

Universität  
Zürich<sup>UZH</sup>



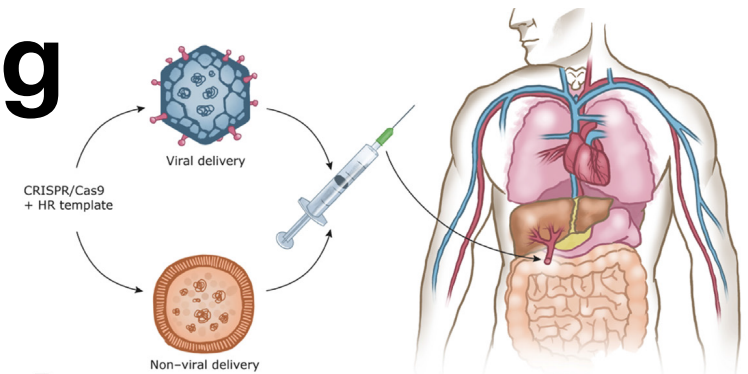
@schwanklab

# Correcting metabolic liver diseases by *in vivo* genome editing

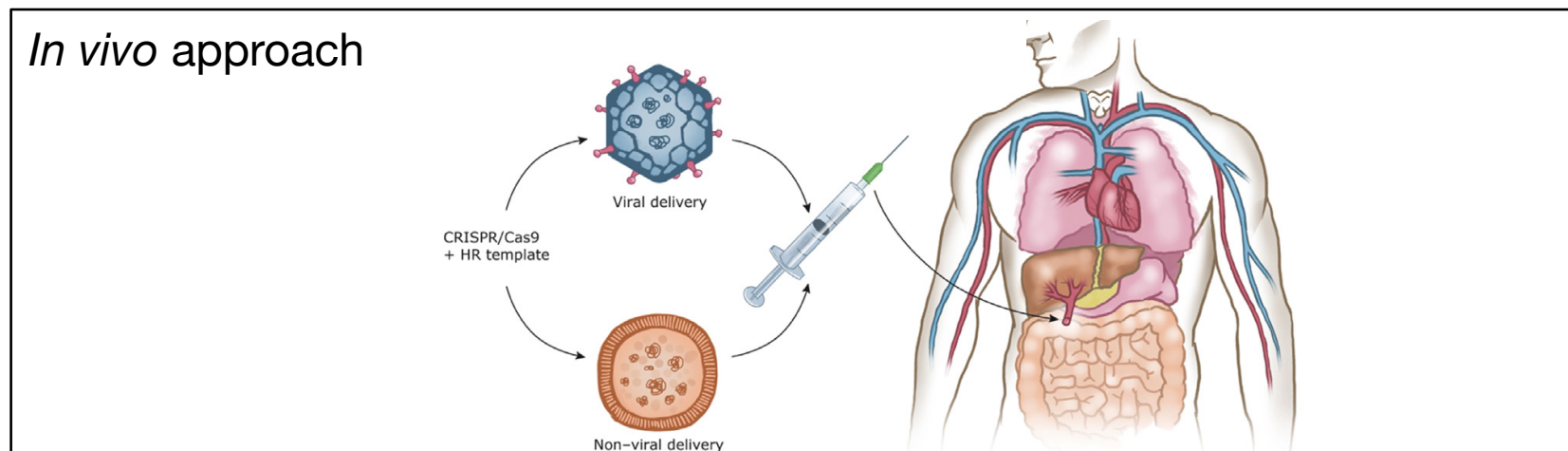
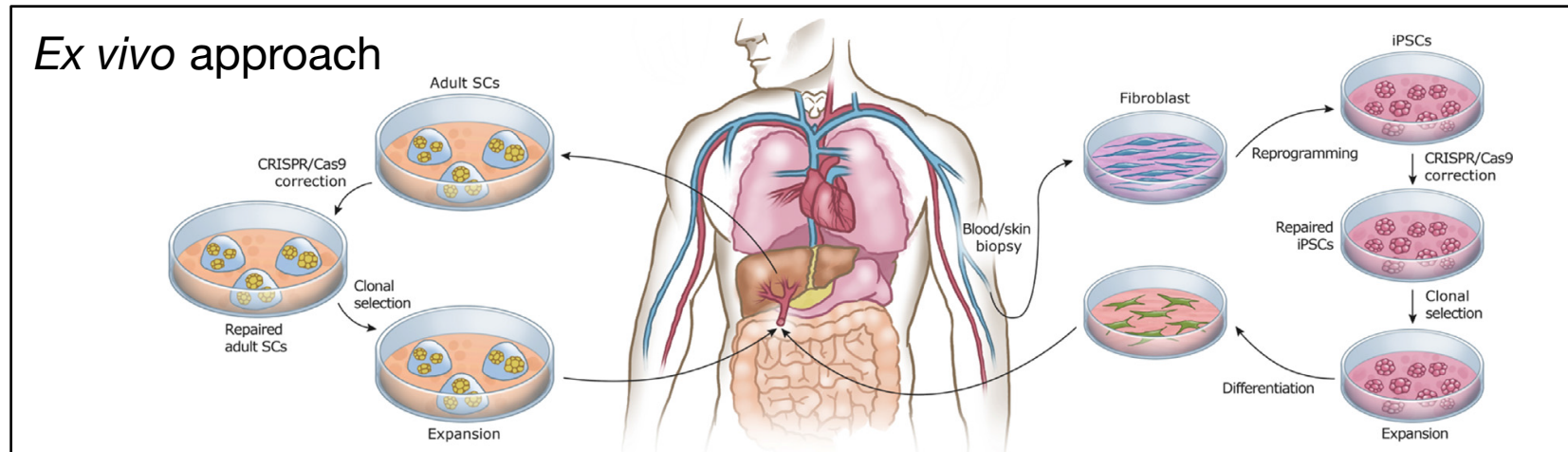
Gerald Schwank

Institute of Pharmacology and Toxicology, University of Zürich

Zürich – Nov. 12, 2021



# Approaches for gene editing therapies



# *In vitro* expansion and transplantation of hepatocytes

## hepOrgs

Hu et al., Cell 2018



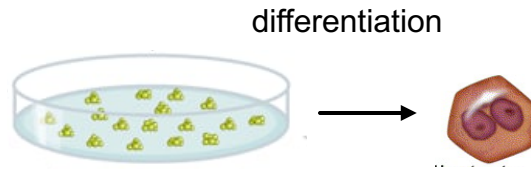
## CLiPs

Katsuda et al., Cell Stem Cell 2017



## iPSCs

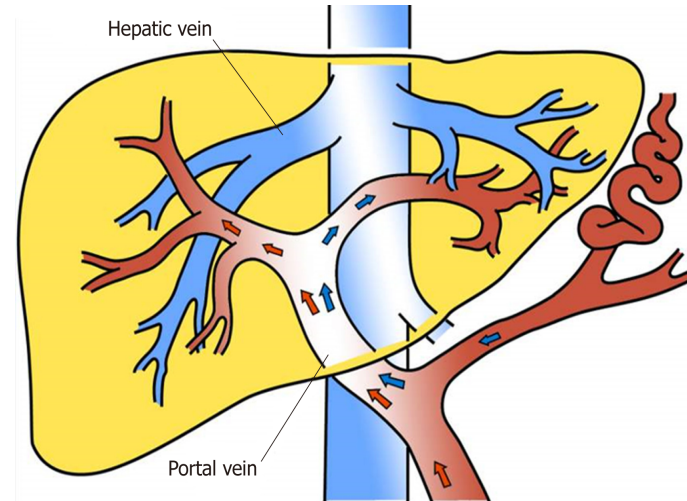
Takahashi et al., Cell 2007



## Clinical trials for hepatocyte transplantation

Crigler-Najjar syndrome type 1 (CN-1), urea cycle defects and factor VII (fVII) deficiency:

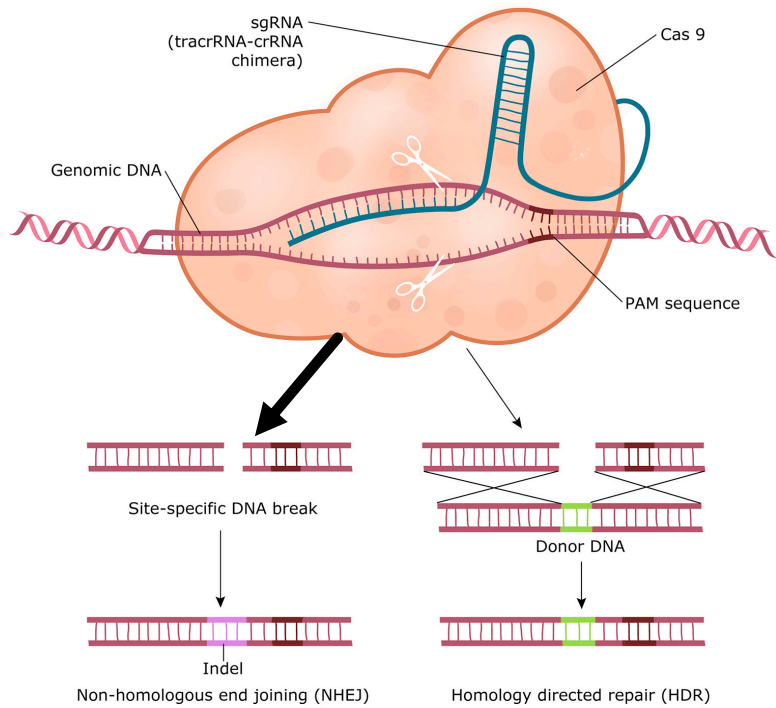
**No long-term benefit observed!**



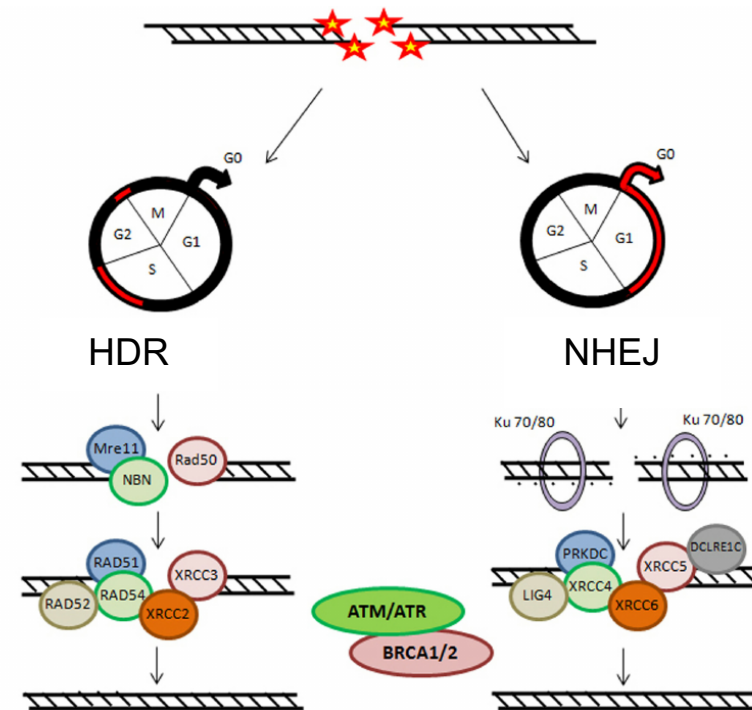
Lee et al., (2018), *J Mol Med*; 96(6): 469–481.

# In non-dividing cells DNA double-strand breaks mainly induce indel mutations

NHEJ vs. HDR



HDR is inactive in postmitotic cells



# DNA double strand breaks can induce complex DNA damage

nature  
medicine

LETTERS

<https://doi.org/10.1038/s41591-018-0050-6>

## p53 inhibits CRISPR–Cas9 engineering in human pluripotent stem cells

Robert J. Ihry<sup>1</sup>, Kathleen A. Worringer<sup>1</sup>, Max R. Salick<sup>1</sup>, Elizabeth Frias<sup>2</sup>, Daniel Ho<sup>1</sup>, Kraig Theriault<sup>1</sup>, Sravya Kommineni<sup>1</sup>, Julie Chen<sup>3</sup>, Marie Sondey<sup>4</sup>, Chaoyang Ye<sup>5</sup>, Ranjit Randhawa<sup>1</sup>, Tripti Kulkarni<sup>1</sup>, Zinger Yang<sup>2</sup>, Gregory McAllister<sup>2</sup>, Carsten Russ<sup>2</sup>, John Reece-Hoyes<sup>2</sup>, William Forrester<sup>2</sup>, Gregory R. Hoffman<sup>2</sup>, Ricardo Dolmetsch<sup>1</sup> and Ajamete Kaykas<sup>1\*</sup>

nature  
medicine

BRIEF COMMUNICATION

<https://doi.org/10.1038/s41591-018-0049-z>

## CRISPR–Cas9 genome editing induces a p53-mediated DNA damage response

Emma Haapaniemi<sup>1,2,4</sup>, Sandeep Botla<sup>1,4</sup>, Jenna Persson<sup>1</sup>, Bernhard Schmierer<sup>1,5\*</sup> and Jussi Taipale<sup>1,2,3,5\*</sup>

BRIEF COMMUNICATIONS ARISING

## Inter-homologue repair in fertilized human eggs?

ARISING FROM H. Ma et al. *Nature* **548**, 413–419 (2017); <https://doi.org/10.1038/nature23305>

LETTERS

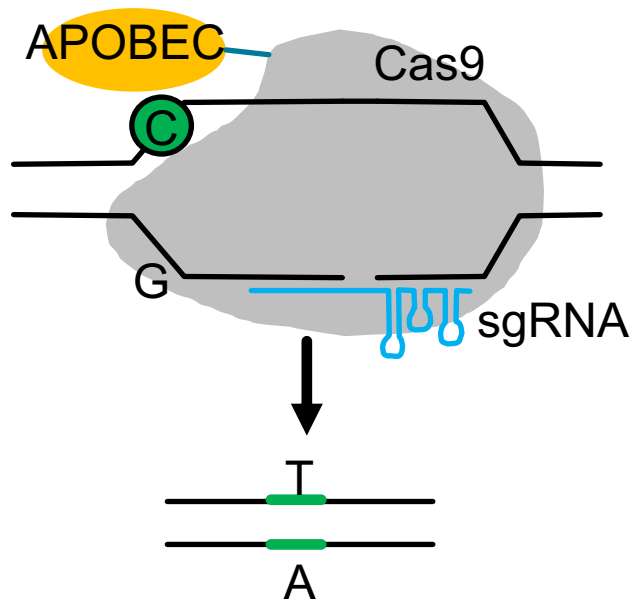
nature  
biotechnology

Repair of double-strand breaks induced by CRISPR–Cas9 leads to large deletions and complex rearrangements

Michael Kosicki, Kärt Tomberg & Allan Bradley

# Base editors can install/correct transition mutations without inducing DNA double-strand breaks

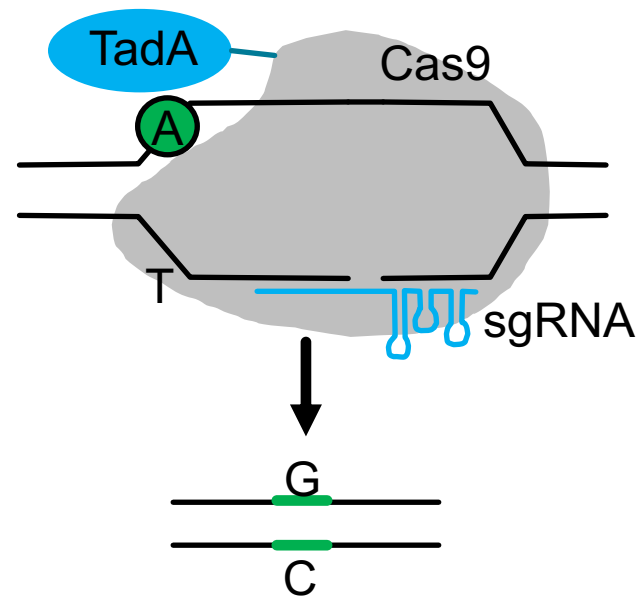
## Cytidine Base Editor



C•G to T•A conversion

*Komor et al. (2016), Nature; 533, pages420–424.*

## Adenine Base Editor



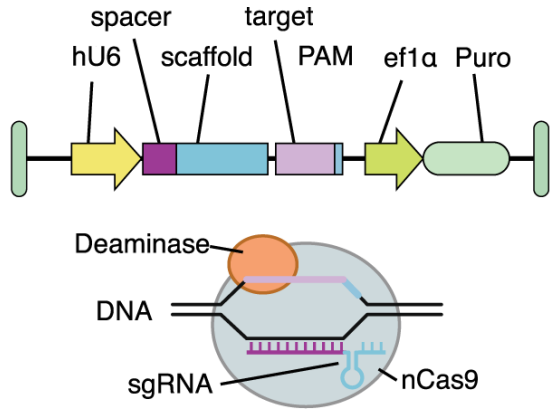
A•T to G•C conversion

*Gaudelli et al. (2017), Nature; 551(7681):464-471.*

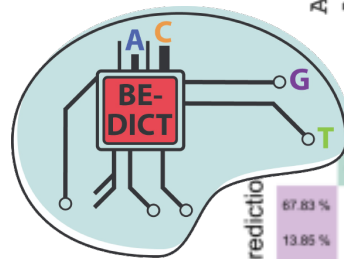
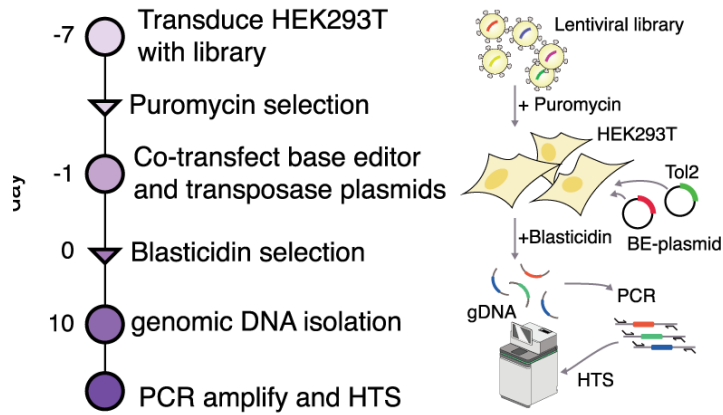
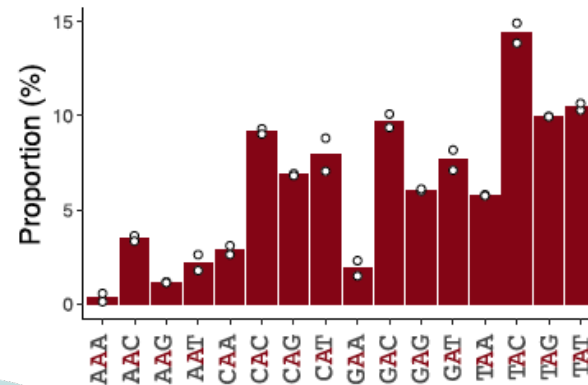
Limitations:

- Transition mutations
- PAM availability
- Bystander edits

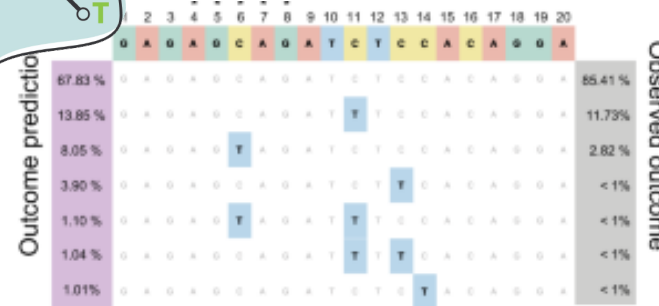
# Predicting base editing efficiencies



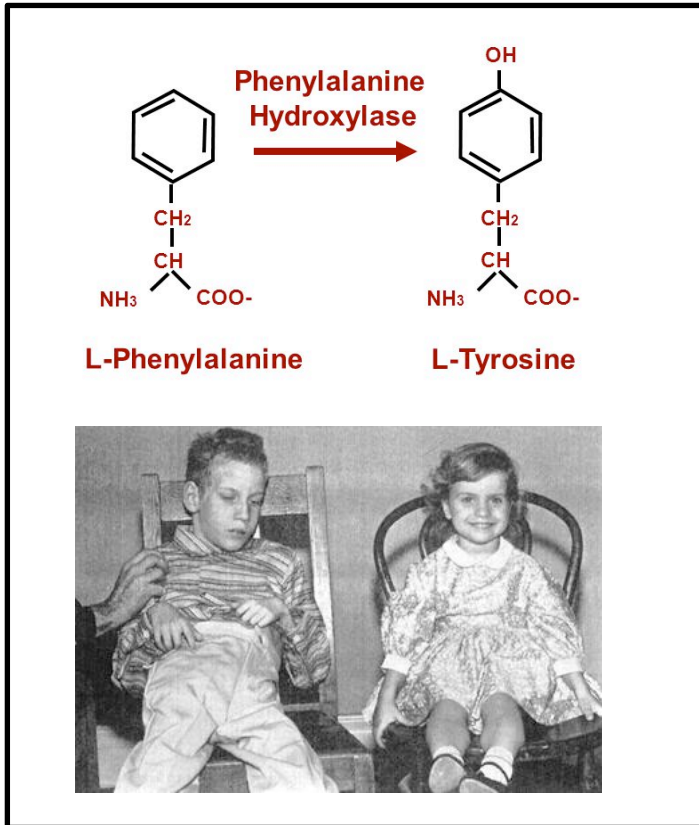
ABE-max trinucleotide motifs



[www.be-dict.org](http://www.be-dict.org)



# The *Pah<sup>enu</sup>* mouse model for Phenylketonuria



- PAH deficiency leads to excess amounts of Phe in the blood, causing damage of the central nervous system
- The pathogenic mutation is a T>C mutation that can be targeted by cytidine base editors



GGC CTG GCC TTC CGA GTC TcC CAC TGC ACA CAG TAC ATT (+)  
 CCG GAC CGG AAG GCT CAG AgG GTG ACG TGT GTC ATG TAA (-)

Gly Leu Ala Phe Arg Val Ser His Cys Thr Gln Tyr Ile

c.835T>C PAH

Gly Leu Ala Phe Arg Val Phe His Cys Thr Gln Tyr Ile

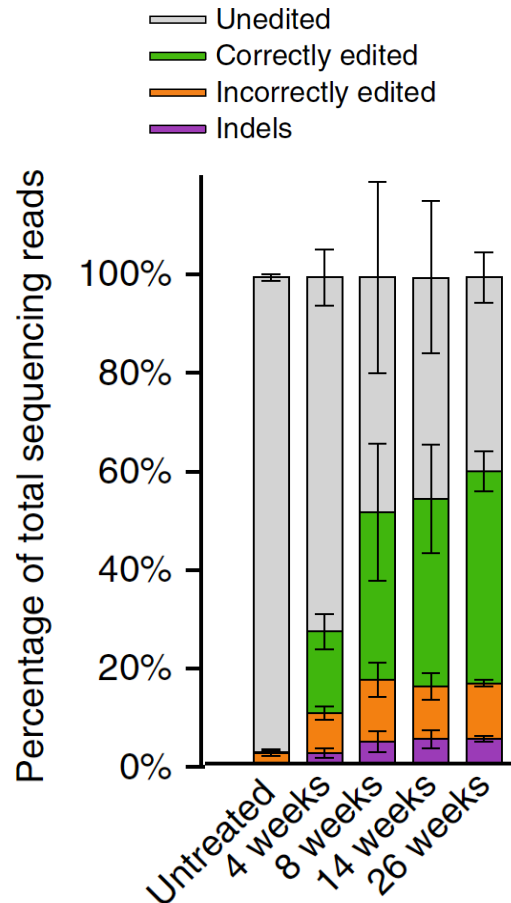
Wild-type PAH

C to T correction  
 using SaKKH-CBE3

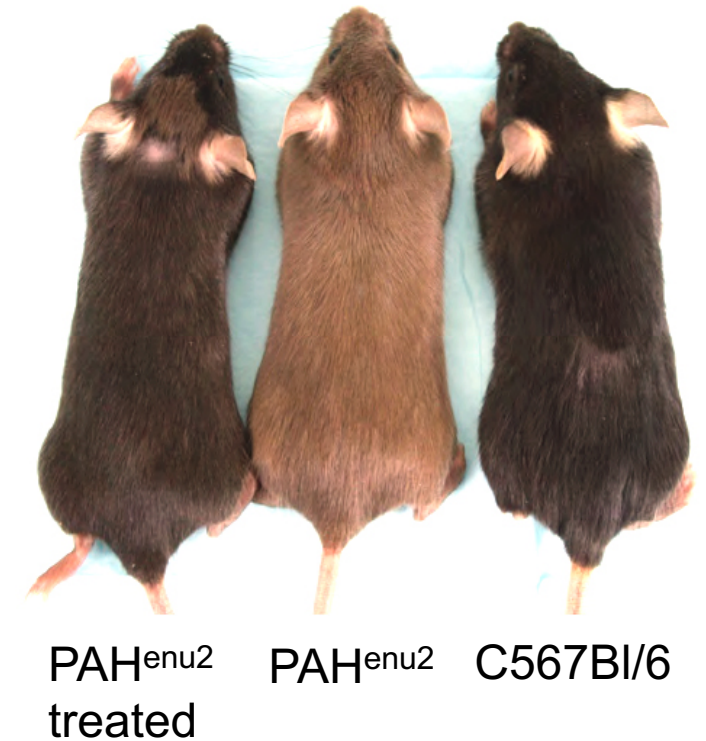
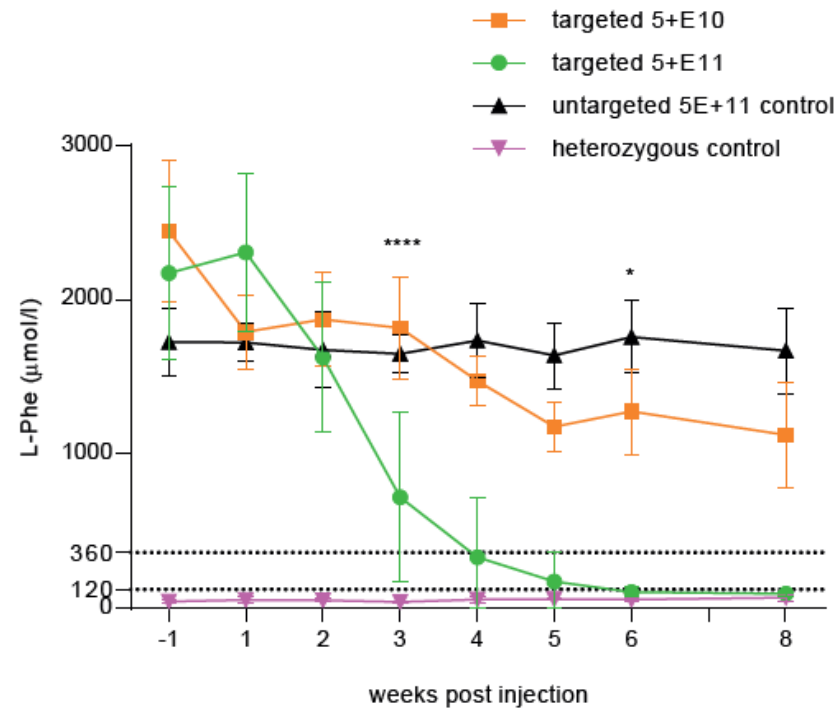


# AAV-mediated base editor delivery restores physiological blood phenylalanine levels

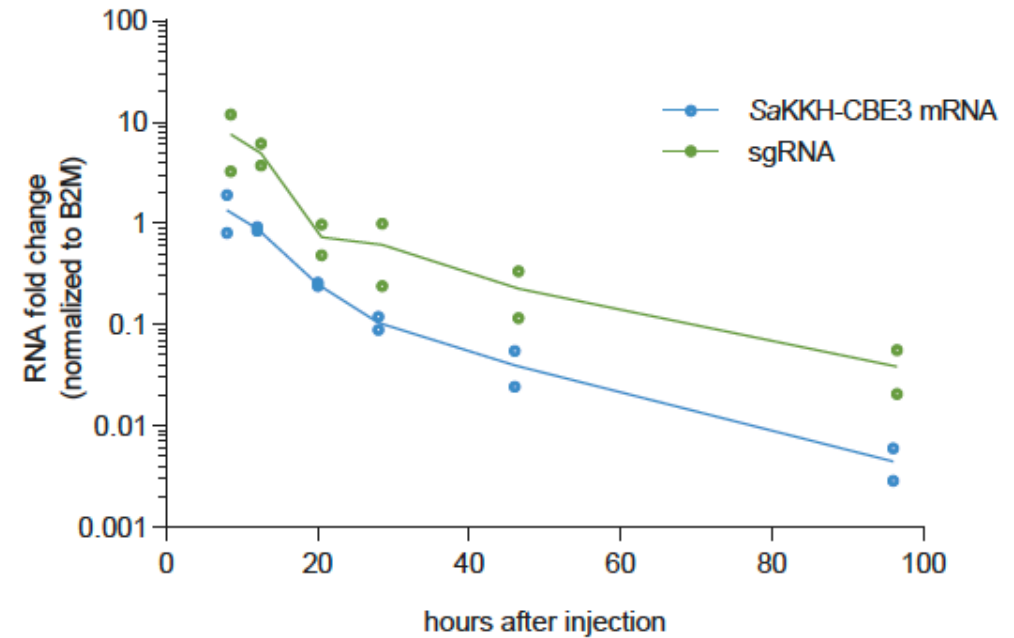
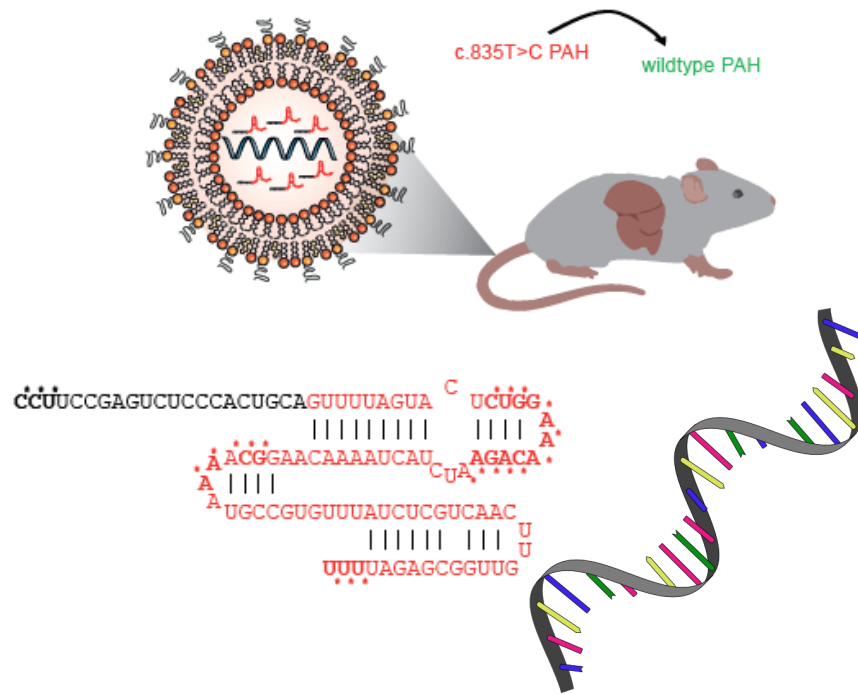
Targeting the *Pah<sup>enu</sup>* mouse model with SaKKH-CBE3



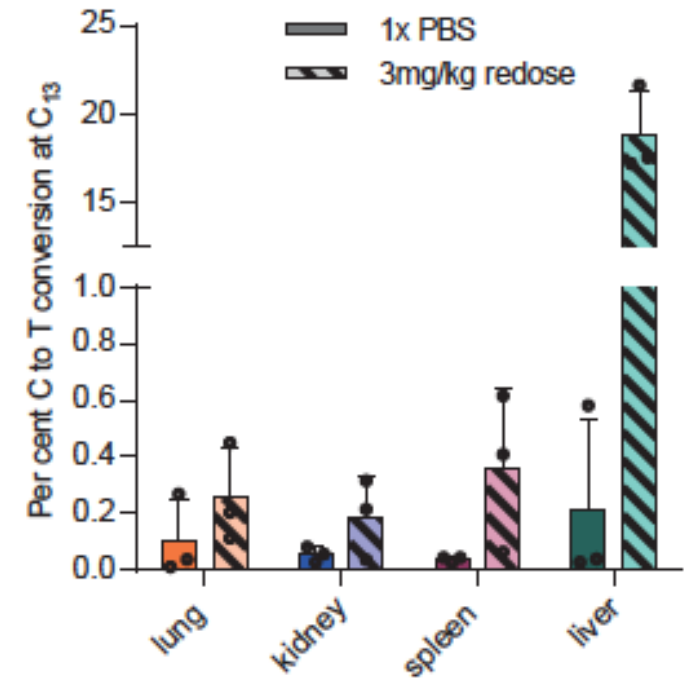
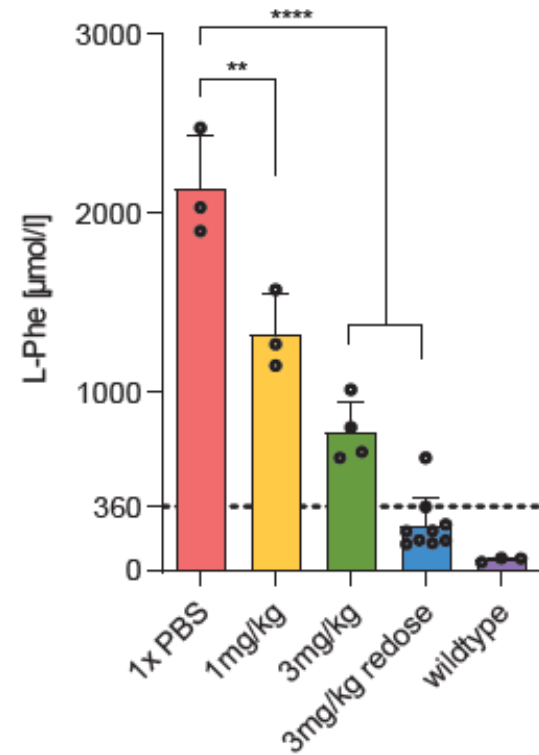
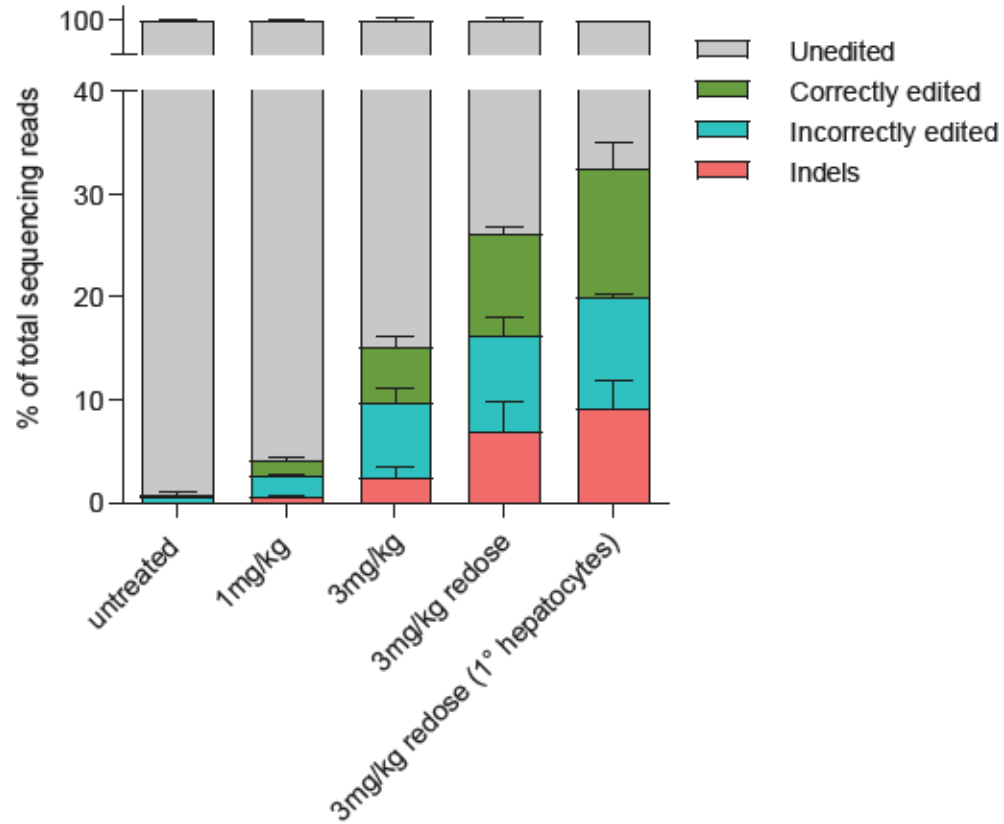
### Blood phenylalanine levels



# *In vivo* cytidine base editing using RNA encapsulated in lipid nanoparticles



# *In vivo* cytidine base editing using RNA encapsulated in lipid nanoparticles



# Base editors can generate sgRNA-independent off-target mutations on RNA and DNA

LETTER

<https://doi.org/10.1038/s41586-019-1161-z>

## Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors

Julian Grünewald<sup>1,2,3,4</sup>, Ronghao Zhou<sup>1,2,3</sup>, Sara P. Garcia<sup>1,6</sup>, Sowmya Iyer<sup>1,6</sup>, Caleb A. Lareau<sup>1,5,6</sup>, Martin J. Aryee<sup>1,2,3,4,5</sup> & J. Keith Joung<sup>1,2,3,4\*</sup>

LETTER

<https://doi.org/10.1038/s41586-019-1314-0>

## Off-target RNA mutation induced by DNA base editing and its elimination by mutagenesis

Changyang Zhou<sup>1,2,9</sup>, Yidi Sun<sup>2,3,4,9</sup>, Rui Yan<sup>5,9</sup>, Yajing Liu<sup>2,6,9</sup>, Erwei Zuo<sup>1,7,9</sup>, Chan Gu<sup>5</sup>, Linxiao Han<sup>1</sup>, Yu Wei<sup>1</sup>, Xinde Hu<sup>1,2</sup>, Rong Zeng<sup>3,6</sup>, Yixue Li<sup>5,6,8\*</sup>, Haibo Zhou<sup>1\*</sup>, Fan Guo<sup>5\*</sup> & Hui Yang<sup>1\*</sup>

Science

## Cytosine base editor generates substantial off-target single-nucleotide variants in mouse embryos

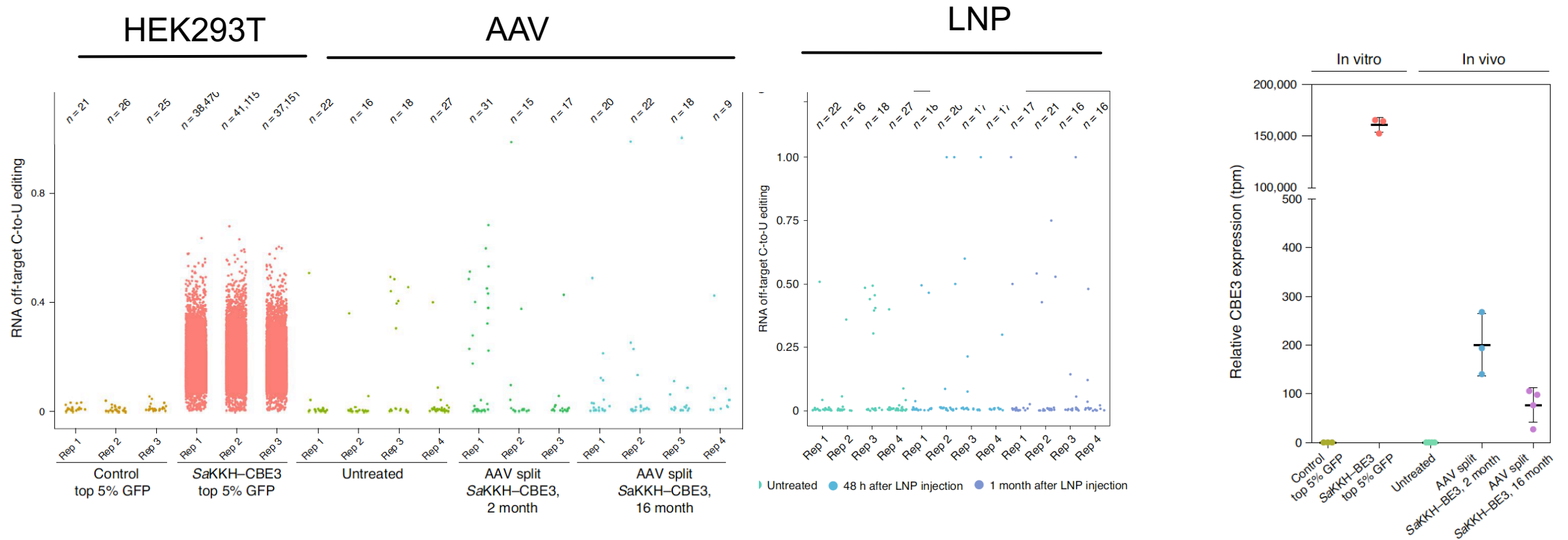
Erwei Zuo<sup>1,2\*</sup>, Yidi Sun<sup>3\*</sup>, Wu Wei<sup>3,4,5\*</sup>, Tanglong Yuan<sup>2\*</sup>, Wenqin Ying<sup>1</sup>, Hao Sun<sup>6</sup>, Liyun Yuan<sup>3</sup>, Lars M. Steinmetz<sup>4,7,8†</sup>, Yixue Li<sup>3,9,10†</sup>, Hui Yang<sup>1†</sup>

BIOTECHNOLOGY

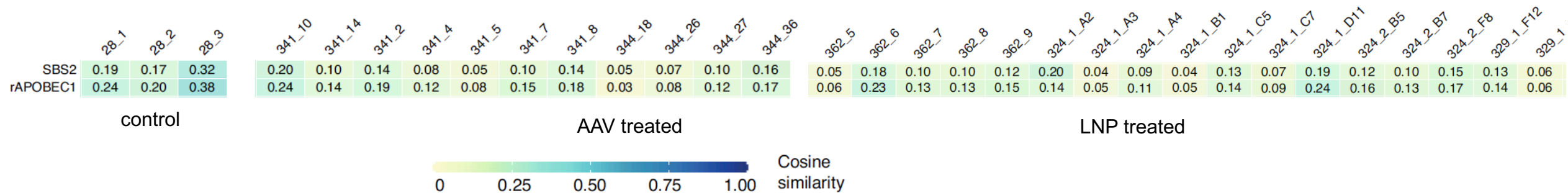
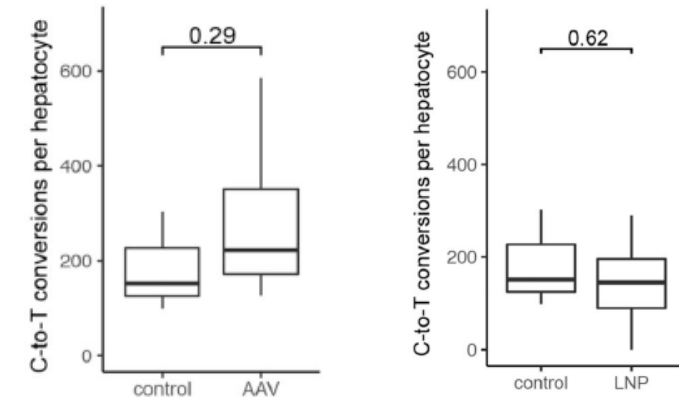
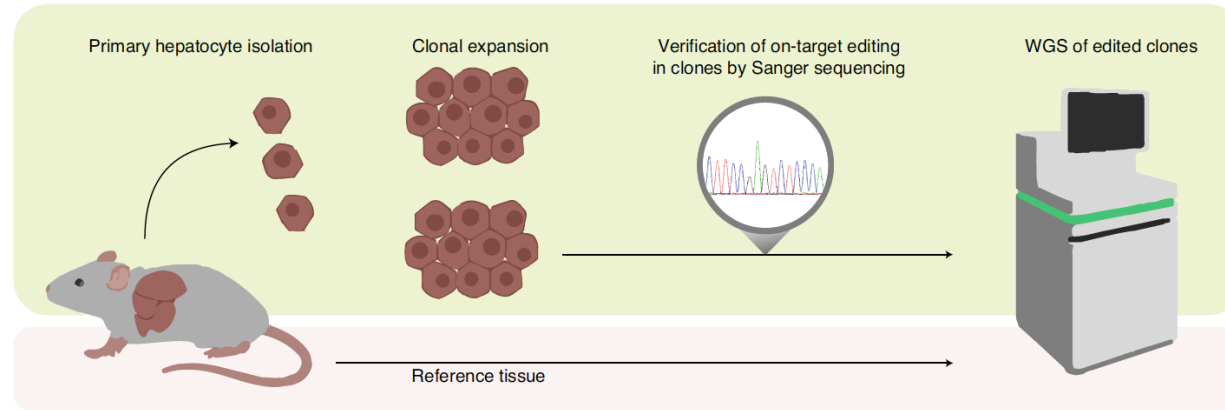
## Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice

Shuai Jin<sup>1,2\*</sup>, Yuan Zong<sup>1,2\*</sup>, Qiang Gao<sup>3\*</sup>, Zixu Zhu<sup>1,2</sup>, Yanpeng Wang<sup>1</sup>, Peng Qin<sup>4</sup>, Chengzhi Liang<sup>2,3</sup>, Daowen Wang<sup>1,2</sup>, Jin-Long Qiu<sup>5</sup>, Feng Zhang<sup>6</sup>, Caixia Gao<sup>1,2†</sup>

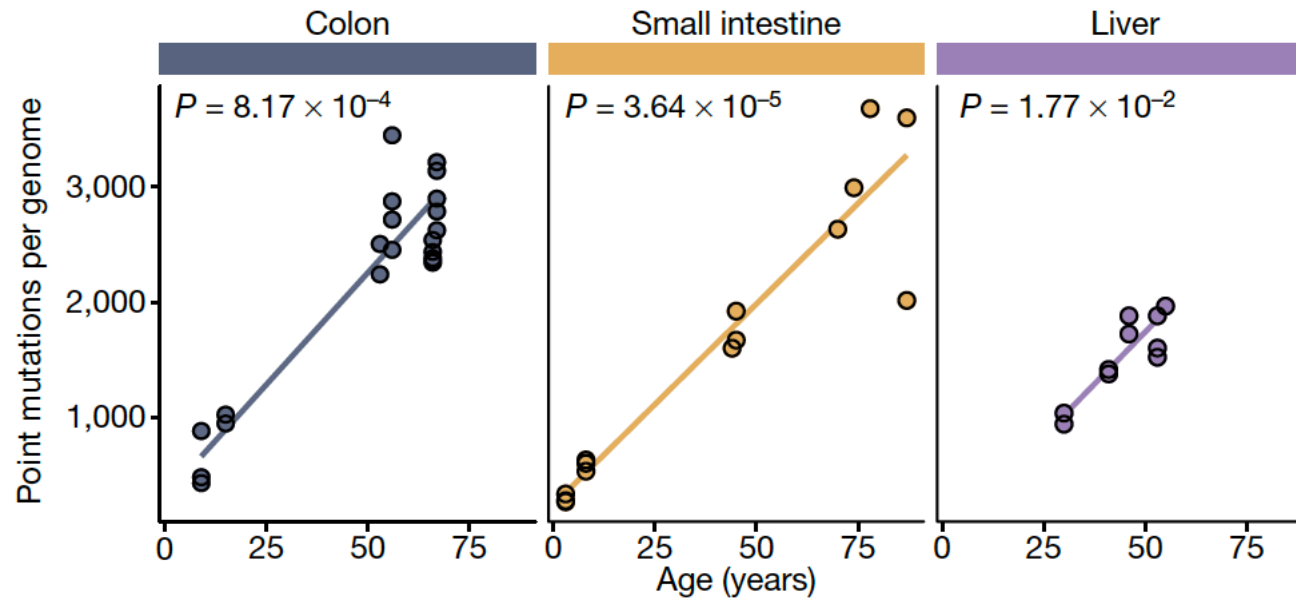
# *In vivo* cytidine base editing did not induced RNA off-target deamination



# *In vivo* cytidine base editing did not induced DNA off-target deamination



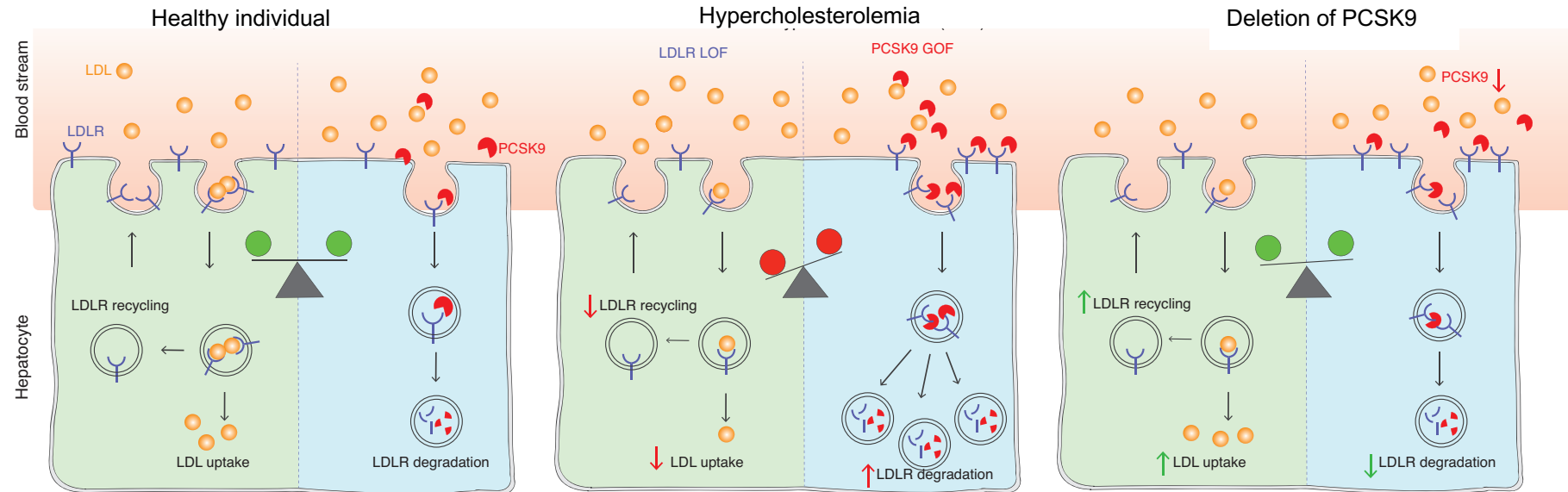
# SNPs are well tolerated in humans



Blokzijl et al. (2016) *Nature*. Oct 13;538(7624):260-264.

# Targeting *PCSK9* via adenine base editing

PCSK9 is a negative regulator of LDL receptor

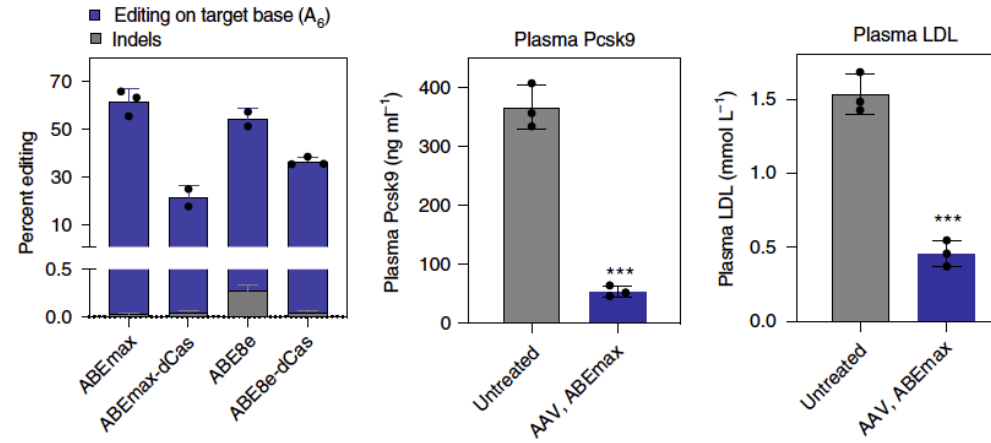




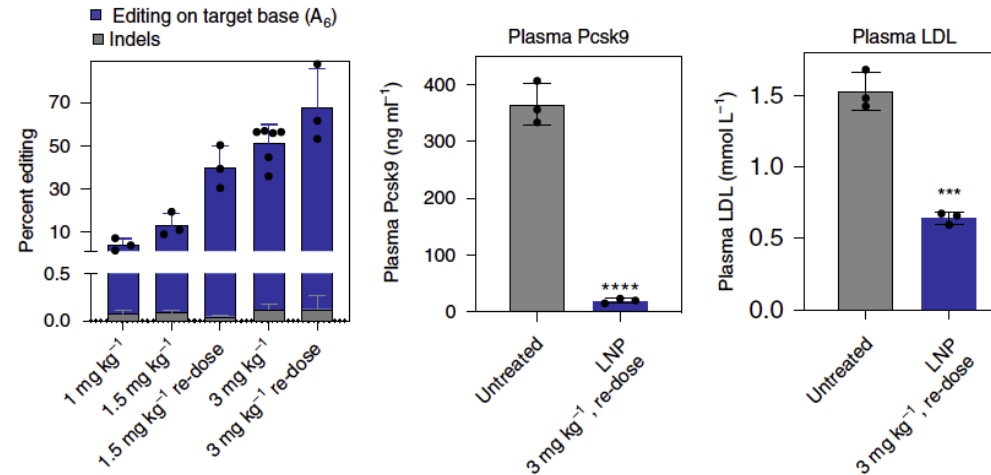
# Inactivating PCSK9 *in vivo* reduces LDL cholesterol



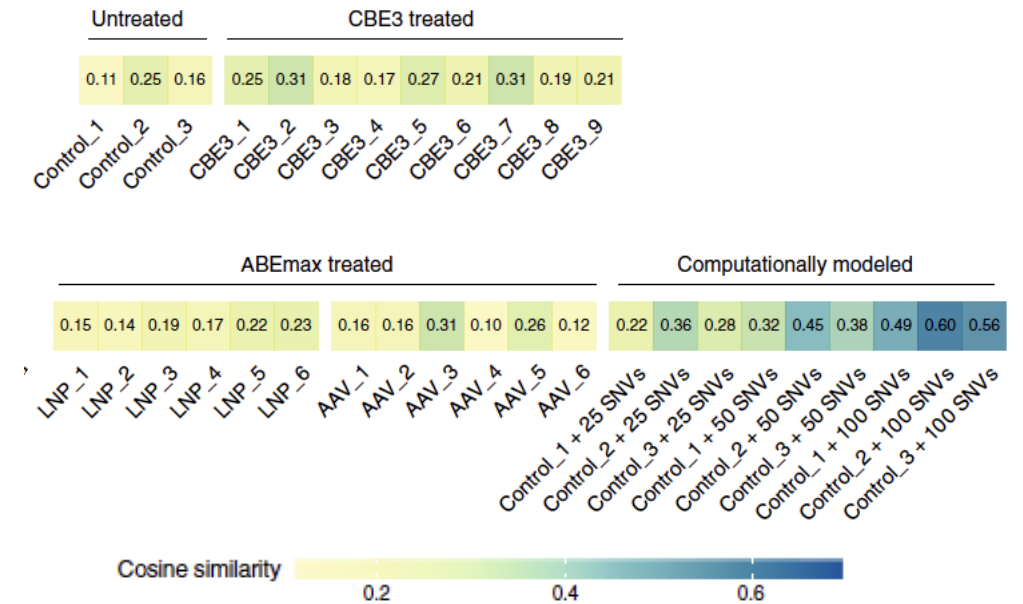
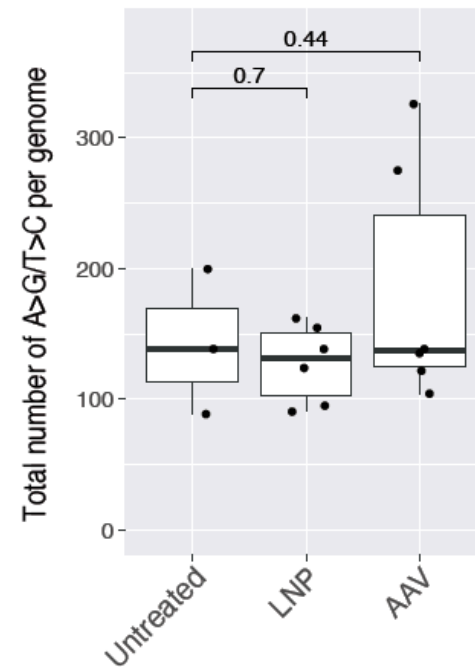
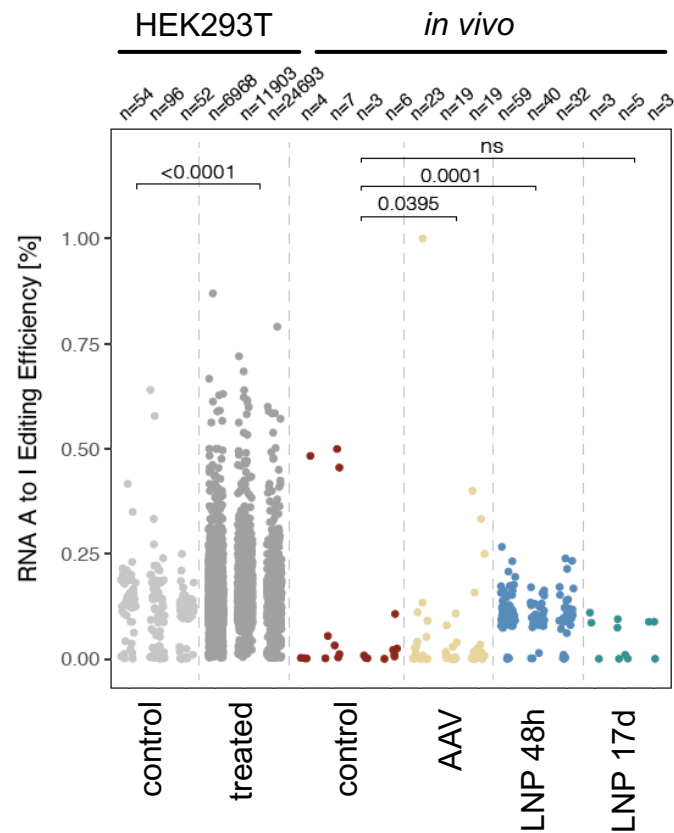
AAV-treated mice



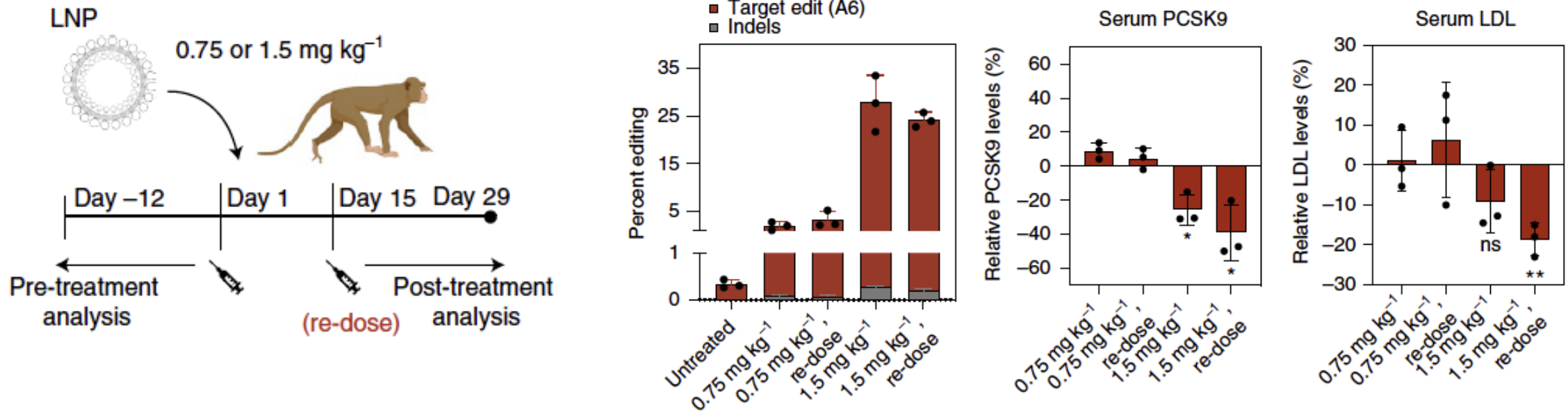
LNP-treated mice



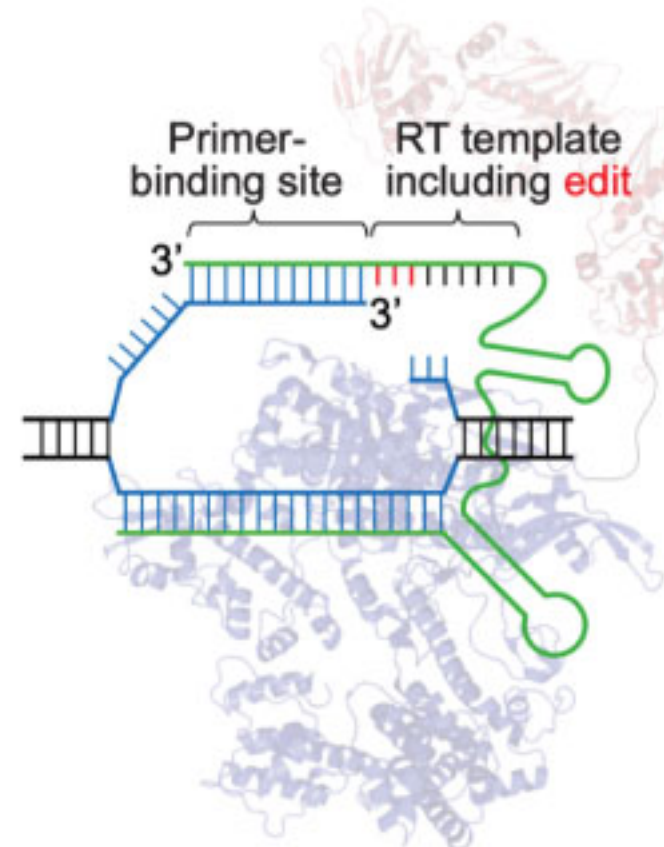
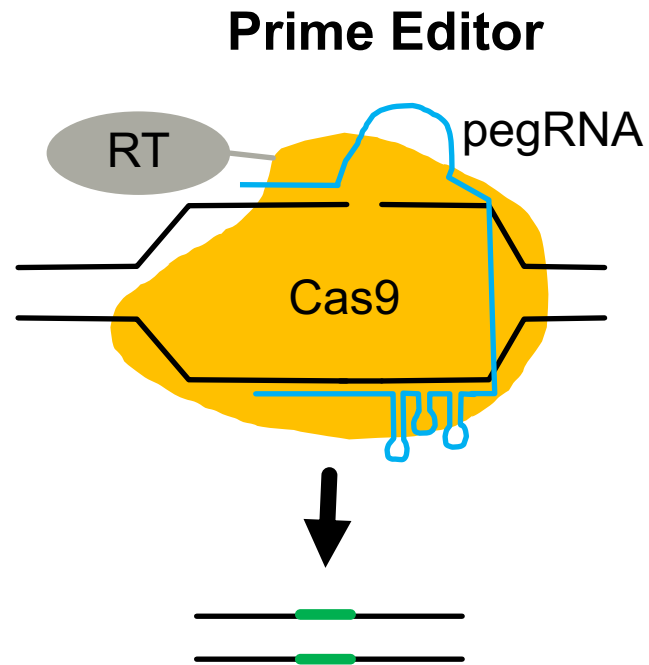
# In vivo adenine base editing did not induced RNA and DNA off-target deamination



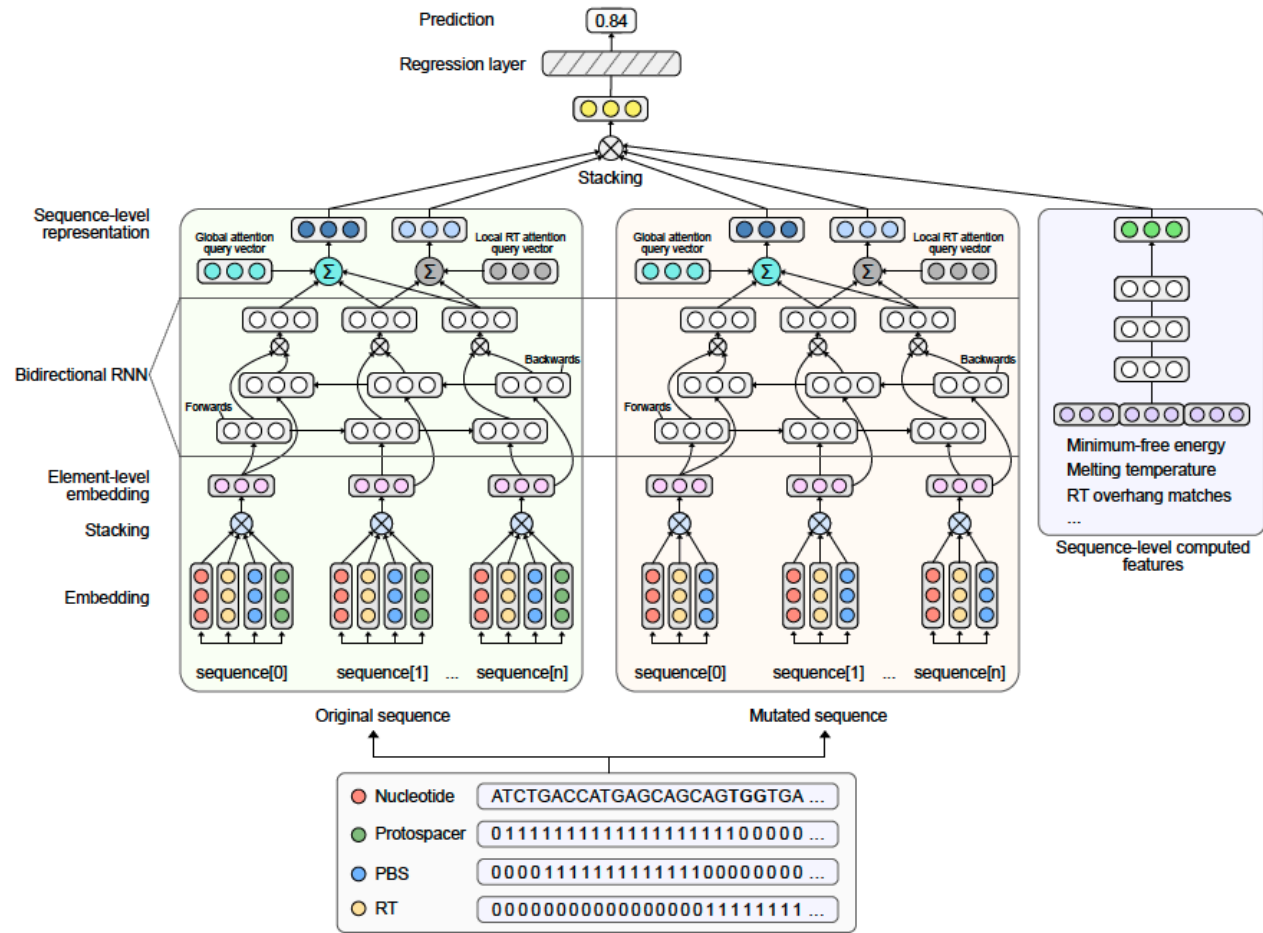
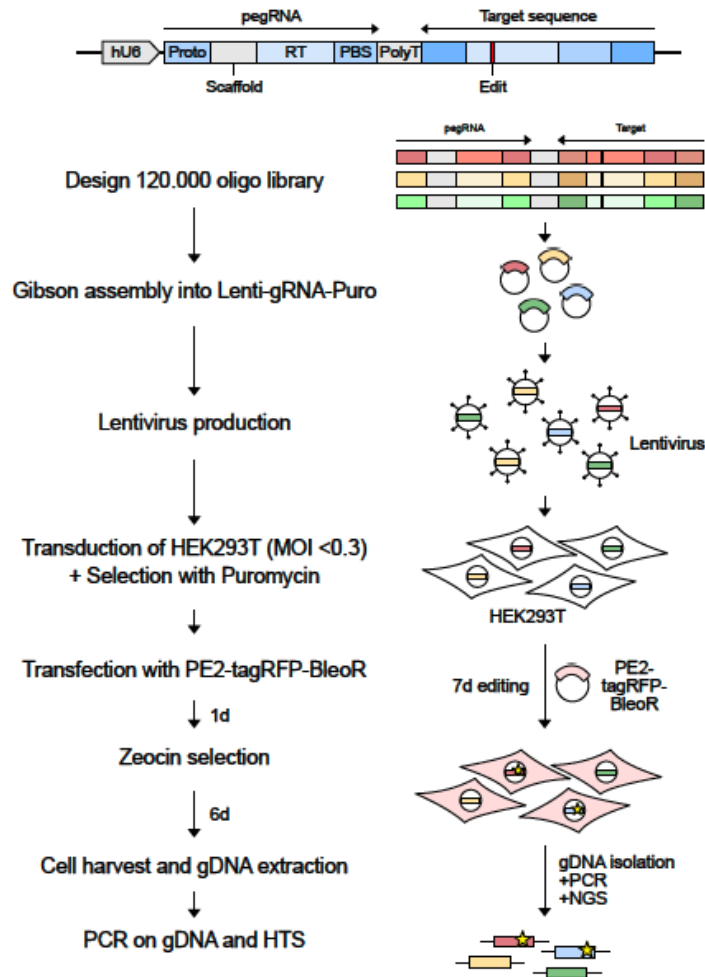
# LNP-mediated adenine base editing of *PCSK9* in primates



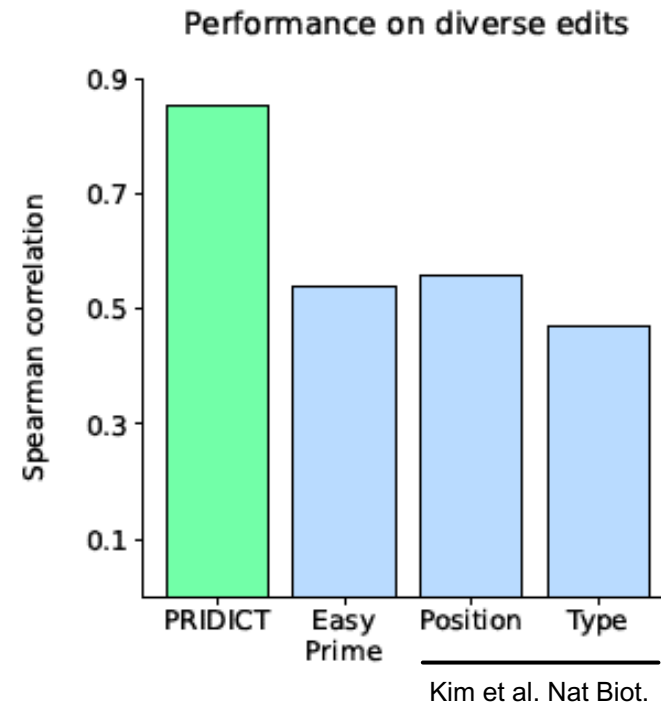
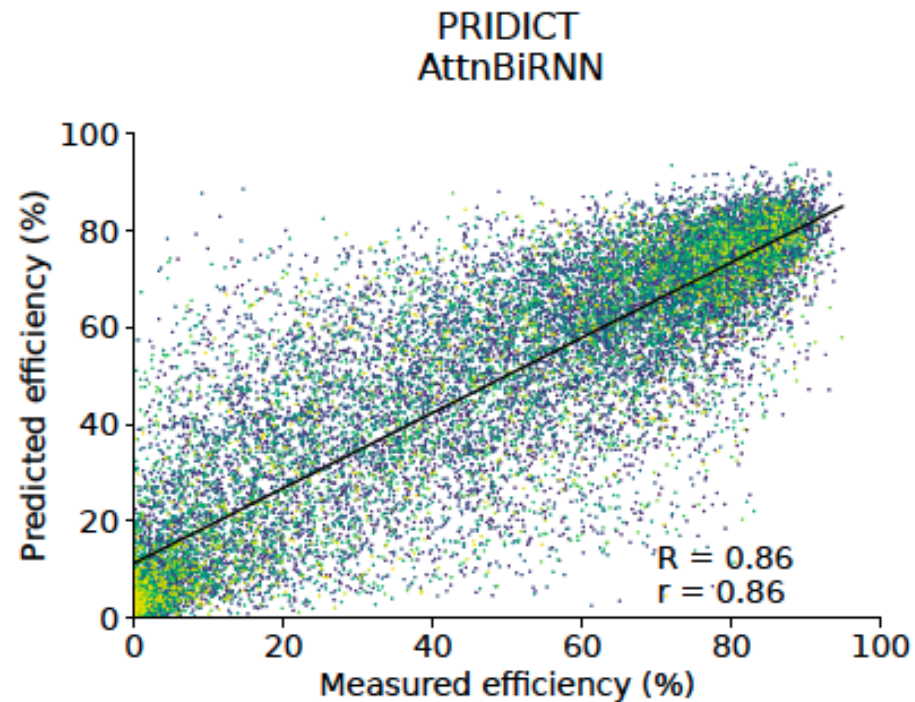
# Prime editors: A highly versatile DNA double strand break-independent genome editor



# PRIDICT: Predicting prime editing efficiencies

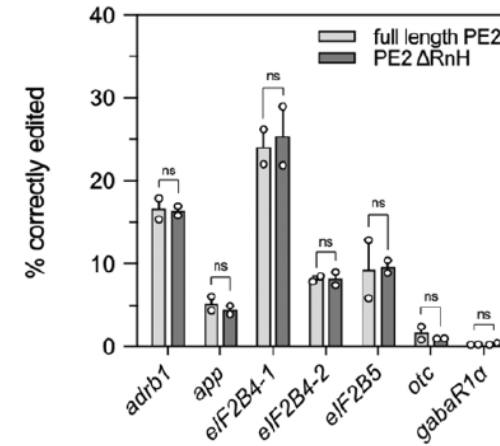
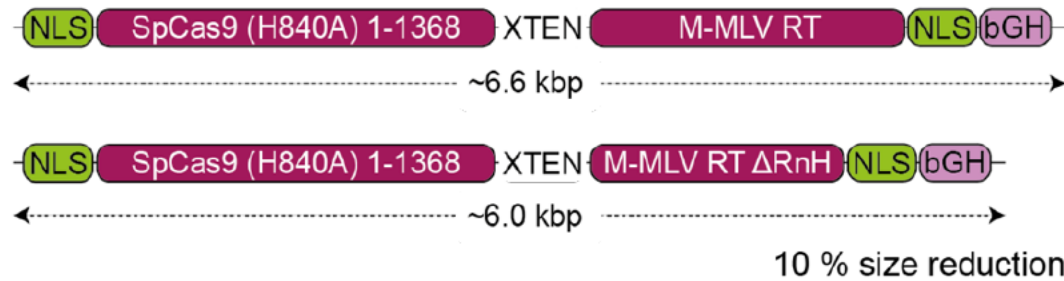


# PRIDICT: Predicting prime editing efficiencies

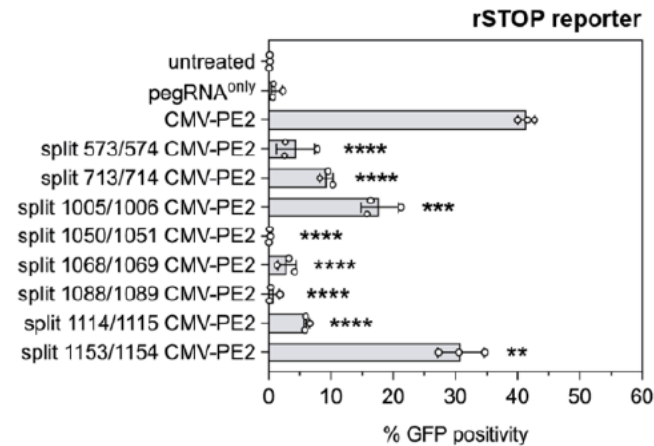
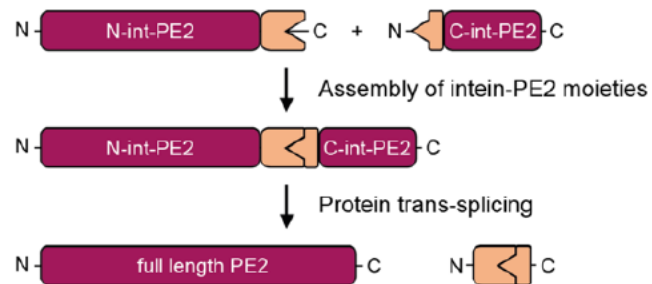


# Generation of size-optimized prime editors

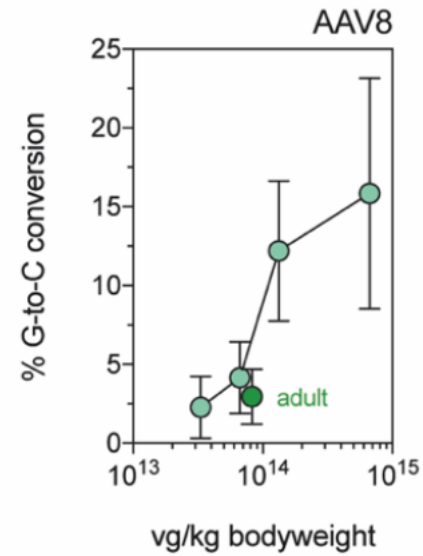
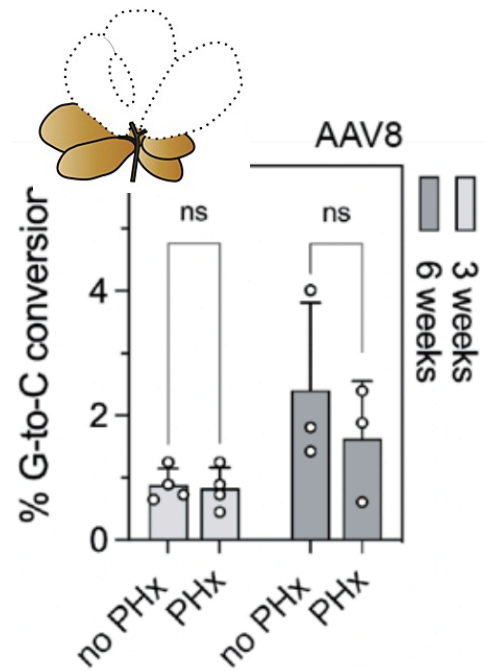
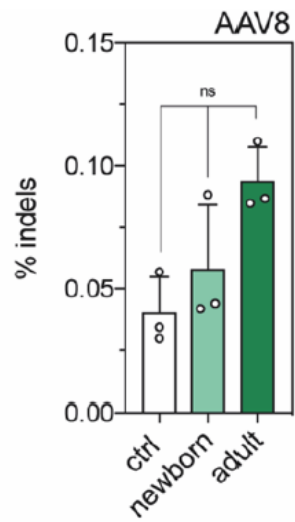
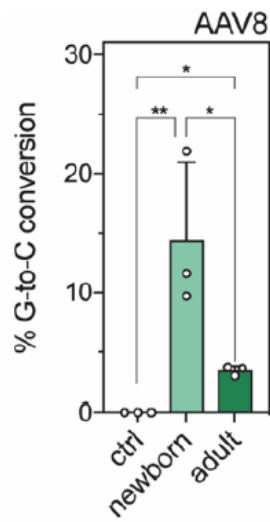
## PE2 $\Delta$ RnH



## split PE2



# Installing a G-to-C edit in *Dnmt1* via AAV-mediated prime editing

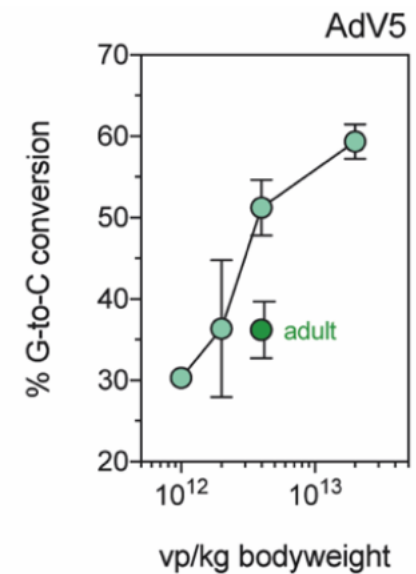
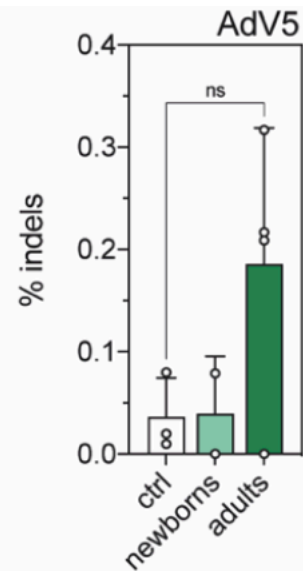
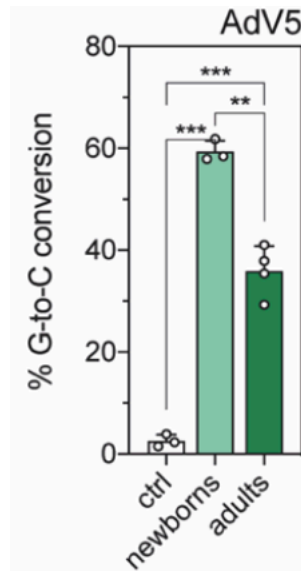
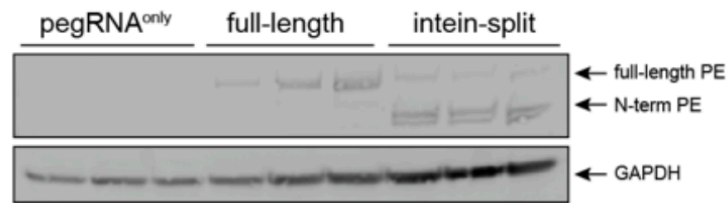




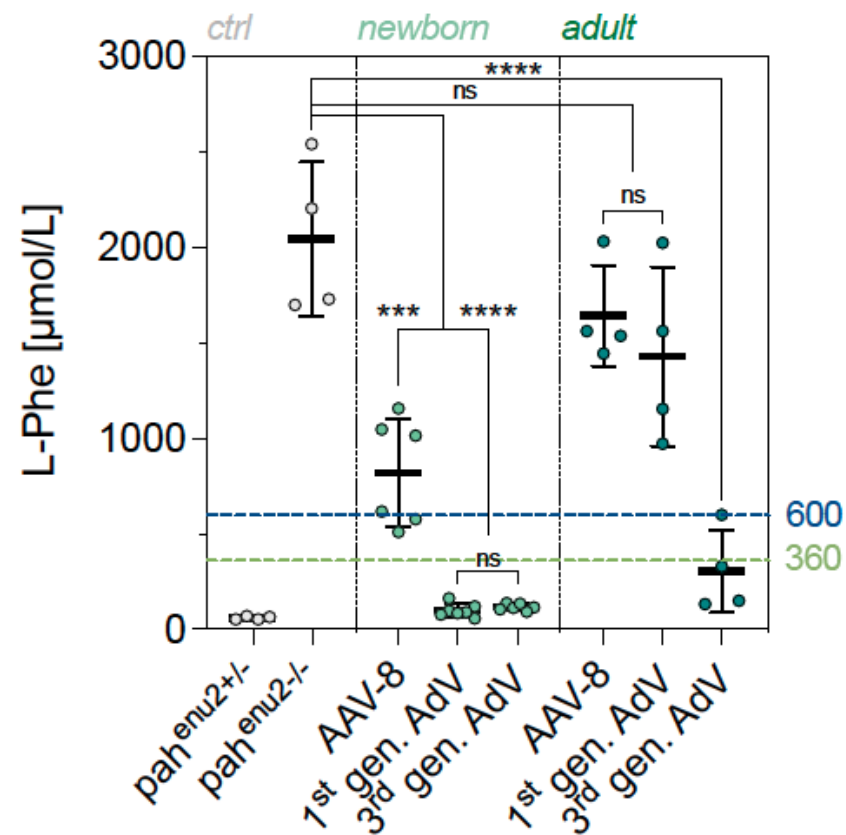
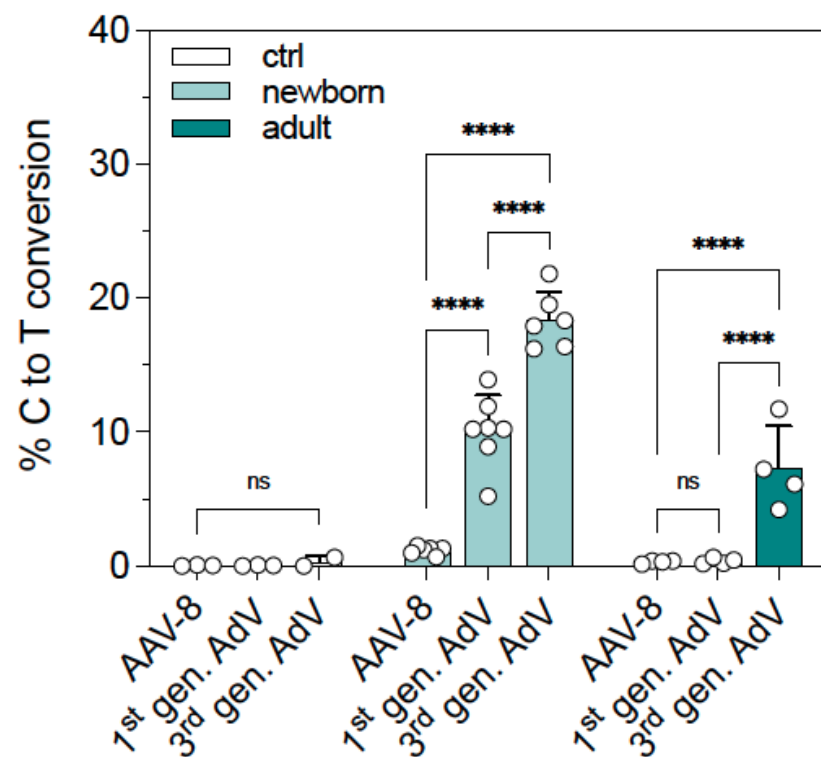
# Installing a G-to-C edit in *Dnmt1* via AdV5-mediated prime editing



## PE expression

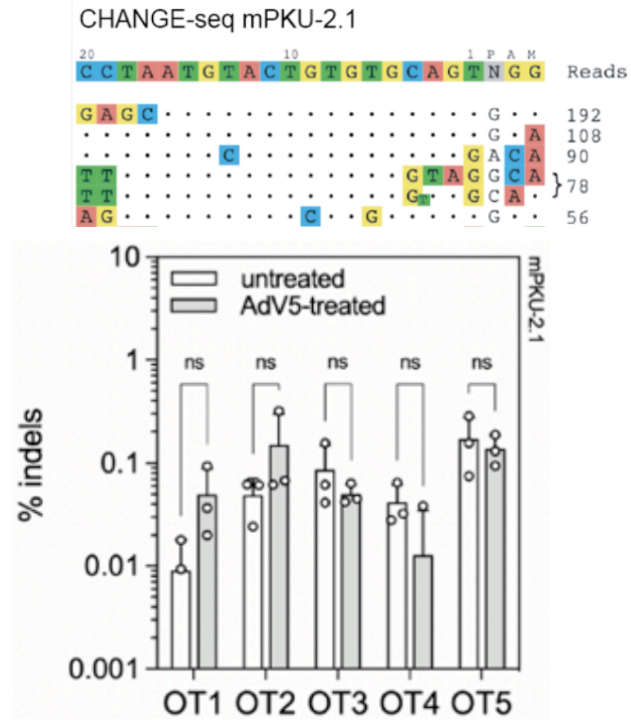


# Correction of the *Pah<sup>enu</sup>* mutation via AdV5-mediated prime editing

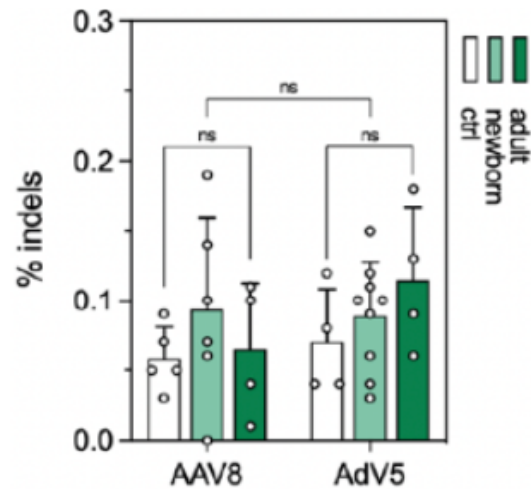


# *In vivo* prime editing is highly precise

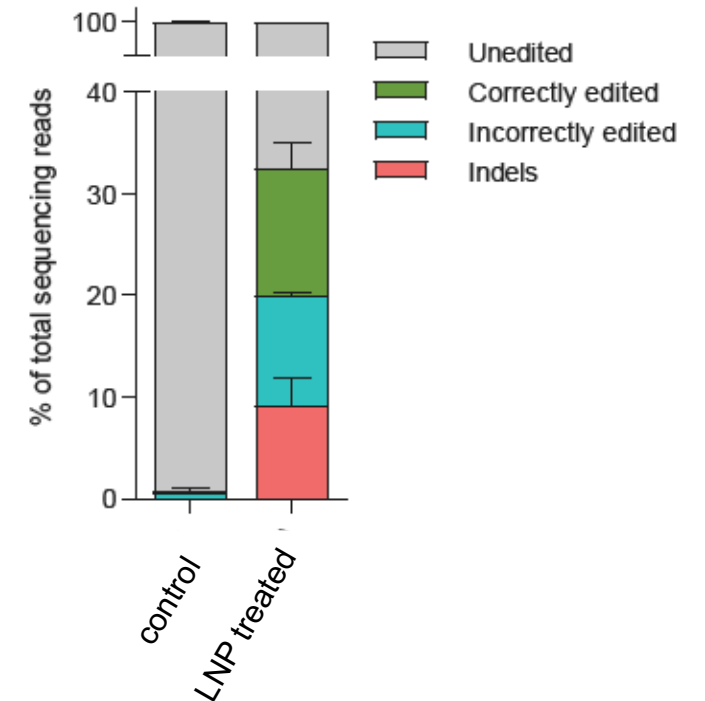
Prime editing off targets



Prime editing bystanders



Cytidine base editing bystanders



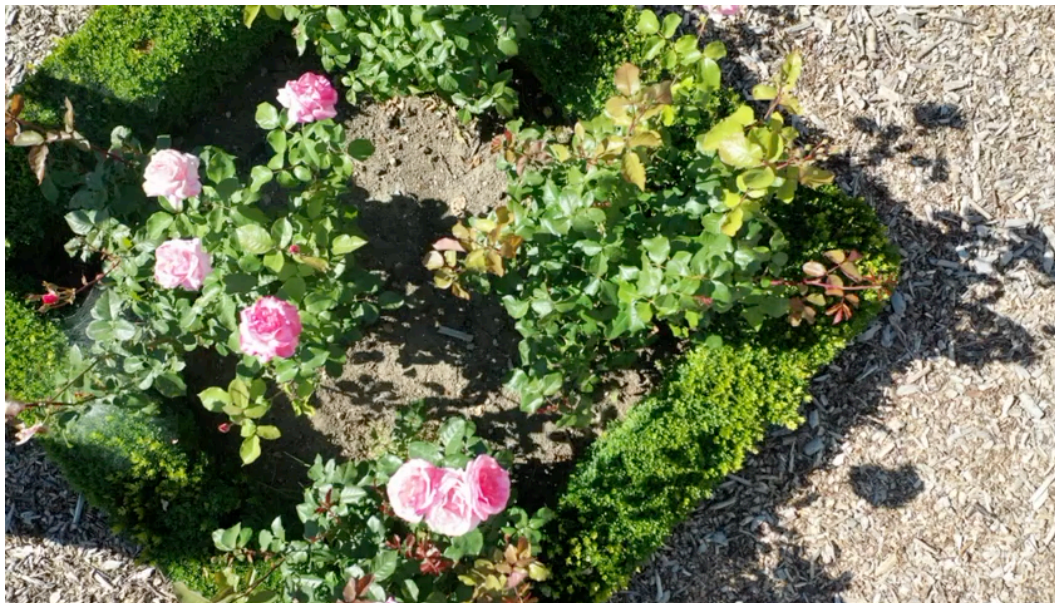


[schwanklab.org](http://schwanklab.org)  
Translational Genome Editing



# Acknowledgements

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Tanja Rothgangl  
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Sharan Janjuha  
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## **FGCZ**

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## **UPenn**

Drew Weissmann, Norbert Pardi

## **UBC**

Dominik Witzigmann

## **UZH**

Michael Krauthammer, Ahmed Allam

