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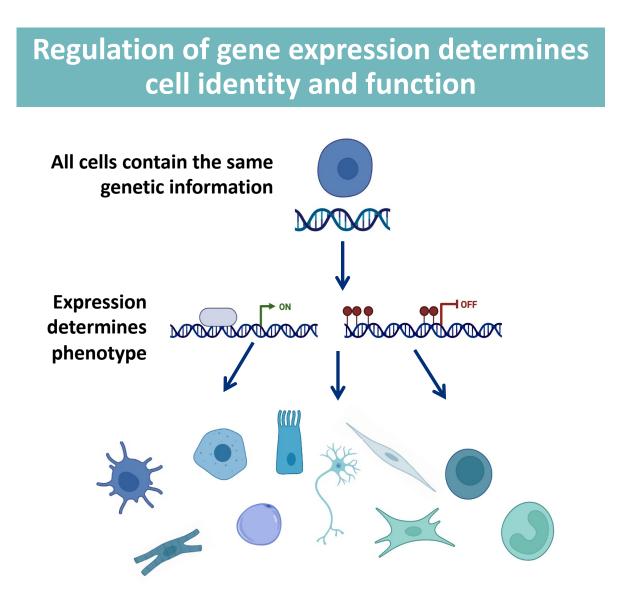
Therapeutic Development of Epigenetic Editors

Morgan Maeder, PhD

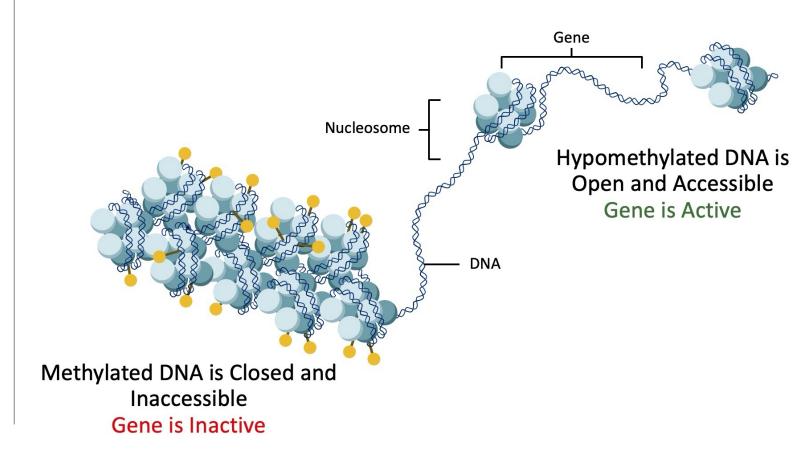
Senior Director, Payload Sciences

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Epigenetics regulates gene expression to determine cell identity and function



Chromatin packaging and epigenetics regulates DNA transcription





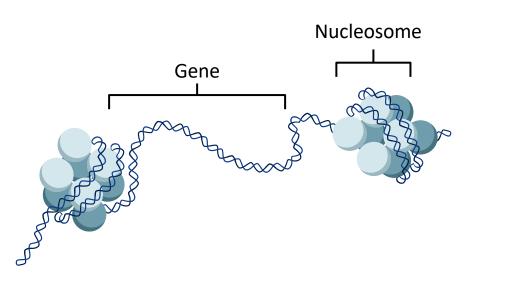
Epigenetic editing leverages the endogenous system to precisely control gene expression

Durable change in phenotype without a change in genotype

Epigenetic Repressor

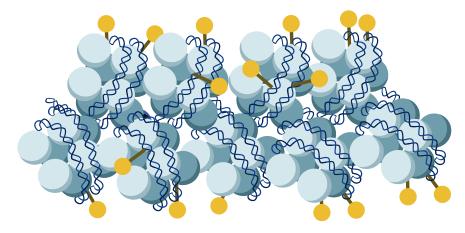
Methylates Targets

Transient Application



Gene is Active DNA is Open and Accessible Epigenetic Activator Demethylates Targets

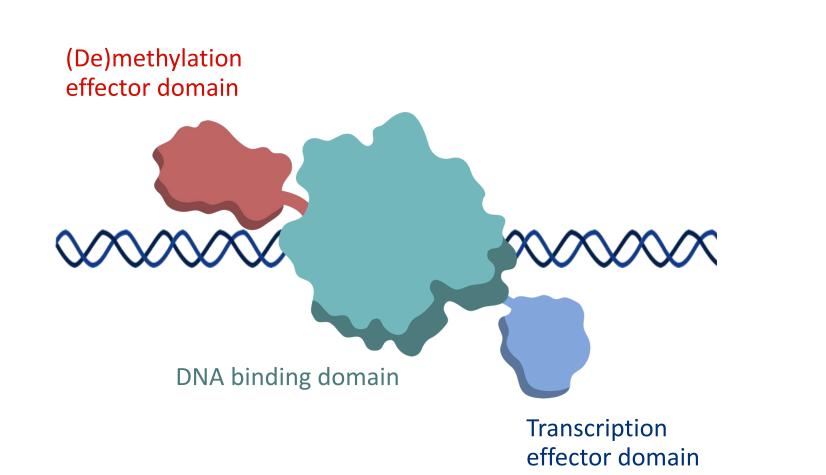
Gene is Inactive DNA is Closed and Inaccessible





Chroma's epigenetic editors are designed to be modular and versatile

Chroma's Epigenetic Editors

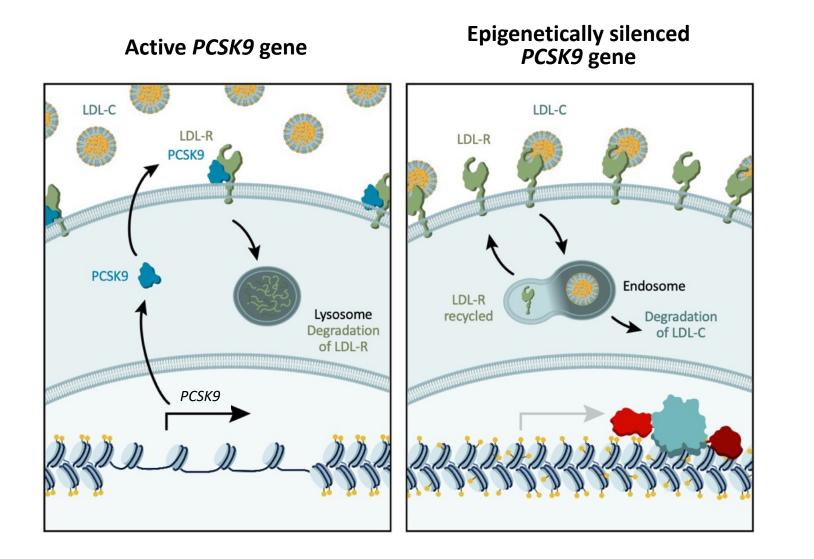


- DNA binding domain precisely localizes effector domains to target sequence
- Transcription effector domain transiently represses or activates target gene
- Methylation / Demethylation effector domain durably silences / activates target gene



Nuñez JK, Chen J, Pommier GC, et al. Genome-wide programmable transcriptional memory by CRISPR-based epigenome editing. *Cell*. 2021;184(9):2503-2519.e17. Amabile A, Migliara A, Capasso P, et al. Inheritable silencing of endogenous genes by hit-and-run targeted epigenetic editing. *Cell*. 2016;167(1):219-232.e14.

Epigenetic editor targeting PCSK9 to lower LDL-C



Epigenetic editor is designed to:

- Silence *PCSK9* through DNA methylation
- Prevent degradation of LDL-R, which increases removal of LDL-C from blood
- Not cause undesirable genomic consequences from cutting or nicking the DNA
- Be durable for lifetime of the patient

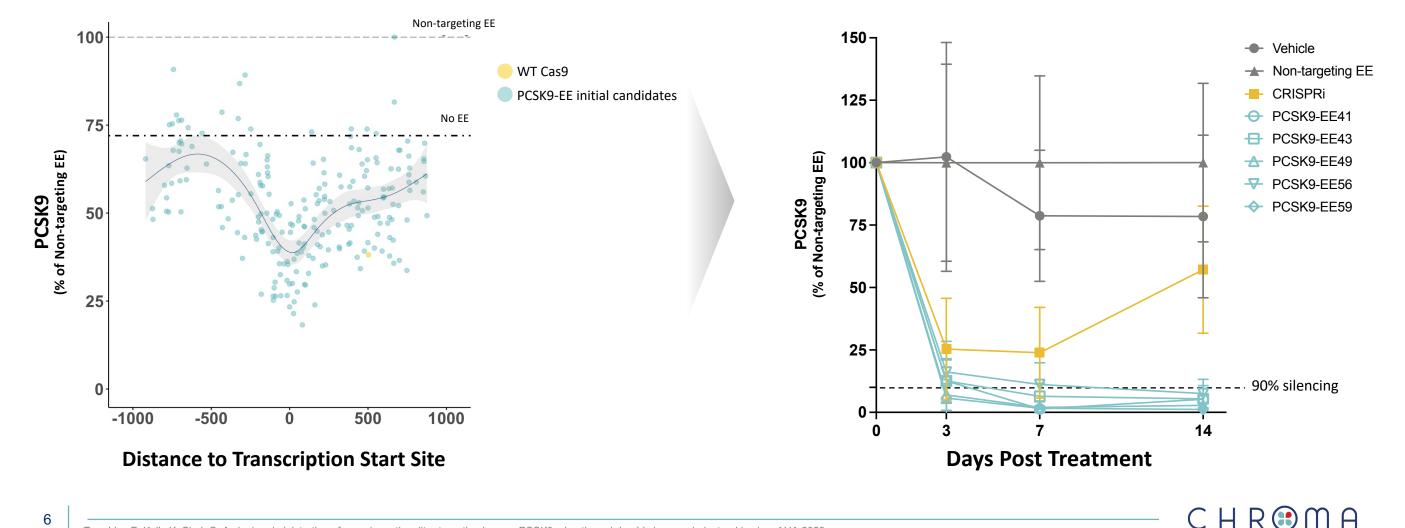


PCSK9-EE screen identified hits with robust activity in primary human hepatocytes (PHH)

PCSK9-EE Screen in Immortalized Liver Cells

PCSK9-EE Hit Confirmation in PHH

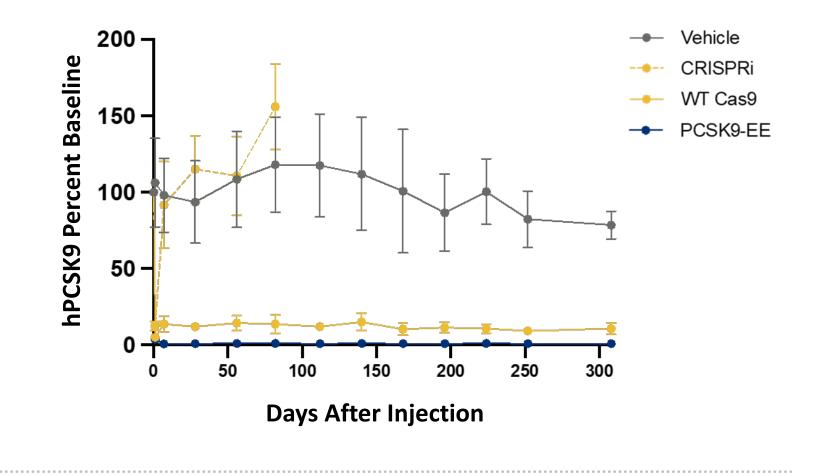
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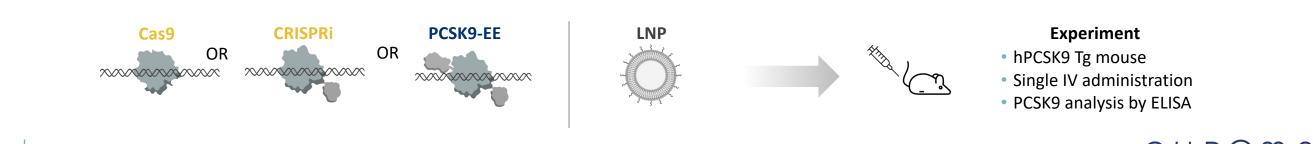


Tremblay F, Kelly K, Shah S, A single administration of an epigenetic editor targeting human PCSK9 robustly and durably lowers cholesterol in vivo, AHA 2023 EE = epigenetic editor; PHH = primary human hepatocyte; WT = wild type; error bars represent standard deviation

Near-complete PCSK9 silencing achieved in transgenic mice

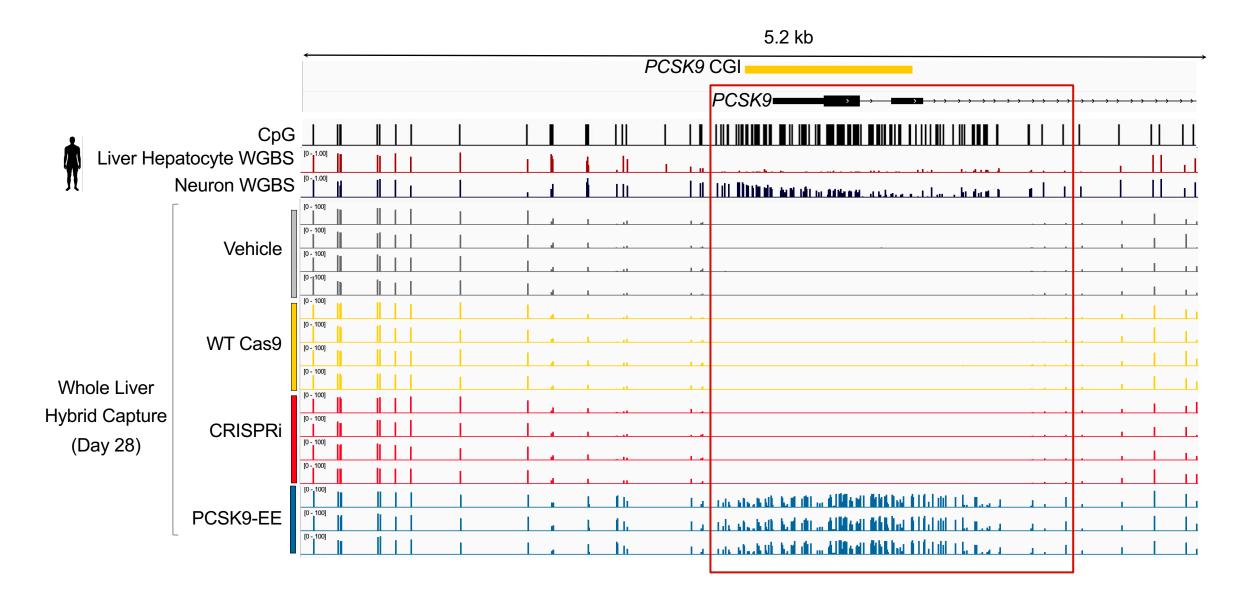
- Transgenic mouse containing the human PCSK9 locus
- Tested optimized single construct epigenetic editor
- >98% silencing maintained for over 300 days post single IV injection





Tremblay F, Kelly K, Shah S, A single administration of an epigenetic editor targeting human *PCSK9* robustly and durably lowers cholesterol in vivo, AHA 2023 EE = epigenetic editor; ELISA = enzyme-linked immunosorbent assay; IV = intravenous; hPCSK9 = human proprotein convertase subtilisin/kexin type 9; LNP = lipid nanoparticles; Tg = transgenic; WT = wild type; error bars represent standard deviatio

PCSK9-EE induced durable, targeted CpG methylation at the human *PCSK9* locus in vivo

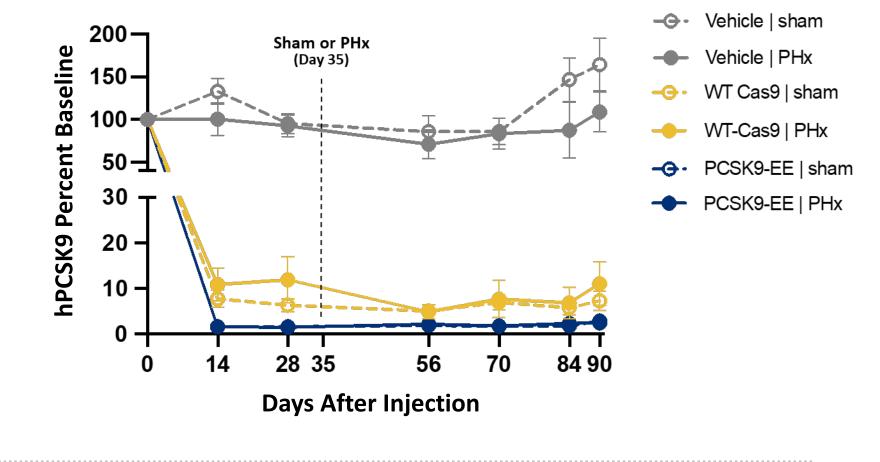


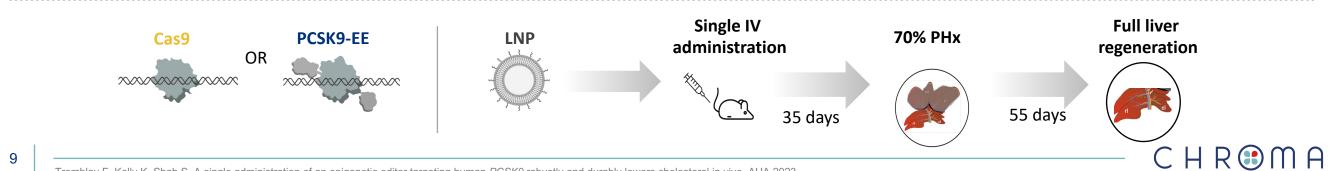


8

PCSK9 silencing was maintained through liver regeneration

- 70% partial hepatectomy (PHx) is a gold standard surgical model to induce liver regeneration in rodents
- Single administration of PCSK9-EE demonstrated durable PCSK9 silencing pre- and post- partial hepatectomy





Tremblay F, Kelly K, Shah S, A single administration of an epigenetic editor targeting human *PCSK9* robustly and durably lowers cholesterol in vivo, AHA 2023

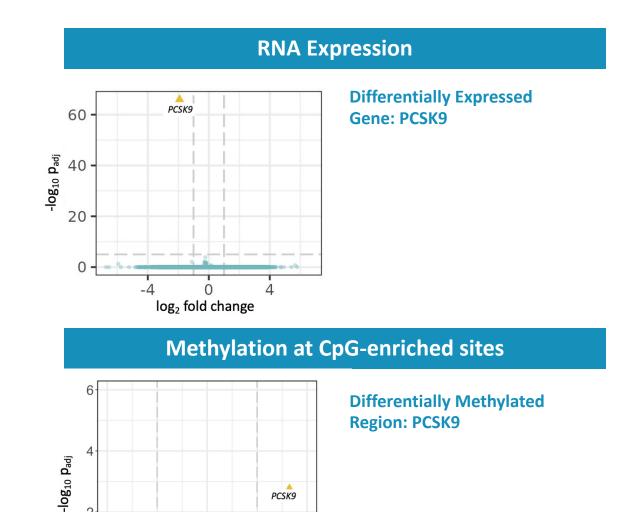
EE = epigenetic editor; IV = intravenous; hPCSK9 = human proprotein convertase subtilisin/kexin type 9; LNP = lipid nanoparticles; PHx = partial hepatectomy; WT = wild type; error bars represent standard deviation.

PCSK9-EEs demonstrated durable DNA methylation at PCSK9 locus pre- and post-partial hepatectomy (PHx)

*					11 kb	
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Tremblay F, Kelly K, Shah S, A single administration of an epigenetic editor targeting human PCSK9 robustly and durably lowers cholesterol in vivo, AHA 2023 EE = epigenetic editor; WT = wild type

PCSK9-EEs can be highly specific with no off-target changes in expression or methylation in primary human hepatocytes



PCSK9

PCSK9

0.4

0.2

-0.4

11

-0.2

0.0

Methylation Difference

Genome-wide Methylation Differentially methylated PCSK9 CpGs in EE-treated CpG density PXB cells relative to effector-only treated cells 3858 7716 11574 15432 19290 23148 27006 30864 34722 PCSK9 P<1E-5, DMR:109 CpGs (1.4 kb) -log 10 FDR 10

- PCSK9-EEs can be highly specific
- No off-target changes in gene expression with epigenetic repressor in primary human hepatocytes as measured by RNA-seq

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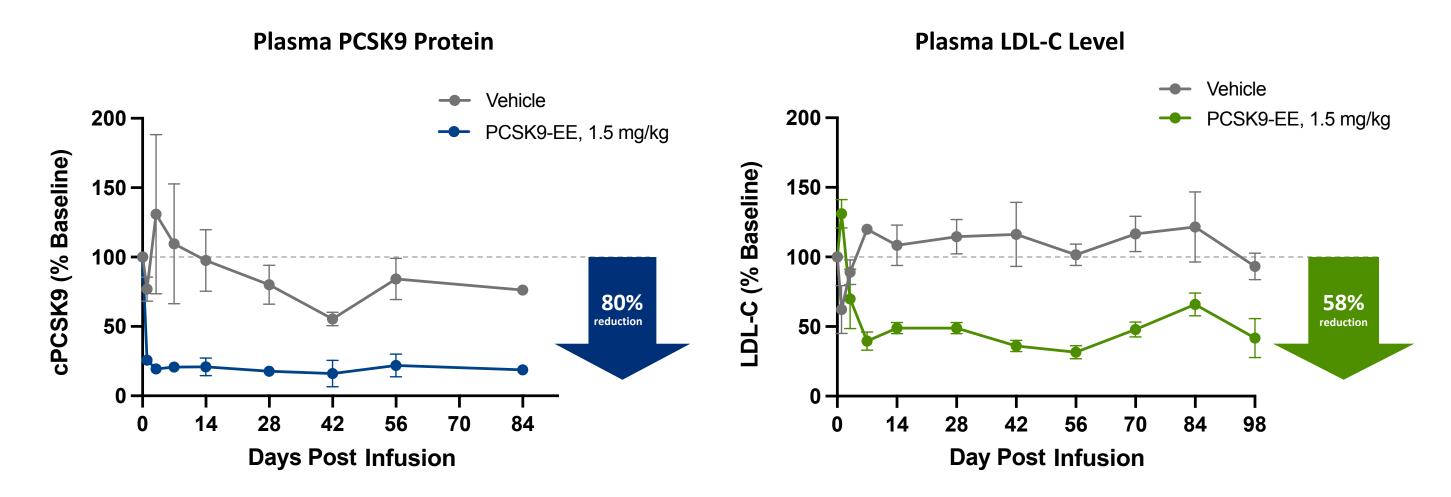
14 15

16 17

No off-target changes in methylation with epigenetic repressor in primary human hepatocytes as measured by Illumina Methylation Array and whole genome bisulfite sequencing

Tremblay F, Kelly K, Shah S, Development of a human PCSK9-targeting epigenetic editor with durable, near-complete in vivo silencing, ASGCT 2023; Tremblay F, Kelly K, Shah S, A single administration of an epigenetic editor targeting human PCSK9 robustly and durably lowers cholesterol in vivo, AHA 2023

In NHPs, PCSK9-EE achieved 80% reduction in PCSK9 and 58% in LDL-C with durability out to 3 months



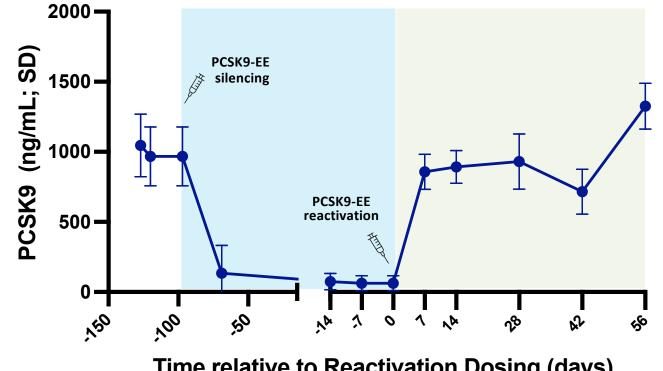


Tremblay F, Kelly K, Shah S, A single administration of an epigenetic editor targeting human *PCSK9* robustly and durably lowers cholesterol in vivo, AHA 2023 cPCSK9 = cyno proprotein convertase subtilisin/kexin type 9; EE = epigenetic editor; IV = intravenous; LDL-C = low-density lipoprotein cholesterol; LNP = lipid nanoparticles; NHP = non-human primates; WT = wild type; error bars represent standard deviation

12

Achieved early proof-of-concept for reactivation of PCSK9 in mice

- Transgenic mouse containing the human PCSK9 locus
- Single administration of epigenetic editor to silence PCSK9 was given 100 days prior to reactivation
- Single administration of epigenetic activator restored PCSK9 expression by day 7 and was durable to day 56



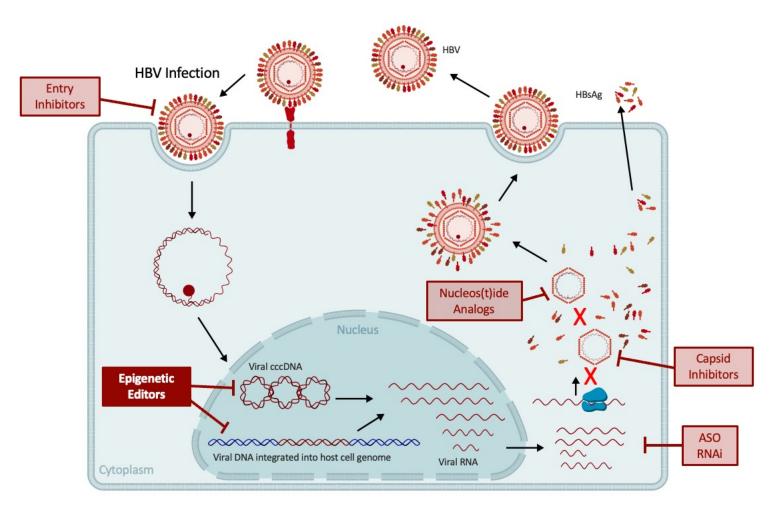
Time relative to Reactivation Dosing (days)



13

Kelly K, Shah S, A single administration of an epigenetic editor targeting human PCSK9 robustly and durably lowers cholesterol in vivo, AHA 2023 EE = epigenetic editor; hPCSK9 = human proprotein convertase subtilisin/kexin type 9; IV = intravenous; LNP = lipid nanoparticles; error bars represent standard deviation

HBV epigenetic editors target both cccDNA and intDNA



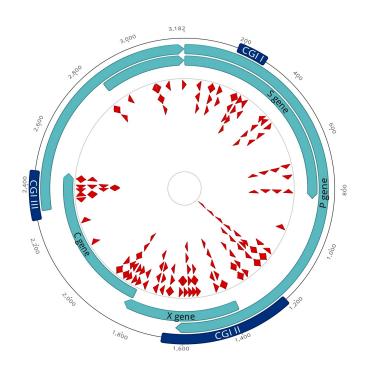
Epigenetic editors are designed to:

- Target both sources of pathogenesis, cccDNA and intDNA, in infected cells
- Prevent production of all viral transcripts and proteins
- Avoid introducing risk of increasing viral integrations
- Be durable for lifetime of the patient



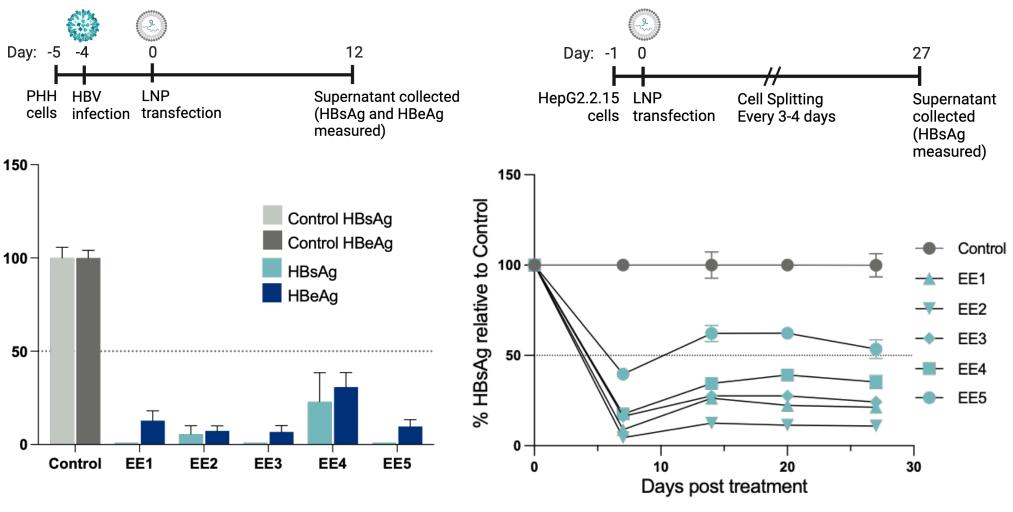
HBV-EE screen identified hits with robust activity in primary human hepatocytes (PHH)

Epigenetic editors were designed to cover the entire HBV genome and are conserved for most common genotypes of HBV



Strong reduction of viral markers in HBV infected primary human hepatocytes

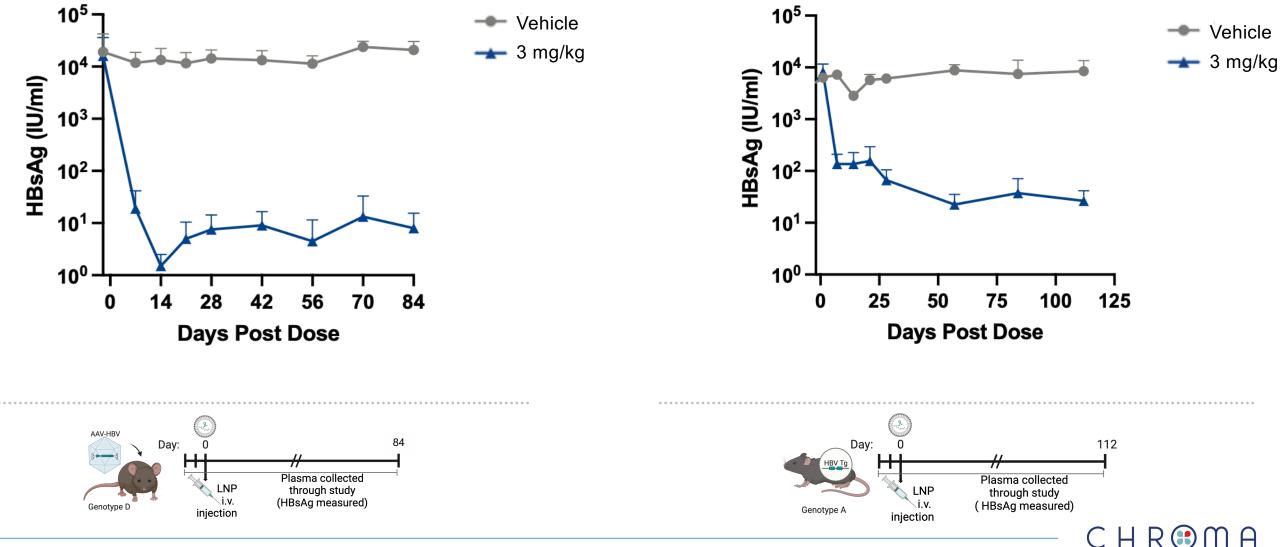
Epigenetic repression of HBsAg is maintained in vitro for nearly a month in dividing cells containing integrated HBV



Anglero-Rodriguez Y, Abubucker S, Xiong J et al Development of HBV-targeting epigenetic repressors with deep, durable in vivo silencing of viral markers. International HBV Meeting 2023 EE= epigenetic editor; HBsAg = hepatitis B surface antigen; LNP = lipid nanoparticle.

% antigen expression

HBV epigenetic editors deeply and durably reduced HBsAg in both AAV8-HBV and Tg-HBV mice

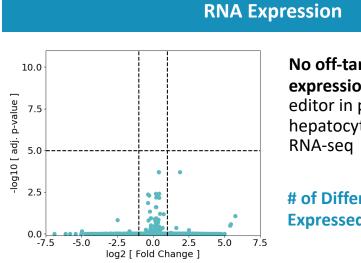


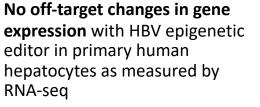
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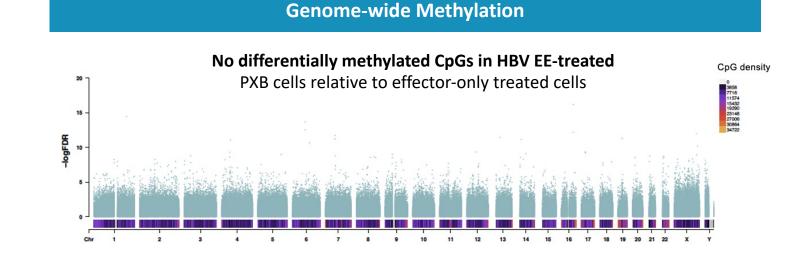
AAV = adeno-associated virus; HBsAg = hepatitis B surface antigen; IV = intravenous; LNP = lipid nanoparticles; Tg = transgenic.

HBV epigenetic editors were highly specific, with no off-target changes in gene expression or methylation in PHH

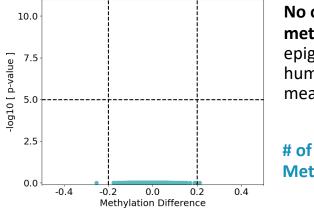




of Differentially Expressed Genes: 0



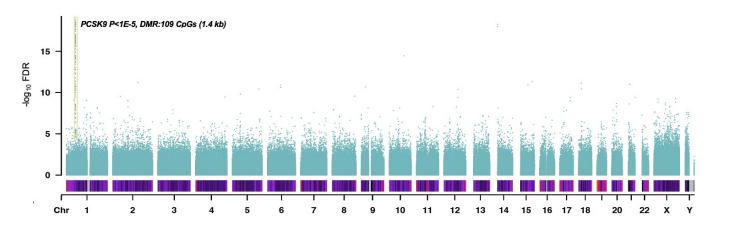
Methylation at CpG-enriched sites



No off-target changes in methylation with HBV epigenetic editor in primary human hepatocytes as measured by methylation array

of Differentially Methylated Regions: 0

PCSK9-EE positive control



Epigenetic gene regulation is designed to be highly efficient, specific, and durable without any cuts, nicks, or changes to the underlying DNA

Potential to enable multiplexing without genotoxic consequences

• Simultaneous silencing of a large number of targets without introducing DNA damage



Potential to streamline manufacturing

- Accomplish a high number of multiplex edits in a single step; eliminates need for sequential administration required with nuclease editing
- No requirement for in-depth characterization of edited T cells for translocations and chromosomal rearrangements

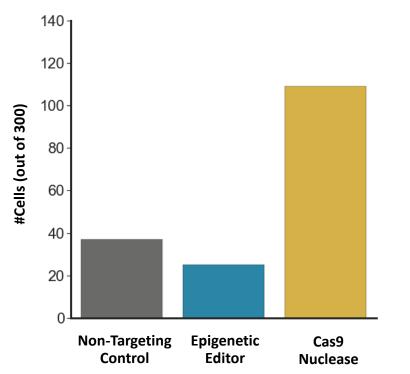


Multiplexing with epigenetic editors did not induce translocations or genomic rearrangement events

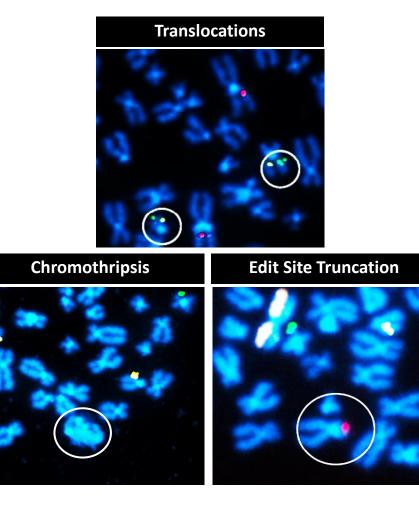
Triple epigenetically silenced cells were compared to triple Cas9 knockout T cells

Number of Cells With Genomic Rearrangement Events

(Translocations, centromere abnormalities, chromothripsis, loss, gain, sister chromatid exchanges/inversions and truncations)

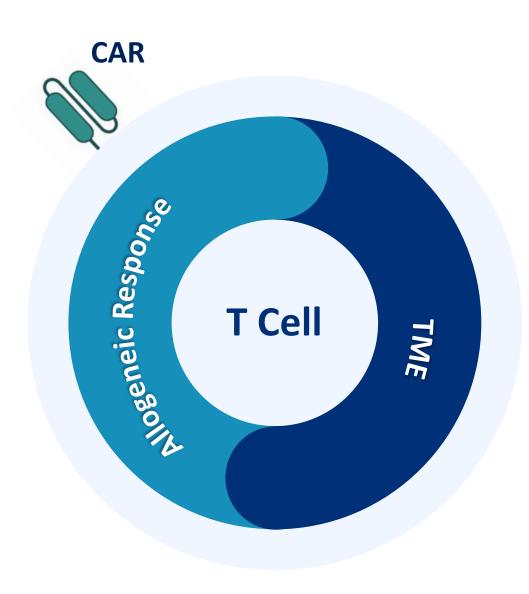


Gross chromosomal abnormalities evident in Cas9 nuclease-treated cells





Modular cassette approach is designed to maximize cell therapy flexibility and functionality



Allogeneic Response

 Enables "off-the shelf" CAR T therapy that maintains potency and durability to treat a greater number of patients



Tumor Microenvironment

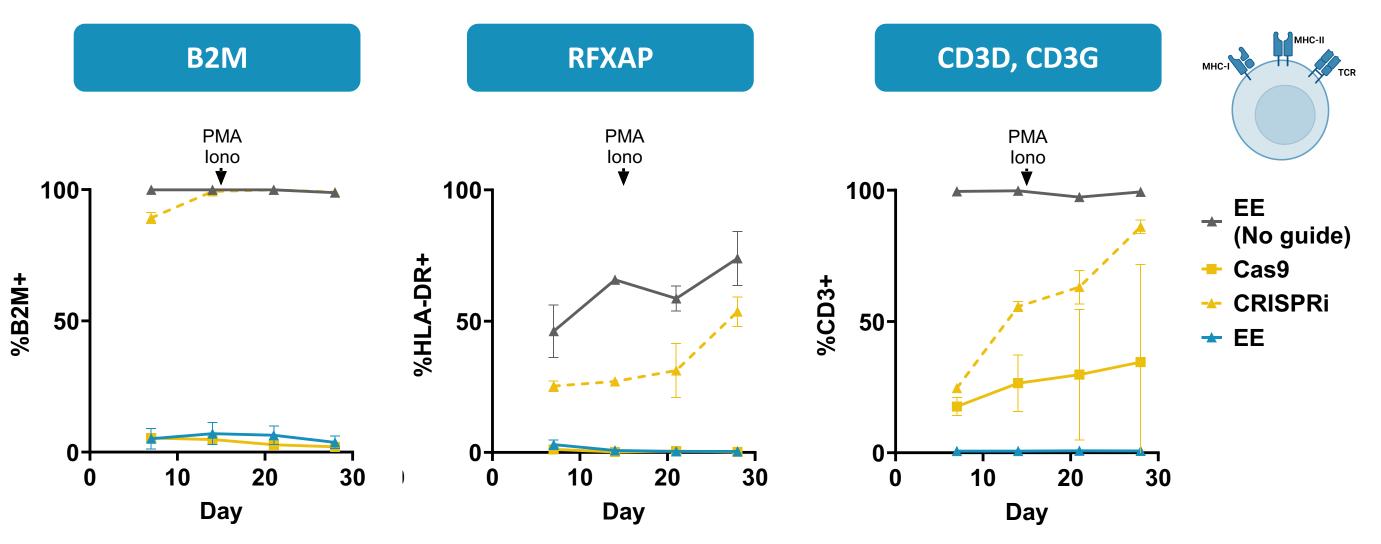
 Overcomes immunosuppressive tumor environment to create a more persistent and efficacious CAR T

Targets:

TGFβR2 Evade TGFβ ADORA2A Reduce immunosuppression



Efficient and durable multiplex silencing of three allogeneic targets

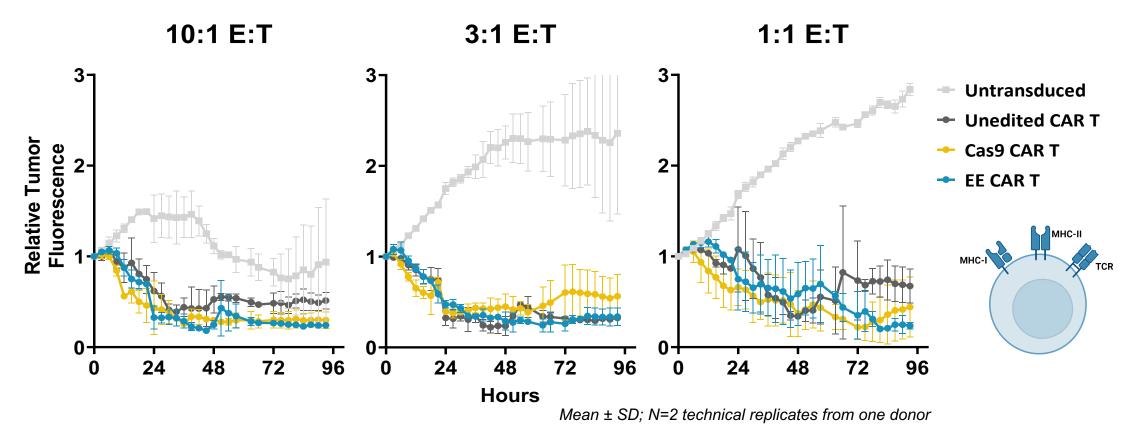


Mean ± SD; N=3 biological replicates from one donor; representative of results obtained with two donors



21

Multiplex epigenetically-edited CAR T have comparable cytotoxic function to unedited CAR T in vitro

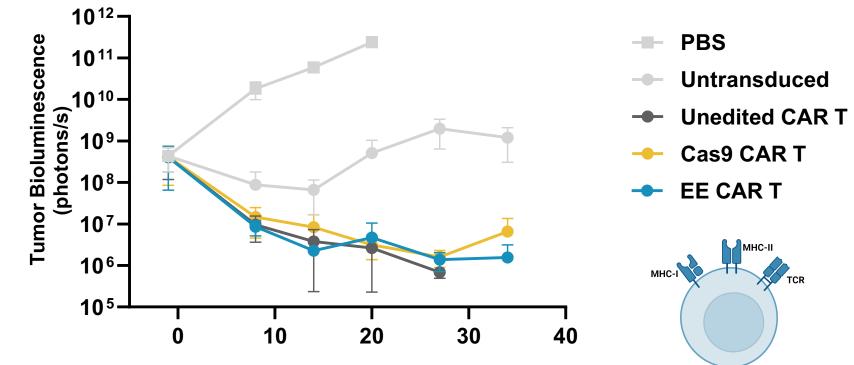


- Multiplex epigenetically-edited CAR T kill tumor cells as effectively as unedited CAR T and demonstrates comparable tumor killing vs. triple Cas9 knock out CAR T for the same three targets
- Additional functional data demonstrates no GvHD response by, or alloresponse to, our epigenetically silenced T cells

22

Multiplex epigenetically-edited CAR T have comparable cytotoxic function to unedited CAR T in vivo

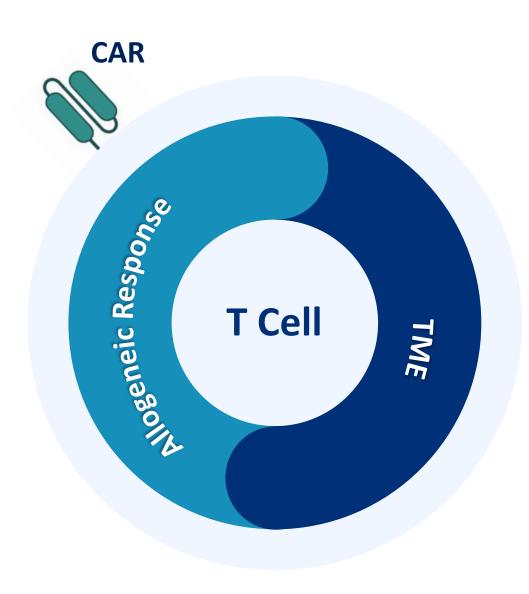
- In vivo control of tumor in an NSG MM.1S model is equivalent for multiplex allogeneic EE CAR T and unedited CAR T
- GvHD response observed in unedited CAR T-treated animals required early euthanization
- Prolonged GvHD-free survival in EE CAR T- and Cas9 CAR Ttreated animals



Days after CAR T administration



Modular cassette approach is designed to maximize cell therapy flexibility and functionality



Allogeneic Response

 Enables "off-the shelf" CAR T therapy that maintains potency and durability to treat a greater number of patients



Tumor Microenvironment

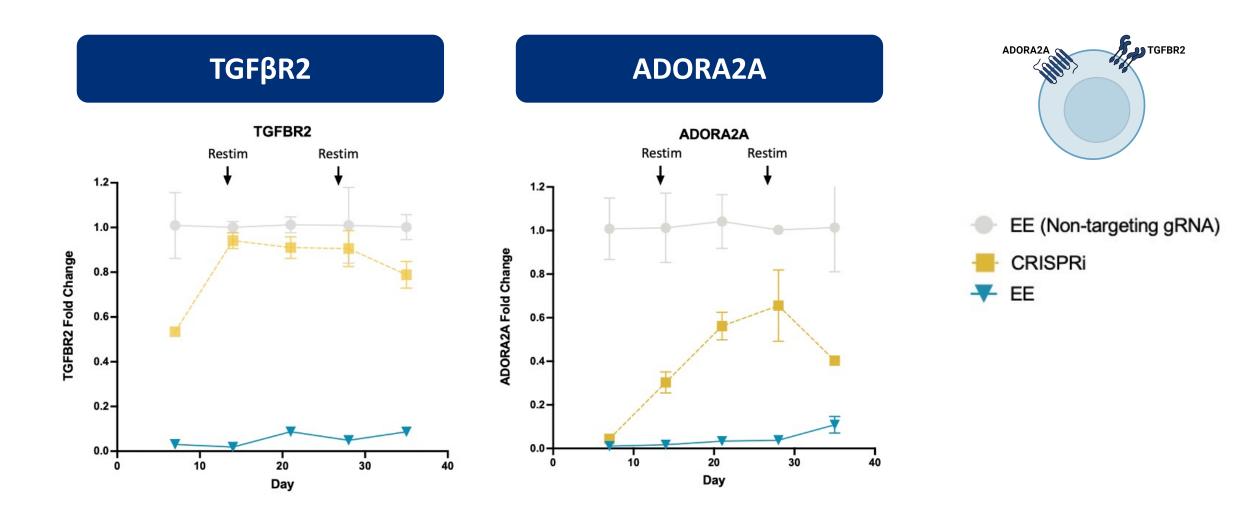
 Overcomes immunosuppressive tumor environment to create a more persistent and efficacious CAR T

Targets:

TGFβR2 Evade TGFβ ADORA2A Reduce immunosuppression

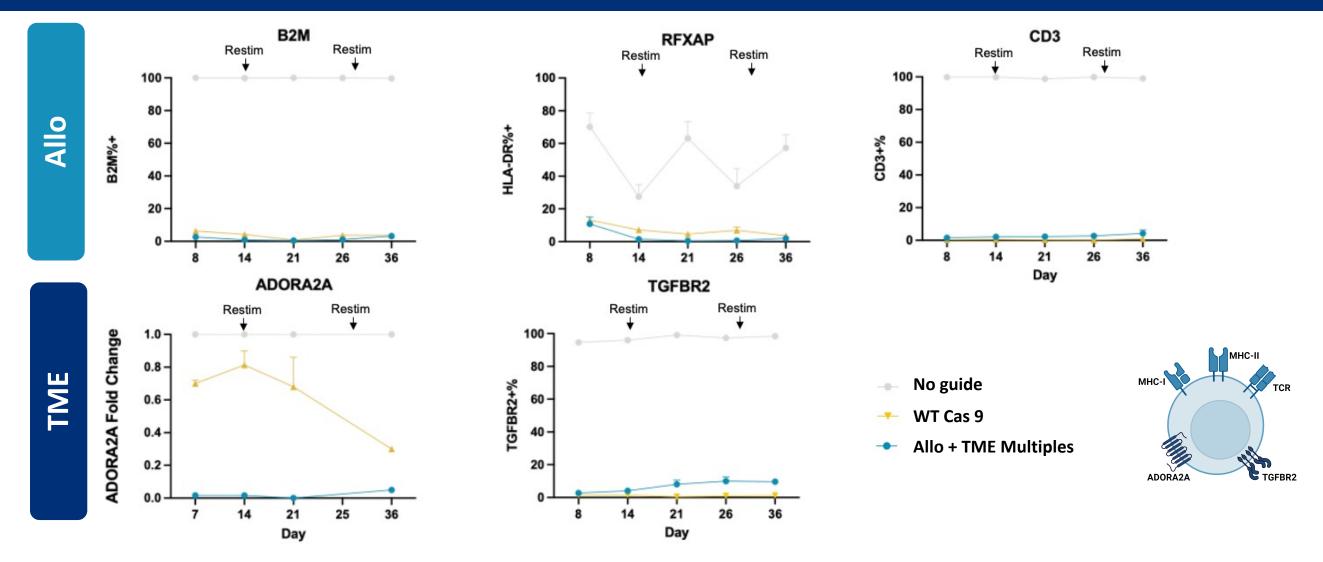


Efficient and durable multiplex silencing of TME resistance targets



 Efficient and durable multiplex silencing of two TME-resistance targets, ADORA2A and TGFBR2, was achieved in primary human T cells

Allo/TME five-target multiplexing is both highly efficient and durable



 Efficient 5-target silencing out to 35 days shows minimal impact of multiplexing on overall silencing efficiency through two PMA/ionomycin restimulations on Days 14 and 28

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Acknowledgements

Thank you to the entire Chroma team, our collaborators, and partners!







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