

20.109

LABORATORY FUNDAMENTALS IN
BIOLOGICAL ENGINEERING

MODULE 2

EXPRESSION ENGINEERING

Lecture # 4

Leona Samson

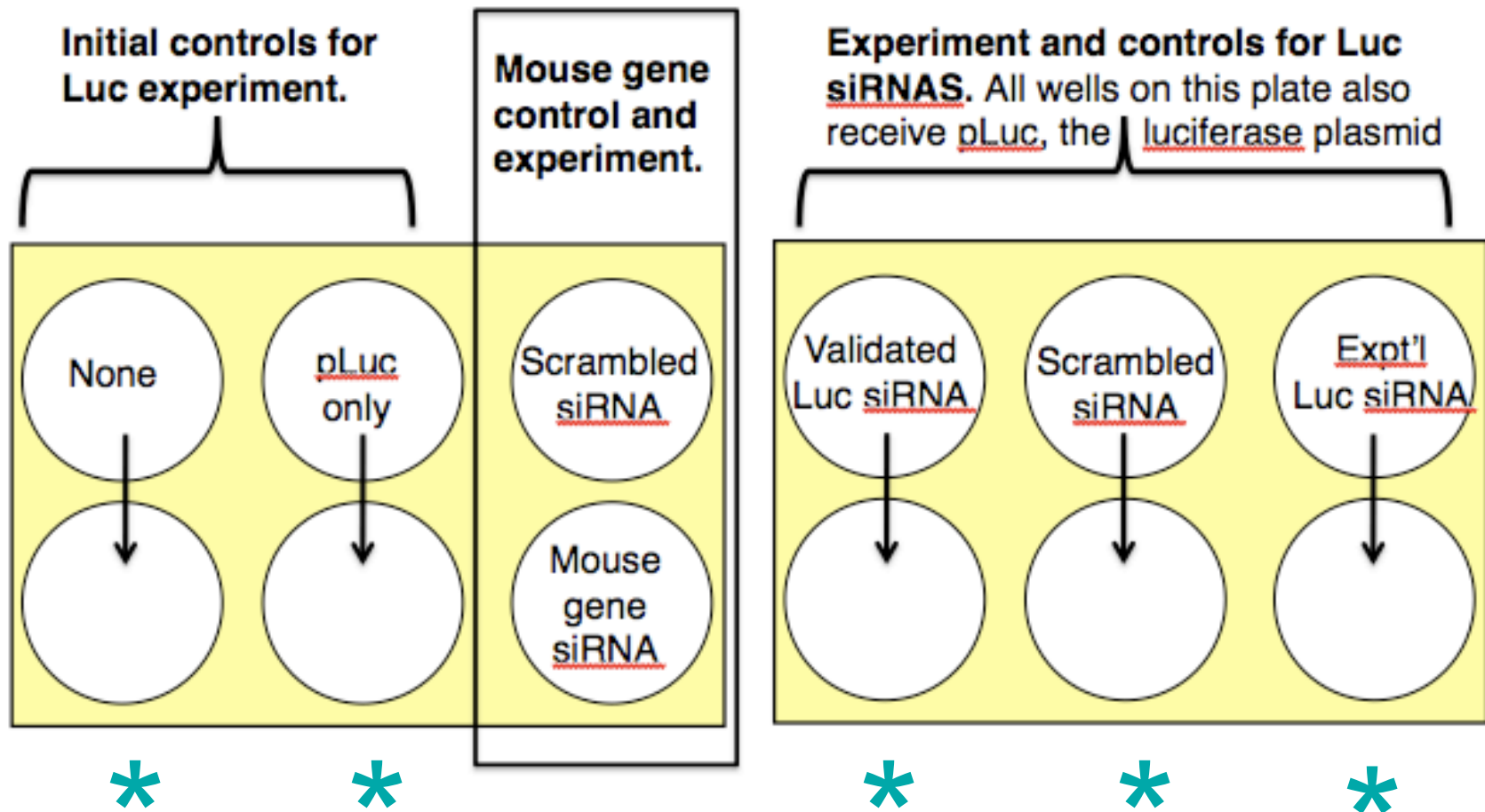
April 2nd 2009

Snapshot of the next four weeks

We will eliminate the expression of various genes using

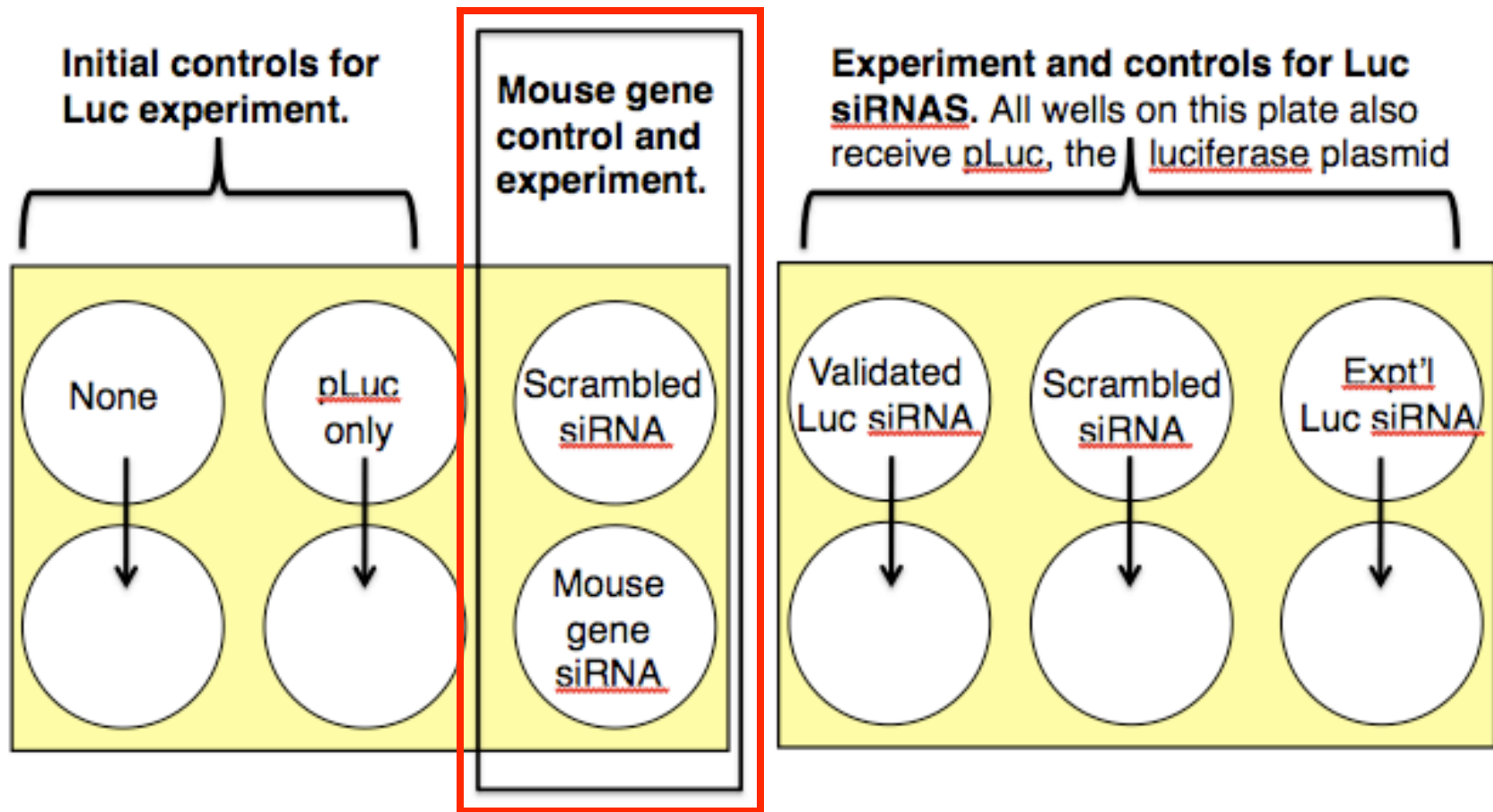
- (i) RNA interference technology
- (ii) Cultured mouse ES cells
- (iii) Chemiluminescent proteins
- (iv) DNA microarrays

siRNA knockdown of expression of Renilla Luciferase plus various mouse gene



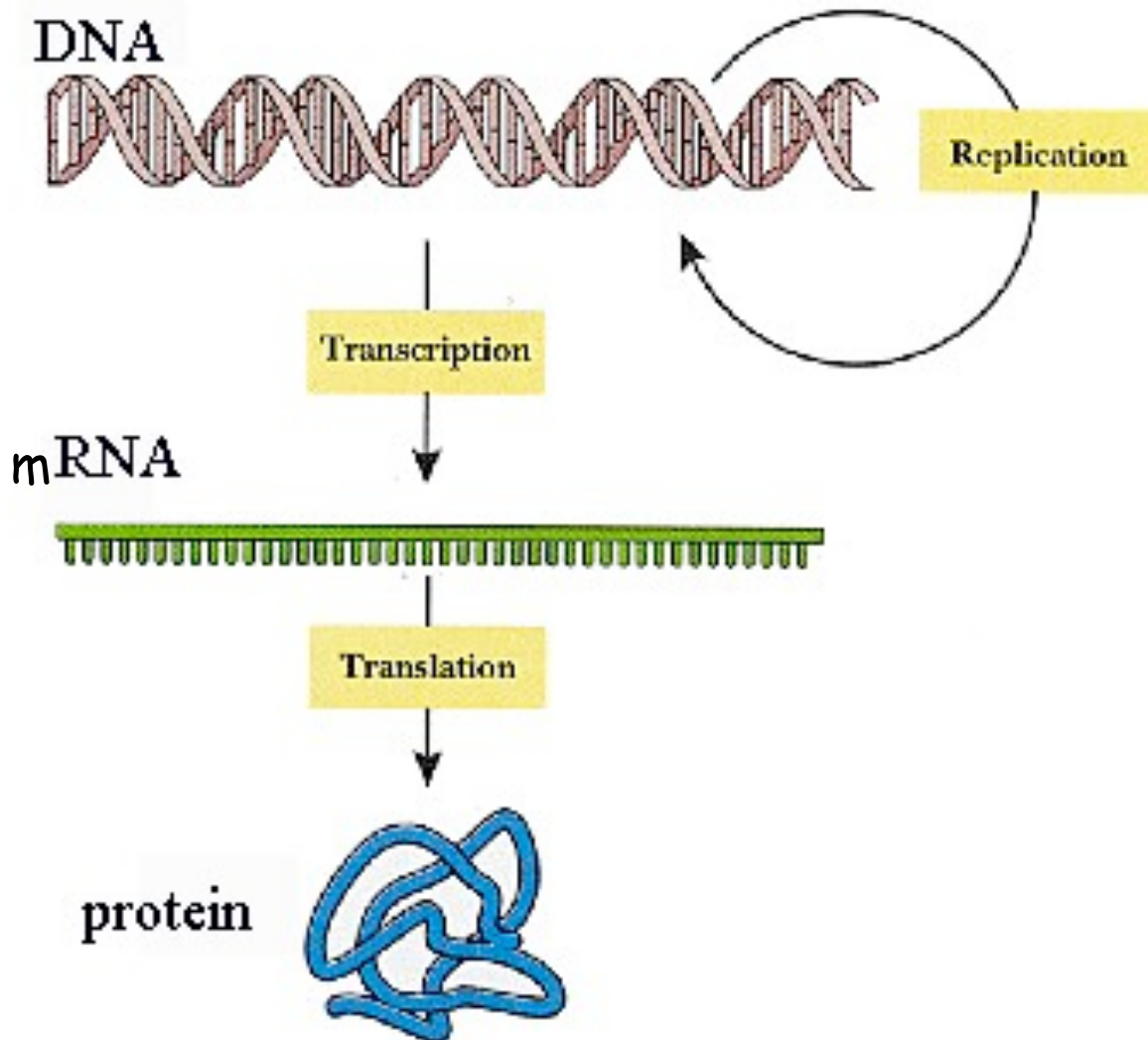
* Prepare cell extracts and measure Luciferase activities

siRNA knockdown of expression of Renilla Luciferase plus various mouse gene



Isolate total RNA in order to measure relative levels of all mRNAs – with special attention to YGI

Monitor mRNA expression level for every mouse gene in one single experiment.

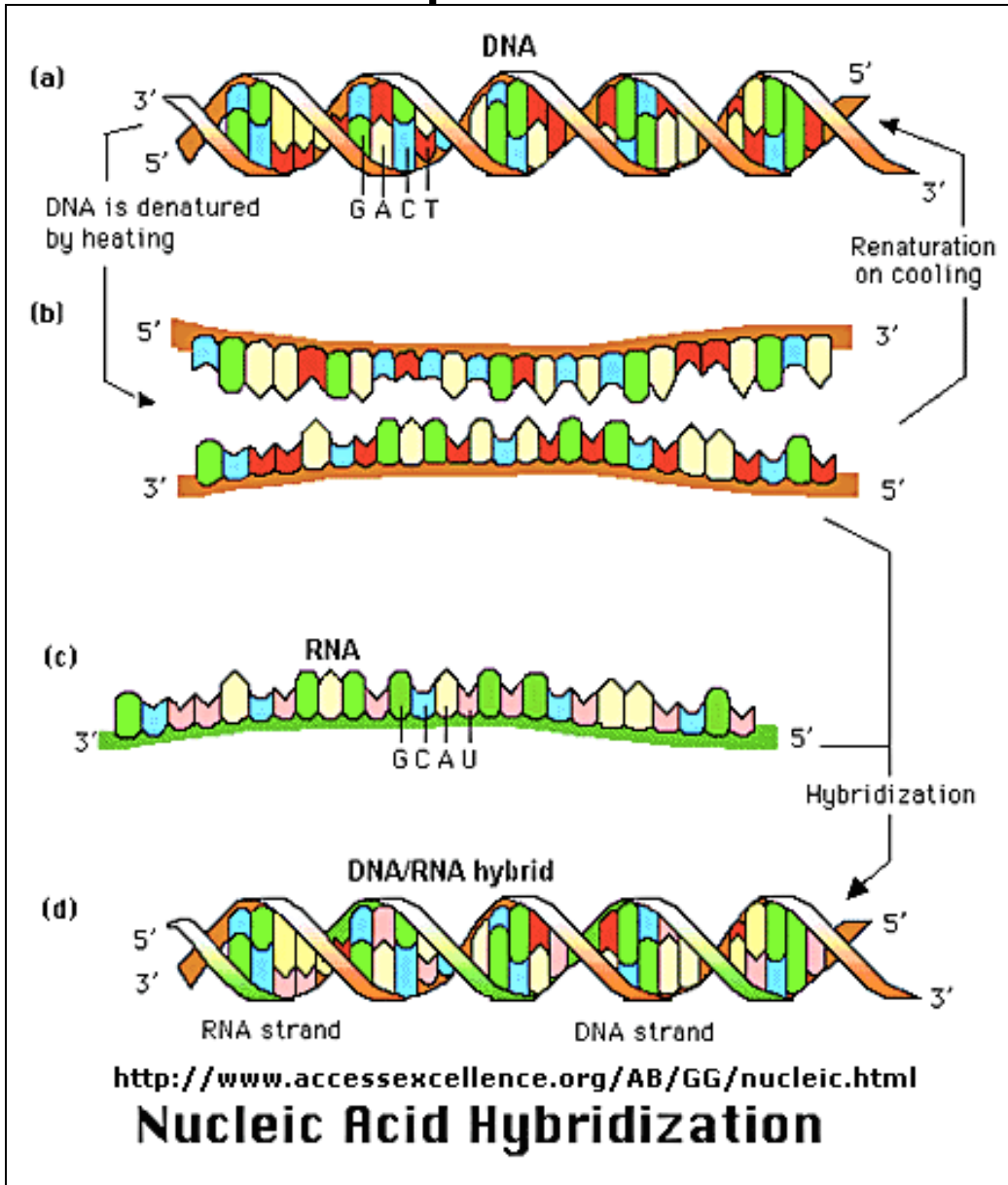


How can we measure the level of **thousands** of mRNA species present in a particular cell type?

Now that we know the DNA sequence for every gene, this is possible!

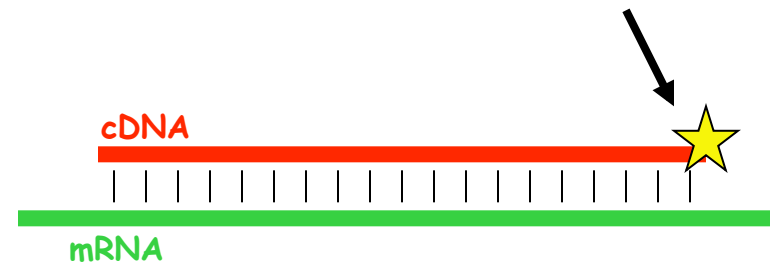
How did we measure mRNA levels one at a time?

This depends on Nucleic Acid **Hybridization**

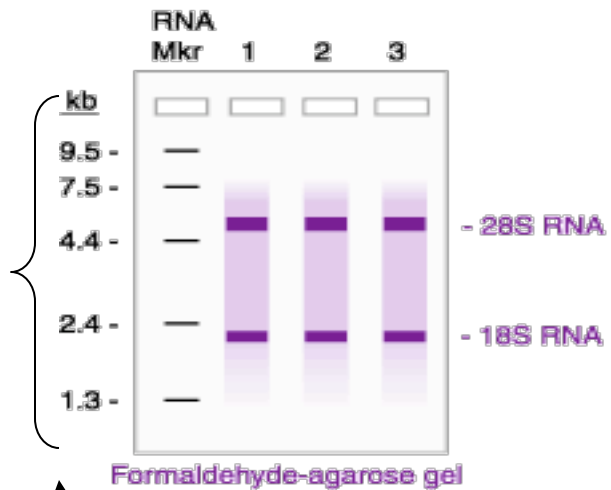


The specificity of G pairing with C and A pairing with T (or U) drives hybridization and provides a mechanism for quantitatively assessing the amount of a specific mRNA species in cells.

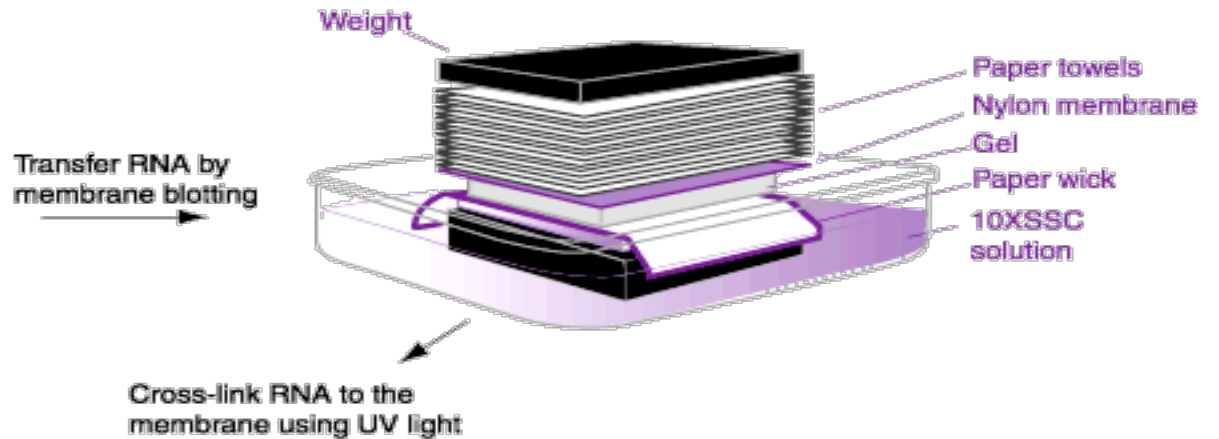
^{32}P - label



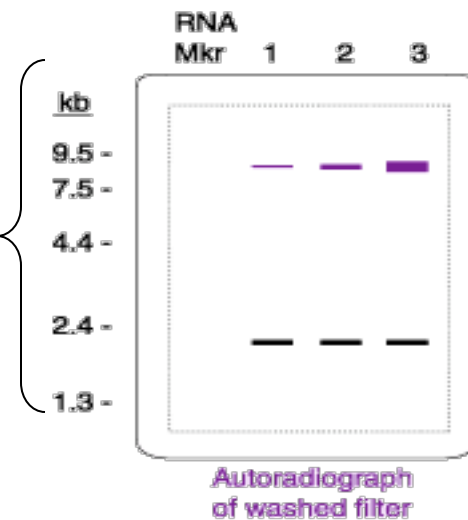
Lets first back-up. How did we measure mRNA levels one or two at a time? Northern Blots



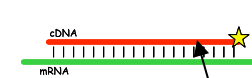
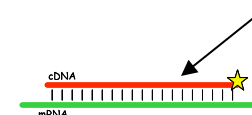
All mRNAs separated by size



Hybridize membrane with denatured ³²P-cDNA probe



AMG probe

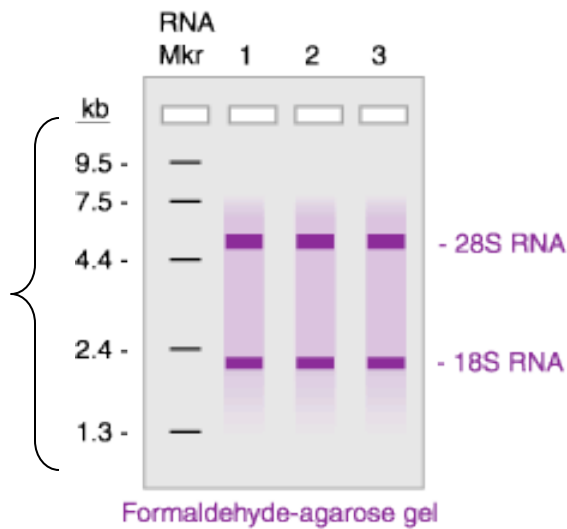


GAPDH probe

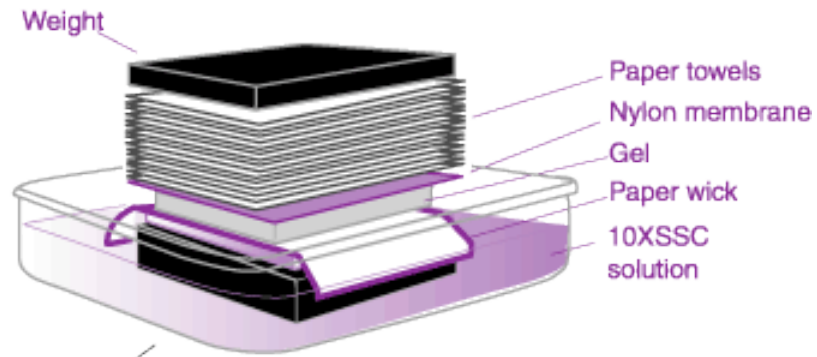
Specific mRNAs Lit-up by radioactive cDNA probes

How to monitor mRNA expression level for every gene: Global transcriptional profiling

- Carry out thousands Northern Blots?
- Instead - DNA microarrays were developed
- DNA microarrays for global transcriptional profiling were not feasible before the sequencing of whole genomes.

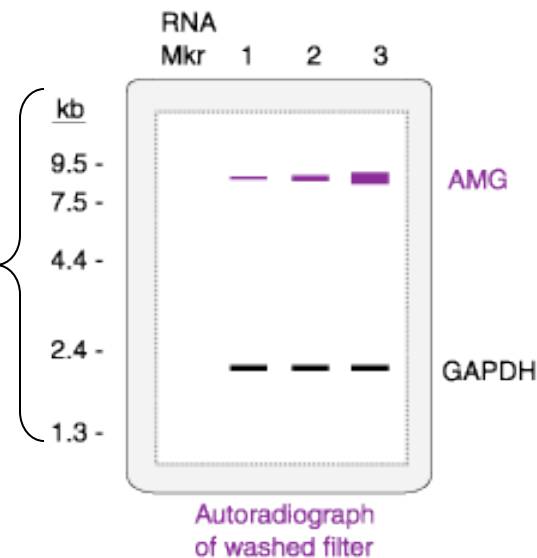


Transfer RNA by
membrane blotting



Cross-link RNA to the
membrane using UV light

Hybridize membrane with
denatured ^{32}P -cDNA probe



All mRNAs
separated by
size

The immobilized mRNA population is probed (hybridized) with ^{32}P -labeled DNA sequences specific for one or two genes

Northern Blots

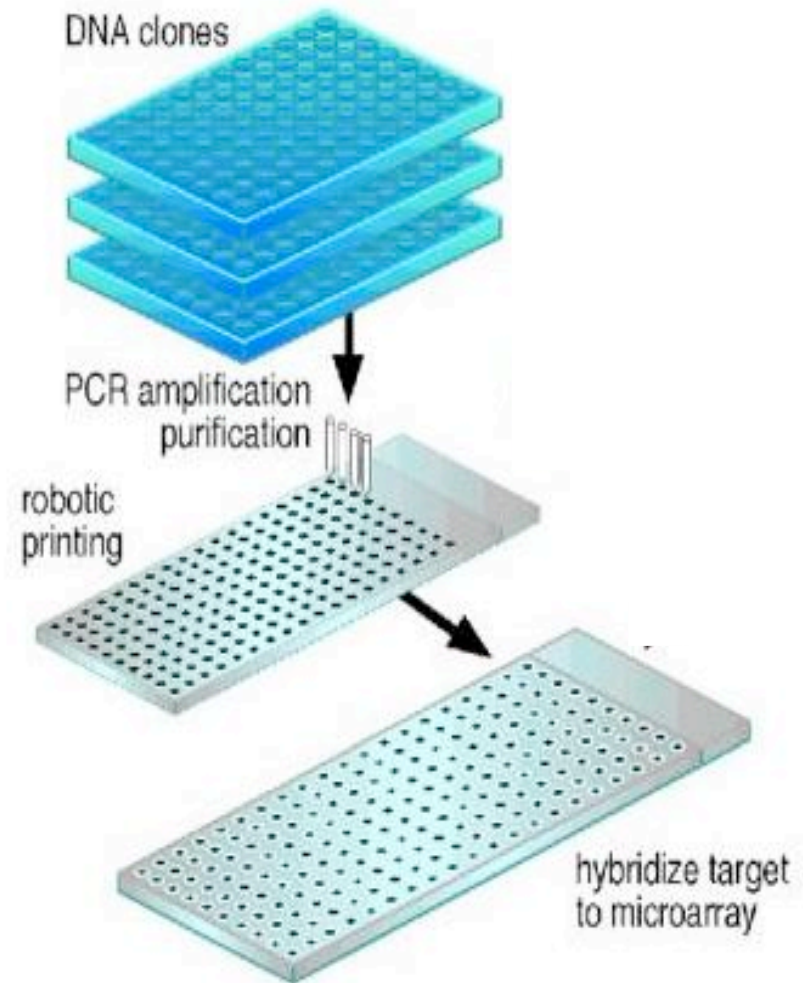
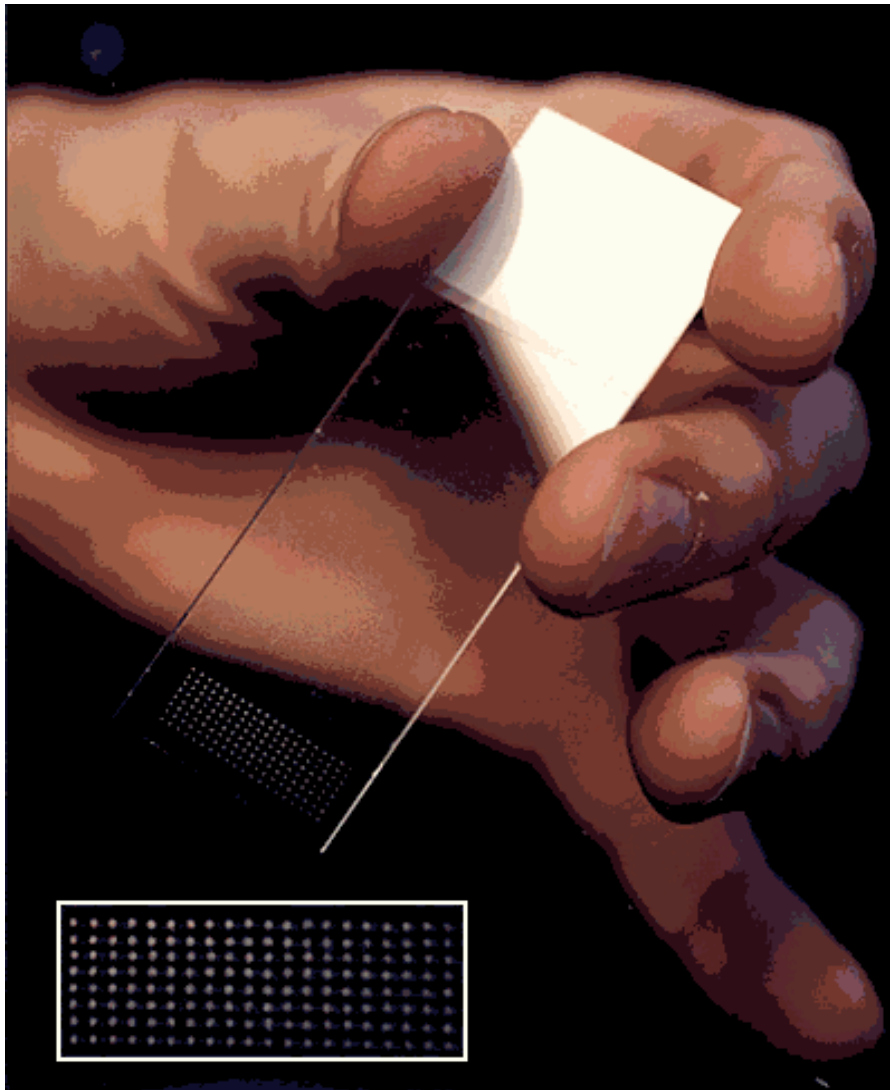
Immobilized mRNA population hybridized with labeled DNA probe representing one or two genes

DNA Microarrays

Immobilized DNA probes representing all possible genes hybridized with labeled mRNA population

Need to achieve two things:

- (i) Immobilize (array) thousands of DNA probes specific for each individual mRNA gene product
- (ii) Label mRNA populations



Up to 20,000 probes per slide

**The probes can be cDNAs (~ 1Kb) or oligonucleotides
(20-70 mers)**

Robots designed to spot up to 20,000 DNA probes per slide

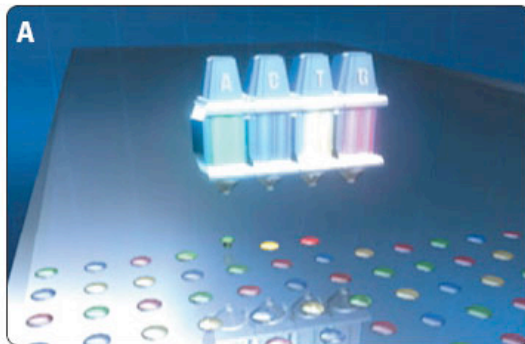


The probes can be cDNAs (~ 1Kb) or oligonucleotides (20-70 mers)

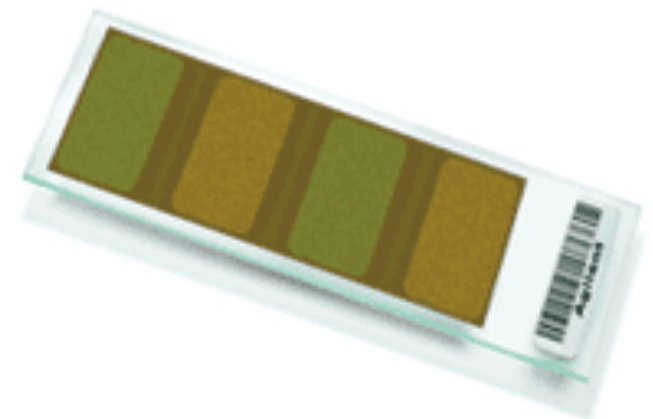
The arrays we'll be using.....

Agilent's non-contact industrial inkjet printing process uniformly deposits oligo monomers onto specially-prepared glass slides. Both the catalog and custom microarrays are manufactured using Agilent's non-contact in situ synthesis process of printing 60-mer length oligonucleotide probes, base-by-base, from digital sequence files. This is achieved with an inkjet process which delivers extremely small, accurate volumes (picoliters) of the chemicals to be spotted. Standard phosphoramidite chemistry used in the reactions allows for very high coupling efficiencies to be maintained at each step in the synthesis of the full-length oligonucleotide. Precise quantities are reproducibly deposited "on the fly." This engineering feat is achieved without stopping to make contact with the slide surface and without introducing surface-contact feature anomalies, resulting in consistent spot uniformity and traceability.

Ink-jet Technology



4x44K
spots
"features"




Need to achieve two things:

(i) Immobilize (array) thousands of probes specific for each individual gene

(ii) Label mRNA populations


Copy the population of purified mRNA species such that they are fluorescently labeled - hybridize to the array

RNA Sample 1

5'  AAAAAAAAAA 3'

Anneal primer containing
capture sequence I



5'  AAAAAAAAAA 3'
TTTTTTT 5' { }

cDNA synthesis




5'  AAAAAAAAAA 3'
3'  TTTTTTT 5' { }

degrade RNA, hybridize
array then bind Cy3




3'  TTTTTTT 5' 

RNA Sample 2

5'  AAAAAAAAAA 3'

Anneal primer containing
capture sequence II



5'  AAAAAAAAAA 3'
TTTTTTT 5' { }

cDNA synthesis



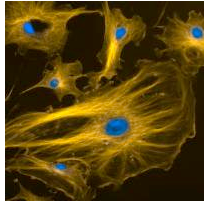
5'  AAAAAAAAAA 3'
3'  TTTTTTT 5' { }

degrade RNA, hybridize
array then bind Cy5

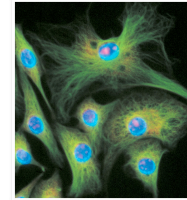


3'  TTTTTTT 5' 

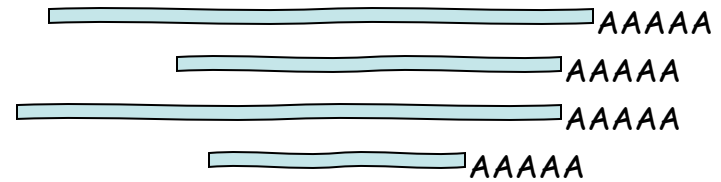
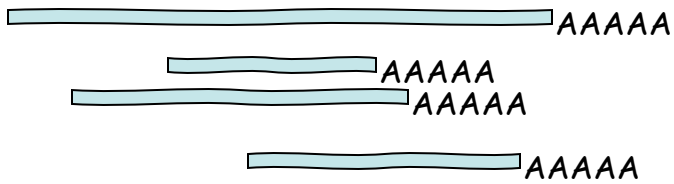
Cells in state A



Cells in state B



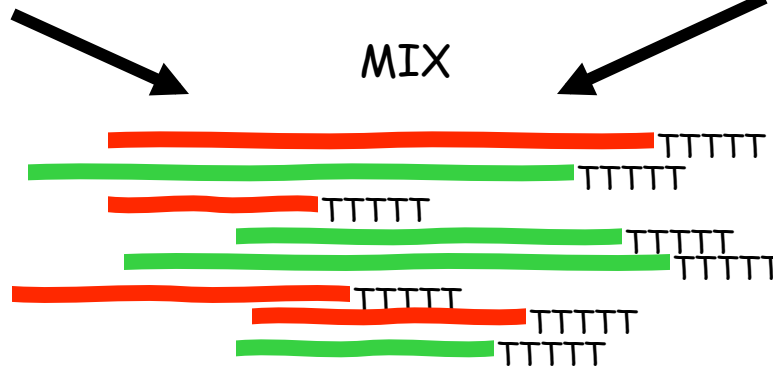
Isolate mRNA populations



Label copies of mRNA species with RED or GREEN

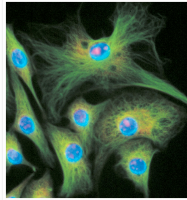


MIX

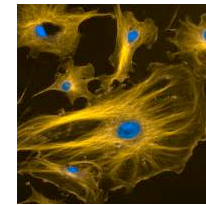


Hybridize to the microarray

Cells in state B

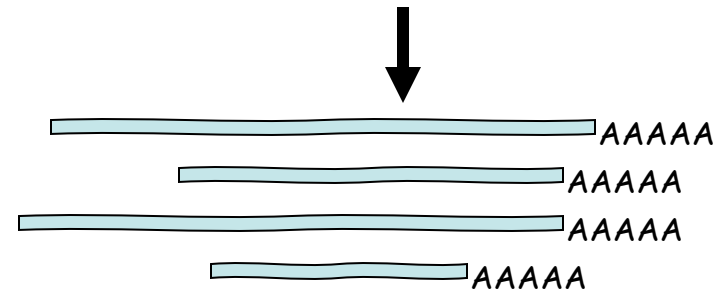
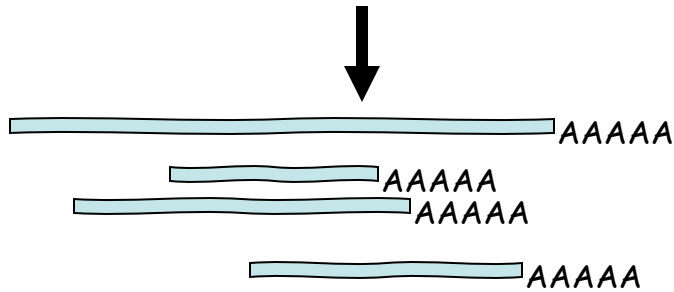


Cells in state A

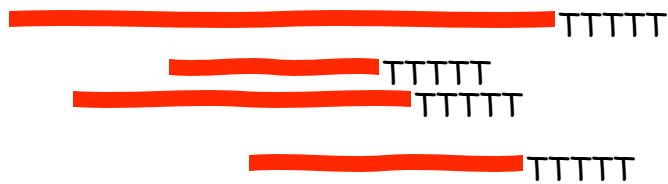


DYE SWAP

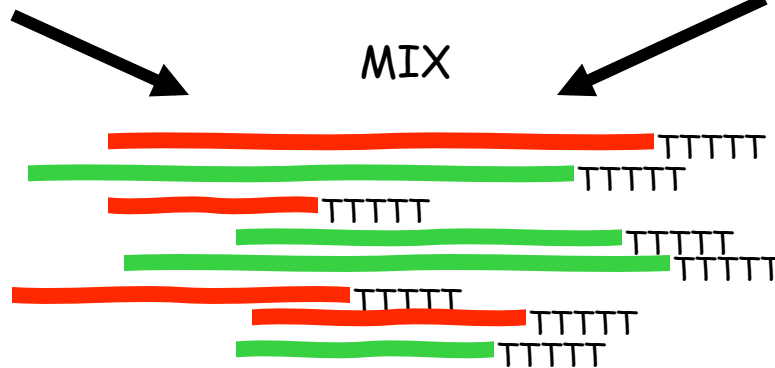
Isolate mRNA populations



Label copies of mRNA species with RED or GREEN

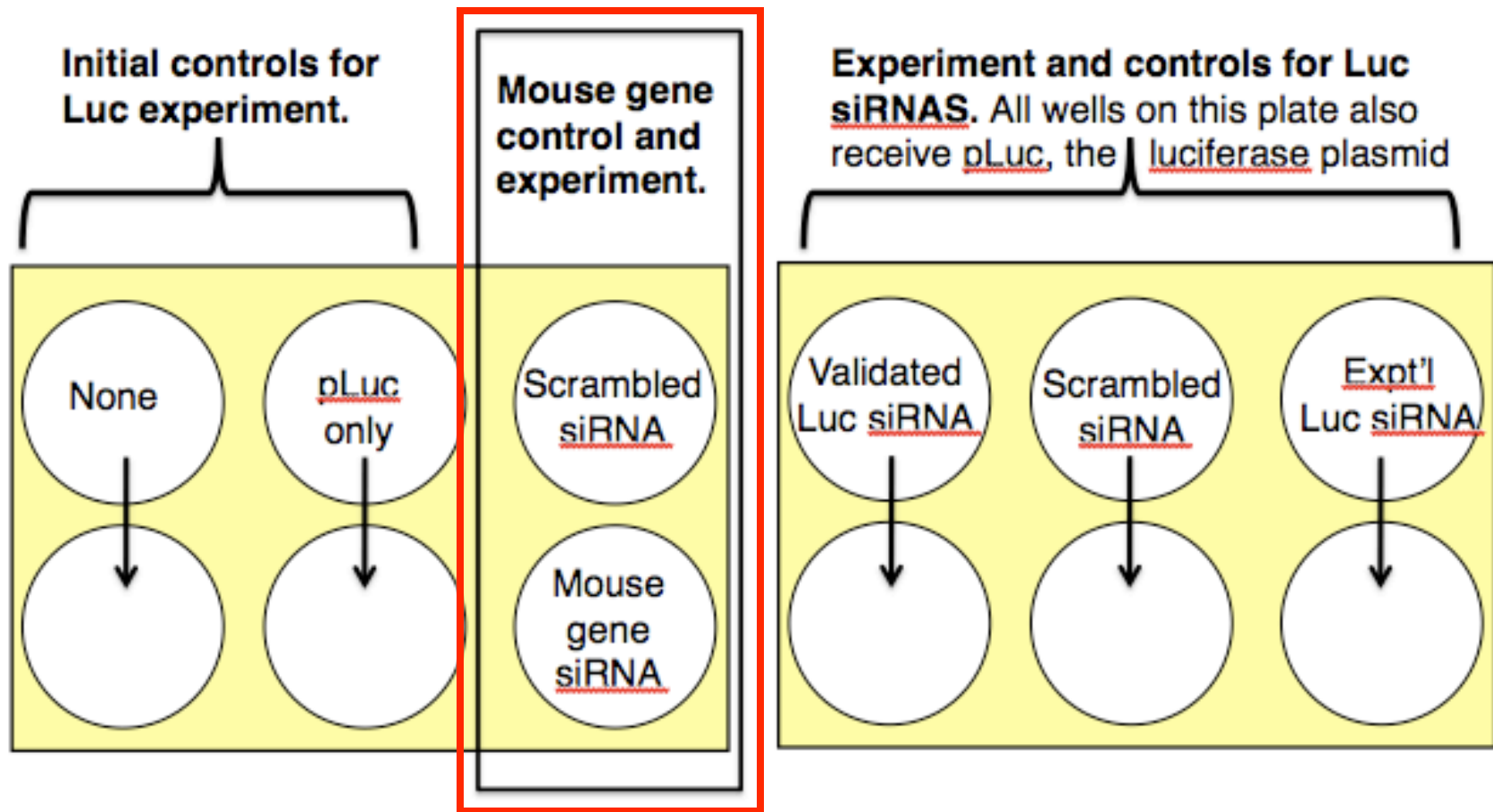


MIX



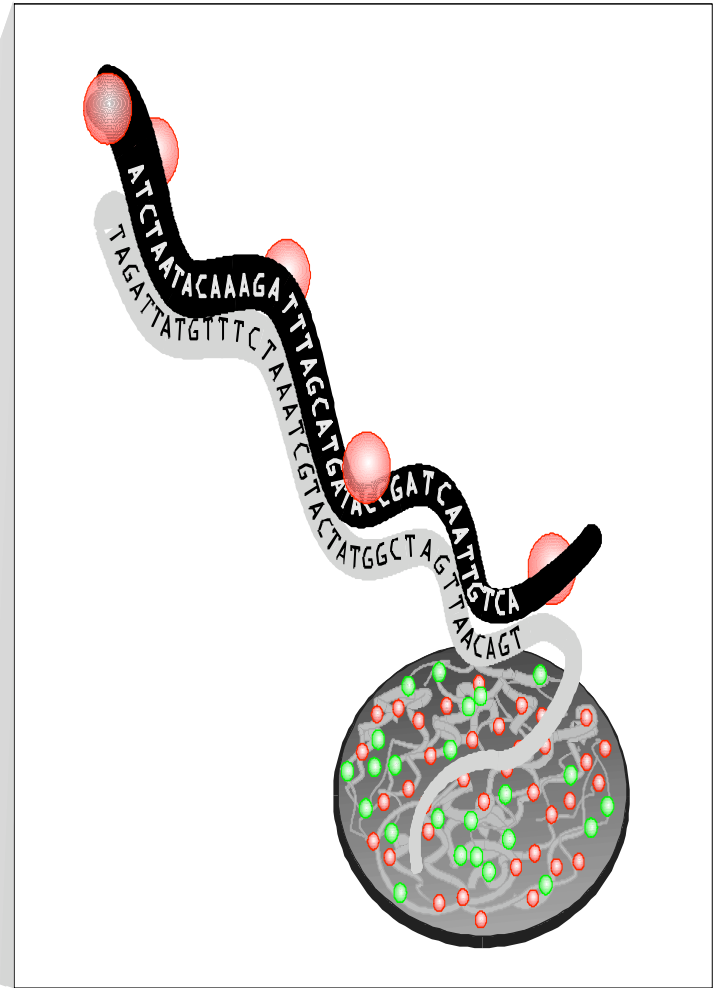
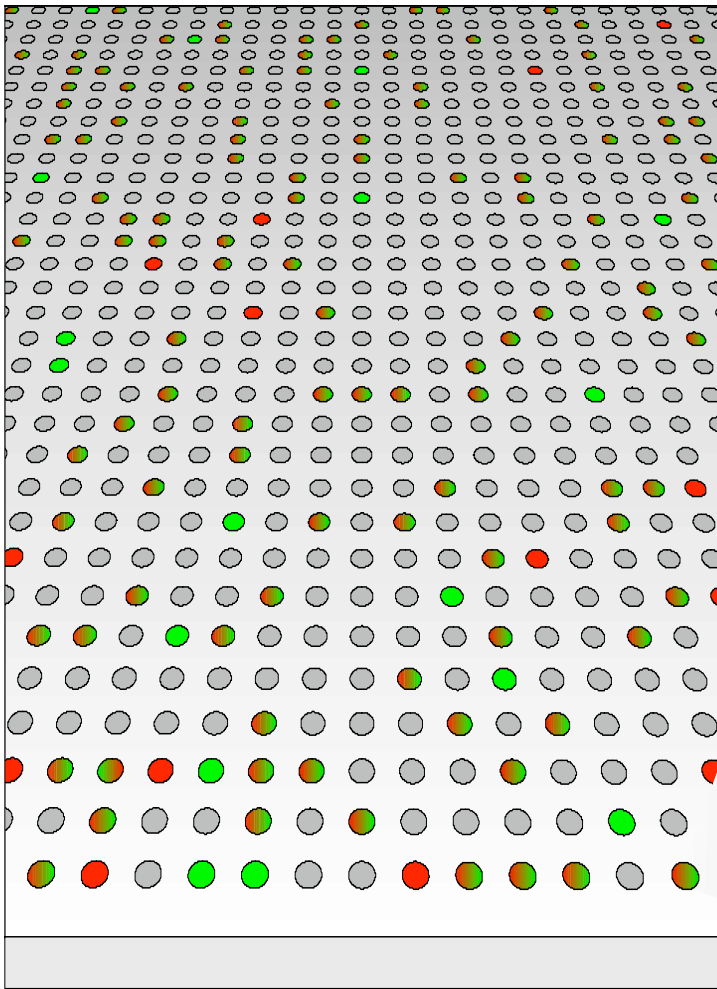
Hybridize to the microarray

siRNA knockdown of expression of Renilla Luciferase plus various mouse gene

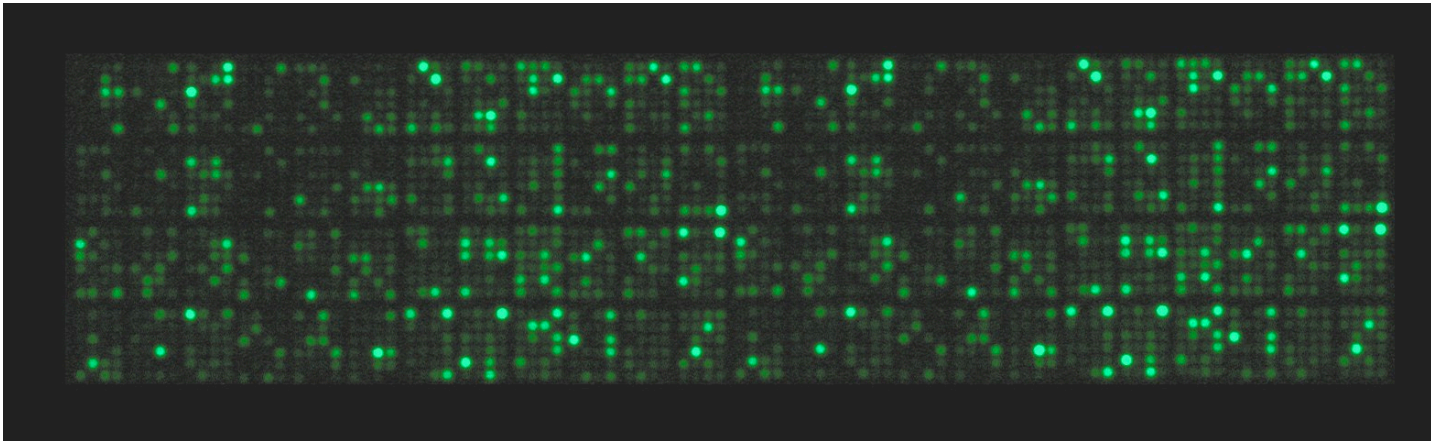
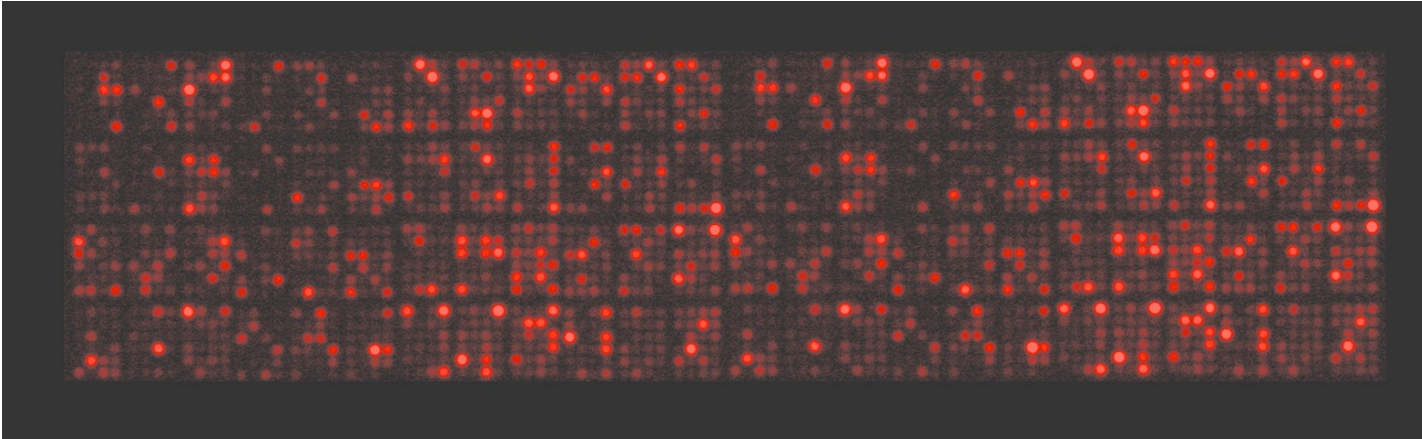


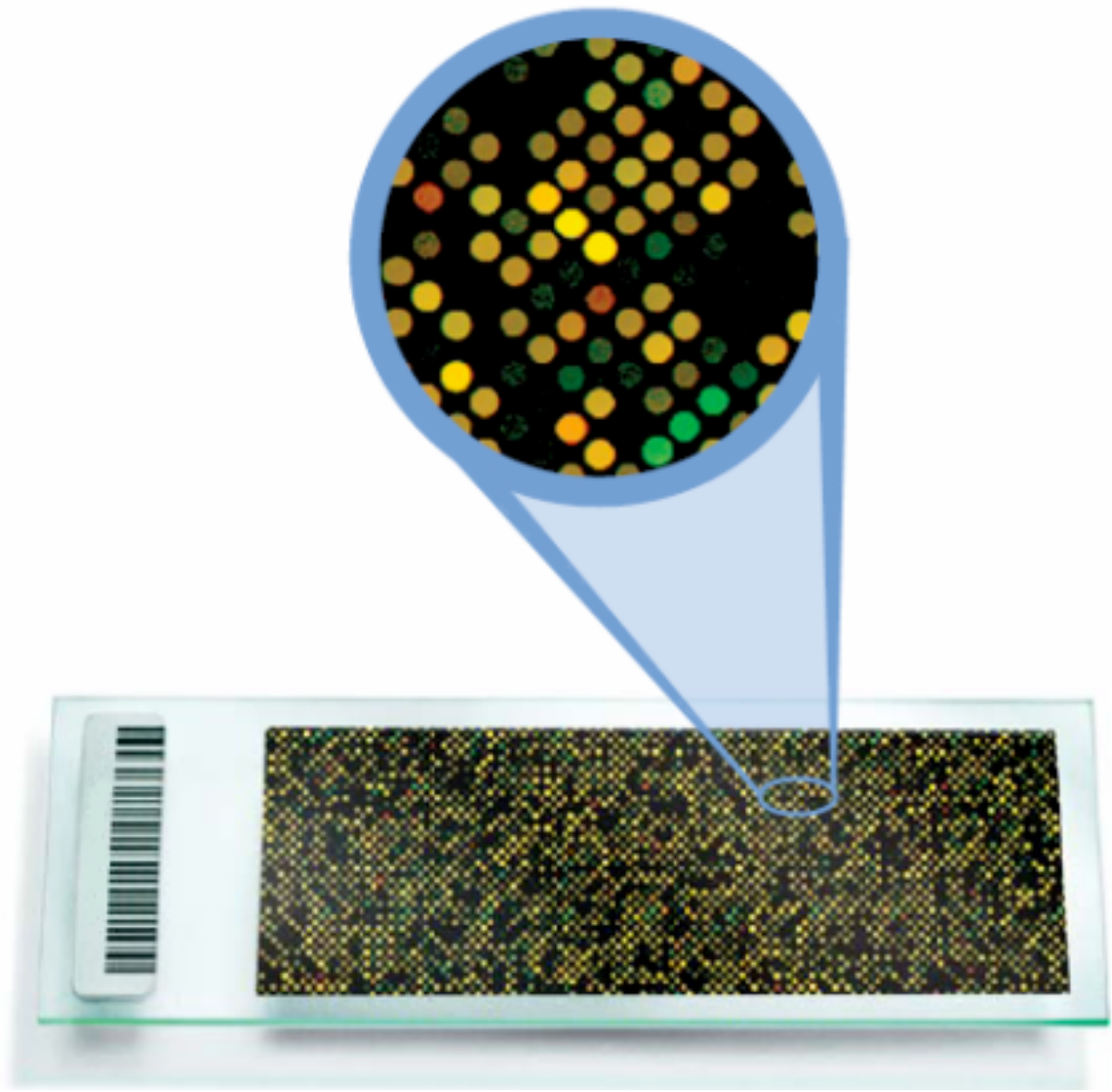
Isolate total RNA in order to measure relative levels of all mRNAs – with special attention to YGI

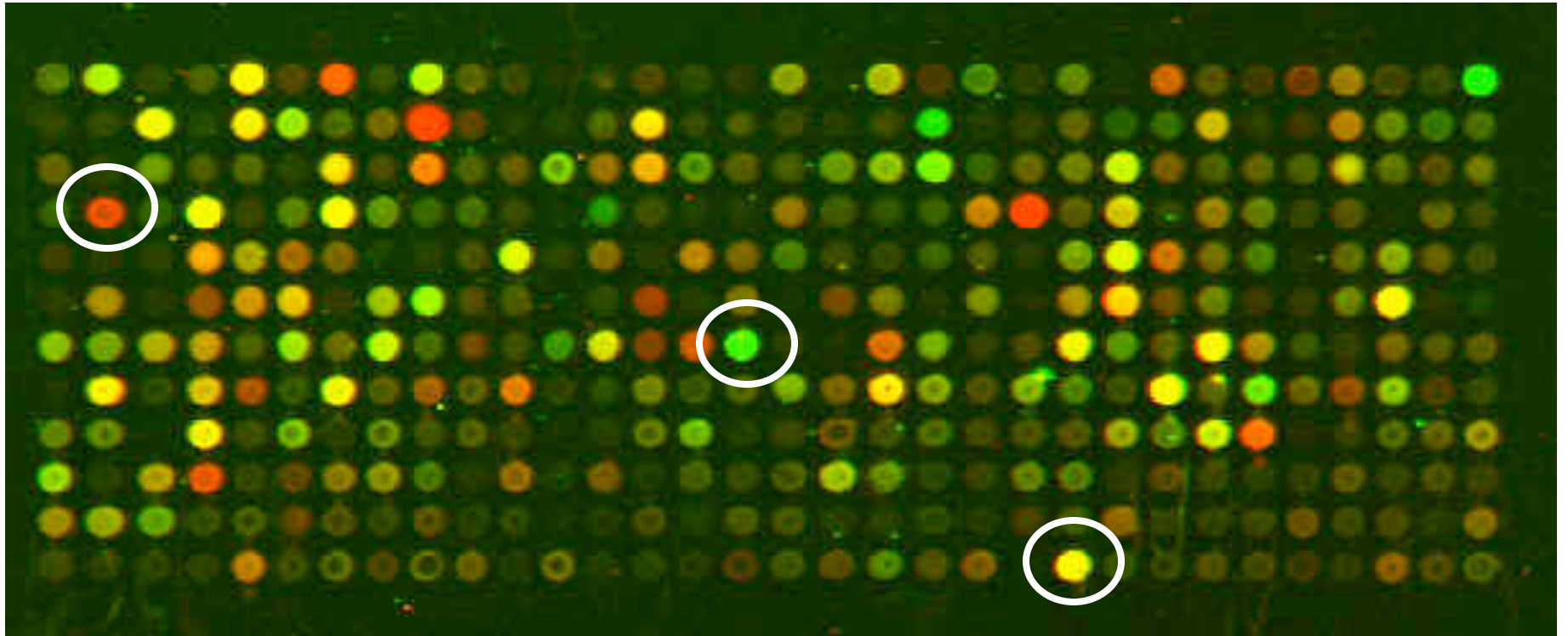
What's happening at each spot?



Hybridization







- mRNA present much higher in State A than State B
- mRNA present much higher in State B than State A
- mRNA present at equal levels in States A and B

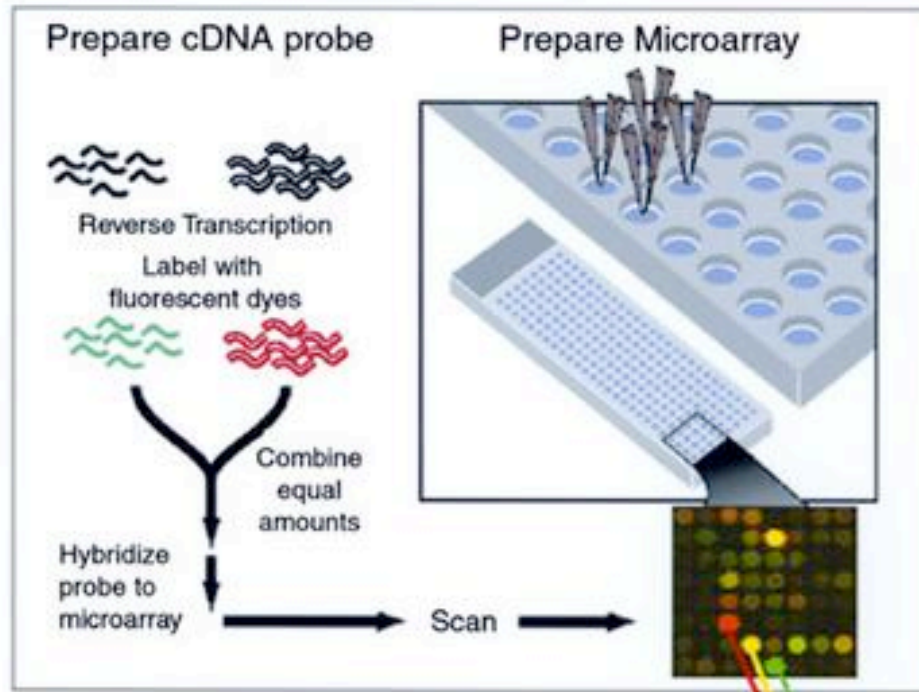
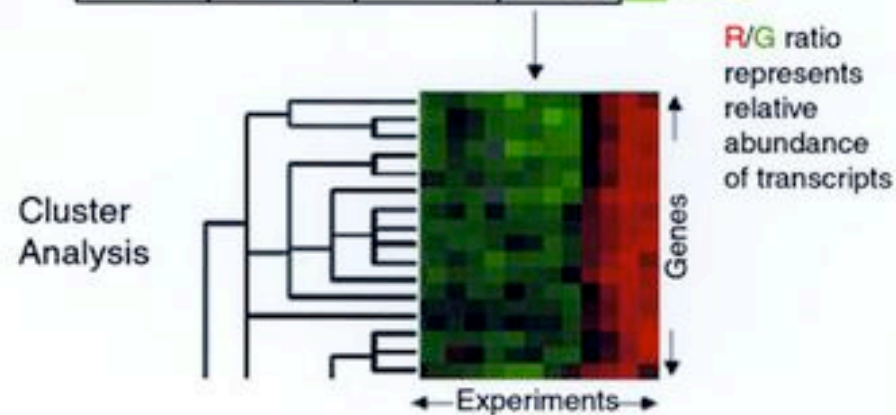


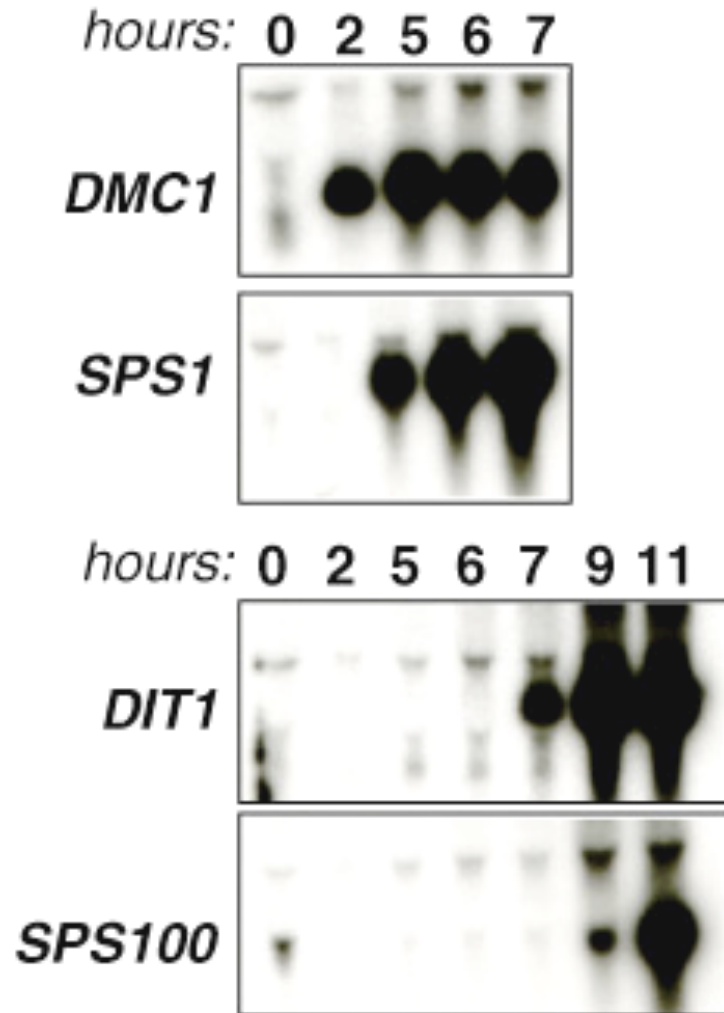
Image Analysis

Cy3	Cy5	$\frac{Cy5}{Cy3}$	$\log_2 \frac{Cy5}{Cy3}$
200	10000	50.00	5.64
4800	4800	1.00	0.00
9000	300	0.03	-4.91

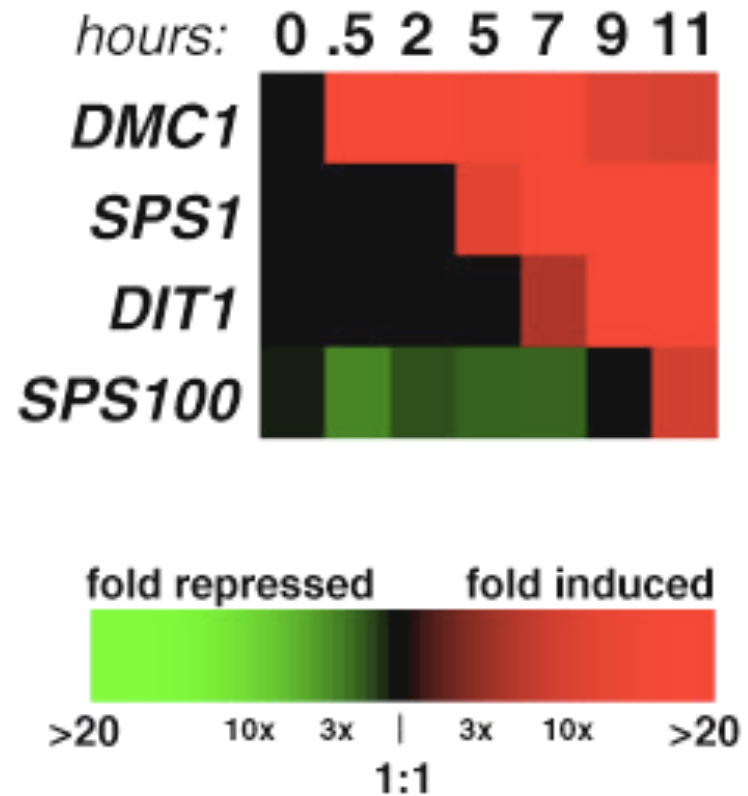


Northern Blot vs. Microarray

A

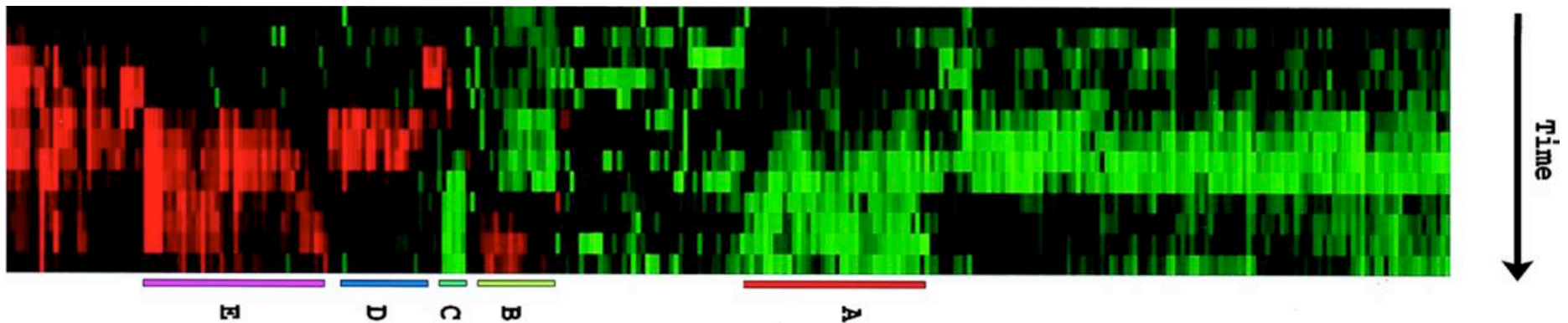


B



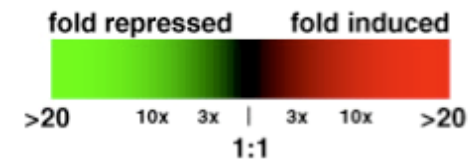
Hierarchical clustering to group together similarly regulated genes

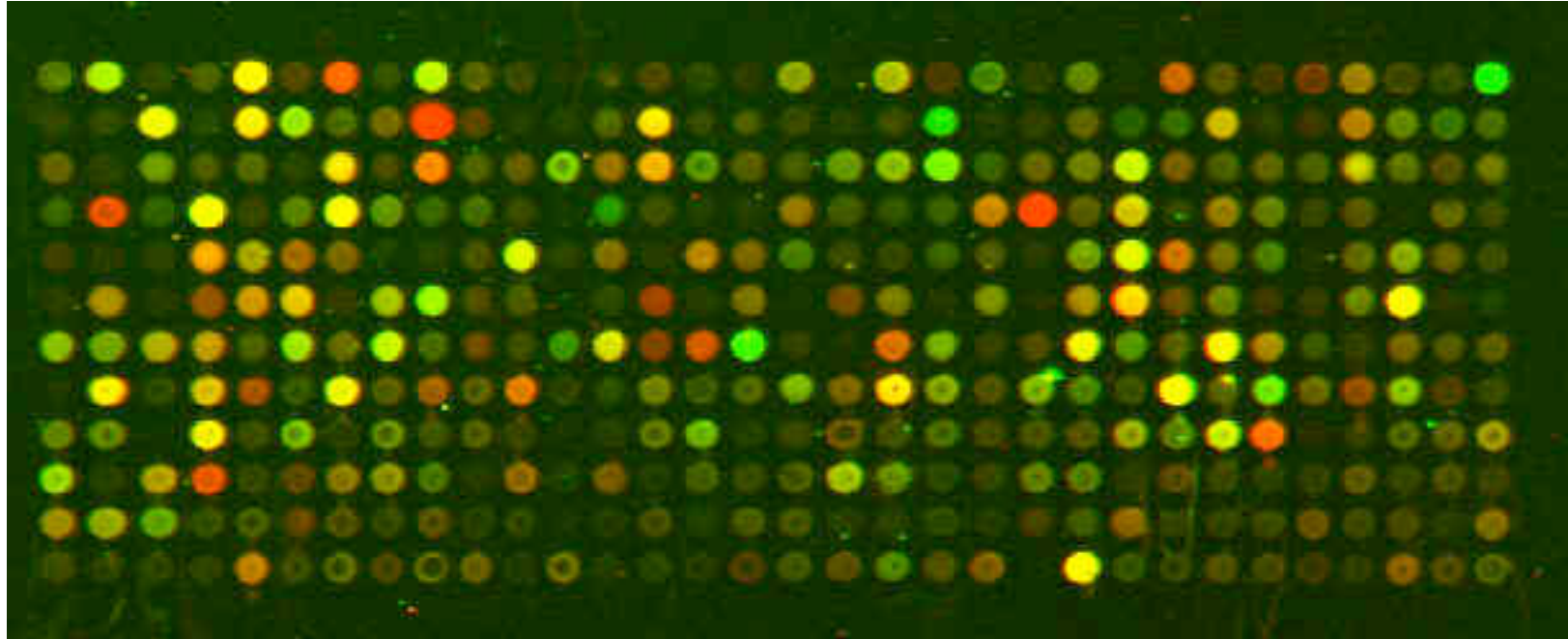
Each colored vertical line in the horizontal lane displays the relative expression level of a single mRNA



13 time points, and several thousand genes

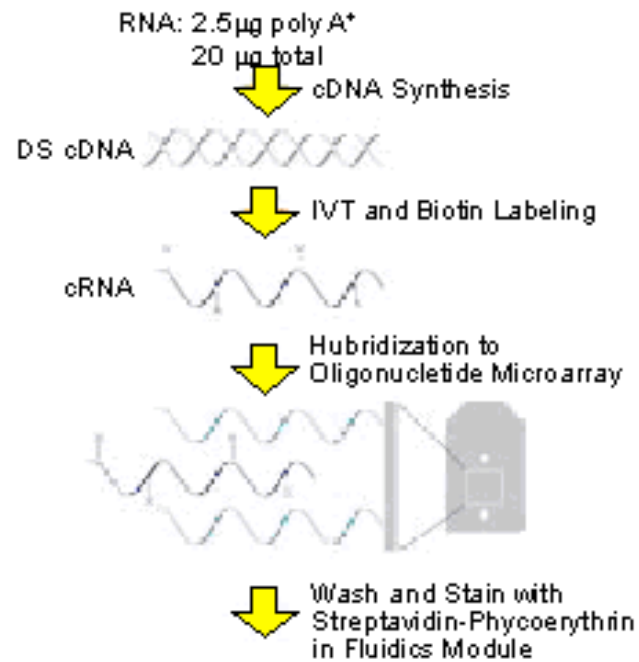
Proc. Natl. Acad. Sci. USA
Vol. 95, pp. 14863-14868, December 1998
Cluster analysis and display of genome-wide expression patterns





This is the "two color" technology (you will use something similar), but there is another common technology that uses one color....

Affymetrix Technology



↓ Scan with Confocal Laser Scanner and Analyze Data



Affymetrix has focused on light-directed synthesis for the construction of high-density DNA probe arrays using two techniques: photolithography and solid-phase DNA synthesis. Synthetic linkers are attached modified with photochemically removable protecting groups to a glass substrate and direct light through a photolithographic mask to specific areas on the surface to produce localized photodeprotection.

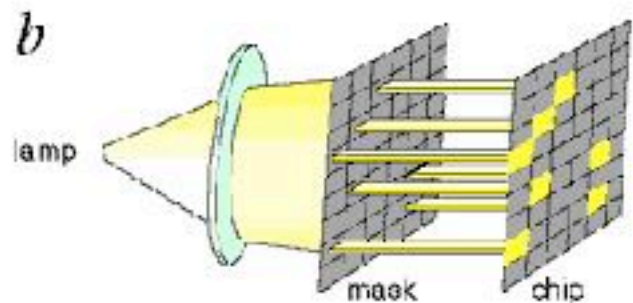
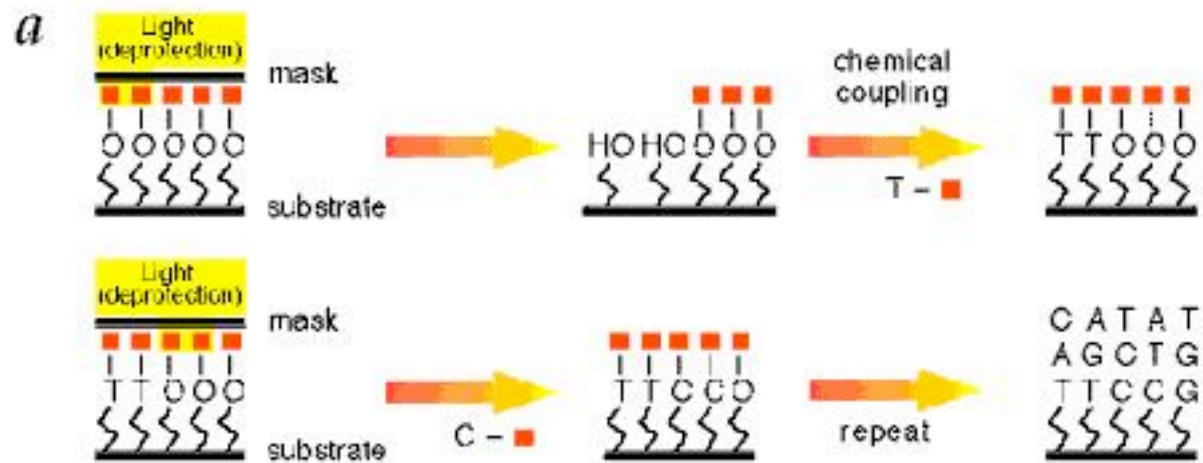
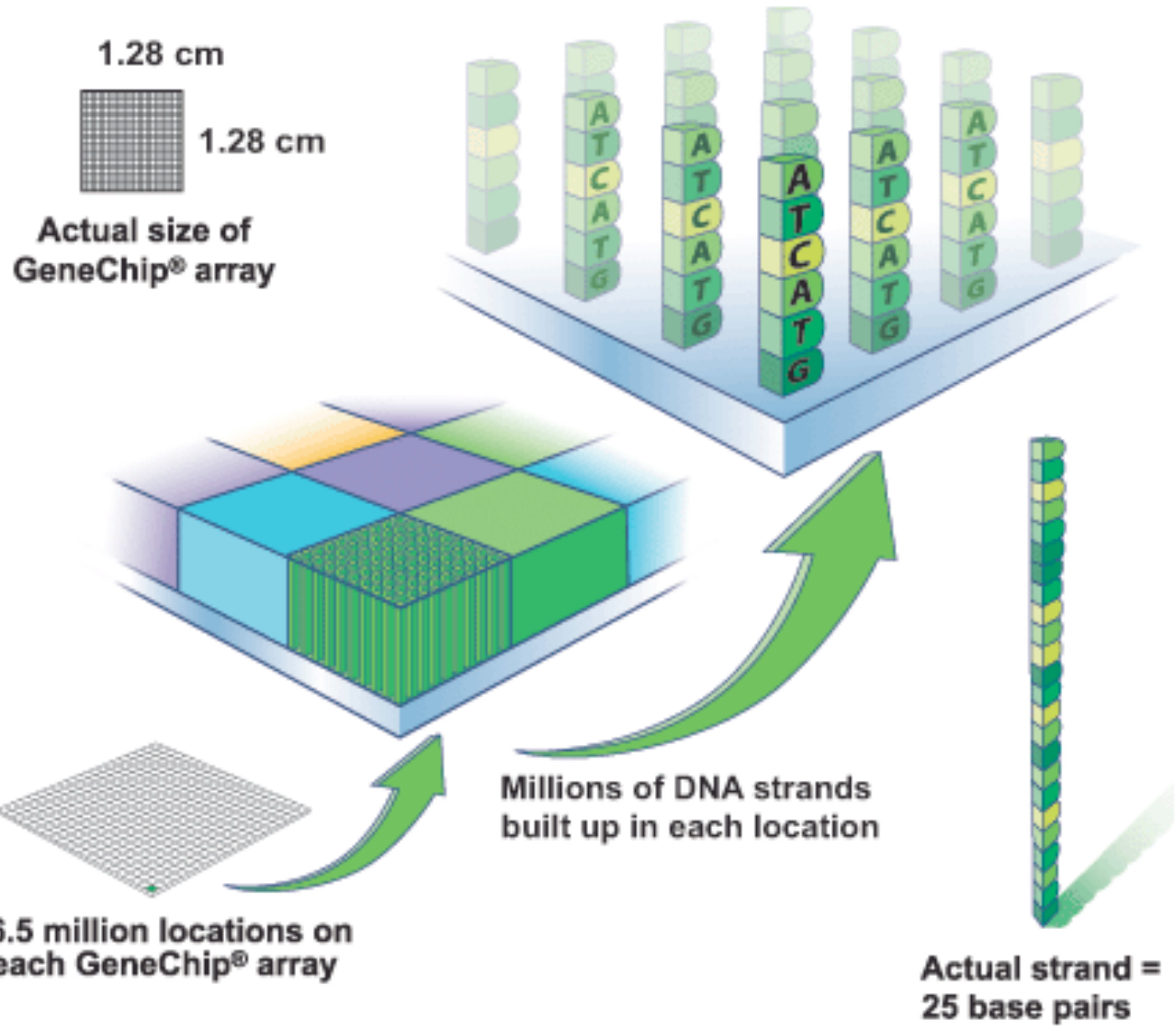


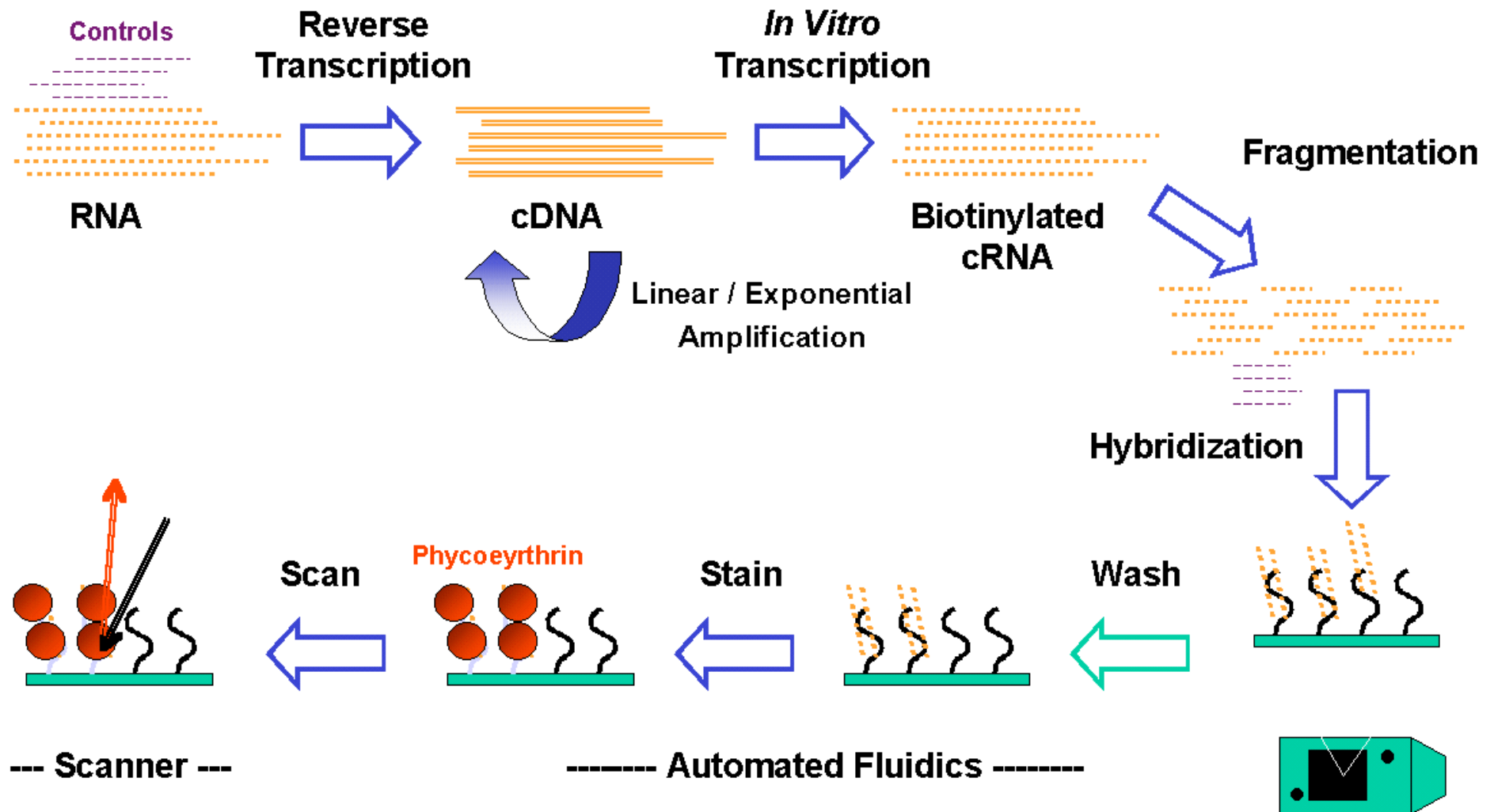
Figure 1. Synthesis Confirmation.

Mask Cycles	1	2	3	4	5	6	7	8	Probes Synthesized
	A	C	G	T	A	C	G	T	
Probe 1	A	C	-	T	-	C	-	-	A C T C
Probe 2	-	-	G	-	A	-	G	T	G A G T
Probe 3	A	-	G	-	A	-	G	-	A G A G
Probe 4	-	C	-	T	-	C	-	T	C T C T

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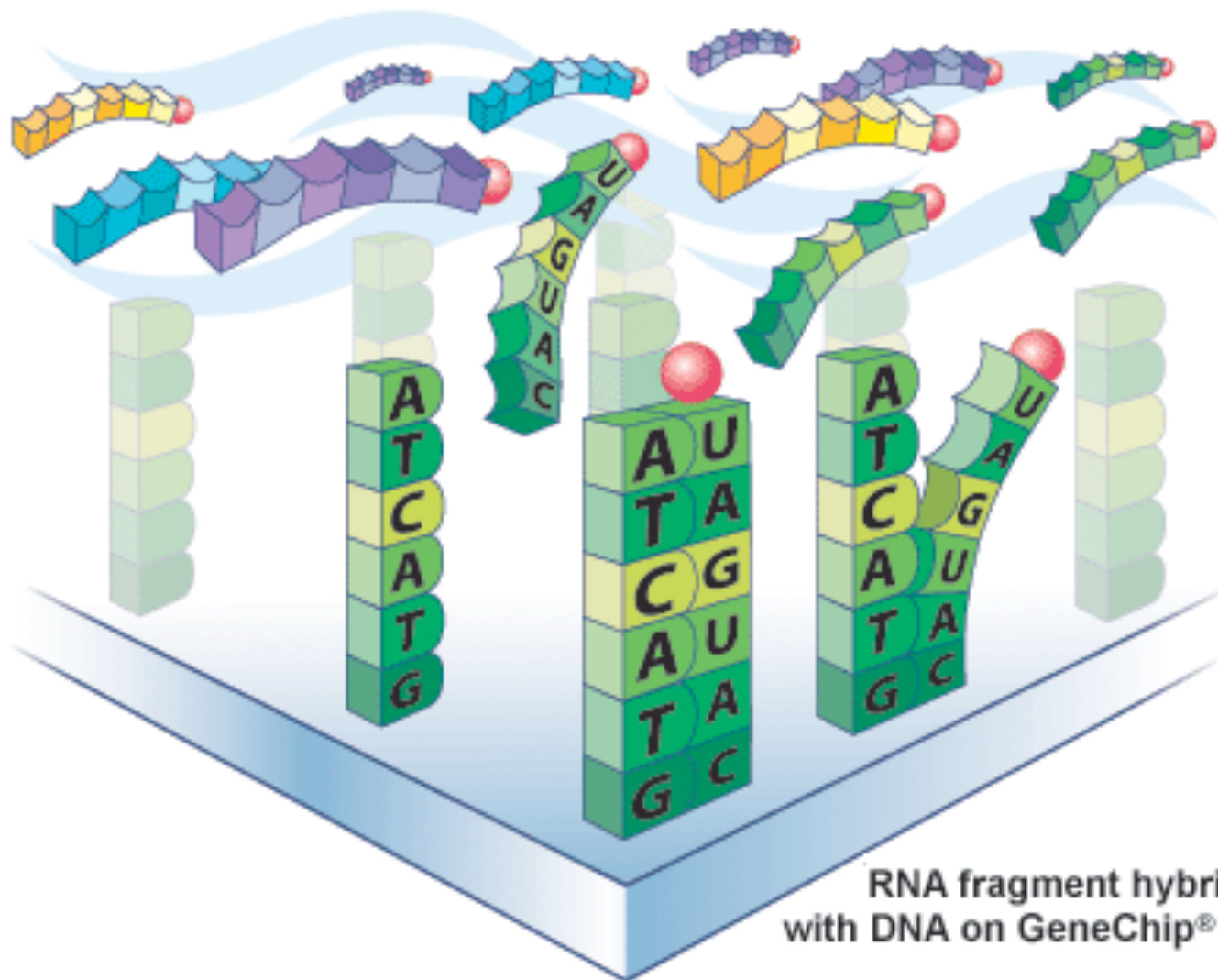


Affymetrix Technology



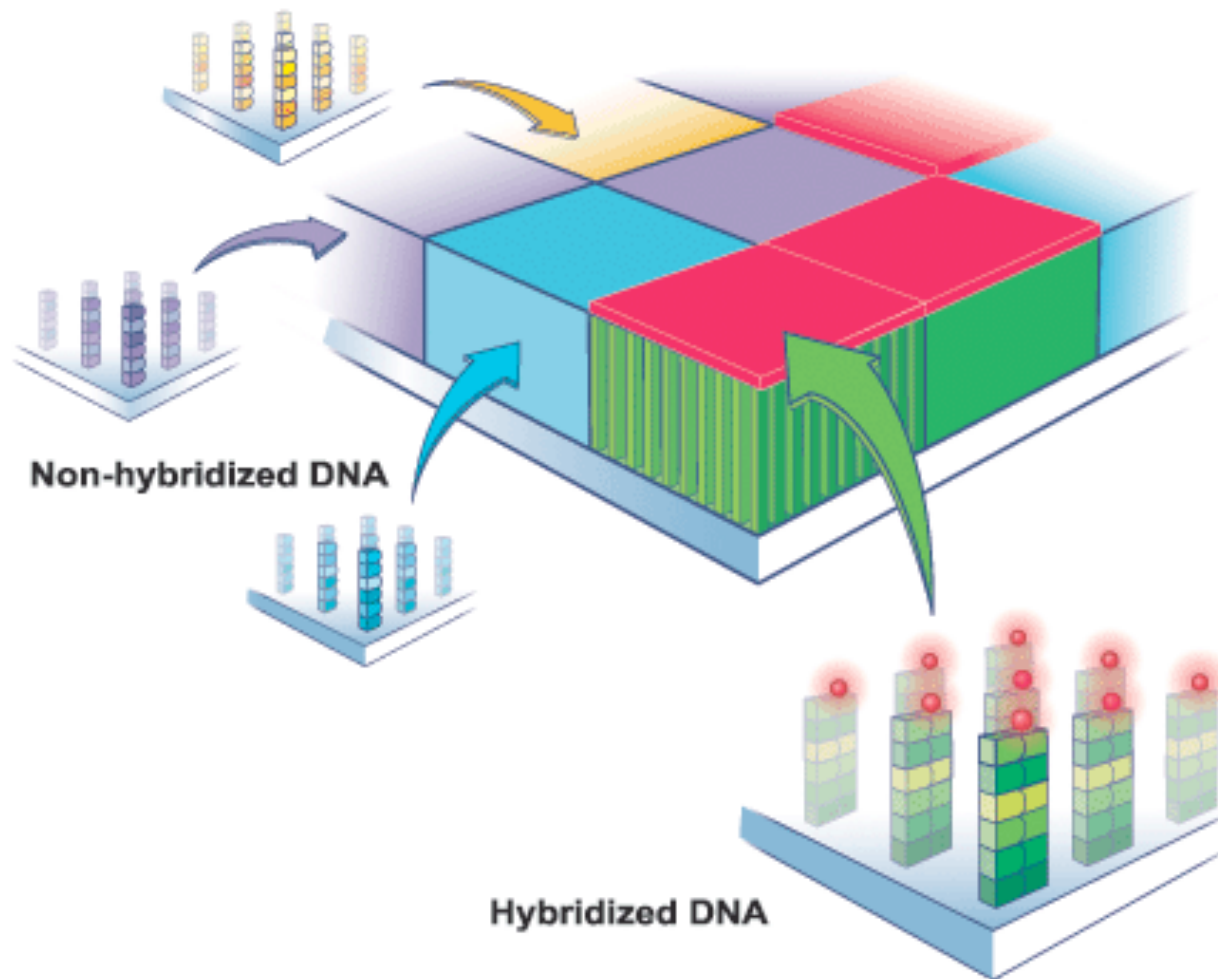
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RNA fragments with fluorescent tags from sample to be tested

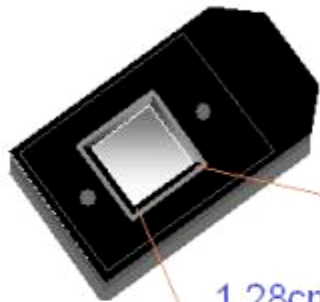


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**Shining a laser light at GeneChip® array causes
tagged DNA fragments that hybridized to glow**



GeneChip Probe Array



1.28cm

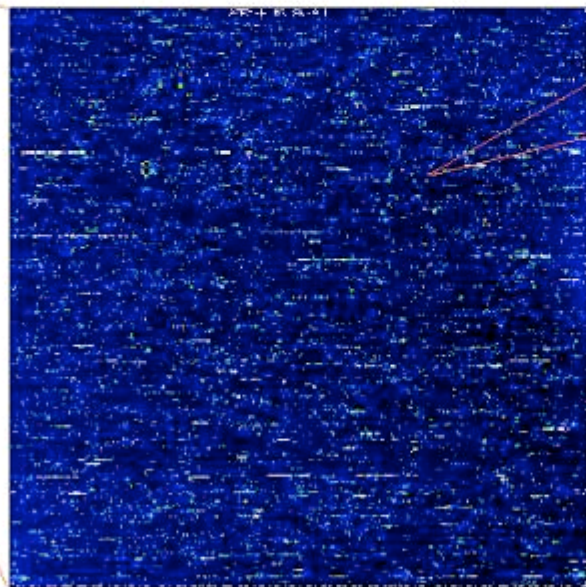
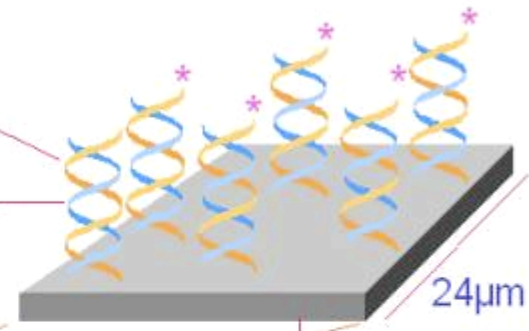


Image of Hybridized Probe Array

Hybridized Probe Cell

Single stranded, labeled RNA target

Oligonucleotide probe



24 μ m

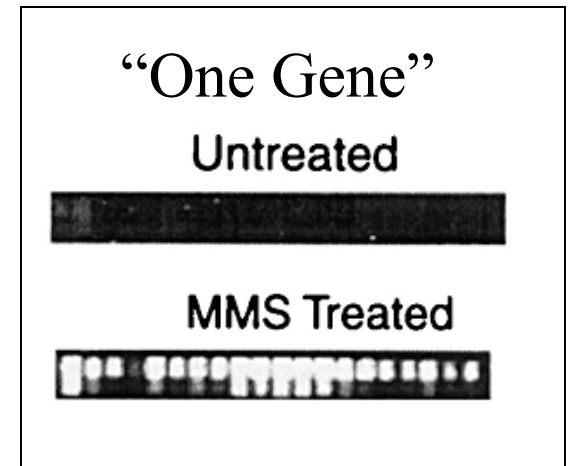
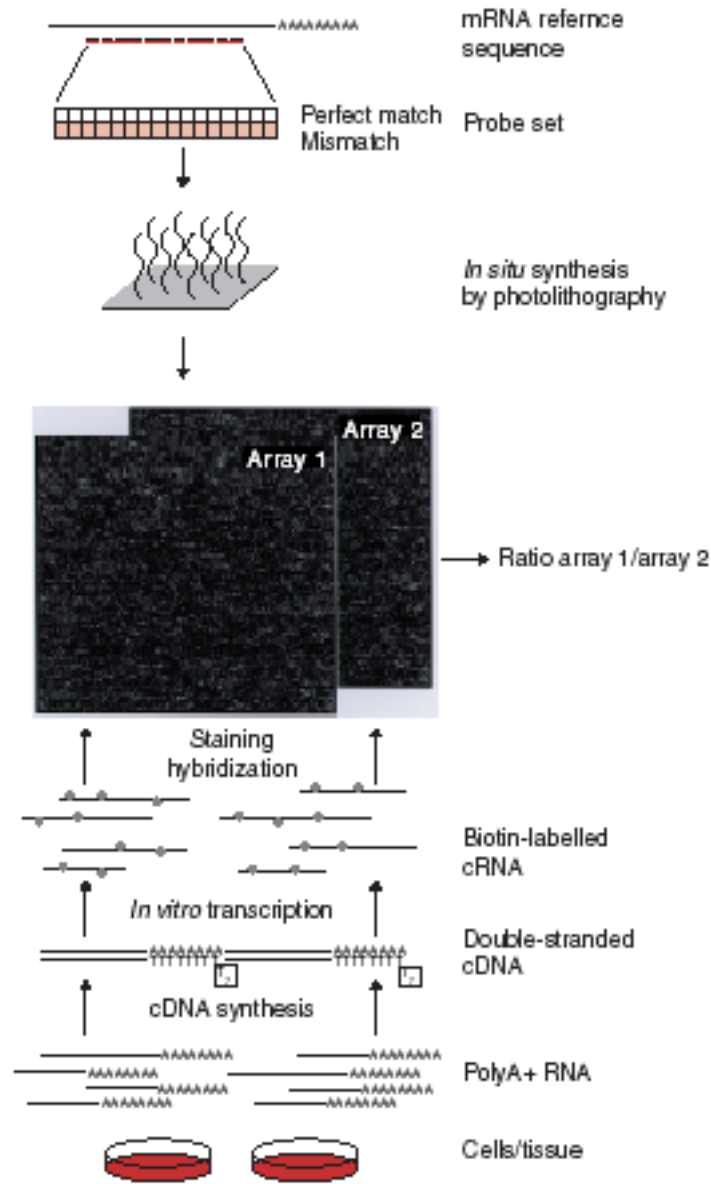
Millions of copies of a specific oligonucleotide probe

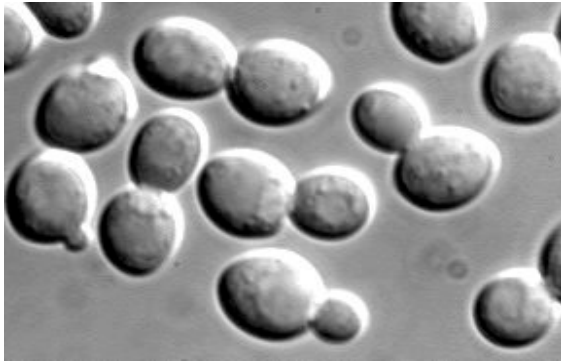
>200,000 different complementary probes

Oligonucleotide "One Color Chips"

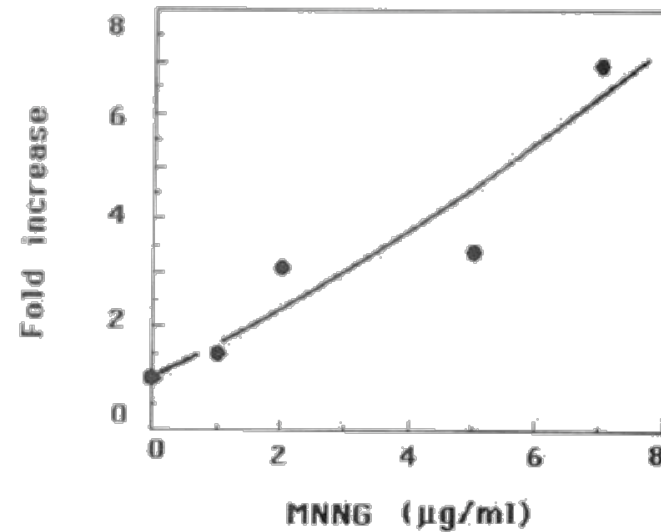
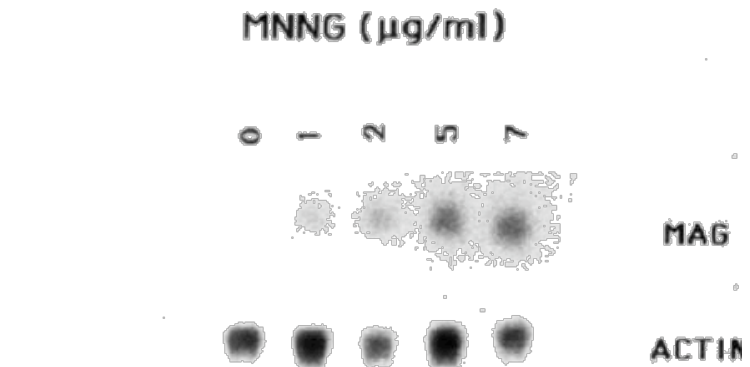
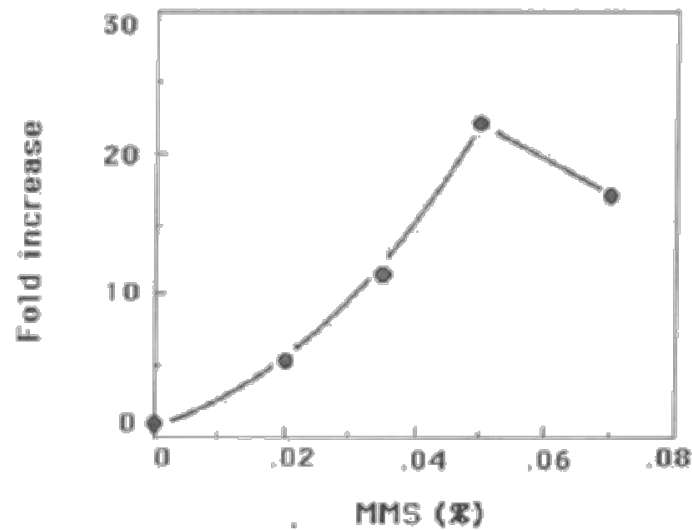
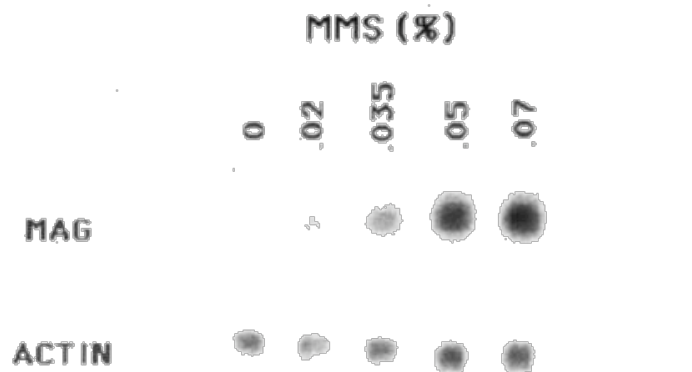
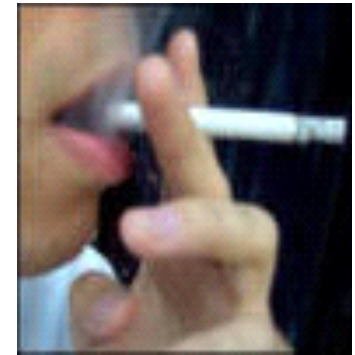
Array preparation

Target preparation

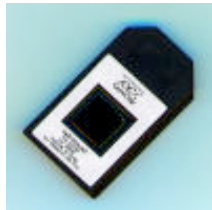




Yeast cells treated with DNA damaging agents like those in tobacco smoke



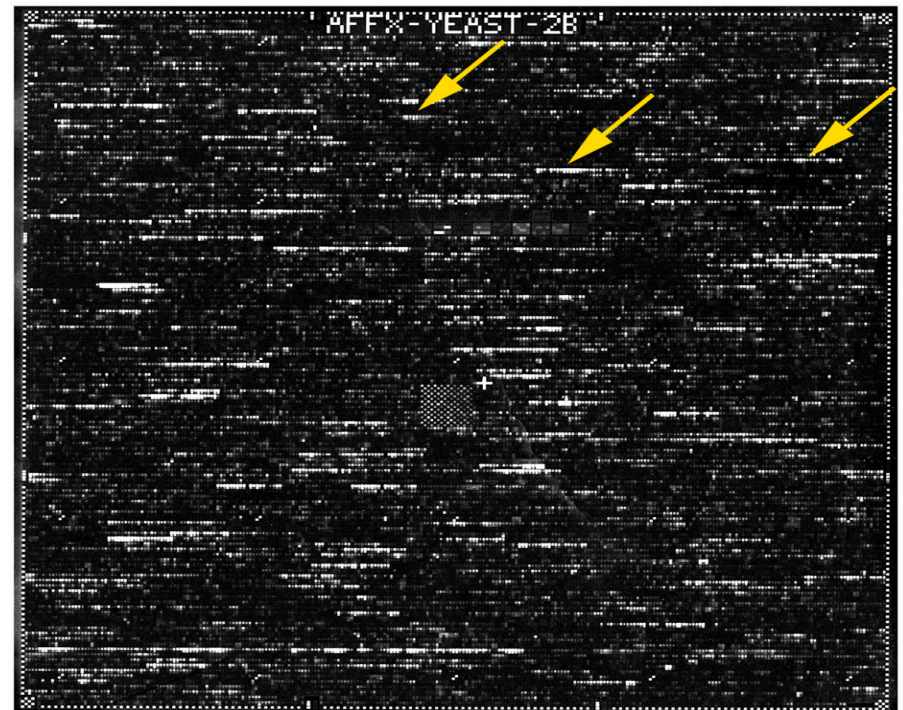
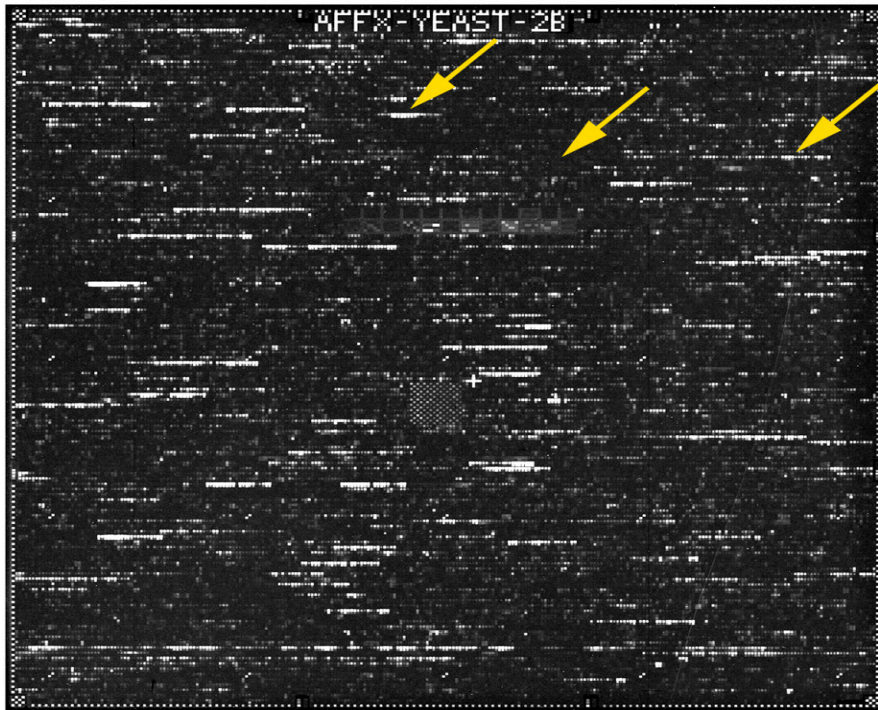
Affymetrix Oligonucleotide Based Expression Arrays



Untreated

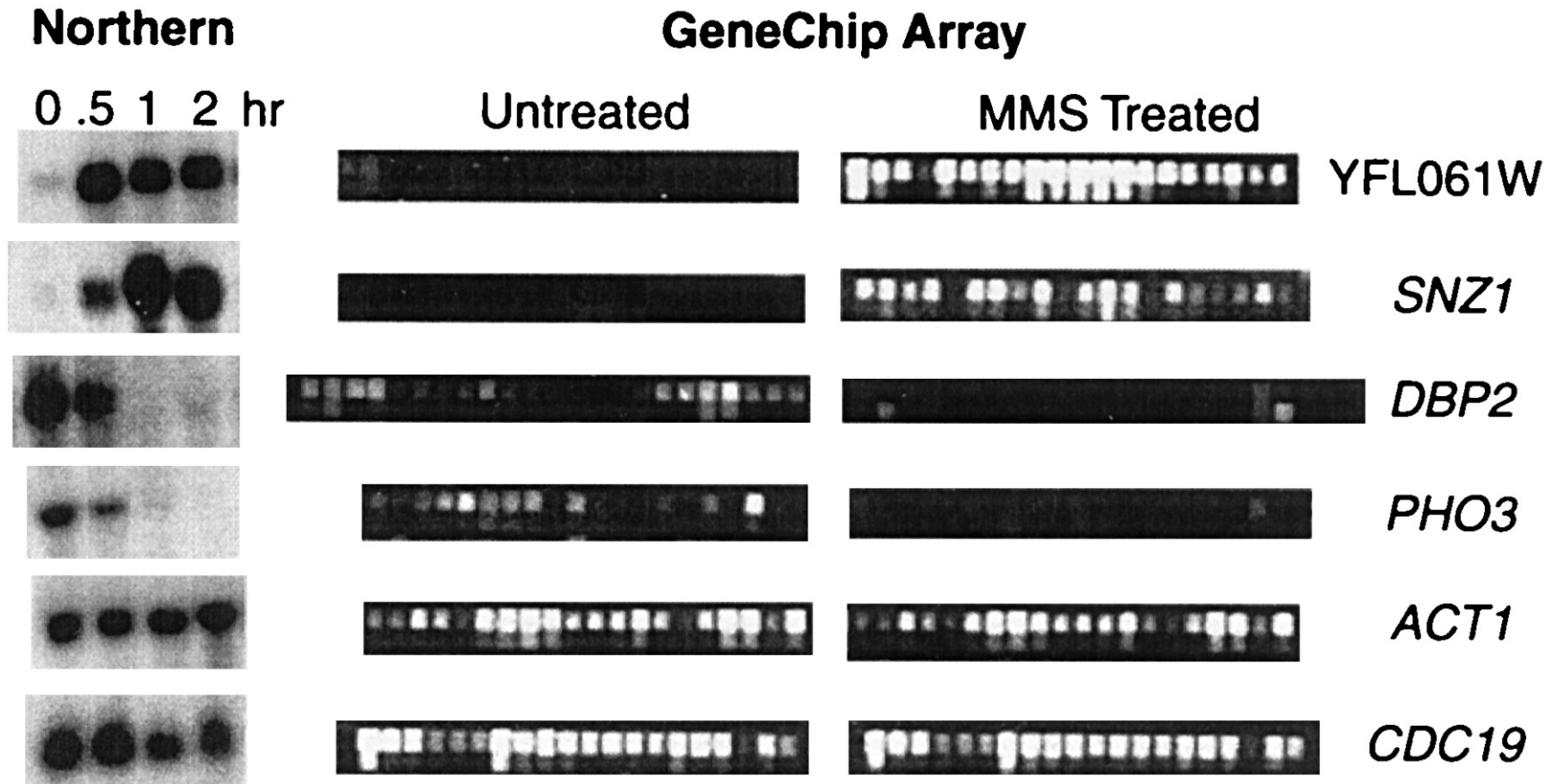


MMS treated

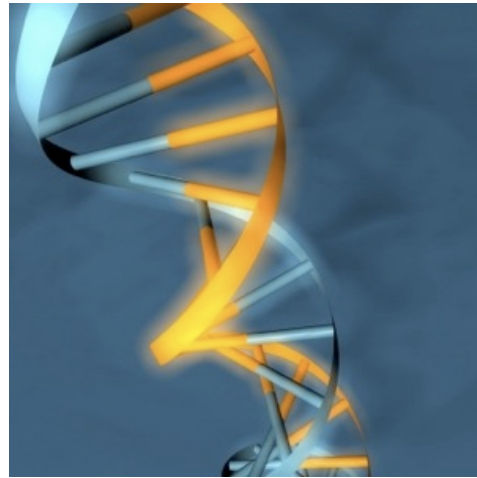


Jelinsky and Samson, 1999

Northern Blot vs. Affymetrix Chip

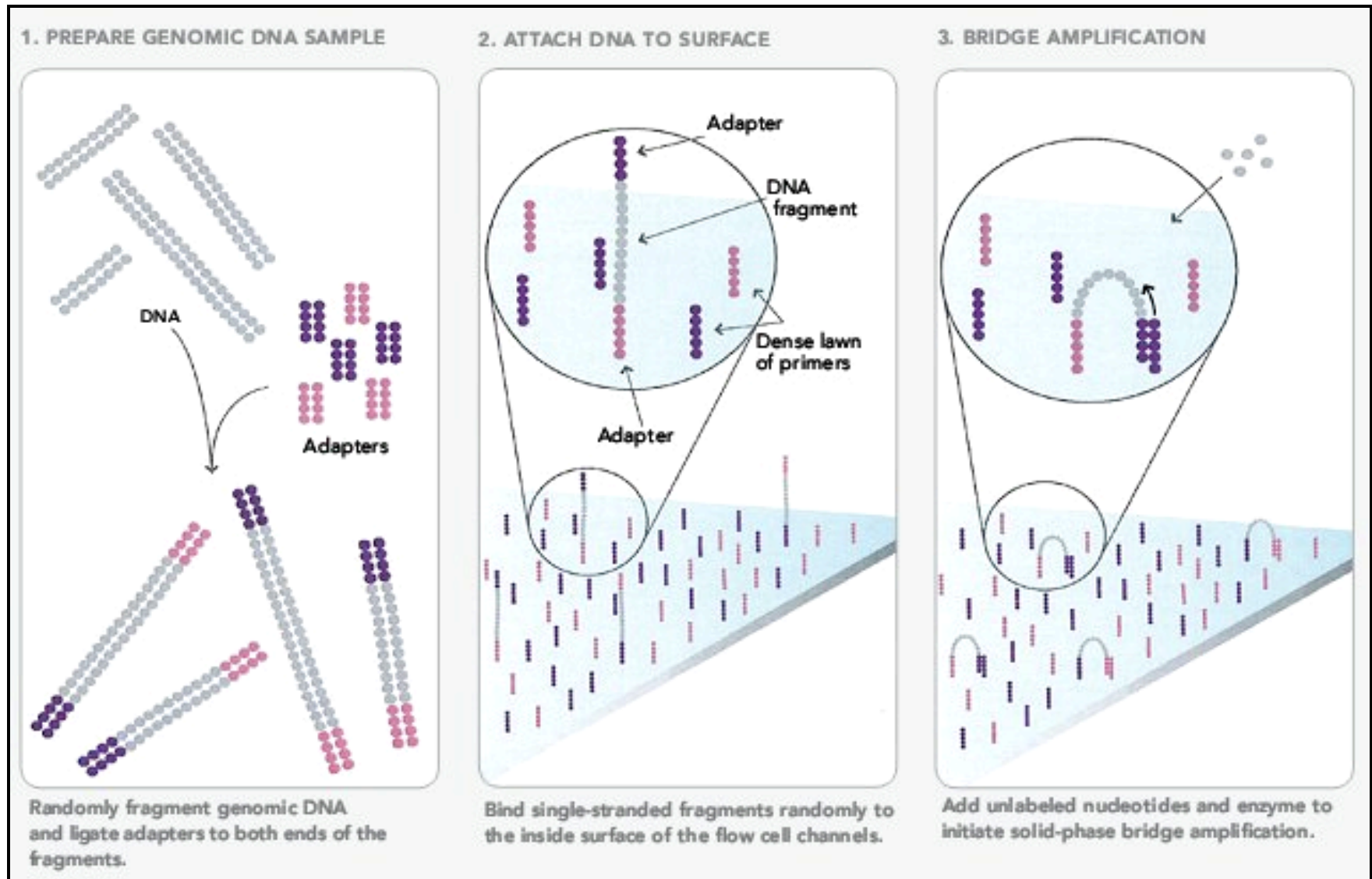


'Next Generation' Sequencing Technologies

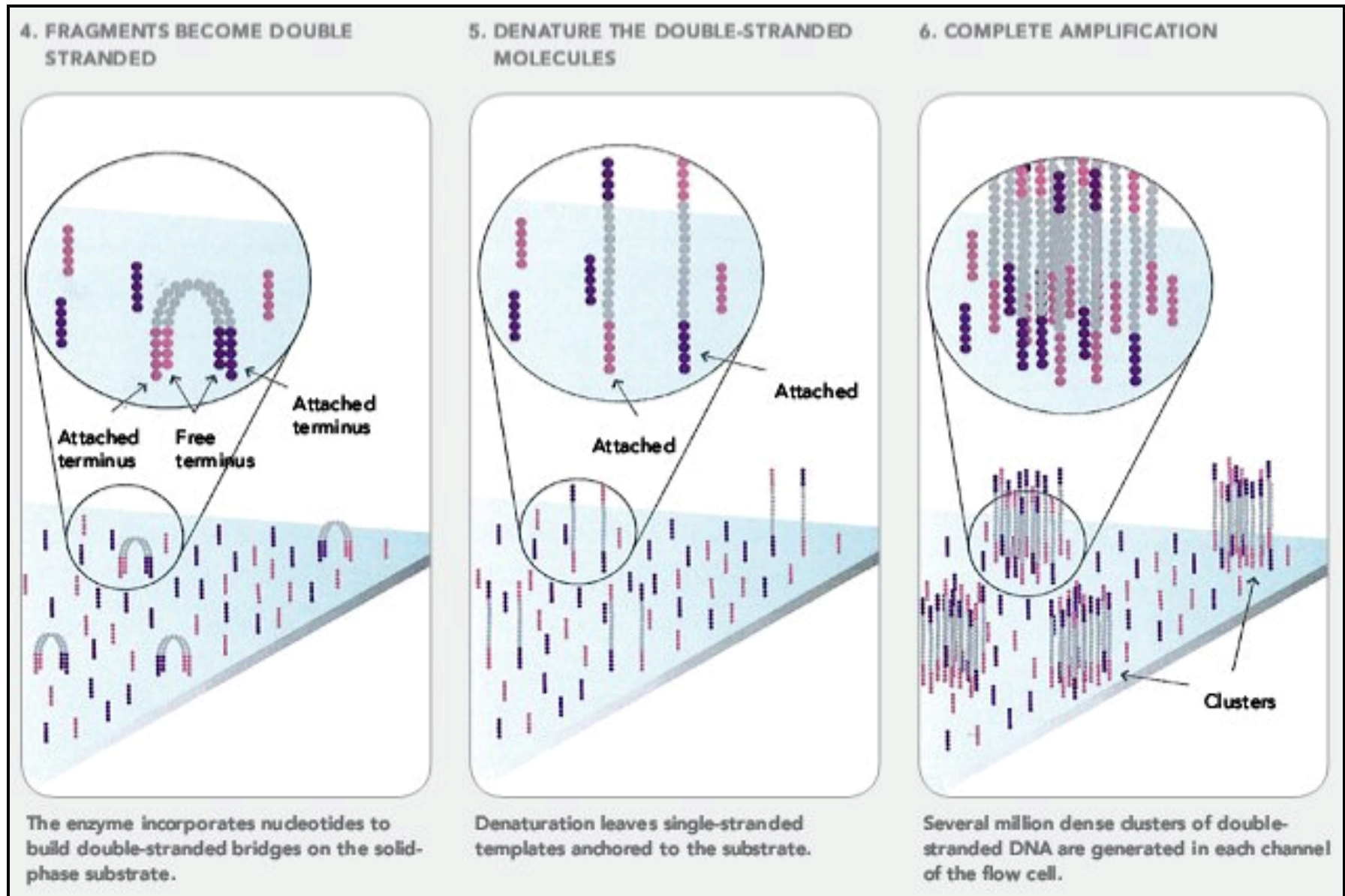


Platform	Amplification	Sequencing
Harvard/Danaher/Agencourt/ABI	Emulsion PCR	Ligase
454 Life Sciences / Roche	Emulsion PCR	Polymerase - pyrosequencing
Solexa/Illumina	Bridge PCR	Polymerase - reversible terminator
Helicos	None	Polymerase - single base extension
Pacific Biosciences occupancy	None	Polymerase - active site

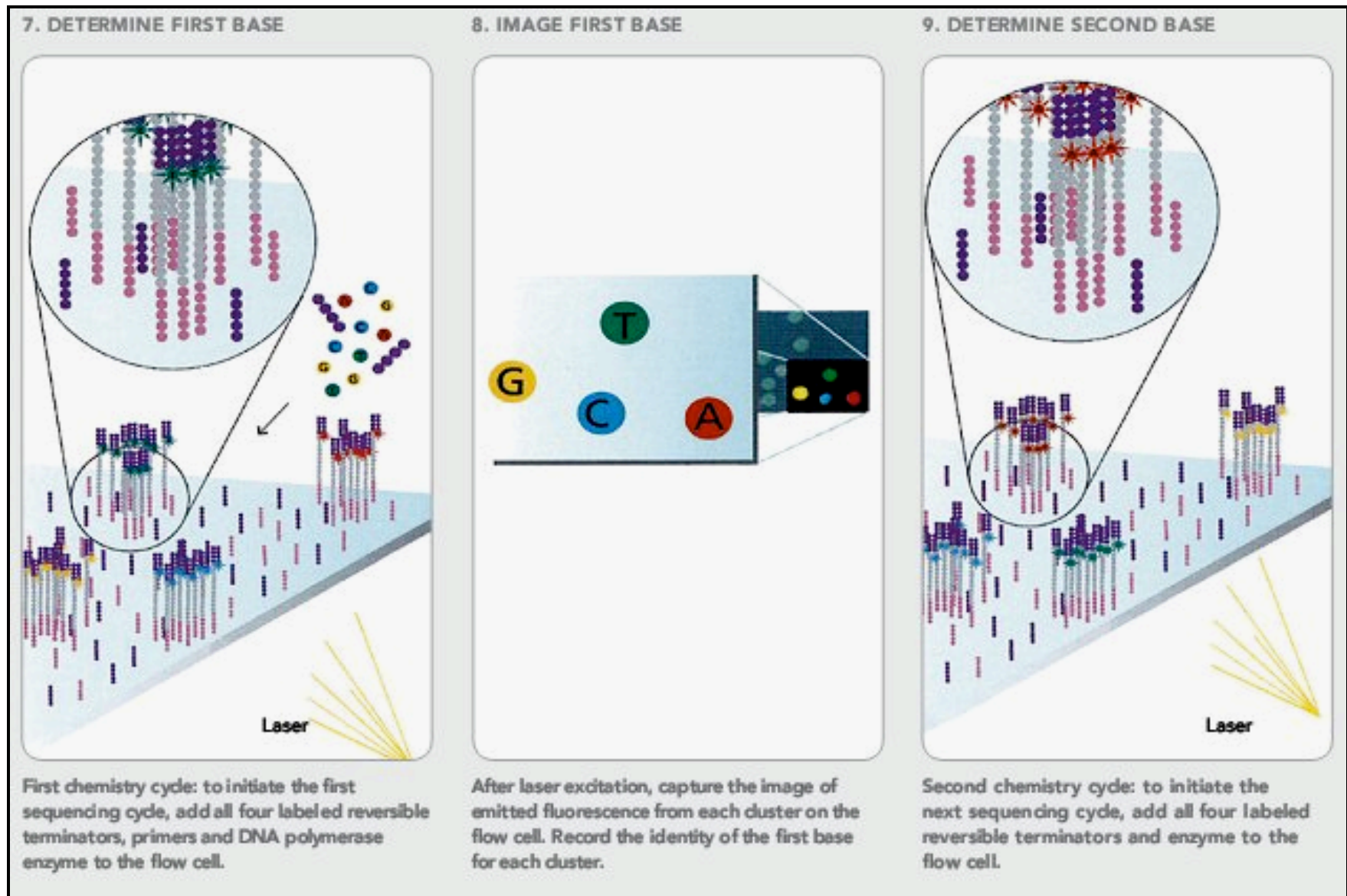
Solexa/Illumina DNA Sequencing Platform



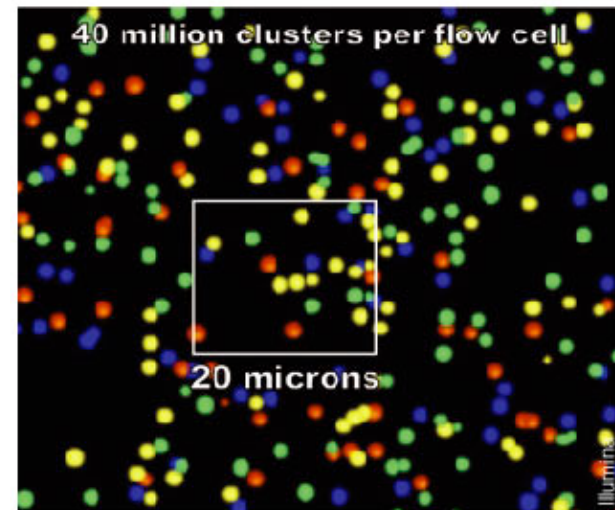
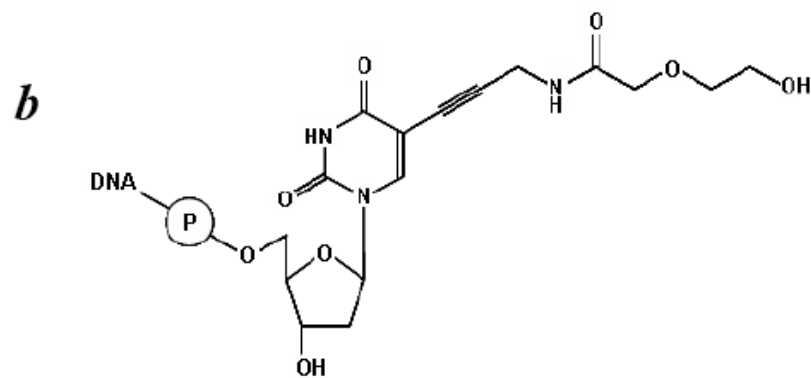
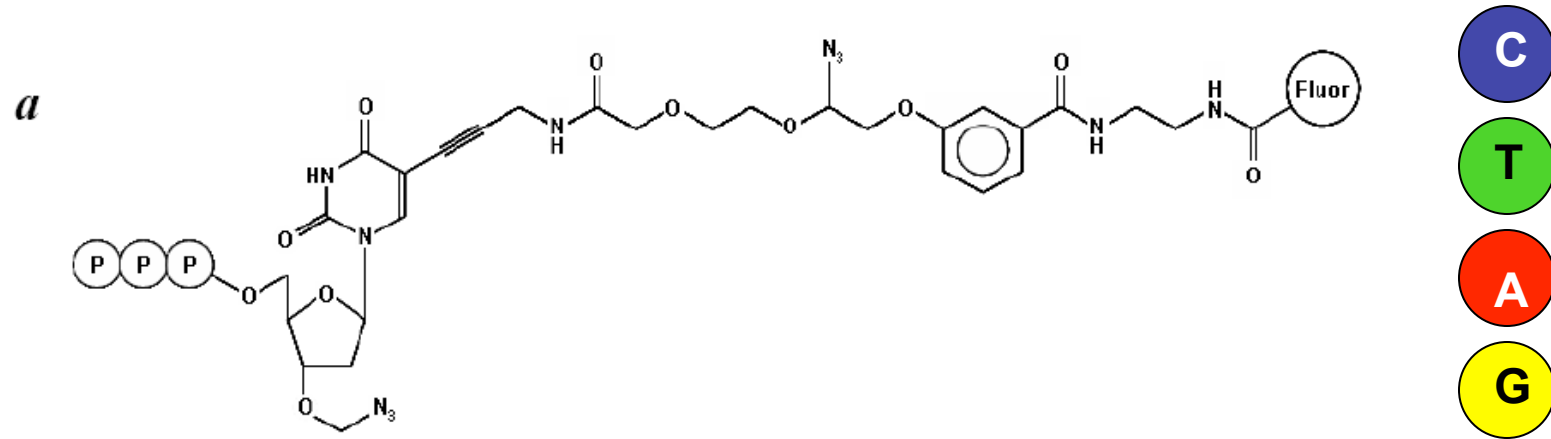
Solexa/Illumina DNA Sequencing Platform



Solexa/Illumina DNA Sequencing Platform

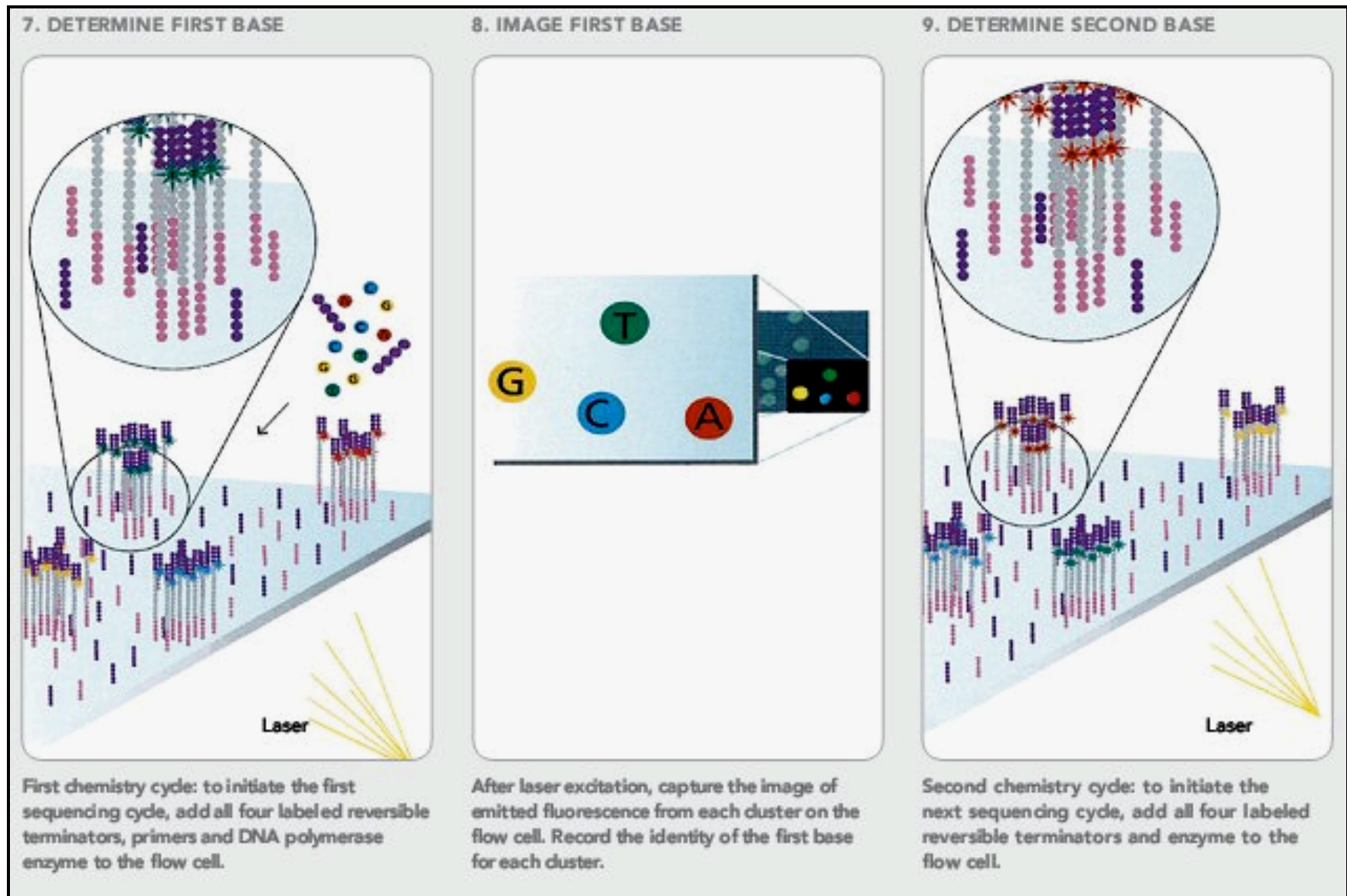


Reversible Terminator Chemistry



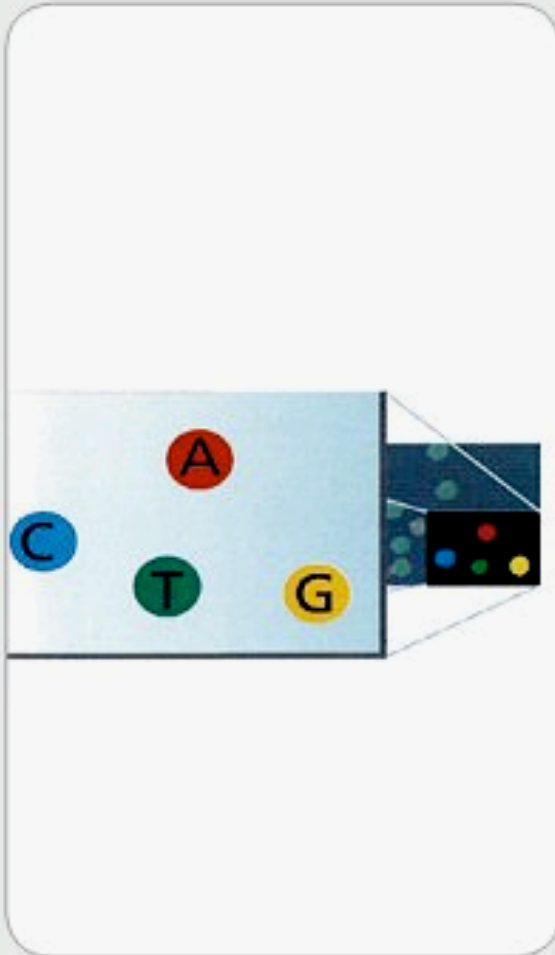
Bentley et al. Nature 456, 53-, 2008.

Solexa/Illumina DNA Sequencing Platform



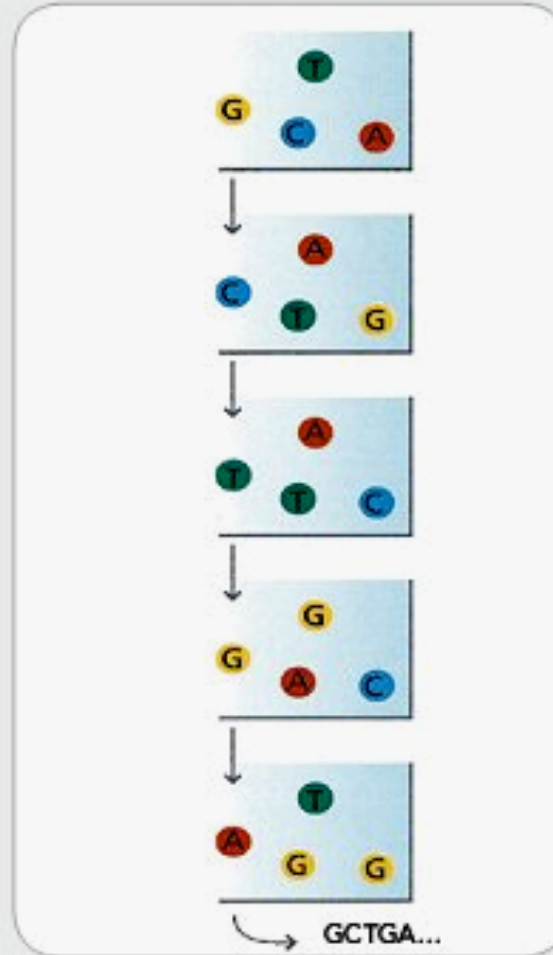
Solexa/Illumina DNA Sequencing Platform

10. IMAGE SECOND CHEMISTRY CYCLE



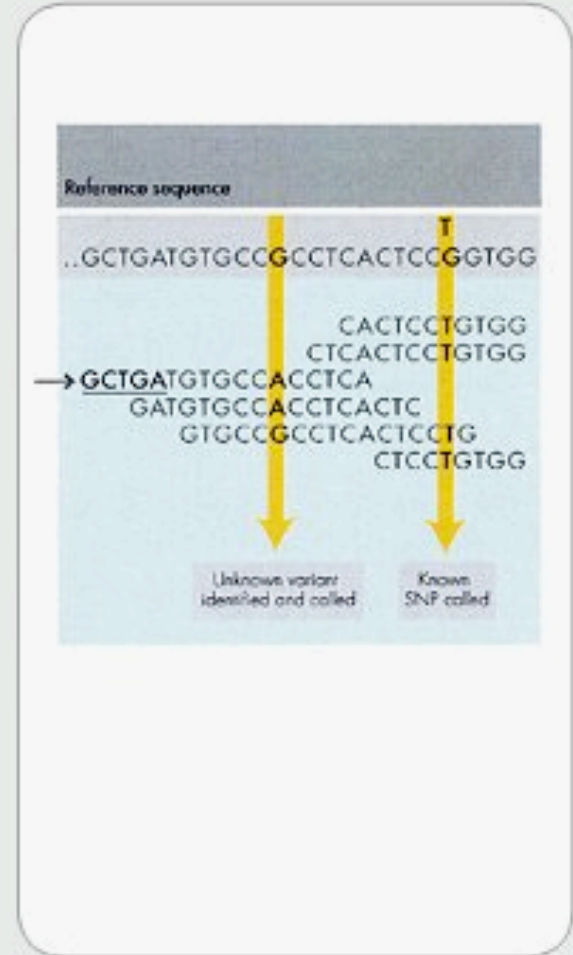
After laser excitation, collect the image data as before. Record the identity of the second base for each cluster.

11. SEQUENCE READS OVER MULTIPLE CHEMISTRY CYCLES

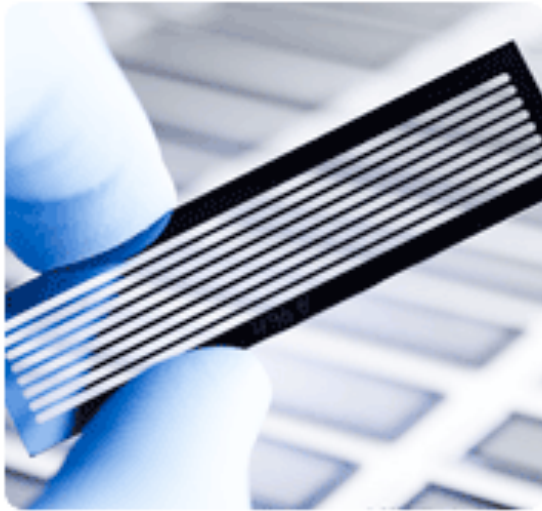


Repeat cycles of sequencing to determine the sequence of bases in a given fragment a single base at time.

12. ALIGN DATA



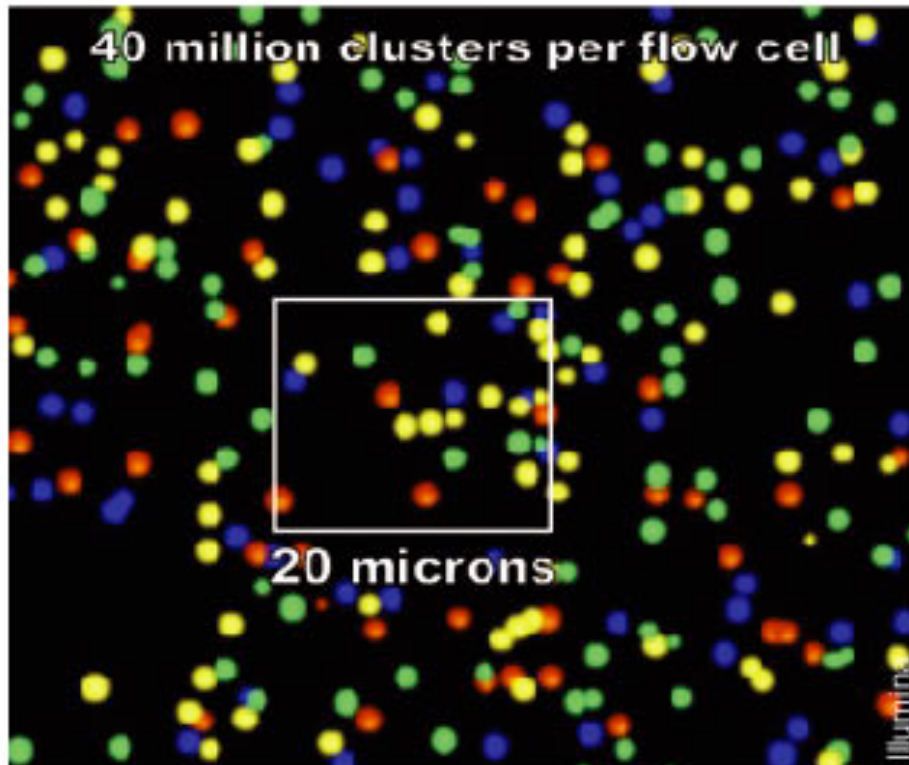
Align data, compare to a reference, and identify sequence differences.



In the MIT BioMicro Center

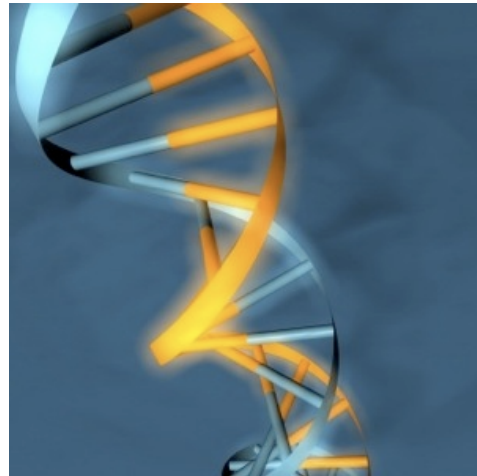
~70bp "reads"

7 million reads per
channel (flow cell)!!!



From 7 million
sequences can count/
calculate the relative
abundance of each
original mRNA species -
i.e. the transcriptional
profile

'Next Generation' Sequencing Technologies



Platform

Harvard/Danaher/Agencourt/ABI

454 Life Sciences / Roche

Solexa/Illumina

Helicos

Pacific Biosciences
occupancy

Amplification

Emulsion PCR

Emulsion PCR

Bridge PCR

None

None

Sequencing

Ligase

Polymerase - pyrosequencing

Polymerase - reversible terminator

Polymerase - single base extension

Polymerase - active site