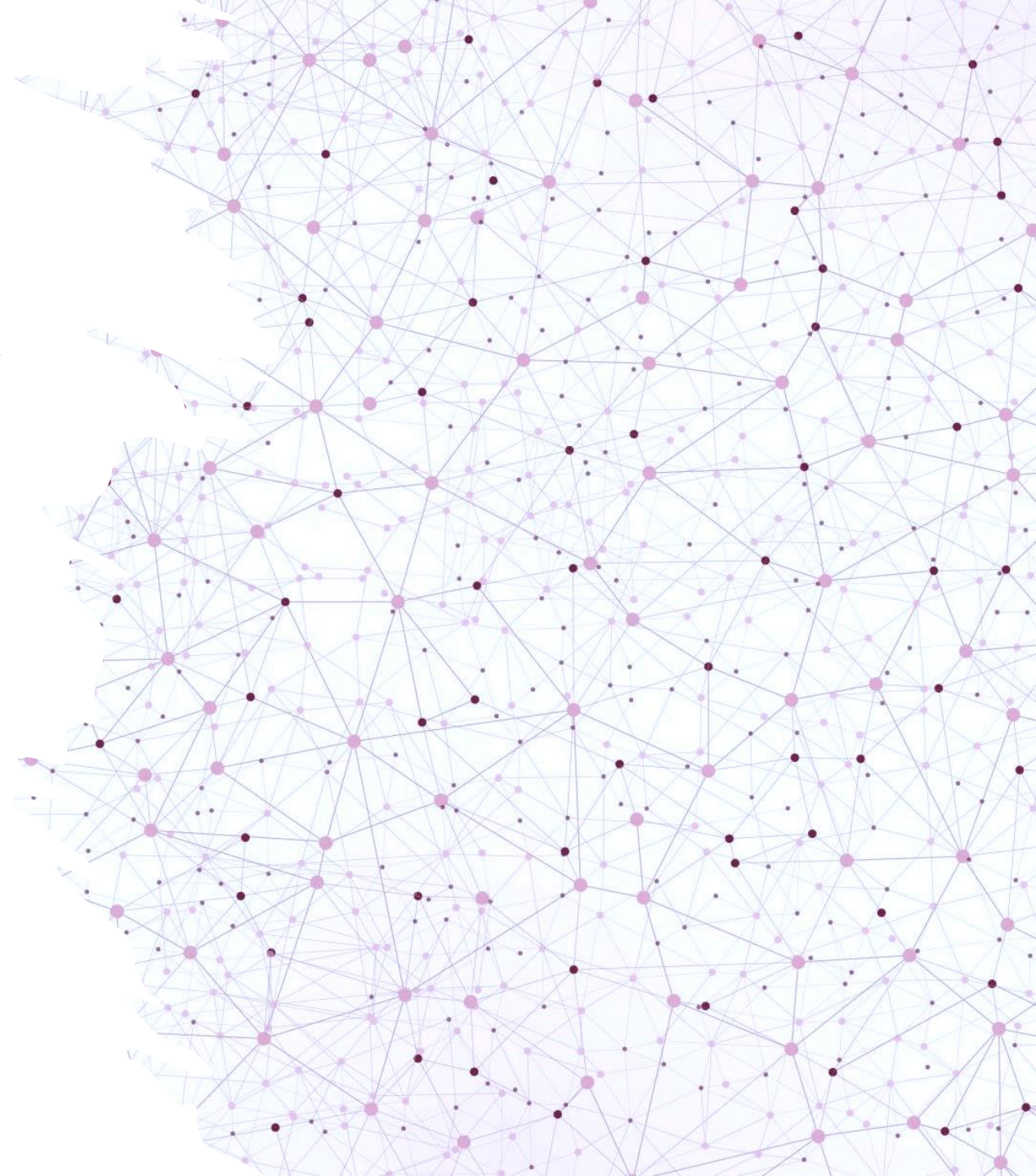


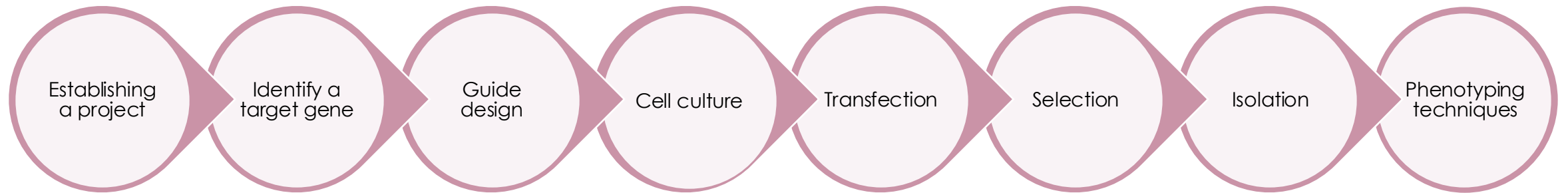
# ***Workflow for creating a CRISPR model***

## ***An undergraduate project***

Munuse C Savash Ishanzadeh  
Oxford University

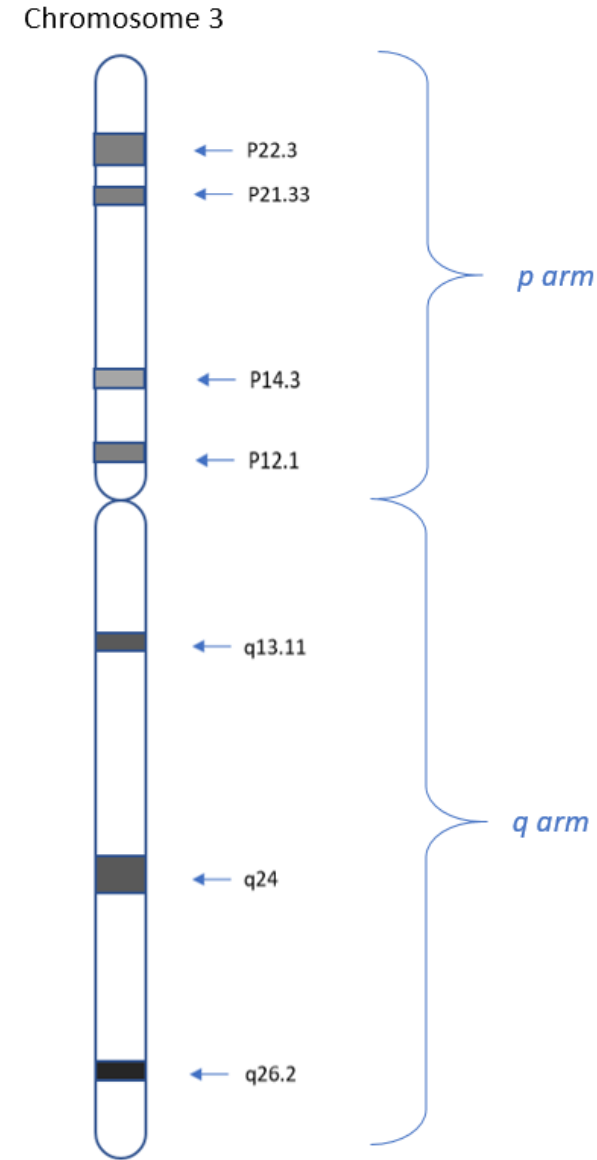


# ***CRISPR Workflow***



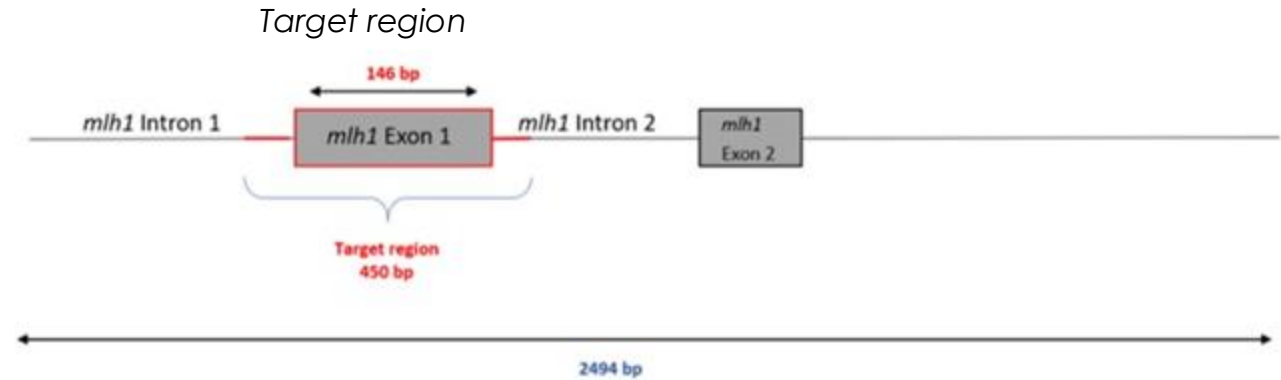
# ***Establishing a project and target gene***

- Targeted the MMR gene, *mlh1* of human chromosome 3
- Defective gene can result in hereditary non-polyposis colon cancer and lynch syndrome
- Cellular model used was a childhood bone cancer cell line tagged with a green fluorescent protein.



# Guide design

- Access the genetic sequence of your target location.
- Design your guide on sites such as Benchling.



Snippet from Ensembl

```

1  gaagagaccc agcaaccac agagttgaga aatttgactg gcattcaagc tgtccaatca
61  atagctgccg ctgaagggtg gggctggatg gcgtaagcta cagctgaagg aagaacgtga
121 gcacgaggca ctgaggtgat tggctgaagg cacttccgtt gagcatctag acgtttcctt
181 ggctcttctg gcgccaaaat gtcgttcgtg gcaggggtta ttcggcggct ggacgagaca
241 gtggtgaacc gcatcgcggc gggggaagtt atccagcggc cagctaagtc tatcaaagag
301 atgattgaga actgaaagaa gatctggata ttgtatgtga aaggttcact actagtaaac
361 tgcagtcctt tgaggattta gccagtattt ctacctatgg ctttcgaggt gaggctttgg
421 ccagcataag ccatgtggct catgttacta ttacaacgaa aacagctgat ggaaagtgtg
481 catacagagc aagt tactca gatggaaaac tgaaagcccc tcctaaacca tgtgctggca
541 atcaagggac ccagatcacg gtggaggacc ttttttaca catagccacg aggagaaaag
601 ctttaaaaaa tccaagtga gaaatggga aaattttgga agttgttggc aggtattcag
661 tacacaatgc aggcattagt ttctcagtta aaaaacaagg agagacagta gctgatgtta
721 ggacactacc caatgcctca accgtggaca atattcgctc catctttgga aatgctgtta
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1201 gtctgacctc gtcttctact tctggaagta gtgataaggt ctatgcccac cagatggttc
1261 gtacagattc cggggaacag aagcttgatg catttctgca gcctctgagc aaaccctgtg
1321 ccagtcagcc ccaggccatt gtcacagagg ataagacaga tatttctagt ggagggtcta
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```



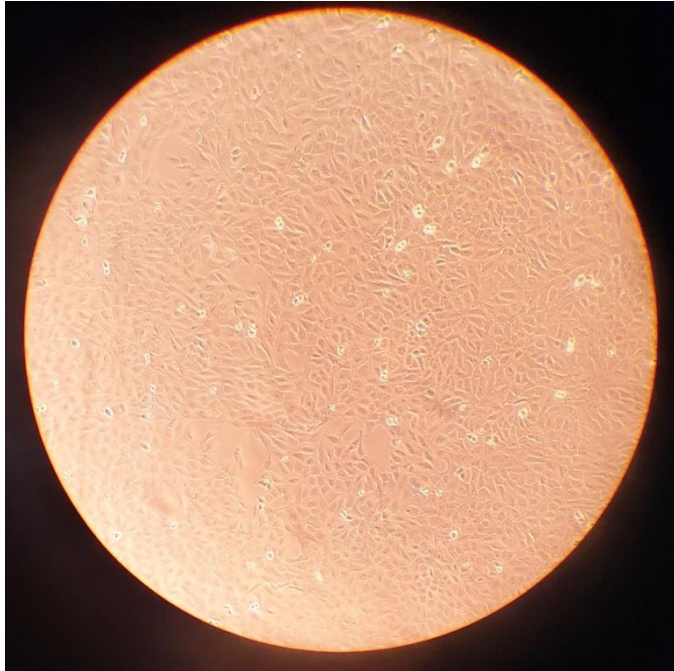
# *Cell culture*

- Growth of chosen cell line

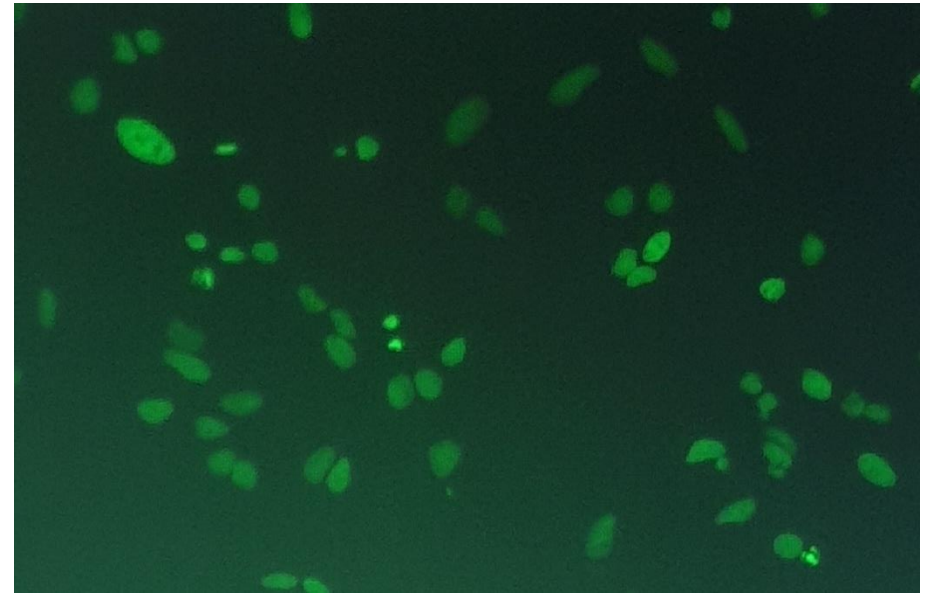
*Low confluence*



*High confluence*



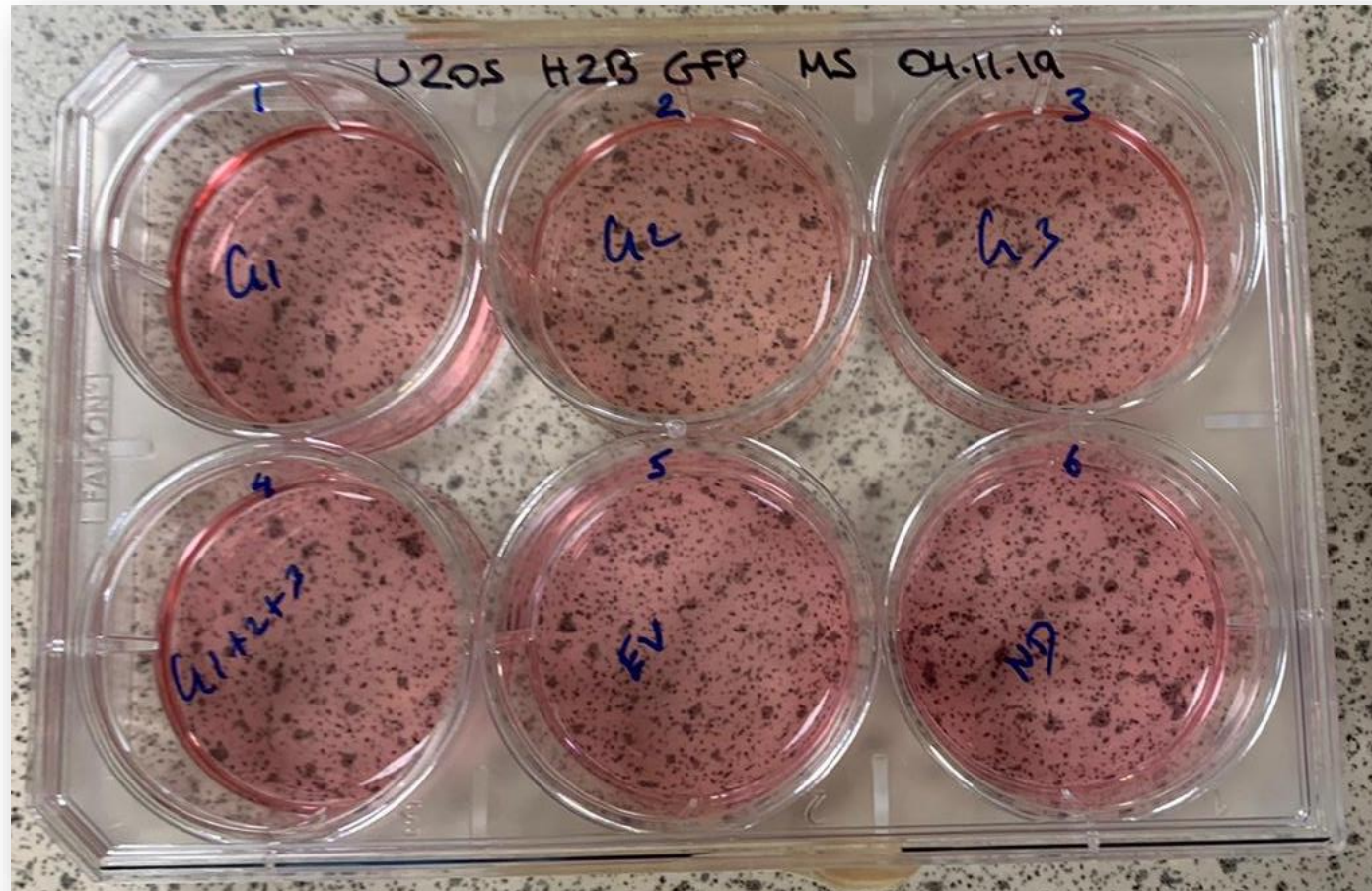
*Fluorescent microscopic image*



# *Transfection*

- Introducing CRISPR complex into cultured cells

6 well plate



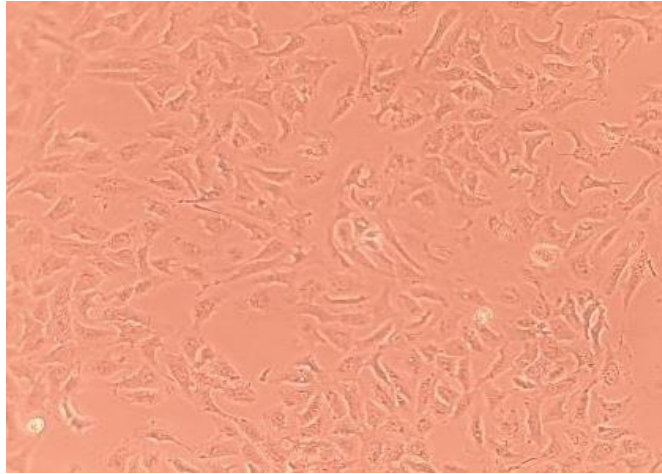


# ***Selection***

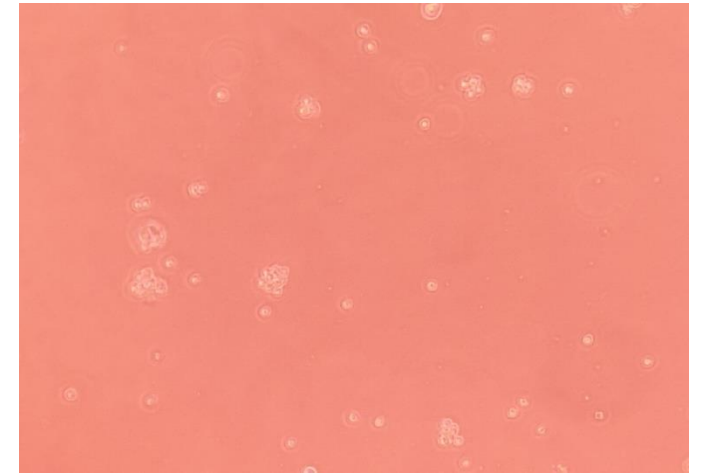
**Before  
Transfection**



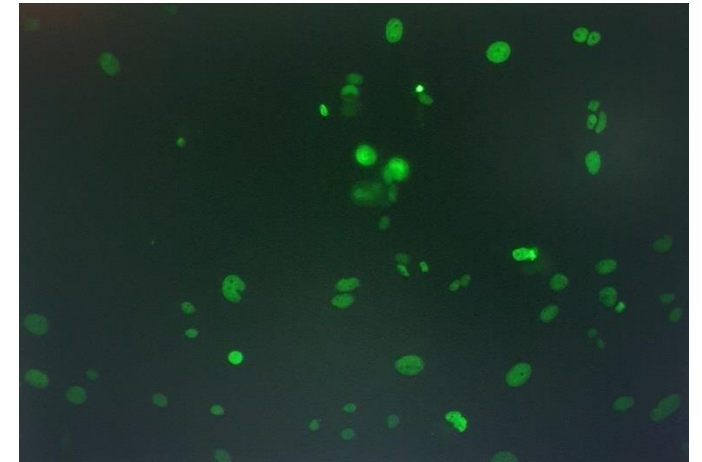
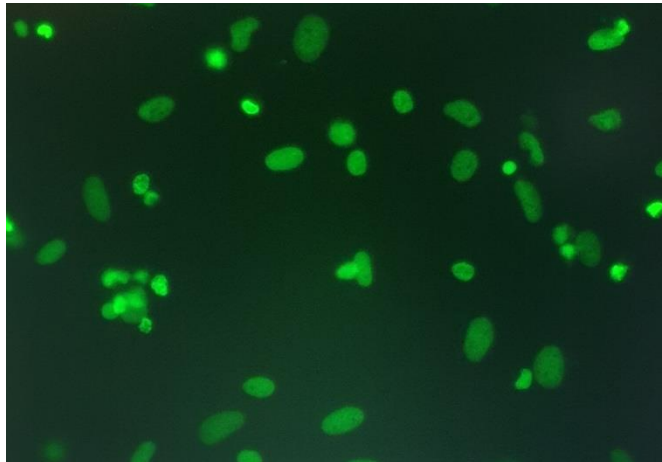
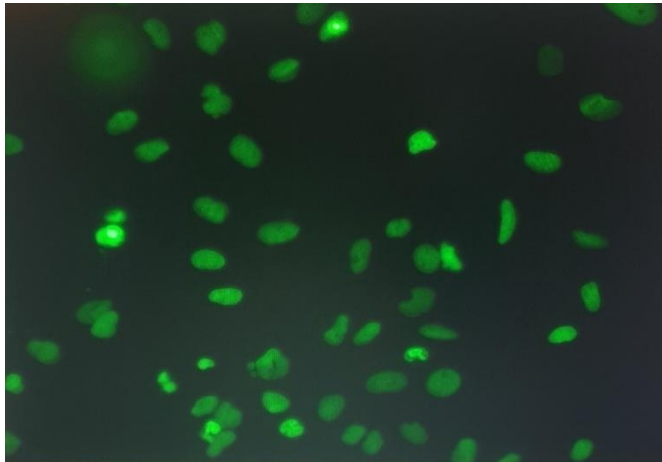
**Post  
Transfection**



**72h post selection release**



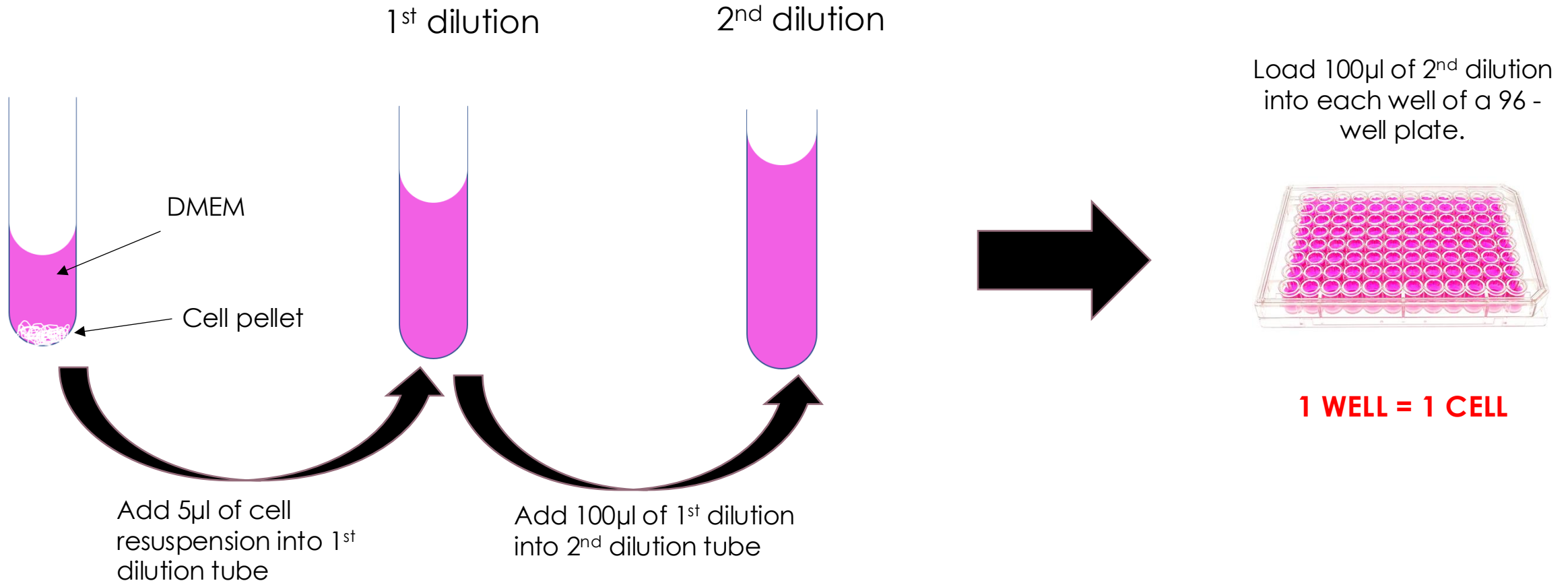
*Brightfield images*



*Fluorescent  
images*

- Selection of cells which contain the CRISPR complex

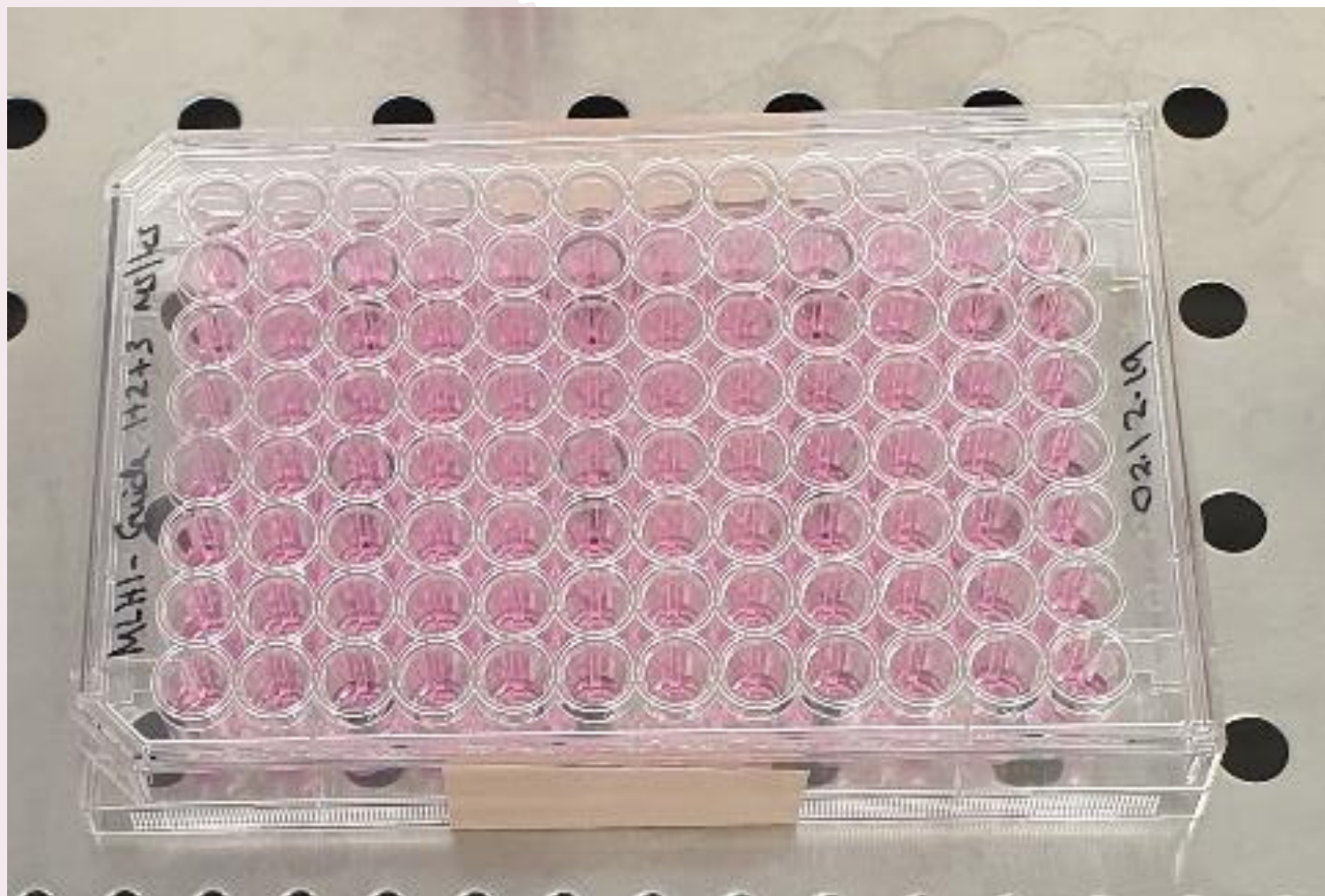
# *Isolation*



- Isolating edited cells into single colonies



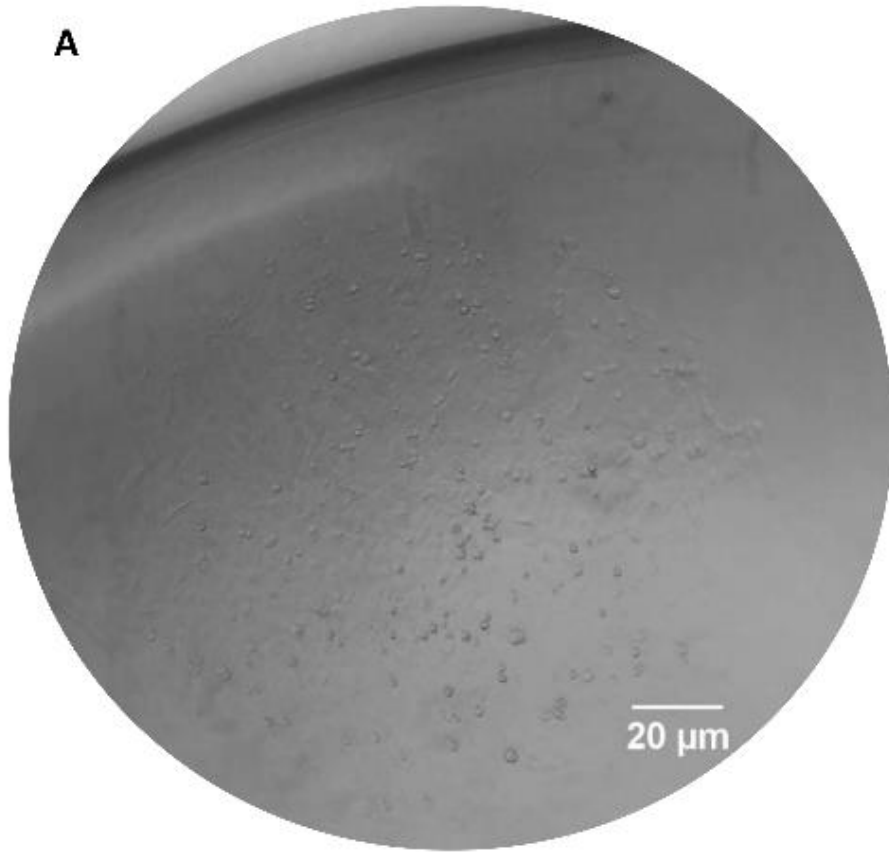
96 well monoclonal isolation plate



# ***Monoclonal culture***

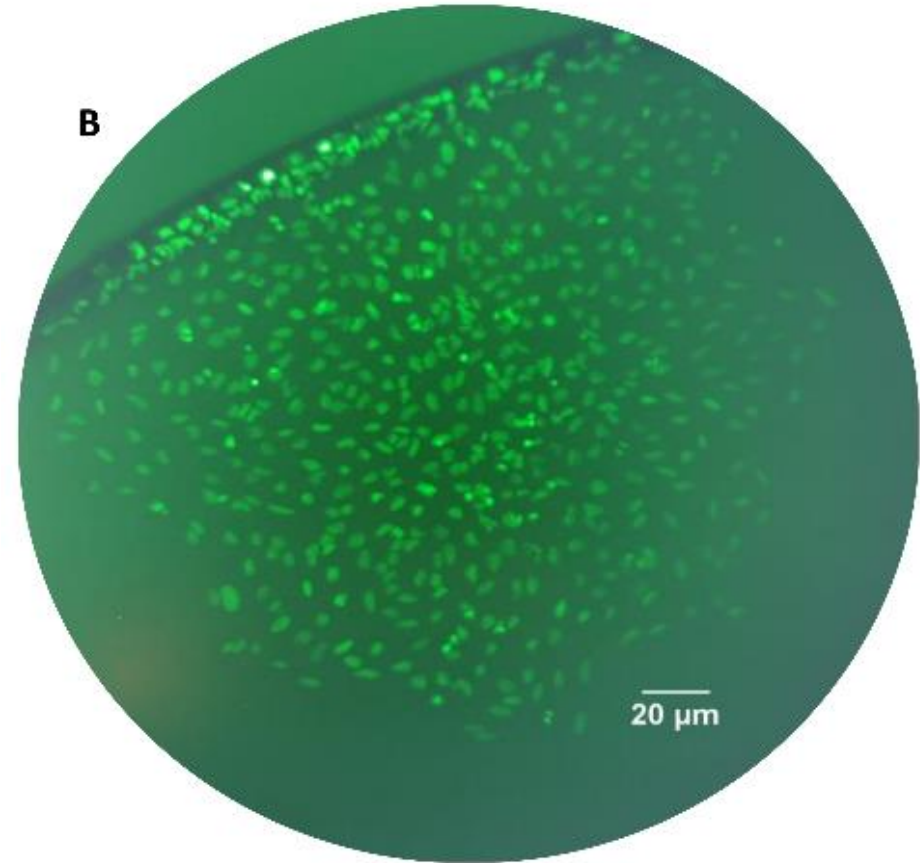
Brightfield images

**A**

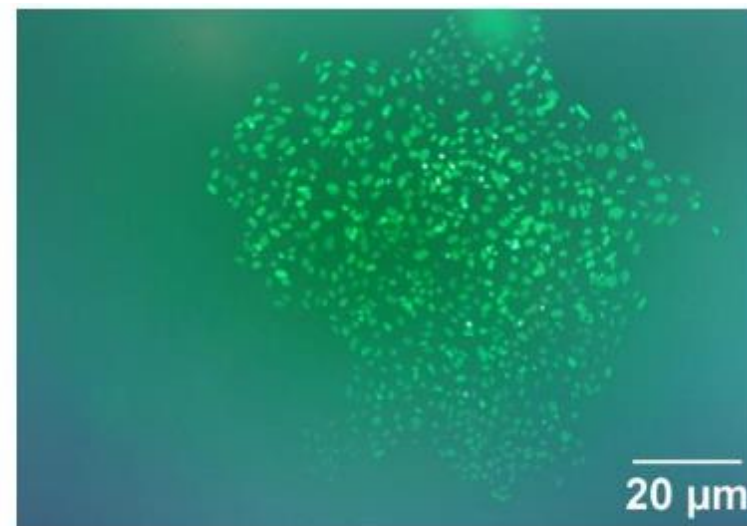
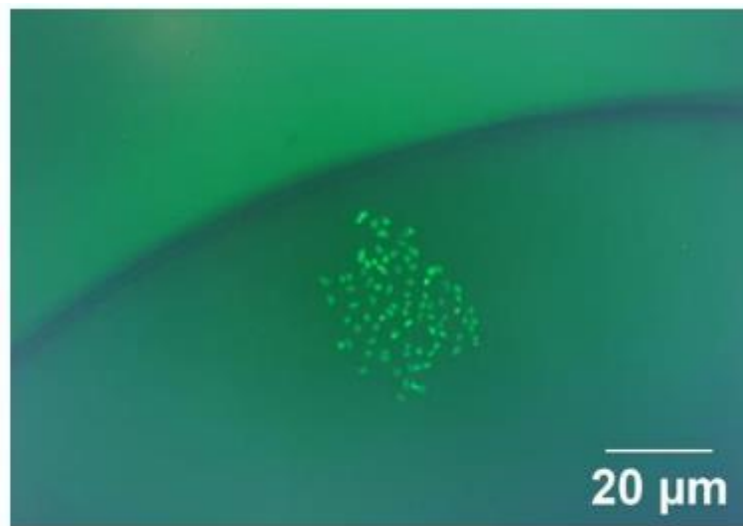
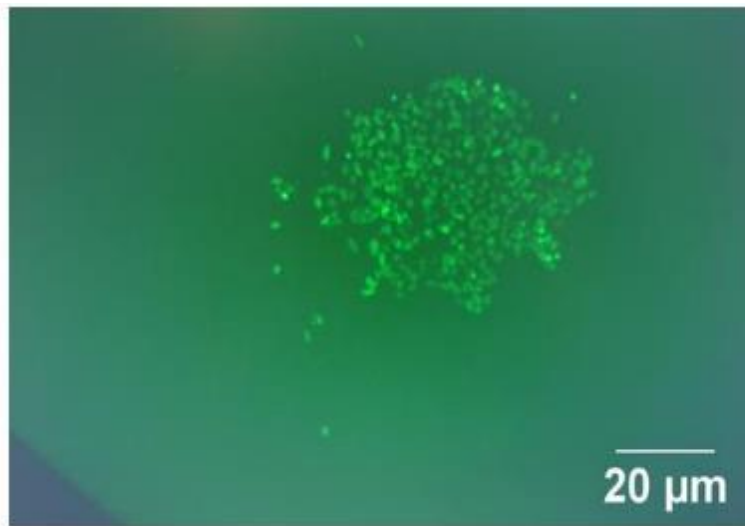


Fluorescent images

**B**

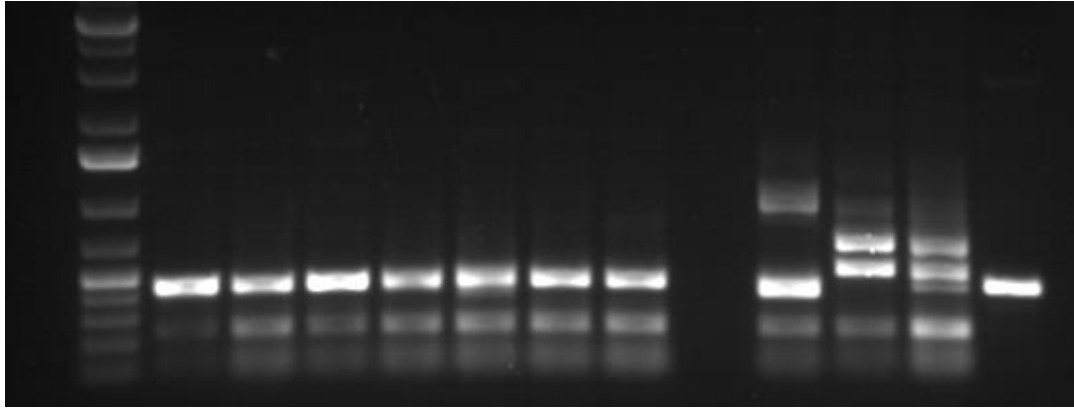


Fluorescent  
images

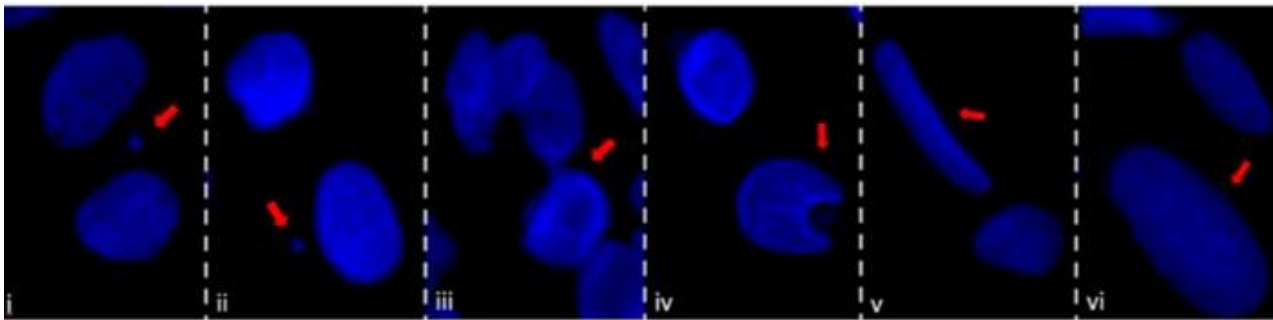


# *Phenotyping techniques*

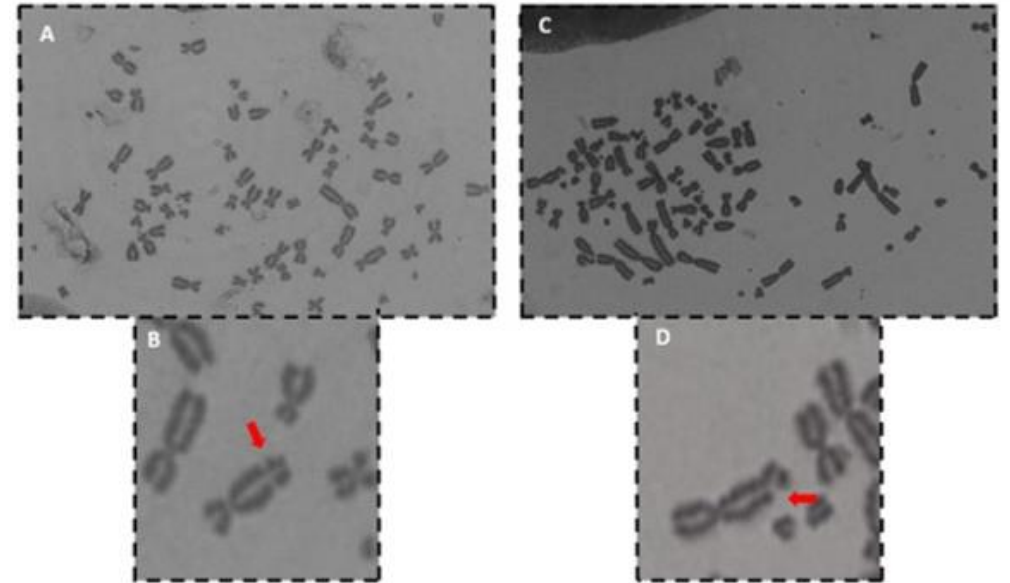
Gel electrophoresis



Nuclear morphology



Metaphase spread





G123C6

Deleted region

ATGTCGTTCTGTGGCAGGGGTTATTCGGCGGGCTGGACGAGACAGTGGTGAACCGCATCGCGGCGGGGGAAGTTATCCAGCGGCCAGCTAAT

Guide 1

Nucleotide percentage

ATGTCGTTCTGTGGCAGGGGTTATTCGGCGGGCTGGA ----- GGCGGGGGAAGTTATC CAGCGGCCAGCTAAT 44.72%

ATGTCGTTCTGTGGCAGGGGTTATTCGGCGGGCTGGA ----- GCGGCGGGGGAAGTTATCCAGCGGCCAGCTAAT 44.63%

Cleavage site PAM

Guide 2

Nucleotide percentage

ATGTCGTTCTGTGGCAGGGGTTATTCGGCGGGCTGGACGAGACAGTGGTGAACCGCA --- GGCGGGGGAAGTTATCCAGCGGCCAGCTAAT 43.78%

ATGTCGTTCTGTGGCAGGGGTTATTCGGCGGGCTGGACGAGACAGTGGTGAACCGCA --- CGGCGGGGGAAGTTATCCAGCGGCCAGCTAAT 43.70%

Guide 3

Nucleotide percentage

ATGTCGTTCTGTGGCAGGGGTT ----- GGTGAACCGCATCGCGGCGGGGGAAGTTATCCAGCGGCCAGCTAAT 44.34%

ATGTCGTTCTGTGGCAGGGGTTATT ----- GGTGAACCGCATCGCGGCGGGGGAAGTTATCCAGCGGCCAGCTAAT 44.27%

*Transcribed  
sequence*

atgtcgttcgtggcaggggttattcggcggctggacgagacagtggatgaaccgcatcg  
cggcgggggaagttatccagcggccagctaatactatcaaagagatgattgagaactg



Translation

*Protein profile*

**MSFVAGVIRRLDET**VVNR**IAAGEVIQRPANA**IK**EM**IEN

Altered protein profile

G123C4

Guide 1 :

**MSFVAGVIRRLDSGQL**MLSKR

Guide 2 :

**MSFVAGVIRRLDET**VVNR**TNAIKEM**IEN

Guide 3 :

**MSFVAGVIGEPH**RGGSYPAA**S**

G123C6

Guide 1 :

**MSFVAGVIRRL**EAGEVIQRPANA**IKEM**IEN

Guide 2 :

**MSFVAGVIRRLDET**VVNR**RRGKLSSGQL**MLSKR

Guide 3 :

**MSFVAGVGEPH**RGGSYPAA**S**

# ***Why is this workshop valuable?***

- Join a revolutionary field
- Enhance laboratory skills
- Open several opportunities
- Networking opportunities
- Assist in further education

# ***Most current research***

A research fellow at Oxford University designed a project to introduce CRISPR into human embryos at two different stages of development.

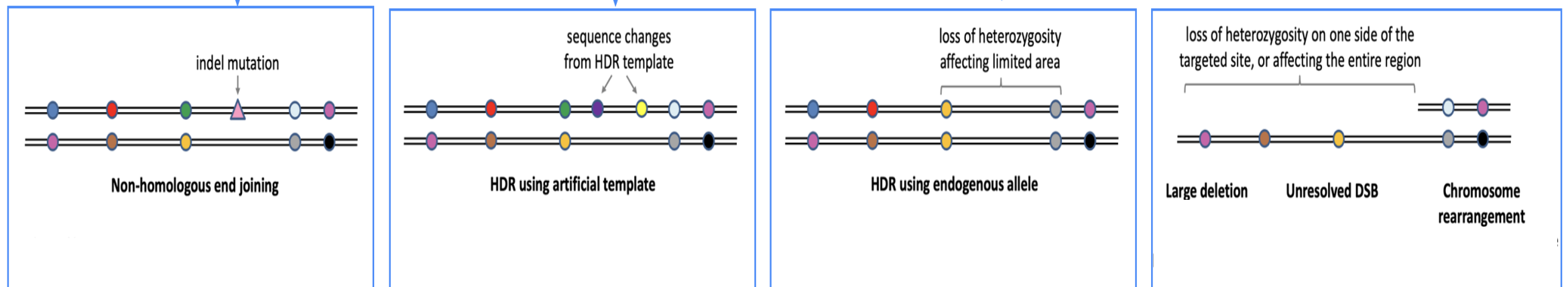
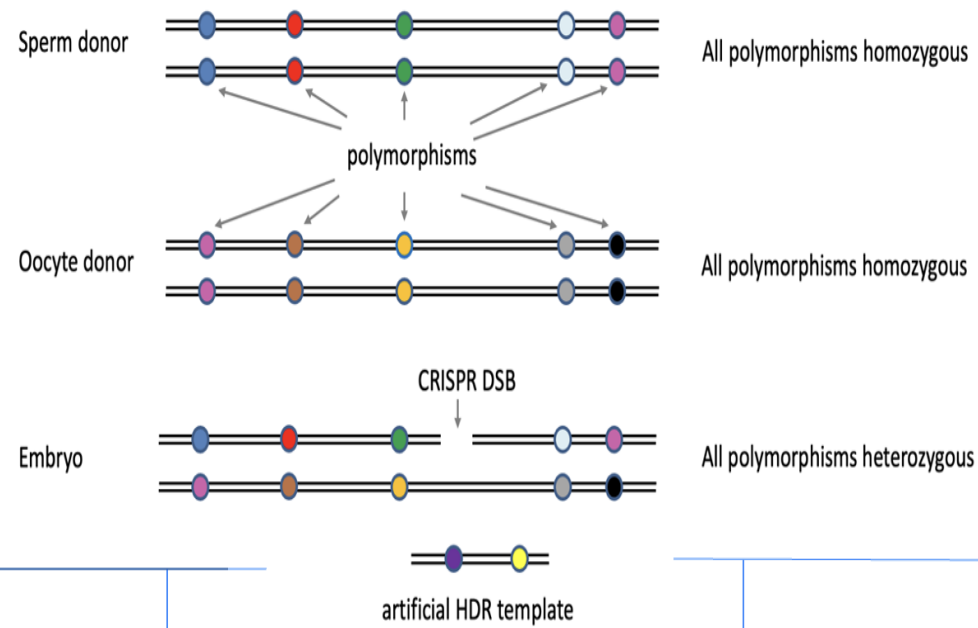


At fertilisation



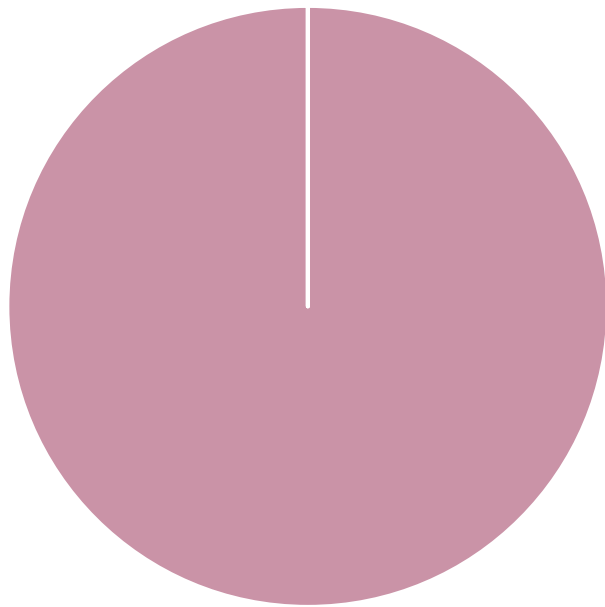
Day 3 embryo





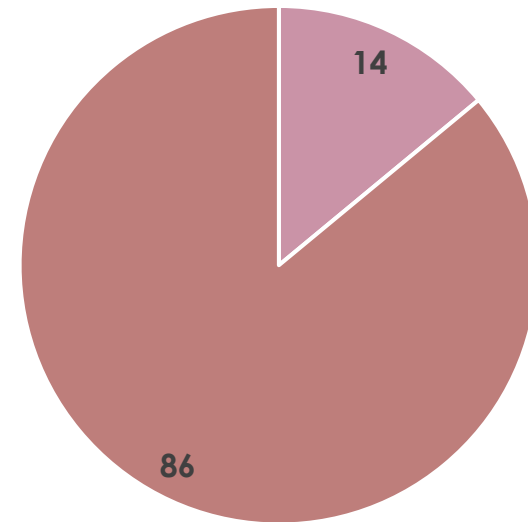
# ***Results***

Editing efficiency of ICSI group



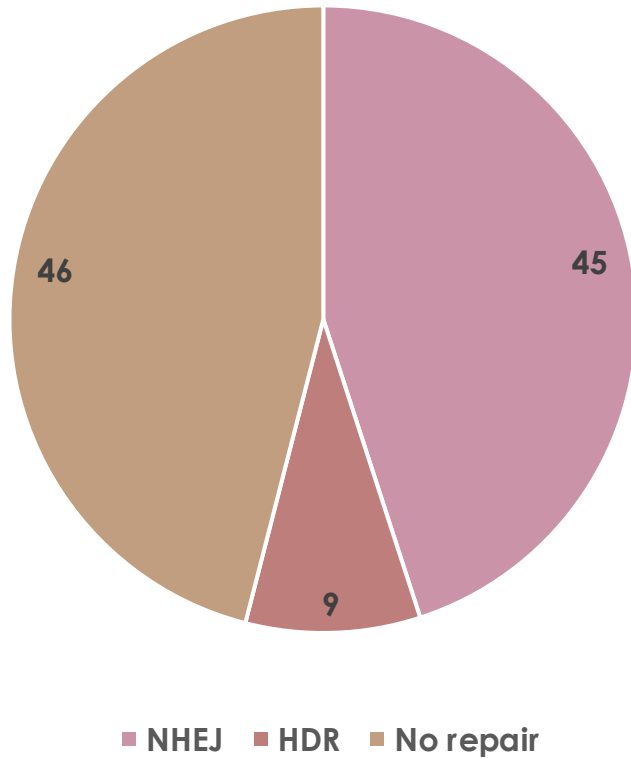
■ Successful ■ unsuccessful

Editing efficiency of cleavage group

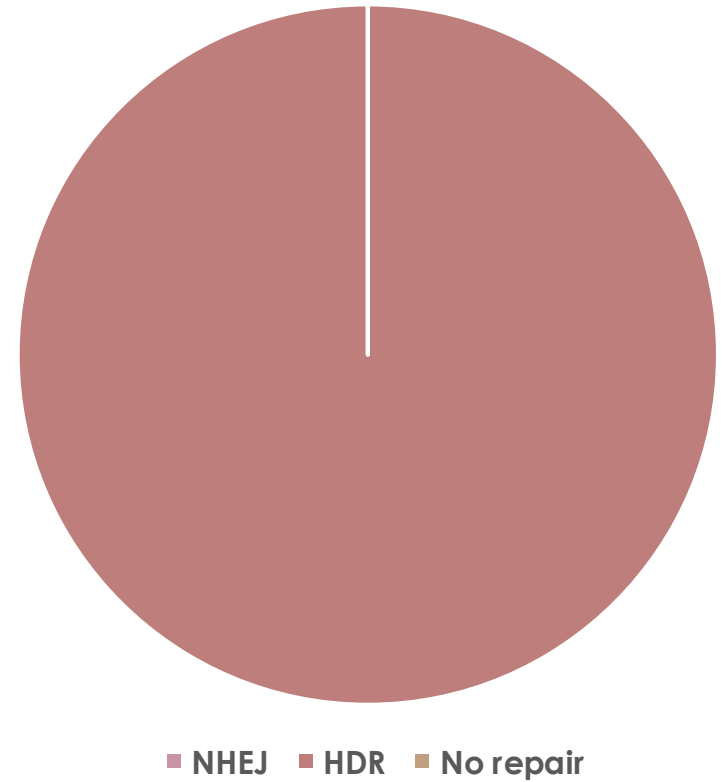


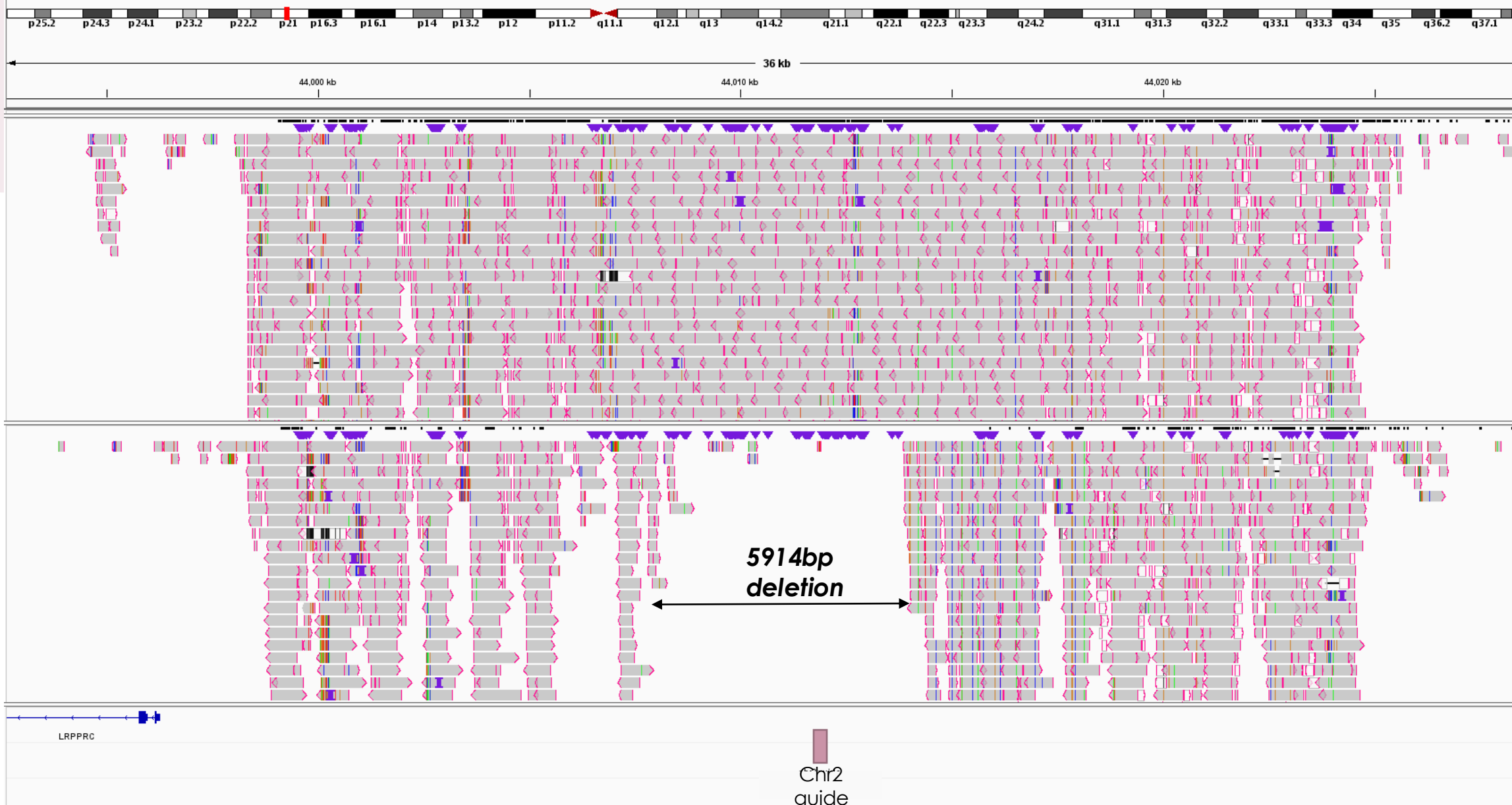
■ Successful ■ unsuccessful

Repair mechanism of ICIS repair group



Repair mechanism of cleavage group







# ***Conclusion***

- Successfully developed a method to detect large deletions.
- Embryos at an early stage have little capacity for DNA repair.
- Embryonic genome activation is crucial.
- HDR most desired but NHEJ is the dominant repair mechanism.