



Molecular Biology (10)

Analysis of gene expression and RNA levels

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School of Medicine
Second year, First semester, 2024-2025



Analysis of gene expression

RNA level

Basic methods: Northern blotting, in situ hybridization

Advanced methods: real-time PCR, DNA microarray

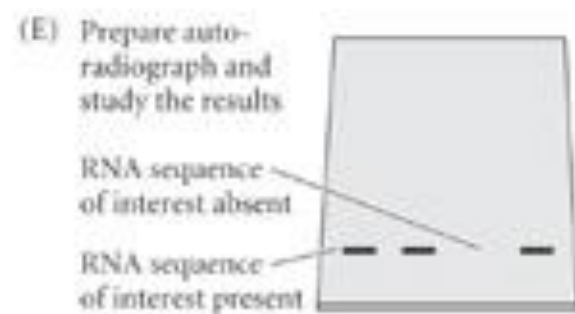
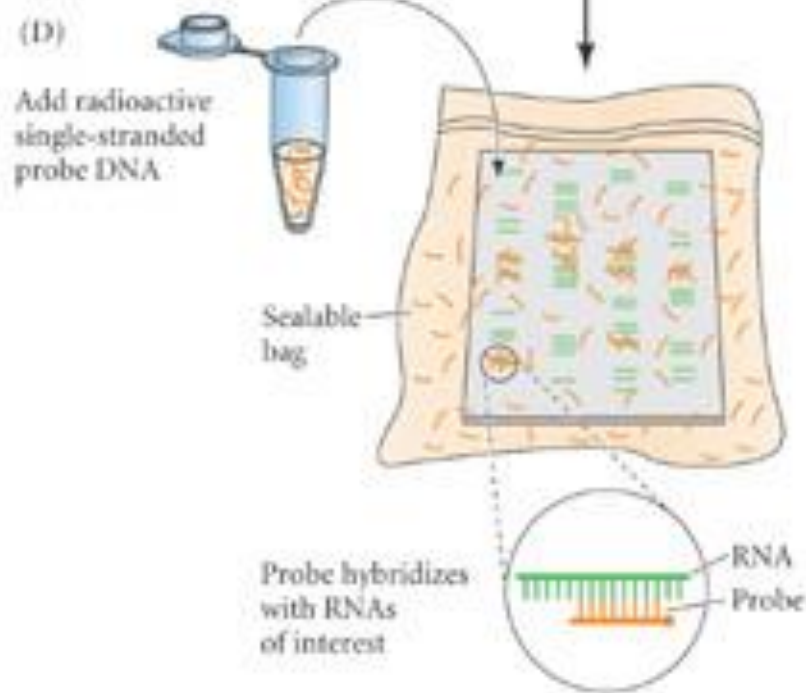
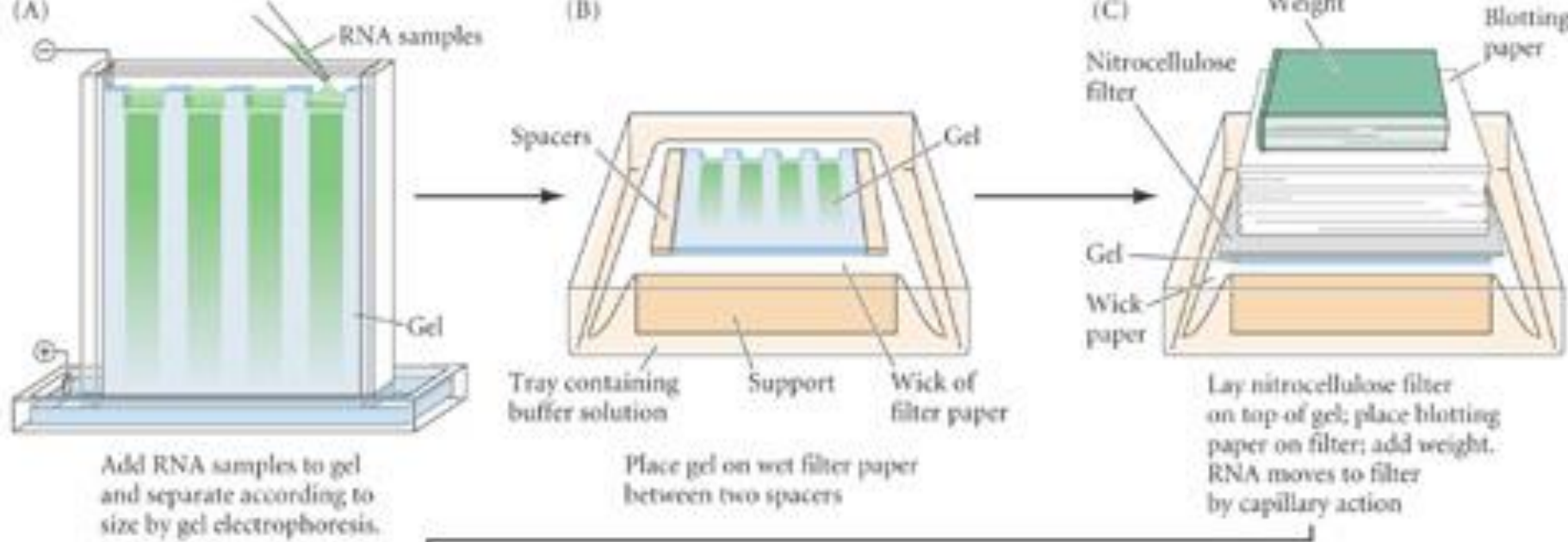
Very advanced methods: RNA-seq

Northern blotting

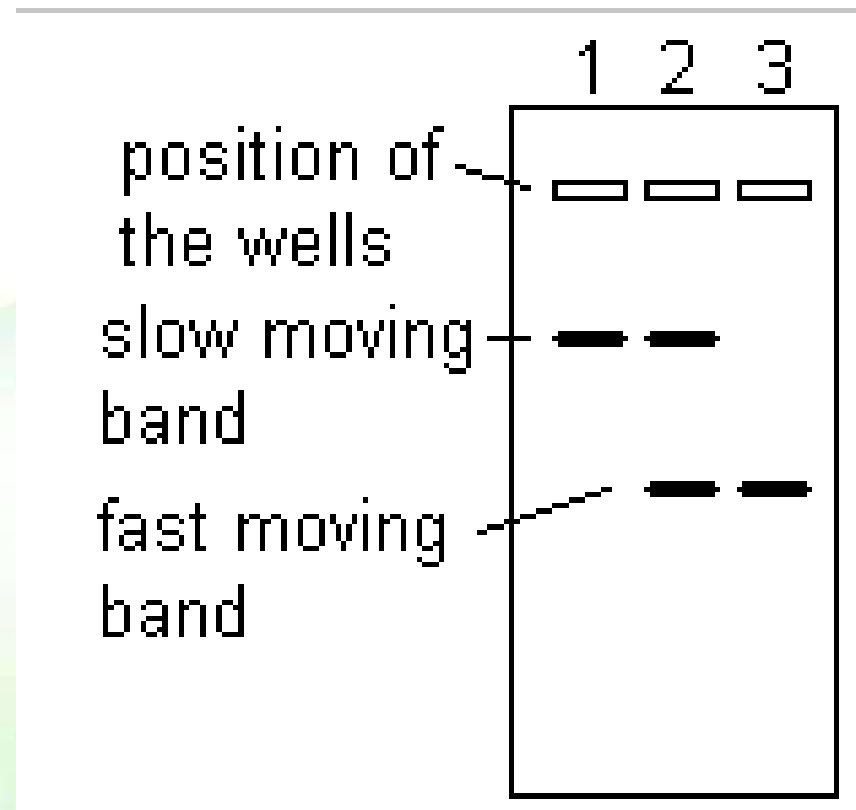


- This is done exactly like Southern blotting except that:
 - RNA from cells is isolated instead of DNA.
 - RNA molecules are fractionated based on size by gel electrophoresis.
 - The fractionated RNA molecules are transferred onto a membrane.
 - RNA molecules are targeted by a labeled DNA probe with a sequence that is complementary to a specific RNA molecule.

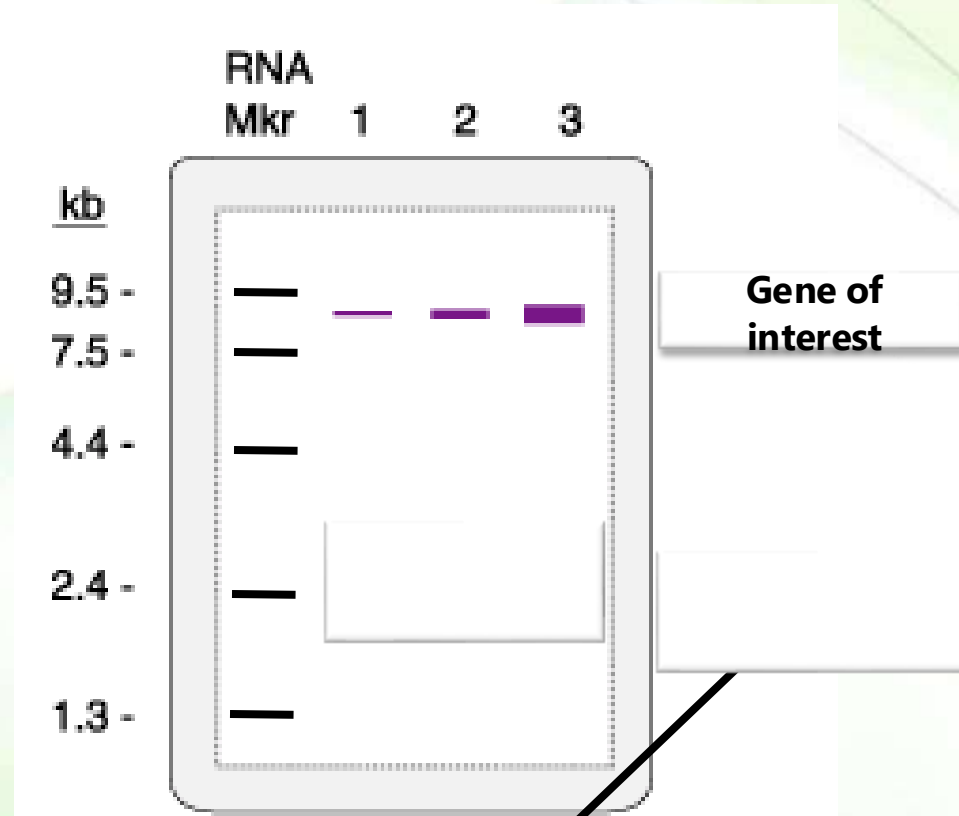
What information can you deduce from it?



What are your interpretations?

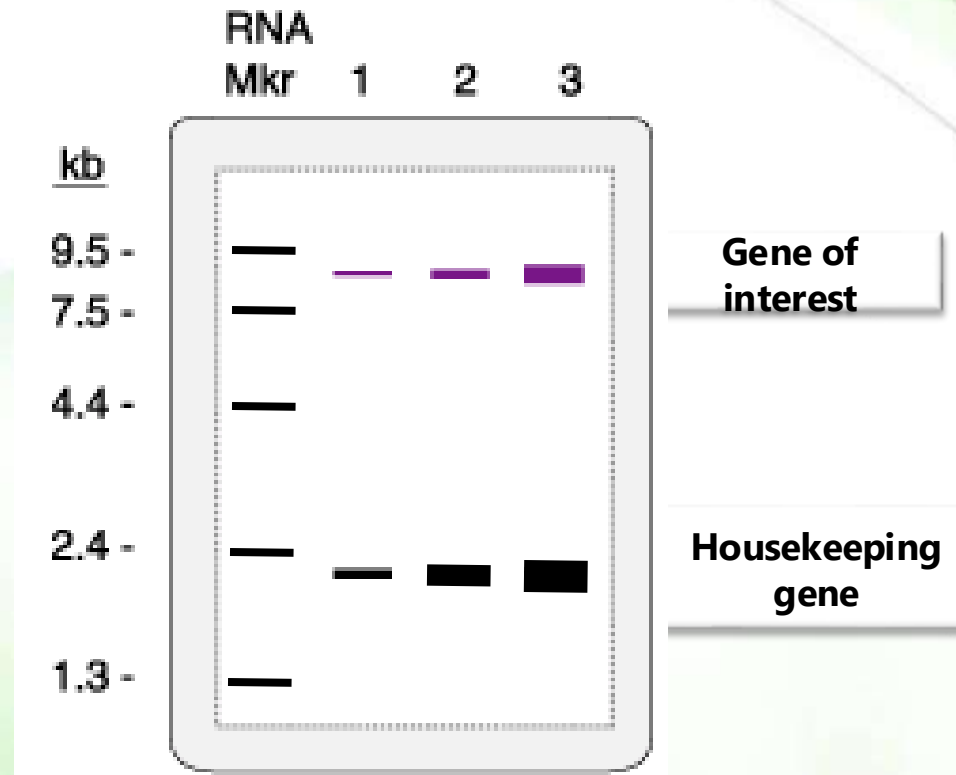


What are your interpretations?



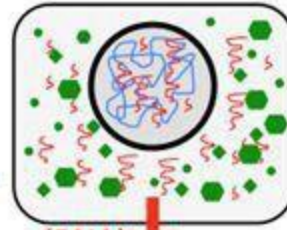
A gene with constant expression
(examples: actin, tubulin)

What are your interpretations?





Cell with DNA,
RNA, & Protein



(DNA)

(Protein)

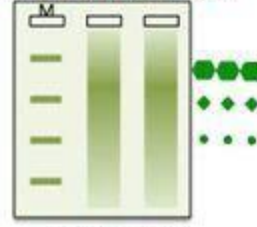
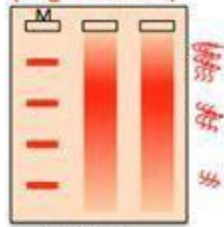
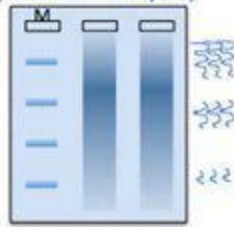
(RNA)

Southern Blot
(Restriction Enzyme)

Northern Blot
(Single stranded)

Western Blot
(Deaturated polypeptides)

Gel
Electro-
phoresis



Agarose
0.5-50Kbp

Agarose
0.5-10 Kb

Acrylamide
10-120 Kd

Transfer separated samples to membrane

Probe
Mem-
brane:

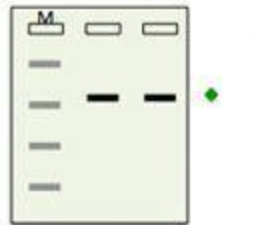
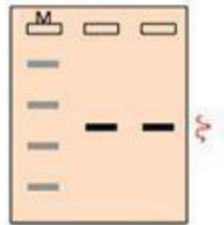
Single stranded
complementary
DNA or RNA to
specific sequence
(restriction fragment)

Single stranded
complementary
DNA or RNA to
specific sequence
(transcript)

Primary antibody
to specific polypeptide
Use Secondary antibody
to detect/amplify primary

Detect labeled probe on membrane

Results:



Sample contains specific
DNA restriction fragment

Sample contains specific
RNA transcript (e.g. mRNA)

Sample contains specific
Polypeptide

Can measure fragment size
and amount (single vs. repeated)

Can measure fragment size
and amount (level of expression)

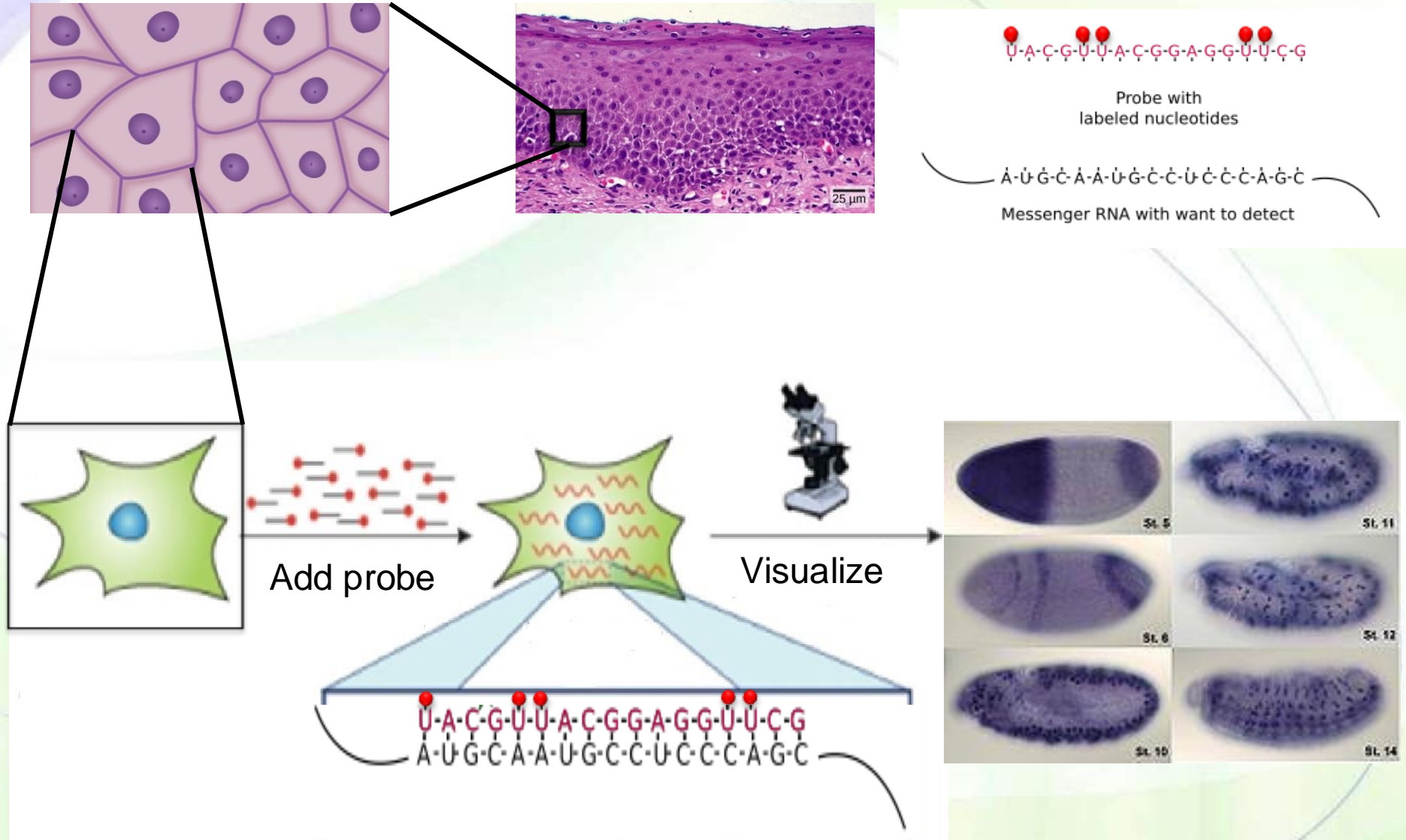
Can measure polypeptide size
and amount (level of expression)

In situ hybridization



- In situ hybridization methods reveals the distribution of specific RNA molecules in cells in tissues.
- RNA molecules can hybridize when the tissue is incubated with a complementary DNA or RNA probe.
- In this way the patterns of differential gene expression can be observed in tissues, and the location of specific RNAs can be determined in cells.

Procedure of in situ hybridization

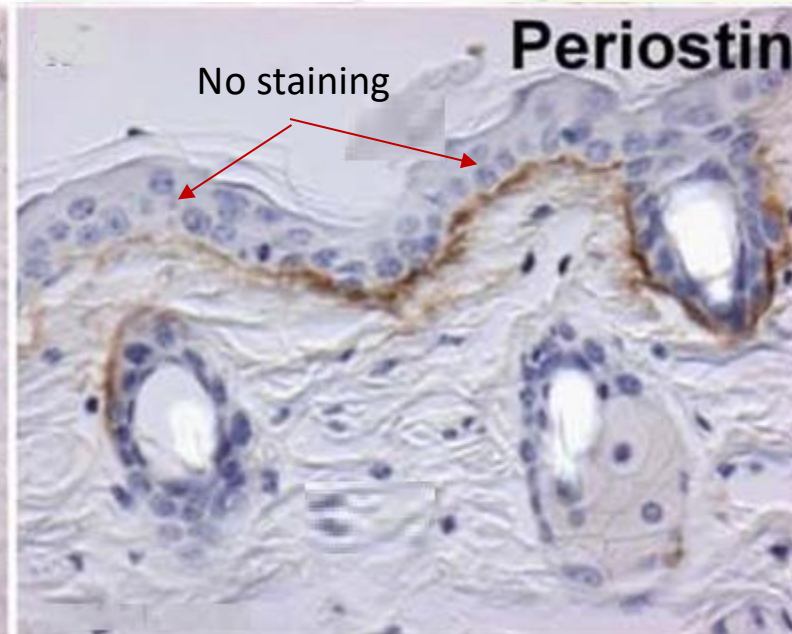




ISH (RNA)



IHC (protein)



RNA and protein molecules do not coexist and are present in different places.

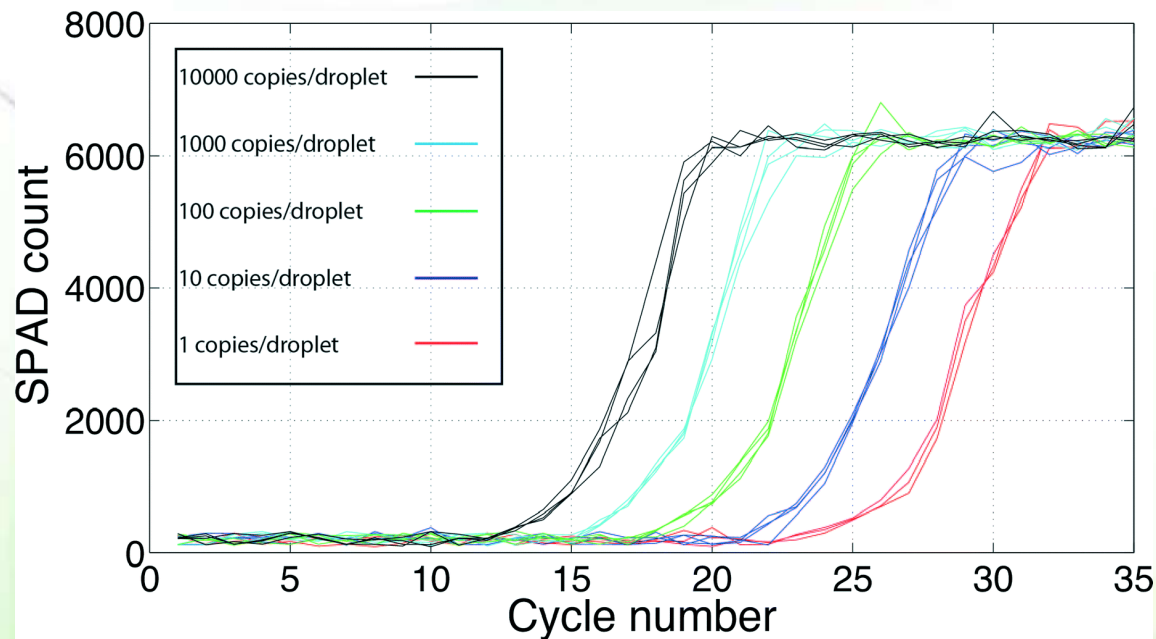
mRNA: inside cells along the basement membrane

Protein: outside cells in the basement membrane

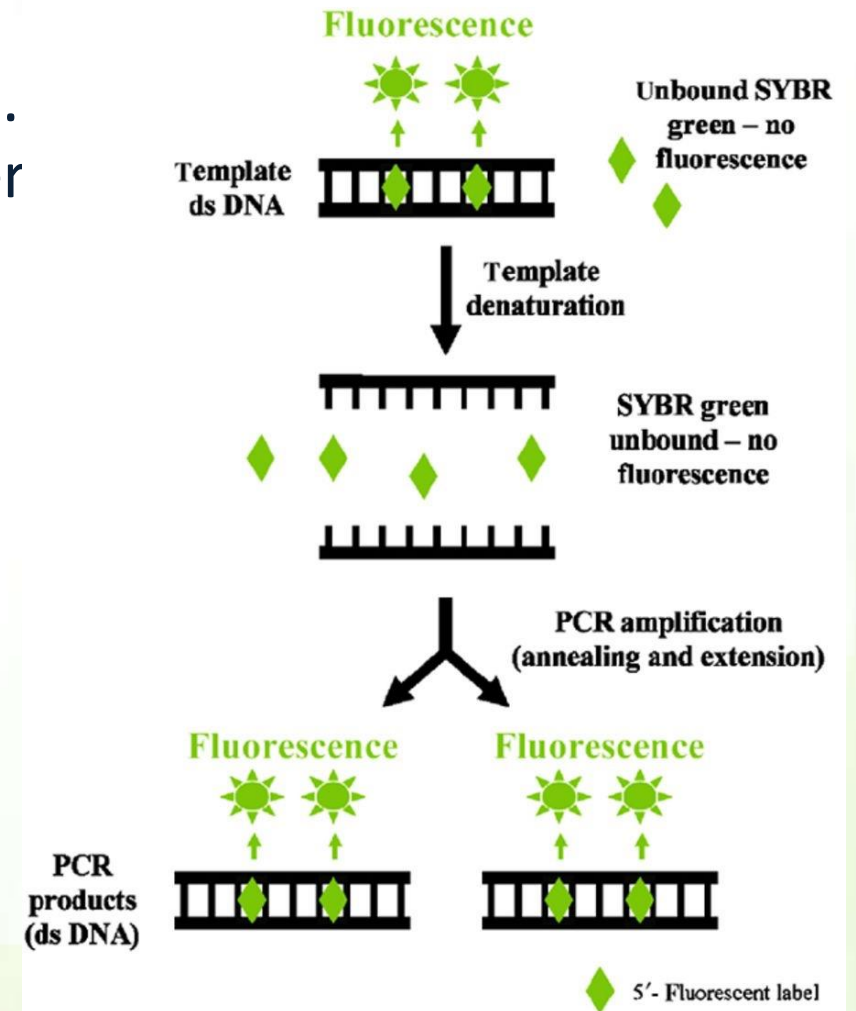
Quantitative reverse transcriptase real-time RT-qPCR of mRNA



- Another way of relative quantitation of RNA expression is by converting RNA into cDNA followed by PCR in the presence of SYBR green.
- The higher the amount of RNA (cDNA), the sooner is detected.



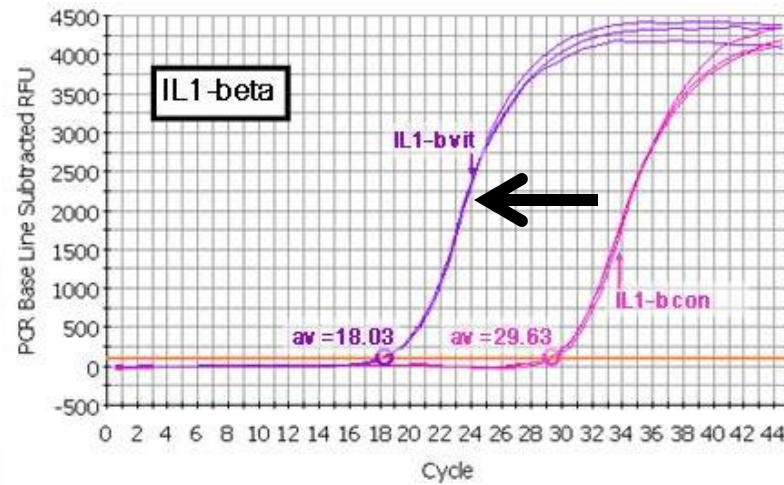
(a) SYBR green assays



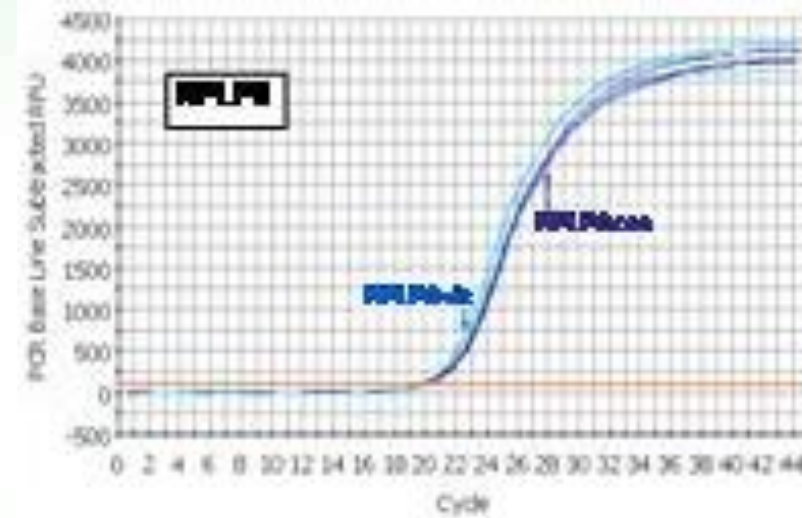
Example



A gene of interest



Housekeeping gene



Unaltered expression

Detection of SARS-Co-2



Tube with inactivated nasopharyngeal swabs

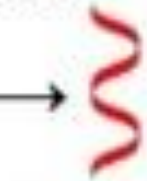


200 μ L aliquot



Automated-based extraction & one-step RT-qPCR

RNA extraction



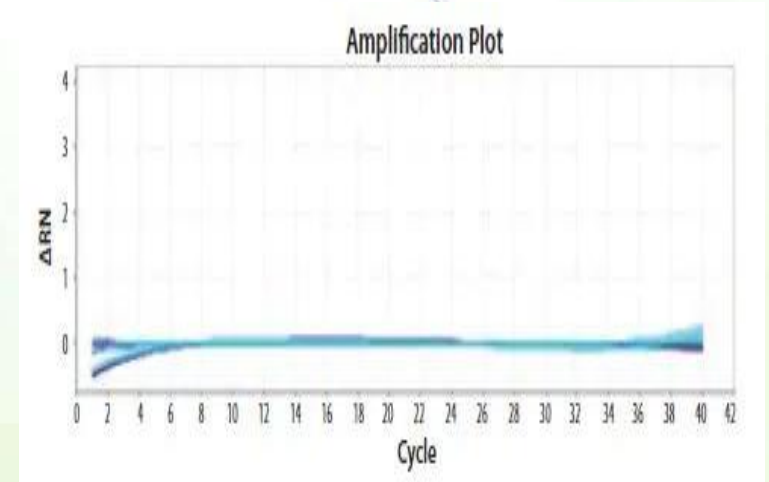
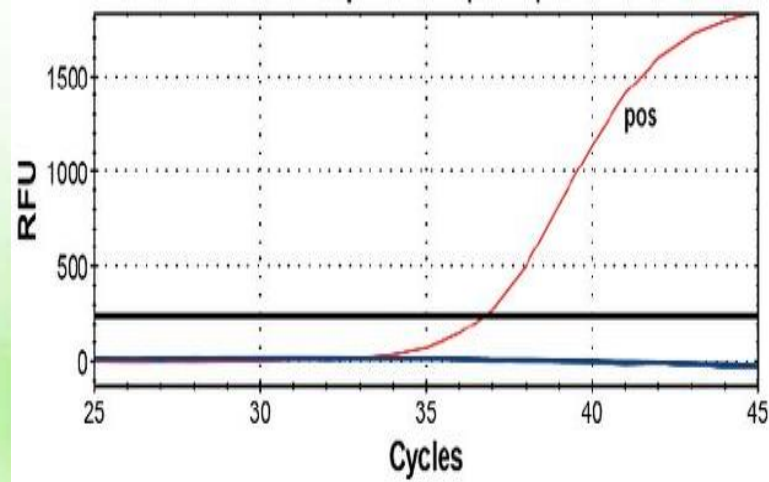
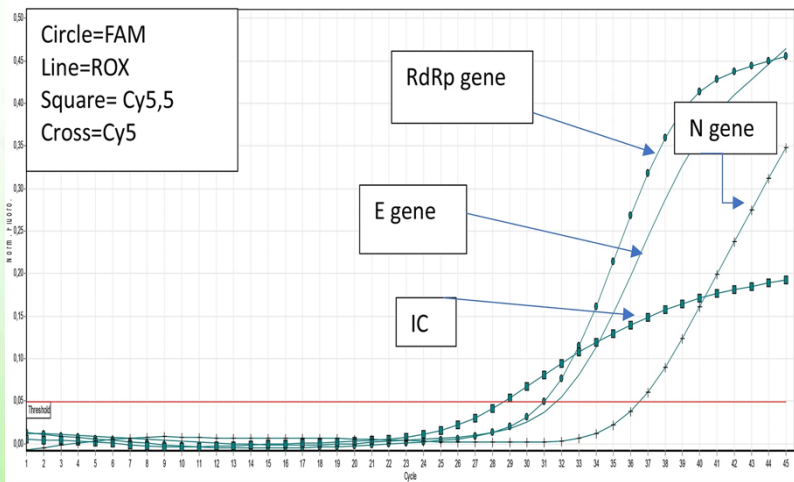
Viral RNA

Amplified E-gene DNA

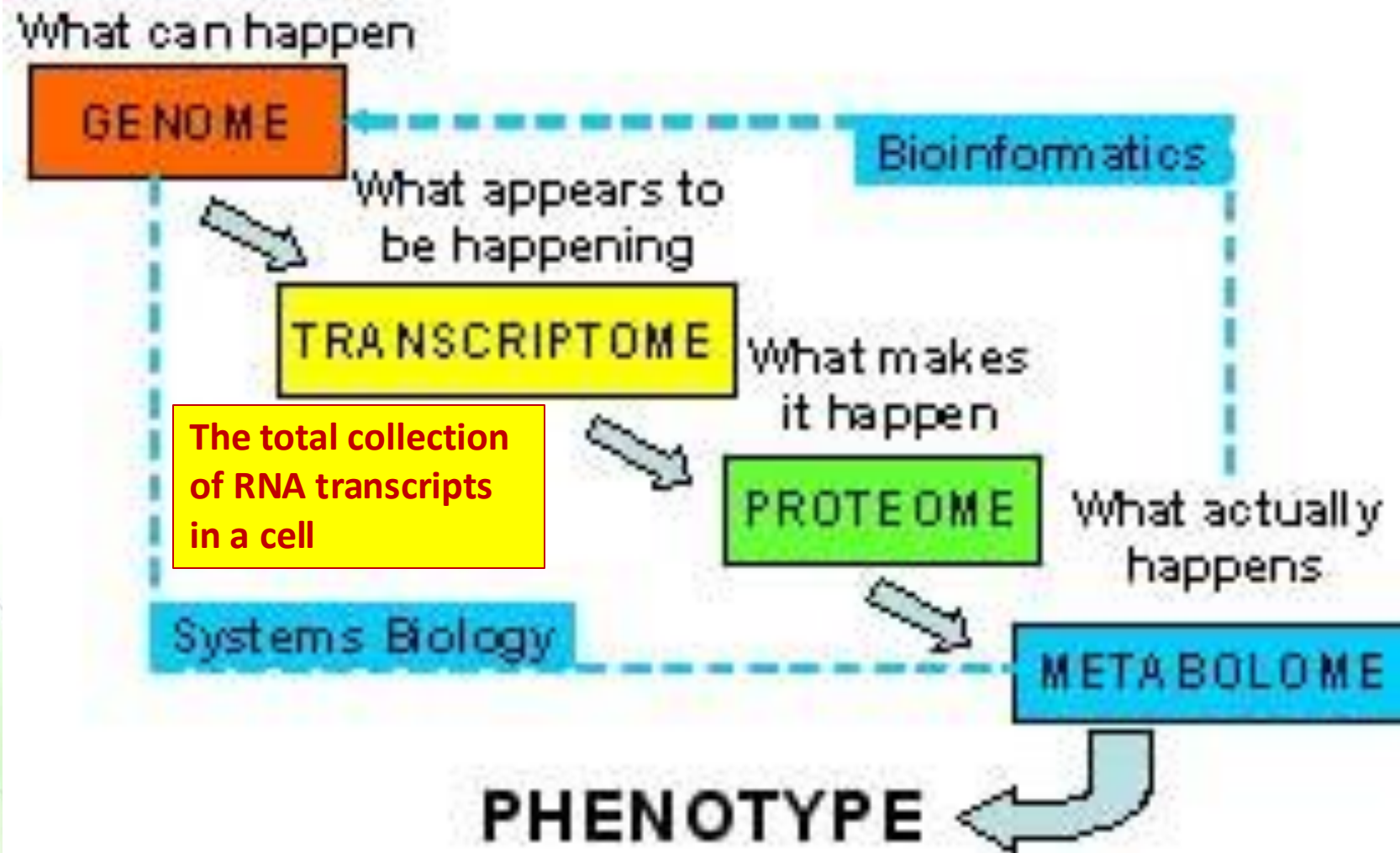


Quantitative detection of E-gene DNA*

5 μ L



The science of -omics



Studying the transcriptome



One such method in studying transcriptomes is DNA microarrays, which allow the analysis of the RNA products of thousands of genes all at once.

By examining the expression of so many genes simultaneously, we can understand gene expression patterns in physiological and pathological states.

DNA microarrays

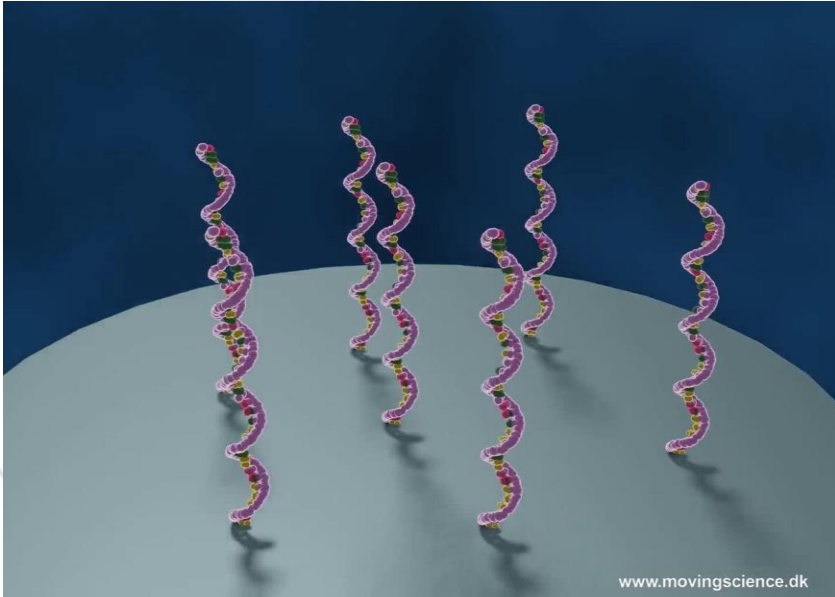


DNA microarrays are solid surfaces (glass microscope slides or chips) spotted with up to tens of thousands of DNA fragments in an area the size of a fingernail.

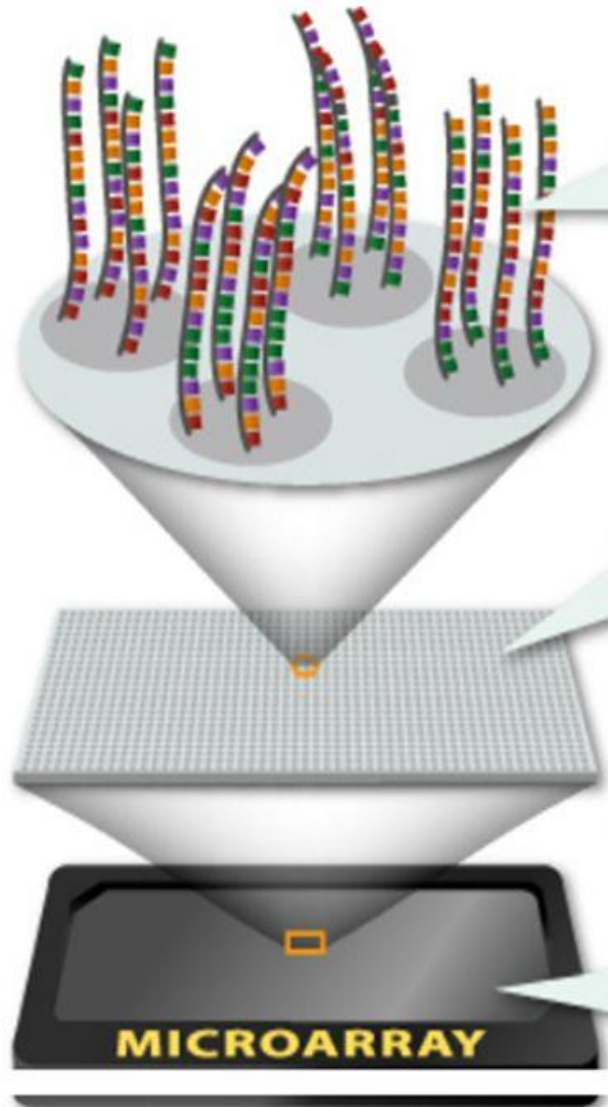
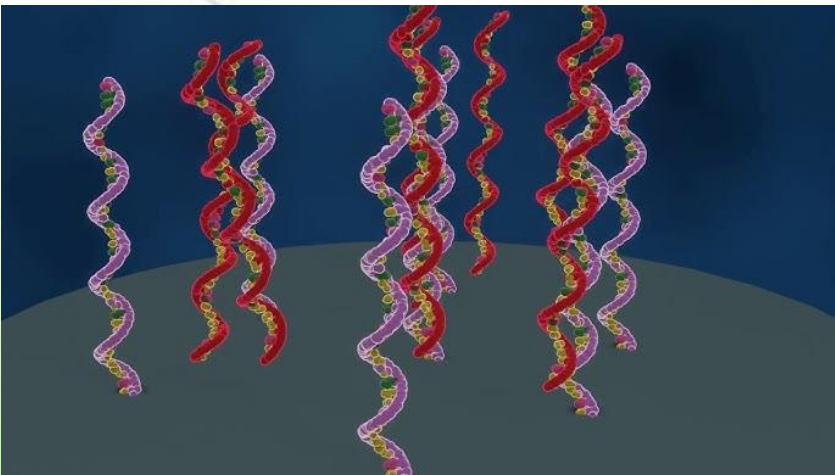
The exact sequence and position of every DNA fragment on the array is known.

<http://learn.genetics.utah.edu/content/labs/microarray/>

<http://www.sumanasinc.com/webcontent/animations/content/dnachips.html>



www.movingscience.dk



A DNA microarray allows scientists to perform an experiment on thousands of genes at the same time.

Each spot on a microarray contains multiple identical strands of DNA.

The DNA sequence on each spot is unique.

Each spot represents one gene.

Thousands of spots are arrayed in orderly rows and columns on a solid surface (usually glass).

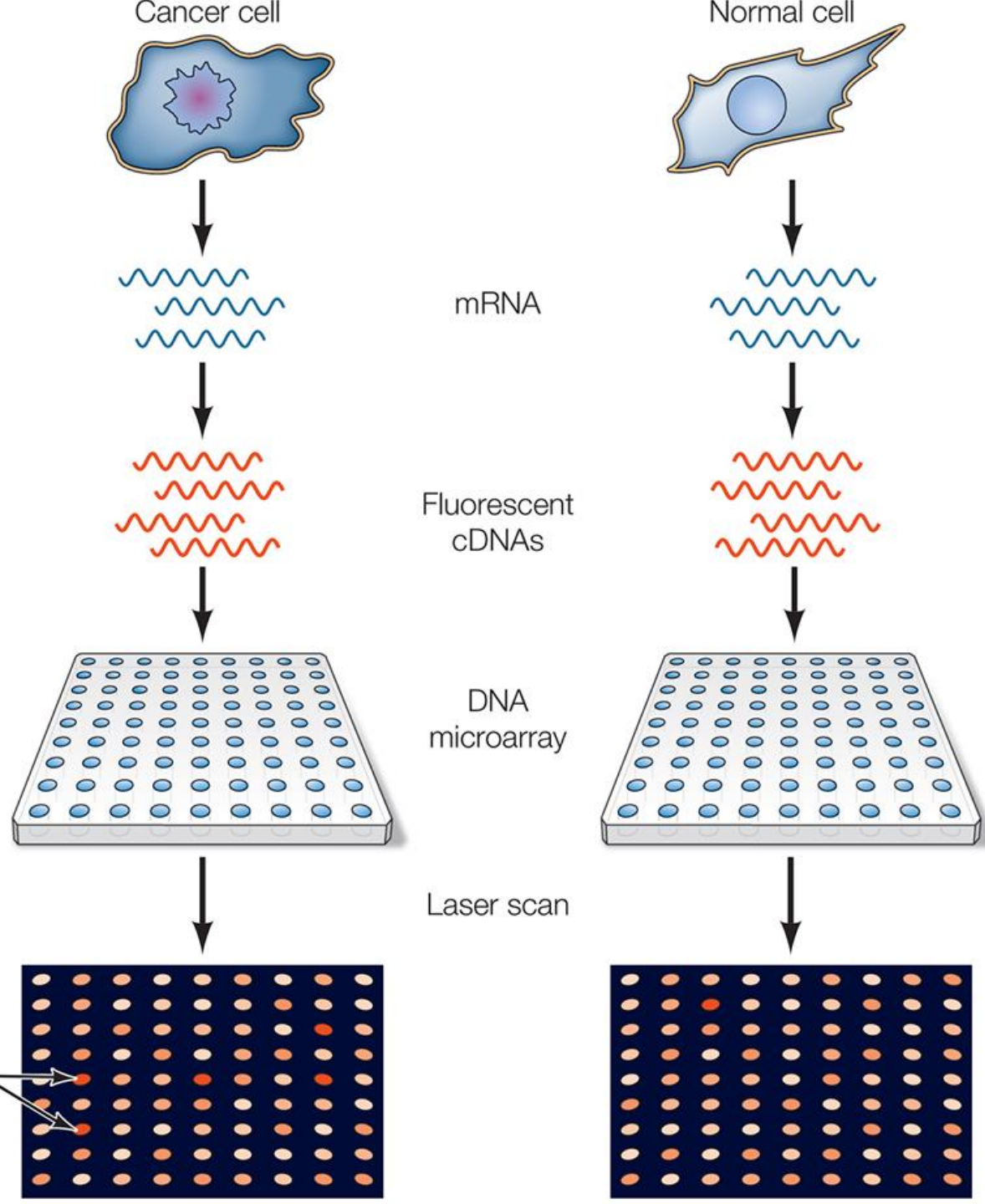
The precise location and sequence of each spot is recorded in a computer database.

Microarrays can be the size of a microscope slide, or even smaller.

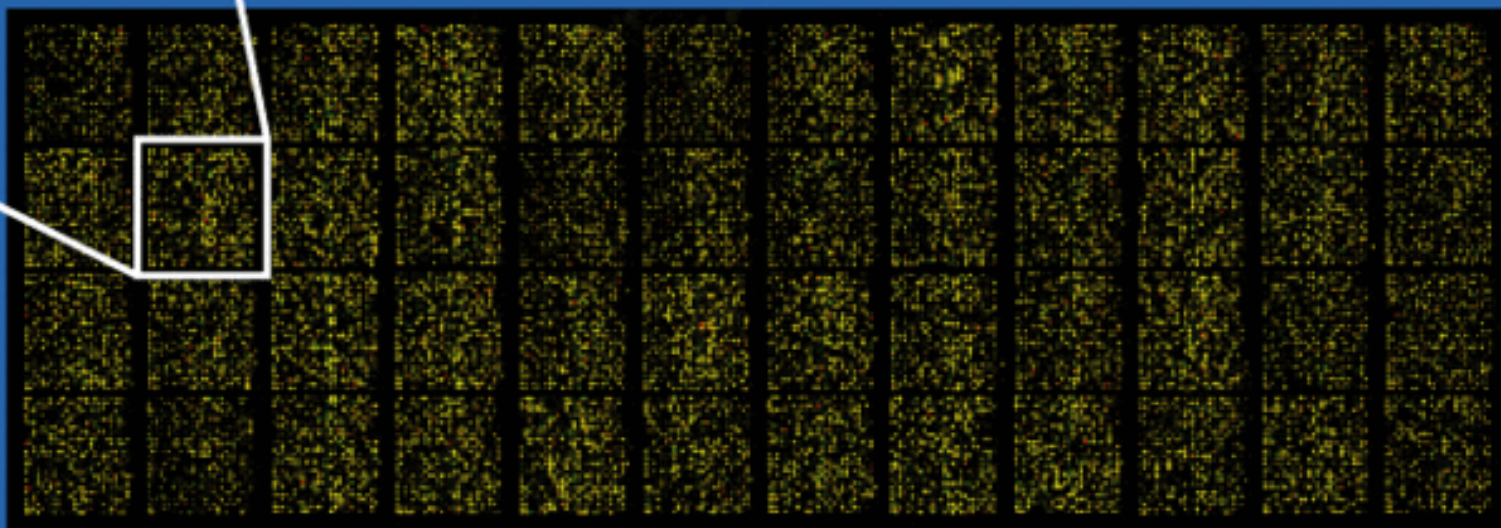
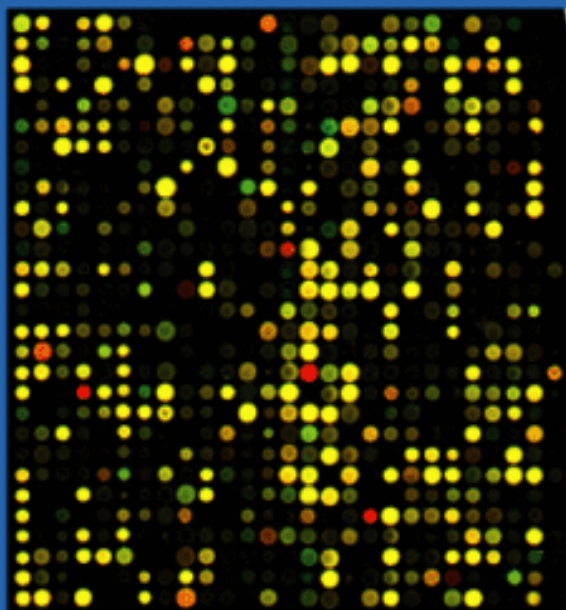




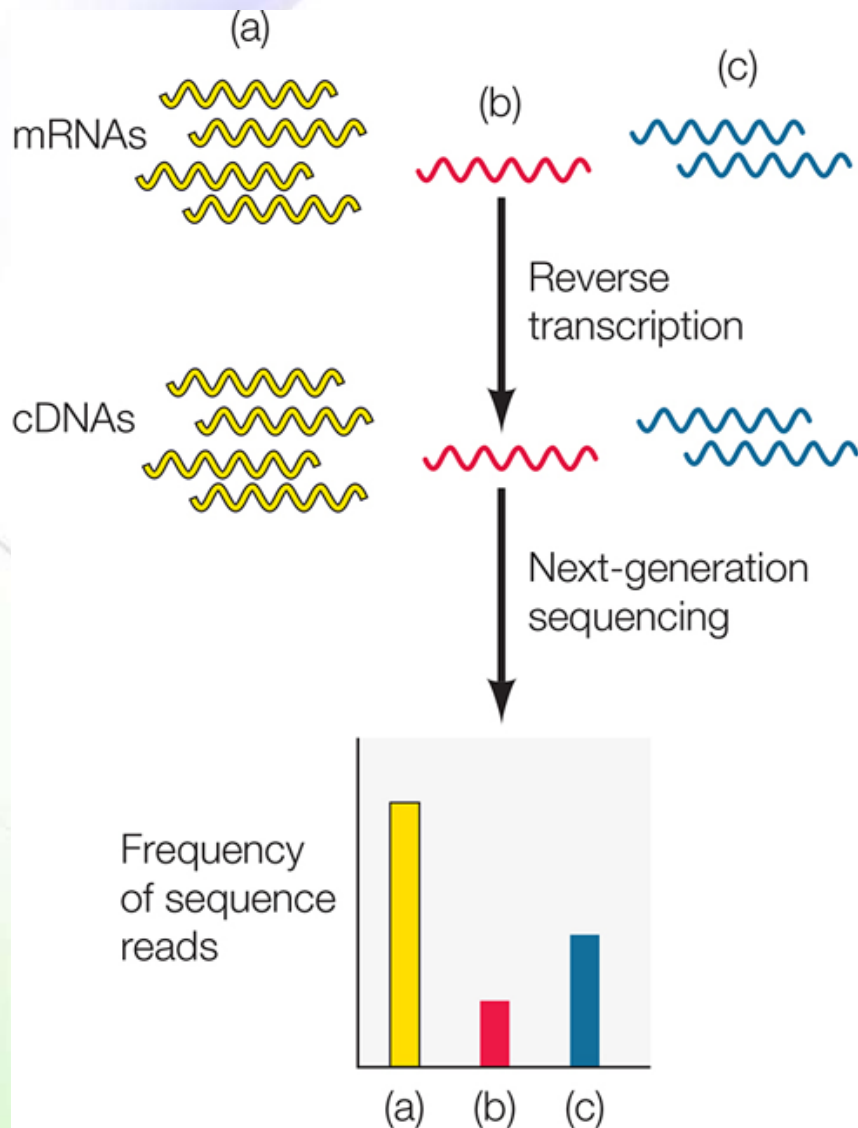
The procedure



- mRNAs are extracted from cancer cells and normal cells and converted to cDNAs, which are labeled with a fluorescent dye.
- The cDNAs are then hybridized to a DNA microarray containing spots of oligonucleotides corresponding to 20,000 or more distinct human genes.
- The relative level of expression of each gene is indicated by the intensity of fluorescence at each position on the microarray, and the levels of expression in cancer cells and normal cells can be compared.



RNA sequencing (RNA-seq)



Cellular RNA is reverse transcribed to cDNAs, which are subjected to next-generation sequencing. The relative amount of each cDNA (mRNA) is indicated by the frequency at which its sequence is represented in the total number of sequences read.

RNA-seq vs. microarray



RNA-seq can be used to

- characterize novel transcripts
- Identify splicing variants
- profile the expression levels of all transcripts

Microarrays are limited to detect transcripts corresponding to known genomic sequences.