



# Metagenomi

Unlocking 4 Billion Years  
of Microbial Evolution to Create  
Curative Genetic Medicines

Nasdaq: MGX

September 2024



# Forward Looking Statements

This presentation includes forward-looking statements, including forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995. All statements other than statements of historical facts contained in this presentation are forward looking statements, including statements regarding our cash runway, strategy and plans, industry environment, potential growth opportunities, and the therapeutic potential of our programs. The words “believe,” “may,” “will,” “estimate,” “continue,” “anticipate,” “design,” “expect,” “could,” “plan,” “potential,” “predict,” “seek,” “should,” “would,” or the negative version of these words and similar expressions are intended to identify forward-looking statements.

We have based these forward-looking statements on our current expectations and projections about future events and trends that we believe may affect our financial condition, results of operations, strategy, short and long term business operations and objectives, and financial needs. These forward-looking statements are subject to a number of risks, uncertainties and assumptions, including but not limited to, our ability to develop and advance our programs and product candidates, our ability to maintain and establish collaborations or strategic partnerships, our regulatory approvals and filings, and other risks, uncertainties and assumptions identified in our filings with the Securities and Exchange Commission (the “SEC”), including our most recent Form 10-K and Form 10-Q filed with the SEC, and any subsequent filings with the SEC.

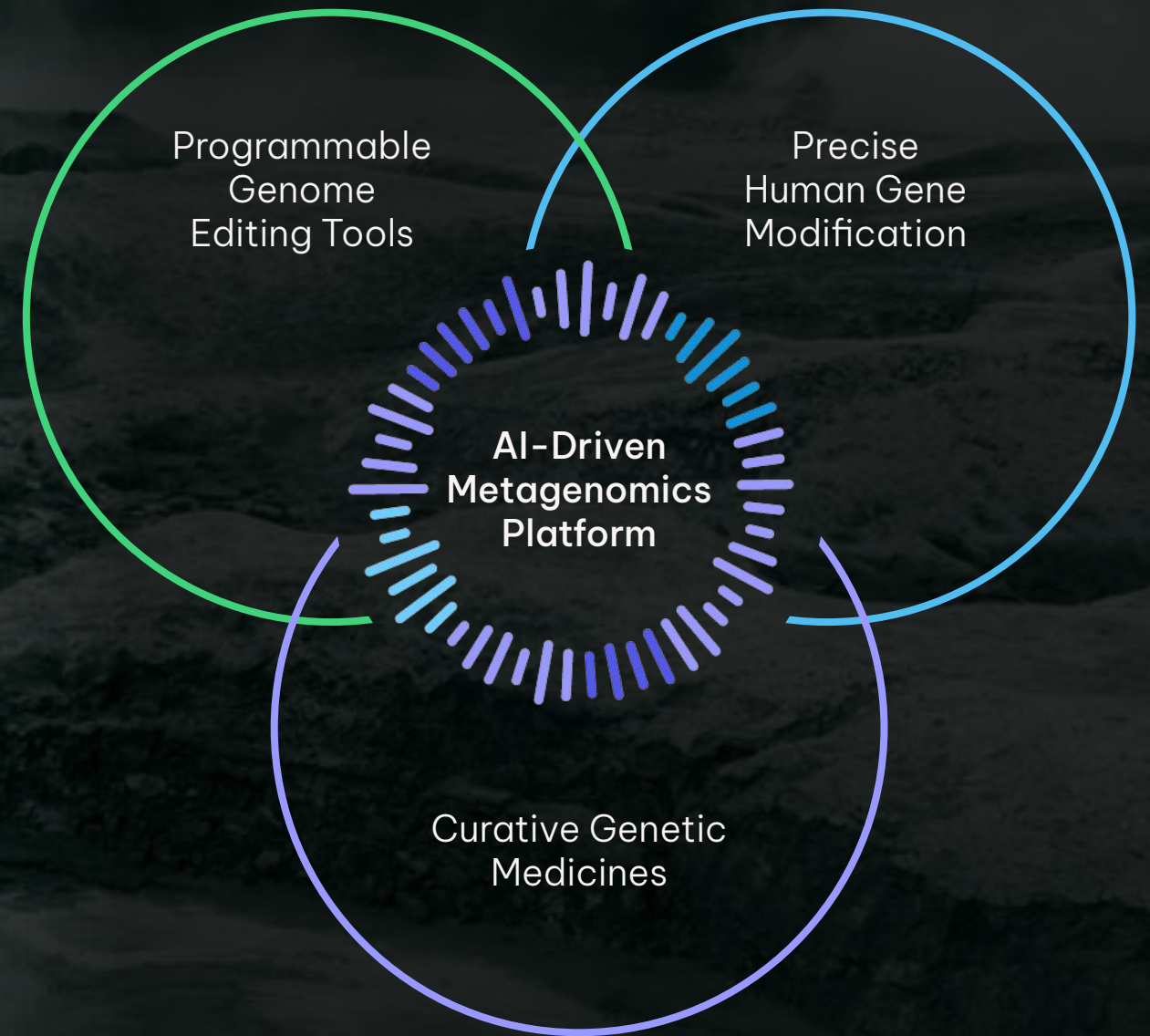
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# Our Vision:

Harness the power of our metagenomics platform to create curative genetic medicines for patients



# The metagenomics platform is the foundation of our gene editing toolbox



## Proprietary Sampling

Exploring diverse microbe-rich ecosystems to extract DNA from environmental samples



## AI-powered Screening

Leveraging AI, ancestral reconstruction, proprietary algorithms, robotics, and automation to reveal novel cellular machinery



## Engineering & Optimization

Designing and optimizing novel gene editing tools to set new standards in targetability, precision, efficiency, and scope of editing capabilities



## Complete Genome Editing Capabilities

Building a proprietary toolbox capable of correcting any genetic mutation anywhere in the human genome



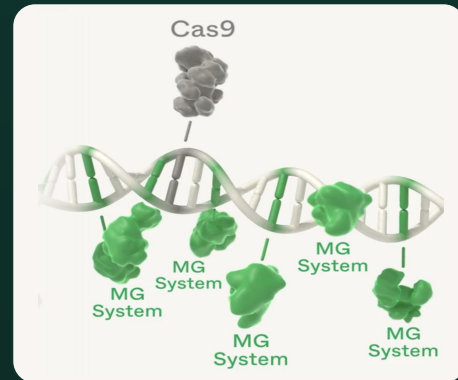


# Our proprietary toolbox enables precise edits of the human genome



## MG Tool

### Nuclease



Proprietary library of highly precise and efficient nucleases, including ultra-small systems (SMARTs), provides programmable chassis for other gene editing tools

## Genomic Correction

*Knockdown, knock-in, exon skipping*

### Base Editors



Programmable chassis with additional effector enzymes to cause single nucleotide changes

*Single nucleotide changes*

### RIGS: Replacement



RNA-mediated integration systems (RIGS) use programmable chassis with additional reverse transcriptase for edits encoded in RNA templates

*1-100 base pair replacement, insertion, or deletion*

### RIGS: Integration



RIGS with expanded RNA template for site-specific integration of genes

*>100 base pair integrations*

### CAST



CRISPR-associated transposases (CAST) use DNA templates to allow for site-specific gene integration

*>10,000 base pair integrations*



# Precise gene edits unlock development of curative medicines



## Disease Target Selection Criteria:

Well understood disease biology

Readily available translational biomarkers

Established development pathways

Important unmet medical need

Choose the right genome editing tool and delivery technology to engineer precision human therapeutics

**FOCUS**  
Liver targeting for hematologic, cardiometabolic and hepatic diseases



Various LNP & AAV delivery options

**ADDITIONAL FOCUS**  
Extrahepatic Disease



Various AAV and novel non-viral delivery options

# Internal development capabilities power a fully integrated gene editing company



*The ability to develop and characterize complex human gene editing components is essential to pursue a successful regulatory pathway in genetic medicine development*

## AI and automation

Integrated screening and characterization to streamline development

## mRNA & gRNA optimization

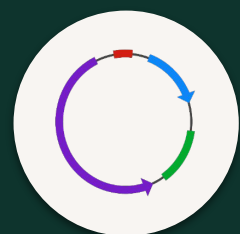
RNA optimizations to enhance genome editing performance

## Delivery

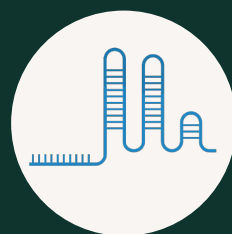
LNP and AAV delivery technologies to expand therapeutic targeting

## GMP Manufacturing

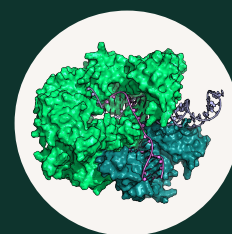
CMC development and GMP manufacturing to enable pipeline advancement to clinic



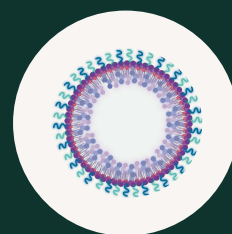
Plasmid



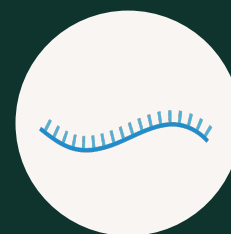
sgRNA



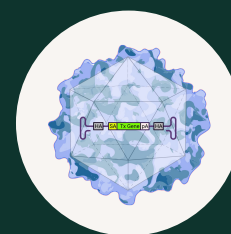
Nuclease



LNP



mRNA



AAV



# Strategic collaborations compliment our development capabilities



- *in vivo* genome editing therapeutics focusing on cardiometabolic diseases
- Up to 8 targets with 4 co-development and co-commercialization options
- \$80 million cash upfront, plus up to \$2.9B in potential milestone payments and royalties to Metagenomi



- Next-generation cell therapies enhanced by multiplex genome editing targeting TCR *ex vivo* immuno-oncology cell therapies
- Co-founded by world-renowned experts in cancer immunotherapy
- Metagenomi to receive options, milestones and royalties

Continuing partnering efforts to expand therapeutic impact to patients

Development Capability

Complementary Technology






Market Presence

Compatible Vision



# Broad pipeline built on our metagenomics platform



Editing Platform	Delivery	Indication / Editing Target	Discovery	Lead Optimization	IND-Enabling	Clinical	Partner	
 LIVER <i>Knock-in</i> <hr/> <i>Knockdown</i>	LNP + AAV	Hemophilia A / ALB	[Progress bar]					
		Undisclosed secreted protein diseases	[Progress bar]					
	LNP	Transthyretin Amyloidosis / TTR	[Progress bar]					IONIS
		Refractory Hypertension / AGT	[Progress bar]					IONIS
		Undisclosed cardiovascular disease	[Progress bar]					IONIS
		Undisclosed cardiovascular disease	[Progress bar]					IONIS
		Other Program: Primary Hyperoxaluria Type 1 / HAO1						
<i>Small gene corrections</i>	LNP	Alpha 1 Antitrypsin Deficiency / SERPINA1	[Progress bar]					
<i>Large gene insertion</i>	LNP	Wilson's Disease / ATP7B	[Progress bar]					
 CELL THERAPY <i>Multiplex editing</i>	Ex vivo	Solid tumor indications / TCR T Cells	[Progress bar]					affini 
		Multiplex editing: Undisclosed cell therapy applications						
 NEURO-MUSCULAR <i>Ultra small systems</i>	LNP / AAV	Programs in Research: Familial ALS, Duchenne Muscular Dystrophy, Charcot Marie Tooth Disease						
 LUNG, KIDNEY <i>Large gene insertion</i>	LNP / AAV	Programs in Research: Undisclosed renal diseases, Cystic Fibrosis						

\*Pipeline as of Q2 earnings (August 13, 2024)

# Recent and upcoming milestones drive towards the clinic



	Recent milestones achieved	2H' 2024	2025
<b>Hemophilia A Program</b>	<ul style="list-style-type: none"> <li>✓ Generated robust proof-of-concept data in multiple NHP studies</li> <li>✓ Engaged with FDA for regulatory advice</li> <li>✓ Nominated Development Candidate</li> </ul>	<ul style="list-style-type: none"> <li>• Confirm 12-month durable expression of Factor VIII in NHP study</li> <li>• Initiate GMP manufacturing and related IND enabling activities</li> </ul>	<ul style="list-style-type: none"> <li>• Continue IND enabling activities to support an IND filing in 2026</li> </ul>
<b>Cardiometabolic Programs</b>	<ul style="list-style-type: none"> <li>✓ Advanced all four targets in wave one of Ionis collaboration in lead optimization</li> </ul>	<ul style="list-style-type: none"> <li>• Demonstrate <i>in vivo</i> proof-of-concept supporting Development Candidate nominations</li> </ul>	<ul style="list-style-type: none"> <li>• Nominate one to two Development Candidates</li> </ul>
<b>Other Therapeutic Programs</b>	<ul style="list-style-type: none"> <li>✓ Established GMP genome editing reagents for cell therapy and regulatory filing to support Affini-T IND</li> </ul>	<ul style="list-style-type: none"> <li>• Present multiplex base editing data at scientific meeting for cell therapy applications</li> </ul>	<ul style="list-style-type: none"> <li>• Continue to advance early-stage pipeline for multiple future IND filings</li> </ul>

Cash runway into 2027





# Technology innovations continue...



## Technology milestones achieved

- ✓ MGX Toolbox with **large selection of nucleases**
- ✓ Theoretical ability to **target any codon** in the human genome

2021-2022

- ✓ Discovered **large gene integration systems** (CAST and RIGS)
- ✓ Discovered **compact systems** (SMART)
- ✓ Developed **base editing** platform
- ✓ Proof-of-concept (PoC) for **in vivo liver editing with nuclease**

2023

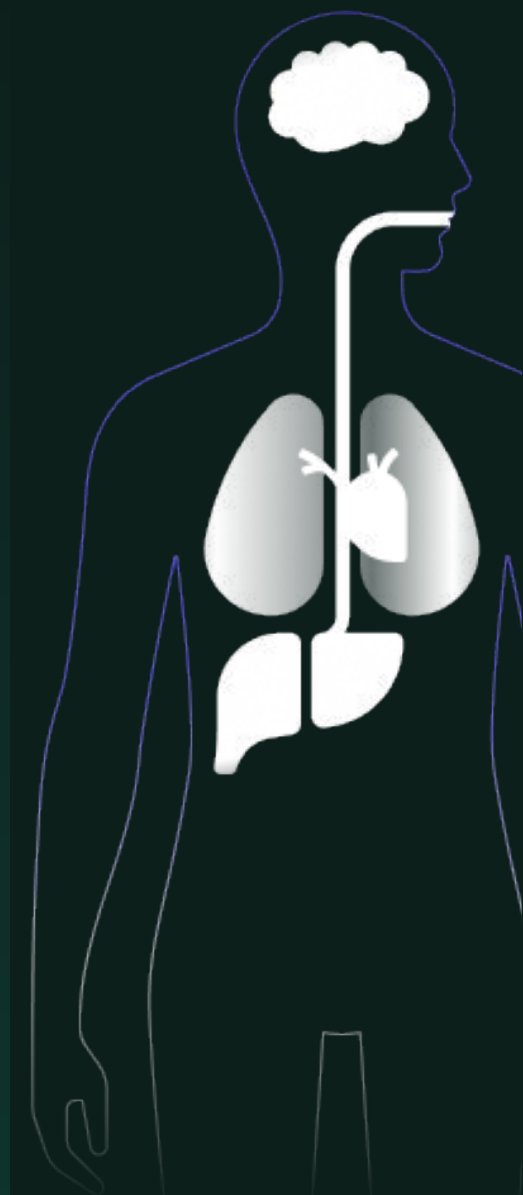
- ✓ **Compact systems:** *in vitro* PoC for neuromuscular target
- ✓ **RIGS:** *in vitro* PoC for small gene correction in liver targets
- ✓ **Multiplex base editing:** PoC for cell therapy (presentation pending)
- ✓ **CAST:** *in vitro* PoC for large gene integration (publication submitted)

2024

## Future Technology Milestones

- **RIGS or Base Editing:** *In vivo* PoC for small gene correction  
*Example disease: A1AT deficiency*
- **RIGS:** *in vivo* PoC for site-specific large gene integration with non-viral, single vector delivery  
*Example disease: Wilson's*
- **RIGS + CAST:** *in vivo* PoC for large gene integration  
*Example diseases: Cystic Fibrosis, Duchenne Muscular Dystrophy*

2025 and beyond



# Pipeline Overview





## THERAPEUTIC CHALLENGES

Available treatments do not eliminate breakthrough bleeds which can result in progressive joint damage

Available gene therapy for adults lacks durability

Available gene therapy not feasible for infants or children

## OUR APPROACH (MGX-001)

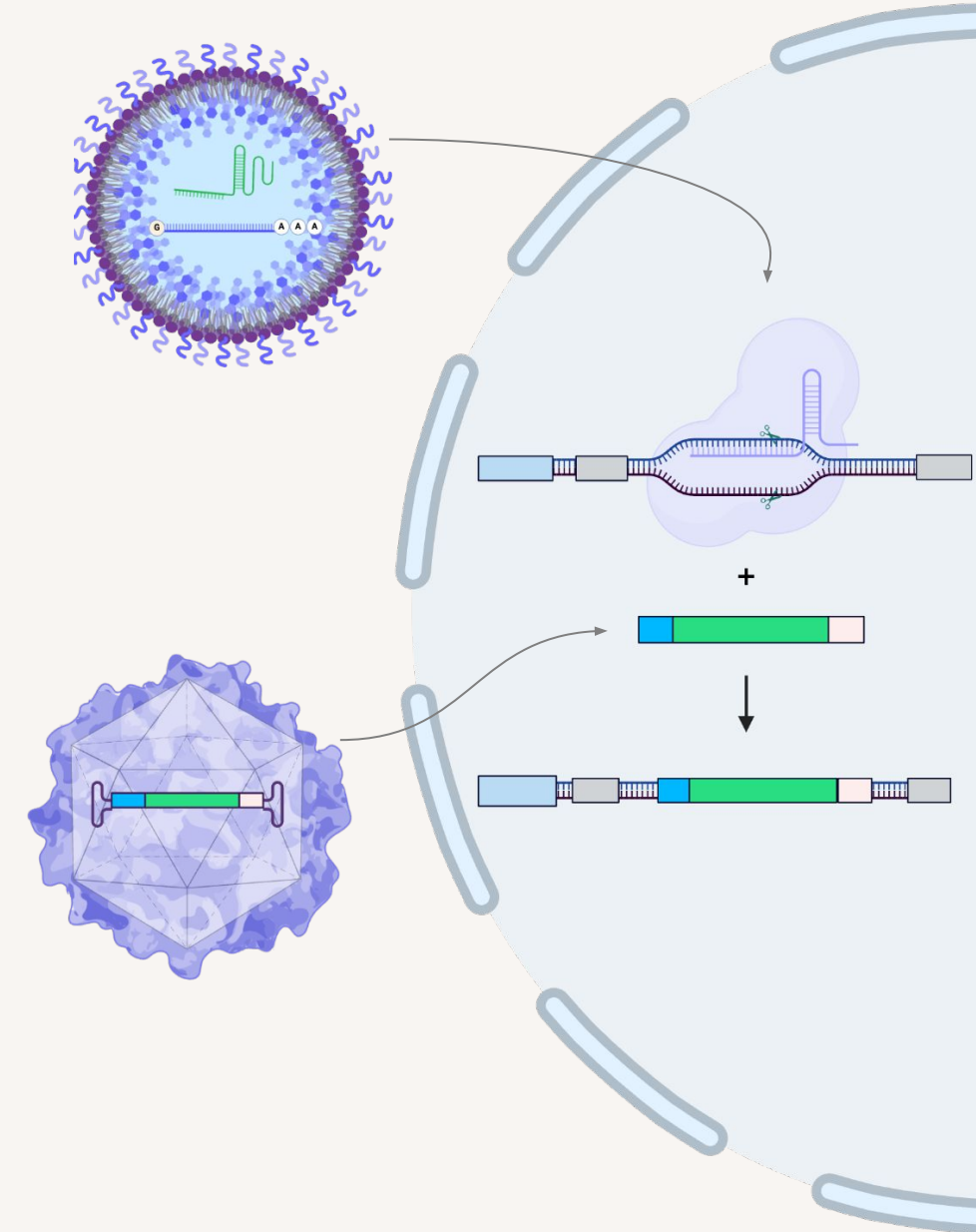
Highly efficient and specific nuclease creates precise cut at albumin safe harbor gene locus after delivery by LNP

AAV vector delivers FVIII DNA template inserted into nuclease cut site by naturally occurring DNA repair process

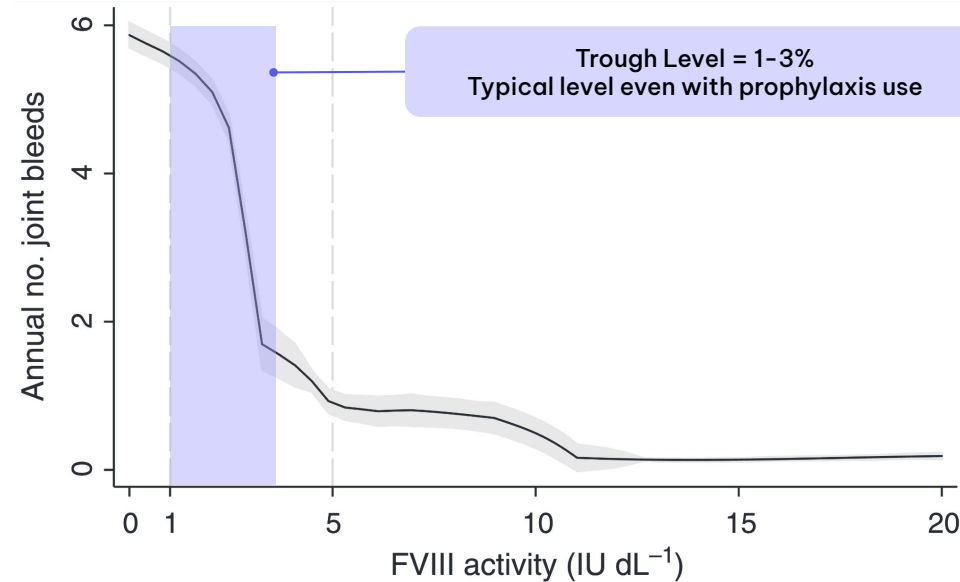
## POTENTIAL BENEFIT

Lifelong, stable FVIII expression due to insertion in safe harbor gene locus

Eliminate need for life long therapy for both adults and children



**MGX-001 approach presents opportunity to accelerate development into similar secreted protein disorders**



Adapted from Den Uijl et al, *Haemophilia* 2011

## DISEASE BACKGROUND

Most common X-linked inherited bleeding disorder; vast majority of patients are male

Caused by large variety of mutations in the FVIII gene leading to loss of functional FVIII protein

Intracranial bleeding is of greatest concern as this can lead to major morbidity and mortality

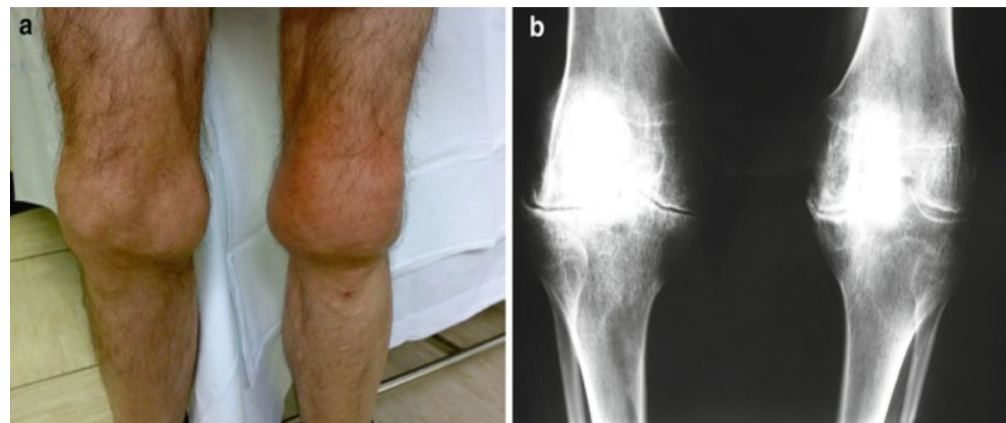
Bleeding into joints leads to cumulative joint damage and is a major cause of morbidity

Diagnosis typically occurs in infancy due to exaggerated bleeding in response to minor injury or routine medical procedures

## PREVALENCE

Up to **26,500** patients in US;\*

More than **500,000** patients globally\*\*



<https://www.ihtc.org/hemophilia-joint-bleeds>

\*Soucie, John Michael, et al. "Occurrence..." *Haemophilia*, vol. 26, no. 3, pp. 487-493

\*\*Stonebraker, J. S., et. al. "A study..." *Haemophilia* 16, 20-32



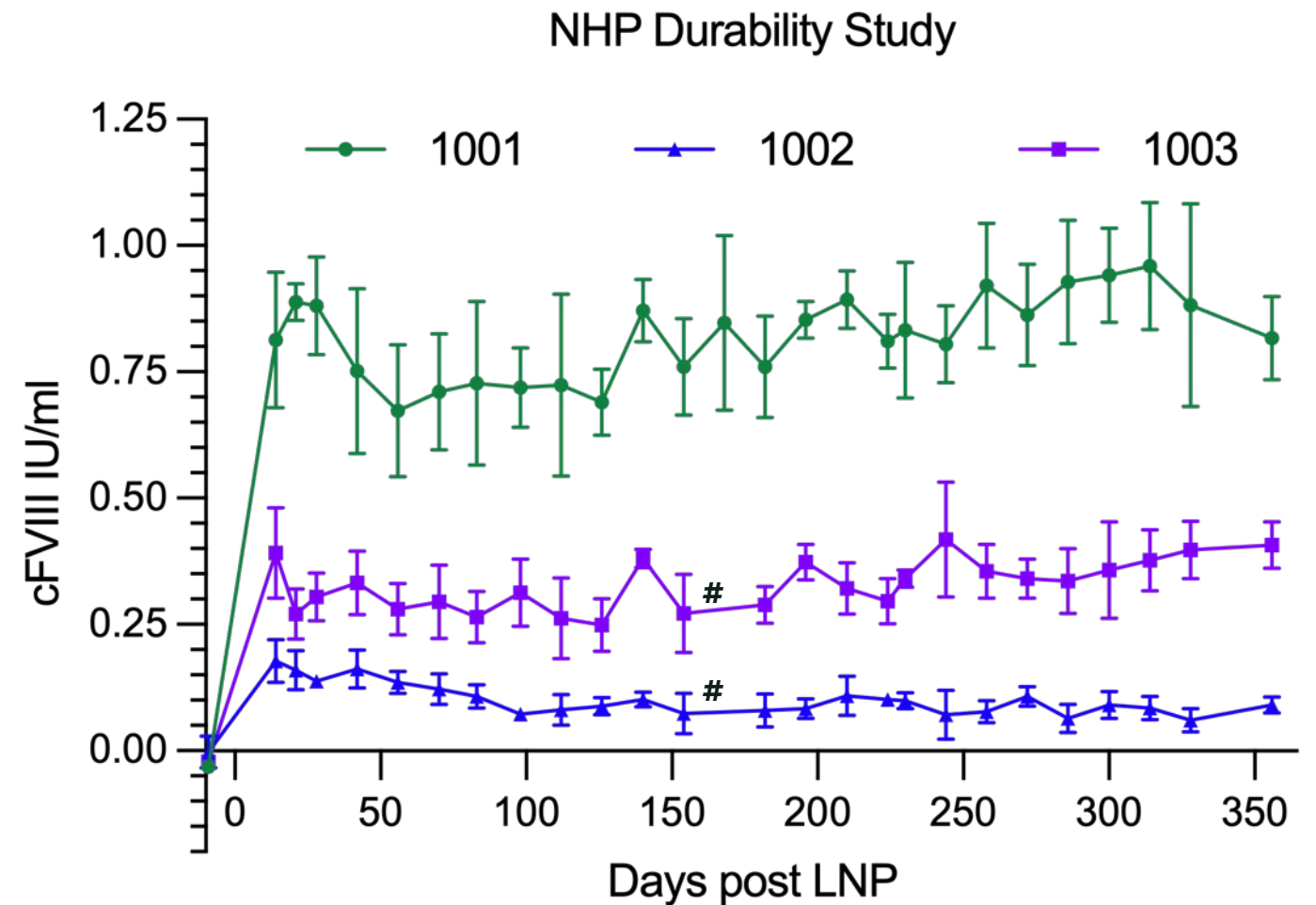


## Proof of concept for durable and therapeutically relevant FVIII levels achieved in nonhuman primates

- FVIII activity levels do not decrease over time
- FVIII activity levels at 12 month time point are:
  - 1001: 0.81 IU/ml (81.7% normal FVIII values)
  - 1002: 0.09 IU/ml (9.1% normal FVIII values)
  - 1003: 0.41 IU/mL (41% normal FVIII values)
- FVIII activity levels correlate with gene integration frequency from biopsy samples (0.7 – 2.9%)

### FVIII levels (IU/ml) over specific time periods

Animal	3–6 months post LNP (d83–d182)		9–12 months post LNP (d272–d356)	
	Mean	Stdev	Mean	Stdev
1001	<b>0.762</b>	0.064	<b>0.898</b>	0.054
1002	<b>0.086</b>	0.014	<b>0.083</b>	0.018
1003	<b>0.290</b>	0.045	<b>0.369</b>	0.029



FVIII activity values are the mean and standard deviation of at least 3 independent assay runs with each sample run in at least duplicate in each assay

# The day 168 plasma sample for 1002 and 1003 were excluded because they appear to have been switched (mis-labelled) at the CRO

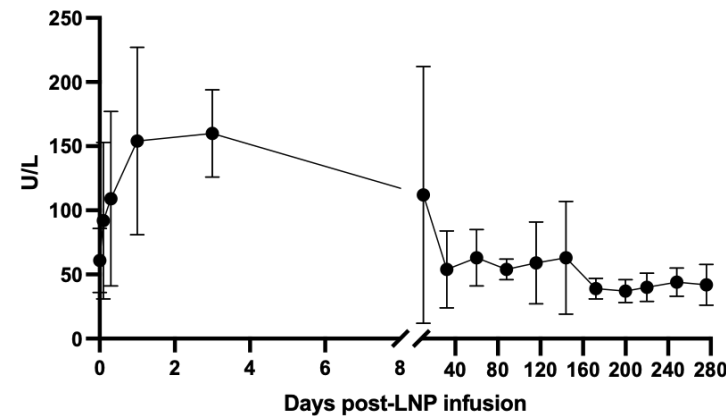
Cyno FVIII gene sequence used to avoid immune response, detection of transgene derived cFVIII achieved by incorporating a single amino acid change that blocks binding of a monoclonal antibody



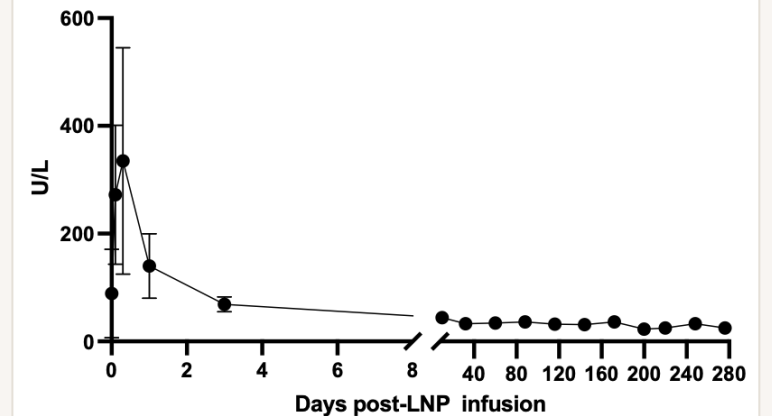
### SUMMARY OF SAFETY FINDINGS:

- Transient elevation of liver function tests after the infusion of AAV and LNP
- No significant change in total bilirubin post AAV and LNP
- Integration of the FVIII gene at the albumin locus had no impact on circulating albumin levels
- Animals are healthy and exhibit normal weight gain

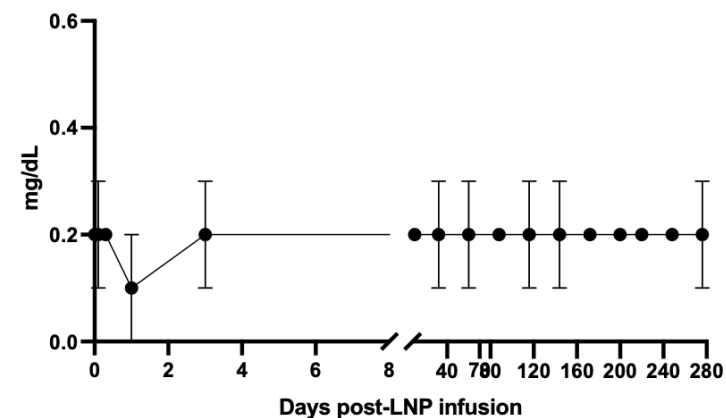
#### Alanine transaminase (ALT) levels post LNP infusion



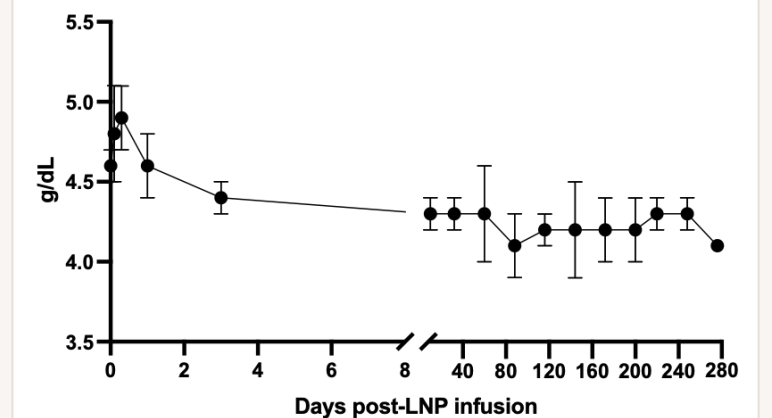
#### Aspartate transaminase (AST) levels post LNP infusion



#### Total bilirubin levels post LNP infusion



#### Albumin levels post LNP infusion





## THERAPEUTIC CHALLENGES

Despite available approaches, disease still associated with significant morbidity and mortality

Currently lifelong course of treatment

## OUR APPROACH

Use our programmable nucleases to knock down wild type or mutated versions of TTR

## POTENTIAL BENEFIT

Single-dose treatment for lifelong, stable knockdown of TTR

## DISEASE BACKGROUND

Caused by misfolded and aggregated transthyretin (TTR) protein

Potential for organ dysfunction, primarily in the heart and / or peripheral nerves

Potential for progressive heart failure and death within 3 - 5 years of disease onset

## PREVALENCE

Up to **40,000** patients worldwide with hereditary ATTR\*

**300,000–500,000** patients worldwide with wild-type ATTR\*\*

\*Hawkins, P. N., et al. "Evolving..." *Annals of Medicine*, 47(8), 625–638.

\*\*Mohamed-Salem L, et al. "Prevalence..." *Int J Cardiol*. 270:192–196.





## THERAPEUTIC CHALLENGES

Many patients do not reach their blood pressure goals despite multiple approved classes of drugs

Significant issues of adherence to taking large number of daily oral pills

## OUR APPROACH

Use our programmable nucleases to knock down AGT

AGT is a novel target which inhibits a pathway known to be associated with multiple diseases

## POTENTIAL BENEFIT

Single-dose treatment for lifelong, stable knockdown of AGT

Reliably and consistently control blood pressure throughout the day

Reduce risk of cardiac and other adverse events

## DISEASE BACKGROUND

Uncontrolled high blood pressure despite use of at least five antihypertensive agents without achieving goal BP

Potential for heart attack, stroke, vision and kidney damage

## PREVALENCE

**900,000** patients in the US with refractory hypertension\*

\*Yoon, Minjae, et al. "Prevalence..." *Hypertension Research*, vol. 45, no. 8, pp. 1353-1362

# Targeting disease with small gene corrections and large gene insertions



## Alpha-1-antitrypsin (A1AT deficiency): Protein deficiencies impacting lung & liver

### THERAPEUTIC CHALLENGES

- Protein augmentation therapy has limited longer term protection of lung function
- Approach is costly and not available for many patients
- Infusions sometimes associated with adverse events
- Organ transplantation may be required

### OUR APPROACH

- Use RIGS for gene correction and to avoid bystander edits
- Alternative: Use base editor for gene correction of PiZ mutation in SERPINA1 gene

### POTENTIAL BENEFITS

- Single-dose treatment provides lifelong, stable A1AT protein expression

## Wilson's Disease: Serious disease of copper metabolism

- Copper chelators have many side effects that can lead to discontinuation
- Discontinuation can lead to hepatic decompensation potentially requiring liver transplant
- Fatal if left untreated

- Use of RIGS to insert a section of the ATP7B gene encoding the majority of disease causing mutations

- Single dose treatment eliminates need for life-long therapy
- Eliminate risk of adverse events
- Approach provides potential to treat majority of patients irrespective of specific mutations

 Metagenomi

# Technology Platform

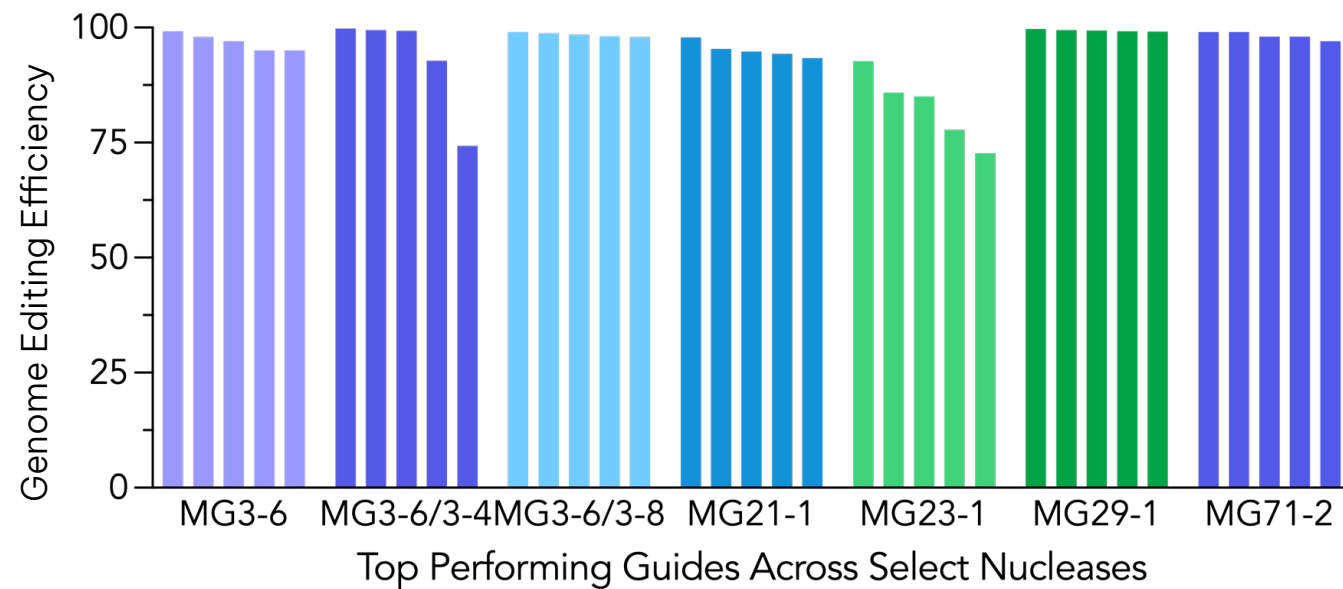


# Highly efficient nucleases designed for any target in the human genome



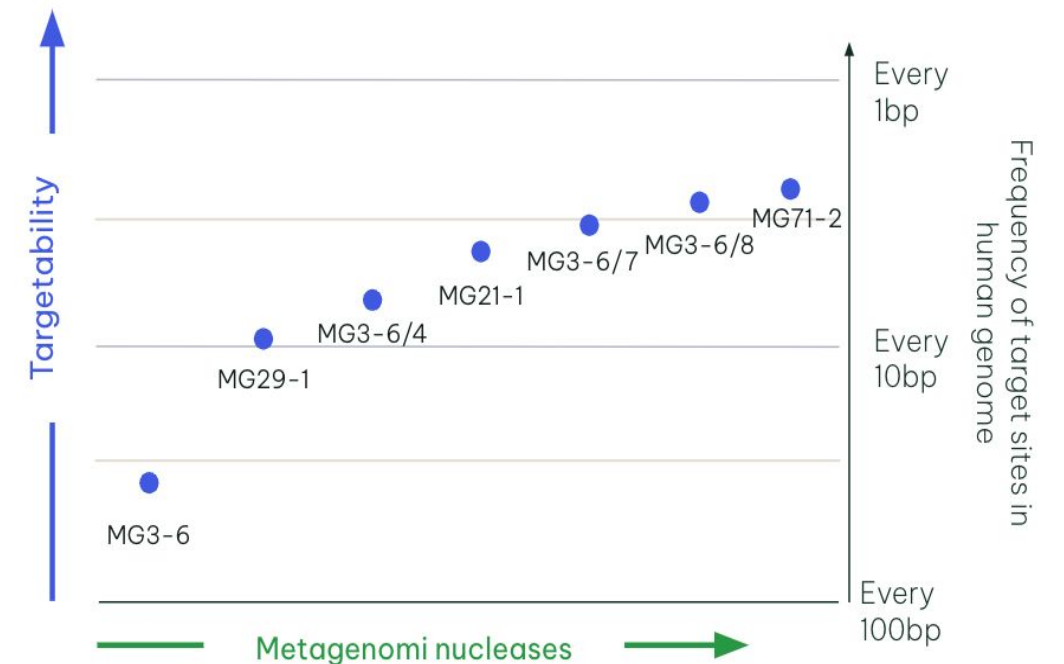
Our nucleases, selected for their native high-efficiency, expand targeting options within genes of interest

## Efficient across multiple guides and targets



Editing efficiency in mammalian cells determined based on the frequency of InDels detected by next generation sequencing (“NGS”) at genomic sites targeted by each nuclease

## Estimated potential to target every codon in the human genome



Targetability is the average distance between nuclease target sites in the human genome

# Generative AI trained on proteins from nature informs optimization of efficient SMART nucleases



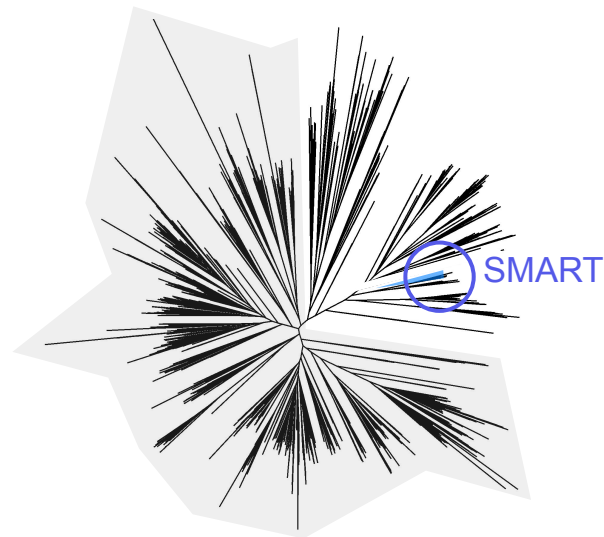
**Search** our metagenomics database for novel compact nucleases

**Characterize** small CRISPR-associated nucleases (Small ARginine-rich systems: "SMART")

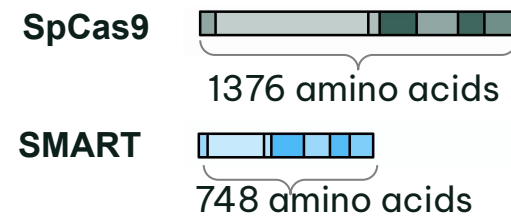
**Design** SMART nucleases with generative AI and ancestral sequence reconstruction (ASR)

**Optimize** SMART nucleases with fine-tuned AI models and protein structure

**Protein sequence comparisons highlight novelty of SMART CRISPR systems**

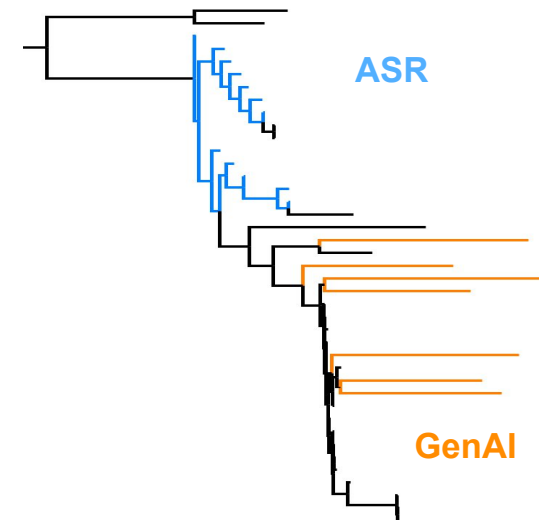


\*Phylogenetic tree comparing CRISPR nucleases  
\*Gray shaded area indicates previously known nucleases including SpCas9



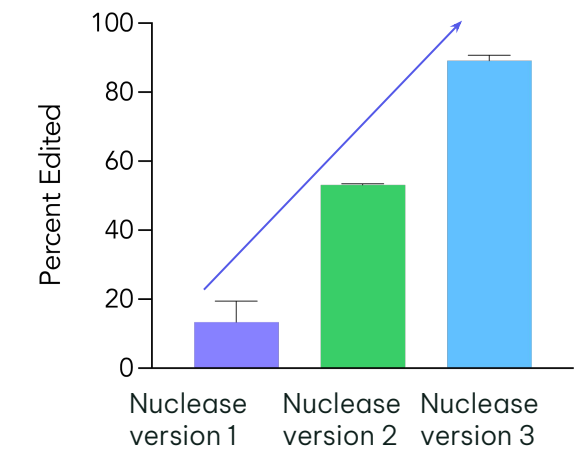
\*Protein structure defined in collaboration with David Taylor, UT Austin

**De novo SMART proteins from ASR and GenAI are unique from natural systems**



\*Phylogenetic tree comparing natural and de novo designed SMART nuclease protein sequences

**Editing efficiency improved to >90% with engineered SMART nucleases <750aa**



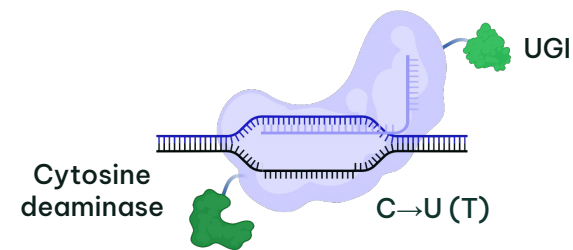
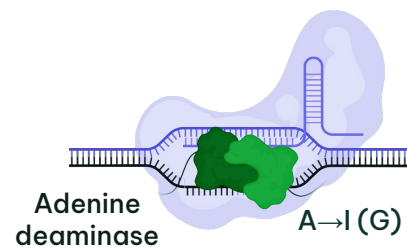
\*Gene editing in human cells with engineered SMART nucleases measured by NGS  
\*Compact size enables all-in-one AAV delivery

# Base editing platform with broad targetability achieves efficient multiplex editing for cell engineering

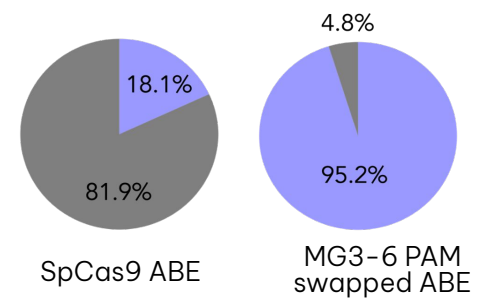
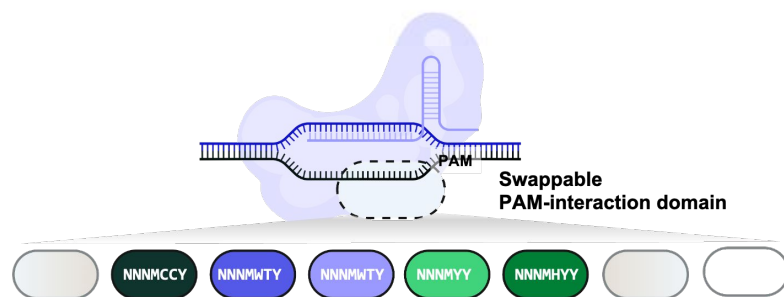


**ABE** (Adenine Base Editor)

**CBE** (Cytosine Base Editor)



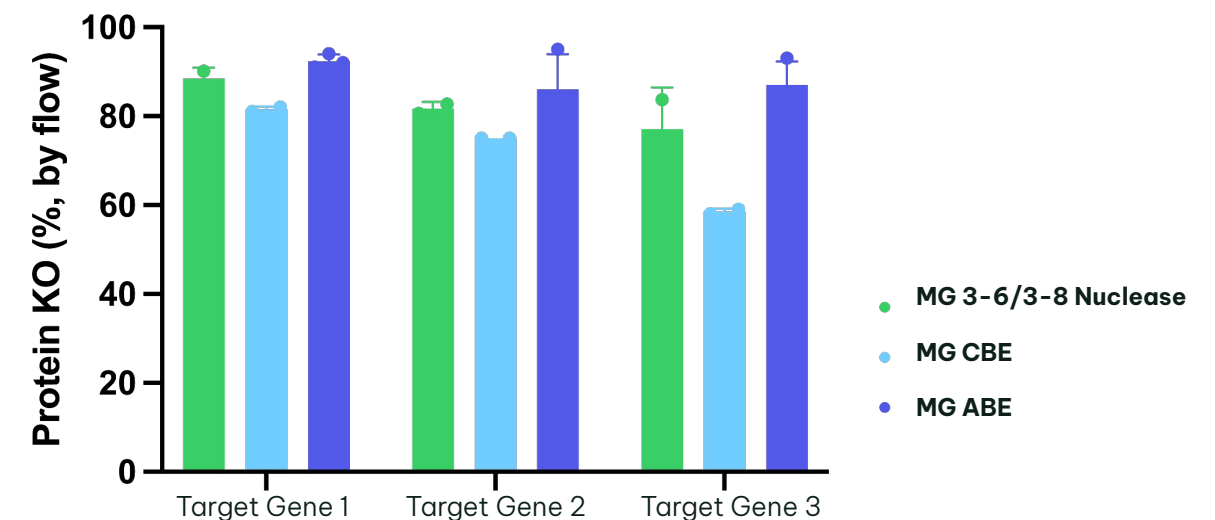
## Reprogrammed chassis increases genome targetability of Base Editors



ABE: SpCas9 = 18% and MG3-6 = 95% targetability  
 CBE (not shown): SpCas9 = 5% and MG3-6 = 53%  
 \*SpCas9 analysis with NGG PAM

Targetable (Blue)  
 Nontargetable (Grey)

## ABE, CBE and nuclease are efficient for multiplexed knockout in primary T cells



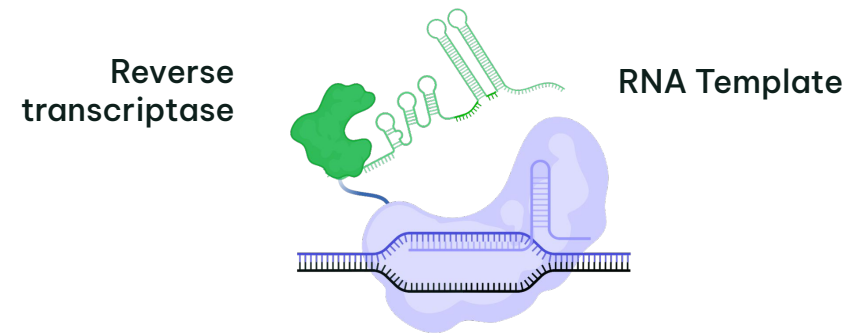
1. Top guides for three cell therapy knockout targets were tested in a multiplexed fashion
2. Edits durable over 10 days and do not impact cell viability or expansion (not shown)



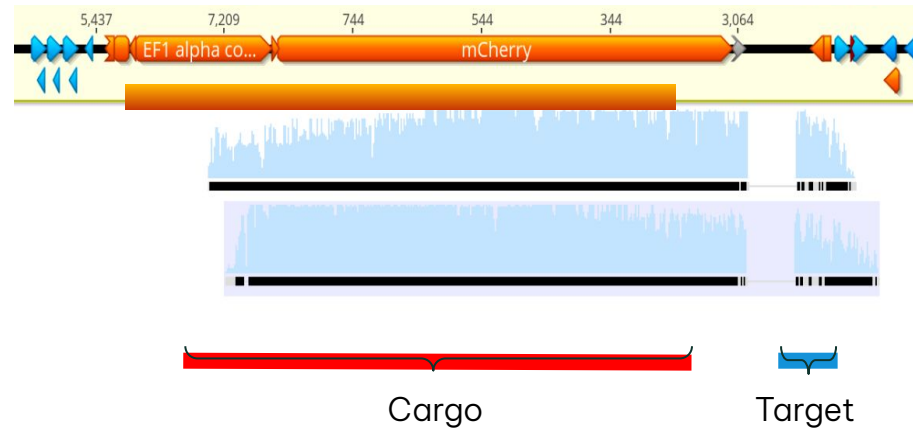
# Next generation technology for programmable large genome integration to address complex genetic diseases



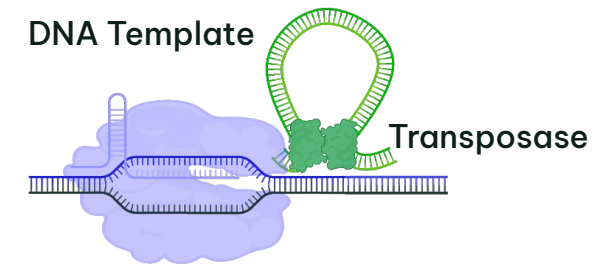
## RIGS (RNA-Mediated Integration Systems)



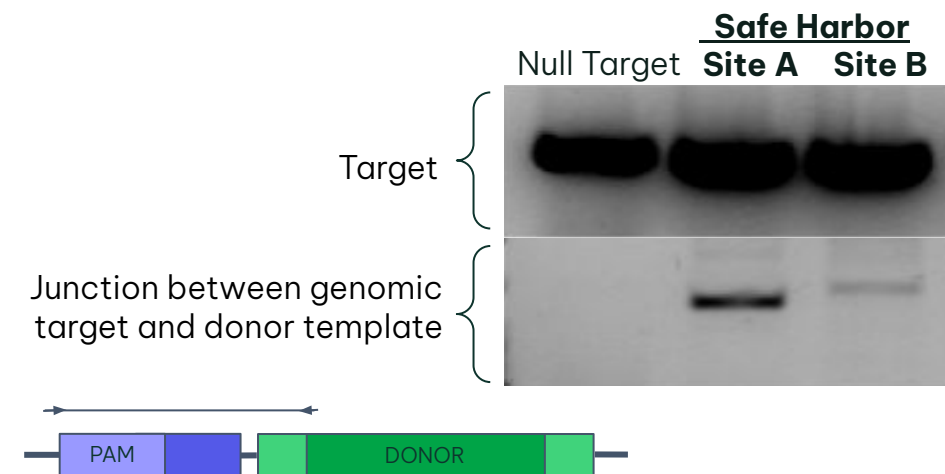
**First-ever report of targeted integration of >900 bp with all-RNA delivery**



## CAST (DNA-Mediated Integration Systems)



**Demonstrated large targeted genome integration using compact CAST in human cells**



# Corporate Highlights

# Recent and upcoming milestones drive towards the clinic



	Recent milestones achieved	2H' 2024	2025
<b>Hemophilia A Program</b>	<ul style="list-style-type: none"> <li>✓ Generated robust proof-of-concept data in multiple NHP studies</li> <li>✓ Engaged with FDA for regulatory advice</li> <li>✓ Nominated Development Candidate</li> </ul>	<ul style="list-style-type: none"> <li>• Confirm 12-month durable expression of Factor VIII in NHP study</li> <li>• Initiate GMP manufacturing and related IND enabling activities</li> </ul>	<ul style="list-style-type: none"> <li>• Continue IND enabling activities to support an IND filing in 2026</li> </ul>
<b>Cardiometabolic Programs</b>	<ul style="list-style-type: none"> <li>✓ Advanced all four targets in wave one of Ionis collaboration in lead optimization</li> </ul>	<ul style="list-style-type: none"> <li>• Demonstrate <i>in vivo</i> proof-of-concept supporting Development Candidate nominations</li> </ul>	<ul style="list-style-type: none"> <li>• Nominate one to two Development Candidates</li> </ul>
<b>Other Therapeutic Programs</b>	<ul style="list-style-type: none"> <li>✓ Established GMP genome editing reagents for cell therapy and regulatory filing to support Affini-T IND</li> </ul>	<ul style="list-style-type: none"> <li>• Present multiplex base editing data at scientific meeting for cell therapy applications</li> </ul>	<ul style="list-style-type: none"> <li>• Continue to advance early-stage pipeline for multiple future IND filings</li> </ul>

Cash runway into 2027





# Technology innovations continue...



## Technology milestones achieved

- ✓ MGX Toolbox with **large selection of nucleases**
- ✓ Theoretical ability to **target any codon** in the human genome

2021-2022

- ✓ Discovered **large gene integration systems** (CAST and RIGS)
- ✓ Discovered **compact systems (SMART)**
- ✓ Developed **base editing** platform
- ✓ Proof-of-concept (PoC) for **in vivo liver editing with nuclease**

2023

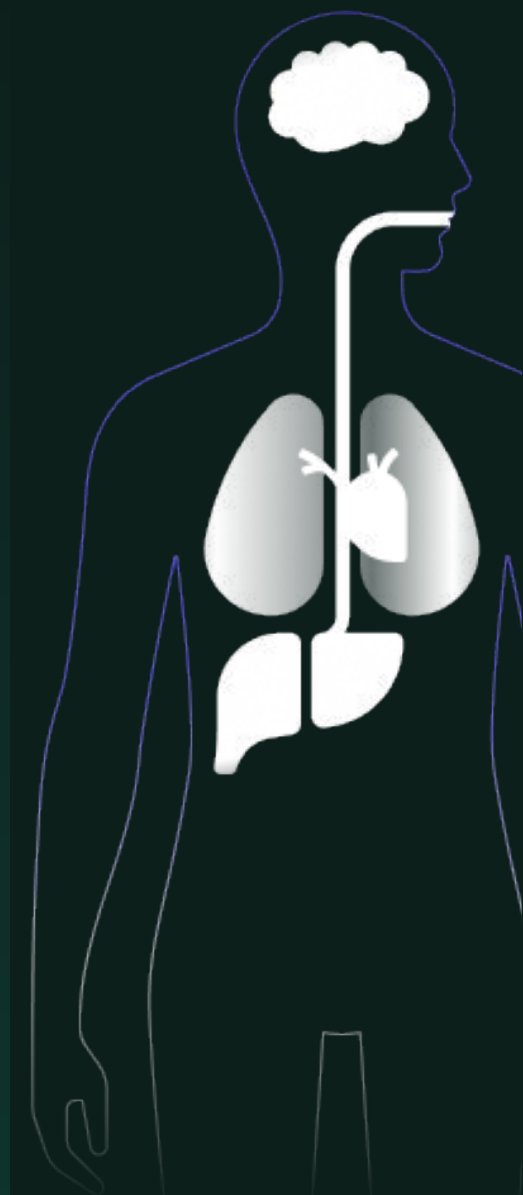
- ✓ **Compact systems:** *in vitro* PoC for neuromuscular target
- ✓ **RIGS:** *in vitro* PoC for small gene correction in liver targets
- ✓ **Multiplex base editing:** PoC for cell therapy (presentation pending)
- ✓ **CAST:** *in vitro* PoC for large gene integration (publication submitted)

2024

## Future Technology Milestones

- **RIGS or Base Editing:** *In vivo* PoC for small gene correction  
*Example disease: A1AT deficiency*
- **RIGS:** *in vivo* PoC for site-specific large gene integration with non-viral, single vector delivery  
*Example disease: Wilson's*
- **RIGS + CAST:** *in vivo* PoC for large gene integration  
*Example diseases: Cystic Fibrosis, Duchenne Muscular Dystrophy*

2025 and beyond





Thank you

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