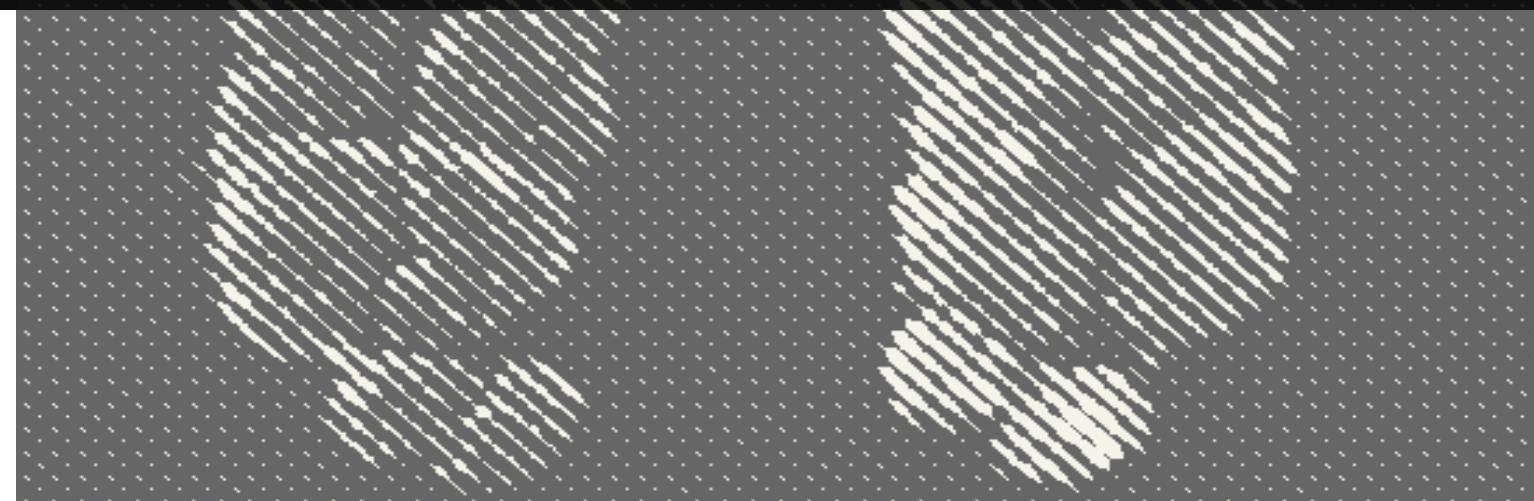




# **Engineering human tumour-associated chromosomal translocations with the RNA-guided CRISPR-Cas9 system**

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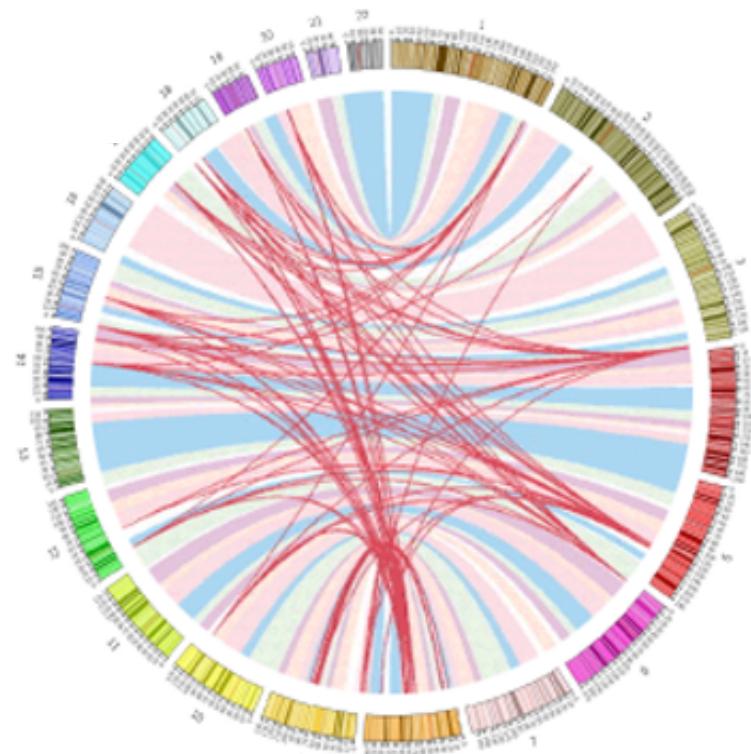
4-7 July 2015



# Chromosome Translocation

## & CANCER

**Chromosome translocations:**  
primary cause of many cancers  
involved in the progression of tumors



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# Chromosome Translocation

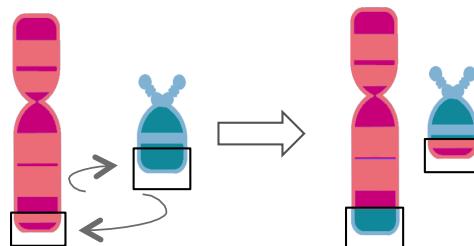
## MODELS

The most widely used models:

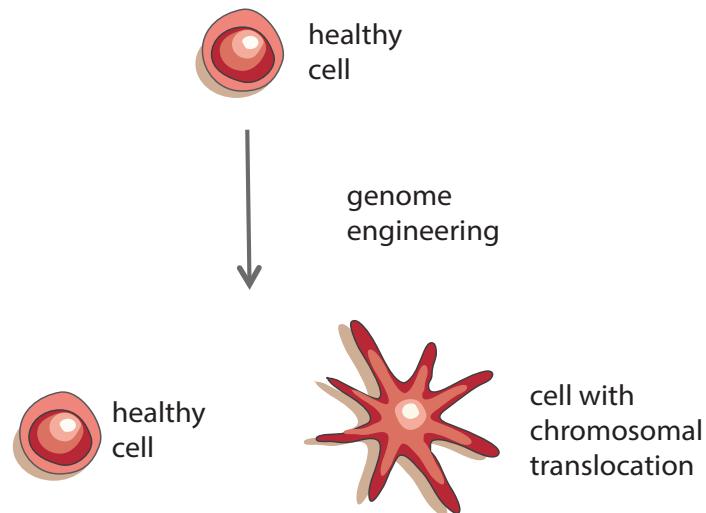
- Patient-derived cell line  
(accumulate secondary mutations)
- Overexpression model



*de novo* generation of the translocation



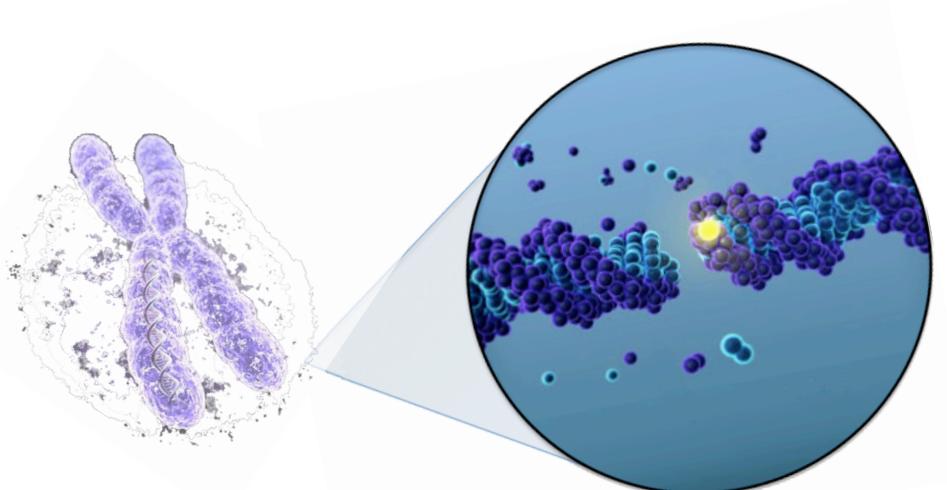
## GE MODELS



# Chromosome Translocation

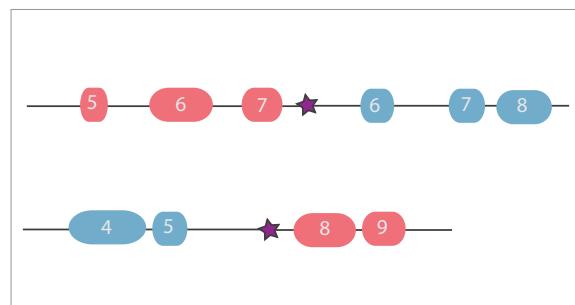
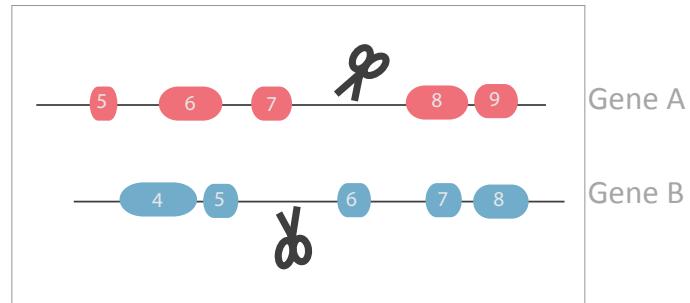
## CAUSES

Two double strand breaks (DSBs)

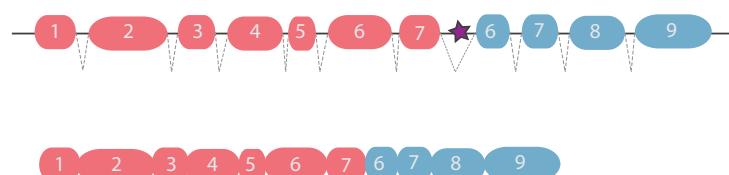


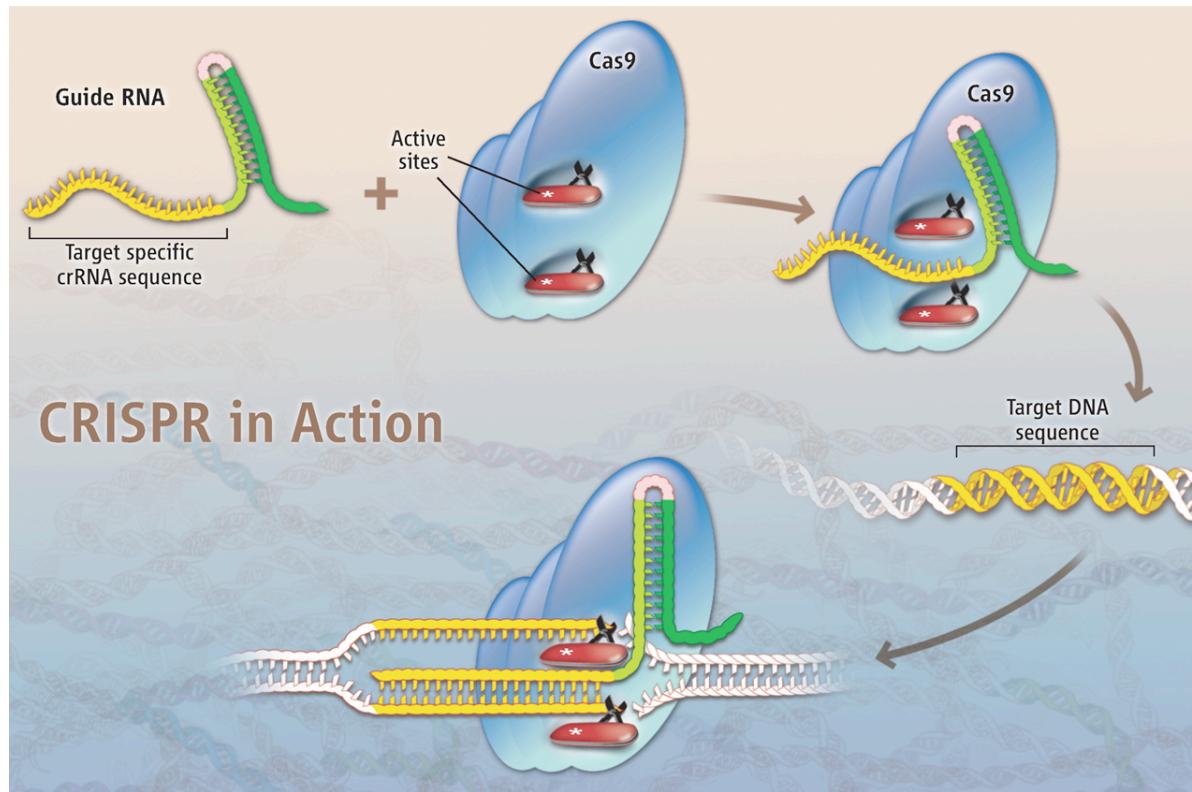
## DSBs

DSB introduction within the targeted regions in the genome

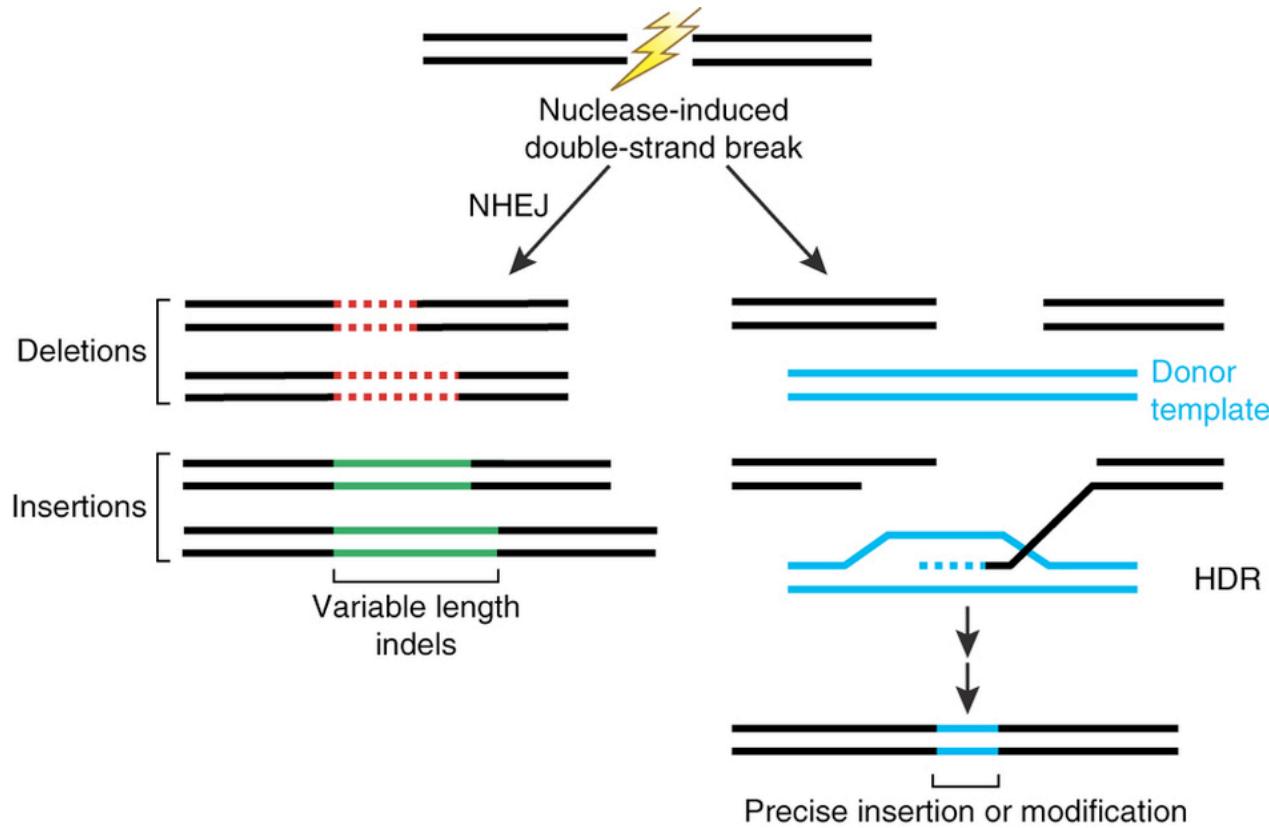


### Splicing machinery

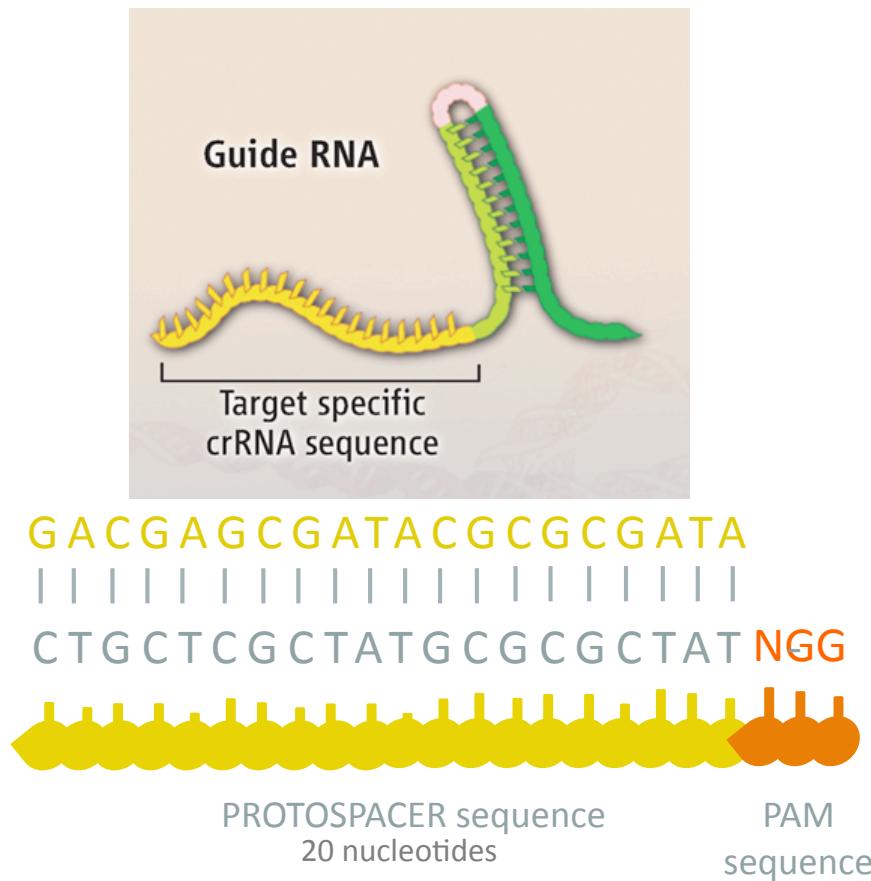




Small guide RNAs (sgRNAs) that lead Cas nucleases to target DNA specific sequences and induce nucleic acid cleavage

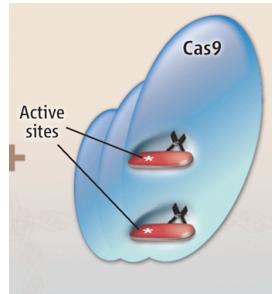


The specificity of DNA recognition is achieved through a short RNA sequence and so by simply altering the composition of this RNA code we can very easily change the specific location to the target genome

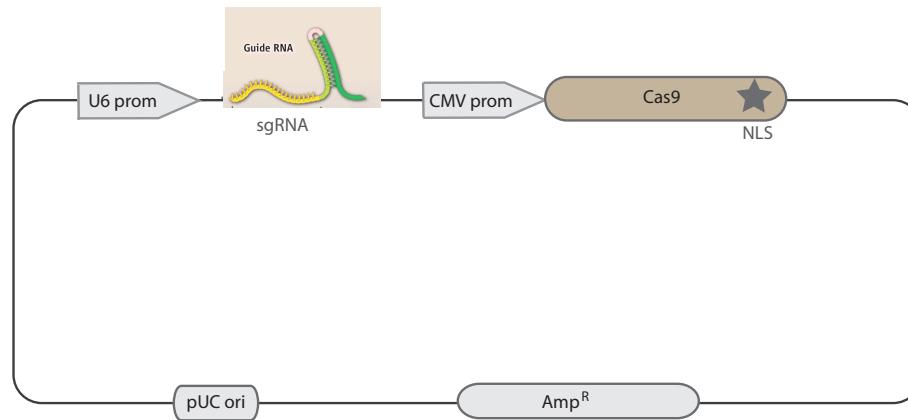
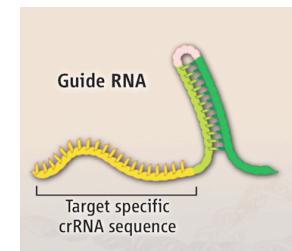


Two components must be introduced into the cell to perform genome editing

The Cas9 nuclease



The programmable guide RNA that target at a specific 20nt region

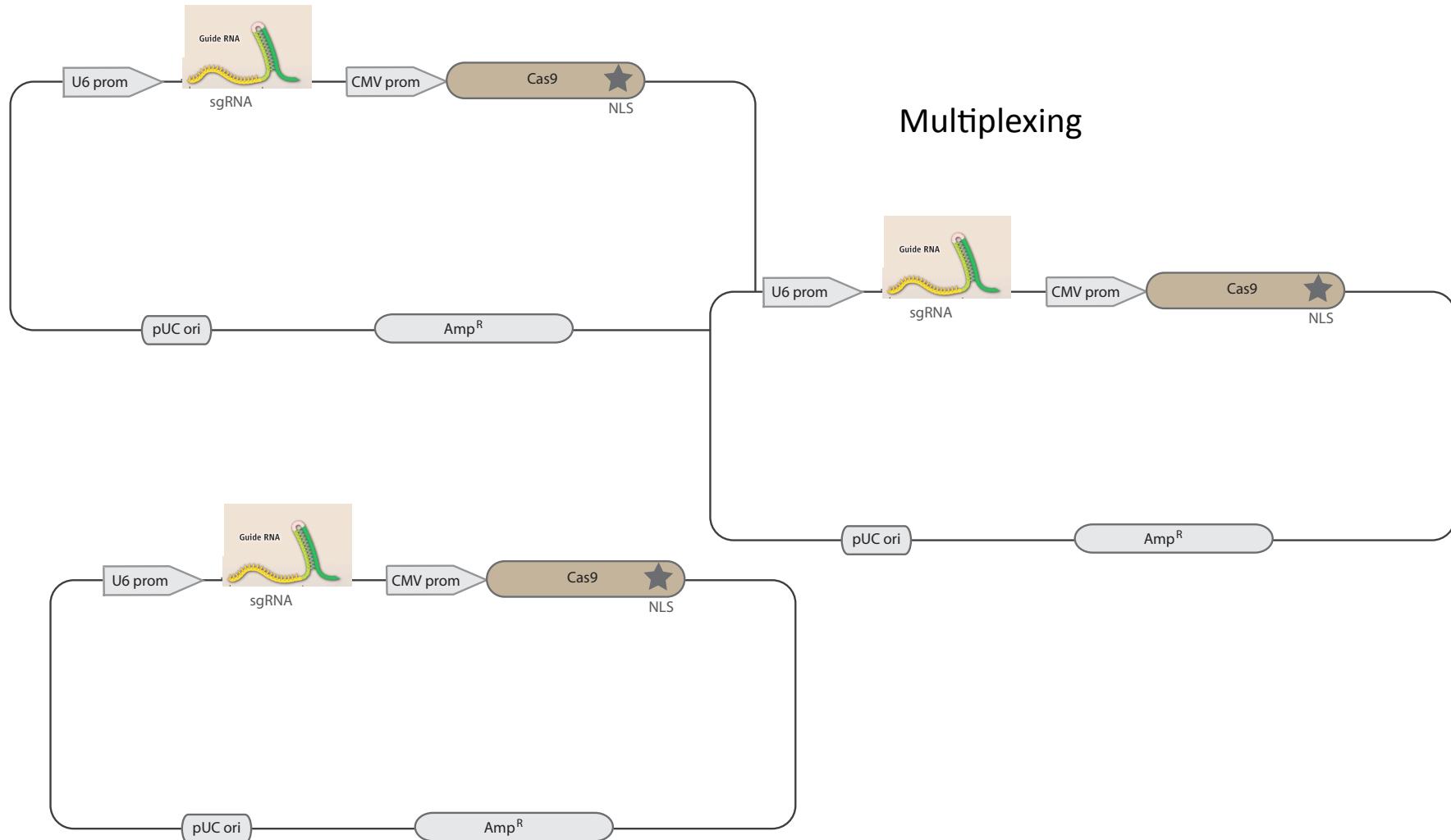


Modified from Church Lab's plasmid (obtained from ADDGENE)

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## Chromosomal Manipulation

## CRISPR System



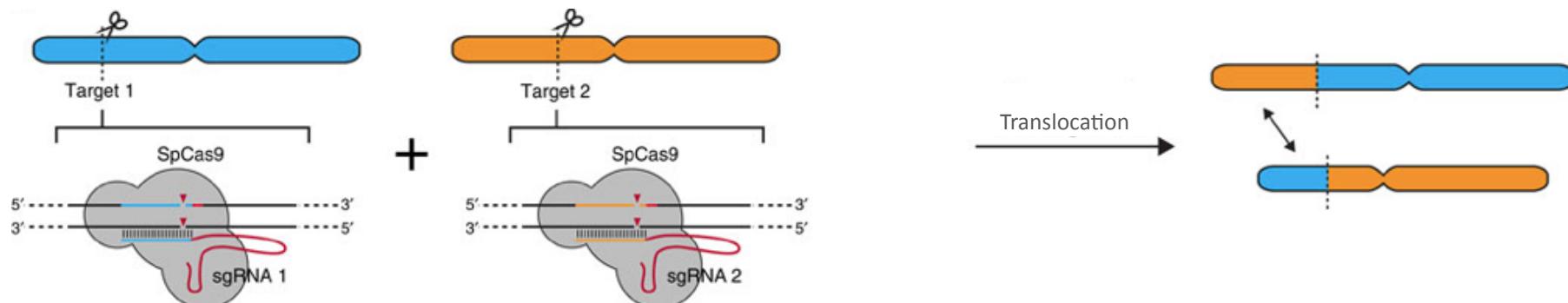
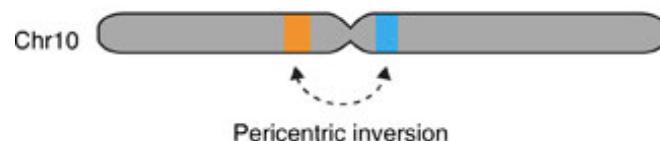
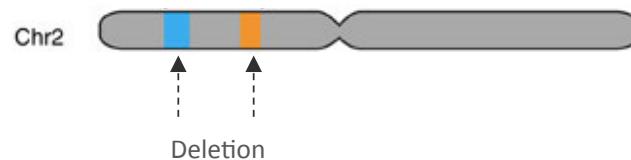
Modified from Church Lab's plasmid (obtained from ADDGENE)

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## Chromosome Translocation

## CRISPR System

## Engineering a Translocation

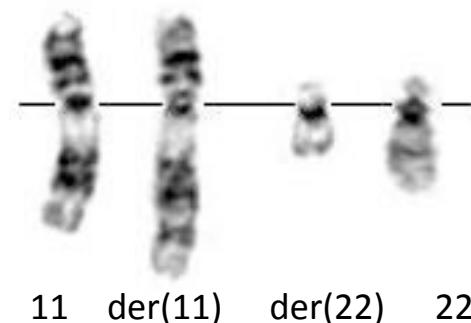


Ewing Sarcoma is a prototype of a solid tumor

Occurs in children and adolescents

Arise in tissues of mesenchymal origin

t(11;22)(q24;q12)

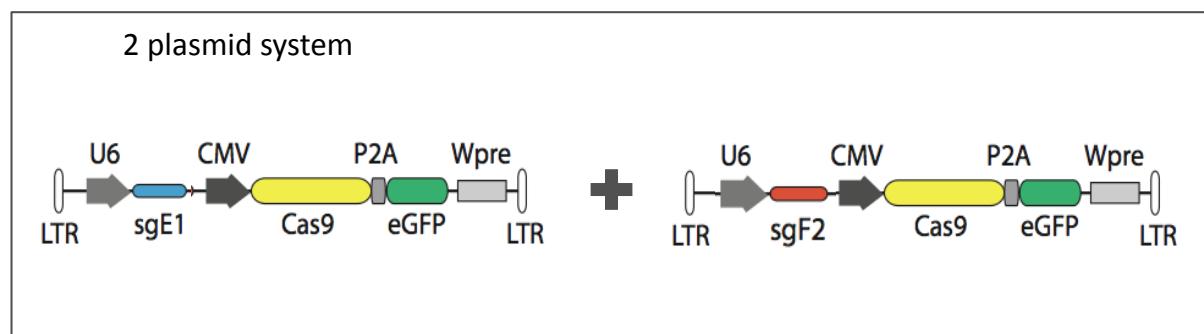
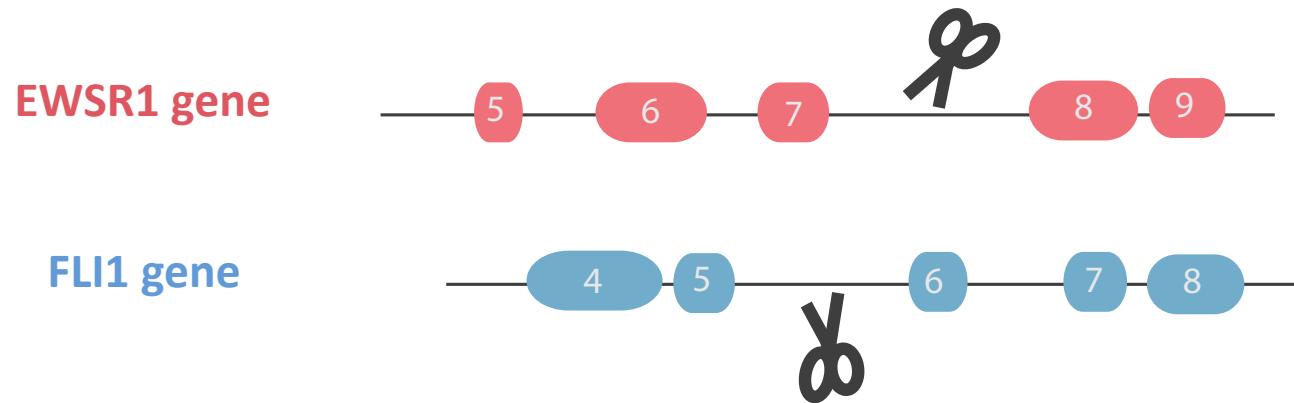


11    der(11)    der(22)    22

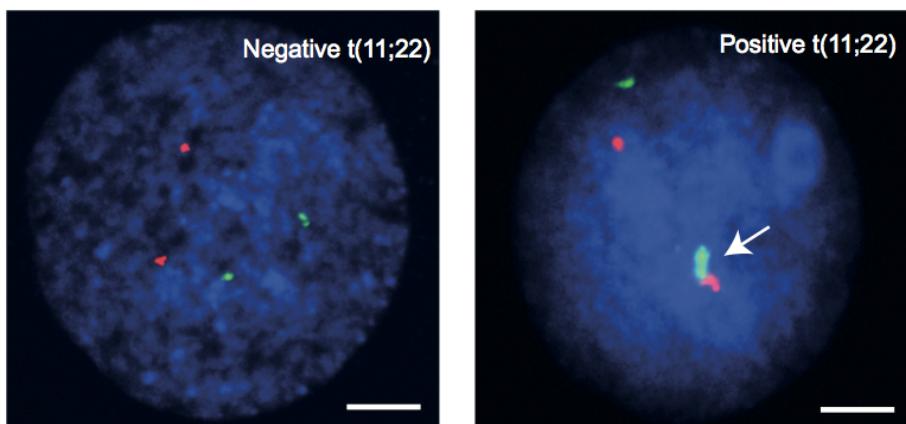


EWSR1-FLI1 chimeric protein (transcription factor)

To induce t(11;22)(q24;q12), 2 sgRNAs were designed



To quantify translocations  
FISH



FISH probe:  
*EWS*(green)/*FLI1*(red)  
Single fusion probe

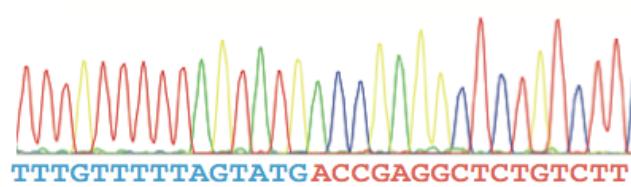
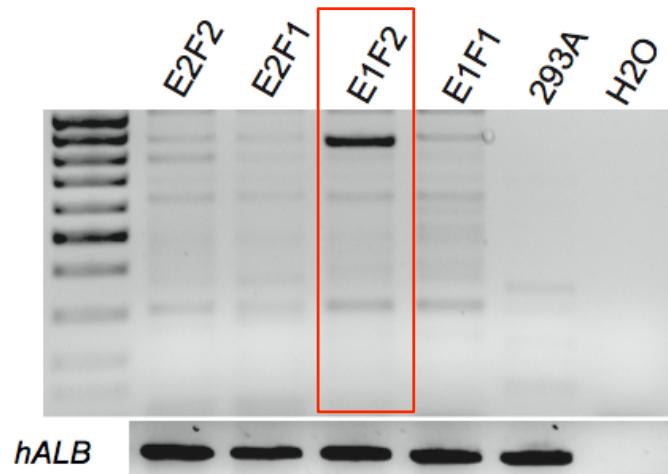
Total transfected cells, no selection

Cell Type	Total cell nuclei	t(11;22)	Frequency (%)
HEK293	285	5	1,75
hMSCs	300	1	0,3

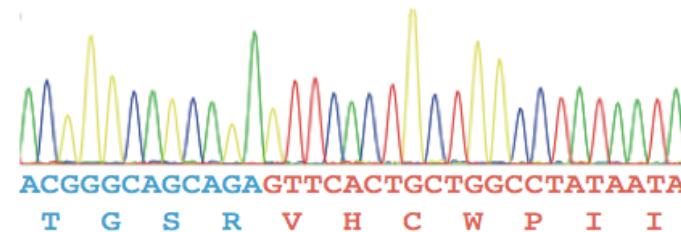
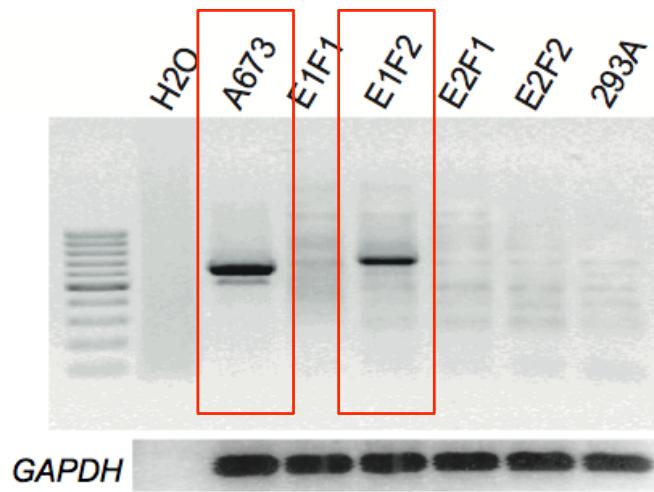
CRISPR efficiency can vary depending on  
the cell type

## MOLECULAR ANALYSIS

### DNA sequencing



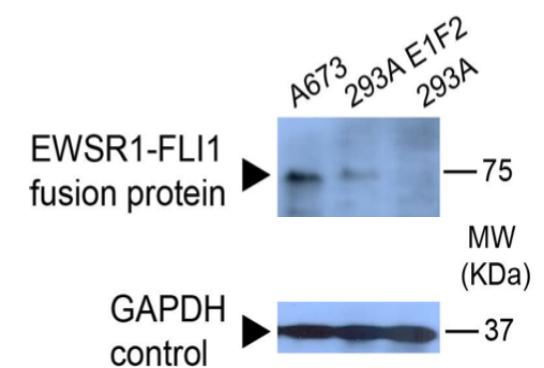
### cDNA sequencing (RT-PCR of RNA)



A673: ewing sarcoma cell line

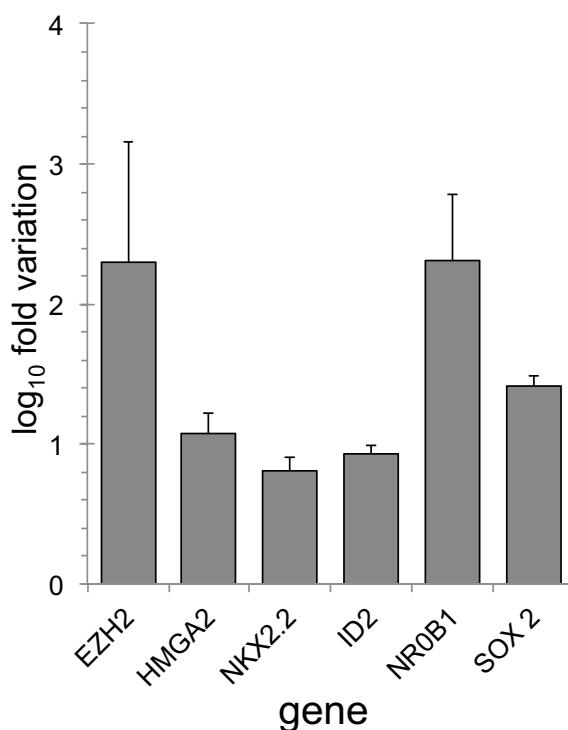


### Western blot

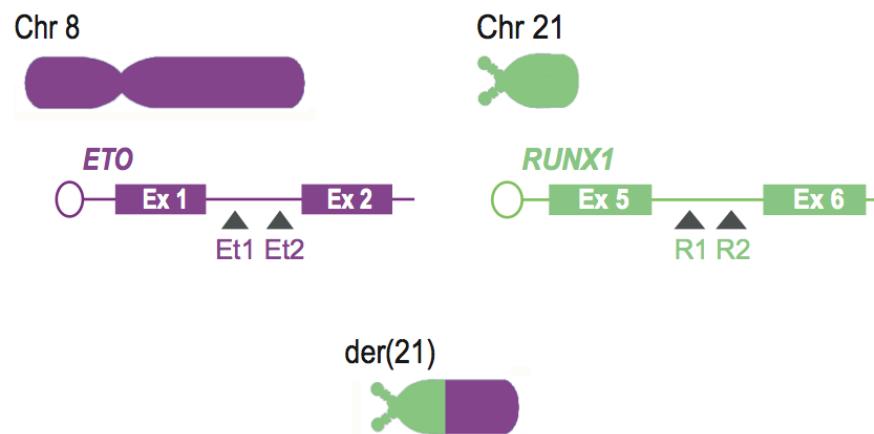


## FUNCTIONALITY OF THE FUSION PROTEIN

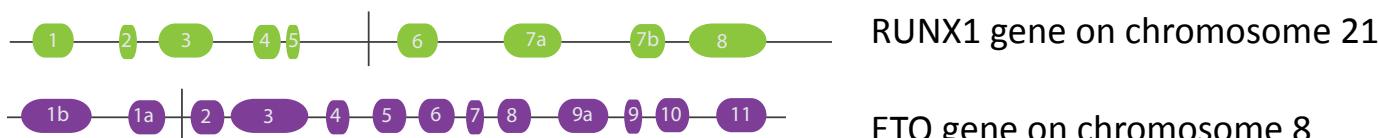
The levels of expression EWSR1-FLI1 target known genes were quantified by real-time reverse transcription-PCR (quantitative PCR)



Increased over the normal expression  
of HEK293 non-t(11;22) cells



The translocation fuses:



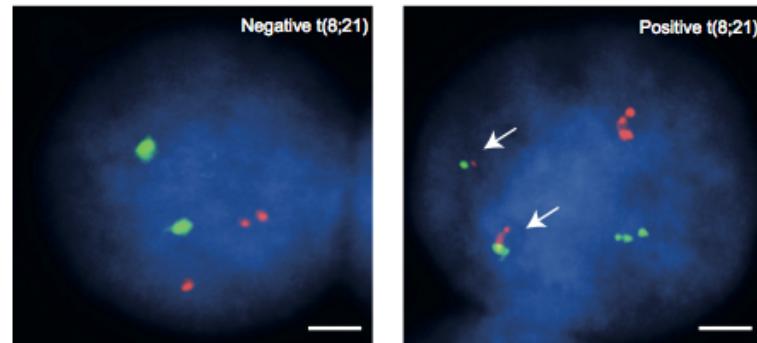
*RUNX1* gene on chromosome 21

*ETO* gene on chromosome 8



RUNX1/ETO fusion gene

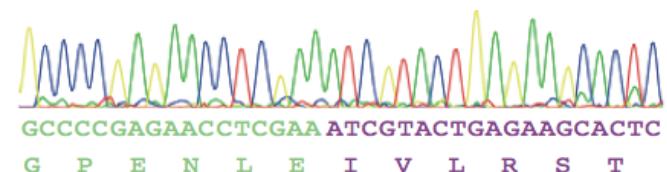
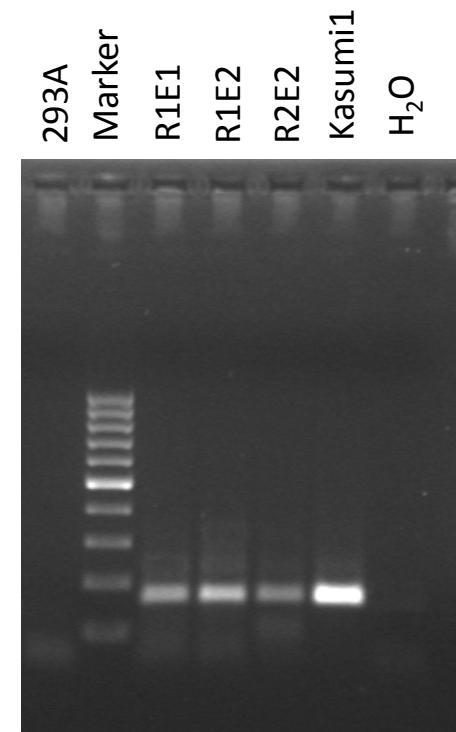
## FISH ANALYSIS



Dual fusion probe

Cell type	Total cell nuclei	t(11;22)	Frequency (%)
HEK293	310	12	3,8
CD34+	1200	2	0,16

## cDNA sequencing (RT-PCR of RNA)

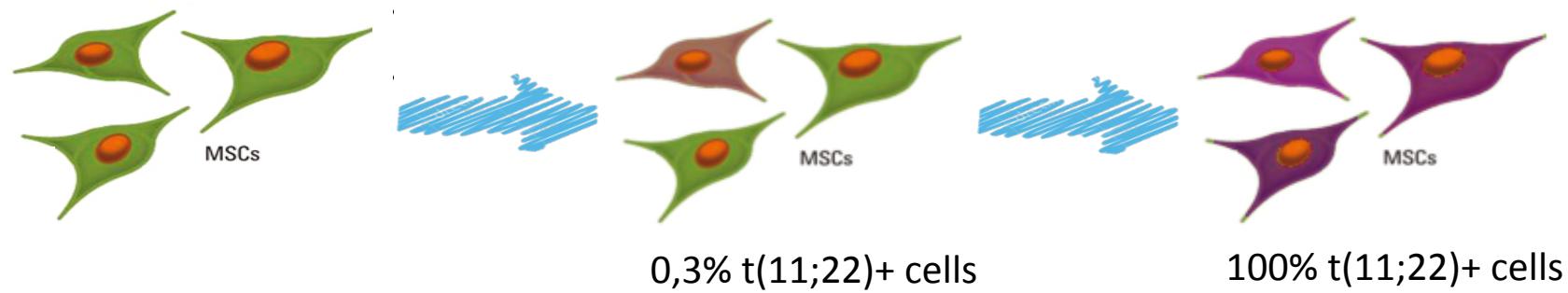


Cell Type	Cell nuclei	t(11;22)	Freq (%)		Cell nuclei	t(8;21)	Freq (%)
HEK293	285	5	1,75	HEK293	310	12	3,8
hMSCs	300	1	0,3	CD34+	1200	2	0,16

Generation of an Ewing sarcoma human cellular model using the CRISPR system

Hallmark: t(11;22)

Cell type: hMSC

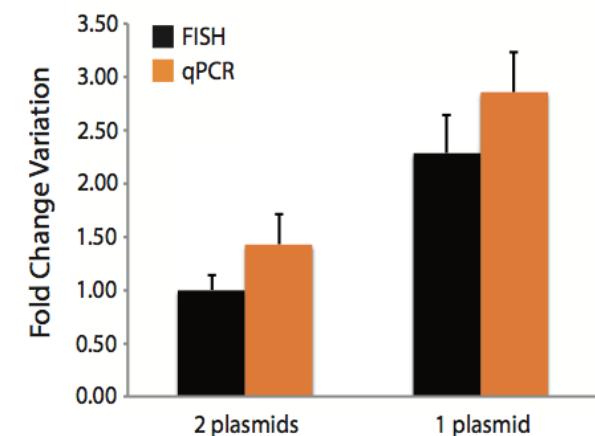
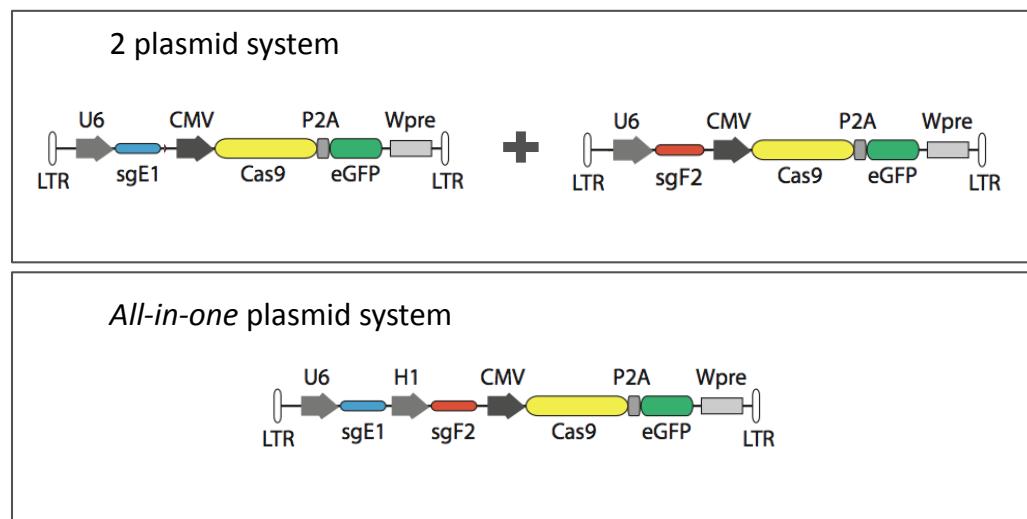


An optimized strategy is needed, especially when mimicking translocations in HUMAN PRIMARY CELLS

Conditions optimized:

1. CRISPR expression plasmid
2. Amount of transfected plasmid
3. CRISPR delivery system
4. Selection of transfected cells

## 1.- CRISPR expression plasmid



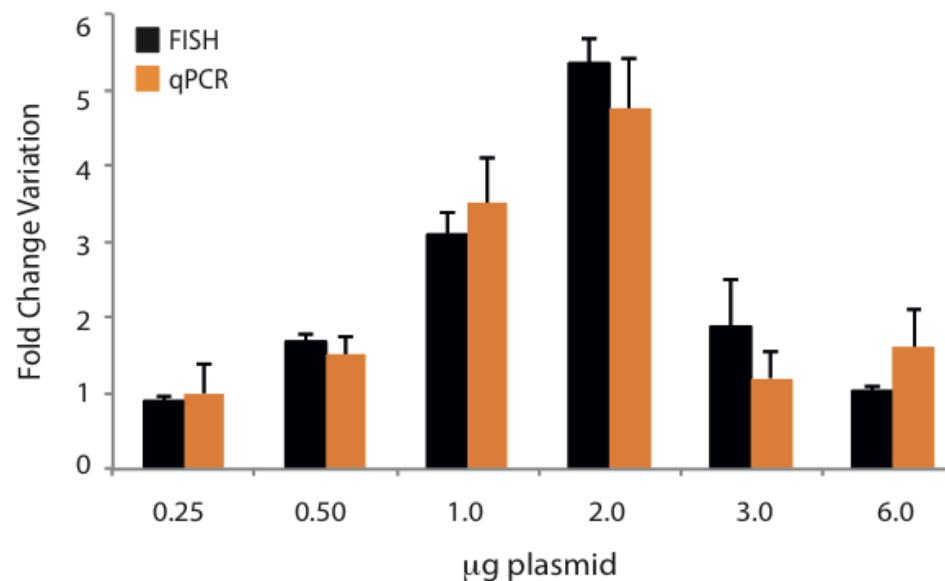
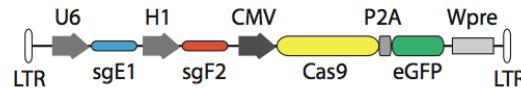
Torres et al, In press

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## 2.- Amount of transfected plasmid

*All-in-one* plasmid system

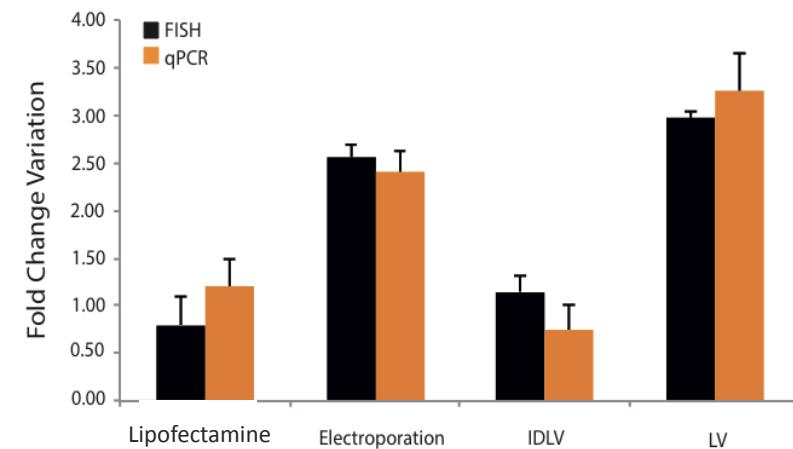
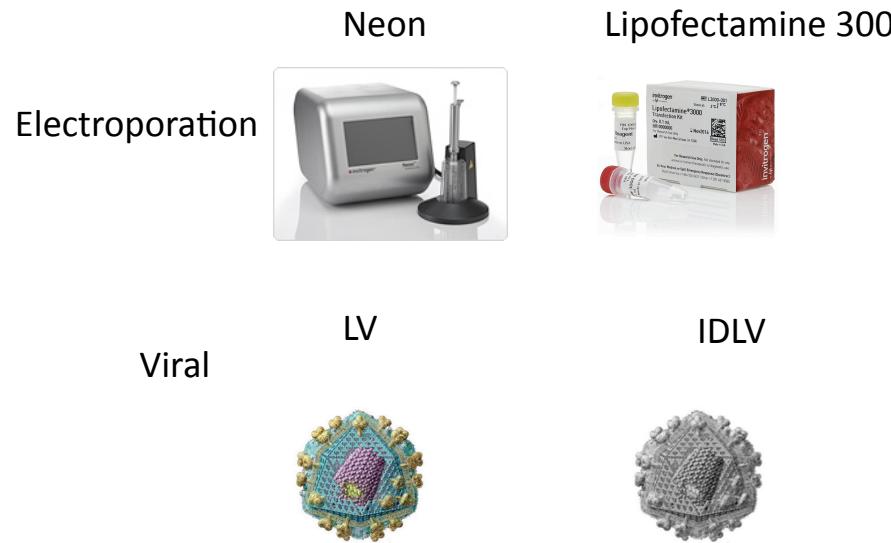


Torres et al, In press

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### 3.- CRISPR delivery system

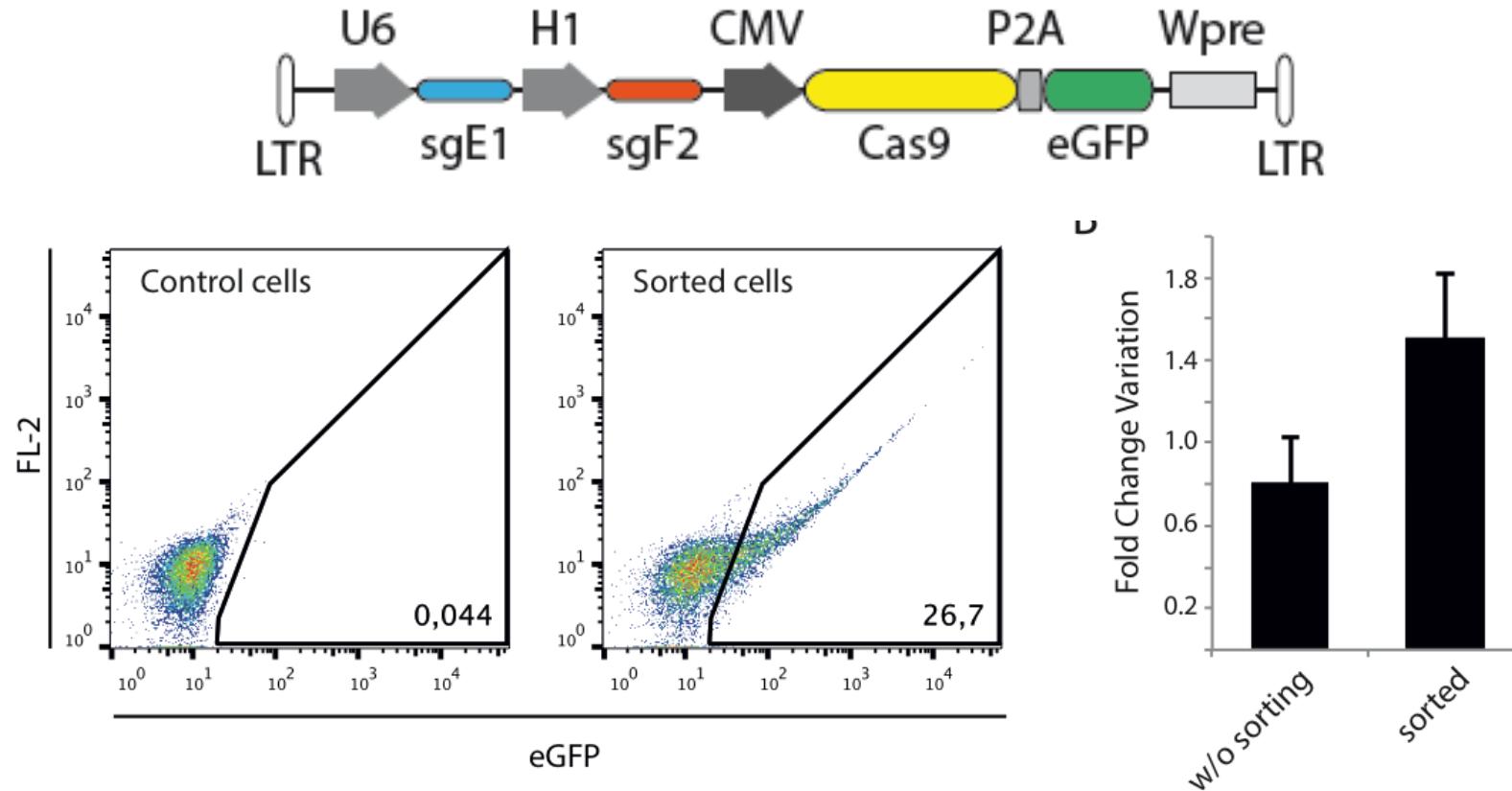


Torres et al, In press

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#### 4.- Selection of transfected cells



Torres et al, In press

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Chromosome  
Translocation

CRISPR  
System

Engineering a  
Translocation

Method  
Optimization

Acknowledgments



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