AFTER THE SEQUENCE:

WHOLE GENOME APPROACHES TO BIOLOGICAL QUESTIONS

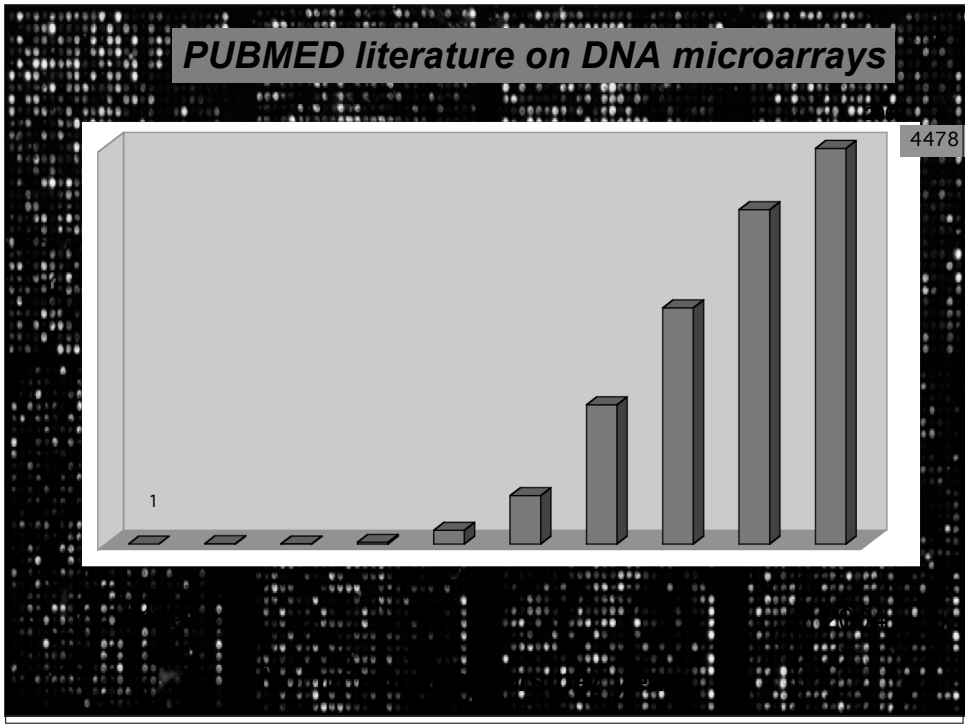
GENE EXPRESSION

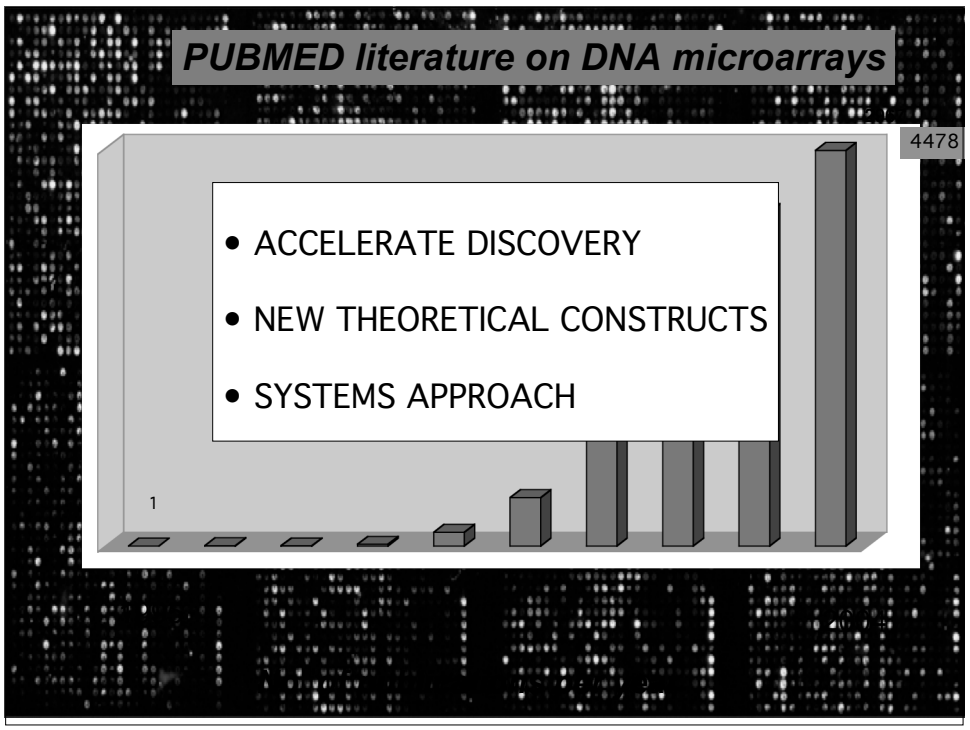
GENE VARIATION

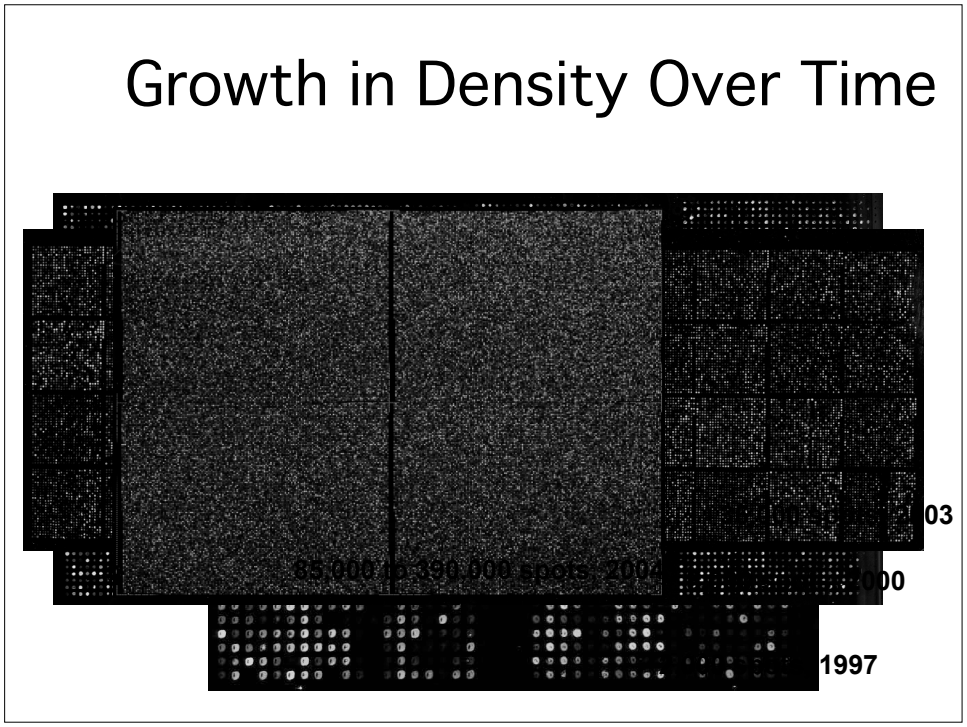
GENE FUNCTION

MICROARRAYS PROVIDE A TOOL FOR WHOLE GENOME ANALYSIS

PRIMARY IMPACT:
ACCELERATED DISCOVERY AND HYPOTHESIS GENERATION




PUBMED literature on DNA microarrays
4478
• ACCELERATE DISCOVERY
• NEW THEORETICAL CONSTRUCTS
• SYSTEMS APPROACH
1


Growth in Density Over Time
03
85,000 to 390,000 spots 2004
000
1997

MICROARRAY TERMINOLOGY

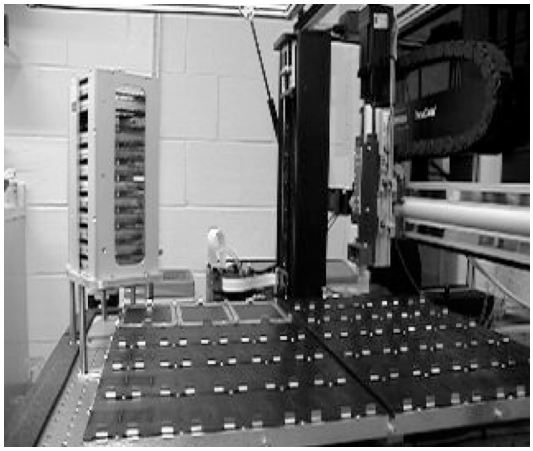
- Feature--an array element
- Probe--a feature corresponding to a defined sequence
- Target--a pool of nucleic acids of unknown sequence

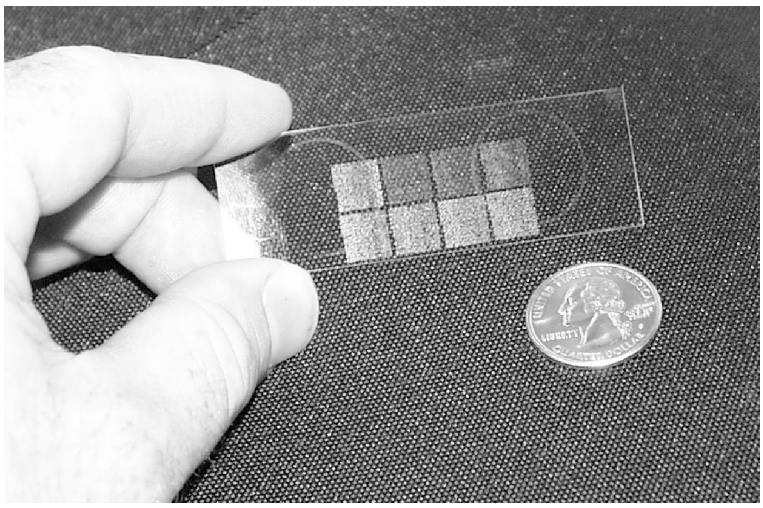
POSSIBLE ARRAY FEATURES

- Synthetic Oligonucleotides
- PCR products from
  - Cloned DNAs
  - Genomic DNA
- Cloned DNA

Microarray Manufacture

- **Printing**

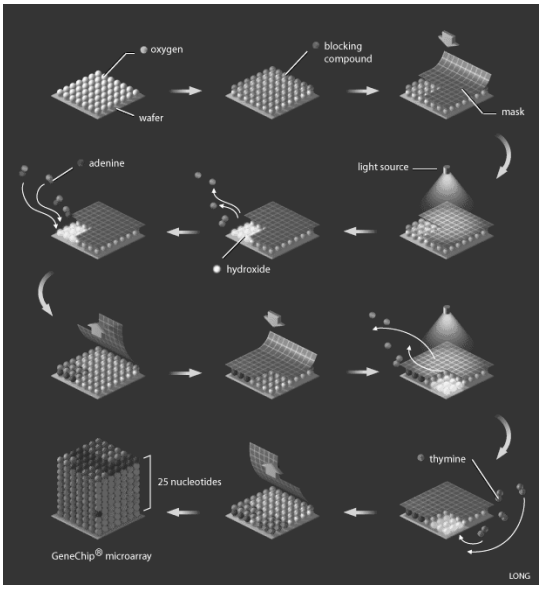




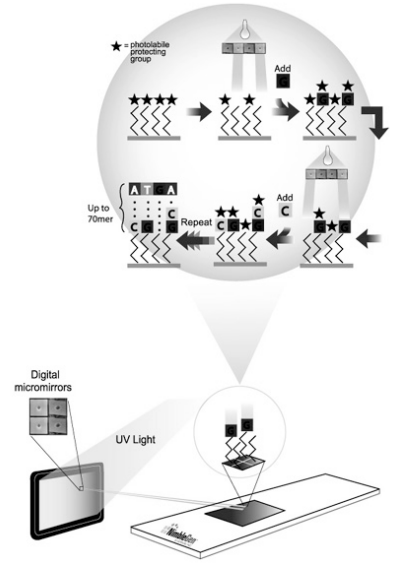
Microarray Manufacture

- **Printing**
- **Synthesis *in situ***
  - light directed
  - mechanically directed

LIGHT DIRECTED OLIGONUCLEOTIDE SYNTHESIS



LIGHT DIRECTED OLIGONUCLEOTIDE SYNTHESIS



MICROARRAY READOUT

- Determine quantity of target bound to each probe in a complex hybridization
- Must have high sensitivity, low background
- High spatial resolution essential
- Dual channel capability
- Fluorescent tags meet these demands

Building Microarrays

- Methods are applicable to any organism
- Sequenced organisms: oligonucleotides
- Unsequenced organisms: cloned DNAs

Building Microarrays

- Density depends on specific technology
- Printing based methods limited to 40-50K
- In situ synthesis: 100K and up
- Array design is linked to purpose.

Laboratory Essentials

- Arrays
- Scanner
- Software for processing array image
- Software for data analysis and display

DNA Microarray Applications

- Resequencing
- Comparative Genomic Hybridization
- Gene Expression
- Transcription factor localization
- Chromatin/DNA modification

DNA Microarray Applications

- Resequencing
- Comparative Genomic Hybridization
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DNA Microarray Applications

- **Resequencing**

  Mutations

  Polymorphisms

SINGLE NUCLEOTIDE POLYMORPHISM

AGGTTACCAGTA

AGGTTGCCAGTA

OCCUR ABOUT 1: 1250 BASES

•Dense SNP maps provide a basis to design microarrays for genome scanning

LABELLING SNPs

Genomic DNA

↓

Reduced complexity PCR product

↓

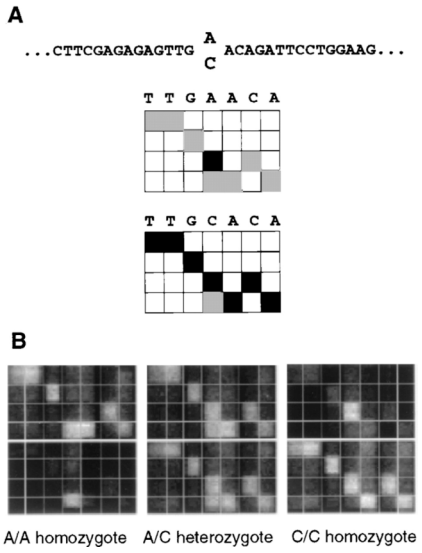
Label

↓

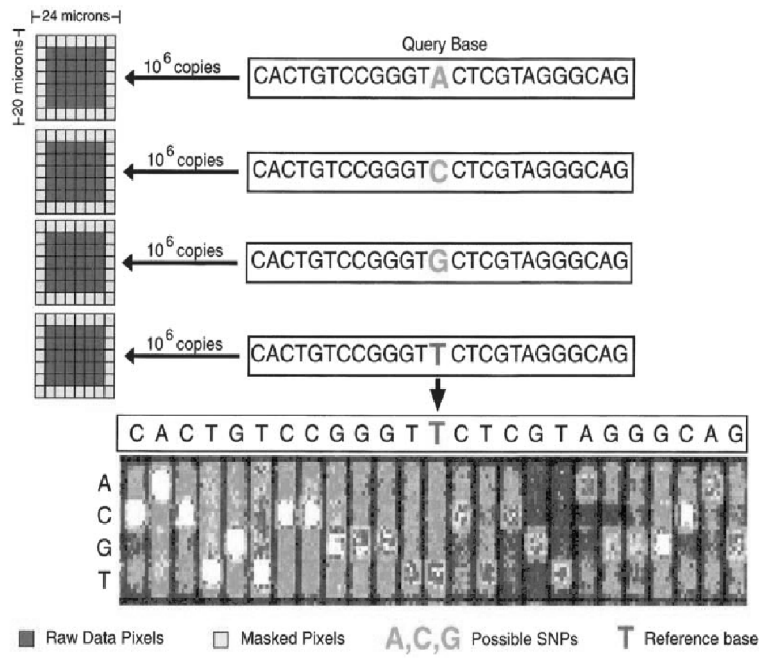
pool, denature, dilute into buffer

Hybridize to microarray

SNP CHIP*



*Wang et al. Science 280:1077 1998



Cutler DJ et al. Genome Res. 2001 11:1913-25.

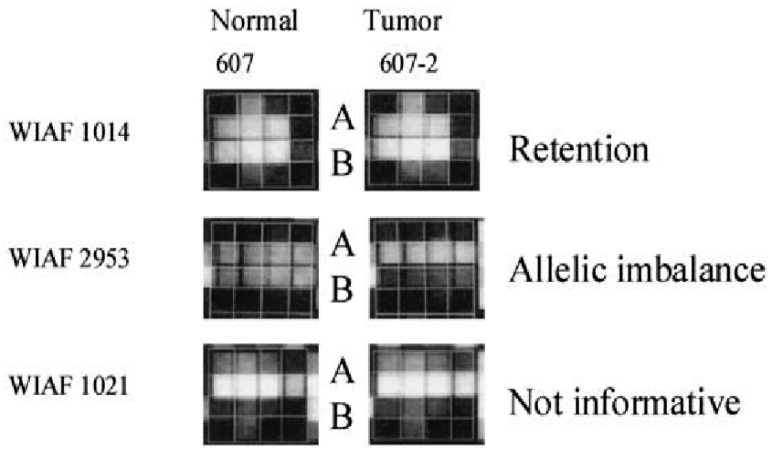
ACCURACY OF SNP CHIP

Table 3. ABACUS SNP Detection and Genotyping Accuracy

	Verified	Total Possible
A. Accuracy of autosomal SNPs detection		
Singleton SNPs	17	17
Non-singleton SNPs	91	91
Total SNPs	108	108
B. Number of autosomal SNPs electronically verified		
Number of SNPs electronically verified	371	
C. Accuracy of autosomal genotype calls		
Number of verified homozygous genotype calls	1515	
Number of incorrect homozygous genotype calls	0	
Percent correct homozygote calls	100.00%	
Number of verified heterozygous genotype calls	423	
Number of incorrect heterozygous genotype calls	3	
Percent correct heterozygote calls	99.30%	
D. Accuracy of haploid genotype calls		
Number of bases sequenced (6X coverage)	17,423	
Number of bases different from microarray chip calls	0	
Percent of bases identical	100.00%	

Cutler DJ et al. Genome Res. 2001 11:1913-25.

SNP CHIP FOR ALLELIC IMBALANCE



Primdahl H et al. J Natl Cancer Inst. 2002, 94:216-223

SNP CHIPS

HAVE ACHIEVED HIGH DENSITY

1,586,383 SNPS

HINDS ET AL. SCIENCE 307:1072 (2005)

COMMERCIAL CHIPS AVAILABLE: 500,000 SNPS

WILL INCREASE

CHOICE OF TECHNOLOGY PLATFORMS

VIABLE OPTION FOR:
GENOTYPING.
CANCER ALLELIC IMBALANCE.

ROLE OF SNP CHIPS IN RESEQUENCING CODING AND FUNCTIONAL SNPS

TECHNICAL CHALLENGE FOR LARGE SCALE ANALYSIS

AMPLICHIP CYP450 NOW FDA APPROVED

(31 POLYMORPHISMS IN 2D6 AND 2C19 P450 GENES)

LIKELY TO BE OF GROWING CLINICAL AND RESEARCH SIGNIFICANCE

DNA Microarray Applications

- **Resequencing**
- **Comparative Genomic Hybridization**
- **Gene Expression**
- **Transcription factor localization**
- **Chromatin/DNA modification**

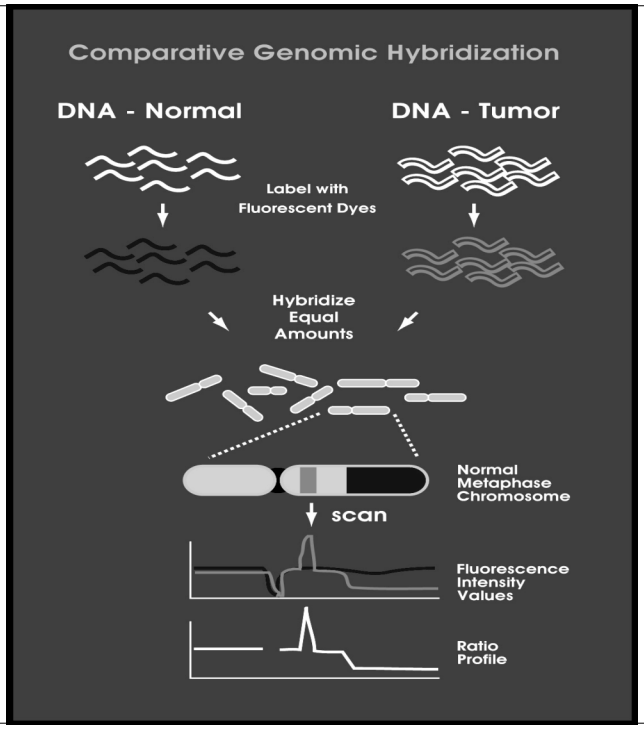
COMPARATIVE GENOMIC HYBRIDIZATION

- Method for gene copy number determination.

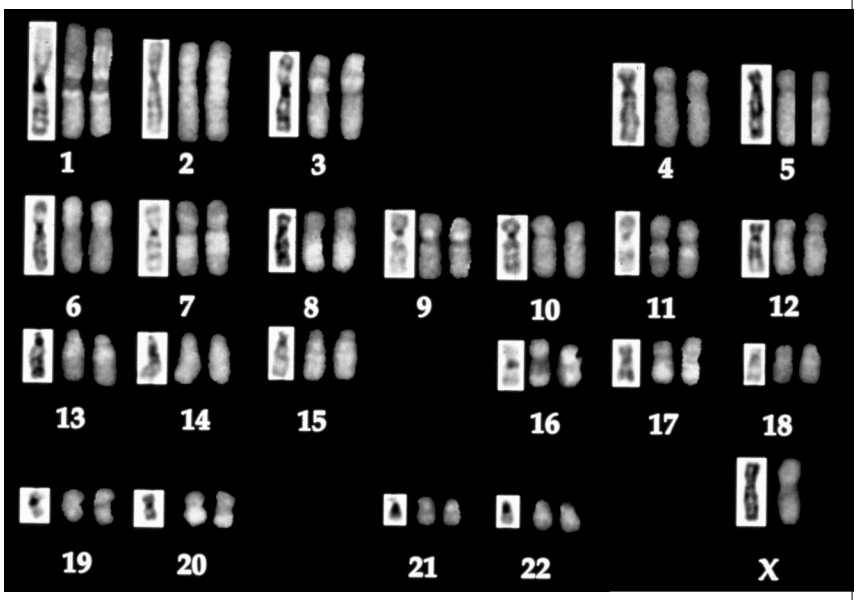
- Useful in cancer research to localize regions containing candidate oncogenes (gains) and tumor suppressor genes (losses).

- Useful in hereditary disease research to localize regions containing constitutional gains or losses of chromosome segments and copy number polymorphisms.

Cancer Genetics Branch

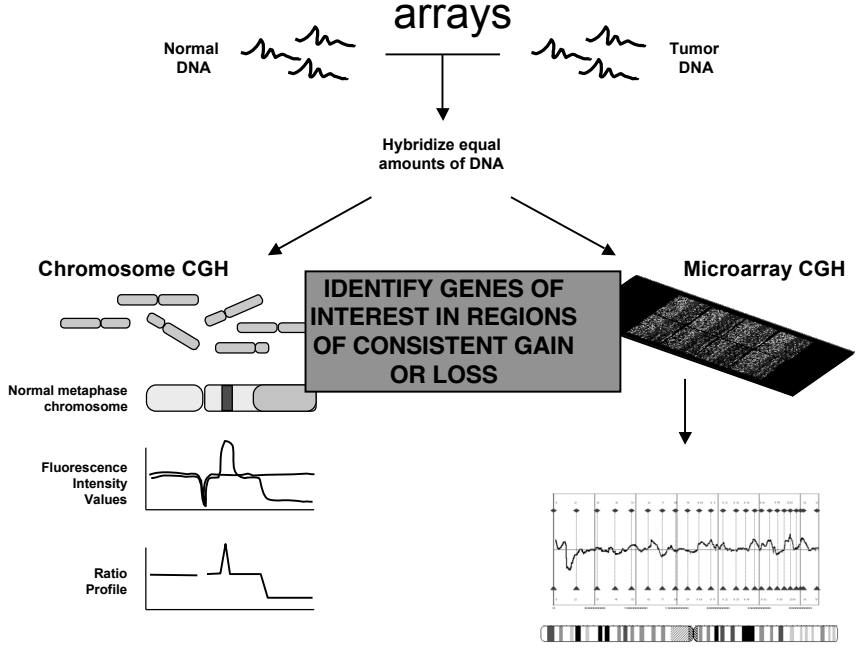


COMPARATIVE GENOMIC HYBRIDIZATION



Cancer Genetics Branch

Comparative Genomic Hybridization (CGH) arrays



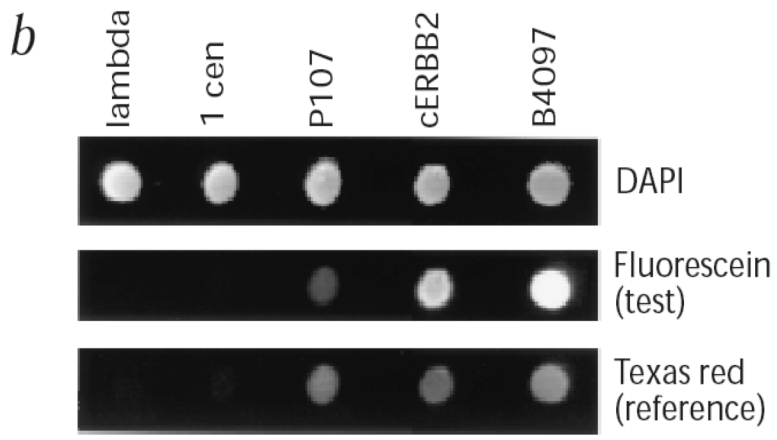
PLATFORMS FOR ARRAY BASED COMPARATIVE GENOMIC HYBRIDIZATION (CGH)

- BACs
- cDNAs
- Oligonucleotides

ARRAY CGH

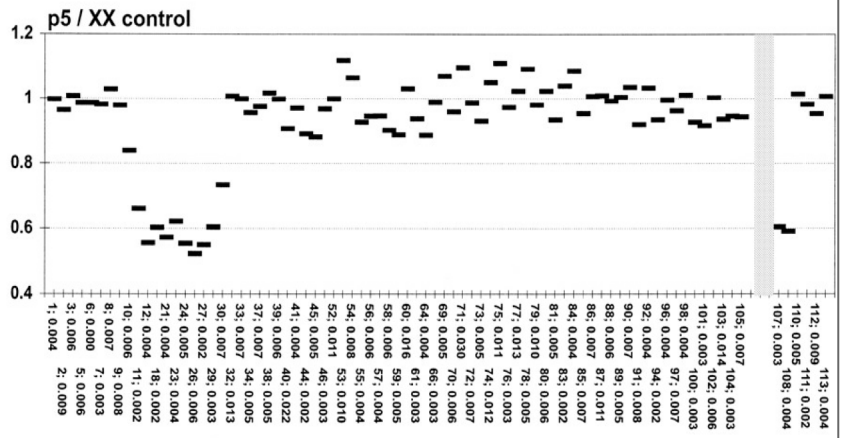
- HIGH RESOLUTION.
- SIMPLIFIED IMAGE ANALYSIS.
- HIGH THROUGHPUT.
- OLIGO STRATEGY ALLOWS GENOME BASED DESIGN.

CGH BAC ARRAYS

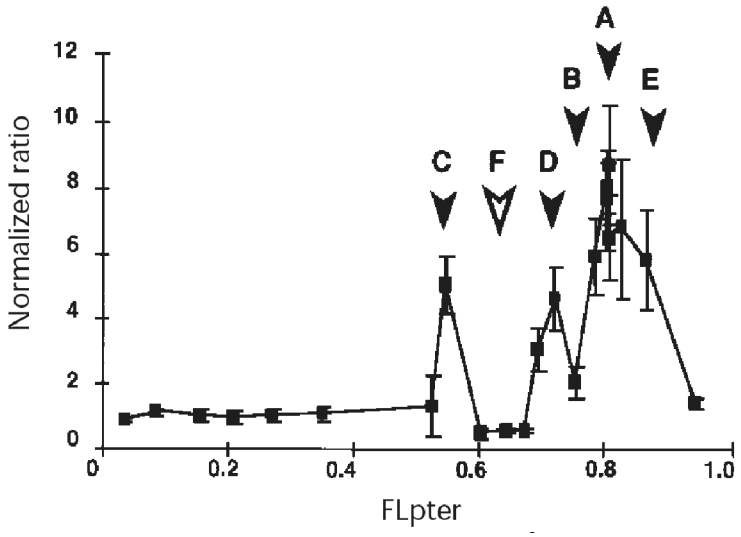


Pinkel D et al., Nature Genetics 20, 207 - 211 ,1998.

CGH BAC ARRAYS

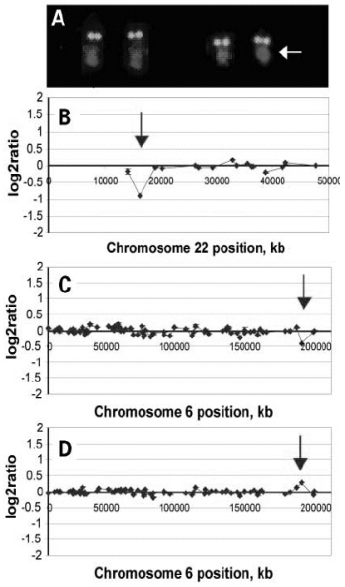


Bruder CE et al., Hum Mol Genet. 2001;10:271-82.



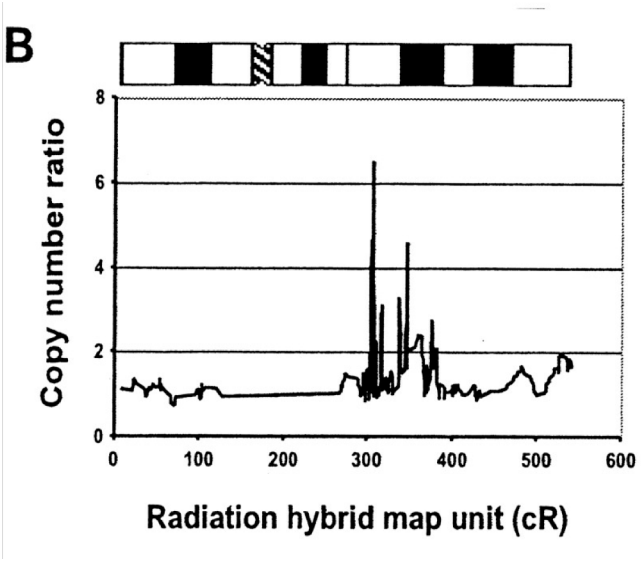
Pinkel et al. Nat Gen 20:207

CGH BAC ARRAYS



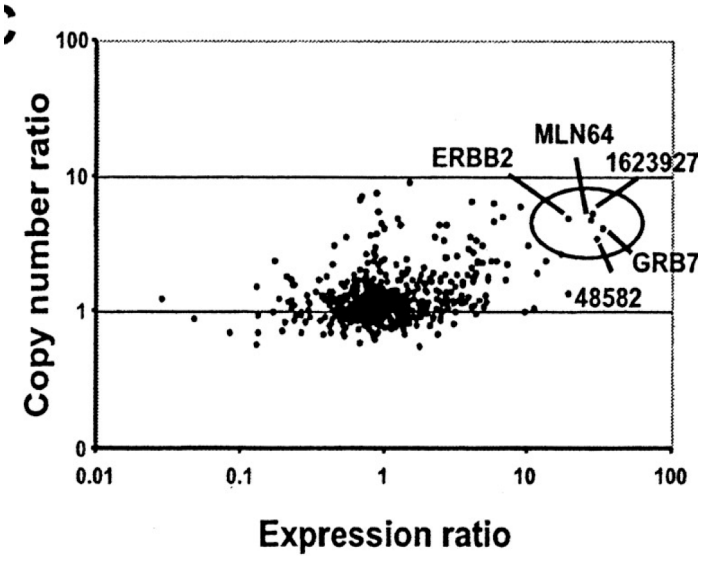
Albertson and Pinkel Hum Mol Genet 2003 12:145

CGH cDNA



Kauraniemi P et al., Cancer Res. 2001 ;61:8235-40.

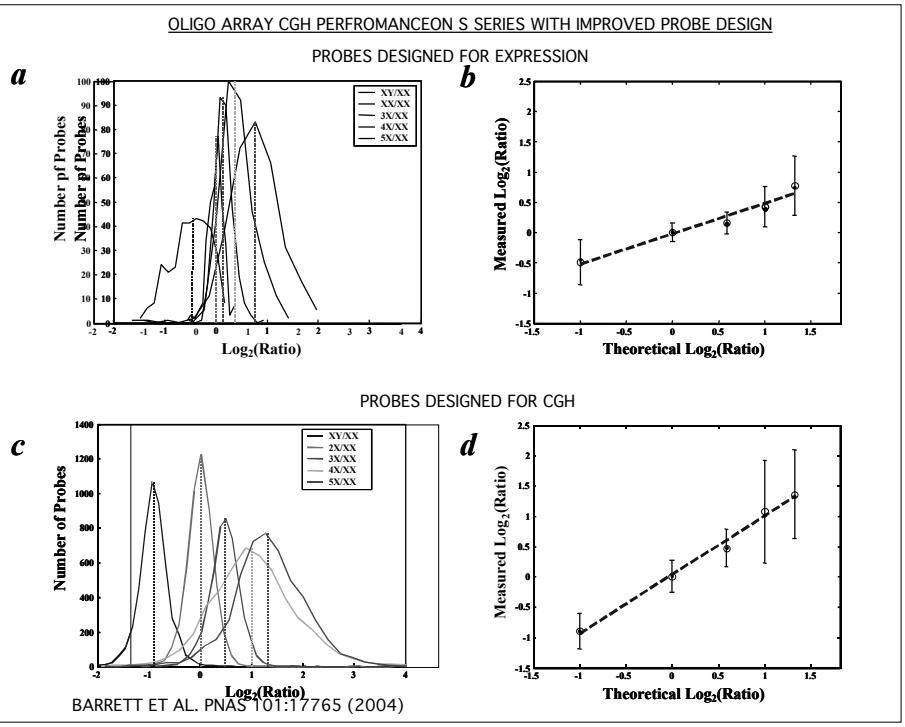
CGH cDNA



Kauraniemi P et al., Cancer Res. 2001 ;61:8235-40.

OLIGONUCLEOTIDE BASED CGH

- No bacterial cultures.
- Flexible in silico design.
- Resolution limited only by feature density
- Challenge: complex hybridization



BARRETT ET AL. PNAS 101:17765 (2004)

COMPARISON OF cDNA AND OLIGONUCLEOTIDE CGH

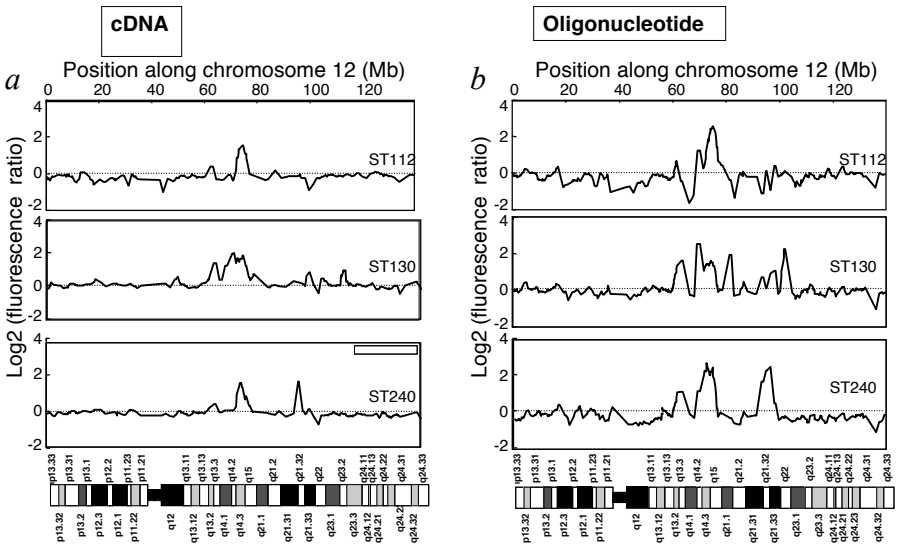


Figure 4

IDENTIFICATION OF GAINS AND LOSSES IN CANCER CELLS

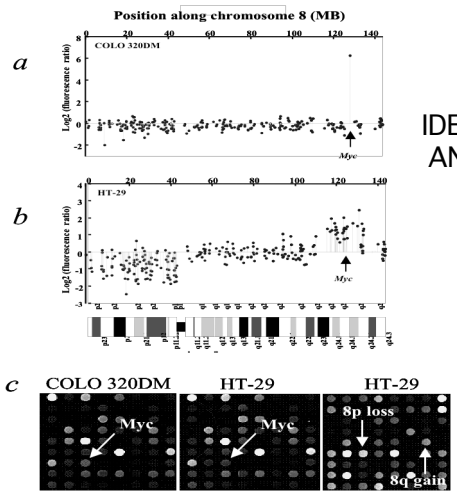
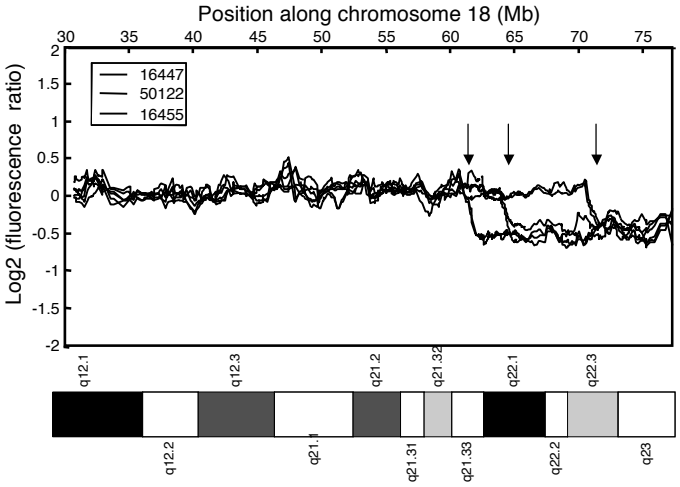
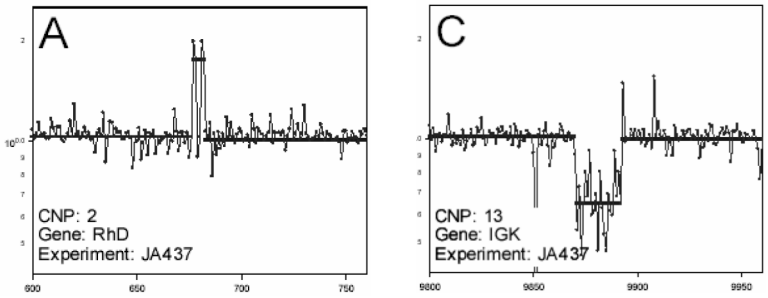


Figure 1. Barrett et al.

LOCATING CONSTITUTIONAL DELETIONS



HIGH DENSITY OLIGO ARRAYS FOR DETECTING COPY NUMBER POLYMORPHISM



Sebat et al., Science 2004;305:525.

DNA Microarray Applications

- Resequencing
- Comparative Genomic Hybridization
- Gene Expression
- Transcription factor localization
- Chromatin/DNA modification

Gene Expression ProfilingTechnologies

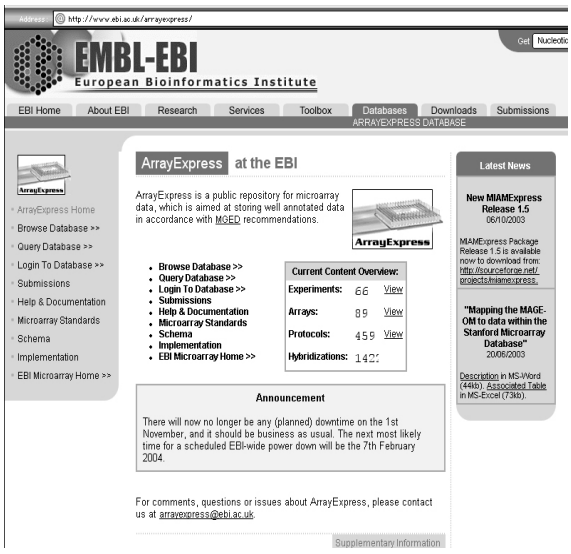
- cDNA library sequencing
- Serial analysis of gene expression (SAGE)
- MPSS (massively parallel signature sequencing)
- Microarray hybridization

Accessing Expression Data

•Individual Lab and Journal Sites; public databases

GEO

Accessing Expression Data



Publishing Expression Data

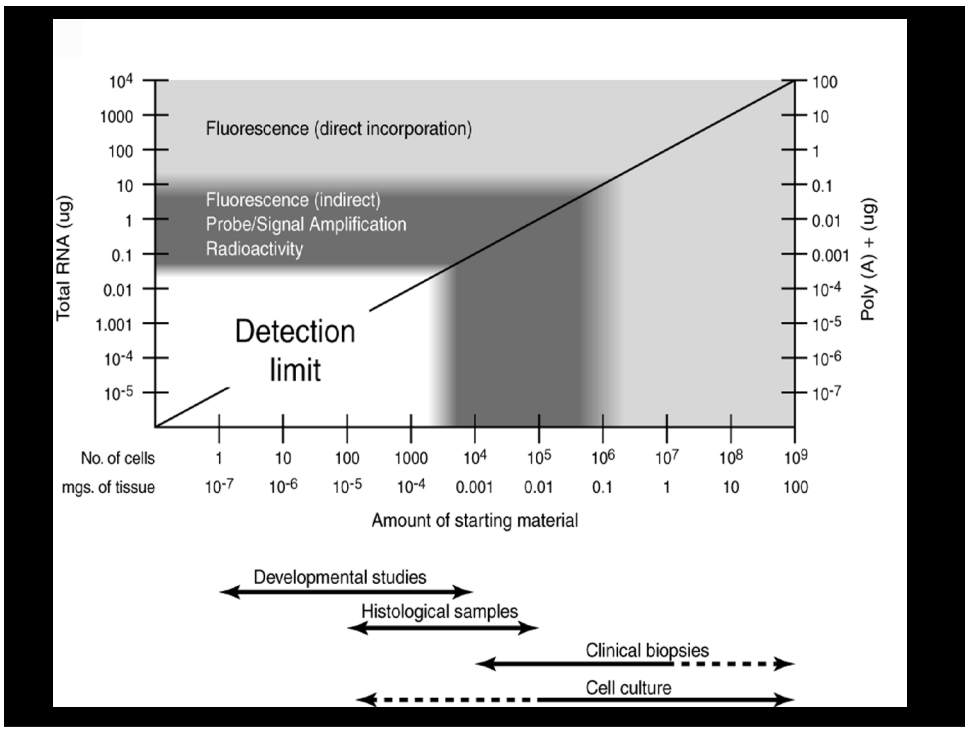
•MIAME standard

Minimum Information about a Microarray Experiment

Format required by many journals

STRATEGIES FOR SIGNAL GENERATION FROM mRNA

- **Fluorochrome conjugated cDNA**
- **Ligand substituted nucleotides with secondary detection (e.g. biotin-streptavidin)**
- **Radioactivity**
- **RNA amplification**


Fluorescence (direct incorporation)
Fluorescence (indirect)
Probe/Signal Amplification
Radioactivity
Detection limit
Total RNA (ug)
Poly (A) + (ug)
No. of cells
mgs. of tissue
Amount of starting material
Developmental studies
Histological samples
Clinical biopsies
Cell culture

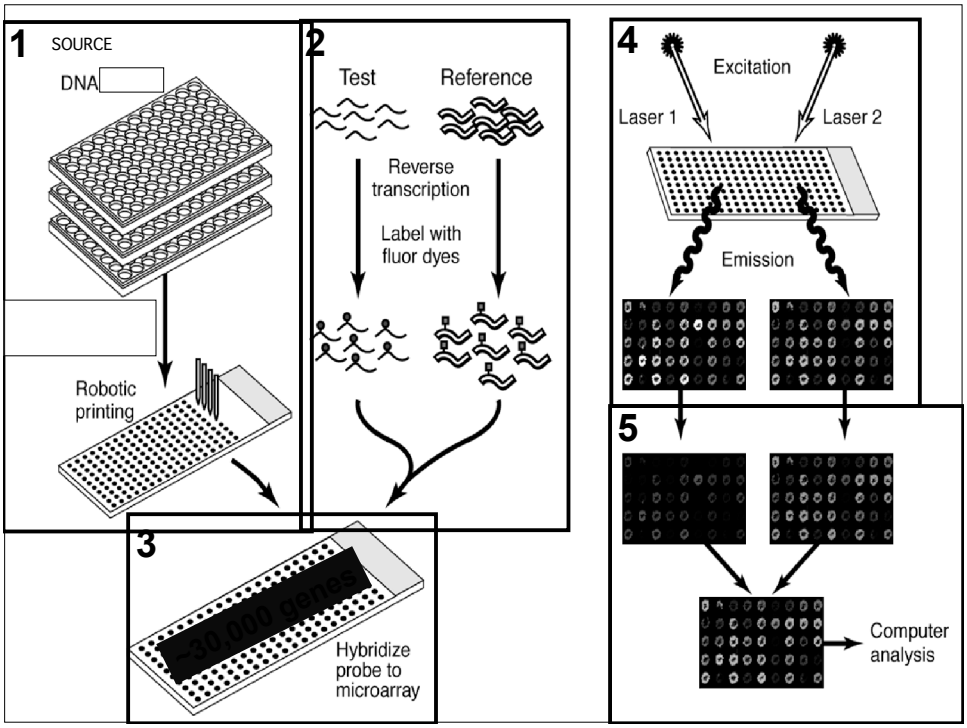
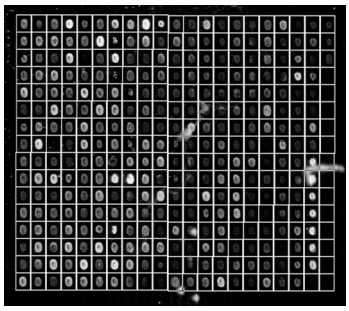

1
SOURCE
DNA
Robotic printing
2
Test
Reference
Reverse transcription
Label with fluor dyes
3
~30 000 genes
Hybridize probe to microarray
4
Excitation
Laser 1
Laser 2
Emission
5
Computer analysis

Image Analysis: DeArray

Grid Overlay



Target detection

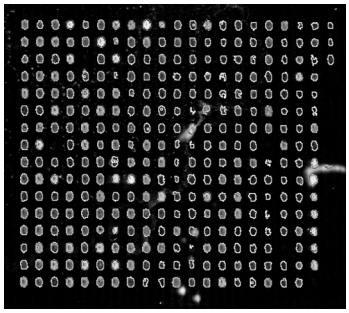
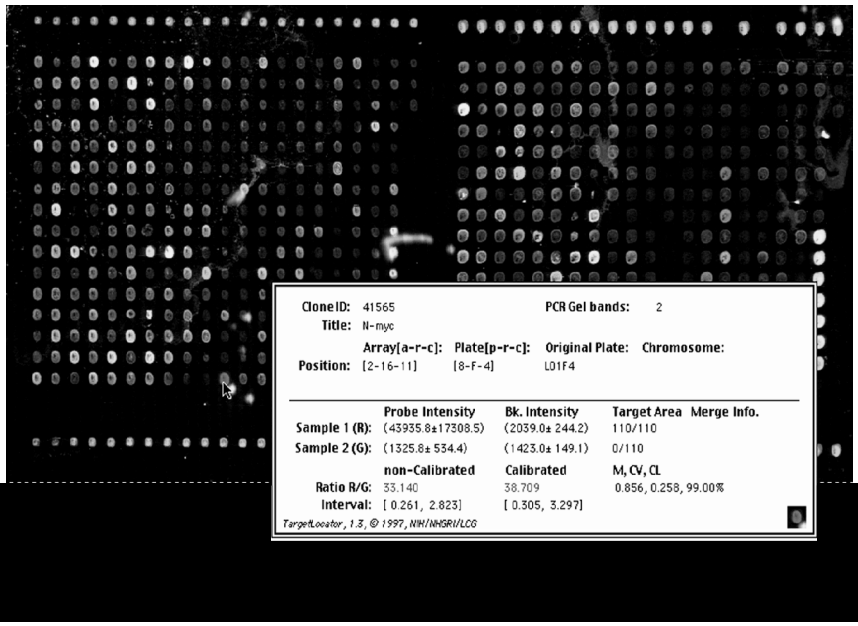
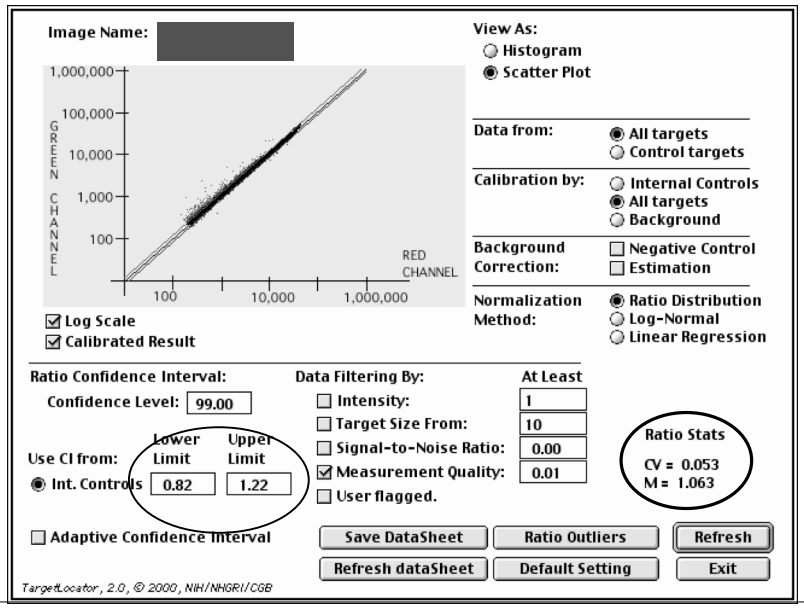
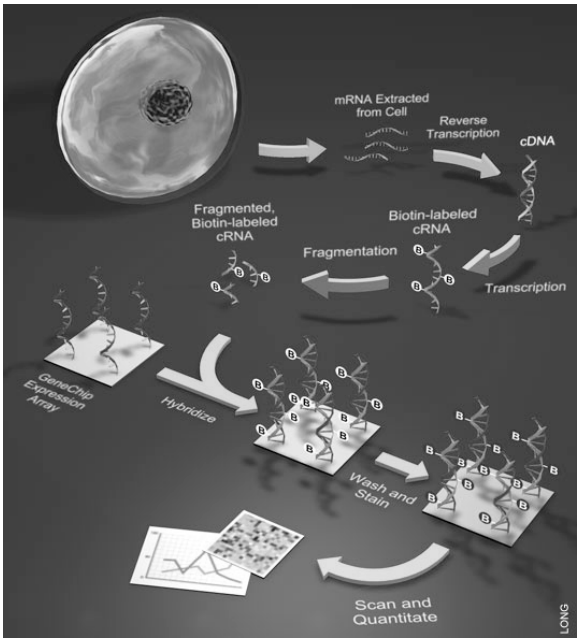


Image Analysis: DeArray



DATA QUALITY IS CRITICAL





ONE COLOR HYBRIDIZATION ON AN OLIGO ARRAY

Output of Microarray Analysis:

expression ratio
(2 color hybridization)

or

relative expression level
(1 color hybridization)

Both types of data can be analyzed with essentially the same tools.

APPLICATIONS OF EXPRESSION ARRAYS

•Expression profiling

Power arises from increasing sample number

•Direct comparisons (Induction)

Biological system critical

•Genome Annotation

A RECURRING PROBLEM

Disease Genes

Transcription factors

Hormones/growth factors

Drugs

Toxins

Infectious agents

Physical agents

?????

<u>Downstream Genes</u>

- **Direct targets**
- **Indirect targets**

EXPRESSION DATA ANALYSIS

- **Large amount of data**
- **Requires visualization and analysis tools**

EXPRESSION DATA ANALYSIS

- Check quality of individual experiments
- **Preprocessing**
  - Normalization
  - Remove genes which are not accurately measured
  - Remove genes which are similarly expressed in all samples
- **Unsupervised Clustering**
- **Supervised Clustering**

Unsupervised Clustering

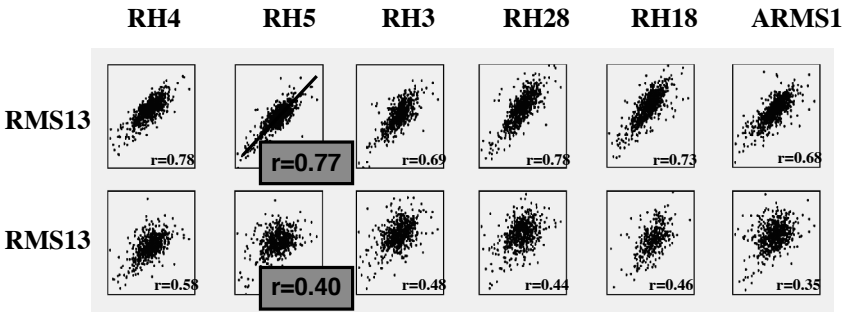
How do genes and samples organize into groups?

Powerful method of data display.

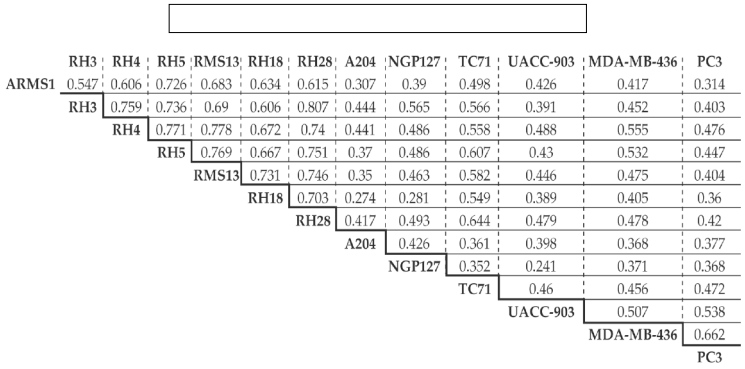
Does not prove the validity of groups.

- Clustered Samples Are Biologically Similar
- Clusters of Co-expressed genes
  - May be functionally related
  - May be enriched for pathways

UNSUPERVISED CLUSTERING IS BASED ON A GLOBAL SIMILARITY METRIC

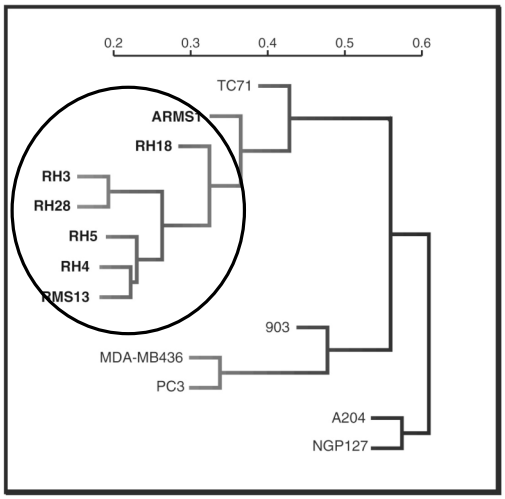


Matrix of Pearson Correlation Coefficients Distance Map

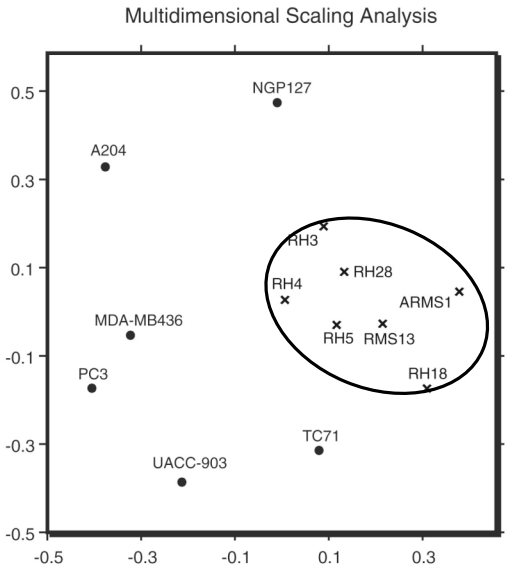


	RH3	RH4	RH5	RMS13	RH18	RH28	A204	NGP127	TC71	UACC-903	MDA-MB-436	PC3
ARMS1	0.547	0.606	0.726	0.683	0.634	0.615	0.307	0.39	0.498	0.426	0.417	0.314
RH3		0.759	0.736	0.69	0.606	0.807	0.444	0.565	0.566	0.391	0.452	0.403
RH4			0.771	0.778	0.672	0.74	0.441	0.486	0.558	0.488	0.555	0.476
RH5				0.769	0.667	0.751	0.37	0.486	0.607	0.43	0.532	0.447
RMS13					0.731	0.746	0.35	0.463	0.582	0.446	0.475	0.404
RH18						0.703	0.274	0.281	0.549	0.389	0.405	0.36
RH28							0.417	0.493	0.644	0.479	0.478	0.42
A204								0.426	0.361	0.398	0.368	0.377
NGP127									0.352	0.241	0.371	0.368
TC71										0.46	0.456	0.472
UACC-903											0.507	0.538
MDA-MB-436												0.662
PC3												

Hierarchical Clustering Dendrogram

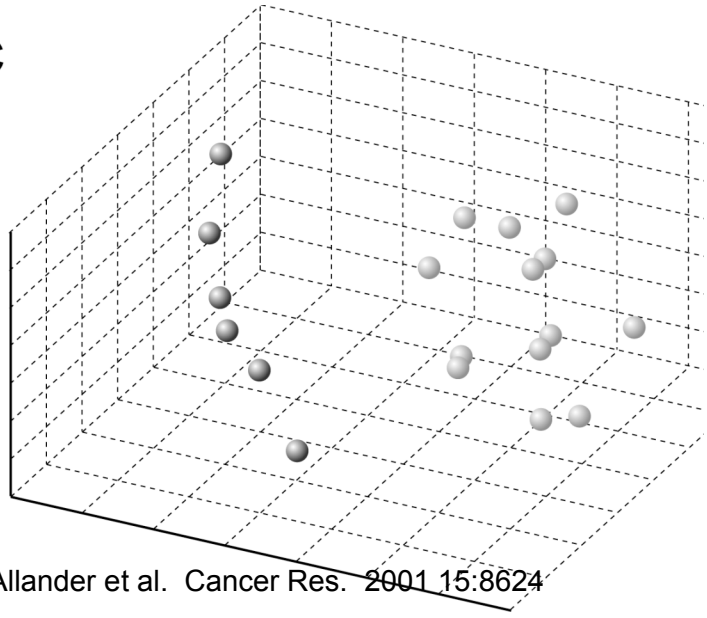


DATA DISPLAY BY MULTIDIMENSIONAL SCALING



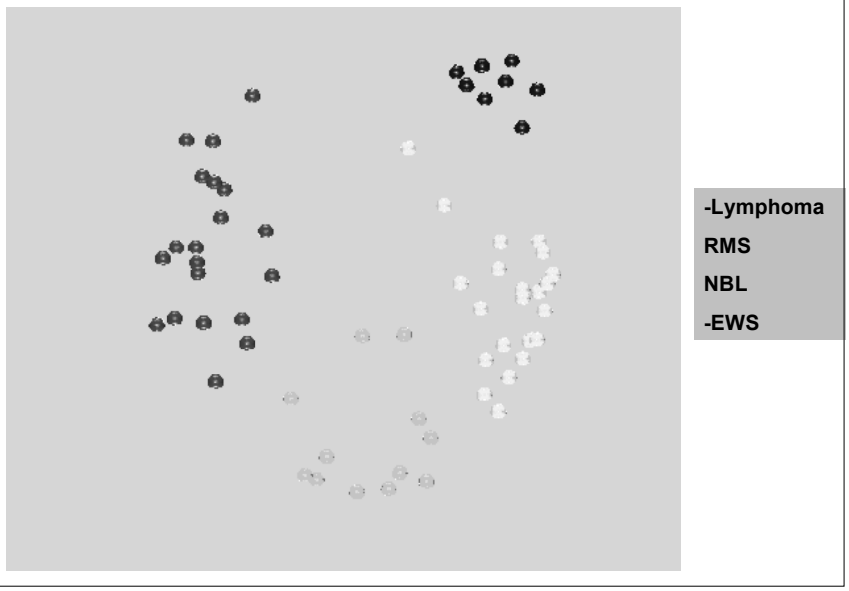
MDS PLOT

C

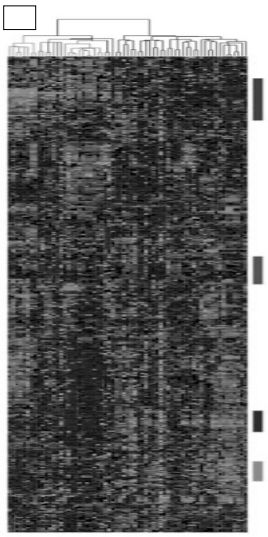


Allander et al. Cancer Res. 2001 15:8624

MULTIDIMENSIONAL SCALING



CLUSTERING GENES AND SAMPLES

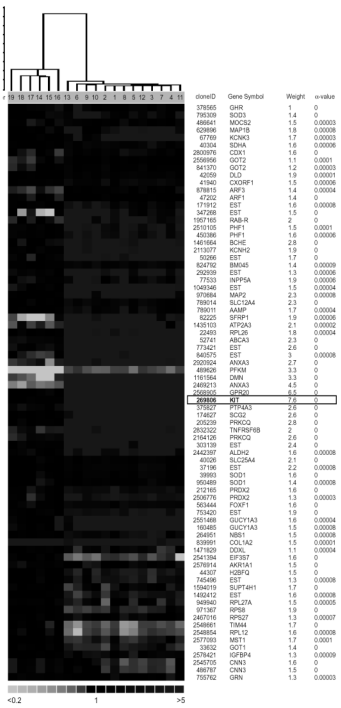


Perou et al. Nature 2000 406:747

Supervised Clustering

What genes distinguish samples in selected groups from each other?

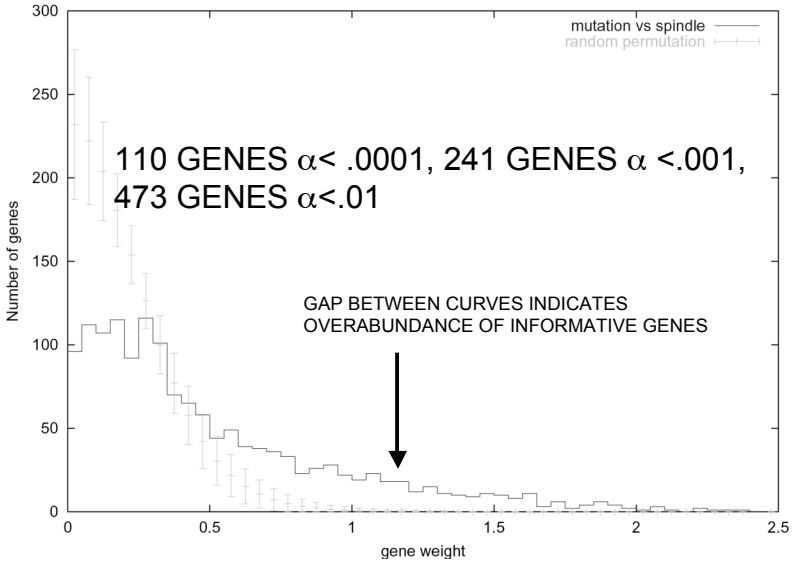
- **Choice of groups can be based on any known property of the samples.**
- **Many possible underlying methods: t-test or F-statistic frequently used.**
- **Output includes ranked gene list.**
- **Leads to the development of classifiers which can be applied to unknown samples.**
- **Must address the problem of false discovery due to multiple comparisons and discrepancy between sample/gene numbers.**



HIERARCHICAL CLUSTERING OF SAMPLES/GENES USING THE GENES SELECTED BY SUPERVISED ANALYSIS

Allander et al. Cancer Res. 2001 15:8624

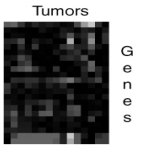
OVERABUNDANCE OF INFORMATIVE GENES DEMONSTRATED BY RANDOM PERMUTATION TEST



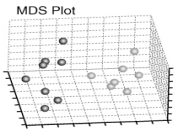
Allander et al. Cancer Res. 2001 15:8624

GENOMICS FROM BENCH TO BEDSIDE

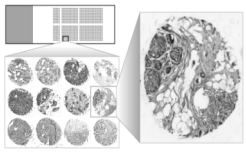
WHOLE GENOME

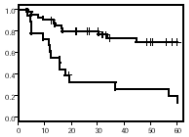


GENE SELECTION



GENE VALIDATION



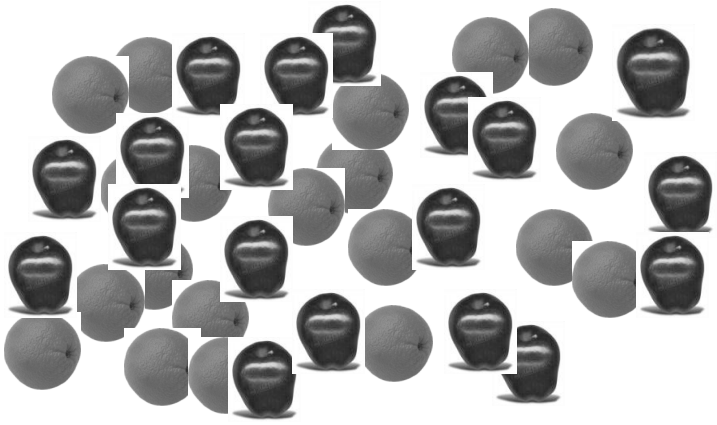


ASSAY DEVELOPMENT

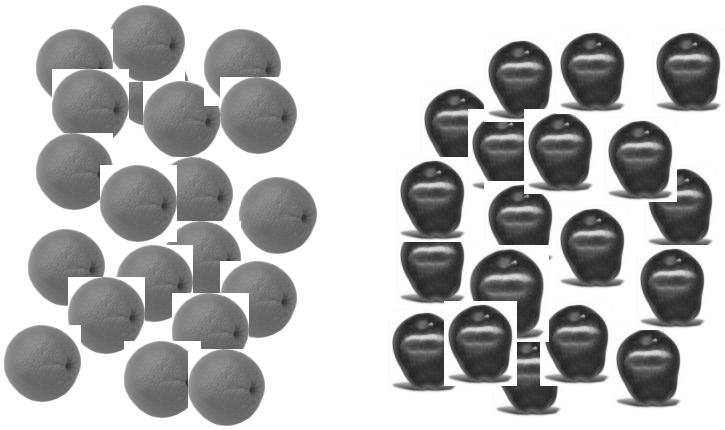
SIGNAL STRENGTH VARIES IN TISSUE PROFILING EXPERIMENTS

THE MOST INTERESTING QUESTIONS TEND TO BE ASSOCIATED WITH WEAKER SIGNAL.

CONSIDER A SAMPLE SET



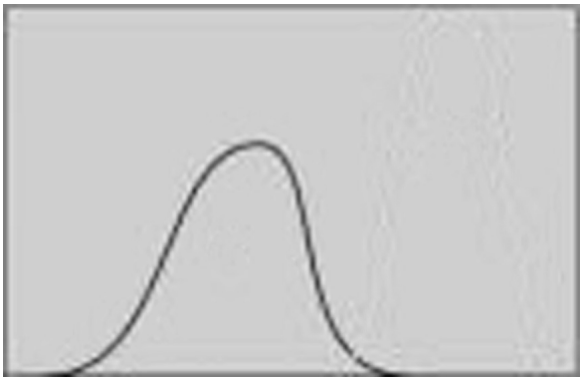
CONSIDER A SAMPLE SET



THESE ARE EASY TO DISTINGUISH BY ONE MEASUREMENT PER INDIVIDUAL.

CONSIDER A SAMPLE SET

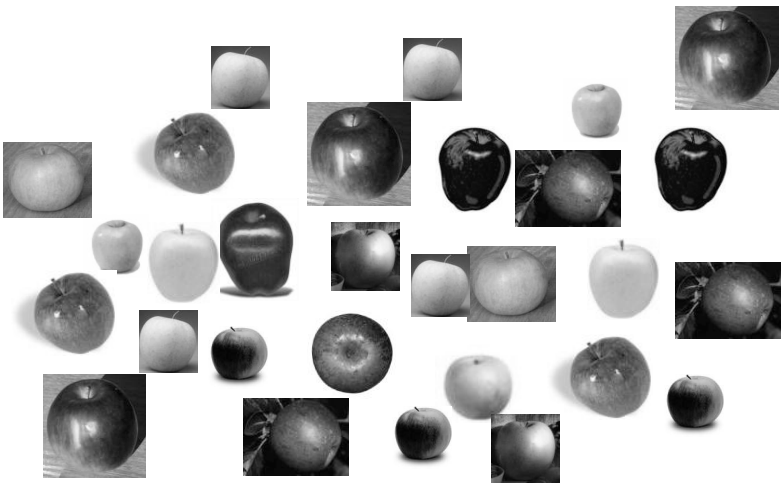
TUMORS



EXPRESSION LEVEL
(HIGHLY INFORMATIVE GENE)

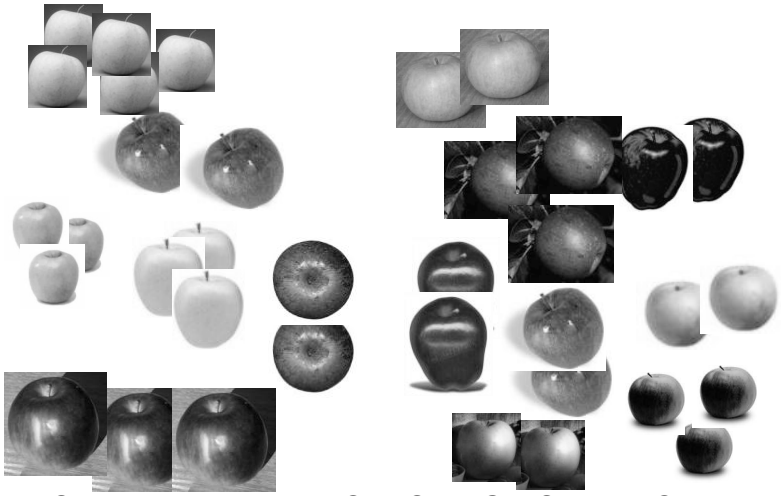
THESE ARE EASY TO DISTINGUISH BY ONE MEASUREMENT PER INDIVIDUAL.

CONSIDER A SAMPLE SET



THESE ARE HARDER TO DISTINGUISH. REQUIRE MORE THAN ONE MEASUREMENT PER INDIVIDUAL.

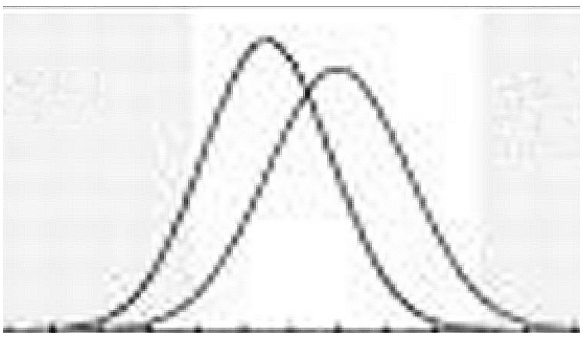
CONSIDER A SAMPLE SET



THESE ARE HARDER TO DISTINGUISH. REQUIRE MORE THAN ONE MEASUREMENT PER INDIVIDUAL.

CONSIDER A SAMPLE SET

TUMORS



EXPRESSION LEVEL
(POORLY INFORMATIVE GENE)

THESE ARE HARDER TO DISTINGUISH. REQUIRE MORE THAN ONE MEASUREMENT PER INDIVIDUAL.

WE CAN TELL APPLES FROM ORANGES.

CAN WE DISTINGUISH DIFFERENT KINDS OF APPLES?

A CONTINUUM OF POSSIBLE OUTCOMES FROM MICROARRAY RESEARCH

- SOME FEATURES WILL SEPARATE TUMORS EASILY INTO CLASSES, AND MIGHT BE REDUCED TO SINGLE GENE TESTS, IMPLEMENTED IN A CONVENTIONAL FASHION.

- OTHERS WILL BE MORE DIFFICULT, AND REQUIRE MULTIPLE GENE MEASUREMENTS.

- MANY CLINICALLY RELEVANT FEATURES APPEAR TO FALL WITHIN THIS DIFFICULT GROUP.

A CONTINUUM OF POSSIBLE OUTCOMES FROM MICROARRAY RESEARCH

- SOME GENES WILL SHOW DIFFERENCES BETWEEN GROUPS OF SAMPLES BY CHANCE ALONE.
- THERE MAY BE NO ONE GENE WHICH SEPARATES GROUPS RELIABLY.
- FIND THE MOST INFORMATIVE GENES AND USE THEM IN COMBINATION .

RISK OF OVERFITTING IN CLINICAL STUDIES WITH SMALL SAMPLE SETS

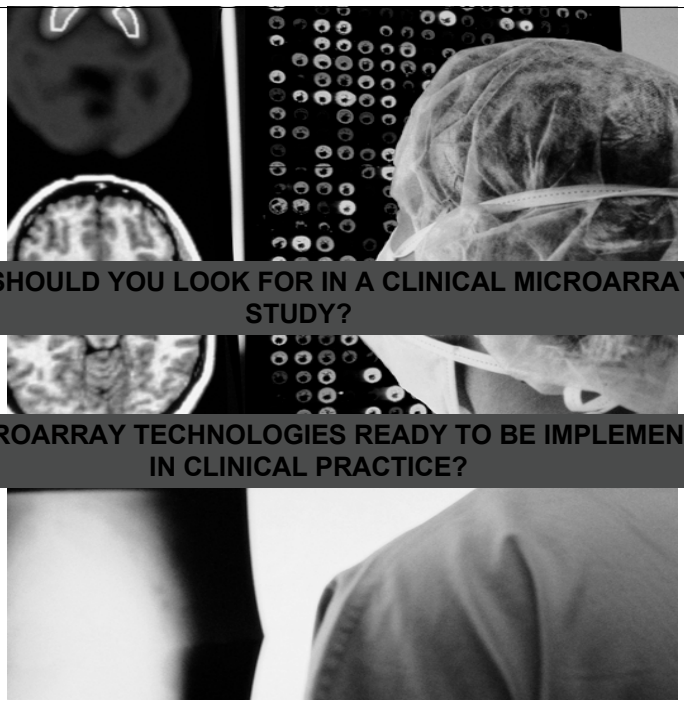
NEED INDEPENDENT VALIDATION SETS.

MICROARRAY STUDIES GENERATE ORGANIZED LIST OF GENES

- Often cryptic and hard to interpret.
- Hypothesis generating, but this is often rather subjective.
- Seldom provide strong evidence for a specific mechanism.
- Expression data is intrinsically limited.

GETTING BEYOND GENE LISTS

- Optimal use of gene annotations.
- Optimizing use of public data.
- Incorporating data from model systems.
- Linking expression data to sequence.
- Adding other types of genome scale data.



WHAT SHOULD YOU LOOK FOR IN A CLINICAL MICROARRAY STUDY?

ARE MICROARRAY TECHNOLOGIES READY TO BE IMPLEMENTED IN CLINICAL PRACTICE?

WHAT TO LOOK FOR IN CLINICAL
CORRELATIVE STUDIES
USING MICROARRAYS

- WELL DEFINED QUESTION AND PATIENT SAMPLE.
- HIGH QUALITY ARRAY MEASUREMENTS (HARD TO ASSESS WITHOUT REFERENCE TO PRIMARY DATA---SHOULD BE MADE PUBLIC).
- APPROPRIATE AND RIGOROUS STATISTICAL ANALYSIS OF ARRAY DATA.
- FORMAL CLASSIFIER THAT CAN BE APPLIED TO NEW SAMPLES.
- VALIDATION SAMPLE SET.

WHAT TO LOOK FOR IN CLINICAL
CORRELATIVE STUDIES
USING MICROARRAYS

• GOAL SHOULD BE TO SEEK AND VALIDATE CLINICALLY RELEVANT SIGNATURES WITHIN DEFINED PATIENT GROUPS FOR WHICH NO CURRENT FEATURES ADEQUATELY ANSWER THE CLINICAL QUESTION POSED.

EXPRESSION PROFILING IN THE CLINIC?

PROBLEMS:

- **SPECIALIZED TECHNOLOGY**
- **RNA IS UNSTABLE**
- **FROZEN TISSUE NOT PART OF USUAL OR SAMPLE FLOW**

EXPRESSION PROFILING IN THE CLINIC?

OPTIONS:

- REFERENCE LABORATORIES
- RNA PRESERVATIVES
- USE OF PARAFFIN EMBEDDED MATERIALS.

EXPRESSION PROFILING IN THE CLINIC?

- COMMERCIAL TESTS BEGINNING TO APPEAR.
- NOT FDA APPROVED
- LIMITED CLINICAL VALIDATION
- ADDITIONAL CLINICAL STUDIES NEEDED

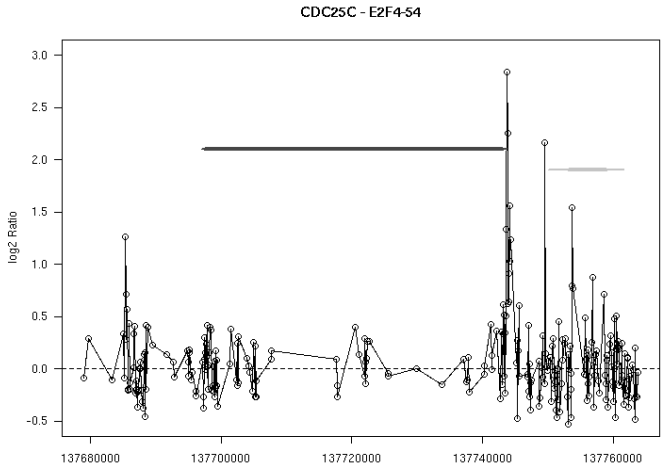
DNA Microarray Applications

- **Resequencing**
- **Comparative Genomic Hybridization**
- **Gene Expression**
- **Transcription factor localization**
- **Chromatin/DNA modification**

APPLICATIONS OF TILING PATH ARRAYS

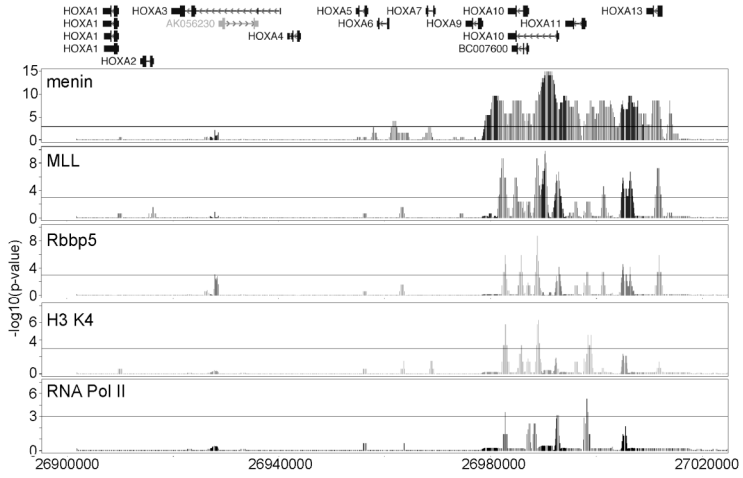
- CGH
- EXPRESSION
- ChIP CHIP
- DNAse HYPESENSITIVE SITES
- ANY ENRICHED PREPARATION OF INTERESTING SEQUENCES

E2F4 IP



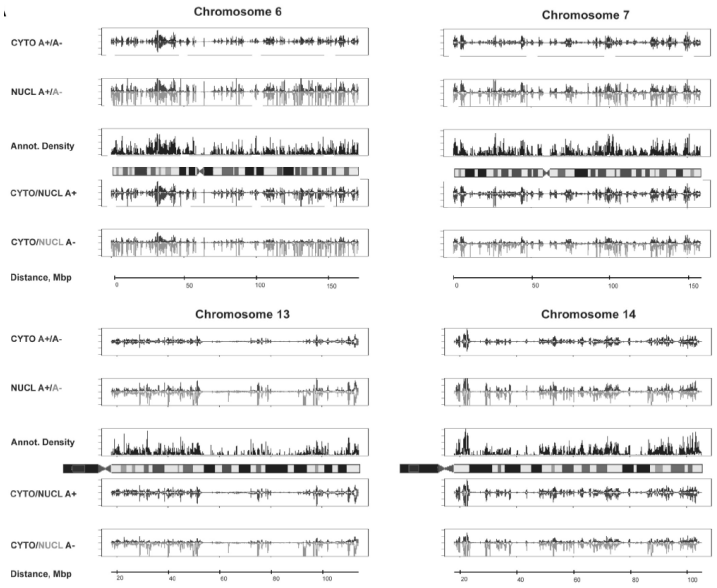
Scacheri et al. PLOS 2006

MULTIPLE IP'S IN HOXA REGION



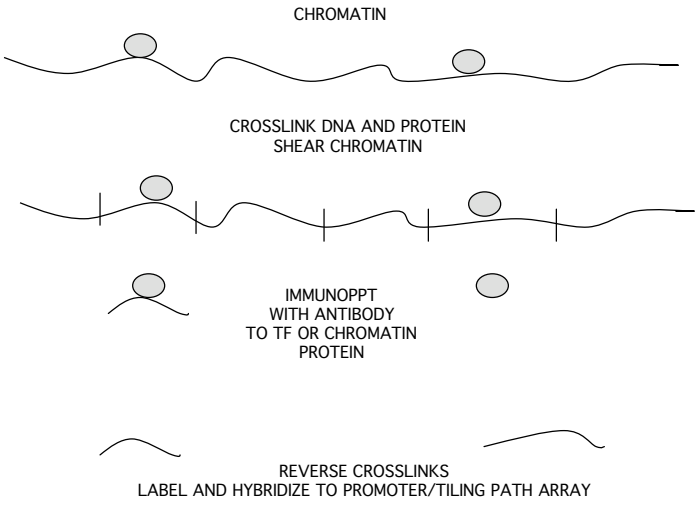
Scacheri et al. PLOS 2006

Scanning Chromosomes with Tiling Path Arrays

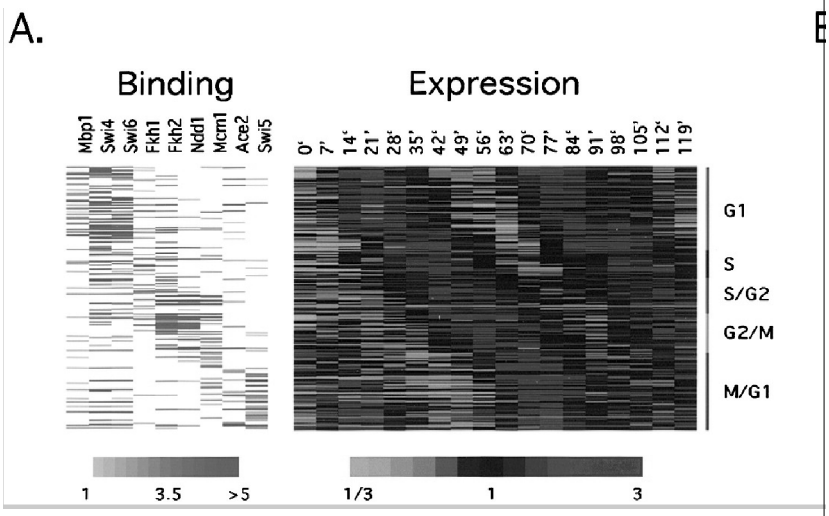


Cheng et al Science March 29, 2005

TRANSCRIPTION FACTOR LOCALIZATION ON ARRAYS

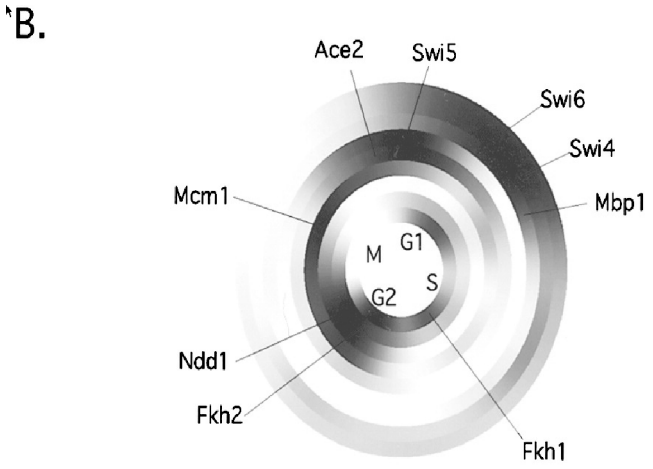


Promoter Occupancy During Yeast Cell Cycle



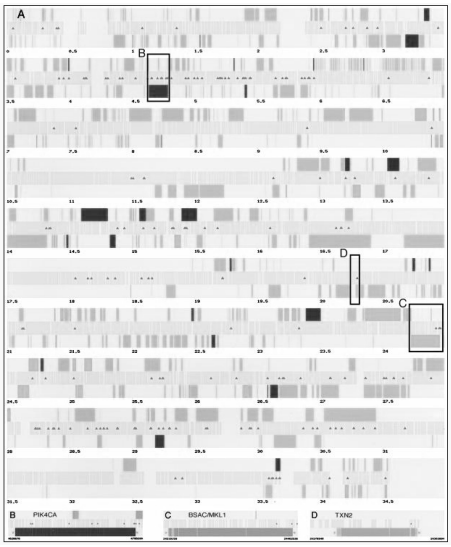
Simon I Cell. 2001 Sep 21;106(6):697-708.

Promoter Occupancy During Yeast Cell Cycle



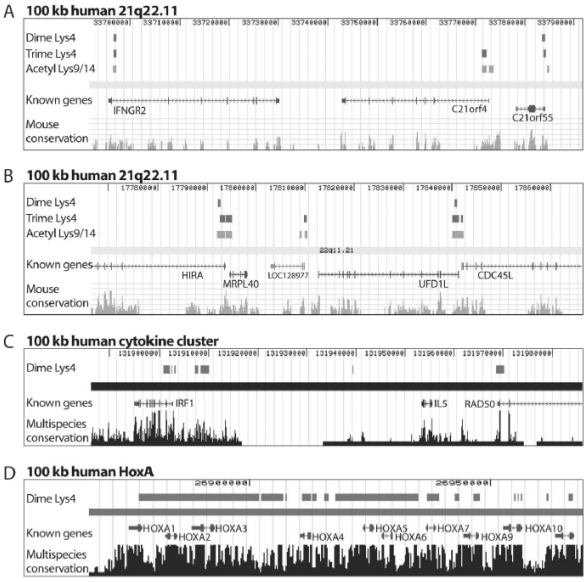
Simon I Cell. 2001 Sep 21;106(6):697-708.

NFKB Binding to Chromosome 22



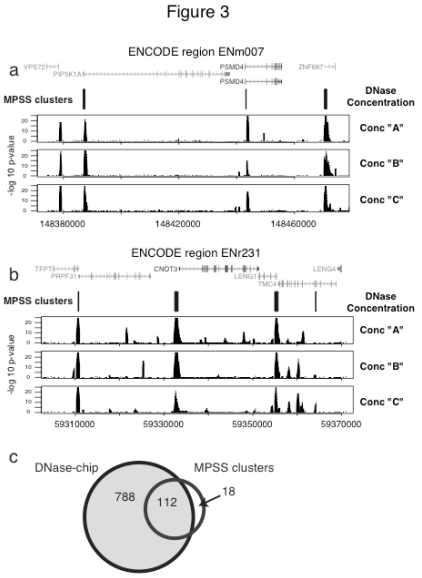
Martone et al. PNAS. 2004 100:12247.

CHROMATIN MODIFICATION BY CHIP CHIP



Bernstein et al. Cell 2005 120:169.

DNASE HS SITES



Crawford et al.

Selected Web Sites for Microarrays

Non-Profit

NHGRI
http://research.nhgri.nih.gov/microarray/
• The National Human Genome Research Institute microarray website

MGED
http://www.mged.org/
• The Microarray Gene Expression Data (MGED) Society is an international organization of biologists, computer scientists, and data analysts that aims to facilitate the sharing of microarray data generated by functional genomics and proteomics experiments.

NCBI
http://ncbi.nih.gov/geo/
• The Gene Expression Omnibus is a gene expression and hybridization array data repository, as well as a curated, online resource for gene expression data browsing, query and retrieval. GEO was the first fully public high-throughput gene expression data repository, and became operational in July 2000.

EBI
http://www.ebi.ac.uk/microarray/index.html
• The microarray informatics group at the EBI addresses the problem(s) of managing, storing and analyzing microarray data.

TIGR
http://www.tigr.org/tdb/microarray/
• The Institute for Genomic Research

Academic

Stanford
http://cmgm.stanford.edu/pbrown/mguide/
• The Brown Lab's complete guide to microarraying for the molecular biologist.

Stanford
http://genome-www5.stanford.edu/MicroArray/SMD/
• The Stanford microarray database

UCSF
http://www.microarrays.org/index.html
• A public source for microarray protocols and software.

MIT
http://www-genome.wi.mit.edu/cancer/
• Focuses on genomic and computational solutions to problems in cancer biology and cancer medicine.