



# **Analysis of pediatric astrocytoma transcriptome at a tumor and cellular level**

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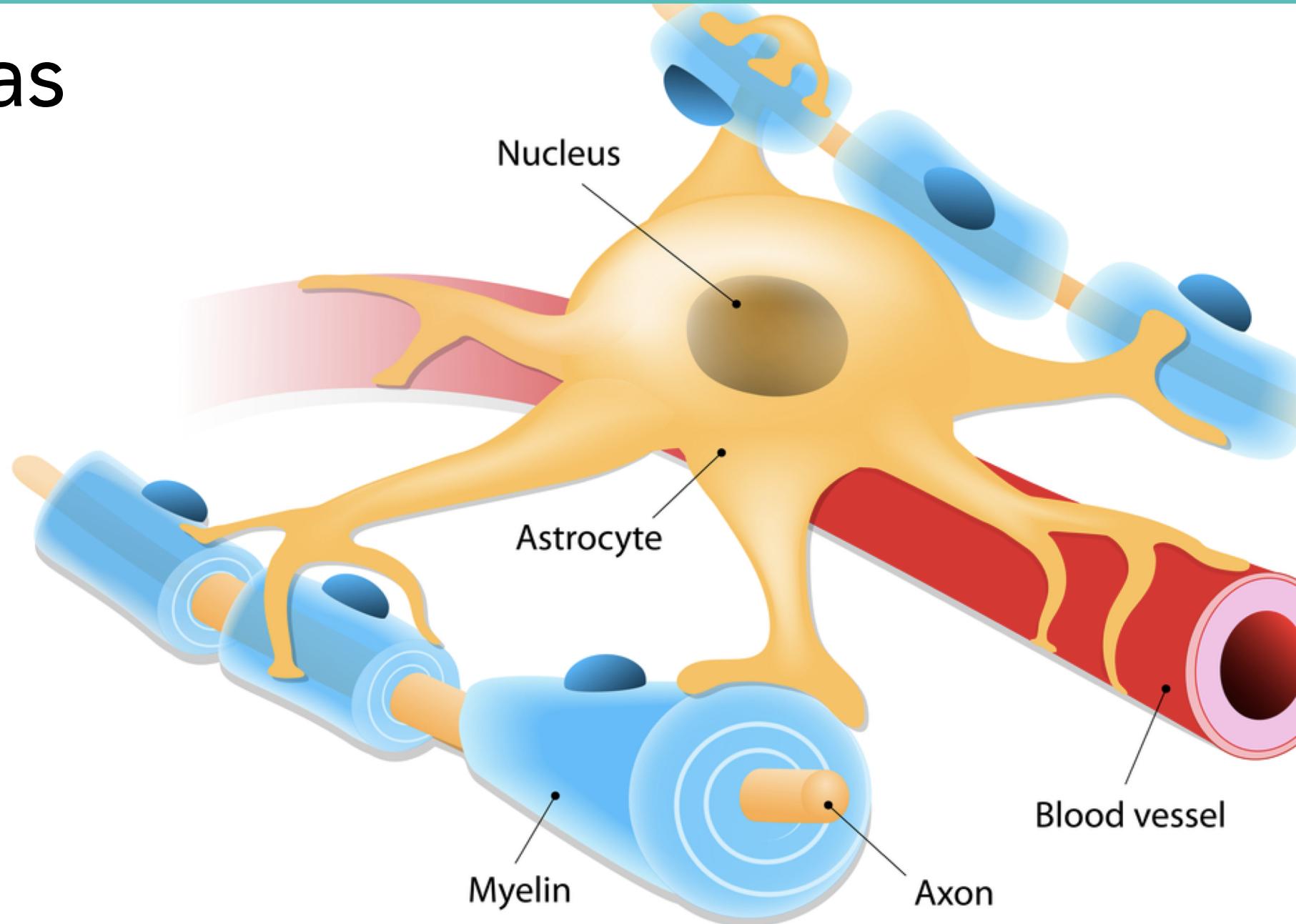
Dra. Lorena Aguilar Arnal



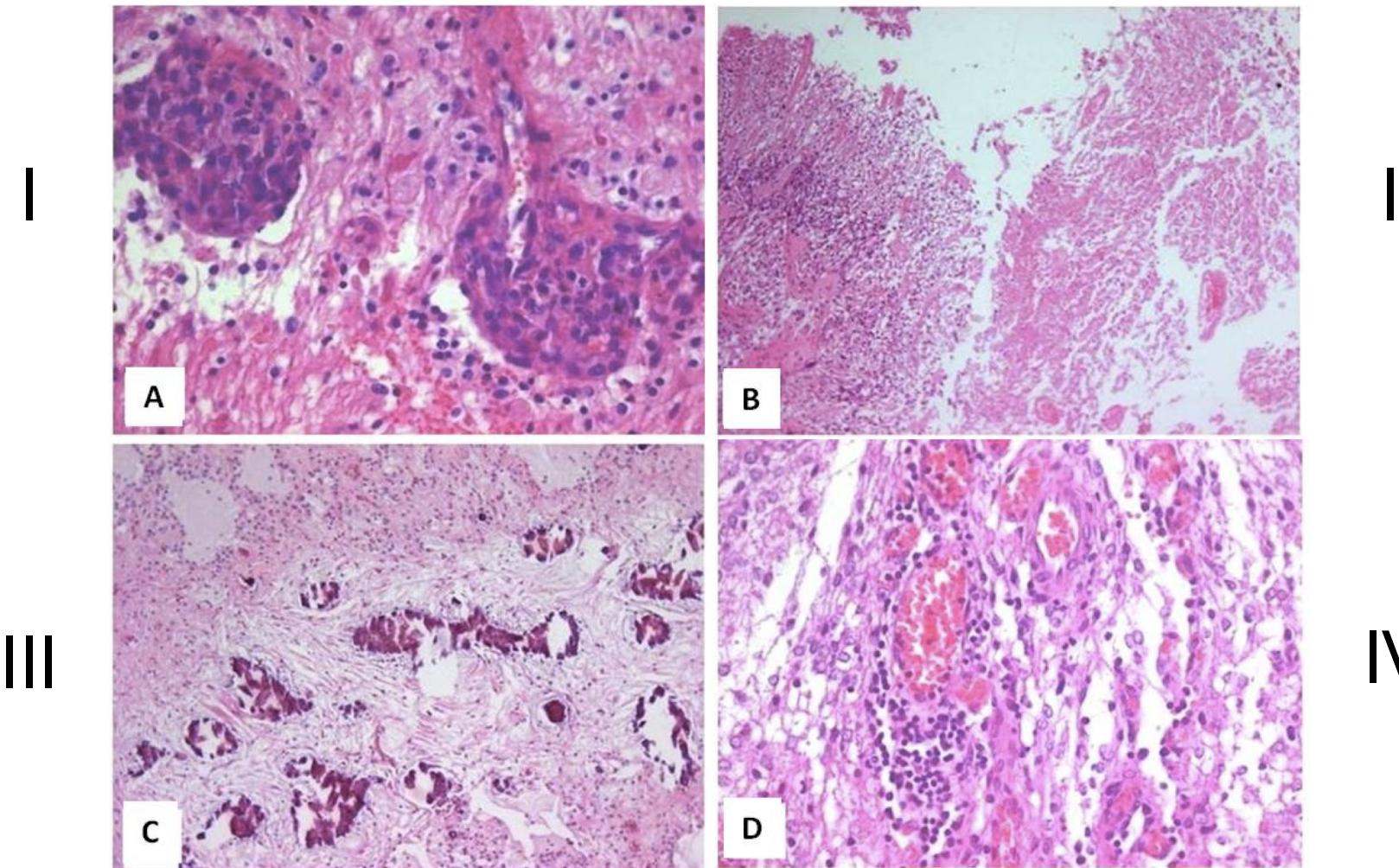
# Astrocytomas

CNS tumors are the most common solid tumors during childhood of humans (Dang & Phillips, 2017)

In Mexico alone, they represent 32% of CNS tumors in infants (Chico-Ponce de León et al., 2006; Eguía-Aguilar et al., 2014).



# Classification



(WHO in Louis et al., 2007)

# Classification

Pediatric astrocytomas were reorganized into two groups (Louis et al., 2016):

1.- Diffuse astrocytomas: Groups anaplastic, diffuse and gliomas astrocytomas according to their recurrent mutations in the IDH1, IDH2 and H3F3A genes.

IDH 1/2

H3F3A

2.- Other astrocytomas: Those astrocytomas with a more restricted growth pattern and absence of the aforementioned recurrent mutations.

WT

(WHO in Louis et al., 2016)

Not common in children

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IDH 1/2

No surgery in Mexico

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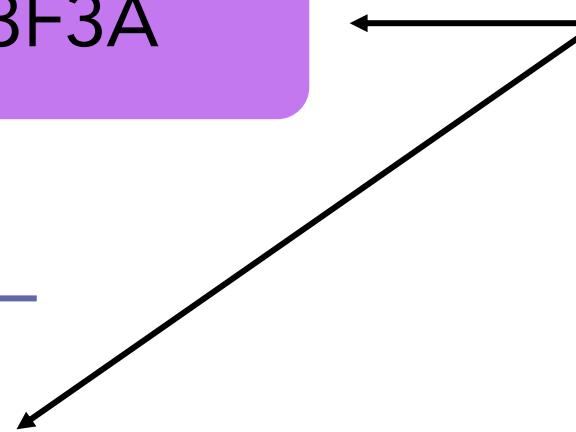
H3F3A

Most common

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WT

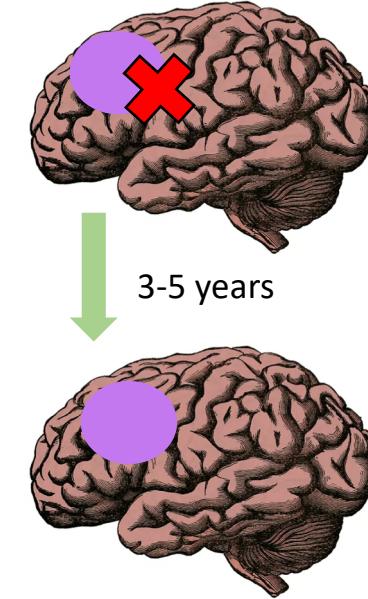
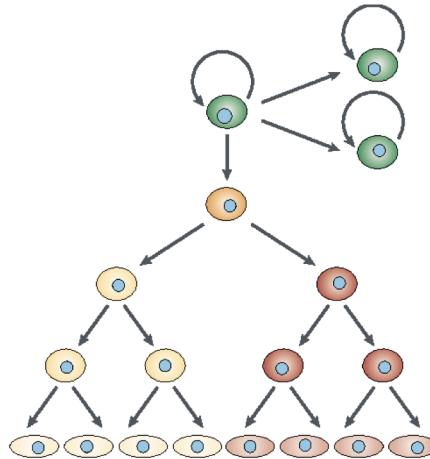
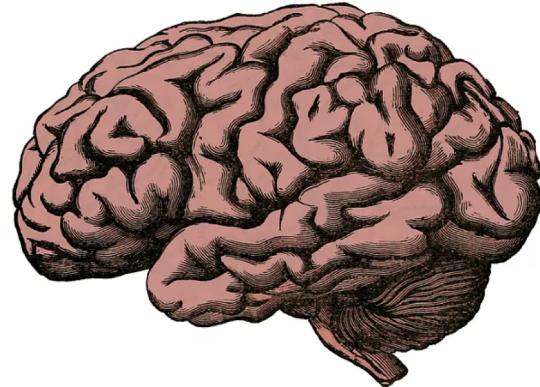
2 in 10 will **NOT**  
relapse



# Objective

Find transcriptional hallmarks  
that can describe the  
characteristics of a recidivist  
astocytome

# General overview



## Bulk RNA-seq

21 samples (WT) 25M  
4 for each histopathology grade  
3 brain controls  
2 cerebellum controls

*IDH 1-2 --*  
*H3F3A --*

## Single Cell RNA-seq

1 for each grade (300 cells)  
1 contiguous control each (300 cells)  
1 distant control (300 cells)

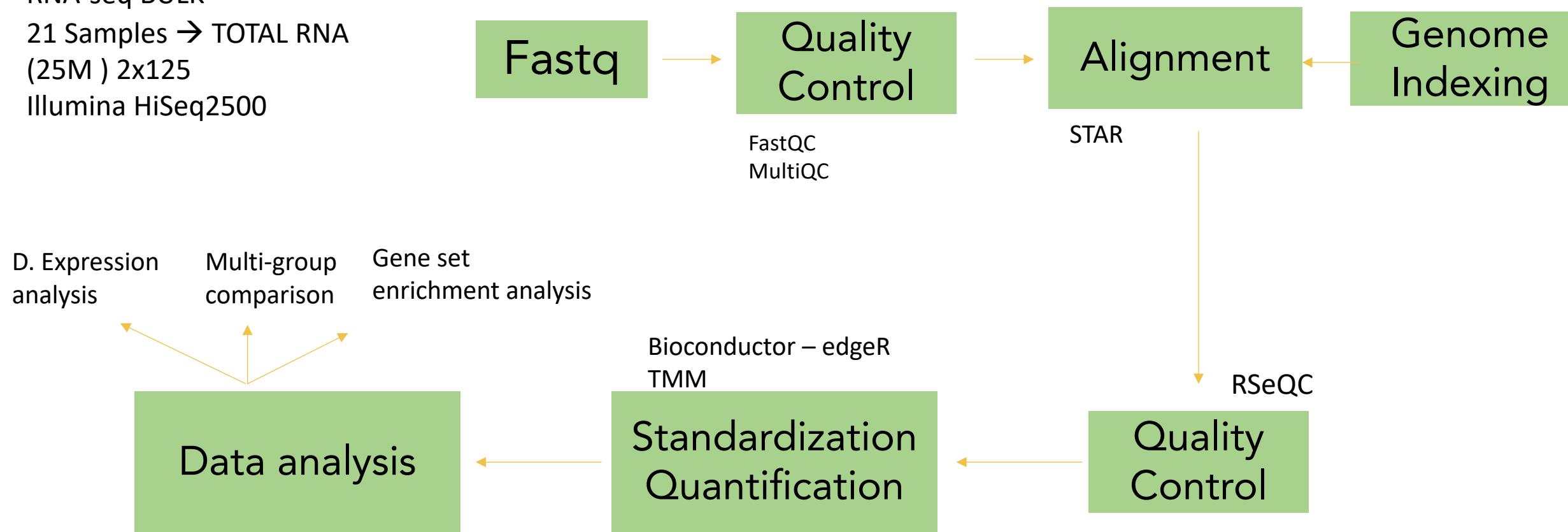
## Bulk RNA-seq

3 samples of kids with relapse  
1 tumor  
1 Contiguous control  
1 Distant control

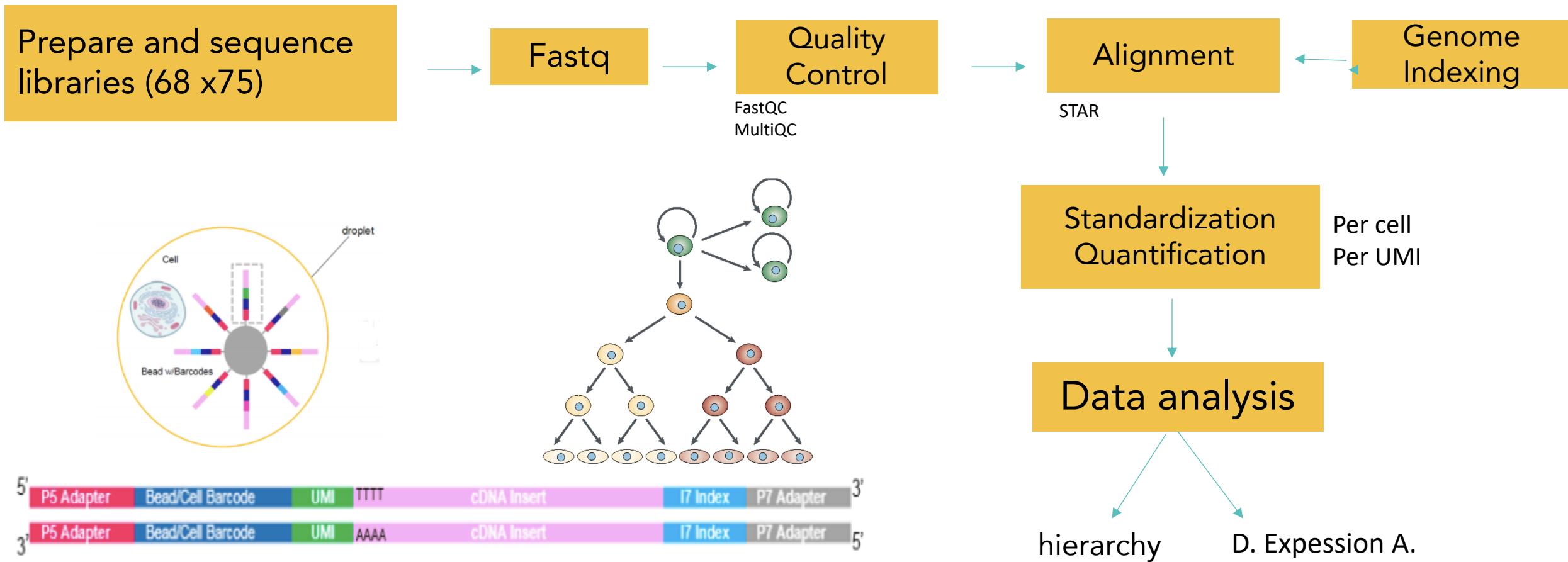
# 1. Characterize the transcriptome of pediatric astrocytomas according to their molecular and histopathological classification

RNA-seq BULK

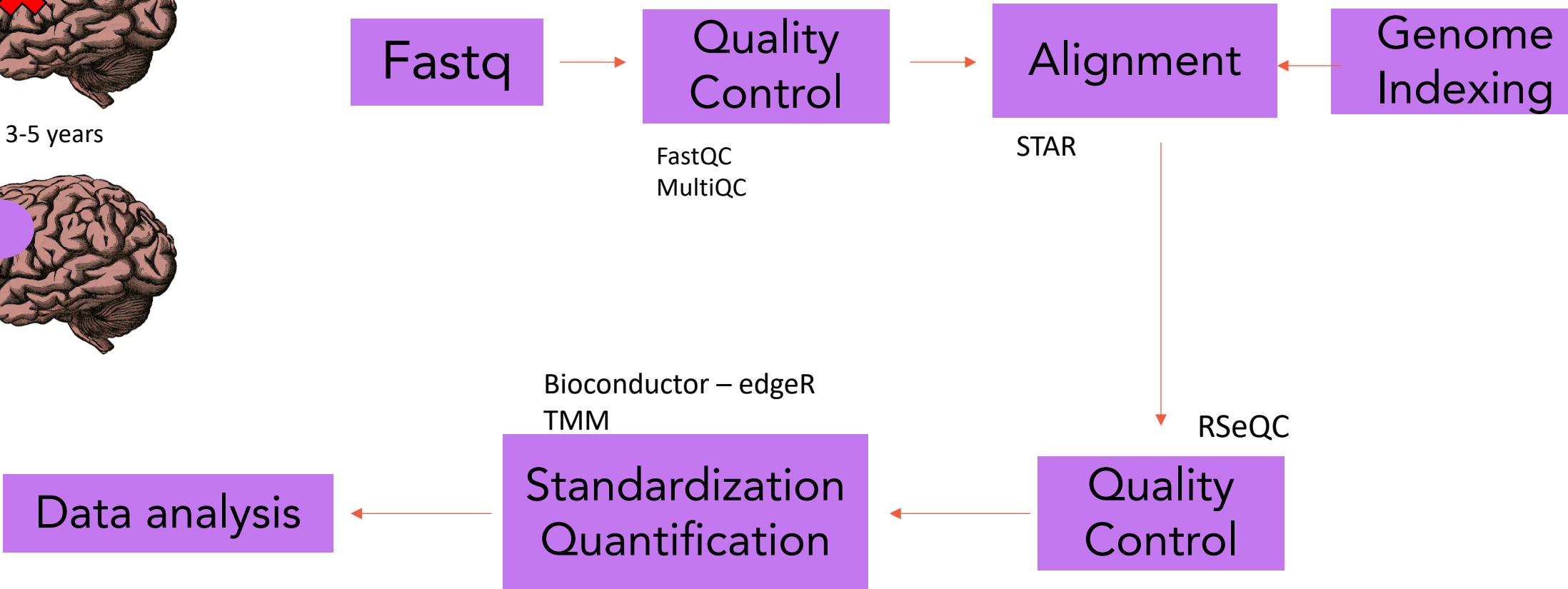
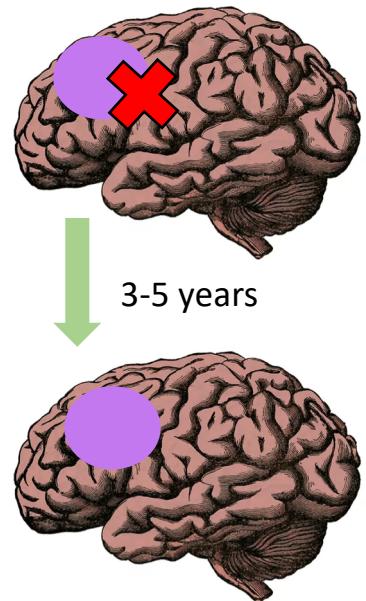
21 Samples → TOTAL RNA  
(25M ) 2x125  
Illumina HiSeq2500



## 2. Characterize the cell hierarchies of tumors according to their transcriptome.



### 3. Search for hallmarks in recidivist patients



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