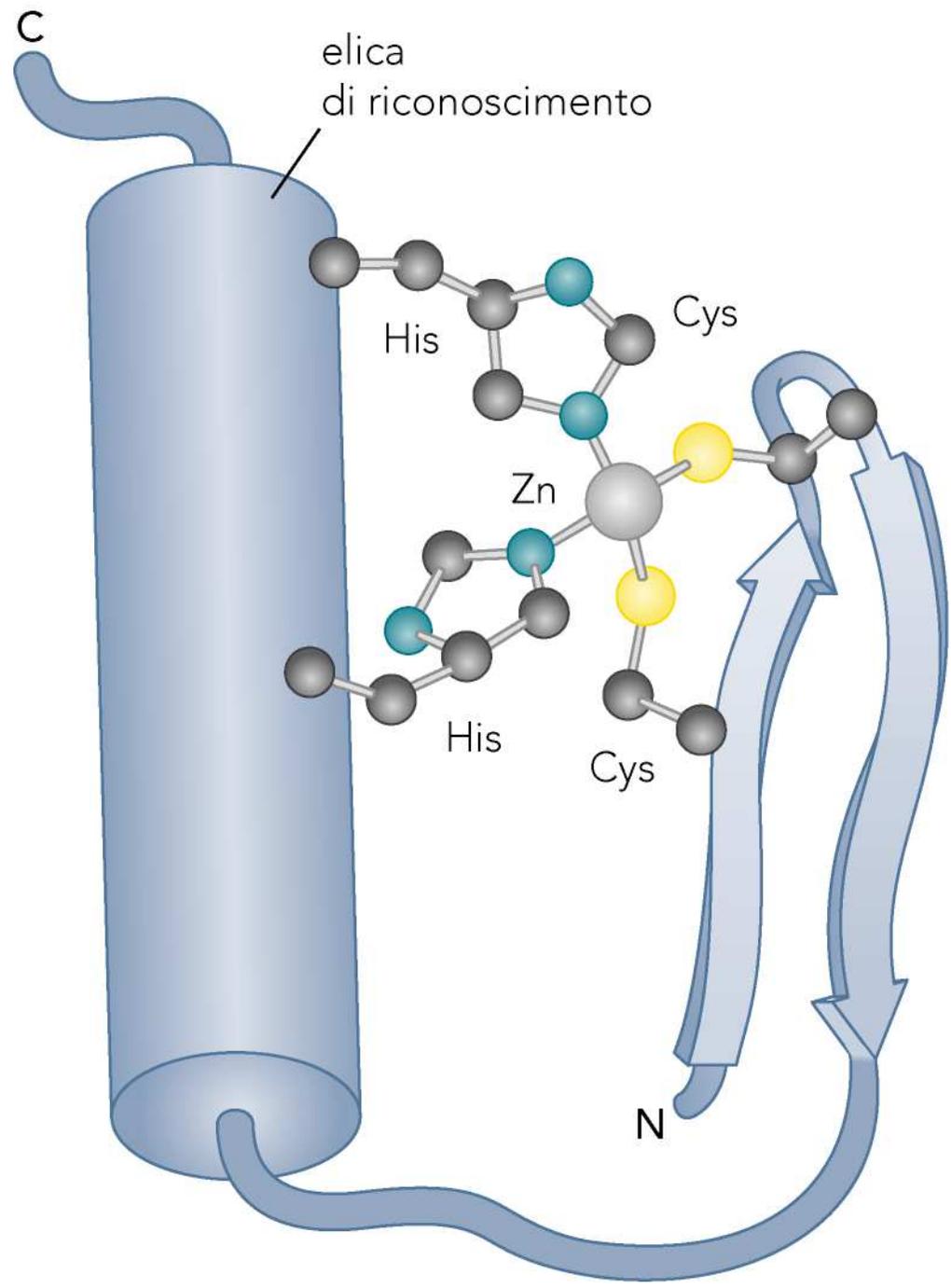
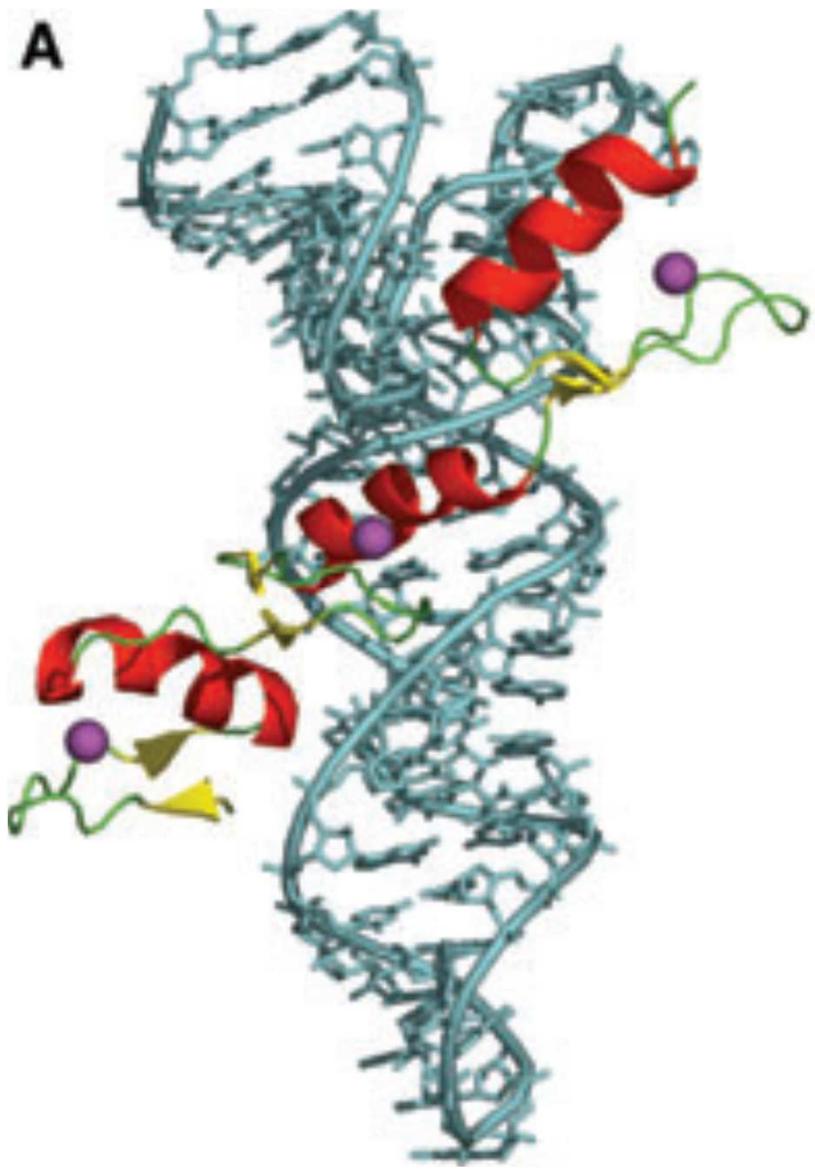


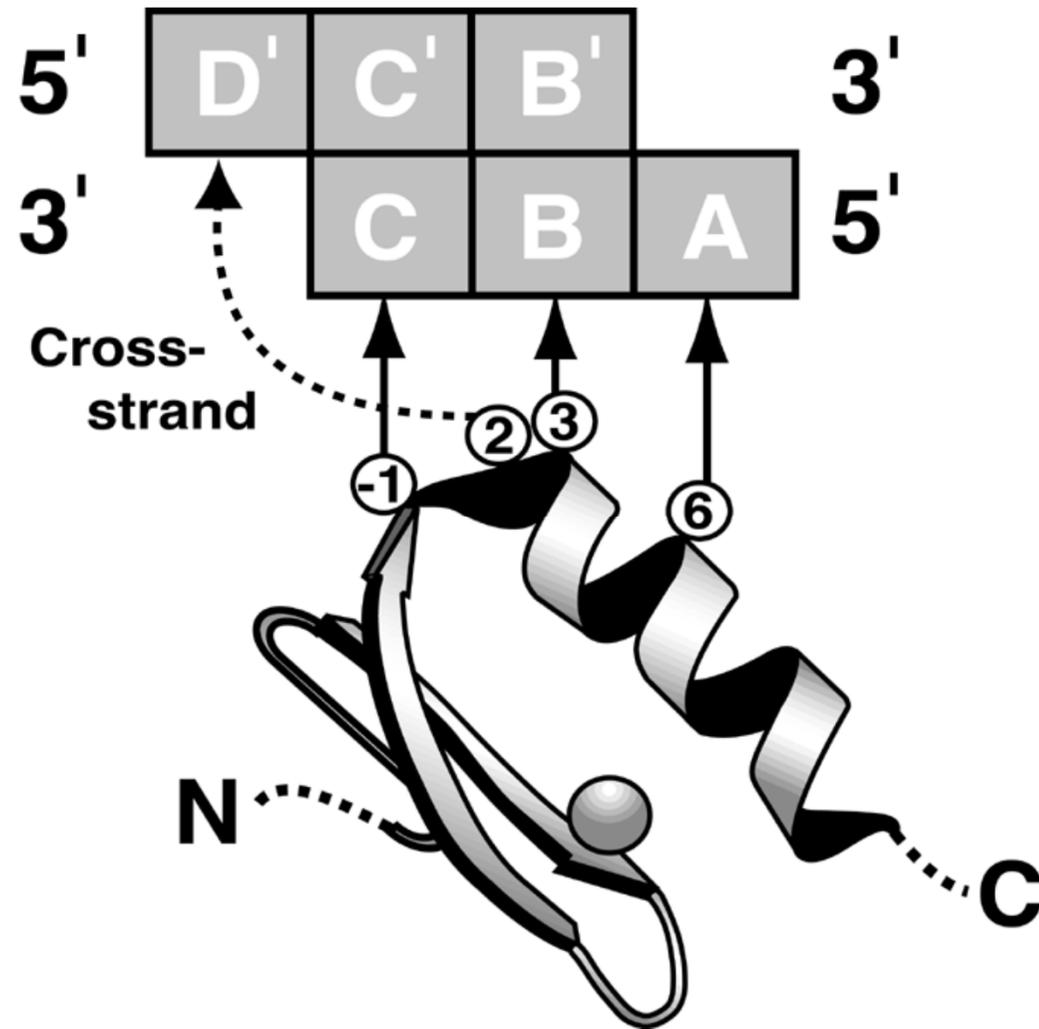
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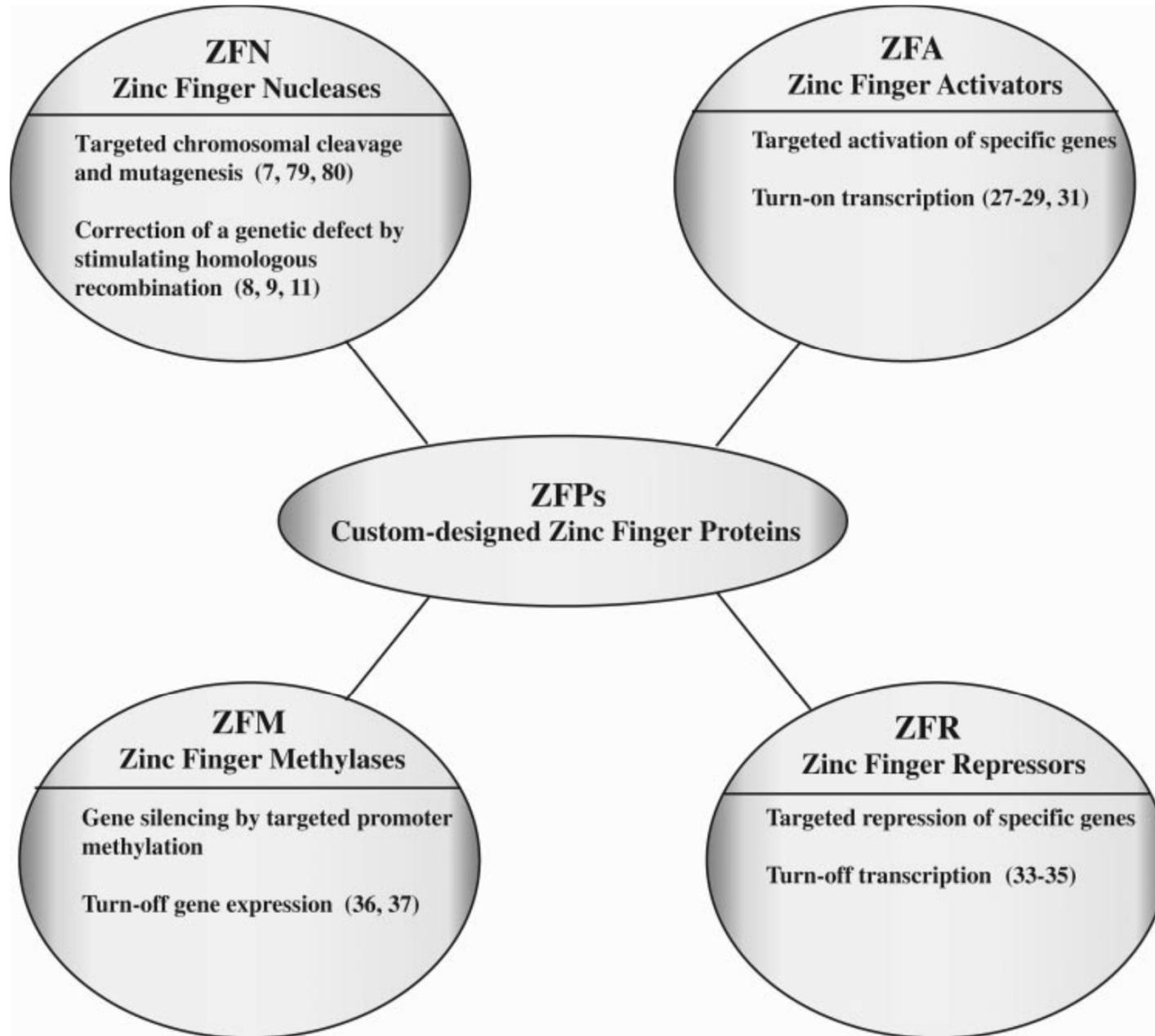
# Highly efficient endogenous human gene correction using designed zinc-finger nucleases

Fyodor D. Urnov<sup>1</sup>, Jeffrey C. Miller<sup>1</sup>, Ya-Li Lee<sup>1</sup>, Christian M. Beausejour<sup>1</sup>, Jeremy M. Rock<sup>1</sup>, Sheldon Augustus<sup>1</sup>, Andrew C. Jamieson<sup>1</sup>, Matthew H. Porteus<sup>2</sup>, Philip D. Gregory<sup>1</sup> & Michael C. Holmes<sup>1</sup>

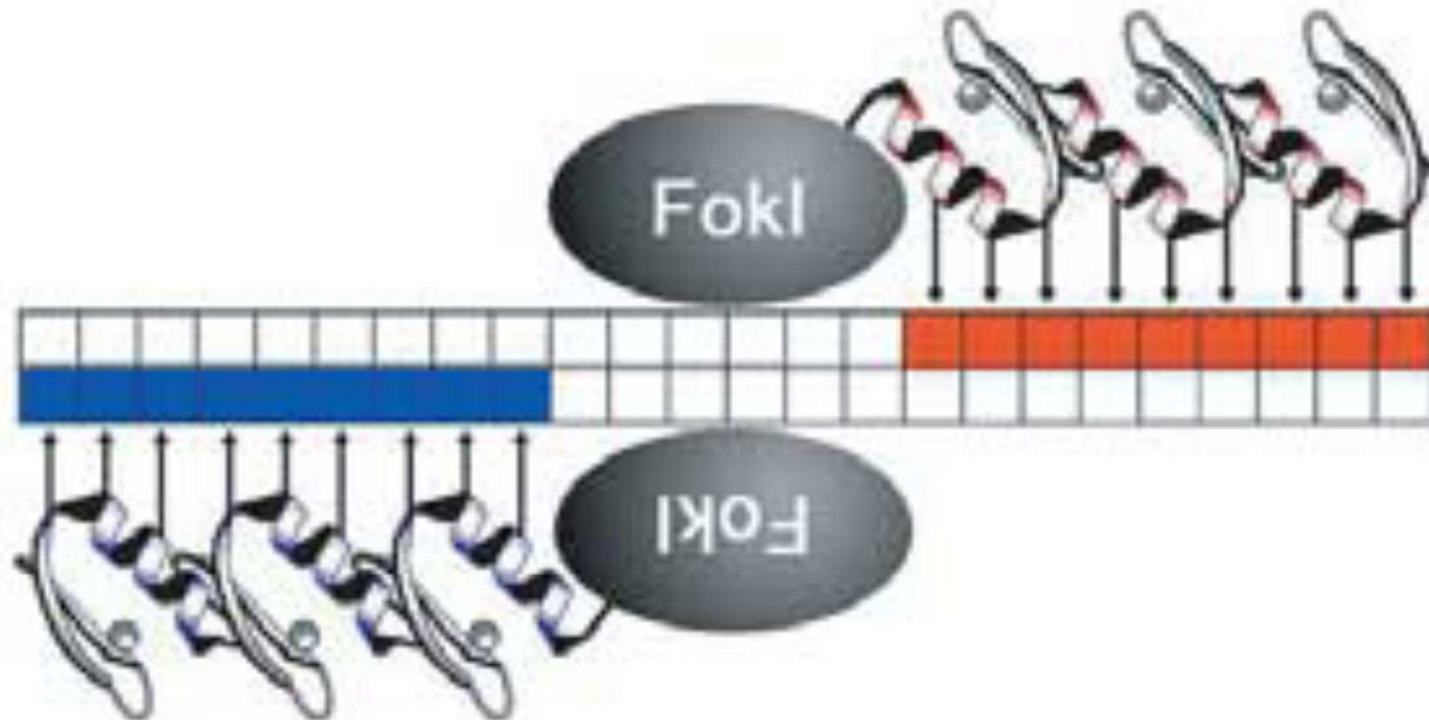








- Two approaches were originally used for zinc finger protein (ZFP) engineering in order to expand the DNA recognition code and to create zinc fingers that bind desired base triplets
- a combinatorial approach using libraries of zinc fingers displayed on the surface of filamentous phage that were selected against target DNA sequences
- a rational design approach that used databases to predict rules for amino acid–base interactions.



Dimerization of FokI domains is required for its DNA binding-dependent endonuclease activity

**Targeted gene knockout in  
mammalian cells by using  
engineered zinc-finger nucleases**

Homology-directed  
repair:

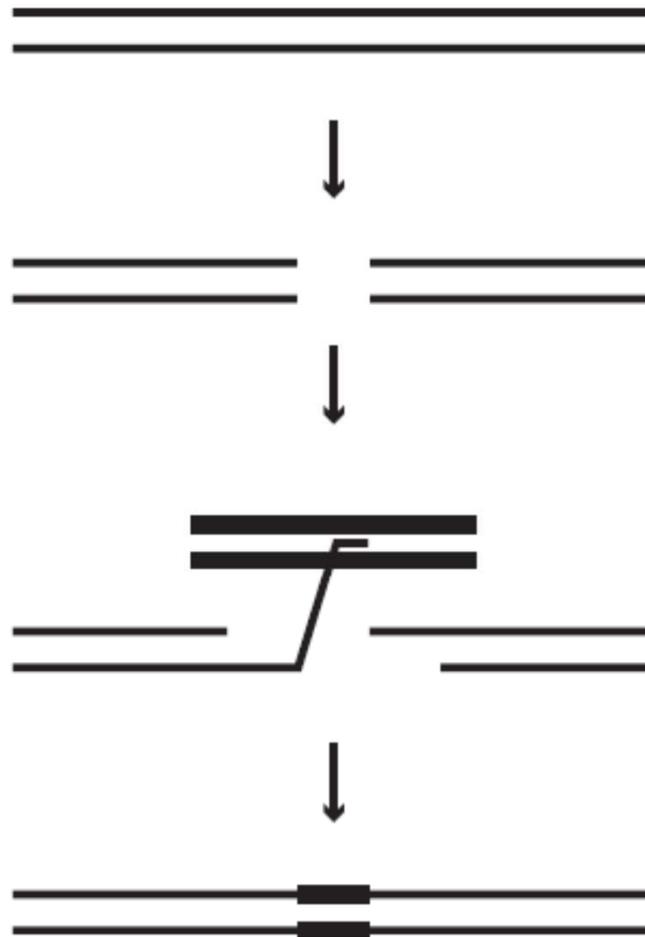
ZFN-driven homology-  
directed repair:

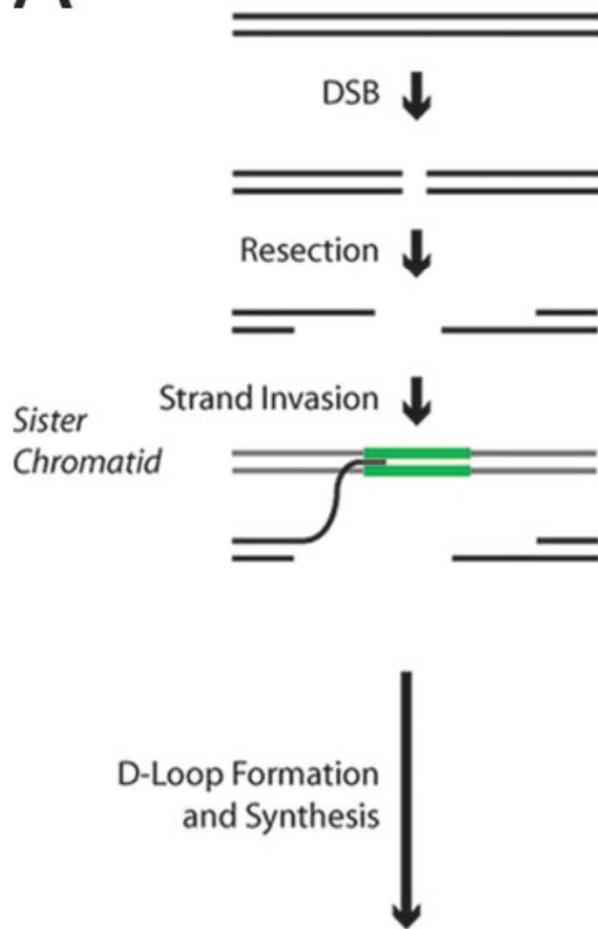
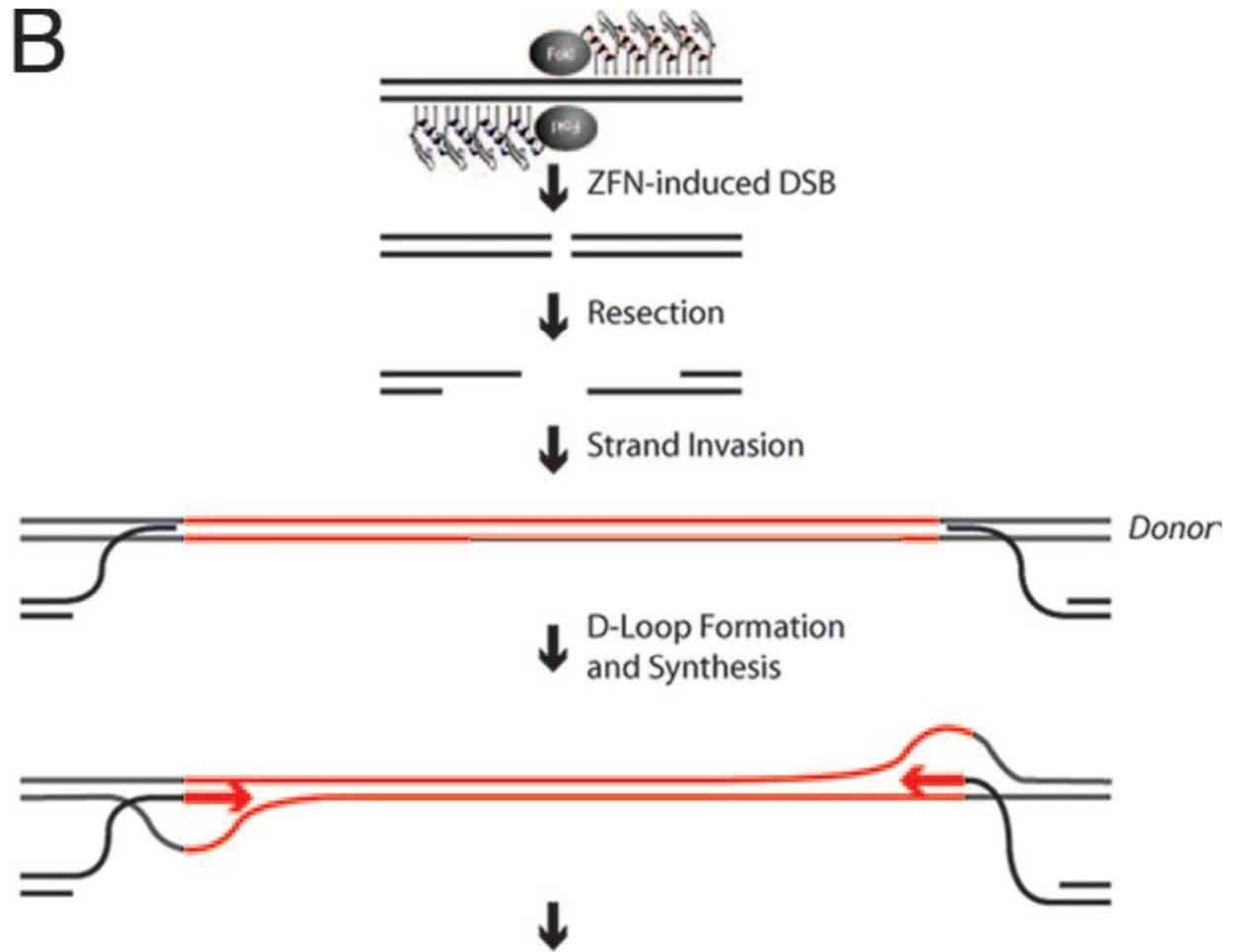
X-ray-induced DSB

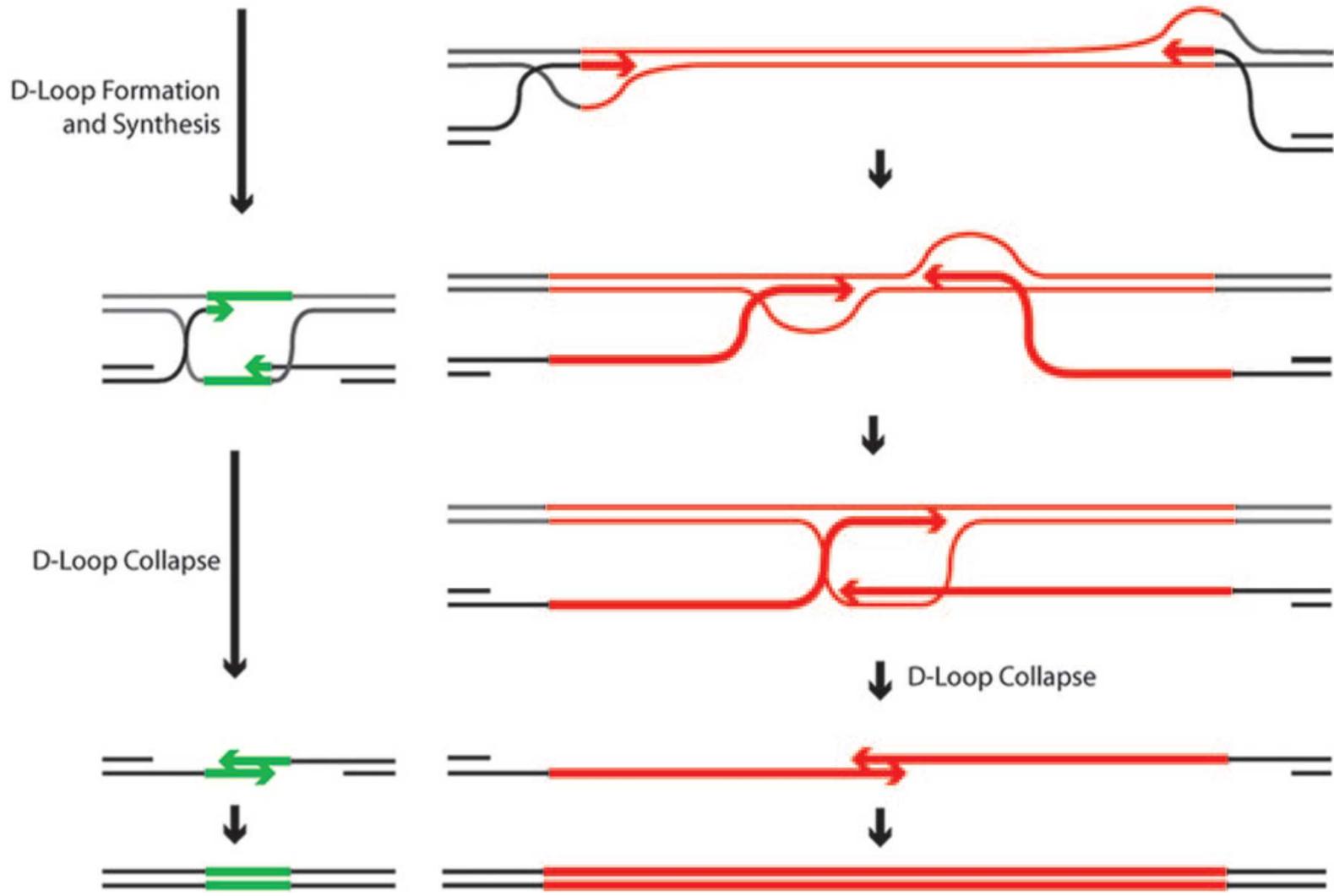
ZFN-induced DSB

Sister chromatid

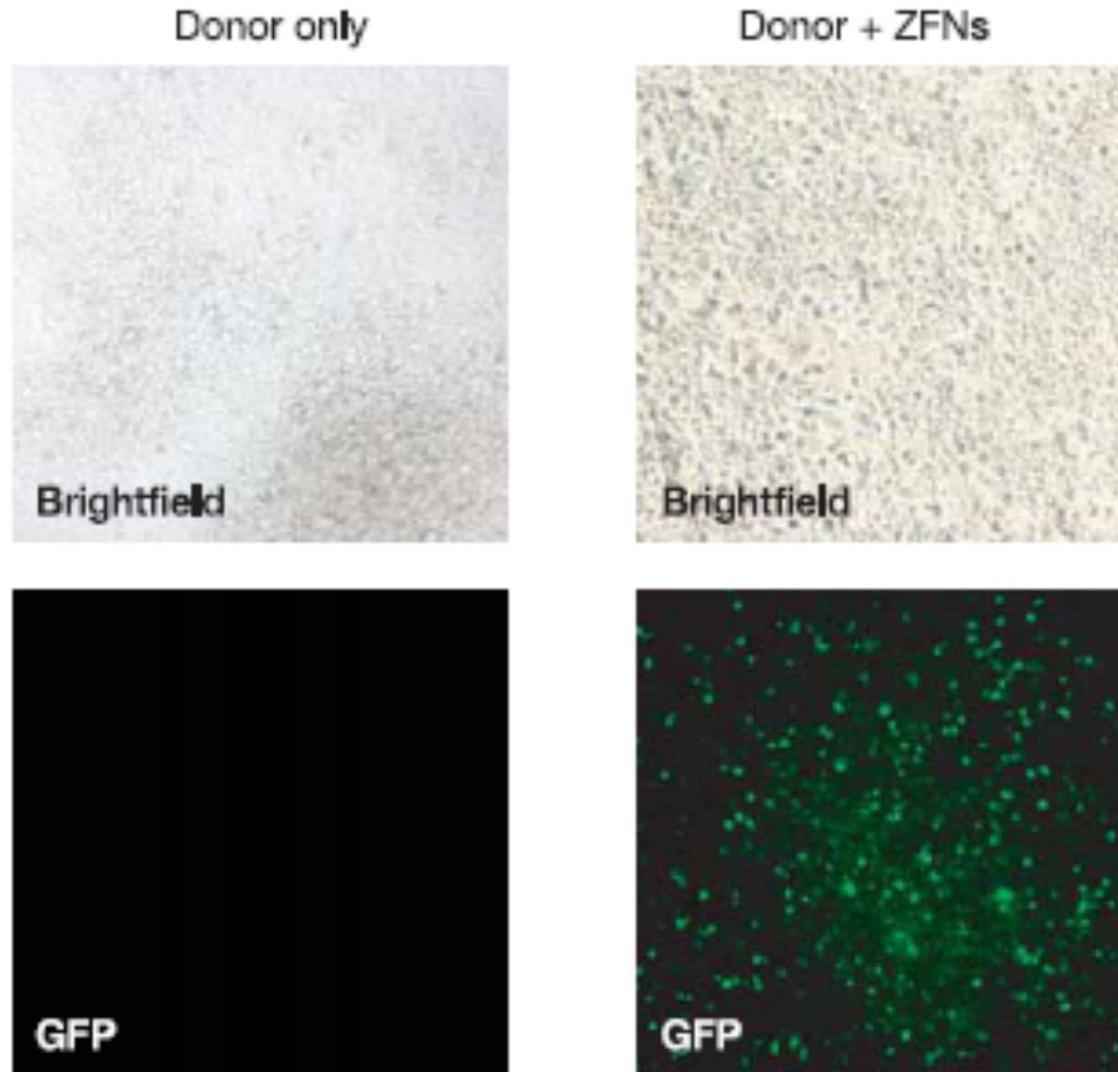
Donor DNA (plasmid)

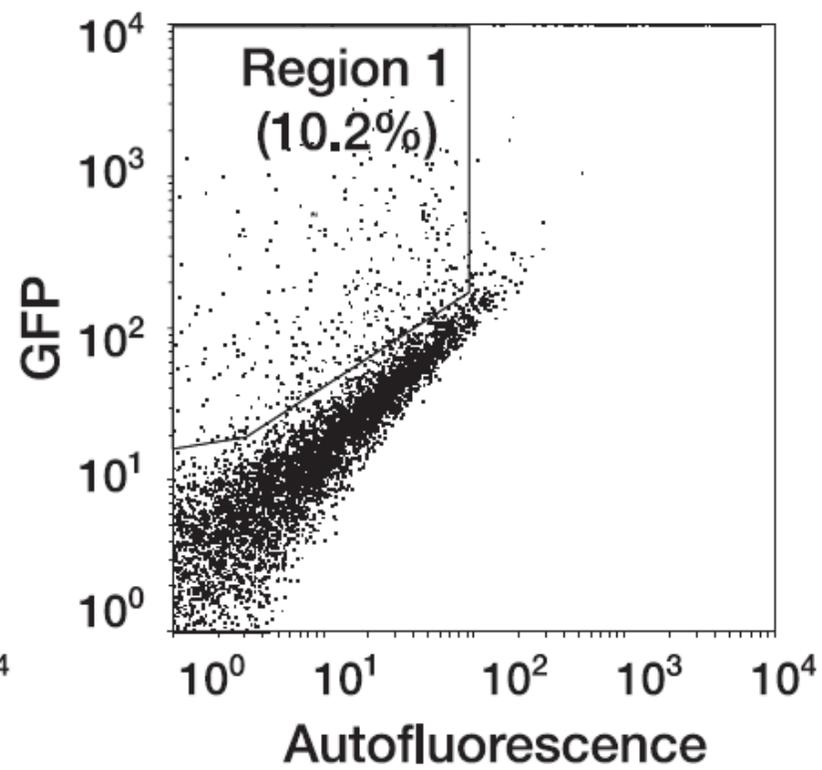
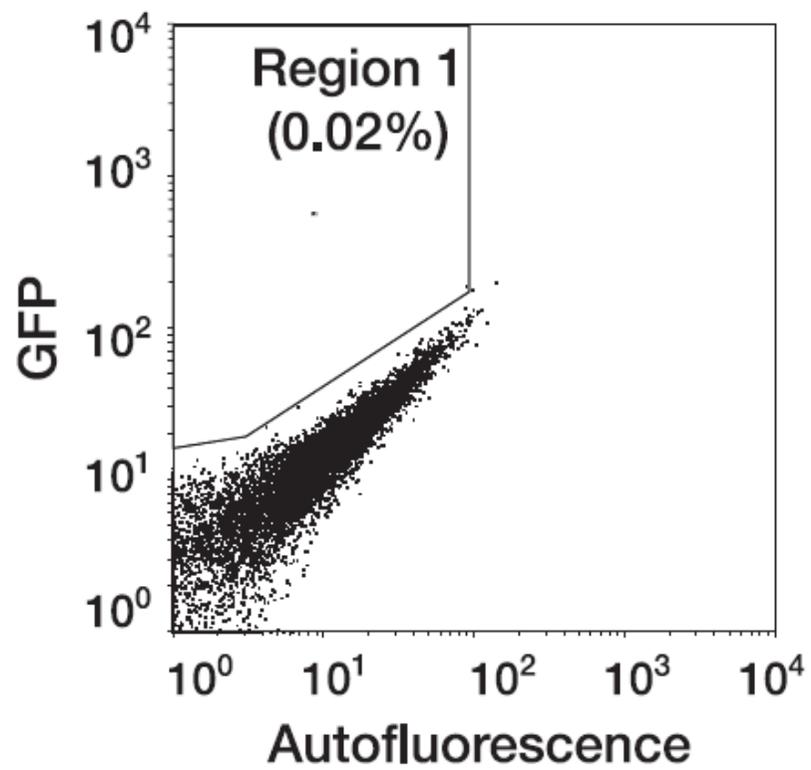


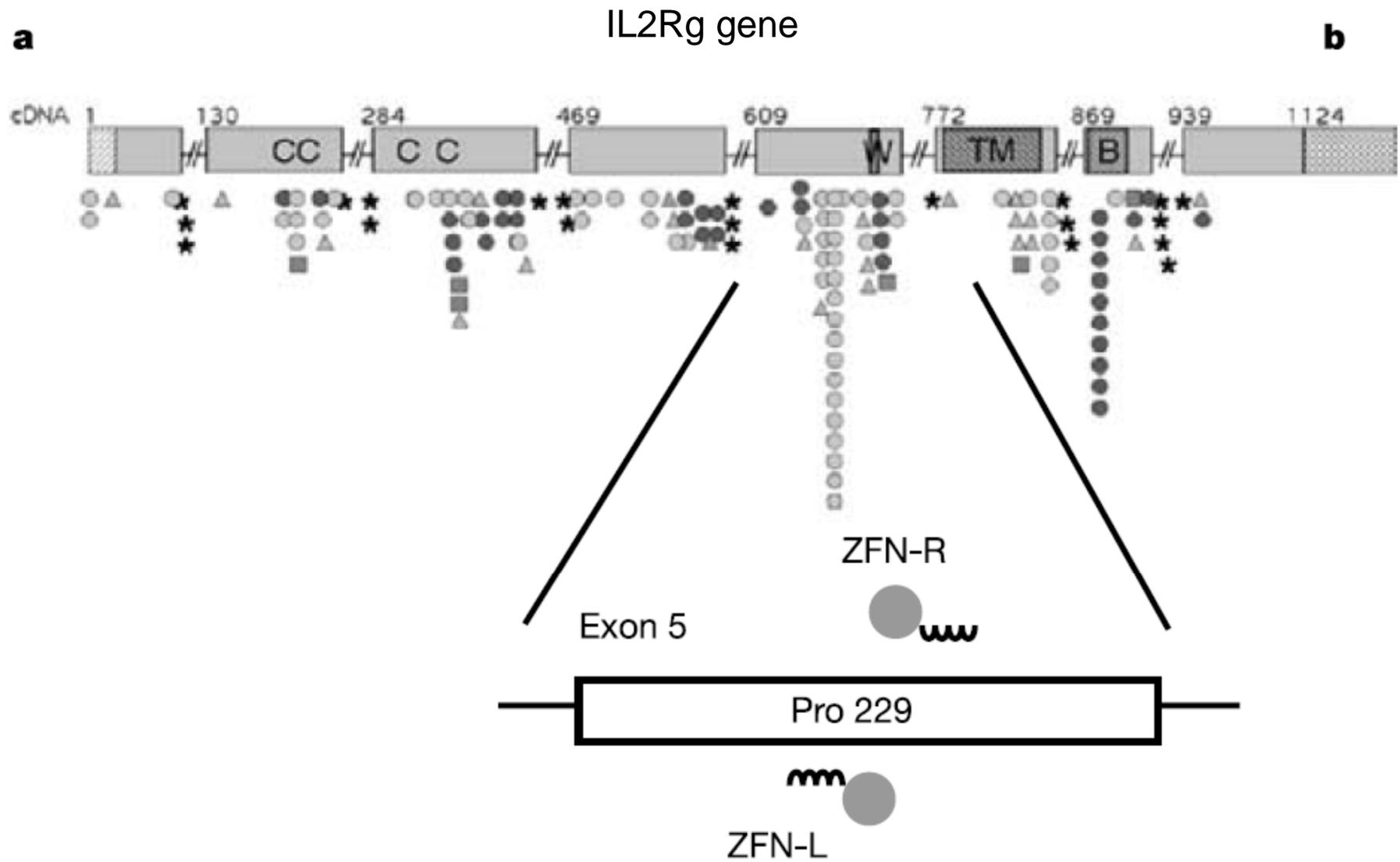
**A****B**



Cells carrying a **mutated** GFP reporter were transiently transfected with a donor plasmid carrying a fragment of wild-type GFP (left column), or the donor plasmid and the ZFNs (right column).







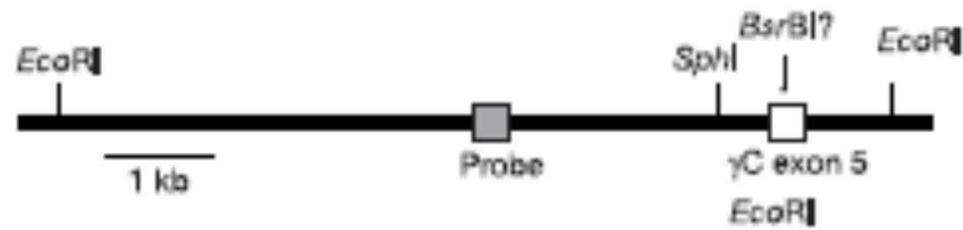
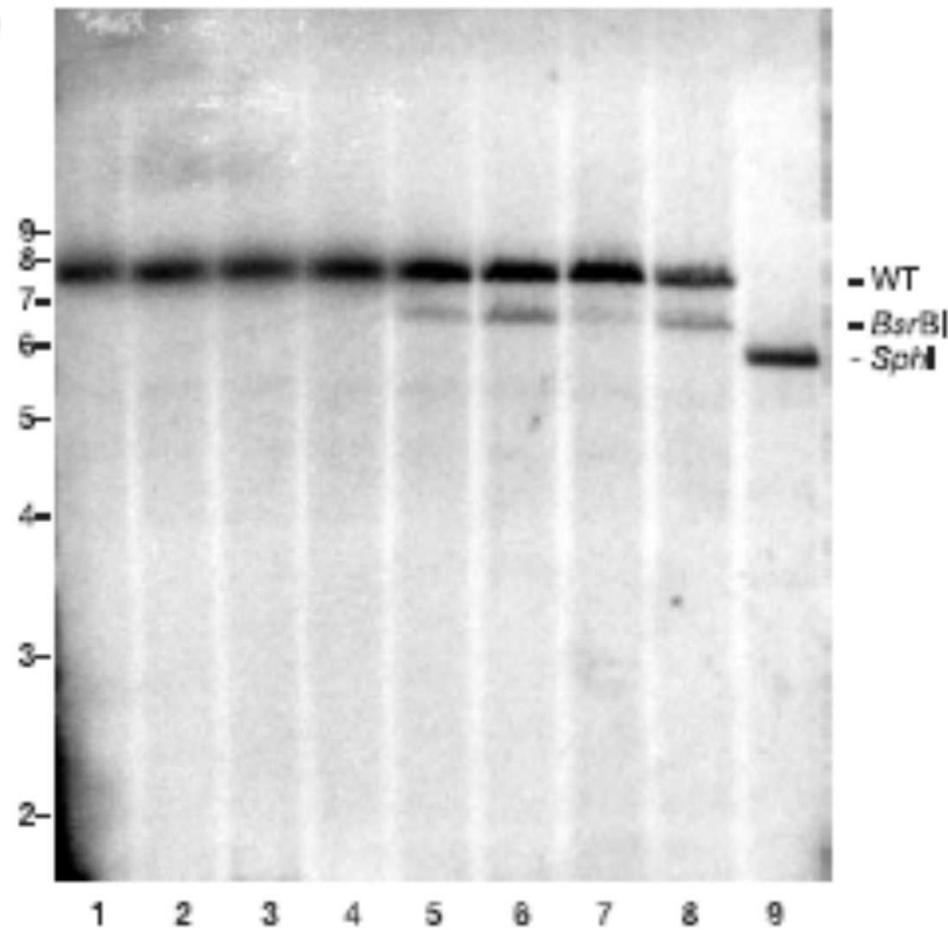
X-linked severe combined immune deficiency (SCID)



# Southern blot

1 month  
(Southern)

7.1 18.0 3.5 21.0 :% HDR



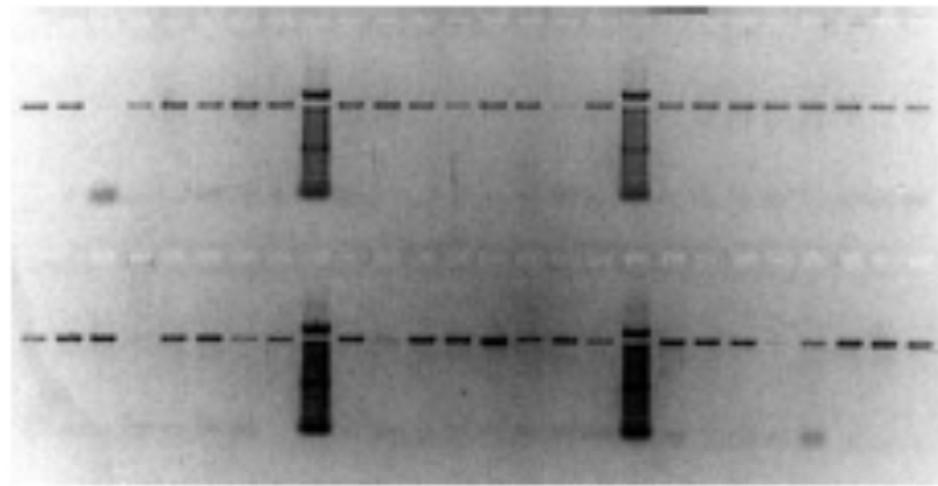
Day 1 : Transfection



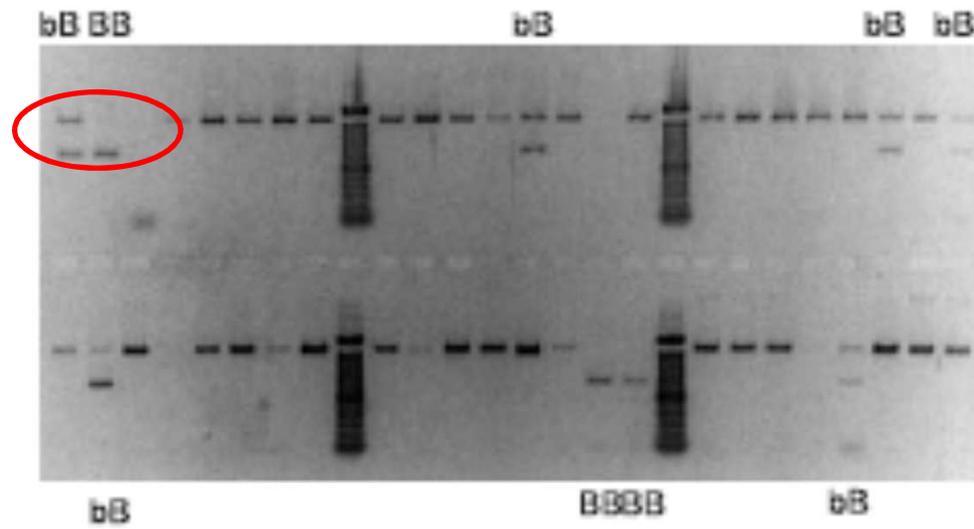
Day 4 : Seed <math>< 1</math> cell per well



Day 30 : Isolate genomic DNA,  
PCR  $\gamma$ C exon 5 (both alleles),  
digest with *BsrBI*, gel



↓ + BsrBI



Alleles altered:	None	One	Both
G2		13.2%	6.6%

# Targeted **gene addition** into a specified location in the human genome using designed zinc finger nucleases Moehle PNAS 2007

A precisely placed double-strand break induced by engineered zinc finger nucleases (ZFNs) can stimulate integration of long DNA stretches into a predetermined genomic location, resulting in high-efficiency site-specific gene addition.

Using an extrachromosomal DNA donor carrying a 12-bp tag, a 900-bp ORF, or a 1.5-kb promoter-transcription unit flanked by locus-specific homology arms, we find targeted integration frequencies of 15%, 6%, and 5%, respectively, within 72 h of treatment, and **with no selection for the desired event.**

The integration event occurs in a homology-directed manner and leads to the accurate reconstruction of the donor specified genotype at the endogenous chromosomal locus, and hence presumably results from synthesis-dependent strand annealing repair of the break using the donor DNA as a template.

This site-specific gene addition occurs with no measurable increase in the rate of random integration. Remarkably, we also find that ZFNs can drive the addition of an 8-kb sequence into an endogenous locus at a frequency of 6%, also in the absence of any selection.

Surprising versatility of the specialized polymerase machinery involved in double-strand break repair

Powerful approach to mammalian cell engineering

Possibility of ZFN-driven gene addition therapy for human genetic disease.

Experimental outline and a schematic of the process whereby a ZFN-induced DSB is repaired by using an extrachromosomal donor as a template

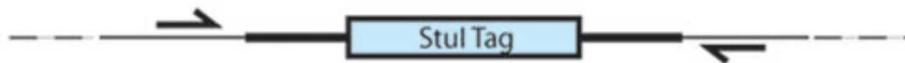
PCR-based measurements of ZFN-driven tag integration frequency into the IL2R locus

**A** Day 1: Introduce ZFNs and Donor

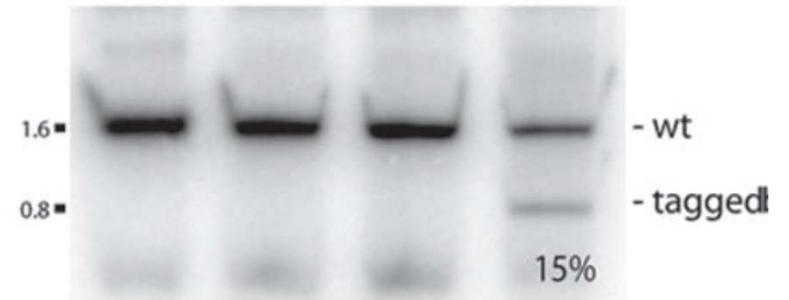


Culture cells 72 hrs in normal medium without selective agent

Day 4: Harvest DNA; analyze tag frequency



**B** DNA: neg. ZFNs donor ZFNs + donor



PCR products were digested with Stul