

2nd International Summit on Human Genome Editing

Towards precise genome engineering *in vivo*



Xingxu Huang

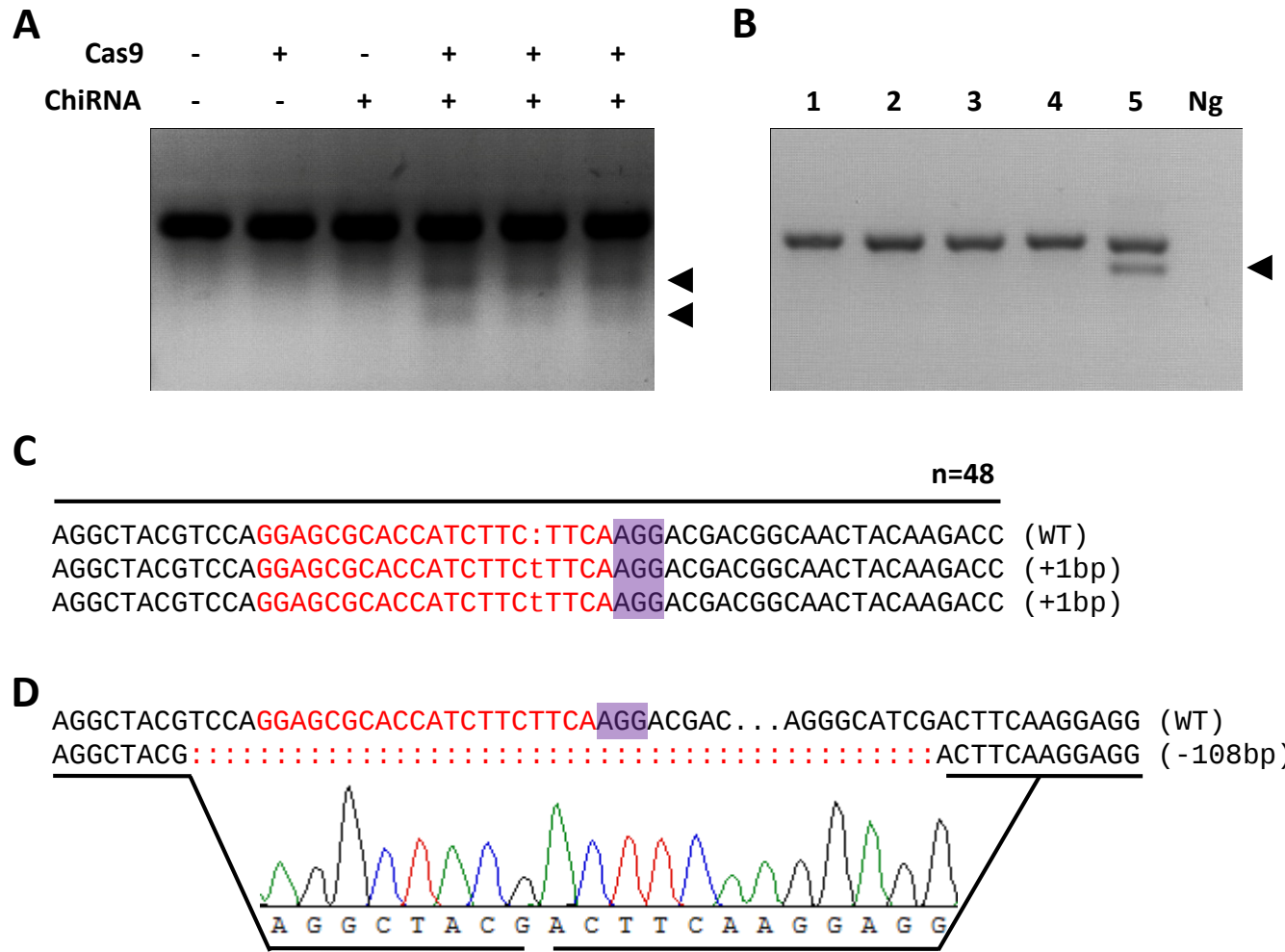
ShanghaiTech University

Huangxx@shanghaitech.edu.cn

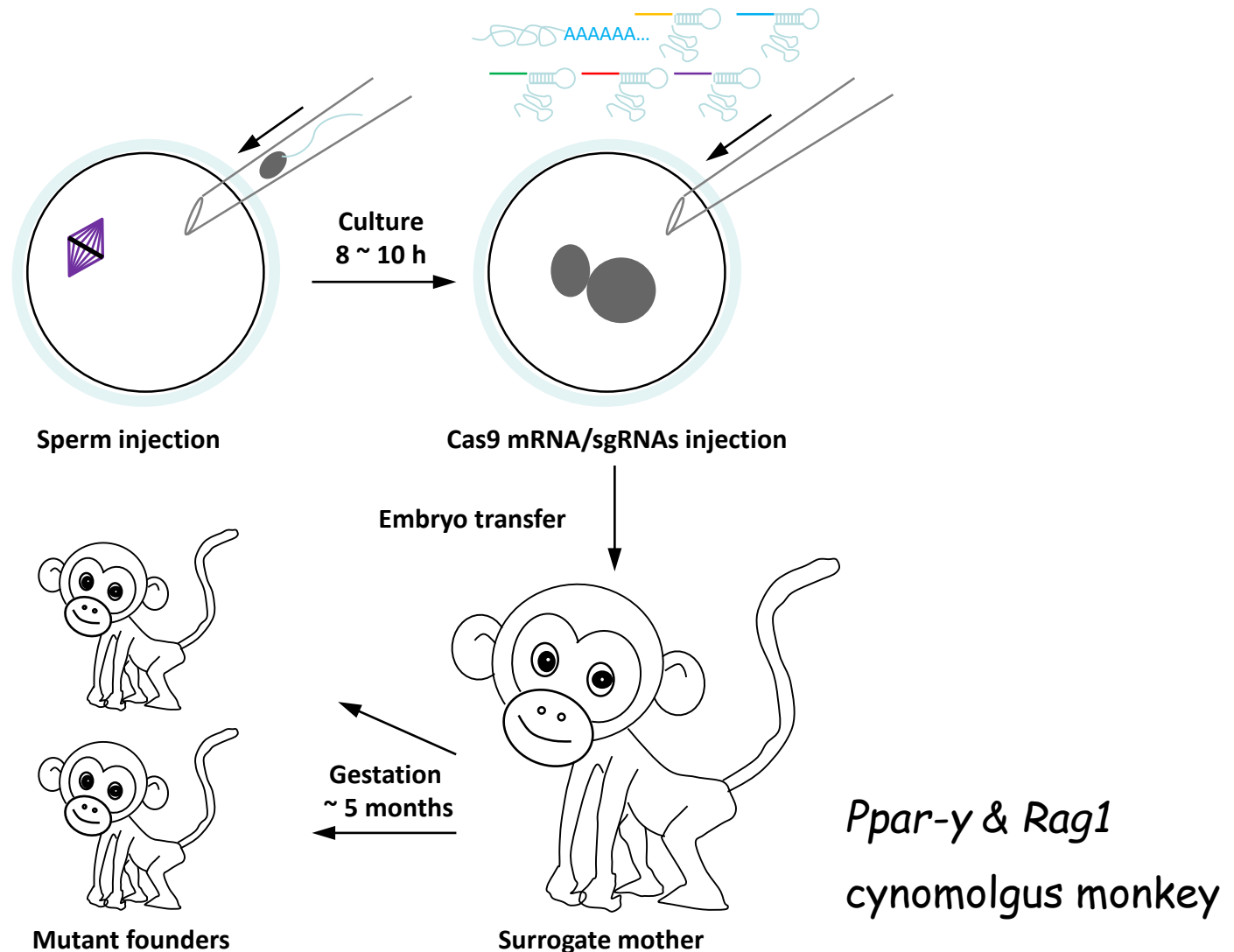


立志成才 报国裕民

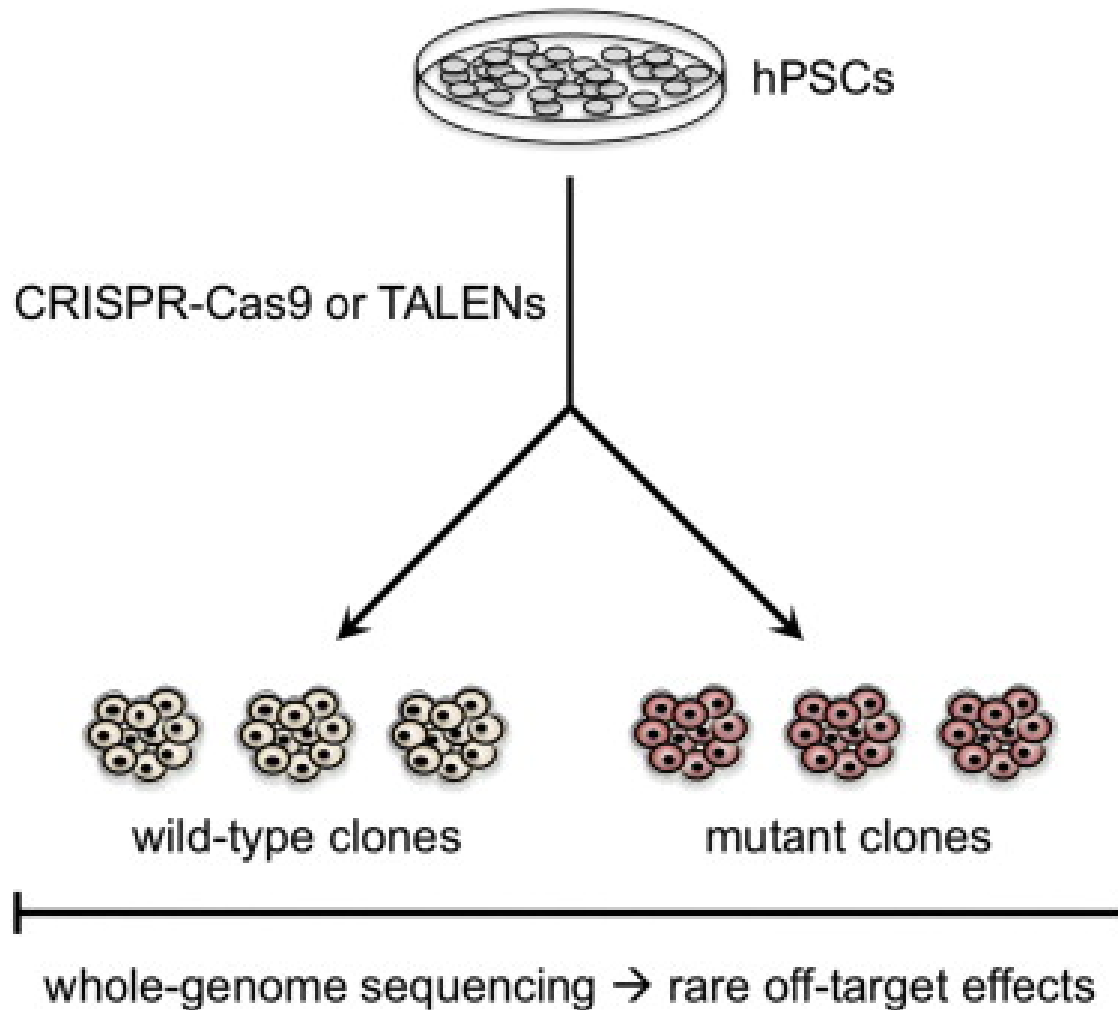
First *in vivo* CRISPR genome editing in mice



Successful *in vivo* genome editing in monkeys



The off-target cleavage in individual clone



Kiskinis E, et al. *Cell Stem Cell* 2014.
Smith C, et al. *Cell Stem Cell* 2014.
Suzuki K, et al. *Cell Stem Cell* 2014.
Veres A, et al. *Cell Stem Cell* 2014.

The off-target cleavage *in vivo*

Species	Number of sgRNA	Tentative off-target sites	Authentic off-target sites
Mouse	7	97	9
Rat	4	119	1
Pig	1	8	0
Goat	4	13	2
Monkey	5	84	0



The human embryo editing

Protein Cell 2015, 6(5):363–372
DOI 10.1007/s13238-015-0153-5



Protein & Cell

RESEARCH ARTICLE

CRISPR/Cas9-mediated gene editing in human tripronuclear zygotes

Puping Liang, Yanwen Xu, Xiya Zhang, Chenhui Ding, Rui Huang, Zhen Zhang, Jie Lv, Xiaowei Xie, Yuxi Chen, Yujing Li, Ying Sun, Yaofu Bai, Zhou Songyang, Wenbin Ma, Canquan Zhou[✉], Junjiu Huang[✉]

Guangdong Province Key Laboratory of Reproductive Medicine, the First Affiliated Hospital, and Key Laboratory of Gene Engineering of the Ministry of Education, School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, China

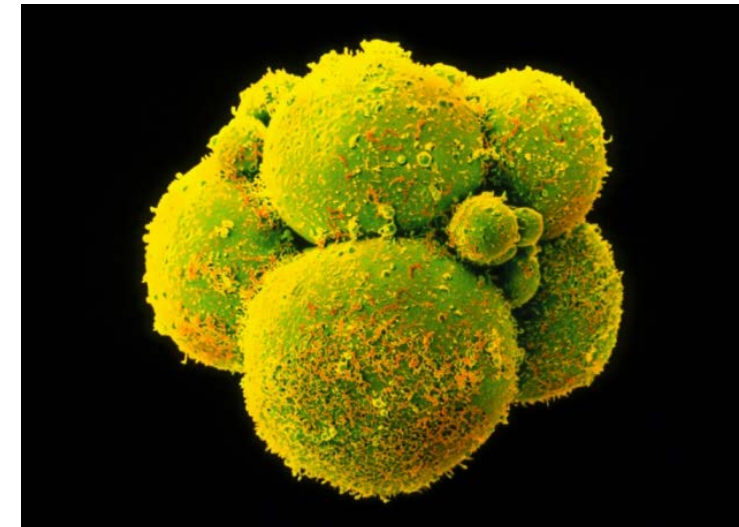
✉ Correspondence: hjunjiu@mail.sysu.edu.cn (J. Huang), zhouchanquan@hotmail.com (C. Zhou)

Received March 30, 2015 Accepted April 1, 2015



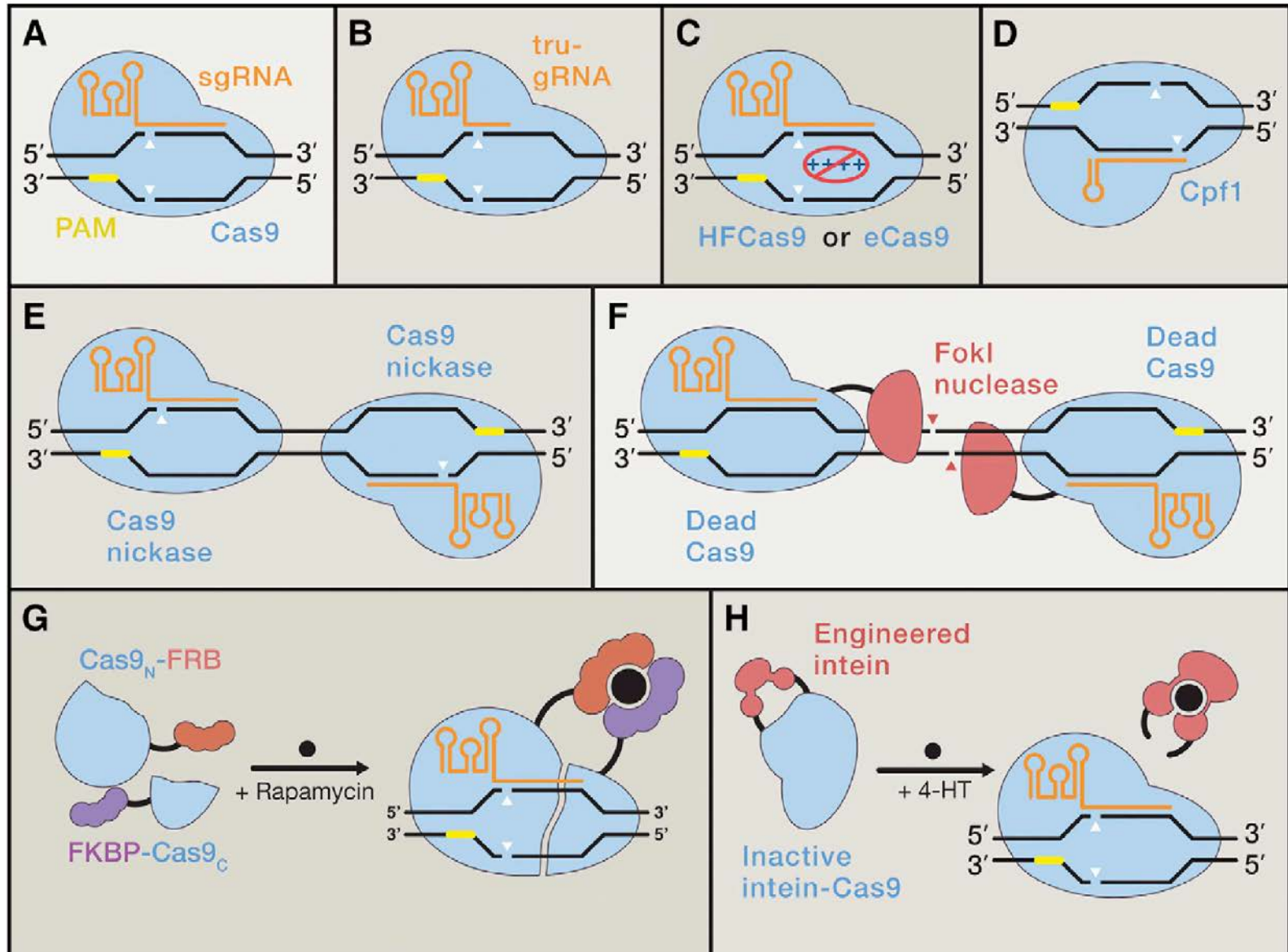
Concerns:

- ◆ Efficacy
- ◆ Safety
- ◆ Mosaicism



<http://www.nature.com/news/embryo-editing-sparks-epic-debate-1.17421>

Strategies for improving the specificities



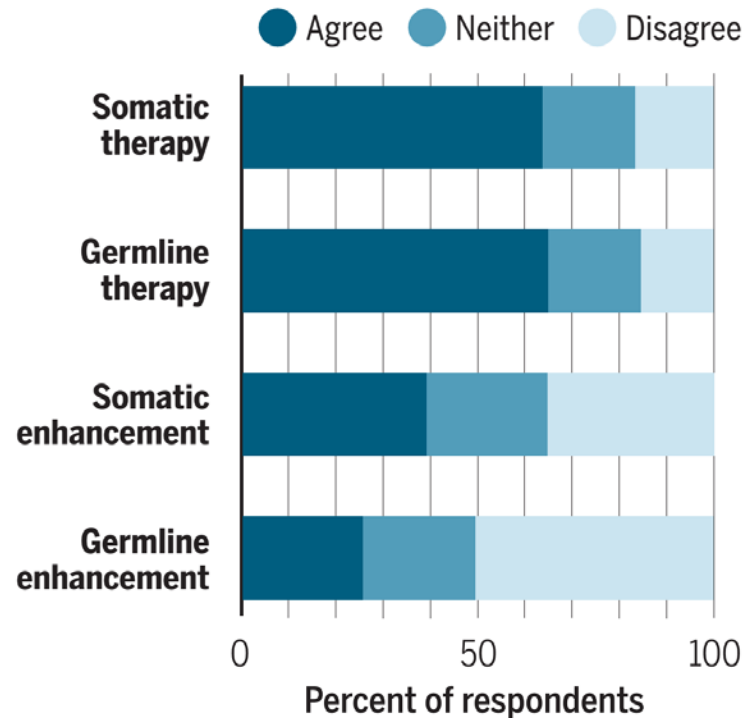
More CRISPR genome editing in human embryos

- ◆ Kang et al. Introducing precise genetic modifications into human 3PN embryos by CRISPR/Cas-mediated genome editing. *Journal Assisted Reproduction Genetics* 2016, 33: 581-588.
- ◆ Tang et al. CRISPR/Cas9-mediated gene editing in human zygotes using Cas9 protein. *Molecular Genetics Genomics* 2016, 292: 525-533.
- ◆ Ma et al. Correction of a pathogenic gene mutation in human embryos. *Nature* 2017, 548: 413-419.
- ◆ Fogarty et al. Genome editing reveals a role for OCT4 in human embryogenesis. *Nature* 2017, 550: 67-73.

Attitudes on human genome editing

- ◆ U.S. panel gives yellow light to embryo editing. Feb. 14, 2017

<http://www.sciencemag.org/news/2017/02/us-panel-gives-yellow-light-human-embryo-editing>

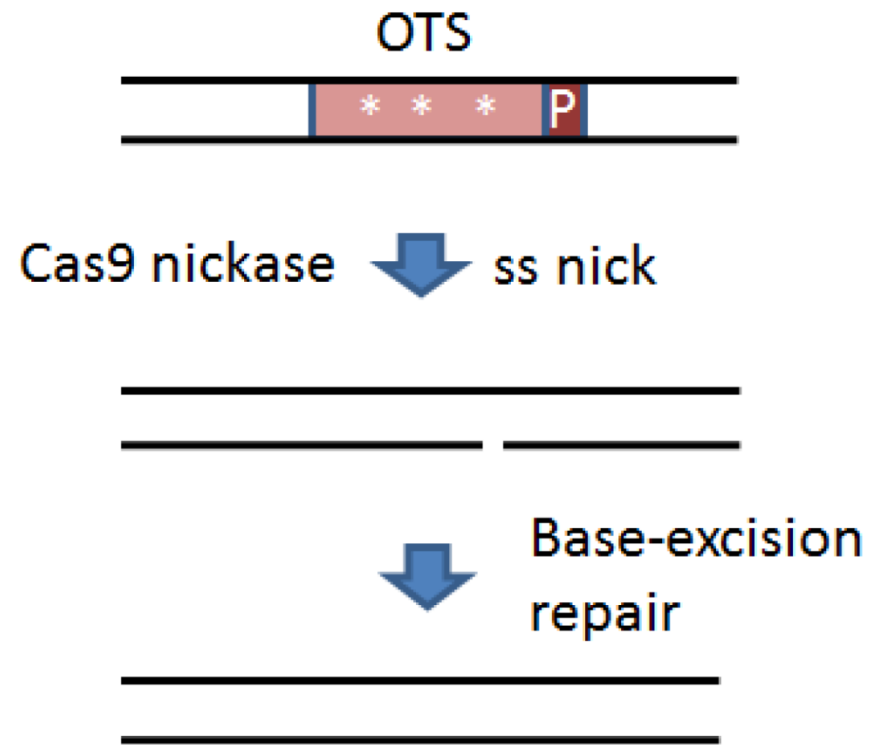
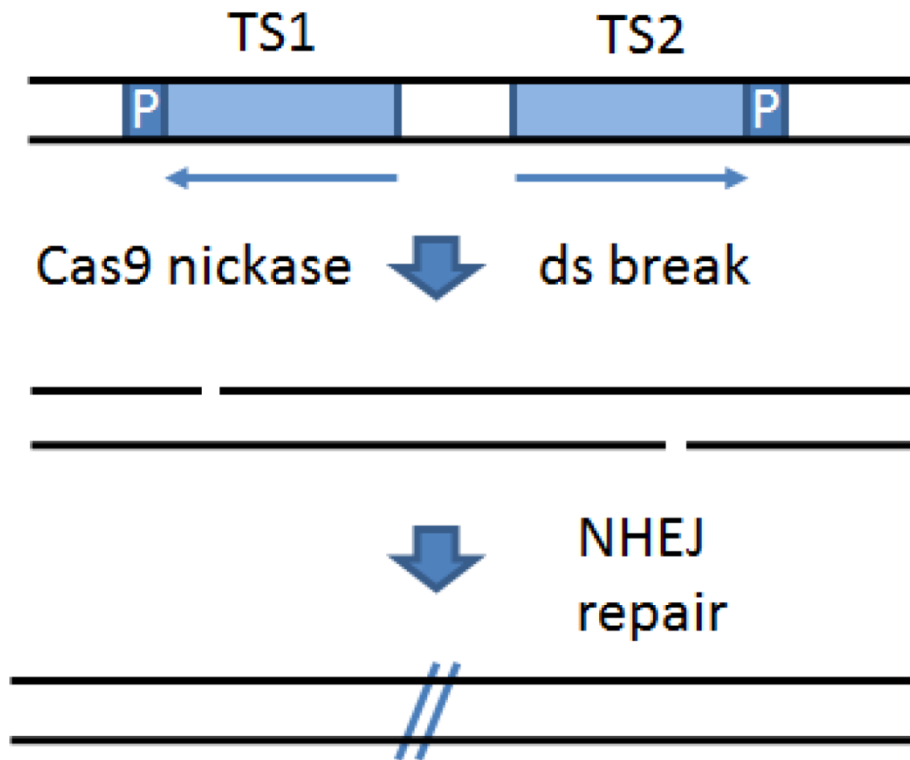


Aug. 11, 2017

- ◆ A majority finds use of human genome editing for therapeutic purposes acceptable, including somatic and germline edits. Public opposition increases for applications aimed at enhancement.

<http://science.sciencemag.org/content/357/6351/553.full>

Minimizing off-target mutagenesis using Cas9-nickase/dual sgRNAs



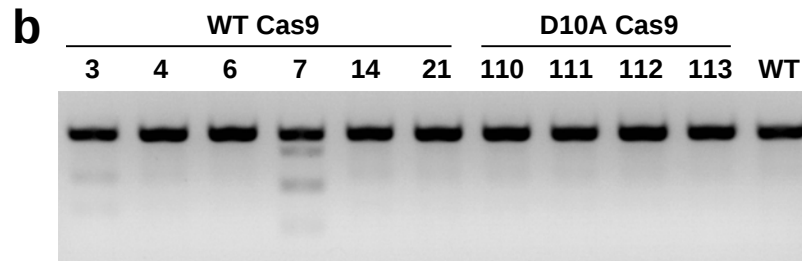
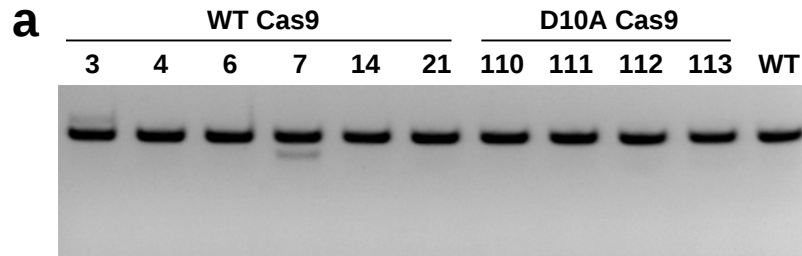
http://www.sanger.ac.uk/htgt/wge/find_crisprs

Off-target mutations are rare *in vivo*



<http://www.bioworld.com/perspectives/>

nCas9/dual sgRNAs strategy reduces off-target

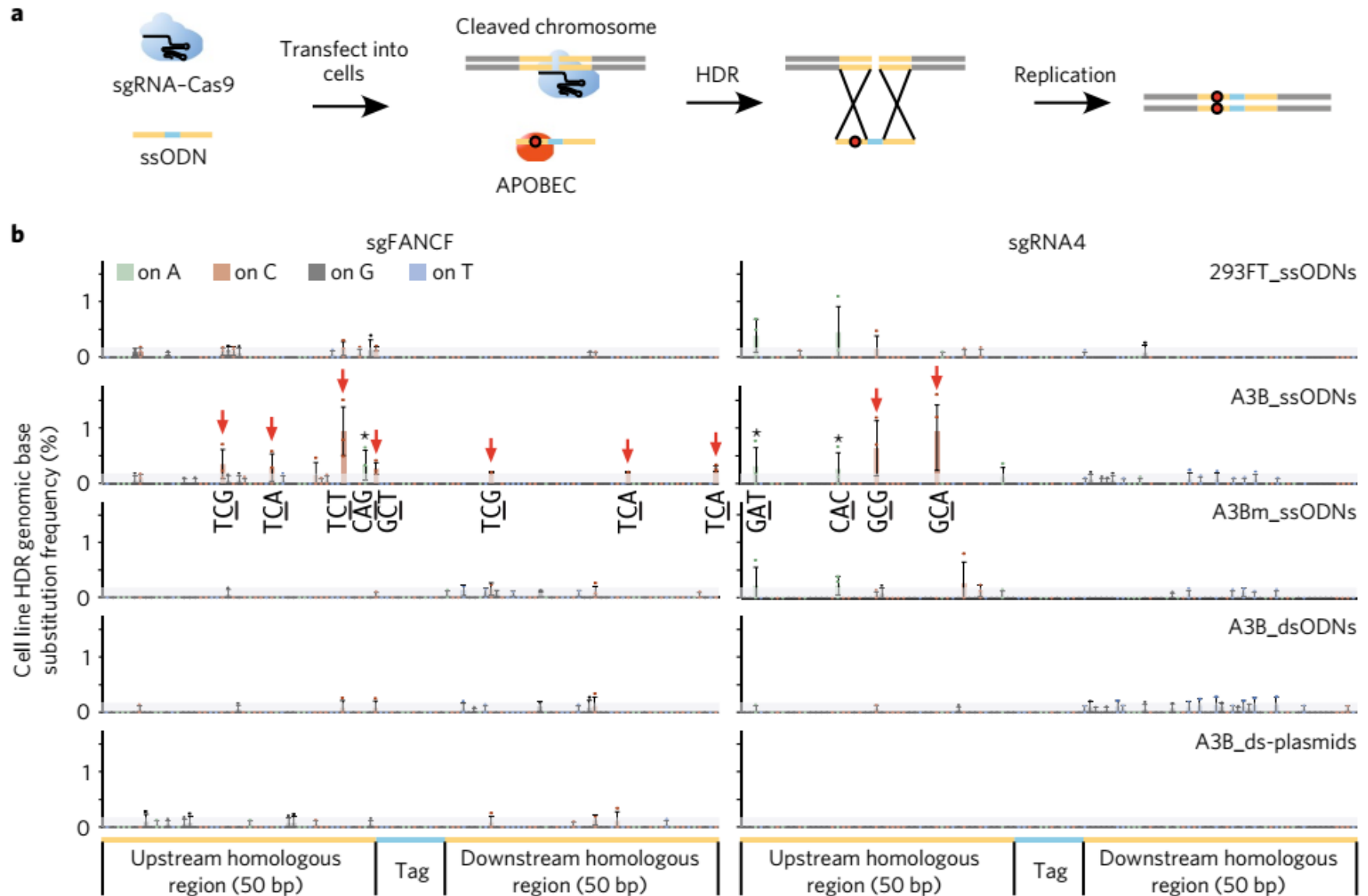


c

	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	N	G	G
RAG1 sgRNAE	G	G	T	G	T	C	T	G	C	T	T	T	G	A	T	G	G	A	C	A	T	G	G
PP13	T	A	T	G	T	C	T	G	C	A	T	T	G	A	T	G	G	A	C	A	A	G	G

PP13 CTTGGAGAAGGGGTCTTCTTTCCCCCTGTGTCATCAATGCAGACATAGCTAGGGCTTCTCCTAAAGAAGCTC (WT)
 #7 CTTGGAGAA-----GCTC (-60, 3/21)

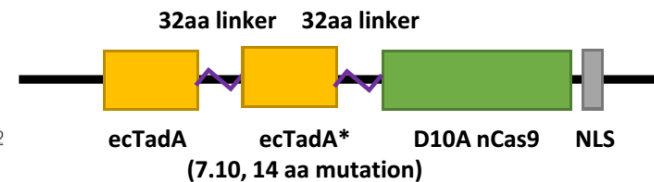
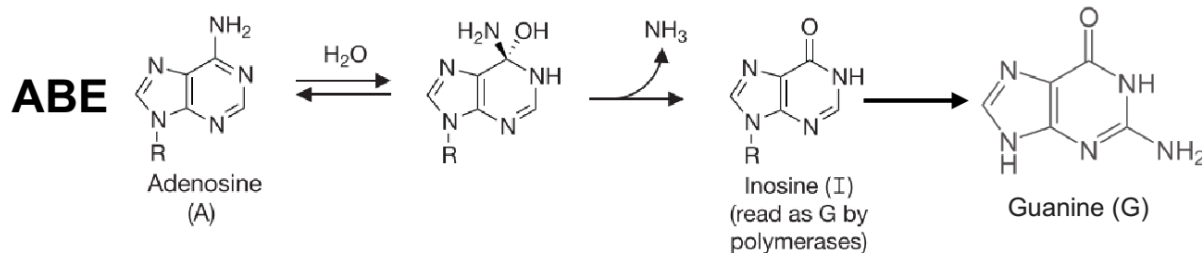
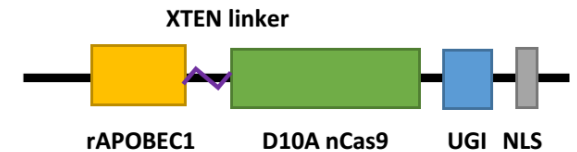
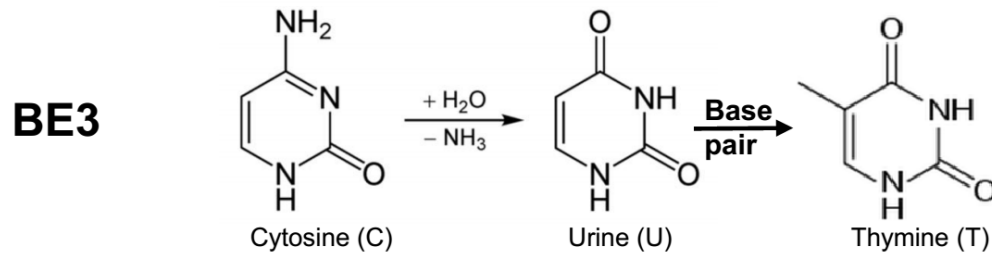
APOBEC3 mediates the formation of unexpected indel mutations near SSBs



Base editing provides a more precise strategy

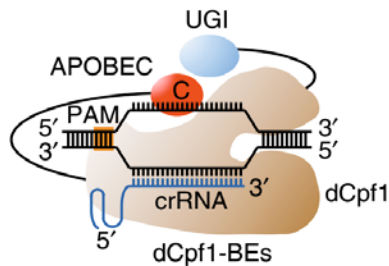
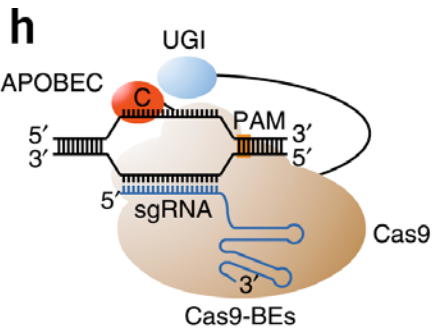
CBE: cytosine base editor

ABE: adenine base editor



Perform programmable editing of a target base in genome by deamination without double-stranded DNA cleavage.

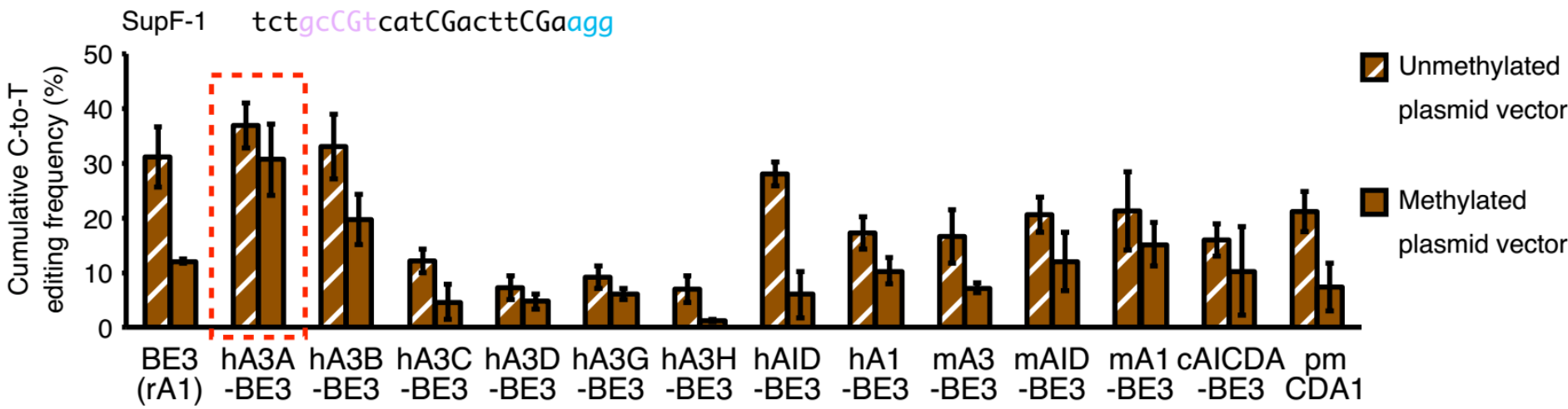
High-fidelity C/T base editing mediated by Cpf1-cytidine deaminase fusion



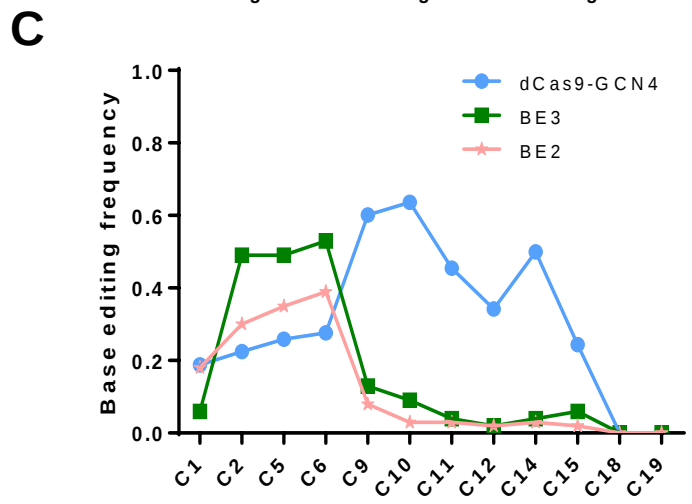
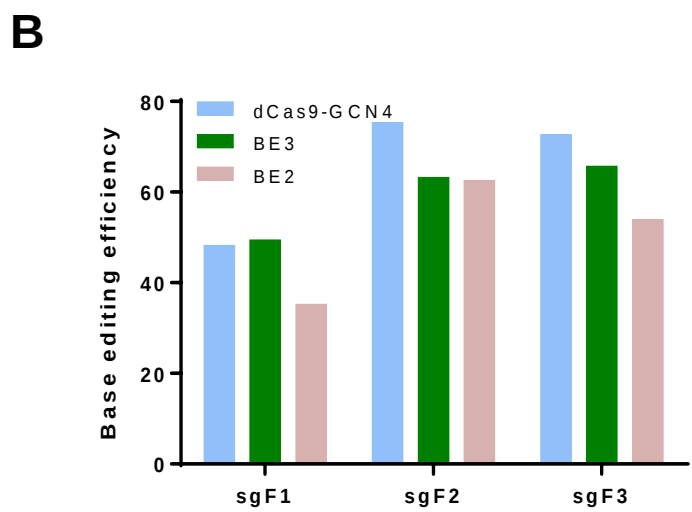
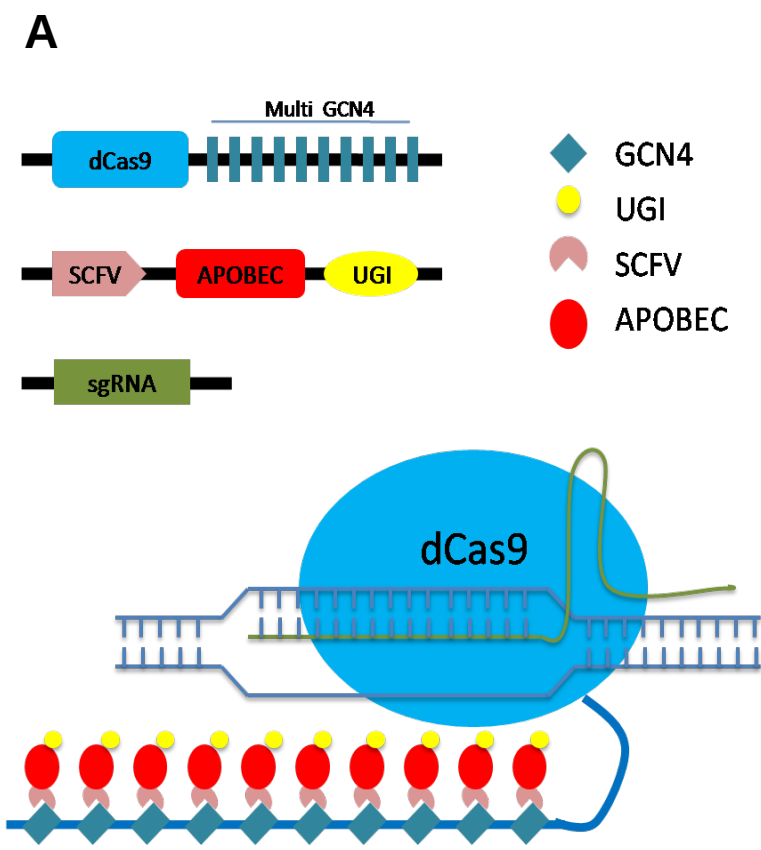
Name	Cas	PAM	APOBEC	N-terminal NLS	Fused UGI	Free UGI	Editing window	Editing efficiency	C-to-T fraction
dCas9-BE2	dCas9	NGG	rA1	–	+	–	4–8	~9–16%	~91–98%
nCas9-BE3	nCas9	NGG	rA1	–	+	–	4–8	~21–46%	~82–99%
dCpf1-BE0	dCpf1	TTTV	rA1	–	+	–	8–13	~10–31%	~89–99%
dCpf1-BE	dCpf1	TTTV	rA1	+	+	–	8–13	~20–44%	~88–99%
dCpf1-BE-YE	dCpf1	TTTV	rA1-YE	+	+	–	10–12	~2–29%	~92–98%
dCpf1-eBE	dCpf1	TTTV	rA1	+	+	+++	8–13	~15–30%	~97–99%
dCpf1-eBE-YE	dCpf1	TTTV	rA1-YE	+	+	+++	10–12	~2–28%	~95–99%

Based on the DYRK1A-, FANCF- and RUNX1-target sites

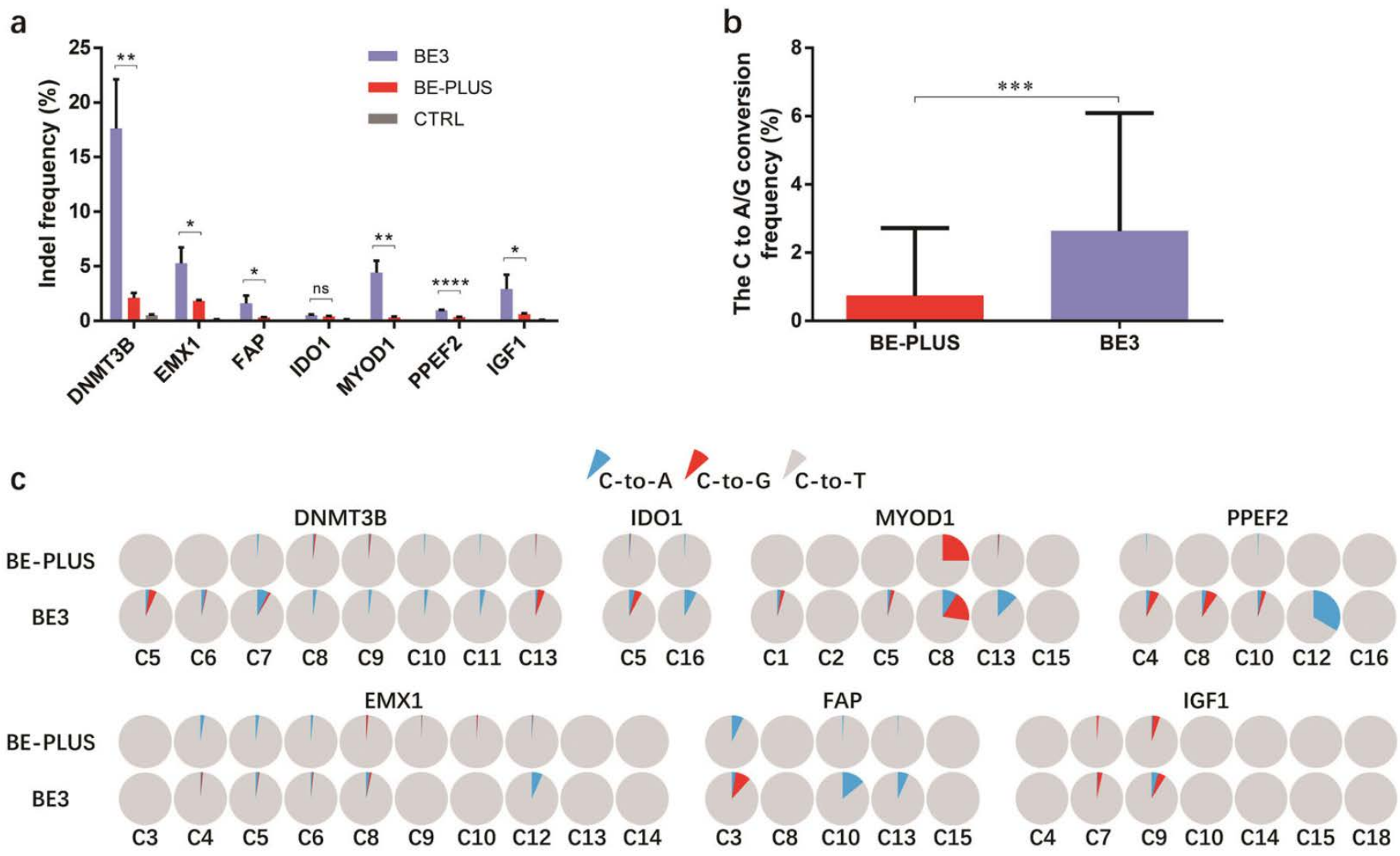
Comprehensive C/T base editing mediated by a new deaminase, A3A



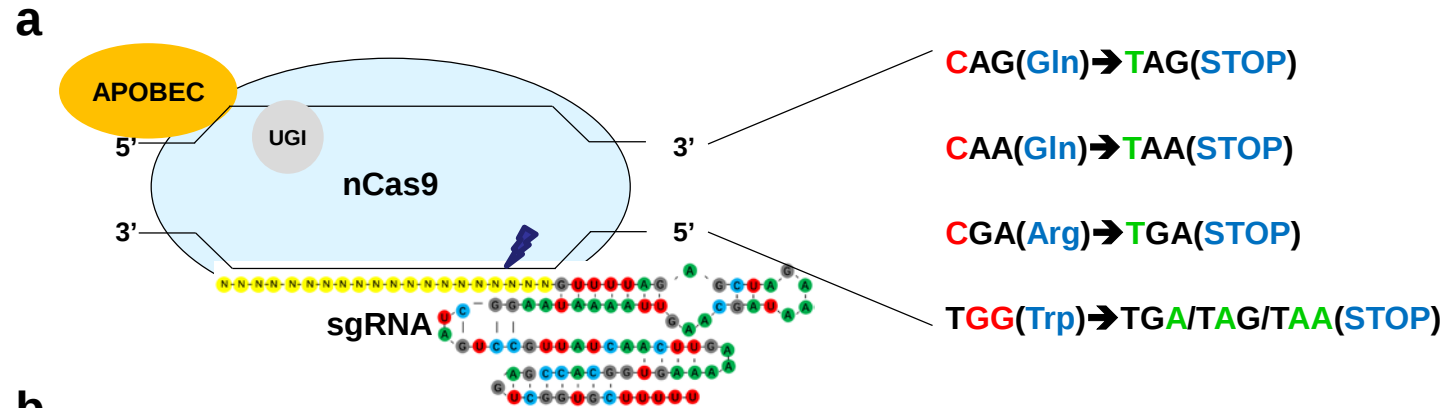
BE-PLUS, to increase the editing scope & precision



BE-PLUS enhances the fidelity of C/T base editing



BE3 mediates isogenic C/T gene editing *in vivo*



VISTA sp-1

CAGCACCACGGAAGCCACCTGAAAGCCAACGCCAGCCATGAC_C₆AGCCCCAGAAGCAT_{GG}₆CTAGAGCTAGCTTCTGAC (WT)
 CAGCACCACGGAAGCCACCTGAAAGCCAACGCCAGCCATGAT_T₆AGCCCCAGAAGCATGGGCTAGAGCTAGCTTCTGAC (14/16, 6/14 homozygote)
 CAGCACCACGGAAGCCACCTGAAAGCCAACGCCAGCCATGAC_T₆AGCCCCAGAAGCATGGGCTAGAGCTAGCTTCTGAC (1/16, 0/1 homozygote)
 CAGCACCACGGAAGCCACCTGAAAGCCAACGCCAGCCATGAT_C₆AGCCCCAGAAGCATGGGCTAGAGCTAGCTTCTGAC (1/16, 0/1 homozygote)

CD160 sp-2

AGCATCCCAGAAAGGAGGGCGACTGGAC_{CT}₆CACCTGTACTTTG_{TG}₆₅CACAAGAAAGACGAAGCTGAGGGGCTAATACT (WT)
 AGCATCCCAGAAAGGAGGGCGACTGGACCTCACCTGTACTTTGT_A₆₅CACAAGAAAGACGAAGCTGAGGGGCTAATACT (3/12, 2/3 homozygote)
 AGCATCCCAGAAAGGAGGGCGACTGGACCTCACCTGTACTTTGT_A₆₅CACAAGAAAGACGAAGCTGAGGGGCTAATACT (2/12, 0/2 homozygote)

Table 1 Summary of the microinjections

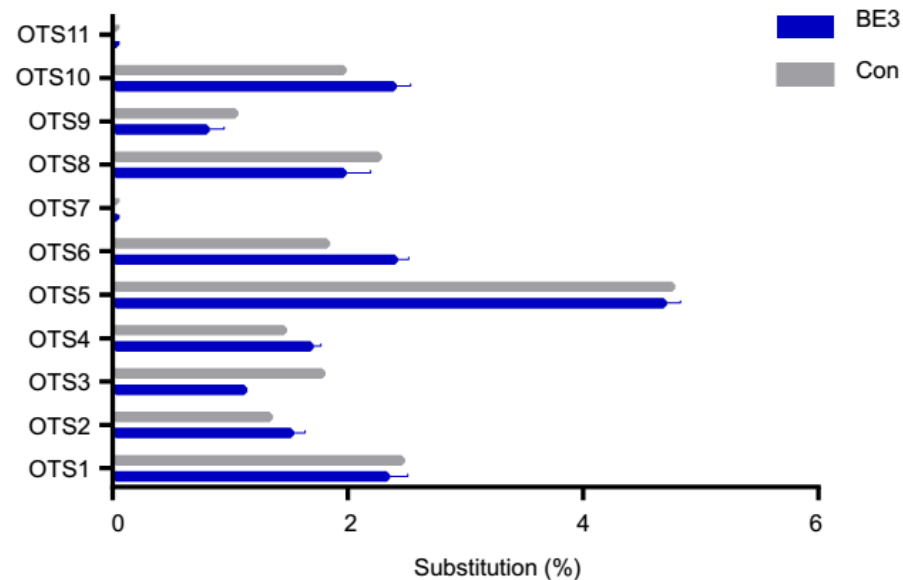
Target genes		Methods	No. of examined embryos	No. of two-cell stage embryos (%)	No. of blastocysts (%)	Mutant ratio (%)	
						No. of mutants/total blastocysts	No. of homozygotes/total mutants
VISTA	VSITA mRNA+BE3 mRNA	Microinjection	20	18 (90) ^a	16 (89) ^b	16 (100)	6/16 (38)
CD160	CD160 mRNA+BE3 mRNA	Microinjection	20	17 (85) ^a	12 (71) ^b	9 (75)	2/9 (22)

Off-target analysis by deep sequencing

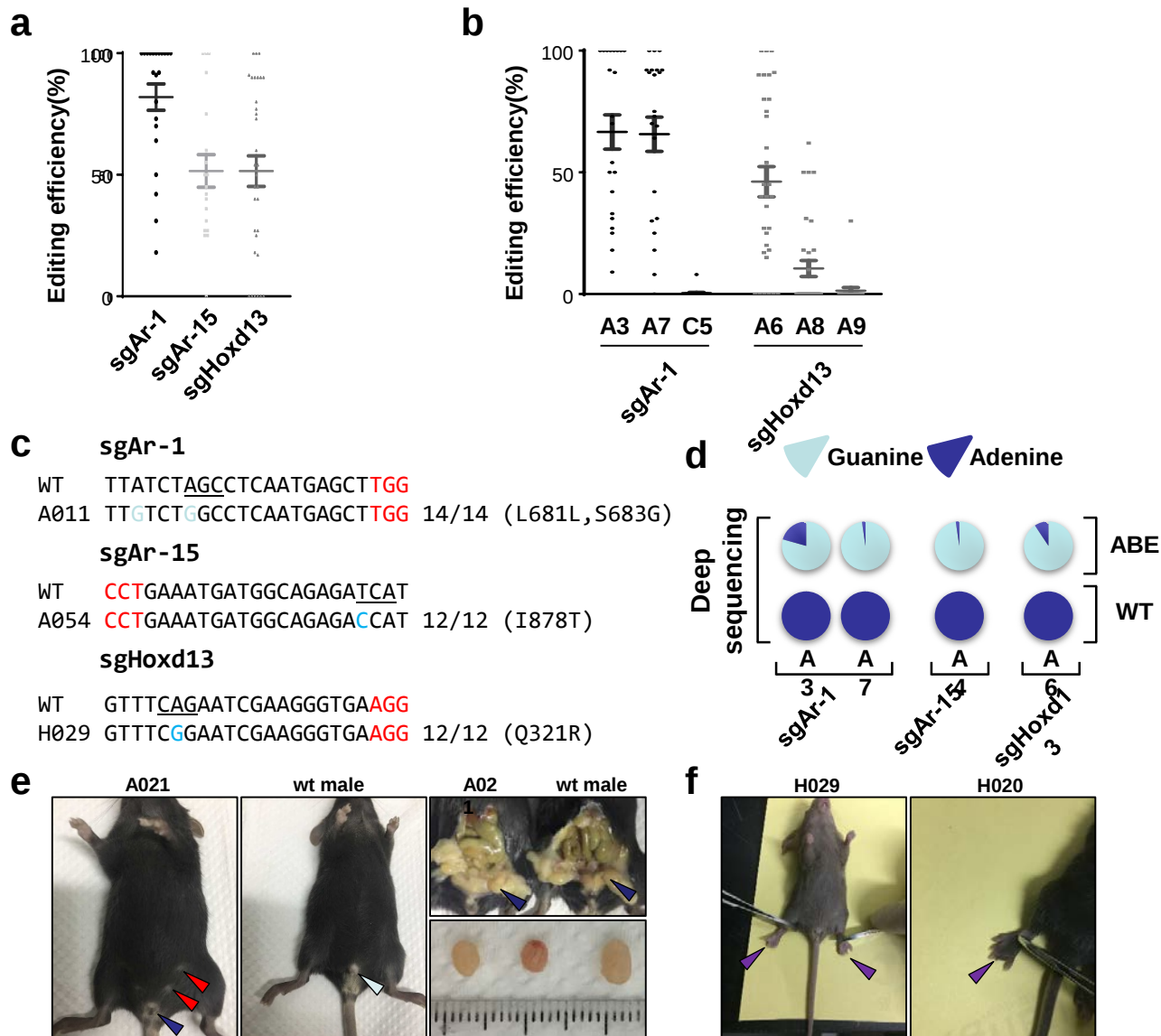
A

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	PAM	Chr.		
On-Target	A	T	G	A	C	C	A	G	C	C	C	C	A	G	A	A	G	C	A	T	G	G	G	10
OTS1	A	T	G	A	a	C	A	t	C	C	C	C	A	G	A	A	G	C	A	a	A	G	G	3
OTS2	A	T	t	A	C	C	A	G	C	C	C	a	A	G	A	A	G	C	c	T	A	G	G	7
OTS3	A	T	G	A	C	C	A	a	C	C	C	C	A	G	A	t	G	C	t	T	T	G	G	4
OTS4	A	g	G	A	C	C	A	G	a	C	C	C	A	G	A	A	c	C	A	T	A	G	G	4
OTS5	c	T	G	A	C	C	A	G	a	C	C	C	A	G	A	A	G	C	A	g	G	G	G	5
OTS6	t	a	G	A	C	C	A	G	C	C	C	C	A	G	A	A	G	C	A	a	A	G	G	5
OTS7	A	T	G	g	C	t	g	G	C	C	C	C	A	G	A	A	G	C	A	T	T	G	G	2
OTS8	A	T	a	c	C	C	A	G	C	C	C	C	A	G	A	A	G	C	c	T	G	G	G	6
OTS9	A	a	a	A	C	C	A	G	C	C	t	C	A	G	A	A	G	C	A	T	G	G	G	14
OTS10	A	T	G	A	t	C	A	G	t	C	C	C	A	G	g	A	G	C	A	T	G	G	G	14
OTS11	A	T	G	A	a	C	A	G	C	t	C	C	A	G	A	A	t	C	A	T	T	G	G	9

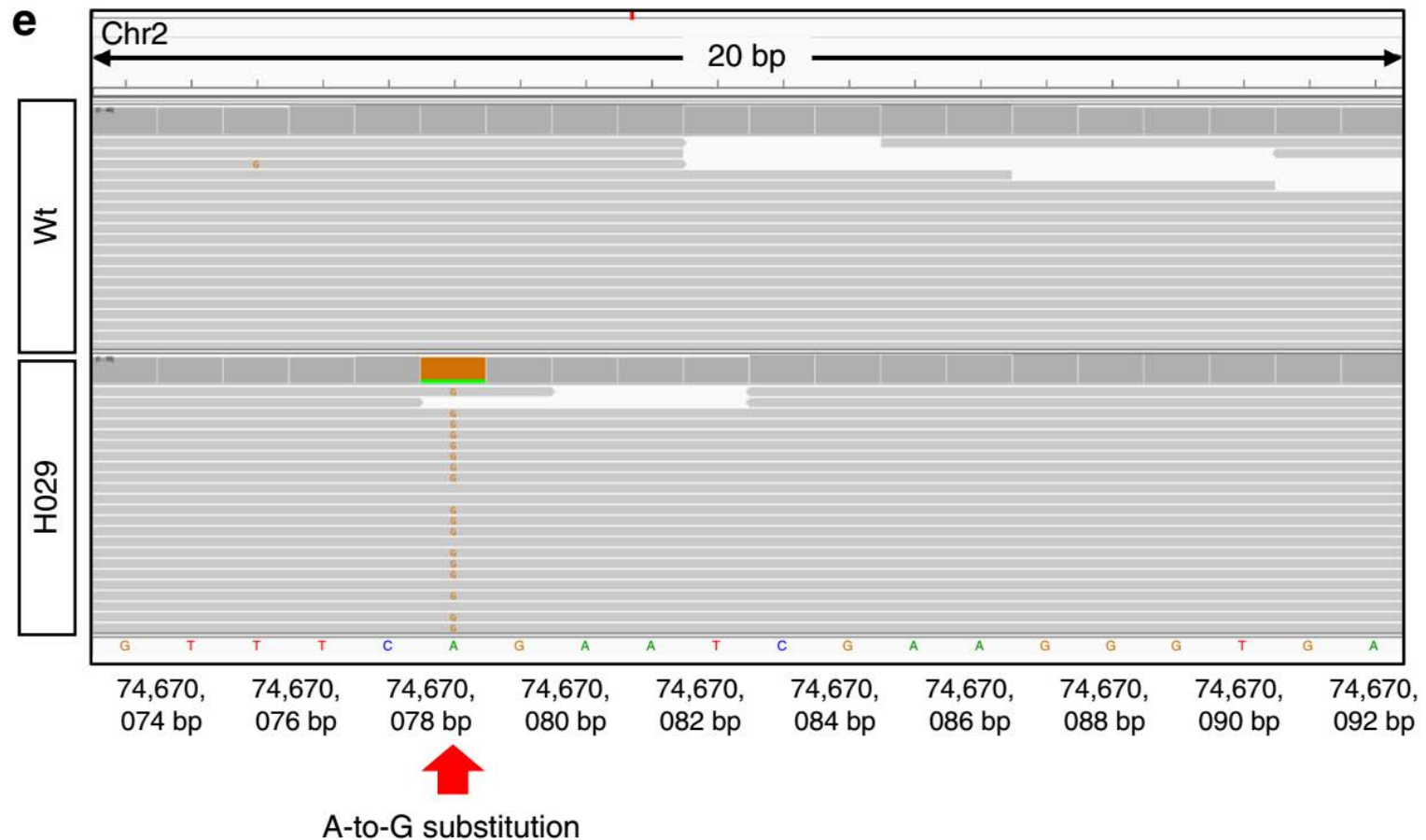
B



ABE mediates efficient A/G base editing *in vivo*



On-target and off-target analysis



A safe & efficient *in vivo* genome editing approach

BE: pinpoint gene editing



Efficient & pure *in vivo* C/T conversion by BE

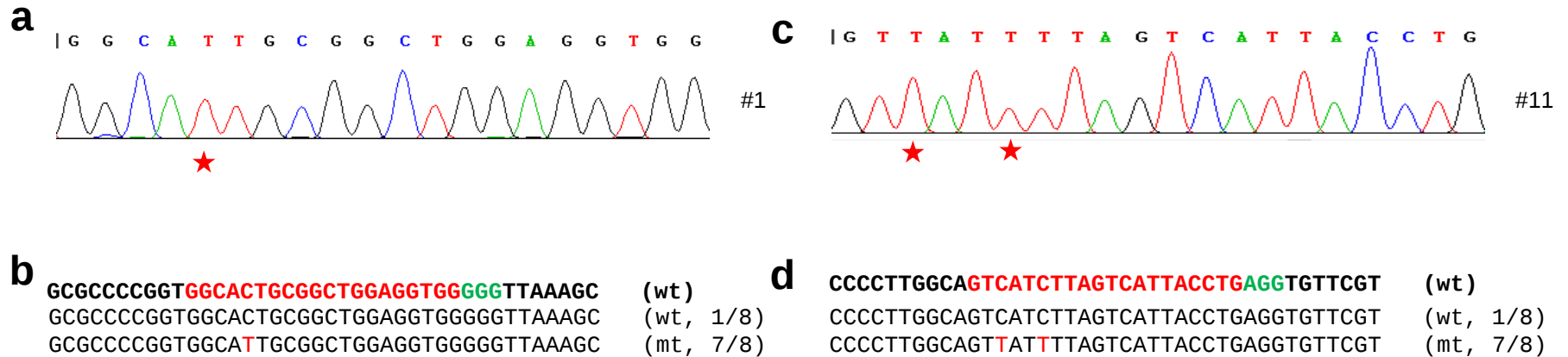


Table 1 Summary of the microinjections

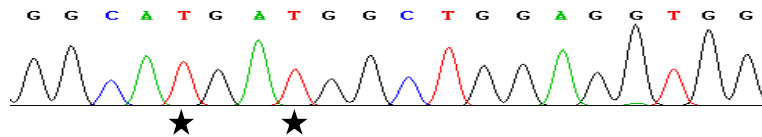
	Injected mixture	Target sites	No. of examined tripronuclear zygotes	No. of mutants/total zygotes	Editing efficiency
Experiment 1	mRNA+sgRNA	SITE 4	8	7/8	87.5%
Experiment 2	mRNA+sgRNA	RNF2	8	7/8	87.5%
Experiment 3	mRNA+sgRNA	SITE4	9	9/9	100%
		RNF2	9	9/9	100%

With very rare off-target

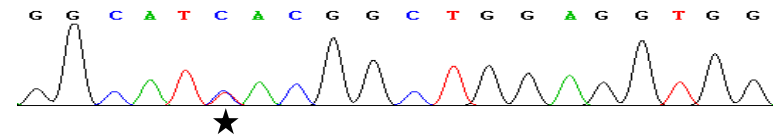
a

	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	N	G	G
SITE4	G	G	C	A	C	T	G	C	G	G	C	T	G	G	A	G	G	T	G	G	G	G	G
OTS3	G	G	C	A	C	G	A	C	G	G	C	T	G	G	A	G	G	T	G	G	A	G	G
OTS4	G	G	C	A	T	C	A	C	G	G	C	T	G	G	A	G	G	T	G	G	A	G	G

b Off-target-3



c Off-target-4



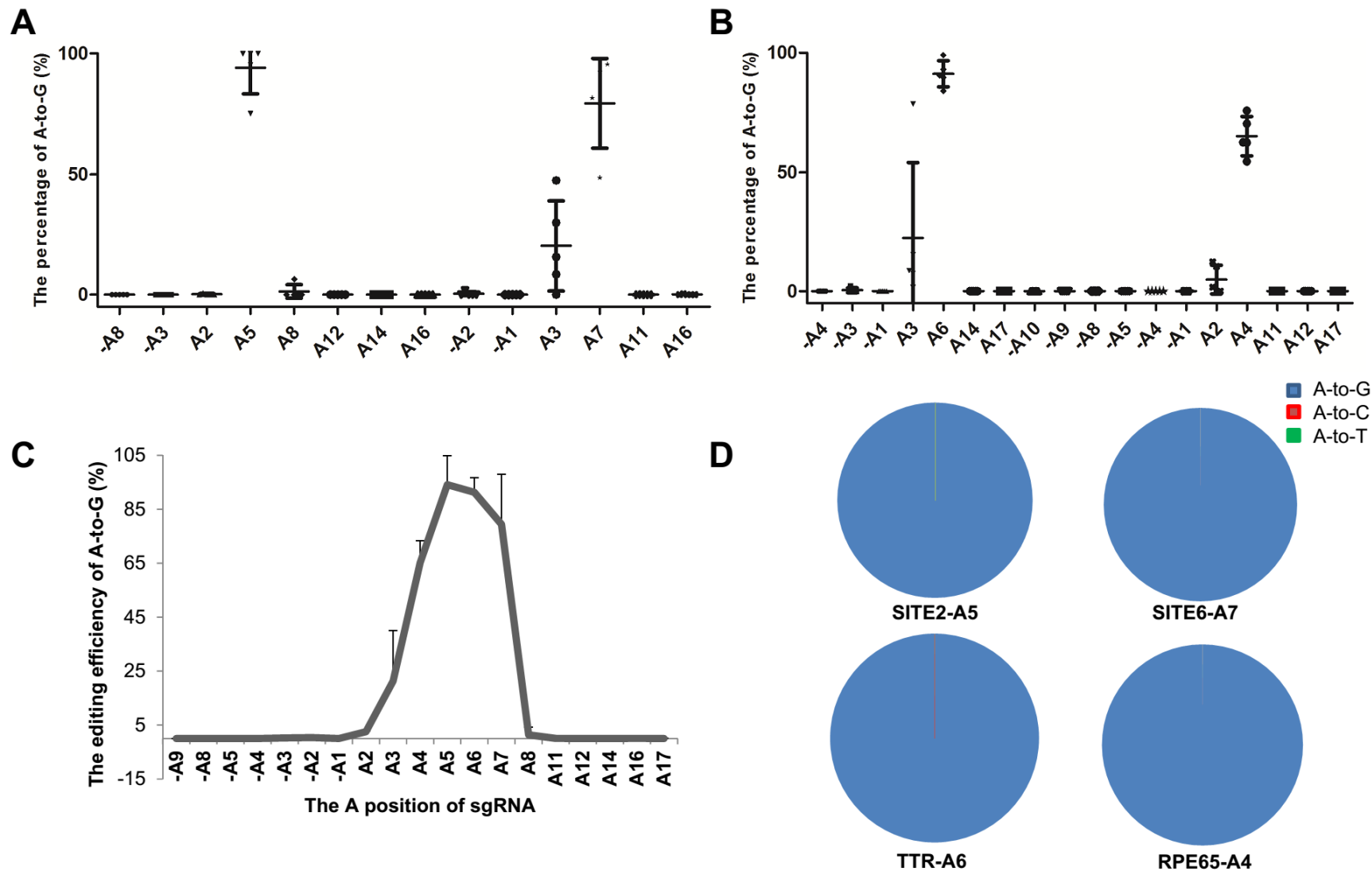
d

Off-target-3	G	G	C	A	C	G	A	C	G	G	C	T	G	G	A	G	G	T	G	G	G	G	G
#2			0.00		0.01			0.00			0.00												
#3			0.00		0.76			0.67			0.00												
#18			0.00		0.18			0.01			0.00												

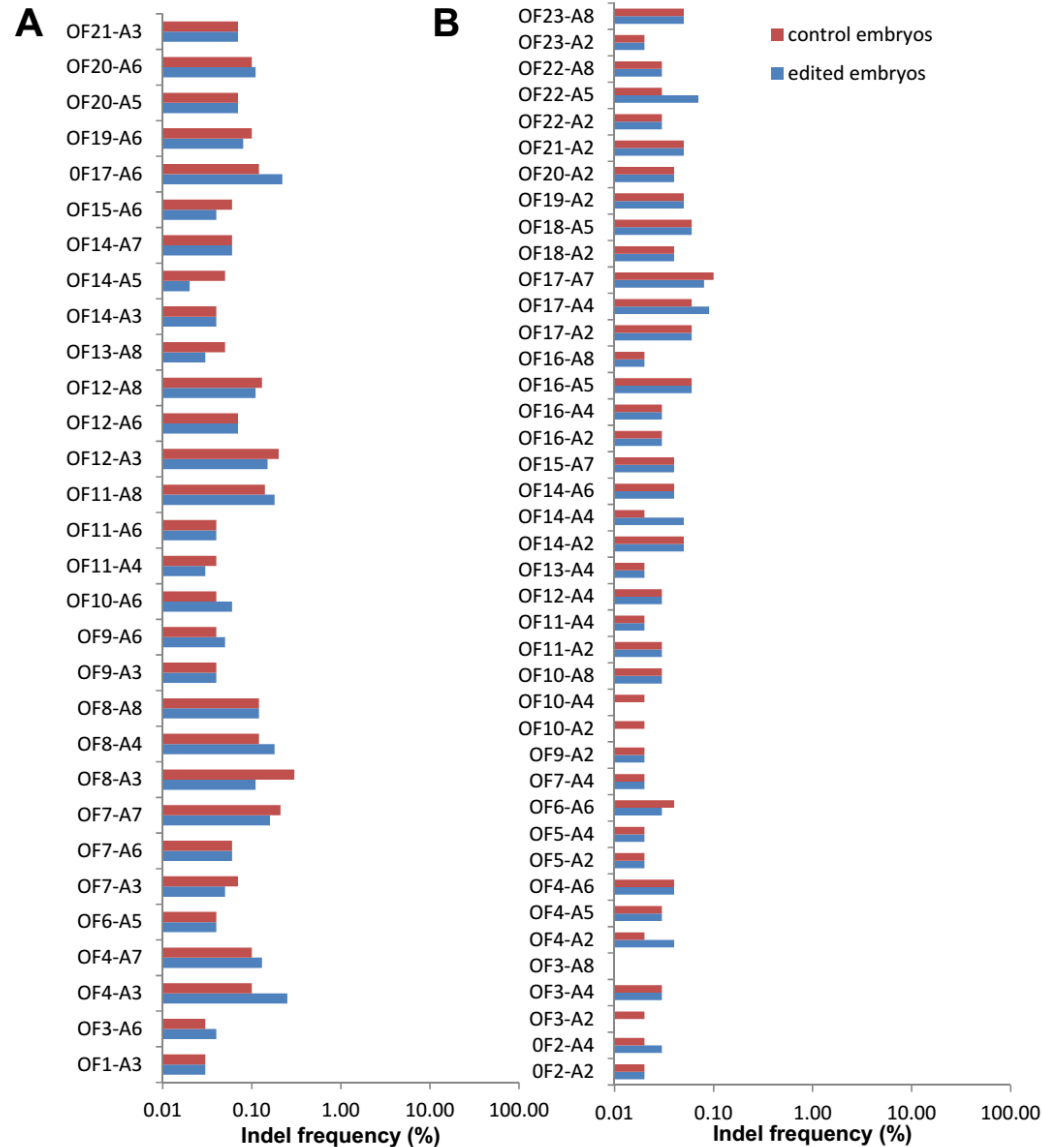
e

Off-target-4	G	G	C	A	T	C	A	C	G	G	C	T	G	G	A	G	G	T	G	G	A	G	G
#2			0.00		0.00			0.02			0.00												
#3			0.00		0.36			0.00			0.00												
#18			0.00		0.01			0.00			0.00												

Efficient & pure *in vivo* A/G conversion by ABE

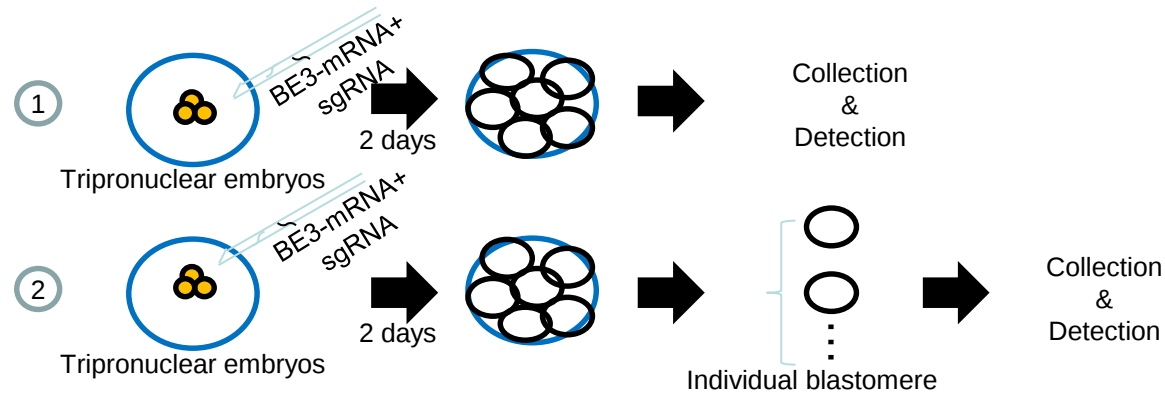


No off-target was detected

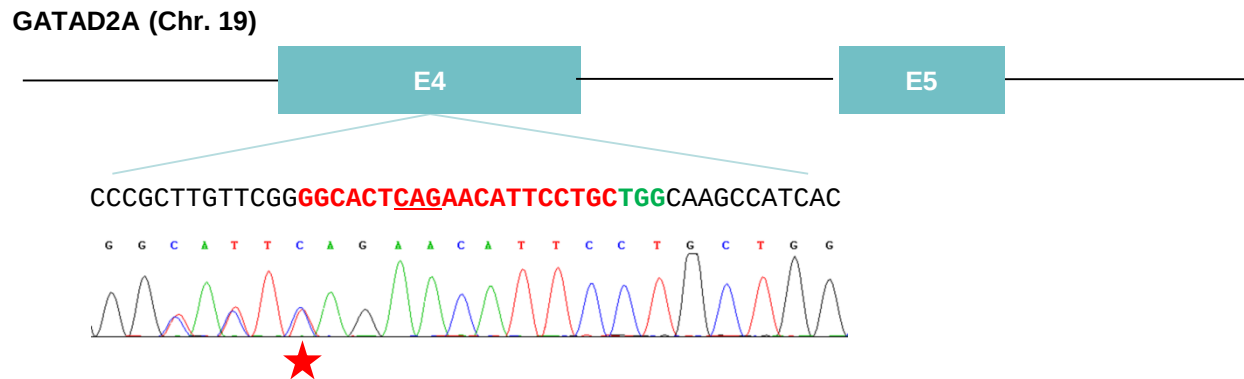


BE mediates isogenic genome editing *in vivo*

a



b



To correct pathogenic mutation of genetic disease

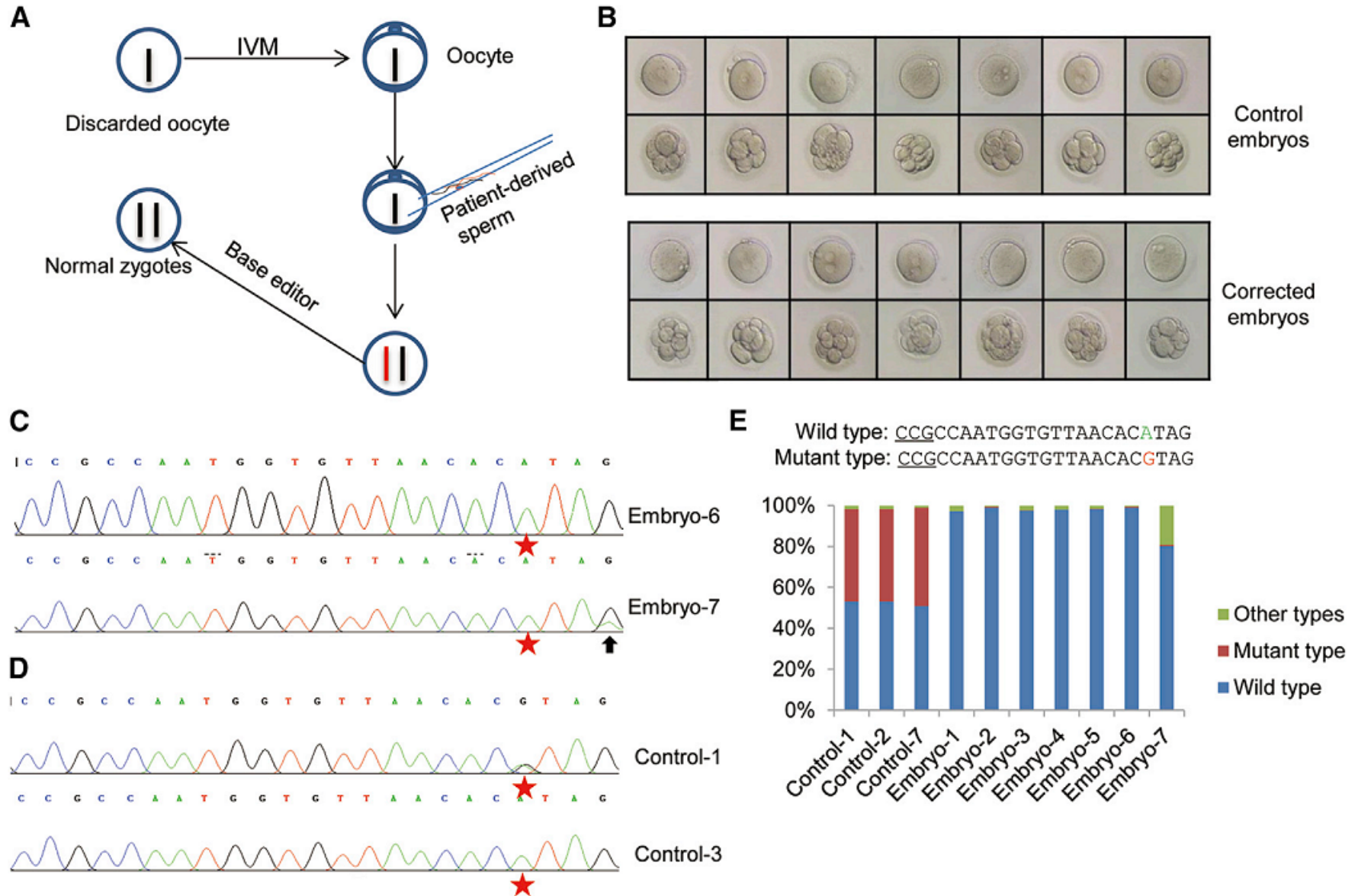
- ◆ There are an estimated 6,000~8,000 rare diseases. The rare diseases are estimated to collectively affect more than 200 million people worldwide;
- ◆ Three-quarters affect children, over half are life limiting;
- ◆ Over 80% of rare diseases are genetic in origin. Most are caused by defects in a single gene;
- ◆ Both the central nervous system (CNS), and peripheral organs and tissues are affected in most rare diseases;
- ◆ There are treatments for only 6% of rare diseases, of which fewer than 1% are curative;
- ◆ It was too expensive, at an average of \$1 million per treatment.

Orkin & Reilly. *Science* 2016, 352: 1059-1061.

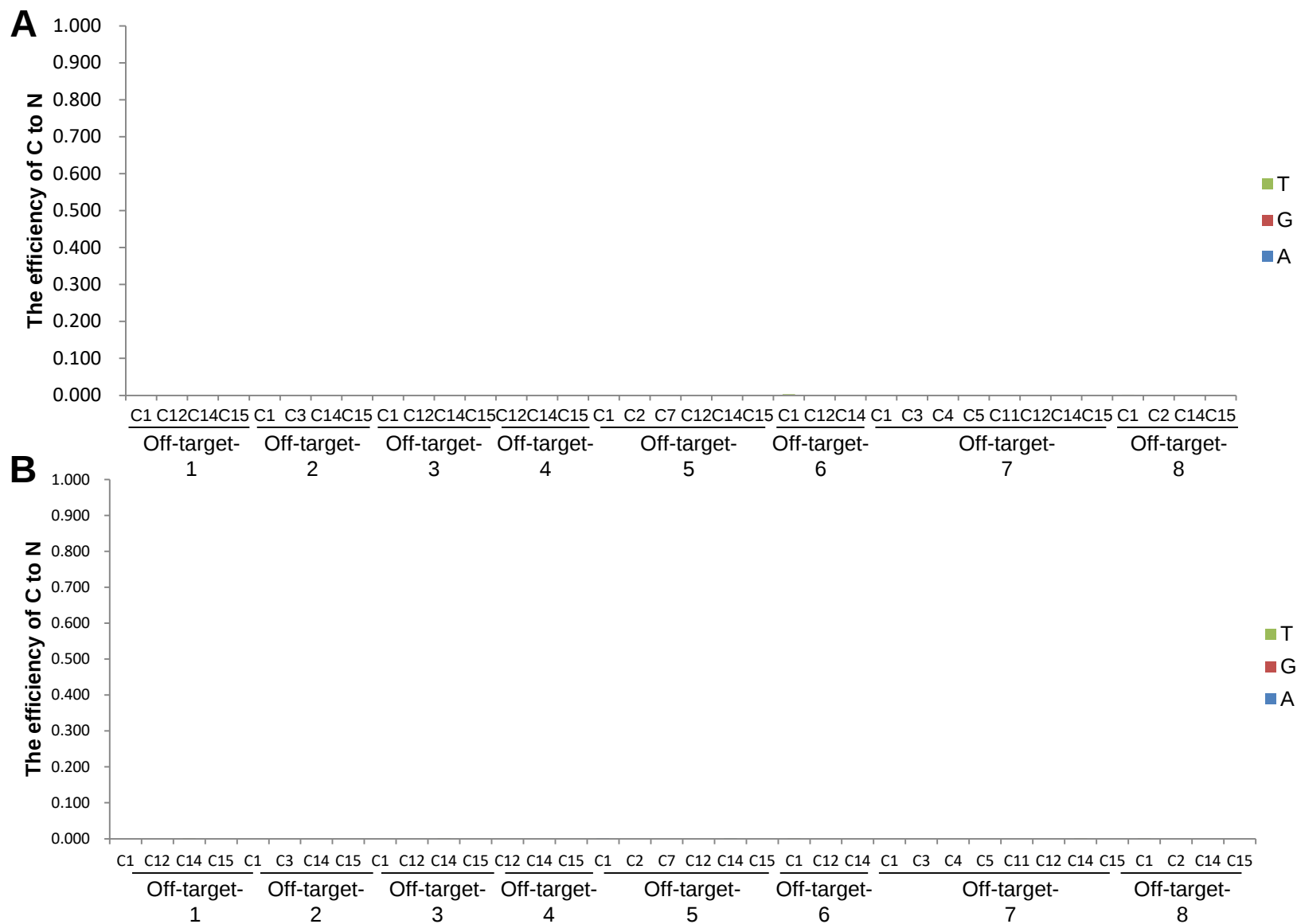
Melnikova. *Nat Rev Drug Dis.* 2012, 11: 267-268.

Boycott & Ardgo. *Nat Rev Drug Dis.* 2018, 17: 151-153.

Correction of the MFS pathogenic $\text{FBN1}^{\text{T7498C}}$ mutation by BE in trippronuclear human embryos



No off-target



BE: a precise strategy for correction of pathogenic mutations in a appropriate way

- ◆ **Ethically: strict regulation (“really the last reasonable option”)**
- ◆ **Technically: efficacy, safety, mosaicism**
- ◆ **Translational cooperation**
- ◆

Pei et al. *Cell Stem Cell* 2017, 21: 423-426.

<http://www.sciencemag.org/news/2017/02/us-panel-gives-yellow-light-human-embryo-editing>

- ◆ **Easy to develop correction for rare genetic disease pathogenic mutations;**
- ◆ **Once intervention with good effect;**
- ◆ **Low cost.**



Acknowledgements



上海科技大学
ShanghaiTech University



立志成才 报国裕民

Acknowledgements

南京医科大学

沙家豪 郭雪江 实验室

中科院动物研究所

周 琪 实验室

中国医科院实验动物研究所

张连峰 马元武 实验室

南京大学鼓楼医院

孙海翔 颜桂军 实验室

上海科技大学

陈 佳 实验室

西南医院

陈洁平 实验室

基金委 (30871429、31171377、31471400、81671516)

科技部 (2009CB918703、2010CB945101、2011CB944301、2016YFA0500903、2016YFC0905901)

云南省灵长类生物医学重点实验室

季维智 牛昱宇 陈永昌 实验室

Wellcome Trust Sanger Institute

Dr. William Skarnes

广州医科大学附属第三医院

刘见桥 实验室

西北农林科技大学

陈玉林 马宝华 实验室

中科院计算生物学所

杨 力 实验室

中科院神经科学研究所

孙 强 刘 真 实验室



上海科技大学
ShanghaiTech University

THANK YOU



立志成才 报国裕民