

*Shifting Heteroplasmy with PBGENE-PMM:
Gene Editing Therapy for m.3243A>G
Associated Mitochondrial Myopathy*

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June 27, 2024



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Disclosures

- I am an employee of Precision BioSciences.



Outline

› Precision BioSciences and ARCUS gene editing

› Applications for ARCUS gene editing of mitochondrial DNA

- Common deletion (del_mtDNA⁴⁹⁷⁷)

- m.3243A>G

- Mouse m.5024C>T

› PBGENE-PMM



ARCUS: Engineering nature's gene editing system

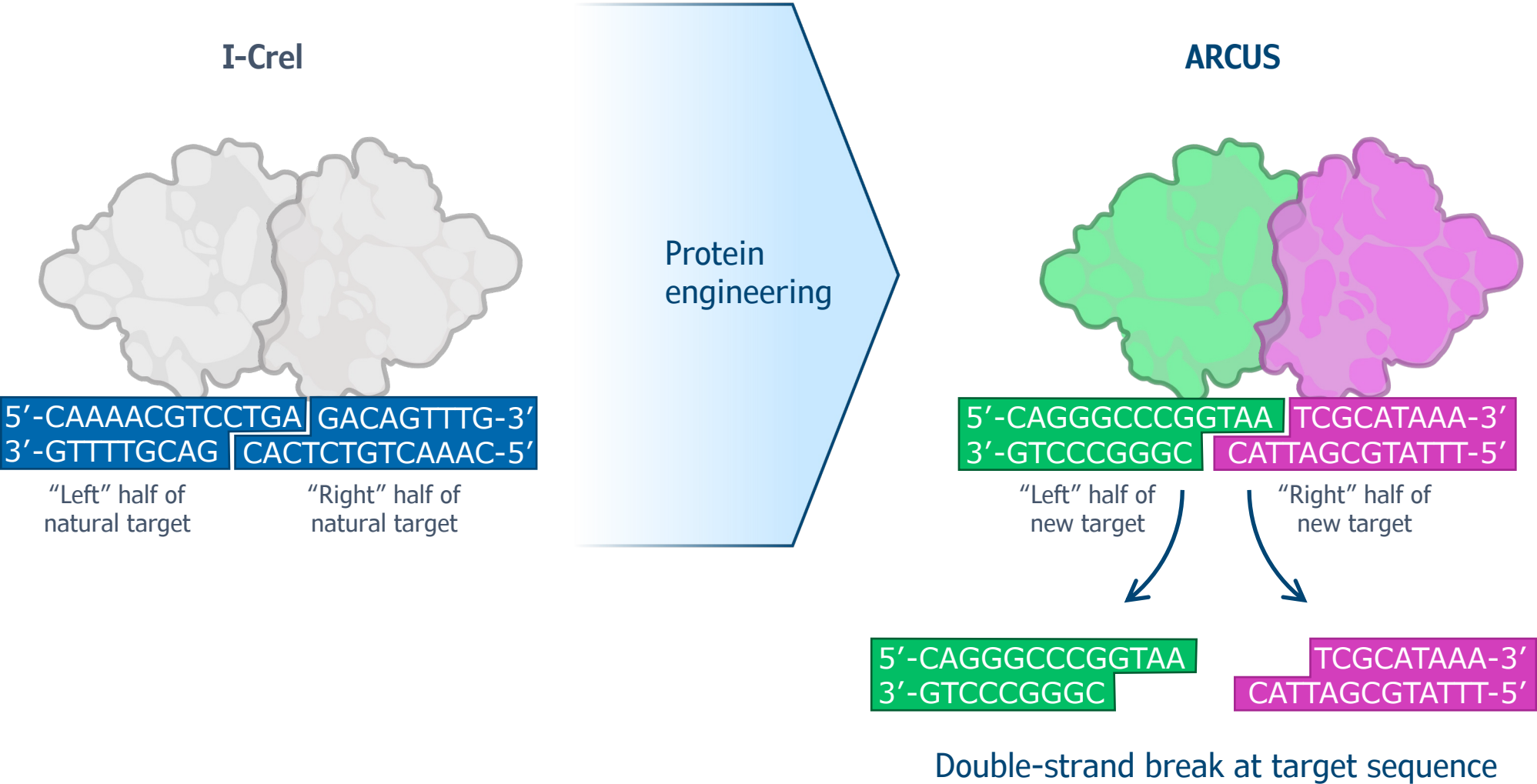


I-CreI bound to target DNA sequence

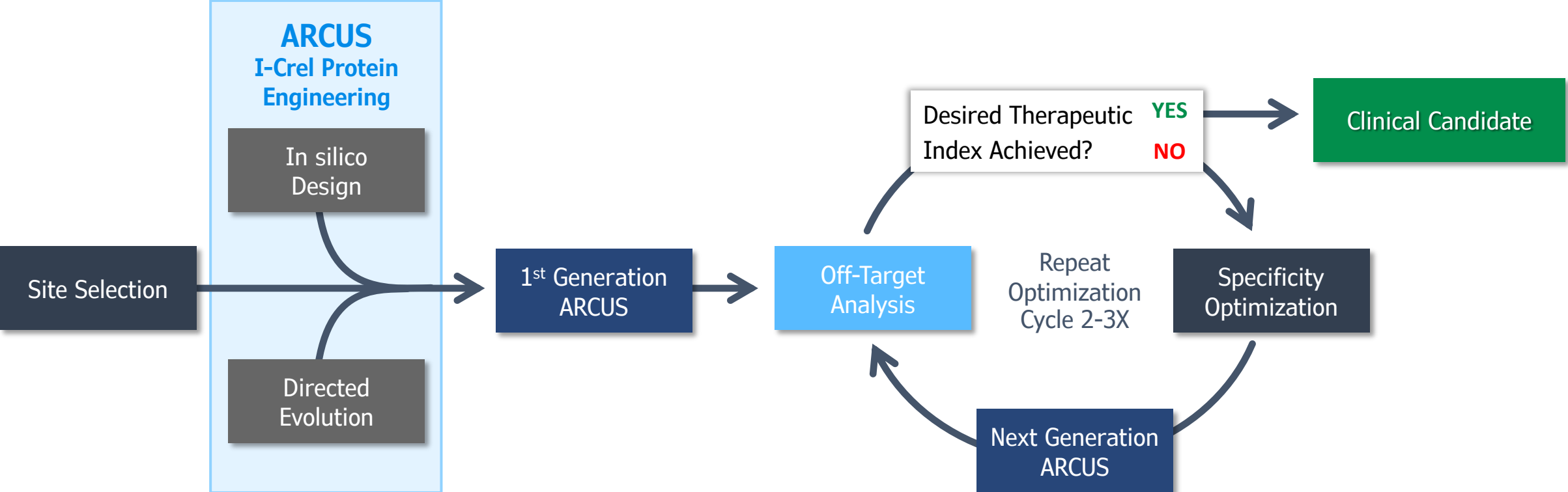
- › ARCUS is derived from **I-CreI**, a homing endonuclease from algae
- › Recognizes 22bp target sequence through extensive **protein-DNA** interactions
- › Does not require guide RNA
- › DNA recognition and cleavage activity are fully integrated into **one protein** for tight regulation



ARCUS generates targeted DNA double-strand breaks



ARCUS protein engineering is an iterative process



Applications for ARCUS



> Nuclear gene editing

- Targeted gene insertion
 - *ECUR-506 IND and CTA approved*
- Elimination of viral DNA
 - *PBGENE-HBV IND/CTA expected 2024*
- Gene knockout
- Excision of precise regions of genome

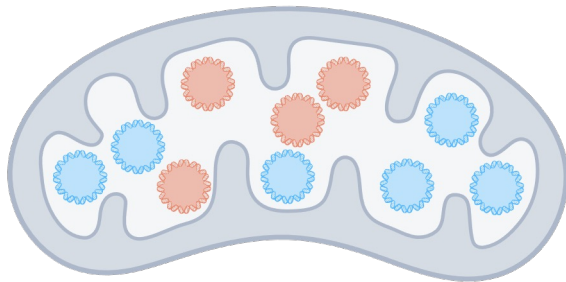
> Mitochondrial gene editing (mitoARCUS)



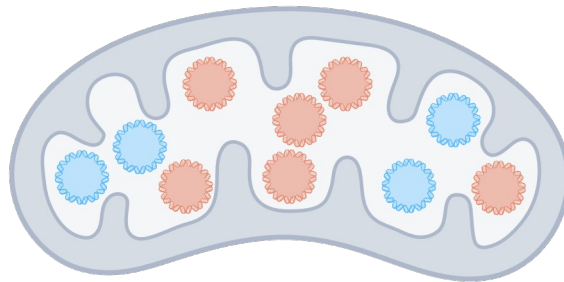
Heteroplasmic mtDNA mutations exhibit a threshold at which symptoms manifest

Clinically asymptomatic

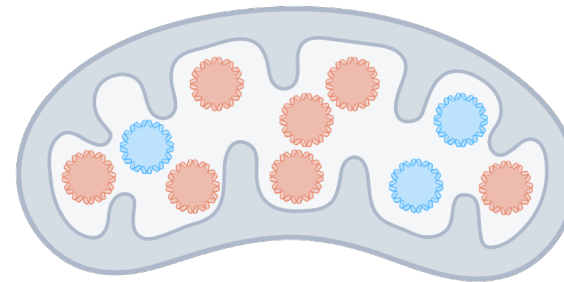
Clinically symptomatic



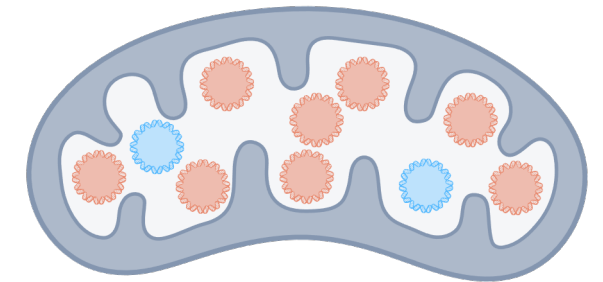
40% mutant



60% mutant



70% mutant



80% mutant

*Biochemical
threshold*



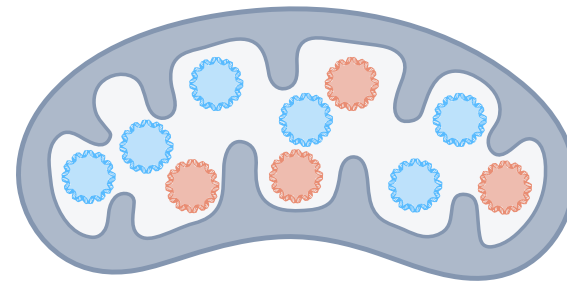
 Mutant mtDNA

 Wild-type mtDNA

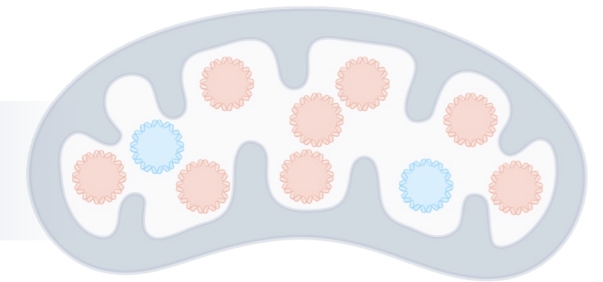
Heteroplasmic mtDNA mutations exhibit a threshold at which symptoms manifest

Clinically asymptomatic

Clinically symptomatic



Less than 80% mutant



80% mutant

*Biochemical
threshold*

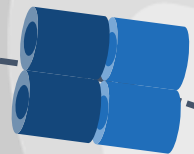
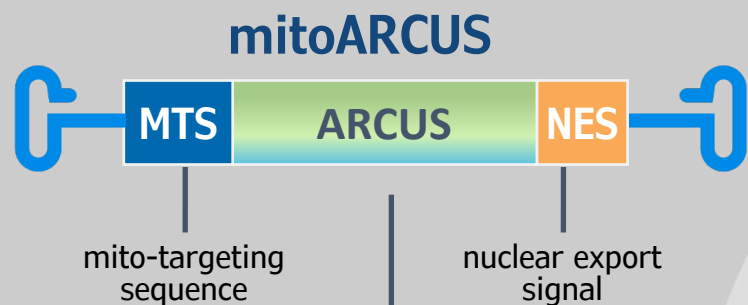
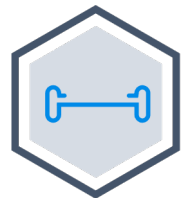
mitoARCUS gene editing



 Mutant mtDNA

 Wild-type mtDNA

mitoARCUS therapeutic approach to shift heteroplasmy



ARCUS

mutant mtDNA

WT mtDNA

Mitochondrial matrix

Cytoplasm



mitoARCUS gene editing seeks to eliminate mutant heteroplasmic mtDNA

Applications

- › Heteroplasmic deletions
- › Heteroplasmic point mutations

Discovery
stage

Common
deletion
(del_mtDNA⁴⁹⁷⁷)

Lead mitochondrial editing
therapeutic program

m.3243A>G

Research
investigation

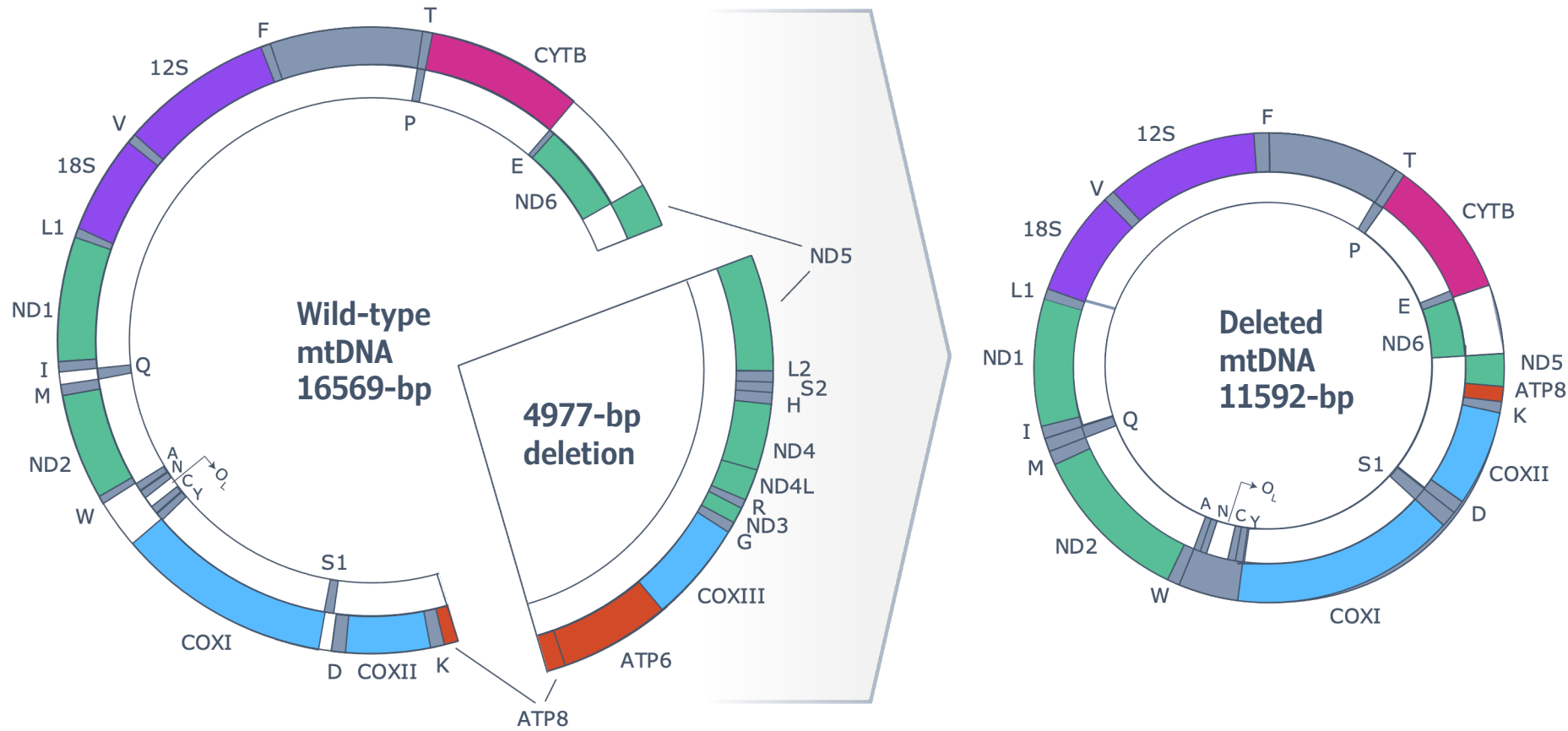
Mouse
m.5024C>T



Common deletion (del_mtDNA^{4977})



4977bp of mtDNA are missing in genomes with the common deletion

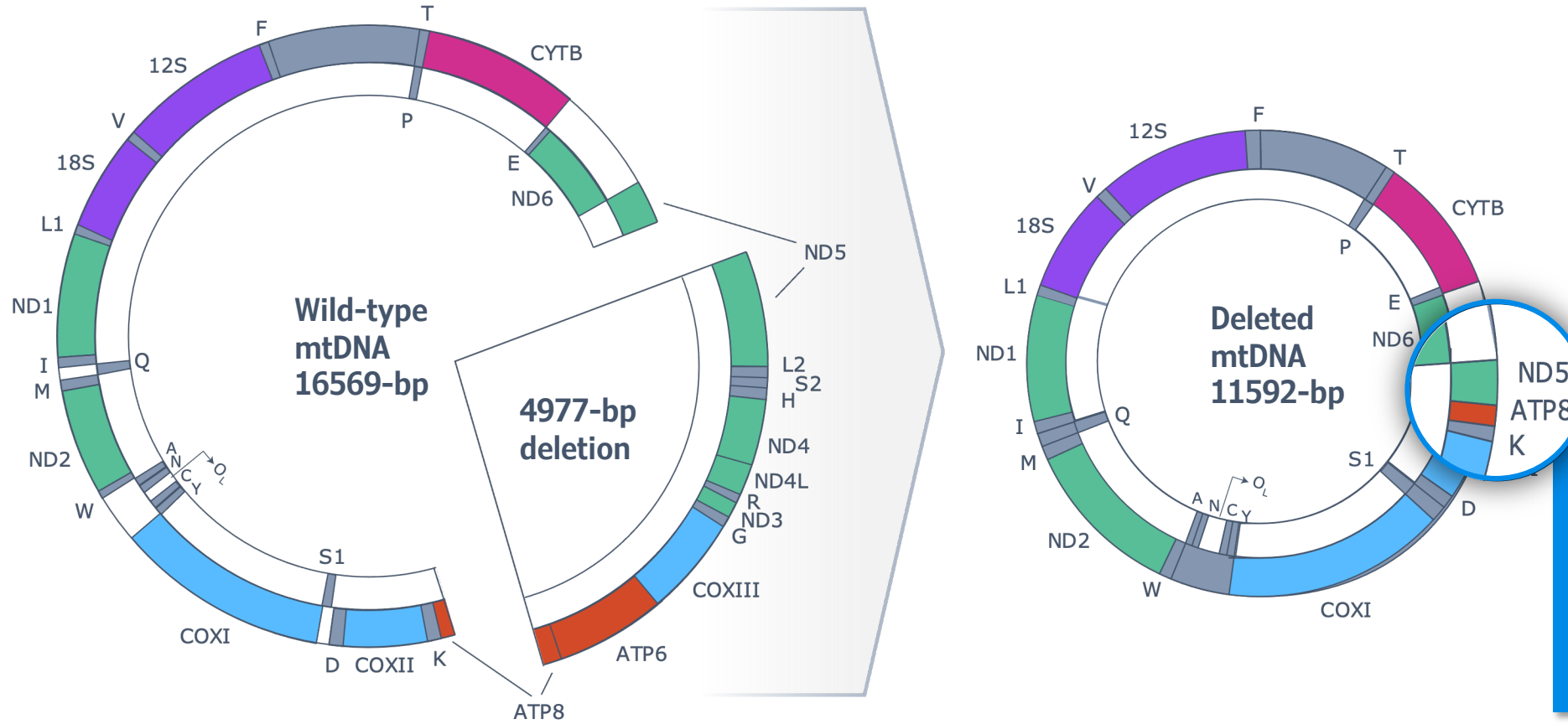


Implicated in:

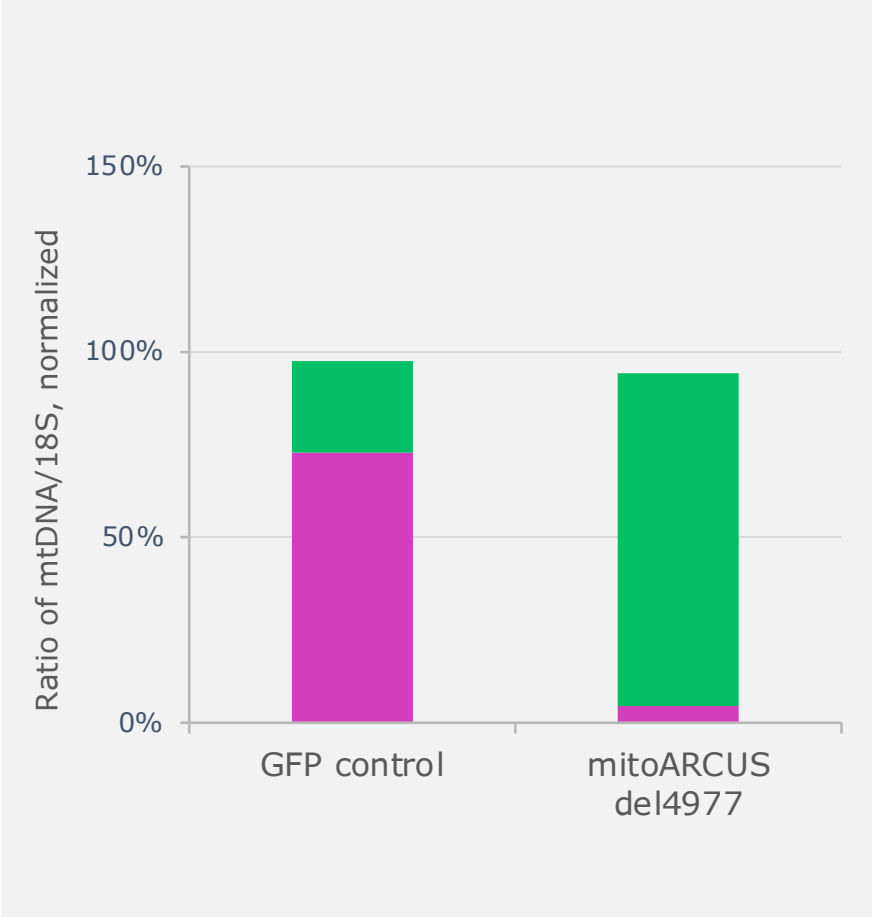
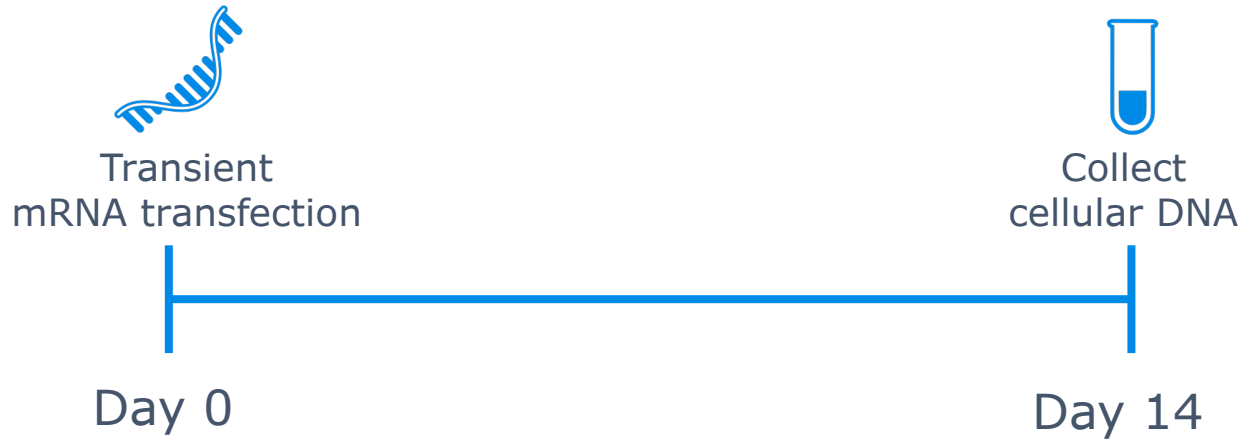
- > Myopathies
- > Kearns-Sayre syndrome
- > Alzheimer's disease
- > Chronic progressive external ophthalmoplegia
- > Pearson syndrome



4977bp of mtDNA are missing in genomes with the common deletion

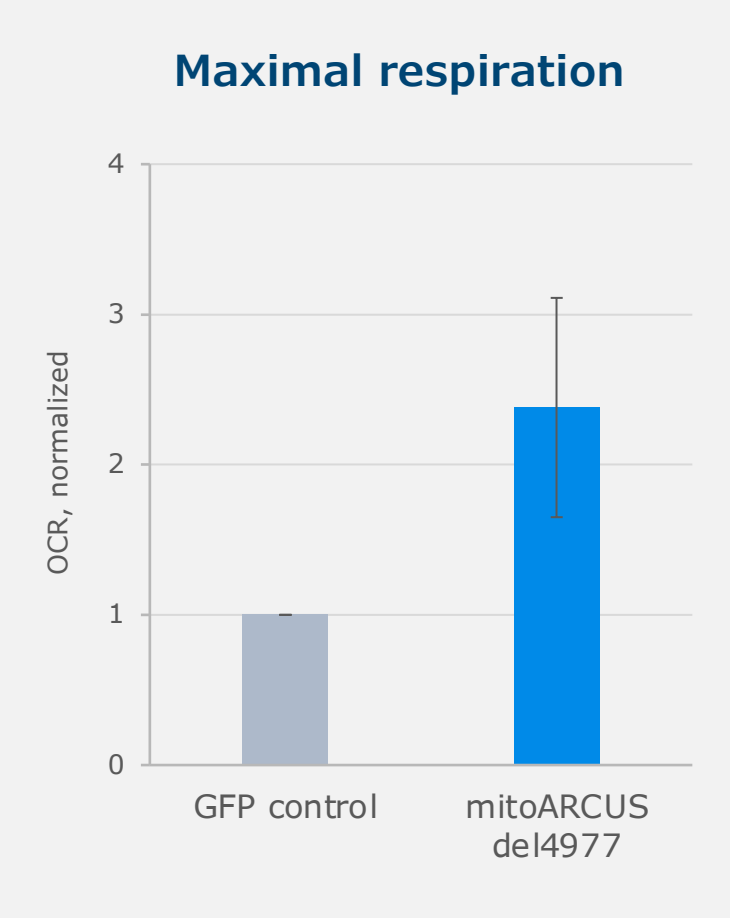
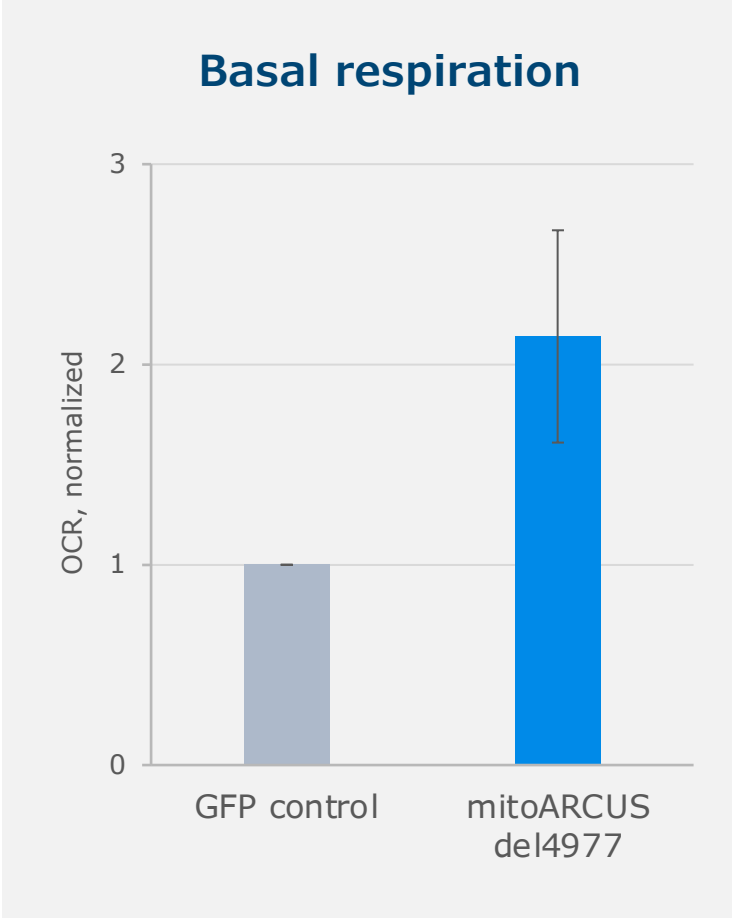
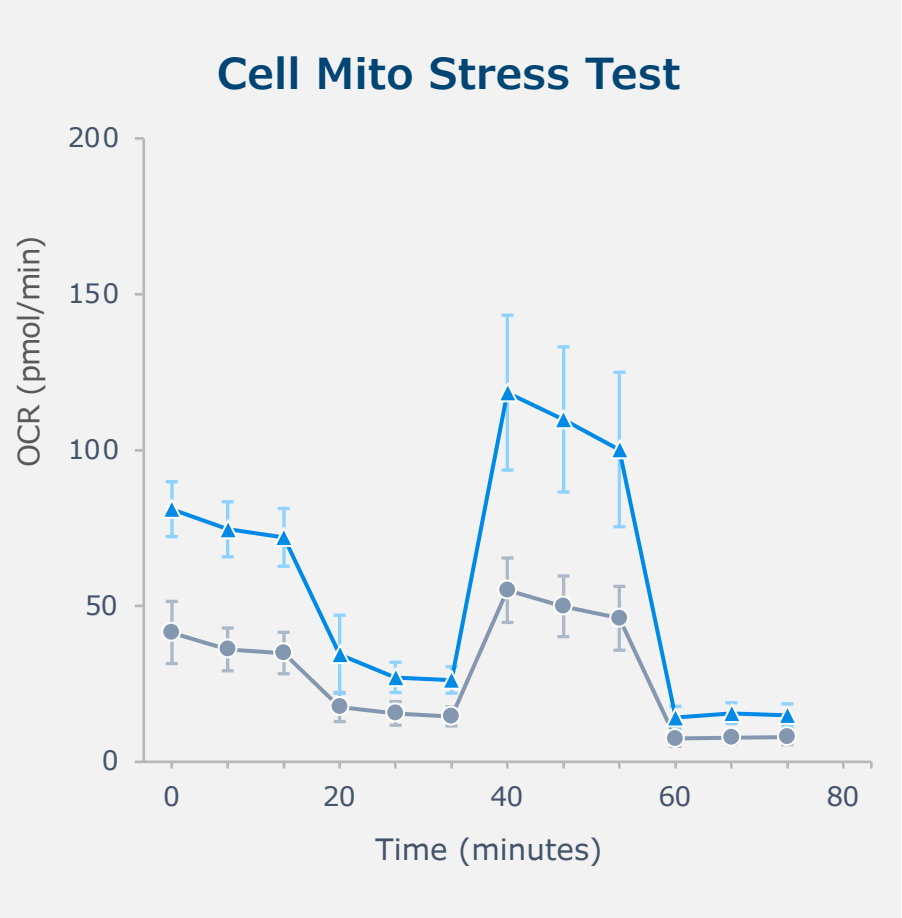


mitoARCUS_del4977 effectively eliminates mtDNA molecules containing common deletion *in vitro*



■ Percentage mutant mtDNA ■ Percentage WT mtDNA

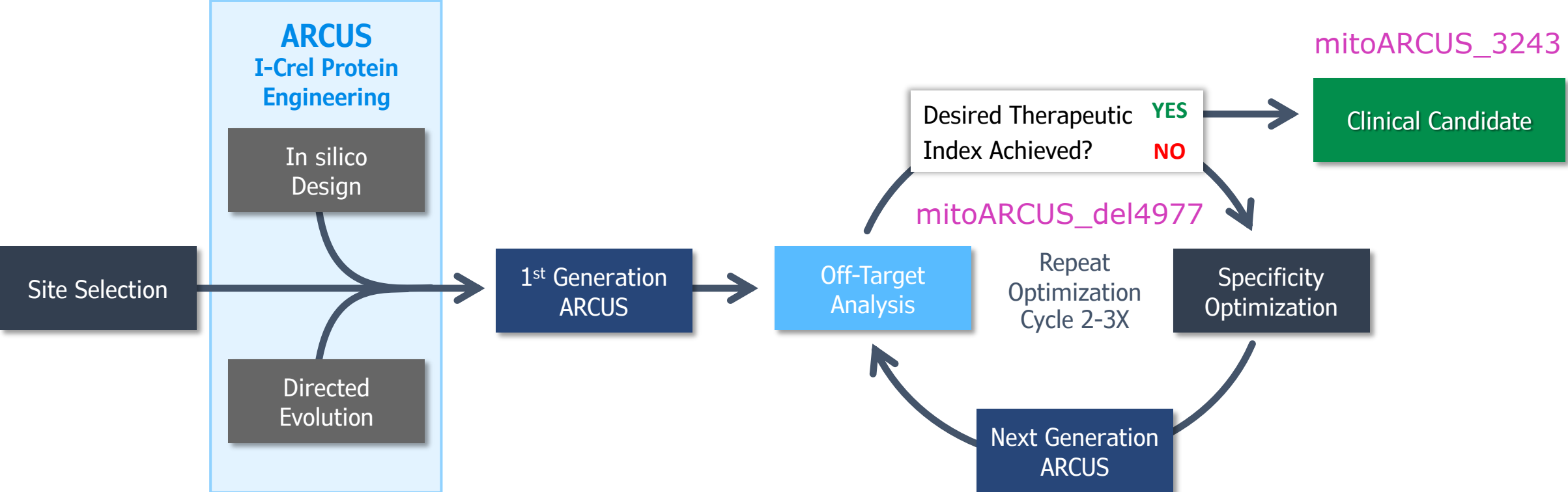
mitoARCUS_del4977-edited cells demonstrates improved mitochondrial function



● GFP control ▲ mitoARCUS_del4977



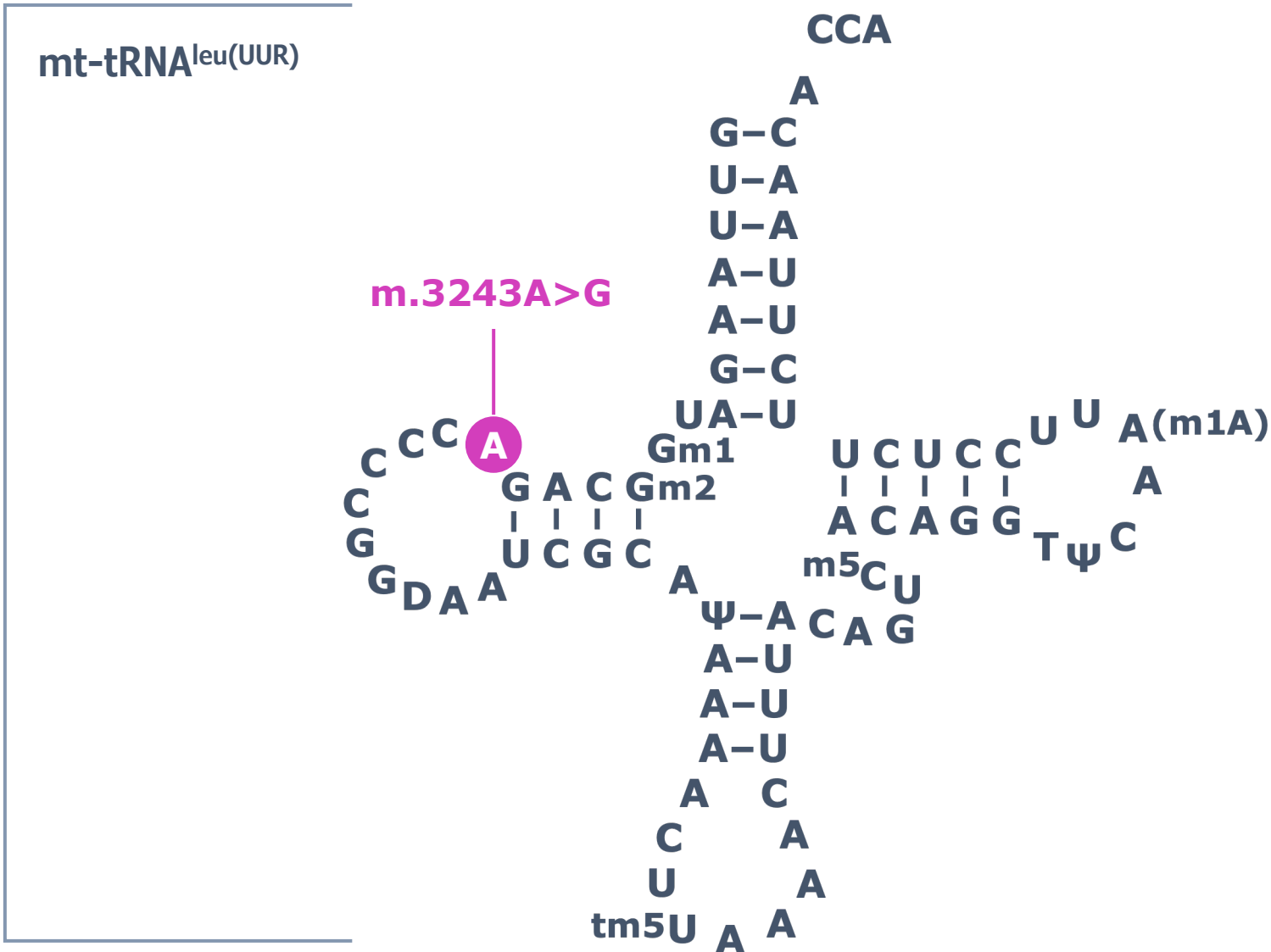
Nuclease optimization for mitoARCUS_del4977 is ongoing



m.3243A>G



m.3243A>G is the most common pathogenic mtDNA point mutation



m.3243A>G

- > Estimated population prevalence of ~1 in 500 individuals¹
- > Impacts tRNA stability/modification and disrupts mitochondrial protein production
- > Implicated in many disorders

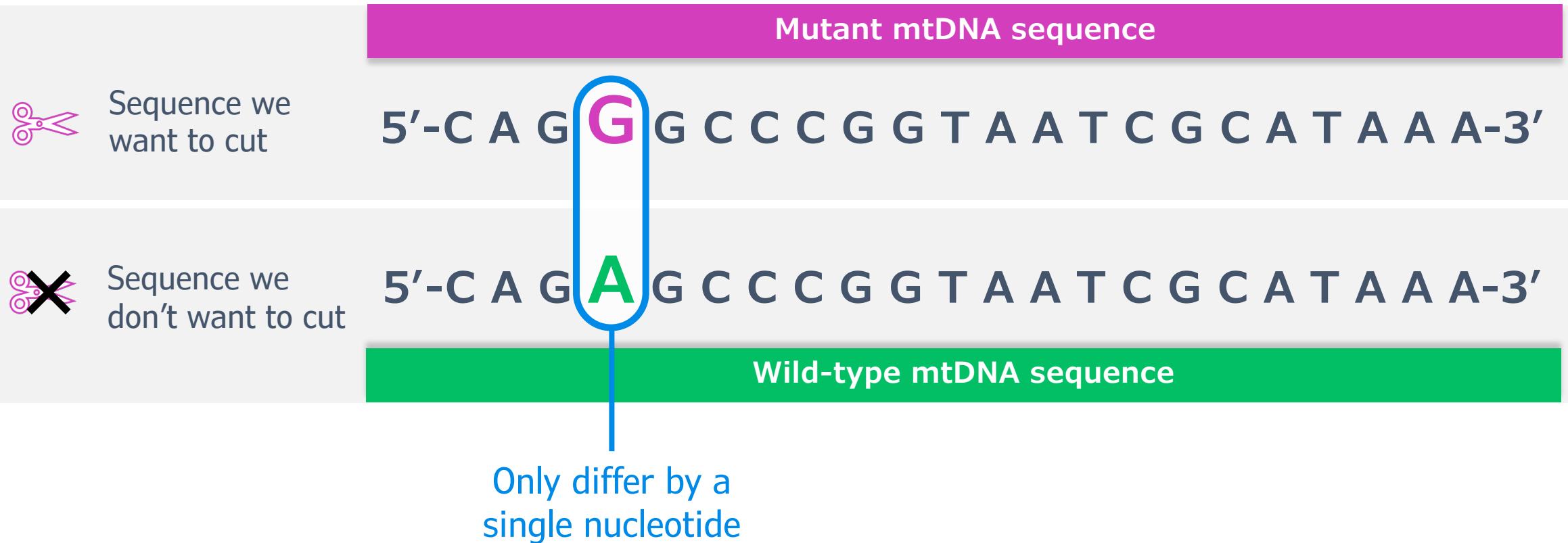


Sources:

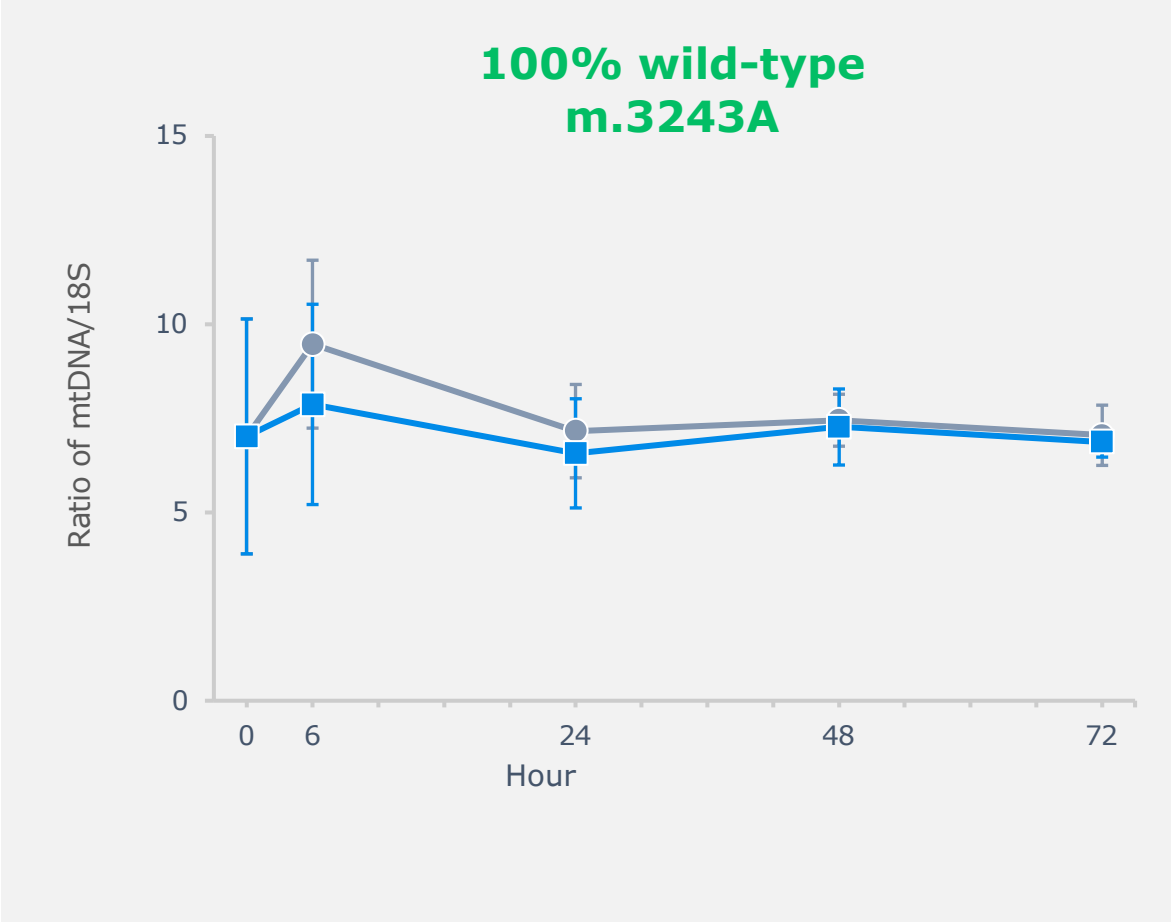
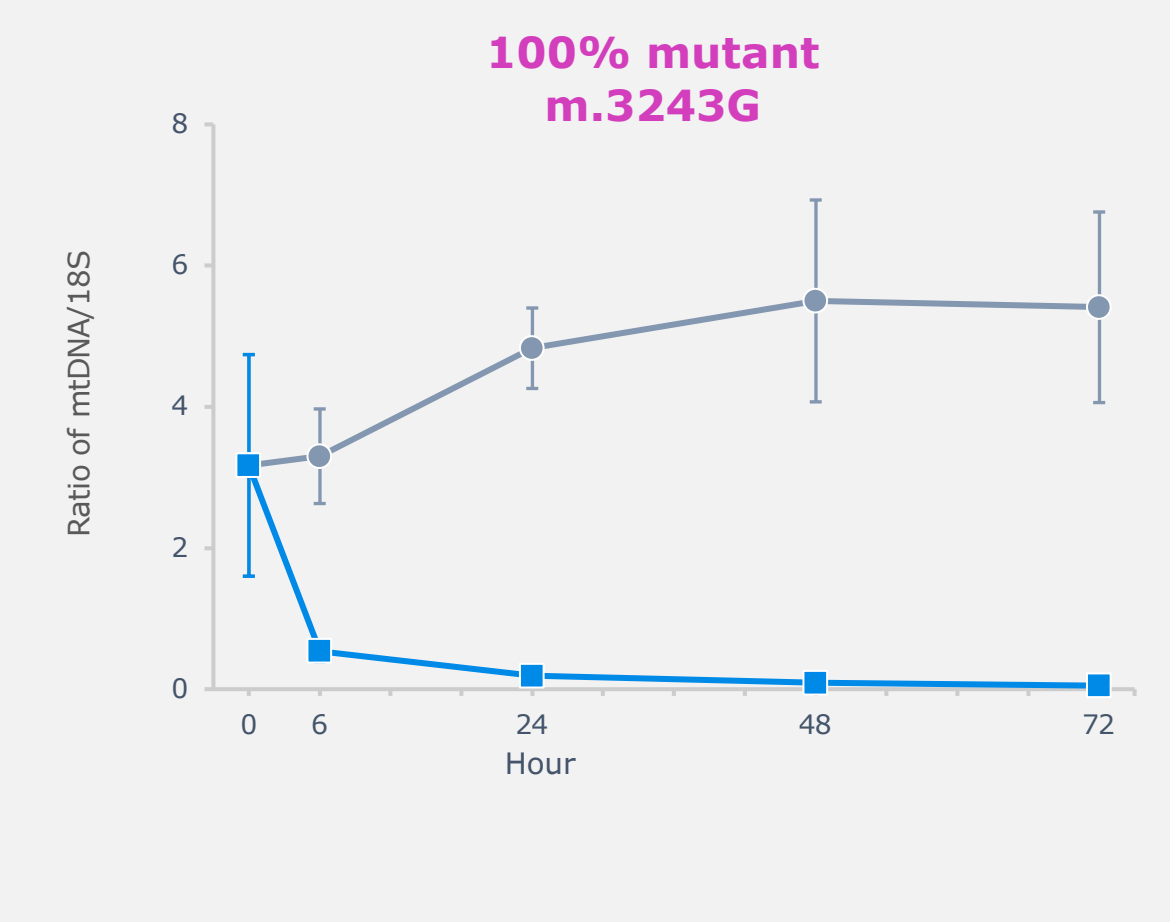
1. Manwaring et al 2007. Population prevalence of the MELAS A3243G mutation. Mitochondrion

Nuclease specificity is crucial to discriminate single nucleotide change

mitoARCUS nuclease specific to mutant m.3243G = **mitoARCUS_3243**



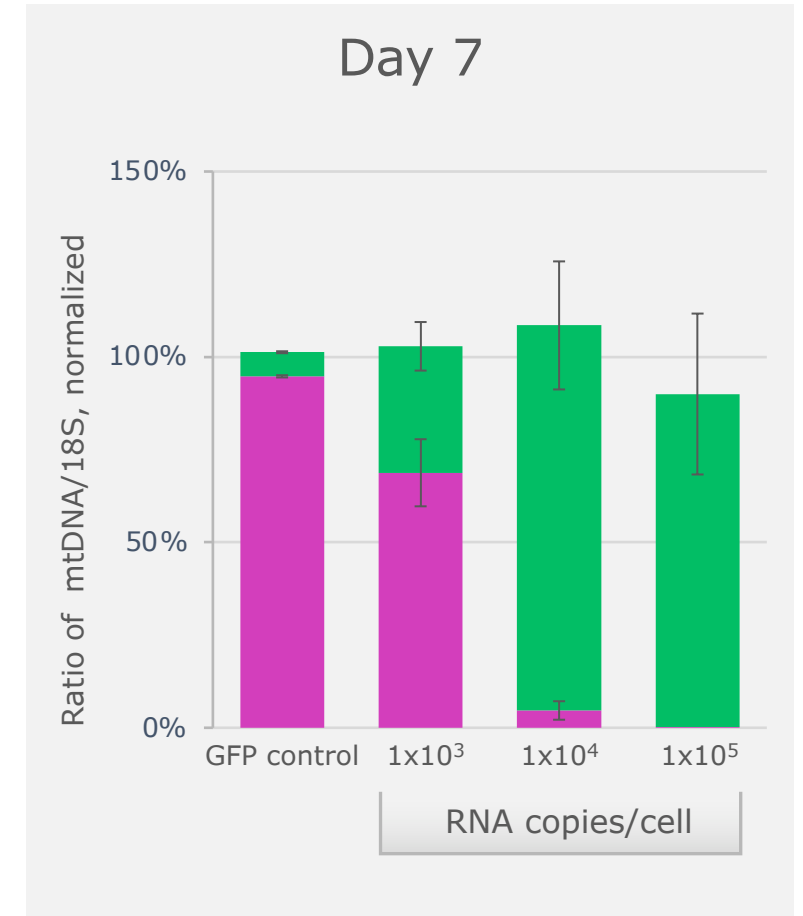
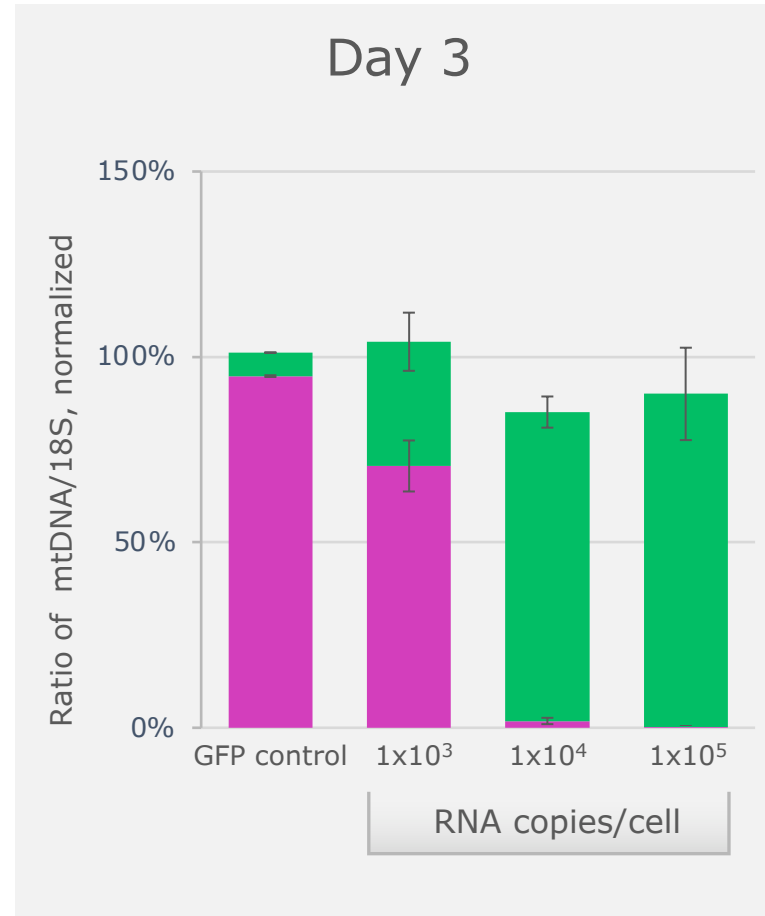
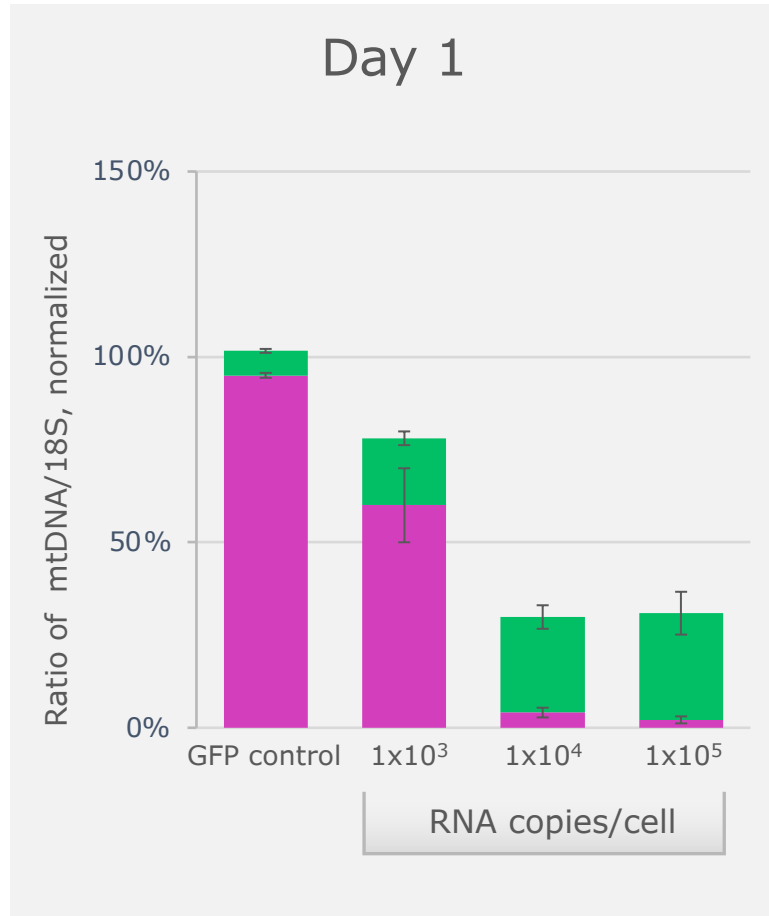
mitoARCUS_3243 efficiently eliminates mutant m.3243G, but does not cut wild-type m.3243A



—●— GFP control —■— mitoARCUS_3243



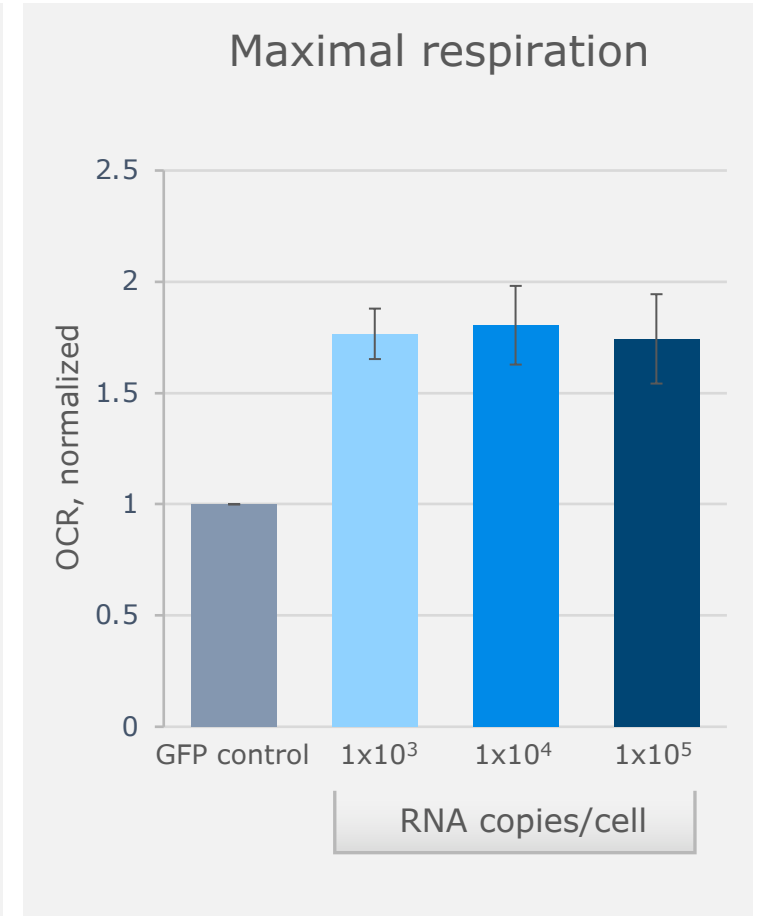
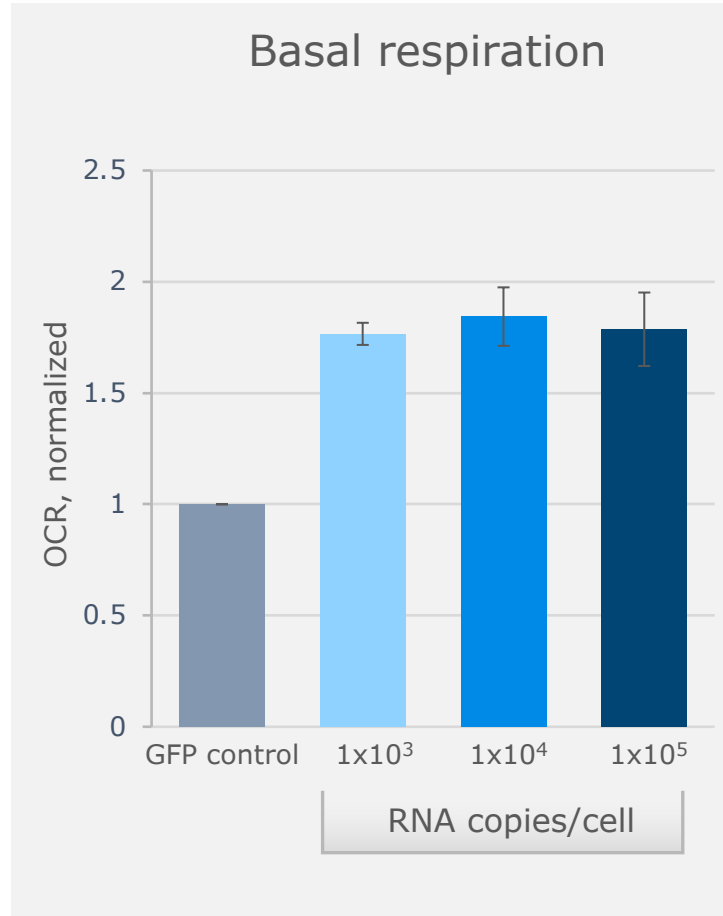
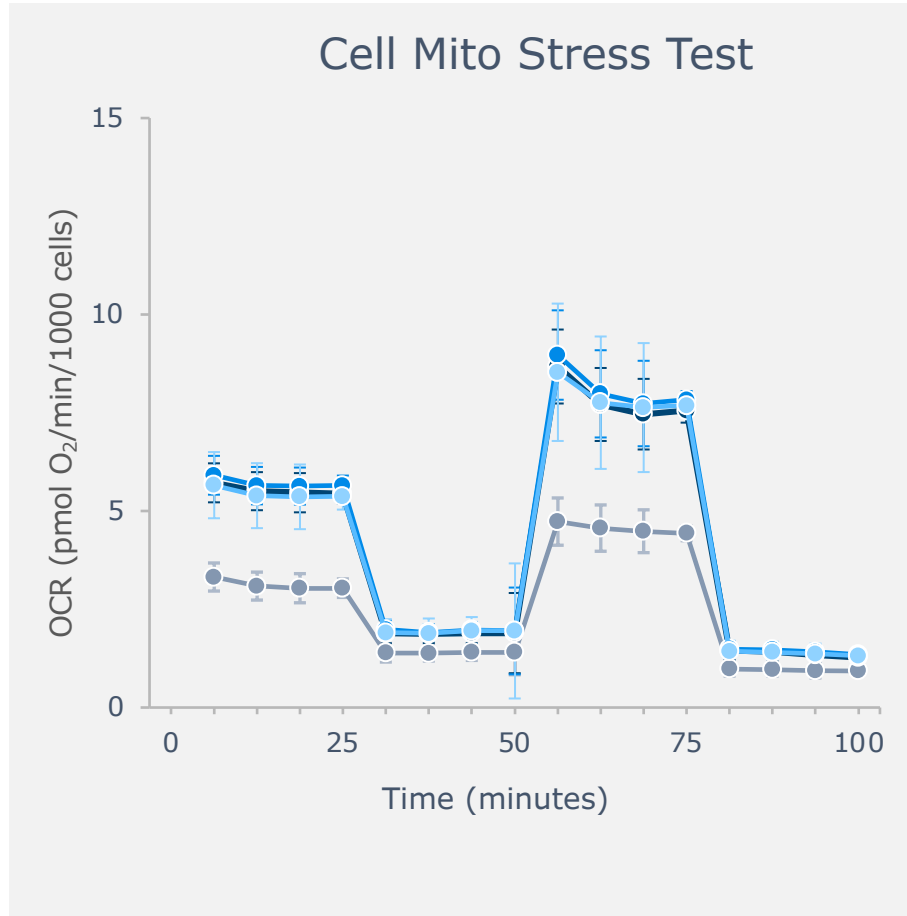
mitoARCUS_3243 shifts heteroplasmy in 95% mutant cybrid cells



■ Percentage mutant mtDNA ■ Percentage WT mtDNA



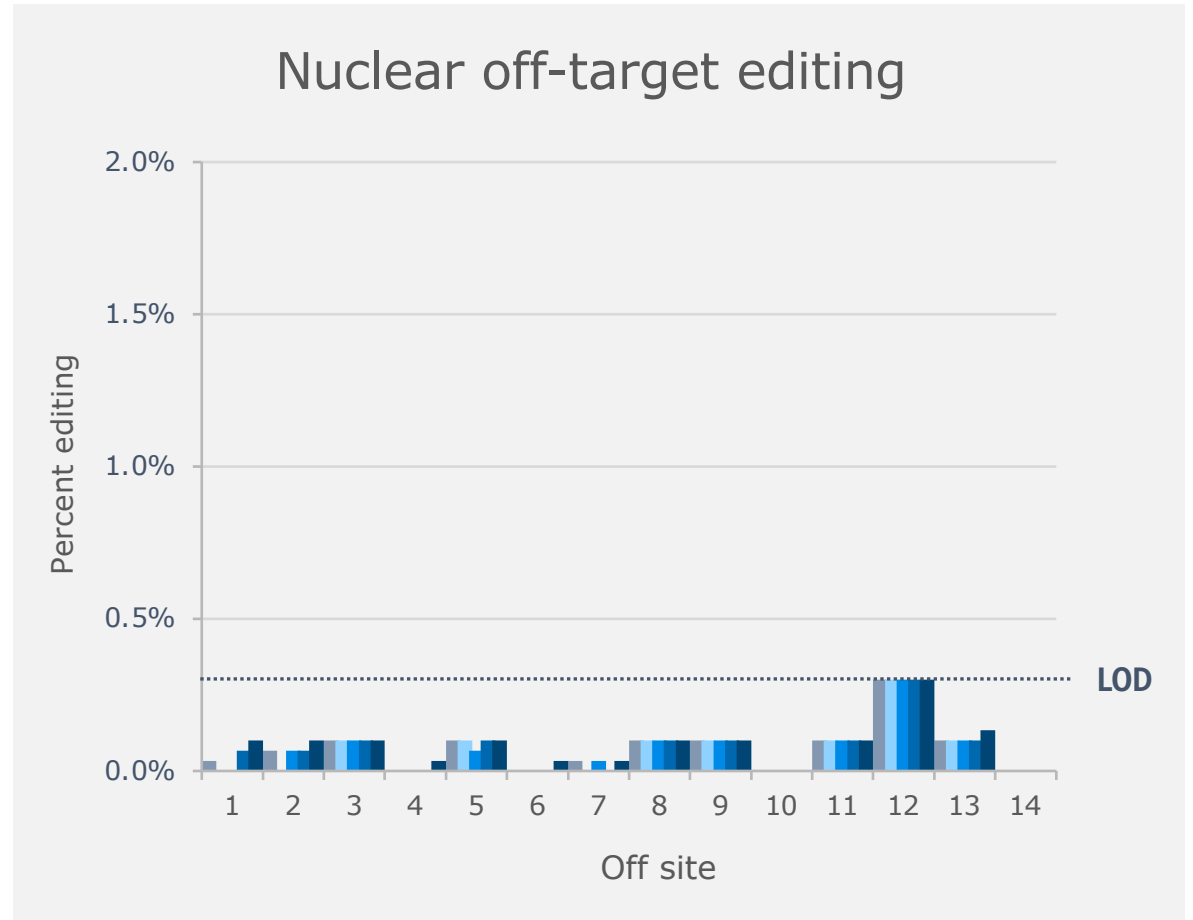
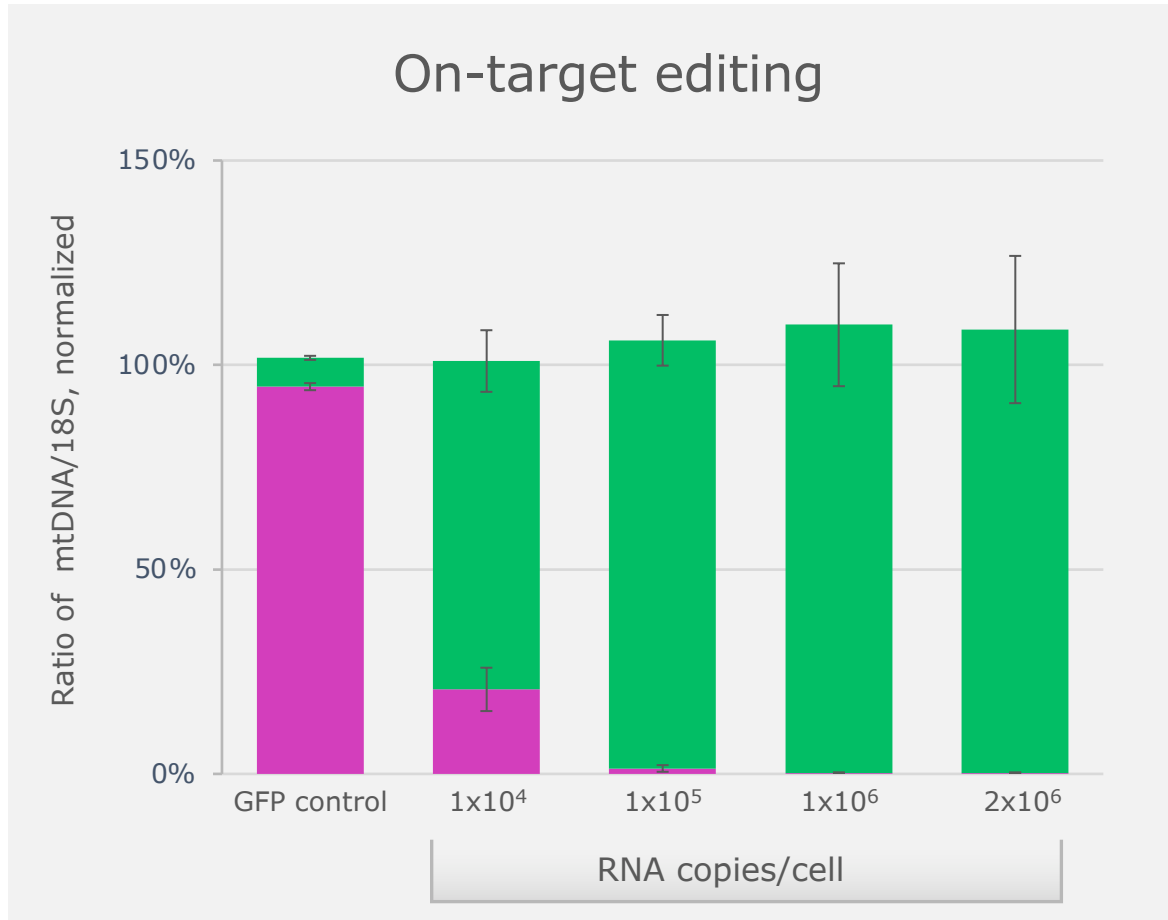
Specific elimination of mutant m.3243G leads to improvements in mitochondrial function



—●— GFP control —●— 1x10³ RNA copies/cell —●— 1x10⁴ RNA copies/cell —●— 1x10⁵ RNA copies/cell



Nuclear off-target editing is eliminated with MTS and NES



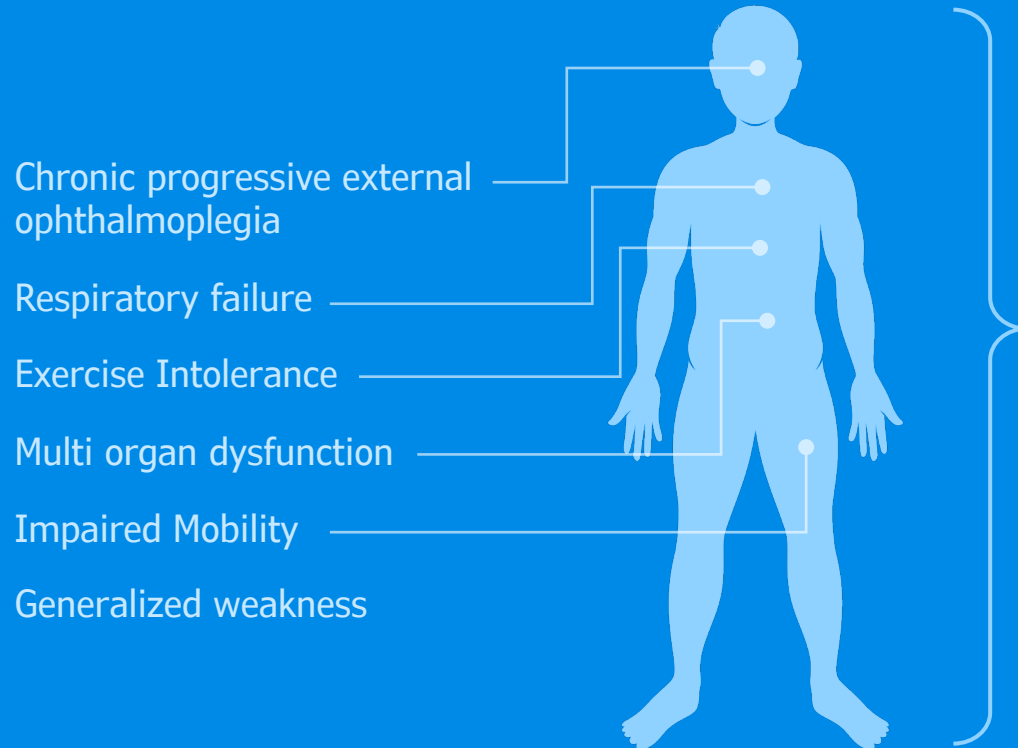
Percentage mutant mtDNA Percentage WT mtDNA

GFP control 1x10⁴ RNA copies/cell 1x10⁵ RNA copies/cell
1x10⁶ RNA copies/cell 2x10⁶ RNA copies/cell



Developing mitoARCUS_3243 for patients with m.3243 mitochondrial disease

m.3243-associated mitochondrial diseases often lead to defects in energy production affecting high energy-demand tissues (e.g. skeletal muscle)



Patients today lack curative treatments and receive supportive care only through "mito cocktails"¹

m.3243A>G

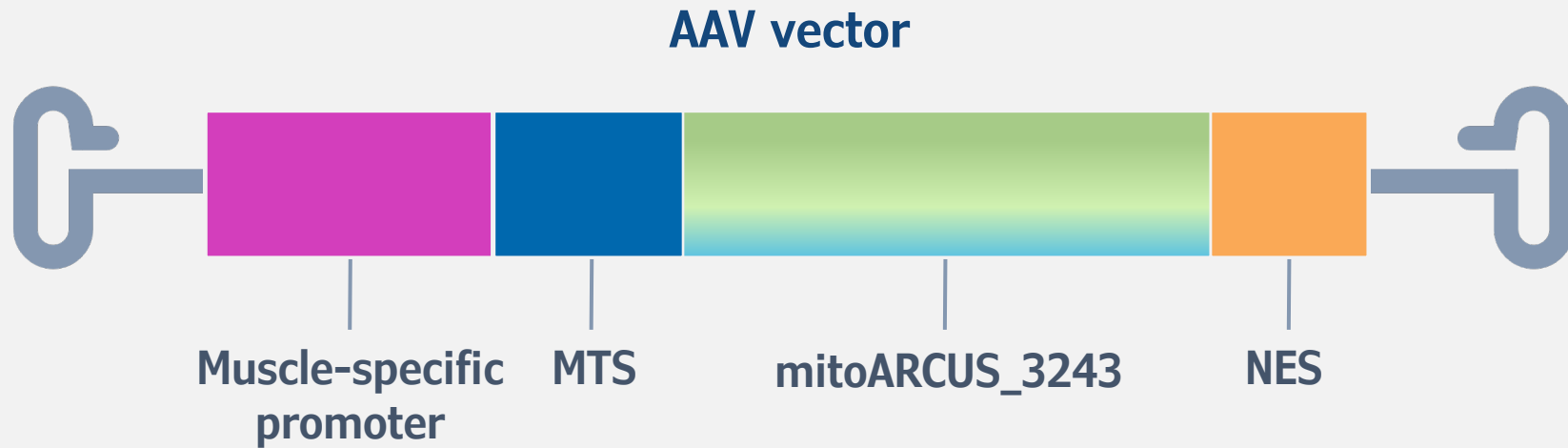
m.3243-associated mitochondrial disease estimated at



Sources:

1. <https://www.ninds.nih.gov/health-information/disorders/mitochondrial-myopathies>; <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6938233/>
2. Calculated based disease epidemiology studies and secondary literature

PBGENE-PMM is the first therapeutic designed to eliminate mutant m.3243G mtDNA



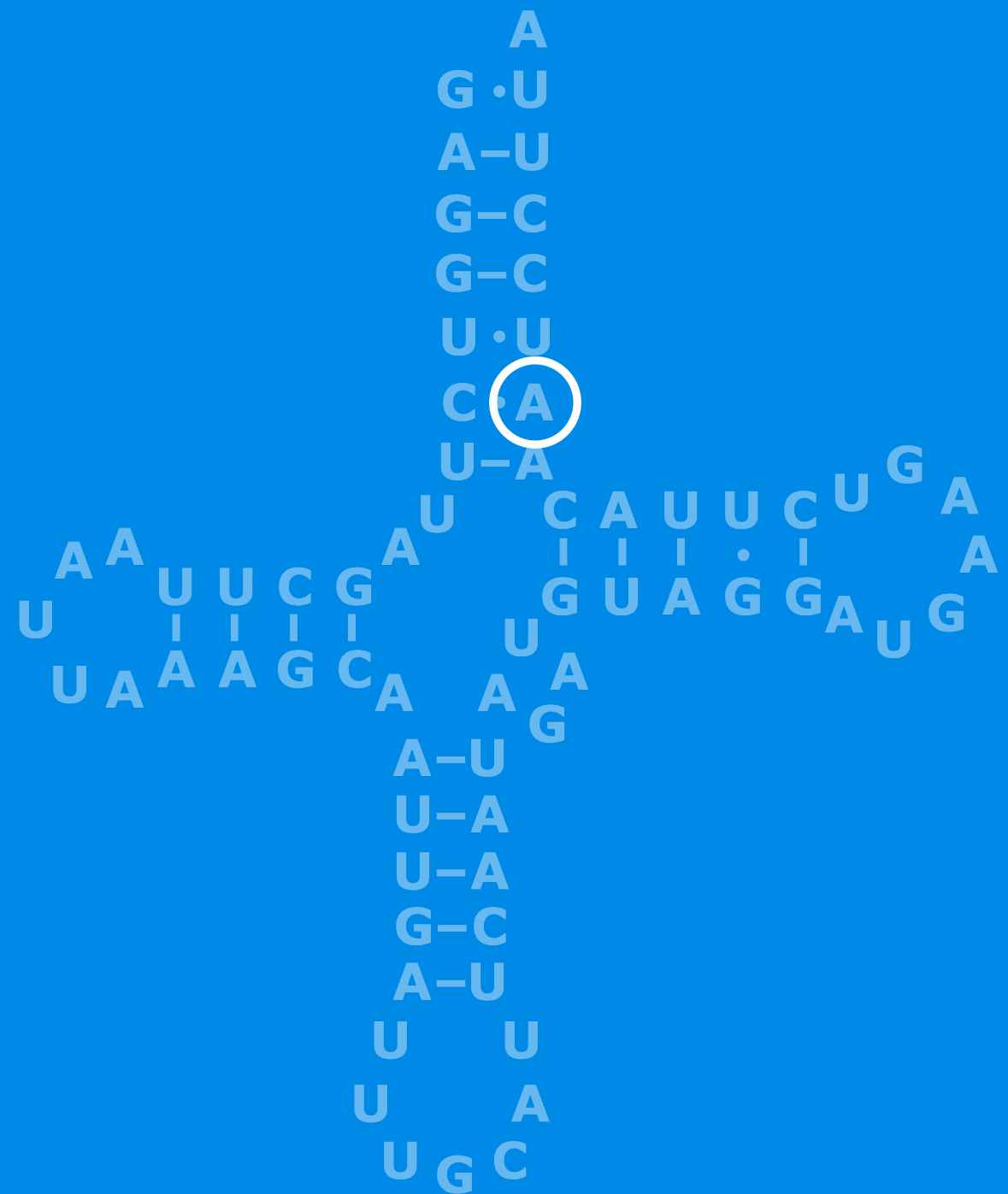
Objective

Systemically administer PBGENE-PMM to patients with m.3243-associated mitochondrial disease to elicit a shift in heteroplasmy in skeletal muscle

Use m.5024C>T mouse model with surrogate nuclease to translate preclinical data

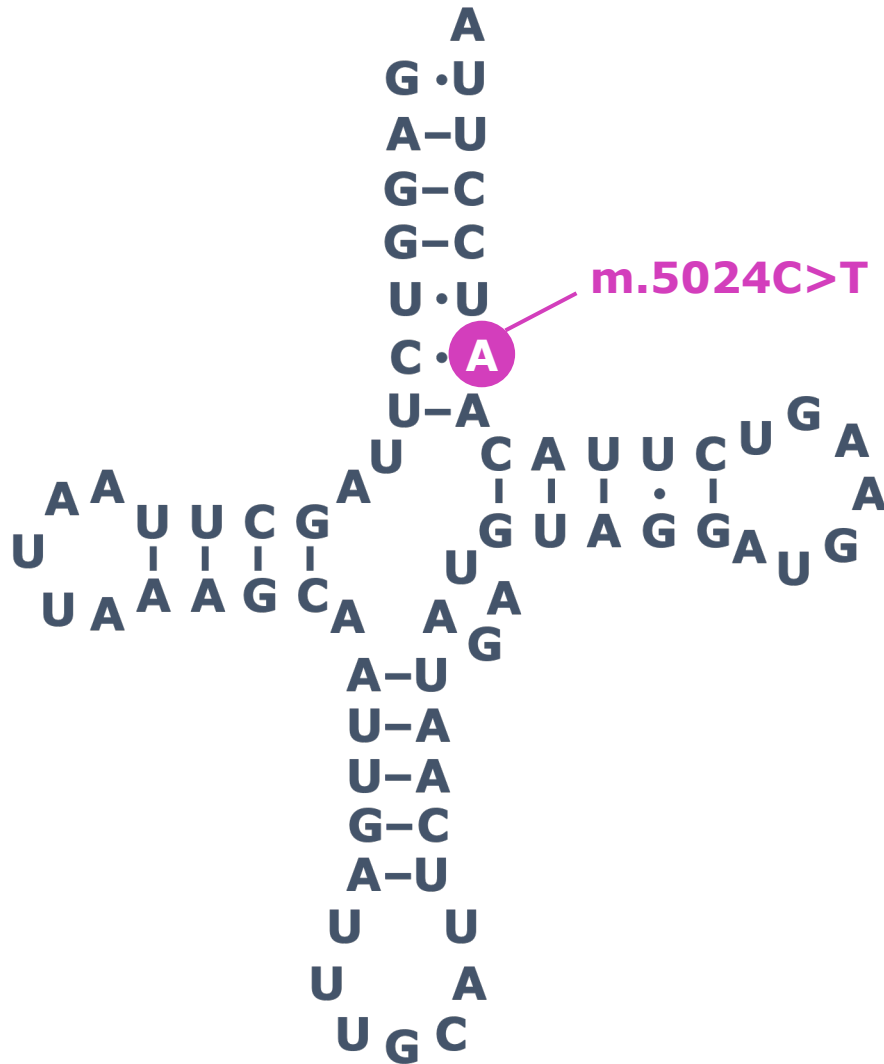


Mouse m.5024C>T



Leveraging the m.5024C>T heteroplasmic mouse model to determine clinical dosing

mt-tRNA^{Ala}

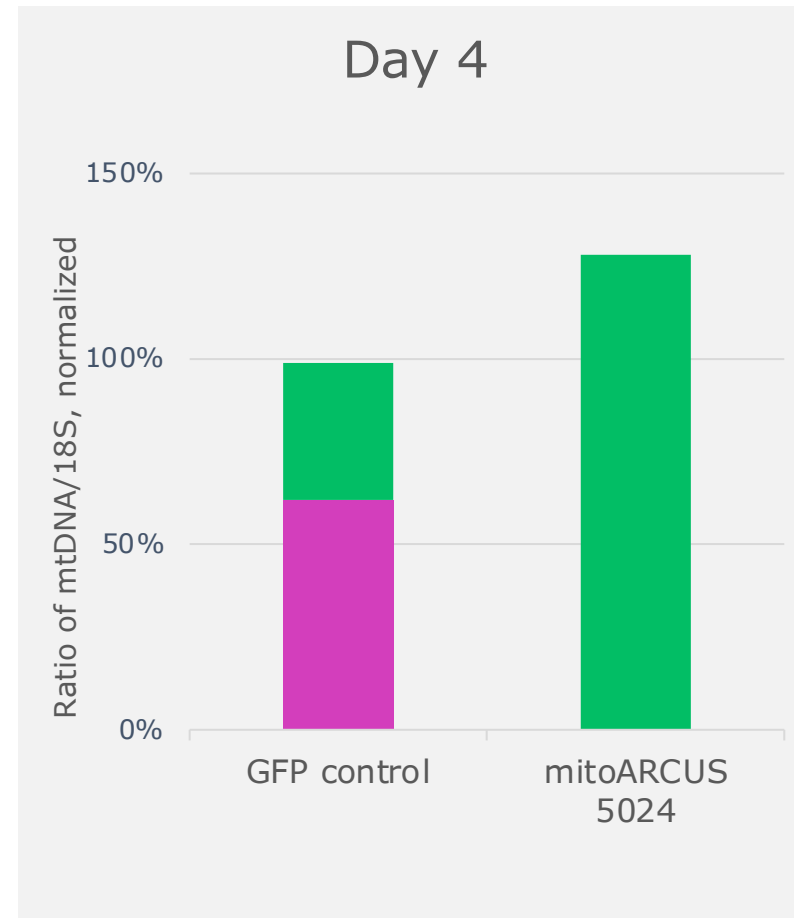
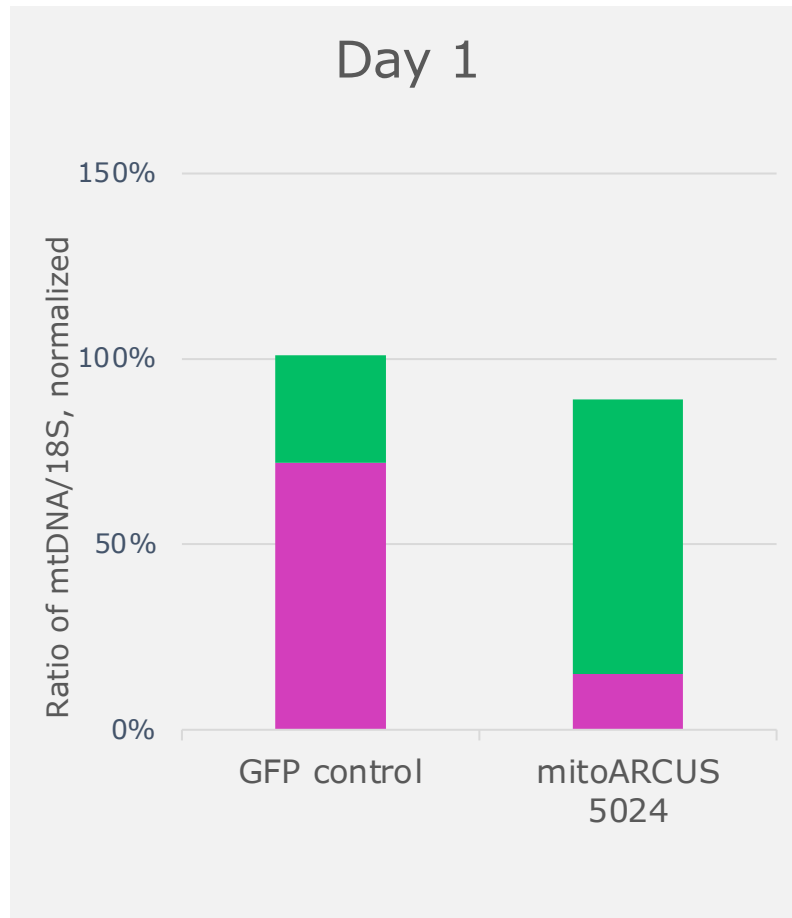


m.5024C>T

- > No overt clinical phenotype
- > Model provides POC for therapeutic approach
- > Surrogate mitoARCUS nuclease developed that is specific for mutant m.5024T mtDNA = **mitoARCUS_5024**



mitoARCUS_5024 effectively eliminates mutant m.5024T mtDNA in vitro

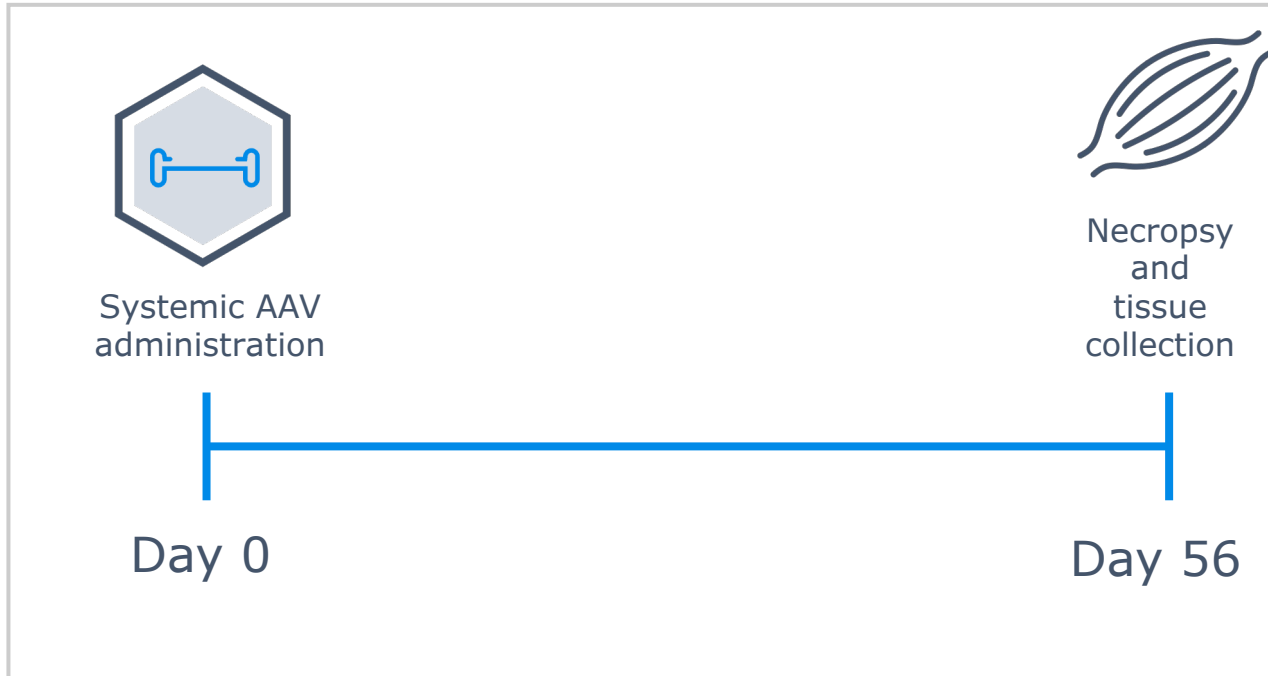


■ Percentage mutant mtDNA

■ Percentage WT mtDNA



mitoARCUS_5024 in vivo study design



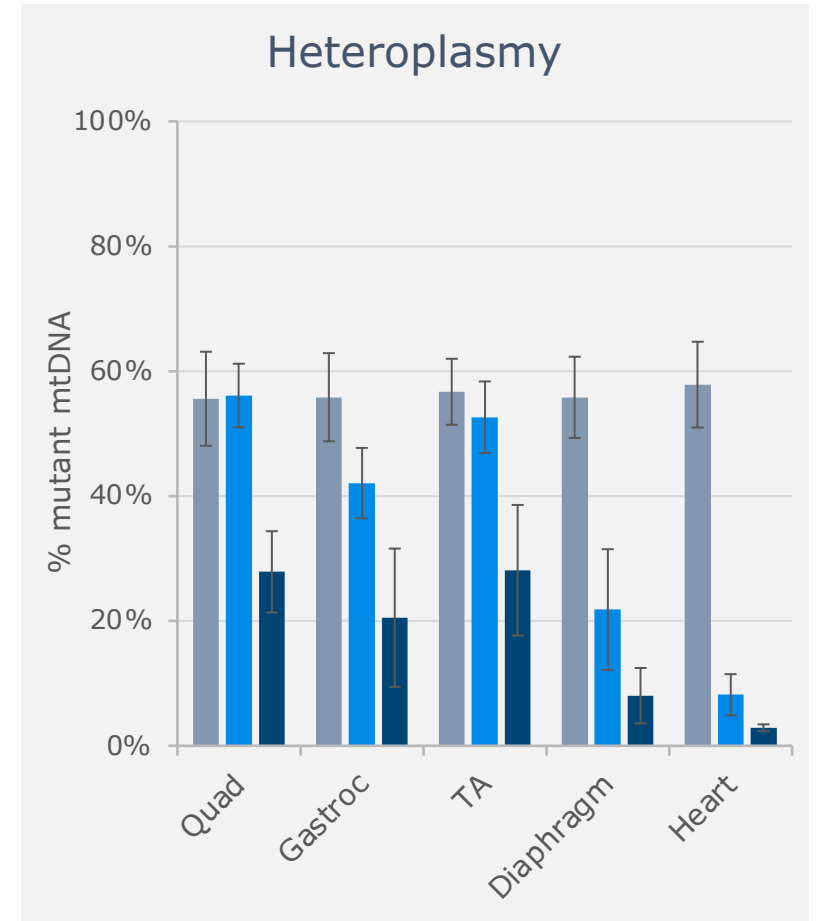
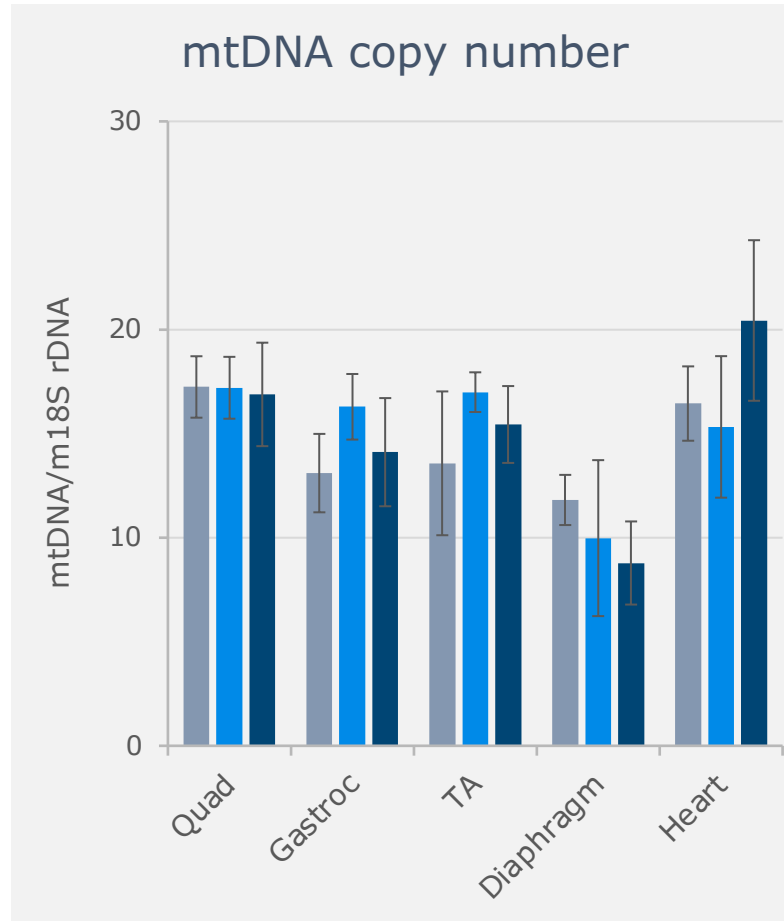
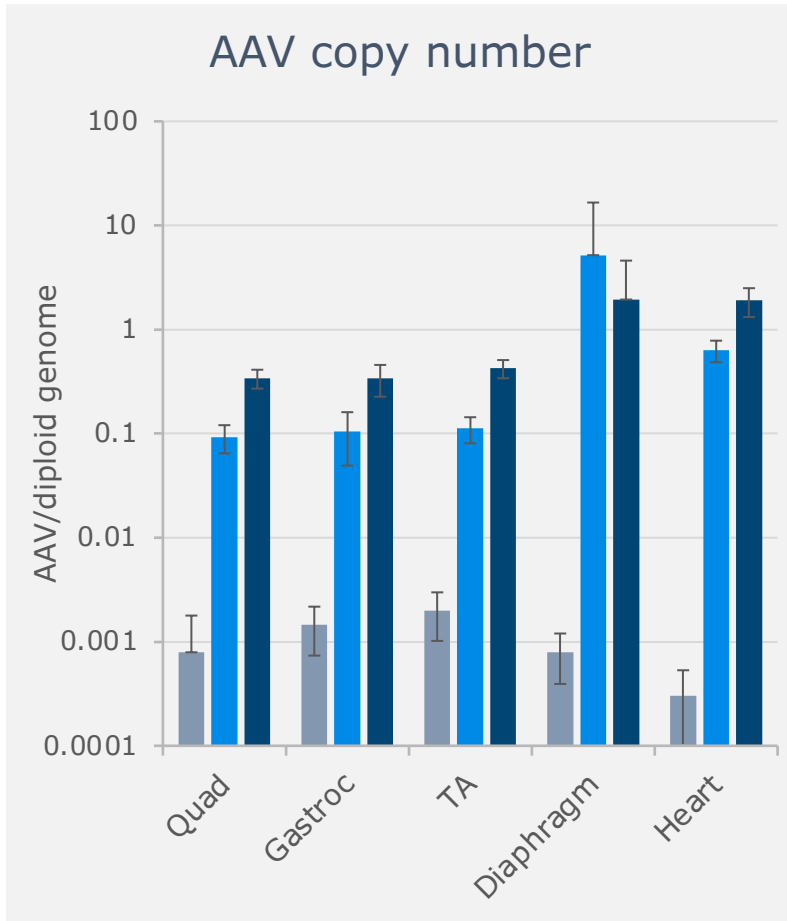
Group	Treatment	Dose	N
1	PBS	N/A	5
2	mitoARCUS_5024	2.5×10^{13} vg/kg	7
3	mitoARCUS_5024	1×10^{14} vg/kg	7

PURPOSE:

To evaluate ability of mitoARCUS_5024 to shift heteroplasmy in target tissues following systemic AAV administration in m.5024C>T heteroplasmic mice



mitoARCUS_5024 effectively transduces target tissues and eliminates mutant mtDNA without inducing mtDNA depletion

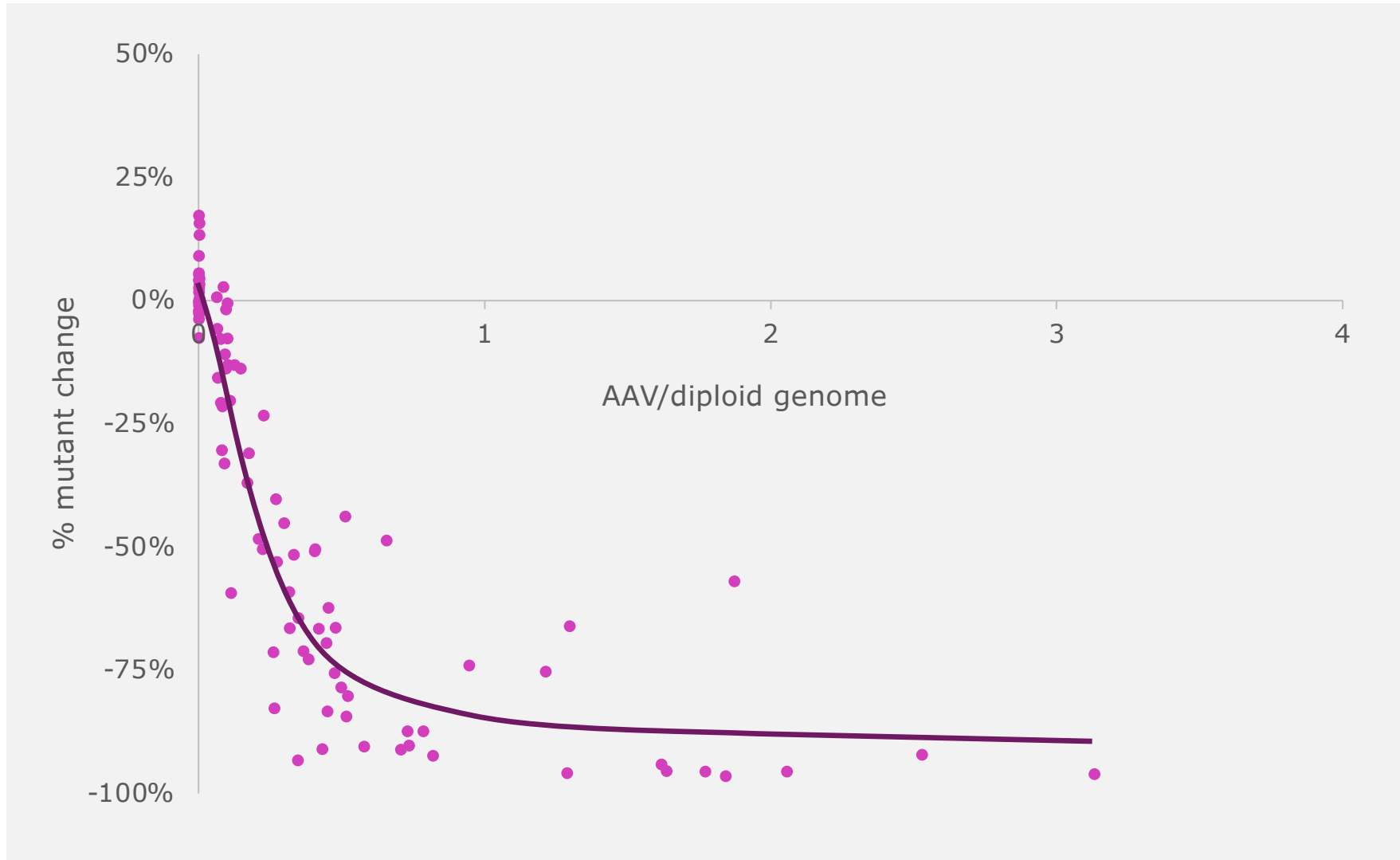


■ PBS control ■ mitoARCUS_5024 2.5x10¹³ vg/kg ■ mitoARCUS_5024 1x10¹⁴ vg/kg



Unpublished data

AAV biodistribution drives mutant mtDNA elimination in target tissues



Minimal amounts of AAV are needed to drive heteroplasmy shift in target tissues



PBGENE-PMM



PBGENE-PMM program overview

- Final Clinical Candidate
- PoC and Dose Finding Studies underway
- on-track* Initiate GLP Tox
- In-process* Identify First-in-Human Study Sites
- on-track* Expected CTA/IND in 2025



Conclusions



ARCUS platform generates highly specific nucleases capable of discriminating a single nucleotide



ARCUS can be trafficked to mitochondria to selectively eliminate mutant mtDNA, both deletions and point mutations



ARCUS-mediated rescue of mtDNA heteroplasmy improves mitochondrial respiration



ARCUS can be systemically delivered using AAV to reach high energy-demand tissues



Preclinical data suggests low levels of AAV presence in target tissues is sufficient to shift heteroplasmy in m.5024C>T mouse model and gives reason to believe in PBGENE-PMM



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- Crystal Gordon
- Kelly Shelton
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- Ugne Zekonyte
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- Flavia Fontanesi

