

# MOD1 – DNA ENGINEERING

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Spring 2008

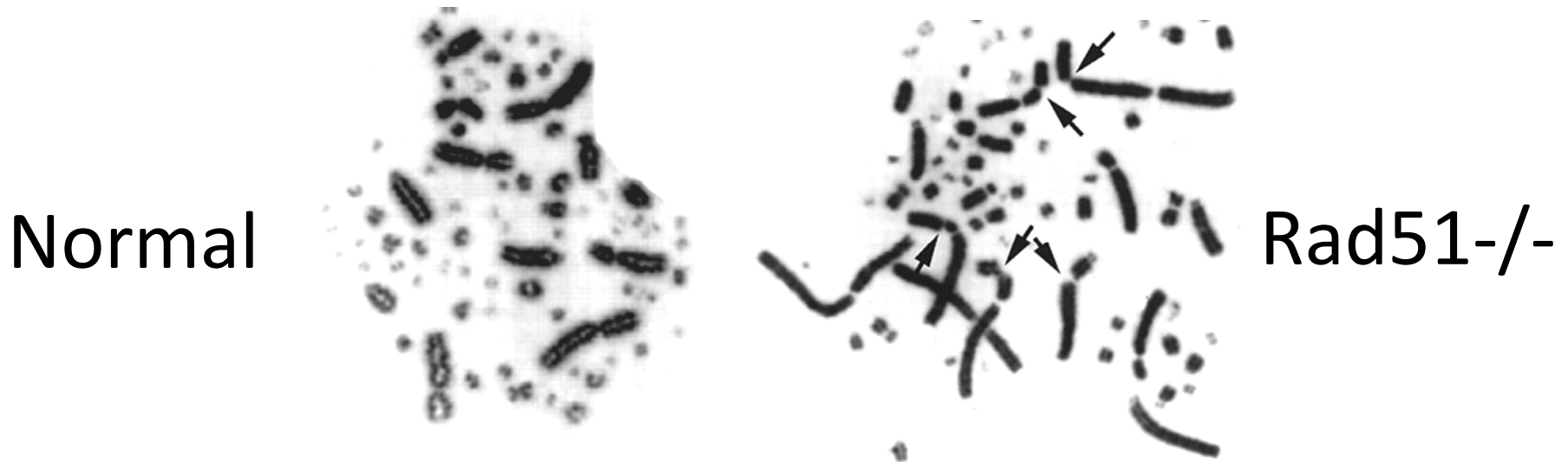
**Day 4**

**Using Homologous Recombination to Engineer Mice**

**Gene Cloning – Tips and Tricks!**

**Your Data – Controls & Interpretation**

# *Why you owe Your Life to Homologous Recombination...*

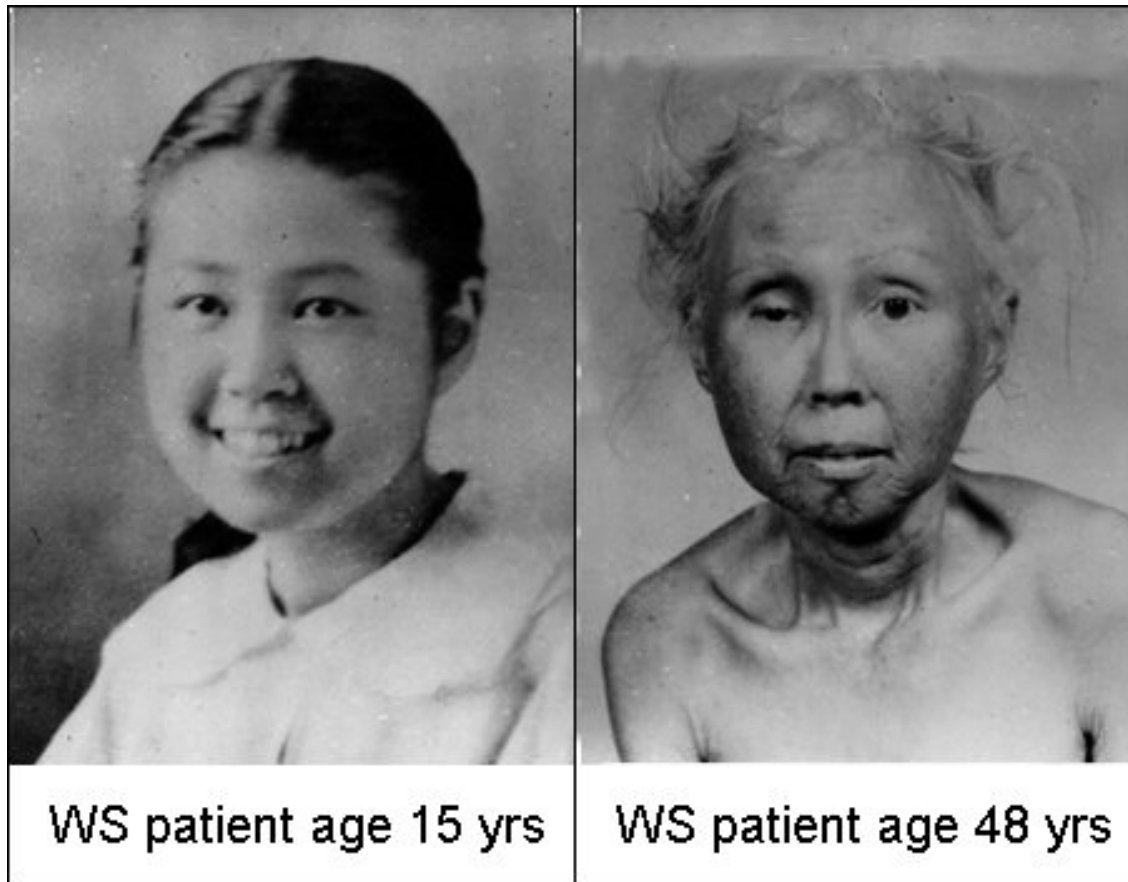


Turn Off Homologous Recombination  
→ Chromosomes Fall Apart

Sonada *et al.*, *EMBO J.* **17**, 598–608 (1998).

# *Why you owe Your Youthfulness to Homologous Recombination...*

Loss of Helicase → Faulty Recomb.



Werner's  
Syndrome

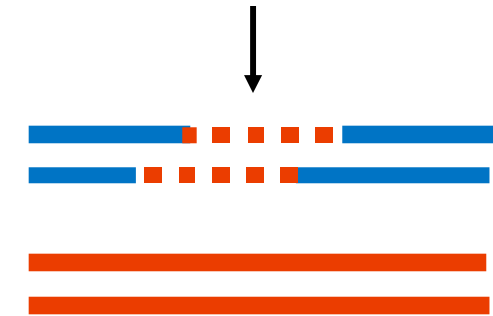
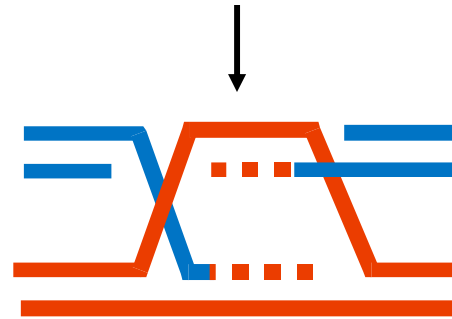
# Double Strand Breaks

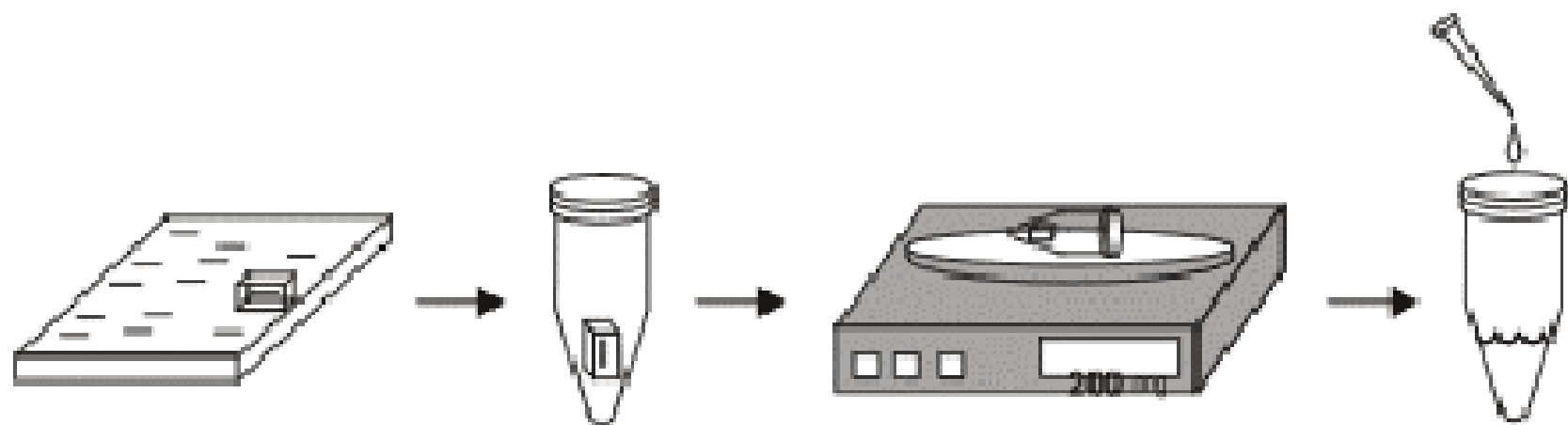
NHEJ

HR



KU heterodimer  
(Ku70&80)  
DNA-PKcs  
DNA ligase IV  
XRCC4





# Exploiting HR for Mouse Engineering

You need to understand gene-targeting in order to understand the paper you will be reading.

# Genetic Engineering in Mice:

## 1) Transgenic Mice

-putting genes in

## 2) Knock-Out Mice

-turning genes off



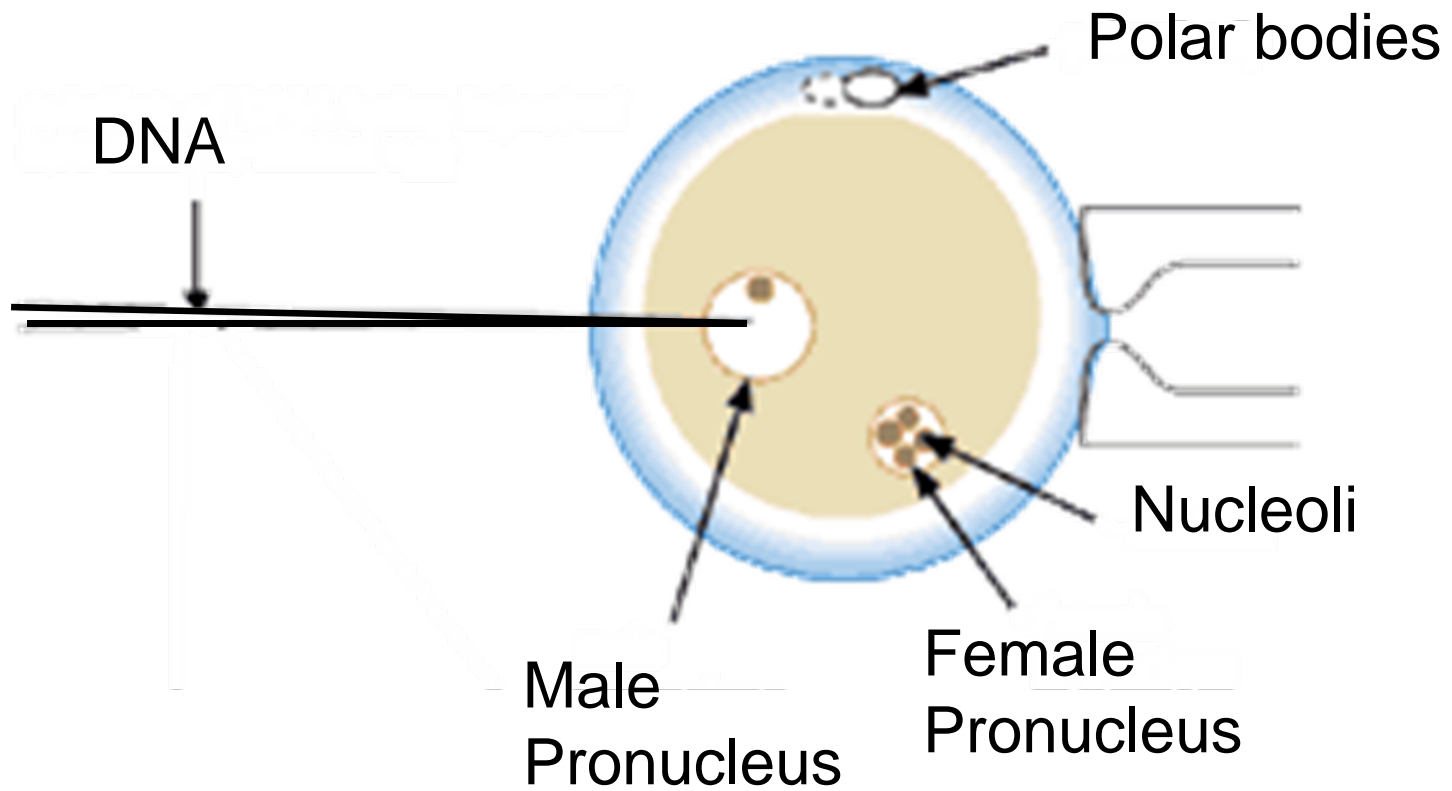
# Genetic Engineering in Mice:

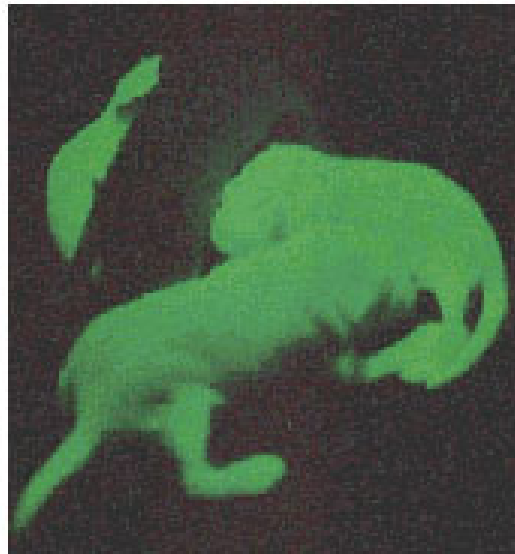
## **1) Transgenic Mice**

-putting genes in

## **2) Knock-Out Mice**

-turning genes off





Okabe *et al.*

# Genetic Engineering in Mice:

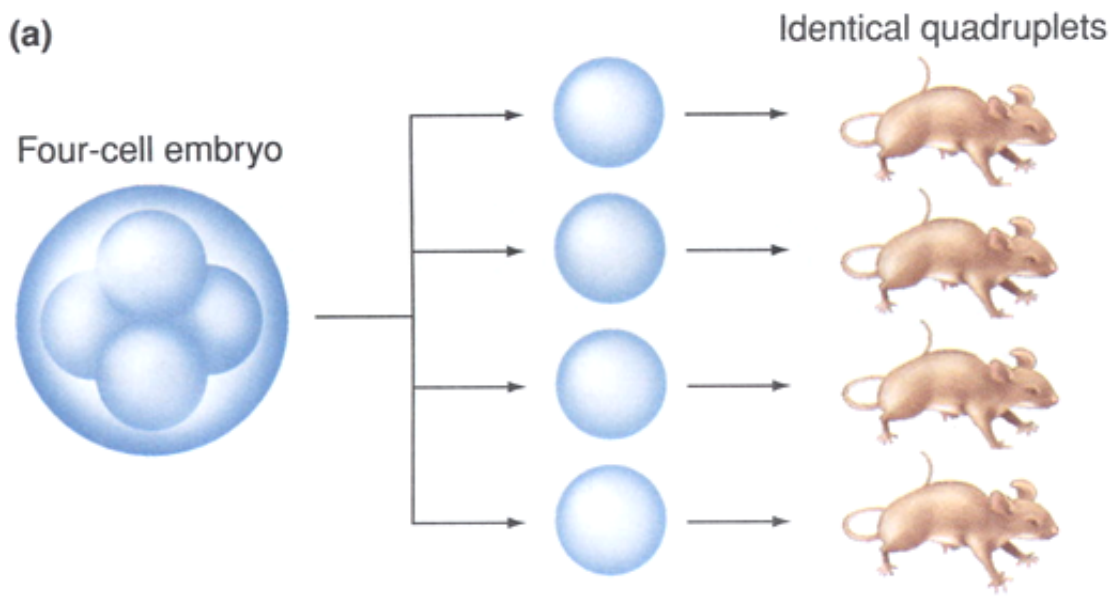
## 1) Transgenic Mice

-putting genes in

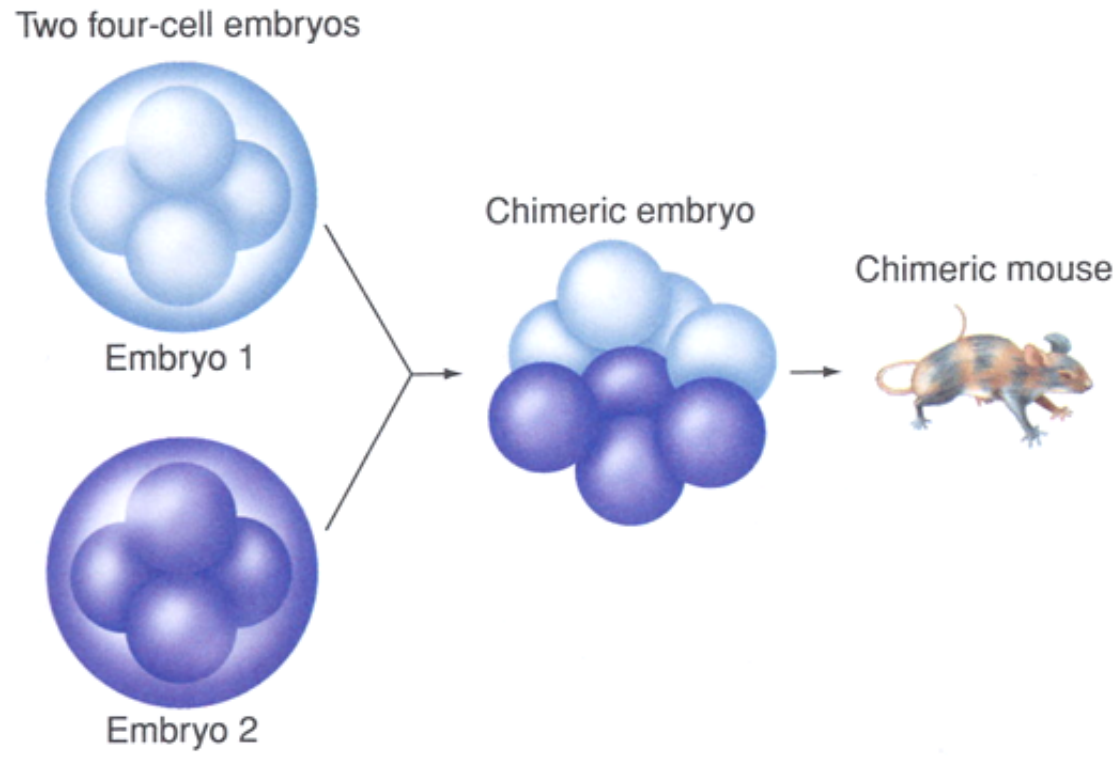
## 2) Knock-Out Mice

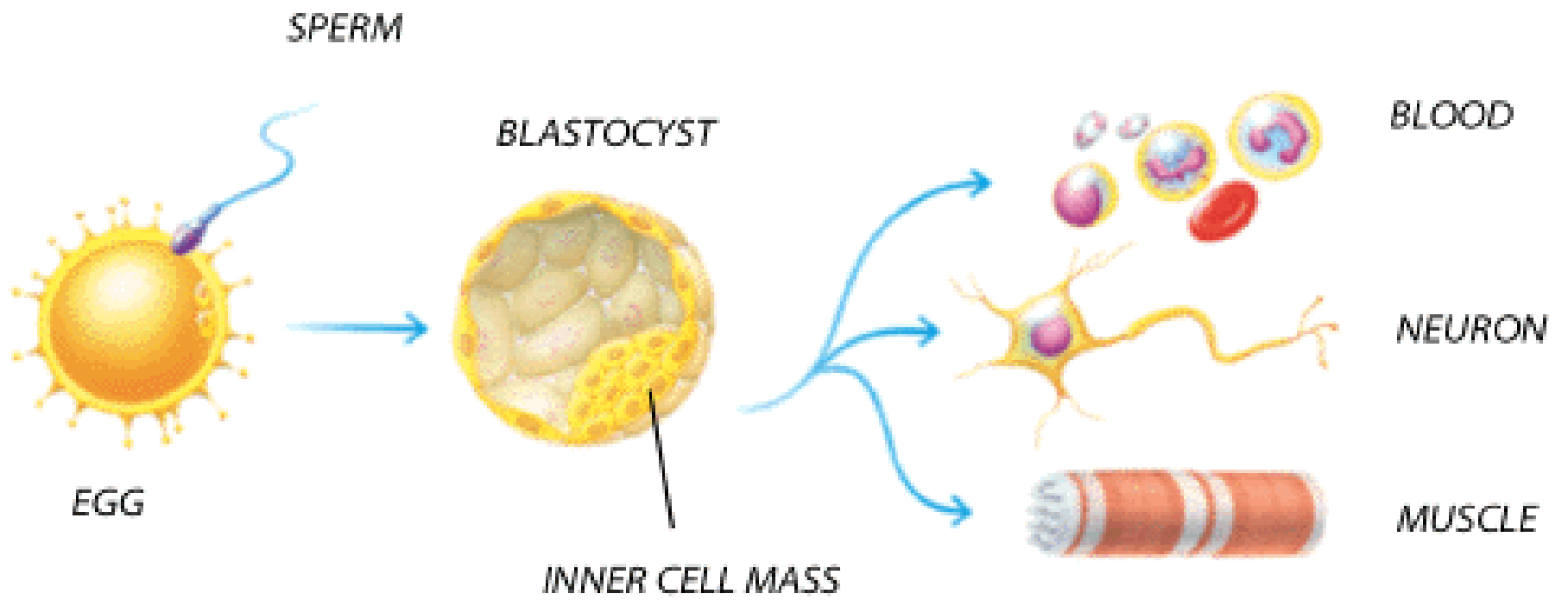
-turning genes off

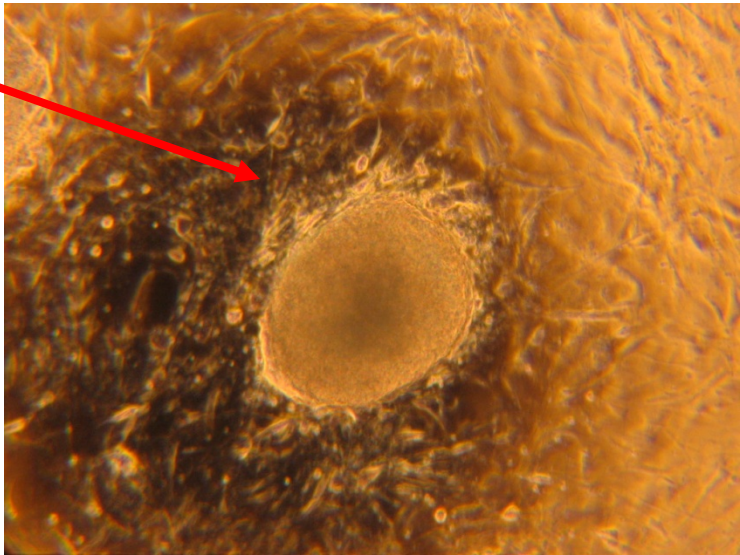
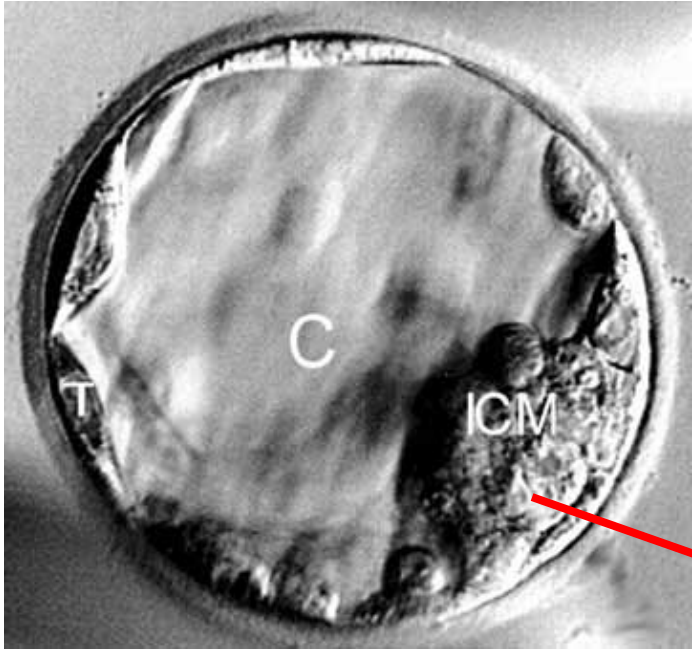
(a)



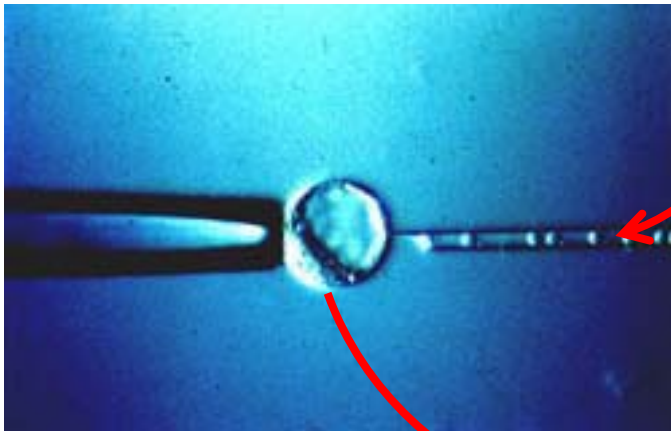
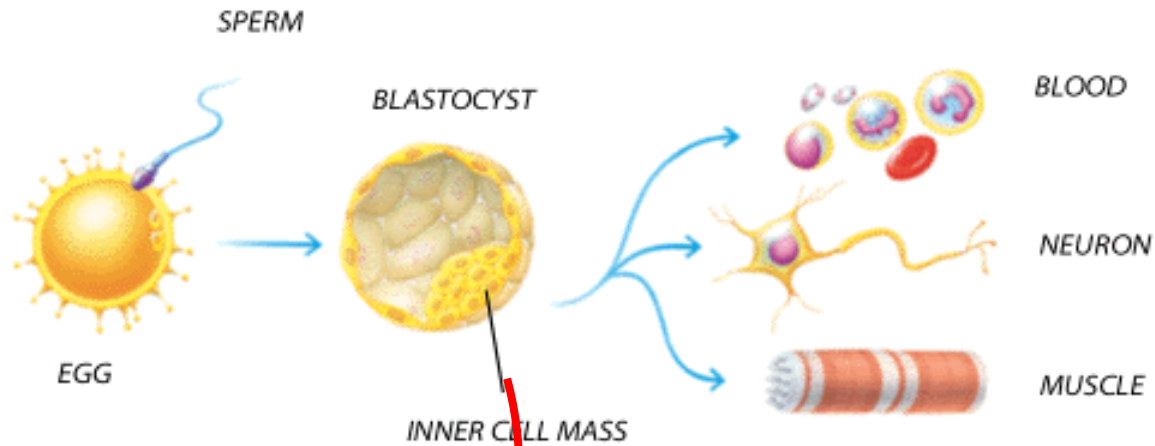
(b)





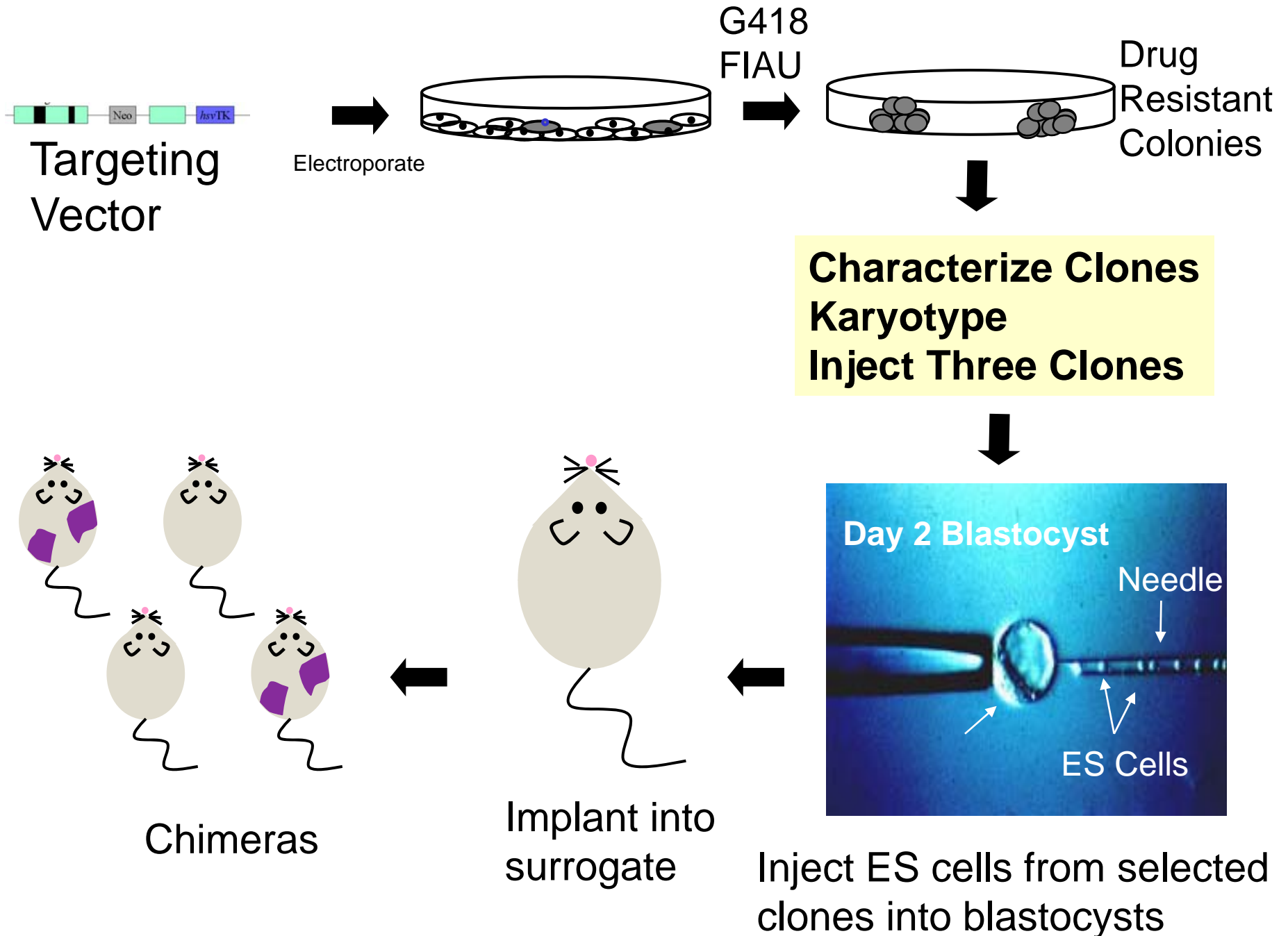


# Traditional ES Knock-Out Technology



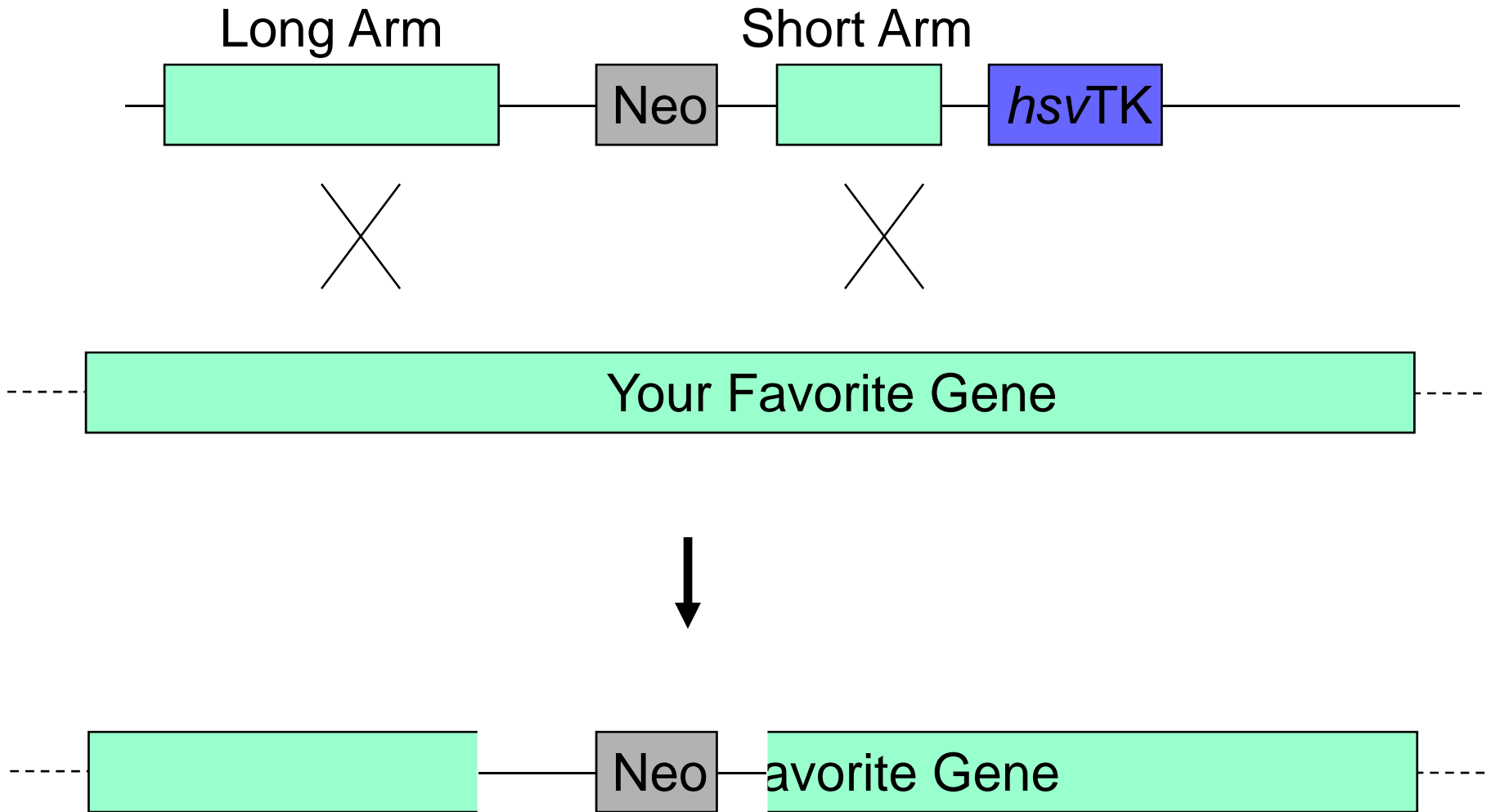
Engineered cells mix with recipient blastocyst to make a chimeric mouse





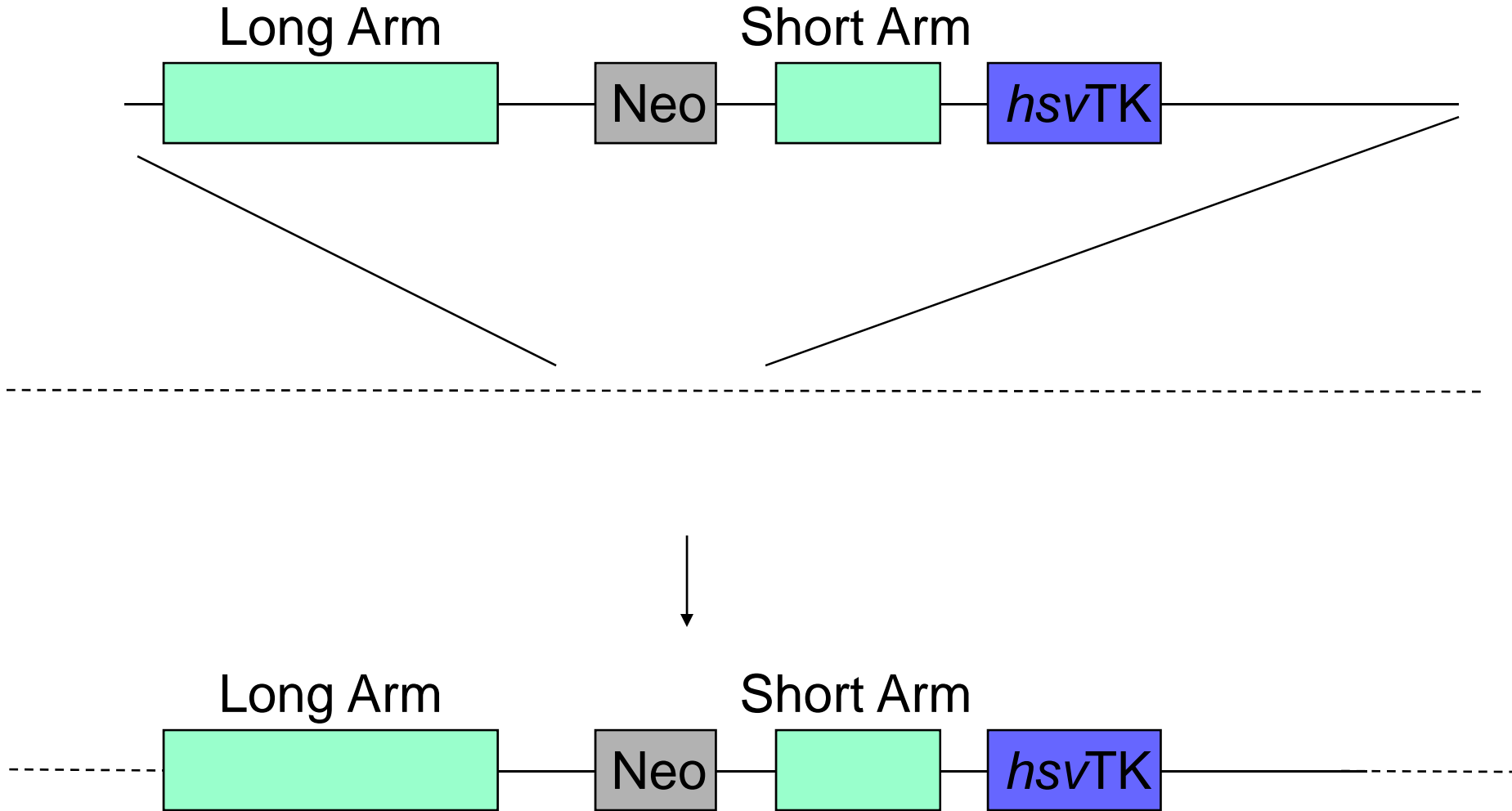
# Traditional ES Knock-Out Technology

## Targeted Homologous Recombination



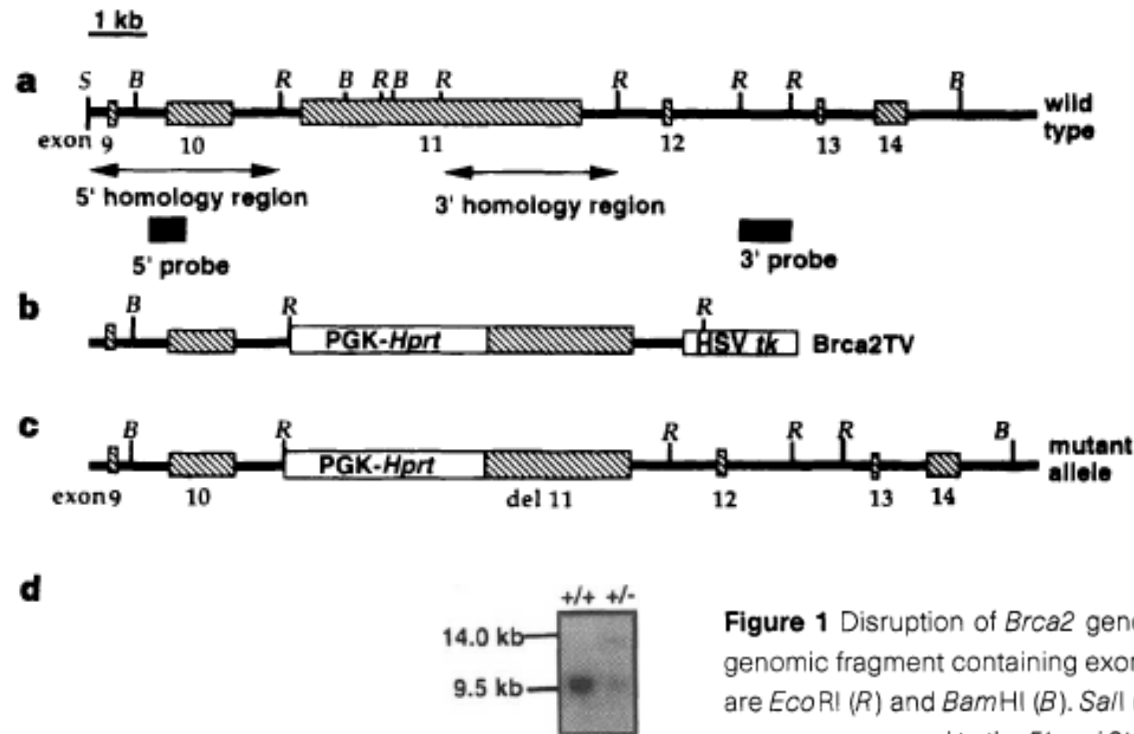
# Traditional ES Knock-Out Technology

## Random Integration

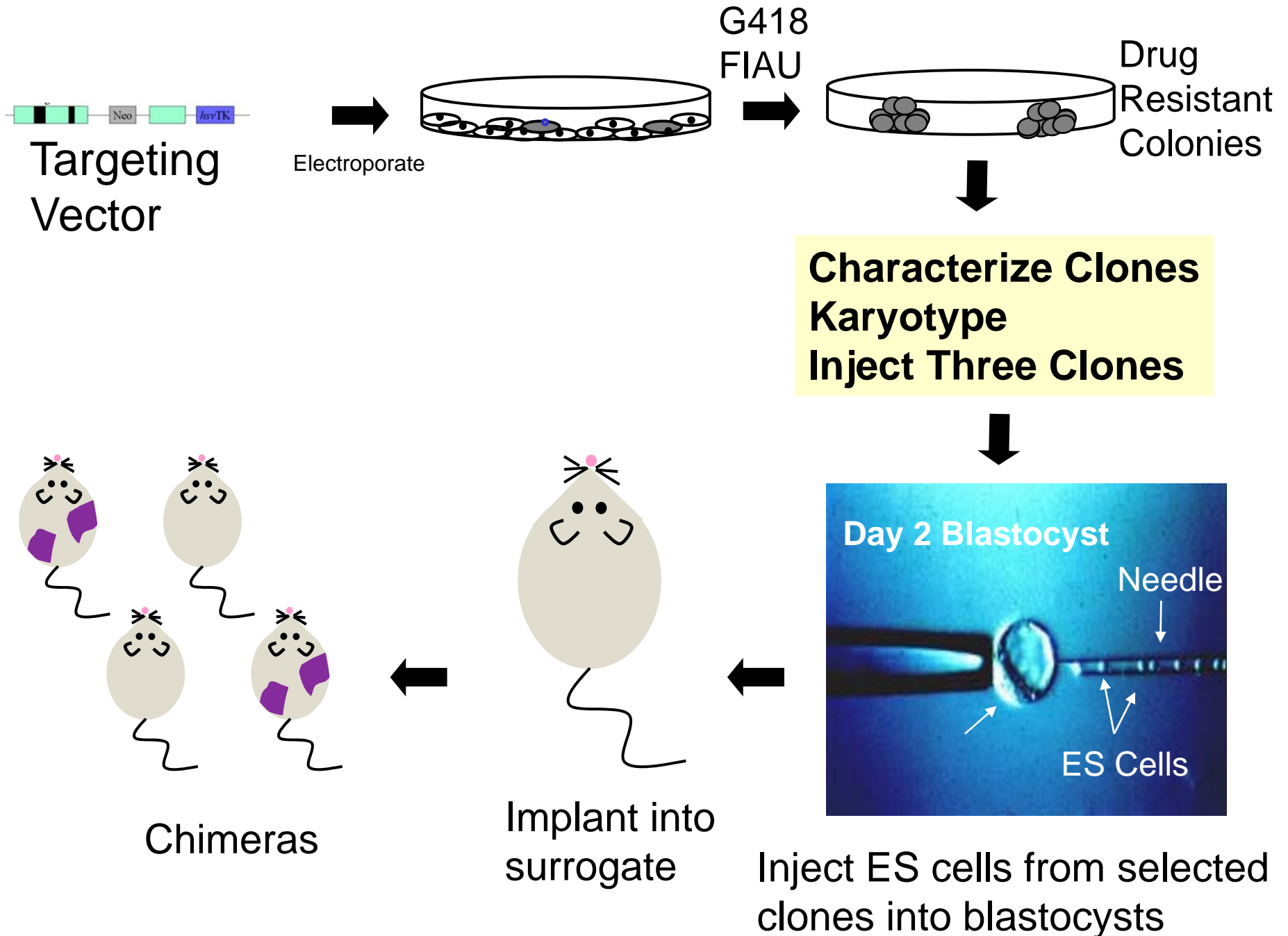


# Embryonic lethality and radiation hypersensitivity mediated by Rad51 in mice lacking *Brca2*

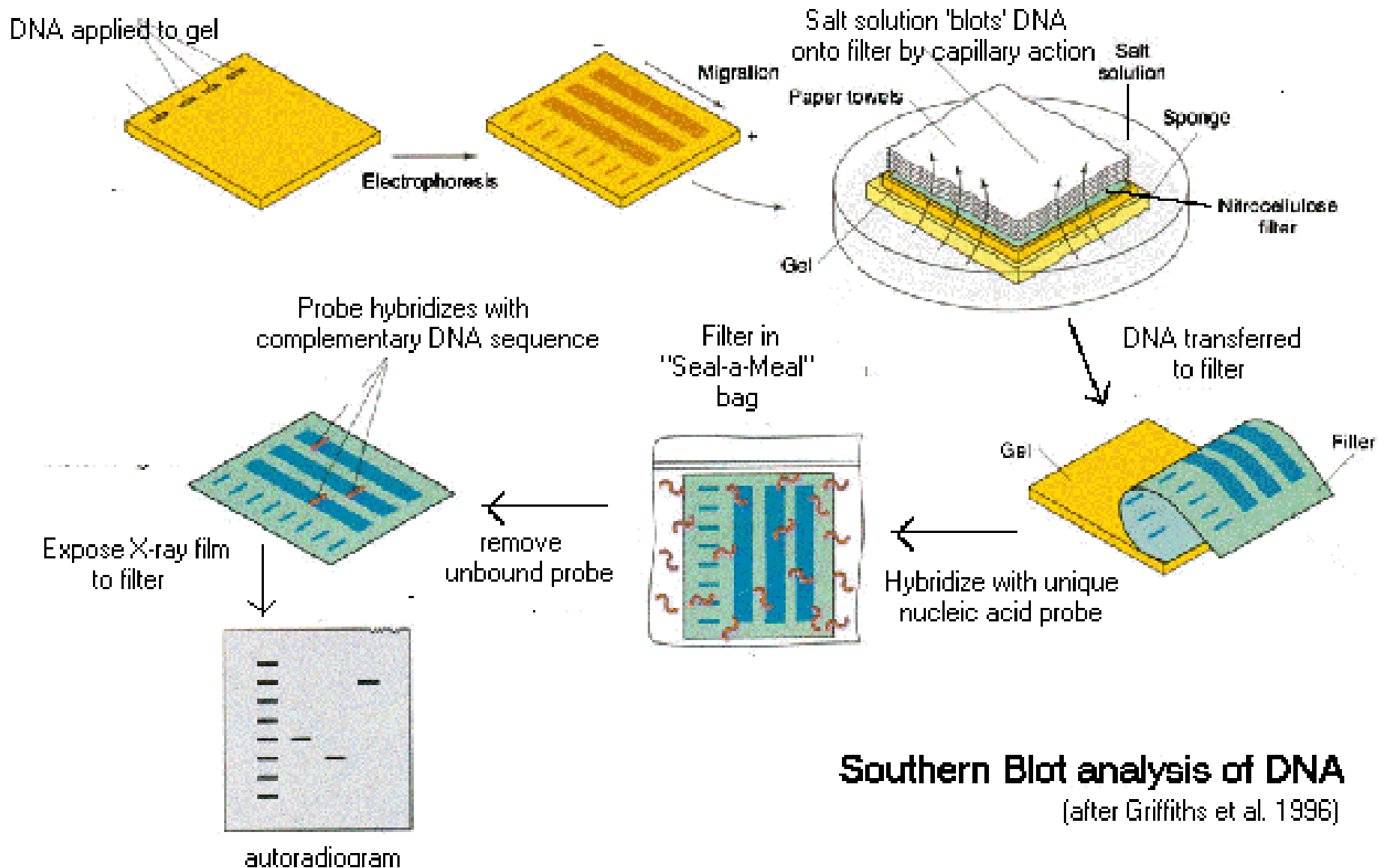
Shyam K. Sharan<sup>†</sup>, Masami Morimatsu<sup>‡§||</sup>, Urs Albrecht<sup>†</sup>, Dae-Sik Lim<sup>‡☆</sup>, Eva Regel<sup>†</sup>, Christopher Dinh<sup>†</sup>, Arthur Sands<sup>‡</sup>, Gregor Eichele<sup>†</sup>, Paul Hasty<sup>‡</sup> & Allan Bradley<sup>††</sup>



**Figure 1** Disruption of *Brca2* gene in ES cells. **a**, Restriction map of the *Brca2* genomic fragment containing exon 9–15 is shown. Restriction sites shown here are *Eco*RI (*R*) and *Bam*HI (*B*). *Sal*I (*S*) is from the cloning vector. Double-headed arrows correspond to the 5' and 3' homology regions and the dark shaded boxes show the probes used. **b**, Restriction map of the targeting vector p*Brca2*TV. **c**, Expected restriction map of the mutated *Brca2* locus. A 2.8-kb genomic region is deleted and replaced by the 3.6-kb *Hprt* gene. **d**, Southern analysis to identify heterozygous ES cells by digesting genomic DNA with *Bam*HI. The 3' probe detects a 9.5-kb wild-type band and a 14.0-kb mutant band. **e**, Restriction map of



# Southern Blot Analysis

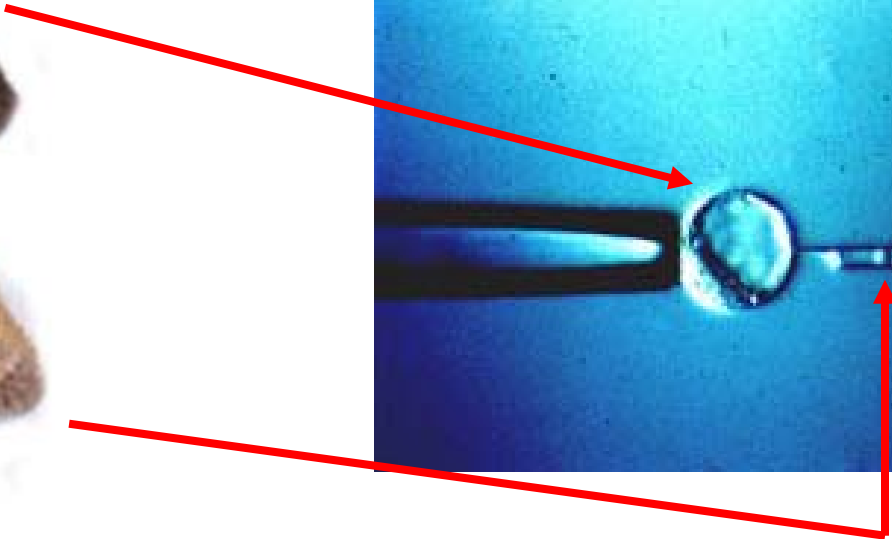
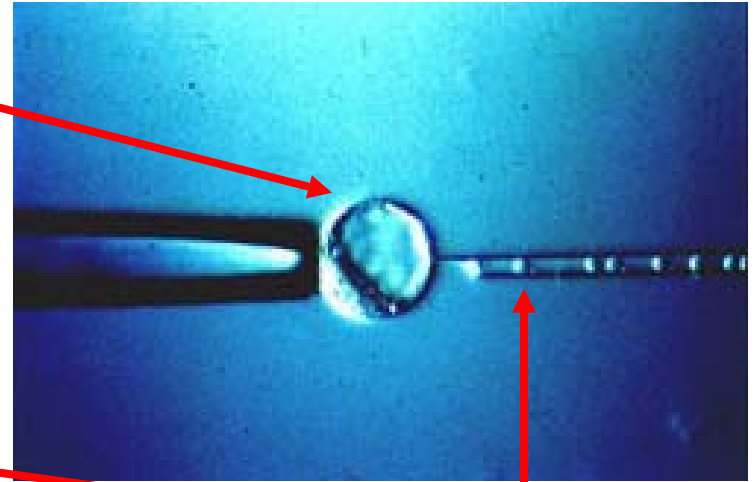


**Southern Blot analysis of DNA**

(after Griffiths et al. 1996)

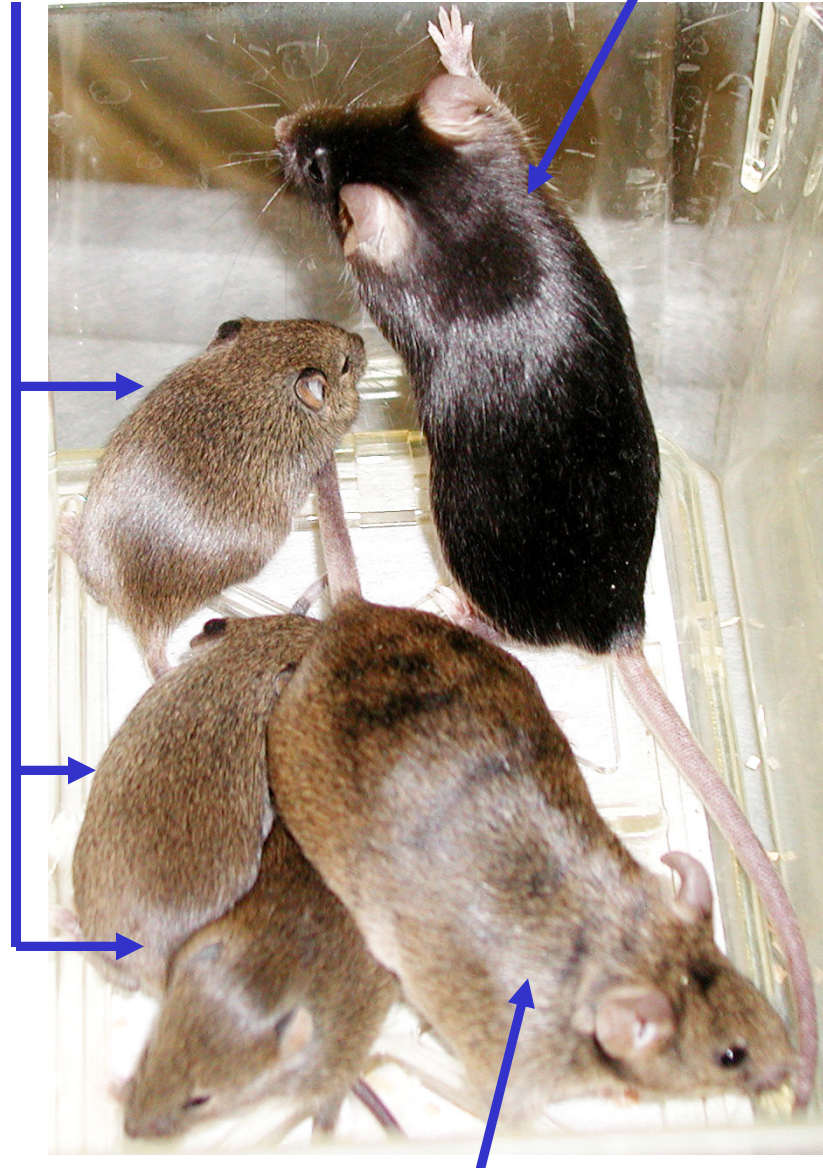
Blastocyst Donor

ES Cell Donor



Germline Offspring

C57BI Male



Germline Chimeric Female



# Gene Cloning:

## Tips and Tricks!



*Not the same as cloning!*

# Know Your Vector!

- Find out as much as you can about your vector

How do you know if your promoter will work?

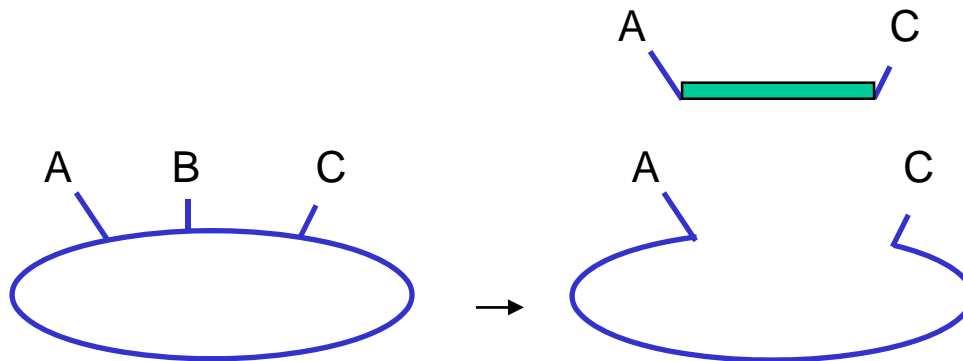
What antibiotic is used?

What is the origin of replication?

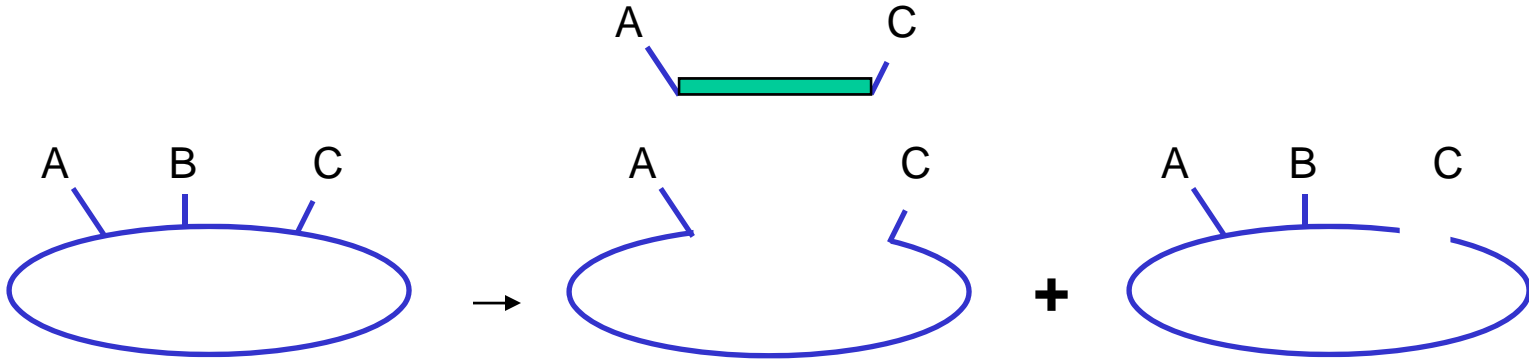
- Watch out for incorrect maps (!)
- Watch out for methylation-sensitive sites

# Picking Restriction Enzyme Sites for PCR Product Insert

- They must not be in the insert
- Each must be unique in the vector
- Ideally they cut in the same buffer (check in catalog)

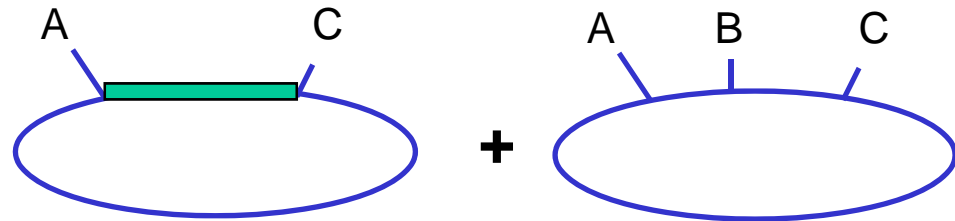


# When possible, use a "Kill" site to get rid of parent-vector

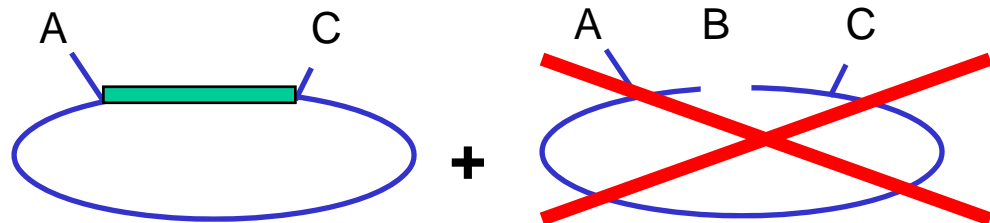


Linear DNA  
is degraded  
in *E. coli*

↓ **Ligase**



↓ **Restriction Enzyme B**



# Common Pitfalls in Preparing Vector

-DNA is not completely digested....

Why might incomplete cutting cause a problem?

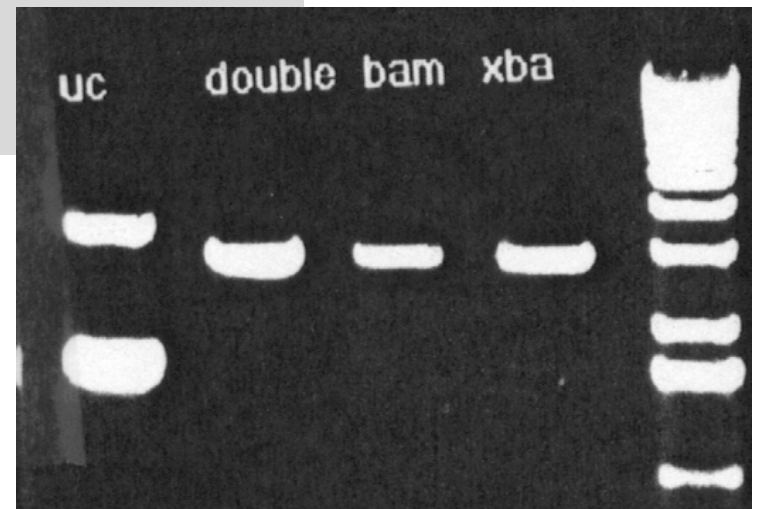
What can cause incomplete digestion?

- EDTA
- contamination with salts
- ethanol
- phenol
- not adding enough enzyme
- not waiting long enough
- incorrect buffer or temp.

## Preparing the Backbone for Ligation

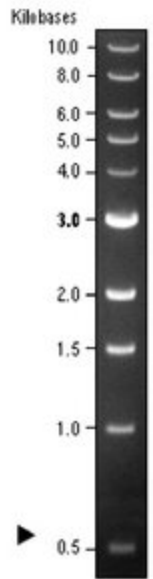
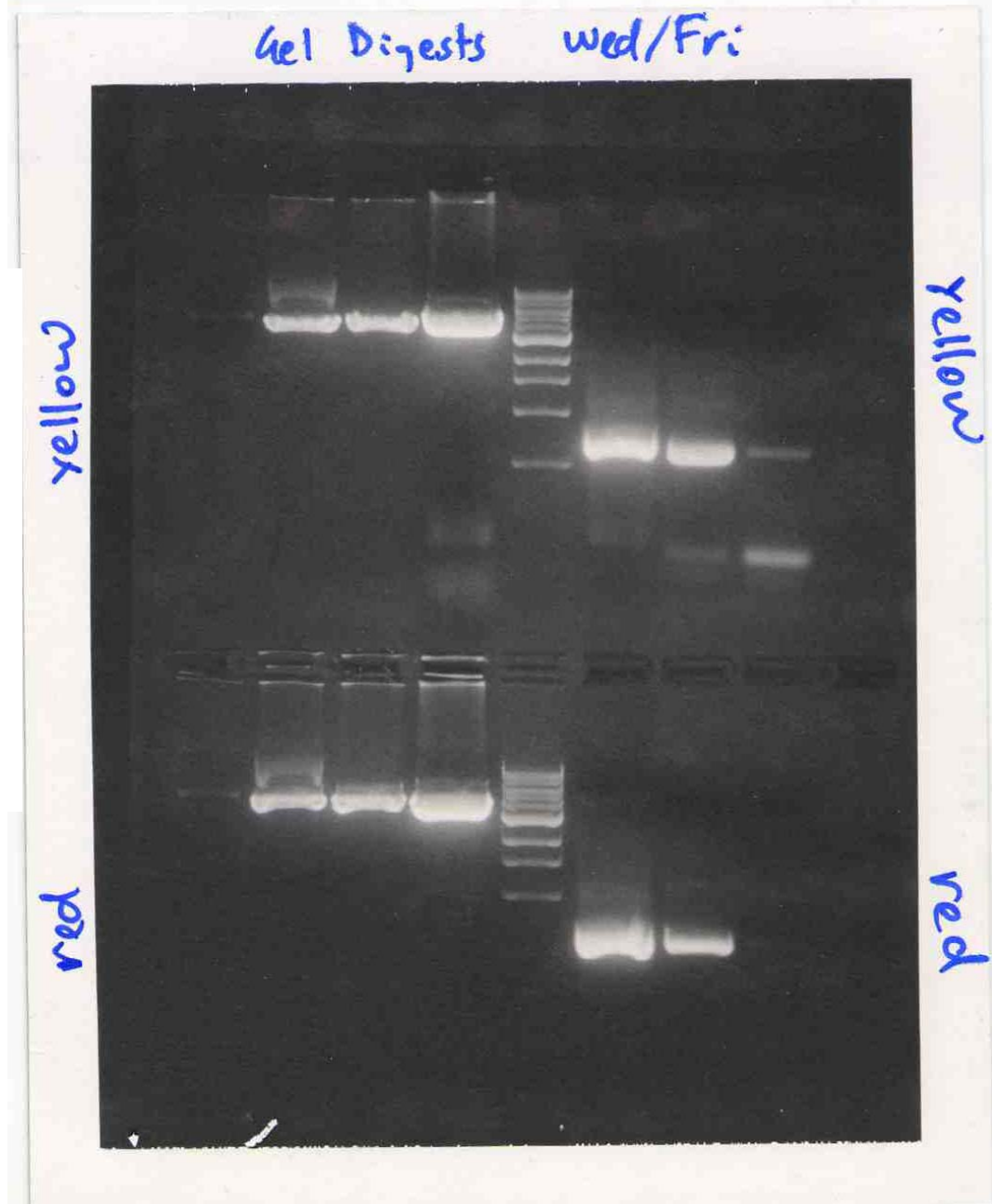
When double digesting, set up four reactions:

- vector with enzyme 1
- vector with enzyme 2
- vector with enzymes 1+2
- vector with *no* enzymes



**Your Data**

- 1 Uncut pCX-NNX
- 2 pCX-NNX XbaI
- 3 pCX-NNX EcoRI
- 4 pCX-NNX XbaI + EcoRI
- 5 DNA Ladder
- 6 PCR Product XbaI + EcoRI
- 7 PCR Product Uncut
- 8 PCR no-template-control

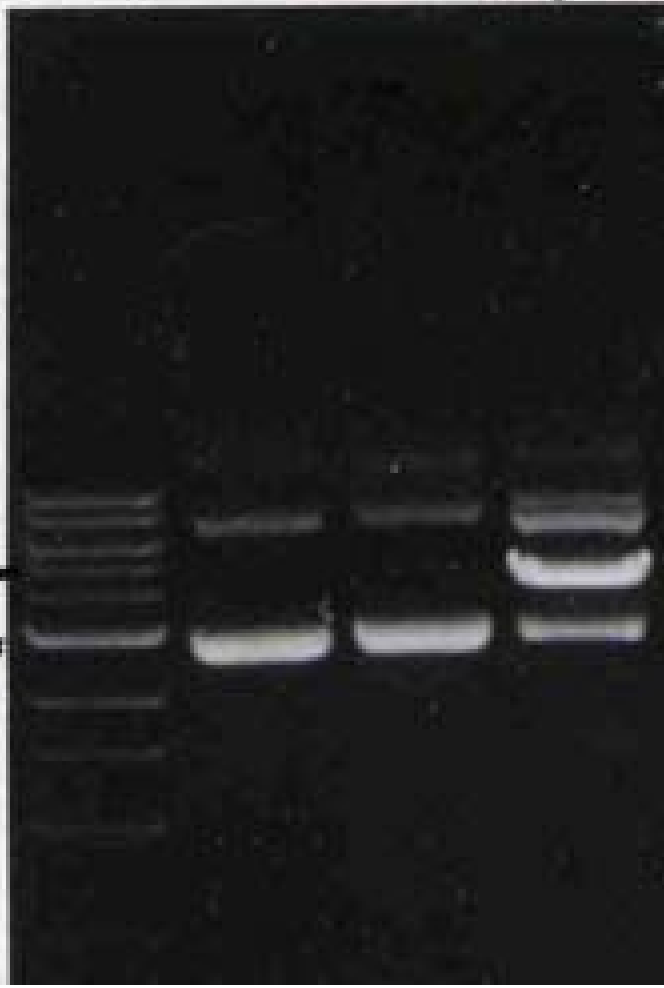




uncut

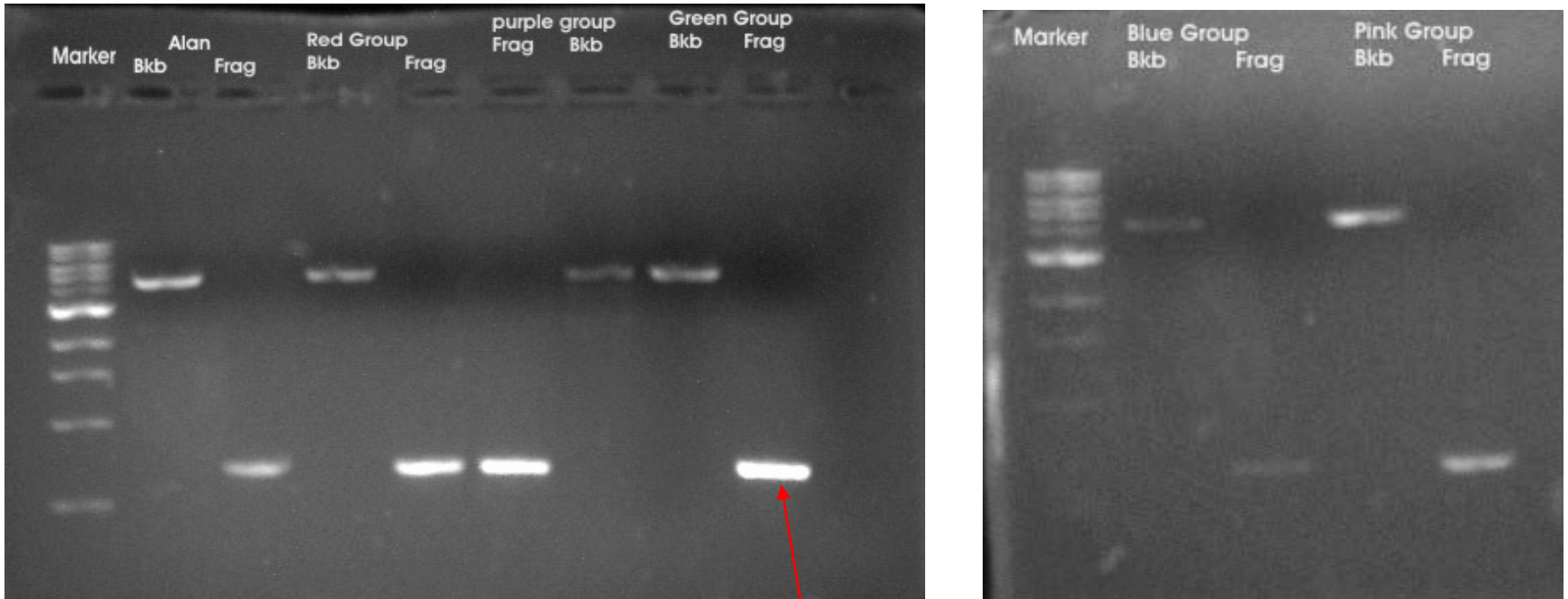
SmaI  
(Xb)

3.5





## Data from a previous year....



Why is it difficult to assess the quantity here?

# Expecting the Unexpected

What might go wrong in your ligation? What controls do you want to have?

Need to be sure your plates are actually selecting for cells that carry the drug resistance marker.

May have uncut plasmid and get original vector back.

May have singly cut vector that recloses.

May get strange products, like multiple inserts.

**Using Homologous Recombination to Engineer Mice**

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