

ciberer isciüü

CNB
CENTRO NACIONAL DE BIOTECNOLOGÍA

ALBA
Asociación de ayuda a personas con albinismo

CSIC

mi+d Un lugar para la ciencia y la tecnología



Aplicaciones del Sistema CRISPR-Cas9 en Enfermedades Raras

Lluís Montoliu

CNB-CSIC, Madrid, Spain



GOBIERNO DE ESPAÑA

MINISTERIO DE ECONOMÍA, INDUSTRIA Y COMPETITIVIDAD





Modifying the Mammalian Genome



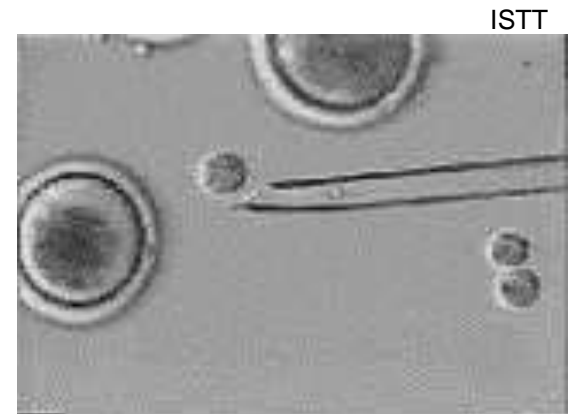
Pronuclear microinjection

1980 → ...



ES / iPS cells

1986 → ...



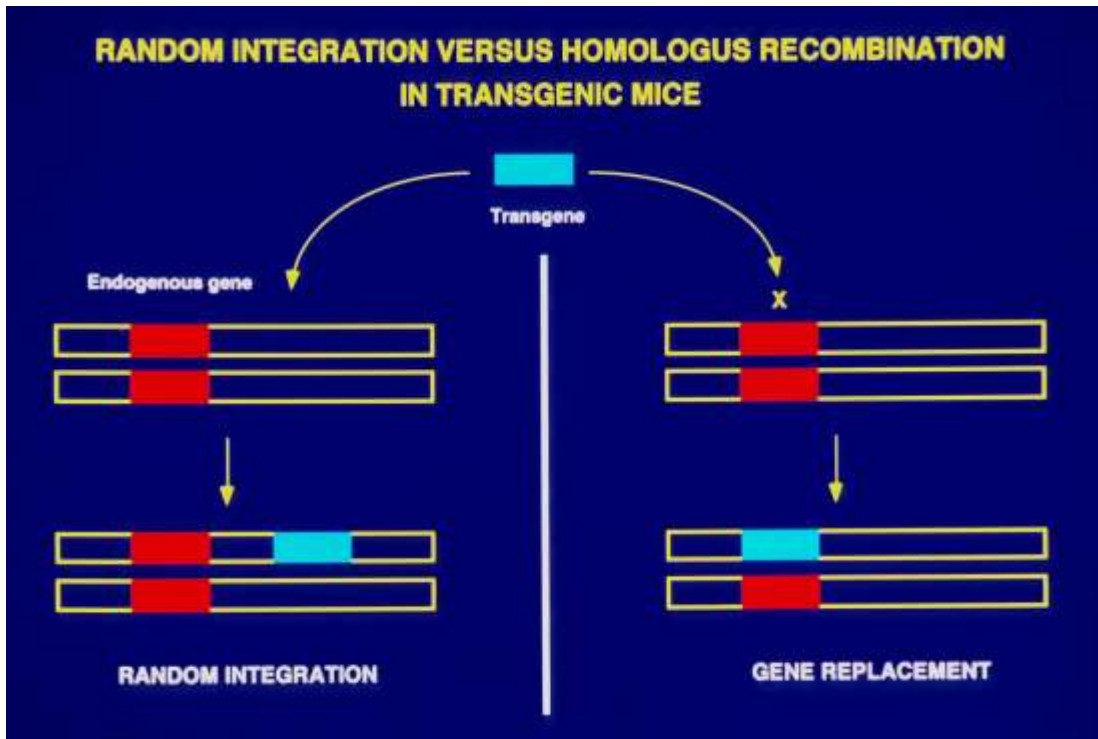
SCNT

1996 → ...

ADDING A GENE

DELETING A GENE

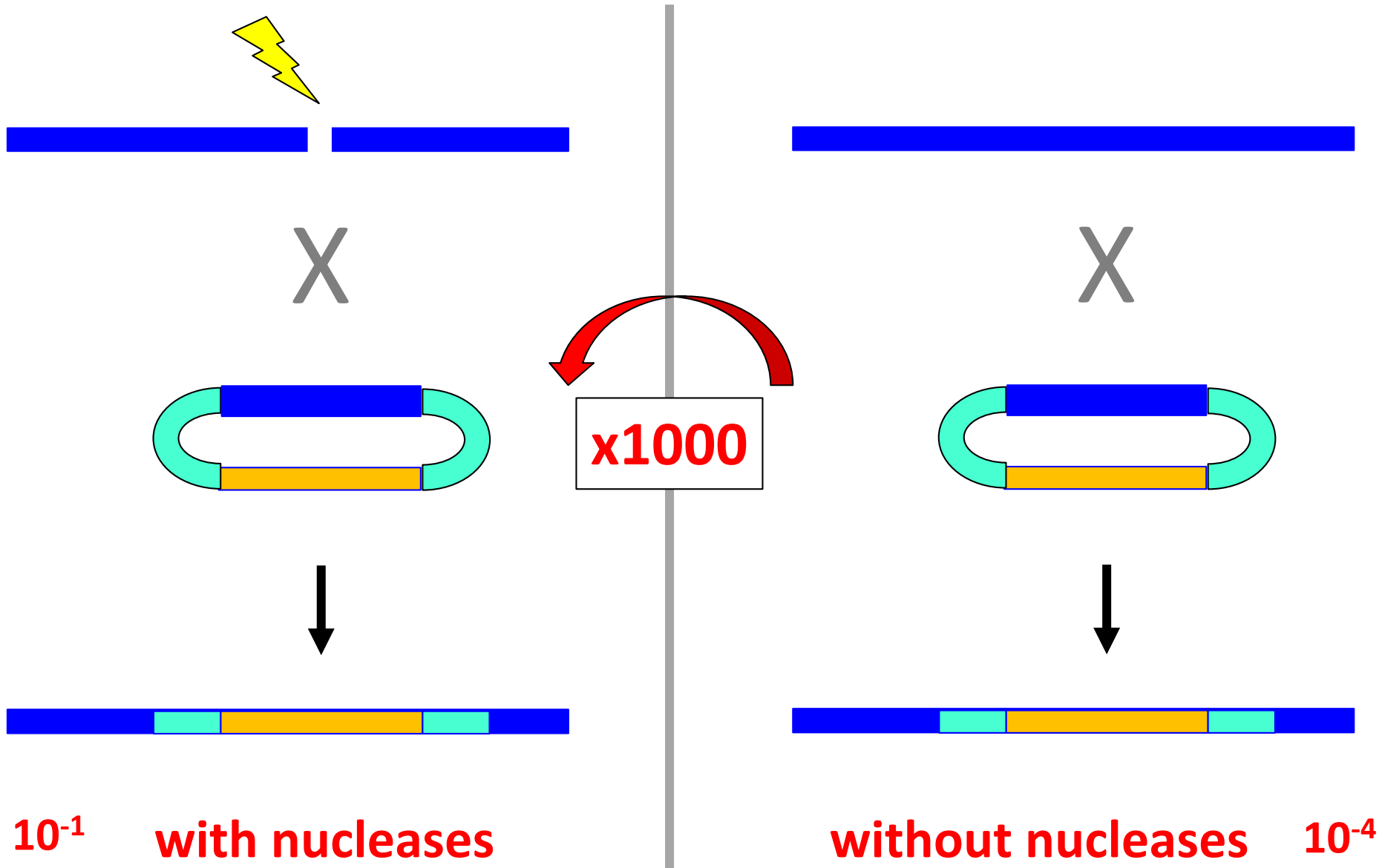
The most relevant and distinctive feature among all gene modifying methods is

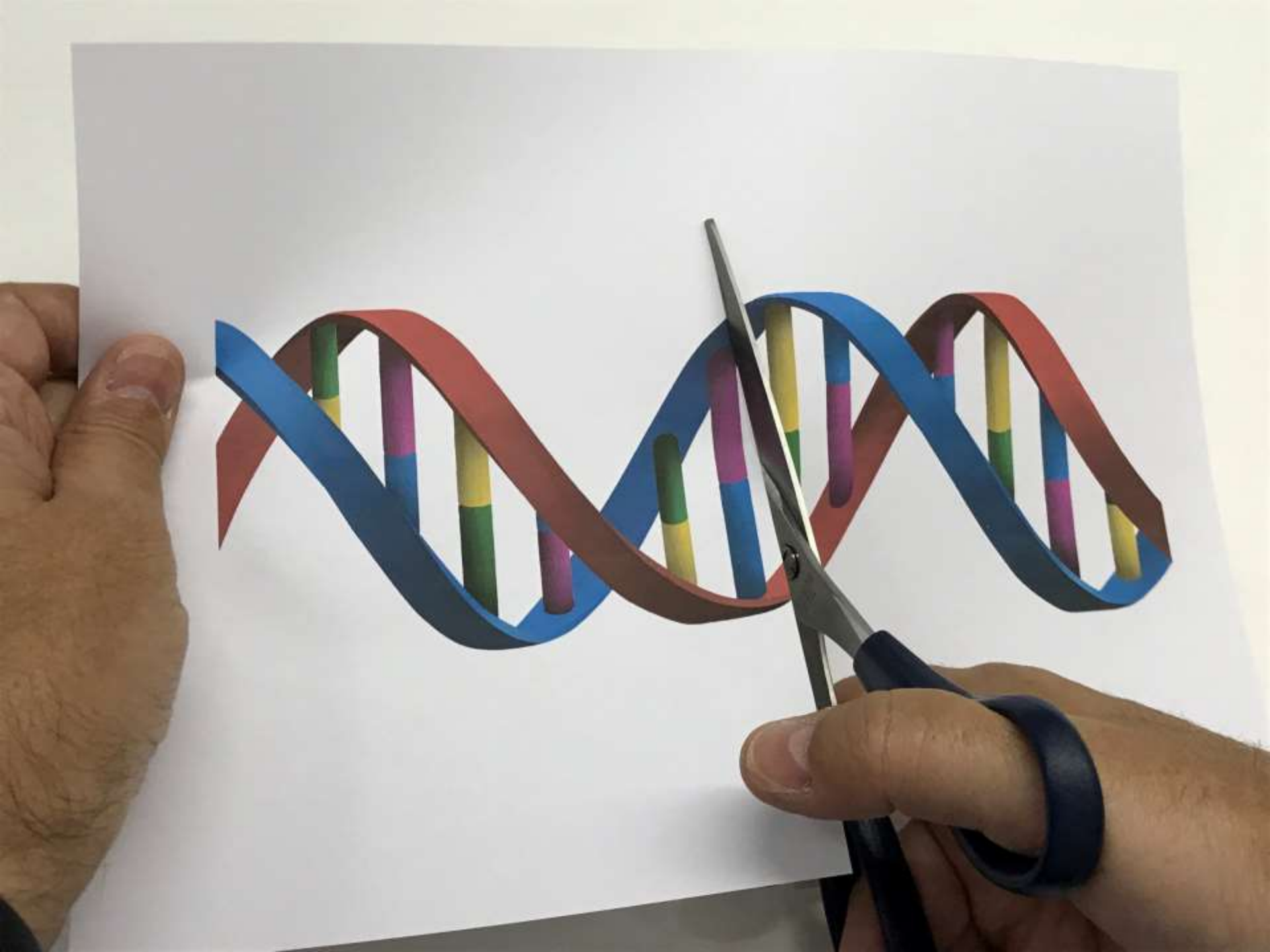


Slides from 1991

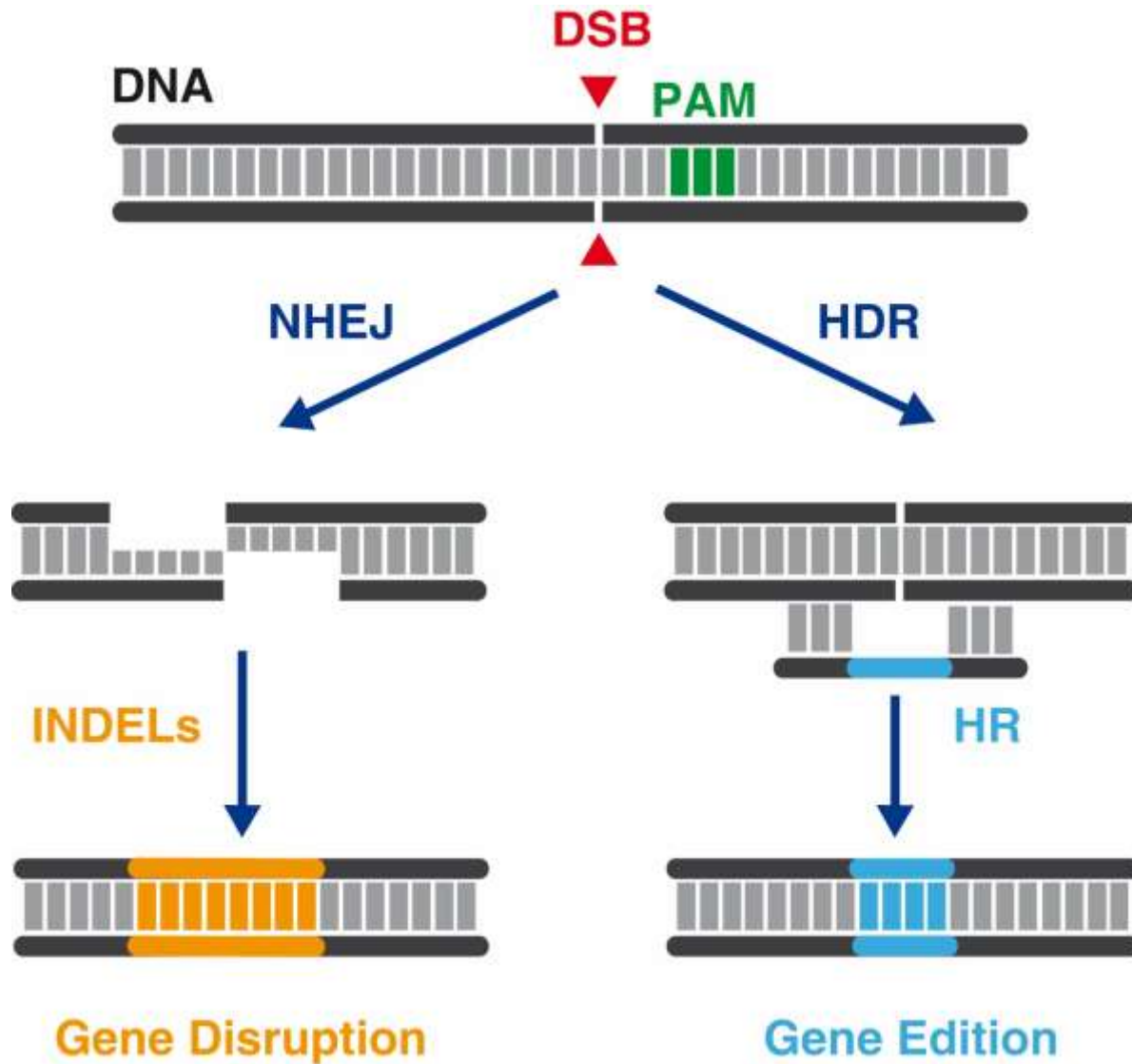
Random versus **Targeted** genetic modification

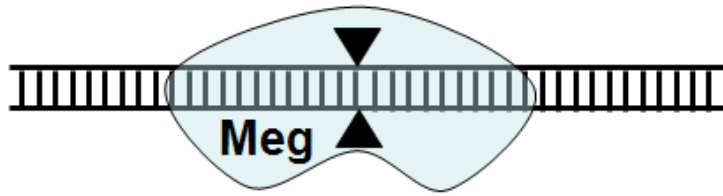
Homologous Recombination and Nucleases





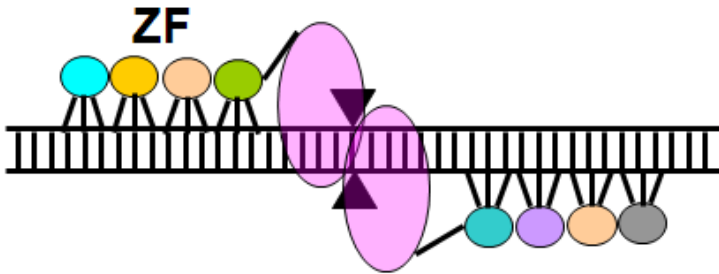
Fixing the DSB: NHEJ vs HDR





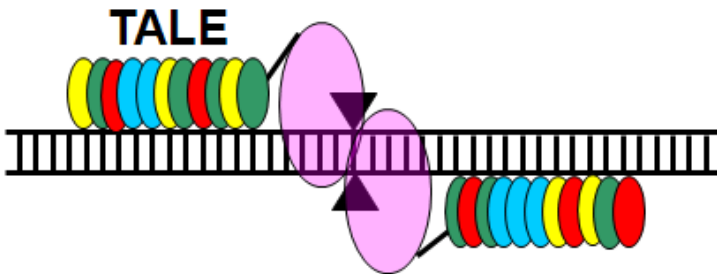
Meganuclease

20-40 bp/Enzyme



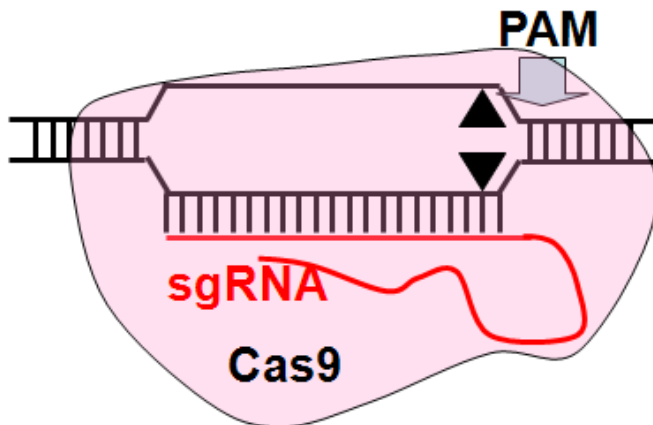
ZFN

3 bp/Finger



TALEN

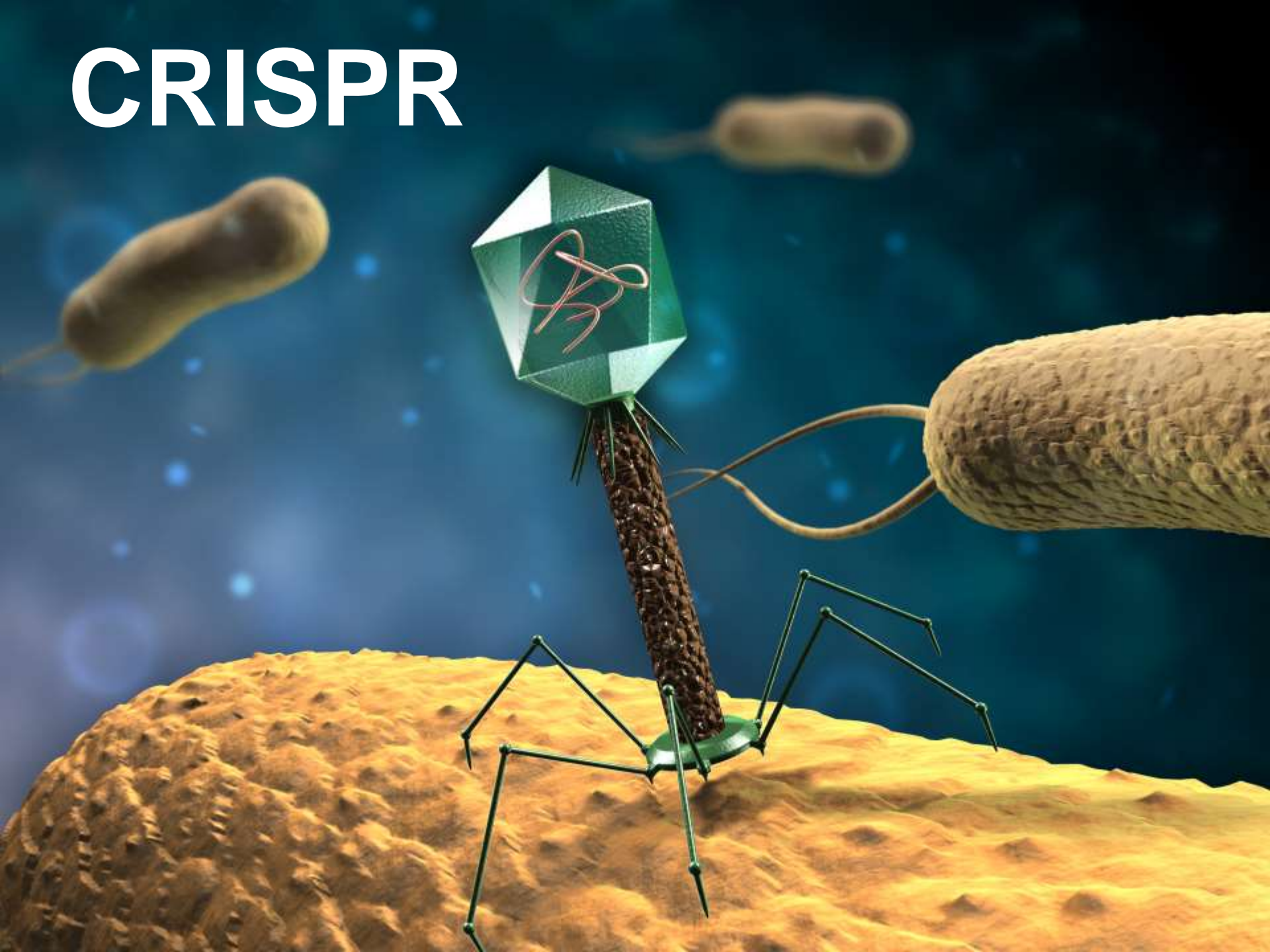
1 bp/Module



CRISPR-Cas

1 bp/Base

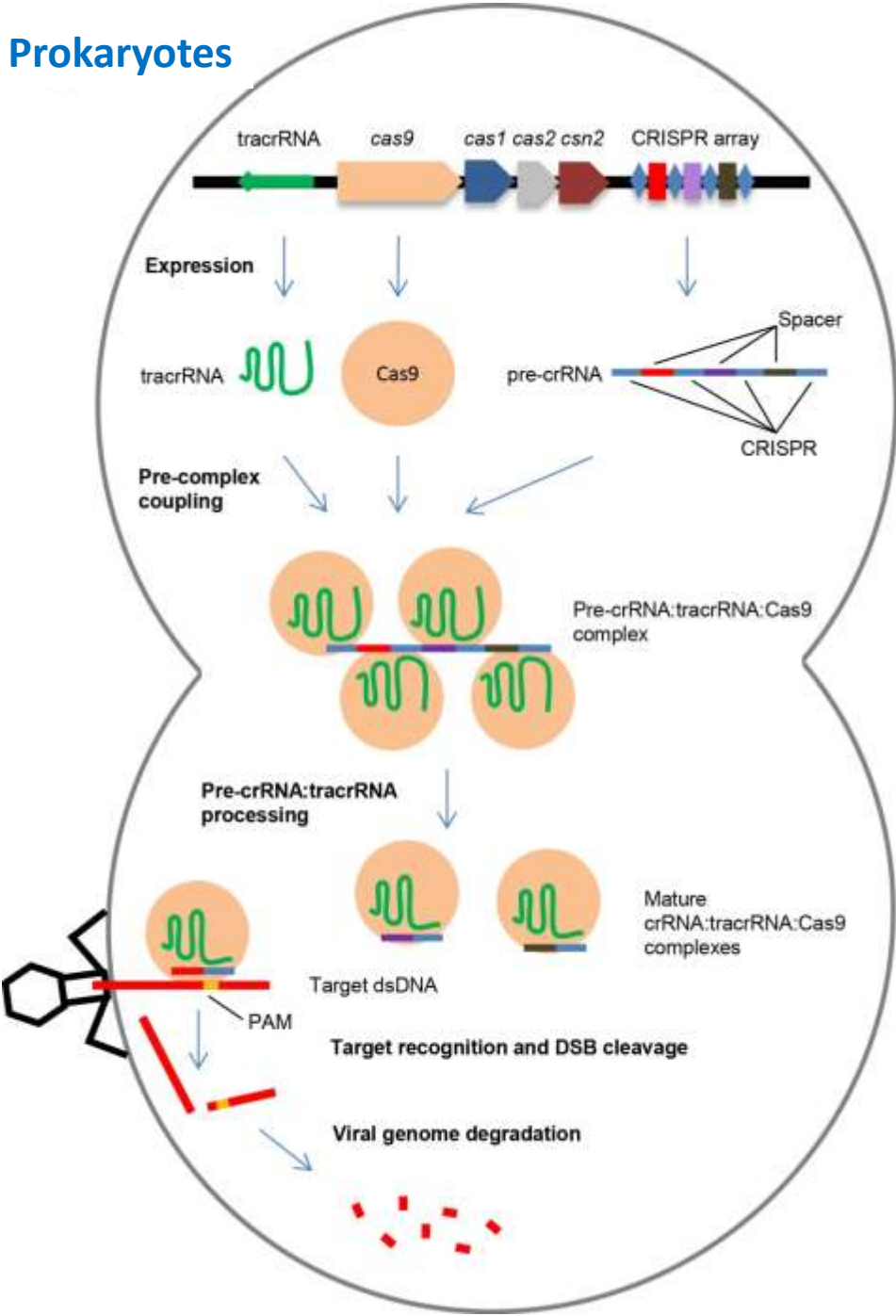
CRISPR



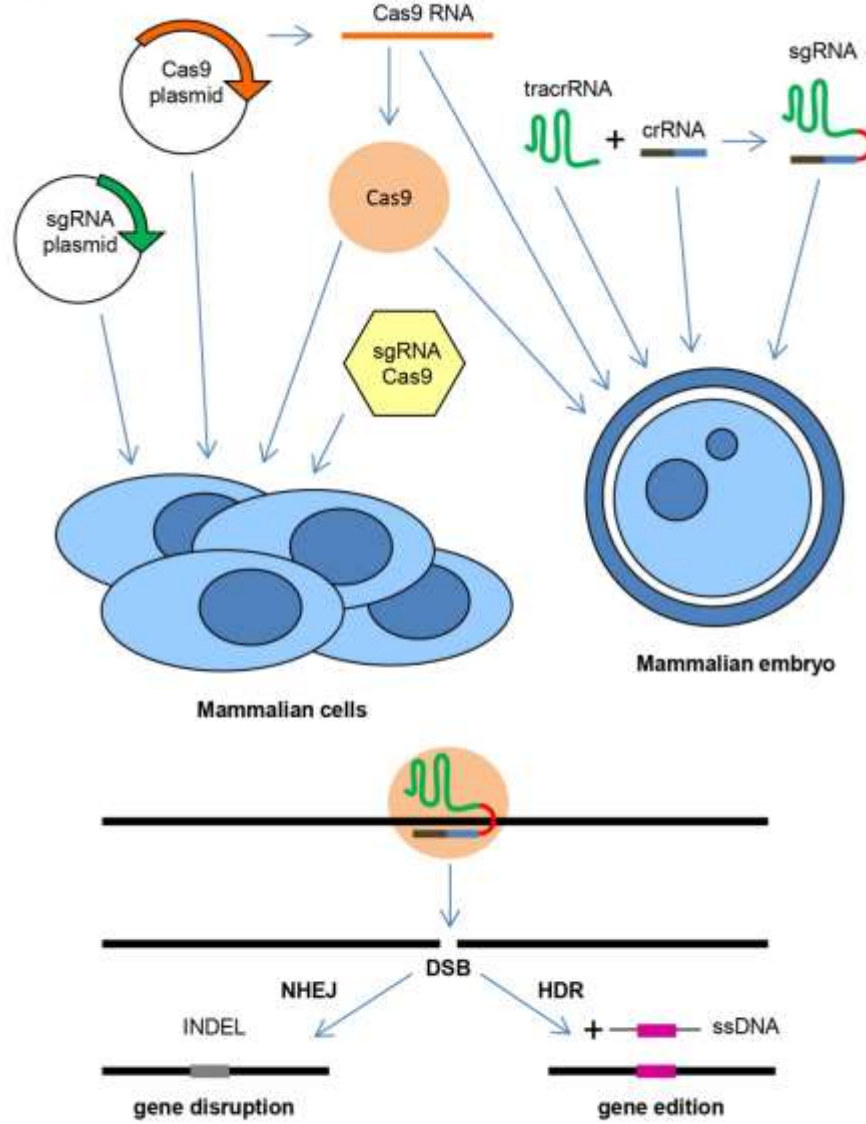


Francisco Juan Martínez Mojica

Prokaryotes



Eukaryotes



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

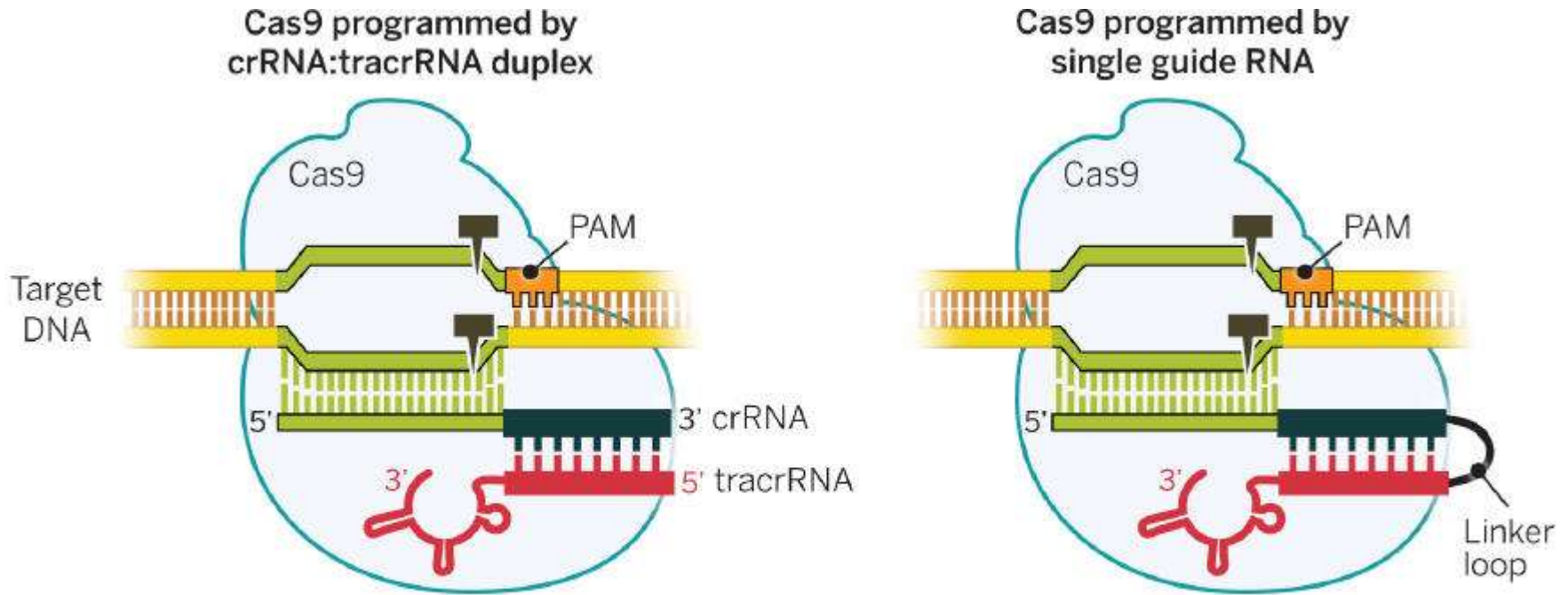
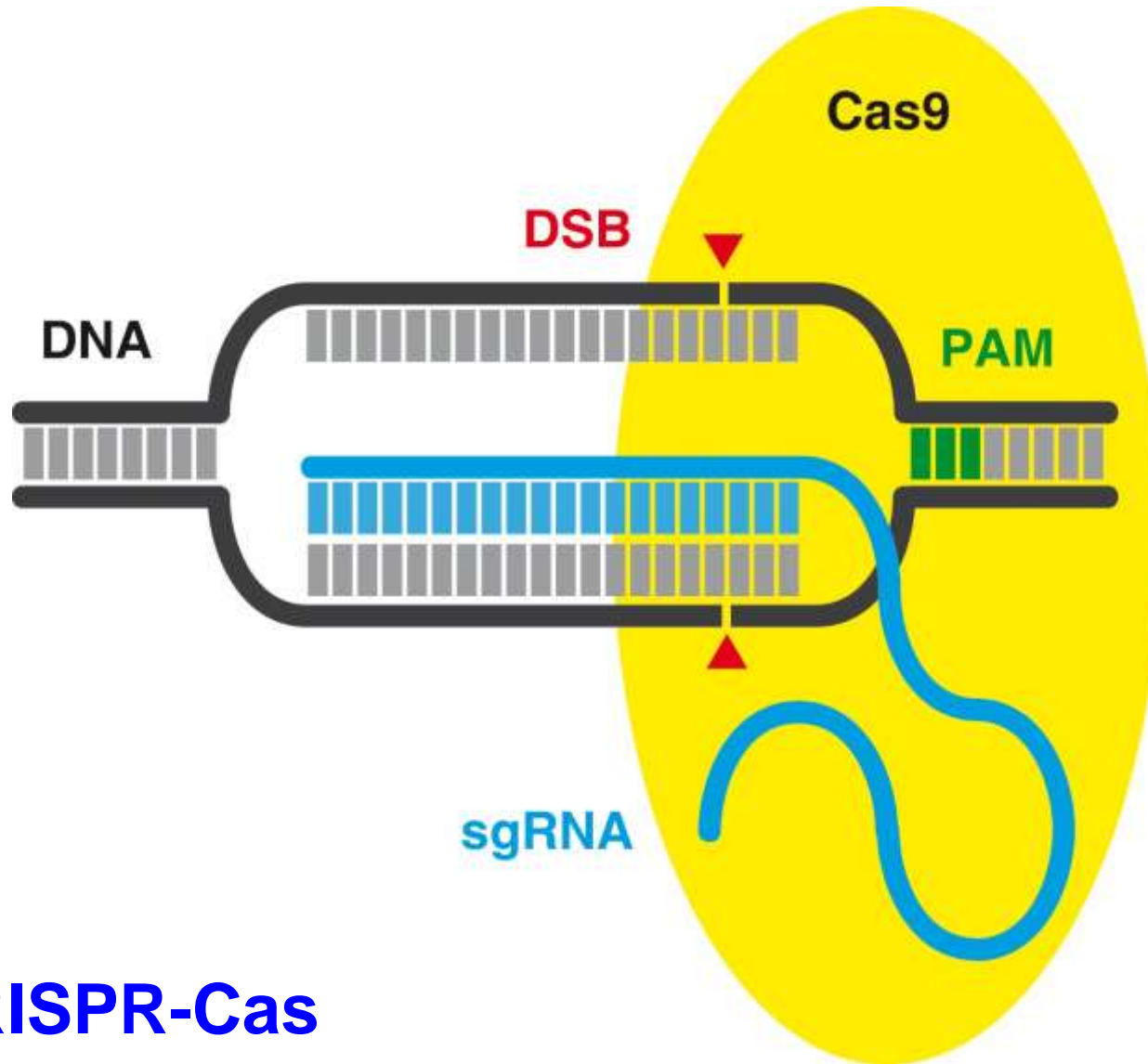


Fig. 3. Evolution and structure of Cas9. The structure of *S. pyogenes* Cas9 in the unliganded and RNA-DNA-bound forms [from (77, 81)].



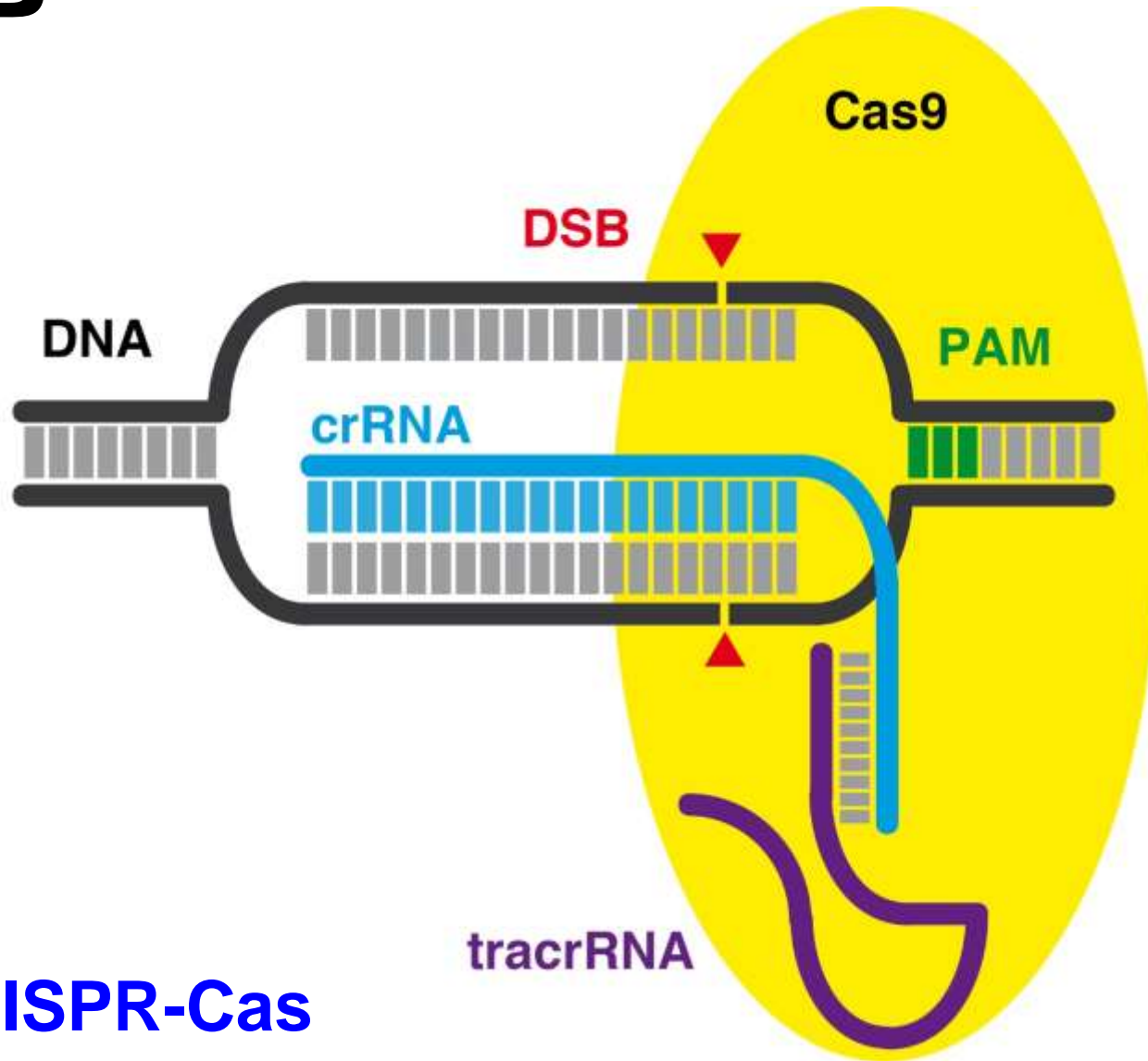
Jennifer Doudna
Emmanuelle Charpentier

Doudna & Charpentier (2014) Science

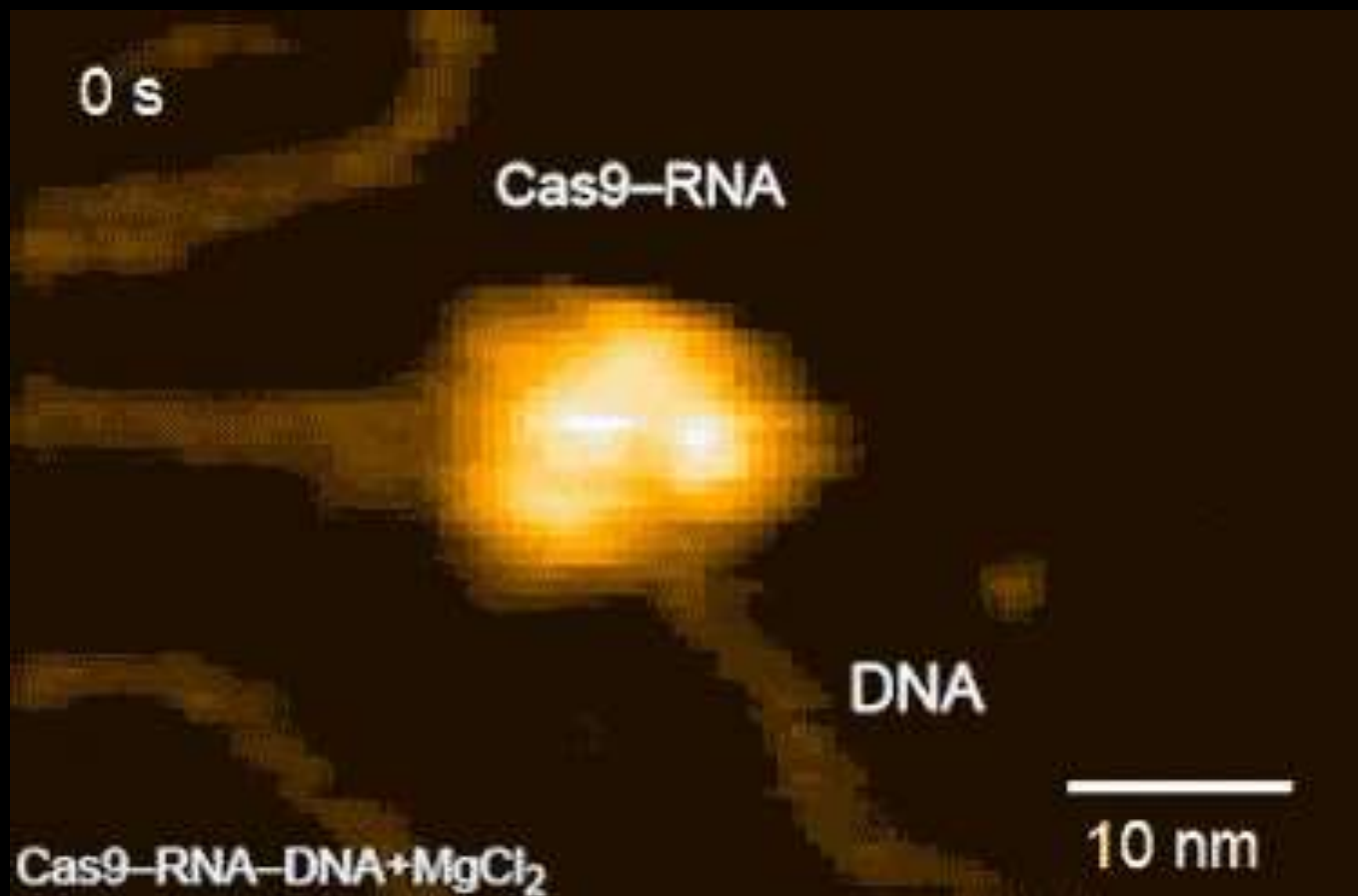


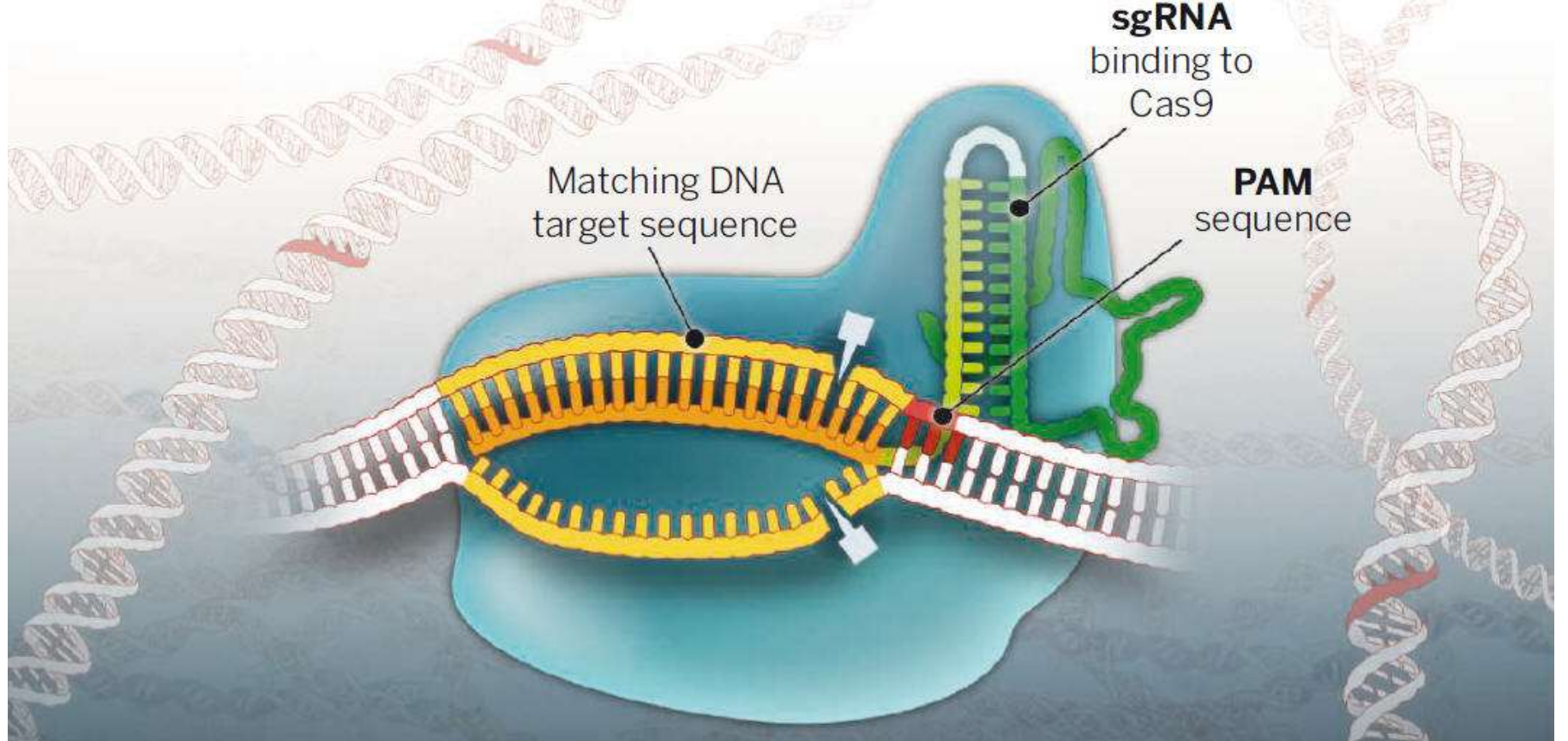
**The CRISPR-Cas
system**

RNP



The CRISPR-Cas system





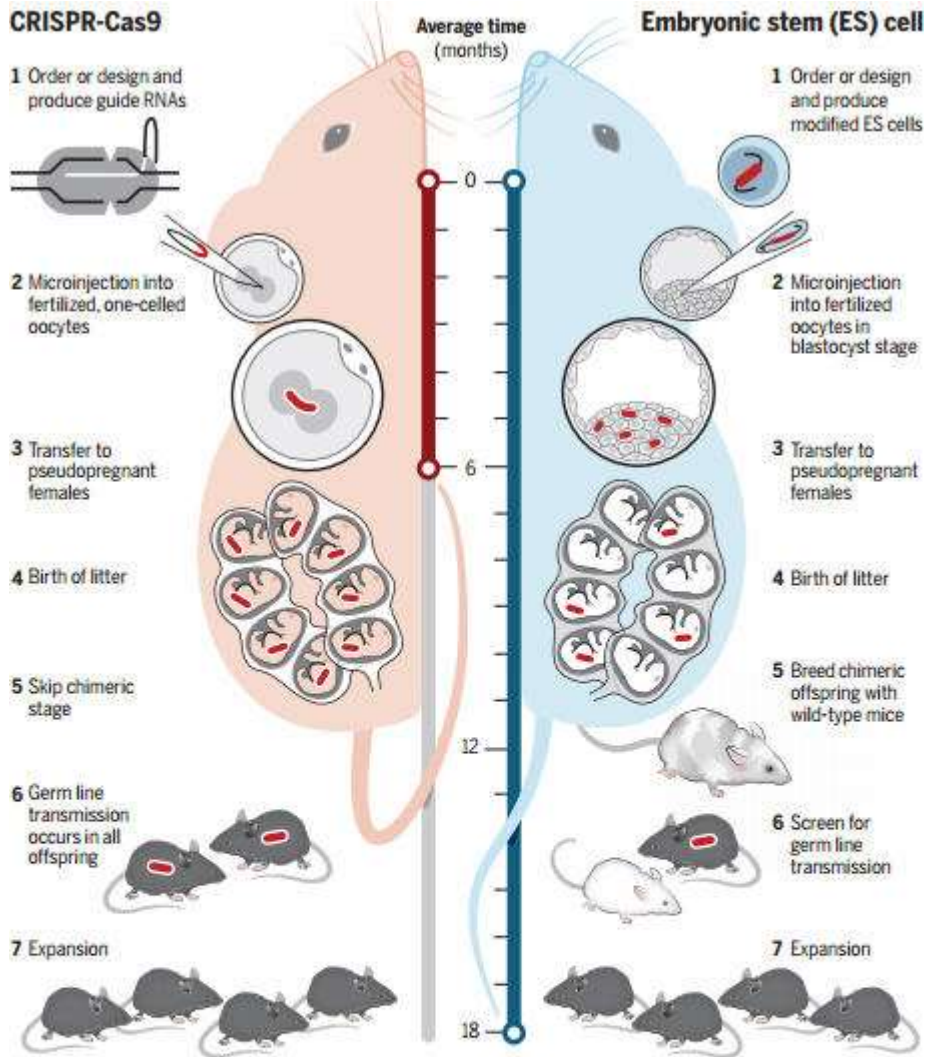
CRISPR-Cas9 development

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

CRISPR-Cas9 applications

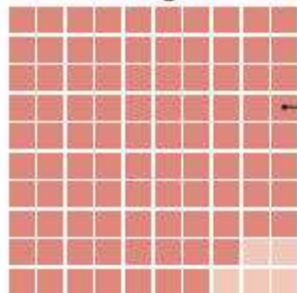
- Biological research
- Research and development
- Human medicine
- Biotechnology
- Agriculture
- ...

Gene Editing CRISPR vs ES cells



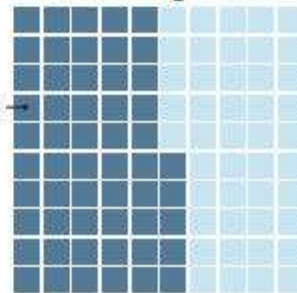
- **Generation of target mutations is faster with CRISPR (x3)**
- **Generation of target mutations is more efficient with CRISPR**

Success rate using CRISPR-Cas9



85%–95%

Success rate using ES cells

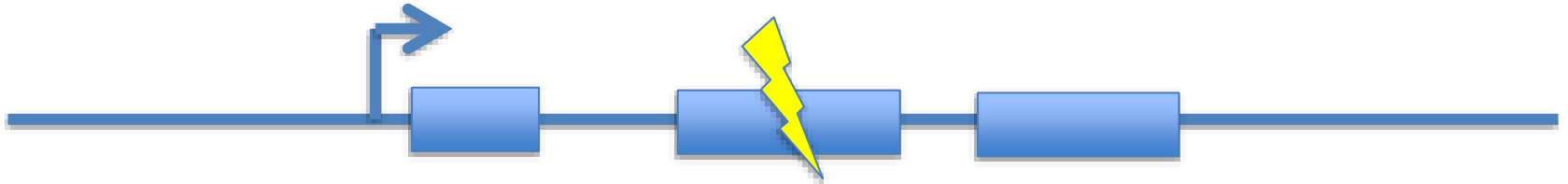


50%–55%

Types of CRISPR-Cas-induced genome editions

- INDELS: small insertions and deletions
- KOs: disrupting ORF
- Gene editions: point mutations
- KIs: introducing specific DNA segments
- Large deletions
- Inversions
- ...

Disrupting a gene: KO



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

We use the Tyrosinase gene (*Tyr*) in mice as experimental model to study mammalian gene regulation and ...

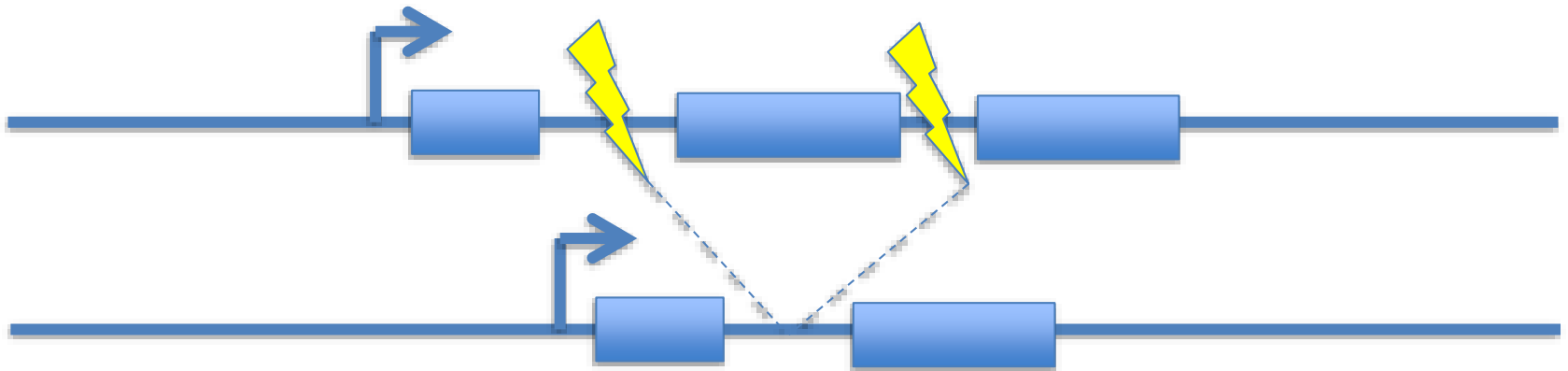


...as animal models of OCA1 albinism, a human rare disease

There are at least **20 genes** associated with albinism

Mouse	Human	Albinism	Mutations (HGMD)	
<i>Tyr</i>	<i>TYR</i>	OCA1	303	melanocytes
<i>Oca2</i>	<i>OCA2</i>	OCA2	154	
<i>Tyrbp1</i>	<i>TYRP1</i>	OCA3	16	
<i>Slc45a2</i>	<i>SLC45A2</i>	OCA4	78	
??	4q24	OCA5	1	
<i>slc24A5</i>	<i>SLC24A5</i>	OCA6	2	
<i>Lrmda</i>	<i>LRMDA</i>	OCA7	6	
<i>Gpr143</i>	<i>GPR143</i>	OA1	114	
<i>Sl38a8</i>	<i>SLC38A8</i>	FHONDA	8	
<i>Lyst</i>	<i>LYST</i>	CHS1	53	Melanosomes/lysosomes
<i>Hps1</i>	<i>HPS1</i>	HPS1	31	
<i>Ap3b1</i>	<i>AP3B1</i>	HPS2	20	
<i>Hps3</i>	<i>HPS3</i>	HPS3	7	
<i>Hps4</i>	<i>HPS4</i>	HPS4	13	
<i>Hps5</i>	<i>HPS5</i>	HPS5	11	
<i>Hps6</i>	<i>HPS6</i>	HPS6	9	
<i>Dtnbp1</i>	<i>DTNBP1</i>	HPS7	2	
<i>Bloc1s3</i>	<i>BLOC1S3</i>	HPS8	2	
<i>Bloc1s6</i>	<i>BLOC1S6</i>	HPS9	2	
<i>Ap3d1</i>	<i>AP3D1</i>	HPS10	1	

Deletions



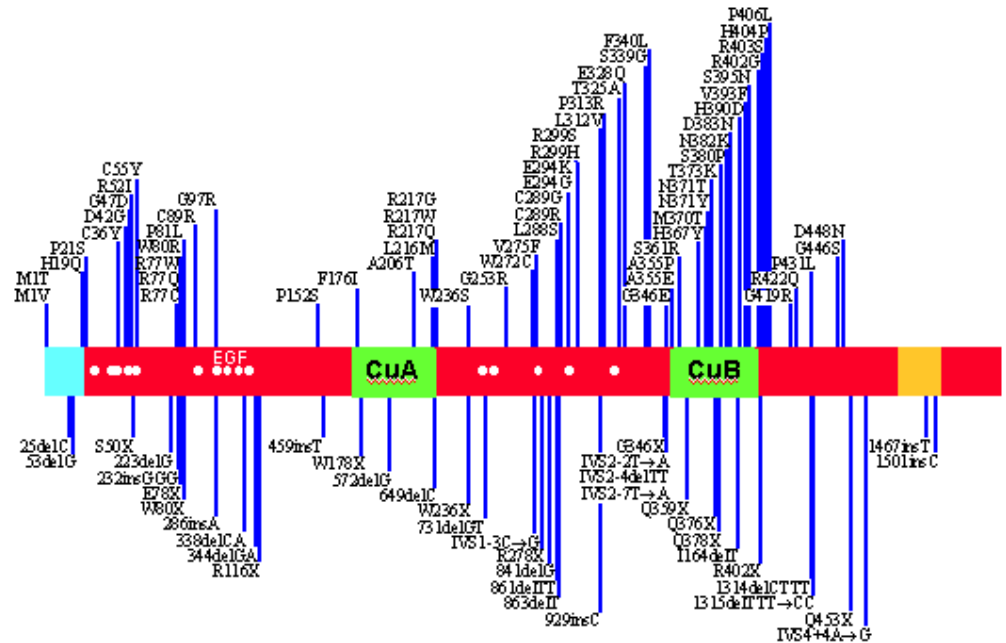
- Relatively straight forward, many alleles will be generated
- INDELS at both targeting sites will be **also** generated
- Consider **inversions** can also be generated
- Efficient protocol

Relevance of regulatory elements at the endogenous *Tyr* locus

Mutations in regulatory elements could possibly account for OCAI individuals (~30%) in which no other alterations are found within the tyrosinase locus



Missense Mutations



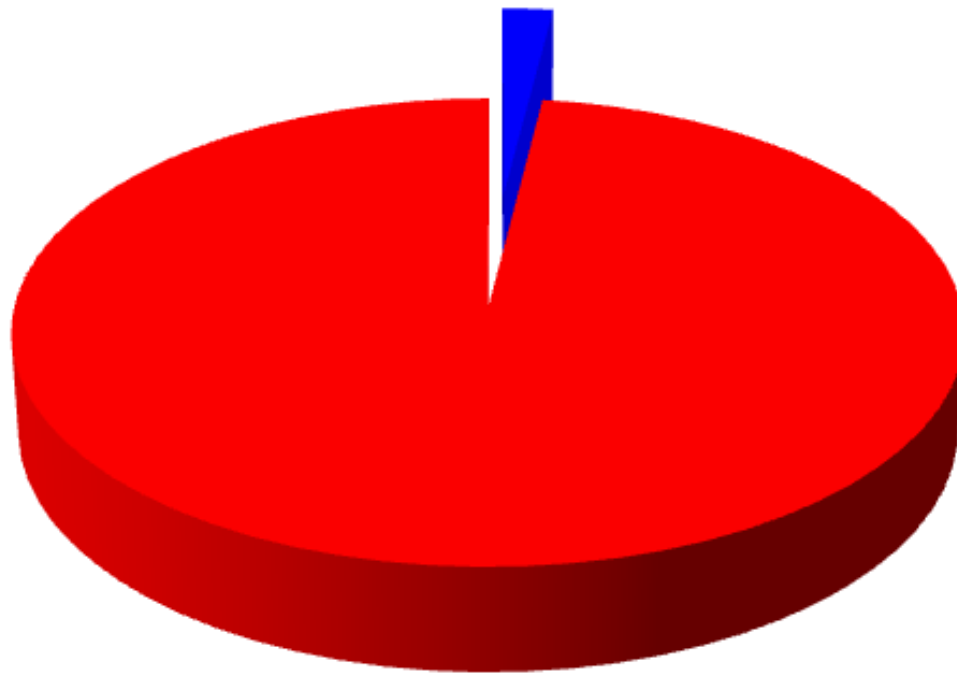
Nonsense, Frameshift and Splice Site Mutations
Oculocutaneous albinism type I

ciberer isciü

The non-coding genome

DNA coding sequences represent 2% genome

DNA non-coding sequences represent 98% genome

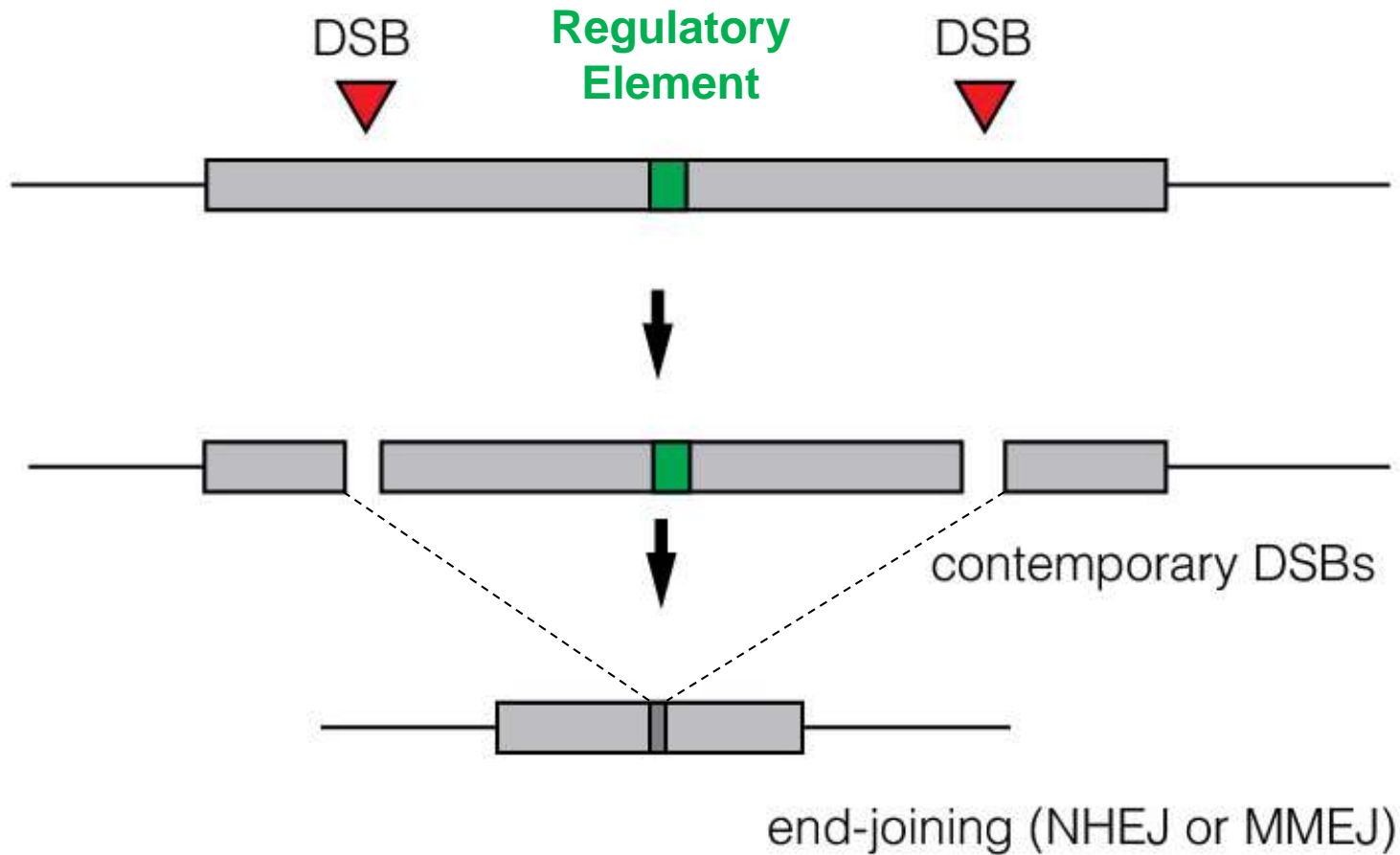


■ coding sequences
■ non-coding sequences



DNA non-coding sequences contain mainly:
DNA repetitive elements, mobile elements and
DNA regulatory elements

Alternative: using CRISPR-Cas9 genome editing to target *Tyr* regulatory elements



CRISPR-Cas9 genome editing

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

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

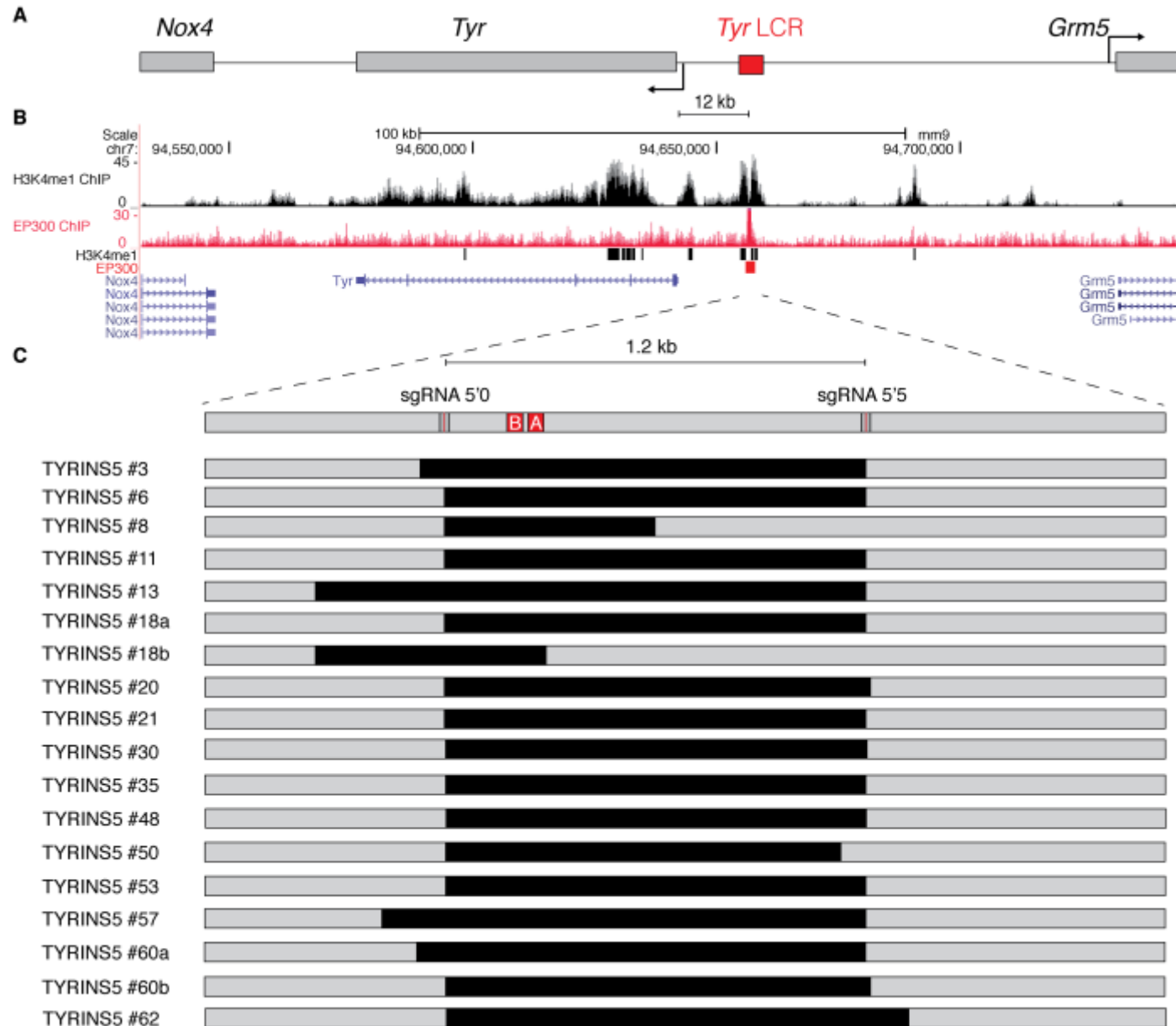


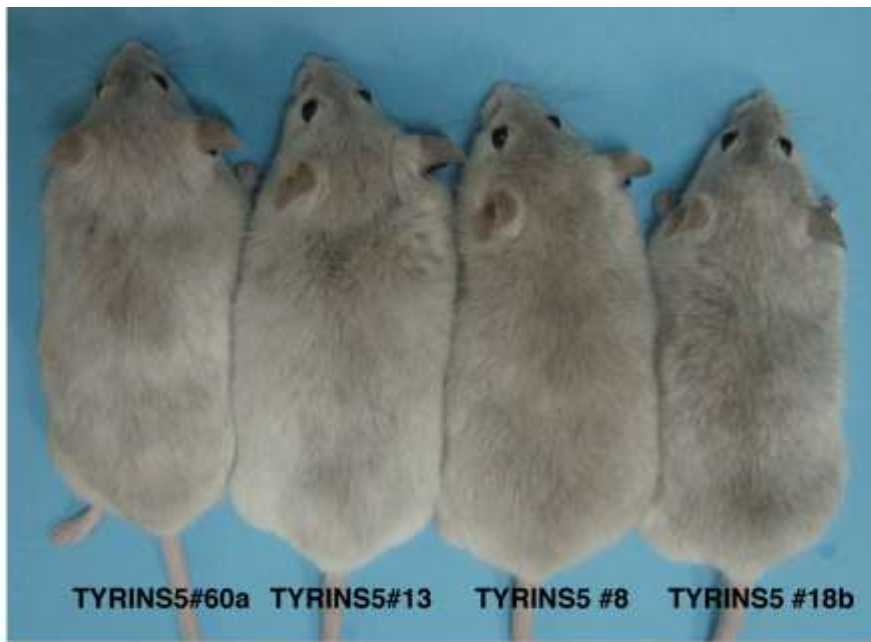
DpnII fragment interacting with Tyr promoter in the 3C assay



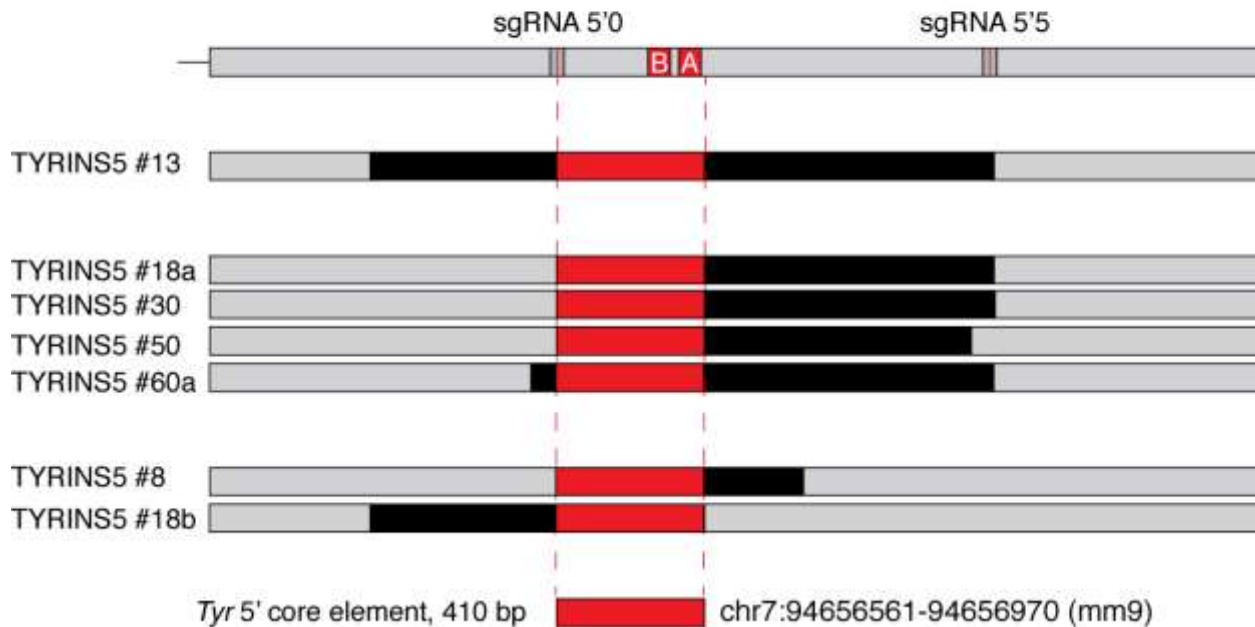
reference: CAAGAATTAAGTGTGACAGTGCAAGATAACAGGAAAATAA.....1170bp.....CTCTAGGCCAAAATTGCCTAGTTTTATCACTACAAAACCT
TYRINS5#18_1: CAAGAATTAAGTGTGACAGTGCAAGAT-----1170bp-----TTGCCTAGTTTTATCACTACAAAACCT
TYRINS5#18_1: CAAGAATTAAGTGTGACAGTGCAAGAT-----1170bp-----TTGCCTAGTTTTATCACTACAAAACCT

Many mutant deletion alleles generated upon targeting the 5' *Tyr* Boundary by CRISPR-Cas9



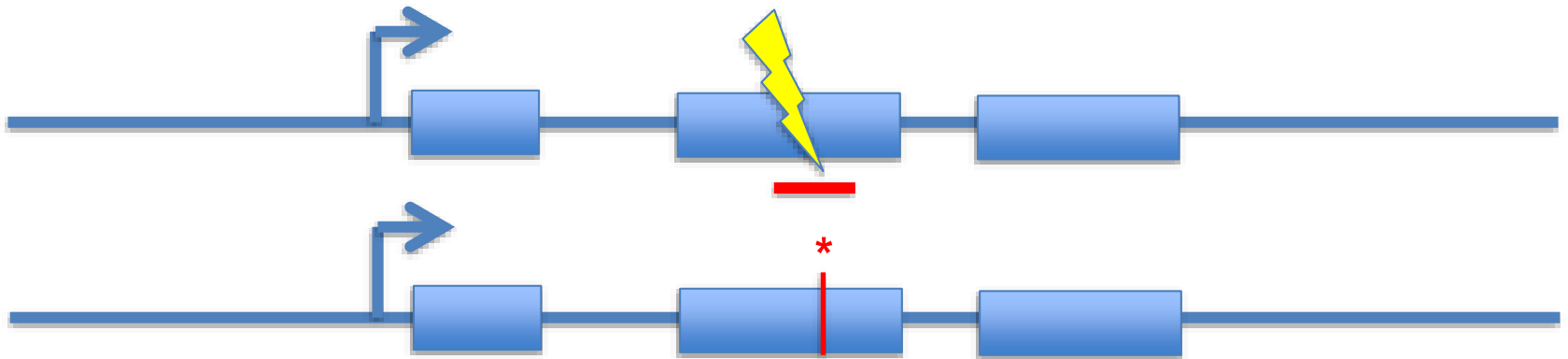


Comparing different *Tyr* 5' Boundary targeted alleles with similar phenotypes reveals the location of the functionally relevant endogenous regulatory DNA sequences



Genetic analysis now possible in mice!

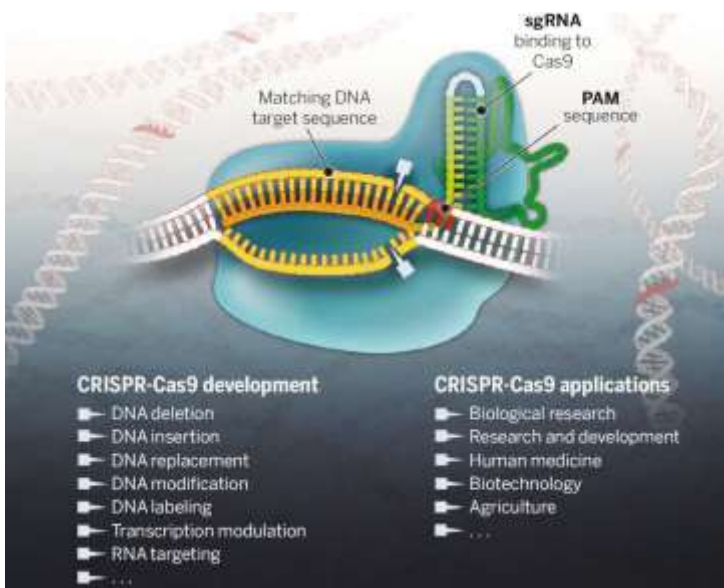
Point mutations



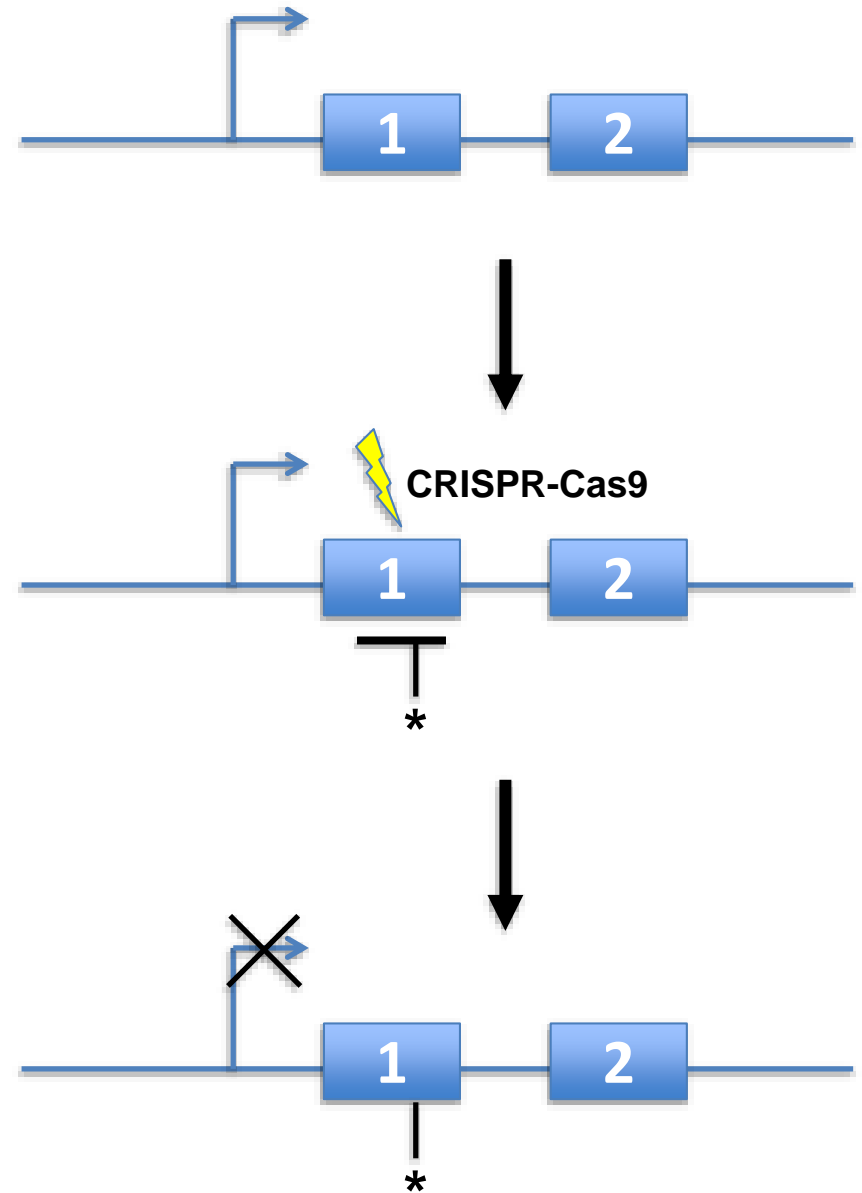
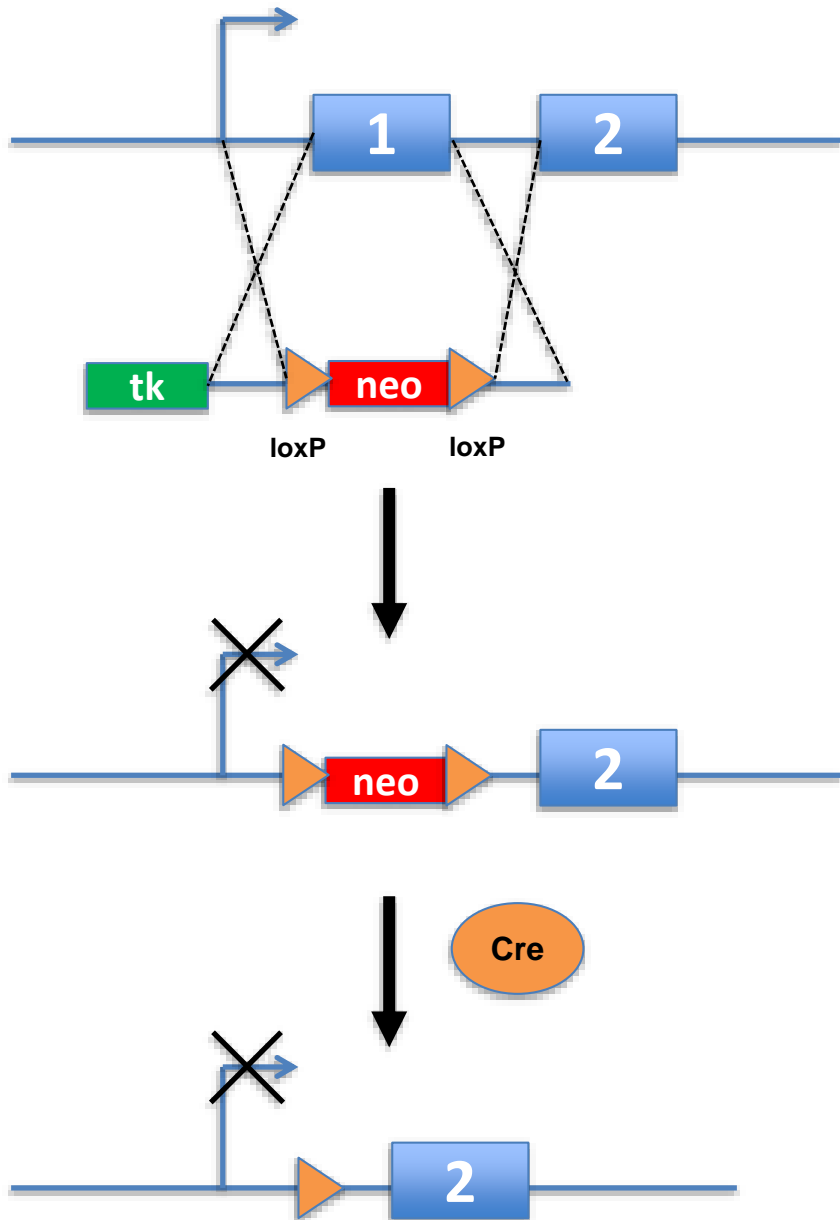
- Relatively straight forward, but can be challenging, many alleles will be generated
- INDELS will mostly be **also** generated
- Relatively doable protocol (however, if expected mutation not found, the number of embryos/animals to be used rapidly increases)
- Optimally: must have screening protocols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

AVATAR CRISPR mice

- Easier approach to reproduce human mutations in animal models



“Classical” versus CRISPR-mediated mutagenesis



El Málaga juega en primera división



El Málaga**a** juega en primera división



El Málaga juega en primera división

El Málagj uegae nprimer adivisió n

El Málagj uegae nprimer adivisió n

El museo Picasso está en Málaga

a



El museo Picasso **o** está en Málaga

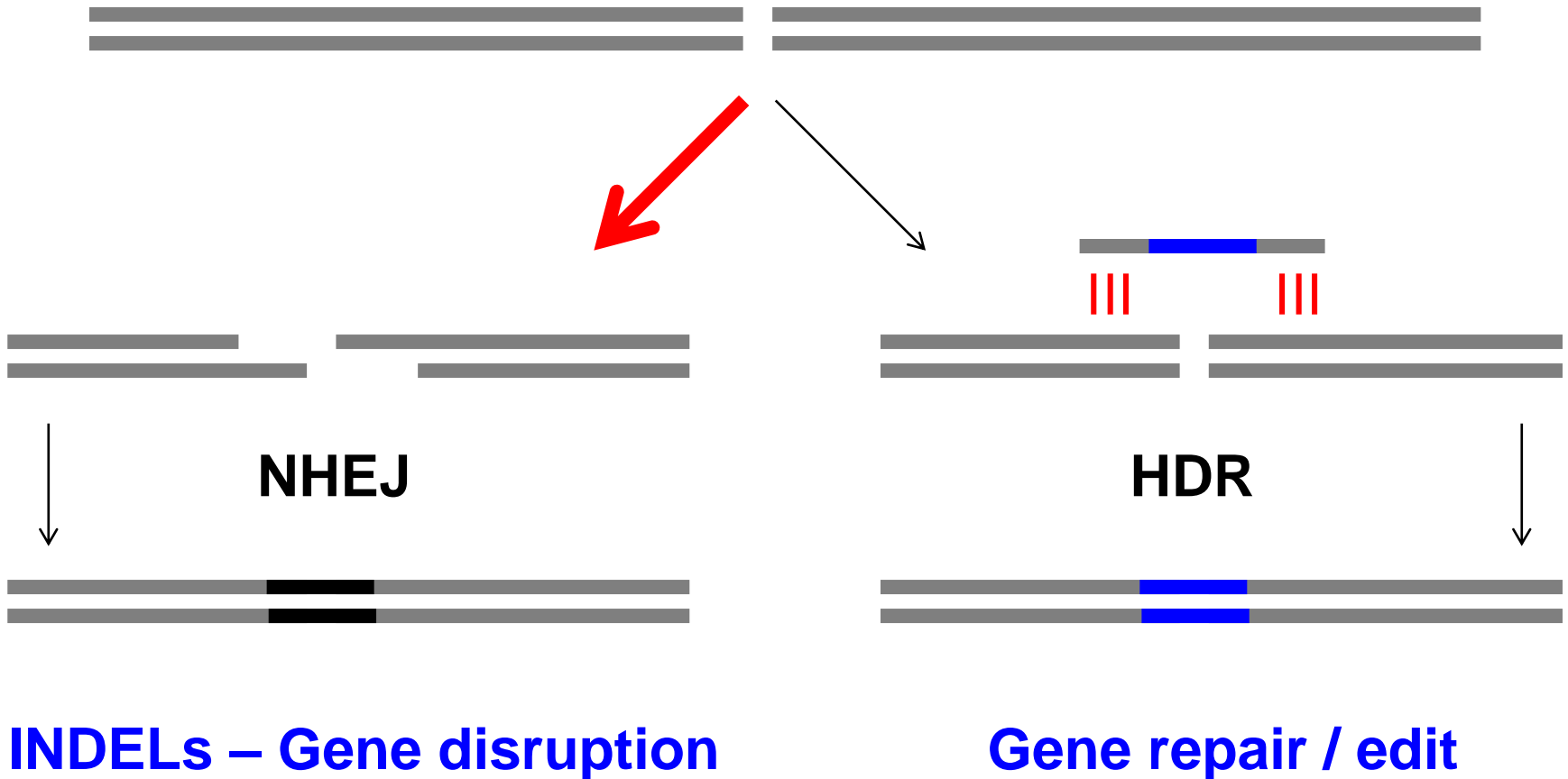
El museo Picassa está en Málaga



Treatments



Improving Gene Edition



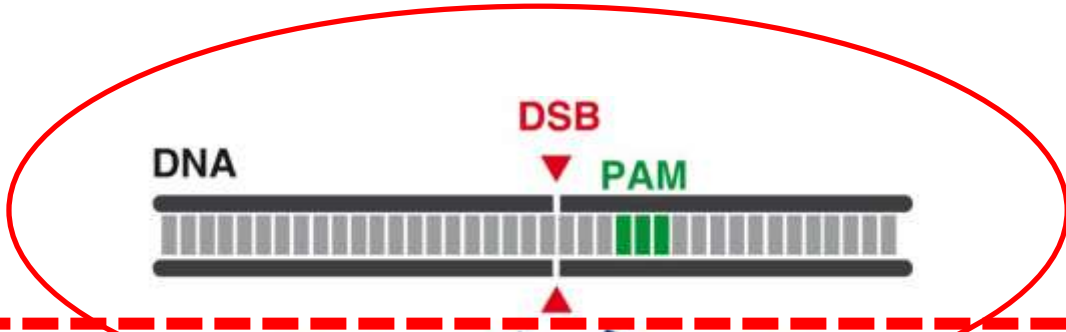
Current limitations of CRISPR

- **On-target uncertainty:** many alleles are generated through NHEJ
- Most/all founder edited-organisms are **mosaic**
- Error-prone NHEJ is the default repairing pathway
- Donor template-specific HDR is not the preferred repairing pathway
- **Off-targets:** similar target sequences can be altered
- Reaching a significant number of target cells (viral & non-viral delivery systems)

Current limitations of genome editing

Off-target effects

Related to CRISPR



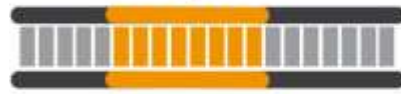
Unrelated to CRISPR

NHEJ

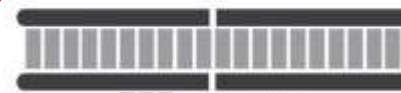
HDR



INDELS



Gene Disruption



HR



Gene Edition

On-target effects
Mosaicism

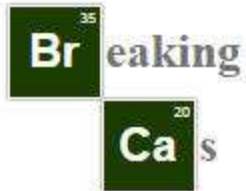
HDR is not the preferred repairing pathway

Off-targets: we can deal with them

- Off-targets depend mainly on the selected guide RNA and, to a lesser extent, on the Cas (different Cas have different properties)
- New algorithms developed for selecting optimal guide RNAs (Breaking-Cas, CRISPOR, Crispr-GOLD...)
- Can be reduced to an acceptable minimum by reducing the amount (Cas protein, not RNA or DNA) and the time of action of Cas nucleases (inhibitors)

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, Mónica 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

Or s

<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	0.388	0.079	0.445	0.508	0.613	0.851	0.732	0.828	0.615	0.804	0.695	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

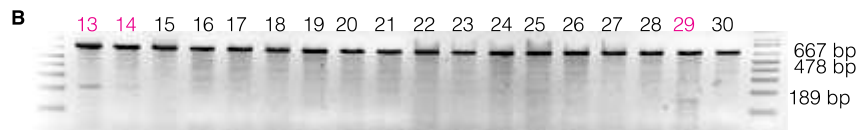
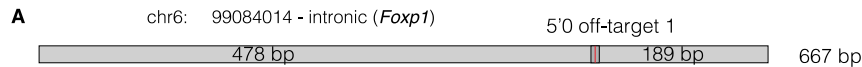
Vivek Iyer, Bin Shen, Wensheng Zhang, Alex Hodgkins, Thomas Keane, Xingxu Huang & William C Skarnes

Affiliations | Corresponding authors

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

Published online 28 May 2015

Confirmed by NGS



C

sgRNA 5'0: CCTGTTATCTTGCACCTGTCACAC

reference: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#13_1: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#13_2: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#13_3: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#14_1: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#14_2: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#14_3: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#13_1: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#29_1: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

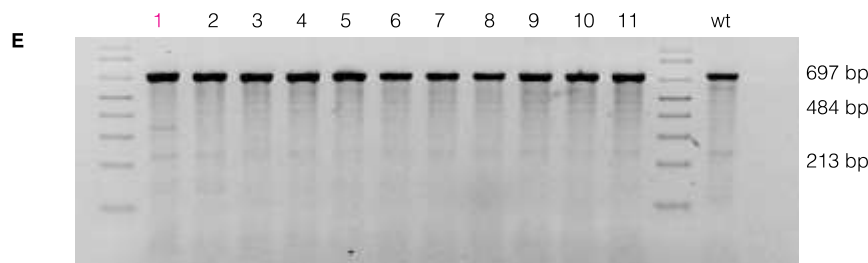
TYRINS5#29_2: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#57_1: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#57_2: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#57_3: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA

TYRINS5#57_4: TGCACAGGGTATTTACTGATCCGGTTATCTTGTCTGTGACAGGCAGAATCAATCAATCAGGA



F

sgRNA 5'5: CCAAAATGCGCTAGTTTTATCAC

reference: GTATTCACGTGCACCTGTTACCAAAAATGCGCTGCTTTTATCTGTGAATCTACCTTTCGTTGAC

TYRINS5#1_1: GTATTCACGTGCACCTGTTACCAAAAATGCGCTGCTTTTATCTGTGAATCTACCTTTCGTTGAC

TYRINS5#1_2: GTATTCACGTGCACCTGTTACCAAAAATGCGCTGCTTTTATCTGTGAATCTACCTTTCGTTGAC

TYRINS5#1_3: GTATTCACGTGCACCTGTTACCAAAAATGCGCTGCTTTTATCTGTGAATCTACCTTTCGTTGAC

TYRINS5#24_1: GTATTCACGTGCACCTGTTACCAAAAATGCGCTGCTTTTATCTGTGAATCTACCTTTCGTTGAC

TYRINS5#24_2: GTATTCACGTGCACCTGTTACCAAAAATGCGCTGCTTTTATCTGTGAATCTACCTTTCGTTGAC

TYRINS5#24_4: GTATTCACGTGCACCTGTTACCAAAAATGCGCTGCTTTTATCTGTGAATCTACCTTTCGTTGAC

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



Reference: AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCAGCGGTAGGGTTGATTTCAGGAAATGTAA
B9040.1 AACATTGGAGGAGCTGC ACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAG-----GTAGGGTTGATTTCAGGAAATGTAA
B9040.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGGTAAGGTAGG-TTGATTTCAGGAAATGTAA
B9040.3 AACACTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAG-----GTAGGGTTGATTTCAGGAAATGTAA
B9040.4 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGC-----AGGGTTGATTTCAGGAAATGTAA
B9040.5 CAAGCTCCTGCCCCACTTTCAAAGCTGTACTGAACGTCAGTTTTCTTCTCCACCAGATTCTGCAAGACCTTGCACCGGG----- (437bp) -----
B9040.6 ----- (561bp) -----
B9041.1 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCTGTTACCTAGGGTTGATTTCAGGAAATG
B9041.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAAC-----AGGGTTGATTTCAGGAAATGTAA
B9041.3 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACA-----GGTAGGGTTGATTTCAGGAAATGTAA
B9041.4 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACG-----GGTAGGGTTGATTTCAGGAAATGTAA
B9041.5 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACA-----GGTAGGGTTGATTTCAGGAAATGTAA
B9042.1 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCAGCGGTAGGGTTGATTTCAGGAAATGTAA
B9042.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAAT-----GGTAGGGTTGATTTCAGGAAATGTAA
B9042.3 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAA-TGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCAGCGGTAGGGTTGATTTCAGGAAATGTAA
B9042.4 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAAT-----GGTAGGGTTGATTTCAGGAAATGTAA
B9043.1 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAAT-----GGTAGGGTTGATTTCAGGAAATGTAA
B9043.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCACACTGGTAGGGTTGATTTCAGGAAATG
B9043.3 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAAT-----GGTAGGGTTGATTTCAGGAAATGTAA
B9043.4 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGATAGACATGTCGAGGA----- (134bp) -----
B9044.1 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAAT-----GGTAGGGTTGATTTCAGGAAATGTAA
B9044.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAAC-----AGGGTTGATTTCAGGAAATGTAA
B9045.1 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTAT-----CAAGGTAGGGTTGATTTCAGGAAATGTAA
B9045.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAAT-----GGTTGATTTCAGGAAATGTAA
B9045.3 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTAT-----CAAGGTAGGGTTGATTTCCGGAAATGTAA
B9046.1 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCACCTAGGTAGGGTTGATTTCAGGAAATG
B9046.2 AACATTG----- (87bp) -----TAGGGTTGATTTCAGGAAATGTAA
B9046.3 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCAATGGTAGGGTTGATTTCAGGAAATGTA
B9046.4 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCACCTAGGTAGGGTTGATTACAGGAAATG
B9060.1 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACA-----GGTAGGGTTGATTTCAGGAAATGTAA
B9060.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACA-----GGTAGGGTTGATTTCAGGAAATGTAA
B9060.3 GACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACA-----GGTAGGGTTGATTTCAGGAAATGTAA
B9060.4 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCT-----GTTGATTTCAGGAAATGTAA
B9064.1 AACATCGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACA-----GGTAGGGTTGATTTCAGGAAATGTAA
B9064.2 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCAAAAATGGTAGGTAGGGTTGATTTCAGG
B9064.3 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGCAAAAATGGTAGGTAGGTAGGGTTGATTTCAGG
B9064.4 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCAGGAGTTGAGAAAAATGGTAGGTAACAGC-----AGGGTTGATTTCAGGAAATGTAA
B9064.5 AACATTGGAGGAGCTGCCACTGCTATTGGGGACCCACCAAATGTTATCATTGTTTCCAATCA-----GGTAGGGTTGATTTCAGGAAATGTAA

CRISPR-Cas is the future

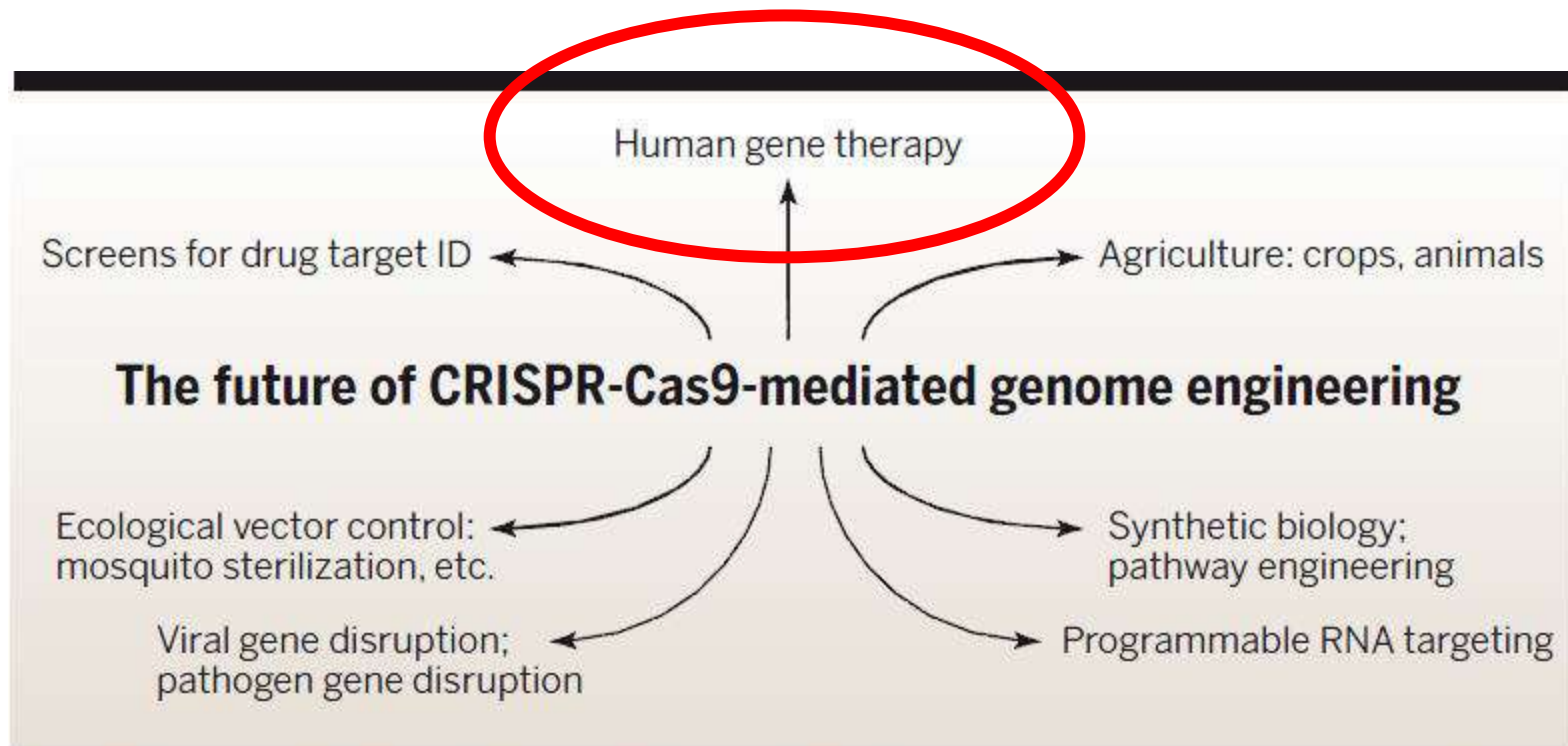
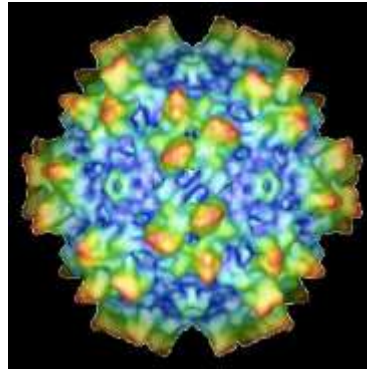


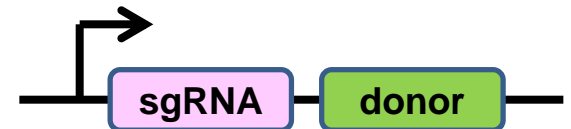
Fig. 6. Future applications in biomedicine and biotechnology. Potential developments include establishment of screens for target identification, human gene therapy by gene repair and gene disruption, gene disruption of viral sequences, and programmable RNA targeting.

CRISPR tools and somatic gene therapy of human rare diseases



Adeno Associated Virus
AAV

Different serotypes
with diverse tropism
to different cellular types
Cargo ~4.7 kb



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

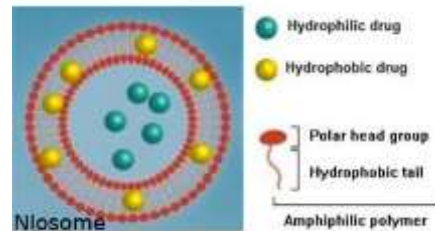


CRISPR-mediated gene therapy of a human rare disease: chronic granulomatous disease (CGD) in human iPS cells

**Challenge:
multiple alleles are
generated**

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



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)



- 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



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



bioRxiv
beta
THE PREPRINT SERVER FOR BIOLOGY

5 Jan 2018

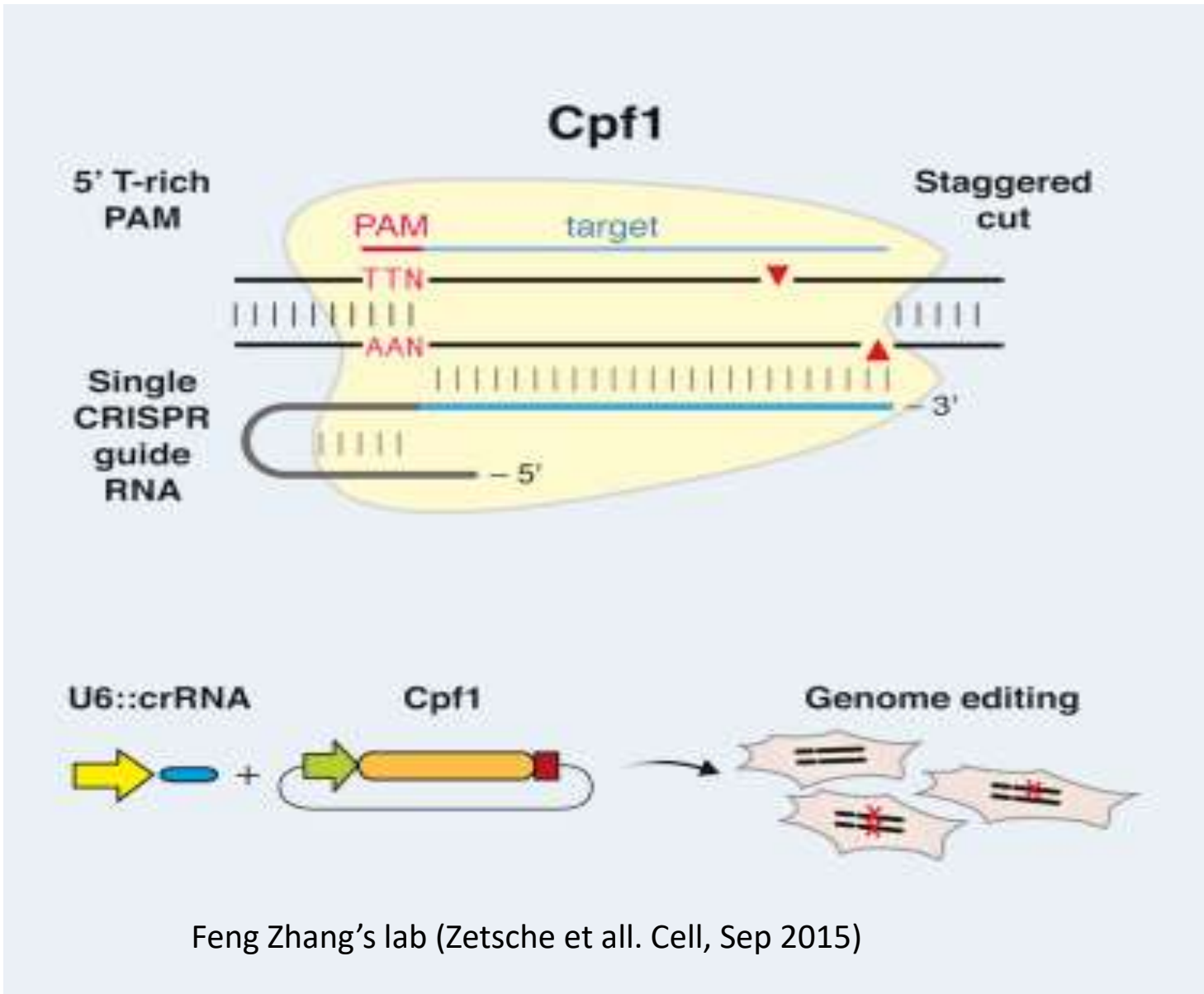
New Results

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

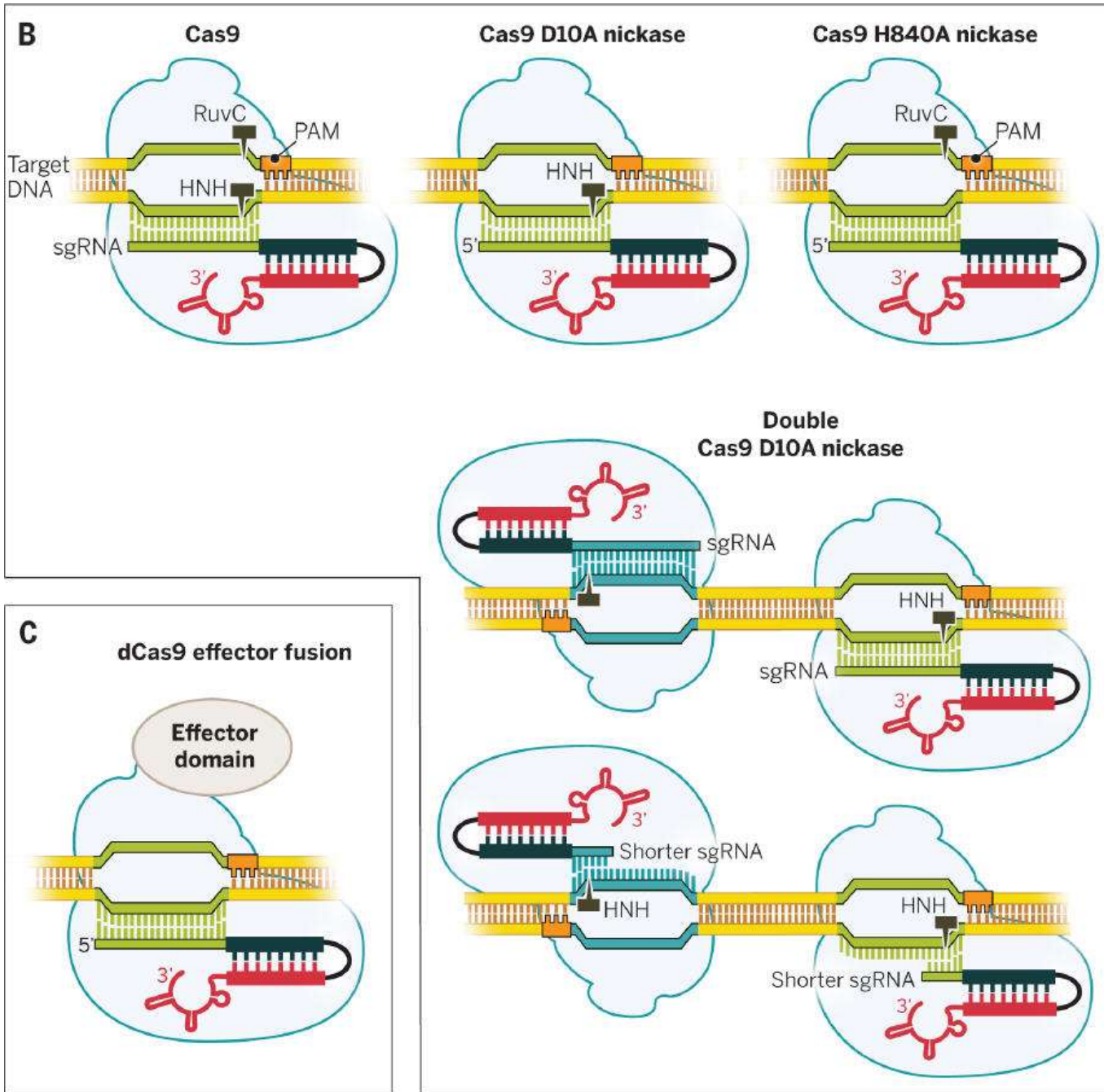
Carsten Trevor Charlesworth, Priyanka S Deshpande, Daniel P Dever, Beruh Dejene, Natalia Gomez-Ospina, Sruthi Mantri, Mara Pavel-Dinu, Joab Camarena, Kenneth I Weinberg, Matthew H Porteus

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

Alternative Cas-like proteins



Feng Zhang's lab (Zetsche et al. Cell, Sep 2015)



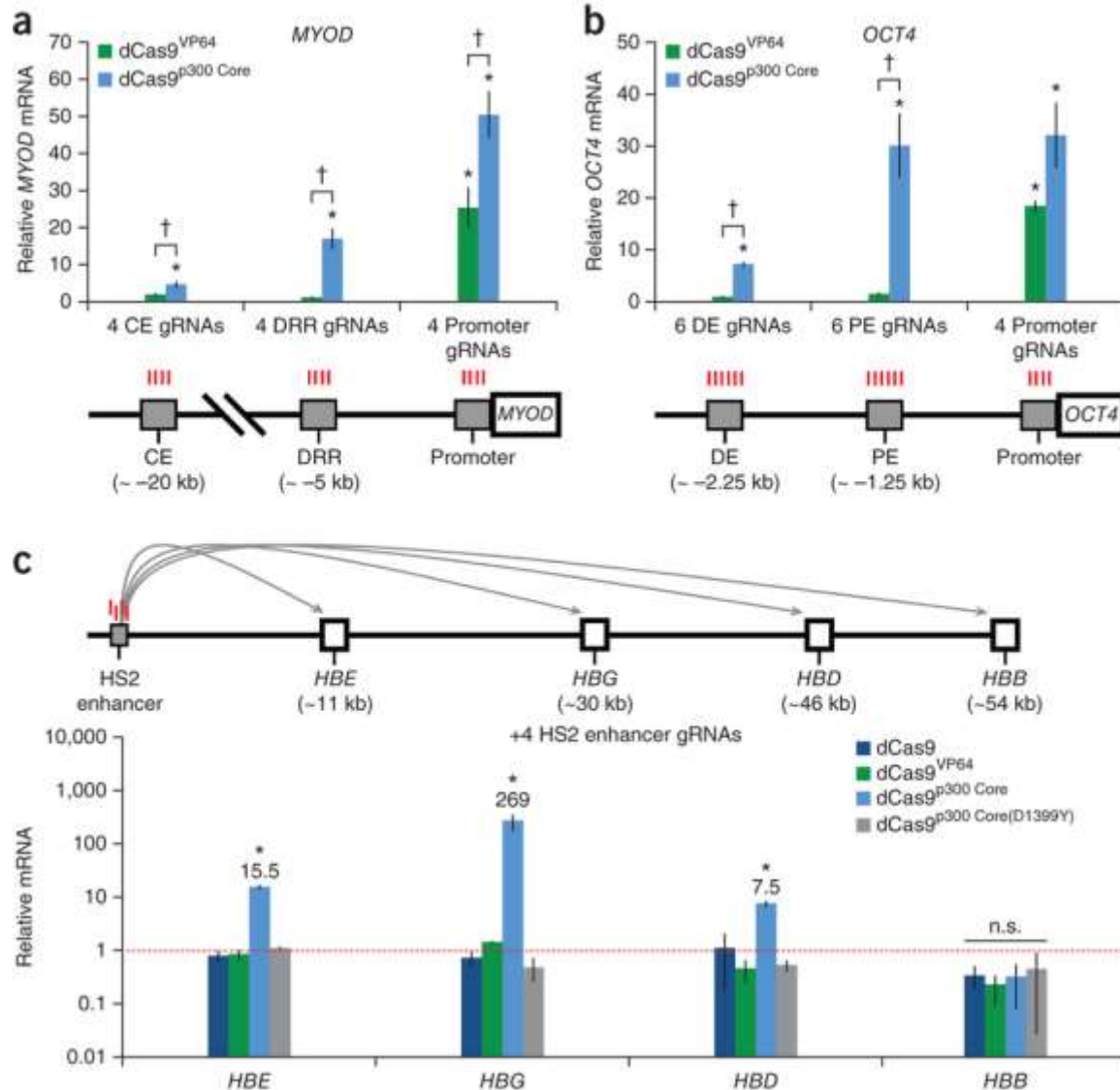
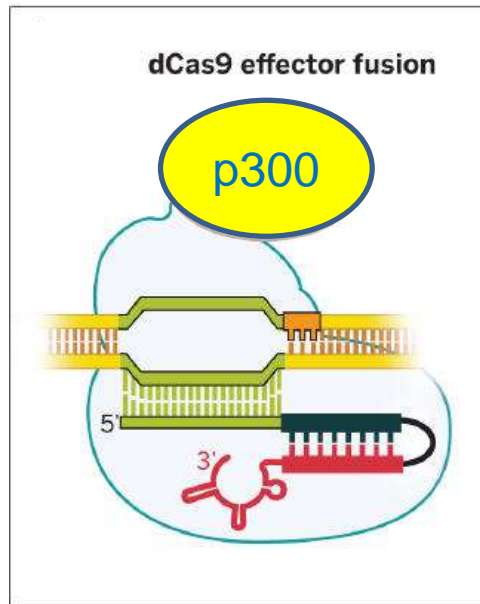
Targeting acetylation of Histone H3 Lysine 27 in the genome

Activating gene expression by CRISPR-dCas9/p300

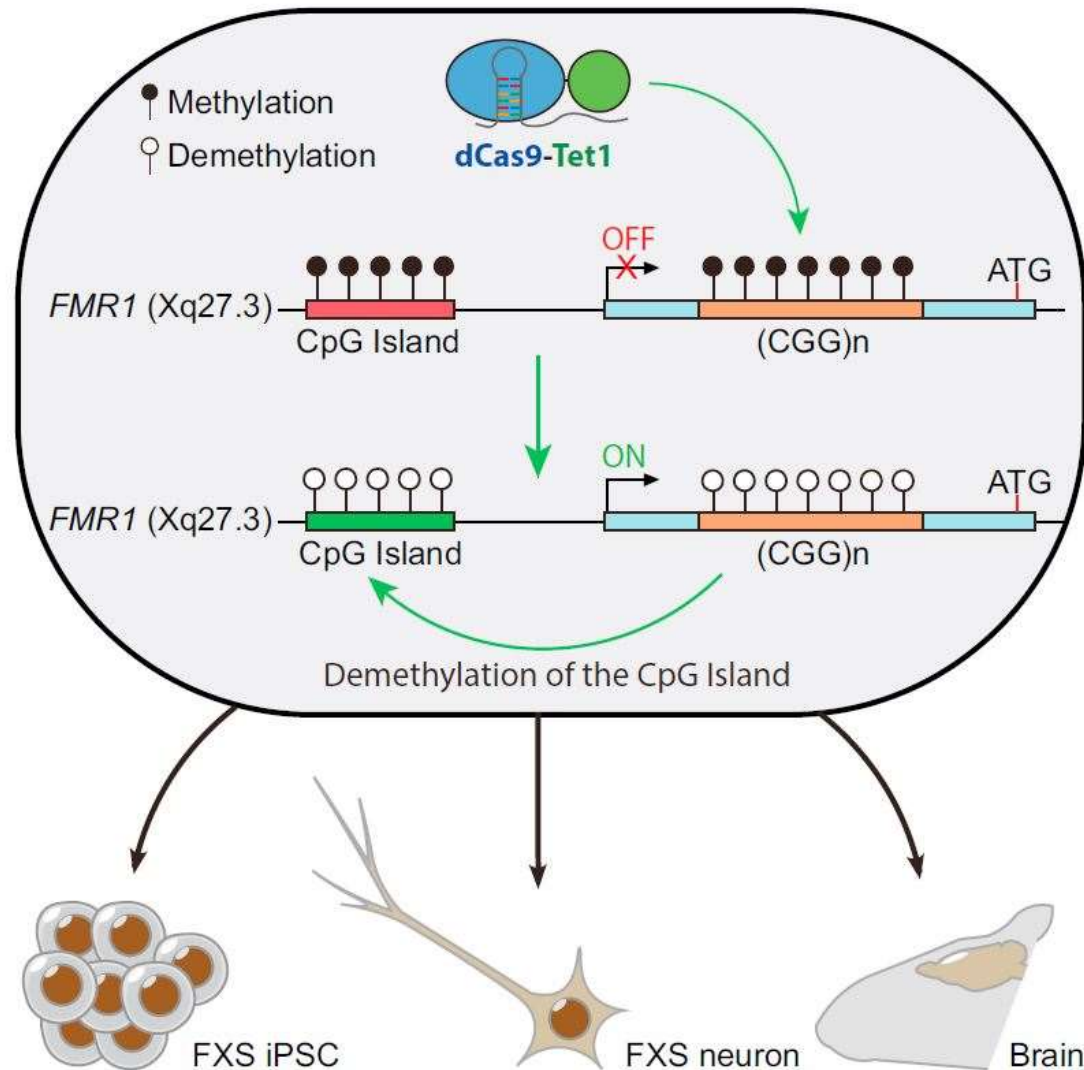
Epigenome editing by a CRISPR-Cas9-based acetyltransferase activates genes from promoters and enhancers

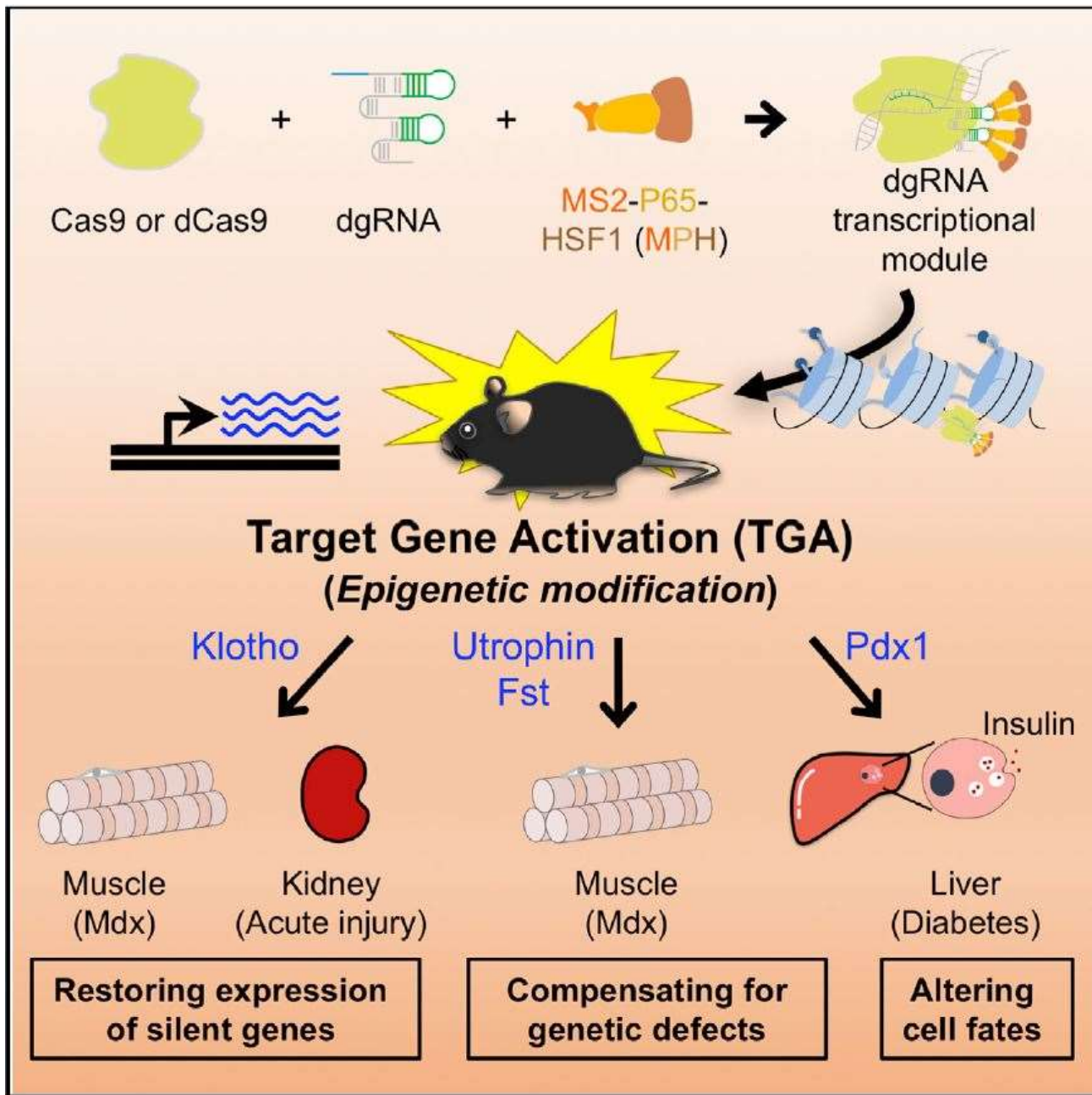
Hilton *et al.*

Nature Biotechnology 33, 510–517 (2015)



CRISPR-Cas rescues Fragile X syndrome

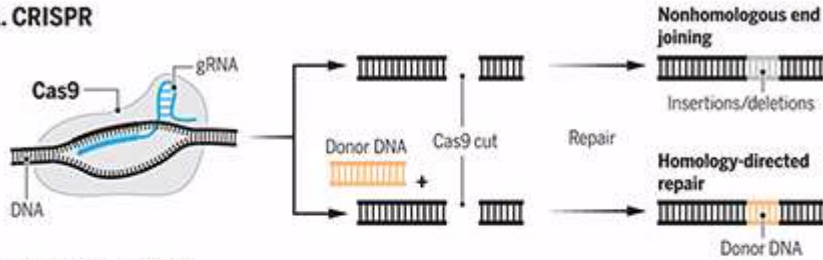




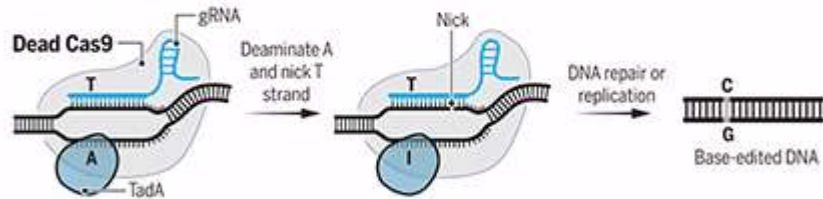
Getting to the point of mutations

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.

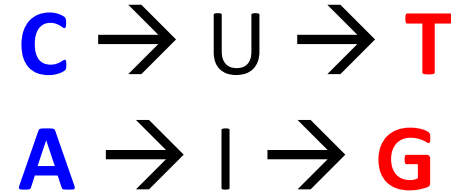
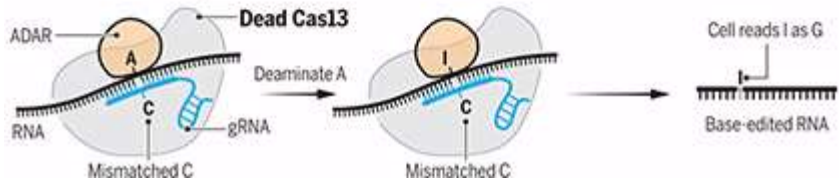
1. CRISPR



2. DNA base editing



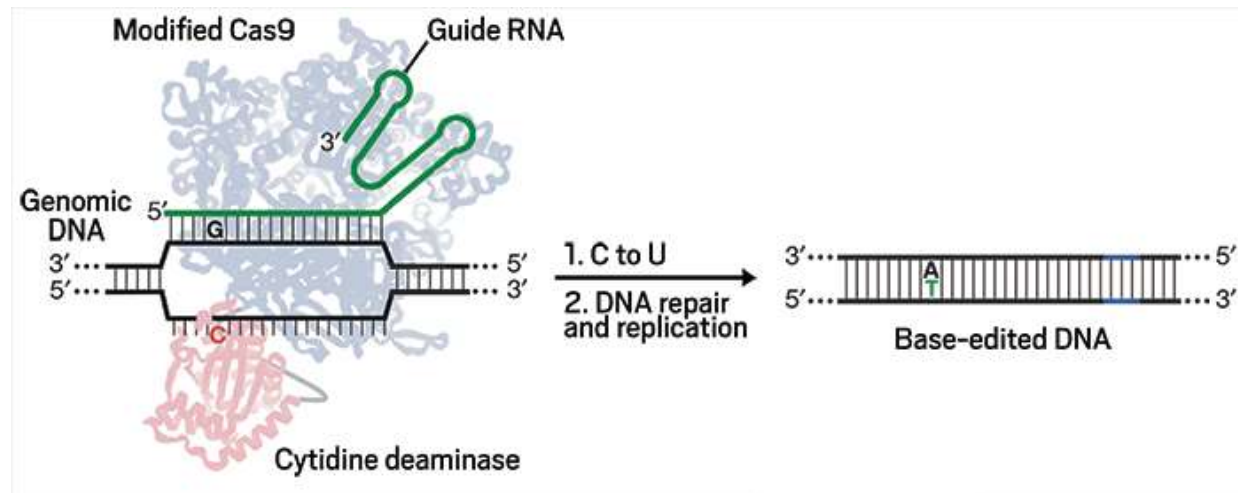
3. RNA base editing



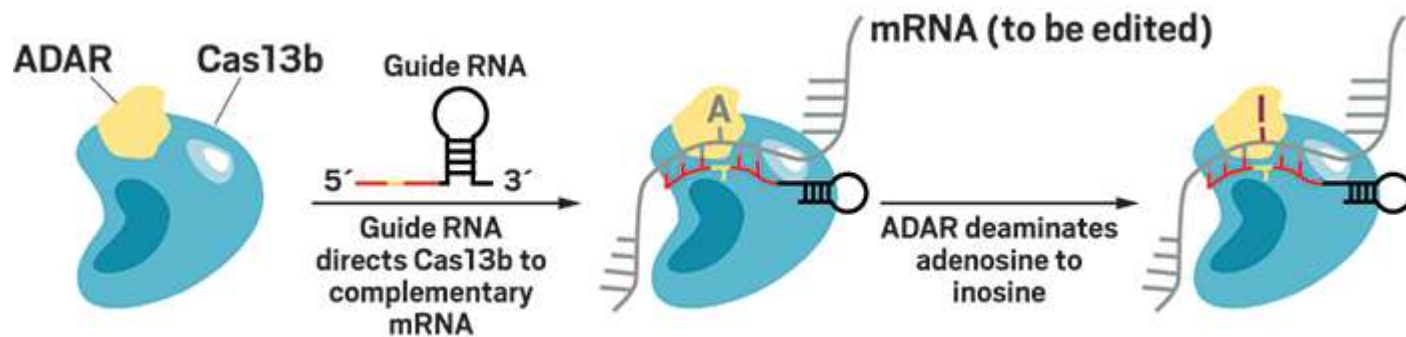
Kim et al. Nat Biotech. 2017

David Liu Lab

CRISPR-derived BASE EDITORS



CRISPR 2.0 (editing RNA)





SHERLOCK

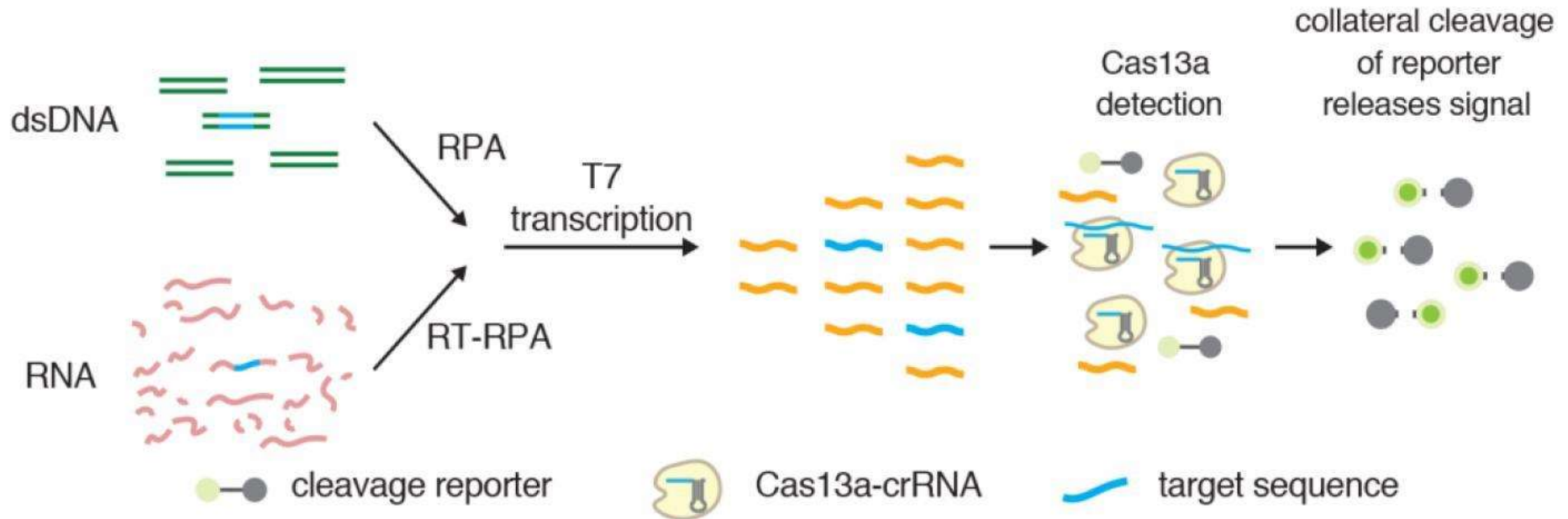


Gootenberg et al. Science 2017

CRISPR-Cas as a diagnostic tool

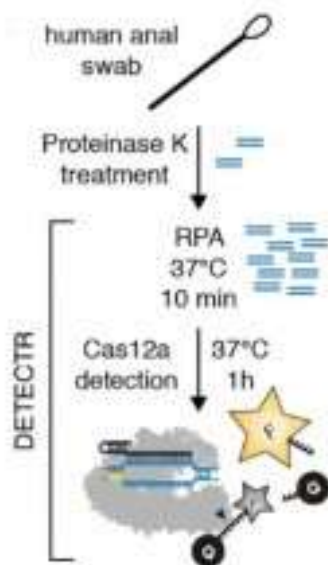
1

Feng Zhang Lab



CRISPR-Cas as a diagnostic tool - 2

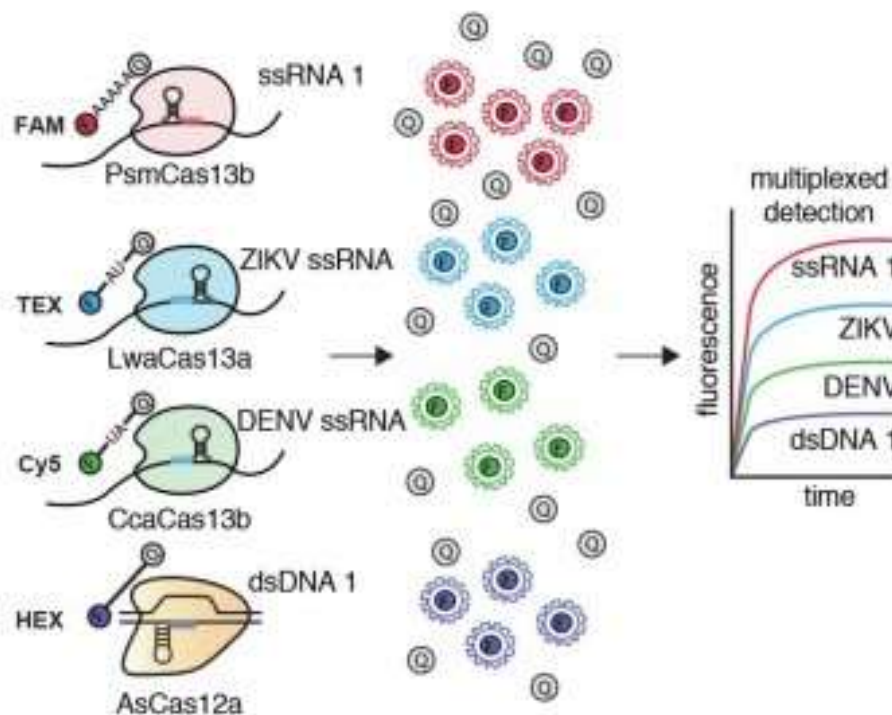
Doudna Lab



J. S. Chen et al., Science
10.1126/science.aar6245 (2018)

DETECTR

Zhang Lab



J. S. Gootenberg et al., Science
10.1126/science.aaq0179 (2018)

SHERLOCKv2



EVERYWHERE

Illustration by Chris Labroy © 2011/12



mi+d Un lugar para la ciencia
y la tecnología



GOBIERNO
DE ESPAÑA

MINISTERIO
DE ECONOMÍA, INDUSTRIA
Y COMPETITIVIDAD



Asociación
de ayuda a
personas con
albinismo



EMMA
mouse repository



INFRAFROntier
mouse disease models

ciberer isciiii

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

Fotos: Ana Ytyrralde

Almudena Fernández
Marcos Rubio
Diego Muñoz
Santiago Josa
Andrea Montero
Julia Fernández
Marta Cantero
Marta Sánchez

Cryopreservation and Histology teams: Julia Fernández, María Jesús del Hierro, Marta Castrillo, Soledad Montalbán, Óscar Sánchez

Former members: Davide Seruggia, Mónica Martínez, Irene Robles, Irene Sánchez, Esther Zurita, Magdalena Hryhorowicz, Barbara Franck, Rafael Jiménez, Cesar Echeverria, Celia de Lara, Iván Caballero, Yaiza López ...

Pawel Pelczar (Univ. Zürich / Univ. Basel) Transgenic Unit
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



ALBA



**Asociación
de ayuda a
personas con
albinismo**

www.albinismo.es