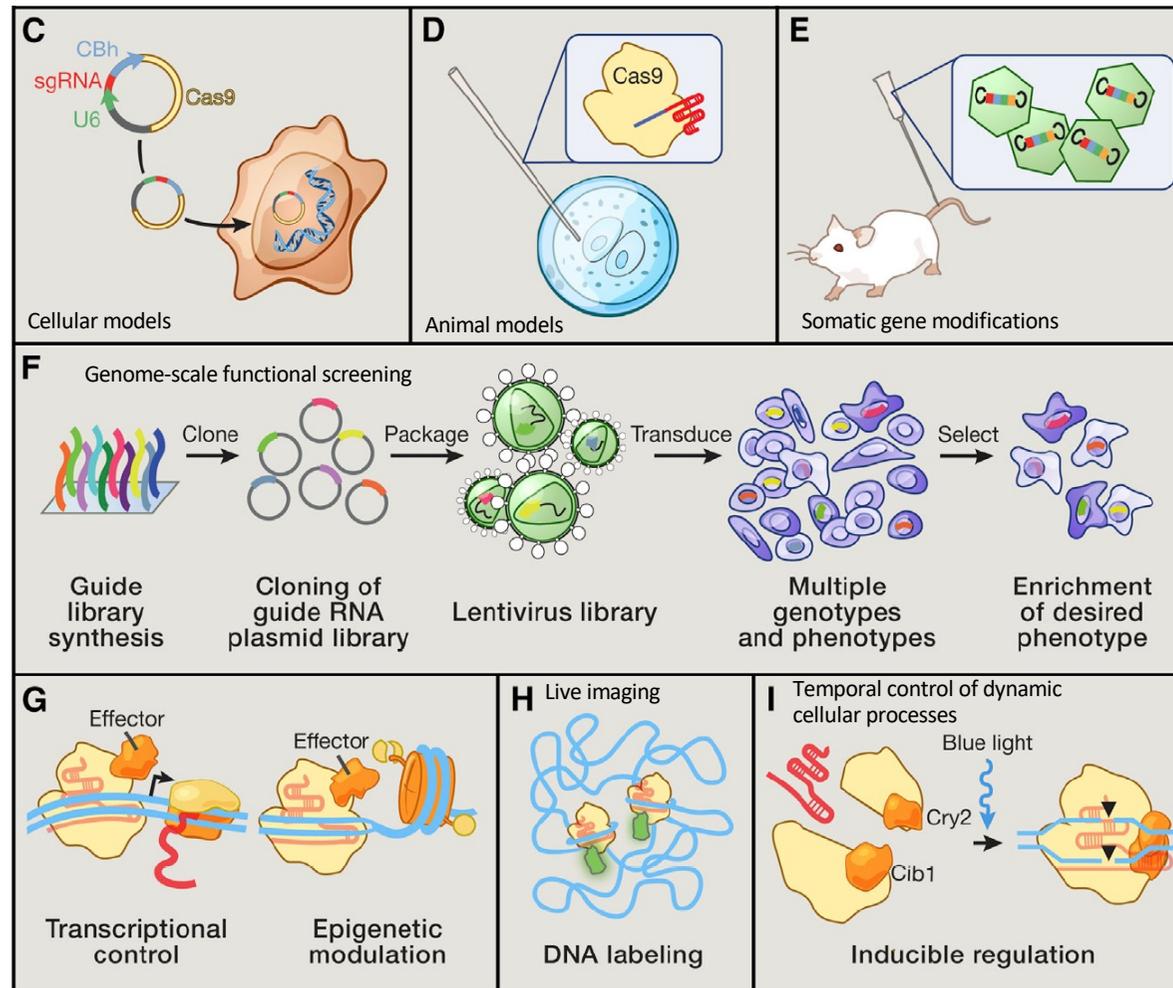


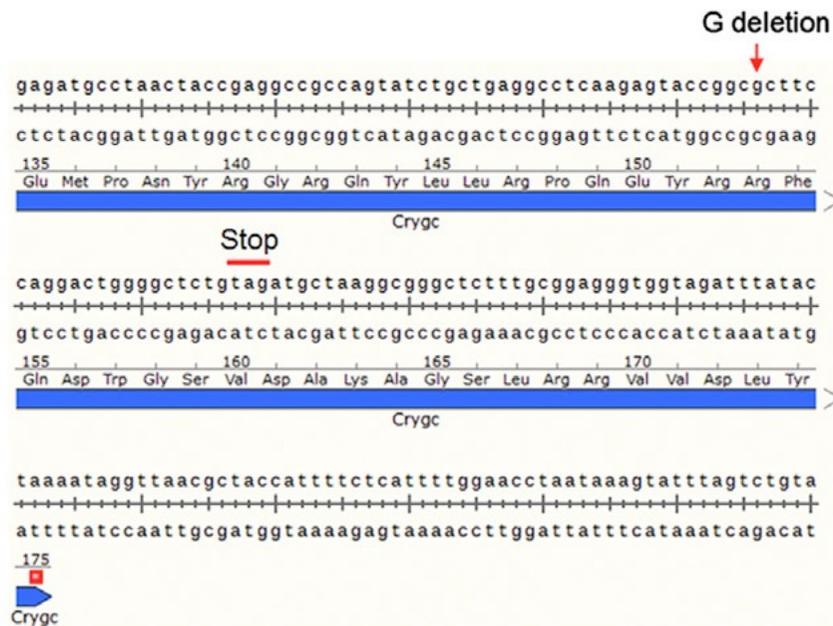
CRISPR/Cas9
APPLICATIONS

CRISPR/Cas engineering is enabling a broad range of applications

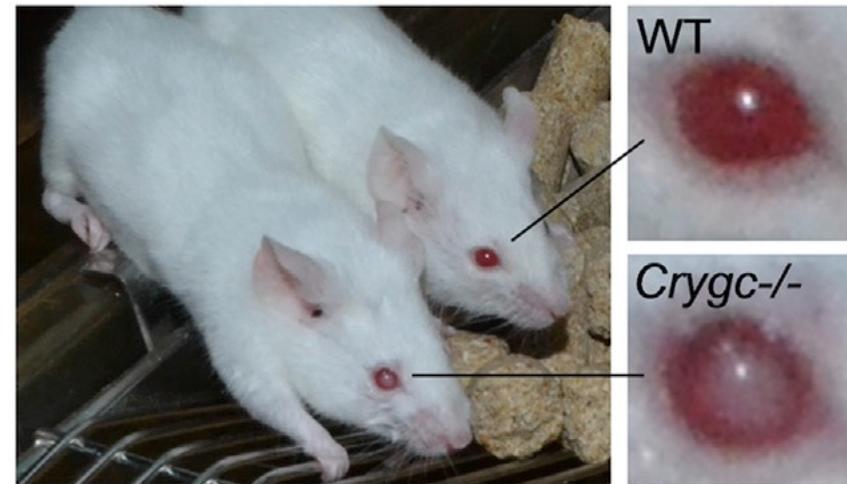


(Hsu et al., Cell, 2014)

Can CRISPR/Cas9 be used for correct genetic disorders?



Crygc mutation (dominant inheritance)

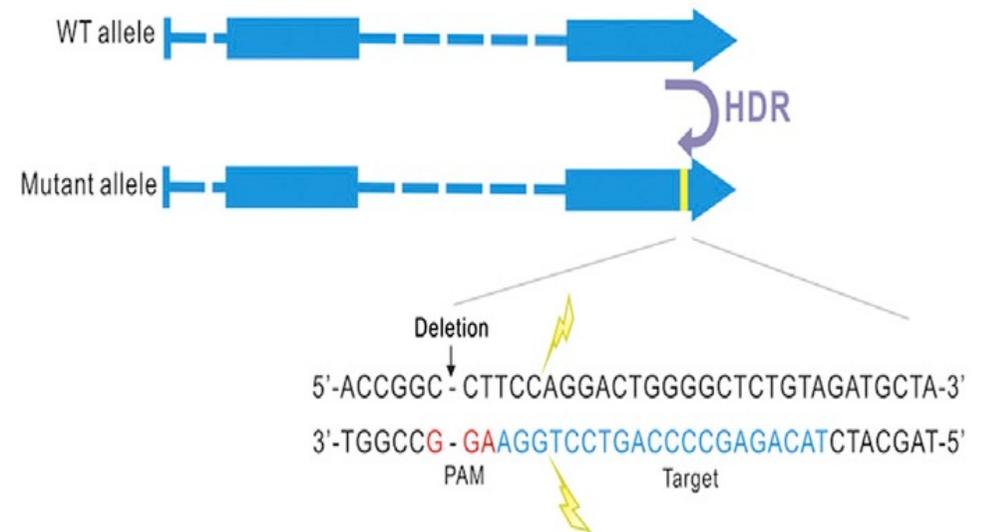
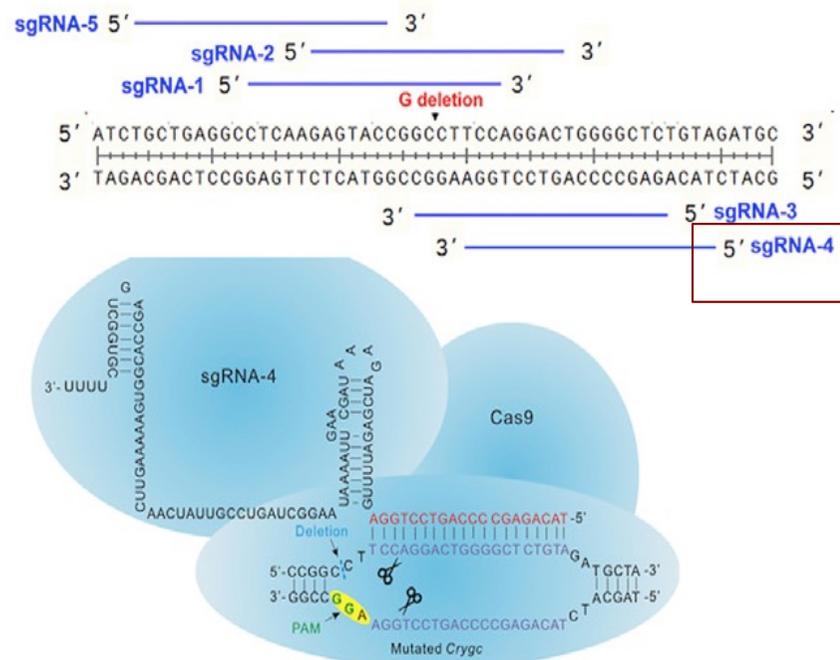


(Wu et al., Cell 2013)

1 bp deletion in exon 3 of *Crygc* gene leads to cataract

Can CRISPR/Cas9 be used for correct genetic disorders?

In vitro



(Wu et al., Cell 2013)

Can CRISPR/Cas9 be used for correct genetic disorders?

In vitro

sgRNA leads to HDR mediated repair

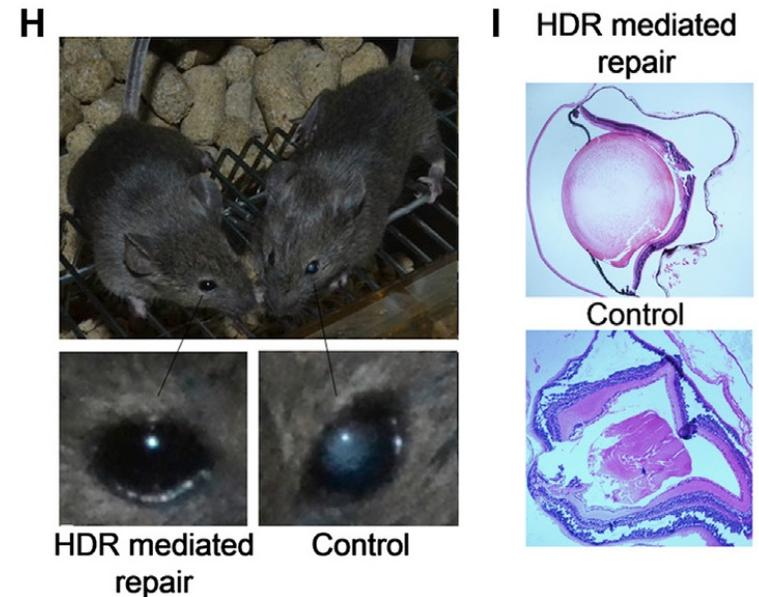
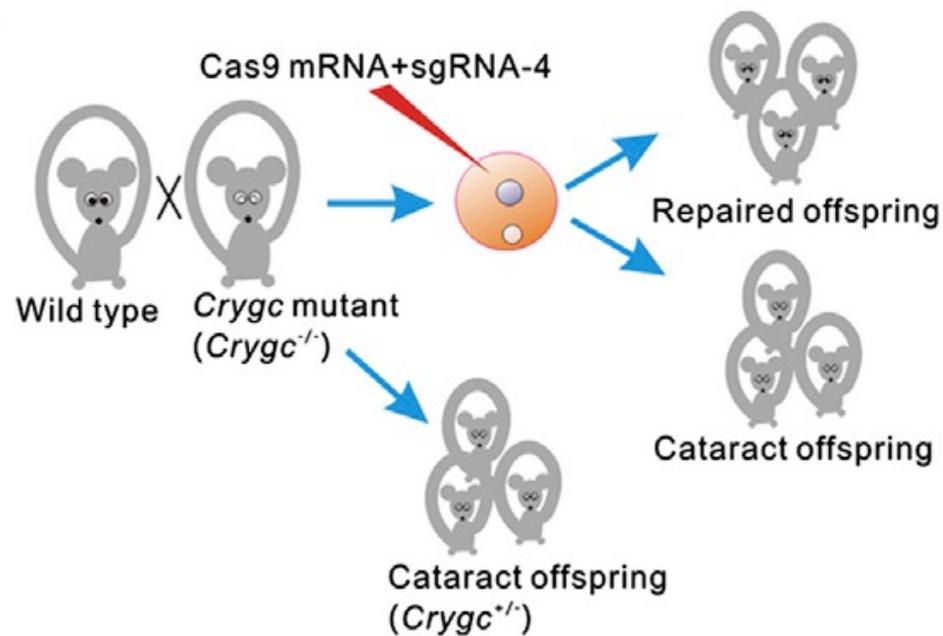
sgRNA	E14 ESC clones		mCrygc (<i>Crygc</i> ^{+/+}) ESC clones		
	Cleavage at 1 Allele/Total	Cleavage at 2 Alleles/Total	Cleavage at WT Allele/Total	Cleavage at Mutant Allele/Total	HDR-mediated Repair/Total
sgRNA-1	4/36	0/36	0/36	10/36	7/36
sgRNA-2	23/36	7/36	17/36	25/36	2/36
sgRNA-3	3/36	0/36	0/36	7/36	5/36
sgRNA-4	0/36	0/36	0/36	11/36	16/36
sgRNA-5	4/36	26/36	27/36	26/36	0/36

(Wu et al., Cell 2013)

sgRNA4 show high specificity for mCrygc allele and mediates HDR

Can CRISPR/Cas9 be used for correct genetic disorders?

In vivo



(Wu et al., Cell 2013)

CRISPR/Cas9 system leads to gene correction via HDR using wt allele on the homologous chromosome

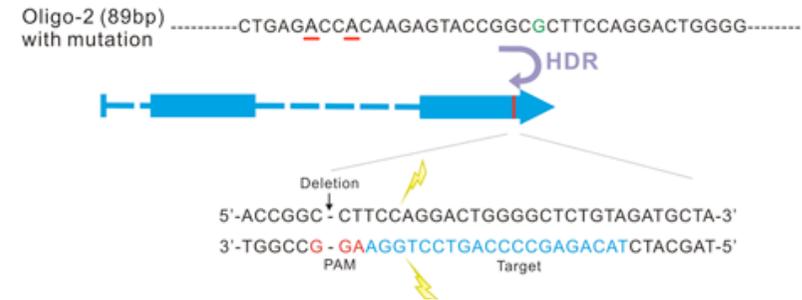
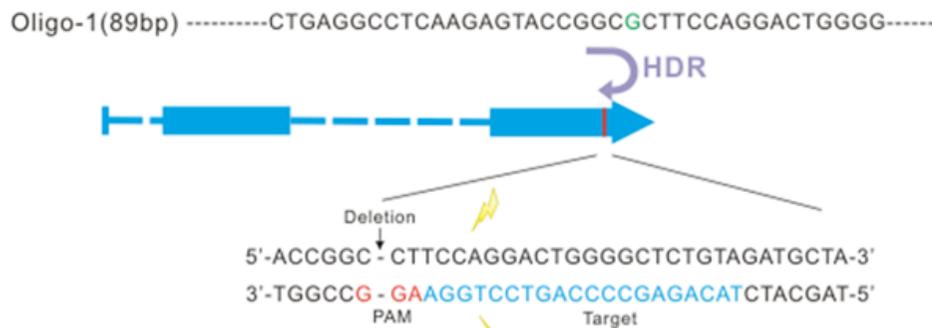
Is it possible to improve CRISPR/Cas9 sgRNA4 gene correction?



(Wu et al., Cell 2013)

Insertion of Oligo-1 that mimic wt allele and Oligo-2 that contains specific in frame mutation

Is it possible to improve CRISPR/Cas9 sgRNA4 gene correction?



Oligo	Injected Embryos	Blastocysts Injected (Percentage of Embryos)	Transferred Blastocysts	Live-Born Pups	Genetic Modification			HDR-Mediated Repair
					WT allele	mutant allele	NHEJ-Mediated Repair/Nonrepair	
-	172	157 (91%)	135	22	0	10	2/4	4
Oligo-1	245	213 (87%)	178	29	0	14	4/5	5
Oligo-2	221	190 (86%)	159	27	0	12	5/3	4

Repair Type	Allele	Sequence	Count
HDR mediated repair	WT allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	HDR with WT (×1)
	Mutant allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	
HDR mediated repair	WT allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	HDR with mutations (×3)
	Mutant allele	CTGAGACCACAAGAGTACCGGCCTTCCAGGACTGGGG	
NHEJ mediated repair	WT allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	+1 (×3)
	Mutant allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	
NHEJ mediated repair	WT allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	-5 (×2)
	Mutant allele	CTGAGGCCTCAAGAGTACCGGC-----CAGGACTGGGG	
NHEJ non-repair	WT allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	-4
	Mutant allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	
NHEJ non-repair	WT allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	-12
	Mutant allele	CTGAGGCCTCAAGAGTACCGGC-----GG	
NHEJ non-repair	WT allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	-3
	Mutant allele	CTGAGGCCTCAAGAGTACCGGCCTTCCAGGACTGGGG	

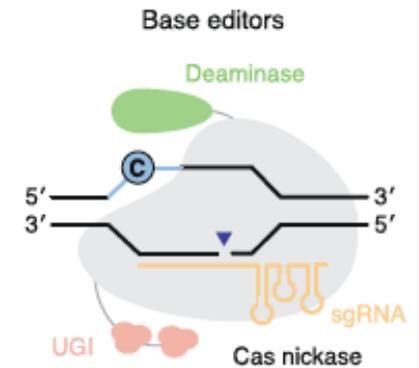
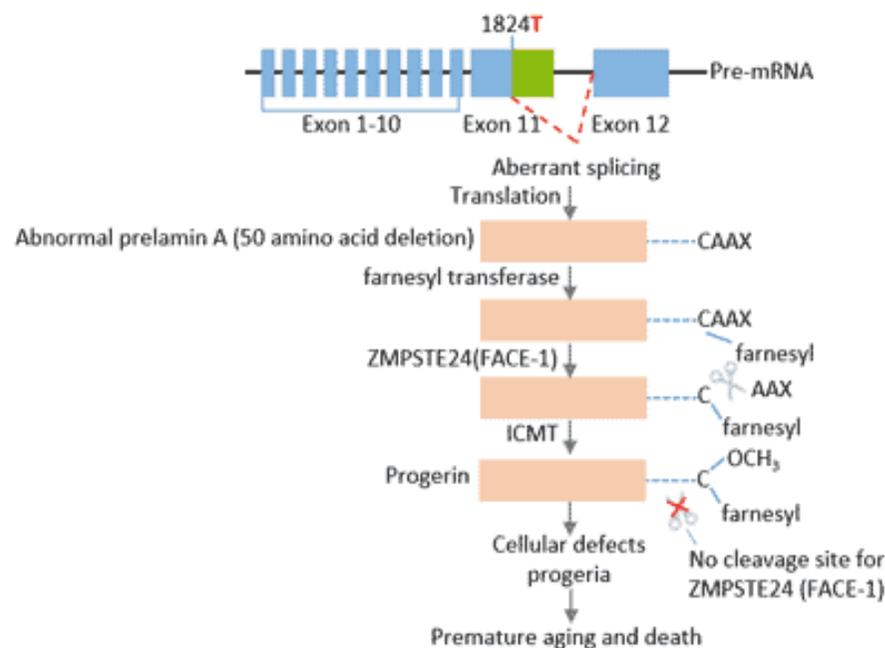
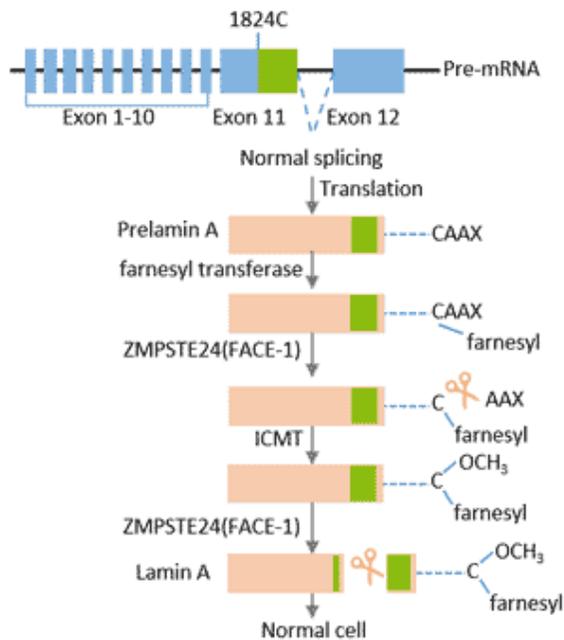
(Wu et al., Cell 2013)

Insertion of Oligo-1 that mimic wt allele and Oligo-2 that contains specific synonymous mutations

In vivo base editing rescues Hutchinson–Gilford progeria syndrome in mice

Luke W. Koblan^{1,2,3,13}, Michael R. Erdos^{4,13}, Christopher Wilson^{1,2,3}, Wayne A. Cabral⁴, Jonathan M. Levy^{1,2,3}, Zheng-Mei Xiong⁴, Urraca L. Tavarez⁴, Lindsay M. Davison⁵, Yantew G. Gete⁶, Xiaojing Mao⁶, Gregory A. Newby^{1,2,3}, Sean P. Doherty⁵, Narisu Narisu⁴, Quanhu Sheng⁷, Chad Krilow⁴, Charles Y. Lin^{8,9,12}, Leslie B. Gordon^{10,11}, Kan Cao⁶, Francis S. Collins⁴, Jonathan D. Brown⁵ & David R. Liu^{1,2,3}

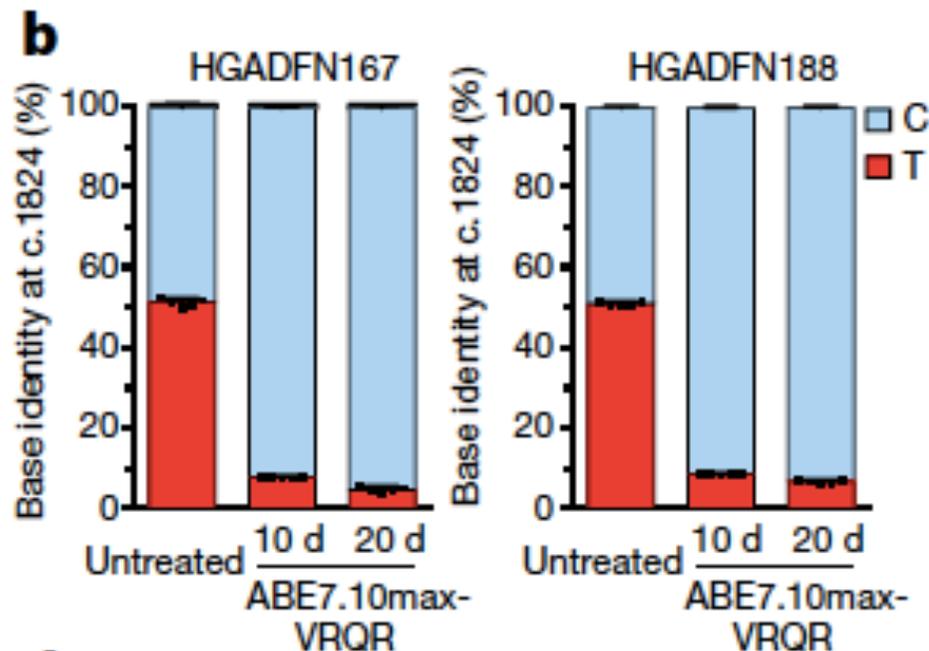
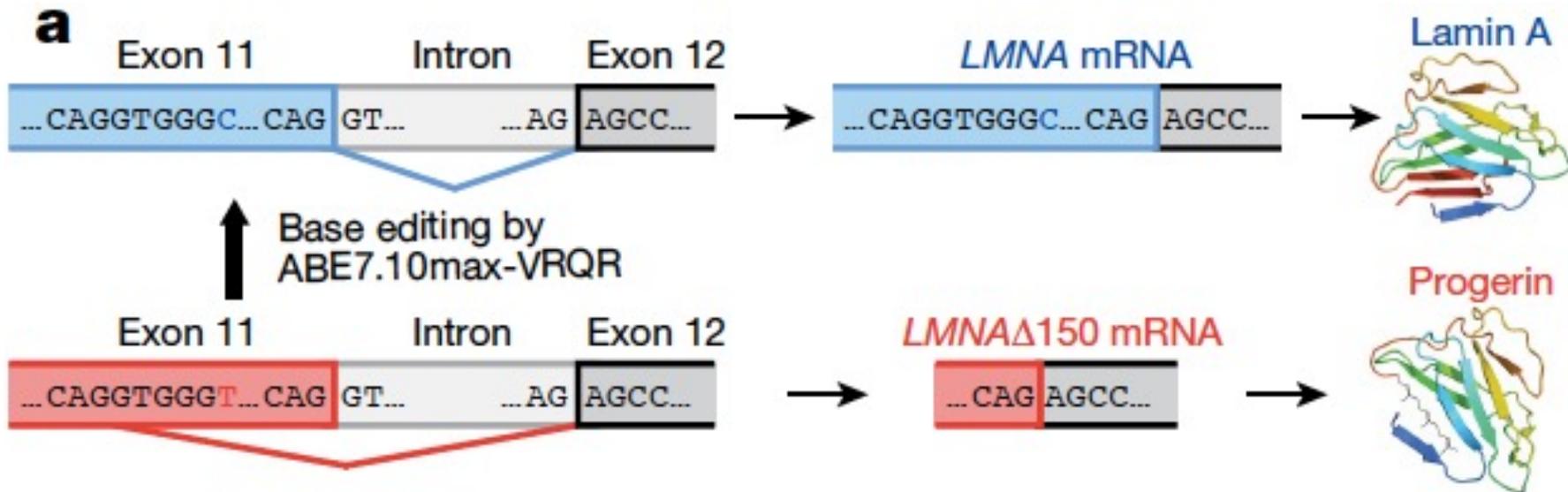
Nature | Vol 589 | 28 January 2021 |



ABE: adenine base editor and converts A-T to G-C.

Adapted from Baek, Erikson, 2013

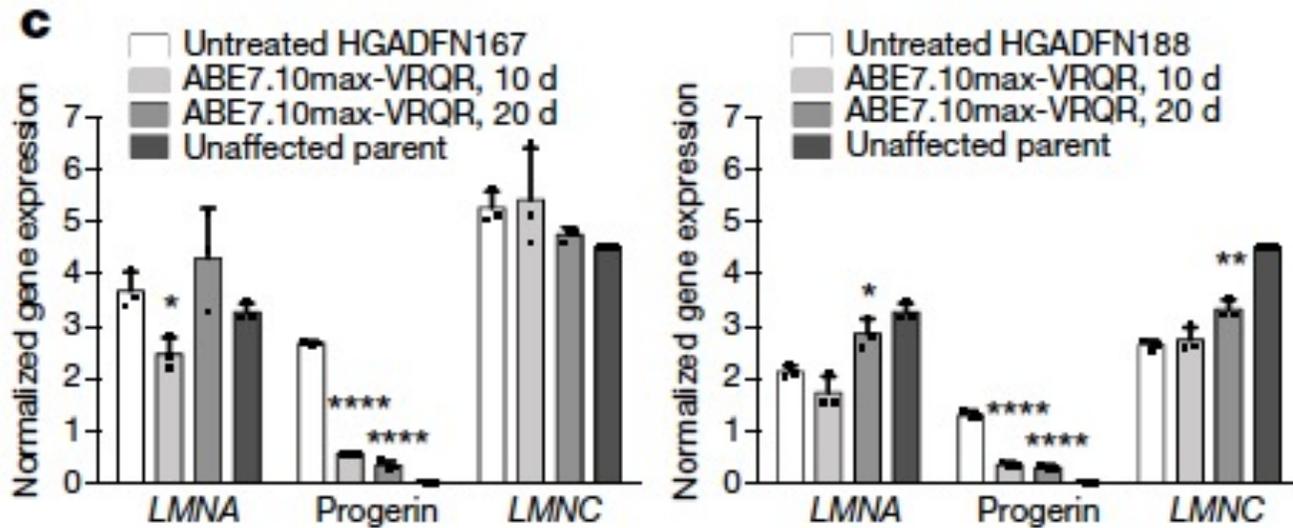
Does ABE approach correct HGPS mutation in patient cells?



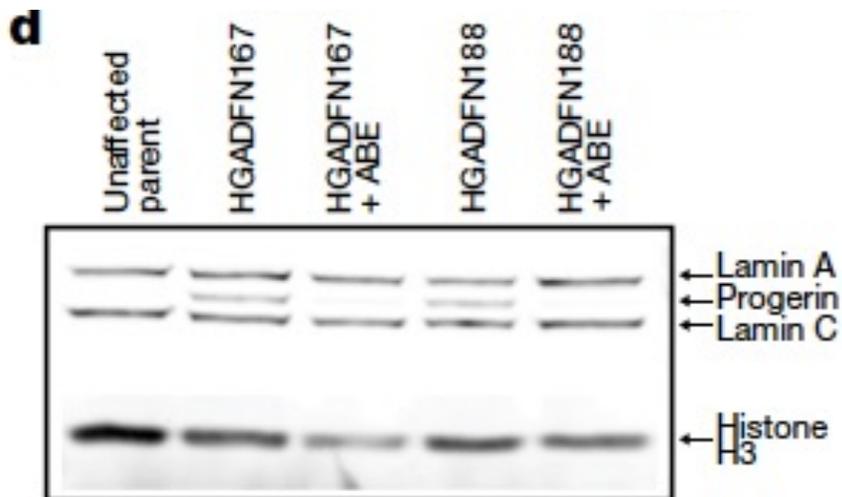
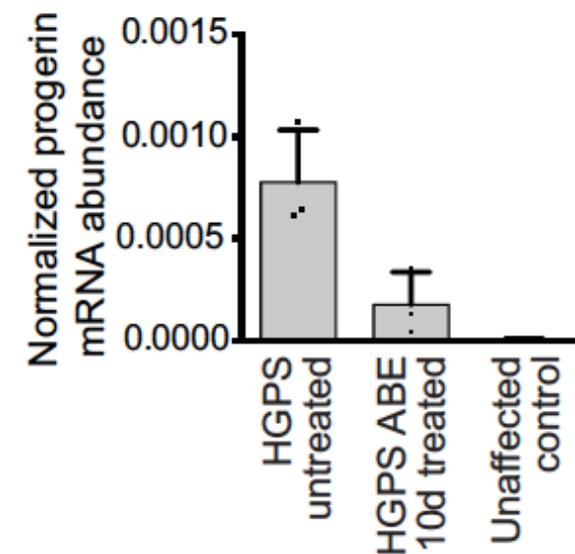
Lentiviral mediated delivery
 ABE7-10fused with optimized SpCas9-VRQR+
 SgRNA targeting HGP mutation

84-85% of correction 10 days
 87-91% of correction 20 days

Does ABE approach correct HGPS mutation in patient cells?

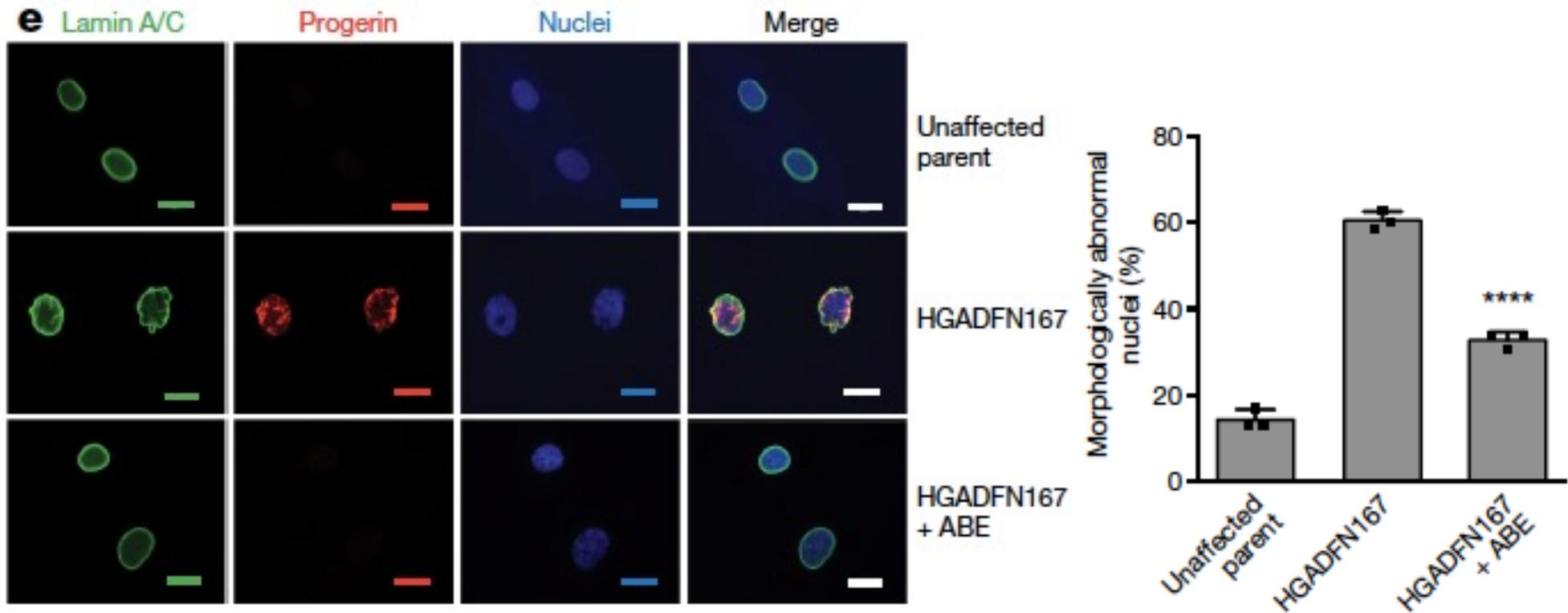


8.8-4.4fold reduction of progerin



6.1-15 fold reduction of progerin protein

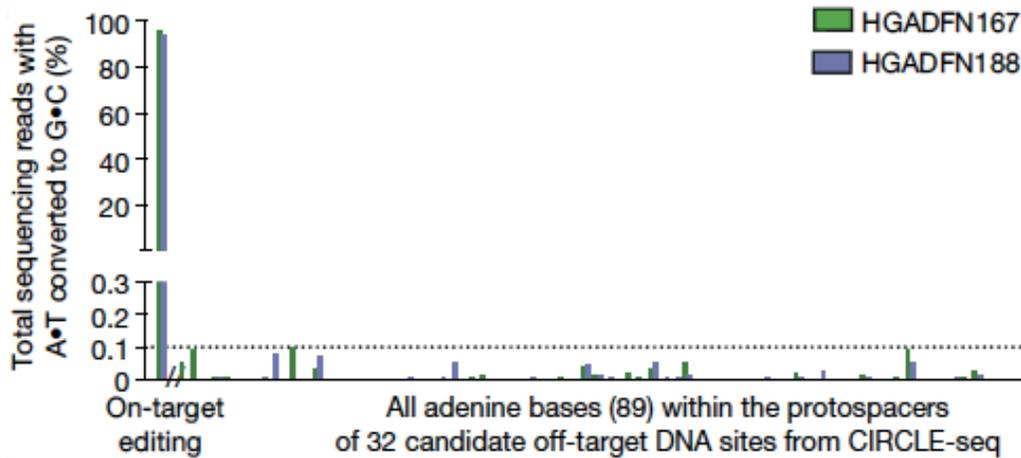
Does ABE approach correct HGPS mutation in patient cells?



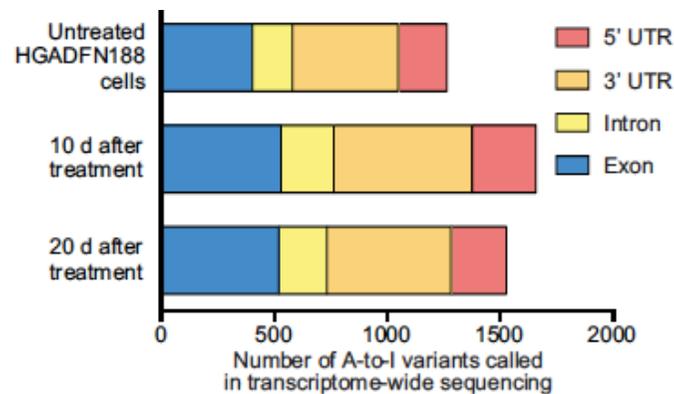
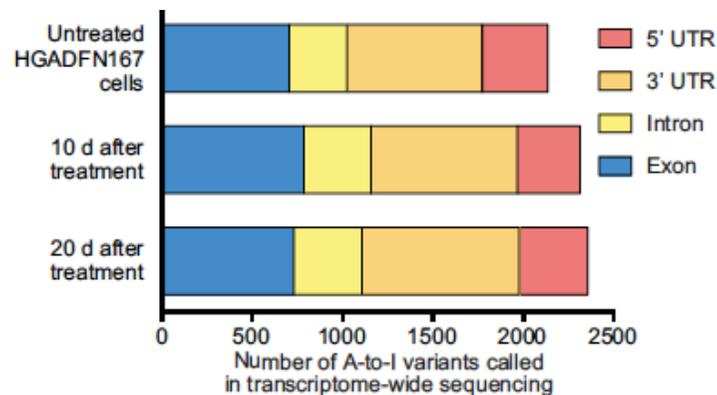
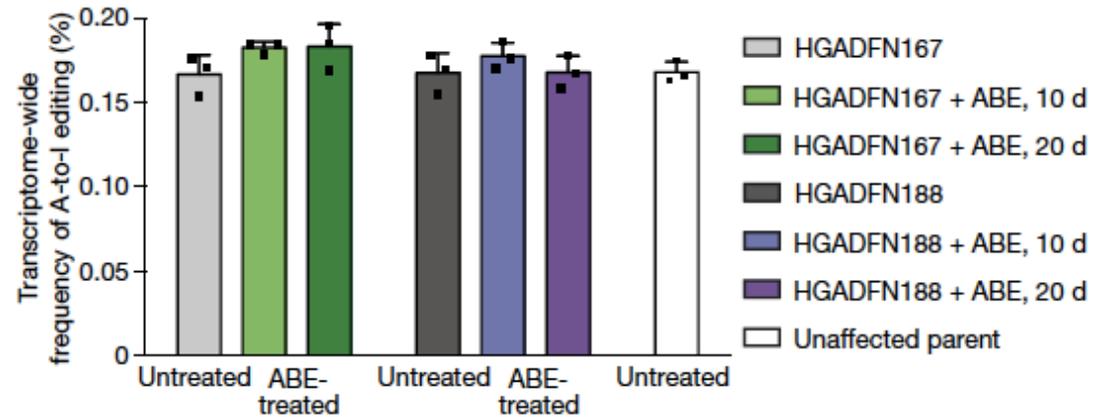
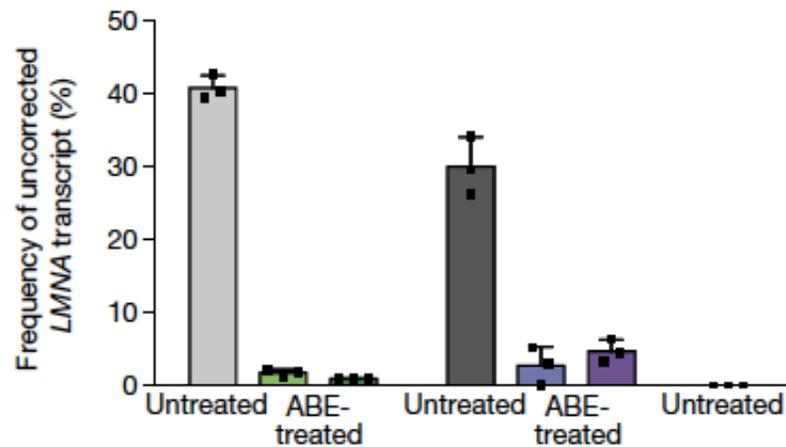
1.8 fold reduction of nuclear abnormalities

Base editing to correct LMNA c.1824 C→T mutation in cells from HGPS patients rescues the molecular and phenotypic consequences of the mutation

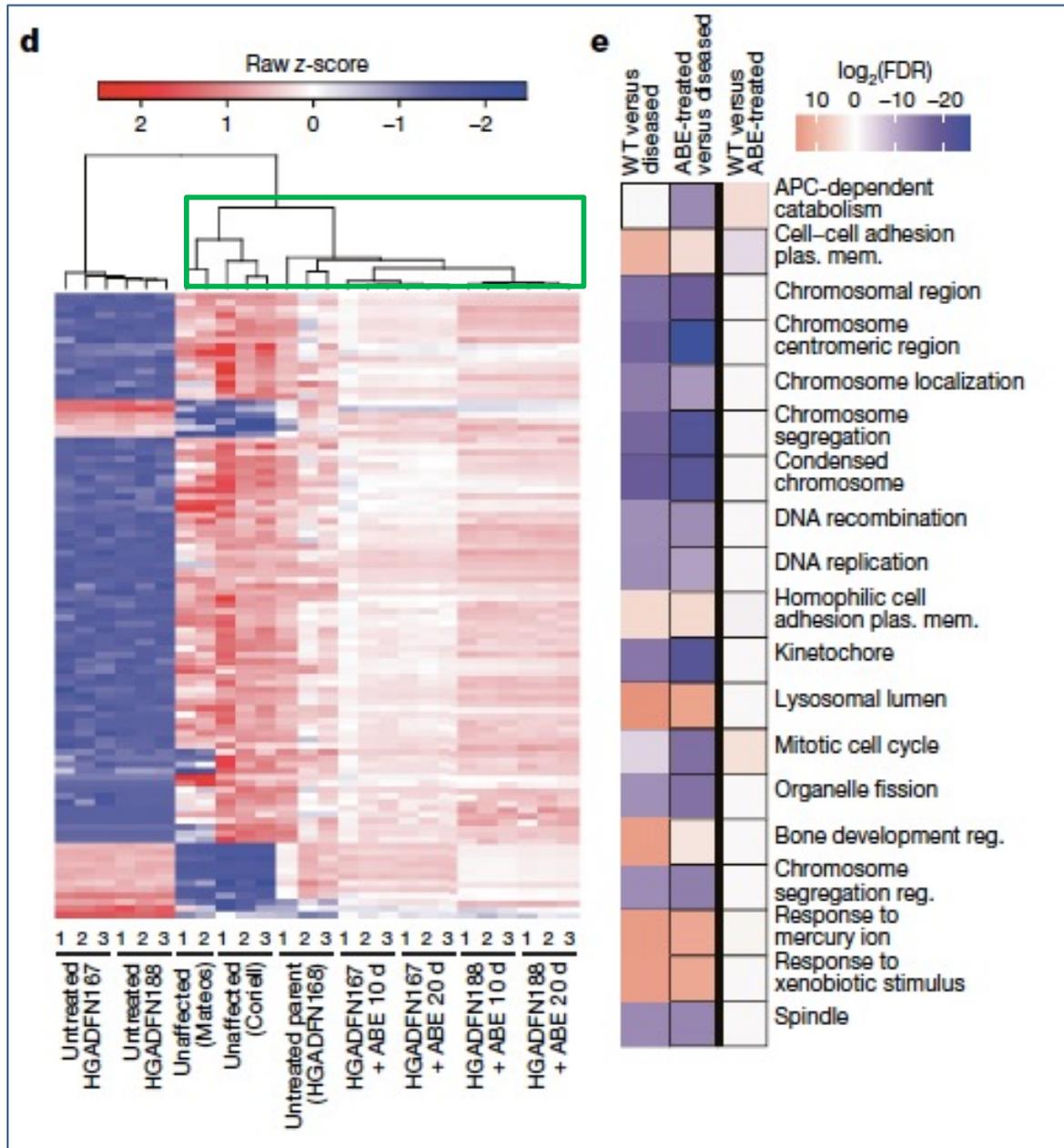
Does LMNA c.1824 C→A BE correction approach induce off targets?



Less than 0.1% off-target DNA editing at 32 candidate off target loci



Does LMNA c.1824 C→ABE correction approach induce off targets?



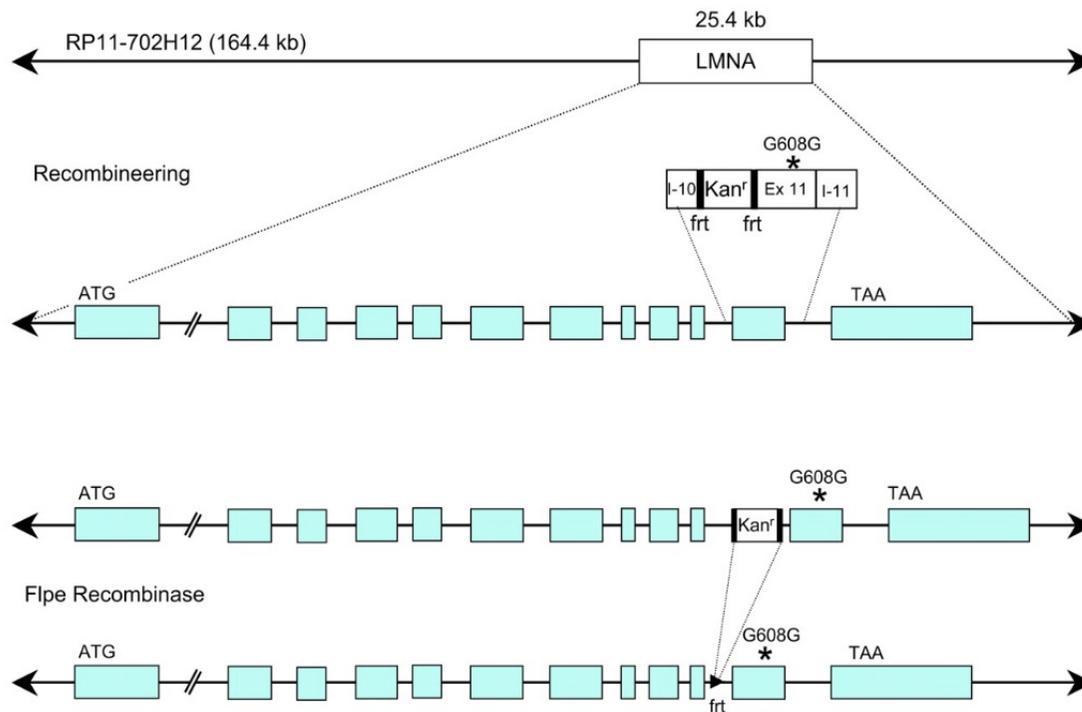
ABE treated transcriptomes cluster with unaffected Fb

Treating cells with LMNA-targeting sgRNA and ABEmax-VRQR didn't result in off-target DNA or RNA editing despite high level of on-target editing

In vivo ABE delivery in mice with progeria

Progeria mouse model:

C57BL/6-tg(LMNA*G608G)HCIns/J: includes complete human LMN c.1824C>T



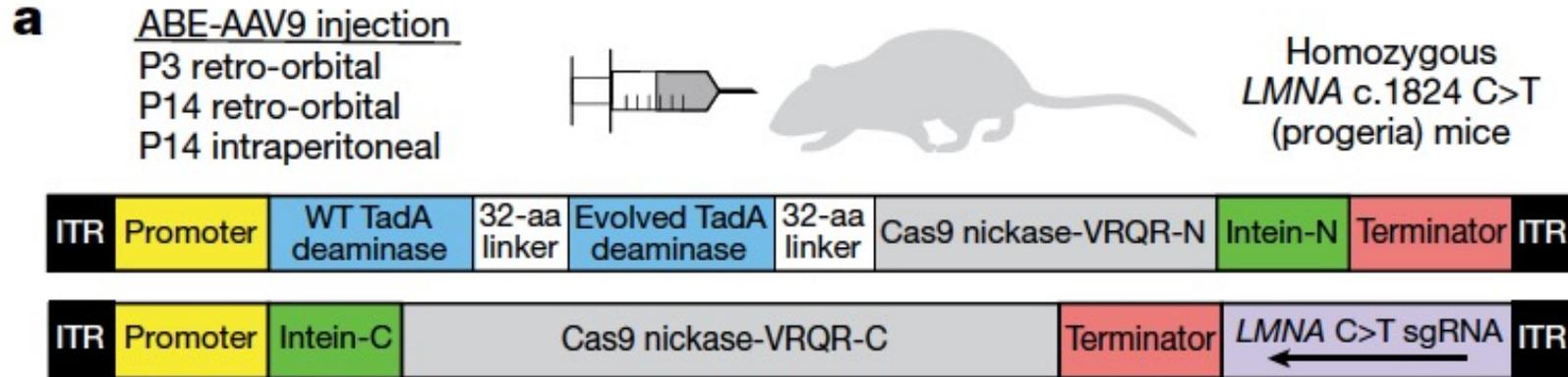
Systemic in vivo delivery of ABE and sgRNA characterized in cells

Varga et al, PNAS 2006

For the first 4 months after birth, homozygotes exhibit a slower rate of weight gain when compared to hemizygotes. In addition to developing kyphosis, hair loss, tight skin, loss of subcutaneous fat and joint contracture, homozygotes develop a significantly more severe vascular damage with VSMC loss in aortic vessel walls, calcification, and periadventitial thickening. Homozygotes die at an average of 7-8 months of age as the result of aortic stiffening and impaired cardiovascular functioning. The Donating Investigator reports that homozygous females are infertile and that a lower than expected number of homozygotes are born.

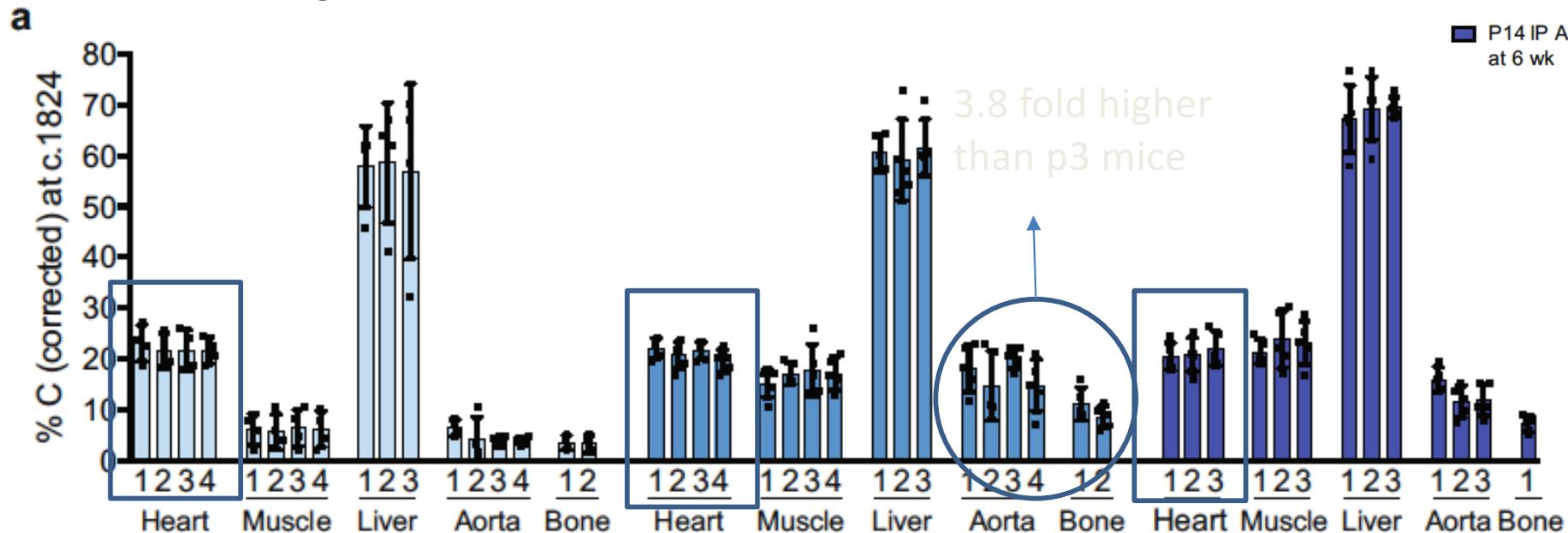
From Jackson Lab

In vivo ABE delivery in mice with progeria



- █ P3 RO ABE-AAV9-injected at 6 wk
- █ P14 RO ABE-AAV9-injected at 6 wk
- █ P14 IP ABE-AAV9-injected at 6 wk

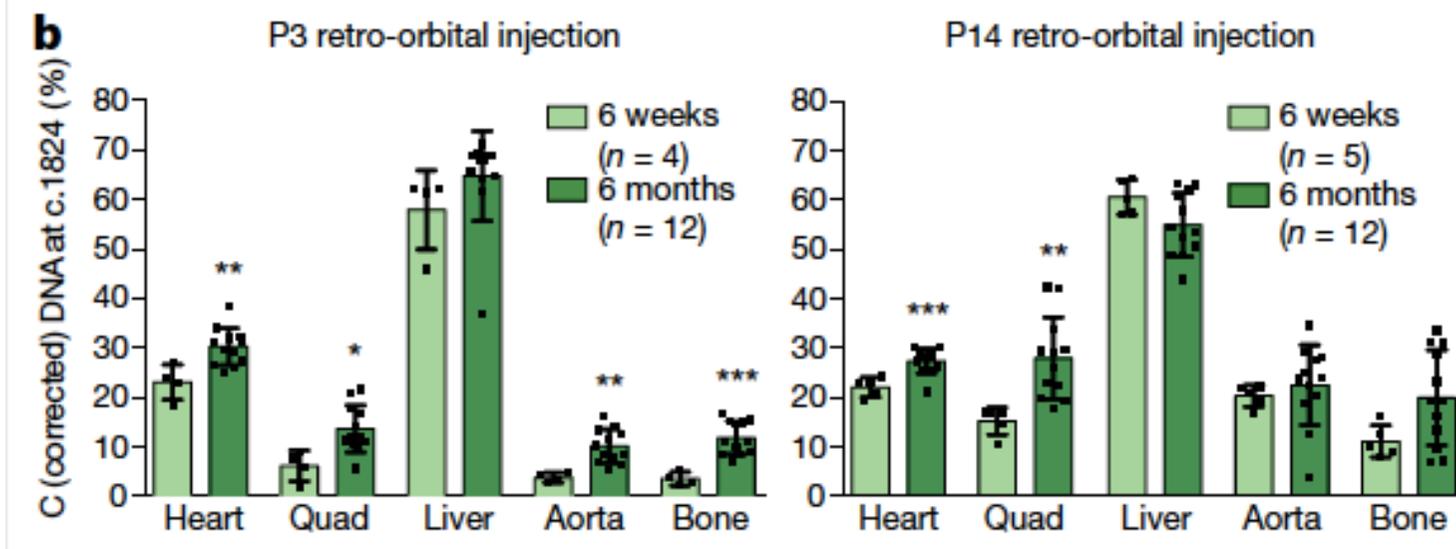
6 weeks of age



A single in vivo AB-encoding AAV results in 10-60% of point mutation correction in the various organs

In vivo ABE delivery in mice with progeria. Long term ABE treatment

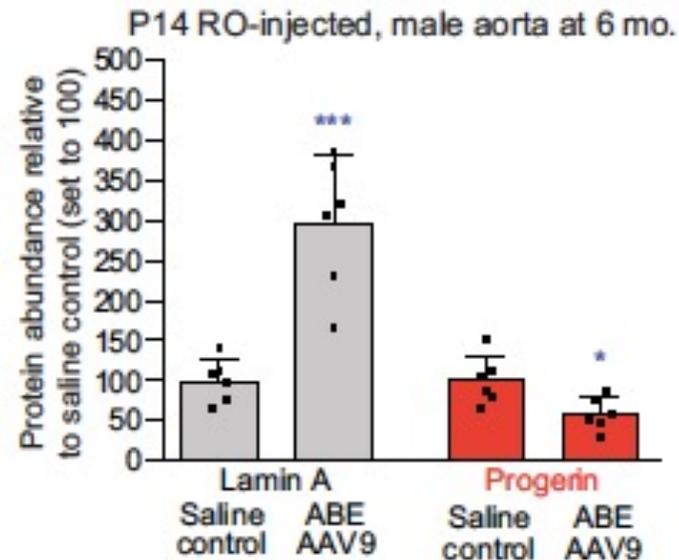
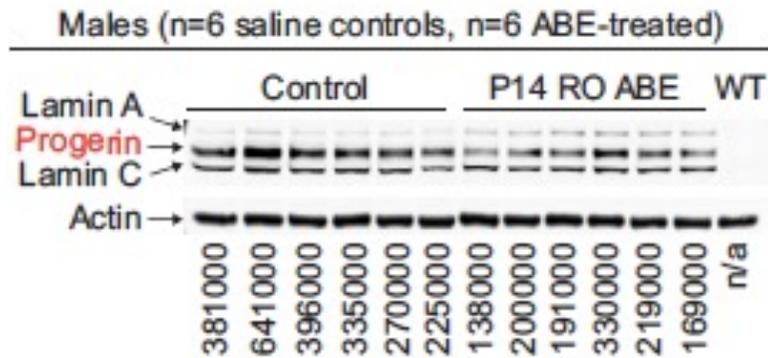
6 months after injection



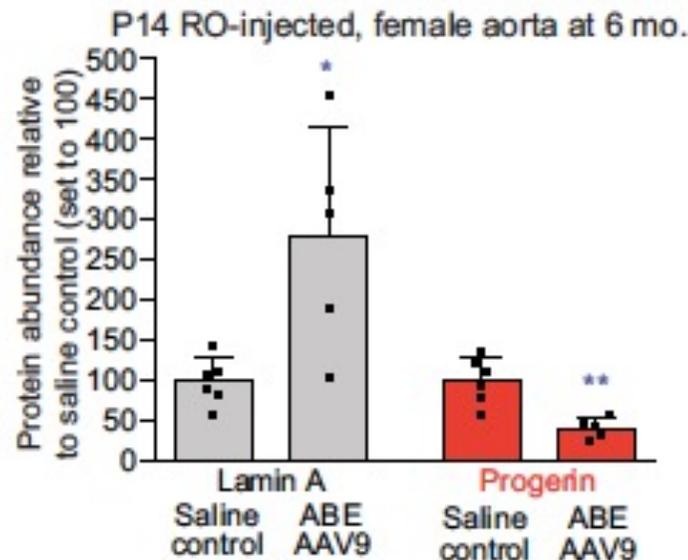
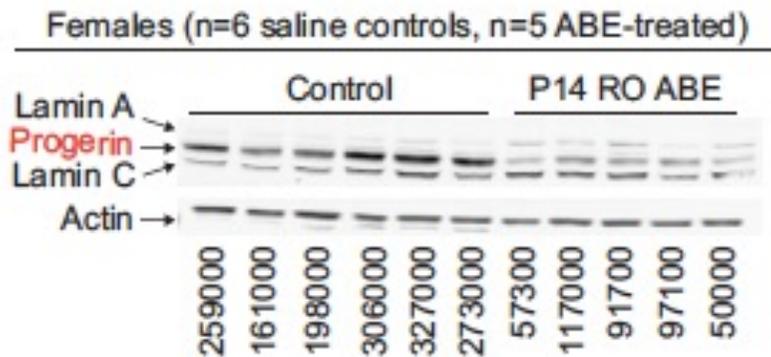
Increase in gene editing at 6 months, mainly for p3 mice but remains higher for p14 mice injected with higher doses of ABE encoding AAVs

Base editing persists in vivo

In vivo ABE delivery in mice with progeria. Long term ABE treatment

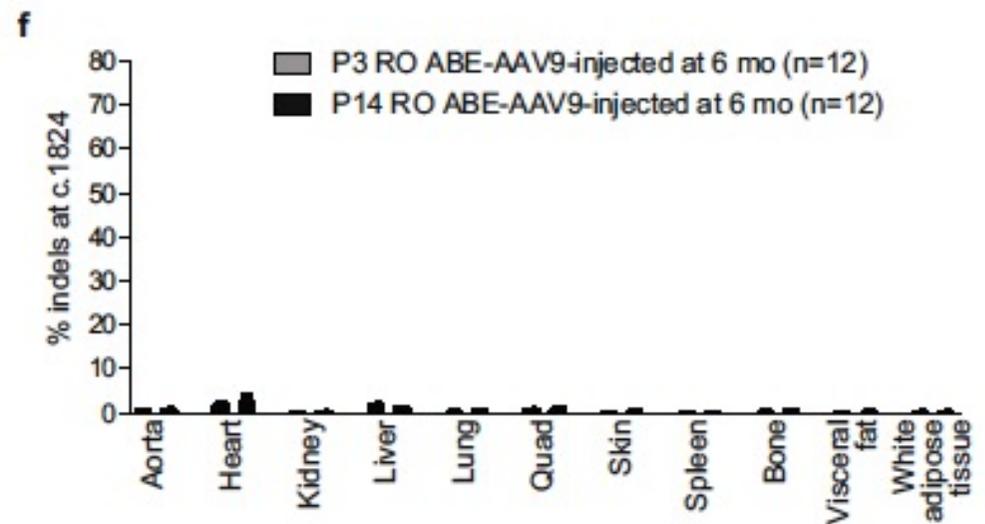
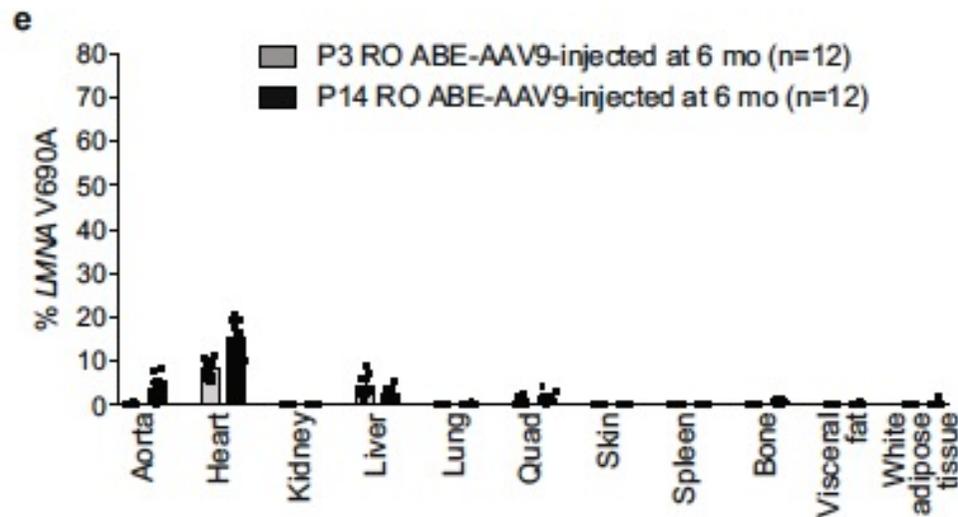


In vivo ABE treatment led to decrease in progerin transcript abundance and robust reduction of progerin protein



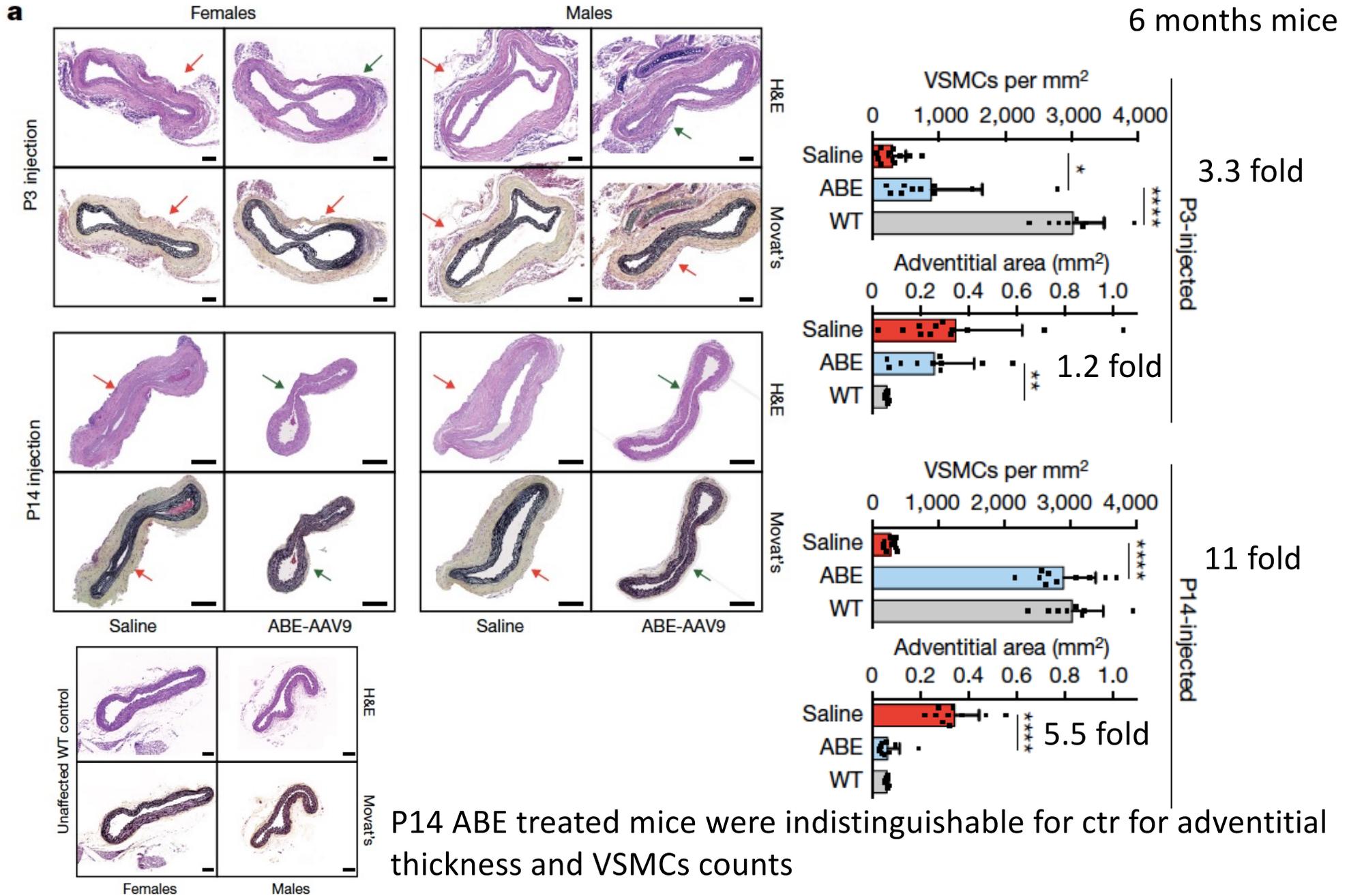
ABE correction of LMNA c.1824C>T alleli in mice can reduce progerin mRNA and protein levels in several clinically relevant tissues

In vivo ABE delivery in mice with progeria. Long term ABE treatment



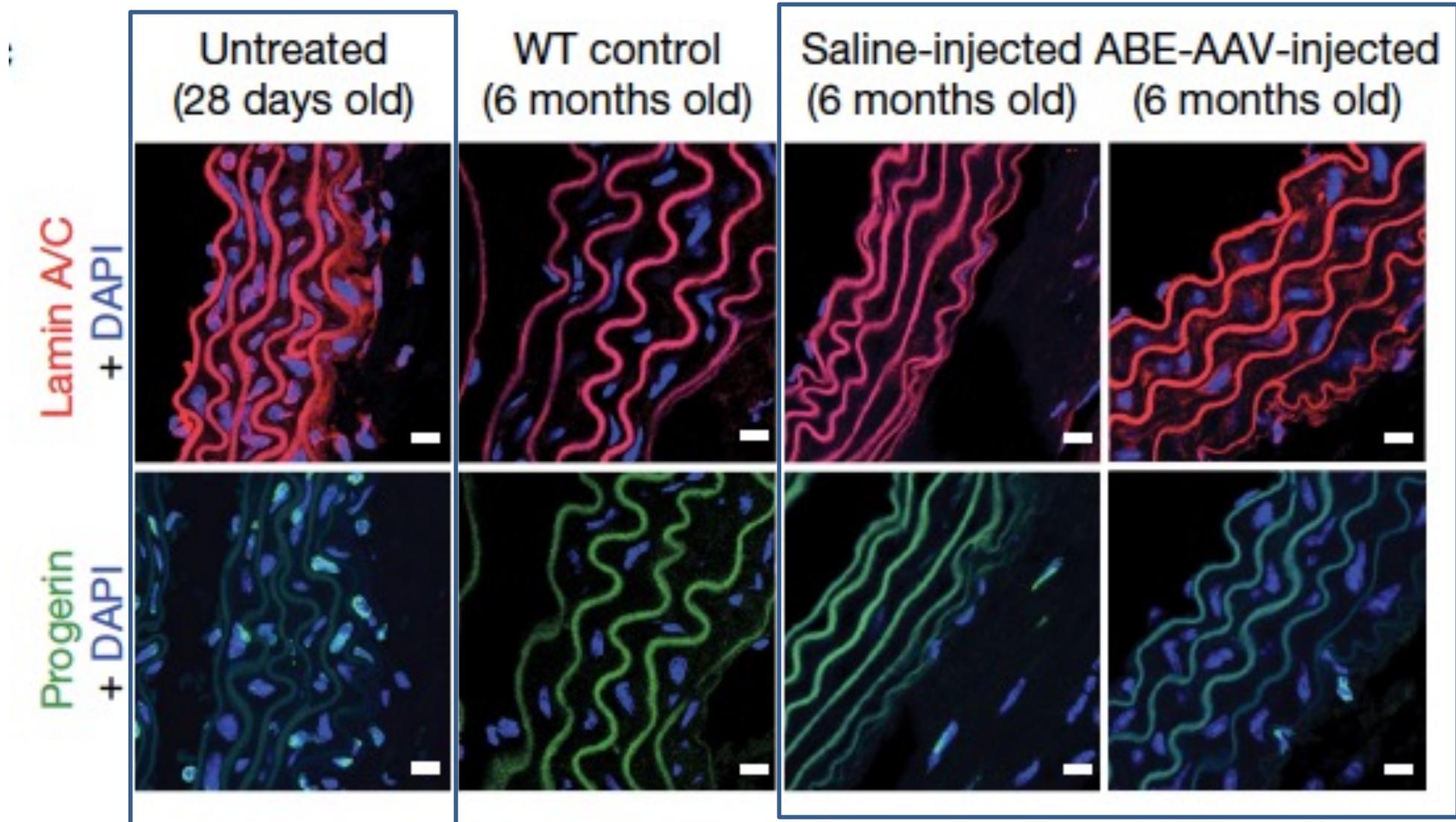
Bystander editing and indels observed at very low frequency compared to on target editing

ABE treatment improves vascular pathology



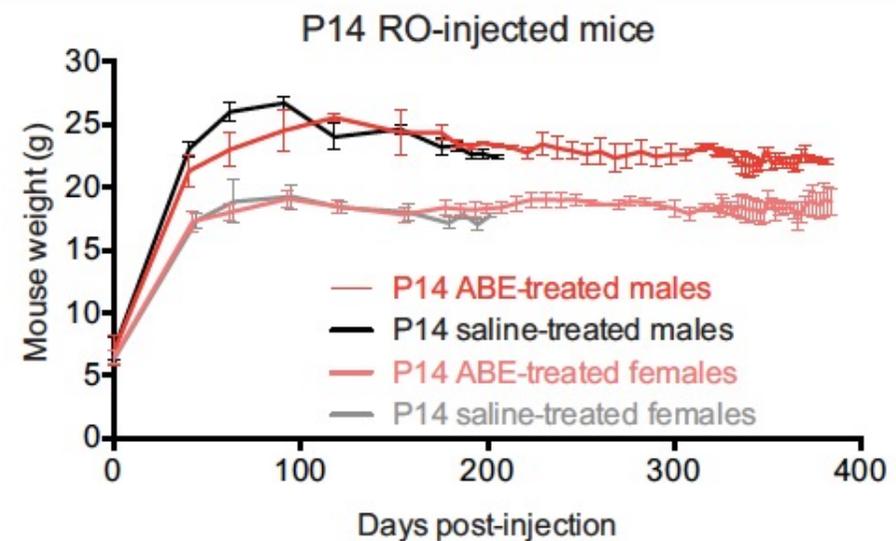
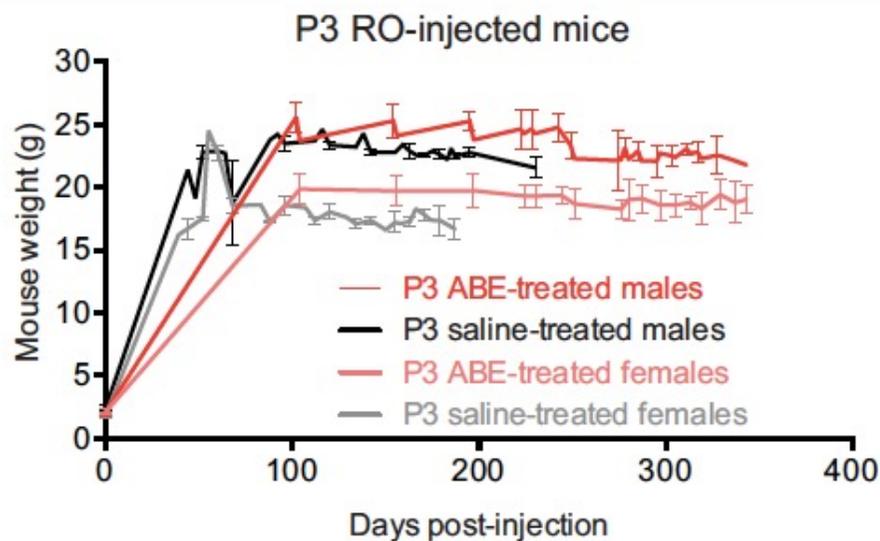
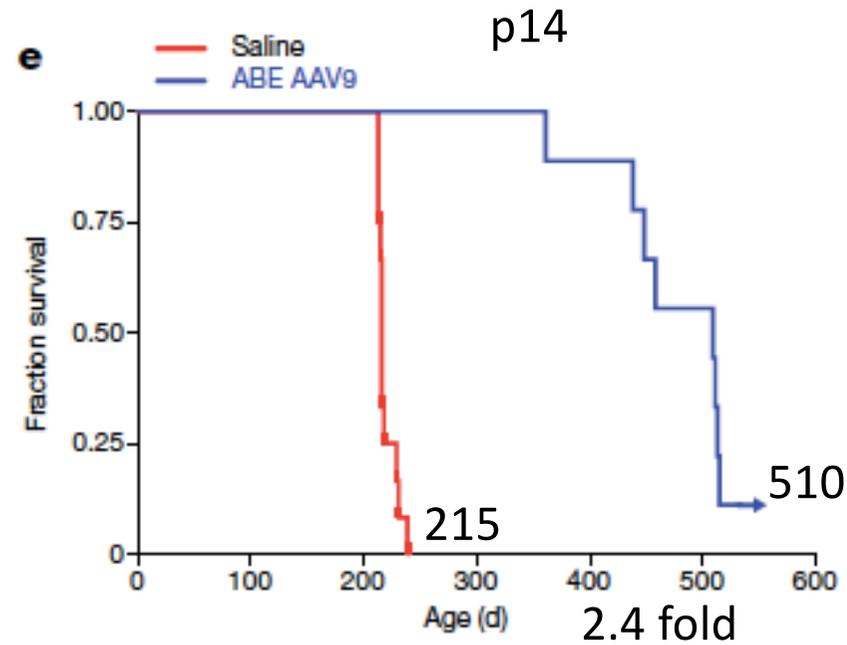
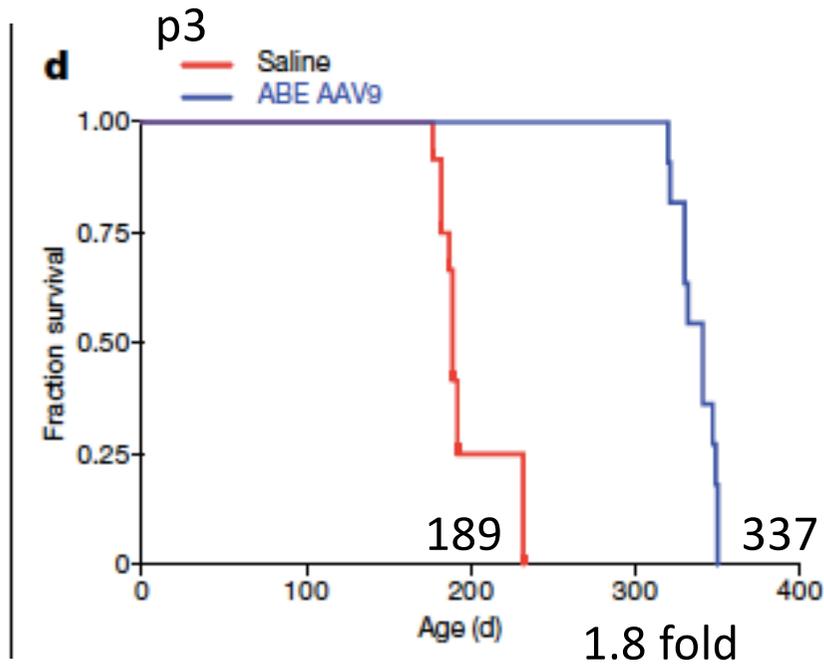
ABE treatment improves vascular pathology

Increase in VSMCs count



Base editing of around 25% in aorta is enough to rescue two key vascular defects of progeria, preserving the expression of Lamin A/C and reducing progerin abundance

ABE treatment extends progeria mouse lifespan



Body weights were maintained

Conclusions

- Patients-derived cells ABE correct pathogenic allele (97-91% of on target editing) with minimal degree of off-target. Reduces mis-splicing and progerin protein reduces nuclear morphology defects
- A single dose of dual AAV9 encoding ABE and sgRNA in a progeria mouse model resulted in durable correction of pathogenic allele, reduction of progerin protein with different efficiency in diverse tissue and organs. Treatment of p14 mice greatly improved cardiac phenotype and aortic health.
- A single dose of dual AAV9 encoding ABE and sgRNA in a progeria mouse model increases mice lifespan

Concerns:

- Immune response to treatment
- Timing of treatment to take account of the time of diagnosis
- Base editing amelioration to obtain results in other tissues
- No direct correlation between base editing, RNA levels and proteins levels