



Transcription-regulation (2)

Resources



- This lecture
- Cooper, pp. 124--132

How do different cells appear?

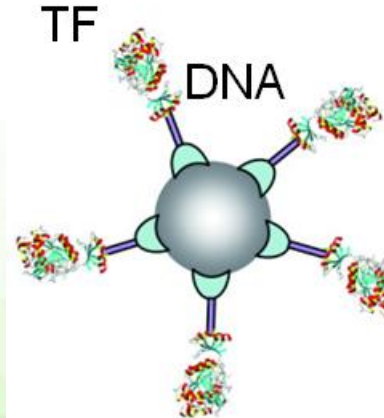
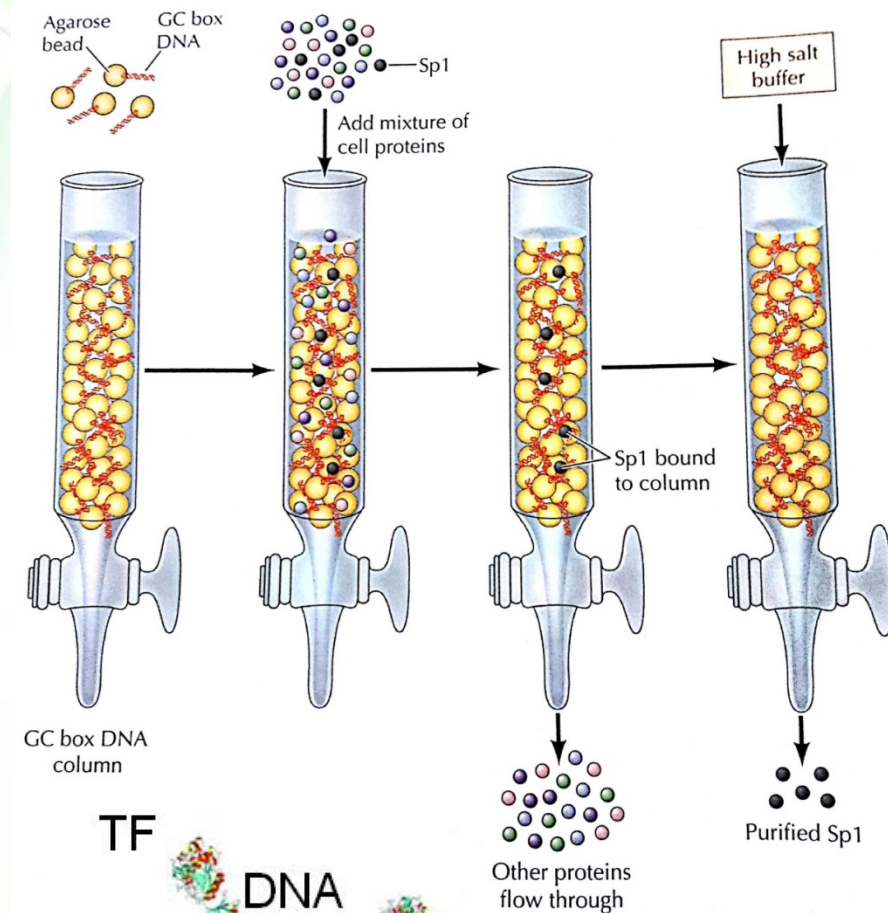


- All cells in one body have the same genome, but cell types in a multicellular organism become different from one another because they synthesize different sets of RNA and protein molecules.
- The patterns of mRNA can differentiate cell types from each other.
- How can we investigate RNA expression and function?

Isolation of transcription factors using affinity chromatography



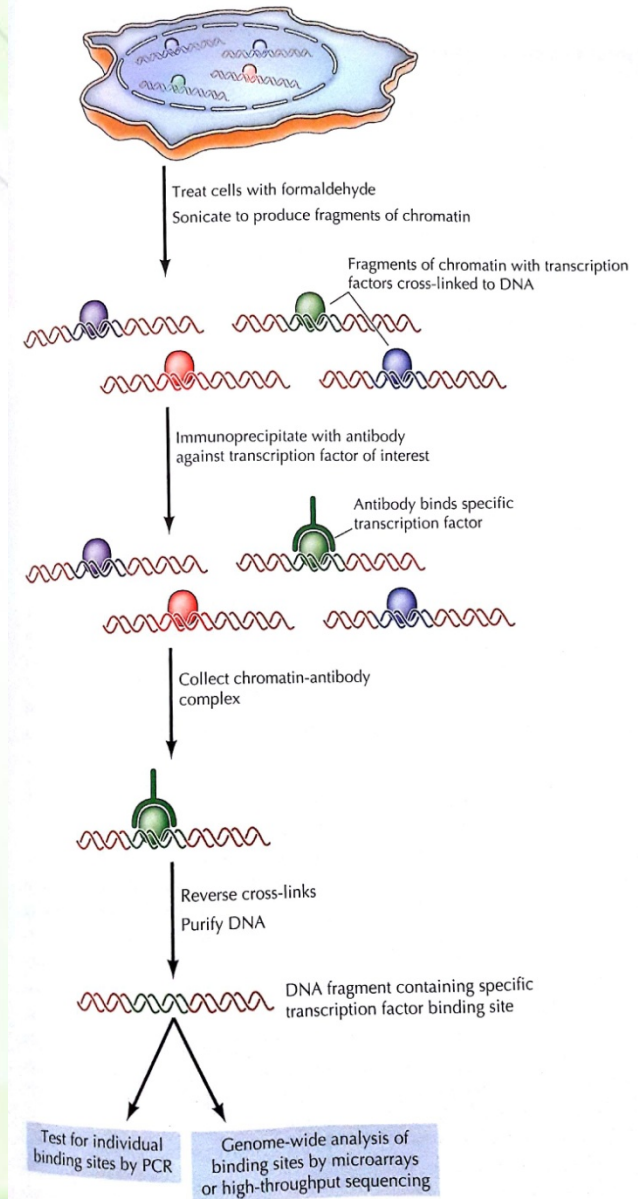
- Attach a DNA fragment with a specific sequence to a bead.
- Pass through nuclear fraction of a cell.
- Elute the bound proteins.

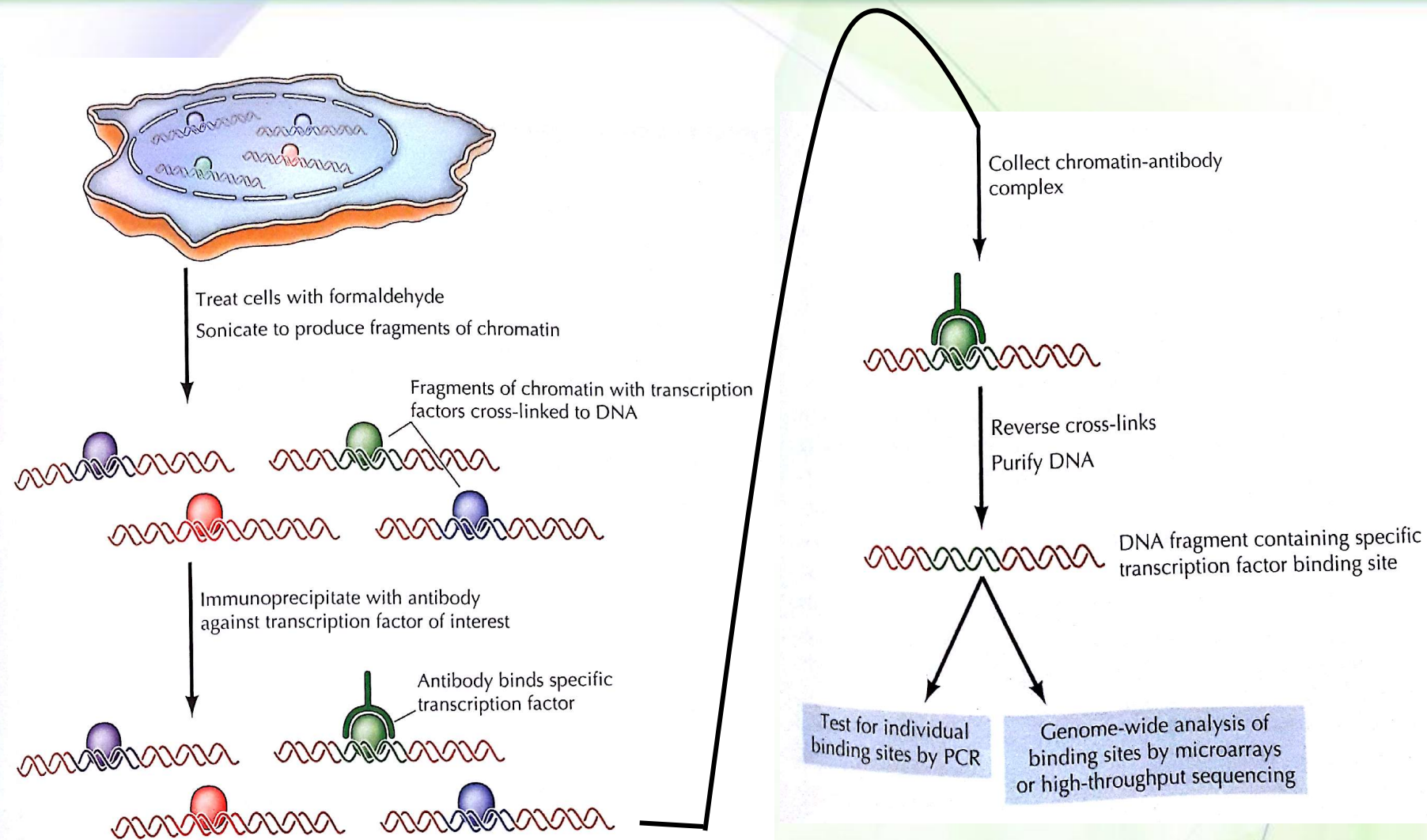


Chromatin immunoprecipitation



- Purpose: identify the DNA sequence to which a transcription factor binds.
- Crosslink proteins bound to DNA.
- Fragments the DNA into smaller pieces.
- Isolate a specific transcription factor by immunoprecipitation.
- Sequence the purified DNA fragment or identify by DNA microarray.

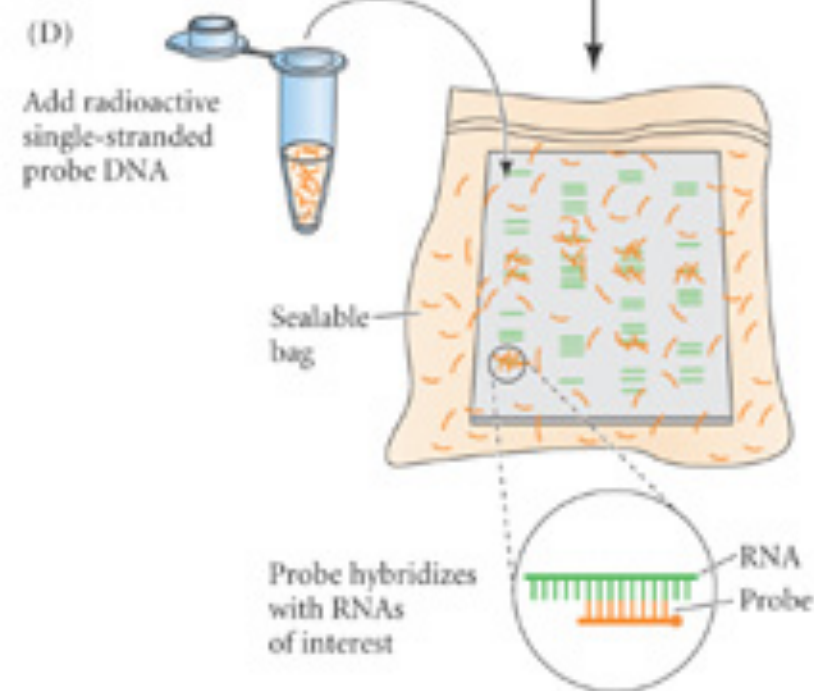
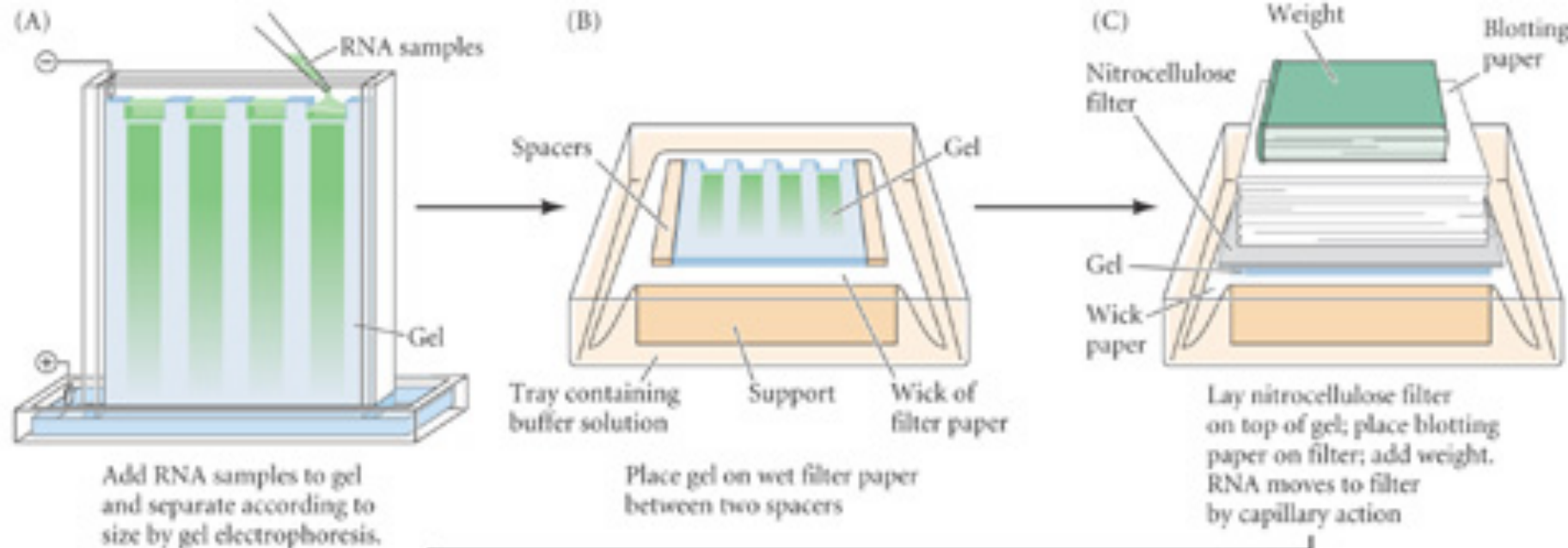


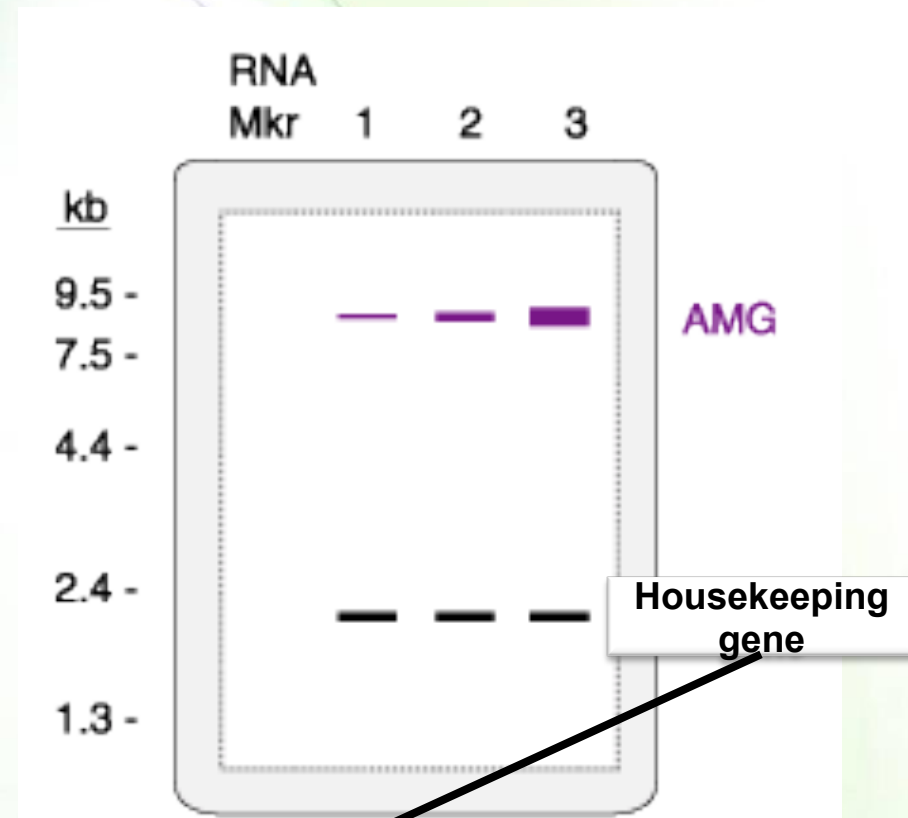
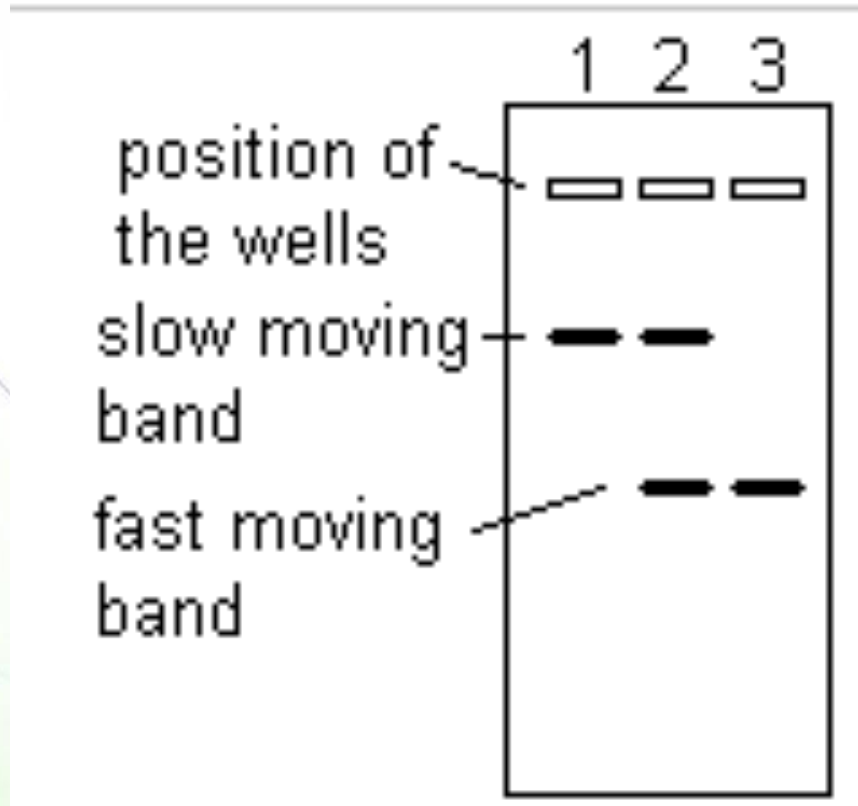


Northern blotting



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





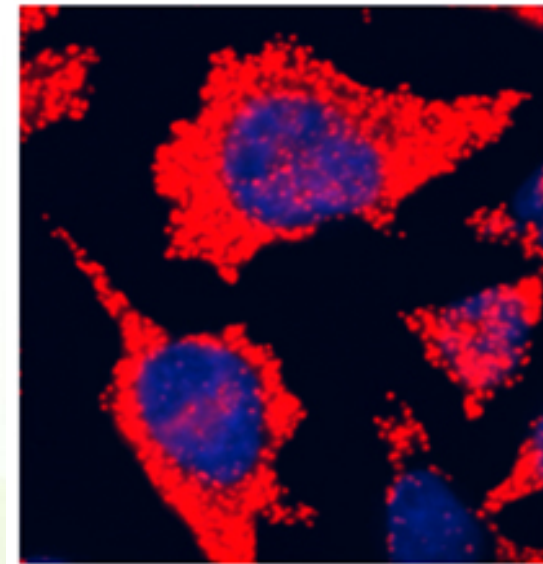
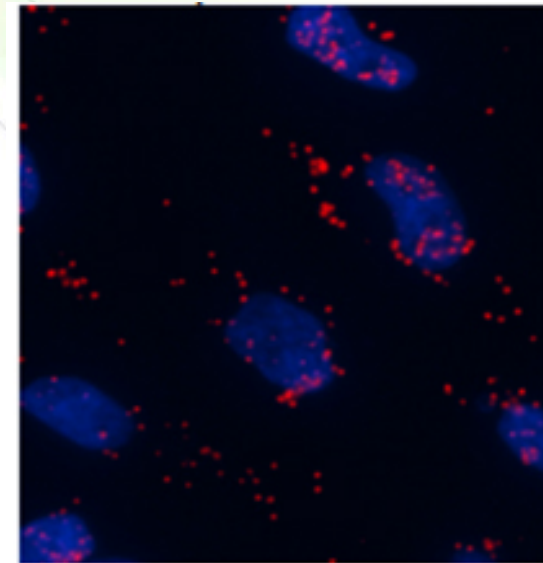
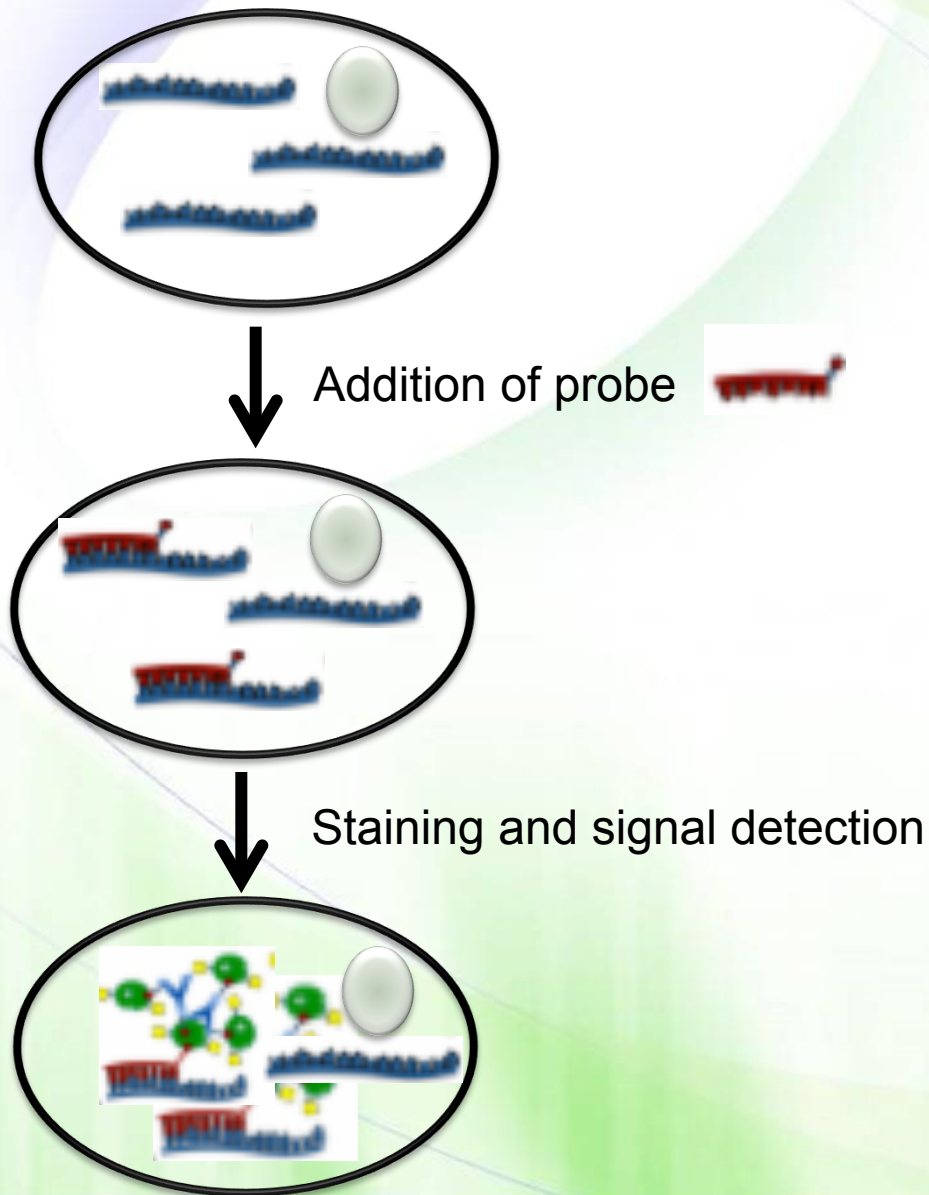
A gene with constant expression like actin

In situ hybridization

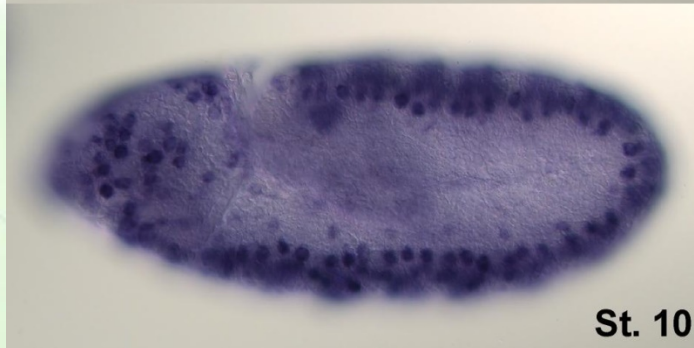
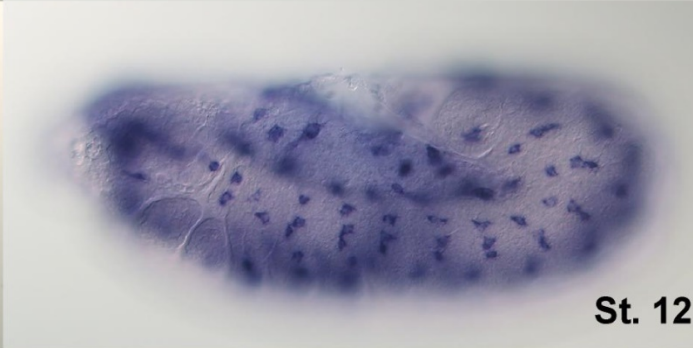
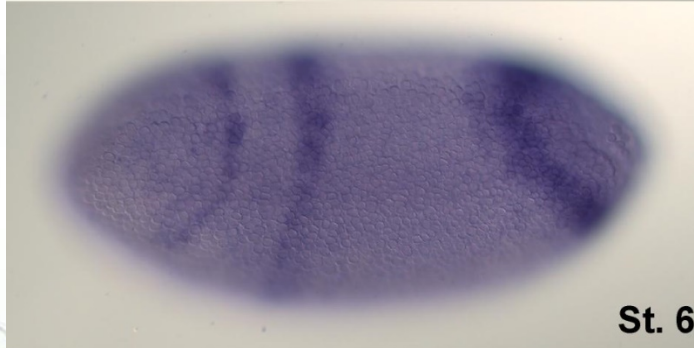
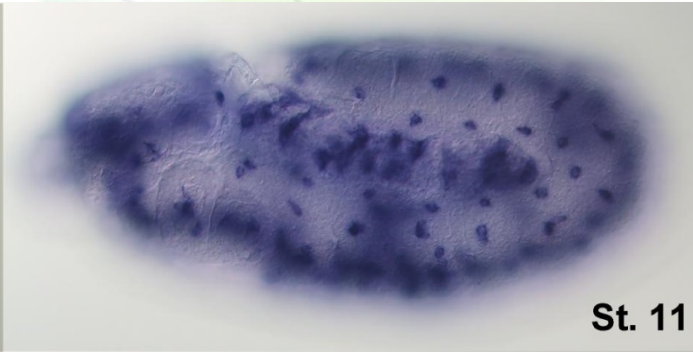


- In situ hybridization methods reveals the distribution of specific RNA molecules in cells in tissues.
- RNA molecules can hybridize when the tissue is incubated with a complementary DNA or RNA probe.
- In this way the patterns of differential gene expression can be observed in tissues, and the location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

Procedure of in situ hybridization



RNA expression in drosophila



Hox gene activity, *Drosophila* embryo

9-13
Abd-B

8
abd-A

lab
1

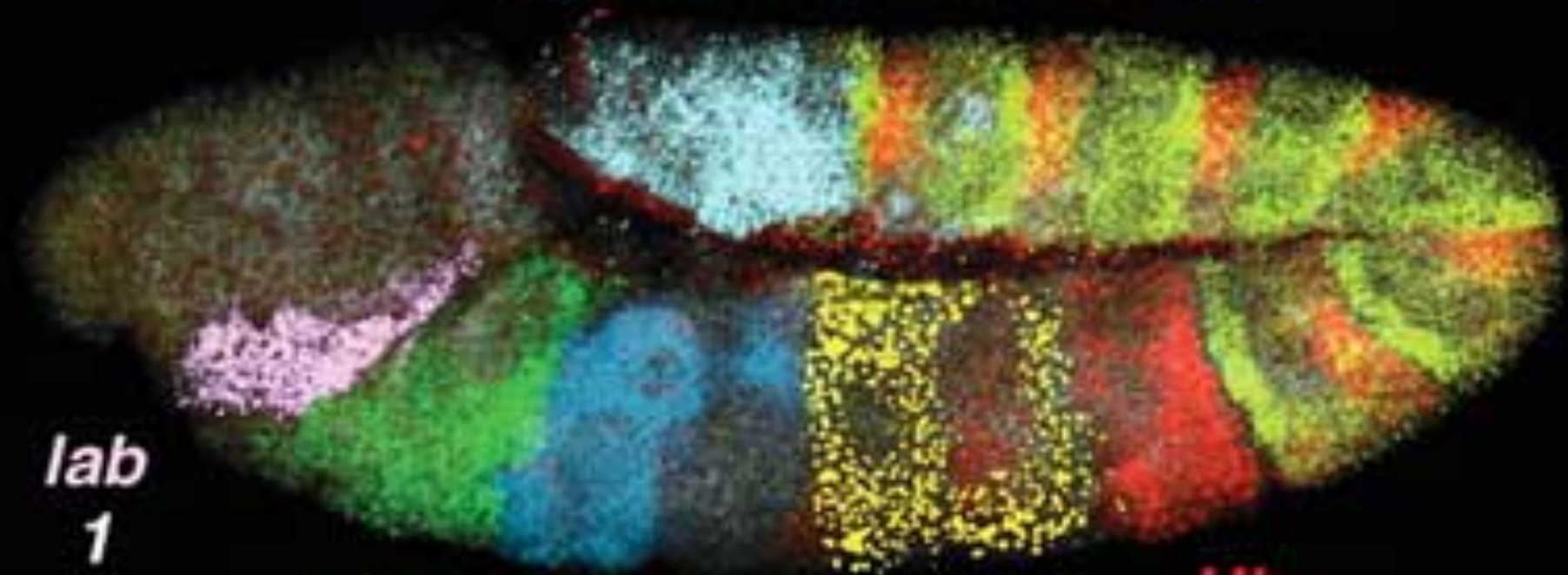
Dfd
4

Scr
5

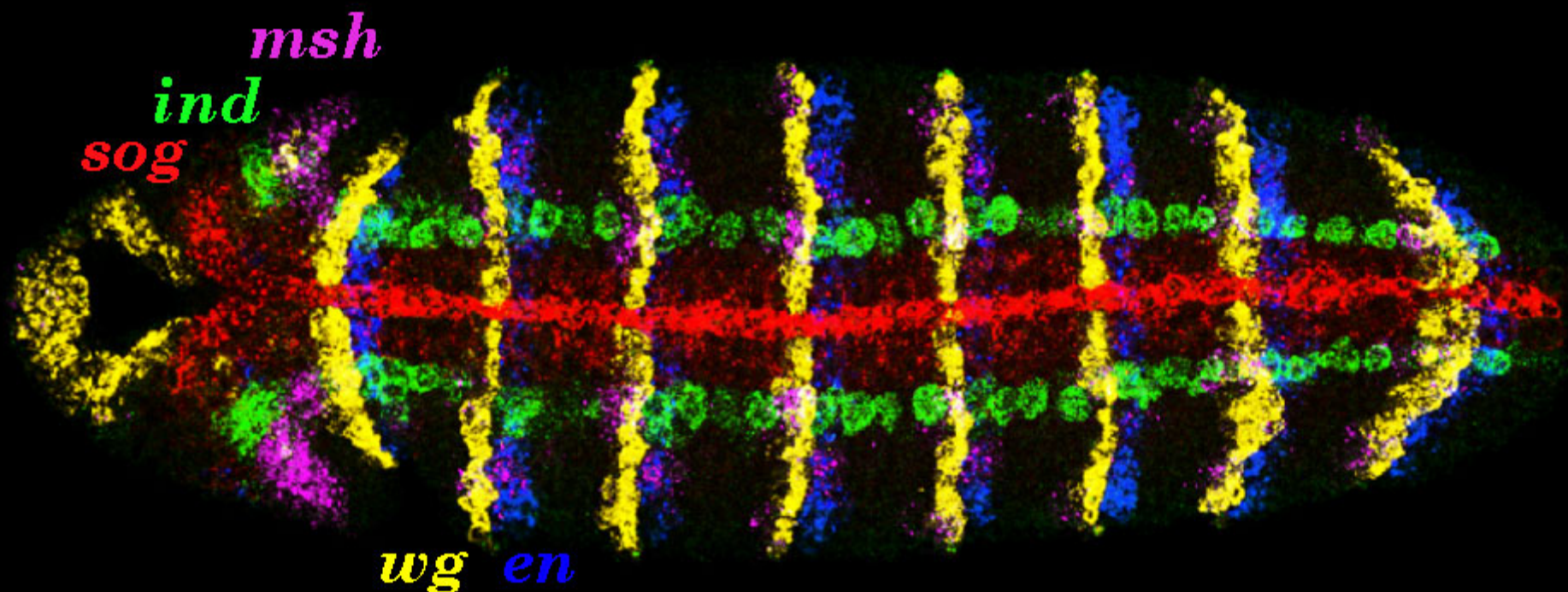
Antp
6

Ubx
7

Hox homology groups



Multiplex detection of 5 different transcripts in a single embryo



msh

ind

sog

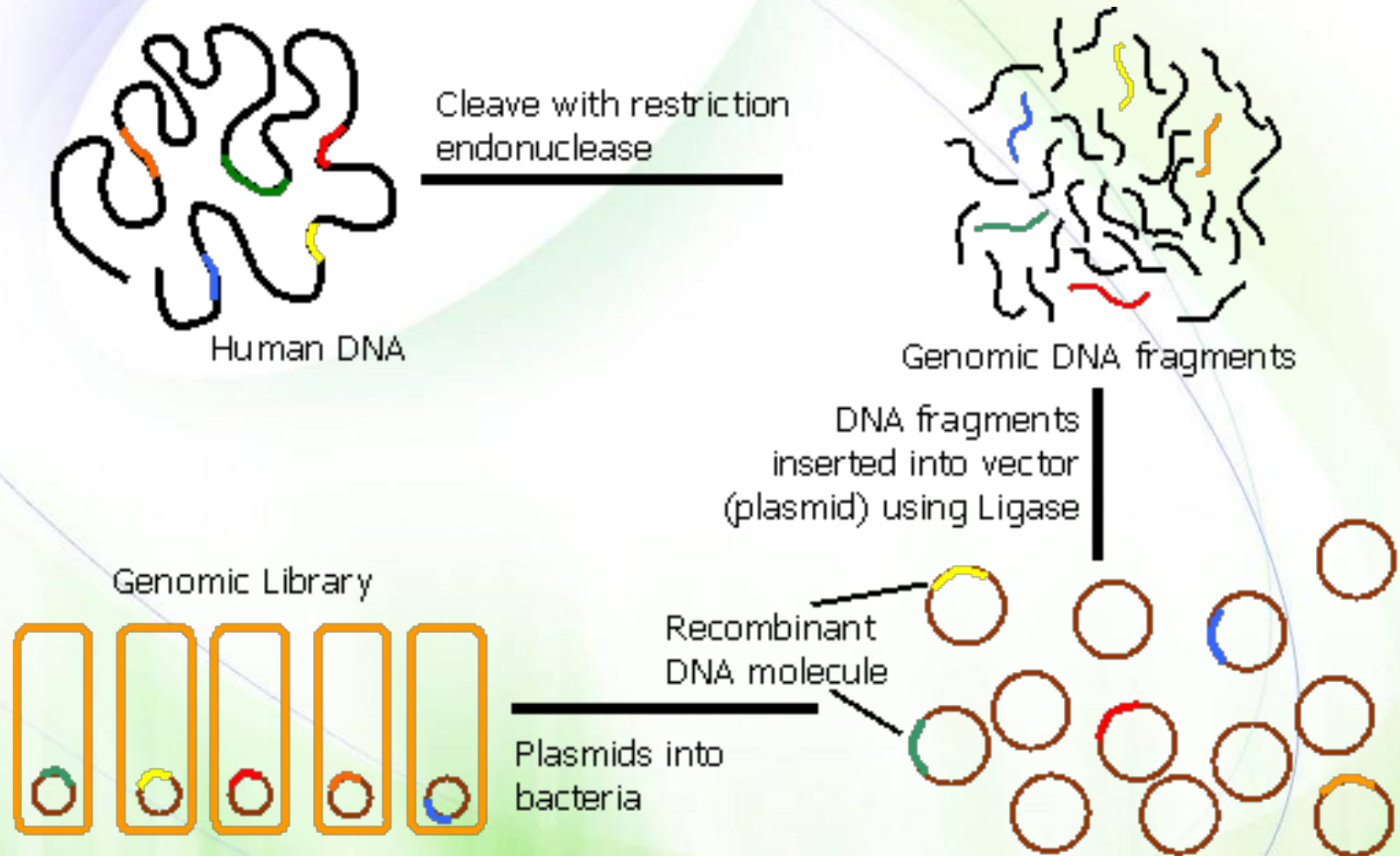
wg en

What is a DNA library?



- A library can be created for DNA fragments just like book libraries.
- You can have clones of bacteria each containing a specific piece of DNA.
- You can save these clones in the freezer and take whichever clone you want to study.
- <http://www.sumanasinc.com/webcontent/animations/content/dnalibrary.html>

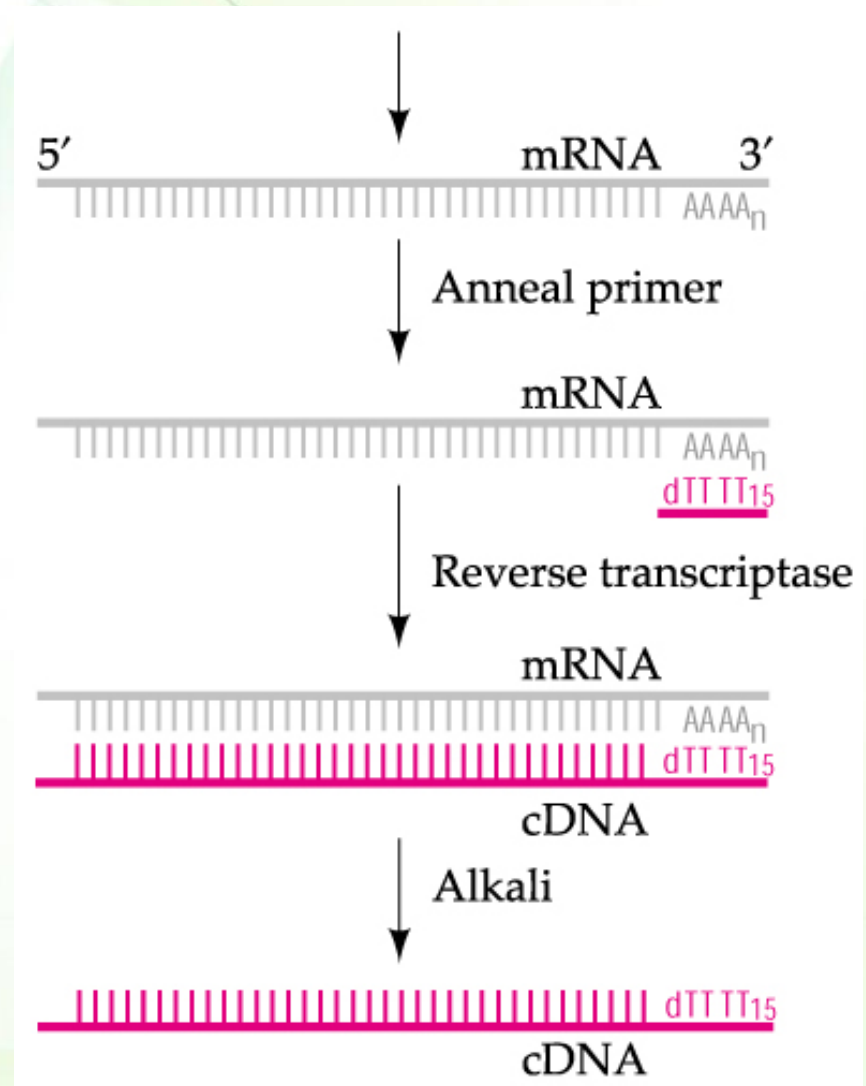
Genomic DNA library



cDNA library



- This library contains only those DNA sequences that are transcribed into mRNA.
- This is done by extracting the mRNA from cells and then making a complementary DNA (cDNA) copy of each mRNA molecule present.
- cDNA is made by retroviral reverse transcriptase.



Genomic vs. cDNA libraries

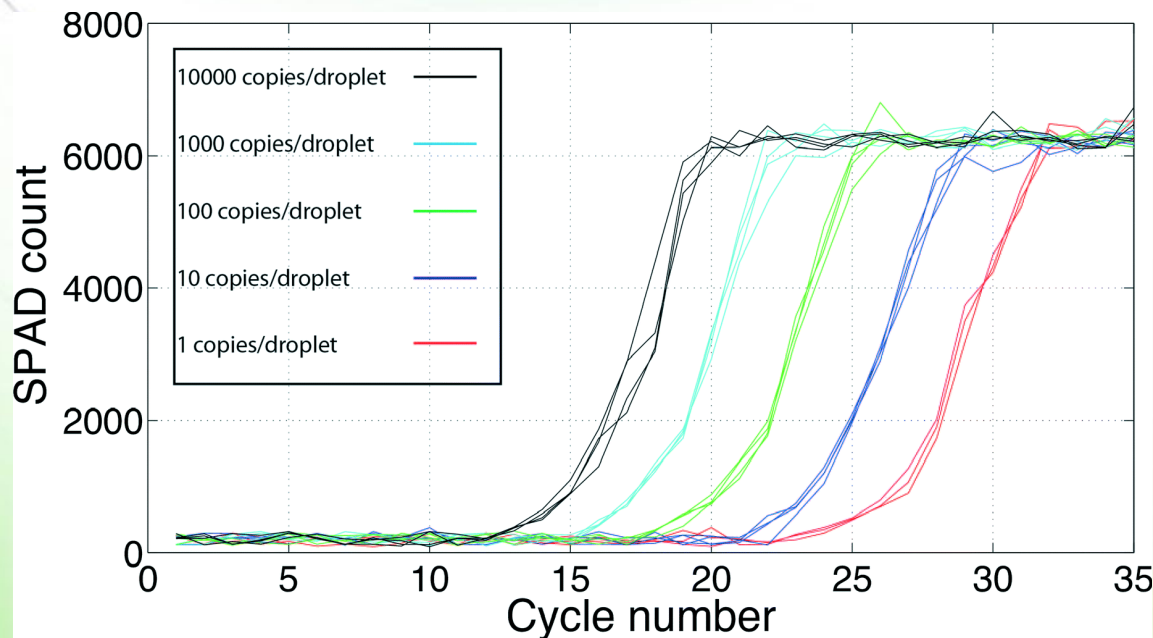


- Genomic clones represent a random sample of all of the DNA sequences in an organism. By contrast, cDNA clones contain only those regions of the genome that have been transcribed into mRNA.
- Because the cells of different tissues produce distinct sets of mRNA molecules, a distinct cDNA library is obtained for each type of cell used to prepare the library.

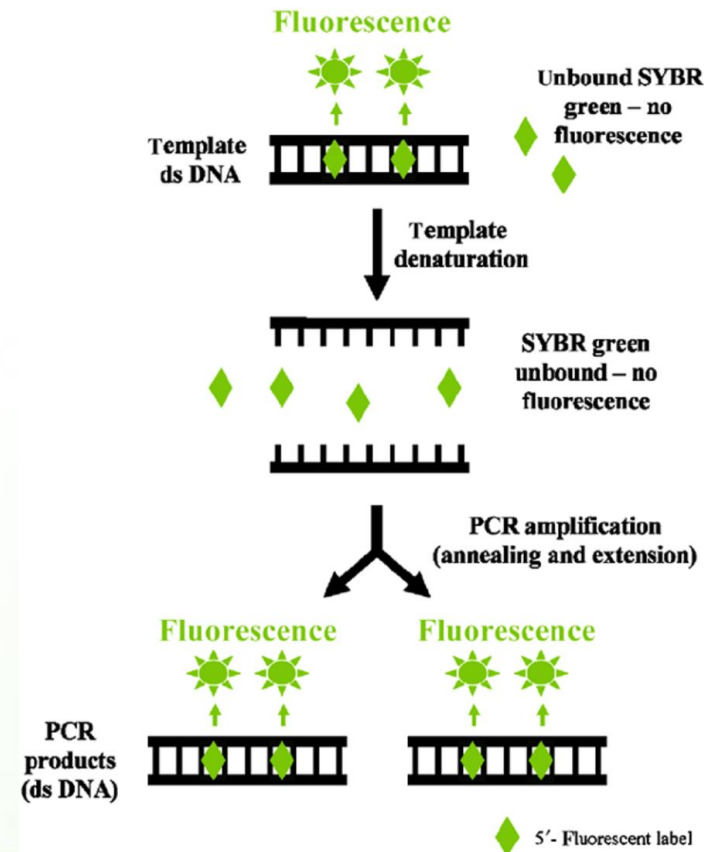
Quantitative real-time PCR of mRNA



- 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 it is detected.



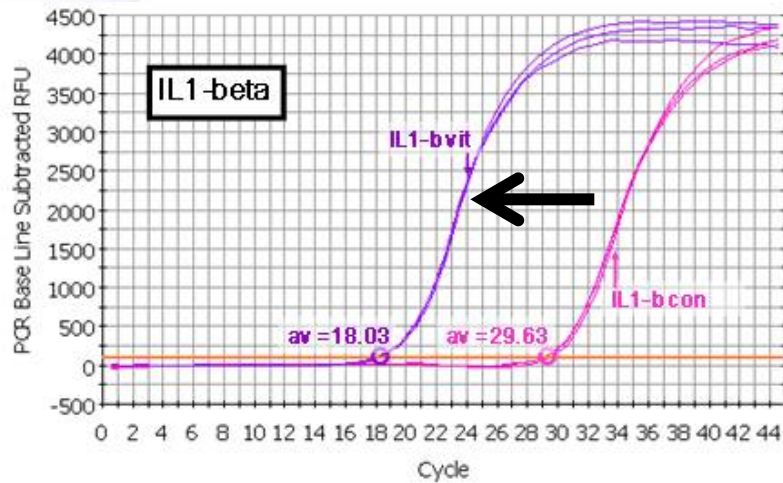
(a) SYBR green assays



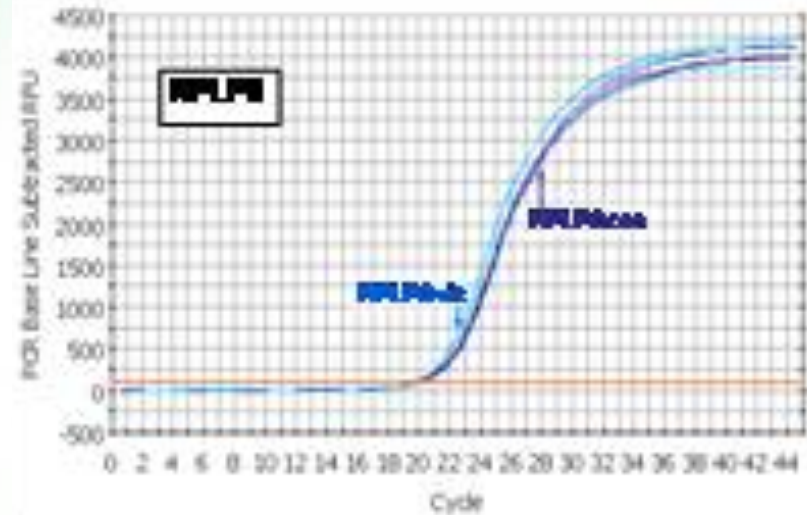
Example



A gene of interest

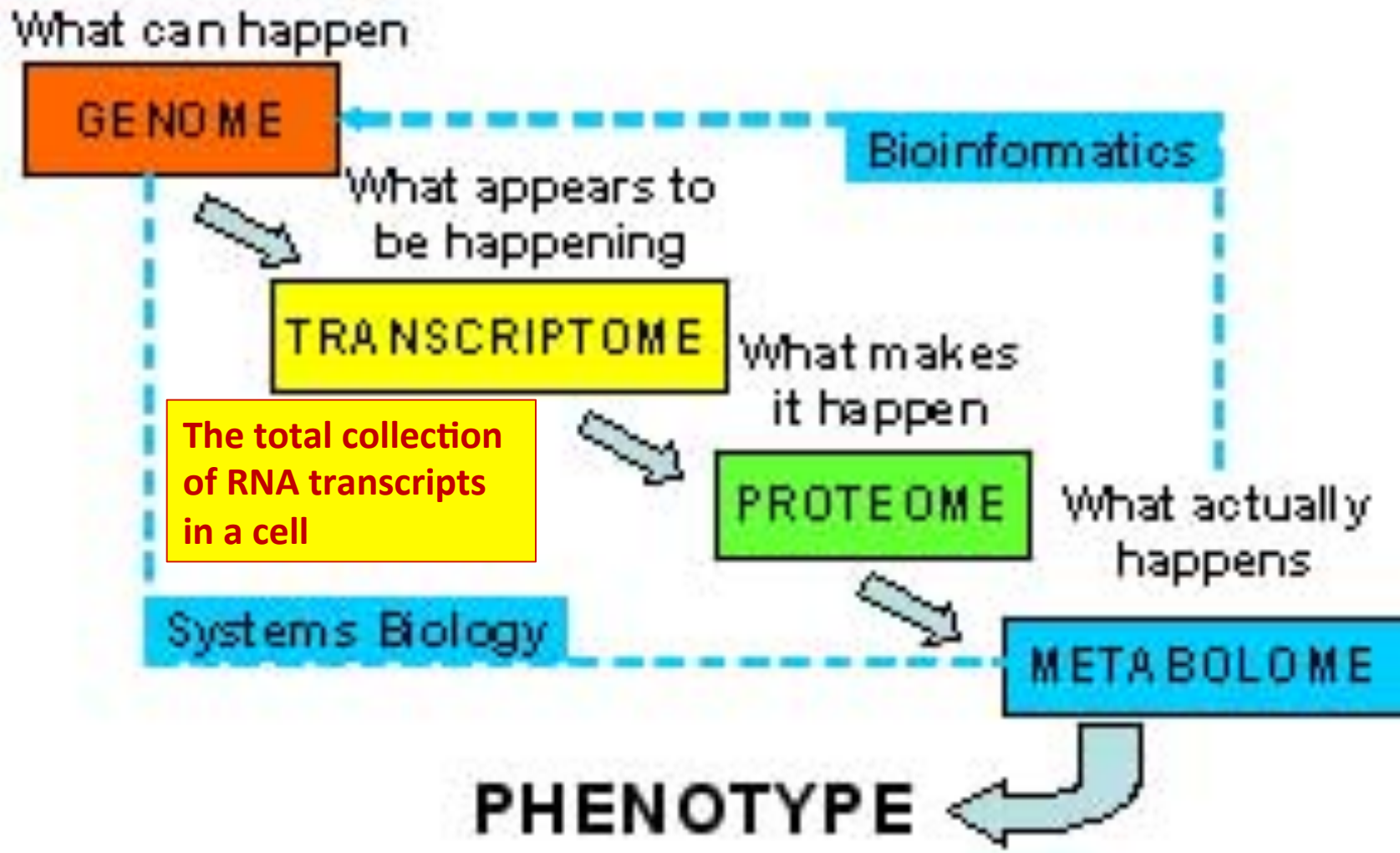


Housekeeping gene



Unaltered expression

The science of -omics



Studying the transcriptome

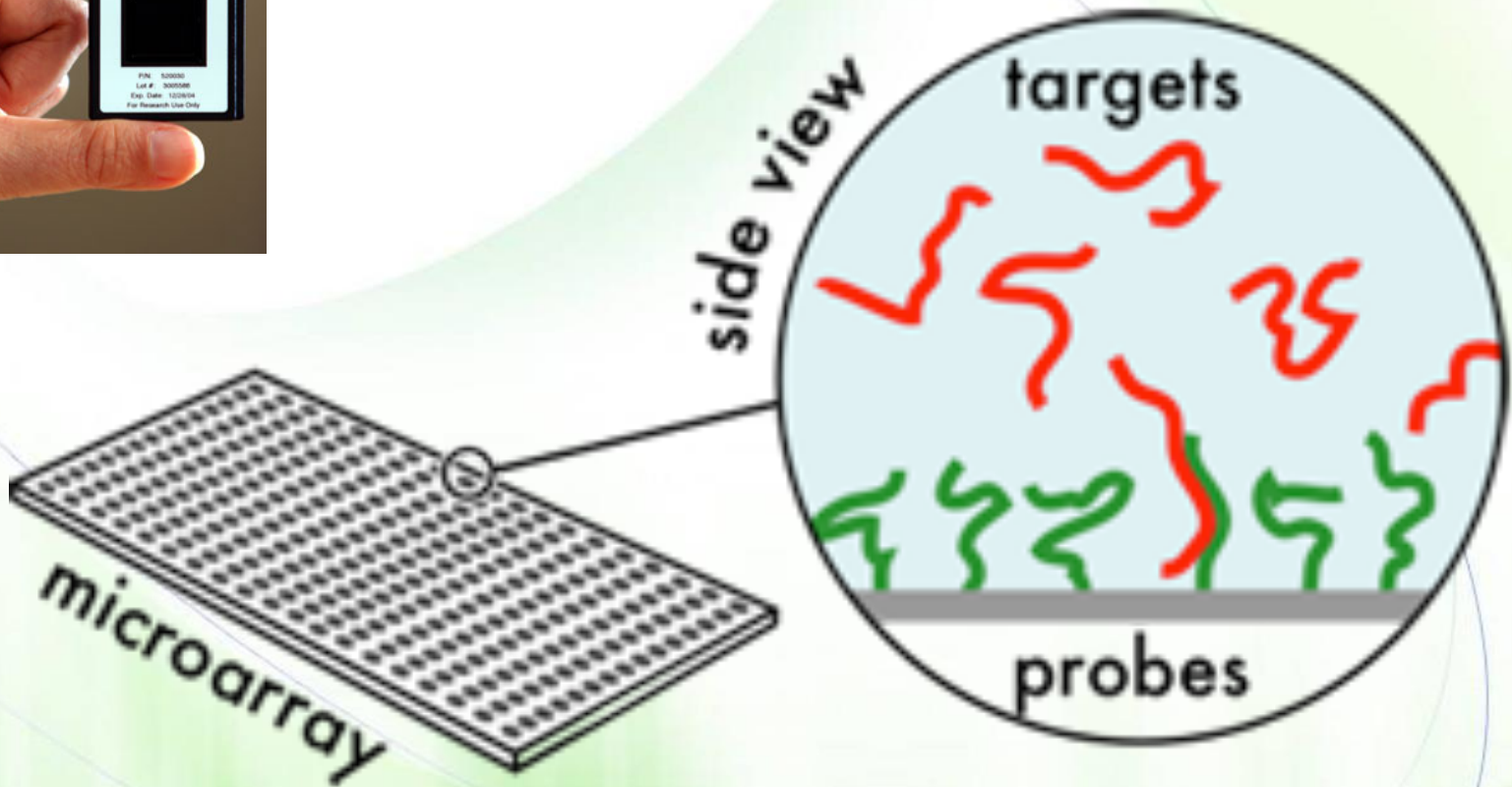


- One such method in studying transcriptomes is DNA microarrays, which allow the analysis of the RNA products of thousands of genes all at once.
- By examining the expression of so many genes simultaneously, we can understand gene expression patterns in physiological and pathological states.

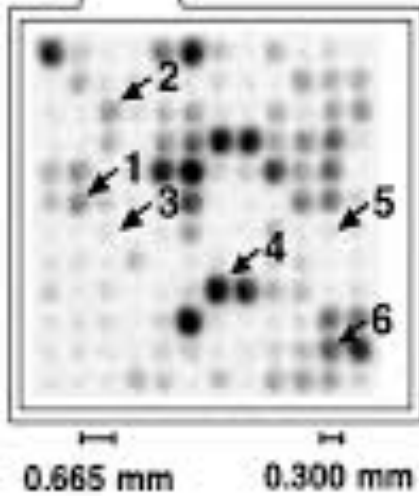
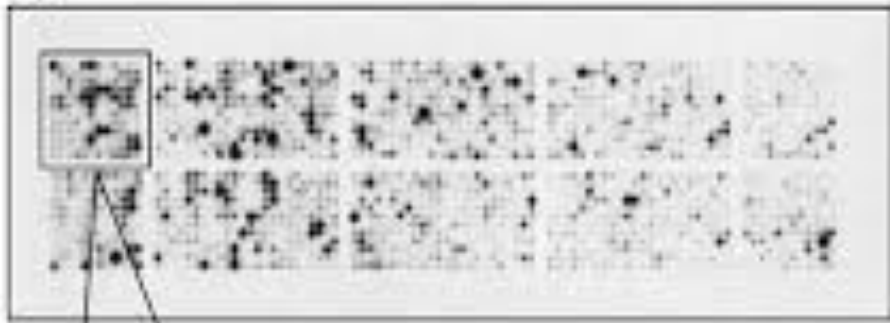
DNA microarrays



- DNA microarrays are glass microscope slides 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>



A DNA microarray



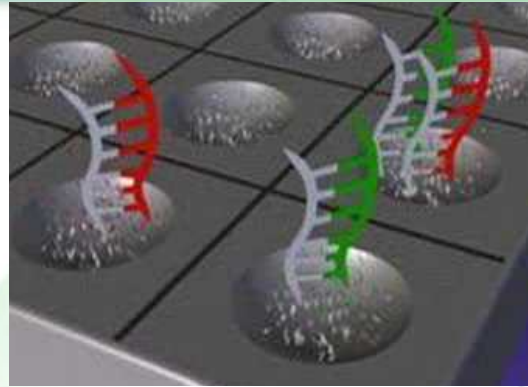
This is done for a single sample using radioactively labeled cDNA.

- mRNA from the cells being studied is first extracted and converted to cDNA.
- The cDNA is labeled with a radioactive probe.
- The microarray is incubated with the labeled cDNA sample for hybridization to occur.
- If a gene is expressed, then the cDNA will exist and bind to a specific complementary DNA fragment on the microarray.
- Binding can be detected since the cDNA is labeled and expression is determined.

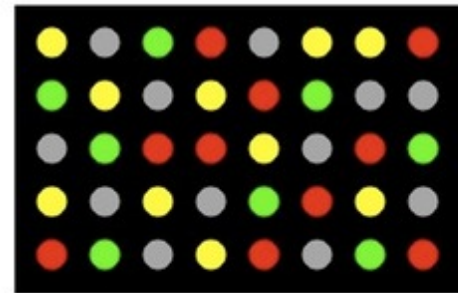
Comparative expression

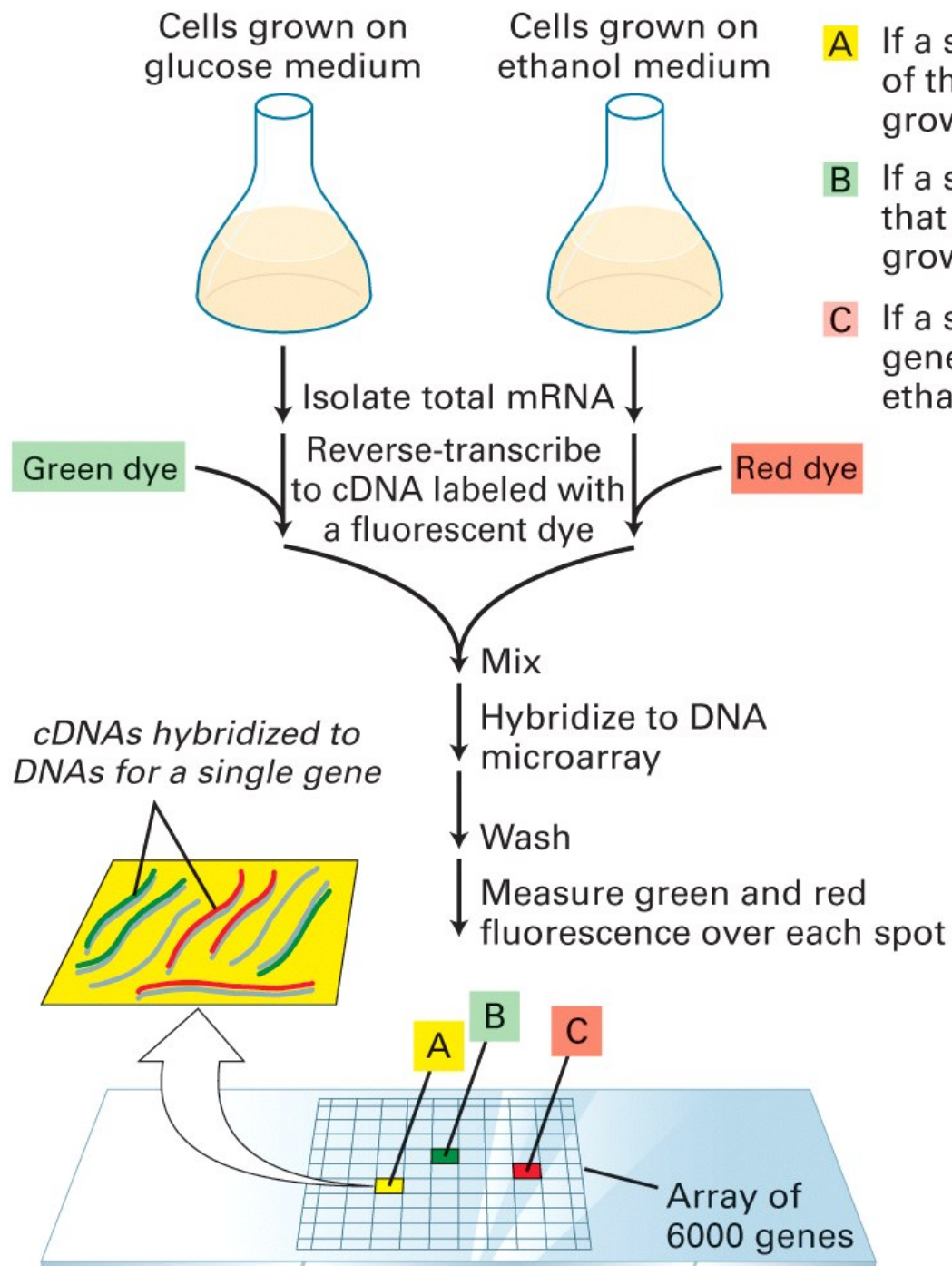


- In order to compare expression of genes two different samples, the cDNA molecules are fluorescently labeled with different colors (green and red) and added to the array.
- An increase in the amount of a RNA molecule in one sample versus the other is reflected by an increase in the amount of produced cDNA and an increase in fluorescence in the bound spot.



- Gene NOT active in either normal or diseased sample
- Gene IS active in both normal and diseased sample
- Gene active in normal only
⇒ *very interesting!*
- Gene active in disease only
⇒ *very interesting!*

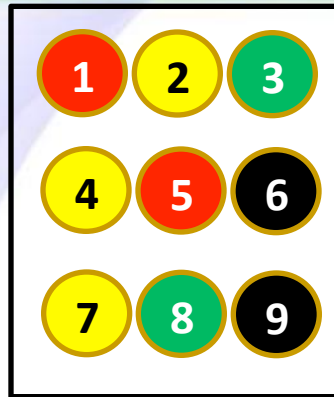




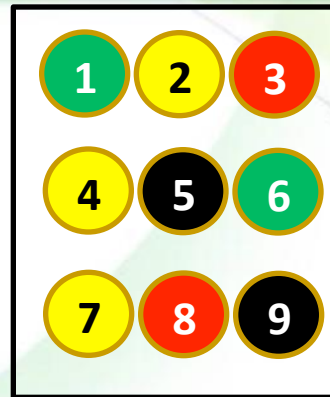
- A** If a spot is yellow, expression of that gene is the same in cells grown either on glucose or ethanol
- B** If a spot is green, expression of that gene is greater in cells grown in glucose
- C** If a spot is red, expression of that gene is greater in cells grown in ethanol



Sample 1



Sample 2



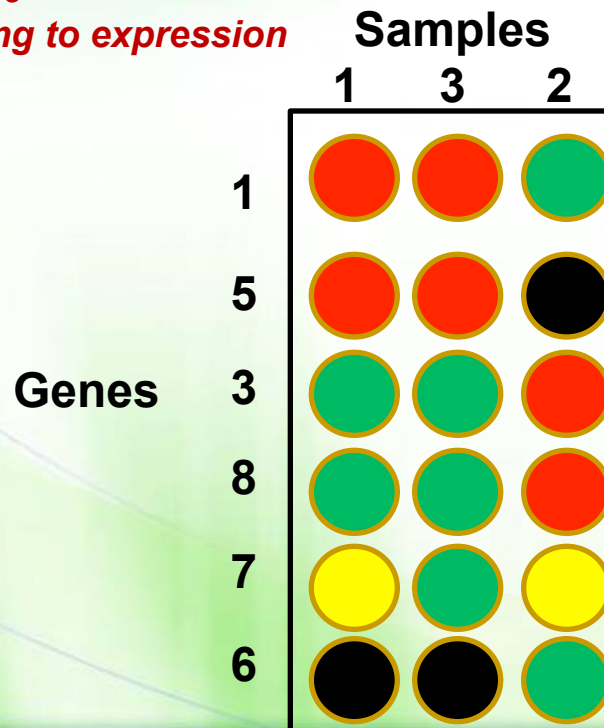
Sample 3



Combine results

Eliminate samples 2, 4, & 9

Cluster samples according to expression



This can be done at a larger scale whereby samples are compared to the same control sample and a computer program combines all data illustrating differences in expression among the samples and classifying them into different groups.

DNA microarrays and breast cancer

