

# State of the Science of Genomic Associations: Current and Future Directions

U.S. Department of Health and Human Services  
National Institutes of Health  
National Human Genome Research Institute

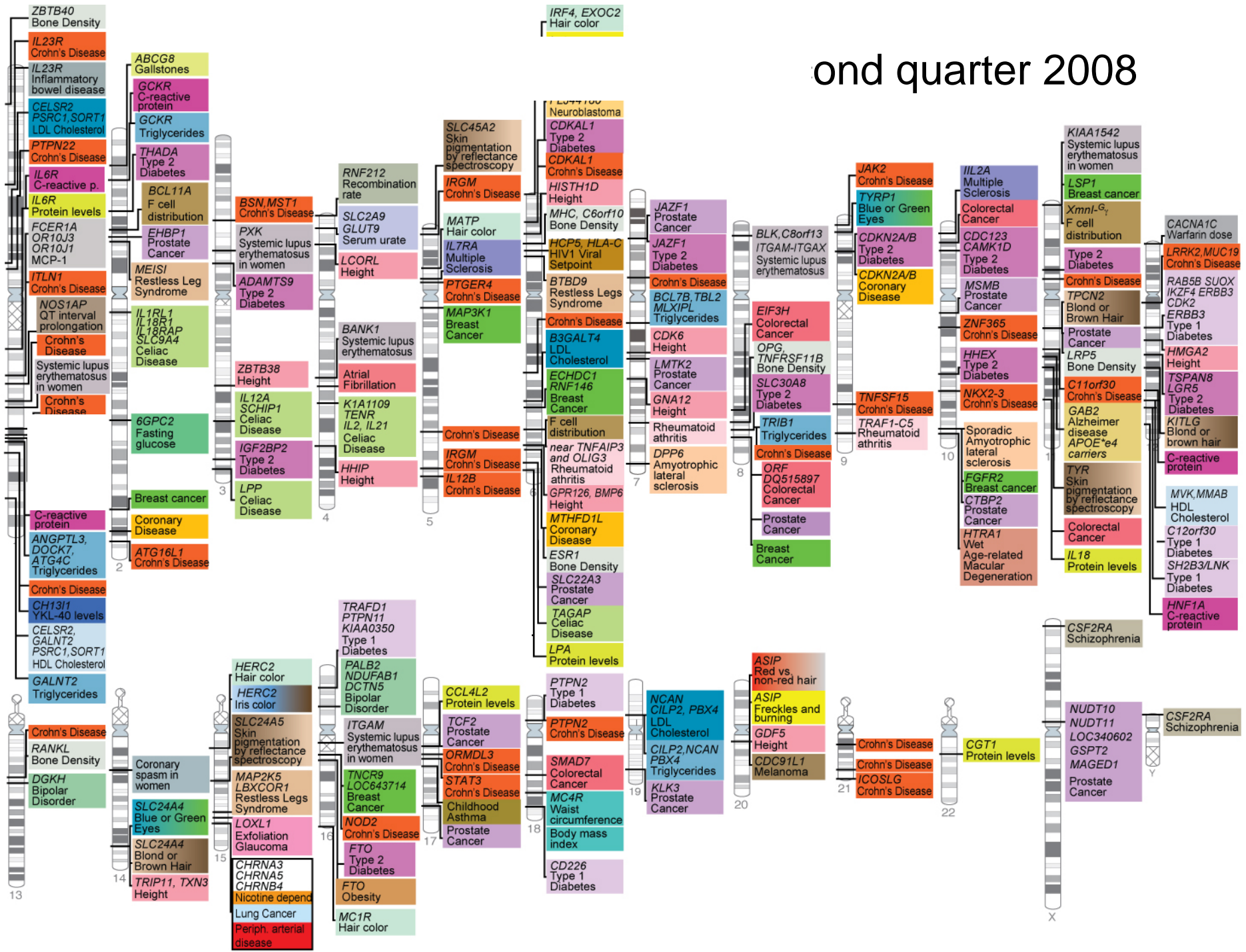
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Director, Office of Population Genomics  
Senior Advisor to the Director, NHGRI,  
for Population Genomics

July 8, 2008

# State of the Science of Genomic Associations

- What are the recent advances in genomics research? How have these advances facilitated the emergence of personal genome services?
- For which diseases are strong genetic associations and/or markers established?
- What criteria should be considered in determining whether the association between a particular genetic marker and phenotype is strong enough for that marker to be included in genetic testing?
- What are the limitations of genetic markers in risk assessment for disease?

ond quarter 2008



# 2007: The Year of GWA Studies

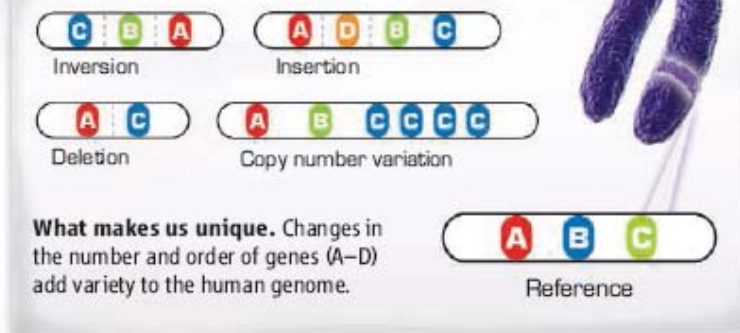
**BREAKTHROUGH OF THE YEAR**

## Human Genetic Variation

Equipped with faster, cheaper technologies for sequencing DNA and assessing variation in genomes on scales ranging from one to millions of bases, researchers are finding out how truly different we are from one another

THE UNVEILING OF THE HUMAN GENOME ALMOST 7 YEARS AGO cast the first faint light on our complete genetic makeup. Since then, each new genome sequenced and each new individual studied has illuminated our genomic landscape in ever more detail. In 2007, researchers came to appreciate the extent to which our genomes differ from person to person and the implications of this variation for deciphering the genetics of complex diseases and personal traits.

Less than a year ago, the big news was triangulating variation between us and our primate cousins to get a better handle on genetic changes along the evolutionary tree that led to humans. Now, we have moved from asking what in our DNA makes us human to striving to know what in my DNA makes me me.



**What makes us unique.** Changes in the number and order of genes (A–D) add variety to the human genome.

Pennisi E, *Science* 2007; 318:1842-43.



[www.hapmap.org](http://www.hapmap.org)

Vol 437|27 October 2005|doi:10.1038/nature04226

nature

Vol 449|18 October 2007|doi:10.1038/nature06258

nature

*Nature* 2007; 449:851-61.

ARTICLES

# A second generation human haplotype map of over 3.1 million SNPs

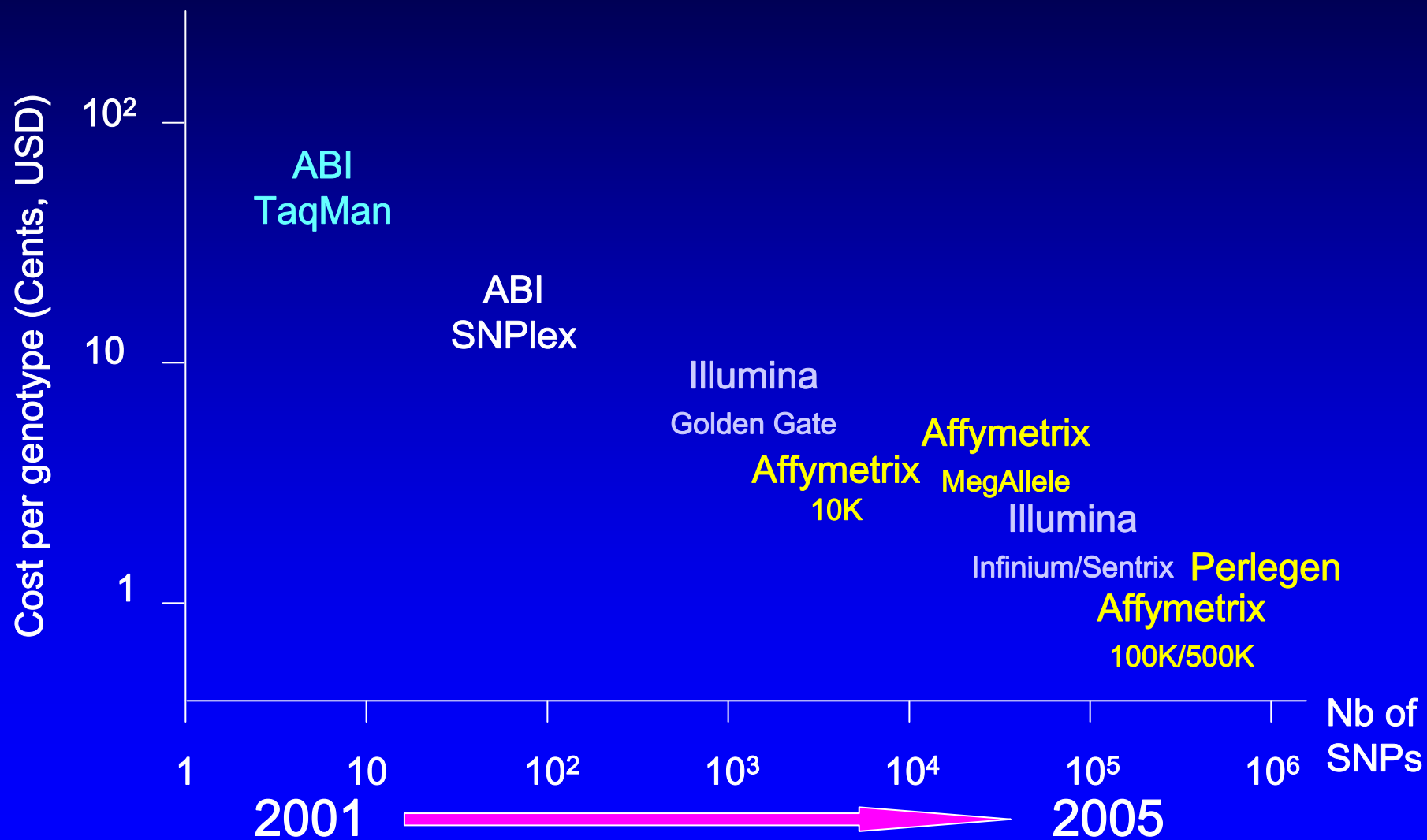
The International HapMap Consortium\*

We describe the Phase II HapMap, which characterizes over 3.1 million human single nucleotide polymorphisms (SNPs) genotyped in 270 individuals from four geographically diverse populations and includes 25–35% of common SNP variation in the populations surveyed. The map is estimated to capture untyped common variation with an average maximum  $r^2$  of between 0.9 and 0.96 depending on population. We demonstrate that the current generation of commercial genome-wide genotyping products captures common Phase II SNPs with an average maximum  $r^2$  of up to 0.8 in African and up to 0.95 in non-African populations, and that potential gains in power in association studies can be obtained through imputation. These data also reveal novel aspects of the structure of linkage disequilibrium. We show that 10–30% of pairs of individuals within a population share at least one region of extended genetic identity arising from recent ancestry and that up to 1% of all common variants are untaggable, primarily because they lie within recombination hotspots. We show that recombination

# A HapMap for More Efficient Association Studies: Goals

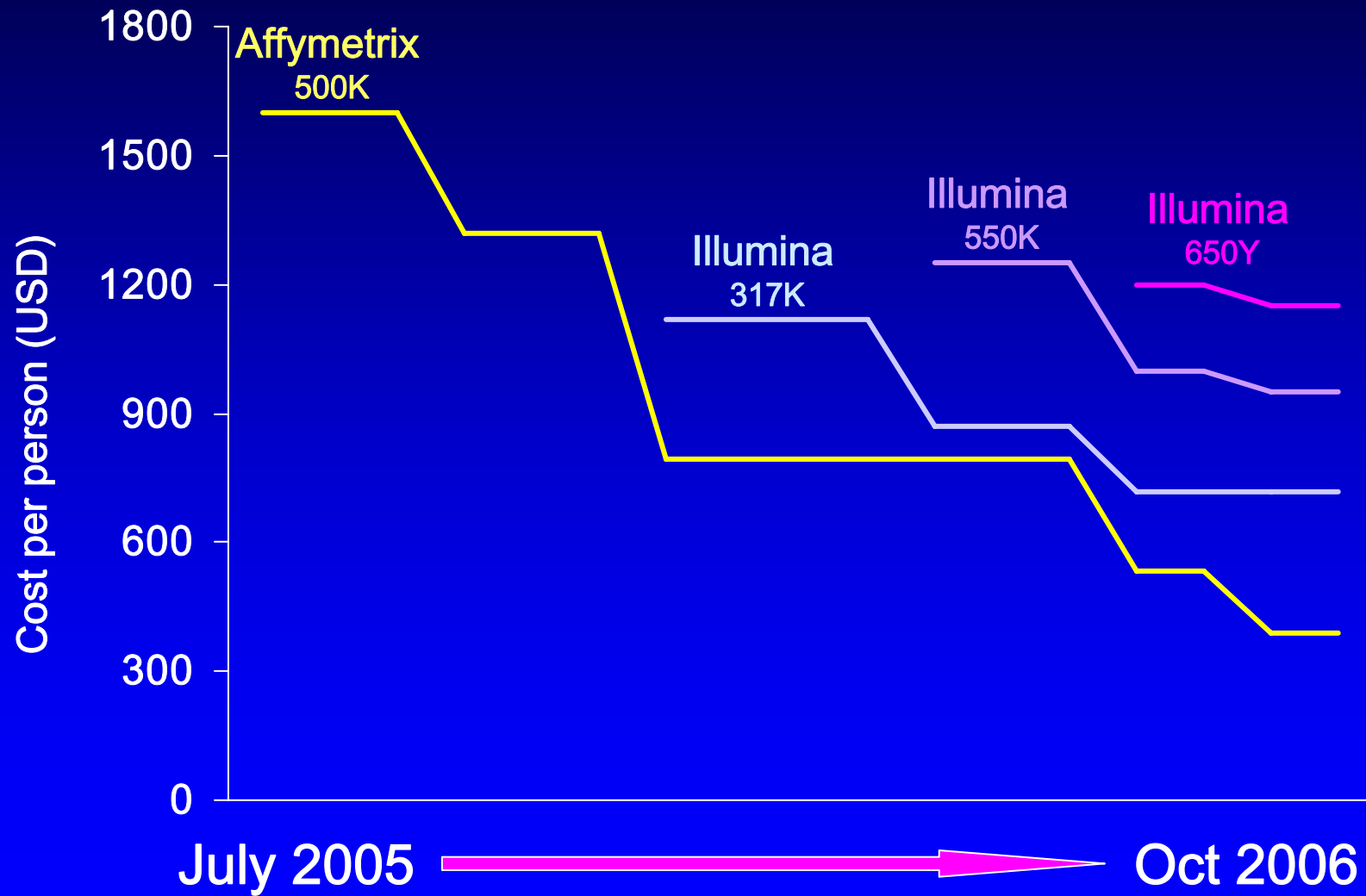
- Use just the density of SNPs needed to find associations between SNPs and diseases
- Do not miss chromosomal regions with disease association
- Produce a tool to assist in finding genes affecting health and disease
- Use more SNPs for complete genome coverage of populations of recent African ancestry populations due to shorter LD

# Progress in Genotyping Technology



Courtesy S. Chanock, NCI

# Continued Progress in Genotyping Technology



Courtesy S. Gabriel, Broad/MIT



# Diseases and Traits with Published GWA Studies (n = 58, 7/7/08)

- Macular Degeneration
- Exfoliation Glaucoma
- Lung Cancer
- Prostate Cancer
- Breast Cancer
- Colorectal Cancer
- Neuroblastoma
- Melanoma
- Inflamm. Bowel Disease
- Celiac Disease
- Gallstones
- Irritable Bowel Syndrome
- QT Prolongation
- Coronary Disease
- Stroke
- Hypertension
- Atrial Fibrillation/Flutter
- Peripheral Artery Disease
- Coronary Spasm
- Lipids and Lipoproteins
- Warfarin Dosing
- Ximelegatran Adv. Resp.
- Parkinson Disease
- Amyotrophic Lat. Sclerosis
- Multiple Sclerosis
- Prog. Supranuclear Palsy
- MS Interferon- $\beta$  Response
- Alzheimer's Disease
- Cognitive Ability
- Memory
- Restless Legs Syndrome
- Nicotine Dependence
- Methamphetamine Depend.
- Neuroticism
- Schizophrenia
- Bipolar Disorder
- Family Chaos
- Rheumatoid Arthritis
- Systemic Lupus Erythematosus
- Psoriasis
- HIV Viral Setpoint
- Childhood Asthma
- Type 1 Diabetes
- Type 2 Diabetes
- Diabetic Nephropathy
- End-St. Renal Disease
- Obesity, BMI, Waist, IR
- Height
- Osteoporosis
- Osteoarthritis
- F-Cell Distribution
- Fetal Hgb Levels
- C-Reactive Protein
- 18 groups of Framingham Traits
- Pigmentation
- Uric Acid Levels
- Recombination Rate
- Protein Levels

STATISTICS AND MEDICINE

## Drinking from the Fire Hose — Statistical Issues in Genomewide Association Studies

David J. Hunter, M.B., B.S., and Peter Kraft, Ph.D.

Related article, page 443

The past 3 months have seen the publication of a series of articles highlighting the need for guessing which genes are likely to harbor variants associated with disease. The main problem with this strategy is that, because of the limited number of samples available, most studies have low power to detect associations with modest relative risks (e.g., 1.3 for heterozygotes and 1.6 for homozygotes), and many true associations are not likely to exceed P values as extreme as  $10^{-7}$  in an initial study. On the other hand, a “statistically significant” finding

*“There have been few, if any, similar bursts of discovery in the history of medical research...”*

and in this issue of the *Journal*, coronary artery disease (reported by Samani et al., pages 443–453). These genomewide association studies have been able to examine interpatient differences in inherited genetic variability at an unprecedented level of resolution, thanks to the development of microarrays, or chips, capable of as-

sociated with disease. Some of these associations have been found in regions not even known to harbor genes, such as the 8q24 region, in which multiple variants have been found to be associated with prostate cancer.<sup>2</sup> Such findings promise to open up new avenues of research, through both the discovery of new genes rele-

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Hunter DJ and Kraft P, *N Engl J Med* 2007; 357:436-439.

# NHGRI Catalog of GWA Studies:

<http://www.genome.gov/gwastudies/>



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### A Catalog of Published Genome-Wide Association Studies

**Search By:**

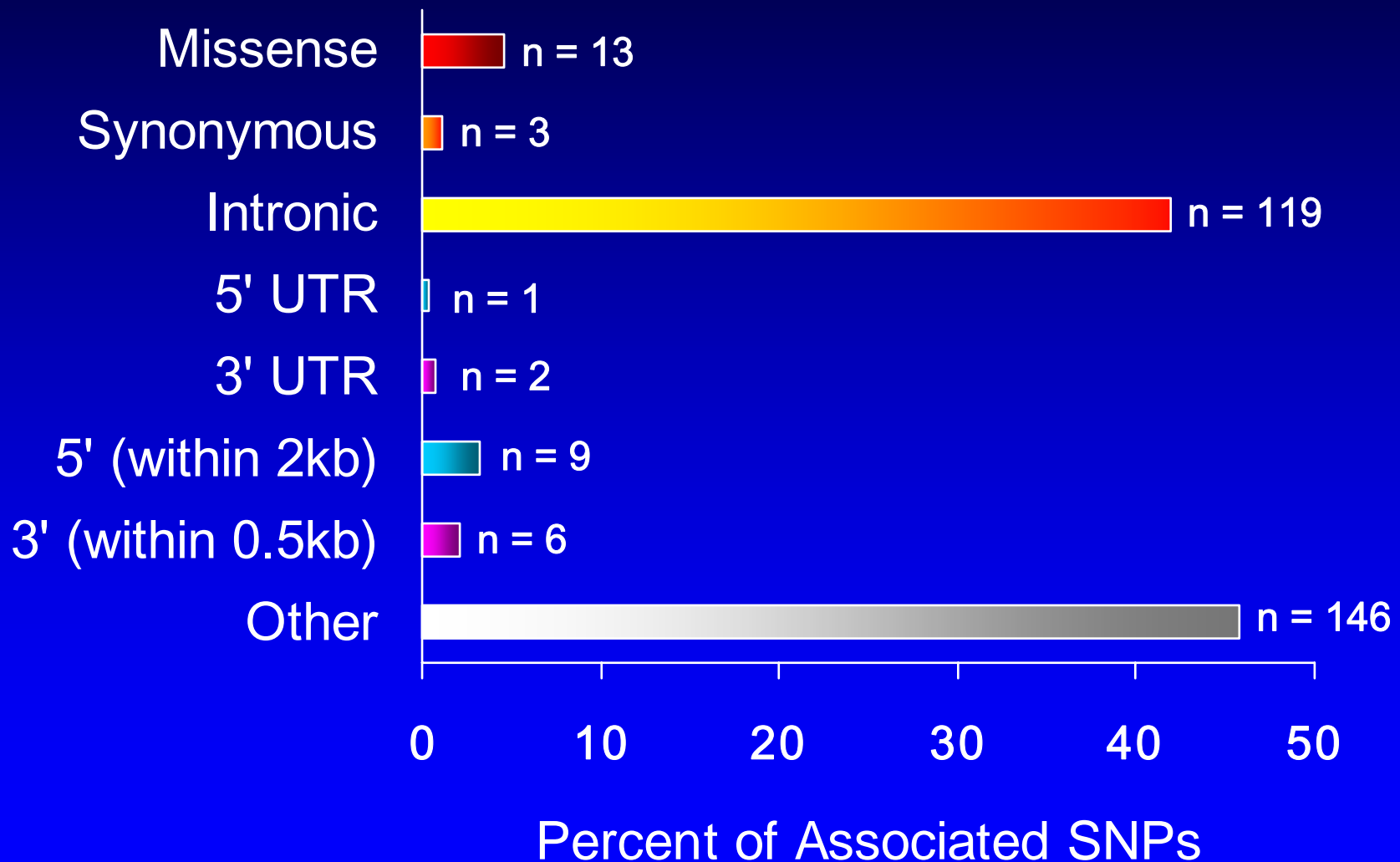
**First Author:**

**Publication:**

**Disease/Trait:**

First Author/Date/ Journal/Study	Disease/Trait	Initial Sample Size	Replication Sample Size	Region	Gene	Strongest SNP-Risk Allele	Risk Allele Frequency in Controls	P-value	OR per copy or B-coefficient for heterozygote and [95% CI]	Platform [SNPs passed]
Amos April 03, 2008 <i>Nat Genet</i> <a href="#">Genome-wide association scan of tag SNPs identifies a susceptibility locus for lung cancer at15q251</a>	Lung cancer	1,154 cases, 1,137 controls	2,724 cases, 3,694 controls	15q25.1	<i>CHRNA3</i>	rs8034191-G	NR	3 x 10 <sup>-18</sup>	1.30 [1.15-1.47]	Illumina [317,498]
				1q23.2	<i>CRP</i>	rs2808630-G	NR	7 x 10 <sup>-6</sup>	1.22 [1.10-1.35]	
				3q28	<i>IL1RAP</i>	rs7626795-G	NR	8 x 10 <sup>-6</sup>	1.16 [1.05-1.28]	
Hung April 03, 2008 <i>Nature</i> <a href="#">A susceptibility locus for lung cancer maps to nicotinic acetylcholine receptor subunit genes on 15q25</a>	Lung cancer	1,926 cases, 2,522 controls	2,513 cases, 4,752 controls	15q25.1	<i>CHRNA3, CHRNA5, CHRN4</i>	rs8034191-C	0.34	5 x 10 <sup>-20</sup>	1.21 [1.11-1.31]	Illumina [310,023]
Spinola January 16, 2007 <i>Cancer Lett</i> <a href="#">Genome-wide single nucleotide polymorphism analysis of lung cancer risk detects the KLF6 gene</a>	Lung cancer	338 Italian lung adenocarcinoma cases, 335 Italian controls	265 Norwegian non-small lung carcinoma cases 356 Norwegian controls	NA	NA	NA	NA	NS	NA	Affymetrix [116,204] (pooled)

# Functional Classification of 284 SNPs Associated with Complex Traits



# Lessons Learned from Initial GWA Studies

## Signals in Previously Unsuspected Genes

Macular Degeneration

*CFH*

Coronary Disease

*CDKN2A/2B*

Childhood Asthma

*ORMDL3*

Type II Diabetes

*CDKAL1*

QT interval prolongation

*NOS1AP*

# Lessons Learned from Initial GWA Studies

## Signals in Previously Unsuspected Genes

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Coronary Disease	<i>CDKN2A/2B</i>
Childhood Asthma	<i>ORMDL3</i>
Type II Diabetes	<i>CDKAL1</i>
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## Signals in Gene “Deserts”

Prostate Cancer	8q24
Crohn’s Disease	5p13.1, 1q31.2, 10p21

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## Signals in Common

Diabetes, CHD, Melanoma, Frailty	<i>CDKN2A/2B</i>
Prostate, Breast, Colorectal Cancer	8q24 region
Crohn’s Disease, Psoriasis	<i>IL23R</i>
Crohn’s Disease, T1DM	<i>PTPN2</i>
Rheumatoid Arthritis, T1DM	<i>PTPN22</i>

# What are the recent advances in genomics research? How have these advances facilitated the emergence of personal genome services?

- Low-cost high-throughput genotyping within reach of large-scale population studies since 2006
- Over 150 such studies completed with over 180 well-replicated loci in nearly 60 diseases/traits
- Genotyping costs now within reach of (well-to-do) consumers

On the horizon...

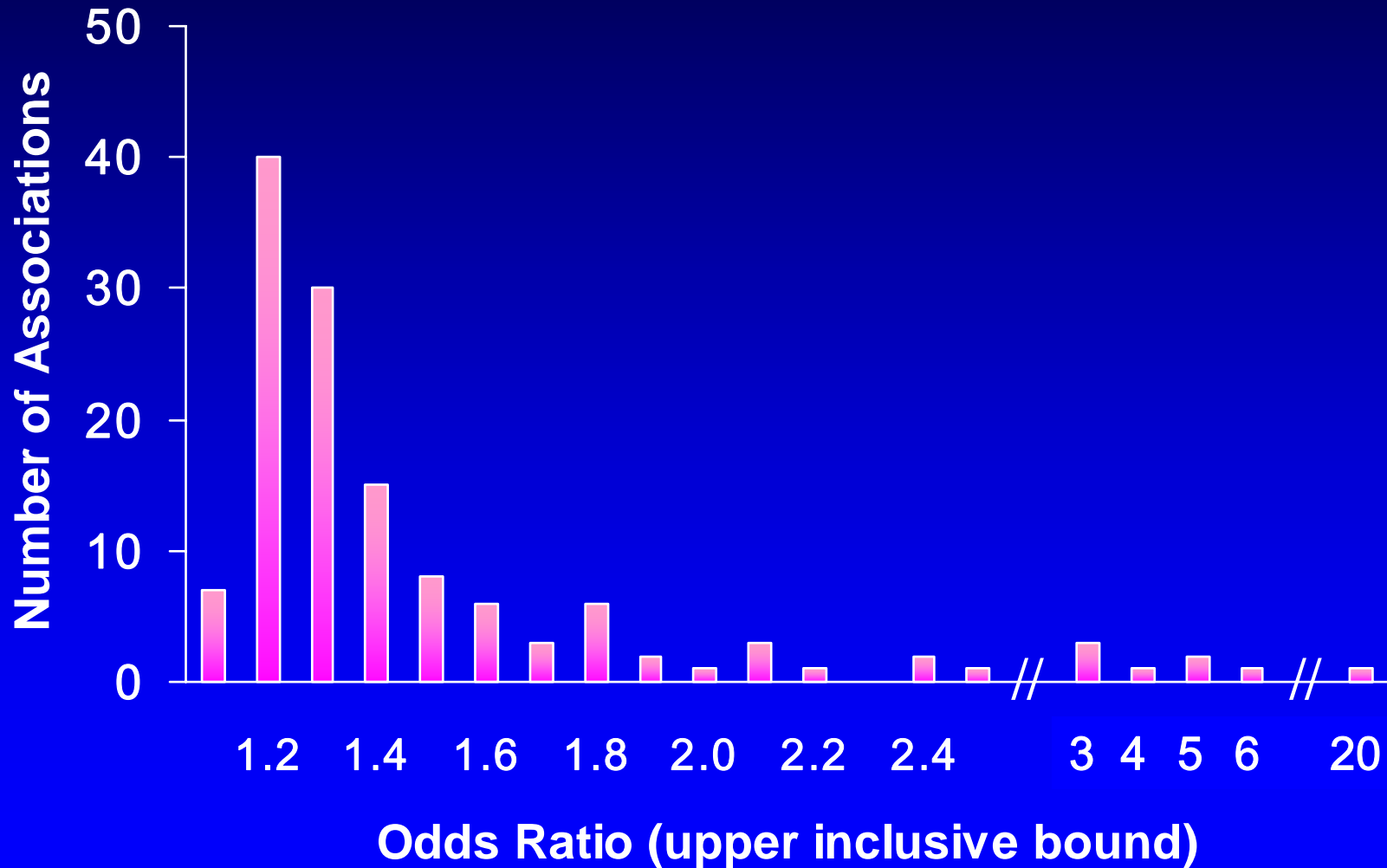
- Copy number variants
- Next generation sequencing; 1,000 Genomes
- DNA methylation and gene expression



# For which diseases are strong genetic associations and/or markers established?

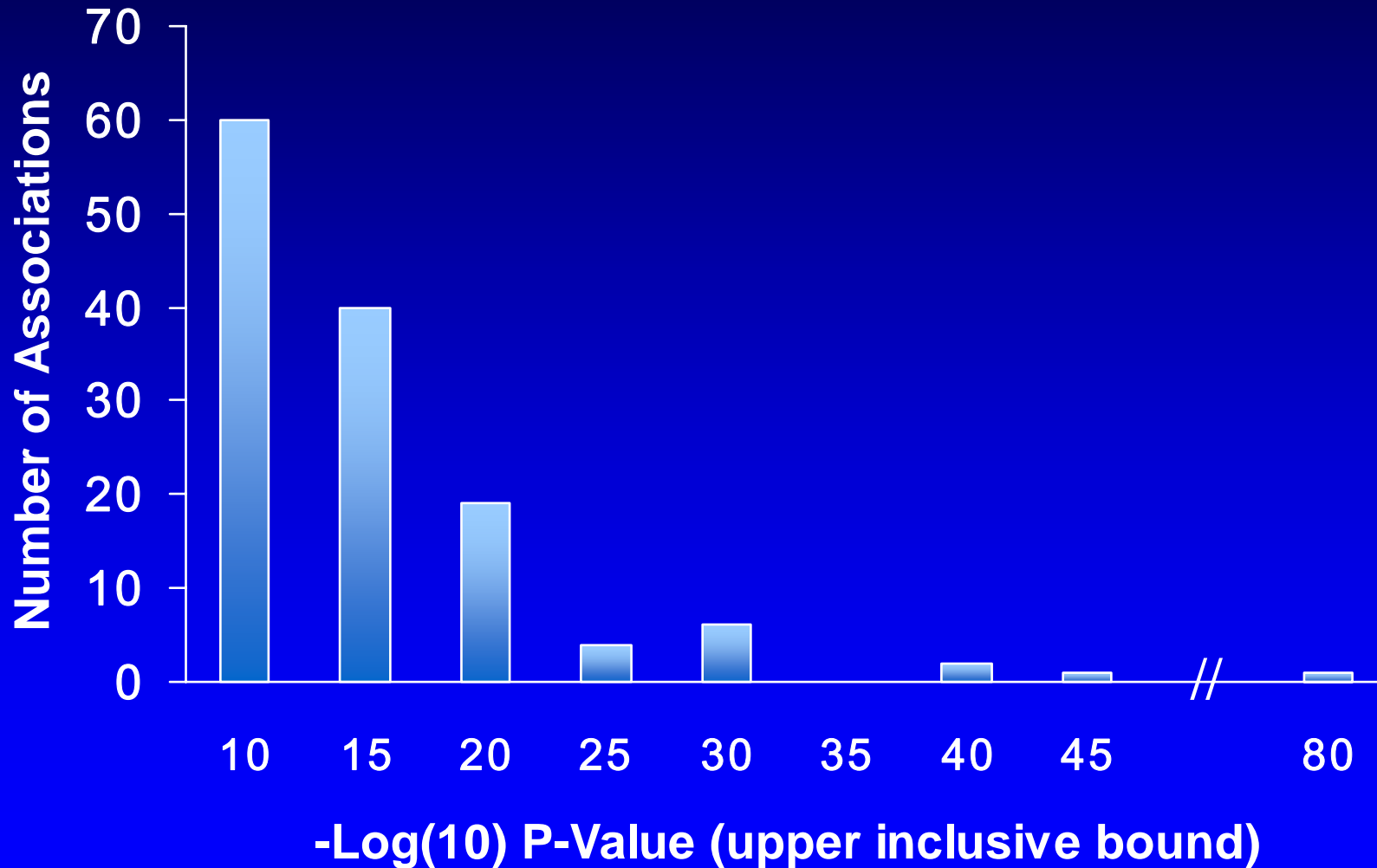
- Define “strong”!
- Large odds ratio?
- Very small p-value?
- Very frequently occurring risk allele?
- Large proportion of disease attributable to risk allele?
- Explaining large proportion of genetic variance?

# Odds Ratios of Discrete Associations



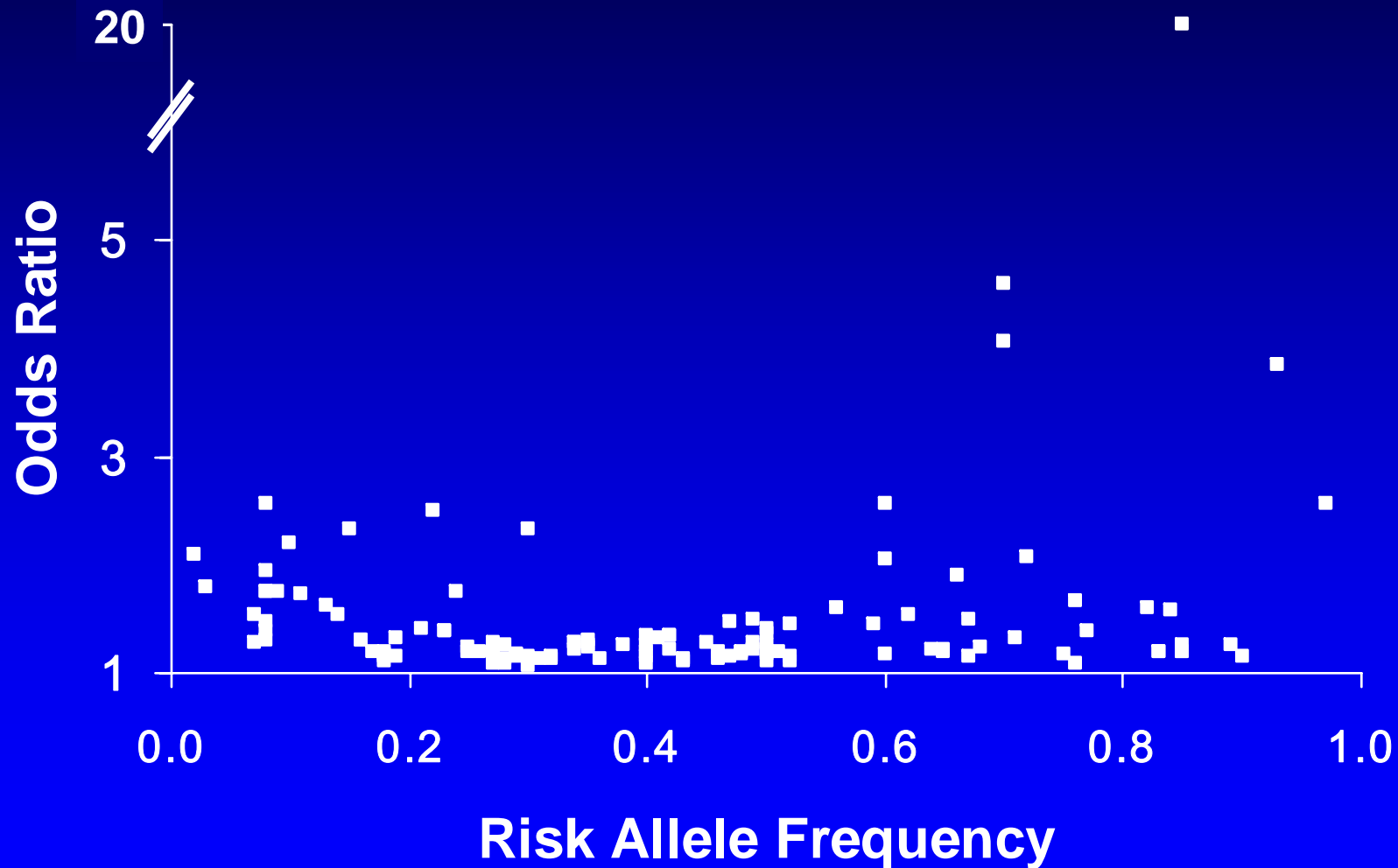
<http://www.genome.gov/gwastudies/>

# - Log<sub>10</sub> P-Values of Discrete Associations

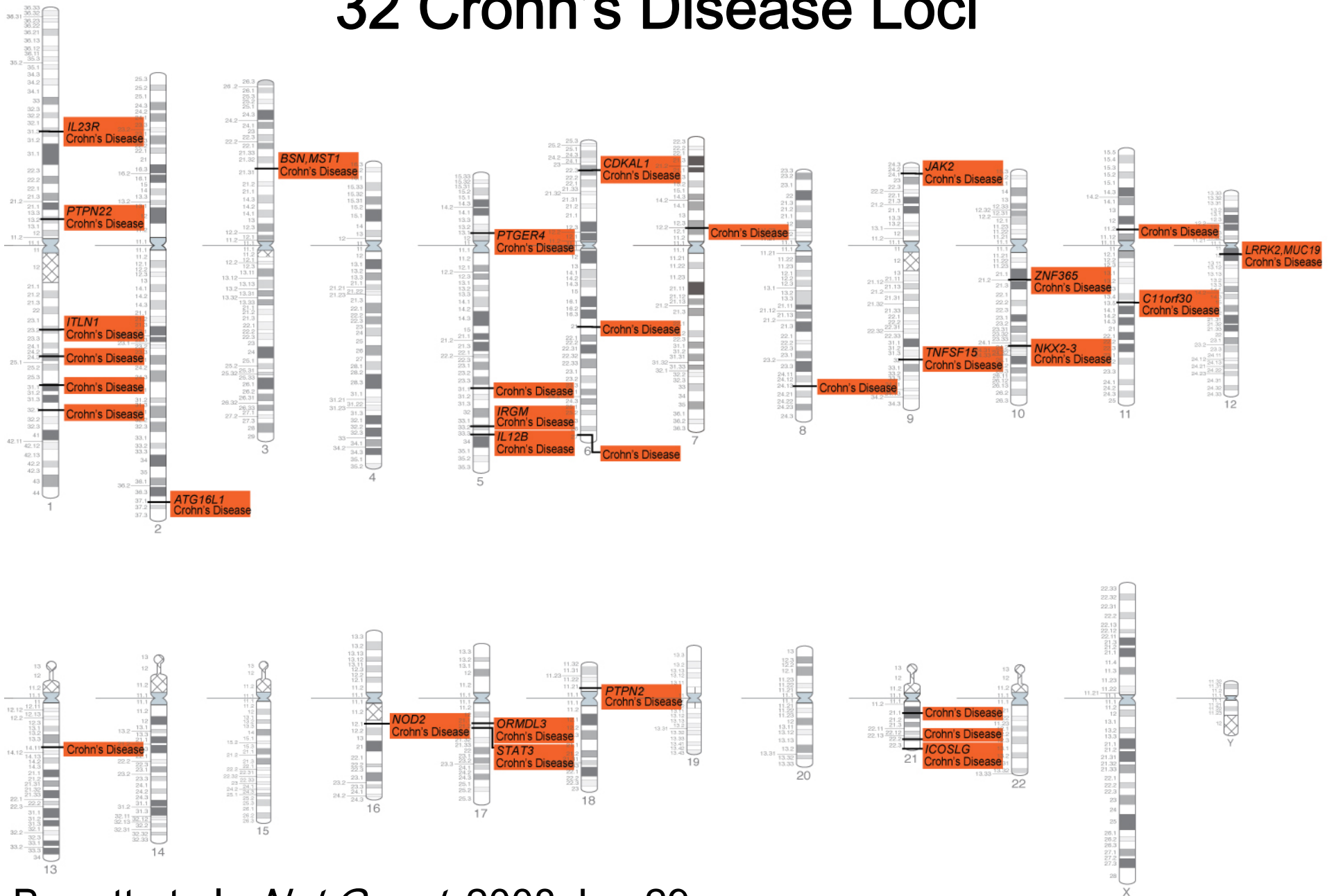


<http://www.genome.gov/gwastudies/>

# Odds Ratio by Risk Allele Frequency for Discrete Associations

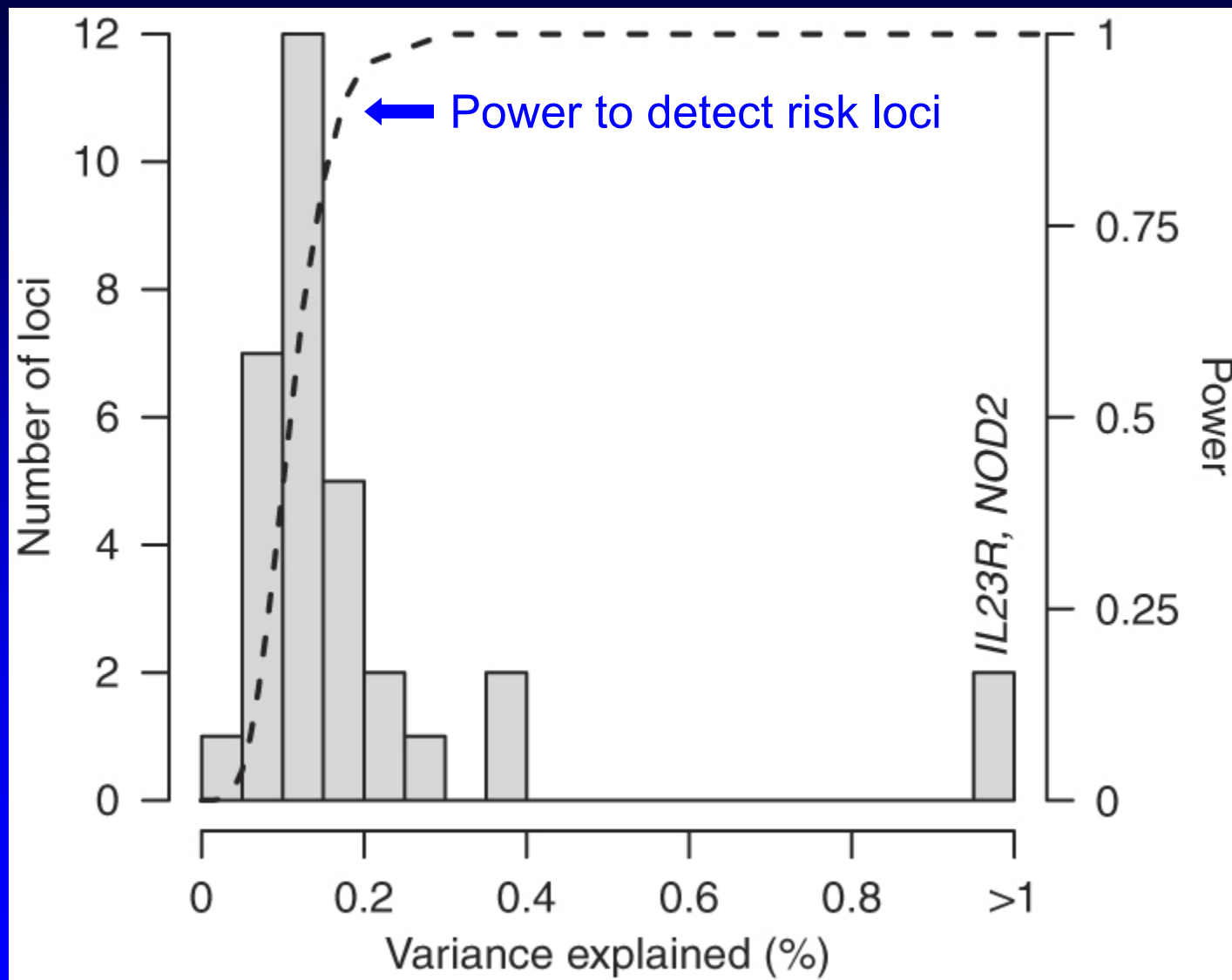


# 32 Crohn's Disease Loci



Barrett et al., *Nat Genet* 2008 Jun 29.

# Percent of Variance in Disease Risk Explained by 32 Established CD Risk Loci



Barrett et al., *Nat Genet* 2008 Jun 29.

What criteria should be considered in determining whether the association between a particular genetic marker and phenotype is strong enough for that marker to be included in genetic testing?

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Depends to very large degree on purpose of testing...

## Possible Purposes of Genetic Testing

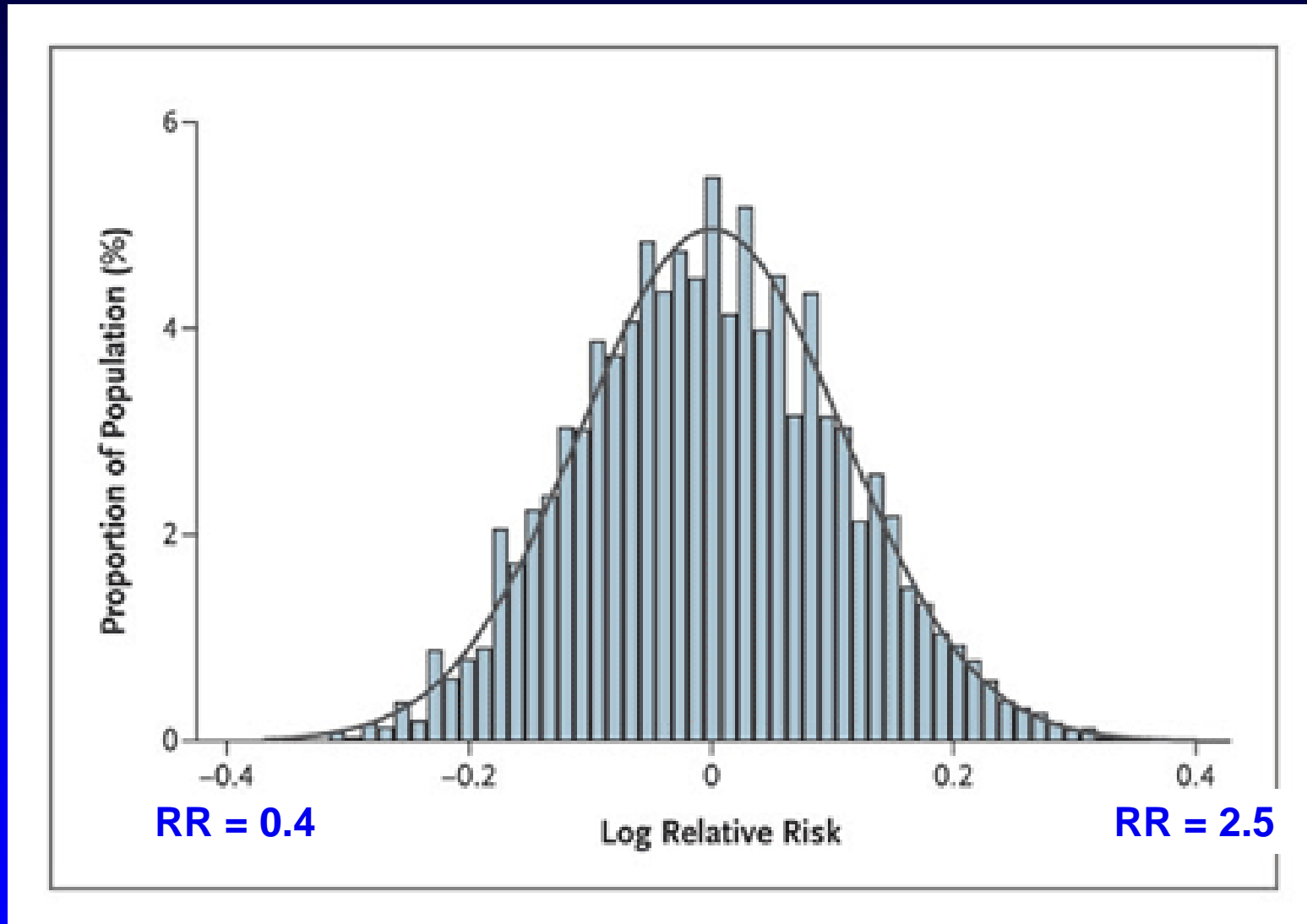
- To improve health and prevent disease
- To provide targeted, proven risk reduction strategies to those at greatest risk
- To identify persons at high risk, for later rapid implementation of newly-proven interventions
- To improve cost efficiency of non-genetic risk reduction strategies
- To facilitate reproductive choices
- To provide information of personal value to individuals, regardless of whether “actionable”



# Criteria to be Considered in Selecting Genetic Variants for Testing

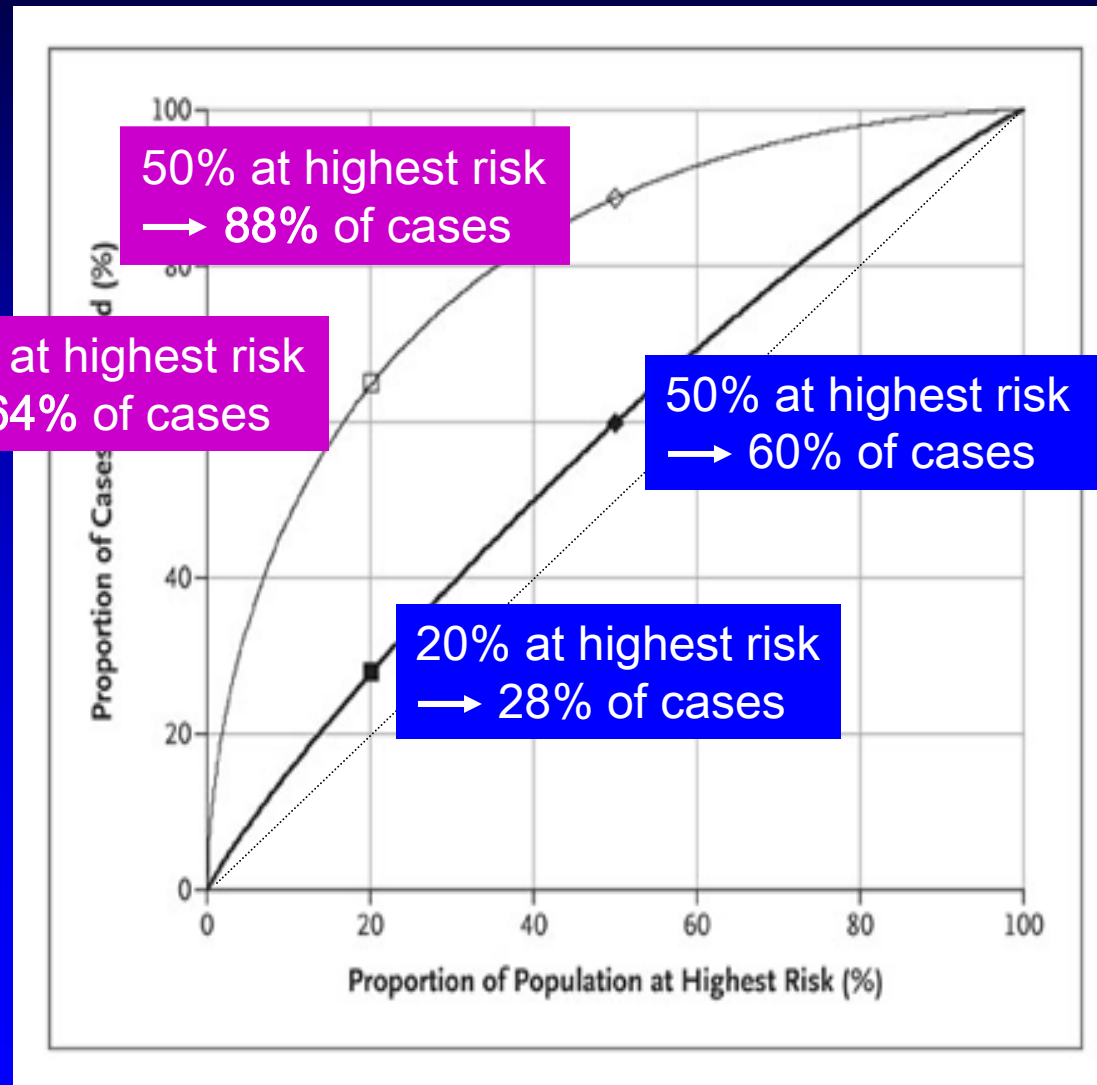
- Strength of evidence for risk association
- Availability and acceptability of proven risk-reducing interventions
- Validity, availability, cost of the test
- Potential anxiety, stigma, cost, additional testing, or other harms from receiving results
- Trade-offs in other testing or care that cannot be paid for within fixed budget

# Distribution of Genetic Risk in the Population



Pharoah et al., *N Engl J Med* 2008; 358:2796-803.

# Proportion of Breast Cancer Cases Explained by Proportion of Population at Highest Risk



Pharoah et al., *N Engl J Med* 2008; 358:2796-803.

# Improving Efficiency of Screening Program for Breast Cancer

- 50-year-old woman in UK has 2.3% risk of breast cancer in next ten years; mammography currently offered to all women over 50
- Offer screening to all women at that risk level?
- Do not offer screening to women not at that risk level?
- Women in 40<sup>th</sup> percentile of population risk have 10-year risk at age 50 of 2.1%
- Women in 5<sup>th</sup> percentile of population risk have 10-year risk at age 50 of 1.5% and *never reach* a 2.3% risk


## What are the limitations of genetic markers in risk assessment for disease?

- Most markers are not deterministic– many people without the markers will develop disease, and many people with the markers will not
- Most of the genetic risk remains unexplained
- Little or no evidence to date that interventions based on genotype improve outcome
- Genetic markers may provide additional risk information for more aggressive risk management in carriers, but again little evidence

## **Randomised trial of cholesterol lowering in 4444 patients with coronary heart disease: the Scandinavian Simvastatin Survival Study (4S)**

PREVENTION OF CARDIOVASCULAR EVENTS AND DEATH WITH PRAVASTATIN IN PATIENTS WITH CORONARY HEART DISEASE AND A BROAD RANGE OF INITIAL CHOLESTEROL LEVELS

## **Primary Prevention of Acute Coronary Events With Lovastatin in Men and Women With Average Cholesterol Levels**

**R**  **MRC/BHF Heart Protection Study of cholesterol lowering with simvastatin in 20536 high-risk individuals: a randomised placebo-controlled trial**

**Executive Summary of the Third Report of the National Cholesterol Education Program (NCEP) Expert Panel on Detection, Evaluation, and Treatment of High Blood Cholesterol in Adults (Adult Treatment Panel III)**

JAMA 2001



# Multiplex Genetic Susceptibility Testing:

*A prototype for applied research to inform  
personalized medicine*

**Colleen M. McBride, PhD. and Larry Brody, Ph.D.**

## **Research Partners:**

National Human Genome Research Institute  
Henry Ford Health System  
Group Health Cooperative  
Cancer Research Network (NCI)



# Multiplex Project Aims

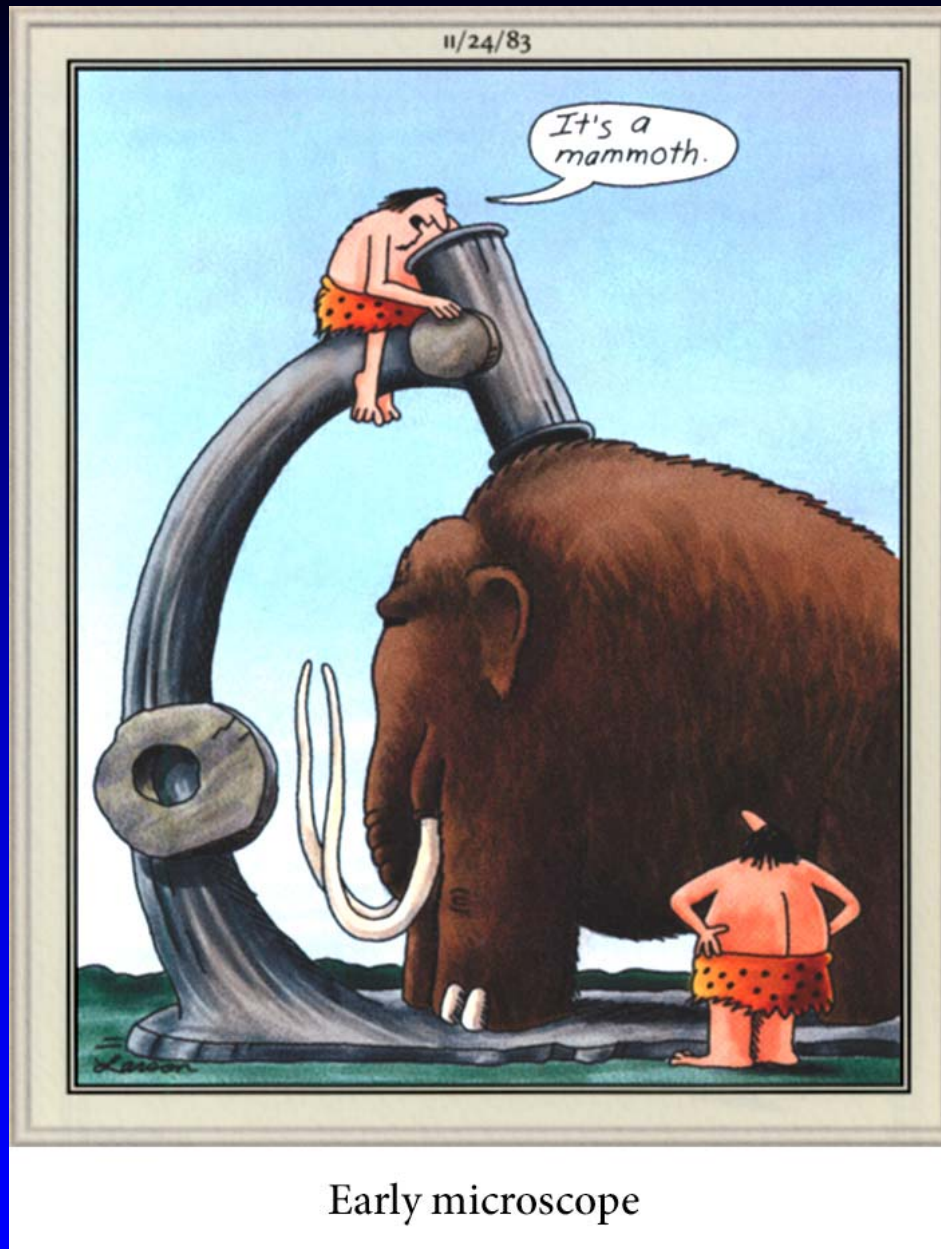
## **To develop a prototype for multiplex genetic susceptibility testing**

- Multiple markers of susceptibility for multiple diseases
- Provide risk feedback to target populations

## **To create an infrastructure to facilitate public health research**

- Decide upon “standard of care” for consent, feedback & support services
- Identify optimal study population(s) and recruitment approach





Larson, G. *The Complete Far Side*. 2003.



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