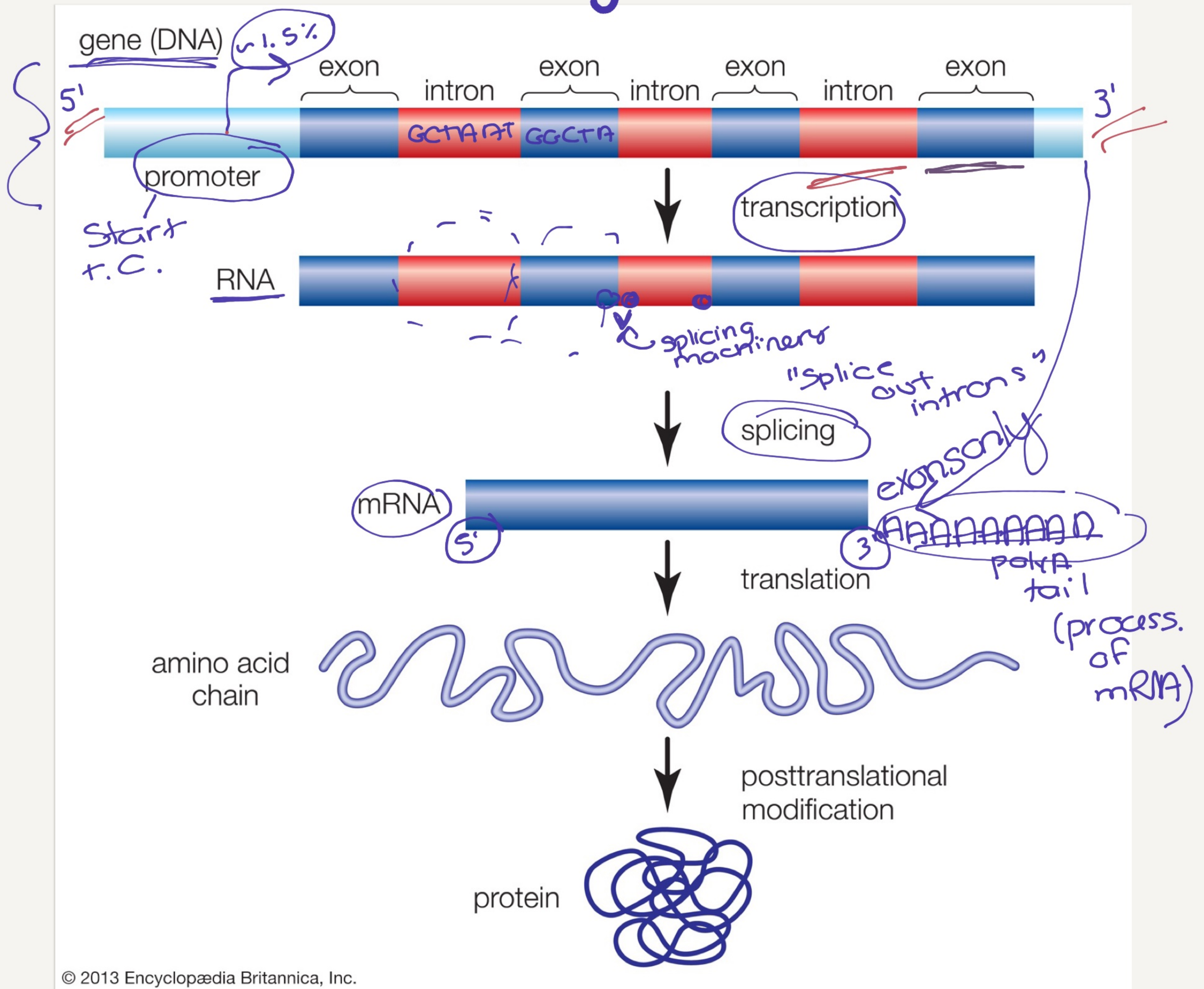


# The structure of the gene





# RNA-Seq: the whole process

## wet-lab

- Designing project
- RNA extraction
- Purification and enriching mRNA
- cDNA synthesis
- Fragmentation
- Adaptor ligation and amplification
- cDNA libraries to be sequenced

## *in equipo*

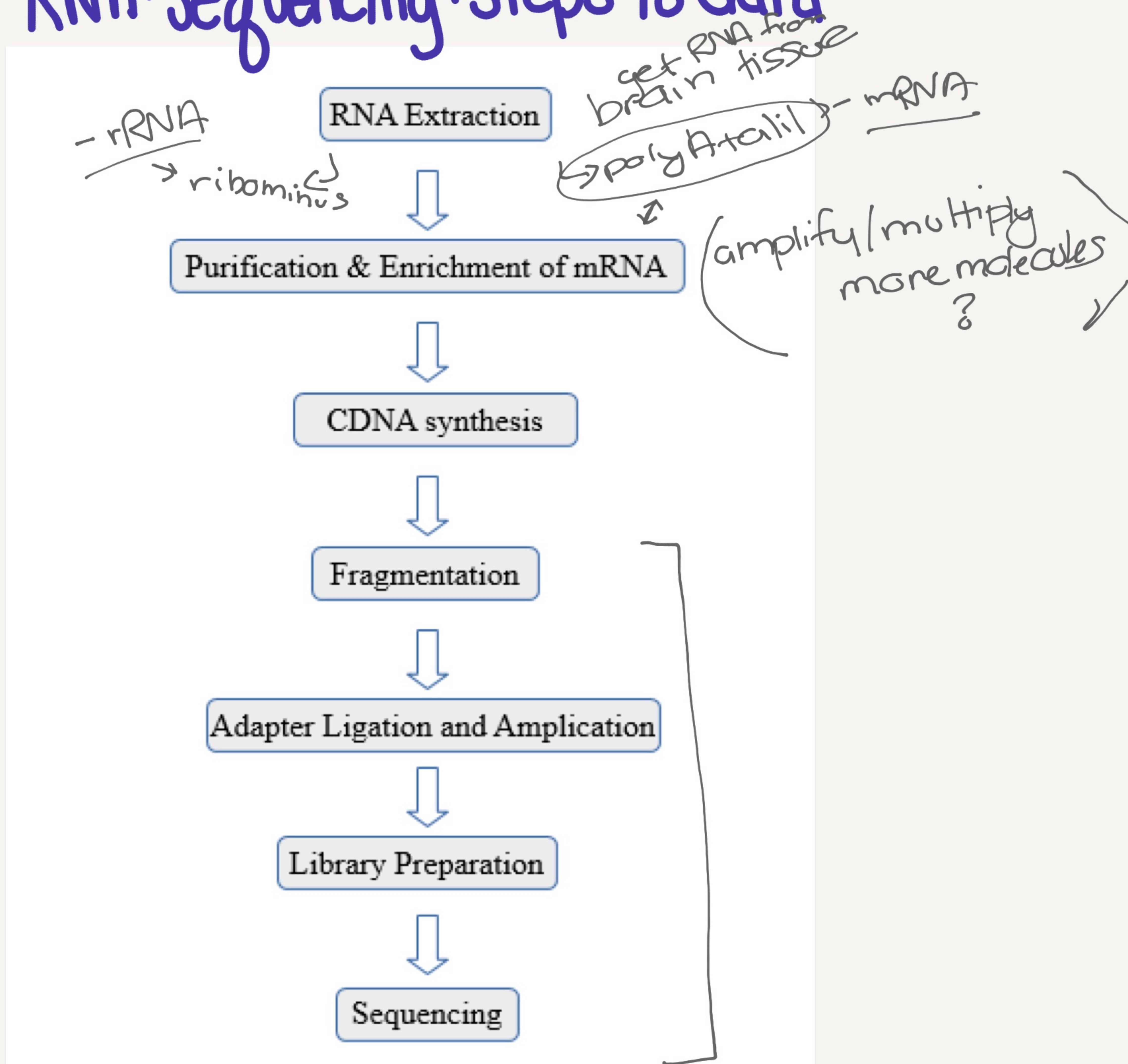
- Choosing suitable platform
- Designing how to run samples
- Sequencing
- Files including sequences to be processed and analyzed

## *in silico*

- Quality control
- Cleaning and trimming
- Alignment
- Mapping
- Annotation
- Further analyses like differential expression, phylogenetics, genetic variation, SNPs, etc.



# RNA Sequencing: Steps to data



gene A : 10 reads

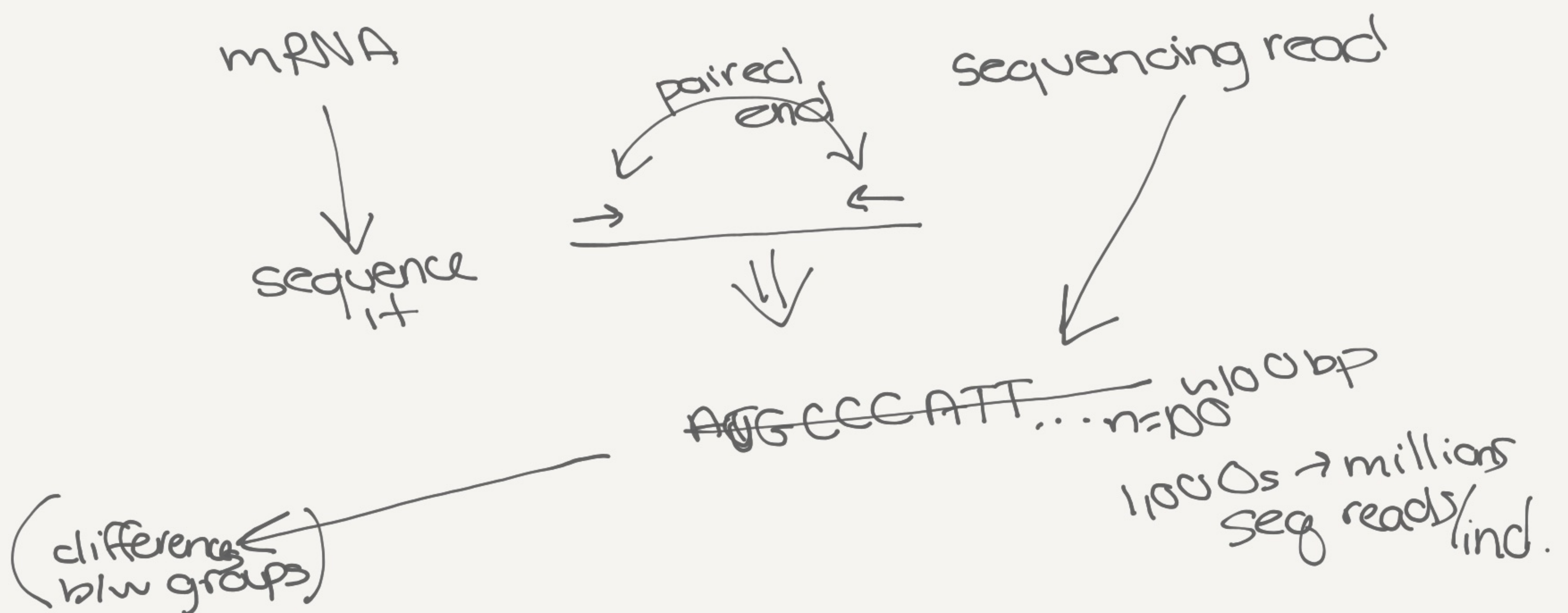
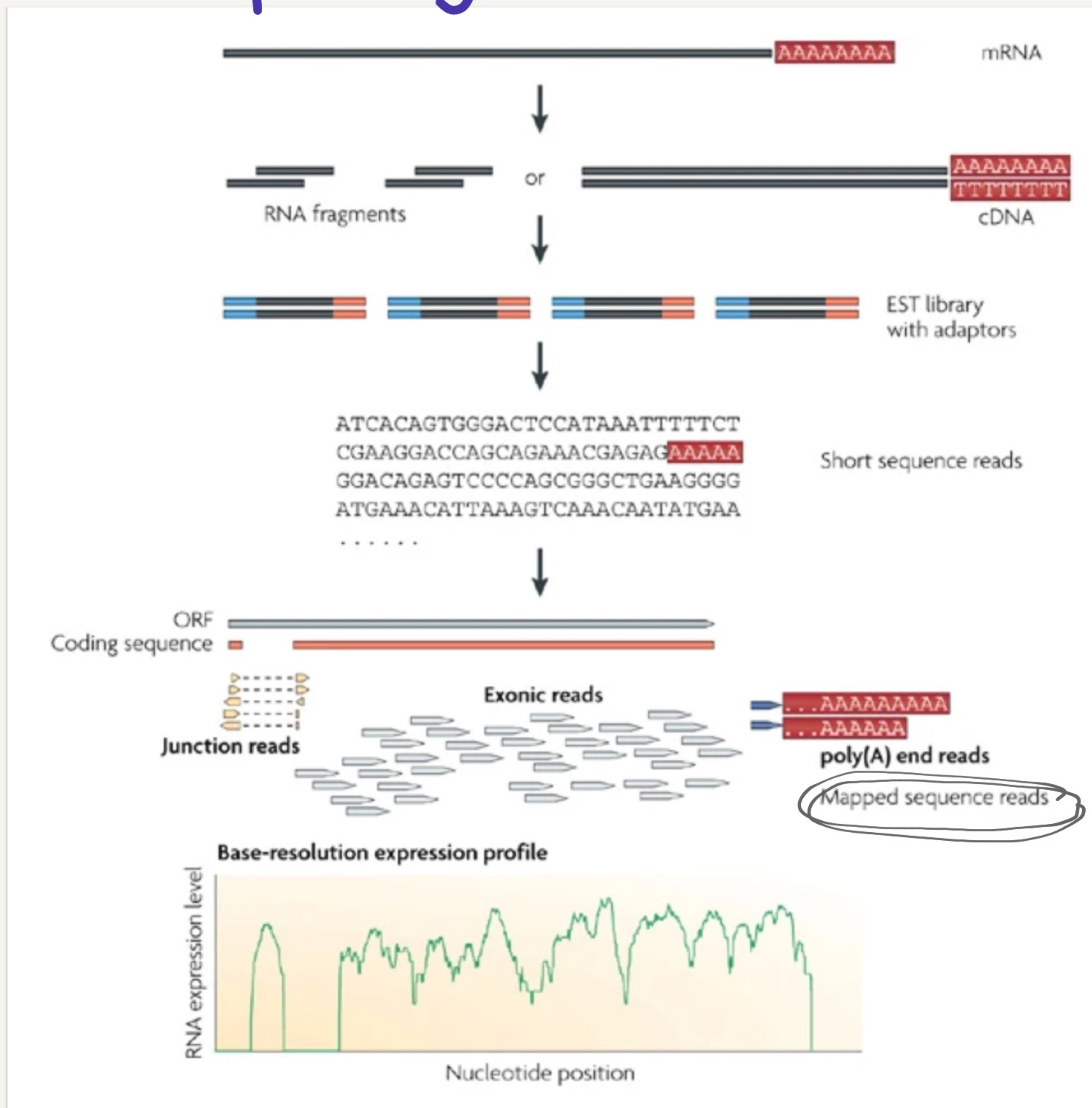
gene B : 100 reads

RNA-Seq:

- profiling transcriptome
- quantify "expression" levels
- mRNA levels in sample across genome



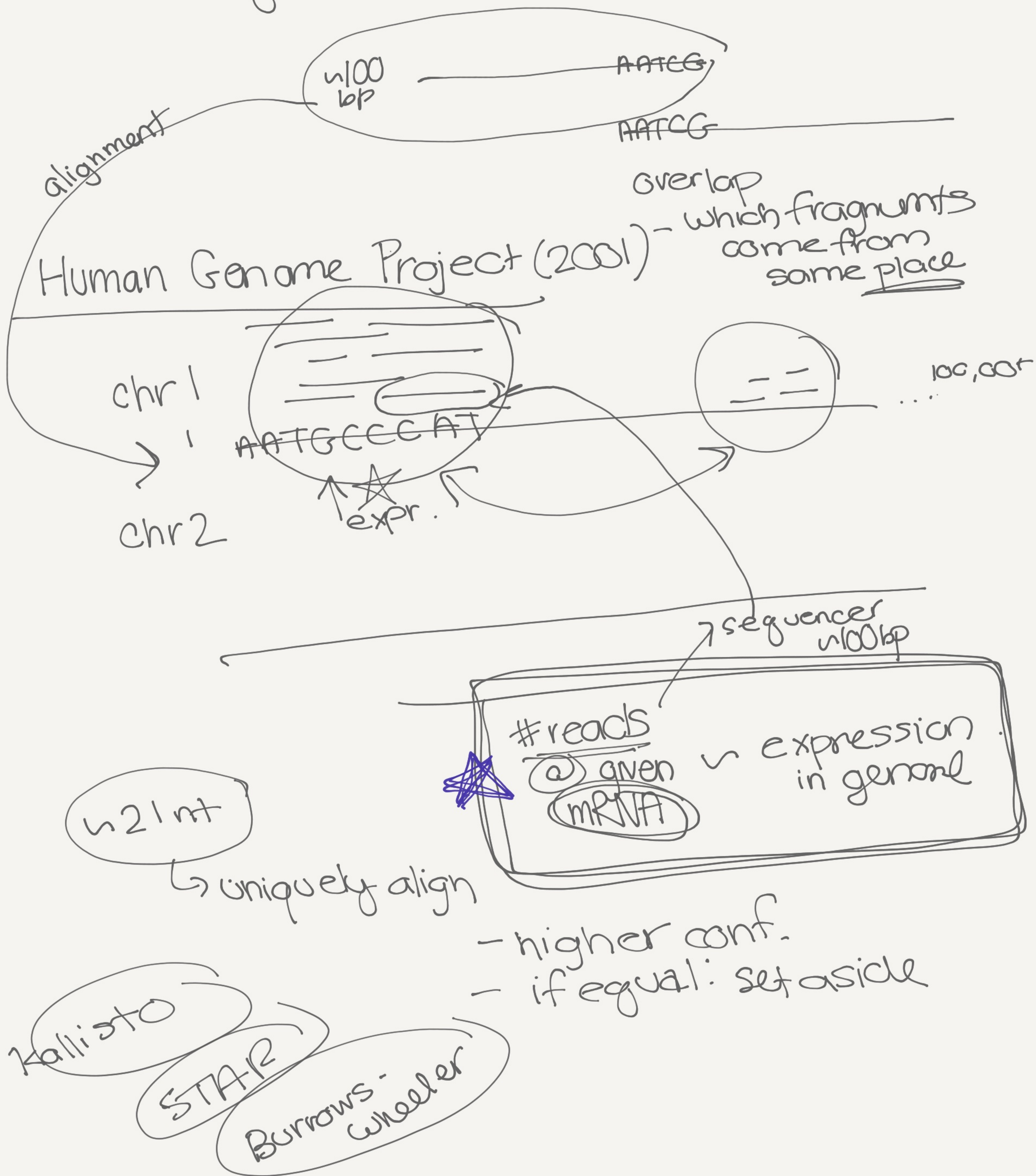
# RNA-Sequencing





# Alignment/Mapping

→ Sequences we already have?





# Terminology

## expression levels

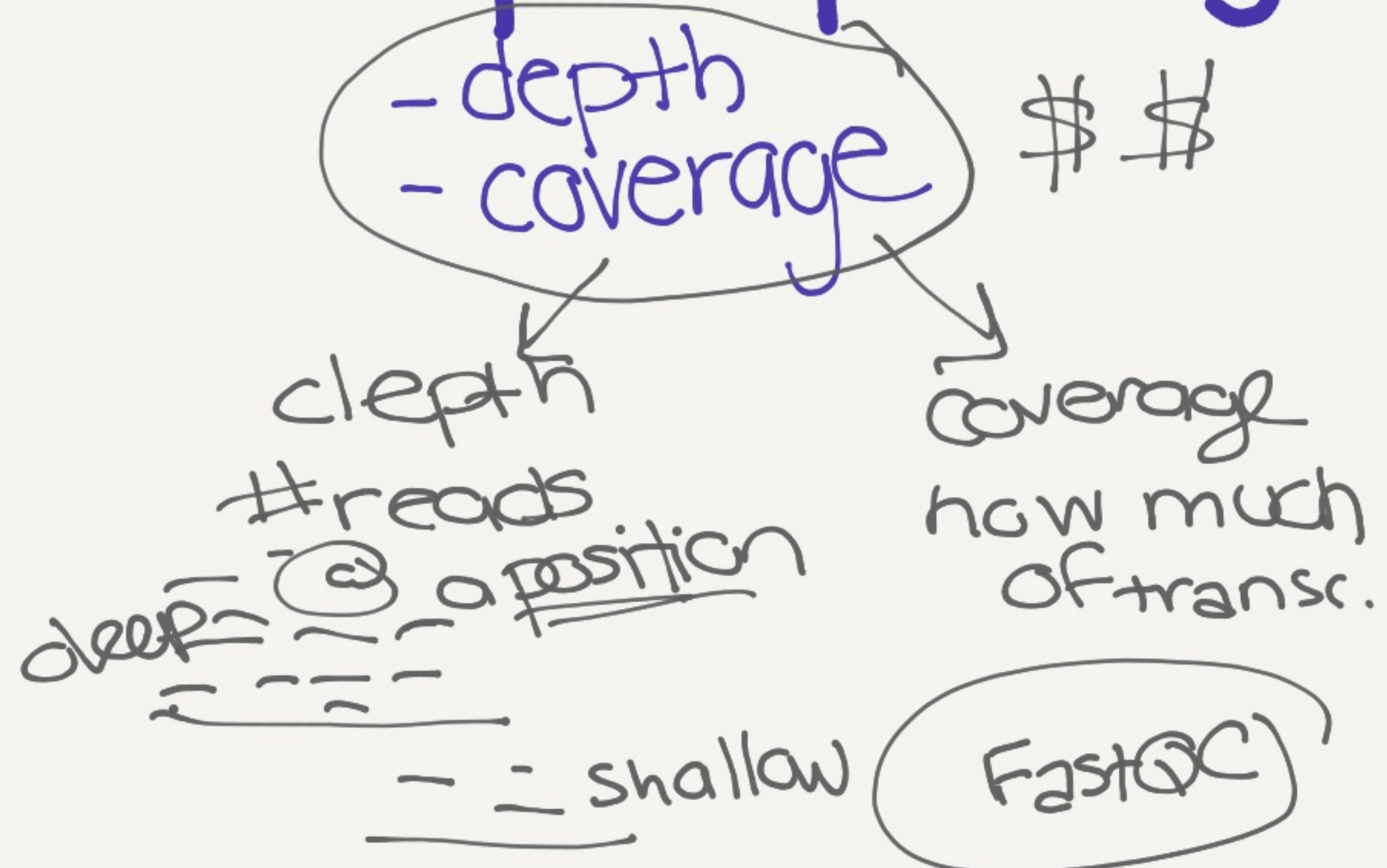
poly A - tags

RNA fragmentation

single-end  
seq.

paired-end  
seq.

"deep" sequencing



"background"