National Human Genome Research Institute

National Institutes of Health

U.S. Department of Health and Human Services

Genomics in the Genome-Wide Association Era: What's Next for Translation?

U.S. Department of Health and Human Services

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Teri A. Manolio, M.D., Ph.D.
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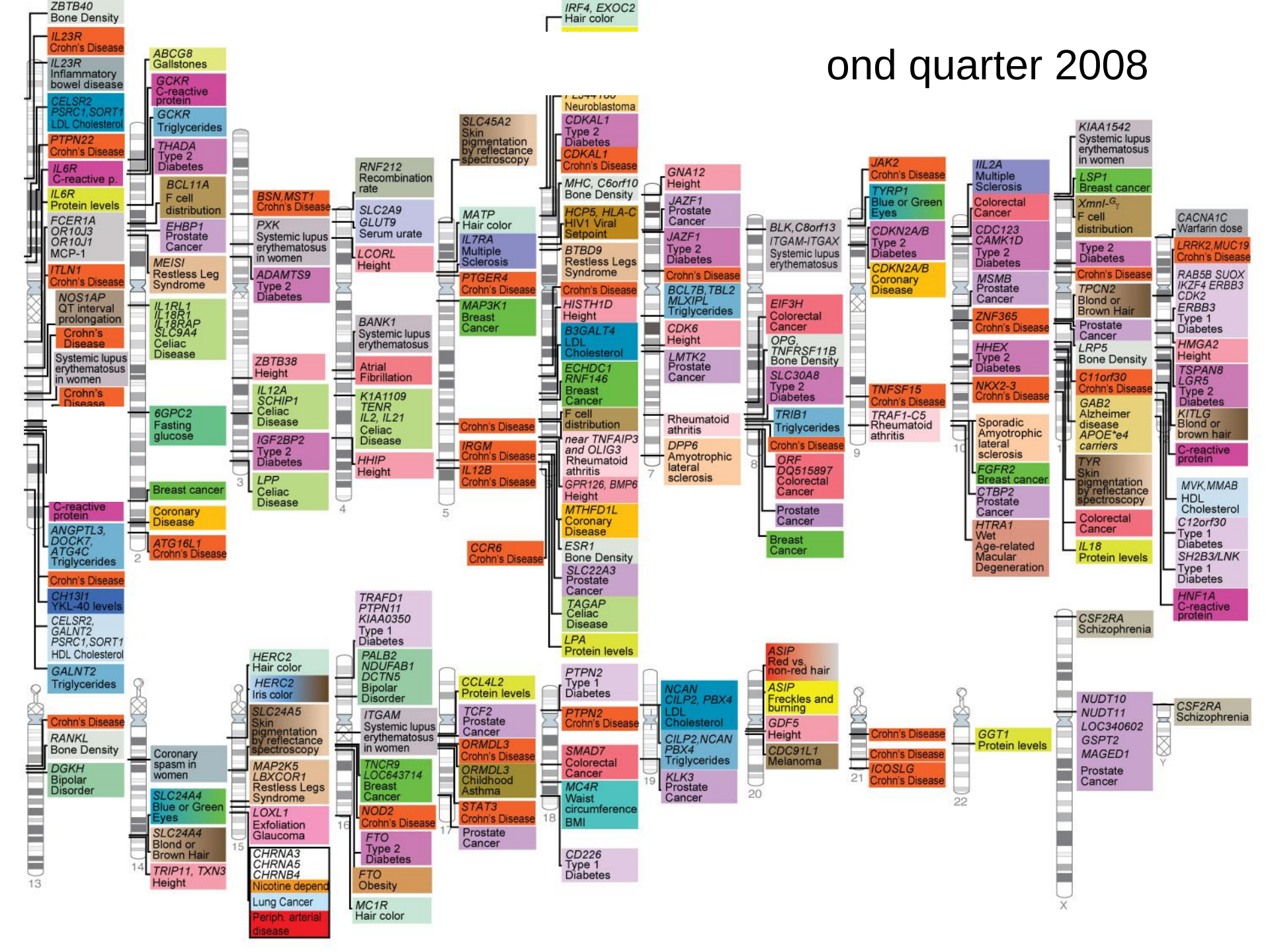
Senior Advisor to the Director, NHGRI,
for Population Genomics

October 22, 2008


ond quarter 2008
ZBTB40 Bone Density
IL23R Crohn's Disease
IL23R Inflammatory bowel disease
CELSR2 PSRC1,SORT1 LDL Cholesterol
PTPN22 Crohn's Disease
IL6R C-reactive p.
IL6R Protein levels
FCER1A OR10J3 OR10J1 MCP-1
ITLN1 Crohn's Disease
NOS1AP QT interval prolongation
Crohn's Disease
Systemic lupus erythematosus in women
Crohn's Disease
C-reactive protein
ANGPTL3, DOCK7, ATG4C Triglycerides
Crohn's Disease
CH13I YKL-40 levels
CELSR2, GALNT2 PSRC1,SORT1 HDL Cholesterol
GALNT2 Triglycerides
Crohn's Disease
RANKL Bone Density
DGKH Bipolar Disorder
ABCG8 Gallstones
GCKR C-reactive protein
GCKR Triglycerides
THADA Type 2 Diabetes
BCL11A F cell distribution
EHBP1 Prostate Cancer
MEISI Restless Leg Syndrome
IL1RL1 IL18R1 IL18RAP SLC9A4 Celiac Disease
6GPC2 Fasting glucose
Breast cancer
Coronary Disease
ATG16L1 Crohn's Disease
Coronary spasm in women
SLC24A4 Blue or Green Eyes
SLC24A4 Blond or Brown Hair
TRIP11, TXN3 Height
BSN,MST1 Crohn's Disease
PXK Systemic lupus erythematosus in women
ADAMTS9 Type 2 Diabetes
ZBTB38 Height
IL12A SCHIP1 Celiac Disease
IGF2BP2 Type 2 Diabetes
LPP Celiac Disease
HERC2 Hair color
HERC2 Iris color
SLC24A5 Skin pigmentation by reflectance spectroscopy
MAP2K5 LBXCOR1 Restless Legs Syndrome
LOXL1 Exfoliation Glaucoma
CHRNA3 CHRNA5 CHRNB4 Nicotine depend
Lung Cancer
Periph. arterial disease
RNF212 Recombination rate
SLC2A9 GLUT9 Serum urate
LCORL Height
BANK1 Systemic lupus erythematosus
Atrial Fibrillation
K1A1109 TENR IL2, IL21 Celiac Disease
HHIP Height
TRAFD1 PTPN11 KIAA0350 Type 1 Diabetes
PALB2 NDUFAB1 DCTN5 Bipolar Disorder
ITGAM Systemic lupus erythematosus in women
TNCR9 LOC643714 Breast Cancer
NOD2 Crohn's Disease
FTO Type 2 Diabetes
FTO Obesity
MC1R Hair color
SLC45A2 Skin pigmentation by reflectance spectroscopy
MATP Hair color
IL7RA Multiple Sclerosis
PTGER4 Crohn's Disease
MAP3K1 Breast Cancer
Crohn's Disease
IRGM Crohn's Disease
IL12B Crohn's Disease
CCR6 Crohn's Disease
CCL4L2 Protein levels
TCF2 Prostate Cancer
ORMDL3 Crohn's Disease
ORMDL3 Childhood Asthma
STAT3 Crohn's Disease
Prostate Cancer
IRF4, EXOC2 Hair color
Neuroblastoma
CDKAL1 Type 2 Diabetes
CDKAL1 Crohn's Disease
MHC, C6orf10 Bone Density
HCP5, HLA-C HIV1 Viral Setpoint
BTBD9 Restless Legs Syndrome
Crohn's Disease
HISTH1D Height
B3GALT4 LDL Cholesterol
ECHDC1 RNF146 Breast Cancer
F cell distribution
near TNFAIP3 and OLIG3 Rheumatoid athritis
GPR126, BMP6 Height
MTHFD1L Coronary Disease
ESR1 Bone Density
SLC22A3 Prostate Cancer
TAGAP Celiac Disease
LPA Protein levels
PTPN2 Type 1 Diabetes
PTPN2 Crohn's Disease
SMAD7 Colorectal Cancer
MC4R Waist circumference BMI
CD226 Type 1 Diabetes
GNA12 Height
JAZF1 Prostate Cancer
JAZF1 Type 2 Diabetes
Crohn's Disease
BCL7B,TBL2 MLXIPL Triglycerides
CDK6 Height
LMTK2 Prostate Cancer
Rheumatoid athritis
DPP6 Amyotrophic lateral sclerosis
NCAN CILP2, PBX4 LDL Cholesterol
CILP2,NCAN PBX4 Triglycerides
KLK3 Prostate Cancer
BLK,C8orf13 ITGAM-ITGAX Systemic lupus erythematosus
EIF3H Colorectal Cancer
OPG, TNFRSF11B Bone Density
SLC30A8 Type 2 Diabetes
TRIB1 Triglycerides
Crohn's Disease
ORF DQ515897 Colorectal Cancer
Prostate Cancer
Breast Cancer
ASIP Red vs. non-red hair
ASIP Freckles and burning
GDF5 Height
CDC91L1 Melanoma
JAK2 Crohn's Disease
TYRP1 Blue or Green Eyes
CDKN2A/B Type 2 Diabetes
CDKN2A/B Coronary Disease
TNFSF15 Crohn's Disease
TRAF1-C5 Rheumatoid athritis
Crohn's Disease
Crohn's Disease
ICOSLG Crohn's Disease
GGT1 Protein levels
IIL2A Multiple Sclerosis
Colorectal Cancer
CDC123 CAMK1D Type 2 Diabetes
MSMB Prostate Cancer
ZNF365 Crohn's Disease
HHEX Type 2 Diabetes
NKX2-3 Crohn's Disease
Sporadic Amyotrophic lateral sclerosis
FGFR2 Breast cancer
CTBP2 Prostate Cancer
HTRA1 Wet Age-related Macular Degeneration
KIAA1542 Systemic lupus erythematosus in women
LSP1 Breast cancer
Xmnl-G(Y) F cell distribution
Type 2 Diabetes
Crohn's Disease
TPCN2 Blond or Brown Hair
Prostate Cancer
LRP5 Bone Density
C11orf30 Crohn's Disease
GAB2 Alzheimer disease APOE*e4 carriers
TYR Skin pigmentation by reflectance spectroscopy
Colorectal Cancer
IL18 Protein levels
CSF2RA Schizophrenia
NUDT10 NUDT11 LOC340602 GSPT2 MAGED1
Prostate Cancer
CACNA1C Warfarin dose
LRRK2,MUC19 Crohn's Disease
RAB5B SUOX IKZF4 ERBB3 CDK2 ERBB3 Type 1 Diabetes
HMGA2 Height
TSPAN8 LGR5 Type 2 Diabetes
KITLG Blond or brown hair
C-reactive protein
MVK,MMAB HDL Cholesterol
C12orf30 Type 1 Diabetes
SH2B3/LNK Type 1 Diabetes
HNF1A C-reactive protein
CSF2RA Schizophrenia

2007: The Year of GWA Studies

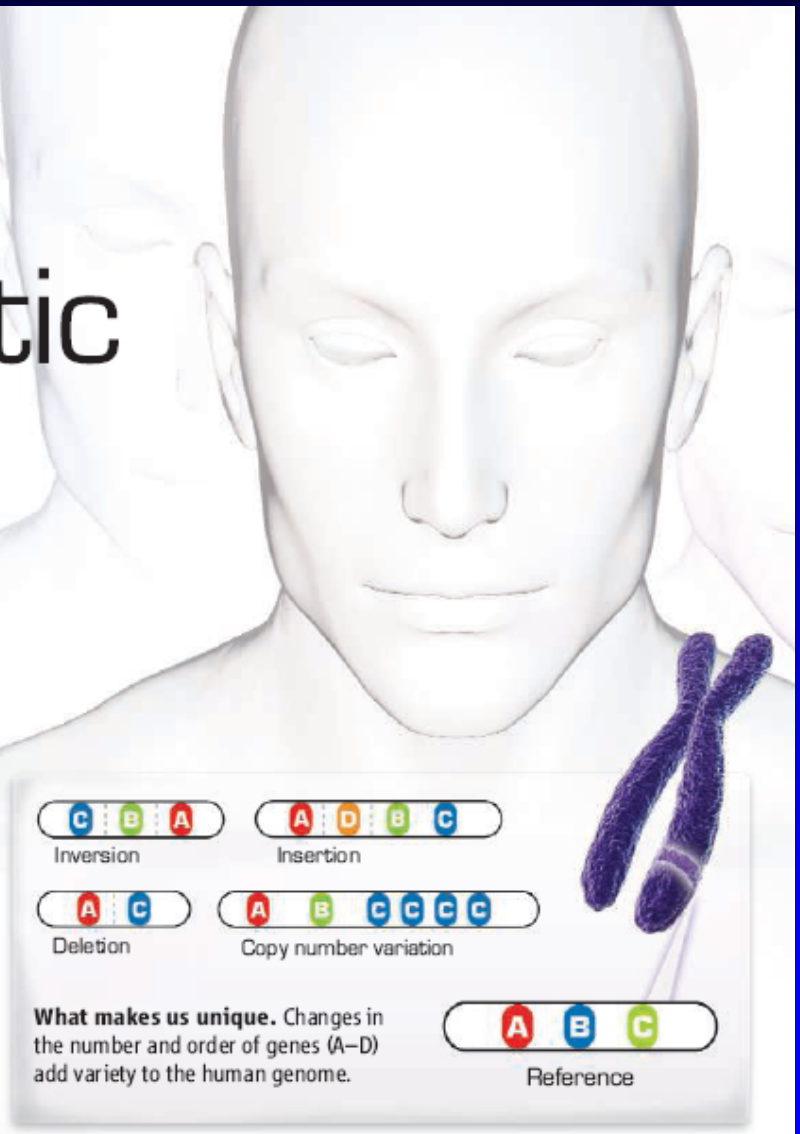
BREAKTHROUGH OF THE YEAR

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.

Diseases and Traits with Published GWA Studies (n = 72, 10/14/08)

- Macular Degeneration
- Exfoliation Glaucoma

- Lung Cancer
- Prostate Cancer
- Breast Cancer
- Colorectal Cancer
- Bladder Cancer
- Neuroblastoma
- Melanoma
- *TP53* Cancer Predispos'n
- Chr. Lymph. Leukemia

- Inflamm. Bowel Disease
- Celiac Disease
- Gallstones
- Irritable Bowel Syndrome

- QT Prolongation
- Coronary Disease
- Coronary Spasm
- Atrial Fibrillation/Flutter
- Stroke
- Subarachnoid Hemorrhage
- Hypertension
- Hypt. Diuretic Response

- Peripheral Artery Disease
- Lipids and Lipoproteins
- Warfarin Dosing
- Ximelegatran Adv. Resp.

- Parkinson Disease
- Amyotrophic Lat. Sclerosis
- Multiple Sclerosis
- MS Interferon-β Response
- Prog. Supranuclear Palsy
- Alzheimer's Disease in ε4+
- Cognitive Ability
- Memory
- Hearing
- Restless Legs Syndrome
- Nicotine Dependence
- Methamphetamine Depend.
- Neuroticism
- Schizophrenia
- Sz. Iloperidone Response
- Bipolar Disorder
- Family Chaos
- Narcolepsy

- Rheumatoid Arthritis
- RA Anti-TNF Response

- Syst. Lupus Erythematosus
- Sarcoidosis
- 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
- Male Pattern Baldness

- F-Cell Distribution
- Fetal Hgb Levels
- C-Reactive Protein
- ICAM-1
- Total IgE Levels
- Uric Acid Levels, Gout
- Protein Levels
- Vitamin B12 Levels
- Recombination Rate
- Pigmentation

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

"There have been few, if any, similar bursts of discovery in the history of medical research…"

The past 3 months have seen the publication of a series of

ating the need for guessing which genes are likely to harbor variants

The main problem with this strategy is that because of the

ost stud-
ained in
samples
ower to

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-

lated to the 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.[2] Such findings promise to open up new avenues of research, through both the discovery of new genes rele-

generate P values as small as 10^{-7}. In addition, most variants identified recently have been associated 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

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

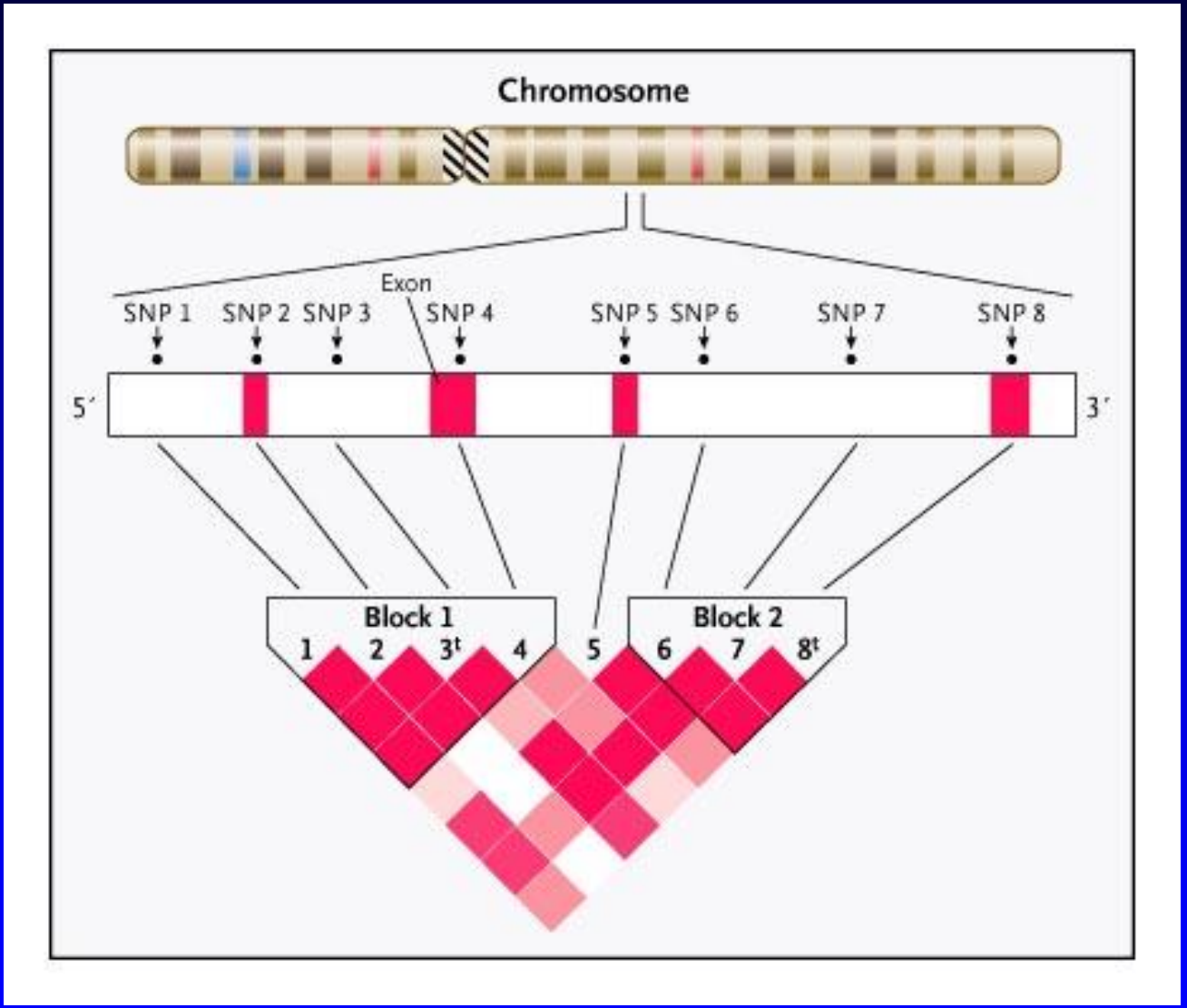
What is a Genome-Wide Association Study?

- Method for interrogating all 10 million variable points across human genome
- Variation inherited in groups, or blocks, so not all 10 million points have to be tested
- Blocks are shorter (so need to test more points) the less closely people are related
- Technology now allows studies in unrelated persons, assuming 5,000 – 10,000 base pair lengths in common (300,000 – 1,000,000 markers)

DNA on Chromosome 7

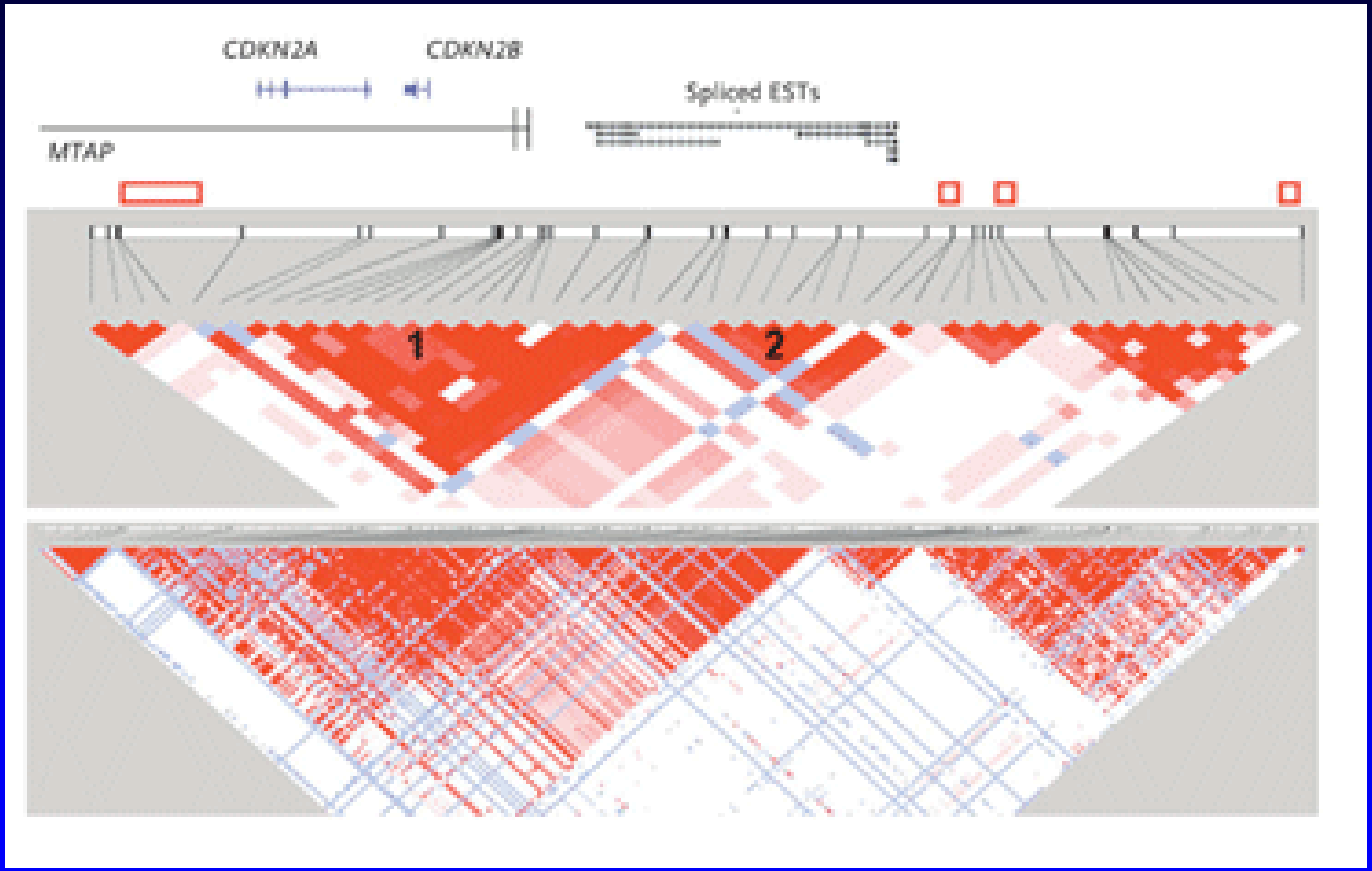
SNPs 1 / 300 bases

Mapping the Relationships Among SNPs



Christensen and Murray, *N Engl J Med* 2007; 356:1094-97.

Chromosome 9p21 Region Associated with MI



Samani N et al, *N Engl J Med* 2007; 357:443-453.

Distances Among East Coast Cities

	Boston	Provi-dence	New York	Phila-delphia	Balti-more
Providence	59				
New York	210	152			
Philadelphia	320	237	86		
Baltimore	430	325	173	87	
Washington	450	358	206	120	34

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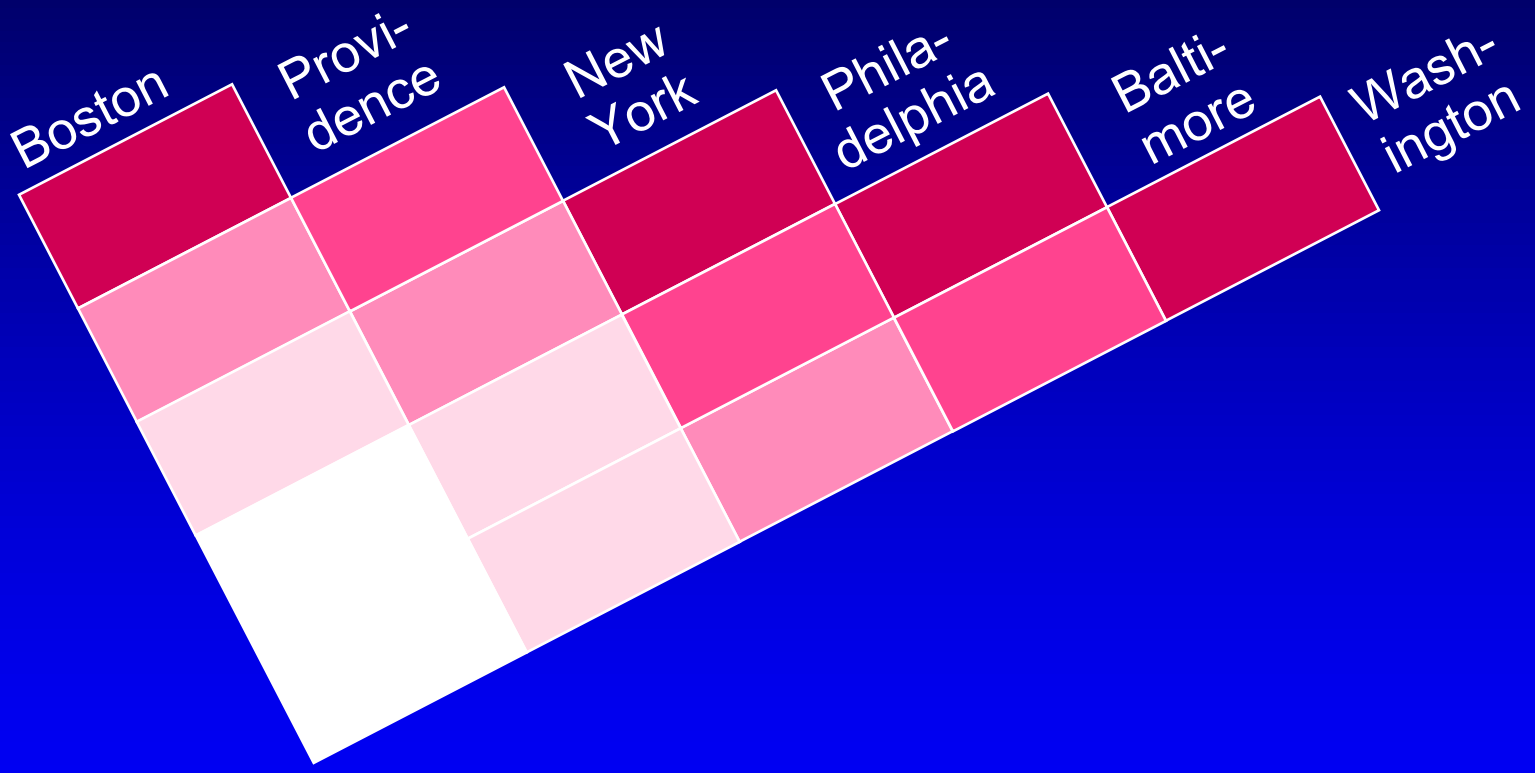

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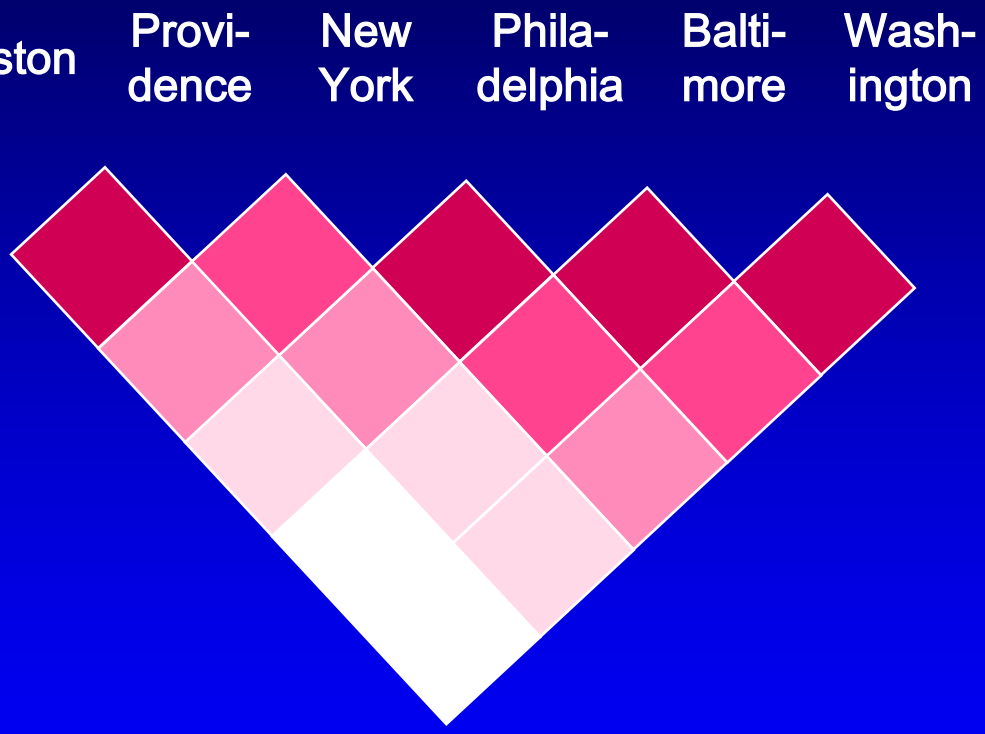

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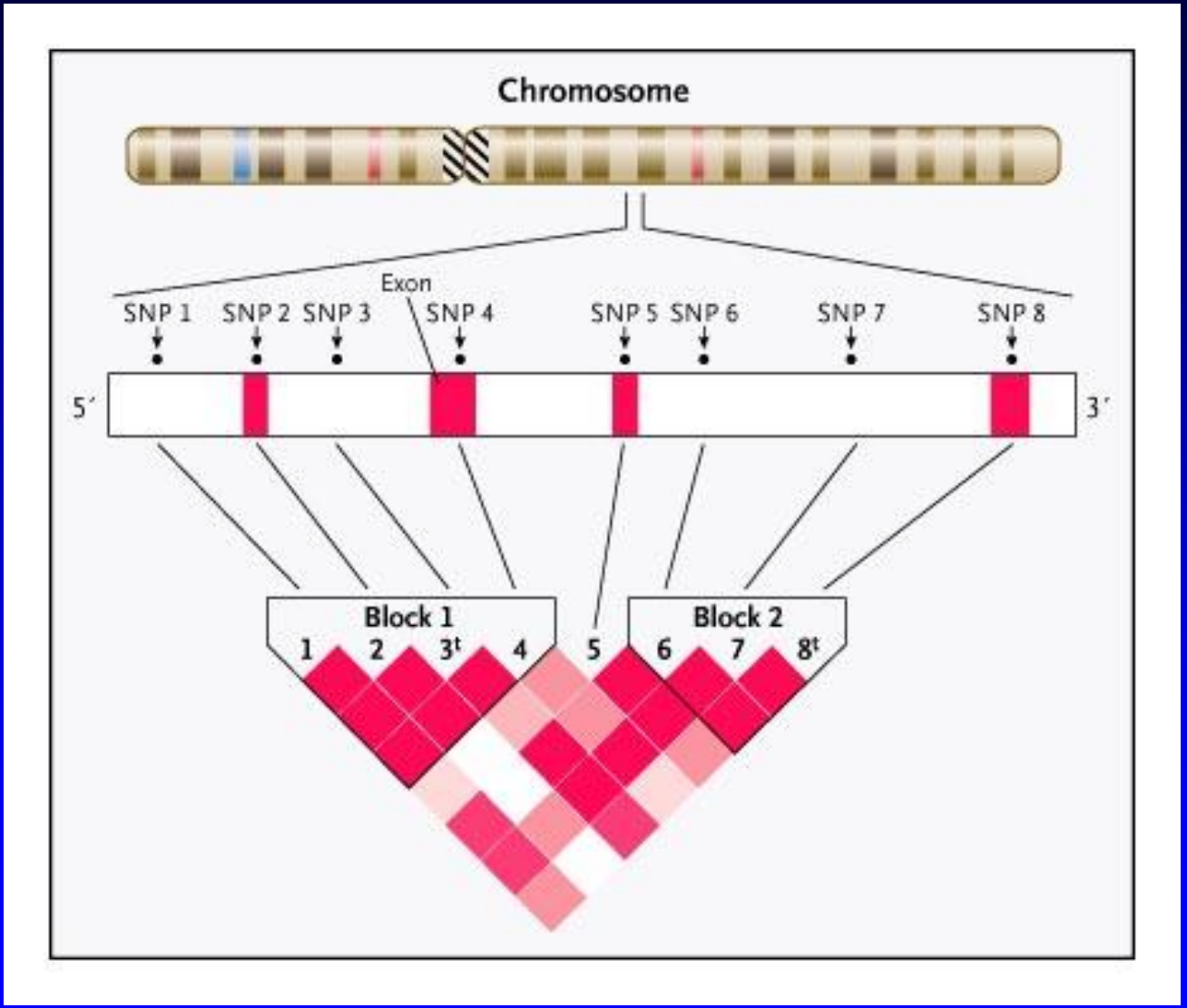
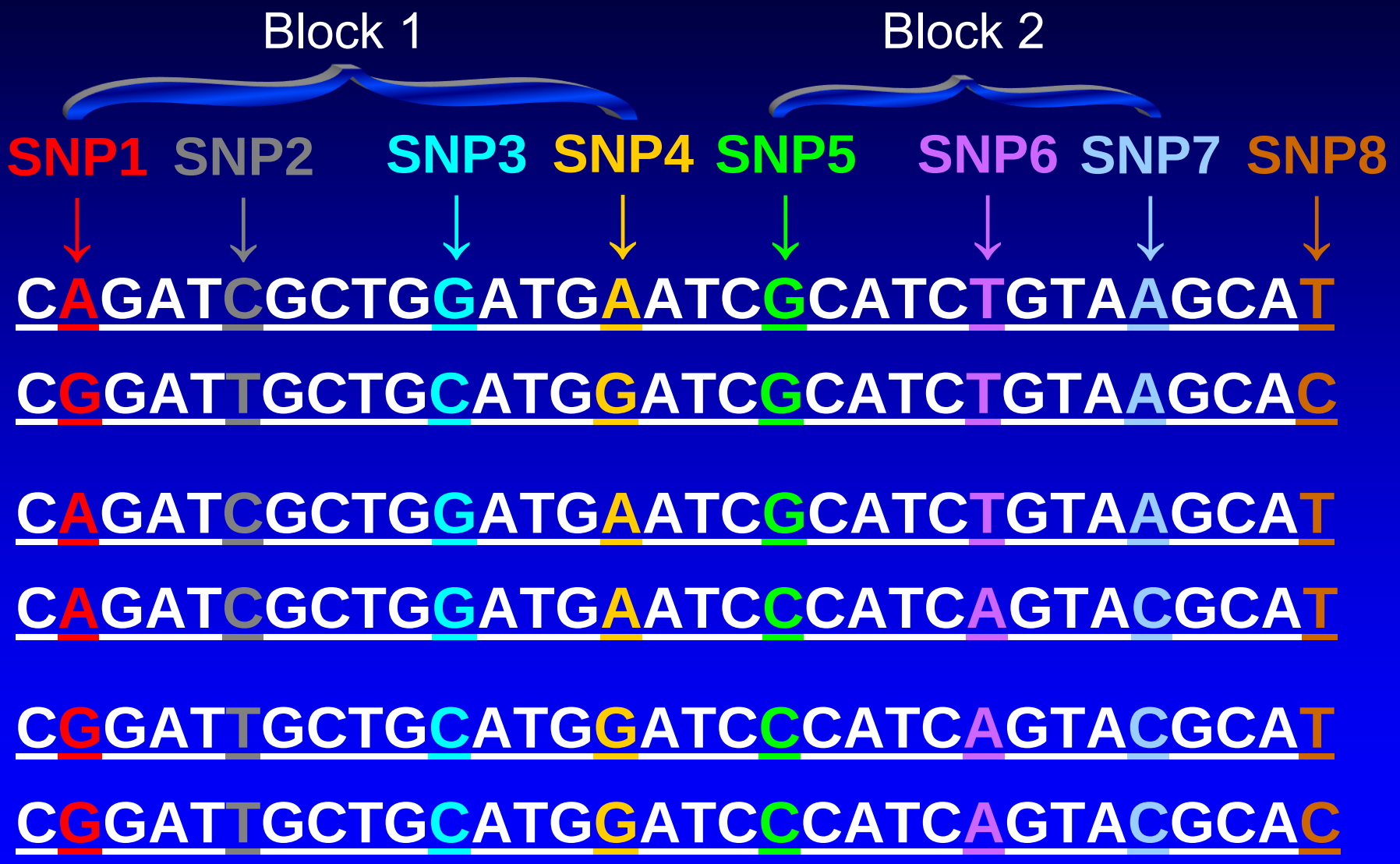


Christensen and Murray, *N Engl J Med* 2007; 356:1094-97.

One Tag SNP May Serve as Proxy for Many



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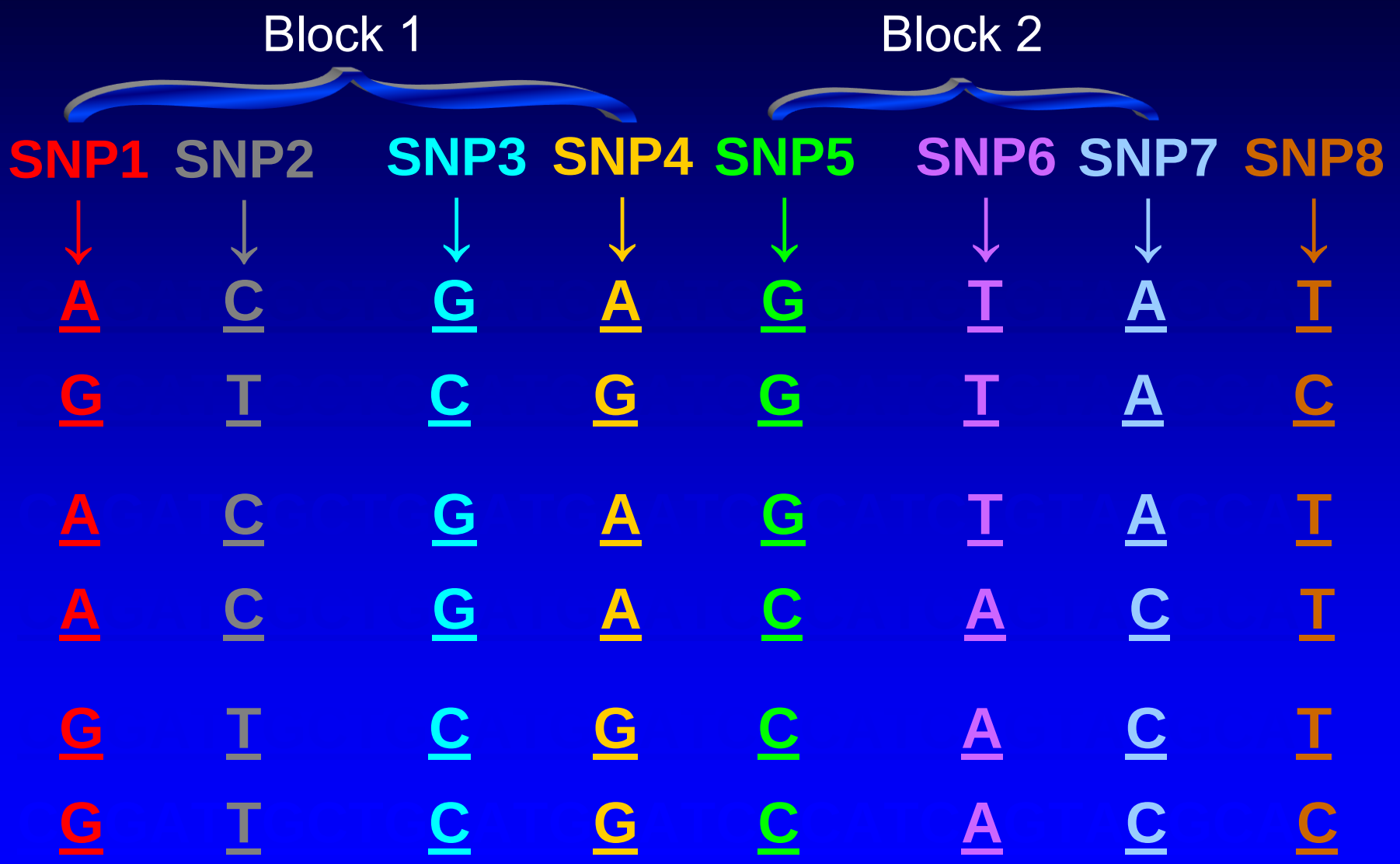

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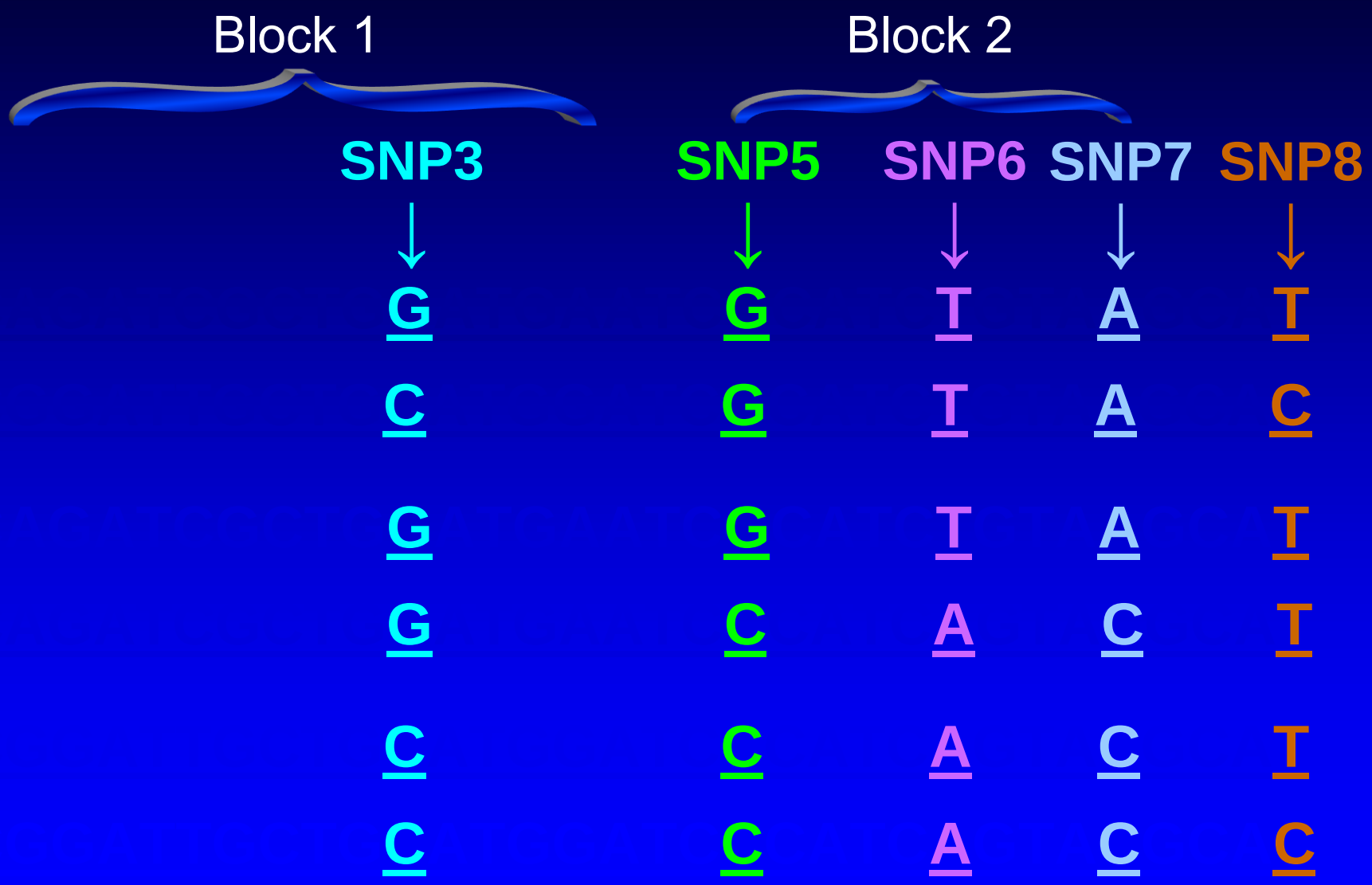

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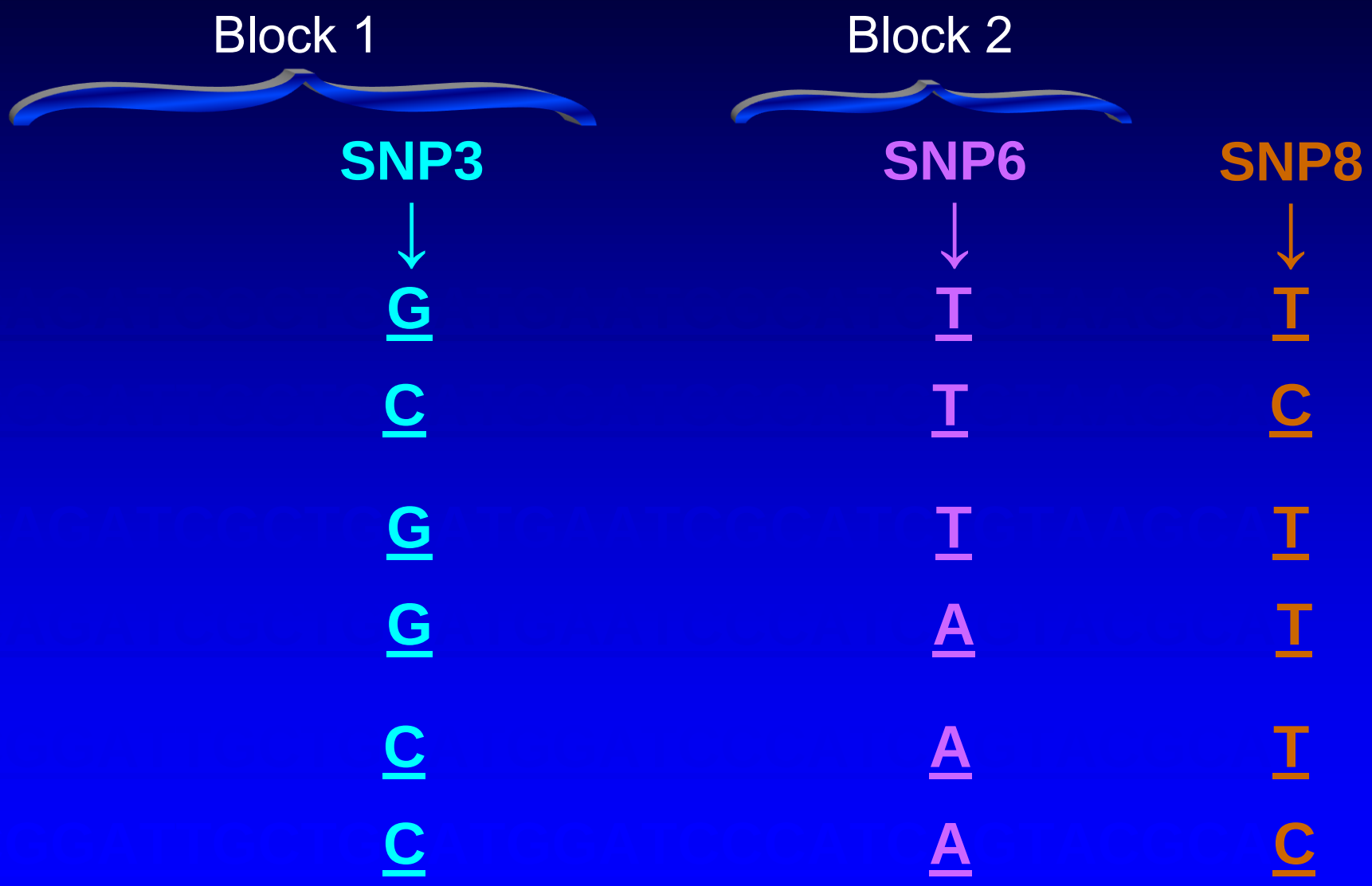

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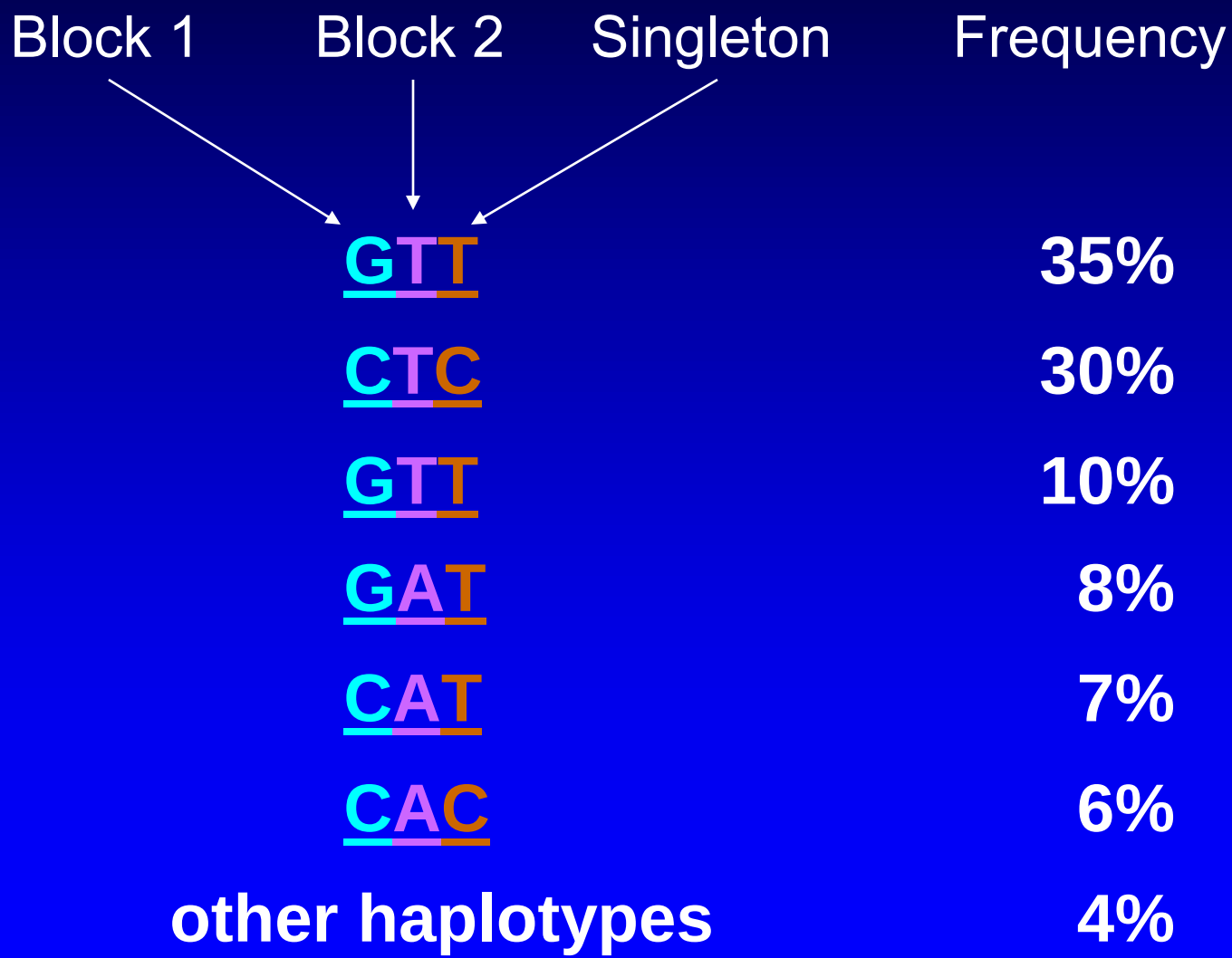


www.hapmap.org

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

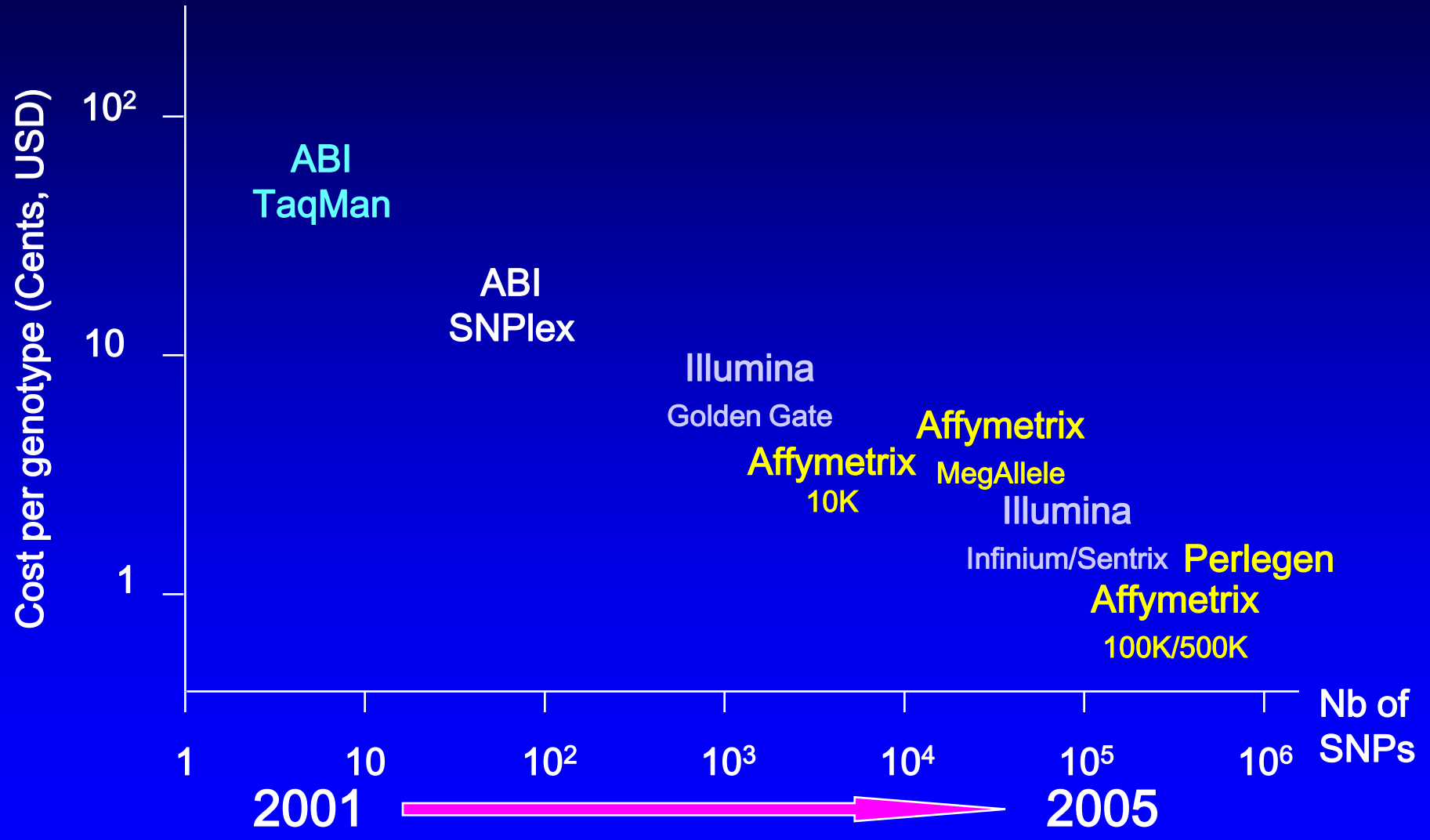
The International HapMap Consortium*

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

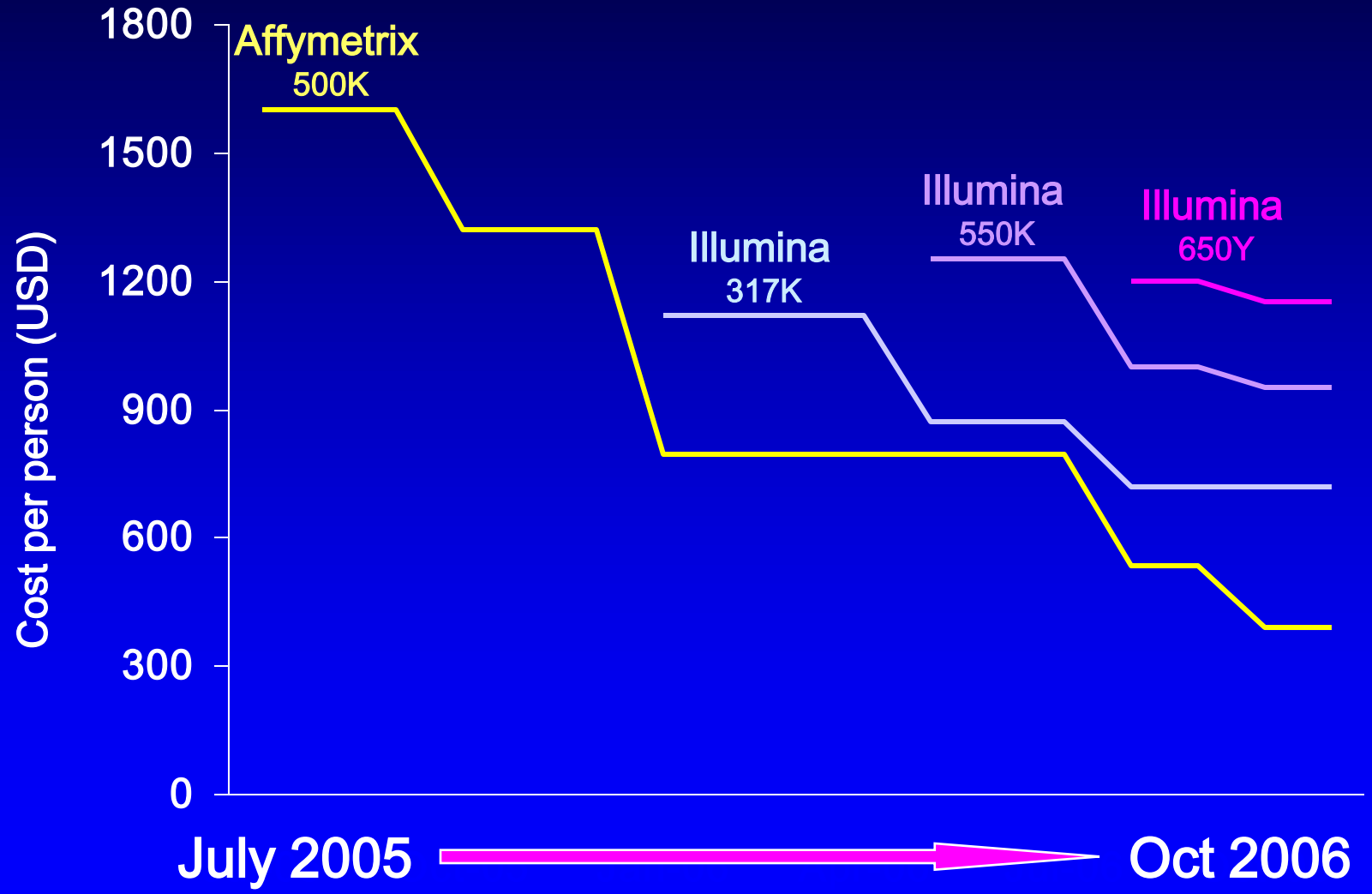
- Use just the density of SNPs needed to find associations between SNPs and diseases
- Do not miss chromosomal regions with disease association
- Produce a tool to assist in finding genes affecting health and disease
- Use more SNPs for complete genome coverage of populations of recent African ancestry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

Progress in Genotyping Technology



Courtesy S. Chanock, NCI

Continued Progress in Genotyping Technology



Courtesy S. Gabriel, Broad/MIT

Association of Alleles and Genotypes of rs1333049 with Myocardial Infarction

	C N (%)	G N (%)	χ^2 (1df)	P-value
Cases	2,132 (55.4)	1,716 (44.6)	55.1	1.2×10^{-13}
Controls	2,783 (47.4)	3,089 (52.6)		
Allelic Odds Ratio = 1.38				

Samani N et al, *N Engl J Med* 2007; 357:443-53.

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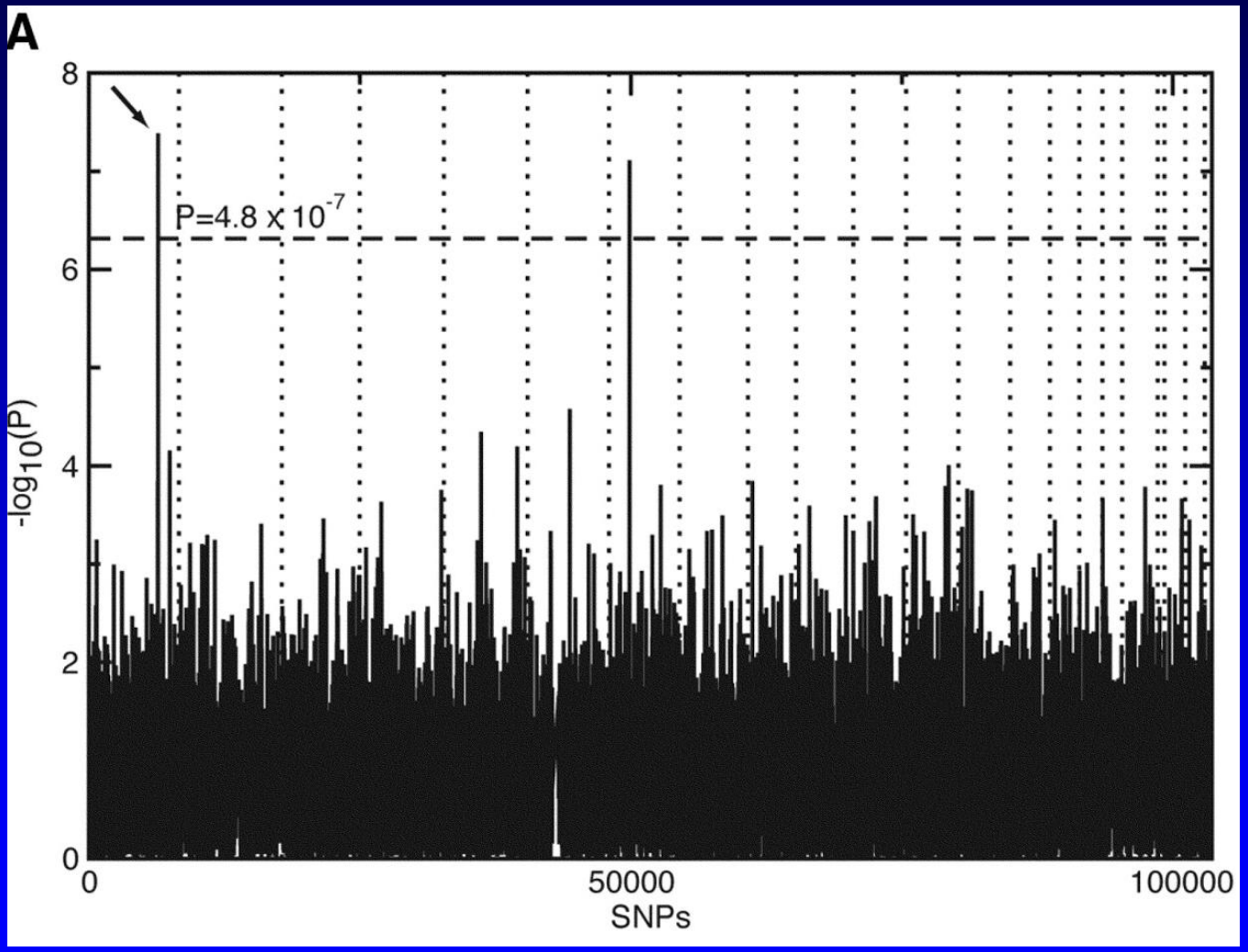
Allelic Odds Ratio = 1.38				

	CC N (%)	CG N (%)	GG N (%)	χ^2 (2df)	P-value
Cases	586 (30.5)	960 (49.9)	378 (19.6)	59.7	1.1×10^{-14}
Controls	676 (23.0)	1,431 (48.7)	829 (28.2)		
Heterozygote Odds Ratio = 1.47					
Homozygote Odds Ratio = 1.90					

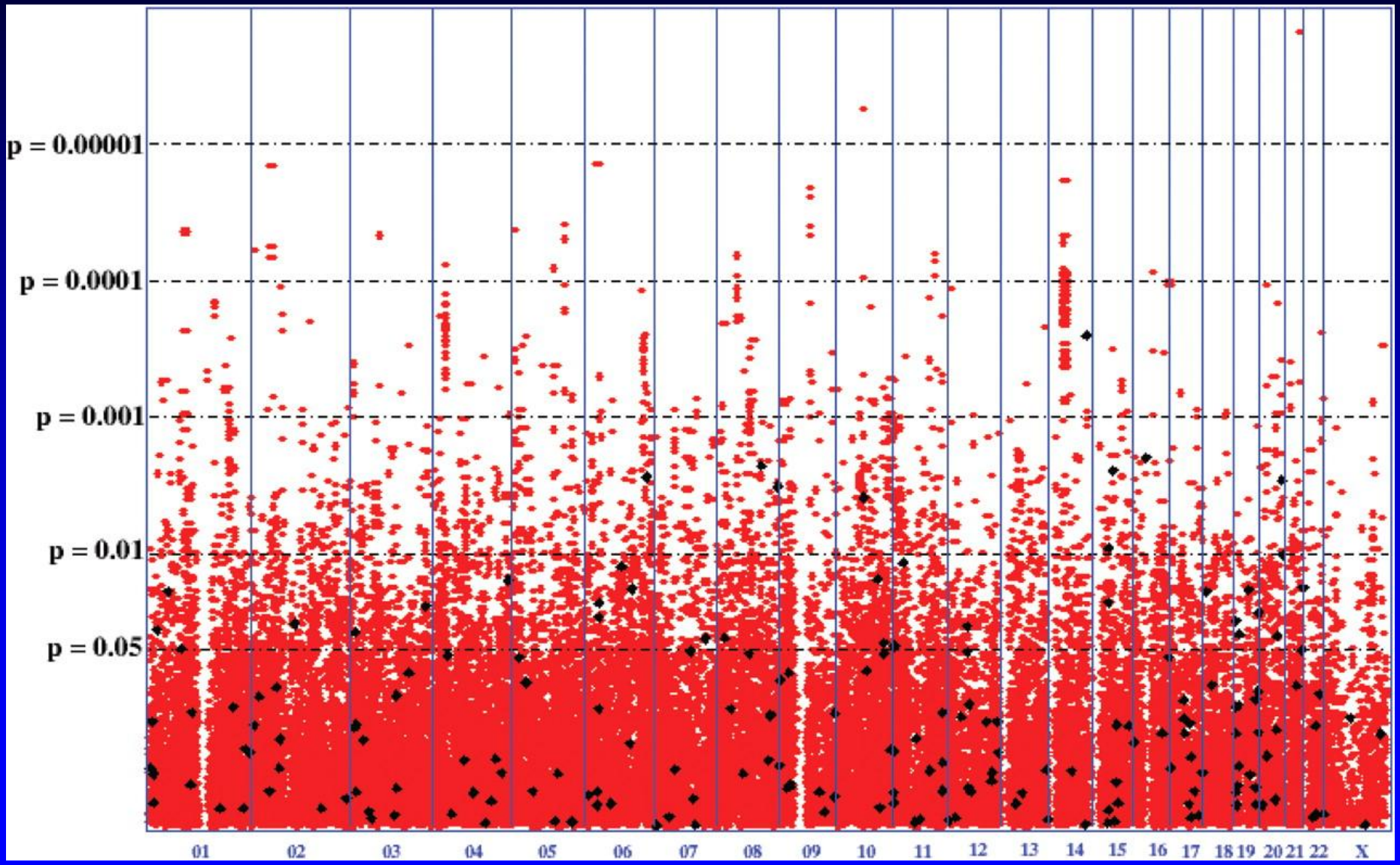
Samani N et al, *N Engl J Med* 2007; 357:443-53.

P Values of GWA Scan for Age-Related Macular Degeneration



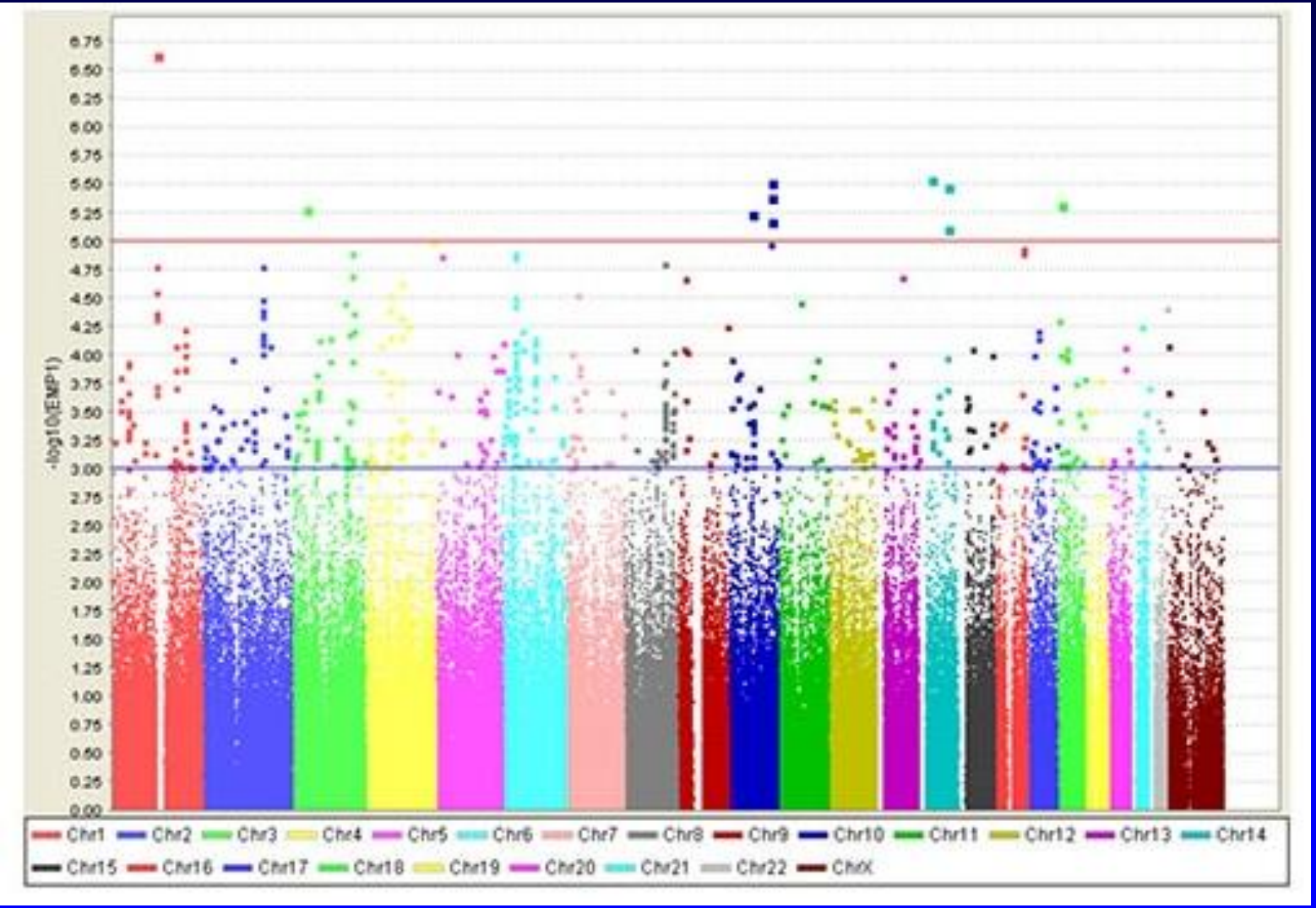
Klein et al, *Science* 2005; 308:385-389.

Nicotine Dependence among Smokers



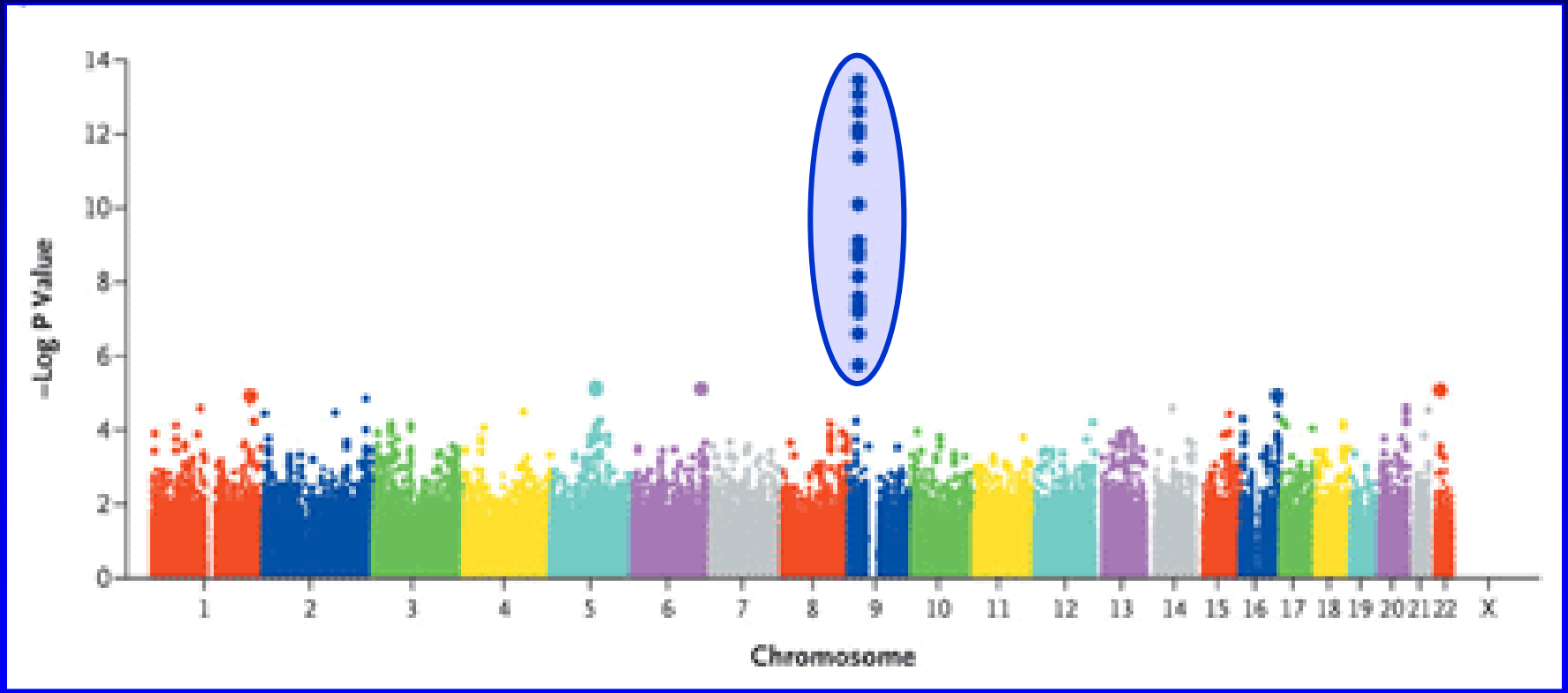
Bierut LJ et al, *Hum Molec Genet* 2007; 16:24-35.

Genome-Wide Scan for Type 2 Diabetes in a Scandinavian Cohort



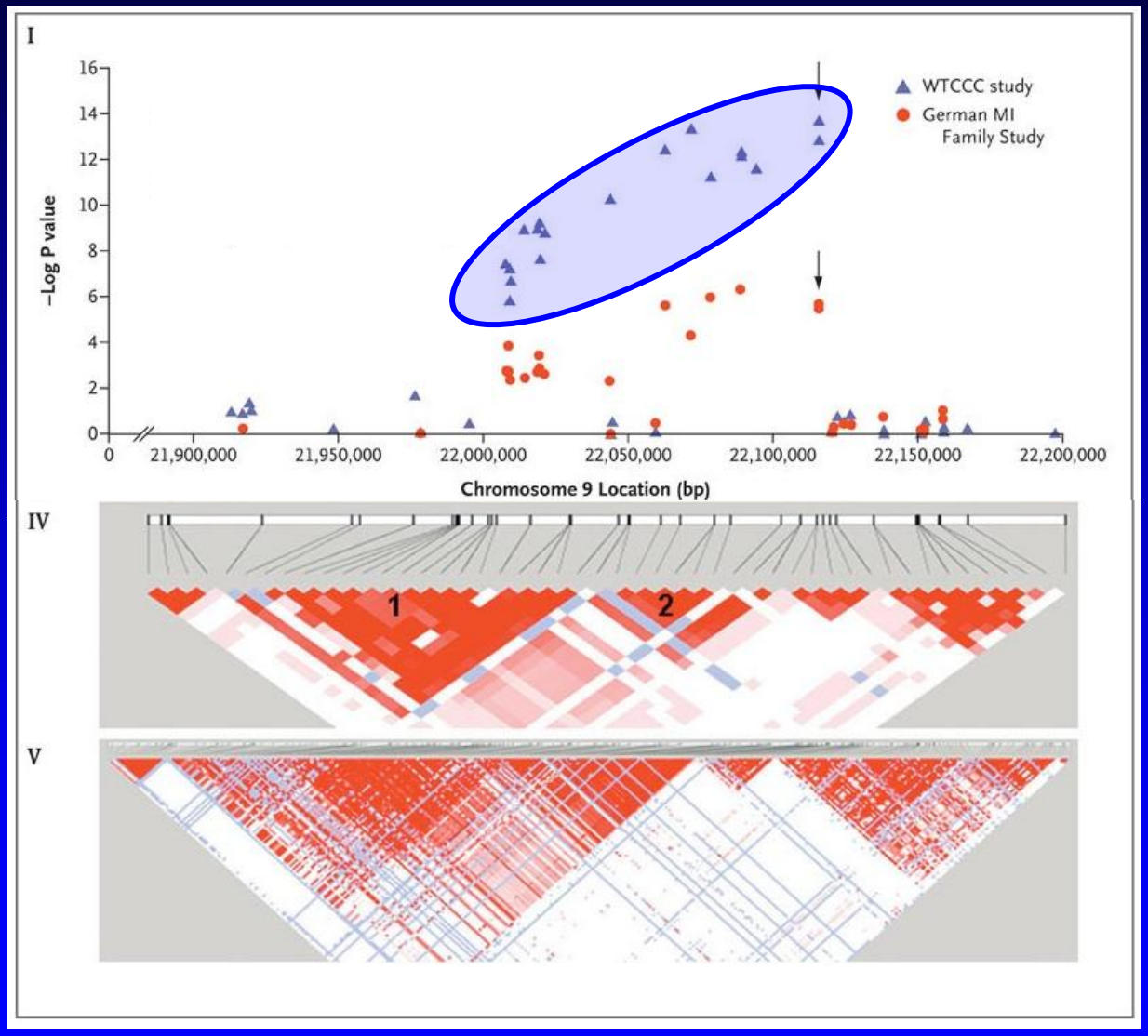
http://www.broad.mit.edu/diabetes/scandinavs/type2.html

$-\text{Log}_{10}$ P Values for SNP Associations with Myocardial Infarction



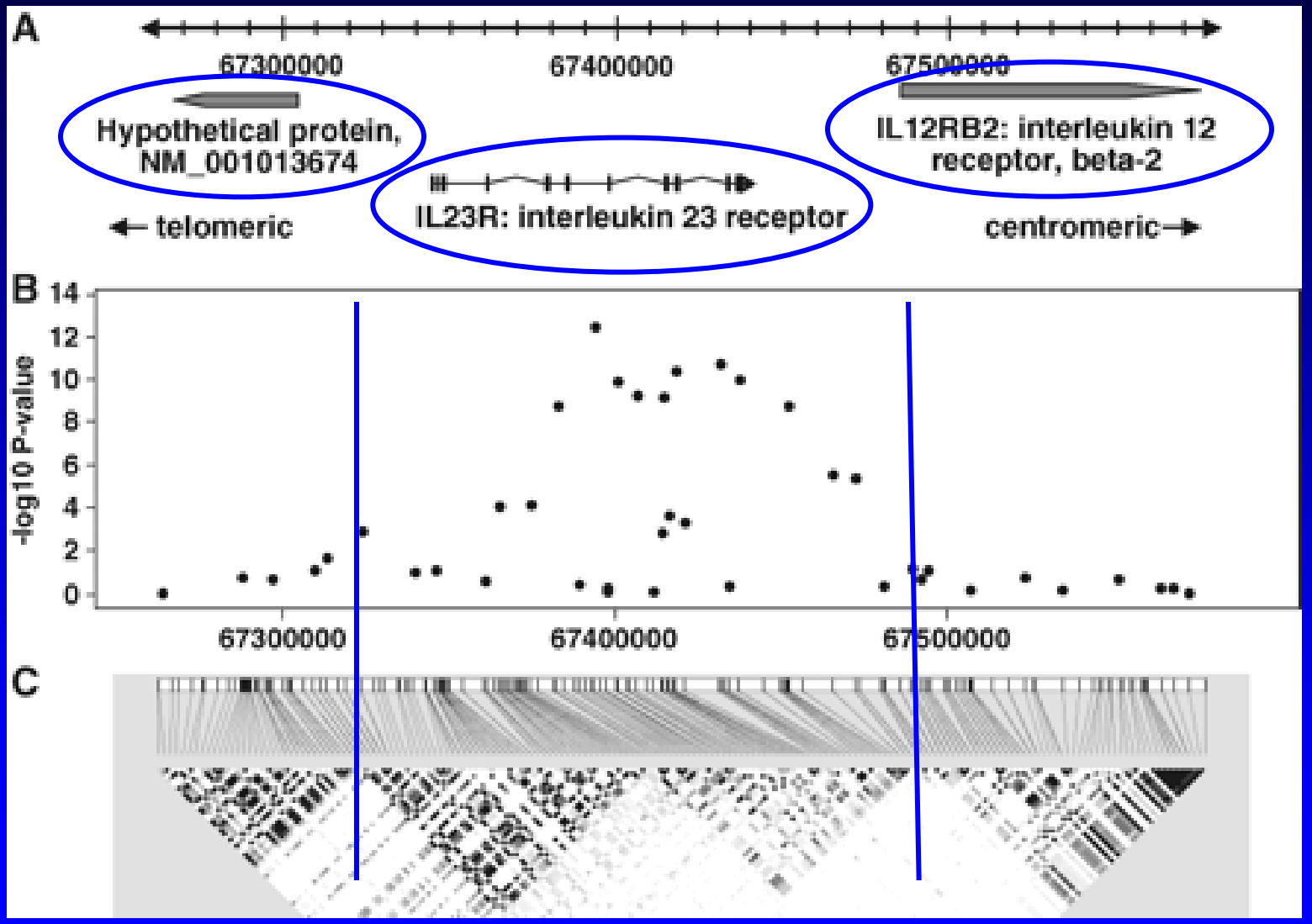
Samani N et al., *N Engl J Med* 2007; 357:443-53.

Association Signal for Coronary Artery Disease on Chromosome 9



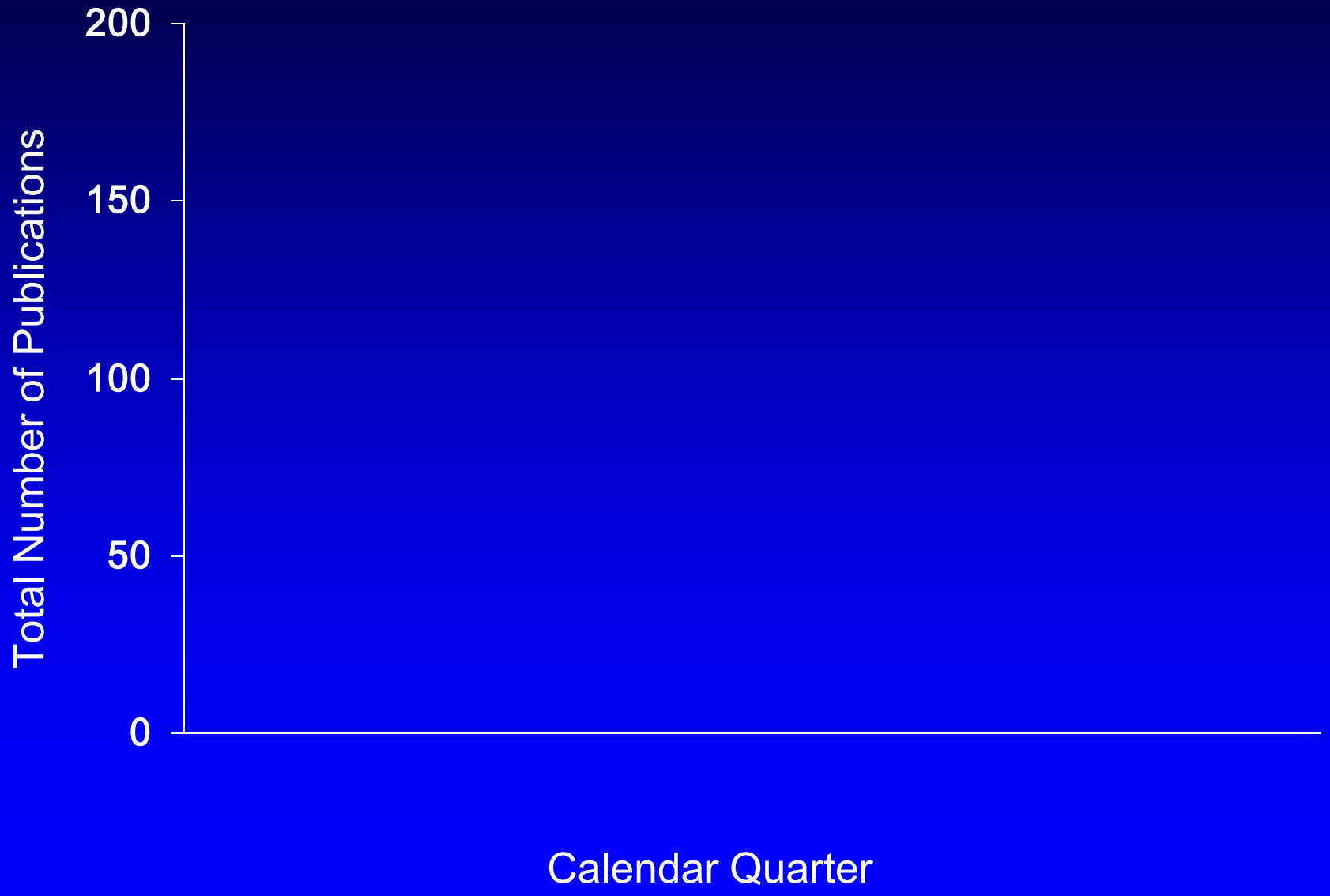
Samani N et al., *N Engl J Med* 2007; 357:443-53.

Region of Chromosome 1 Showing Strong Association with Inflammatory Bowel Disease



Duerr R et al., *Science* 2006; 314:1461-63.

Published GWA Reports, 3/2005 - 9/2008



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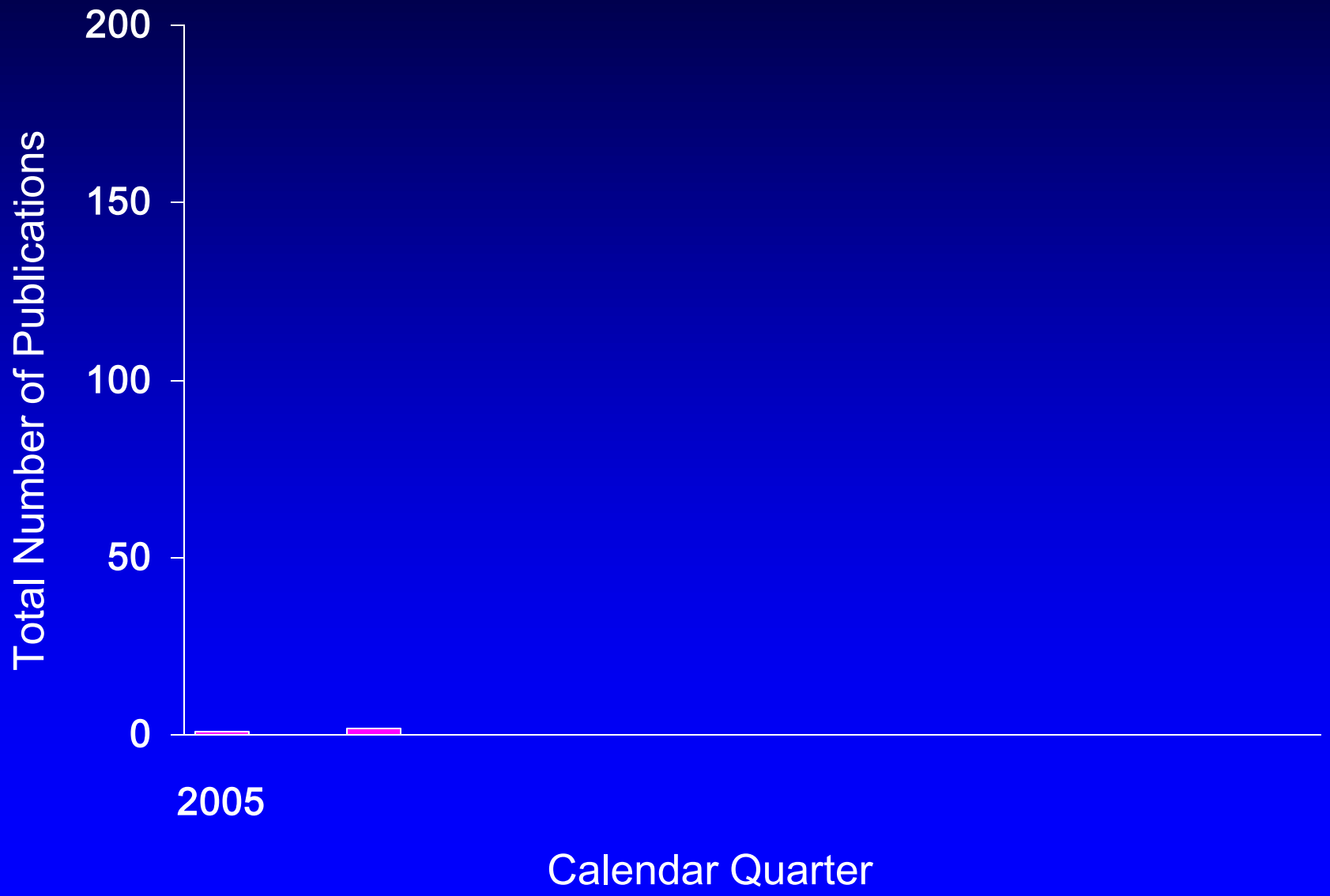

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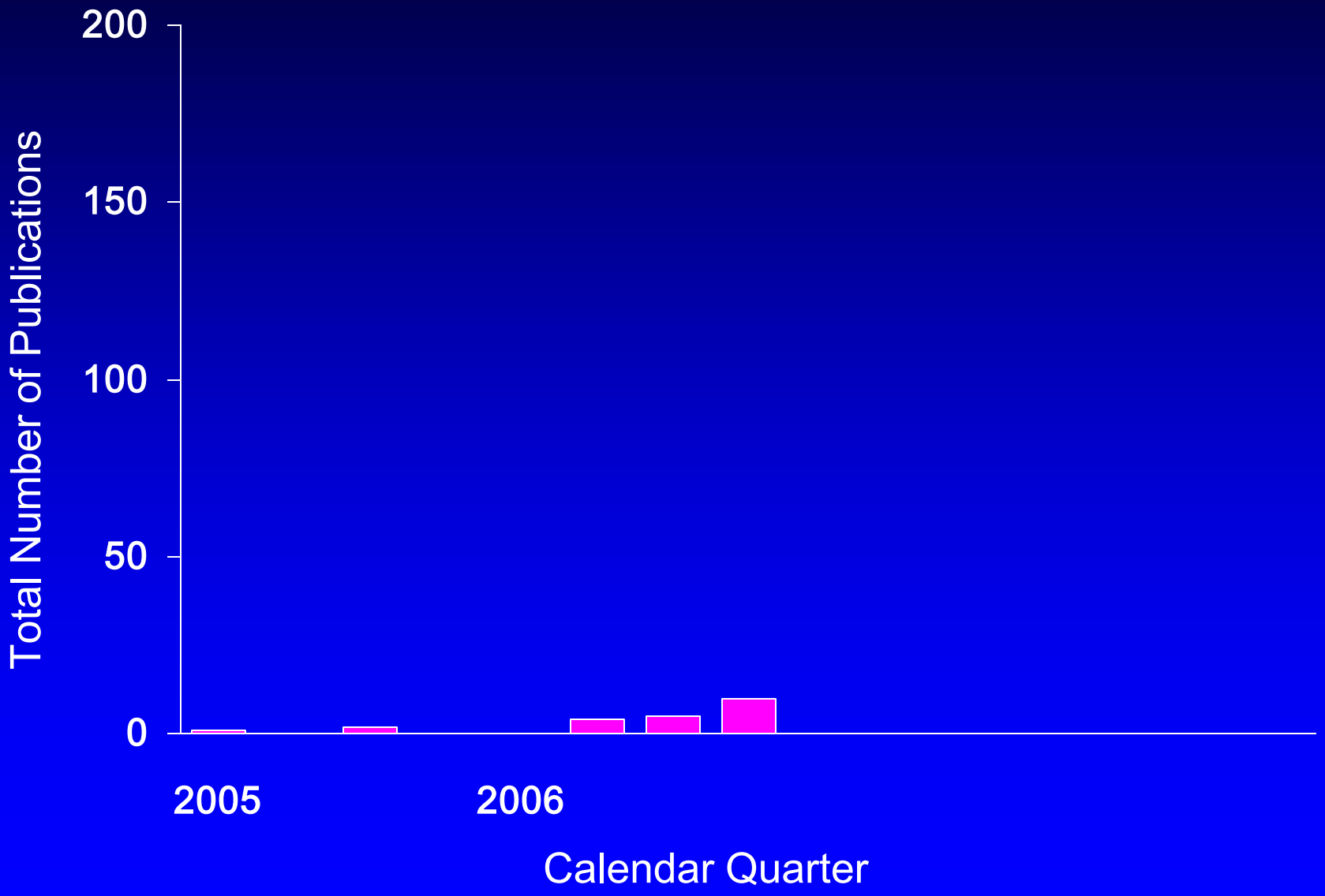

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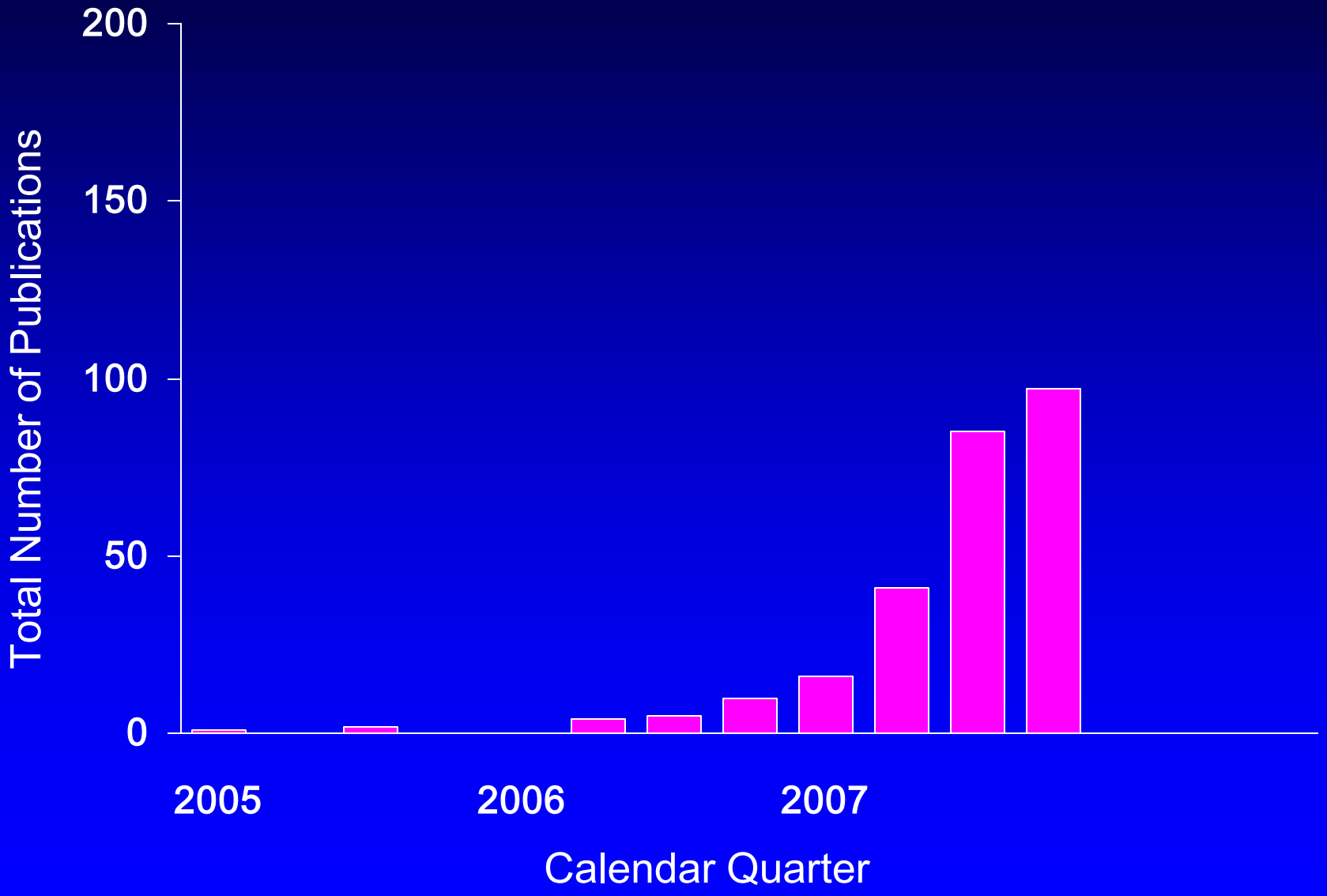

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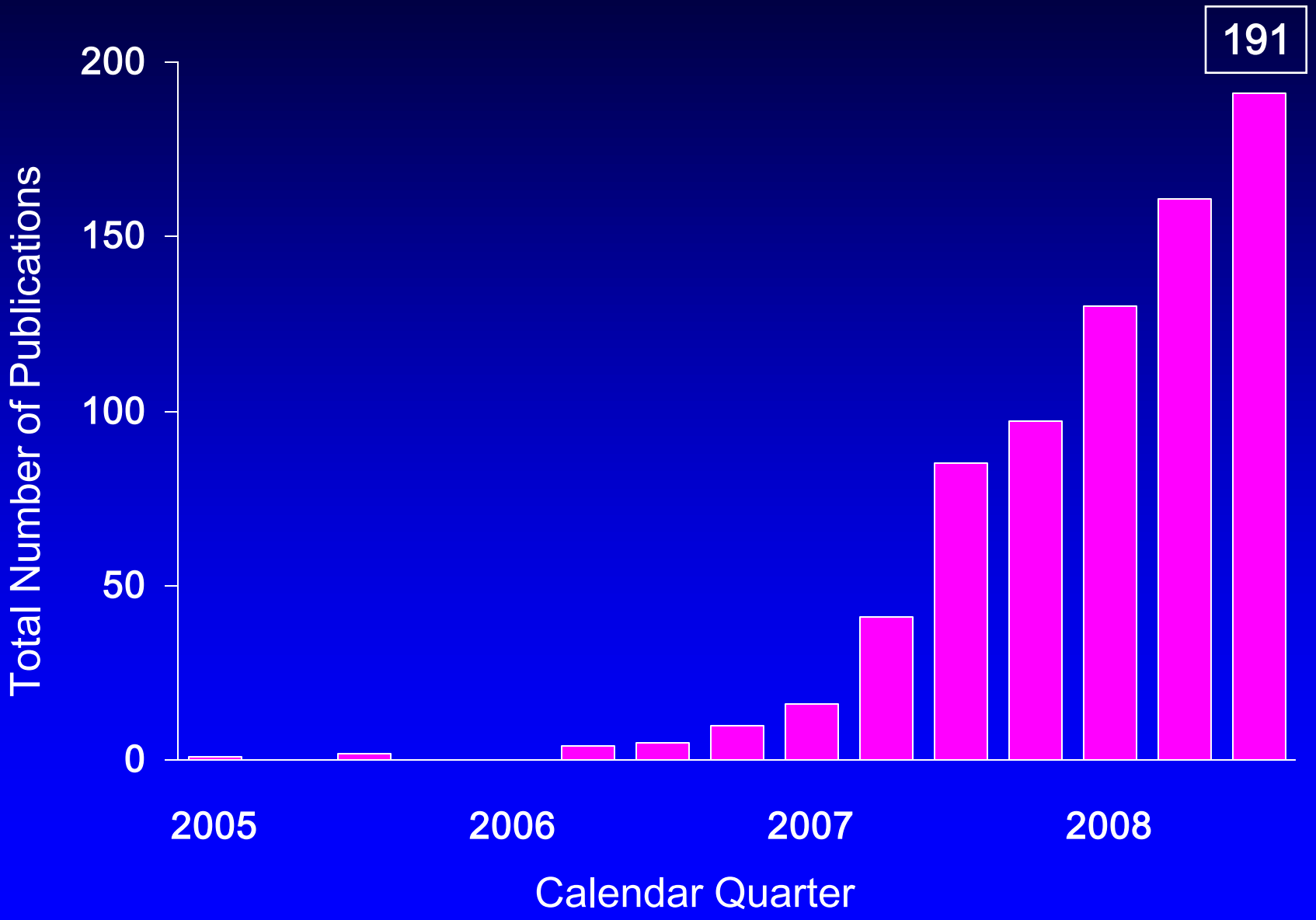
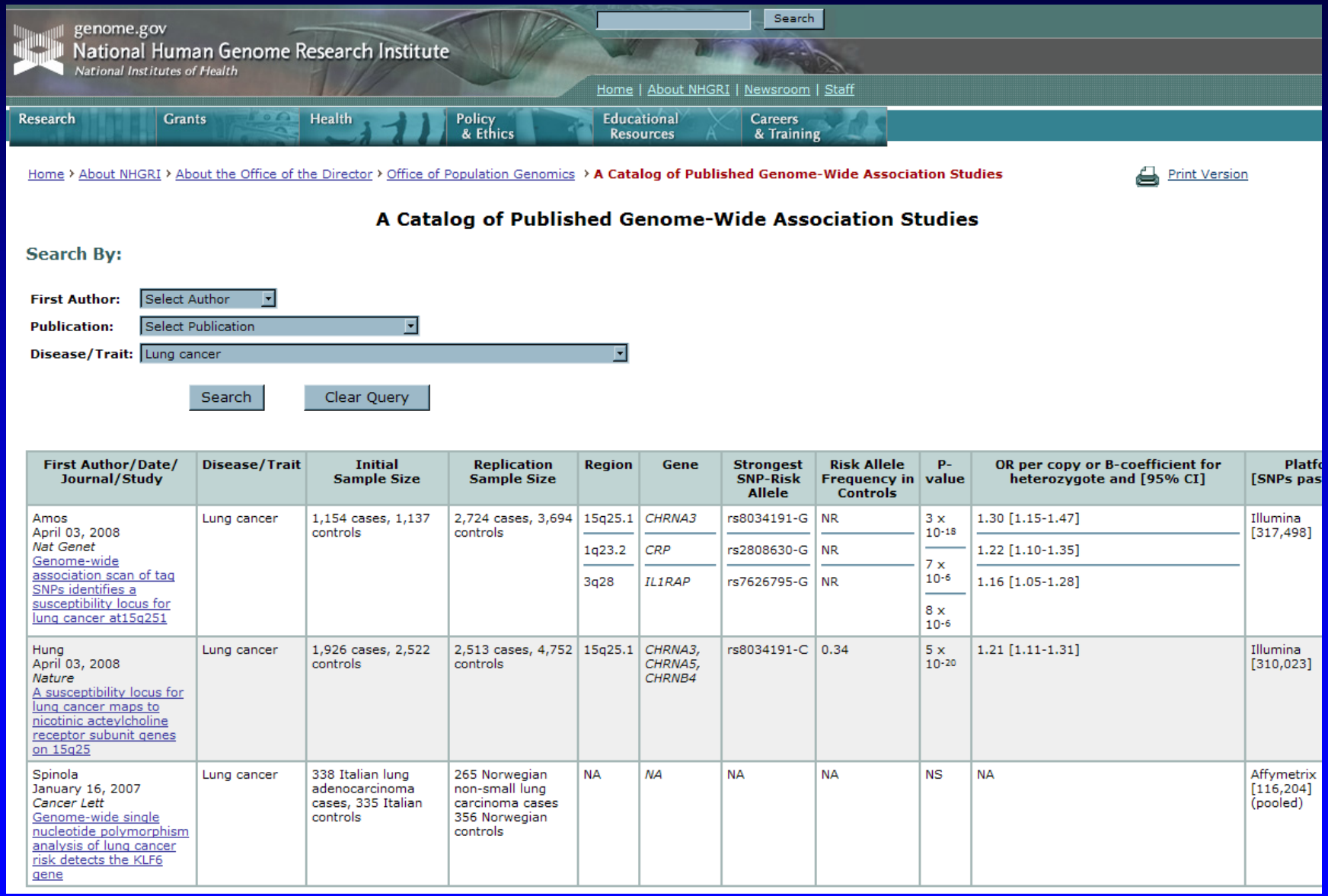


NHGRI Catalog of GWA Studies:
http://www.genome.gov/gwastudies/



genome.gov
National Human Genome Research Institute
National Institutes of Health

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Home › About NHGRI › About the Office of the Director › Office of Population Genomics › A Catalog of Published Genome-Wide Association Studies

Print Version

A Catalog of Published Genome-Wide Association Studies

Search By:

First Author: Select Author

Publication: Select Publication

Disease/Trait: Lung cancer

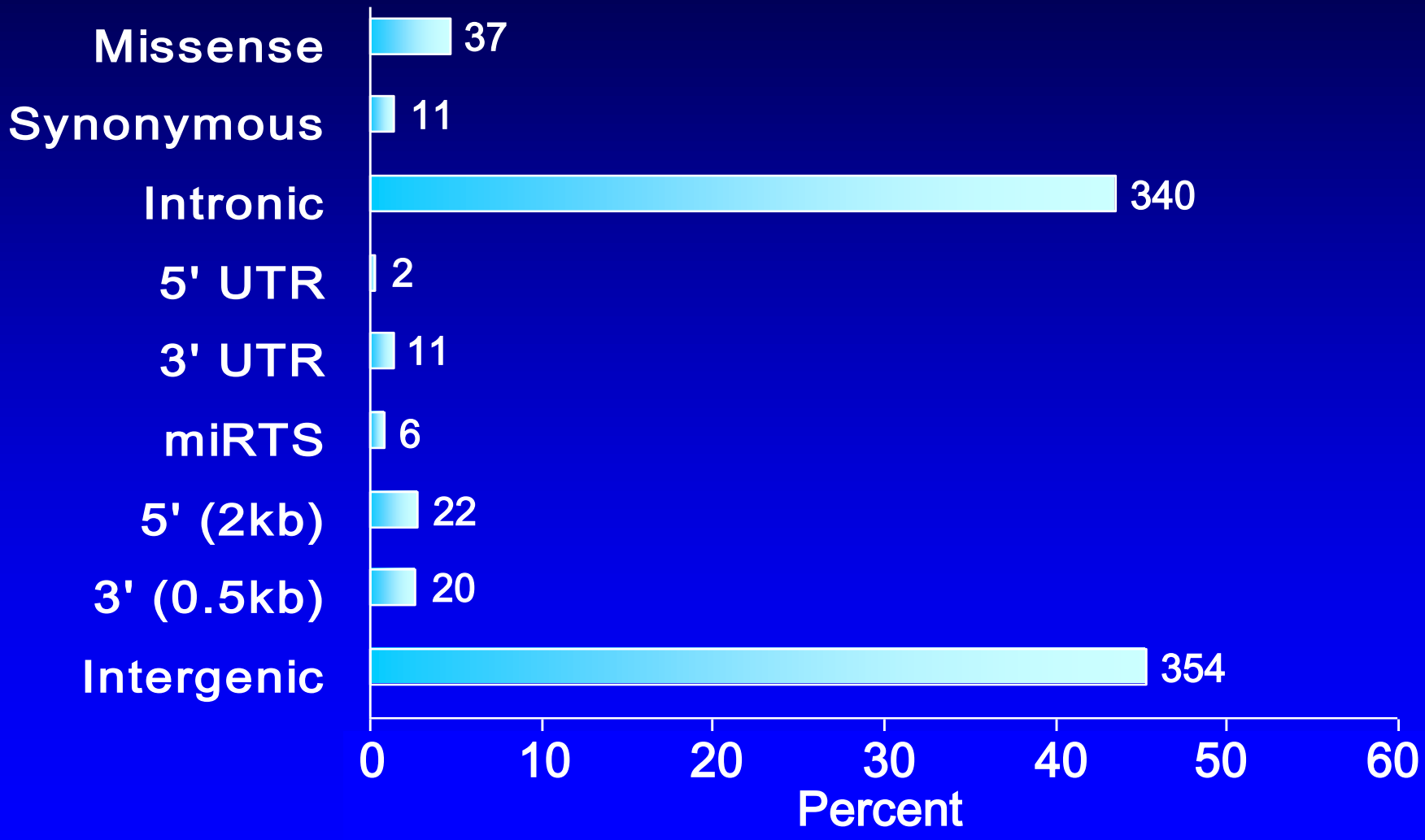
Search | Clear Query

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]	Platfo [SNPs pas
Amos April 03, 2008 *Nat Genet* Genome-wide association scan of tag SNPs identifies a susceptibility locus for lung cancer at15q251	Lung cancer	1,154 cases, 1,137 controls	2,724 cases, 3,694 controls	15q25.1 1q23.2 3q28	*CHRNA3* *CRP* *IL1RAP*	rs8034191-G rs2808630-G rs7626795-G	NR NR NR	3 x 10^{-18} 7 x 10^{-6} 8 x 10^{-6}	1.30 [1.15-1.47] 1.22 [1.10-1.35] 1.16 [1.05-1.28]	Illumina [317,498]
Hung April 03, 2008 *Nature* A susceptibility locus for lung cancer maps to nicotinic acetylcholine receptor subunit genes on 15q25	Lung cancer	1,926 cases, 2,522 controls	2,513 cases, 4,752 controls	15q25.1	*CHRNA3, CHRNA5, CHRNB4*	rs8034191-C	0.34	5 x 10^{-20}	1.21 [1.11-1.31]	Illumina [310,023]
Spinola January 16, 2007 *Cancer Lett* Genome-wide single nucleotide polymorphism analysis of lung cancer risk detects the KLF6 gene	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)

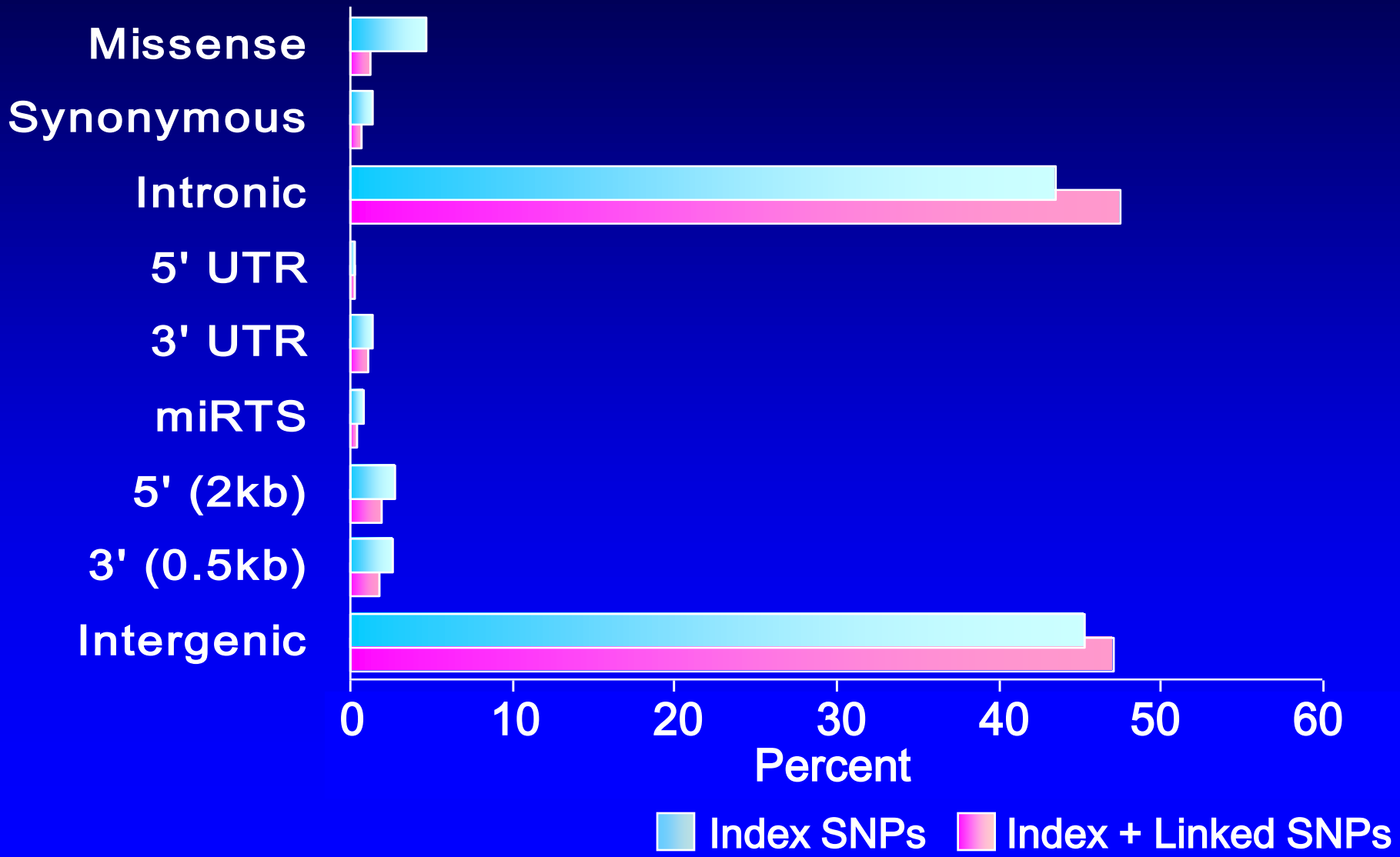
NHGRI GWA Catalog - Objectives

- Identify and track all GWA publications attempting to assay ≥ 100,000 SNPs
- Extract key information regarding associations
- Provide widely as scientific resource, including downloadable datafile
- Seek commonalities across associations genome-wide rather than disease by disease
- Describe approach clearly so others can replicate or expand upon it
- Maintain consistency in approach
- Adapt to evolving technologies: CNVs?

Functional Classification of 782 Index SNPs Associated with Complex Traits



Functional Classification of 782 Index SNPs and 4,623 Index + Linked SNPs



Functional Classes (%) of Linked and Index SNPs vs Randomly-Drawn HapMap SNPs

Functional Class	Index	Linked	HapMap	P-value*
Missense	4.7	1.3	0.6	2×10^{-6}
Synonymous	1.4	0.7	0.5	0.05
Intronic	43.5	47.5	37.5	6×10^{-38}
5' UTR	0.3	0.3	0.1	0.05
3' UTR	1.4	1.0	0.9	0.23
miRTS	0.8	0.5	0.3	0.12
5' (2kb)	2.8	2.0	1.1	2×10^{-7}
3' (0.5kb)	2.6	1.8	1.2	3×10^{-4}
Intergenic	45.3	47.0	58.1	4×10^{-59}

* Multiple comparisons correction $p_{threshold} = 0.006$.

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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*
Crohn's Disease	*ATG16L1*

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Multiple Sclerosis	*IL7R*	Type 1 Diabetes
Sarcoidosis	*C10orf67*	Celiac Disease
RA, T1DM	*PTPN2, PTPN22*	Crohn's

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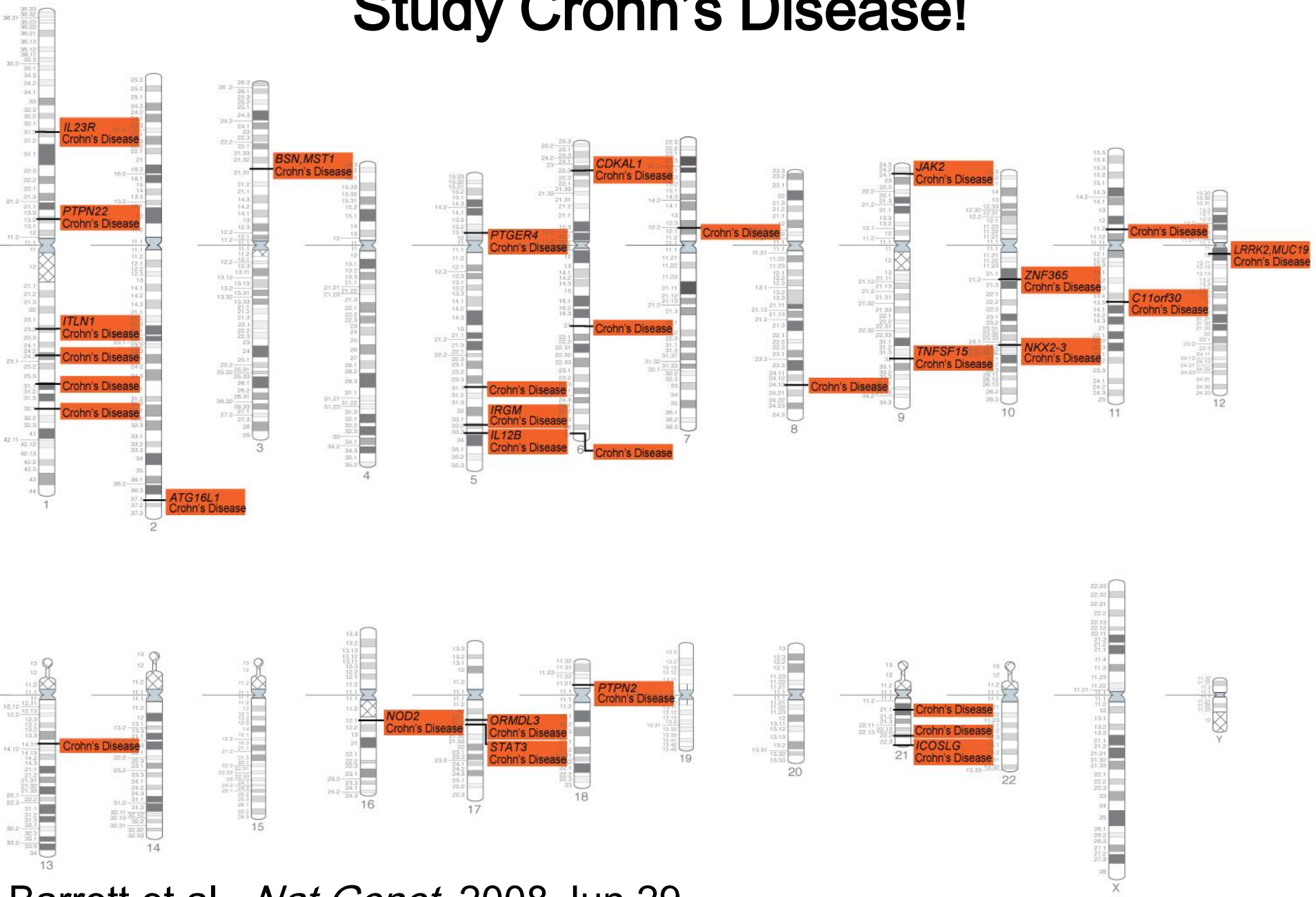
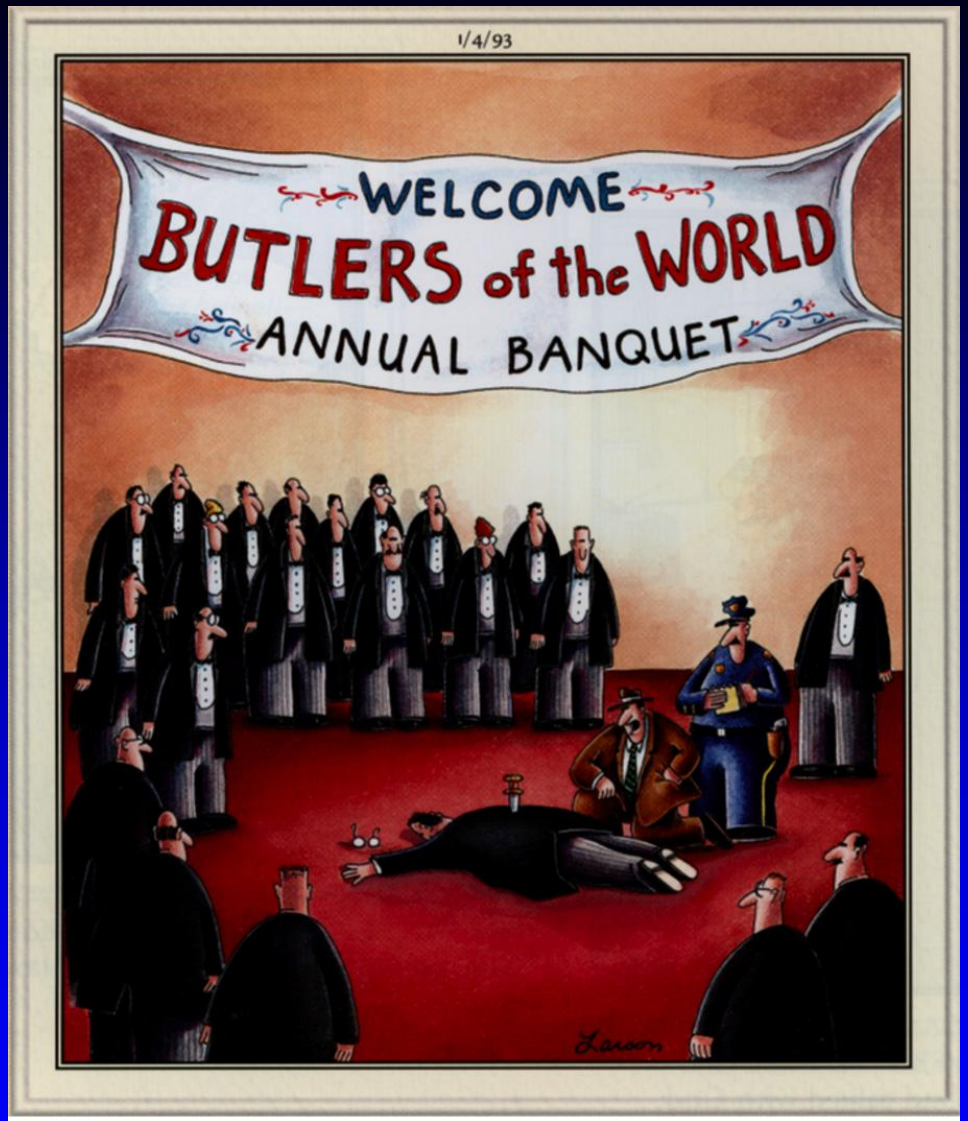
Study Crohn's Disease!



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



"God, Collings, I hate to start a Monday with a case like this."

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

nature genetics
volume 22 no. 1 may 1999

Freely associating

May 1999

Editorial: Once and Again—Issues Surrounding Replication in Genetic Association Studies

PERSPECTIVE

The Future of Association Studies: Gene-Based Analysis and Replication

B

Editorial

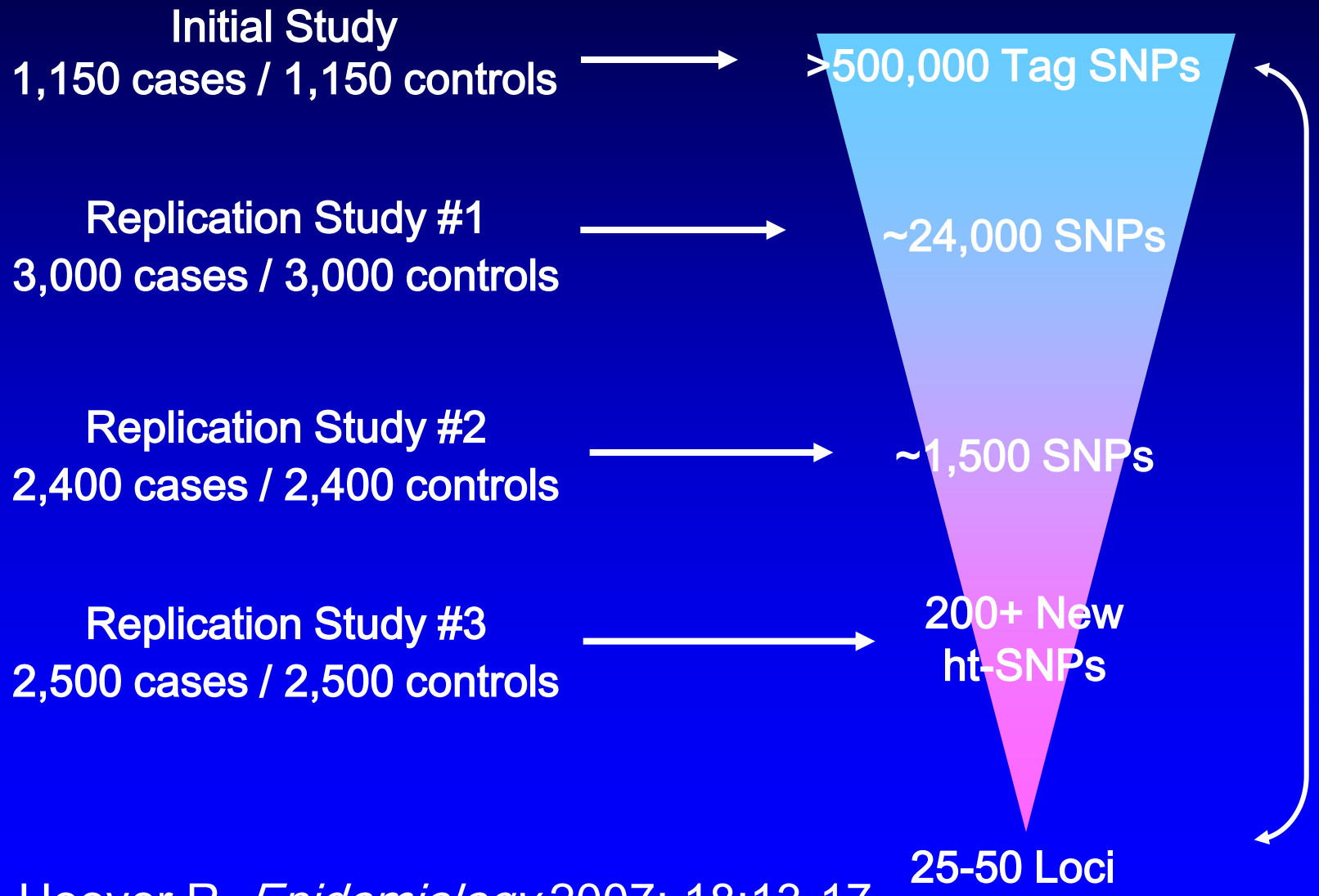
Replication Publication

Statistical false positive or true disease pathway?

John A Todd

Nat Genet July 2006

Replication Strategy for Prostate Cancer Study in CGEMS



Hoover R, *Epidemiology* 2007; 18:13-17.

GWA Efforts at NHGRI and NIH-wide

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Genetic Association Information Network (GAIN) Analysis Workshop III

Philadelphia Marriott Downtown
November 10 - 11, 2008

FOUNDATION FOR THE National Institutes of Health

Partners for Innovation, Discovery, Life

Overview

The Genetic Association Information Network (GAIN) is a public-private partnership of the Foundation for the National Institutes of Health, that currently involves the National Institutes of Health (NIH), Pfizer, Affymetrix, Perlegen Sciences, Abbott, and the Eli and Edythe Broad Institute - of MIT and Harvard University. GAIN is taking the next step in the search to understand the genetic factors influencing risk for complex diseases. Through a series of whole genome association studies, using samples from existing case-control studies of patients with common diseases, GAIN will contribute to the identification of genetic pathways that make us more susceptible to these diseases and thus facilitate discovery of new molecular targets for prevention, diagnosis, and treatment.

GAIN announced the selection of six major studies in common diseases for genotyping at our November 2006 GAIN Kickoff Meeting and Analysis Workshop, including studies in ADHD, diabetic nephropathy, major depression, psoriasis, schizophrenia, and bipolar disorder. Since then GAIN has completed genotyping on all six studies and made the resulting phenotype and genotype data available via the GAIN Database in dbGaP at the National Center for Biotechnology Information (NCBI) at NIH **(dbgap)**. The GAIN Analysis Workshop III will bring together the primary investigators and data analysts from these studies with genetics and data analysis experts from the scientific community to present the results of findings from analysis of the GAIN data, as well as related advances in strategies for analyzing specific genome-wide association data.

GWA-Related Efforts at NHGRI

The eMERGE Network

electronic Medical Records & Genomics

PhenX

consensus measures for Phenotypes and eXposures

Web Site Search

Home

Population Architecture using Genomics and Epidemiology (PAGE)

Part I Overview Information

Department of Health and Human Services

Participating Organizations

National Institutes of Health (NIH), (http://www.nih.gov)

Components of Participating Organizations

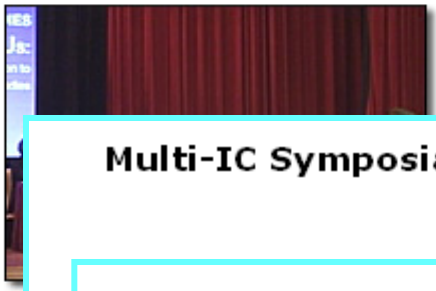
National Human Genome Research Institute (NHGRI), (http://www.genome.gov)

Title: Genome-wide Association Studies of Treatment Response in Randomized Clinical Trials – Study Investigators (U01)

Announcement Type

New

GWA-Related Efforts at NHGRI: Training



Genome-Wide Association Studies for the Rest of Us: Adding Genome-Wide Association to Population Studies

Multi-IC Symposia on Application of Genomic Technologies to Population-Based Studies at NIH Institutes and Centers

Genetics for Epidemiologists Application of Human Genomics to Population Sciences

Epidemiology for Researchers Performing Genetic/Genomic Studies

Natcher Auditorium, NIH Campus

Bethesda
July 18, 2008

Overview

Epidemiology for Researchers Performing Genetic/Genomic Studies, is a short course for investigators and trainees doing research in human genetics, particularly studies employing genomic analyses of samples from human populations. It was conducted by the Office of Population Genomics, NHGRI, on July 18, 2008, in Natcher Auditorium, Building 45, NIH campus.

The course consists of eight lectures and aims at familiarizing researchers studying the human genome with basic principles and potential pitfalls of epidemiology as applied to human genome research. It draws from traditional genetic epidemiology and statistical genetics, but emphasizes the application of genomic technologies to unrelated subjects in human populations. Focus is on the design, conduct, analysis and interpretation of the epidemiologic studies most feasible and appropriate to address the genomic questions of interest.

NIH-Wide Efforts in Gene Discovery and Translation

NATIONAL INSTITUTES OF HEALTH

Genes, Environment and Health Initiative (GEI)

U.S. Department of Health and Human Services

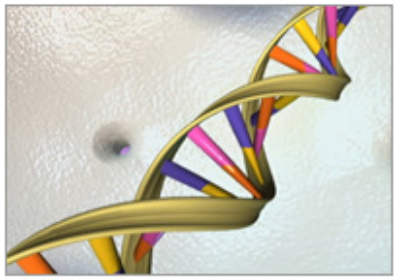
U.S. Department of Health and Human Services

NIH News

National Institutes of Health

NIH's Genes, Environment & Health Initiative Adds Six Studies

Scientists Will Search for Genetic Factors Underlying Stroke, Glaucoma, High Blood Pressure and Other Common Disorders



Bethesda, Md., Wed., Sept. 24, 2008 — The Genes, Environment and Health Initiative (GEI) of the National Institutes of Health (NIH) today awarded grants, estimated to be up to $5.5 million over two years, for six studies aimed at finding genetic factors that influence the risks for stroke, glaucoma, high blood pressure, prostate cancer and other common disorders.

The grantees will use a genome-wide association study to rapidly scan markers across the complete sets of DNA, or genomes, of large groups of people to find genetic variants associated with a particular disease, condition or trait.

"Genome-wide association studies are helping us take major strides towards identifying the genetic variants associated with common diseases," said National Human Genome Research Institute (NHGRI) Acting Director Alan E. Guttmacher, M.D., who is co-chair of the GEI coordinating committee. "This initiative will yield valuable information about the biological pathways that lead to health and disease and about how genetic variants, environmental factors and behavioral choices interact to influence disease risk. Such information is vital to our efforts to develop more personalized approaches to health care."

NIH-Wide Efforts in Gene Discovery and Translation

Part I Overview Information

Receipt Date: 10/17/2008

Part I Overview Information

Receipt Date: 11/25/2008

Part I Overview Information

Receipt Date: 12/1/2008

Department of Health and Human Services

Participating Organizations

National Institutes of Health (NIH) (http://www.nih.gov/)

Components of Participating Organizations

This FOA is developed as a part of the NIH-wide Genes, Environment, and Health Initiative (GEI). All NIH Institutes and Centers participate in NIH-wide initiatives. This FOA will be administered by the National Cancer Institute (NCI, http://www.cancer.gov/) on behalf of the NIH (http://www.nih.gov)

Title: Replication and Fine-Mapping Studies for the Genes Environment and Health Initiative (GEI)(R01)

Announcement Type

New

Request For Applications (RFA) : RFA-CA-09-003