



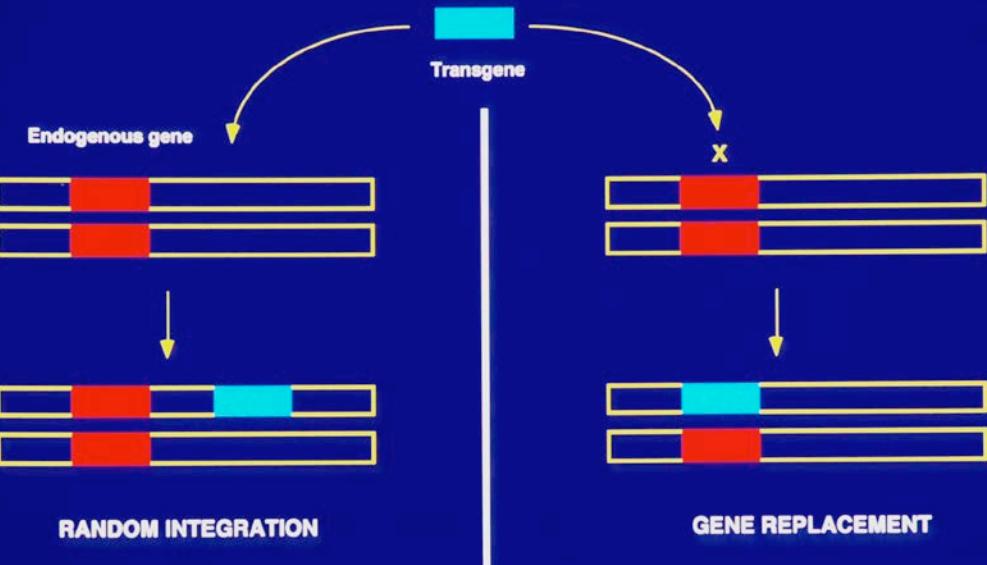
Genome editing with CRISPR: Innovative approaches for gene therapy

Lluís Montoliu

CNB-CSIC, Madrid, Spain

The lasting challenge in transgenesis and in gene therapy

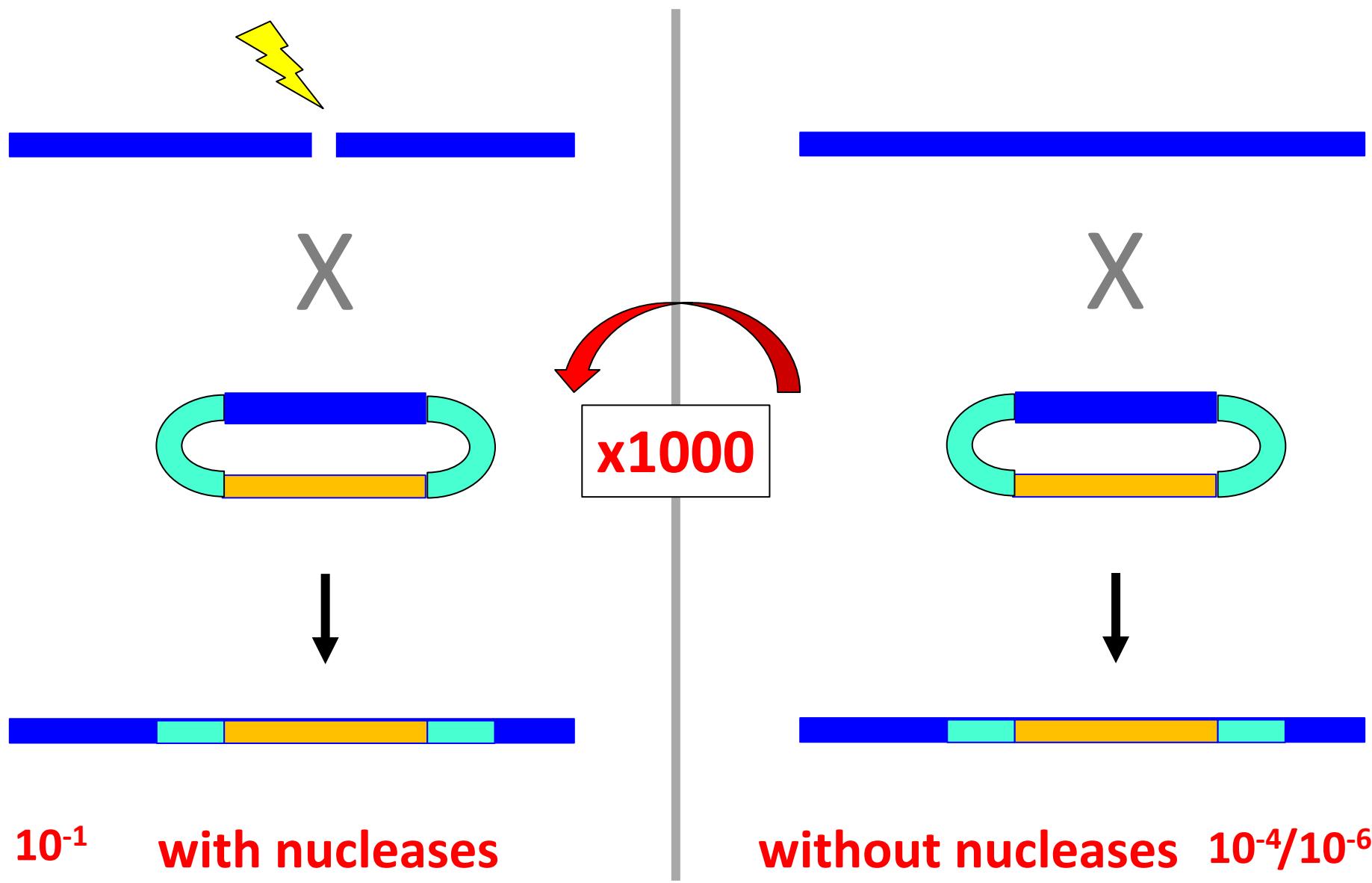
RANDOM INTEGRATION VERSUS HOMOLOGOUS RECOMBINATION IN TRANSGENIC MICE



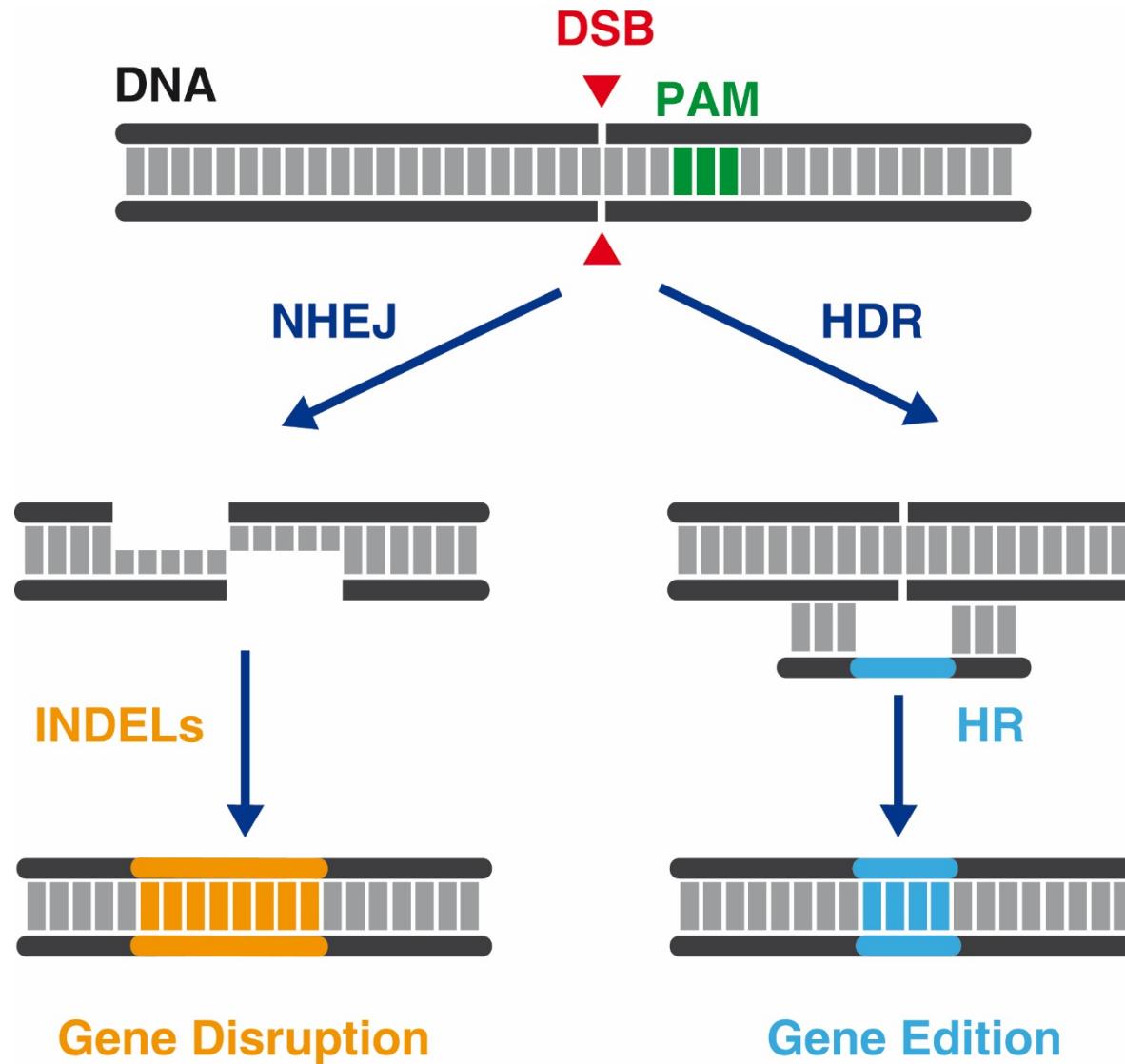
Slides from 1991

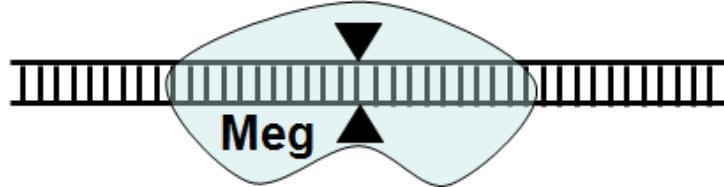
Random versus Targeted genetic modification

Homologous Recombination and Nucleases



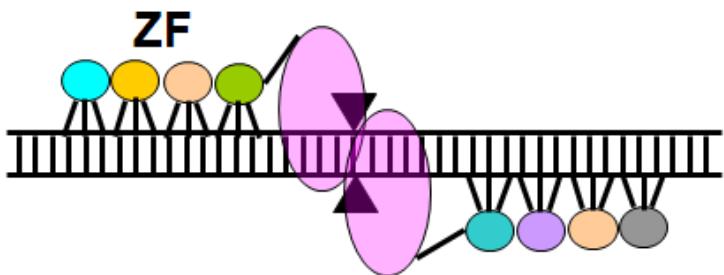
Fixing the DSB: NHEJ vs HDR





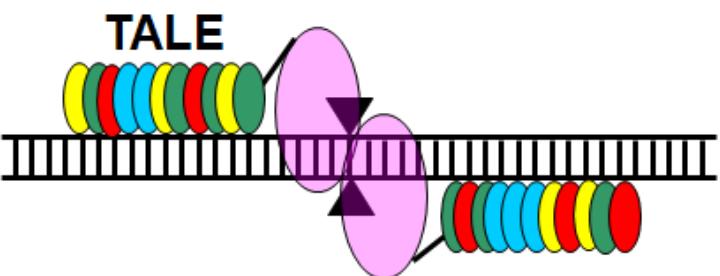
Meganuclease

20-40 bp/Enzyme



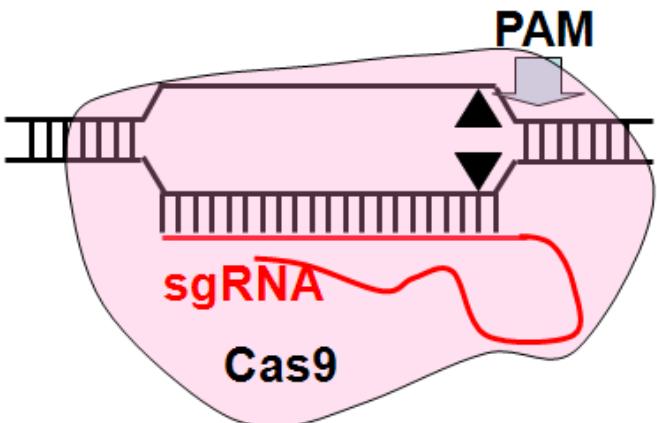
ZFN

3 bp/Finger



TALEN

1 bp/Module



CRISPR-Cas

1 bp/Base

Scientists make first attempt to permanently change a person's DNA to cure a disease

A risky new treatment is being trialled in the US to reverse the effects of an incurable genetic disorder

Josh Gabbatiss | 12 hours ago | [Comment](#)

Associated Press, 15 Nov 2017



Me gus Click to follow
The Independent Online

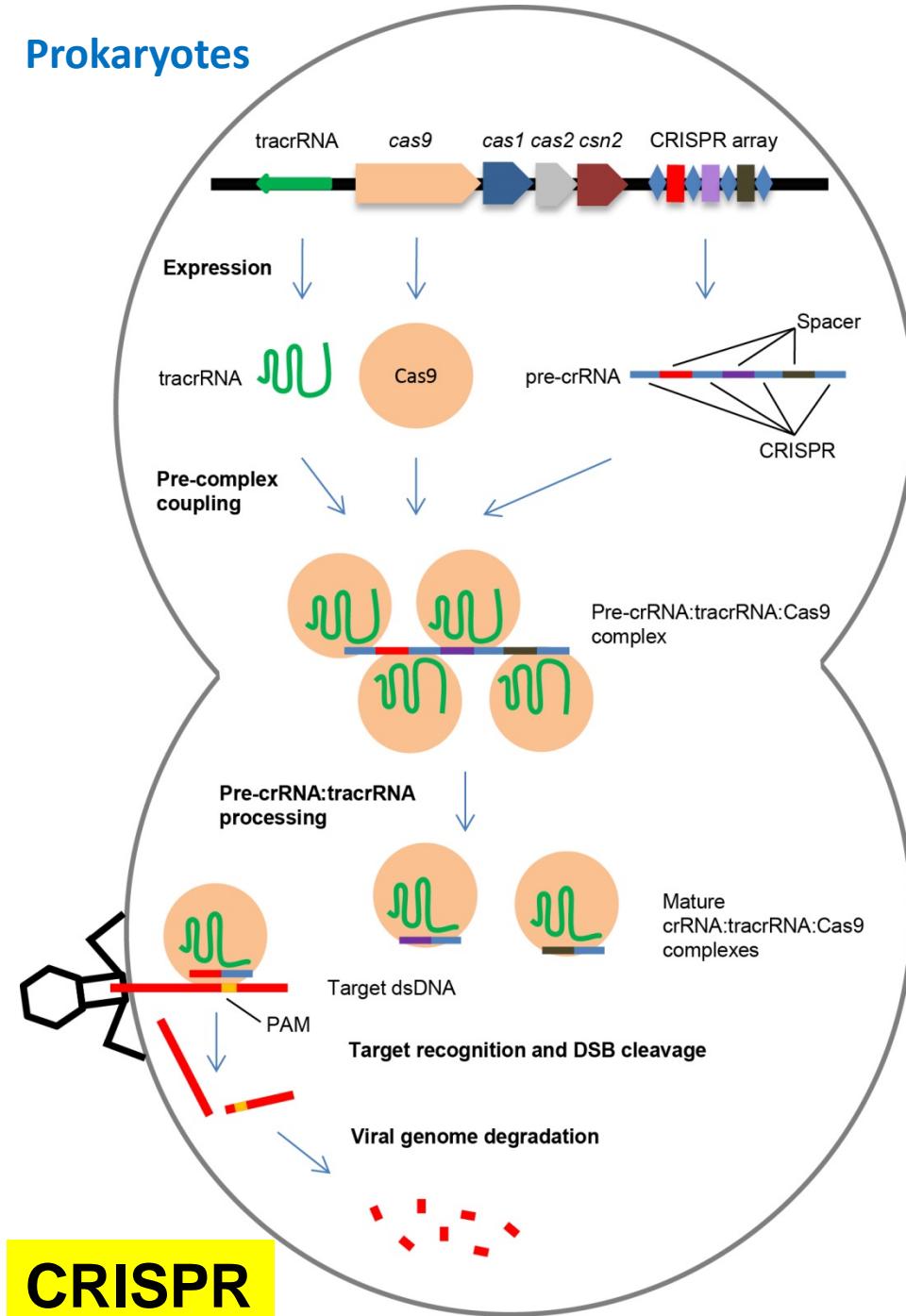


Brian Madeux, 44, looks up at nurse practitioner Jacqueline Madde while receiving the first human gene editing therapy at the UCSF Benioff Children's Hospital in Oakland, California ASSOCIATED PRESS

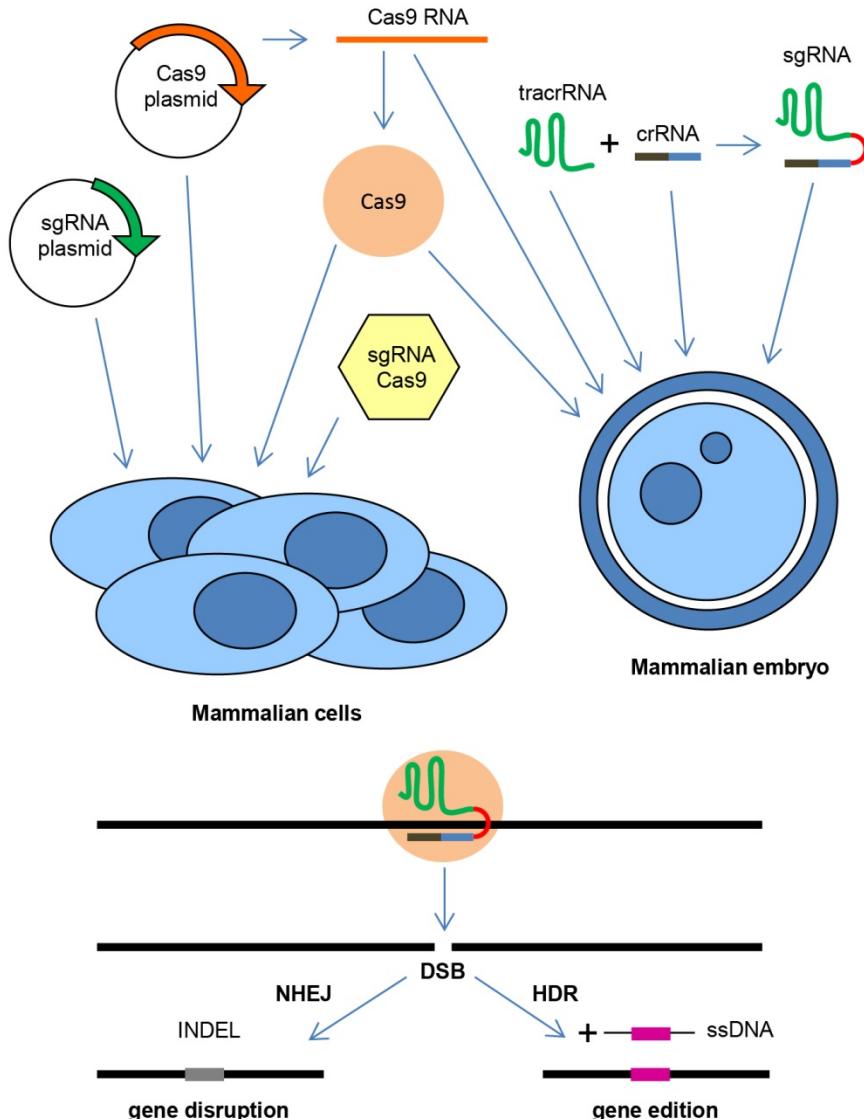
- UCSF Benioff Children's Hospital in Oakland, California
- IV injection of viral particles with ZFNs
- Approved by NIH
- Sangamo
- Hunter's syndrome (I2S gene)
- Mucopolysaccharidosis II (MPS II)
- Lysosomal storage disease
- Injected last Monday **13 Nov 2017**

First genome editing (driven by ZFN) somatic gene therapy in a patient IN VIVO

Prokaryotes



Eukaryotes



CRISPR



Francisco Juan Martínez Mojica

UA

The CRISPR-Cas pioneers



Francisco Mojica
University of Alicante, Spain



Rodolphe Barrangou
North Carolina State Univ, Raleigh, USA



Philippe Horvath
DuPont Nutrition and Health, France



Luciano Marraffini
The Rockefeller Univ, New York, USA



John van der Oost
Wageningen University, The Netherlands



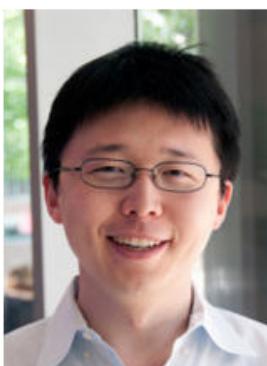
Emmanuelle Charpentier
MPI for Infect. Biol., Berlin, Germany



Jennifer Doudna
Univ California Berkeley, CA, USA



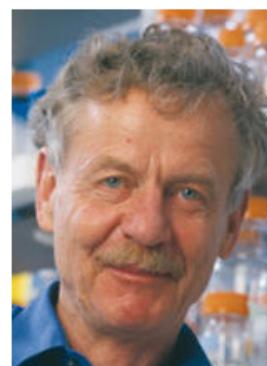
Virginijus Siksnys
Vilnius University, Lithuania



Feng Zhang
BROAD-MIT, Cambridge, MA, USA



George Church
Harvard Med School, Boston, MA, USA



Rudolf Jaenisch
Whitehead Inst, Cambridge, MA, USA



J. Keith Joung
Mass Gen Hosp, Charlestown, MA, USA

The CRISPR-Cas System: targeting nucleases to specific DNA sequences a binary system: Cas9 protein and sgRNA

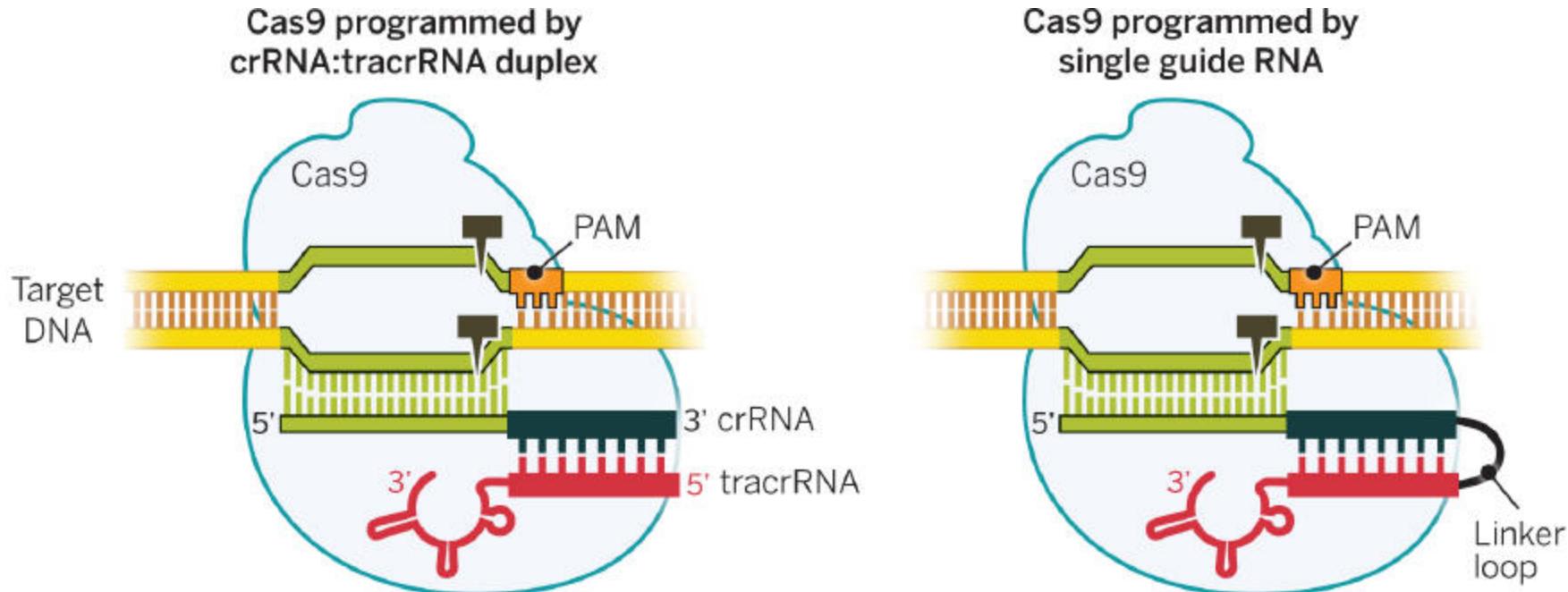
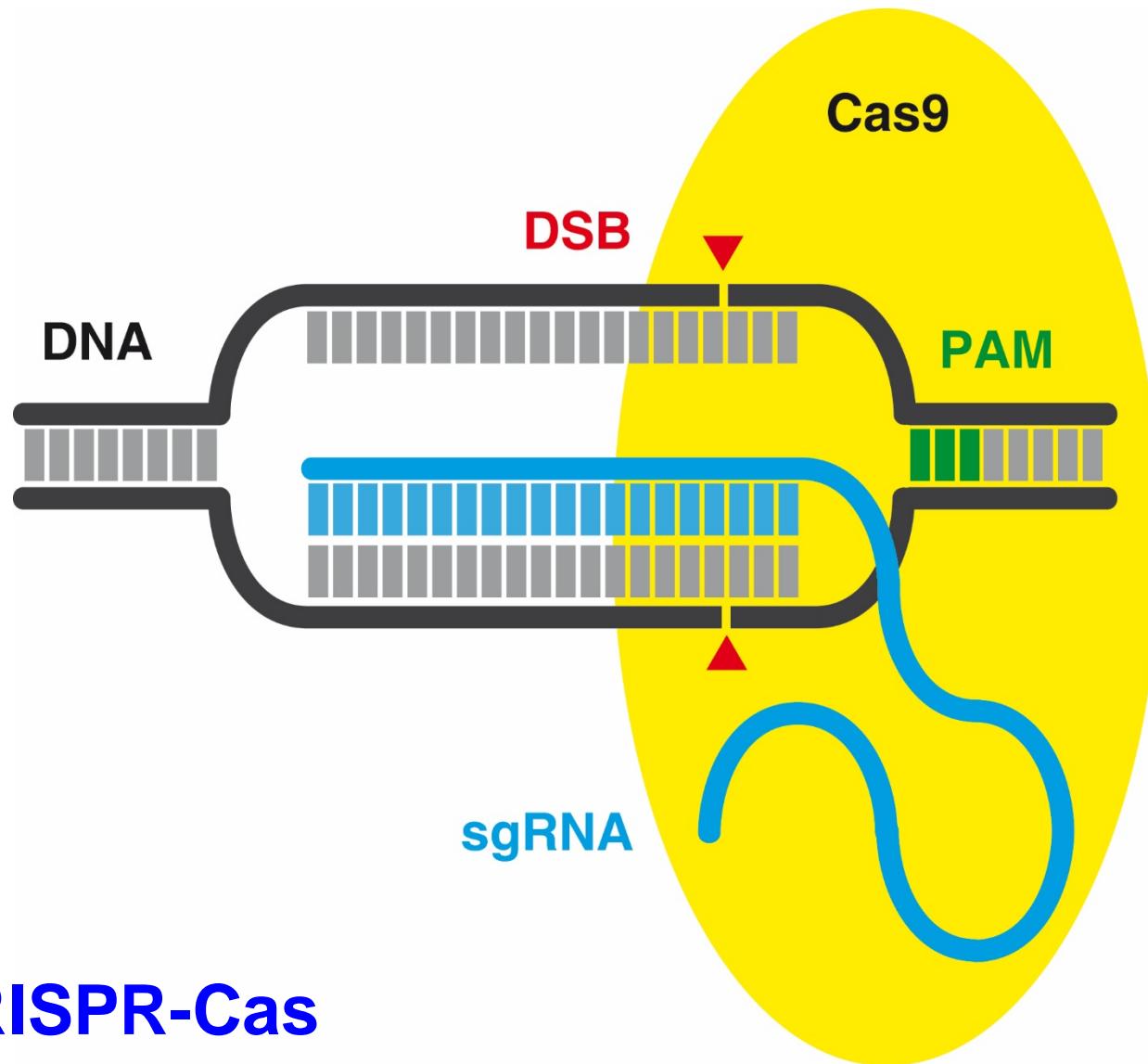


Fig. 3. Evolution and structure of Cas9. The structure of *S. pyogenes* Cas9 in the unliganded and RNA-DNA-bound forms [from (77, 81)].



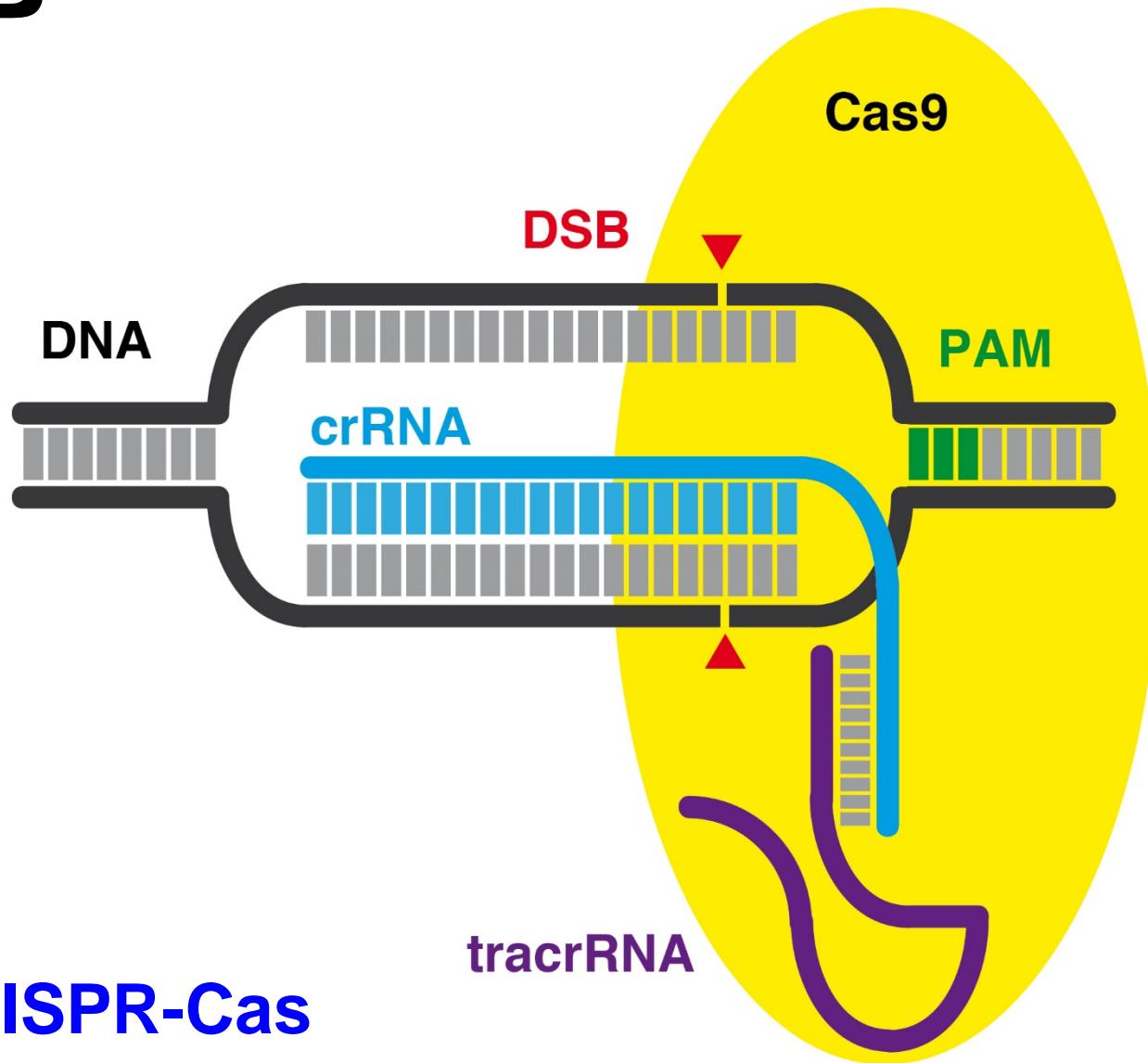
Jennifer Doudna
Emmanuelle Charpentier

Doudna & Charpentier (2014) Science

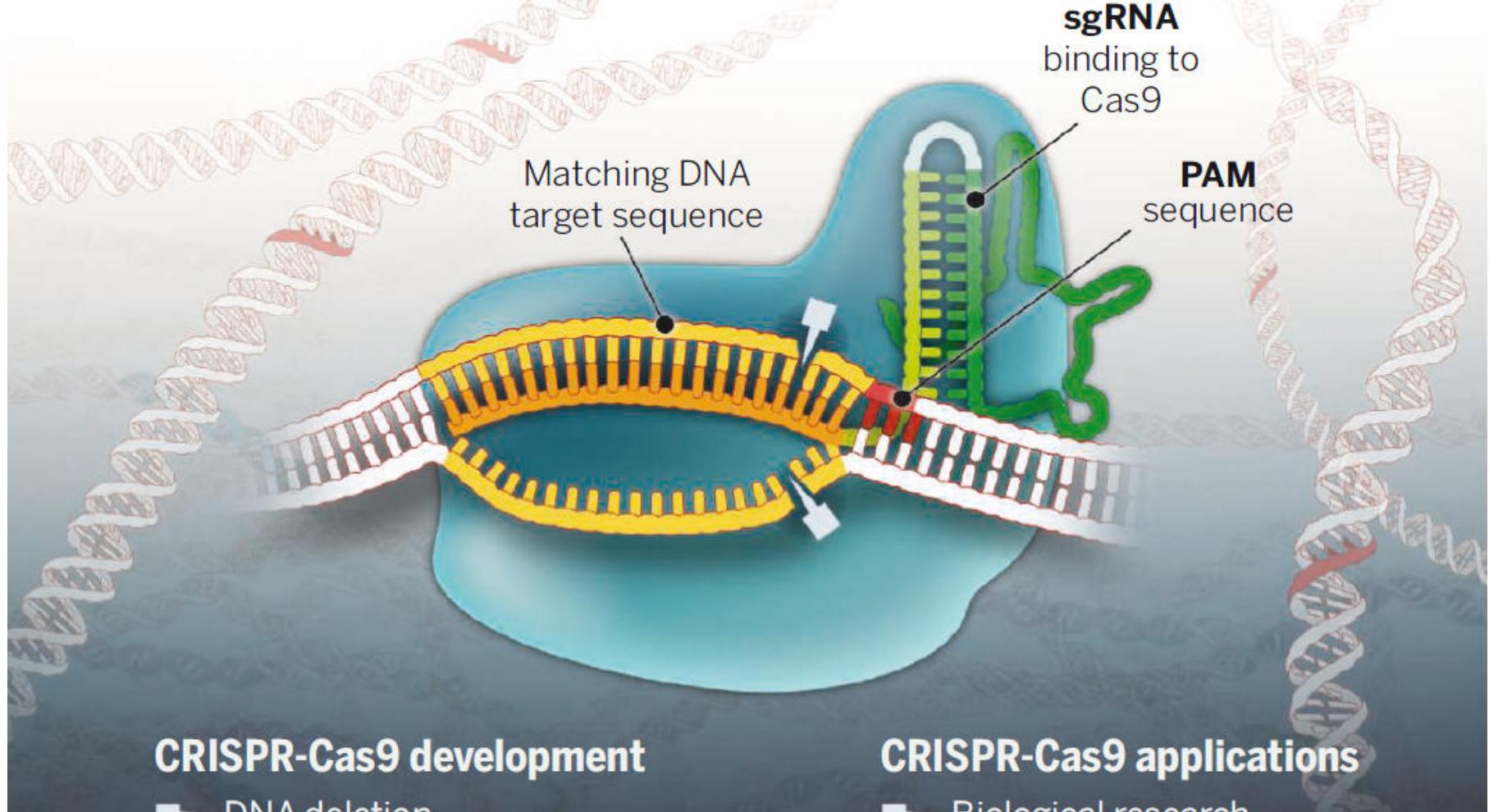


The CRISPR-Cas system

RNP



The CRISPR-Cas
system



CRISPR-Cas9 development

- ▶ DNA deletion
- ▶ DNA insertion
- ▶ DNA replacement
- ▶ DNA modification
- ▶ DNA labeling
- ▶ Transcription modulation
- ▶ RNA targeting
- ▶ ...

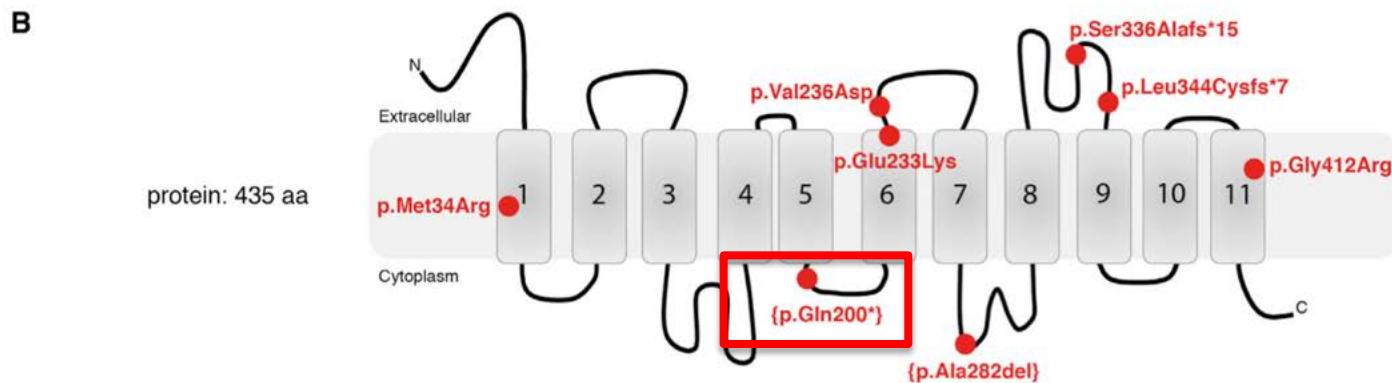
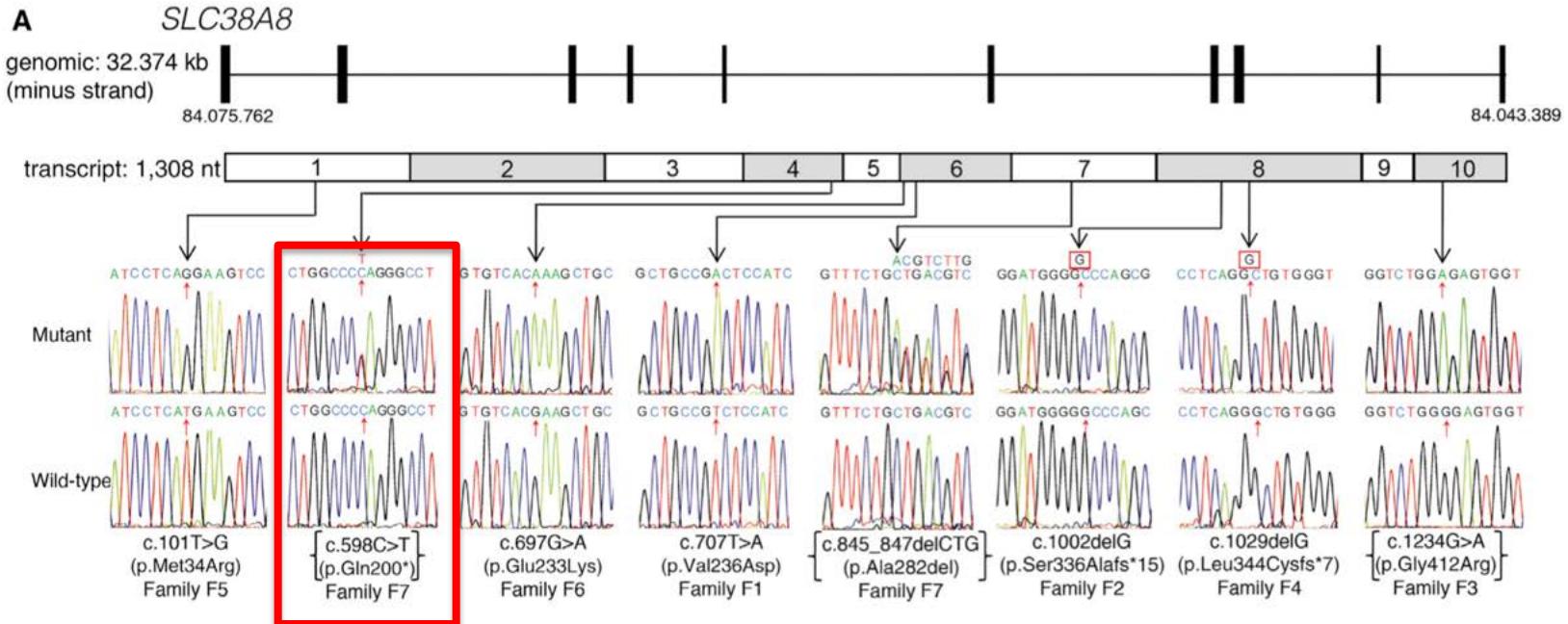
CRISPR-Cas9 applications

- ▶ Biological research
- ▶ Research and development
- ▶ Human medicine
- ▶ Biotechnology
- ▶ Agriculture
- ▶ ...

Disrupting a gene: KO



- The easiest approach
- almost trivial nowadays
- Many similar alleles will be generated
- Efficient protocol



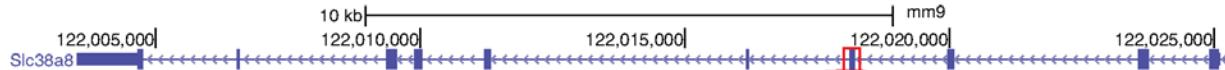
Mouse model of FHONDA

We set to reproduce the Gln200* in mice using CRISPR-Cas9

Mouse model of FHONDA (*Slc38a8*)

Prediction of protein sequence after mutagenesis: 16 different proteins

Scale
chr8:



Val Ile Thr Val Gln Tyr Tyr
GTC • ATC • ACG • GTG • CAA • TAC • TAC

exon 3 exon 4

ALQKYTSILGTLAACYLALVITVQYYLW
ALQKYTSILGTLAACYLALVITVQYY--
ALQKYTSILGTLAACYLALVITVQYYLW
ALQKYTSILGTLAACYLALVITVQYYLW
ALQKYTS**NPRYFAEPVSLDLCV***
ALQKYTSILGTLAACYLALVITVQYYLW
ALQKYTSILGTLAACYLALVITVQYYL**I**
ALQKYTSILGTLAACYLALVITVQYYLW
ALQKYTS**PGPHTPARSFAEPVSLDLCV***
ALQKYTSILGTLAACYLALVITVQYYLW
ALQKYTS**RASYASPVLC***

ALQKYTSILGTLAACYLALVITVQYYLWPRASYASPVLC*****

ALQKYTSILGTLAACYLALVITVQYYLW*

ALQKYTSILGTLAACYLALVITVQYYLRASYASPVLC*****

ALQKYTSILGTLAACYLALVITVQYYLRPHTPARSFAEPVSLDLCV*****

ALQKYTSILGTLAACYLVLVISVQYYLWPTPCRFFELITDYPYFNLLFLALKLGPOQLIHQPGPLLSP**** 91

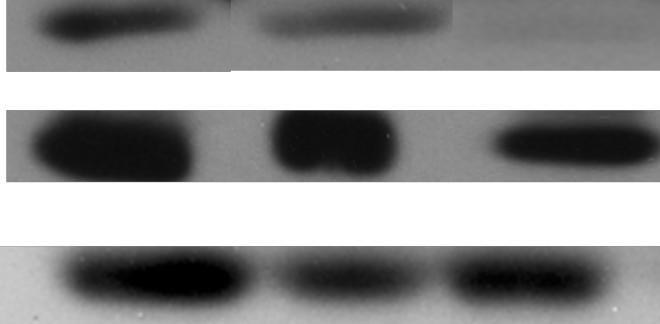
WB Slc38a8 Line # 78

Eye

WT

Hetero

Homo



Ab-Slc38a8 C-end

β- Actin

Ab-Slc38a8 central

75; 80; 83; 87; 88

76; 79; 82; 93; 94

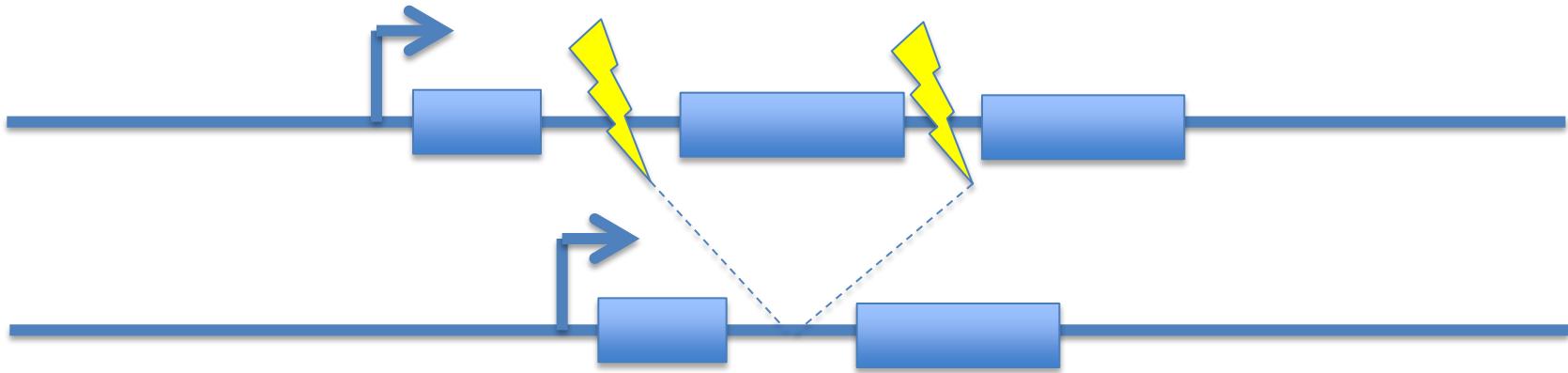
78

79

87

91

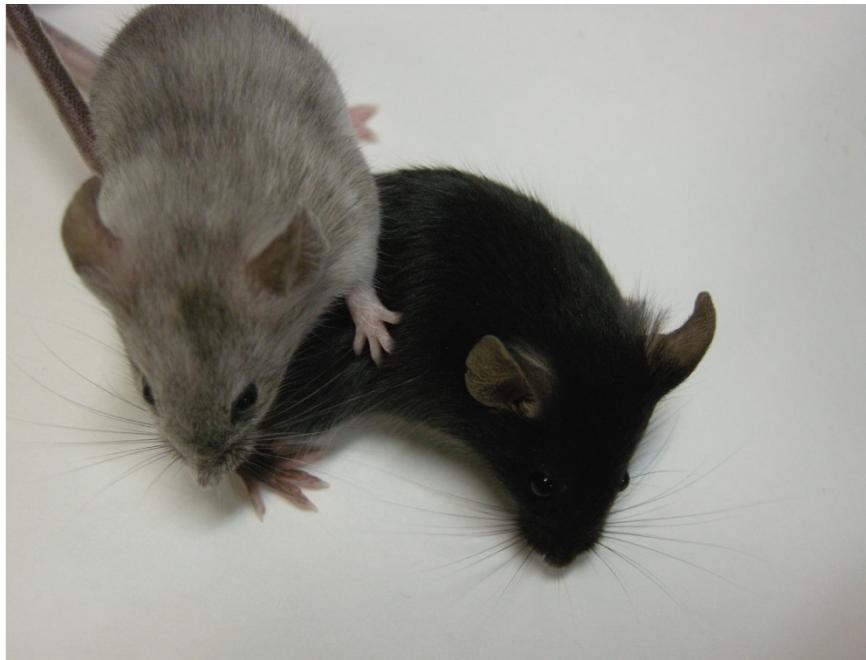
Deletions



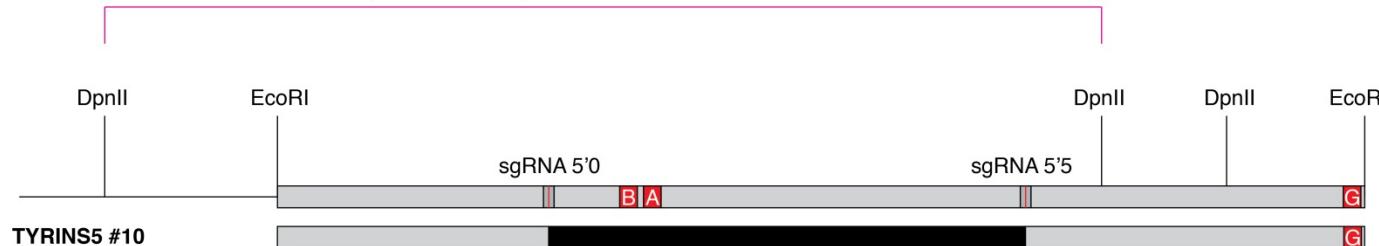
- Relatively straight forward, many alleles will be generated
- INDELs at both targeting sites will be **also** generated
- Consider **inversions** can also be generated
- Efficient protocol

Deleting *Tyr* 5' boundary with CRISPRs *in vivo*

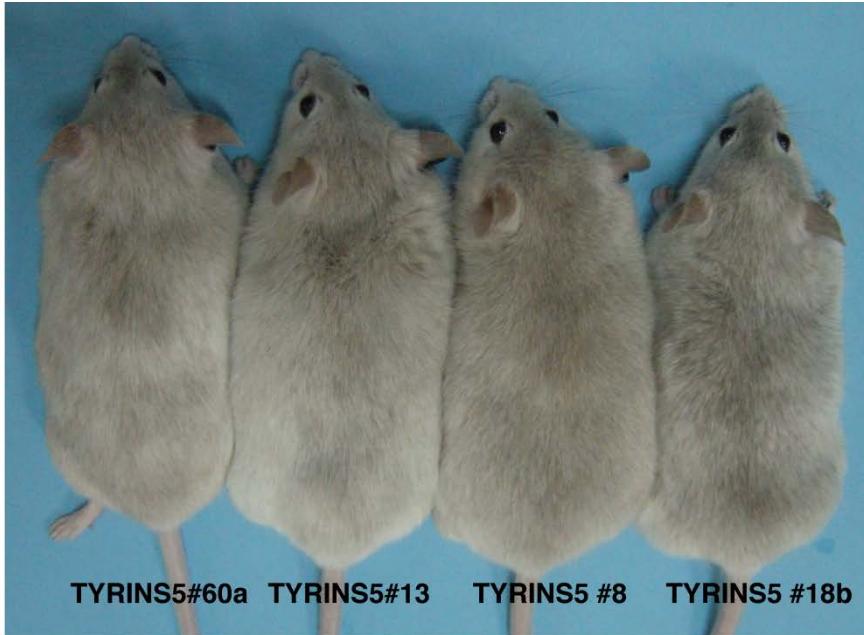
Founder mosaic mice with clear coat colour pigmentation phenotype carrying BIALLELIC deletion of *Tyr* 5' boundary



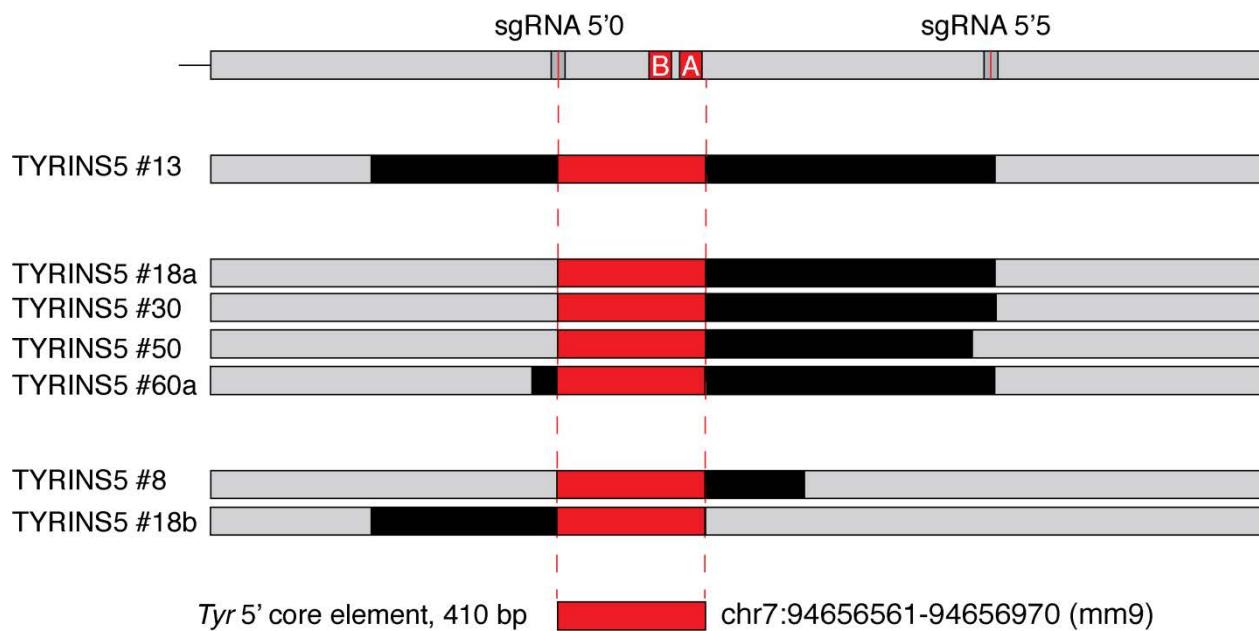
DpnII fragment interacting with *Tyr* promoter in the 3C assay



reference: CAAGAATTAAGTGTGACAGTGCAAGATAAACAGGAAAATAA.....1170bp.....CTCTAGG**CCA**AAATTGCTAGTTTATCACTACAAAACCT
TYRINS5#18_1: CAAGAATTAAGTGTGACAGTGCAAGAT-----1170bp-----TTGCCTAGTTTATCACTACAAAACCT
TYRINS5#18_1: CAAGAATTAAGTGTGACAGTGCAAGAT-----1170bp-----TTGCCTAGTTTATCACTACAAAACCT

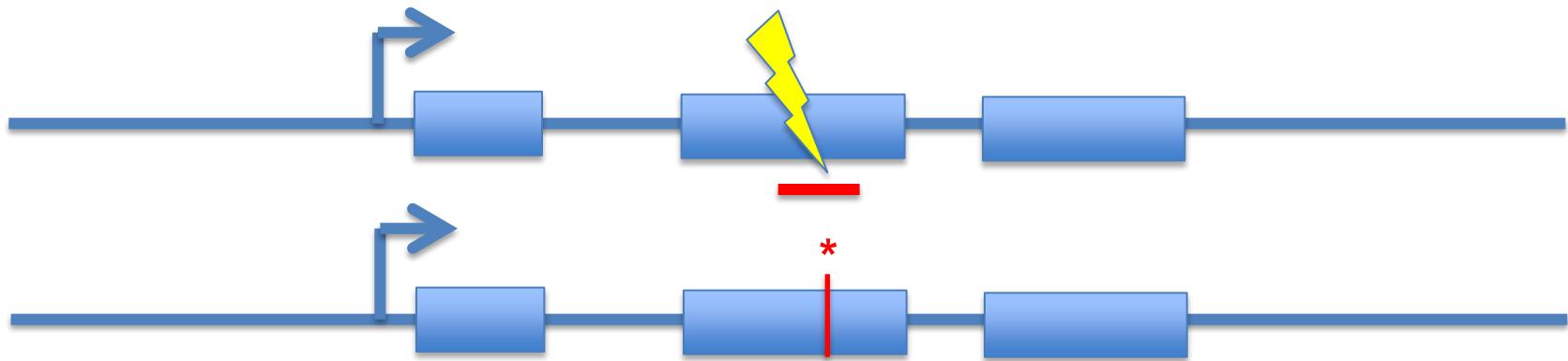


Comparing different *Tyr* 5' Boundary targeted alleles with similar phenotypes reveals the location of the functionally relevant endogenous regulatory DNA sequences



Genetic analysis now possible in mice!

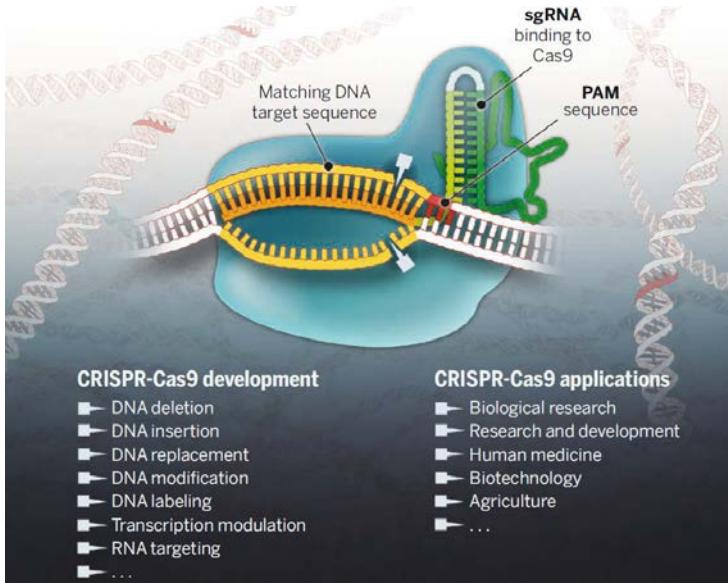
Point mutations



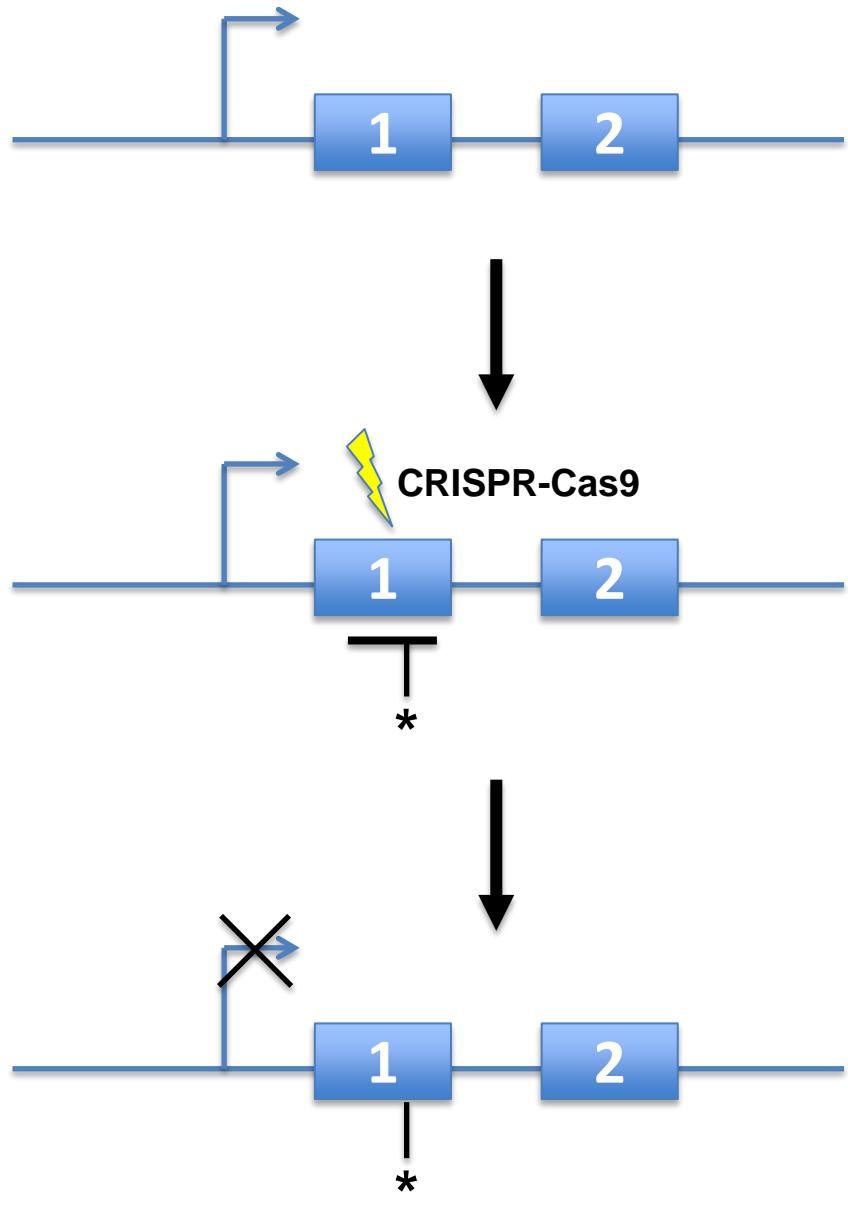
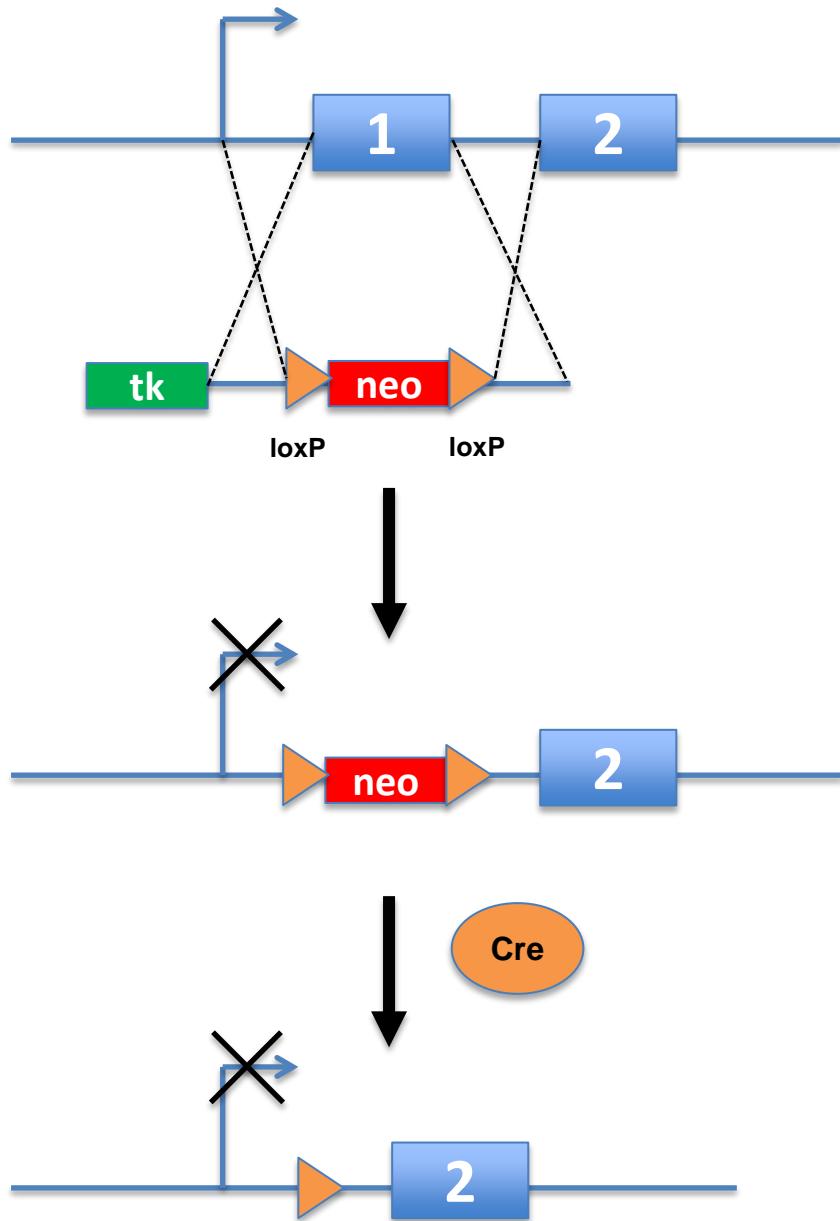
- Relatively straight forward, but can be challenging, many alleles will be generated
- INDELs will mostly be **also** generated
- Relatively doable protocol (however, if expected mutation not found, the number of embryos/animals to be used rapidly increases)
- Optimally: must have screening protocols in place (silent mutations/RFLPs/sequencing...)

AVATAR CRISPR mice

- Easier approach to reproduce human mutations in animal models



“Classical” versus CRISPR-mediated mutagenesis



New specific mouse models of OCA4



Patty & Bea

Patients with oculocutaneous
albinism type 4 (**OCA4**)

Mutation: c.986delC (**SLC45A2**)
homozygous

Celia de Lara



Gene edited Oca4 (*Slc45a2*) mice

OCA4 avatar mouse model

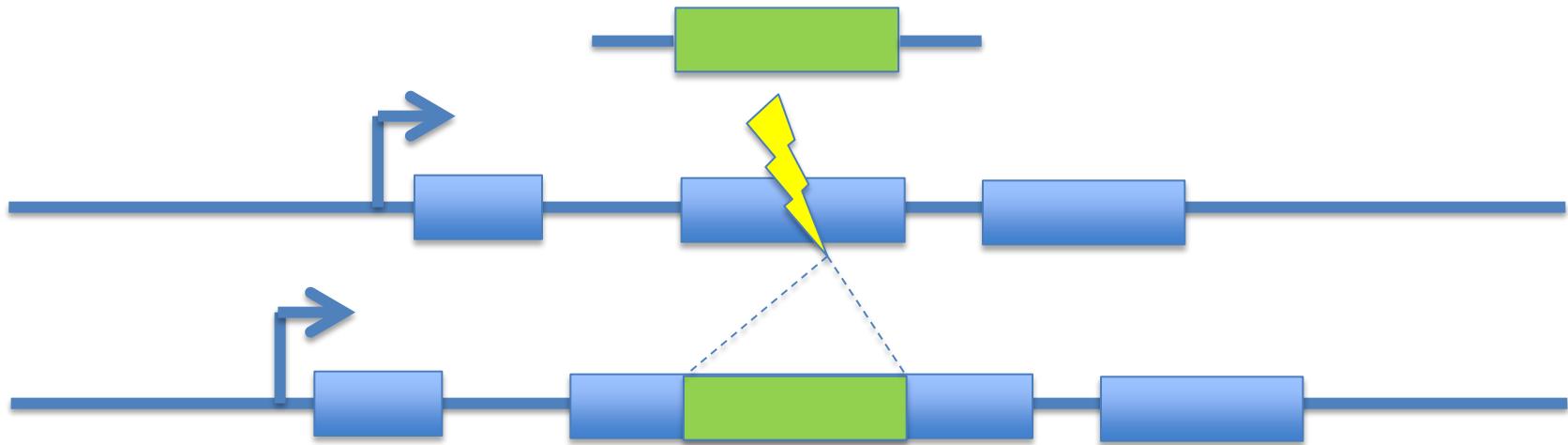
Mutation: c.986delC (*SLC45A2*)



Wt:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCACCTGATTGGATGGACTGCCTTCCTGTCAAACATG
Mu:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCACCTGAT <u>CGGATGGA</u> -TGCCCTCCTGTCAAACATG
63:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCACCTGATTGGATGGACTGCCTTCCTGTCAAACATG
64:	GTAAACATGCCTCCCATTATCGCTGCCTT-----CCTGTCAAACATG
65:	GTAAACATGCCTCCCATTATCGCTGCCTT-----CCTGTCAAACATG
66:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCACCTGATTGGATGGACTGCCTTCCTGTCAAACATG
67:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCAC <u>G</u> ---GATTGGATGGACTGCCTTCCTGTCAAACATG
68:	GTAAACATGCCTCCCATTATCGCTGCC <u>T</u> TGCCTCAGCCAC-TGATTGGATGGACTGCCTTCCTGTCAAACATG
69:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCACCT <u>T</u> GATTGGATGGACTGCCTTCCTGTCAAACATG
70:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCACCT <u>T</u> TGATTGGATGGACTGCCTTCCTGTCAAACATG
71:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCTCAGCCACCT <u>T</u> GATTGGATGGACTGCCTTCCTGTCAAACATG
R1:	GTAAACATGCCTCCCATTATCGCTGCCTTGCCT <u>AACATGCTCTTCCCATTATCGCTGCC</u> -----TTGGATGGACTGCCTTCCTGTCAAACATG

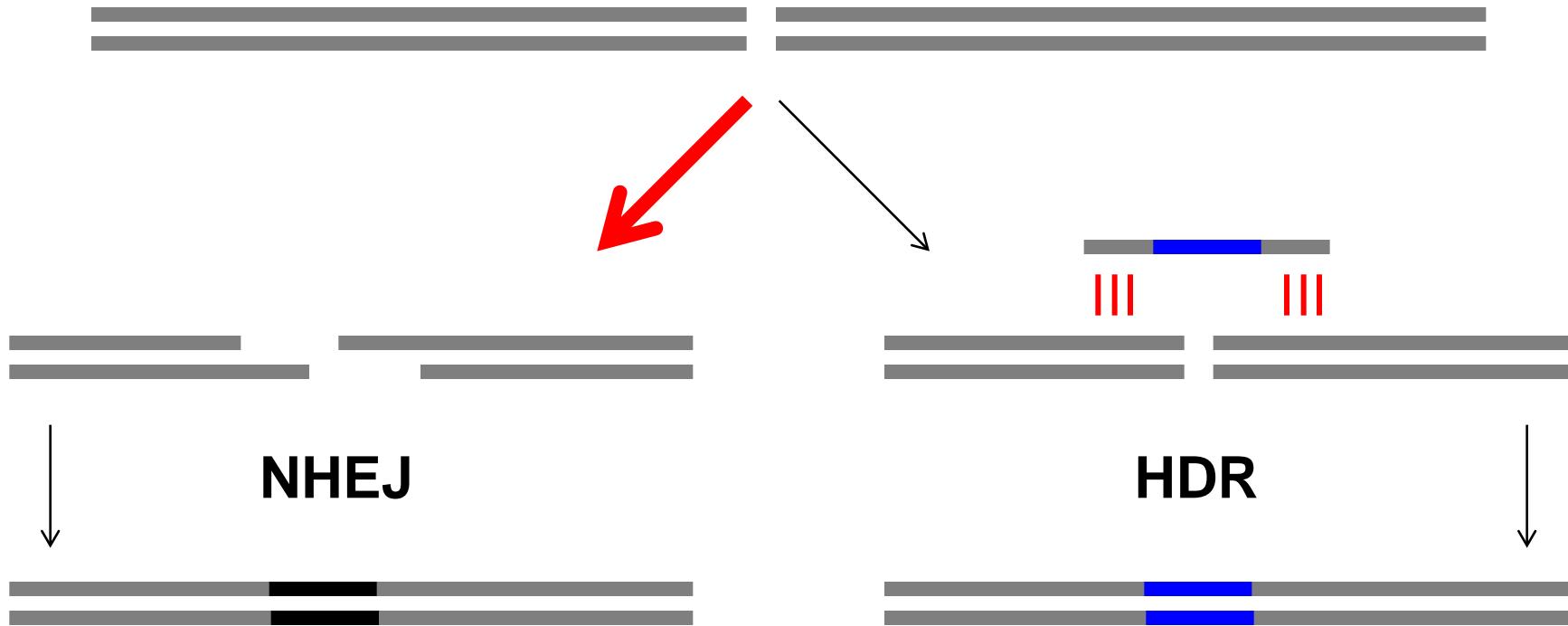


Knock-ins



- Most challenging approach, many protocols, not really optimized
- Useful for small (loxP) and larger (EGFP) insertions
- INDELs will mostly be **also** generated
- Relatively in-efficient approach
- Must have screening protocols in place
(PCR/RFLPs/sequencing...)

Improving Gene Edition



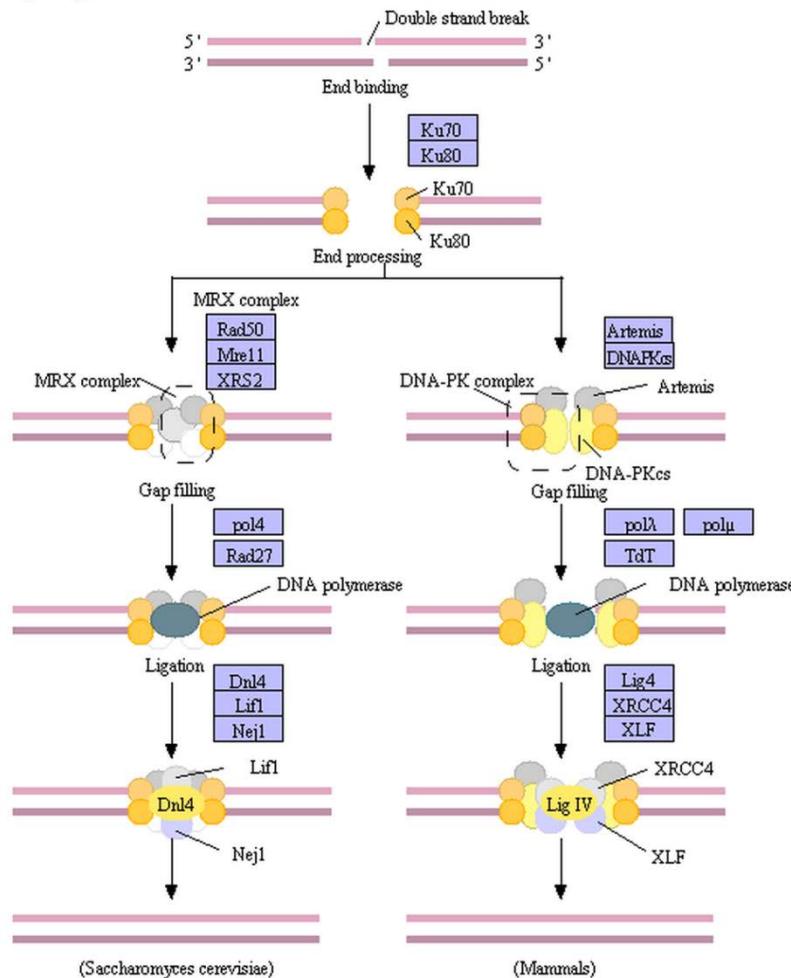
INDELs – Gene disruption

Gene repair / edit

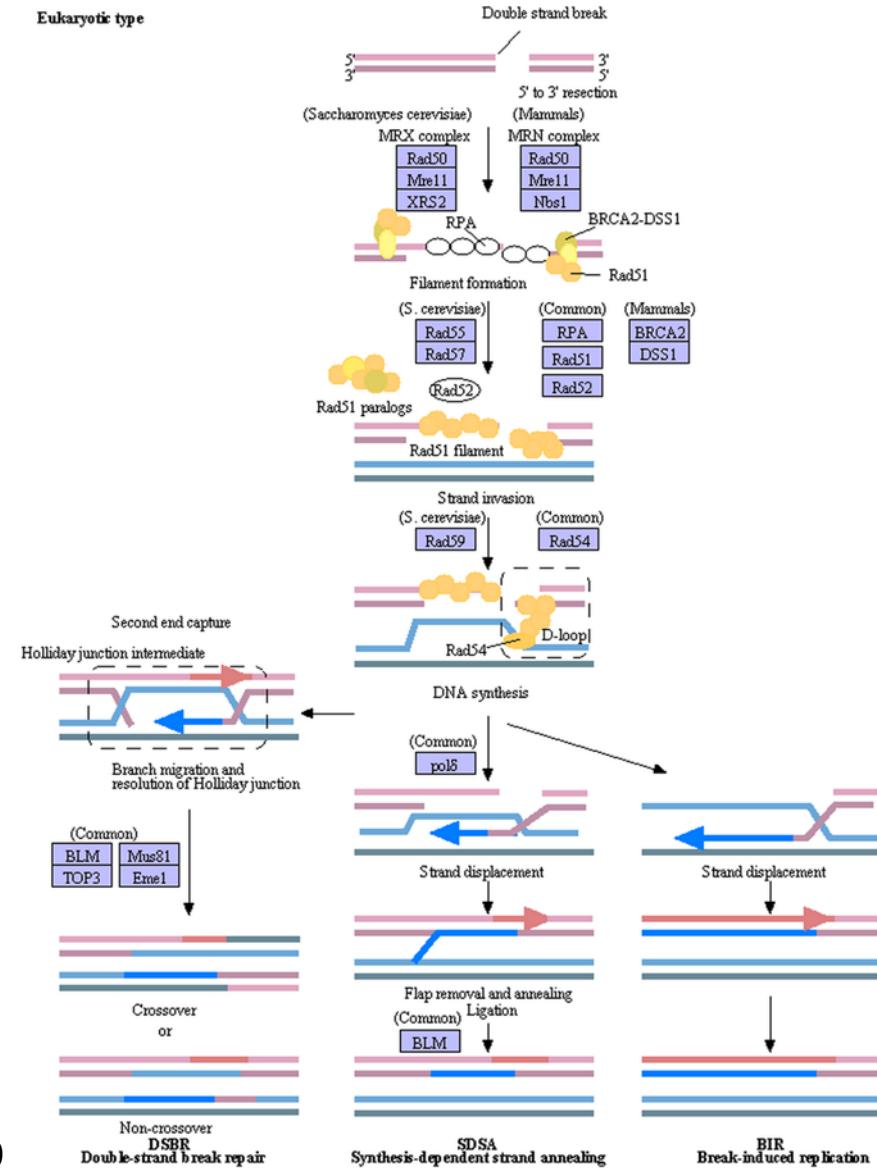
NHEJ

HDR

Eukaryotic type

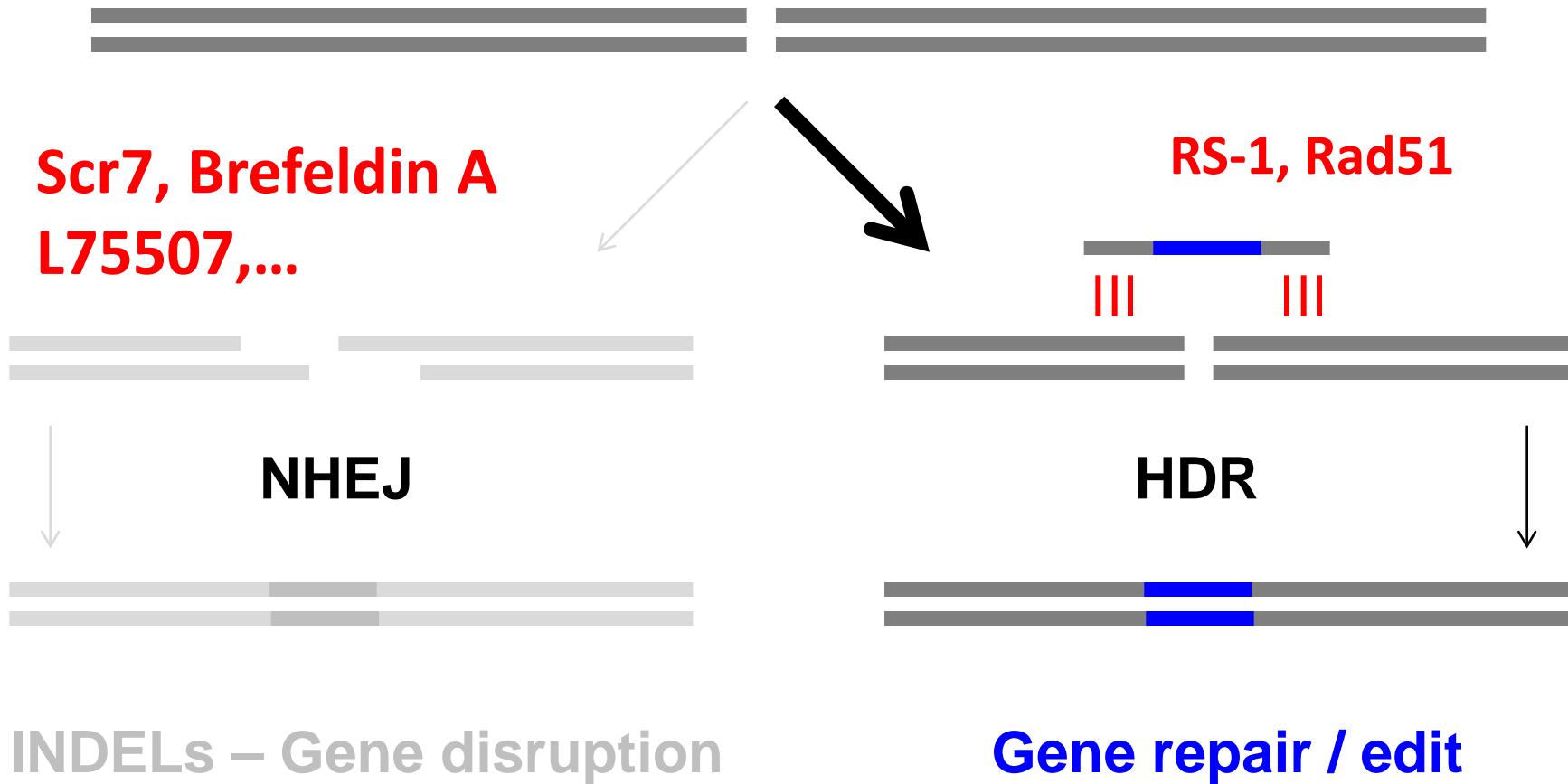


Eukaryotic type

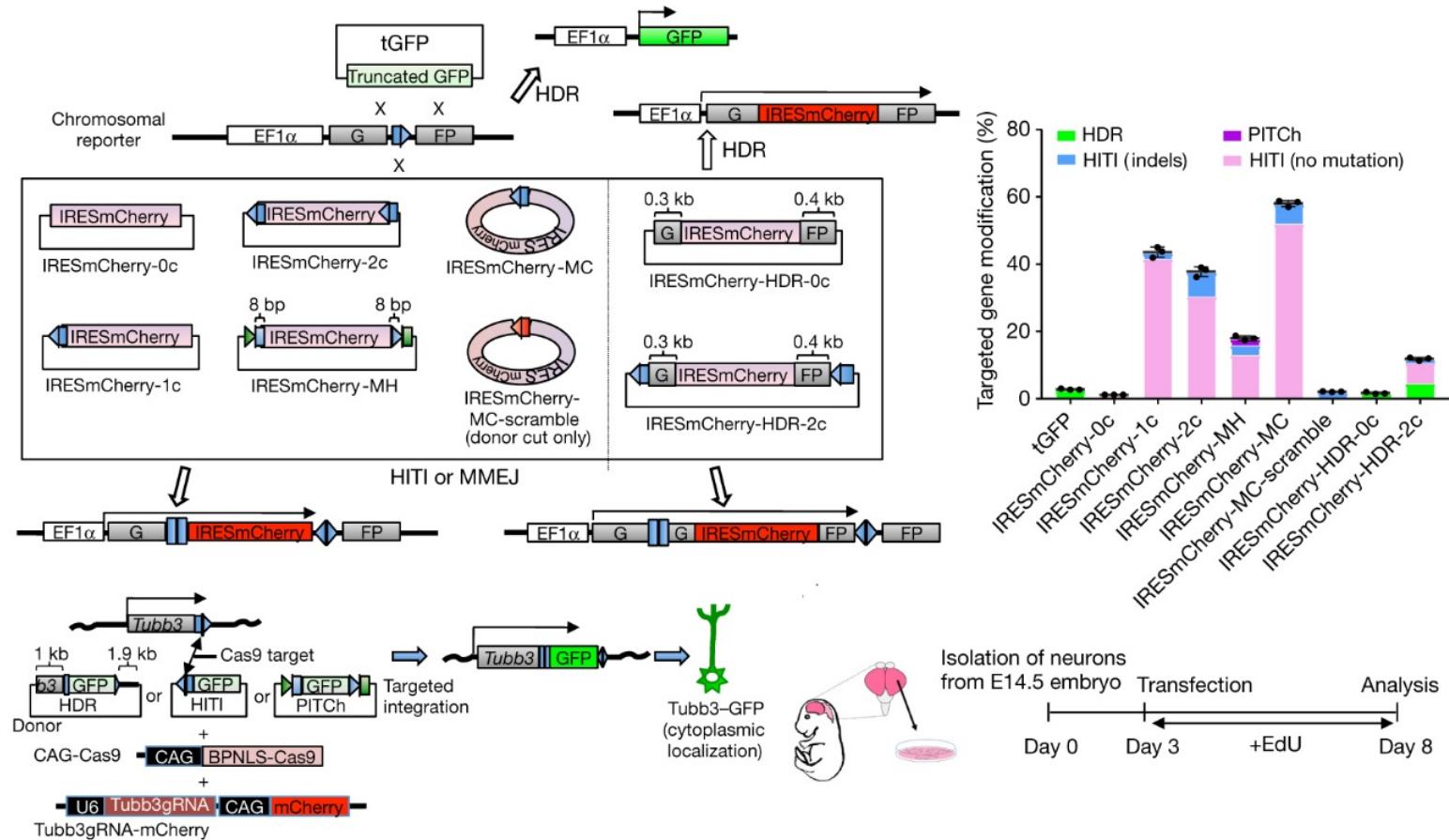


Using NHEJ inhibitors to boost HDR

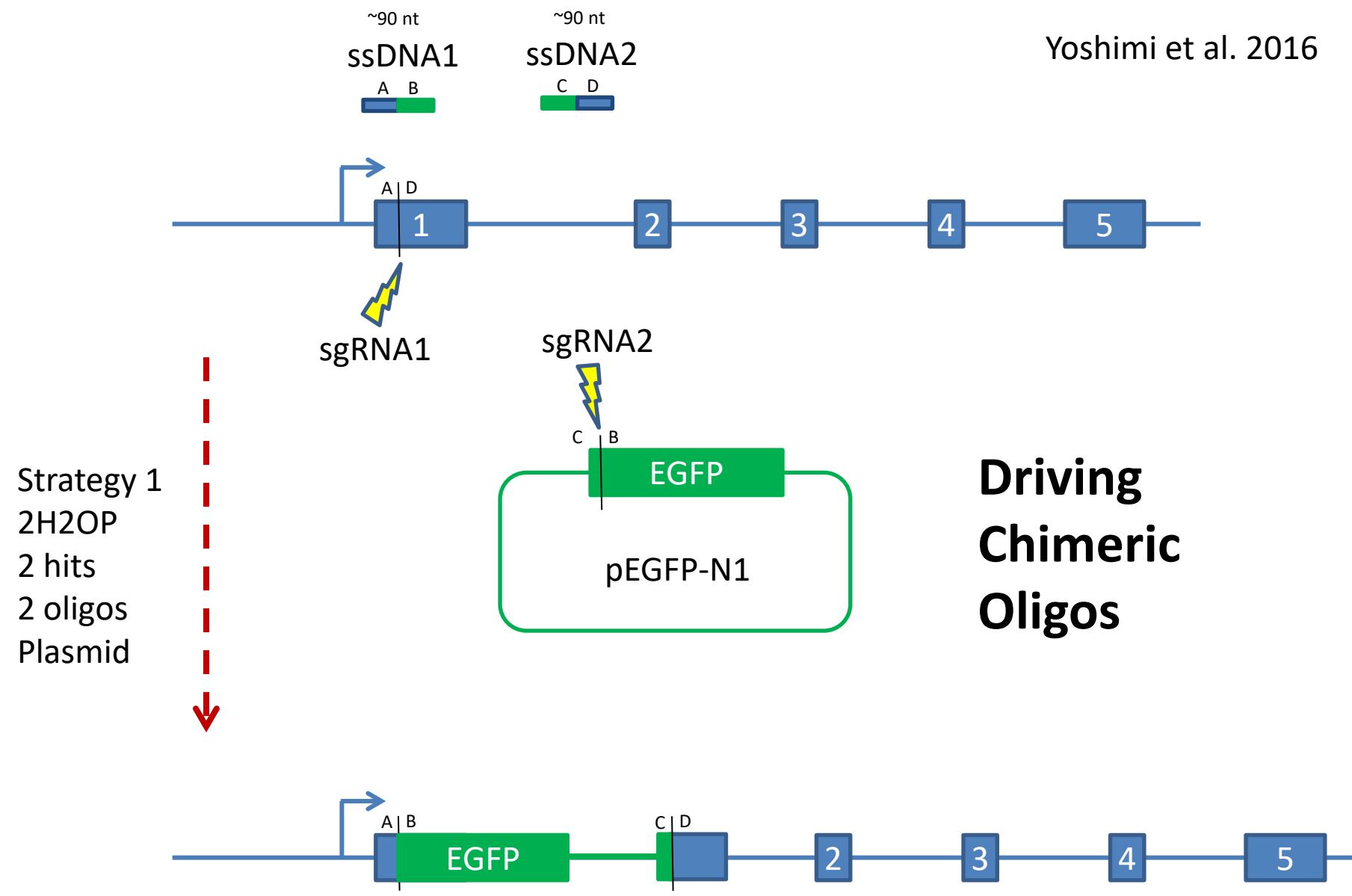
Yu et al. Cell Stem Cell Feb 2015; Maruyama et al. Nat Biotech March 2015;
Chu et al. Nat Biotech March 2015; Song et al. Nat. Comm. 2016



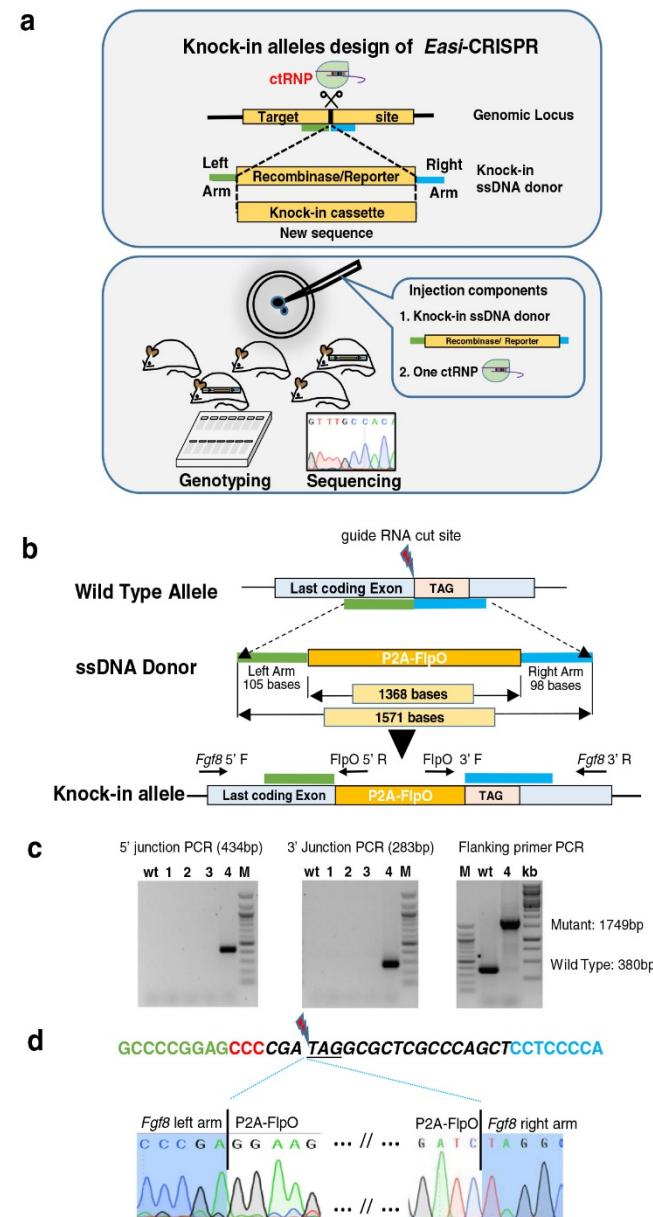
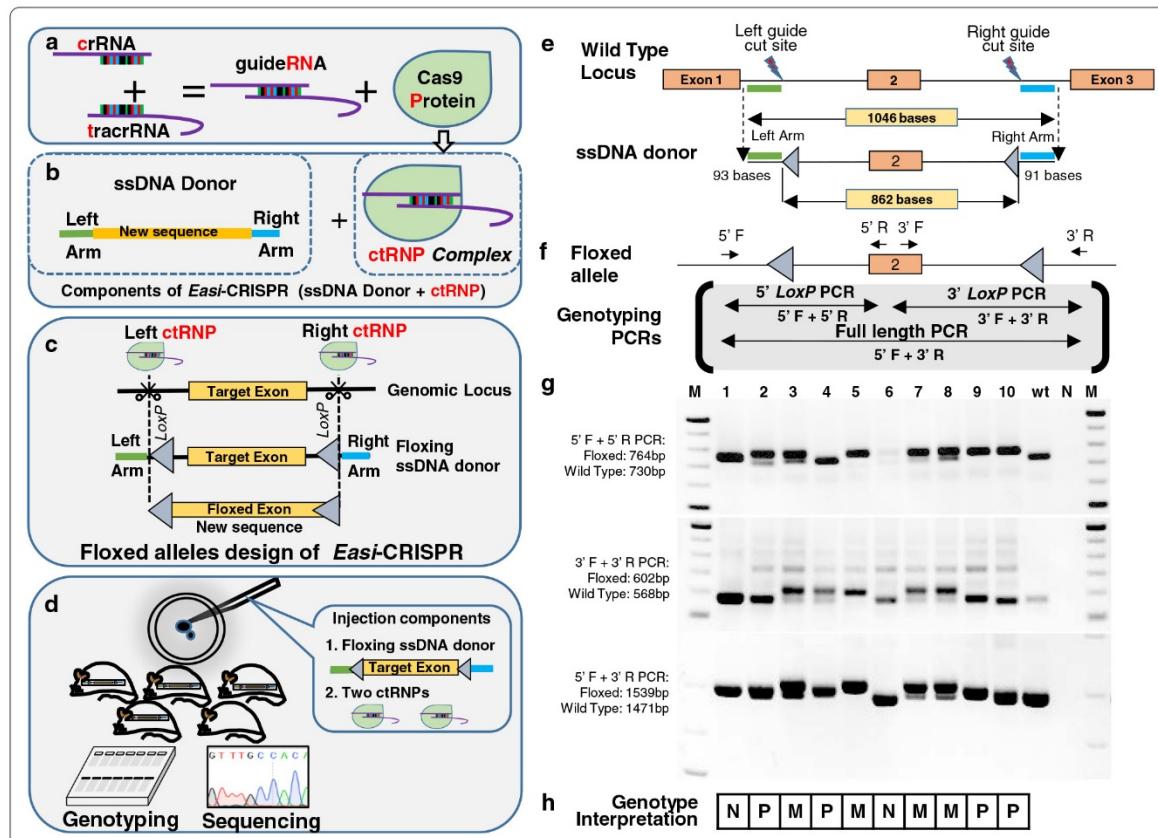
HITI: Homology-independent targeted integration



Alternative strategies for knock-in experiments: 2H2OP



Easi-CRISPR: improved knock-in approach



Combining RNPs + long ssDNA donor template

RNP = crRNA + tracrRNA + Cas9 protein

Current limitations of CRISPR

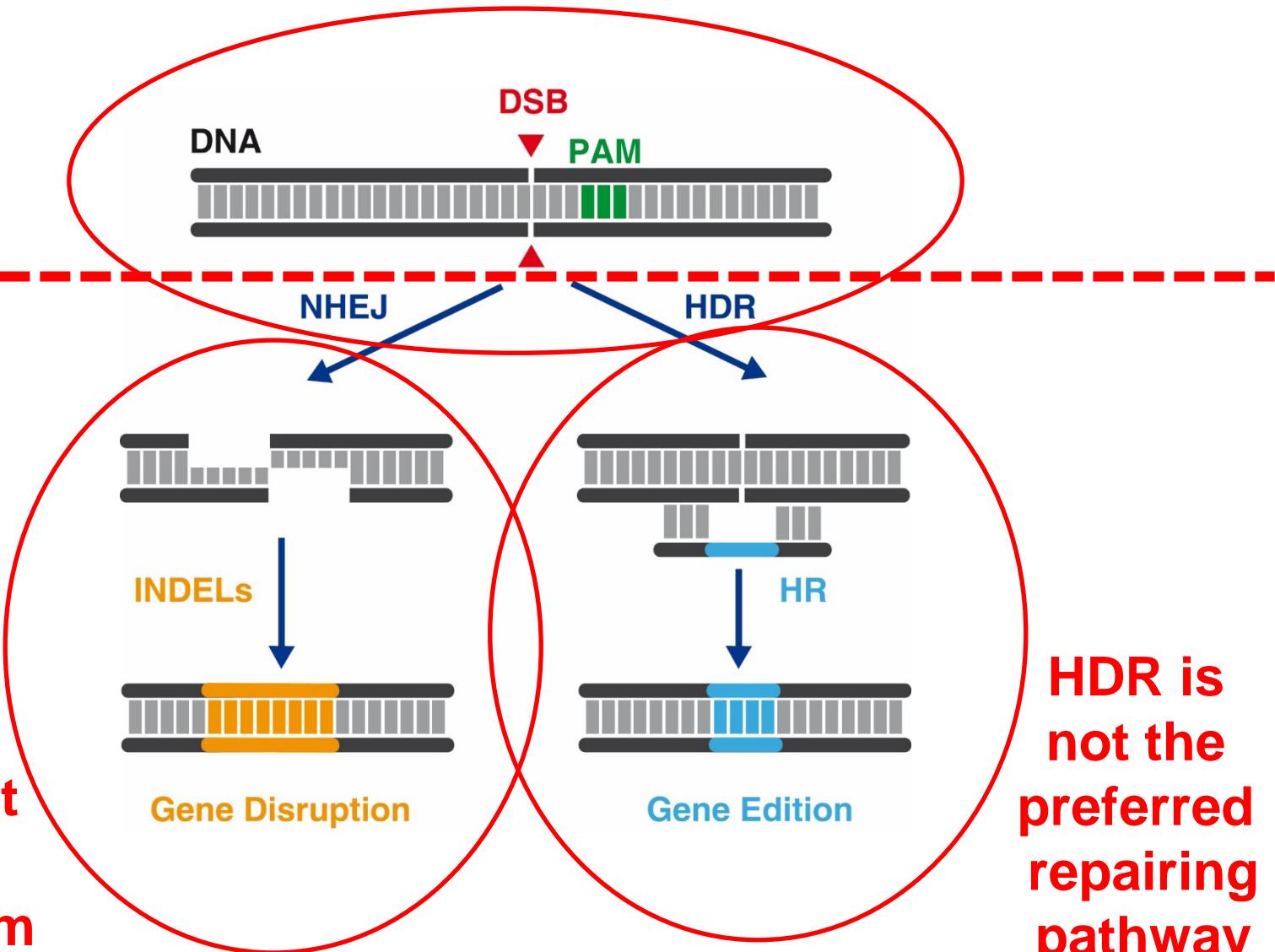
Off-target effects

Related to
CRISPR



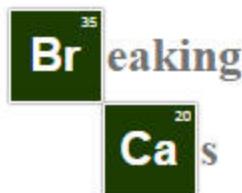
Unrelated to
CRISPR

On-target
effects
Mosaicism



Improved design of RNA guides for optimized CRISPR experiments

[CNB-CSIC](#) | [BioinfoGP](#) | [tools](#)



Breaking-Cas

Oligo guide design tool for CRISPR based genome editing. Any eukaryote genomic sequence available in ENSEMBL (release 84) or ENSEMBLGENOMES (release 31) can be used as reference.

Please cite:

"Juan C. Oliveros, Mònica Franch, Daniel Tabas-Madrid, David San-León, Lluís Montoliu, Pilar Cubas and Florencio Pazos (2016). SUBMITTED.

<http://bioinfogp.cnb.csic.es/tools/breakingcas>"

[Tutorial](#)

1 Choose organism: ([alphabetic list](#)) Write 3 letters or more and select it.

2 Paste one or several query DNA sequences in FASTA format (up to 20.000 nucleotides in total):

Or upload FASTA file (DNA): Ningún archivo seleccionado

3 Sele

<http://bioinfogp.cnb.csic.es/tools/breakingcas/>

ary, write a
3) are used

Google for “Breaking Cas”

Position-dependant weights

#1	#2	#3	#4	#5	#6	#7	#8	#9	#10	#11	#12	#13	#14	#15	#16	#17	#18	#19	#20	(PAM)	
5'-	0	0	0.014	0	0	0.395	0.317	0	0.389	0.079	0.445	0.508	0.613	0.851	0.732	0.828	0.615	0.804	0.685	0.583	NGG -3'

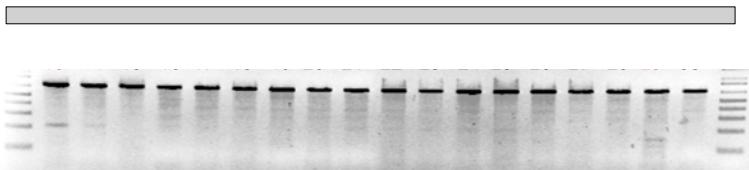
Confirmation email (optional):

To receive a message as soon the job finishes. Write it carefully (it will not be checked).

[Fill with example](#)

[Clear fields](#)

What about off-targets?



Mostly observed in vitro

We have not found
off-target sites with
altered sequences in
genome-edited mice

Off-target mutations are rare in Cas9-modified mice

Vivek Iyer, Bin Shen, Wensheng Zhang, Alex Hodgkins, Thomas Keane, Xingxu Huang & William C Skarnes

Affiliations | Corresponding authors

Nature Methods 12, 479 (2015) | doi:10.1038/nmeth.3408

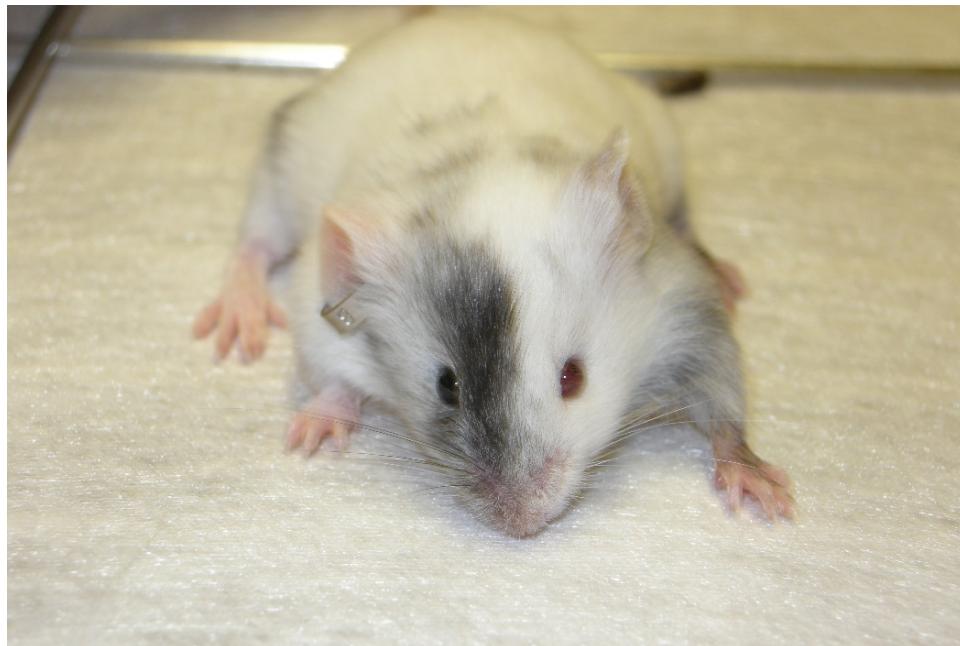
Published online 28 May 2015

E

F

Confirmed by NGS

On-targets: the real problem



- Founder animals are nearly always complex mosaic
- Many different alleles can be present
- Not all of them might transmit through germline



One 8-cell embryo = 16 possible alleles

Multiple alleles present in CRISPR founder gene-edited mice





CRISPR-mediated gene therapy of a human rare disease: chronic granulomatous disease (CGD) in human iPSC cells

Challenge:
multiple alleles are generated

CRISPR-Cas is the future

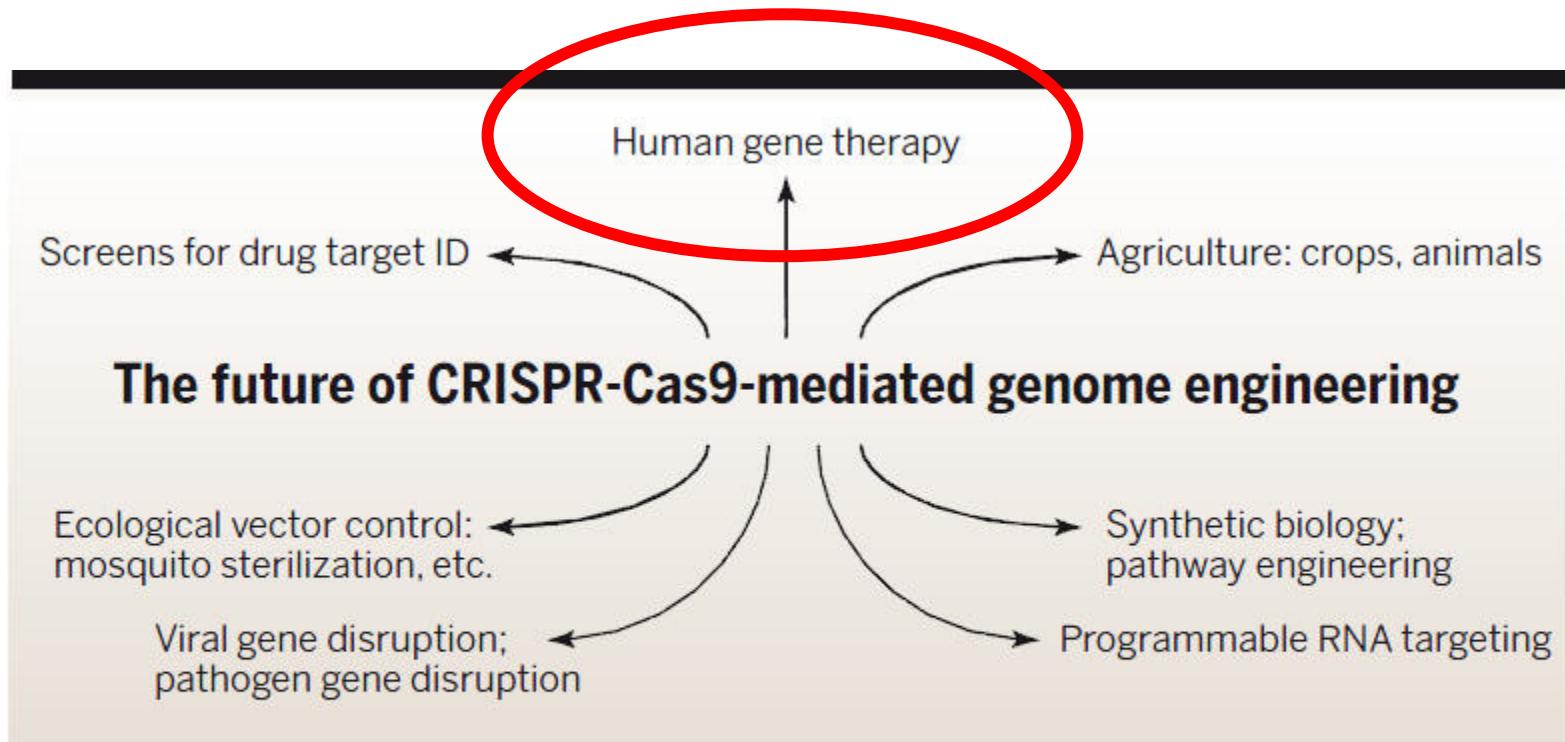


Fig. 6. Future applications in biomedicine and biotechnology. Potential developments include establishment of screens for target identification, human gene therapy by gene repair and gene disruption, gene disruption of viral sequences, and programmable RNA targeting.

CRISPR-Cas9 and *in vivo* somatic gene therapy

Science

REPORTS

Cite as: M. Tabebordbar *et al.*, *Science* 10.1126/science.aad5177 (2015).

In vivo gene editing in dystrophic mouse muscle and muscle stem cells

Mohammadsharif Tabebordbar,^{1,2*} Kexian Zhu,^{1,3*} Jason K. W. Cheng,¹ Wei Leong Chew,^{2,4} Jeffrey J. Widrick,⁵ Winston X. Yan,^{6,7} Claire Maesner,¹ Elizabeth Y. Wu,^{1†} Ru Xiao,⁸ F. Ann Ran,^{6,7} Le Cong,^{6,7} Feng Zhang,^{6,7} Luk H. Vandenberghe,⁸ George M. Church,⁴ Amy J. Wagers^{1,‡}

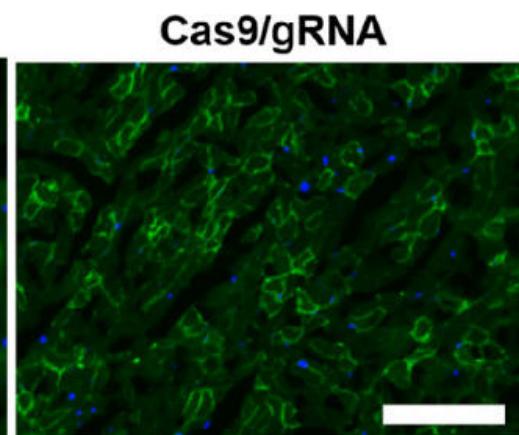
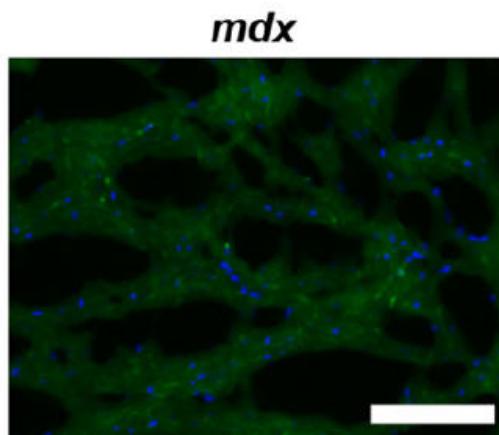
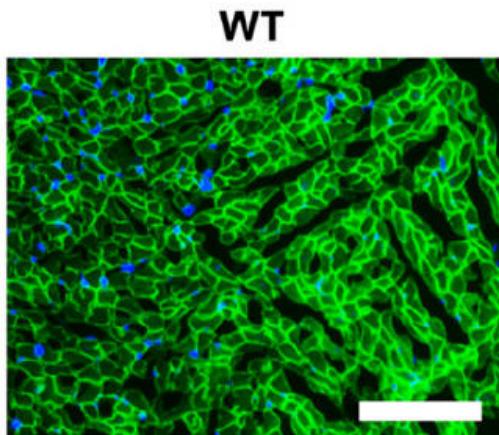
Science

REPORTS

Cite as: C. E. Nelson *et al.*, *Science* 10.1126/science.aad5143 (2015).

In vivo genome editing improves muscle function in a mouse model of Duchenne muscular dystrophy

Christopher E. Nelson,^{1,2} Chady H. Hakim,³ David G. Ousterout,^{1,2} Pratiksha I. Thakore,^{1,2} Eirik A. Moreb,^{1,2} Ruth M. Castellanos Rivera,⁴ Sarina Madhavan,^{1,2} Xiufang Pan,³ F. Ann Ran,^{5,6} Winston X. Yan,^{5,7,8} Aravind Asokan,⁴ Feng Zhang,^{5,8,10,11} Dongsheng Duan,^{3,12} Charles A. Gersbach^{1,2,13*}



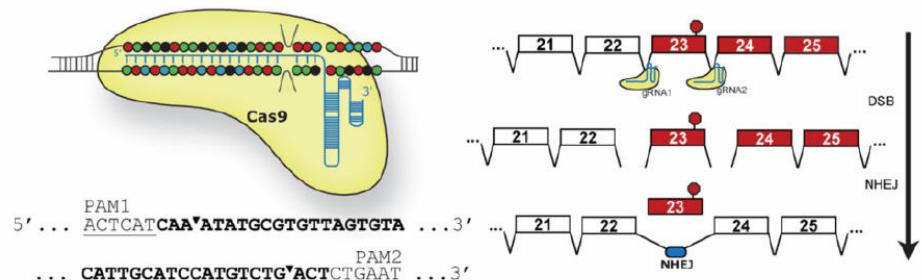
Science

REPORTS

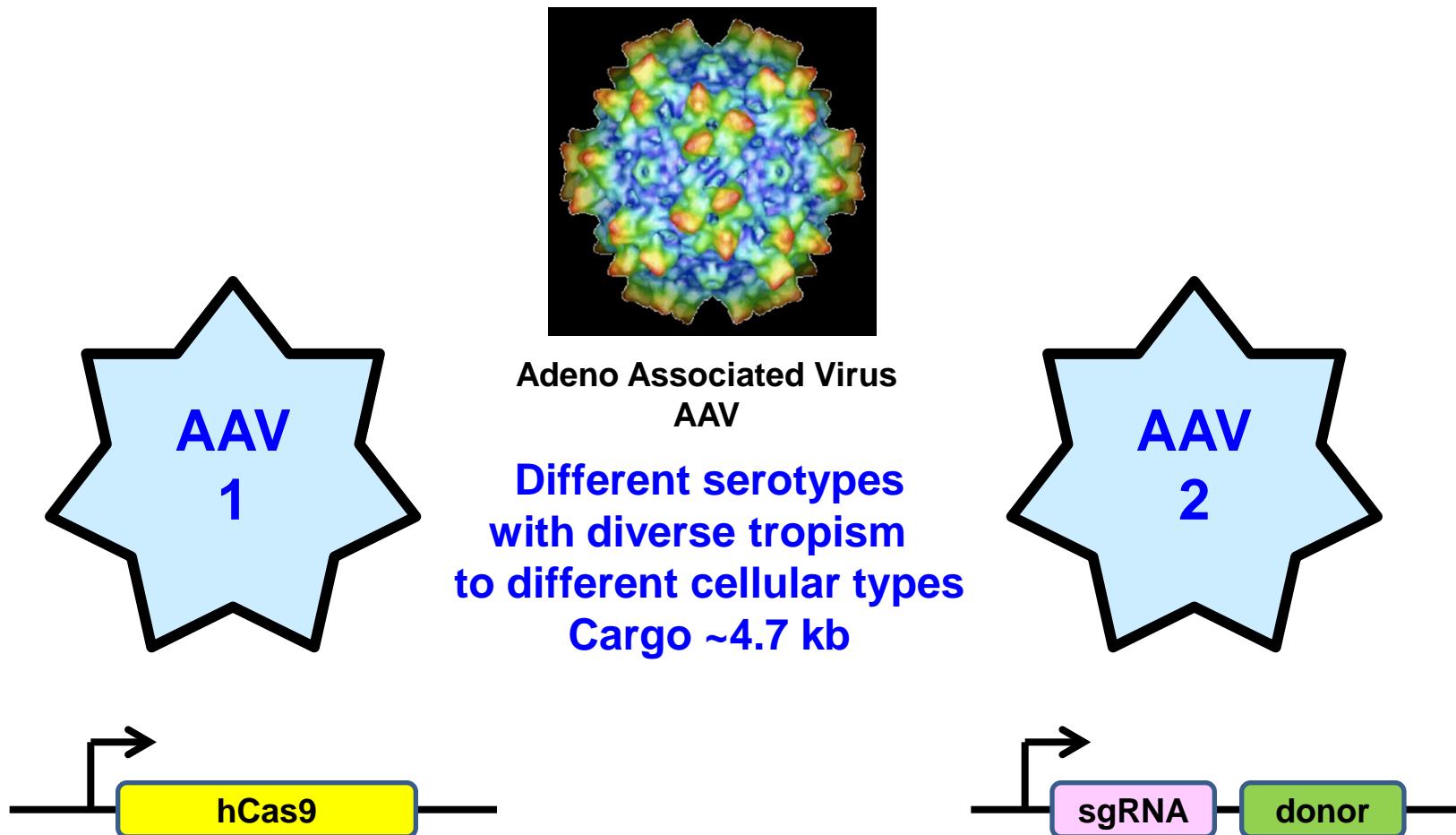
Cite as: C. Long *et al.*, *Science* 10.1126/science.aad5725 (2015).

Postnatal genome editing partially restores dystrophin expression in a mouse model of muscular dystrophy

Chengzu Long,^{1,2,3*} Leonela Amoasi,^{1,2,3*} Alex A. Mireault,^{1,2,3} John R. McAnally,^{1,2,3} Hui Li,^{1,2,3} Efrain Sanchez-Ortiz,^{1,2,3} Samadrita Bhattacharyya,^{1,2,3} John M. Shelton,⁴ Rhonda Bassel-Duby,^{1,2,3} Eric N. Olson^{1,2,3,†}



CRISPR tools and somatic gene therapy of human rare diseases



Increasing number of animal models of rare monogenic diseases corrected via CRISPR

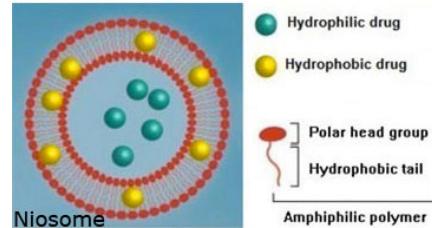
Preclinical animal models

- Duchenne muscular dystrophy (DMD)
- Ornithine transcarbamylase (OTC) deficiency
- Hereditary tyrosinemia I (FAH deficiency)
- Congenital cataract (CRYGC)
- Chronic granulomatous disease (CGD)
- Retinitis pigmentosa (RP)
- Leber congenital amaurosis (LCA)
- Huntington Disease (HD)
- ...
- Also many iPS cells models correcting gene mutations via CRISPR strategies

Challenges for CRISPR-mediated gene therapy in patients

- Immune response against Cas9
- Immune response against AAV
- Finding the right AAV serotype (preferential)
- Non-viral delivery systems (nanoparticles, liposomes) → the future

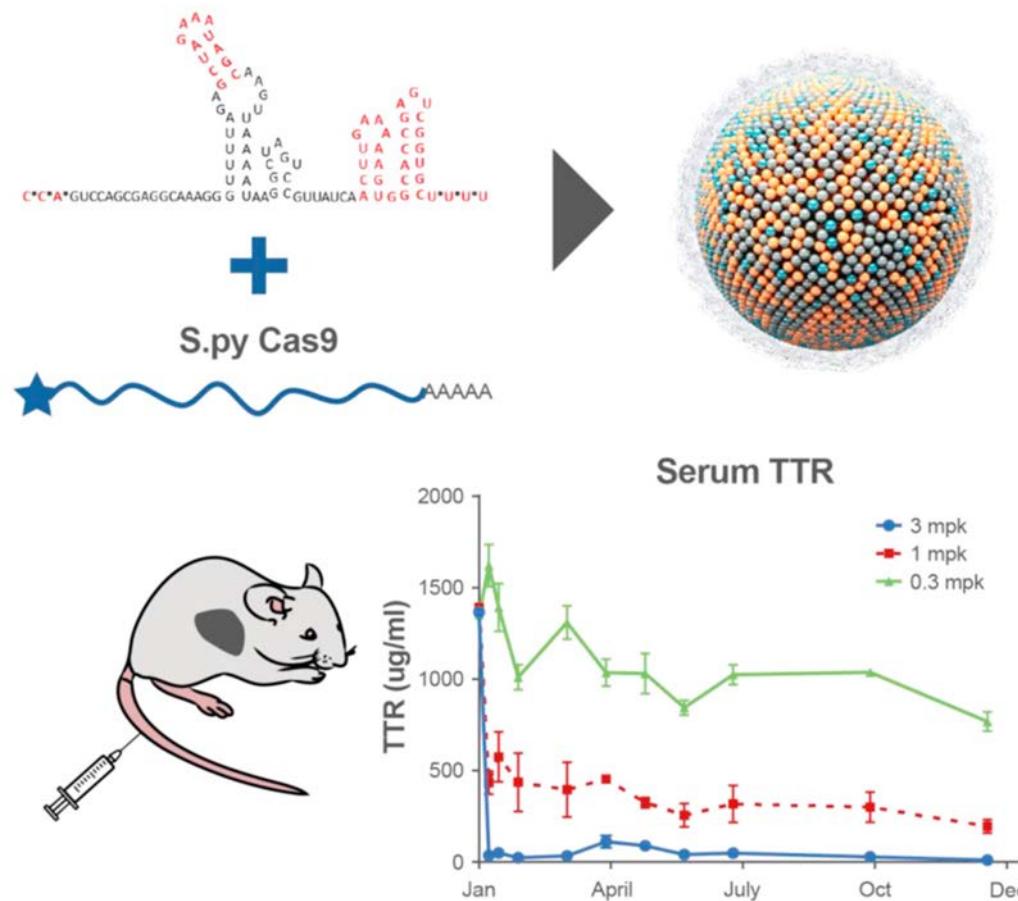
ciber-bbn



NanoCRISPRalbino
Niosomes
J.L. Pedraz (UPV/EHU)

- Reaching a significant number of target cells
- On-target allelic multiplicity (indetermination)
- Off-targets
- HDR (dividing cells) versus NHEJ (quiescent cells/neurons)
→ HITI (homology-independent targeted integration)

Single Administration of CRISPR/Cas9 Lipid Nanoparticles achieves Robust and Persistent In Vivo Genome Editing





Cas9
Streptococcus pyogenes
Staphylococcus aureus

Cas9: Bang Wong, Broad Institute of Harvard and MIT, Cambridge, MA



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New Results

Identification of Pre-Existing Adaptive Immunity to Cas9 Proteins in Humans

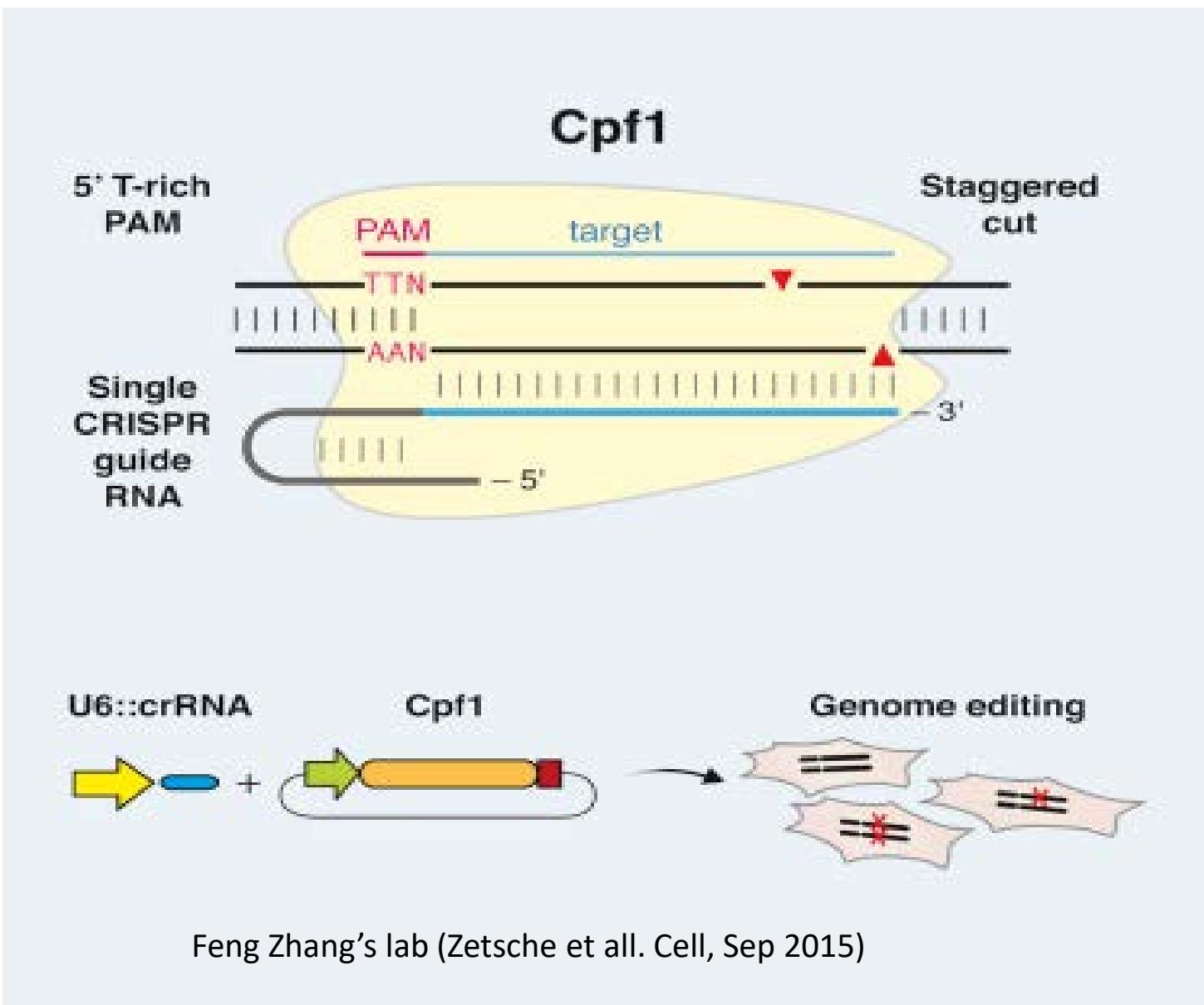
Carsten Trevor Charlesworth, Priyanka S Deshpande, Daniel P Dever, Beruh Dejene, Natalia Gomez-Ospina, Sruthi Mantri, Mara Pavel-Dinu, Joab Camarena, Kenneth I Weinberg, Matthew H Porteus

doi: <https://doi.org/10.1101/243345>



- Cas9 antibodies found in human serum
- Anti-Cas9 T lymphocytes found in human blood
- 79% individuals have antibodies against SaCas9
- 65% individuals have antibodies against SpCas9
- 46% individuals have anti-Cas9 T cells
- Immunosuppression or alternative Cas proteins

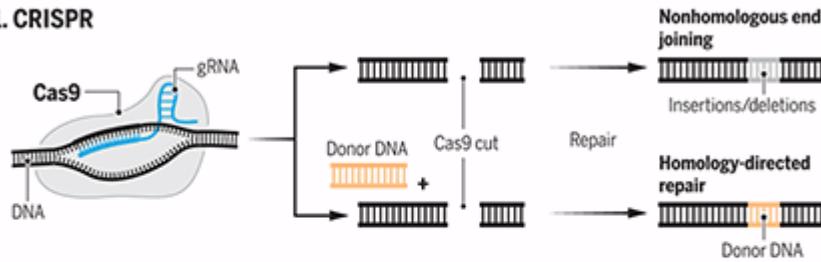
Alternative Cas-like proteins



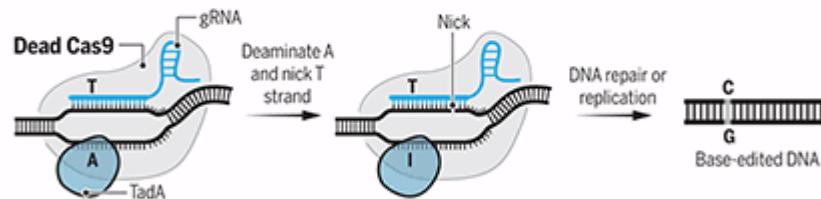
Getting to the point of mutations

Base editors borrow from CRISPR's components—guide RNAs (gRNAs) and Cas9 or other nucleases—but don't cut the double helix and instead chemically alter single bases with deaminase enzymes such as TadA and ADAR.

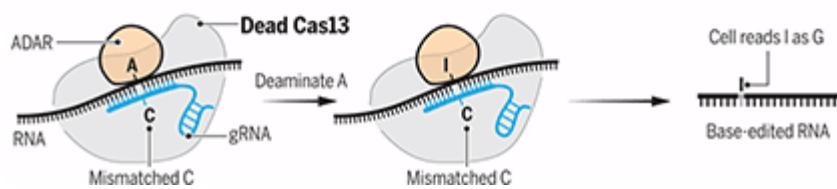
1. CRISPR



2. DNA base editing



3. RNA base editing

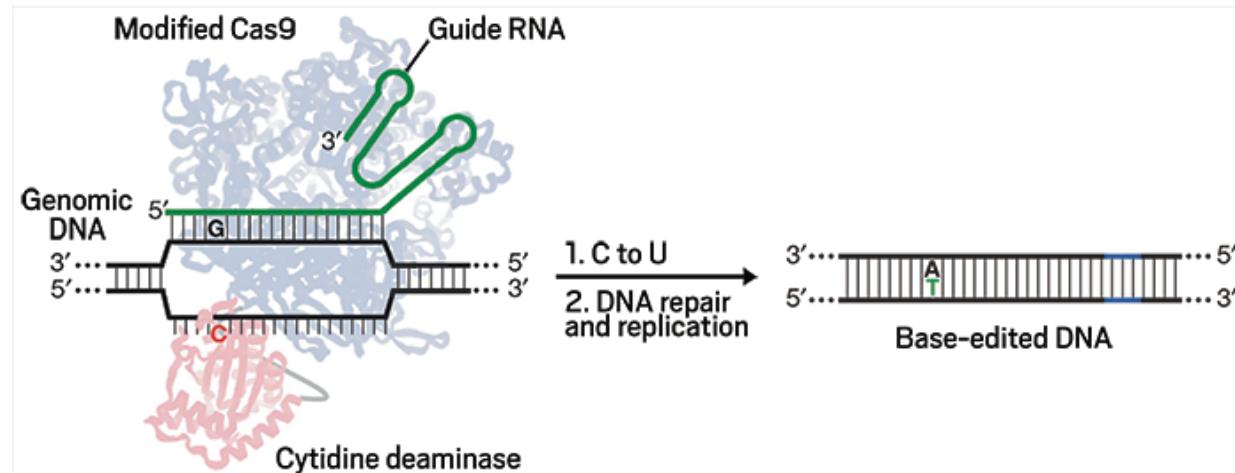


C → U → T
A → I → G

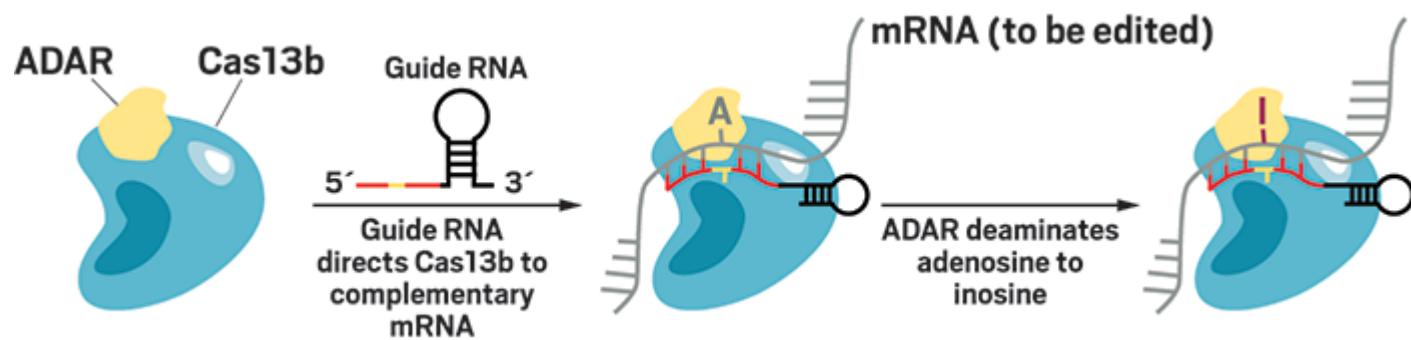
Kim et al. Nat Biotech. 2017

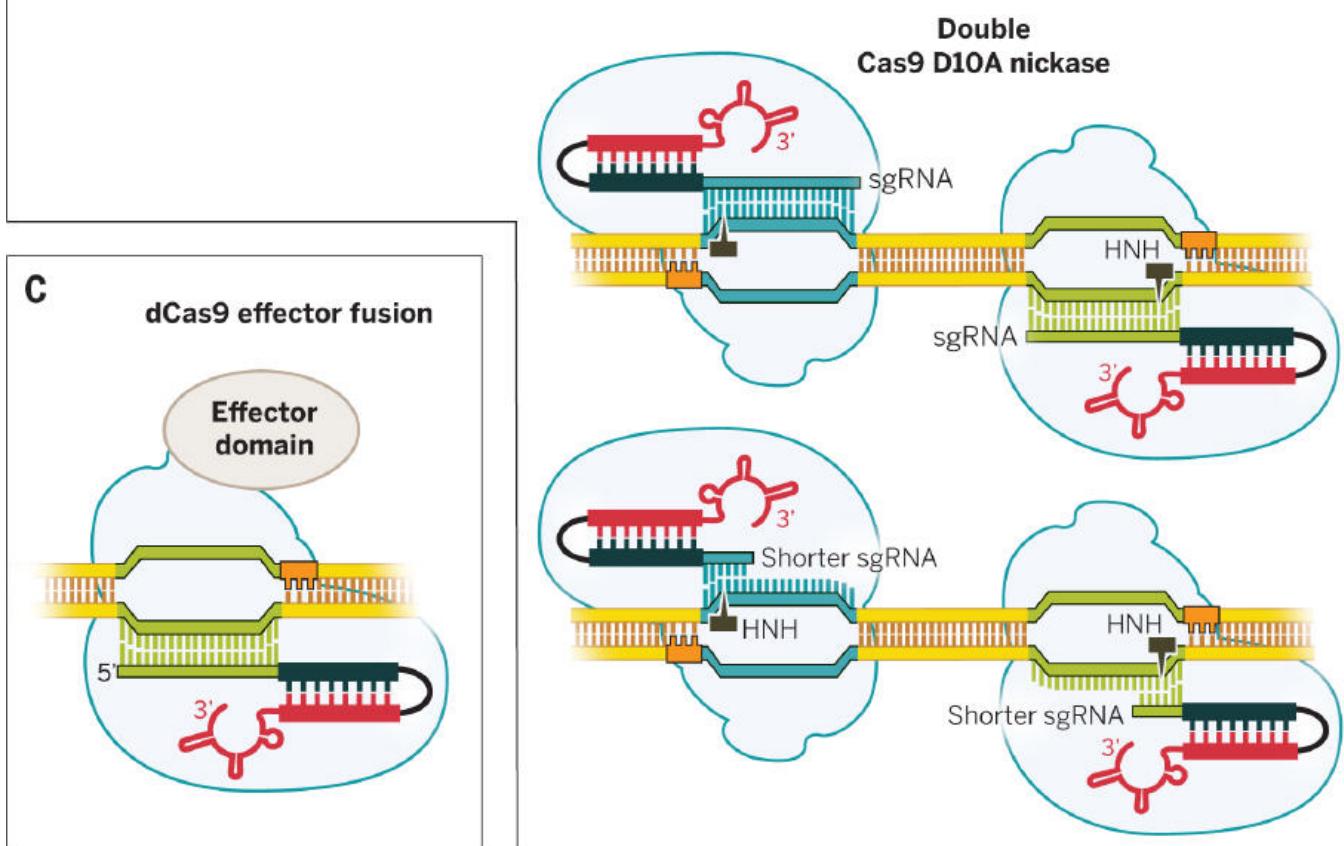
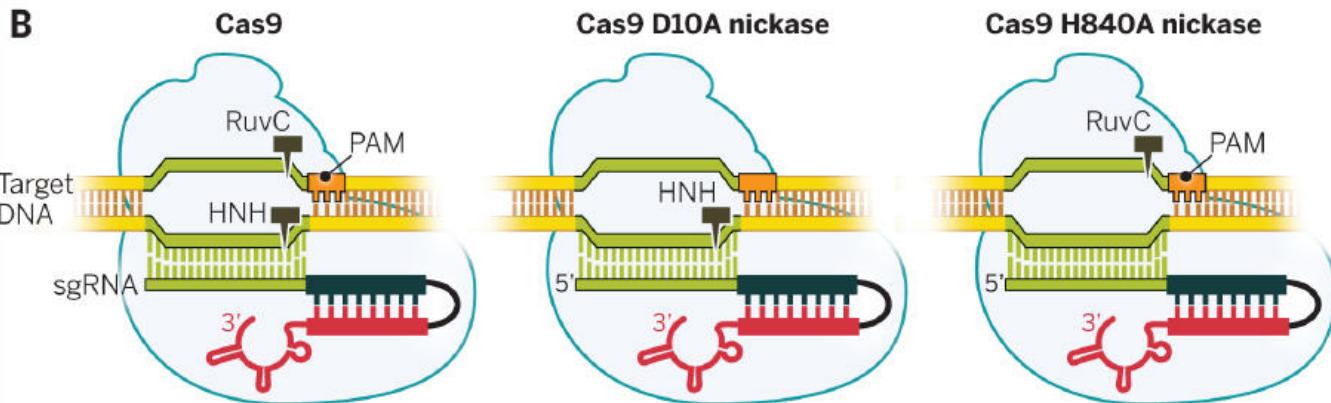
David Liu Lab

CRISPR-derived BASE EDITORS



CRISPR 2.0 (editing RNA)





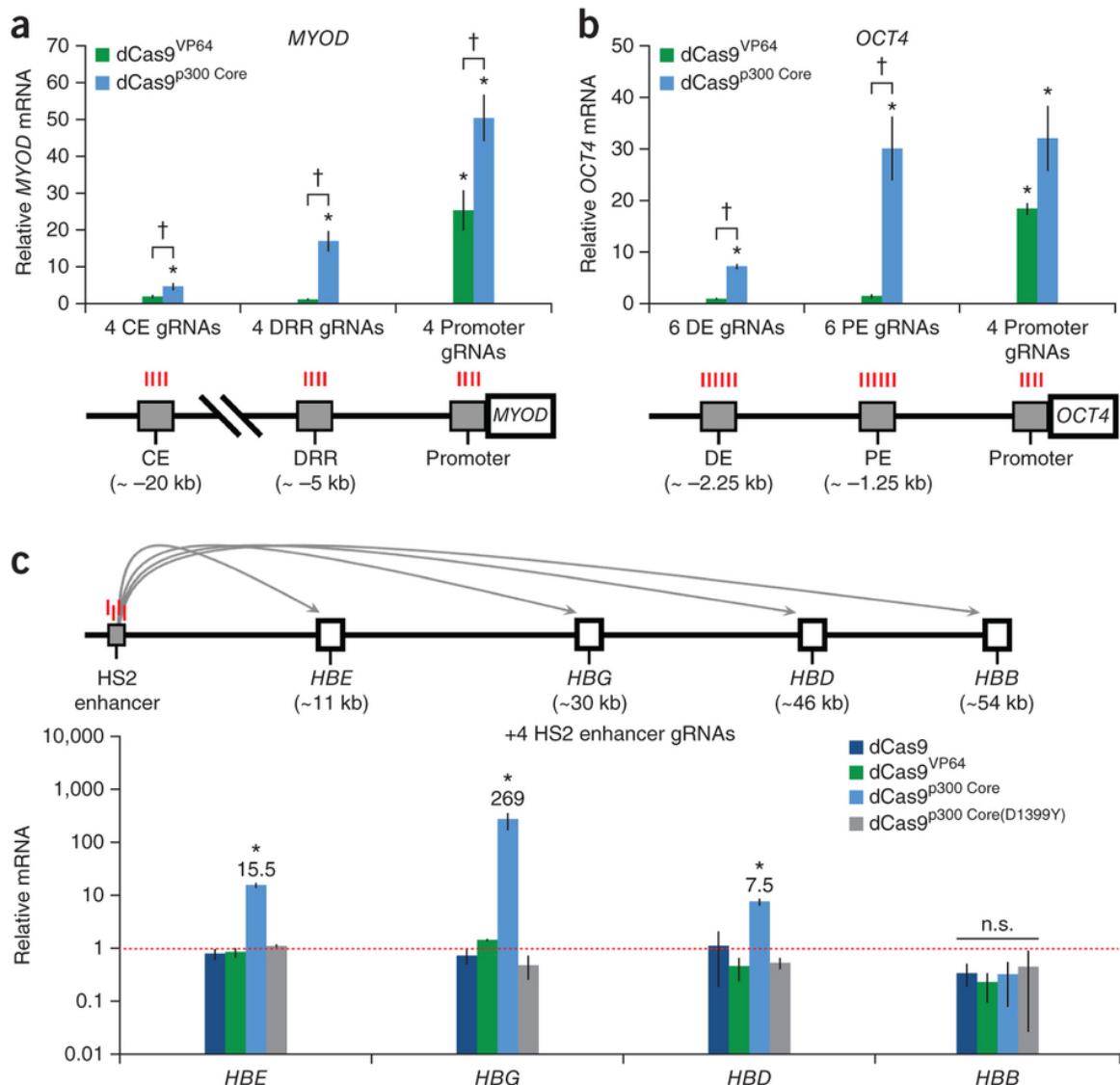
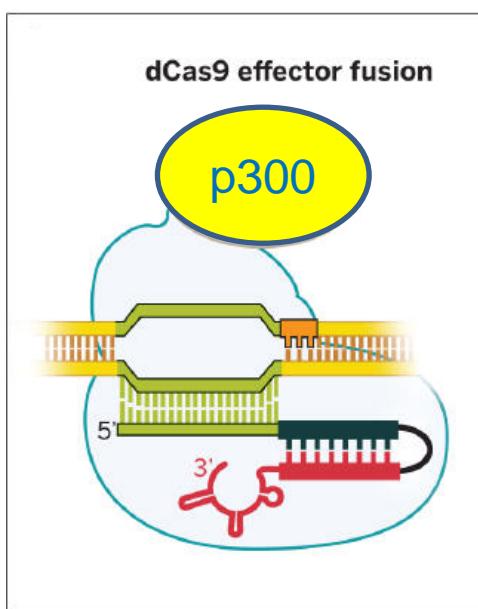
Targeting acetylation of Histone H3 Lysine 27 in the genome

Activating gene expression by CRISPR-dCas9/p300

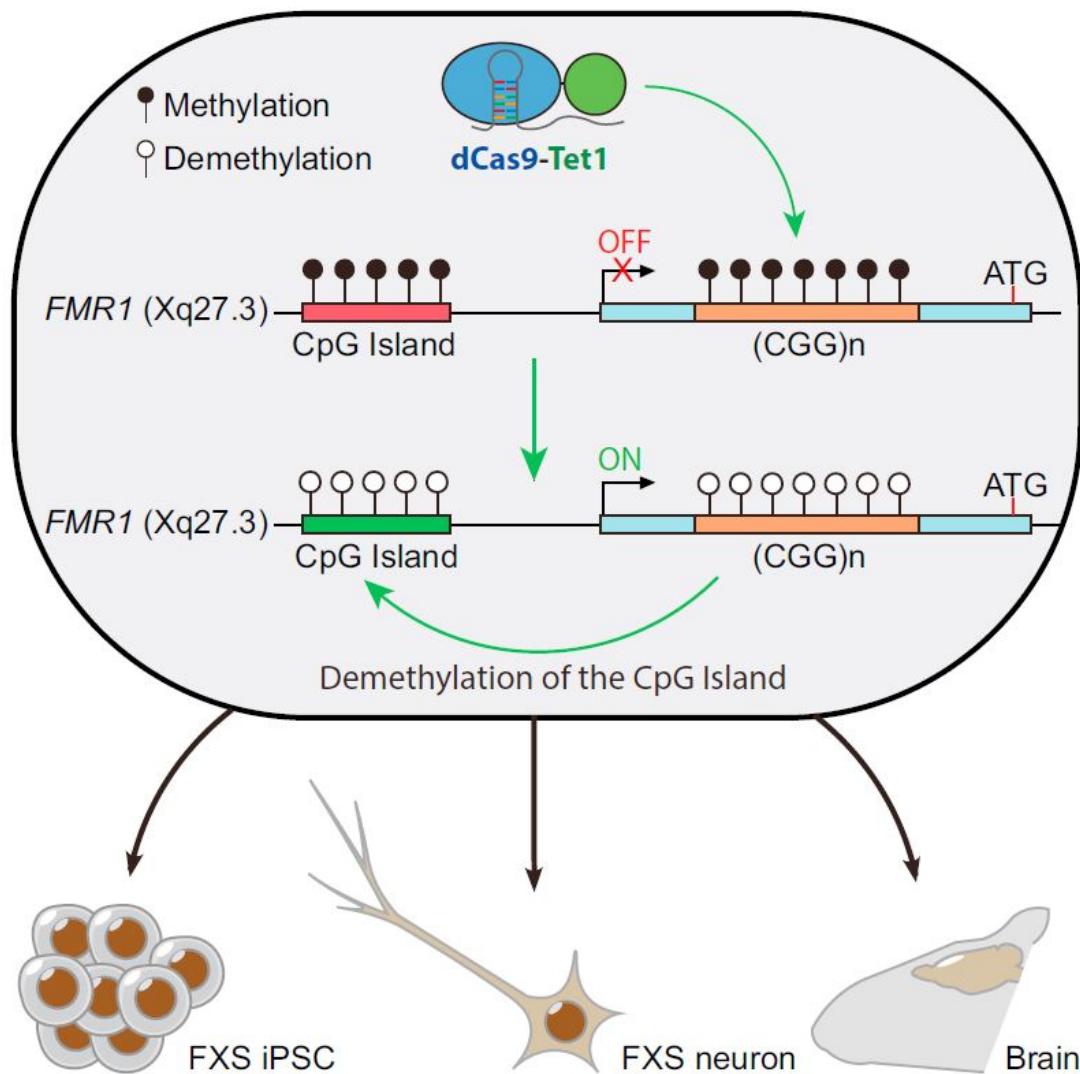
Epigenome editing by a CRISPR-Cas9-based acetyltransferase activates genes from promoters and enhancers

Hilton *et al.*

Nature Biotechnology 33, 510–517 (2015)

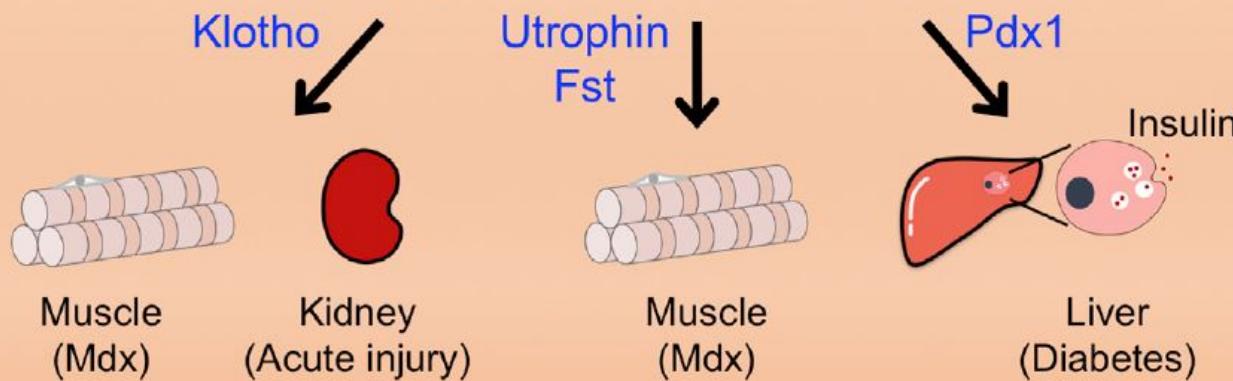


CRISPR-Cas rescues Fragile X syndrome





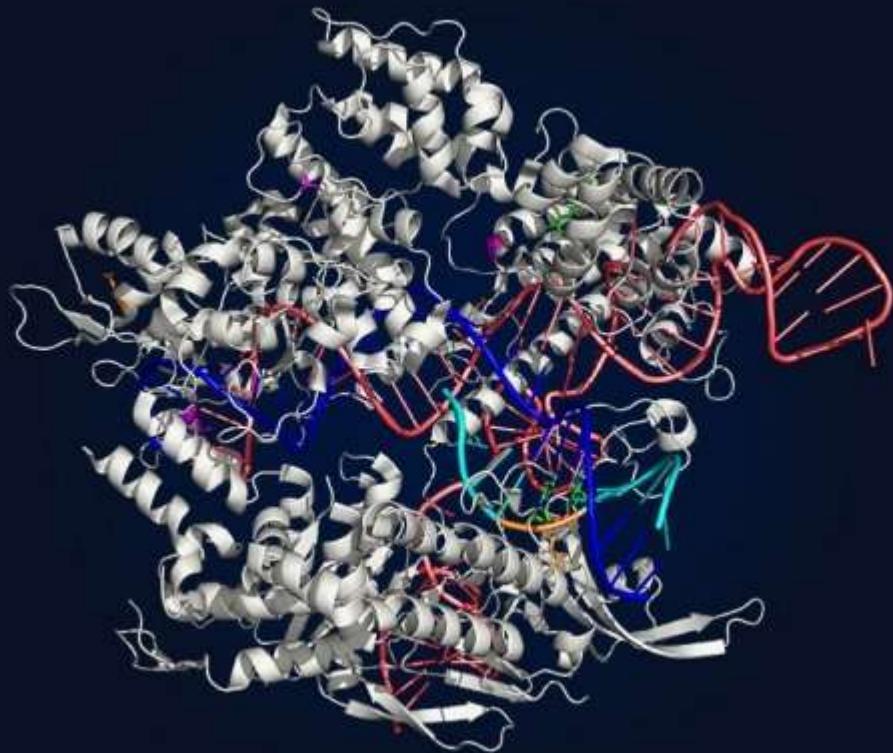
Target Gene Activation (TGA) (Epigenetic modification)



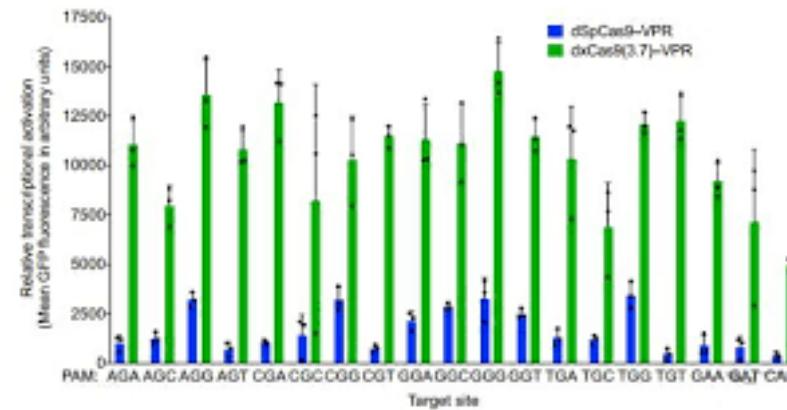
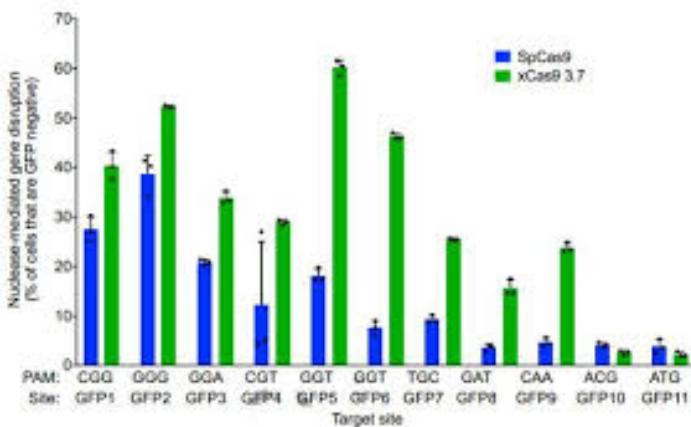
Restoring expression
of silent genes

Compensating for
genetic defects

Altering
cell fates



Evolved Cas9 variants with broad PAM compatibility and high DNA specificity

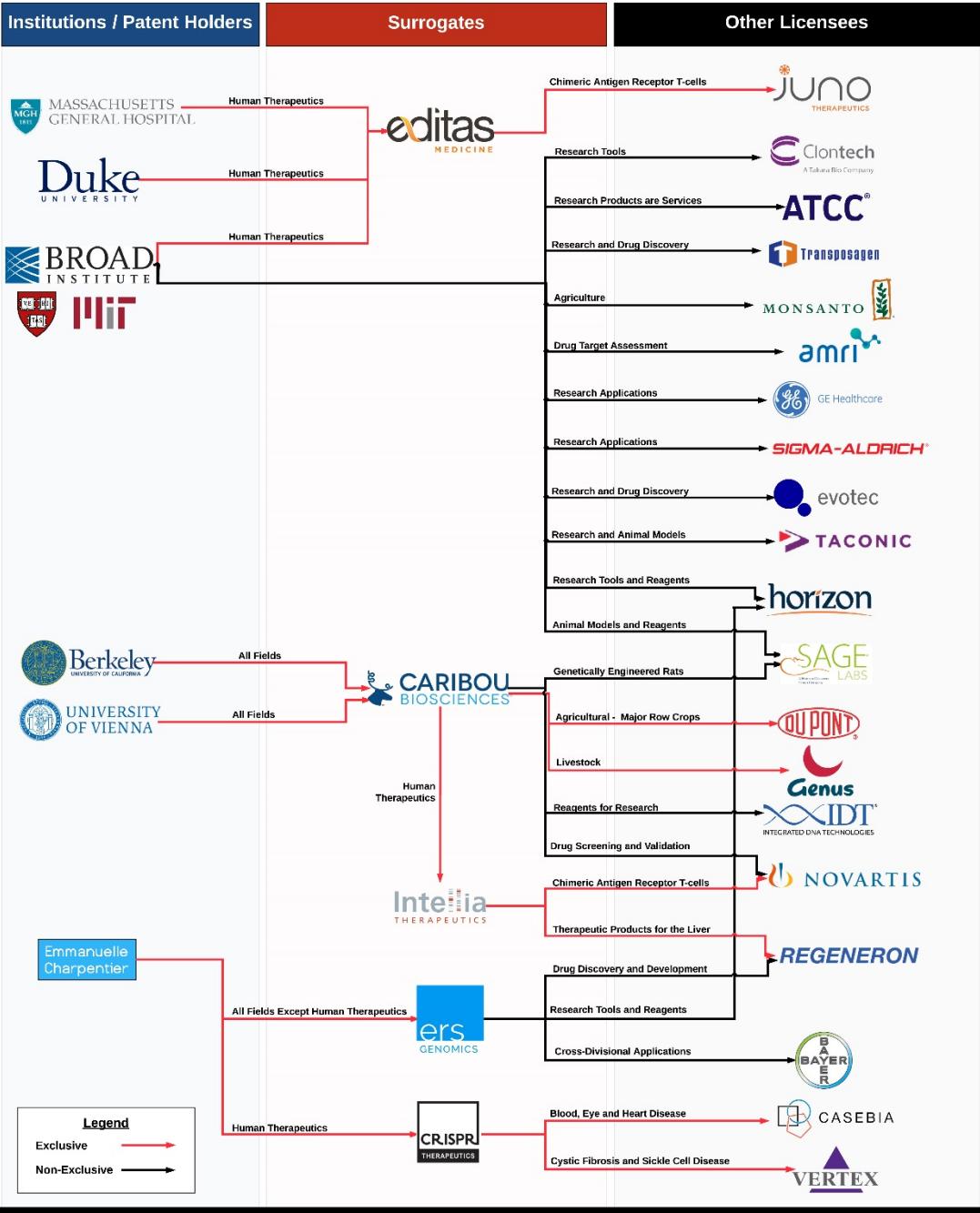




EVERWHERE

Illustration by Chris Labrooy © Hallmark

CRISPR CAS9 Licensing Agreements



BROAD / MIT

Patent filed in December 2012

Paper published January 2013

Patent granted in April 2014

“CRISPR applications in all eukaryotic cells”

UC Berkeley

Patent filed in May 2012

Paper published in August 2012

Interference filed in January 2016

Interference denied in February 2017

Patent still under evaluation

“CRISPR applications in all cells”



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Y COMPETITIVIDAD



ciberer *isci*ⁱⁱ

<http://www.cnb.csic.es/~montoliu/>

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Belén Pintado (CNB-CSIC, Madrid) Transgenic Unit
Juan Carlos Oliveros (CNB-CSIC, Madrid) Bioinformatics

The CRISPR web page at CNB



www.cnb.csic.es/~montoliu/CRISPR/

Google for CNB + CRISPR