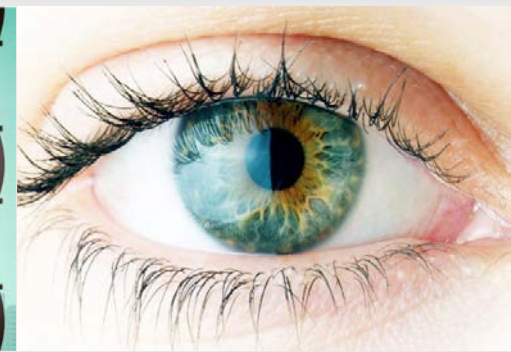




Keeping an Eye on CRISPR

Gerry Cox, MD, PhD
Chief Medical Officer

Creating transformative genomic medicines for patients who have serious diseases with high unmet medical need

Leadership

- **Katrine Bosley**
President & Chief Executive Officer
Avila, Adnexus, Biogen
- **Charles Albright, Ph.D.**
Chief Scientific Officer
BMS, Incyte, DuPont
- **Gerald Cox, M.D., Ph.D.**
Chief Medical Officer
Sanofi Genzyme, Boston Children's Hospital
- **Vic Myer, Ph.D.**
Chief Technology Officer
Novartis, Akceli, Millennium
- **Andrew Hack, M.D., Ph.D.**
Chief Financial Officer
Millennium Management, HealthCor Management, Carlyle-Blue Wave
- **Tim Hunt, J.D.**
Senior Vice President, Corporate Affairs
Cubist, Biogen



Organization

- Founded in 2013 by leading scientists and investors
- IPO in Feb. 2016 (EDIT)
- Over 100 FTEs today with approximately 75% in R&D
- Established capabilities include:
 - Screening, disease biology, pharmacology, specificity, manufacturing, regulatory, clinical development
- Well capitalized with ~\$325M current cash position
- Strong intellectual property position
 - >40 issued patents in US/Europe and 500 pending applications
- 60,000 square foot facility in Cambridge, MA

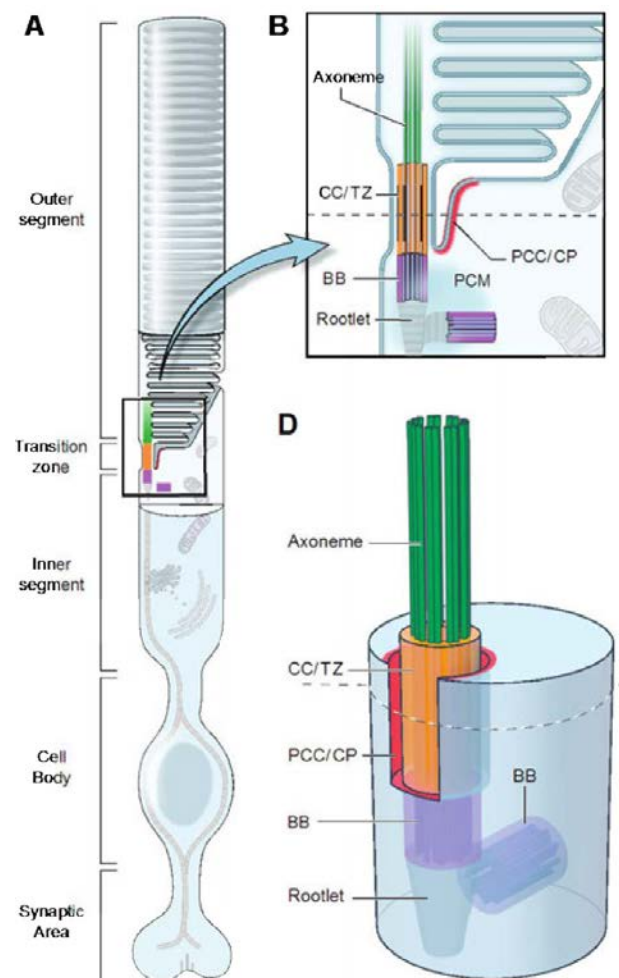
Founders & Advisors

- **Feng Zhang, Ph.D.**
Broad Institute; MIT
- **George Church, Ph.D.**
Harvard Medical School; MIT; National Academy of Sciences
- **David Liu, Ph.D.**
Howard Hughes Medical Institute; Harvard University; Broad Institute
- **Keith Joung, M.D., Ph.D.**
Massachusetts General Hospital; Harvard Medical School



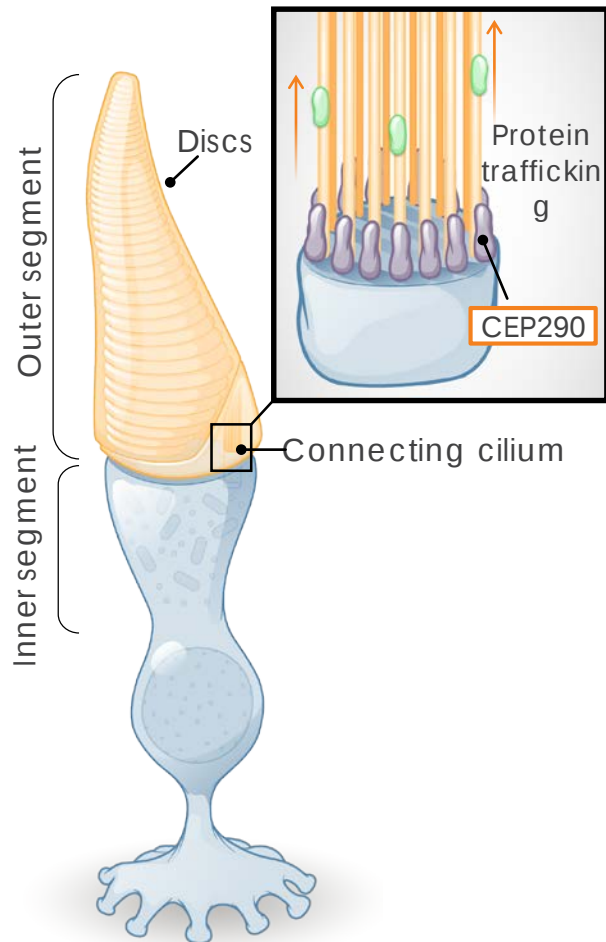
Leber Congenital Amaurosis Type 10

- Infantile-onset of poor vision, nystagmus, and a flat ERG¹
- Visual acuity is typically counting fingers or worse, but can vary widely, even among siblings¹
- LCA10 accounts for ~20-30% of all LCA patients¹
- Caused by autosomal recessive mutations in the CEP290 gene at chromosome12q21.32²
- ~85% of LCA10 patients from north and west Europe have a common mutation in intron 26, c.2991+1655A>G, with geographic variation¹⁻⁷
- CEP290 is present in the connecting cilium and is important for ciliogenesis, ciliary trafficking, and outer segment function and structure⁸

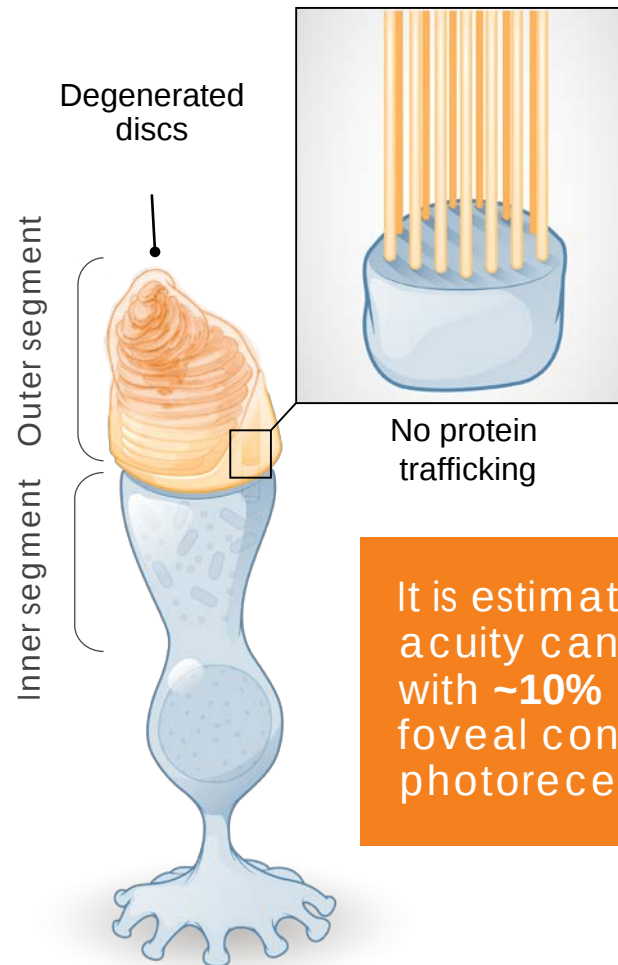


¹Weleber RG, 2013 LCA Gene Reviews; ²den Hollander AI, Koenekoop RK, Am J Hum Genet 2006;79:556-61; ³Stone EM, Am J Ophthalmol 2007;144:791-811; ⁴CEP290_databse 2017; ⁵Perrault I, Hum Mutat 2007;28:416; ⁶Vallespin E, IOVS 2007;48:5653-61; ⁷Simonelli F, IOVS 2008;48:4284-90; ⁸Rachel RA, Cilia 2012;1:22;

WT Photoreceptor



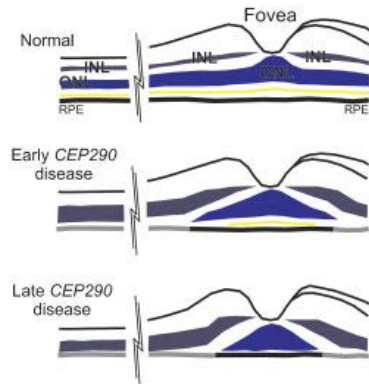
LCA10 Photoreceptor



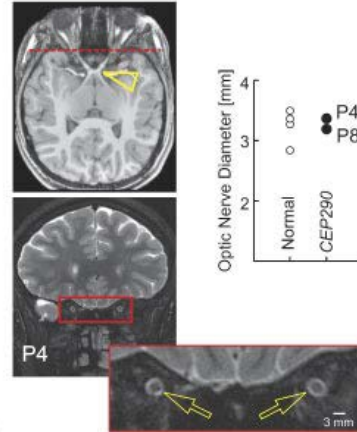
It is estimated that visual acuity can be achieved with ~10% of functioning foveal cone photoreceptors^{1,2}

Visual Pathway is Anatomically Intact in LCA10

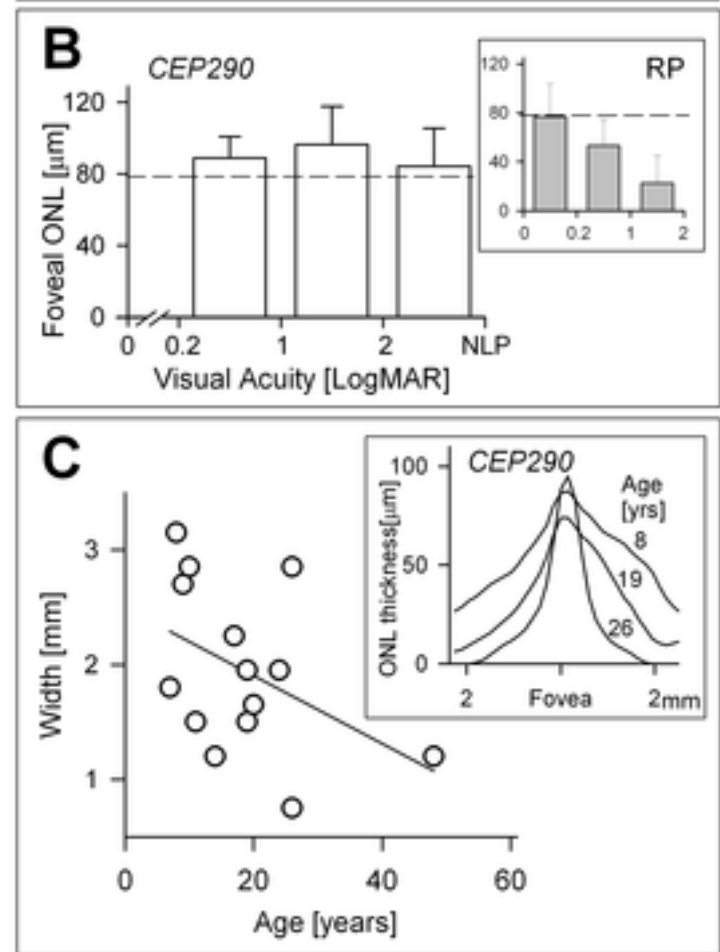
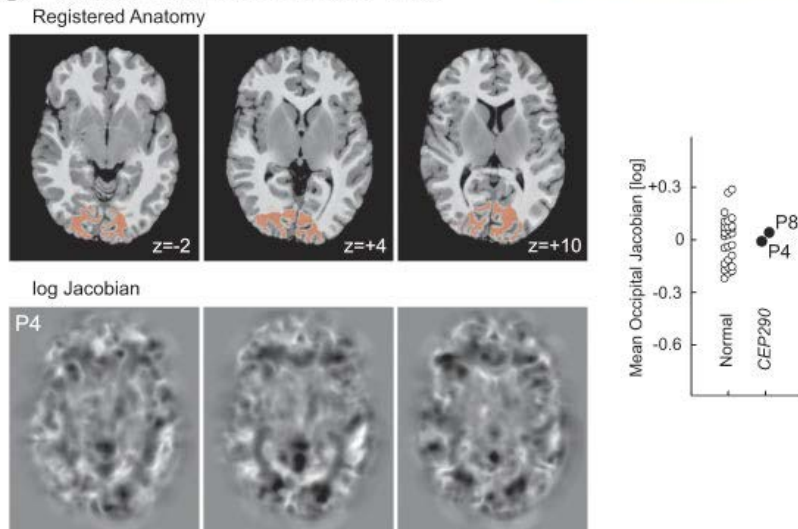
A RETINA



B OPTIC NERVE



C OCCIPITAL WHITE MATTER



Cideciyan AV, Hum Mutat 2007;28:1074-83

Boye SE, PloS One 2014;9(3)e92928

| Visual Acuity is not Related to Age in LCA10

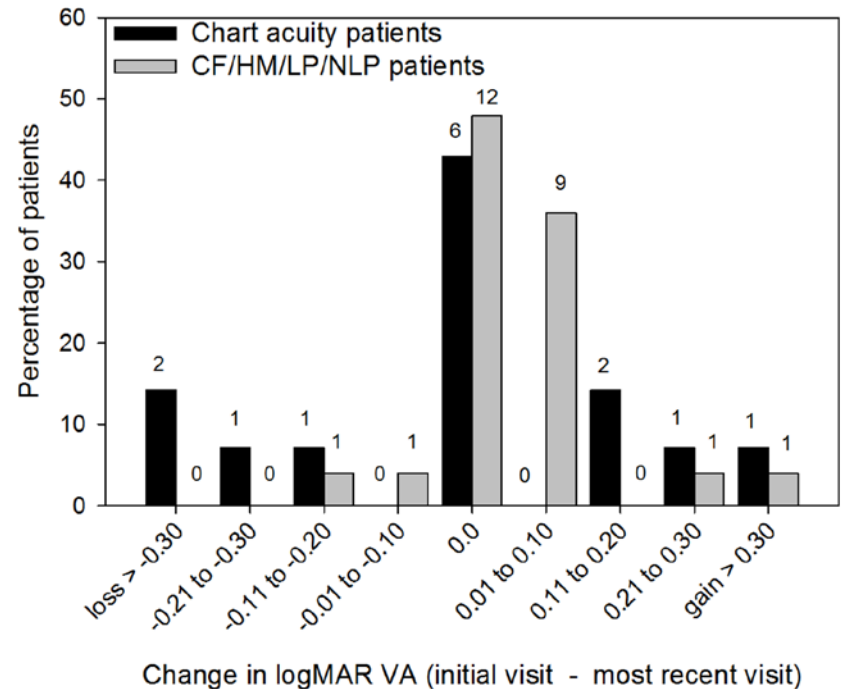
Mean logMAR (n)	
Age (yrs)	CEP290
0–10	2.83 (10)
11–20	2.2 (13)
21–30	2.54 (5)
31–40	2.75 (4)
41–50	2.47 (4)
51–60	0.8 (1)
61–70	None
71–80	None

N=39

82% Counting Fingers or worse

Range 20/50 – No Light Perception

Mean follow-up 10.4 yr (range 2-47 yr)



N=43

64% Counting Fingers or worse

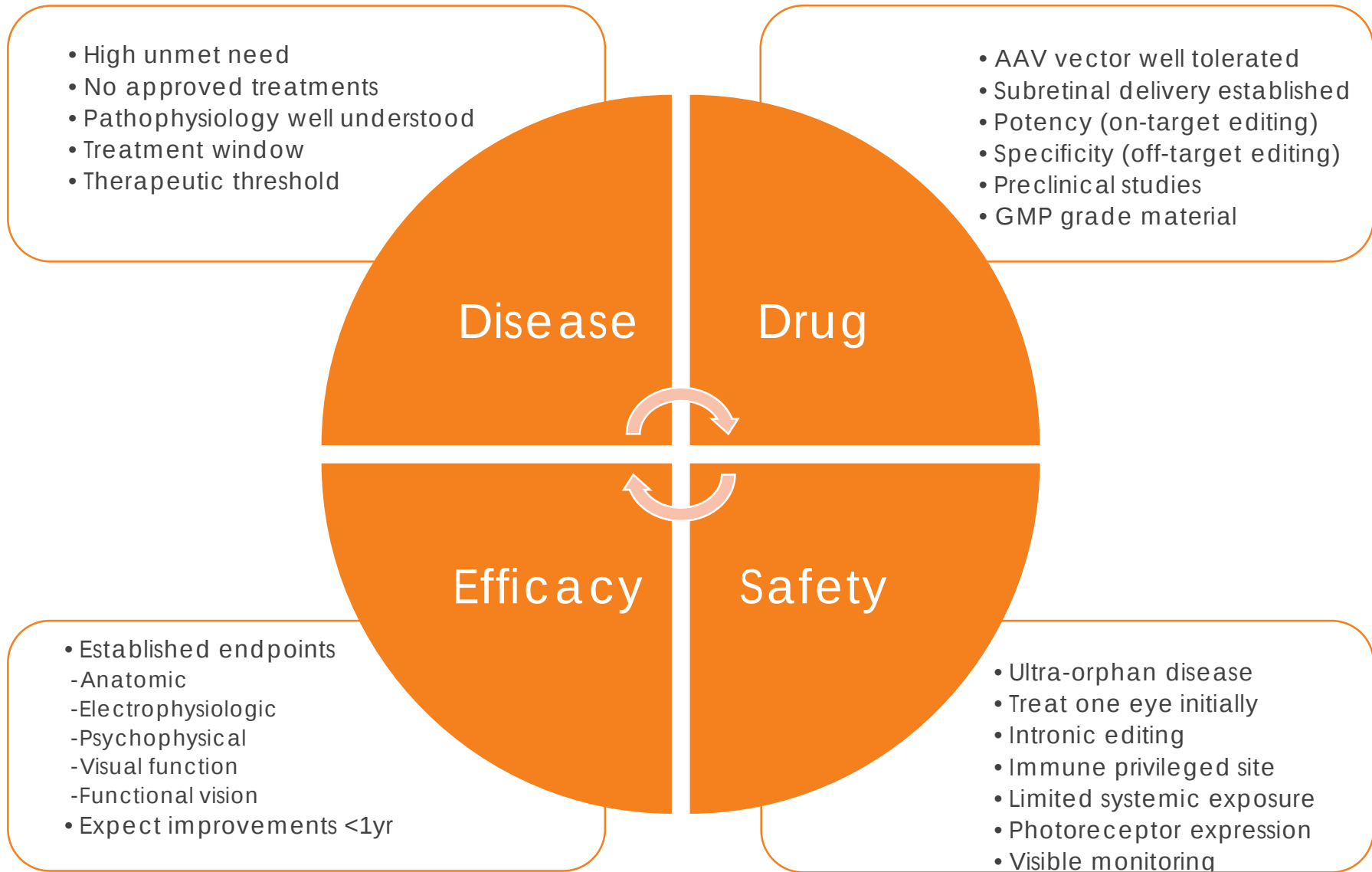
77% with IVS26 mutation

Mean age at initial visit 12.7 yr (0.2-57 yr)

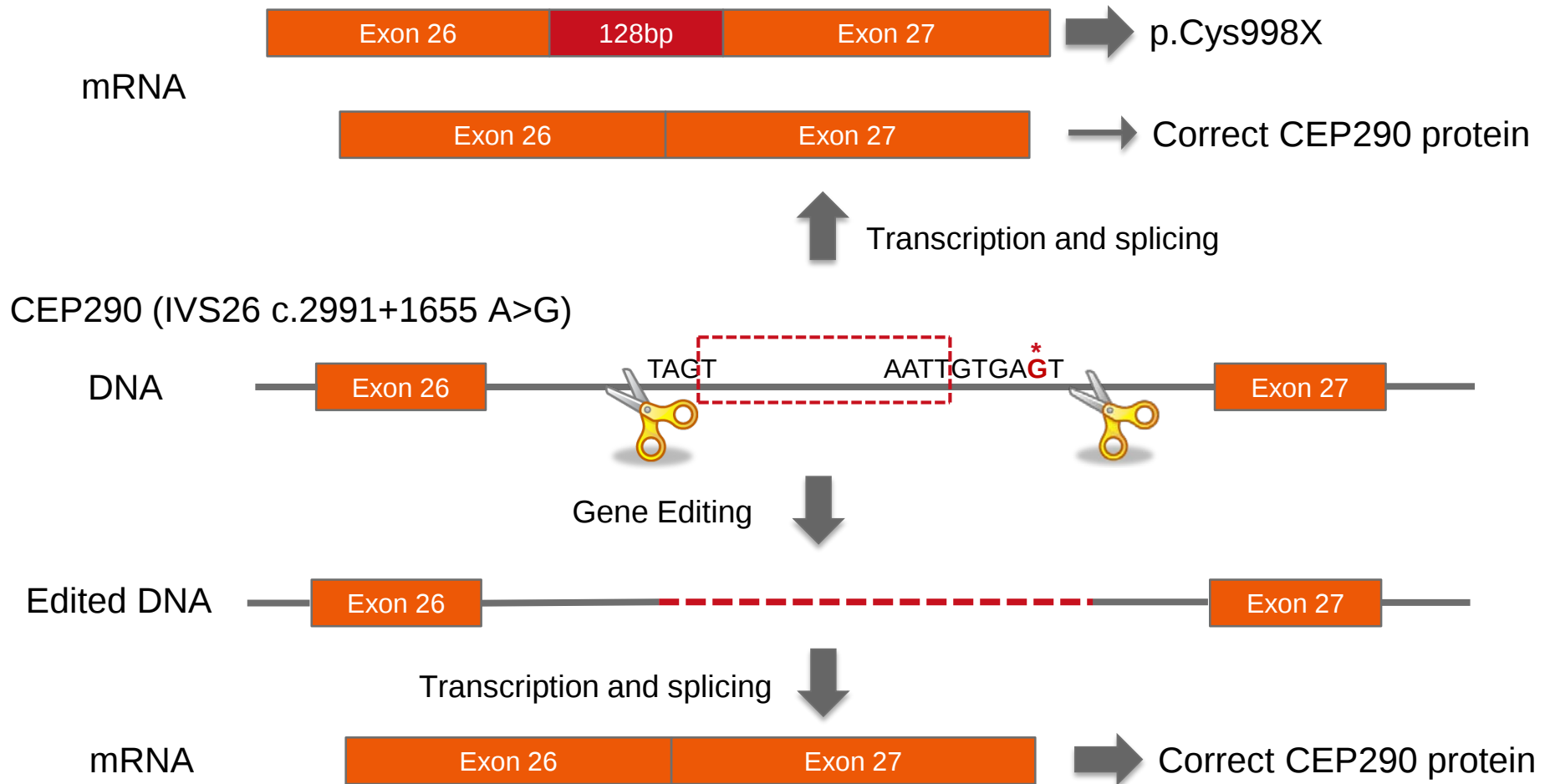


Clinical Development Considerations for LCA10

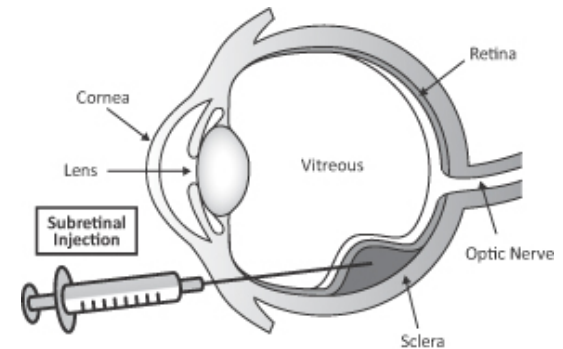
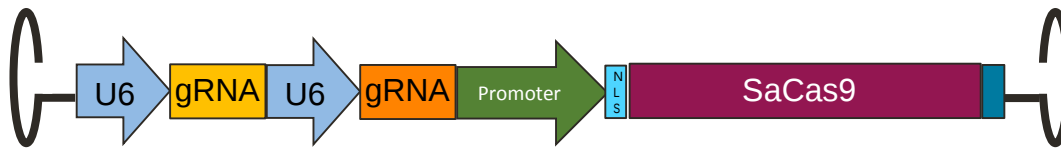
Therapeutic goal is to improve vision



| Gene Editing to Repair *CEP290* Splicing Defect



Subretinal injection of AAV5 vector encoding CRISPR/SaCas9 components intended to delete the IVS26 mutation and restore CEP290 splicing in photoreceptors



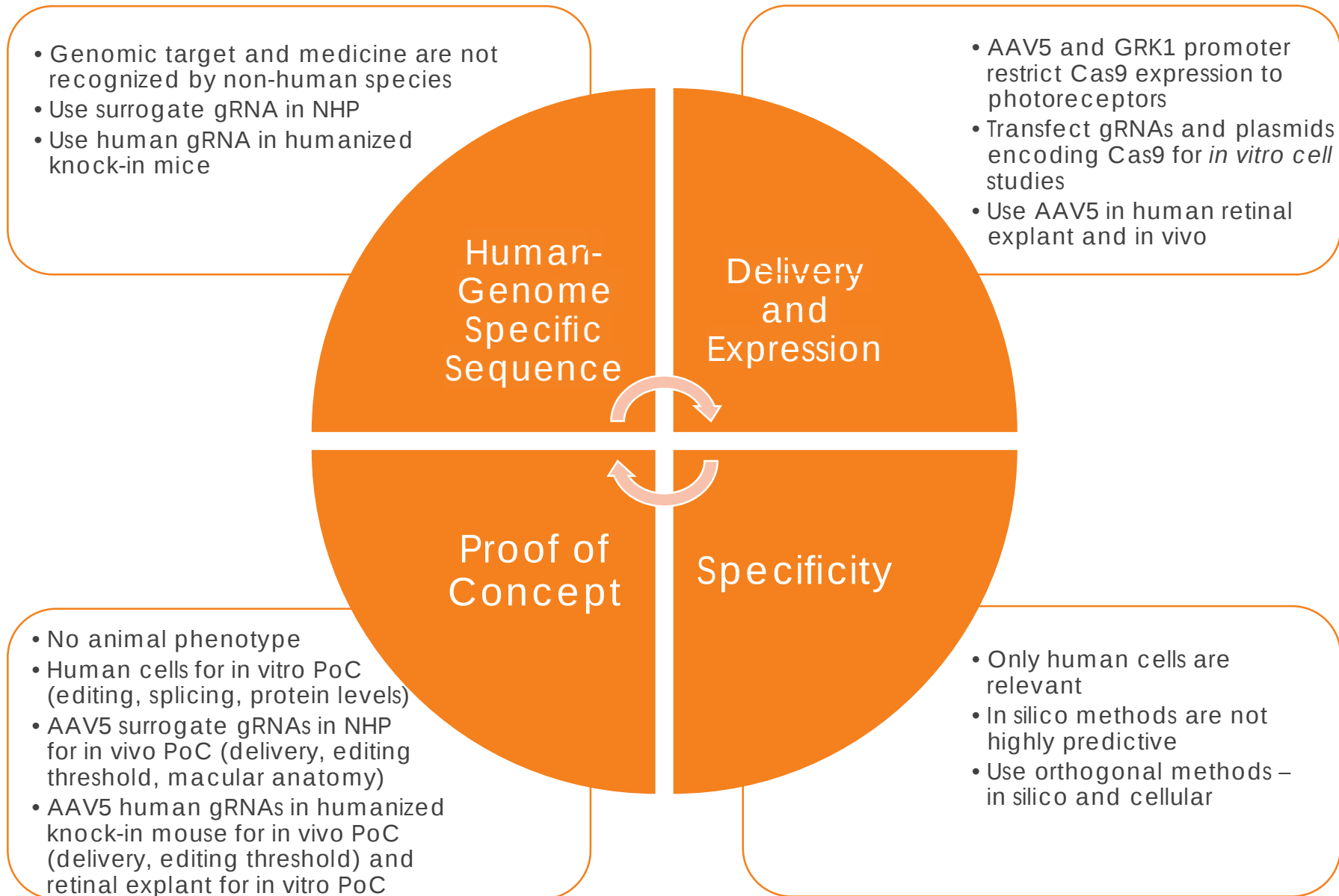
On-going in vivo experiments to understand:

1. Level of gene editing in photoreceptors
2. Specificity
3. Tolerability

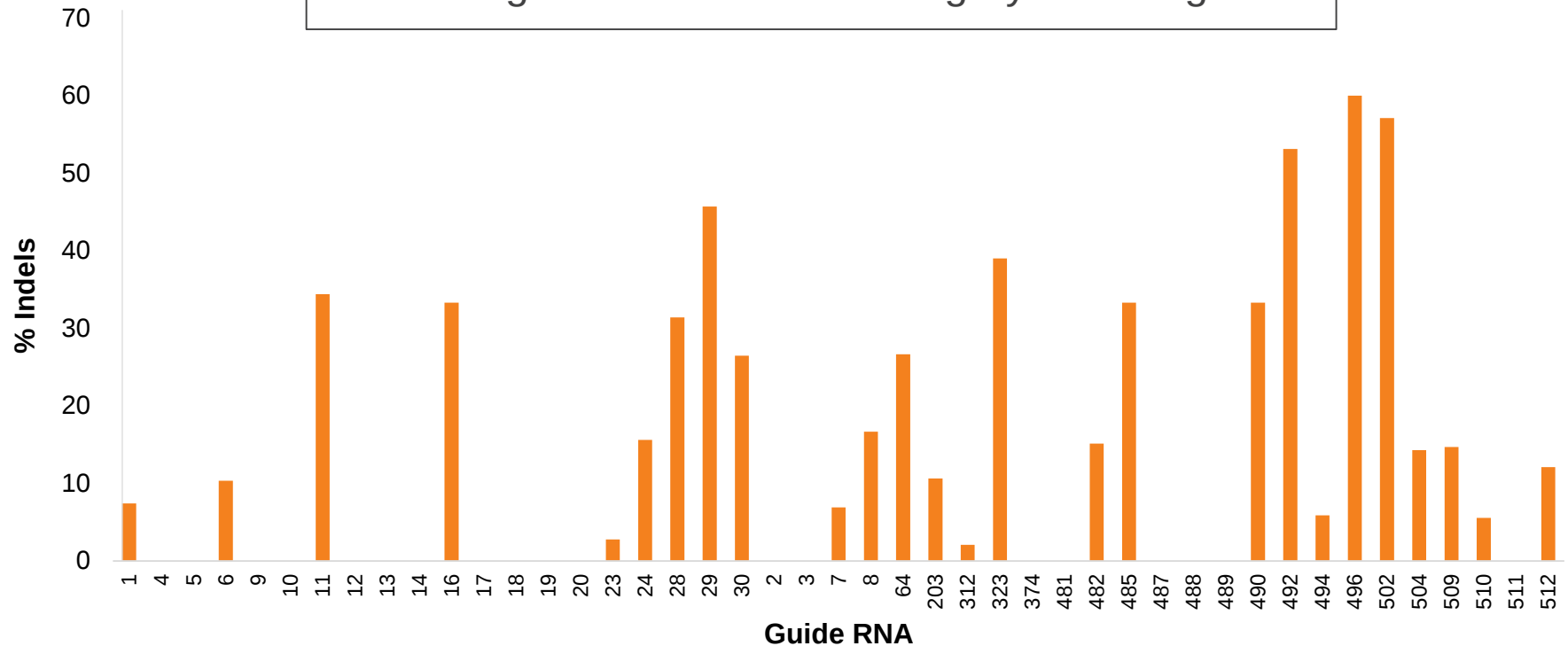
gRNA, guide RNA; NLS, nuclear localization signal
Sa Cas9, *Staphylococcus aureus* Cas9



CRISPR Development Challenges



Screening identified several highly active gRNAs

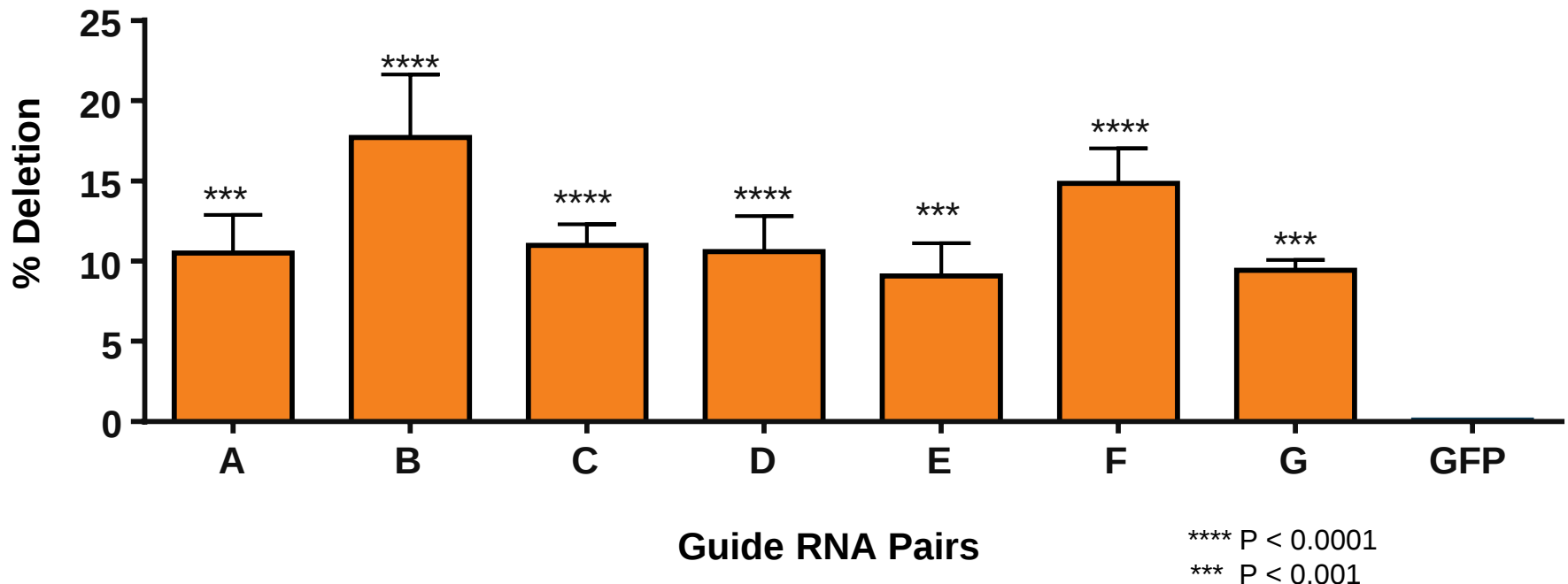


- Single gRNAs were co-transfected with Cas9-encoding plasmid into either patient fibroblasts or HEK293 cells
- Gene editing rates were determined by quantifying indels at the target locus by Sanger sequencing



gRNA Pairs Induce Targeted Deletion

Quantification of targeted deletion by ddPCR following transfection of SaCas9 and gRNA pairs into LCA10 patient fibroblasts with a homozygous IVS26 mutation

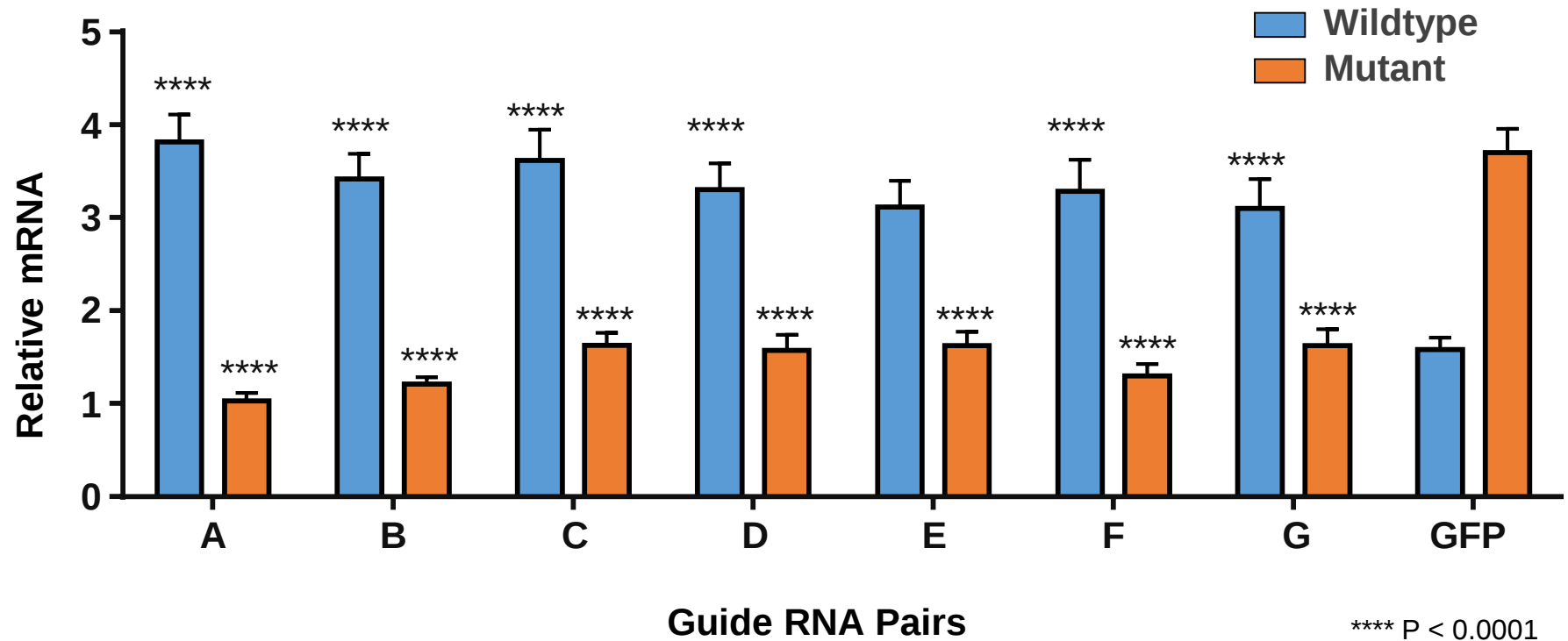


ddPCR, digital droplet PCR; SaCas9, Staphylococcus aureas Cas9;
gRNA, guide RNA; GFP, green fluorescent protein



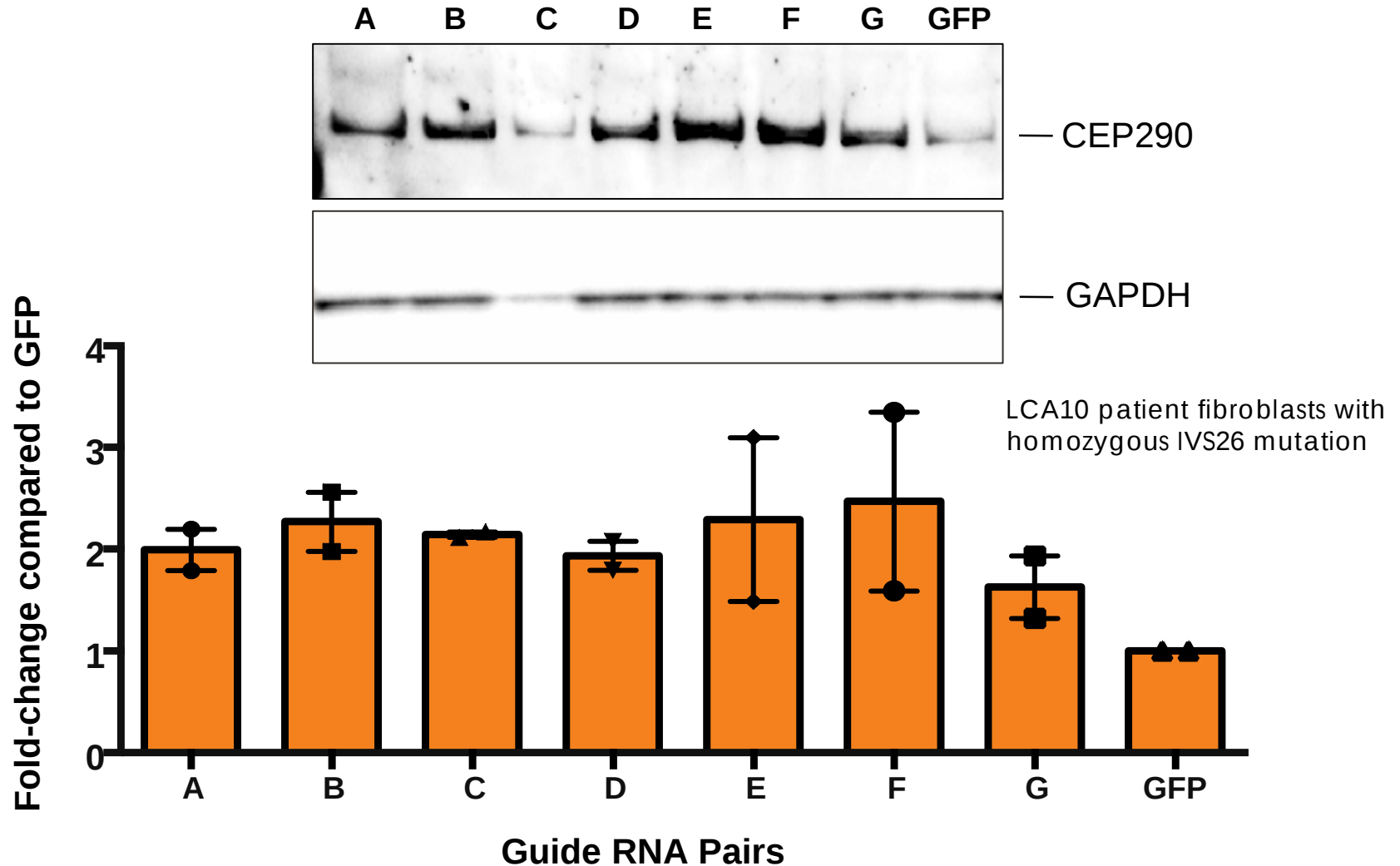
Targeted Deletion Corrects Splicing

Quantification of wildtype and mutant CEP290 mRNA by qRT-PCR in LCA10 patient fibroblasts



qRT-PCR, quantitative real time PCR
GFP, green fluorescent protein

Targeted Deletion Increases CEP290 Level

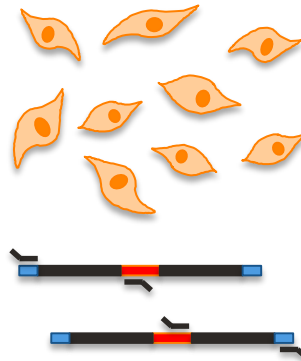
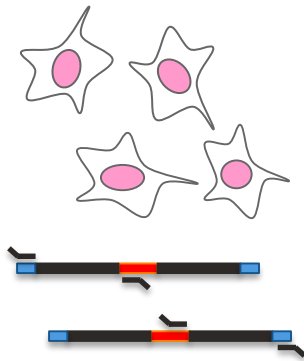


GAPDH, glyceraldehyde 3-phosphate dehydrogenase
GFP, green fluorescent protein



Specificity Analysis of Candidate gRNAs

GUIDE-Seq in multiple
human cell lines
(Unbiased Method)



Computational identification
of closely matched sites
(Biased Method)



TTGCACGTACGTAAACAGGATGG
TTG**G**ACGTACGTAAACAGGATGG
TTGCACG**A**ACGTAA**G**CAGGATGG
TTGCACGTACGT**T**AACAGGATGG
T**A**GCACGTACGTAAACAGG**C**TGG

Panel of sites analyzed by targeted NGS



NGS, next-generation sequencing



GUIDE-Seq Summary for CEP290 gRNAs

5 of 8 gRNAs had no detectable off-targets in 3-4 cell lines

Guide RNA	Cells Used for GUIDE-Seq				# Off-target Sites Identified
	ARPE19	Fibroblasts	SH-SY5Y	U2OS	
1	✓	✓	✓	✓	4
2	✓	✓	✓	✓	0
3	✓	✓	✓	✓	0
4	✓		✓	✓	0
5	✓		✓	✓	1
6	✓		✓	✓	0
7	✓		✓	✓	8
8	✓		✓	✓	0
VEGFA site3, Sp**				✓	59

GUIDE-Seq, Genome-wide Unbiased Identification of Double-stranded breaks Enabled by Sequencing
Sp**, *Streptococcus pyogenes* positive control



Targeted Amplicon Sequencing Summary for CEP290 gRNAs

5 of 8 gRNAs had no detectable off-targets in 2 cell lines

- Hg38 reference genome used for in silico identification of sites
- Variants in the 1,000 Genomes Project with a minor allele frequency >1% and a 3' *S. aureus* PAM (NNGRR) were identified using Cas-OFFinder¹
- Sites prioritized in coding sequence or in non-coding regions of tumor suppressors, oncogenes or IRD genes (GEDi-R)
- Approximate sensitivity of detection = 0.1%

¹Bae S, Bioinformatics 2014;30-1473-75

PAM, protospacer adjacent motif
GEDi-R, genetic eye disease panel for retinal genes
gRNA, guide RNA

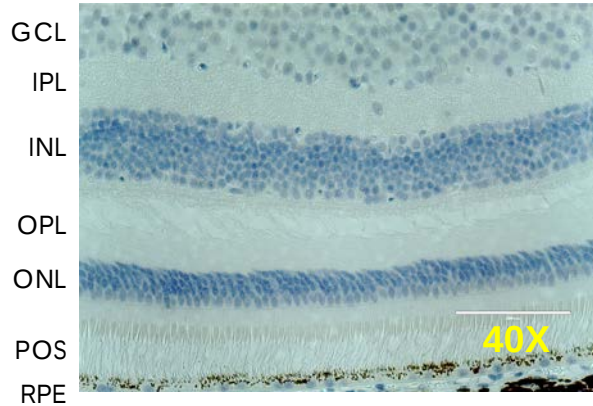
Guide	Cells	# of Sites Sequenced	# Off- target Sites Identified
1	U2OS	6	1
	ARPE19	3	1
2	U2OS	81	0
	ARPE19	61	0
3	U2OS	90	0
	ARPE19	57	0
4	U2OS	74	0
	ARPE19	48	0
5	U2OS	95	1
	ARPE19	56	0
6	U2OS	72	0
	ARPE19	58	0
7	U2OS	12	6
	ARPE19	12	0
8	U2OS	71	0
	ARPE19	53	0



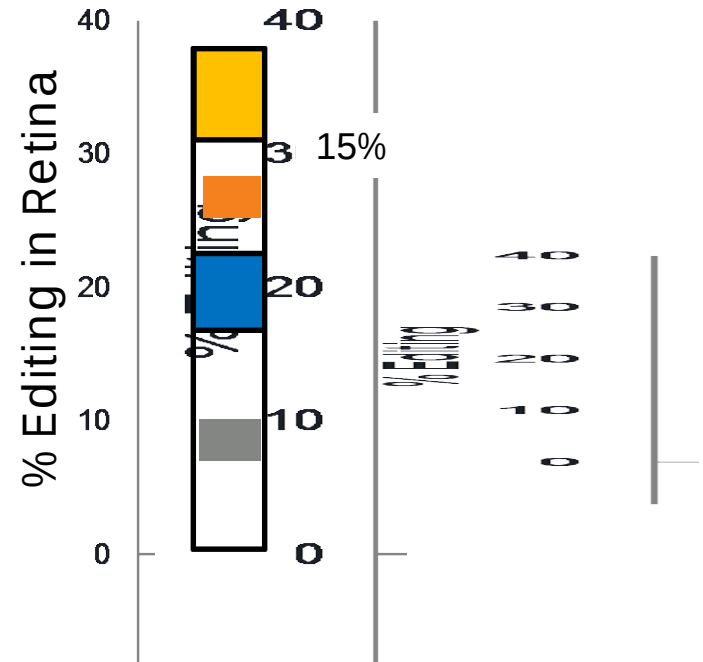
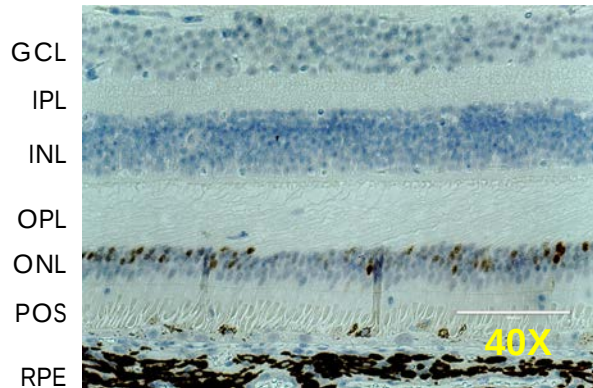
In vivo CEP290 Editing in Non-Human Primate Photoreceptors Using AAV5 and Surrogate gRNAs

Cynomolgus macaque injected sub-retinally with 4×10^{11} vg of AAV5-NHPCEP290gRNAs-GRK1-SaCas9

Vehicle

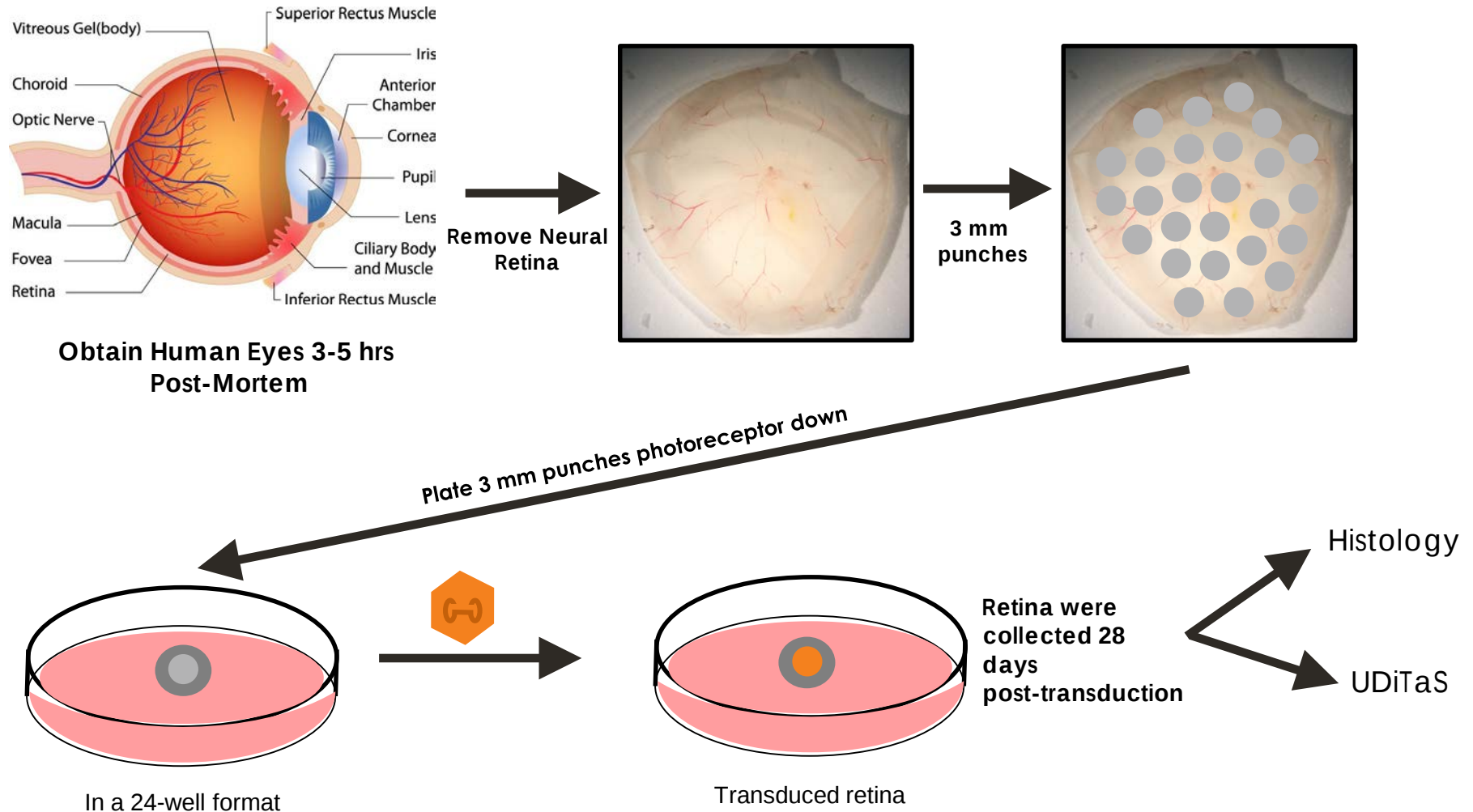


AAV5-NHPCEP290gRNAs-GRK1-Cas9



Proof of concept that CRISPR/SaCas9 can reach >15% productive editing in NHP bulk retina and potentially as high as 50% productive editing in photoreceptors

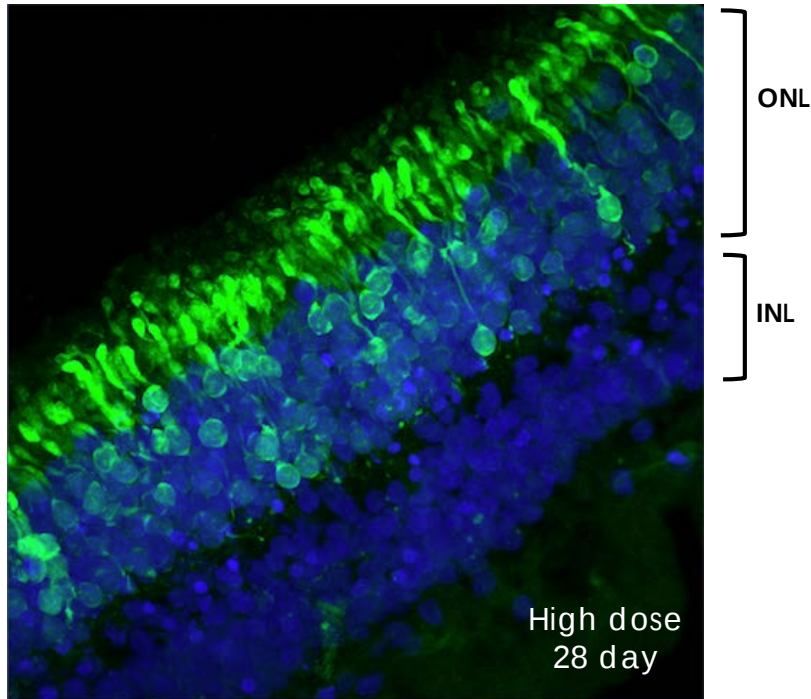
| Developing a Human Retinal Explant System



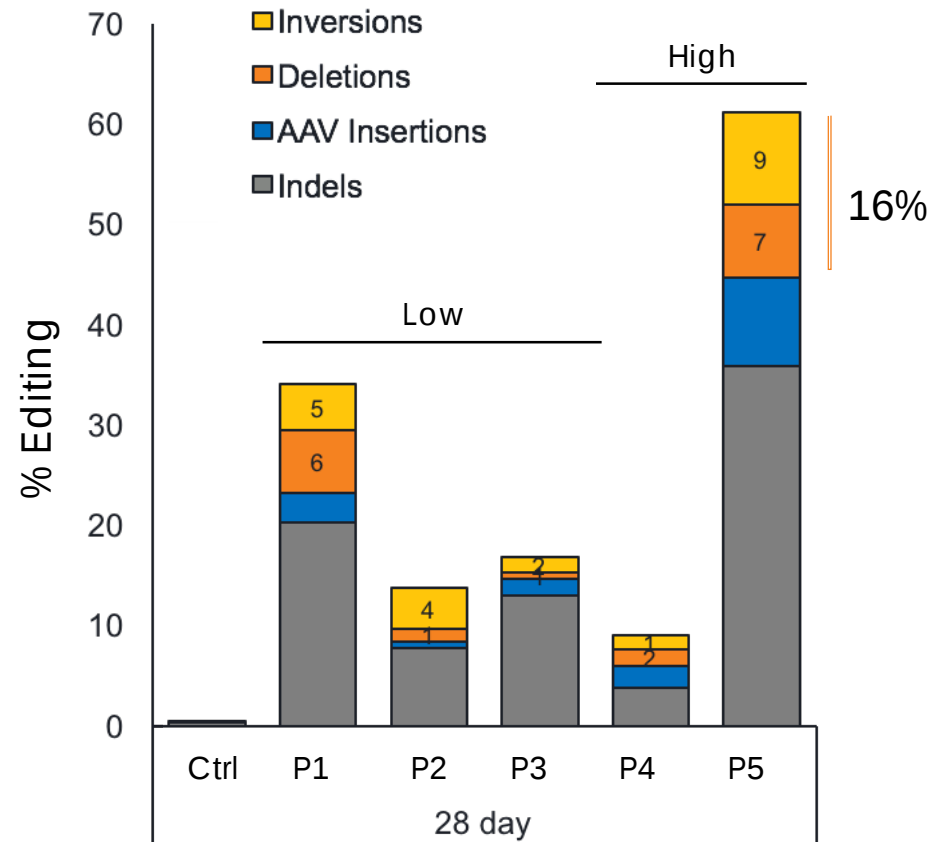


Preliminary Data Demonstrating Editing of CEP290 in Human Retinal Explants using AAV5

Human retina transduced with AAV5-GRK1-GFP



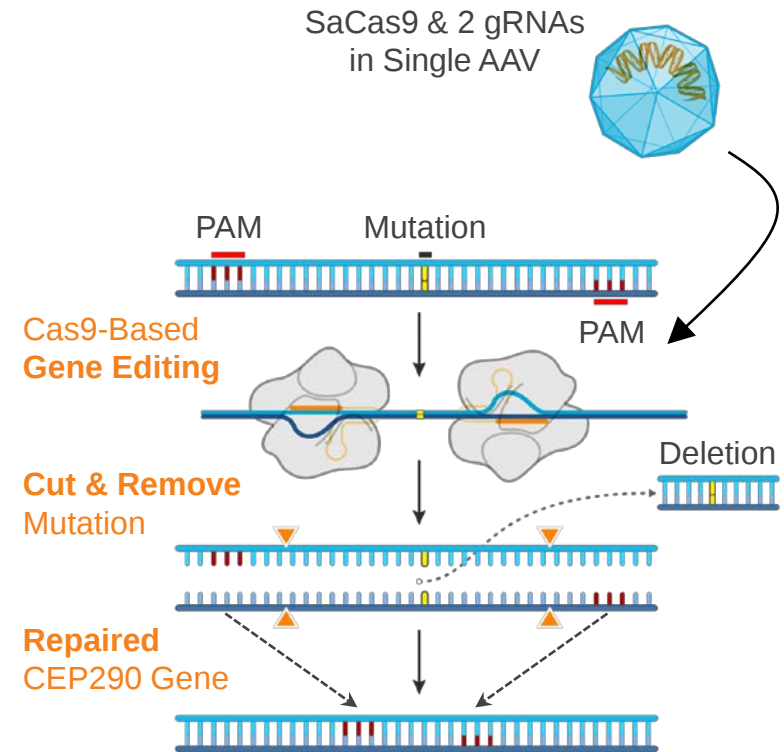
Targeted CEP290 gene editing in normal mature human photoreceptors



Low dose = 1×10^{11} vg
High dose = 5×10^{11} vg

Attractive Target Product Profile Emerging

- ✓ Efficient editing in LCA10 patient-derived cells corrects mutation *in vitro*
- ✓ Highly selective with no off-target editing detected with multiple methods
- ✓ Efficient delivery of all components in a single, well-validated AAV5 vector
- ✓ Optimized configuration to include photoreceptor-specific promoter
- ✓ Demonstrated editing with drug product configuration in human eye explants
- ✓ Demonstrated therapeutically-relevant editing in non-human primates *in vivo*





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Vidya Dhanapal

Mitch McCartney
Nicholas Sprehe



Medicines which Aim to Repair Any Broken Gene



Potentially transformative new category of medicines
for genetically-defined and genetically-treatable diseases