

*Scientific Literature Analysis In Neuroscience*

**EPFL**

# **Methods in Neurobiology**

**BIOENG-451**

Academic year: 2025-2026

Teacher: Prof. Gioele La Manno

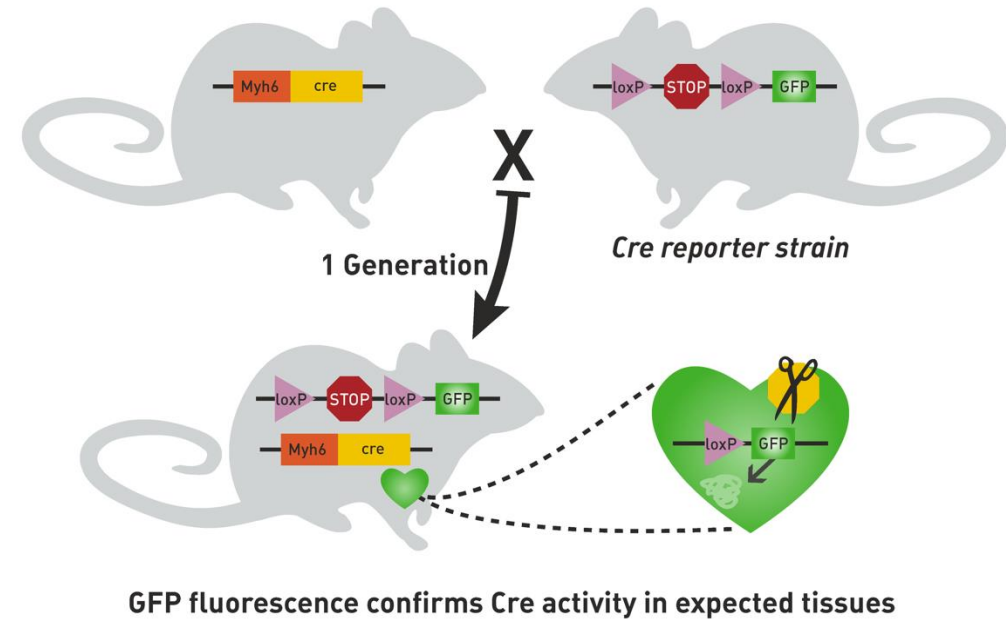
TA: Alessandro Valente

# Genetic Mouse Systems

# Reporter Mice

**Aim:** Visualize gene expression patterns or cellular identities in vivo & live

- Express fluorescent proteins or enzymes under specific promoters
- Allows for labeling of specific cell types or lineages
- Enables live imaging and cell tracking



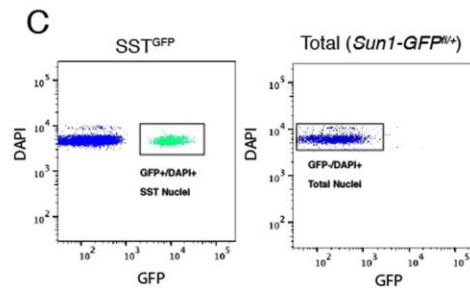
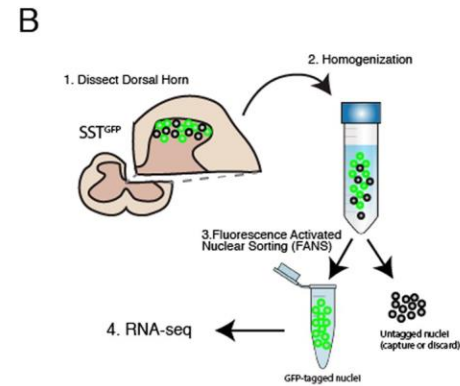
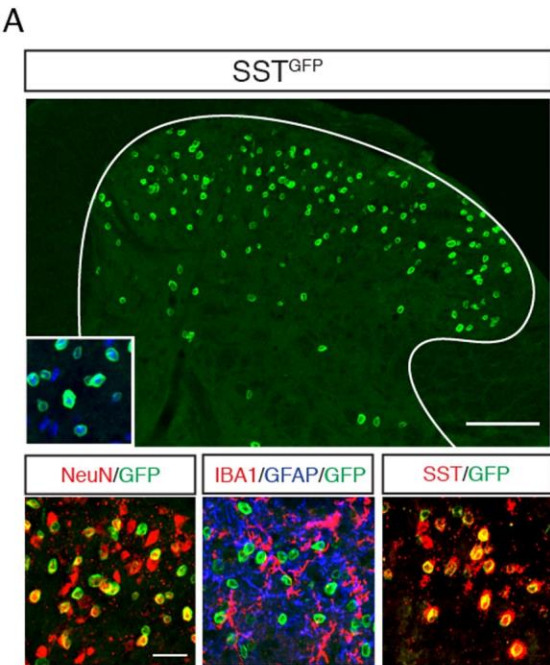
# Reporter Mice

## Controls:

- Comparison with known expression patterns
- Validation with other techniques (e.g., immunostaining)

## Critical points:

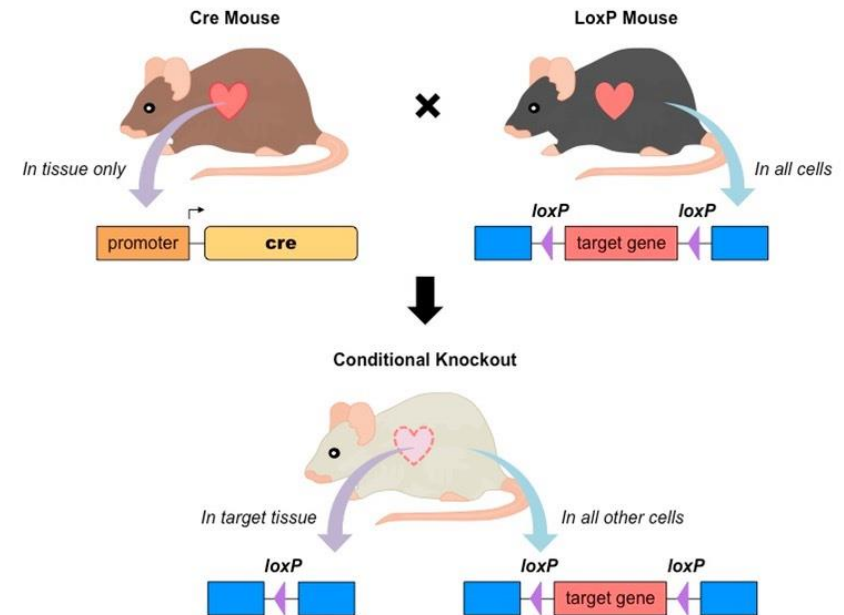
- Fidelity reporter expression / endogenous gene
- Potential interference with normal gene function
- Sensitivity and specificity of the reporter



# Conditional Knockout Mice (Cre-lox System)

**Aim:** Generate tissue-specific or time-specific gene knockouts in mice

- Cre recombinase recognizes loxP sites flanking target gene
- Excises DNA between loxP sites, inactivating the gene
- Cre expression controlled by tissue-specific or inducible promoters
- Results in targeted gene deletion in specific cells or at specific times



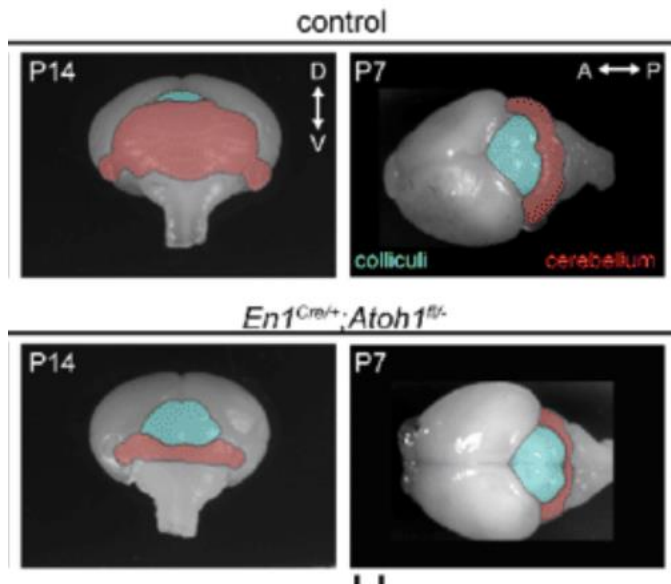
# Conditional Knockout Mice (Cre-Lox System)

## Controls:

- Cre-only and floxed-only controls
- Comparison with wild-type littermates

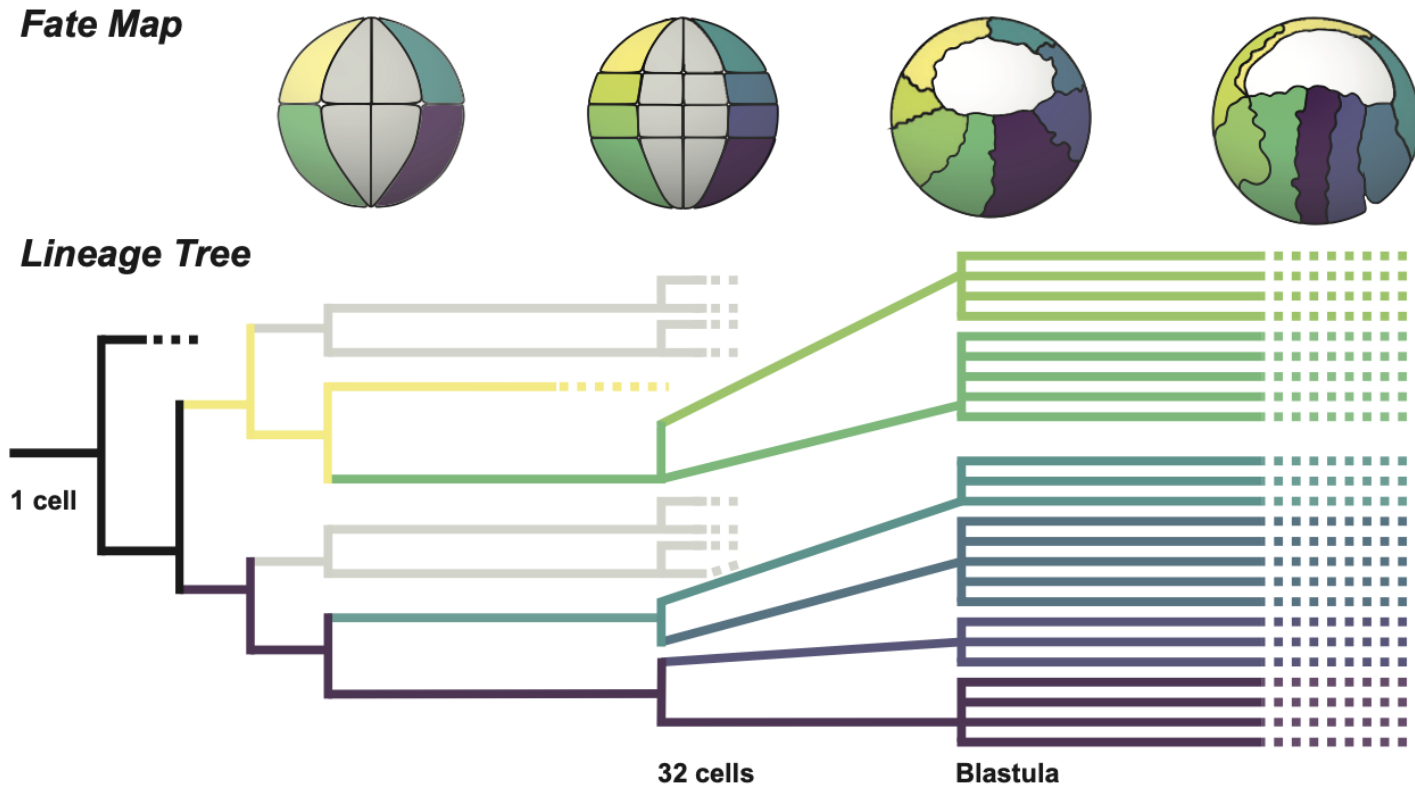
## Critical points:

- Specificity and efficiency of Cre expression
- Potential for unexpected Cre activity
- Importance of confirming gene deletion



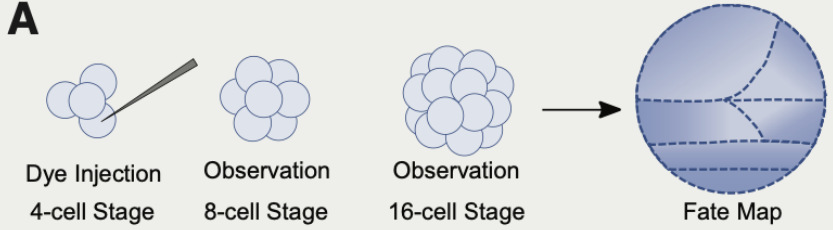
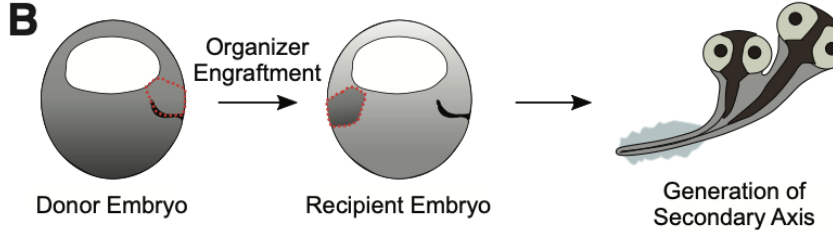
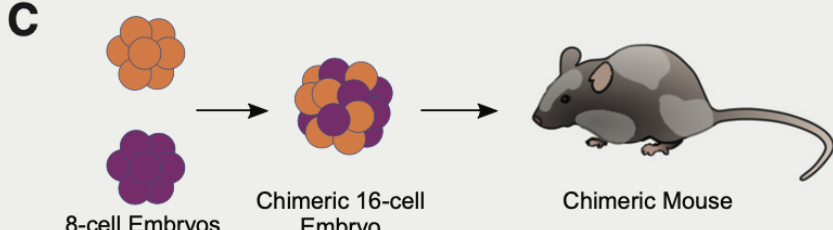
# Developmental Tracing

# Fate Map vs Lineage tree



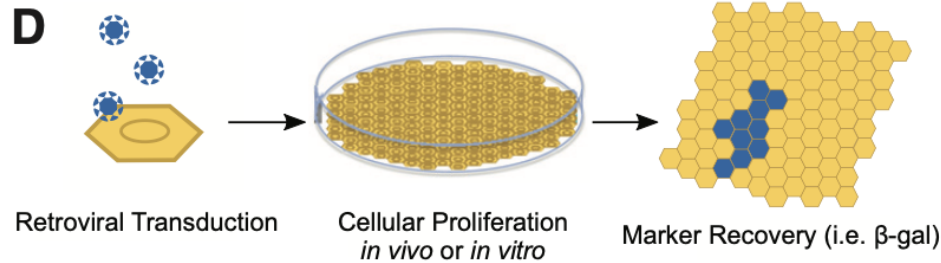
Fate maps are schematics representing the developmental potential of specific cells or regions of cells within an embryo at a defined stage. Upper panels: early *Xenopus* development fate map, retaining cell-cell relationships and position. Lower panels: lineage tracing, the identification of all progeny arising from an individual cell. Each color in the branching tree relates to a region of the corresponding fate map. Dashed lines depict lineages not shown for simplicity.

# Evolution of lineage tracing tech

Era	Year	Lineage Tracing Technique	Resolution	Scalability	Limitation	Technique & Citation
Observational Biology	1890s	<p><b>A</b></p>  <p>Dye Injection 4-cell Stage</p> <p>Observation 8-cell Stage</p> <p>Observation 16-cell Stage</p> <p>Fate Map</p>	Single-cell limited by injection	10s of cells limited by observation	Observational data	<p><b>Dye Injection and Time Lapse</b> Conklin, 1905 Vogt, 1924</p>
	1920-30s	<p><b>B</b></p>  <p>Organizer Engraftment</p> <p>Donor Embryo</p> <p>Recipient Embryo</p> <p>Generation of Secondary Axis</p>	N/A	Tissues	Observational data	<p><b>Organizer Grafts</b> Spemann and Mangold, 1924 Wetzel, 1929</p>
	1960s	<p><b>C</b></p>  <p>8-cell Embryos</p> <p>Chimeric 16-cell Embryo</p> <p>Chimeric Mouse</p>	N/A	Tissues	Only specific to embryo of origin	<p><b>Chimera Generation</b> Tarkowski, 1965 Mintz, 1965</p>

# Molecular Biology

1980s



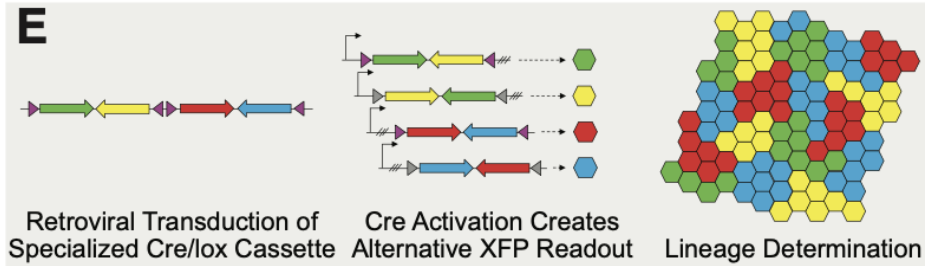
Theoretically single clones

10s of cells limited by observation

Observational data

**Retroviral Labelling**  
Cepko *et al*, 1987

2000s



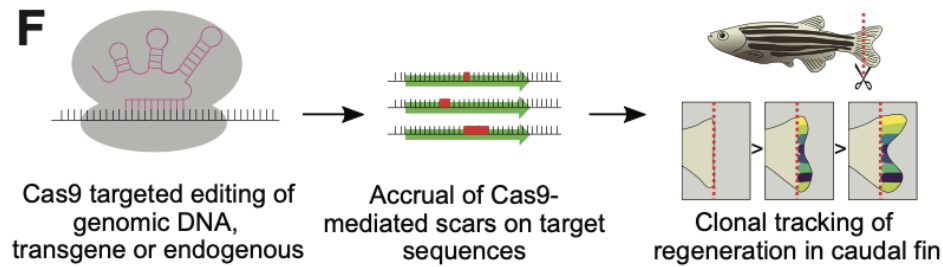
Theoretically single clones

100s of cells limited by observation

Observational data

**Randomized Recombination Cassettes**  
Livet *et al*, 2007  
Snippert *et al*, 2010

2010s



Theoretically single clones

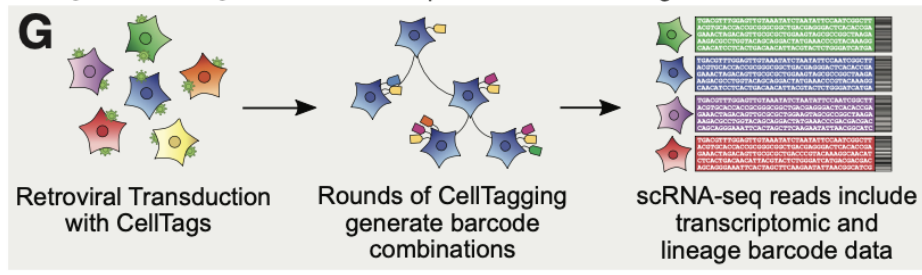
100s of cells limited by observation

Dataset limitation based on collection method

**Cas9 Targeted Scar Accrual**  
McKenna *et al*, 2016  
Junker *et al*, 2017

# Single-cell Biology

2010s-



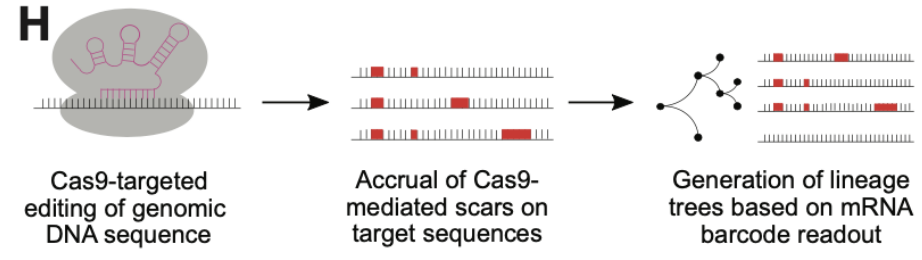
Single-cell

1000s - 10,000s of cells

Resolved to clonal and sub-clonal populations

**Retroviral mRNA Barcode Accrual**  
 Yao *et al*, 2017  
 Bidy *et al*, 2018  
 Weinreb *et al*, 2020

2010s-



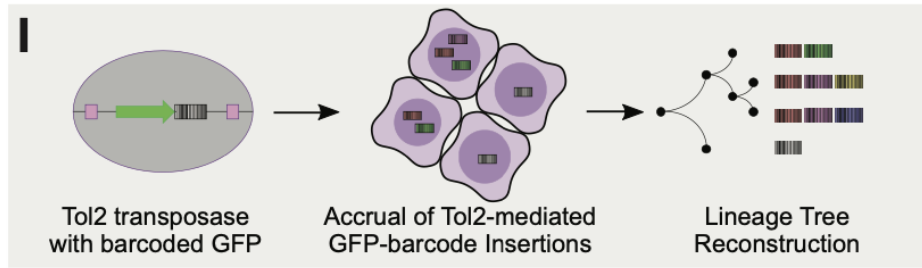
Single-cell

1000s - 10,000s of cells

Information dropout due to Cas9 induced deletion of previous scars

**Cas9 mRNA Scars**  
 Spanjaard *et al*, 2018  
 Raj *et al*, 2018  
 Chan *et al*, 2019  
 Bowling *et al*, 2020

2010s-



Single-cell

1000s - 10,000s of cells

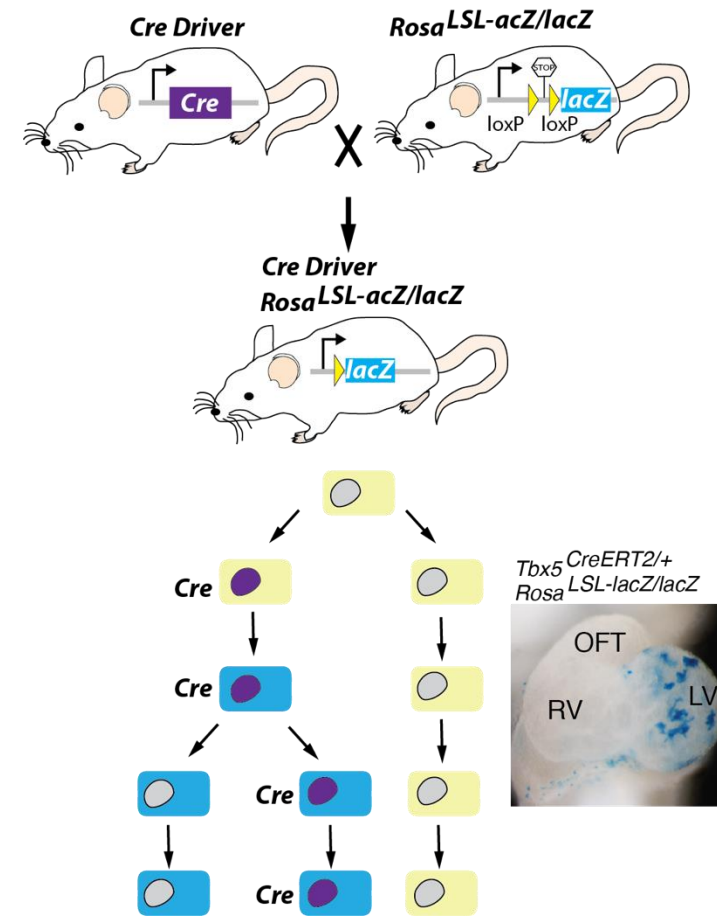
None beyond usual scRNA-seq transgene dropout

**Transposon mRNA Barcode Accrual**  
 Wagner *et al*, 2019

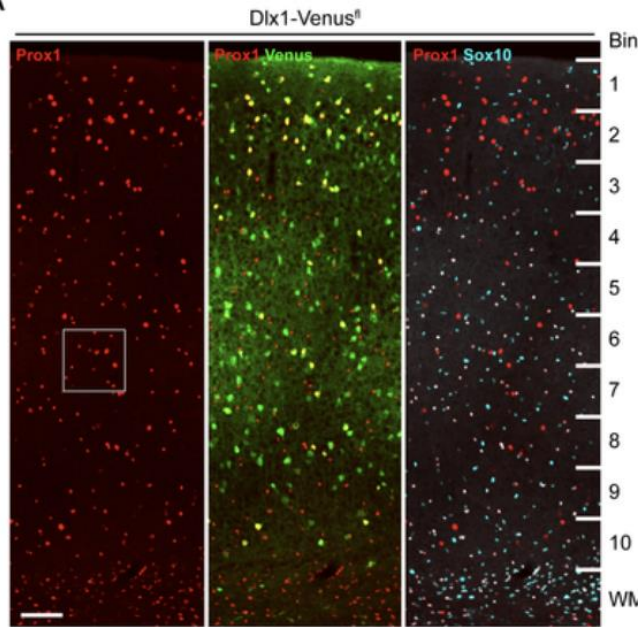
# Inducible Lineage Tracing (CreERT2-loxP System)

**Aim:** Achieve highly efficient, temporally controlled labeling and tracking of specific cell populations and their progeny

- Uses CreERT2 (Cre recombinase fused to mutated estrogen receptor) and loxP-flanked reporter
- Tamoxifen administration activates CreERT2
- Induces permanent genetic labeling of target cells and their progeny
- Allows for precise temporal and spatial control of labeling



# Lineage Tracing (Inducible Dox-based Reporters)



## Controls:

- Vehicle-only (no tamoxifen) controls
- Cre-negative; reporter-positive controls

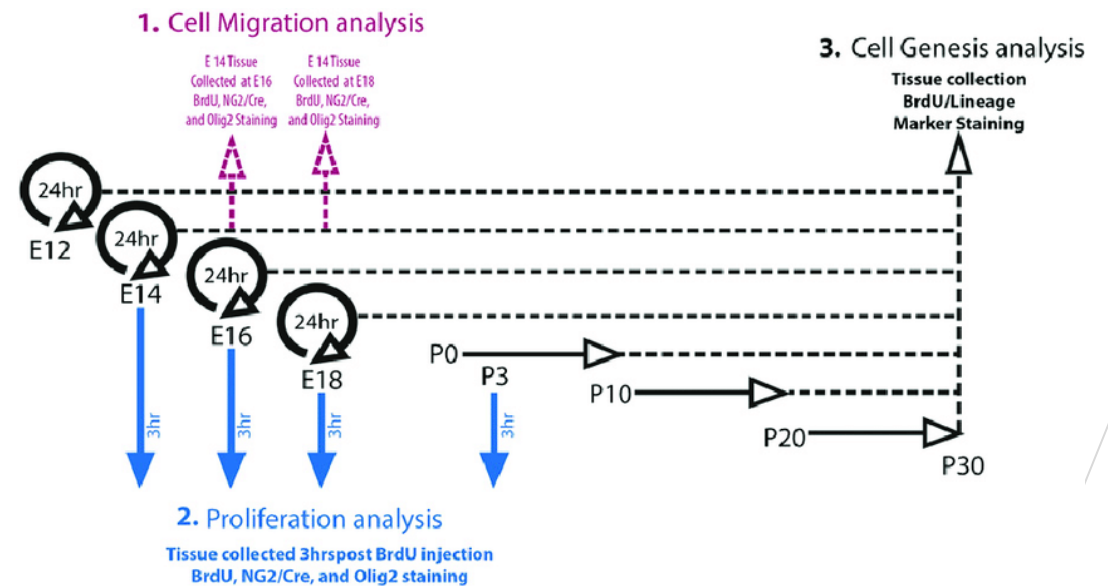
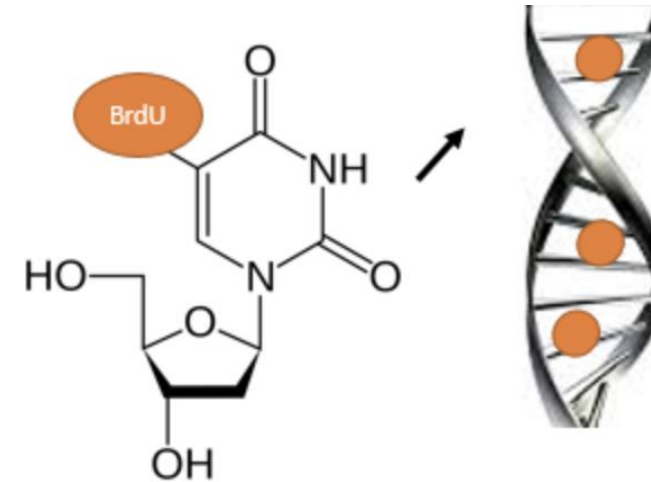
## Critical points:

- Timing, dose, and route of tamoxifen administration
- Background recombination in absence of tamoxifen
- Recombination efficiency and labeling sensitivity

# Birth Dating with EdU/BrdU

**Aim:** Label and track newly born cells in the developing or adult nervous system

- EdU/BrdU are thymidine analogs incorporated into DNA during S-phase
- Pulse-labeling marks cells undergoing division at specific time points
- Detection via immunohistochemistry (BrdU) or click chemistry (EdU)
- Allows determination of cell birth timing and fate



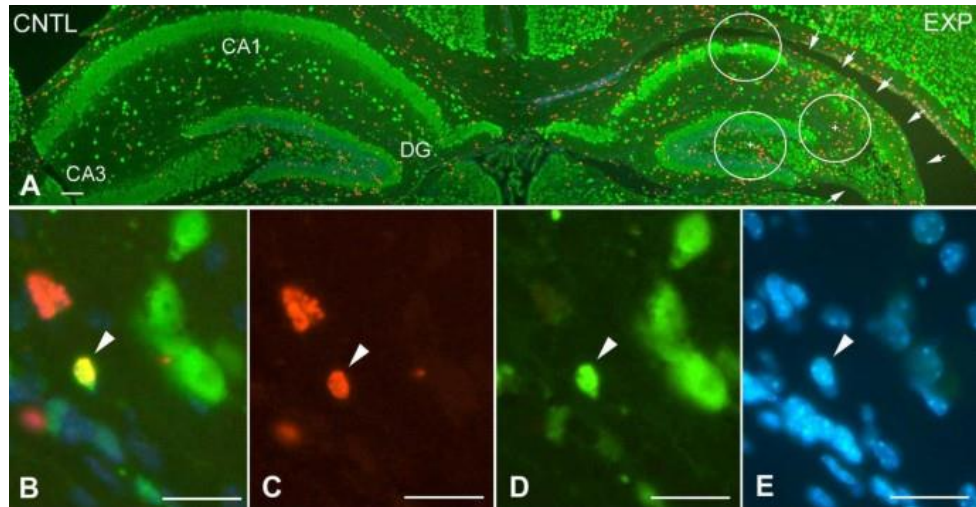
# Birth Dating with EdU/BrdU

## Controls:

- Untreated samples for background
- Known proliferative regions as positive controls

## Critical points:

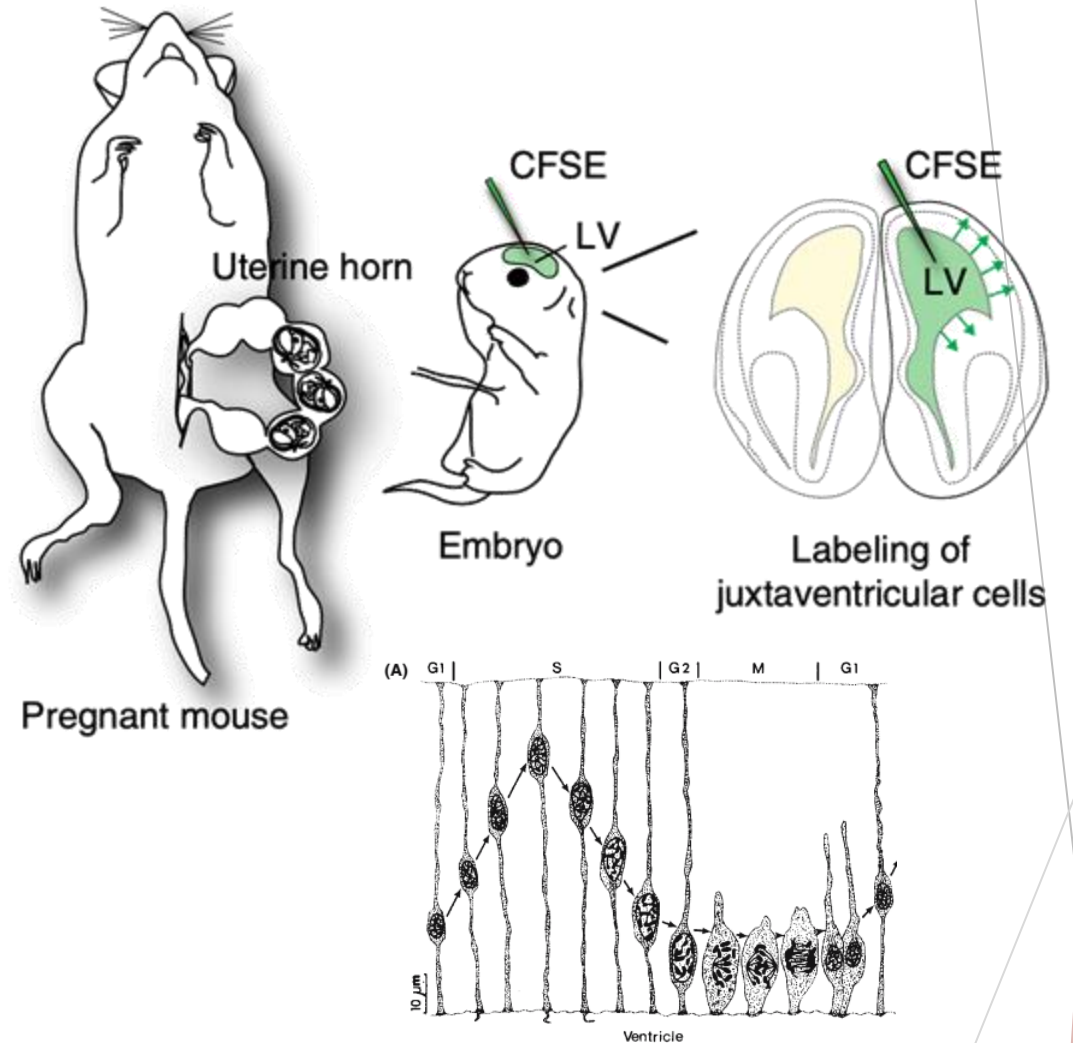
- Toxicity and potential effects on cell cycle
- Dosage and timing of administration
- Sensitivity and specificity of detection methods



# Flash Tag Technique

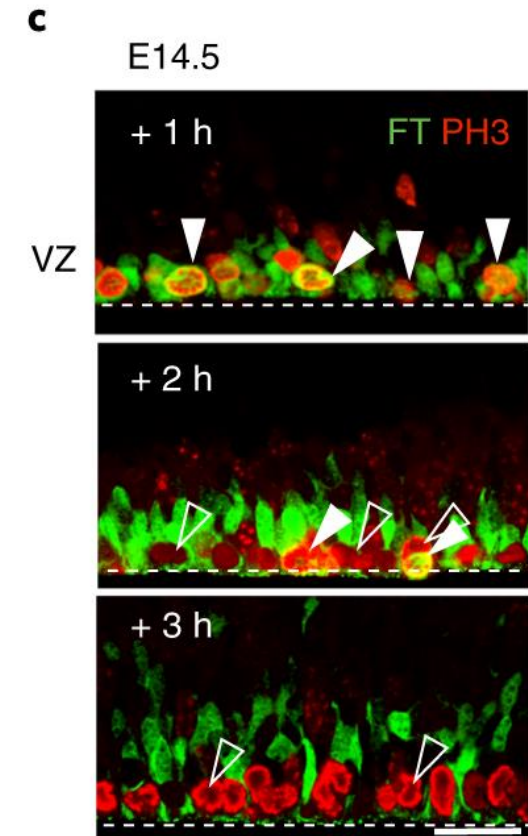
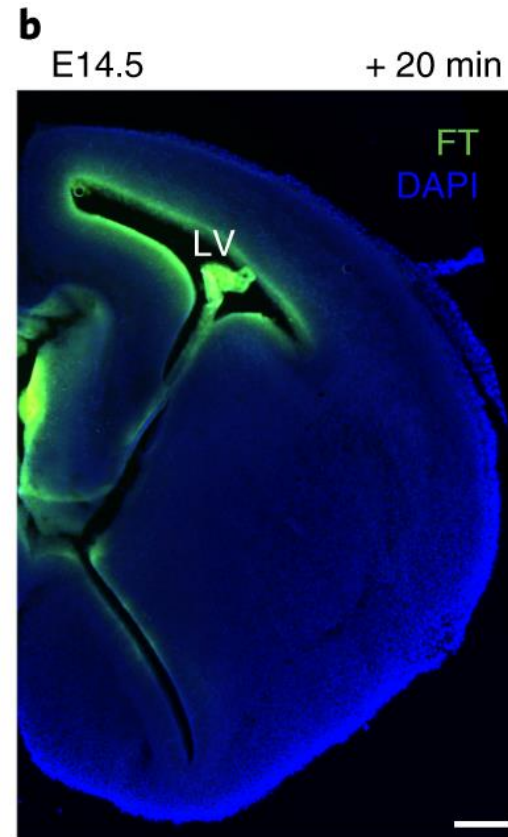
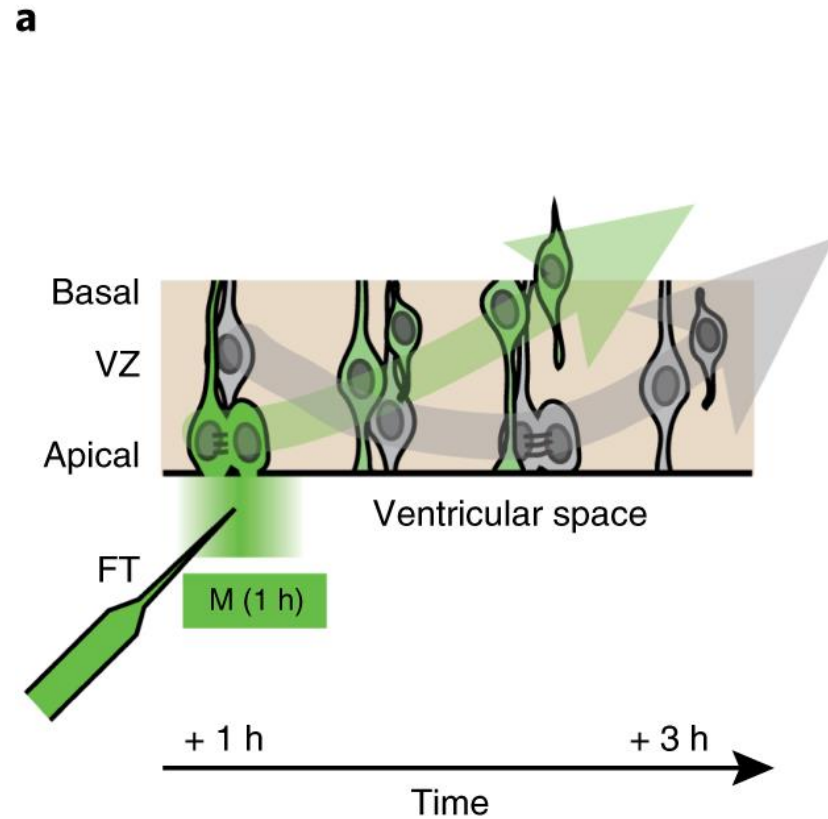
**Aim:** Precisely label and track newborn neurons from the ventricular zone

- Intraventricular injection of fluorescent molecule (e.g., CFSE)
- Rapid uptake by ventricular zone progenitors
- Fluorescence retained in daughter cells
- Allows for high temporal resolution birth dating



# Flash Tag Technique

**Aim:** Precisely label and track newborn neurons from the ventricular zone



# Flash Tag Technique

## Controls:

- Vehicle-only injections
- Comparison with traditional birth dating methods (EdU/BrdU)

## Critical points:

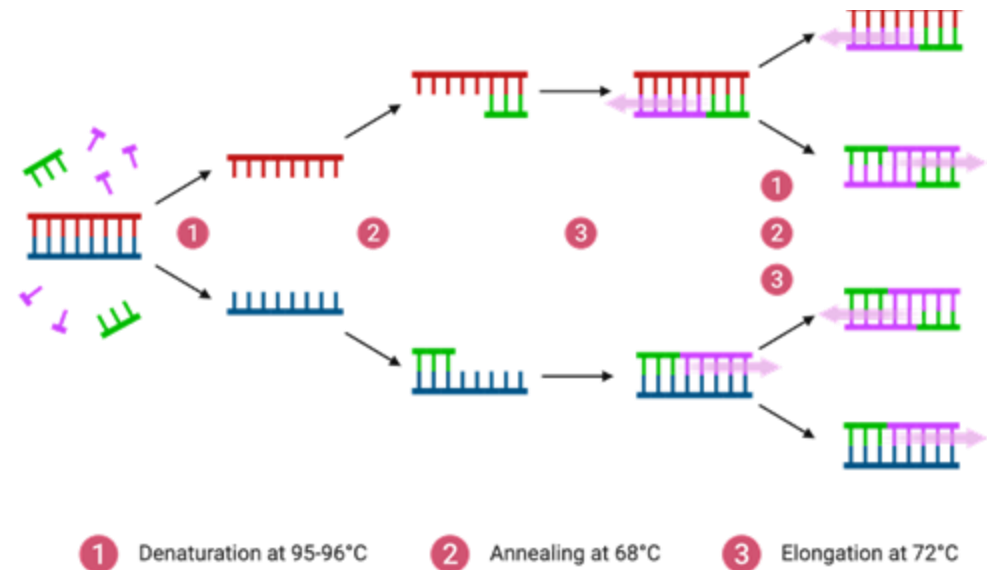
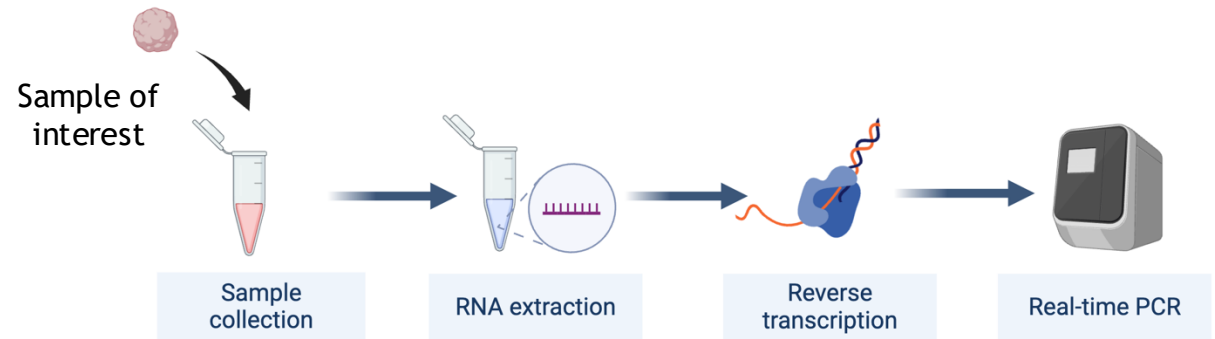
- Injection technique and timing
- Potential for labeling non-dividing cells
- Signal dilution with successive divisions

# Molecular Techniques

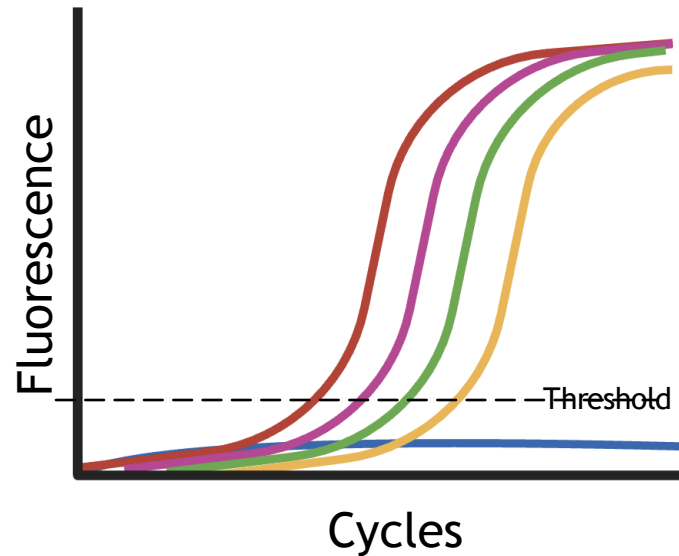
# Quantitative PCR (qPCR)

*Aim: Measure relative or absolute gene expression levels*

- Amplifies and quantifies targeted DNA sequences,
- Uses fluorescent reporters to detect amplification in real-time.
- Cycle threshold (Ct) values indicate relative abundance.



# Quantitative PCR (qPCR)



## Controls:

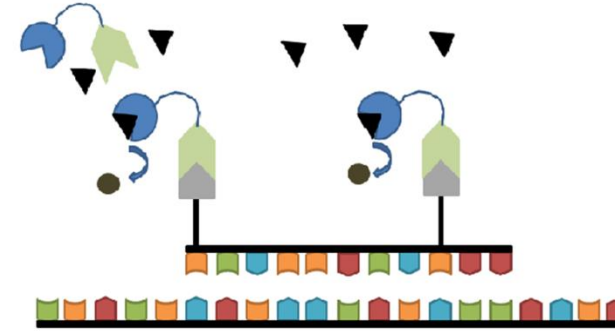
- Housekeeping genes for normalization
- No template control (NTC)

## Critical points:

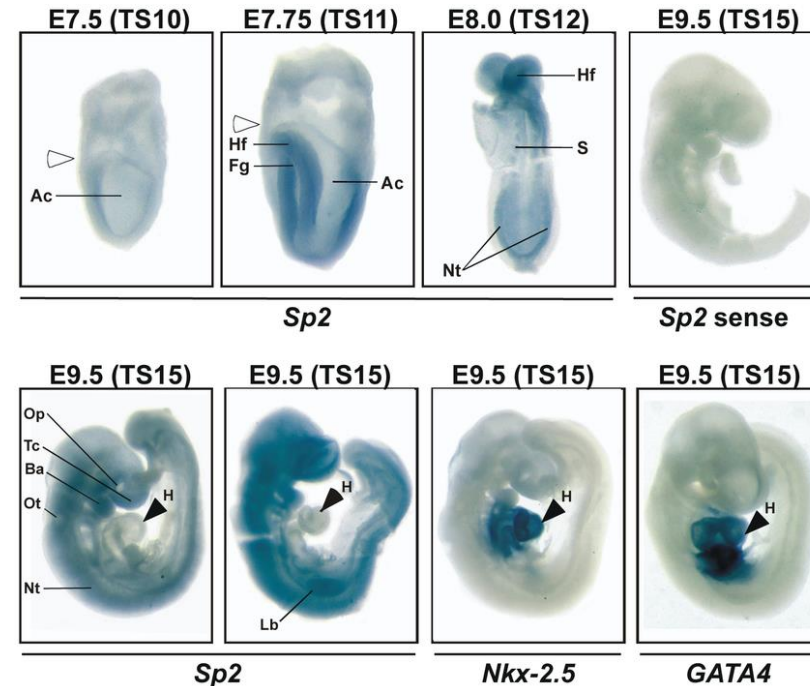
- Primer design and efficiency
- Sample quality and consistency
- Proper data analysis and interpretation

# In Situ Hybridization (ISH)

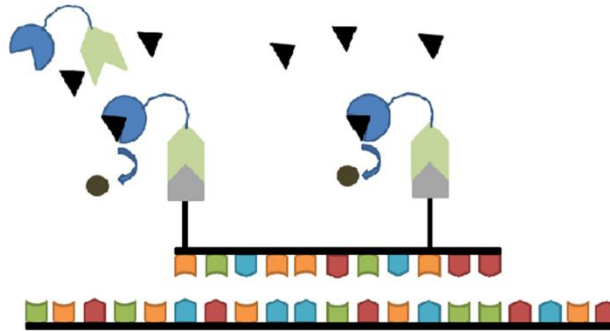
**Aim:** Visualize and localize specific RNA sequences within tissues or cells



- Uses labeled complementary DNA or RNA probes
- Hybridizes to target mRNA in fixed tissue sections
- Colorimetric detection reveals spatial gene expression patterns



# In Situ Hybridization (ISH)



## Controls:

- Sense probe as negative control
- Known expression patterns as positive control

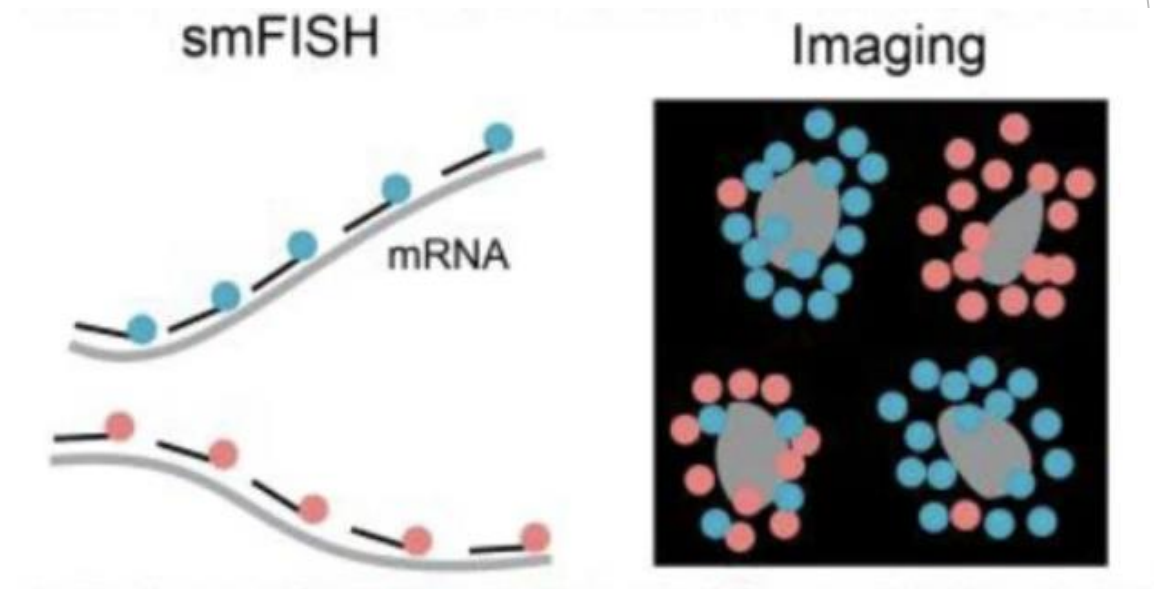
## Critical points:

- Probe specificity and sensitivity
- Tissue fixation and permeabilization
- Signal-to-noise ratio and background

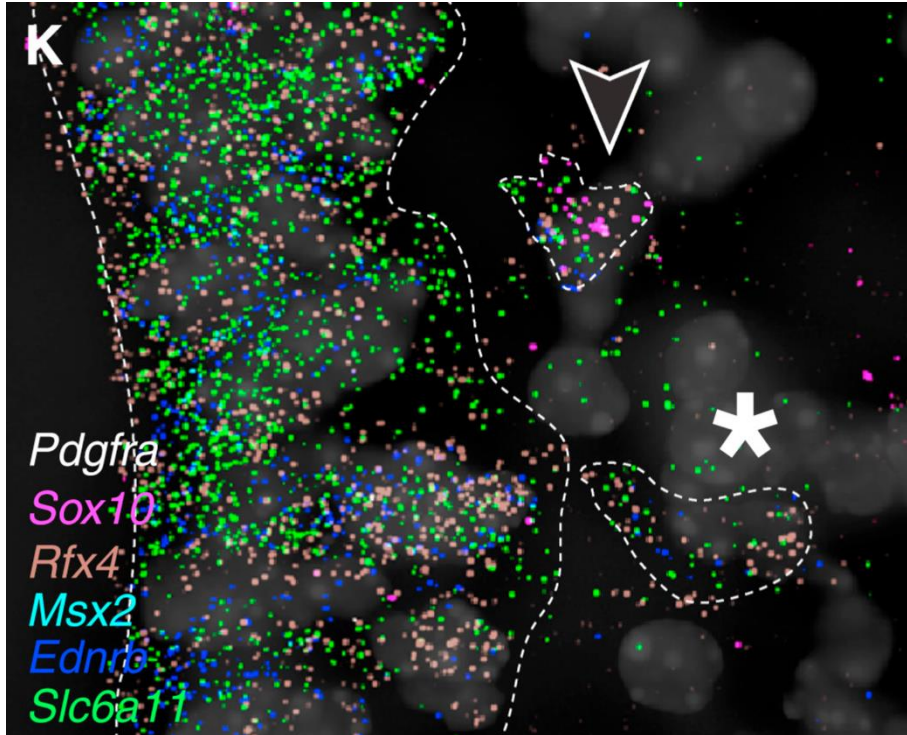
# Quantitative smFISH (single-molecule Fluorescent ISH)

**Aim:** Detect and quantify specific RNA sequences at single-molecule resolution

- Uses fluorescently labeled oligonucleotide probes
- Hybridizes to target mRNA in fixed cells or tissues
- Visualizes individual mRNA molecules as fluorescent dots



# Quantitative FISH (Fluorescent In Situ Hybridization)



## Controls:

- Negative control probes
- Positive control for known abundant transcripts

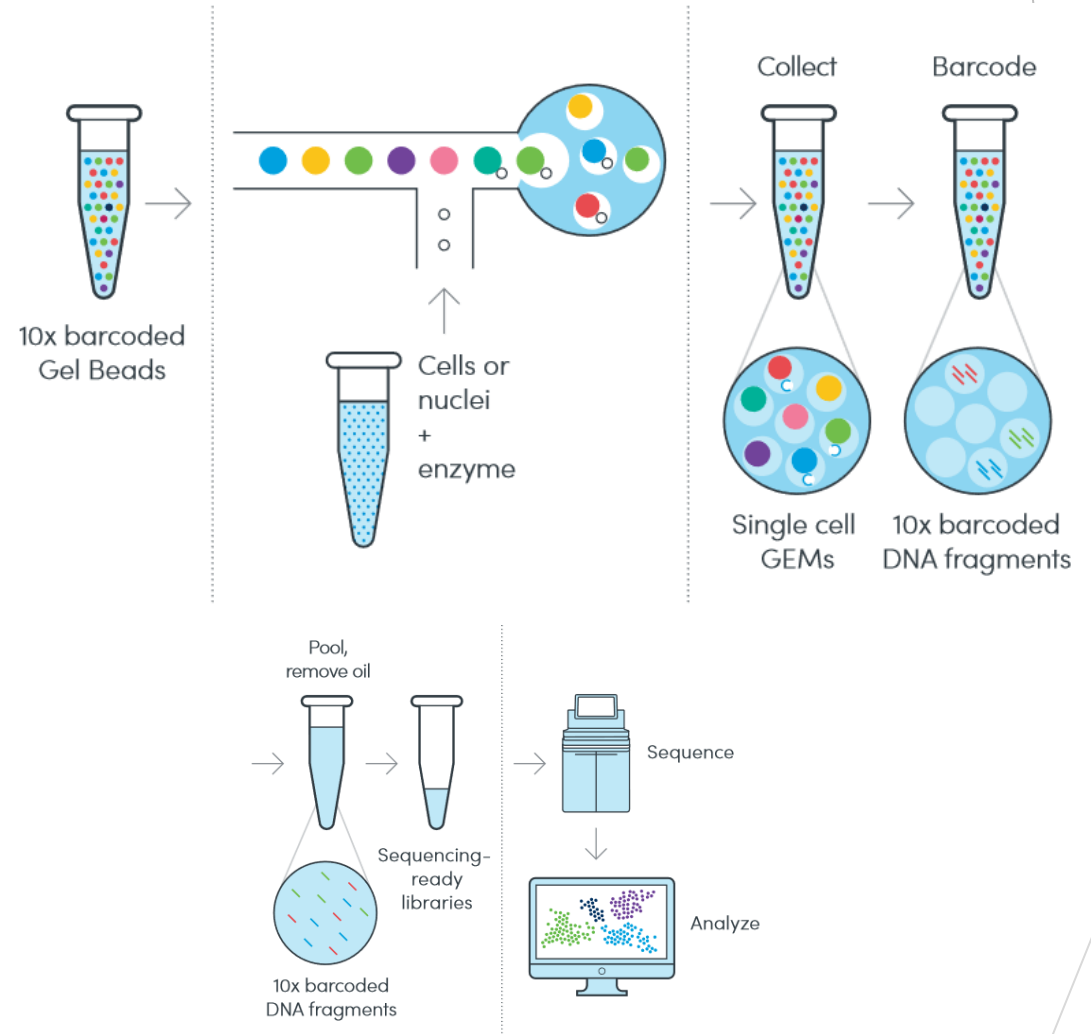
## Critical points:

- Probe design and specificity
- Image acquisition and analysis parameters
- Thresholding and spot counting algorithms

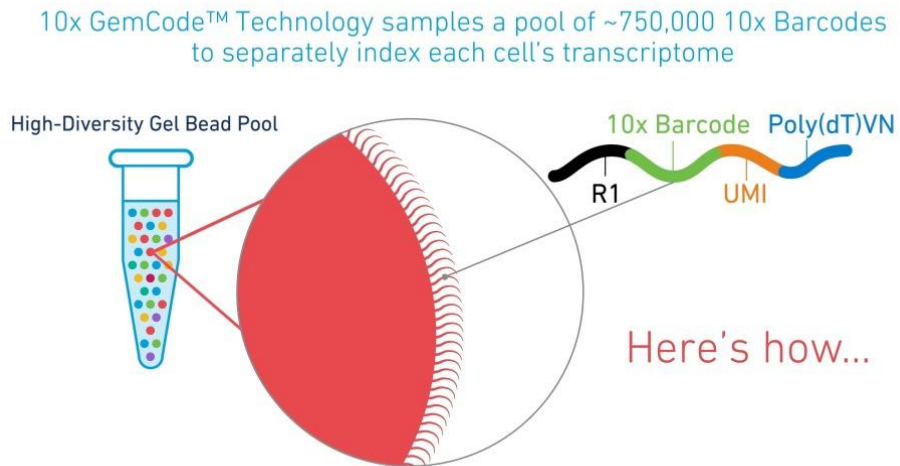
# Single-cell RNA Sequencing (scRNA-seq)

Aim: Profile gene expression at individual cell resolution

- Isolates individual cells
- Captures and amplifies mRNA from each cell
- Sequences and quantifies transcripts
- Computational analysis for cell clustering and gene expression patterns



# Single-cell RNA Sequencing (scRNA-seq)



## Controls:

- Spike-in controls for technical variability
- Cell type-specific markers for validation

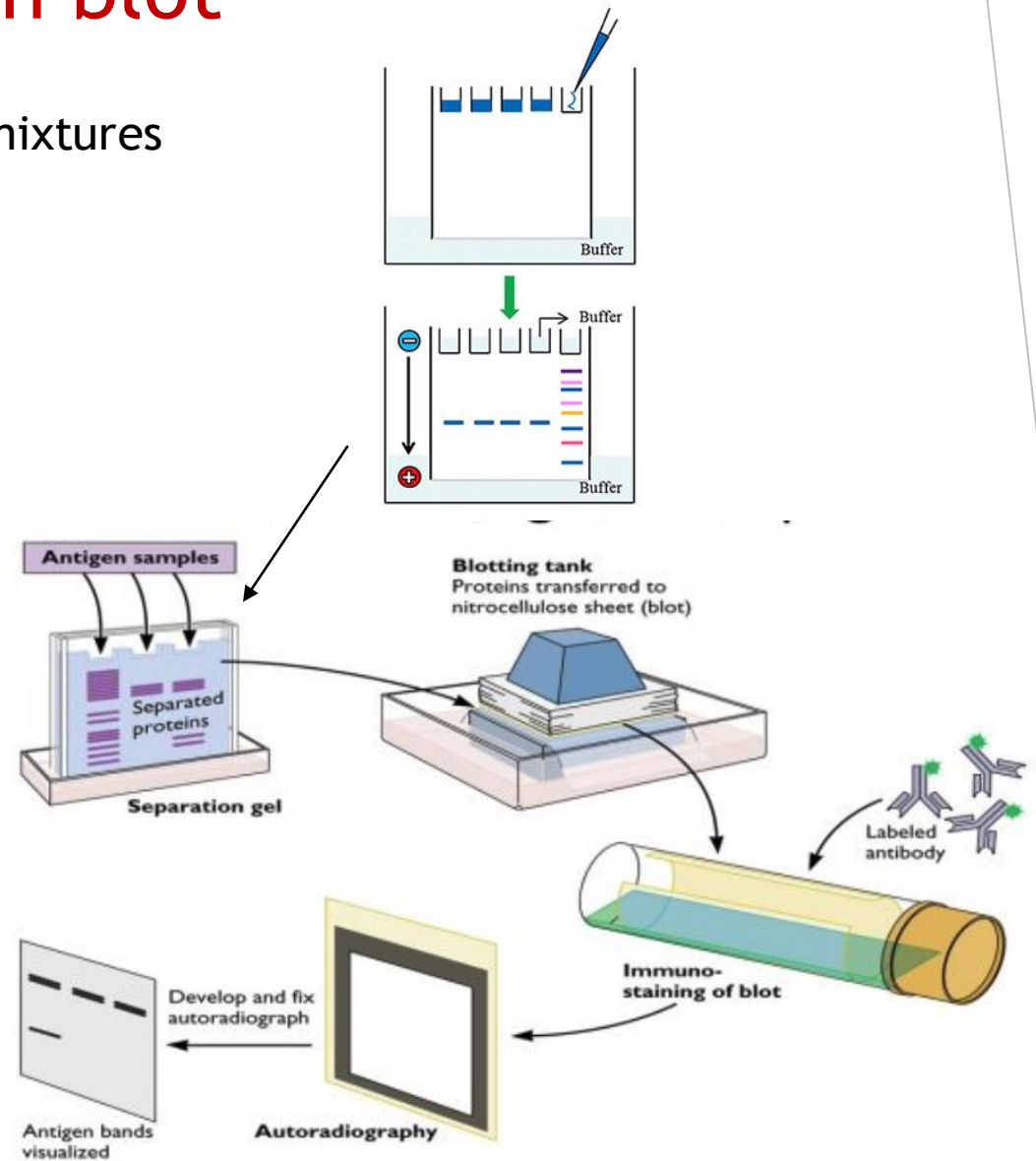
## Critical points:

- Cell dissociation and viability
- Dropout events and technical noise
- Batch effects and data normalization

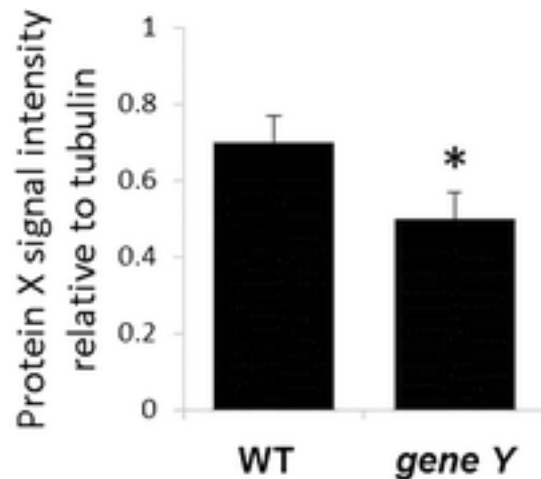
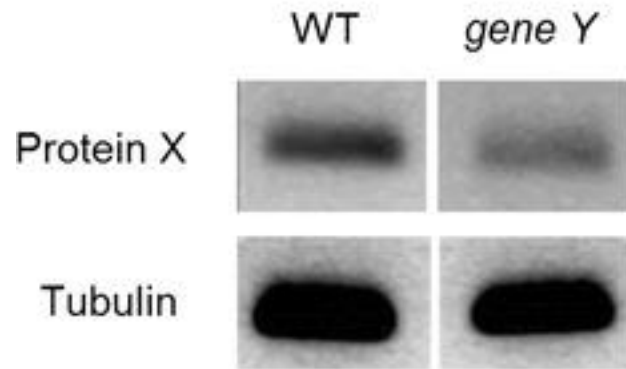
# Western blot

**Aim:** Detect and quantify specific proteins in complex mixtures

- Separates proteins by size using gel electrophoresis.
- Transfers proteins to a membrane.
- Detects target proteins using specific antibodies.
- Visualizes using chemiluminescence or fluorescence.



# Western blot



## Controls:

- Loading control (e.g., housekeeping proteins)
- Positive and negative controls for antibody specificity

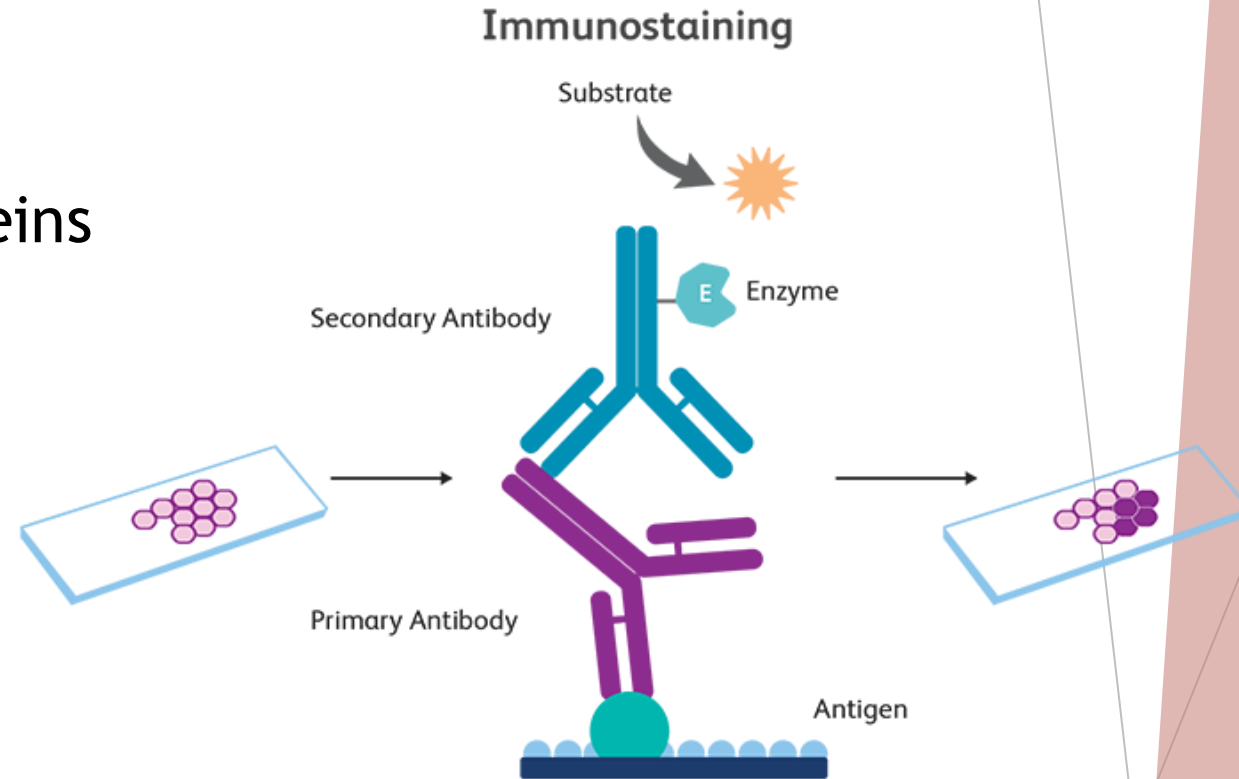
## Critical points:

- Antibody specificity and validation
- Proper normalization for quantification
- Linear range of detection

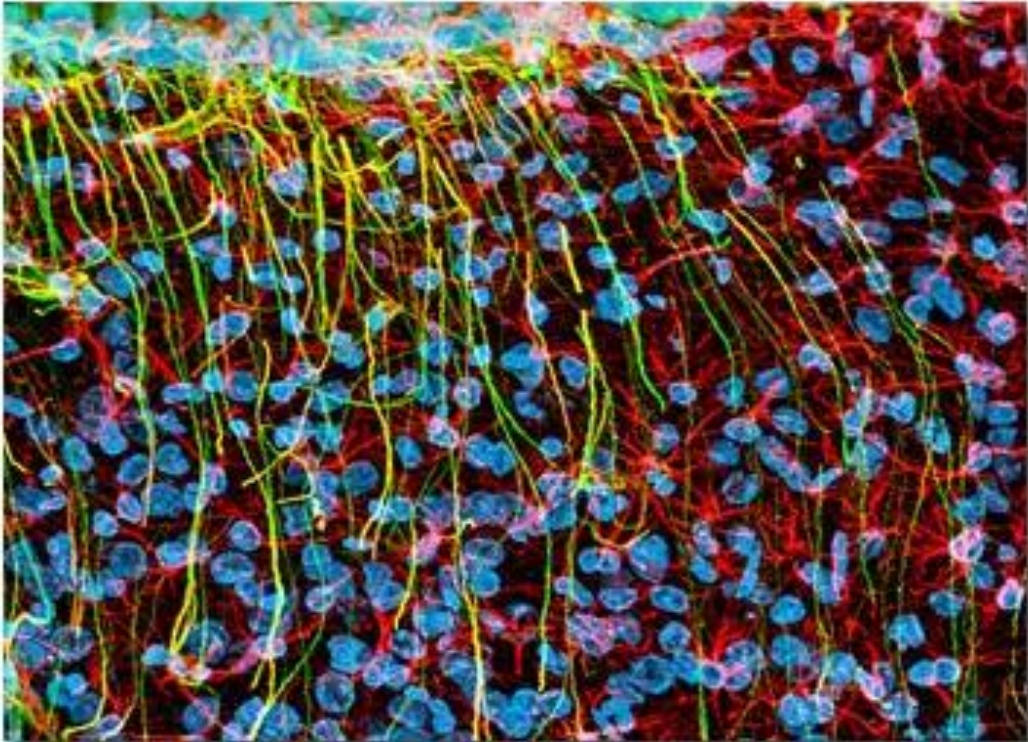
# Immunostaining

**Aim:** Visualize and localize specific proteins within cells or tissues

- Uses antibodies to detect target proteins
- Primary antibody binds to protein of interest
- Secondary antibody (labeled) binds to primary antibody
- Fluorescent (or chromogenic) detection



# Immunostaining



## Controls:

- Negative control (no primary antibody)
- Positive control (known expression pattern)

## Critical points:

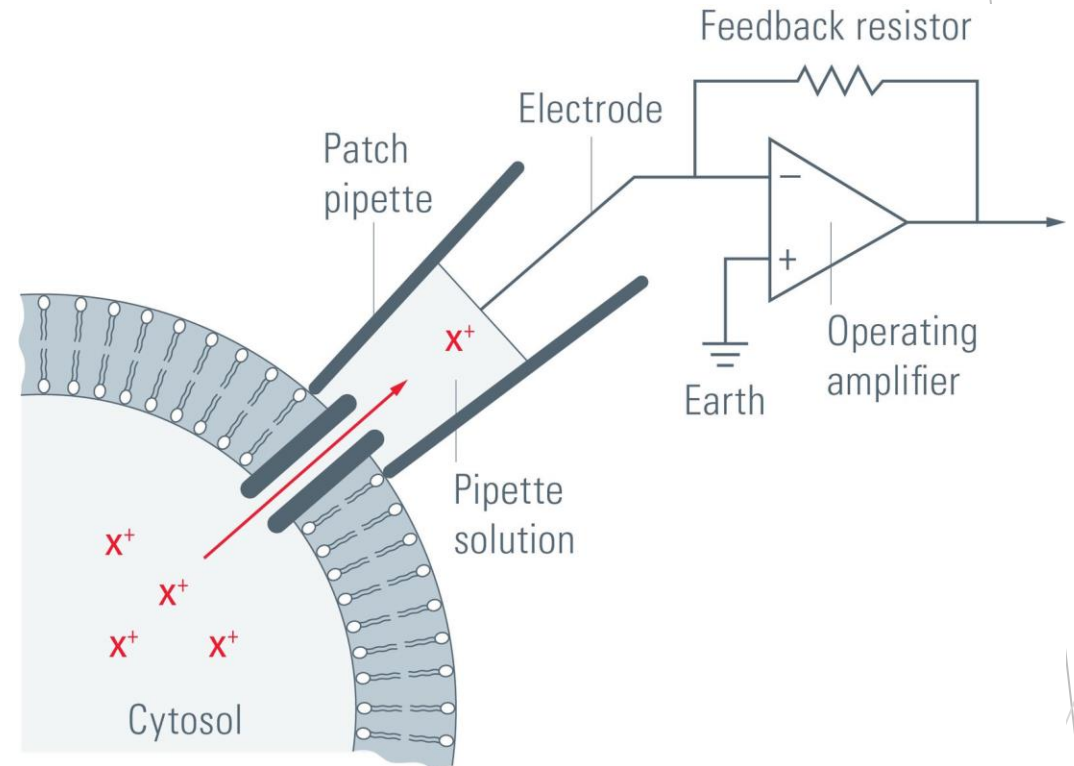
- Antibody specificity and validation
- Fixation and permeabilization methods
- Autofluorescence and background signal

# Neuronal activity

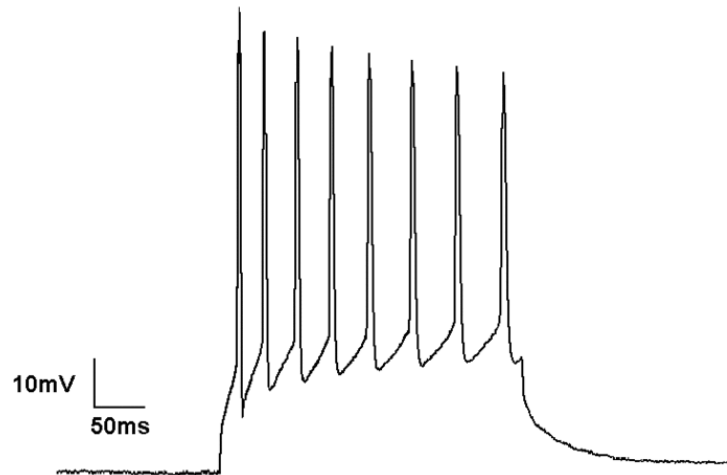
# Patch Clamp Electrophysiology

**Aim:** Measure electrical activity and membrane properties of individual neurons

- Forms tight seal between pipette and cell membrane
- Records current flow through ion channels
- Allows manipulation of intracellular environment
- Provides high-resolution temporal data on neuronal activity



# Patch Clamp Electrophysiology



## Controls:

- Known ion channel blockers or activators
- Comparison with model cell parameters

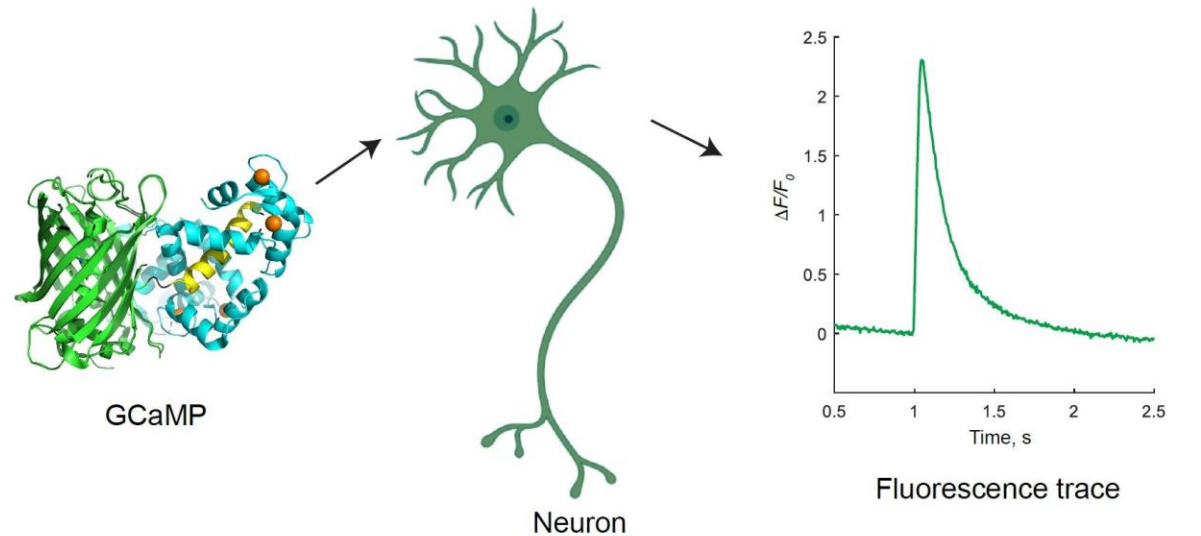
## Critical points:

- Cell health and viability during recording
- Series resistance and capacitance compensation
- Liquid junction potential correction

# Calcium Imaging with GCaMP

Aim: Visualize neuronal activity through calcium-dependent fluorescence changes

- GCaMP: Genetically encoded calcium indicator
- Binds to  $\text{Ca}^{2+}$  upon neuronal firing
- Increases fluorescence intensity
- Optical imaging captures activity patterns



# Calcium Imaging with GCaMP

## Controls:

- Calibration with known stimuli
- Comparison with electrophysiological recordings

## Critical points:

- Temporal resolution and calcium dynamics
- Potential interference with cellular calcium homeostasis
- Relationship between fluorescence and spike rate

