

# Microarray Technology

(Thinking carefully about data)

Lecture 5

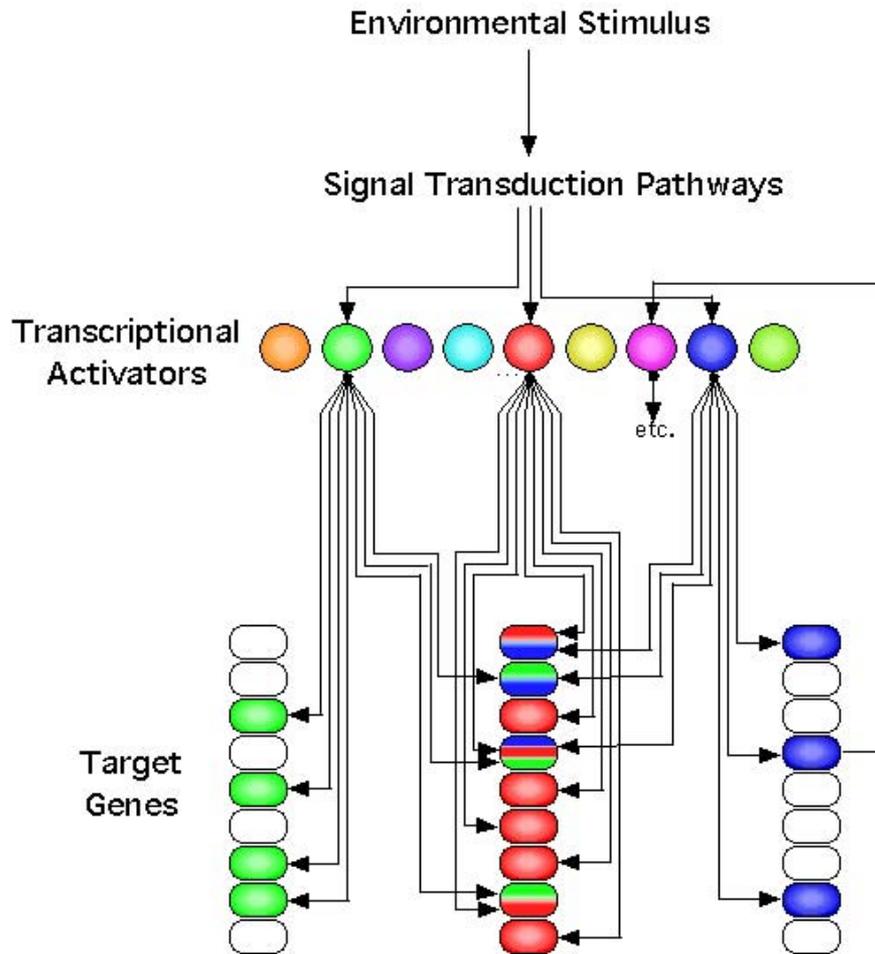
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David Gifford

# Microarrays can access in-vivo data derived from nucleic acid

- What kinds of information would we like to know?
- How do microarrays work?
- What kinds of errors are inherent in microarrays?
- How can we design measurement protocols to derive useful information using microarrays?
  - mRNA expression is just one example of what we can observe
  - Expression arrays are becoming less important over time

# Transcriptional Regulatory Pathways



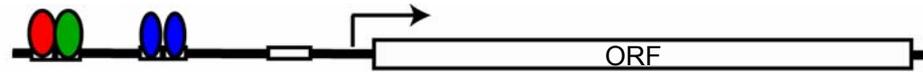
The regulatory pathways that control gene expression programs are uncharted

The mapping of transcriptional regulatory pathways will:

- reveal how cell state, differentiation and response to stimuli are controlled
- suggest new strategies to combat disease

# Transcription of Protein-Coding Genes

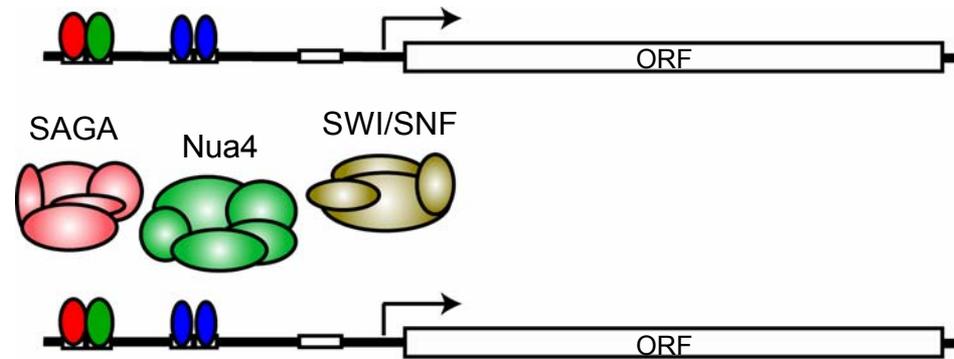
DNA-binding regulators occupy promoter elements



Jacob & Monod, 1961  
Gilbert & Muller-Hill, 1967  
Ptashne, 1967

# Transcription of Protein-Coding Genes

DNA-binding regulators occupy promoter elements



Histone H3 and H4 acetyl transferases and SWI/SNF recruited to promoter

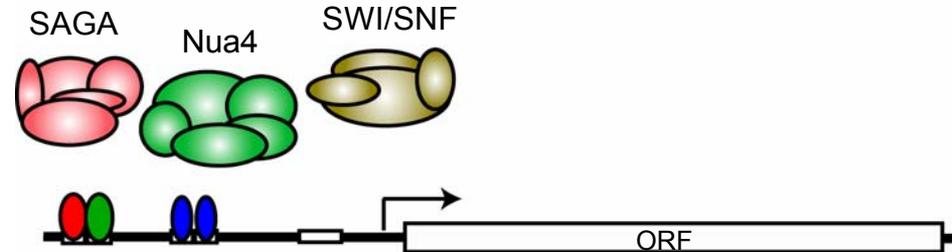
- Peterson & Herskowitz, 1992
- Brownell et al., 1996
- Smith et al., 1998
- Cosma et al., 1999
- Reid et al., 2000
- Bhanmik & Green, 2001
- Larschan & Winston, 2001

# Transcription of Protein-Coding Genes

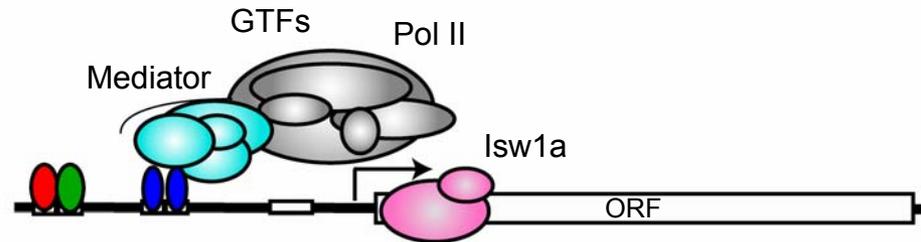
DNA-binding regulators occupy promoter elements



Histone H3 and H4 acetyl transferases and SWI/SNF recruited to promoter



GTFs, Mediator, RNA polymerase II, and additional chromatin regulators recruited



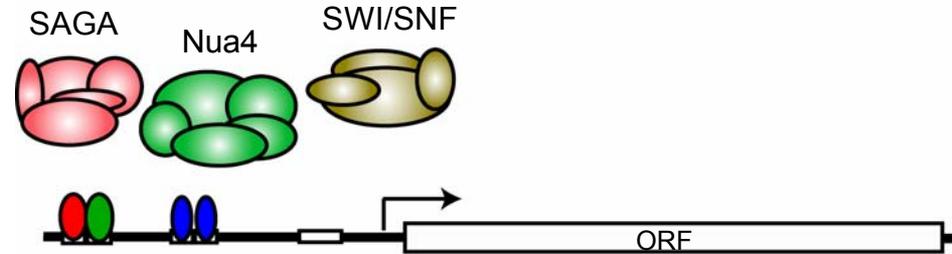
- Reinberg & Roeder, 1987
- Buratowski et al. 1989
- Flores et al. 1992
- Kolenske & Young, 1994
- Kim & Kornberg, 1994
- Li et al., 1999
- Orphanides & Reinberg, 2002
- Pokholok et al., 2002
- Morillon et al., 2003

# Transcription of Protein-Coding Genes

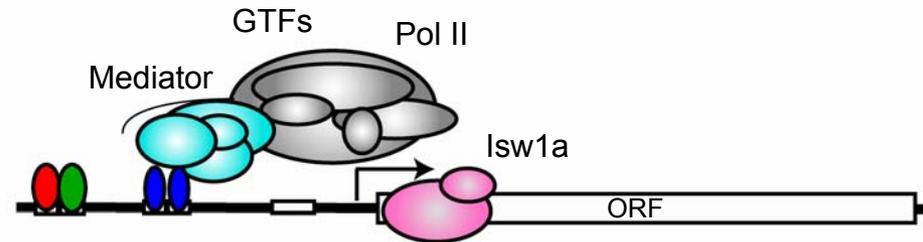
DNA-binding regulators occupy promoter elements



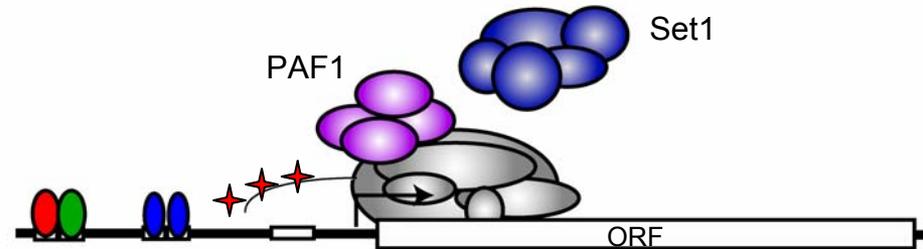
Histone H3 and H4 acetyl transferases and SWI/SNF recruited to promoter



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TFIIH phosphorylates RNA Pol II CTD on Ser5  
Recruitment of Paf1 complex and Set1 histone H3 K4 methyl transferase



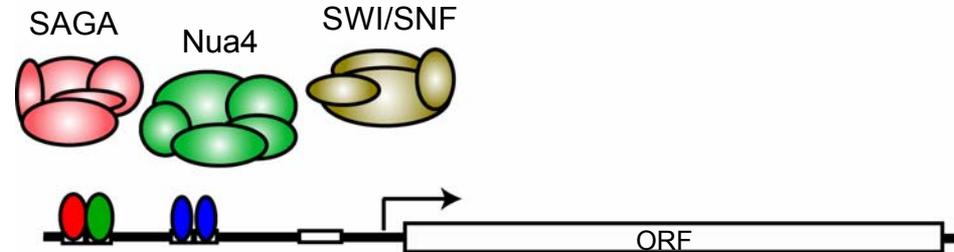
Nislow et al., 1997  
Briggs et al., 2001  
Ng et al., 2003  
Krogan et al., 2003

# Transcription of Protein-Coding Genes

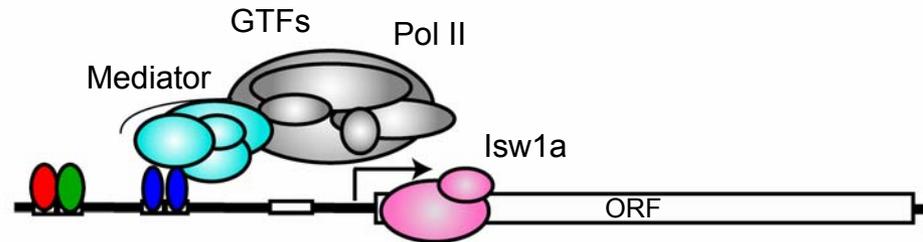
DNA-binding regulators occupy promoter elements



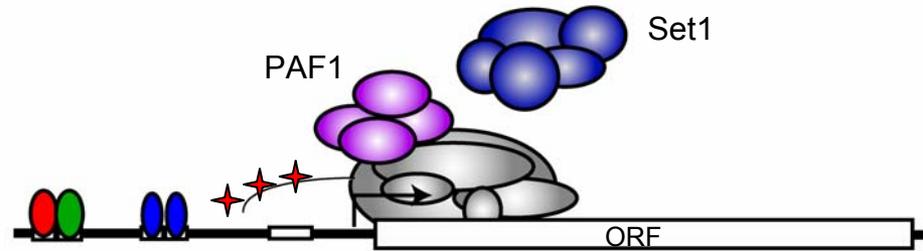
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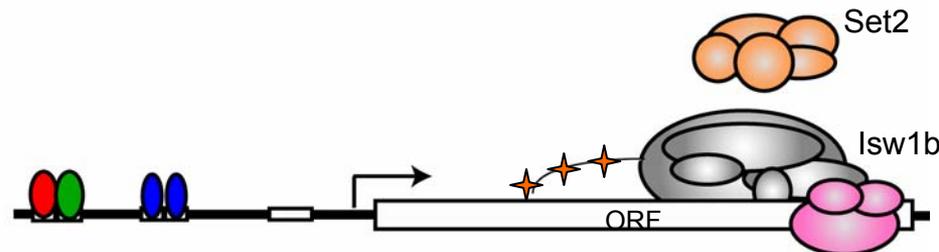
GTFs, Mediator, RNA polymerase II, and additional chromatin regulators recruited



TFIIH phosphorylates RNA Pol II CTD on Ser5  
Recruitment of Paf1 complex and Set1 histone H3 K4 methyl transferase



CTK1 phosphorylates RNA Pol II CTD on Ser2  
Recruitment of Set2 H3 K36 methyl transferase and Isw1b



Strahl et al., 2002; Krogan et al., 2003; Li et al., 2003

# Microarrays can access in-vivo nucleic acid based information

- What kinds of information would we like to know?
- How do microarrays work?
- What kinds of errors are inherent in microarrays?
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# DNA Hybridization

Complimentary strands of  
nucleic acid will bind each  
other by base pairing

Diagram removed for copyright reasons.

# DNA Microarray

By immobilizing different sequences in unique locations on a solid substrate we can measure relative levels of many target DNA or RNA molecules in a complex mixture in parallel

Diagram removed for copyright reasons.

# DNA Microarray Content

## **Oligonucleotides**

- Synthesized in situ or printed
- Short Probes (25-70 Bases)
- Multiple probes/gene
- Homemade or Commercial

## **cDNA**

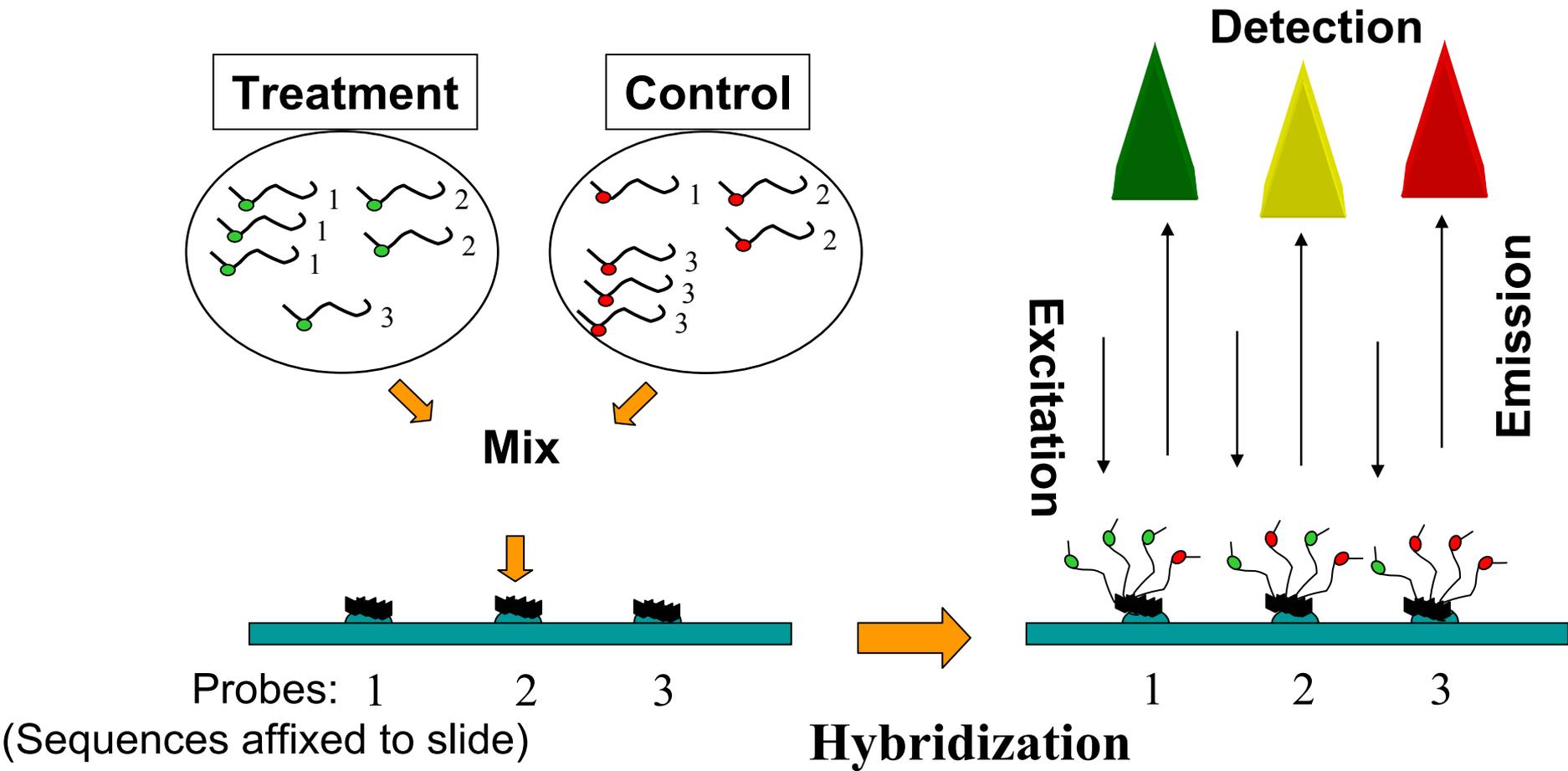
- Prefabricated and printed
- Long Probes (300-1000)
- One probe/gene
- Homemade or Commercial

# Synthesis of Labeled Target From mRNA

- 1) Reverse transcription can be used to make double-stranded DNA from RNA, and DNA molecule can be labeled
- 2) Double stranded DNA molecule can be transcribed by RNA polymerase to produce cRNA

Diagram removed for copyright reasons.

# Measuring Relative Target Abundance



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Diagrams and descriptions of Affymetrix, Agilent, and MAGE-ML technologies.

# Some sources of variation in microarray data

- Sample variation (not noise)
  - Population differences
- Sample preparation (noise)
  - Amplification based artifacts
  - Dye-substrate preferences (dye swap test)
  - Protocol specific issues
- Probe design (noise)
  - Cross-hybridization / non-uniqueness
  - Probe secondary structure
  - T<sub>m</sub> issues
- Array based (noise - can be reduced by technical replicates)
  - Hybridization
  - Scanner noise

# Is noise additive or multiplicative?

- Examples of additive noise
  - Scanner noise
- Examples of multiplicative noise
  - Probe affinity
  - Amplification non-linearity

$$o_i = n_{1i} d_i + n_{2i}$$

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# Microarray based measurement protocols

- Genotype
  - Single nucleotide polymorphisms (SNPs)
  - Comparative genomic hybridization (CGH)
- Expression (mRNA)
  - mRNA transcript levels
  - alternative splice variants
  - ncRNAs (miRNAs)
- Protein / RNA interactions
- Genome interaction
- ChIP – Chip (location analysis)
  - TF Binding
  - Chromatin structure
  - Dam Methylase assay

# CGH and SNP analysis

- Represent probes that correspond to interesting genetic loci
- Fragment and amplify genome; apply to array
- CGH – probes measure relative copy number of loci of two genomes
  - Can detect aneuploidy, certain genetic diseases
- SNP – probes measure presence or absence of SNP at a particular locus
  - Discovering SNPs and linking them to disease is key first step

Image removed for copyright reasons.  
See Figure 1 in source cited below.

Pollack,J., Perou,C., Alizadeh,A., Eisen,M., Pergamenschikov,A., Williams,C., Jeffrey,S., Botstein,D. and Brown,P. (1999) Genome-wide analysis of DNA copy-number changes using cDNA microarrays. *Nat. Genet.*, **23**, 41–46.

# SNP Array (Affymetrix)

The 40 25-mer probes per locus

= 5 groups of probes with SNP at different position

X 8 probes / position (both strands)

(1) a perfect match for one of the allelic states (allele A);

(2) a single base mismatch for allele A;

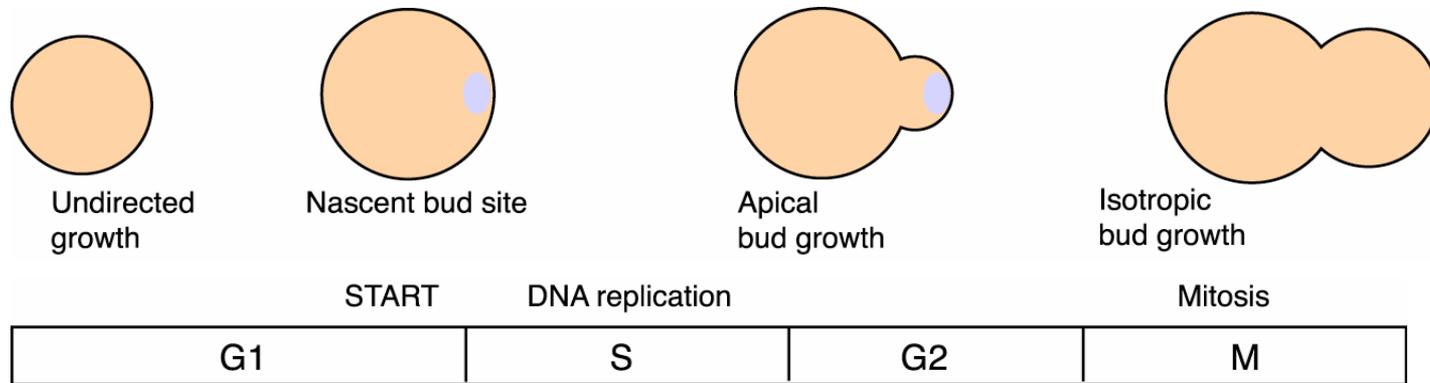
(3) a perfect match for the other allelic state (allele B);

(4) a single base mismatch for allele B

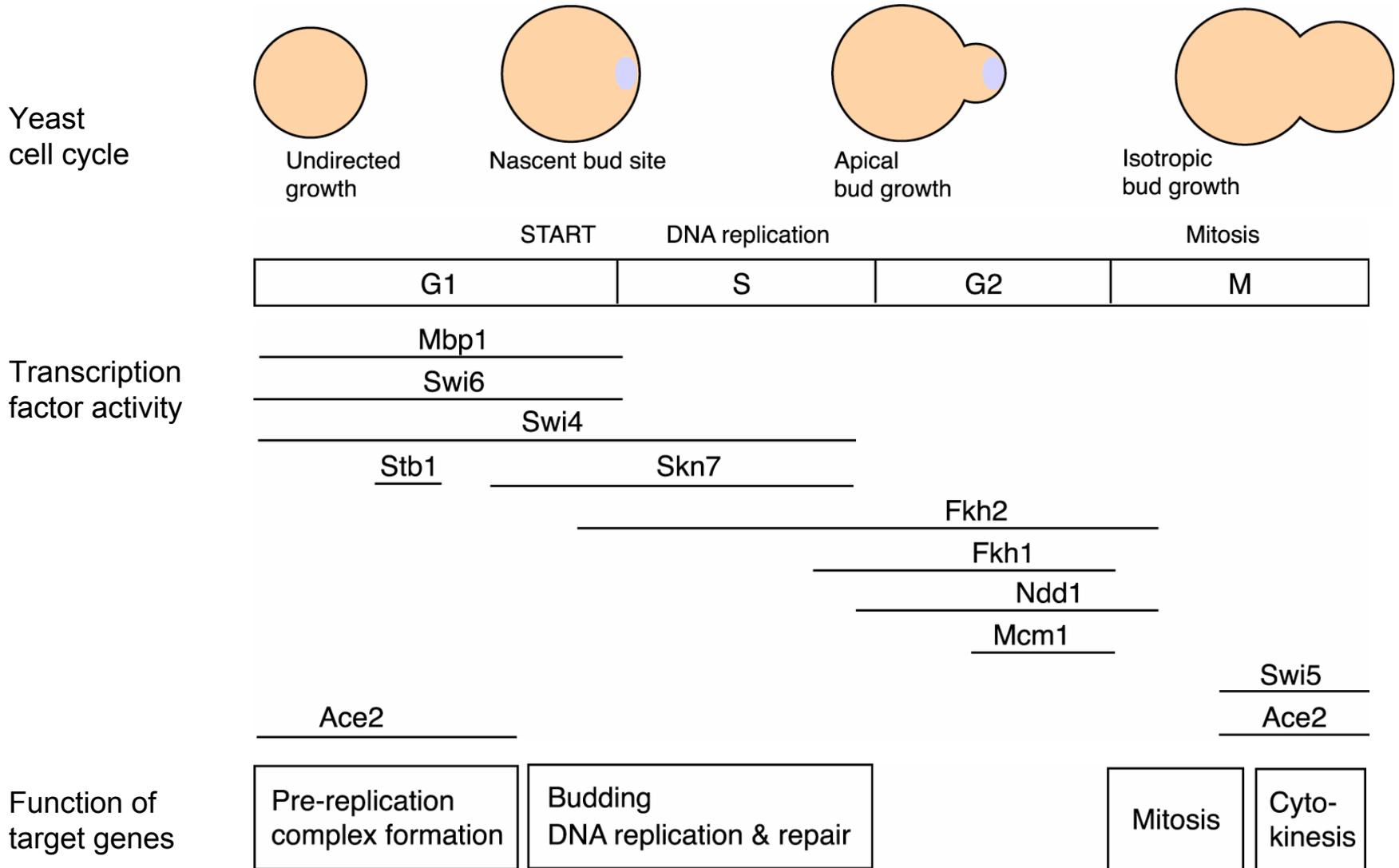
# Expression

- Amplify RNA and label with Cy3 / Cy5
  - Can be used with small number of cells (10,000 or so)
  - Select control sample if two color array
- Hybridize to array

# Transcriptional Regulation of Yeast Cell Cycle



# Transcriptional Regulation of Yeast Cell Cycle



# Master Regulators of Human Transcription

*Misregulation results in developmental problems and/or adult disease*

## Brain and Spinal Cord

SOX1-18, OCT6, MeCP2  
CBP, NGN, NEUROD

Cerebrum  
Cerebellum  
Ganglia & nerves

## Circulatory System

Myocardin, GATA4, TBX5,  
NKX2.5, MEF2, HAND

Heart  
Vascular system

## Digestive System

HNF1, HNF4, HNF6, CBP,  
PGC1, FOXA, PDX1, GATA,  
MAFA, NKX2.2

Esophagus  
Stomach  
Intestines  
Liver  
Pancreas

## Urinary System

HNF1B, HNF4, CDX, FTF  
C/EBP, FOXA, GATA

Kidney  
Urinary tract

## Respiratory System

HNF-3, NKX2.1 and GATA6

Airways  
Lungs

## Reproductive Organs

ESR1, SERM, C/EBP $\beta$

Ovary  
Uterus  
Breast  
Testis

## Skeletal and Muscular

MYOD, MEF2, MRF4, MYF5

Bone  
Muscle  
Cartilage

## Hematopoietic System

TAL1, LMO1, LMO2, E2A,  
XBP1, AFT6, PAX5, BCL6

Bone marrow  
Blood  
Embryonic Liver

## Immune System

AML1, MLL1, HP1, HOXA7,  
HOXA9, HOXC8, C/EBPA,  
NF $\kappa$ B family

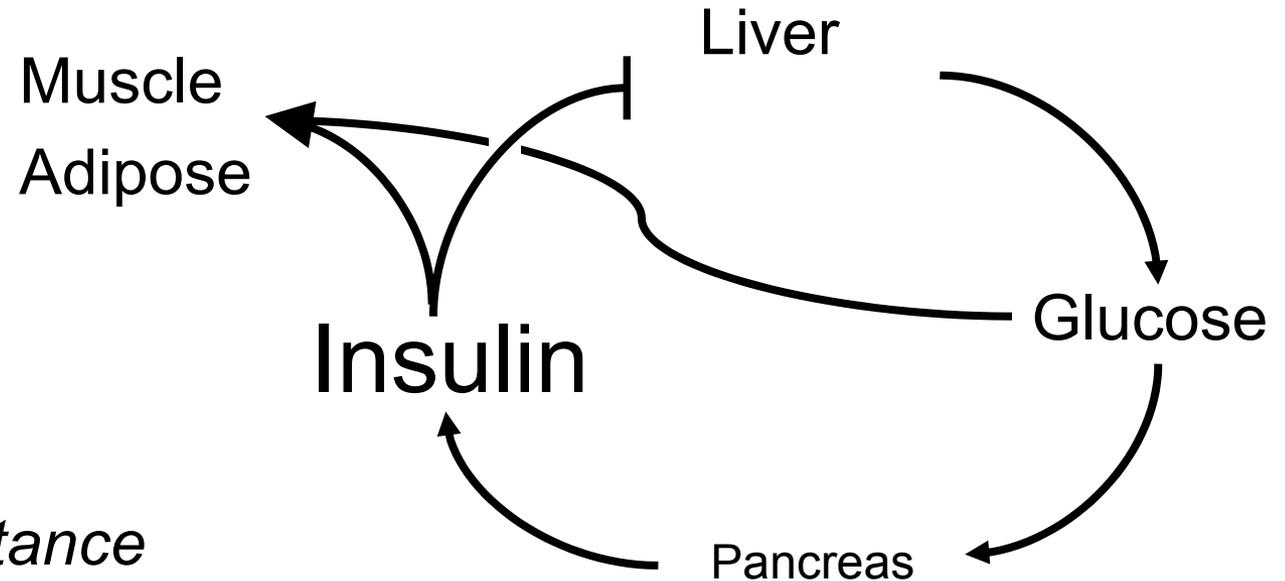
Thymus  
Spleen  
Lymph nodes

## Sensory Organs

SOX1-18, OCT6, PAX3,  
PAX6, NGN, SKIN1

Eye  
Ear  
Olfactory  
Skin  
Tongue

# Glucose Homeostasis and Type 2 Diabetes



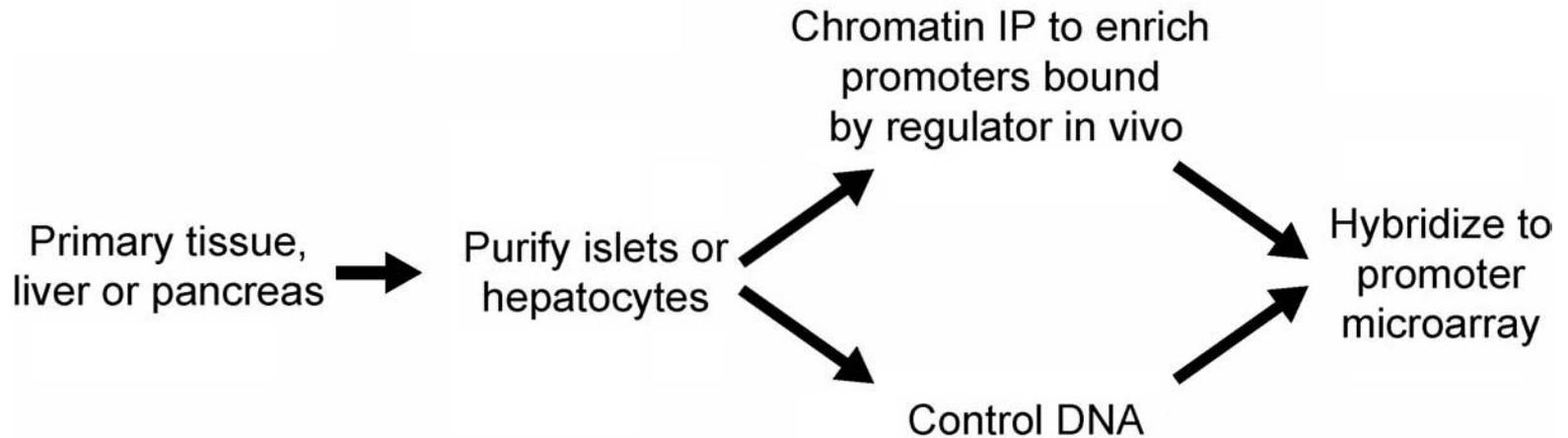
- *Insulin Resistance*
- *Mitochondrial inefficiency*
- *Impaired  $\beta$  cell insulin secretion*

# MODY Diabetes

<u>MODY type</u>	<u>Causative Gene</u>	<u>Protein Class</u>	<u>% Cases</u>
MODY 1	<i>HNF-4<math>\alpha</math></i>	Orphan nuclear receptor protein	1
MODY 2	Glucokinase	Key enzyme in glucose sensing	20
MODY 3	<i>HNF-1<math>\alpha</math></i>	POU-homeodomain protein	60
MODY 4	<i>IPF1/PDX1</i>	Homeodomain protein	1
MODY 5	<i>HNF-1<math>\beta</math></i>	POU-homeodomain protein	1
MODY 6	<i>NeuroD1</i>	Basic helix-loop-helix protein	1

Fajans et al. *N Engl J Med* (2001) 345 : 971

# Genome-Scale Location Analysis in Human Tissues

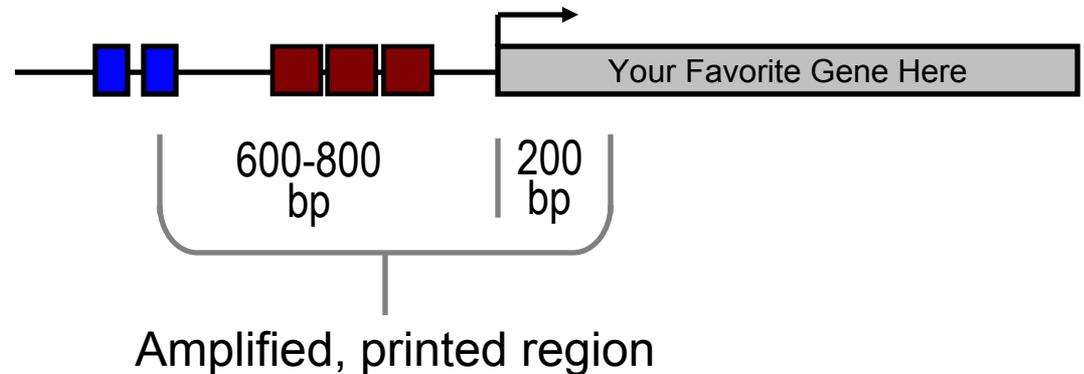


# Hu13K Promoter Chip

13,000 proximal promoter microarray

Targets 600-800 bp upstream and 200 bp downstream of mRNA start site (NCBI).

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# Hu13K Promoter Chip

1. 80% of binding sequences for known factors are promoter proximal.

Diagram and graph removed for copyright reasons.

2. Long range interactions between distal- and proximal-binding transcription factors can be captured by formaldehyde crosslinking.

- Carter et al. Nature Genetics 32:623 (2002)

- Tolhuis et al. Molecular Cell 10:1453 (2002)

# Selected HNF1 $\alpha$ Targets in Human Hepatocytes

## **Apolipoproteins**

APOA2 Apolipoprotein A-II  
APOC3 Apolipoprotein C-III  
COPB2 [Coatomer protein complex, subunit beta 2](#)

## **Complement Proteins**

C1S Complement component 1, s subcomponent  
C4BPA Complement component 4 binding protein, a  
F10 Coagulation factor X  
DAF [Complement decay accelerating factor](#)

## **Hormones, Cytokines, Growth Factors**

ALB Albumin  
IGFBP1 Insulin-like growth factor binding protein 1  
MST1 Macrophage stimulating 1 (hepatocyte growth factor-like)  
SCYA16 [Small cytokine subfamily A, member 16 \(Monotactin-1\)](#)

## **Metabolism**

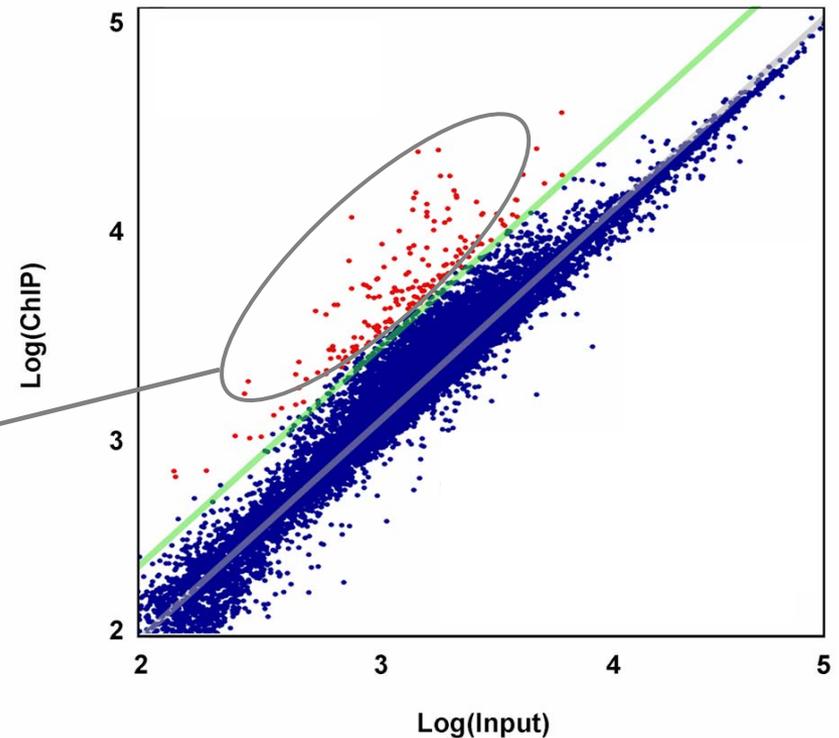
PCK1 Phosphoenolpyruvate carboxykinase 1 (soluble)  
G6PT1 Glucose-6-phosphatase, transport protein 1  
ADH1A [Alcohol dehydrogenase 1A, alpha polypeptide](#)  
XDH [Xanthene dehydrogenase](#)

## **Receptors, Surface Transmembrane**

RBP5 Retinol binding protein 5, cellular  
GJB1 Gap junction protein, beta 1 (connexin 32)  
RARB [Retinoic acid receptor, beta](#)  
SSTR1 [Somatostatin receptor 1](#)

## **Transcription Factors**

HNF4A7 Hnf4alpha  
ELF3 [E74-like factor 3 \(ets domain tf, epithelial-specific\)](#)  
NR0B2 [Small heterodimeric protein \(Nr0B2\)](#)  
NR5A2 [Alpha-fetoprotein transcription factor](#)



222 Targets

