then column purified with NucleoSpin. A heterogeneous pool of the digested target region was ligated to the blunt-digested reporter using T4 Ligase (New England Biolabs) with an overnight incubation at 16°C. The ligation reaction was transformed into Top10 competent *E. coli* (Thermo Fisher Scientific) per manufacturer’s instructions. Transformed cells were spread on LB-Agar plates containing 100 μg/mL ampicillin. Plates were inverted and incubated overnight at 37°C. Clones were screened by colony PCR to identify insert size with the primers acGFP FW2 5′-ATC ACA TGA AGC AGC AC-3′ and V5Tag-RVSeq 5′-GGA GAG GGT TAG GGA TAG GC-3′. Cultures of unique clones were grown and later Sanger sequence verified to generate the binding domain library.

**Generation of Reporter Target Mini-gene**
A 3′ AcGFP trans-splicing target mini-gene was designed encoding human CEP290 exons 25 and 26, intron 26, and the 3′ portion of AcGFP to complete the coding DNA sequence of the 5′ GFP reporter. This mini-gene was generated by in-fusion cloning (Macherey-Nagel) to create a proviral lenti-plasmid with CMV immediate-early promoter, CMV enhancer, Kozak consensus sequence, ATG start codon, CEP290 exon 26 and intron 26, the 3′ portion of GFP, a STOP codon, and the bovine growth hormone poly-adenylation signal sequence.

To generate a positive control for full-length GFP, the 5′ GFP and 3′ GFP sequences were assembled via in-fusion cloning using the respective 5′ and 3′ PTMs as templates. The fragments were inserted into an expression plasmid driven by the CMV immediate-early enhancer and promoter.

**Screening of Binding Domains**
Library screening was performed by co-transfection of PTM Target 3′ GFP and reporter PTM binding domain library clones into HEK293T at an equal molar ratio. At 48 hr post-transfection, cells were dissociated, and the fraction of GFP-positive cells was determined by flow cytometry using BD Accuri C6 (BD Biosciences, San Jose, CA). Samples were gated using a GFP plasmid transfection in which 99.9% of cells were GFP positive (data not shown).

Confirmation of trans-spliced RNA was evaluated by reverse transcription followed by PCR using the primers GFP FW1 5′-TTC GAG GAT GAC GGC AAC TA-3′ and GFP RVseq 5′-GCC ATC CTC GTT GAA ATA TG G-3′. Library clones that showed the highest GFP were assessed for trans-splicing to endogenous CEP290 with...
primers GFP FW 5′-TTC GAG Gat GAC GGC AAC TA-3′ and hCEP290 E27 RVseq 5′-CCC AGG CTT GTT CAA TAG TGT-3′.

**Generation of CEP290 5′ PTM**

PCR was utilized to amplify the 5′ CDS from a codon-optimized human CEP290 coding DNA sequence (CDS) (DNA 2.0 now ATUM, Newark, CA) and a 5′ splice site and the first 20 nucleic acids of hCEP290 intron 26 were added via the oligonucleotide primers. This fragment was cloned into the Scal site of the AAV proviral vector p1107 (Bennett Lab, Philadelphia, PA) to generate PTM_NBD. PTM_07 was generated by amplifying the binding domain 07 sequence from the 5′ GFP clone BD15 and inserting this fragment into the EcoRV site of PTM_NBD. All constructs were validated by Sanger sequencing.

**Immunohistochemistry**

Whole eyes were isolated by enucleation of euthanized animals. Eyes were fixed in 4% paraformaldehyde for 2 hr on ice and then cryoprotected with 30% (w/v) sucrose in DPBS. Eyes were then embedded in Tissue-Tek optical cutting temperature cryopreservation media (Sakura Finetek USA, Torrance, CA) and frozen at −80°C. Embedded eyes were sectioned on a Leica CM1850 cryostat (Leica Biosystems, Buffalo Grove, IL) at 12 µm thickness and transferred to charged glass microscope slides (Globe Scientific, Paramus, NJ). Tissue slices were then incubated for 1 hr at room temperature in blocking buffer comprised of 10% (v/v) goat serum (Sigma-Aldrich) and 0.5% (v/v) Triton X-100 (Roche) in DPBS (Corning). Primary antibodies of Rhodamine labeled Peanut Agglutinin (Vector Laboratories, Burlingame, California) 1:100 and Cone Arrestin (Abcam) 1:100 were diluted in blocking buffer and applied to samples in a humidified chamber and incubated for 4 hr at room temperature. Slides were then washed three times for 5 min per wash in phosphate buffered saline with 0.5% v/v Triton X-100 (PBST) comprised of 0.5% v/v Triton X-100 in DPBS. Secondary antibody goat anti-rabbit Cy5 (SeraCare, Milford, MA) was diluted in blocking buffer 1:100 and applied to cells for 1 hr at room temperature followed by three washes in PBST and a final wash in DPBS. Fluoromount-G mounting media (Thermo Fisher Scientific) supplemented with DAPI was added to slides prior to the addition of No. 1 1/2 cover glass (Corning) and sealed with nail polish (Electron Microscopy Sciences). 10 Z-slices of 1 µM depth were obtained with a FLUOVIEW FV1000 confocal laser scanning microscope with a PLAPON 60× Oil NA:1.42 objective (Olympus, Center Valley, PA). Images were excited with lasers at wavelengths 405, 488, and 559 or 405 and 635 nm. z stacks between images were aligned with FIJI software using Split Channels, then the 635 nm channel was combined with the other three channels using Merge Channels. The composite image was then flattened using Z Project with Standard Deviation. The final image was rotated and cropped for display orientation.

**AAV Vector Production**

Vectors were produced by the Center for Advanced Retinal and Ophthalmic Therapeutics Retinal Research Vector Core (Philadelphia, PA). Viral lots were AAV7m8 p628 9.75e12 vector genomes (vg)/mL CT-117, AAV7m8 CMVie coC290 PTM NBD 8.86e12 vg/mL CT-332, and AAV7m8 CMVie coC290 PTM BD15 7.45e12 vg/mL CT-333.

**In Vivo Studies**

Animals were housed and maintained in accordance with the Association for Research in Vision and Ophthalmology’s Statement for the Use of Animals in Ophthalmic and Visual Research and Institutional Animal Care and Use Committee approval (IACUC #805890). The mini-CEP290 mouse line was generated by pronuclear injection of B6Af1 zygotes with a CEP290 intron 26 mini-gene driven by the 3.8 kb murine rhodopsin upstream sequence (see Figure 5A). The mini-CEP290 mouse line #406 was generated and maintained by brother-sister matings. Subretinal injections were performed as previously described. Each retina received 8 × 105 vector genomes in a volume of 1 µL PBS supplemented with Pluronic F-68 NF Prill Poloxamer 188.

**SUPPLEMENTAL INFORMATION**

Supplemental Information includes one figure and can be found with this article online at https://doi.org/10.1016/j.omtn.2018.05.014.

**AUTHOR CONTRIBUTIONS**

Conceptualization, S.J.D., K.J.F., L.G.M., J.B.; Methodology S.J.D., D.S.M., L.G.M., J.B.; Validation, Formal Analysis, Data Curation, Visualization, and Writing – Original Draft, S.J.D.; Design, Generation and Characterization of Mouse Model, J.B., J.L.B.; Investigation, S.J.D., D.S.M.; Resources, S.J.D., D.S.M., J.L.B., K.J.F.; J.B.; Supervision and Funding Acquisition, J.B. All authors reviewed and edited the final manuscript.

**CONFLICTS OF INTEREST**

S.J.D., J.L.B., L.G.M., and J.B. are co-inventors on patent PCT/US16/62941 relevant to the topic of this article. This patent has been licensed to Limelight Bio, Inc. (Philadelphia, PA), of which J.B. is a co-founder.

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