

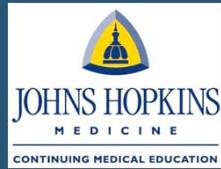


**Human  
The Genomics Landscape  
Circa 2016**

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**Eric Green, M.D., Ph.D.  
Director, NHGRI**

 National Human Genome Research Institute 



*Current Topics in Genome Analysis 2016*

*Eric Green, M.D., Ph.D.*

*No Relevant Financial Relationships with  
Commercial Interests*

  
NATIONAL HUMAN GENOME RESEARCH INSTITUTE  
Division of Intramural Research

The collage is a visual summary of the field of genomics and genetics over two decades. It features a central DNA helix icon with a lightbulb, symbolizing the discovery and illumination of genetic information. The timeline on the left shows major milestones from 1990 to 2016. The right side is filled with logos for various international genome projects, scientific societies (e.g., ACMG, ISMB), and journals (e.g., Nature, Science, PNAS). Numerous small images of researchers, laboratory equipment, and biological samples are scattered throughout, illustrating the breadth of genomic research.

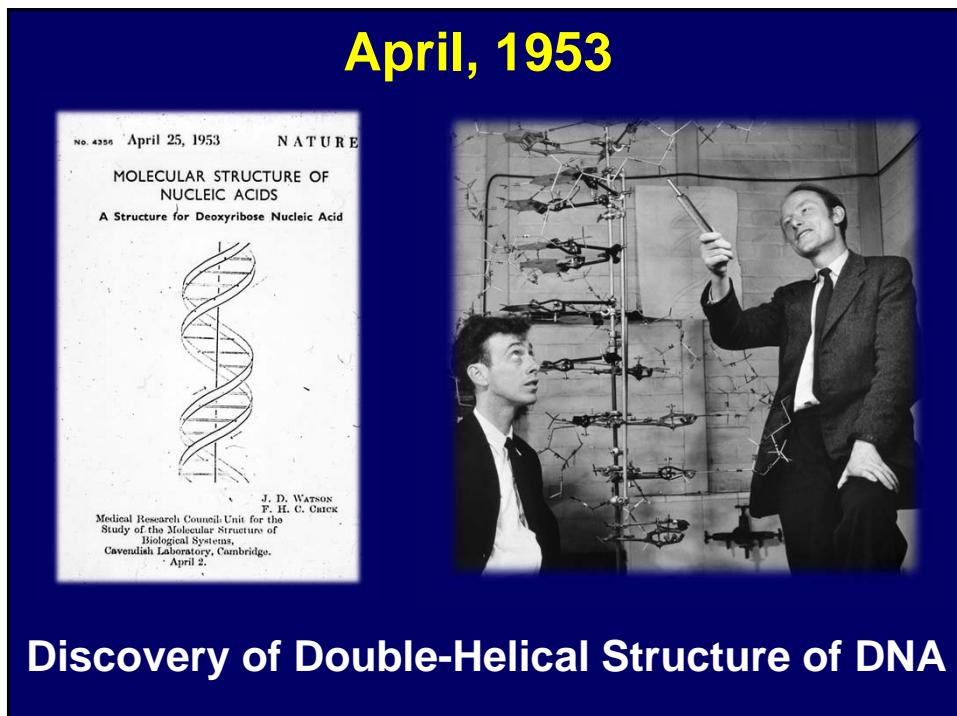
**I. Historical Context for Genomics**  
**II. Major Achievements since the Human Genome Project**  
**III. The Human Genomics Landscape: 2016 and Beyond**

>> Goal: Place Other Speakers into a Broader Context <<

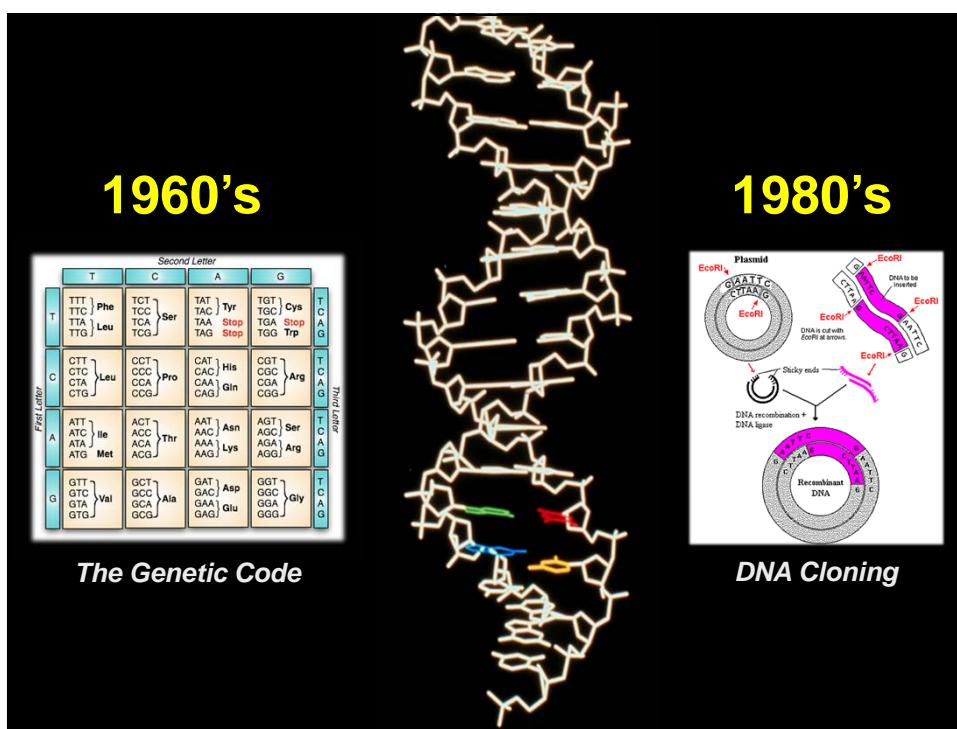
### Foundational Milestones in Genetics & Genomics

This timeline highlights the four most fundamental discoveries in the field of genetics:

- Mendel (1865):** Portrayed as a priest, with his original handwritten notes on inheritance laws.
- Miescher (1871):** Portrayed as a scientist, with his handwritten notes on the discovery of nucleic acid.
- Avery (1944):** Portrayed as a scientist, with a diagram of the Avery-MacLeod-McCarty experiment showing the transformation of live bacteria by heat-killed pneumococcus bacteria.
- Watson & Crick (1953):** Portrayed as co-authors of the DNA double helix model, with the iconic Nature magazine cover of their paper.



## Discovery of Double-Helical Structure of DNA



## The Origin of “Genomics”: 1987

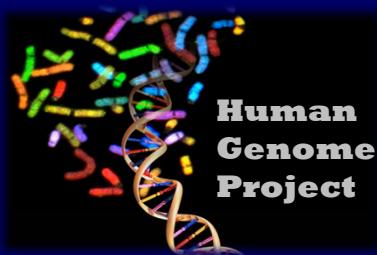
### EDITORIAL

#### A New Discipline, A New Name, A New Journal

*Genomics* (1987)

“For the newly developing discipline of [genome] mapping/sequencing (including the analysis of the information), we have adopted the term GENOMICS...

## Human Genome Project: 1990-2003



## Twenty-five years of big biology

The Human Genome Project, which launched a quarter of a century ago this week, still holds lessons for the consortium-based science it ushered in, say Eric D. Green, James D. Watson and Francis S. Collins.

*Nature* (2015)



## Myriad Applications of Genomics

**G Disease**

**CATG TGTTGG**

### Health, Disease, & Medicine

## Genomic Medicine

An emerging medical discipline that involves using genomic information about an individual as part of their clinical care (e.g., for diagnostic or therapeutic decision-making) and the other implications of that clinical use



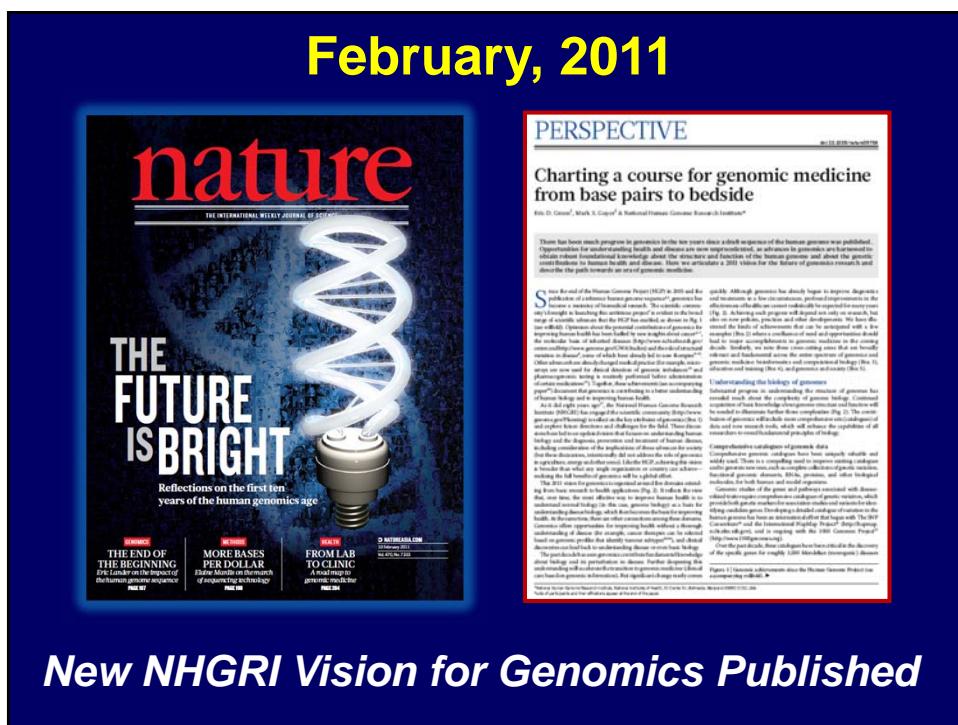
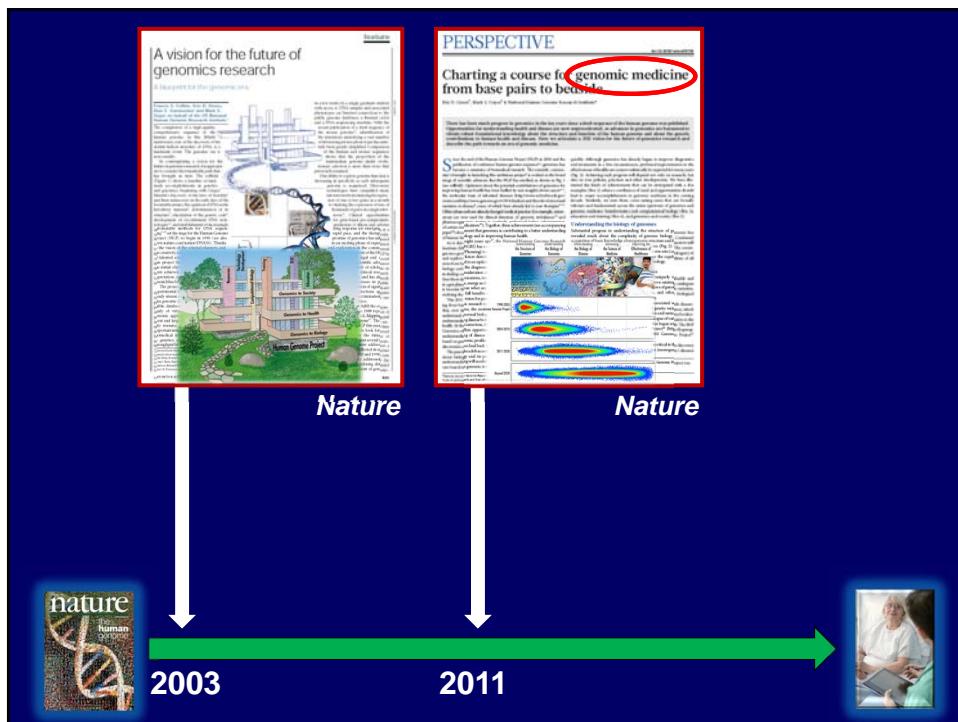
## The Path to Genomic Medicine

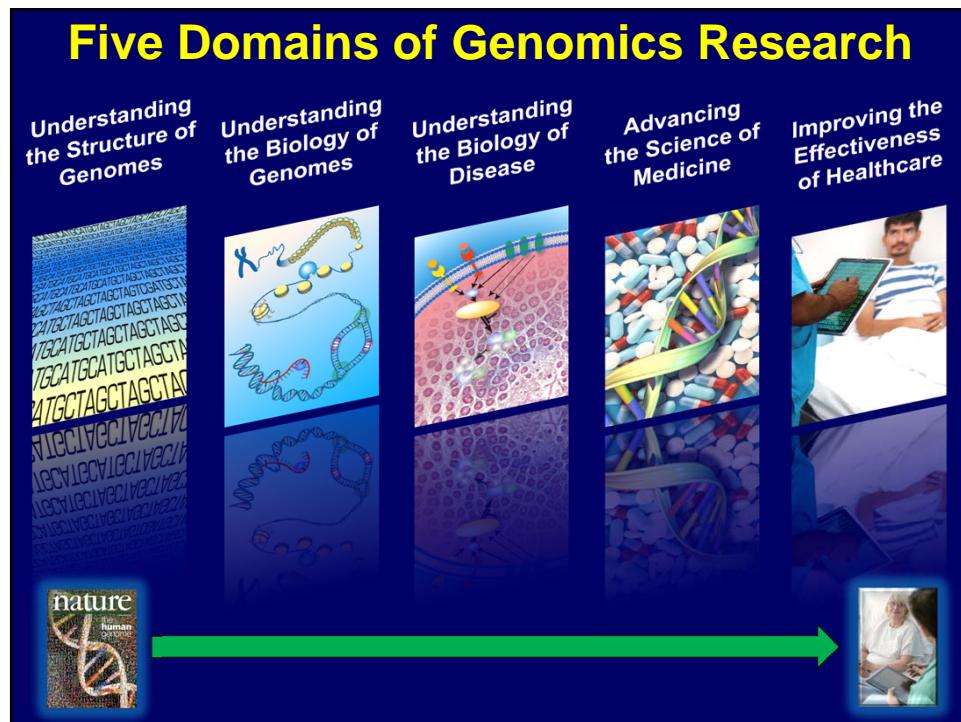


Human  
Genome  
Project



Realization of  
Genomic  
Medicine





A vision for the future of genomics research

A blueprint for the genomic era.

Francine S. Collins, Eric D. Green, Alan E. Guttmacher and Mark S. Giger on behalf of the US National Human Genome Research Institute

The completion of a high-quality, comprehensive sequence of the human genome, just one anniversary year of the discovery of the double helical structure of DNA, is a landmark event. The genomic era is now a reality.

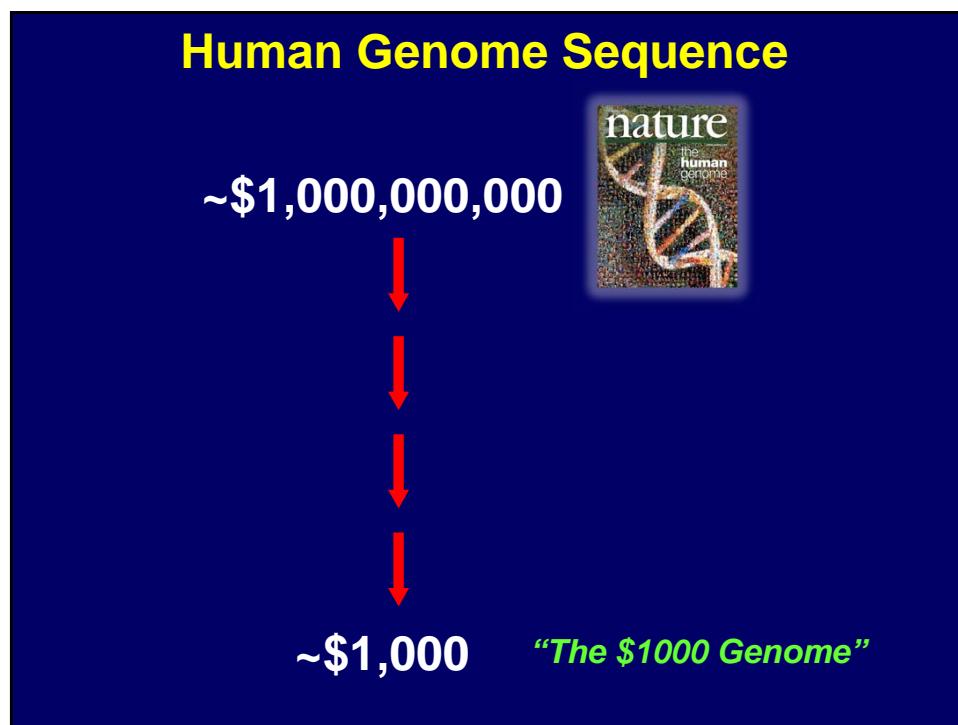
In contemplating a vision for the

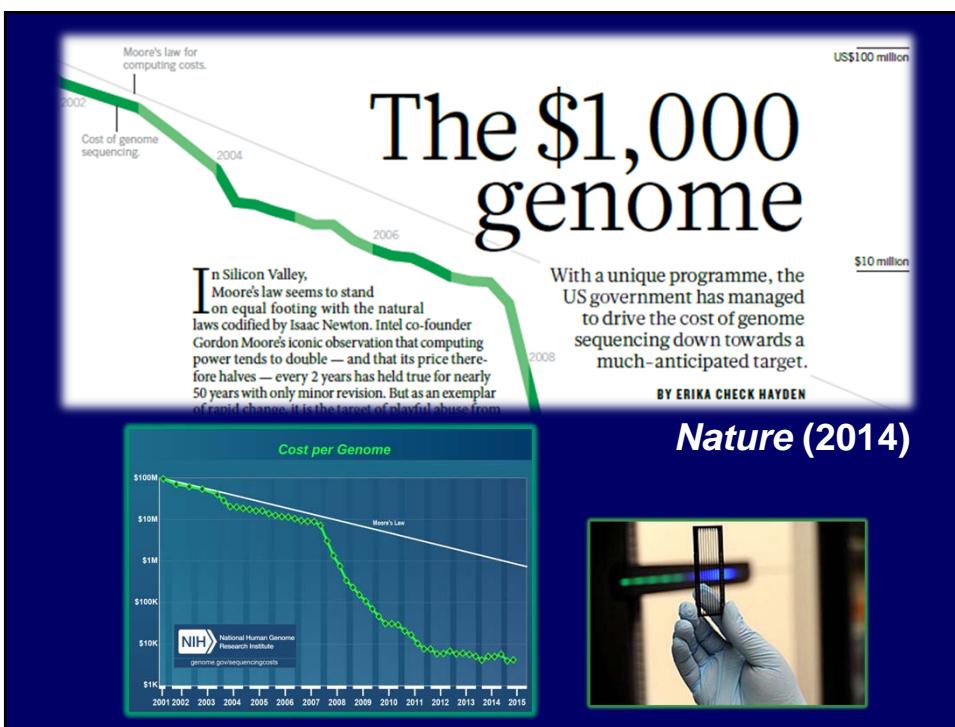
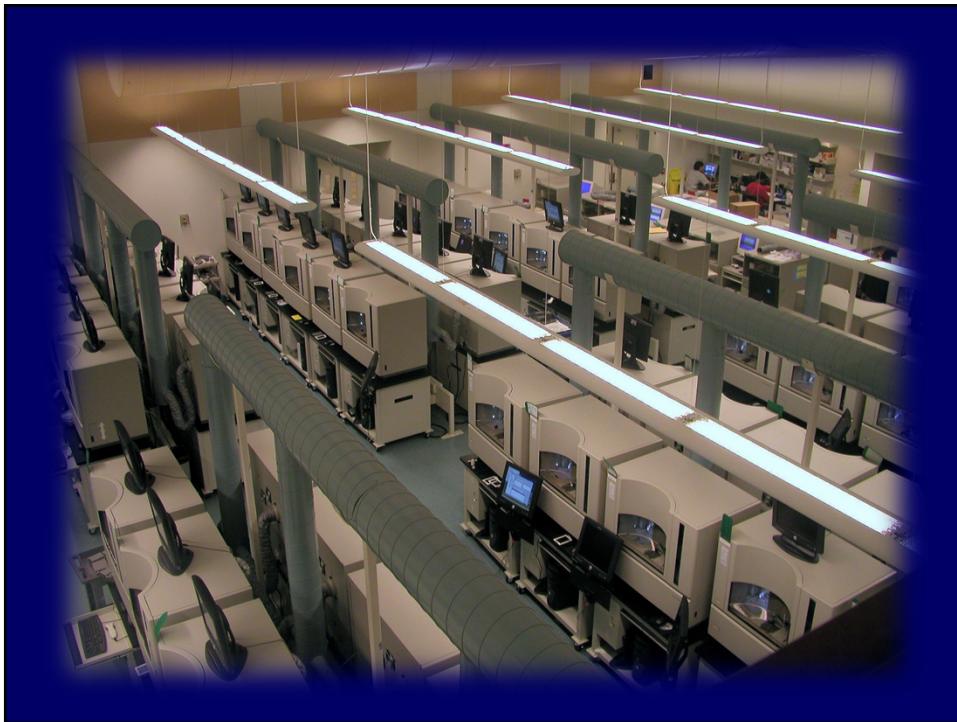
feature

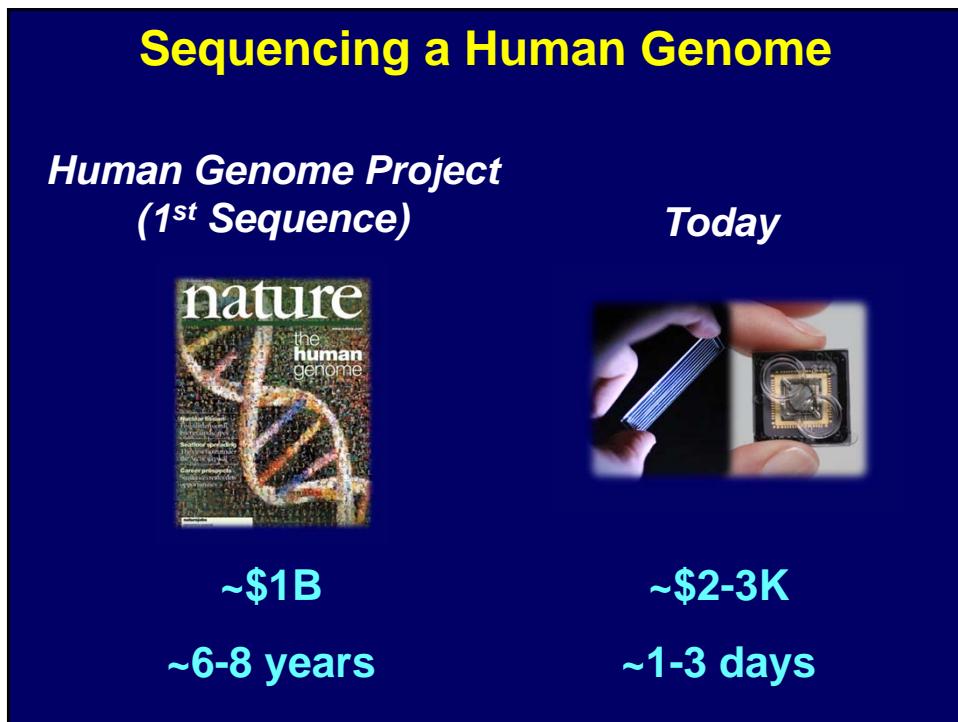
in a few weeks by a single graduate student with access to DNA samples and associated clinical information, a computer, some public genome databases, a thermal cycler and a DNA sequencing machine. With the completion of the genome sequence of the mouse genome, identification of interesting genes and phenotypes has similarly become greatly simplified. Comparison of the mouse and human genomes shows that the proportion of the mammalian genome under evolution

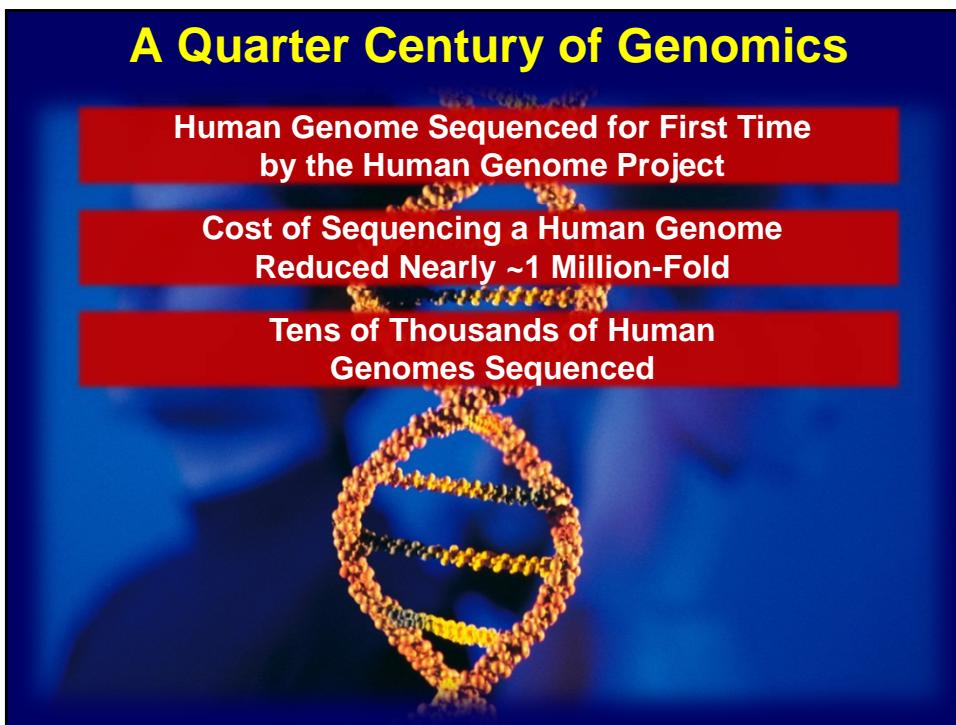
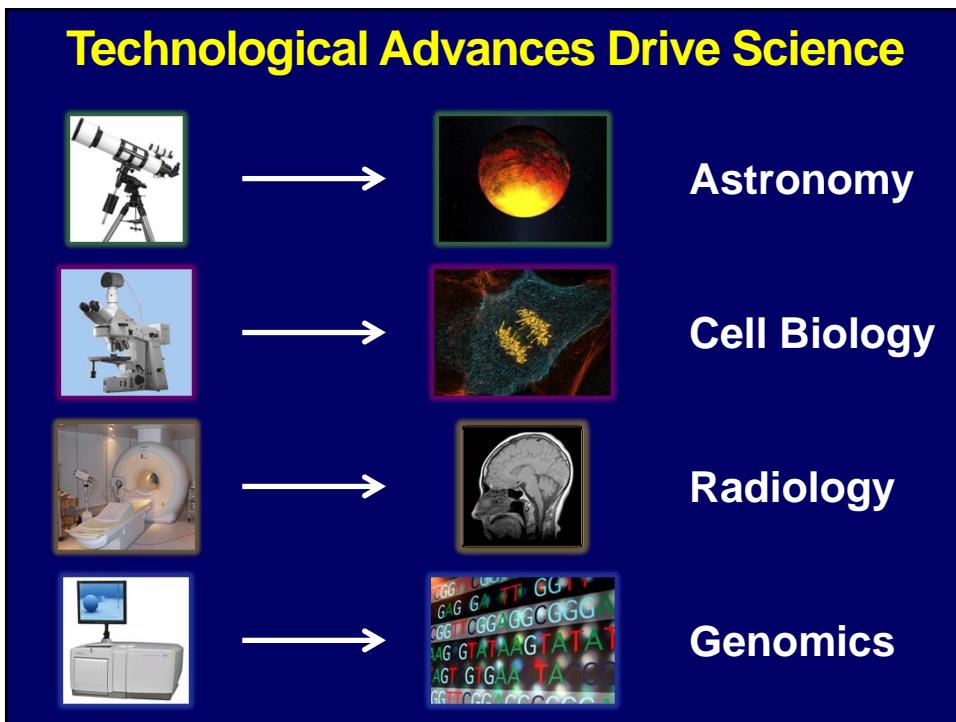
“...‘technological leaps’ that seem so far off as to be almost fictional but which, if they could be achieved, would revolutionize biomedical research and clinical practice.

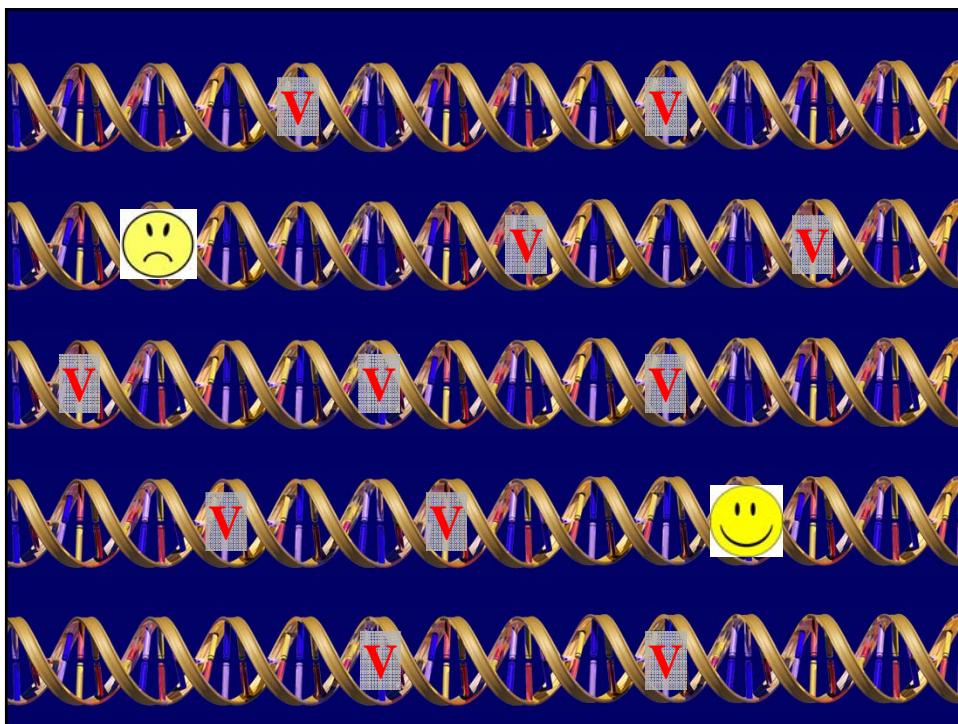
[For example,]...the ability to sequence DNA at costs that are lower by four to five orders of magnitude than the current cost, allowing a human genome to be sequenced for \$1,000 or less.”











**International HapMap Project**

The International HapMap Consortium\*

27 October 2005 | www.nature.com/nature/ | 510 | THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

**nature**

INSIDE  
 Why do we sleep?

OPTOELECTRONICS  
 Germanium boost for silicon chips

LAW OF THE JUNGLE  
 Don't ask a chimpanzee for help

MEN OF LETTERS  
 If Darwin and Einstein had e-mail...

**THE HAPMAP PROJECT**

Chapter and verse on human genetic variation

NATUREJOBS  
 Biodefence boom

A haplotype map of the human genome

The International HapMap Consortium\*

Inherited genetic variation has a critical but as yet largely uncharacterized role in human disease. Here we report a public database of common variation in the human genome: more than one million single nucleotide polymorphisms (SNPs) for which accurate and complete genotypes have been obtained in 269 DNA samples from four populations. The average minor allele frequency is 0.09, and the average linkage disequilibrium with all other SNPs in each population is 0.94. We show that the commonest genes with an average maximum  $r^2$  of 0.95 in African Americans have an average maximum  $r^2$  of 0.8 in European Americans. These data document the generality of recombination hotspots, a block-like structure of linkage disequilibrium and low linkage disequilibrium between SNPs, and the presence of long-range linkage disequilibrium. We show how the HapMap resource can guide the design and analysis of genome association studies, shed light on structural variation and recombination, and identify loci that may have been subject to natural selection during human evolution.

**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) generated in 270 individuals from four geographically diverse populations and includes 25–35% of common SNP variation in the populations. The map is estimated to capture approximately 90% linkage disequilibrium with all other SNPs in each population. The average minor allele frequency is 0.09 and 0.94 across all populations. We show that the commonest genes with an average maximum  $r^2$  of up to 0.8 in African and up to 0.95 in European Americans have an average maximum  $r^2$  of 0.95 in East Asian populations. 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 SNPs are shared between individuals from different populations. We find that linkage disequilibrium distances vary systematically around genes and between genes of different function. Finally, we demonstrate increased differentiation at non-synonymous, compared to synonymous, SNPs, resulting from systematic differences in the strength of natural selection between populations.

**Integrating common and rare genetic variation in diverse human populations**

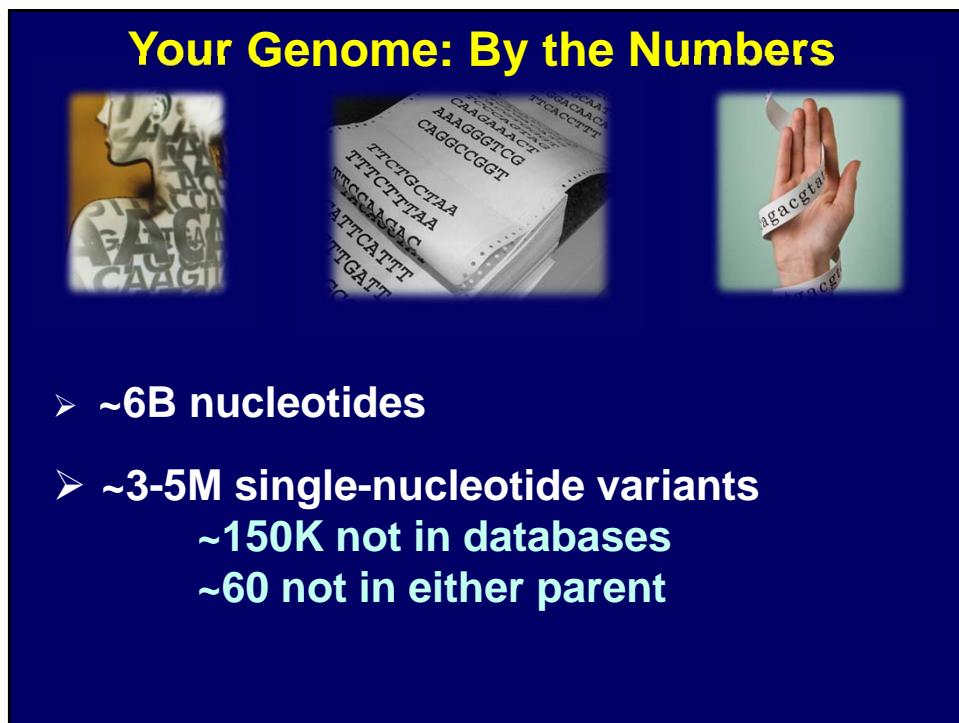
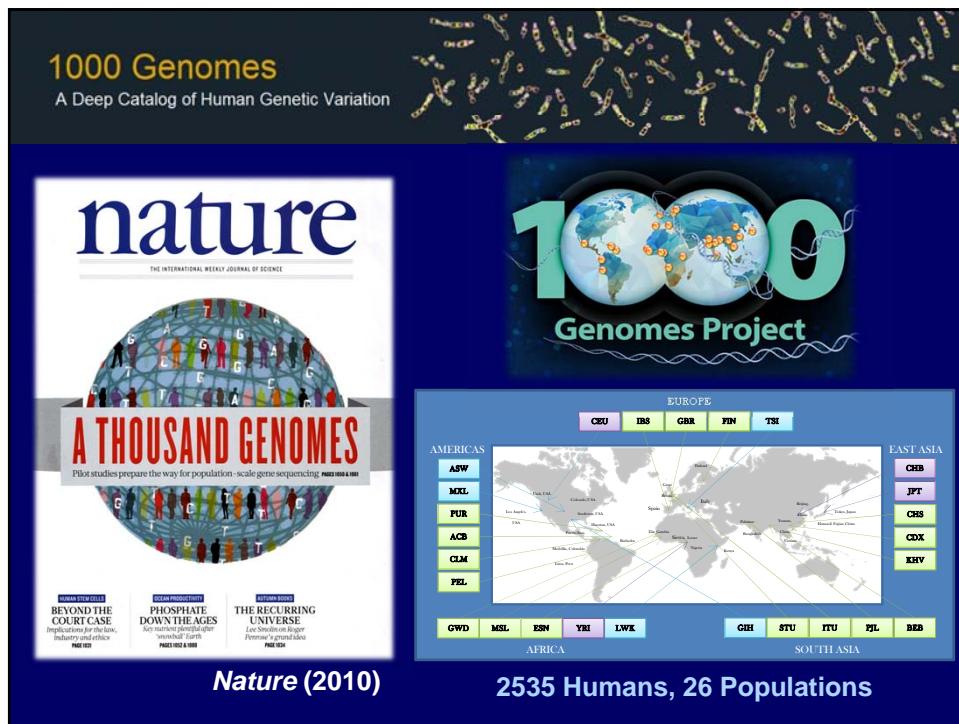
The International HapMap 3 Consortium\*

Despite great progress in identifying genetic variants that influence human disease, most heritable risk remains unexplained. A major challenge is to extend genome-wide studies that fully examine less common alleles in populations with a wide range of ancestry. To inform the design and interpretation of such studies, we generated 1.6 million common single nucleotide polymorphisms (SNPs) in 1808 reference individuals from 11 global populations, and sequenced two 100-kilobase regions of the genome for 100 individuals. This dataset includes 1.3 million SNPs with a minor allele frequency of 1–5%, and 1.3 million SNPs and copy number polymorphisms (CNPs). We characterized population-specific differences among low-frequency variants and found evidence for positive selection on some variants. We identified 1000 new common CNPs, including 100 CNPs with a minor allele frequency of >5%, and demonstrated the feasibility of mapping newly discovered CNPs and SNPs. This expanded public resource of genome variants in global populations supports deeper interpretation of genomic variation and its role in human disease, and serves as a step toward a high-resolution map of the landscape of human genetic variation.

**2005**

**2007**

**2010**



# A Quarter Century of Genomics

## Human Genome Sequenced for First Time by the Human Genome Project

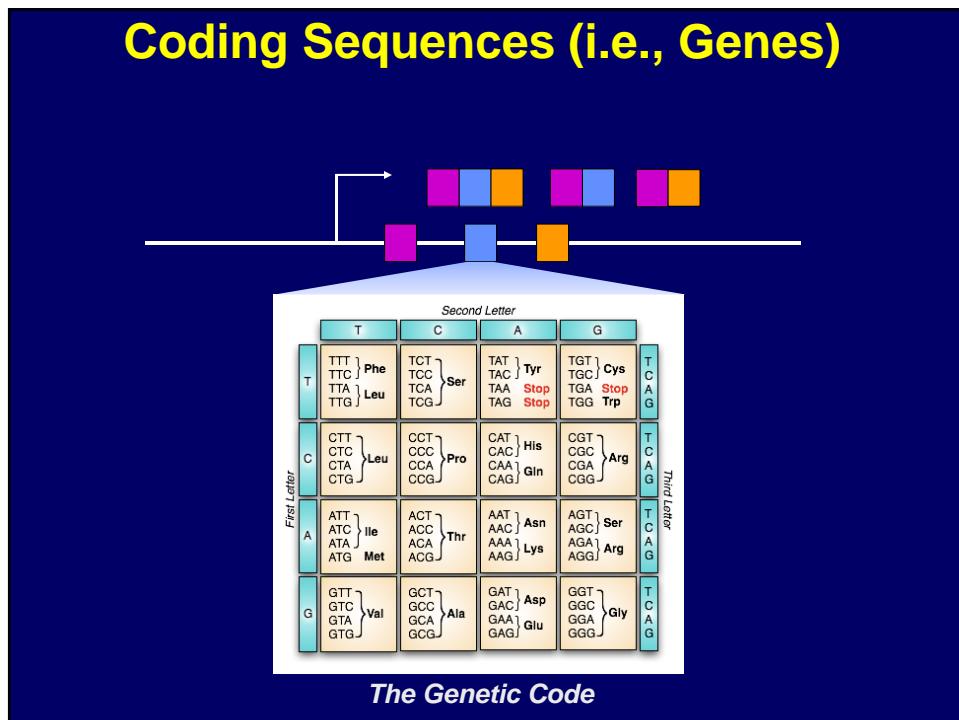
# Cost of Sequencing a Human Genome Reduced Nearly ~1 Million-Fold

## Tens of Thousands of Human Genomes Sequenced

# Profound Advances in Understanding How the Human Genome Functions

**~3,000 bp (0.0001%) of Human Genome Sequence**

TGCGCCGGAACATTTCGGCTCTAAGGCTGTATTTGATATACGAAAGGCACATTTCTCCCTTCAAAATGCACCTTGCAAAGCTAACAG  
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 AGAACATCGGGAAAGGGAGGTGCGGGGCGCGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 GAAAGCCCGTAGACGAAATTGGGGCCGACGGCAGCACCTGGGTTTAACTCGGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
 TGTGGGAGTAGGTGGGTGGGGAAATTTGGAGGAAATGGACATACAGGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
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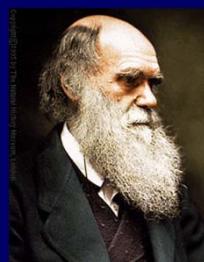


**~3,000 bp (0.0001%) of Human Genome Sequence**



**"It is not the strongest of the species that survives, nor the most intelligent that survives. It is the one that is the most adaptable to change."**

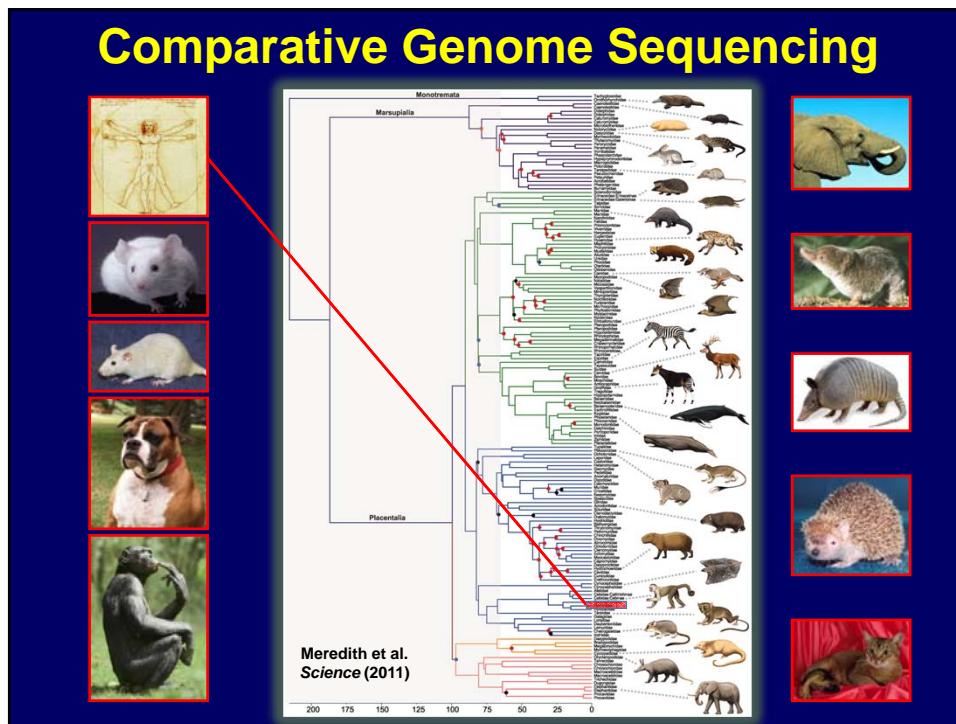
(Attributed to Darwin)



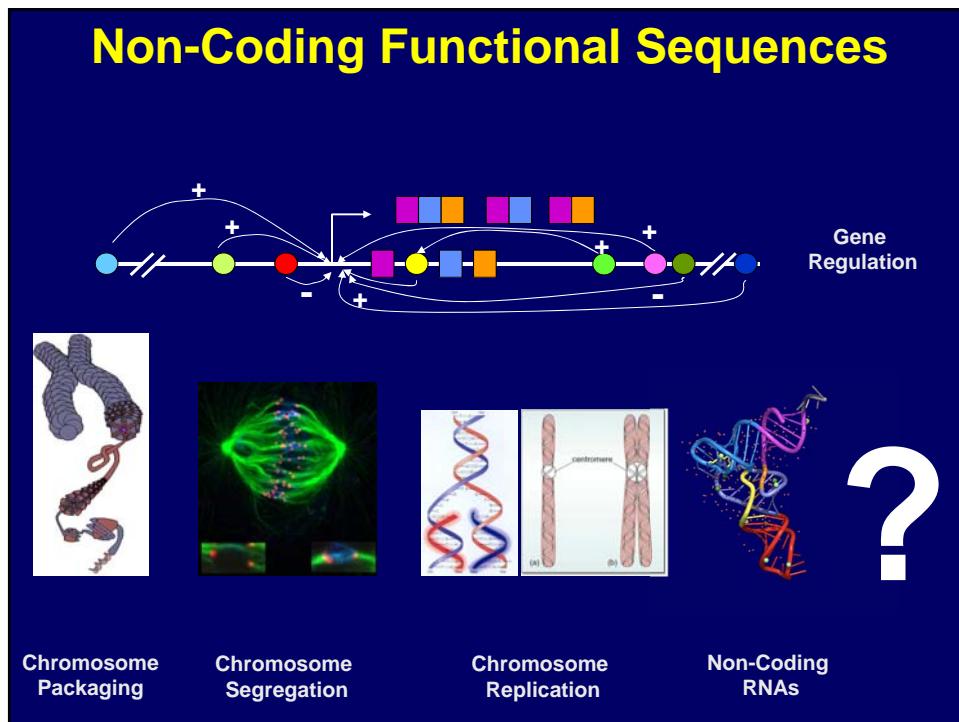
Charles Darwin (1809-1882)

**"For the last three and a half billion years, evolution has been taking notes."**

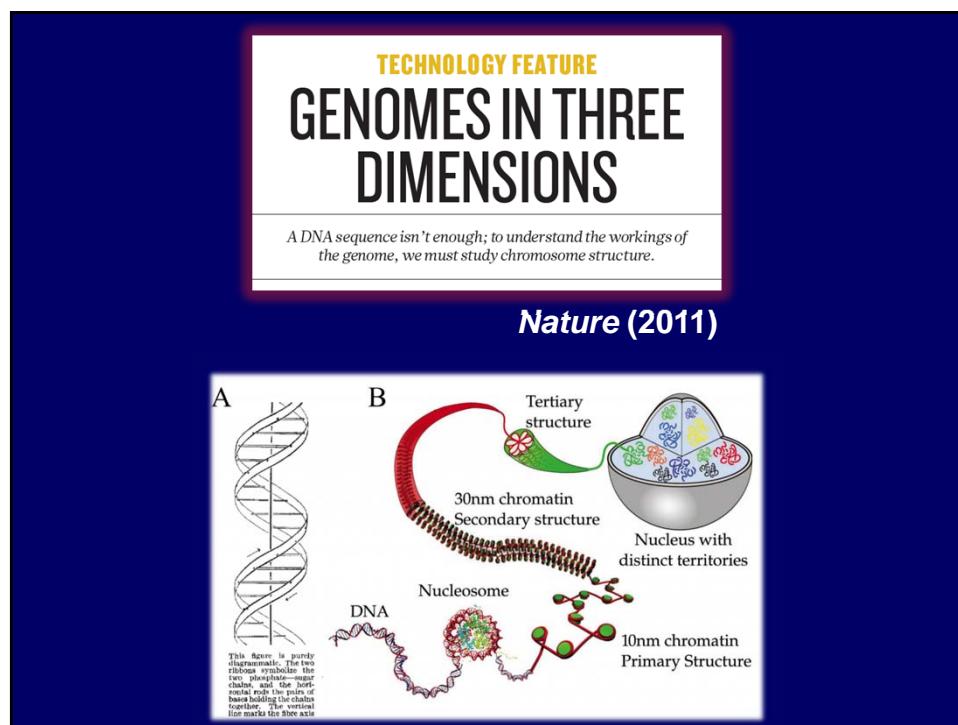
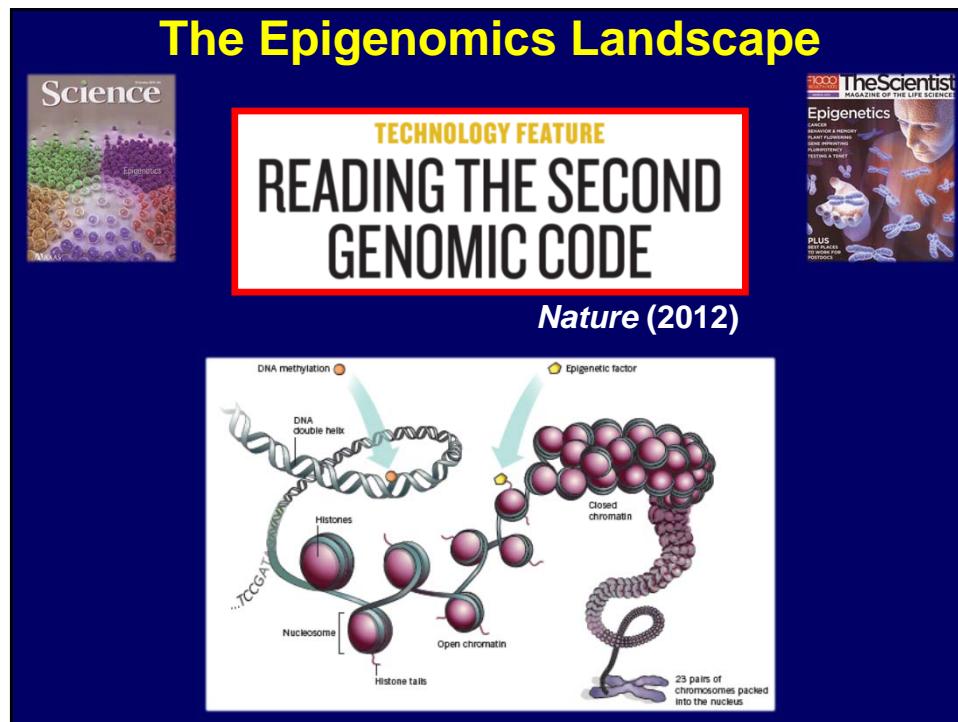
— Eric Lander

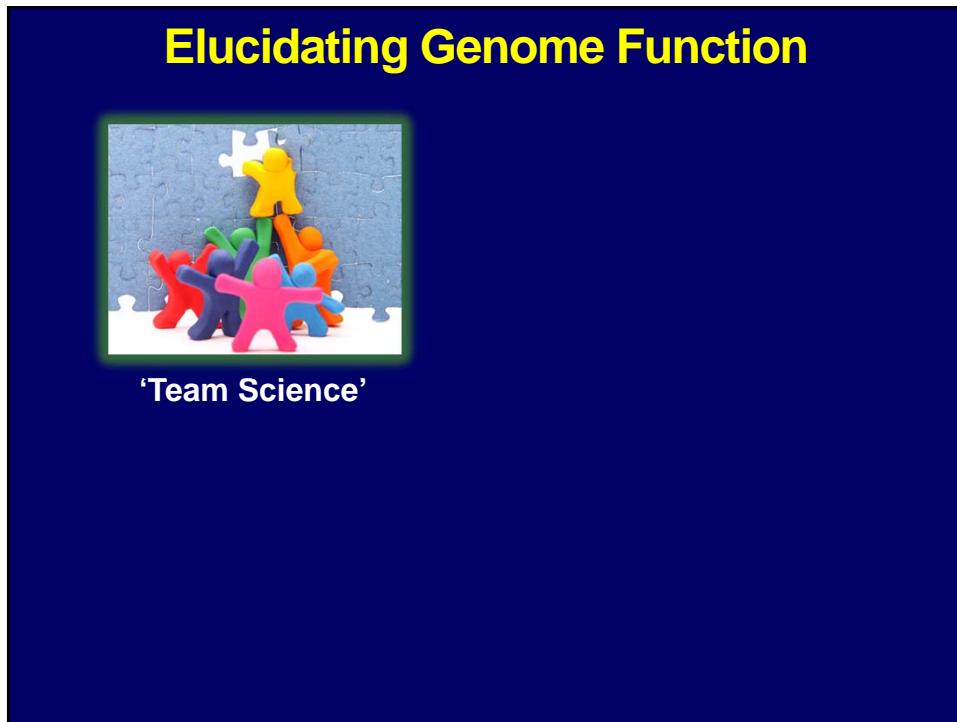


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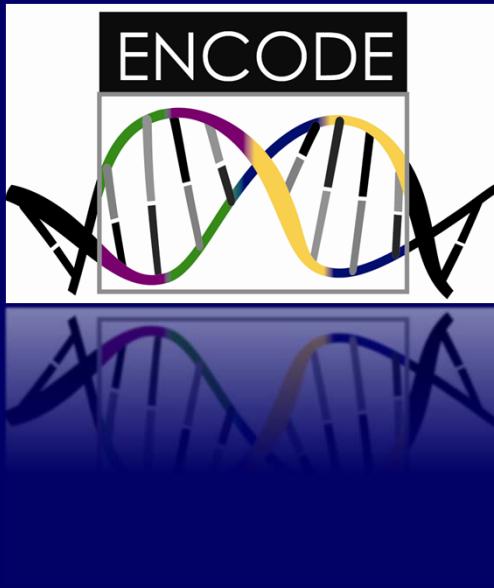


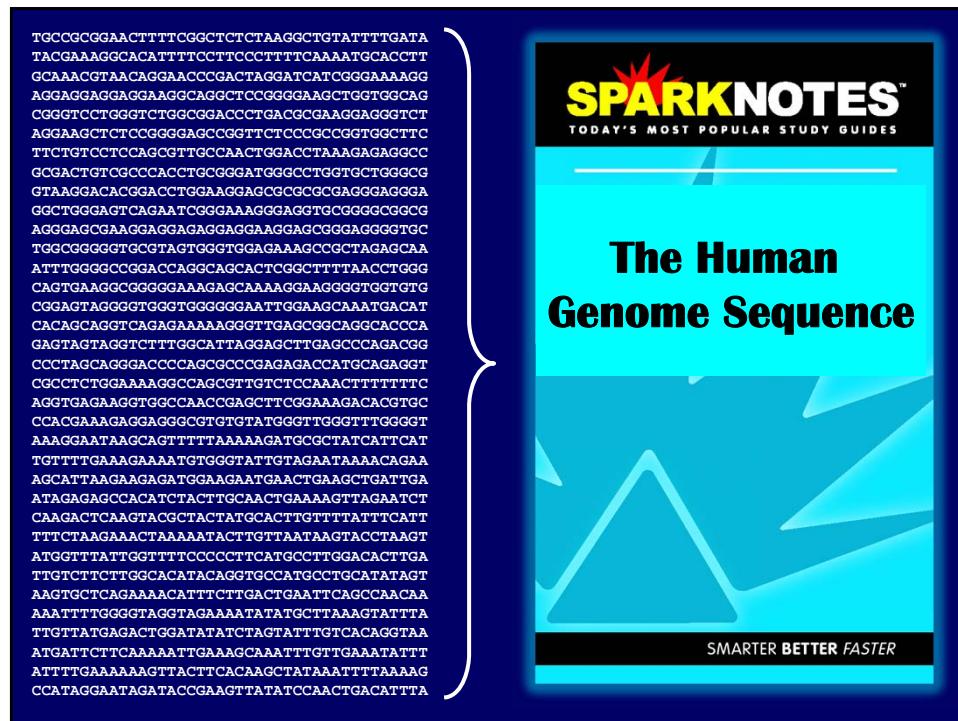
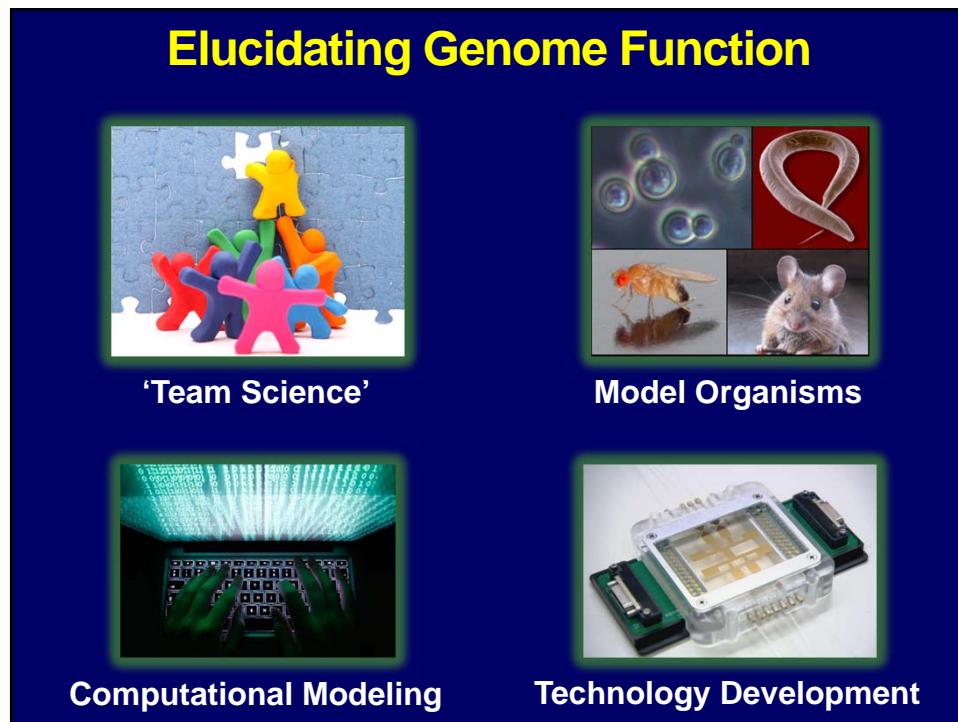
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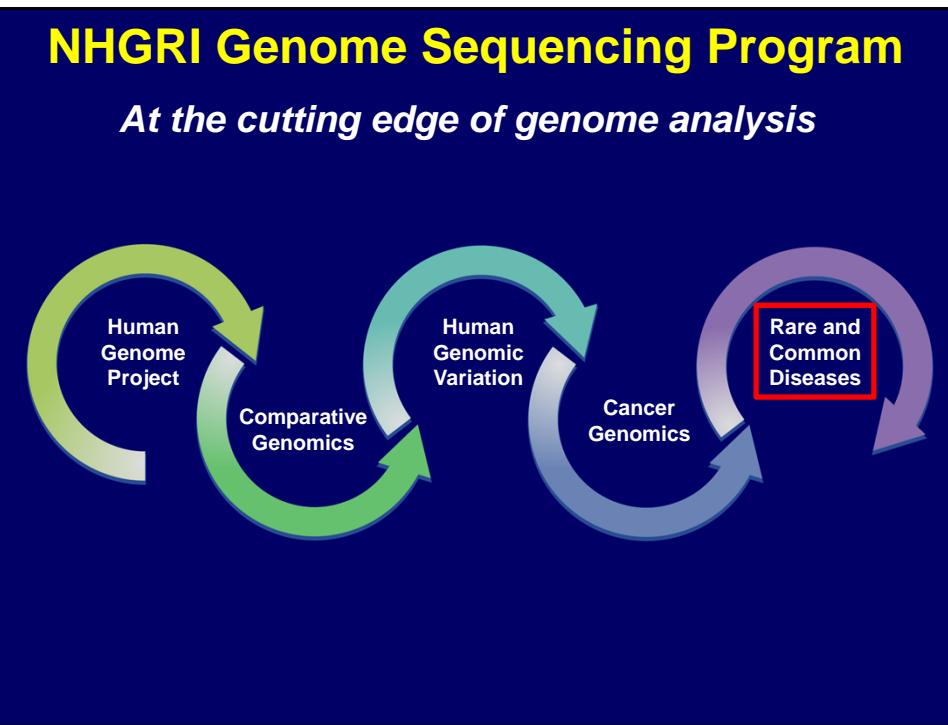
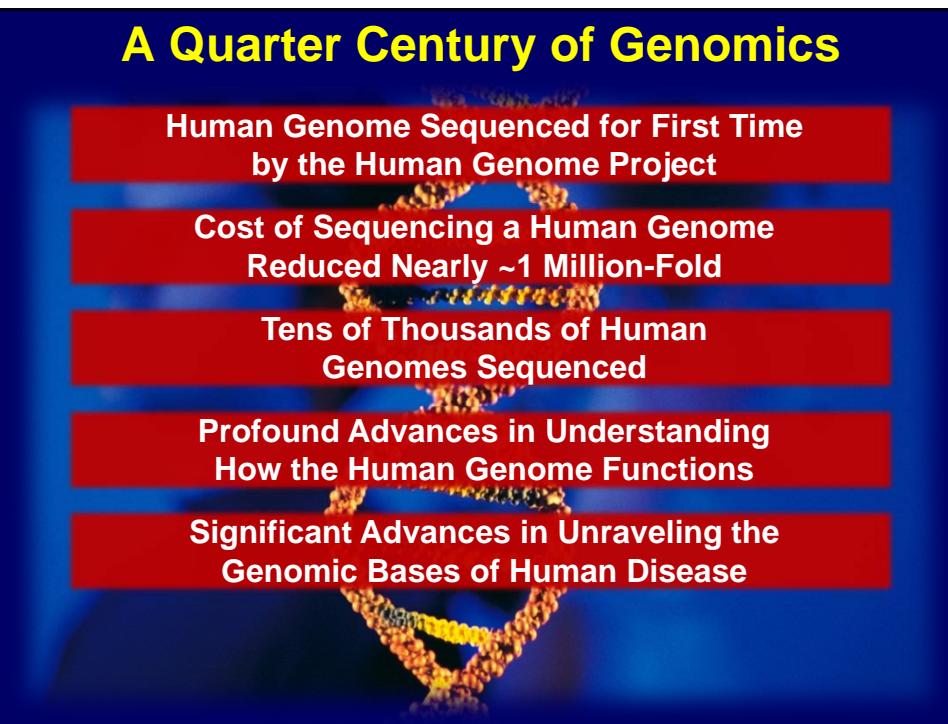


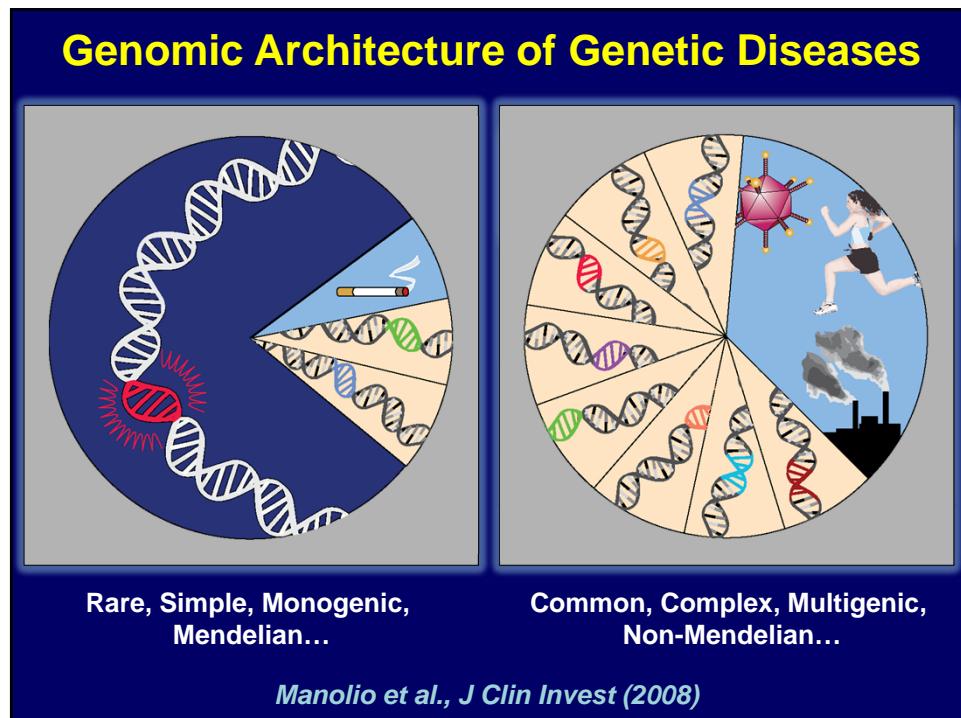


## ENCODE: Giving 'GPS' Views of Genomes









## The Data Analysis Bottleneck



## A Quarter Century of Genomics

Human Genome Sequenced for First Time  
by the Human Genome Project

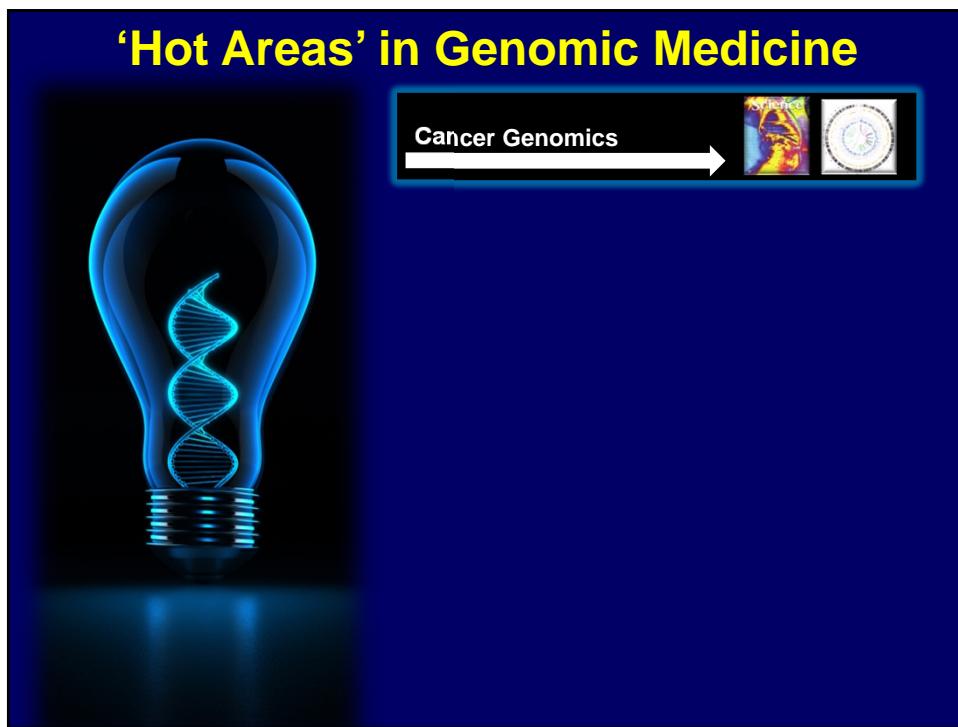
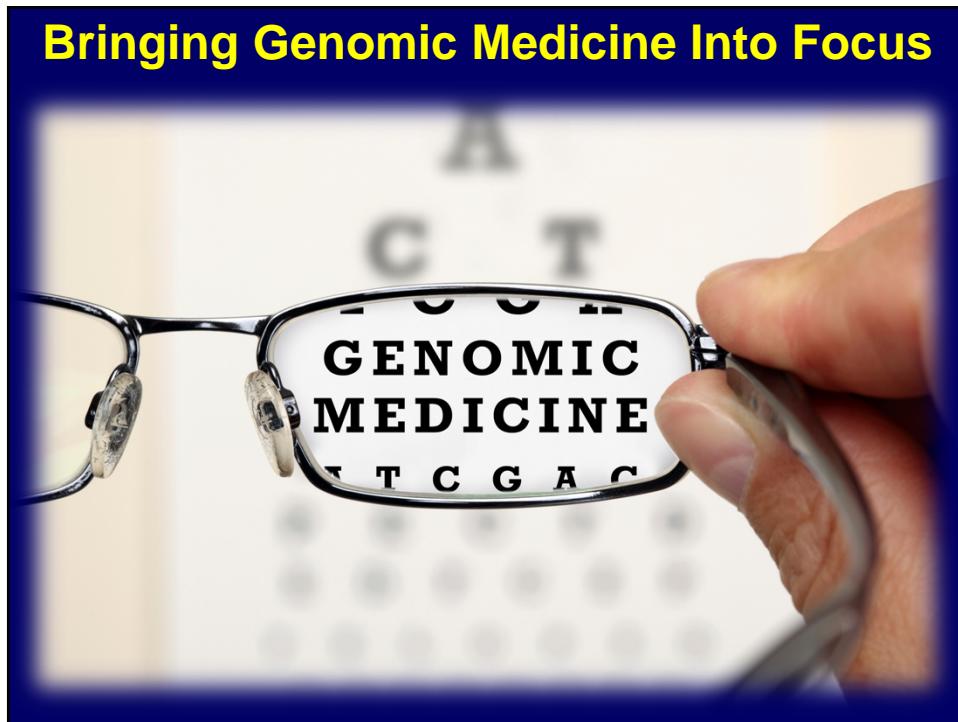
Cost of Sequencing a Human Genome  
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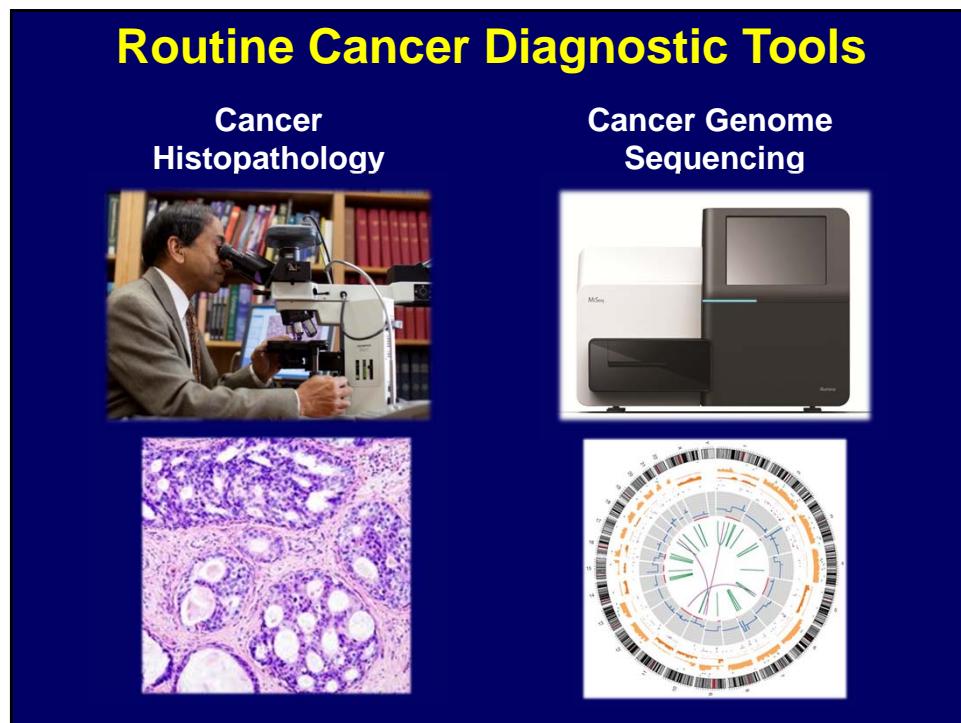
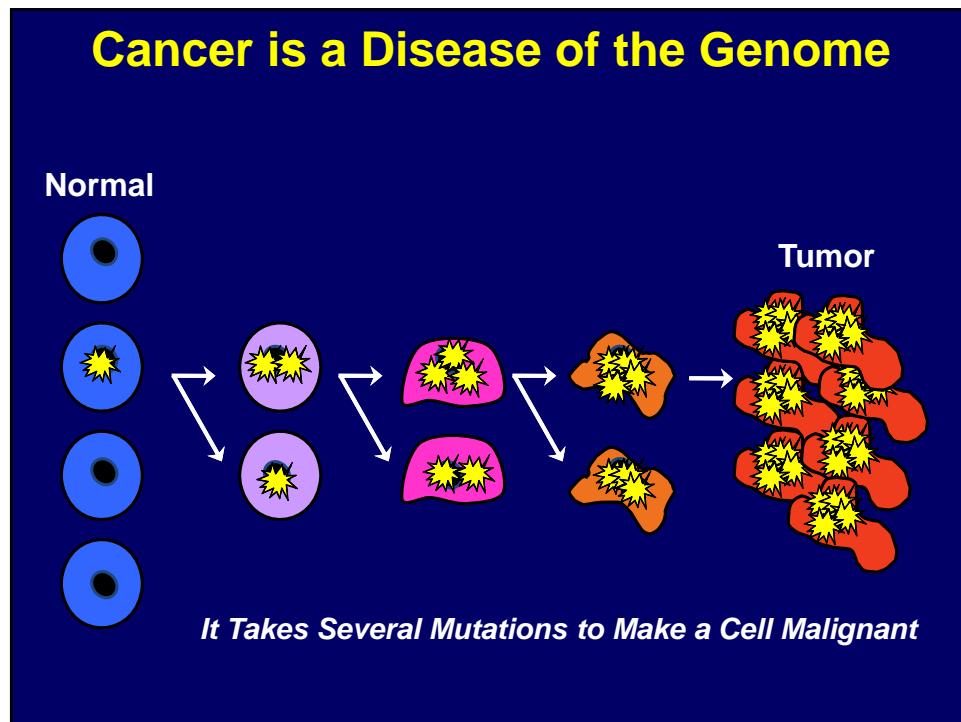
Tens of Thousands of Human  
Genomes Sequenced

Profound Advances in Understanding  
How the Human Genome Functions

Significant Advances in Unraveling the  
Genomic Bases of Human Disease

Vivid Examples of Genomic Medicine  
in Action Now Emerging





## Genomics and Cancer: Here and Now

Cancer Treatment Centers of America

We're available 24/7 to discuss treatment options. Call anytime (800) 931-9299 Chat online now

ABOUT YOUR CANCER | HOW WE TREAT CANCER | OUR HOSPITALS | COMMUNITY & SUPPORT | search

HOW CAN GENOMIC TESTING HELP PATIENTS NOW?

Every cancer is different. Genomic testing helps our doctors understand a patient's cancer at the molecular level and may reveal more personalized treatment options.

LEARN MORE »

“Genomic testing is the future of cancer treatment.”  
Dr. Shayma Kazmi, Medical Oncologist  
Cancer Treatment Centers of America

**HUNTSMAN**  
CANCER INSTITUTE  
UNIVERSITY OF UTAH  
CHANGING THE DNA OF CANCER CARE

[huntsmancancer.org](http://huntsmancancer.org)

## ‘Hot Areas’ in Genomic Medicine



**Cancer Genomics** → 

**Pharmacogenomics** → 

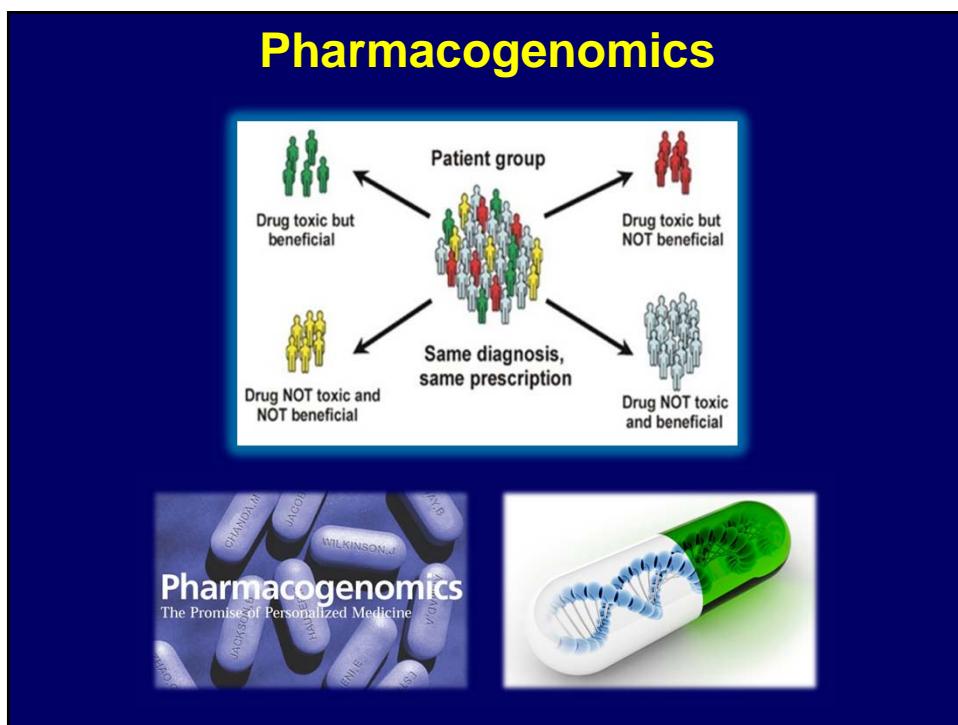
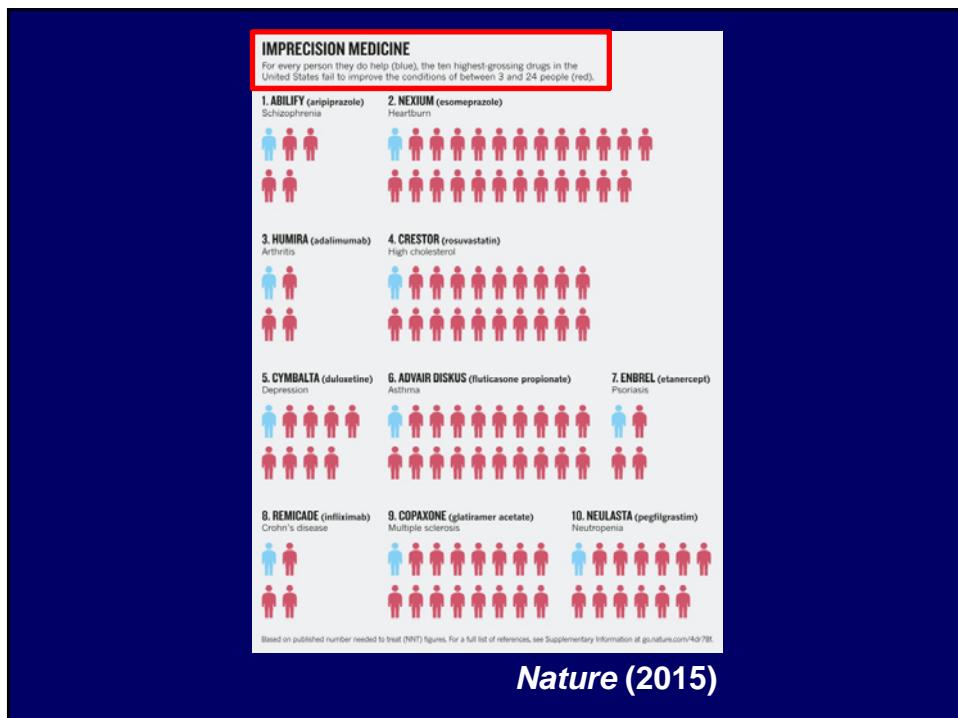


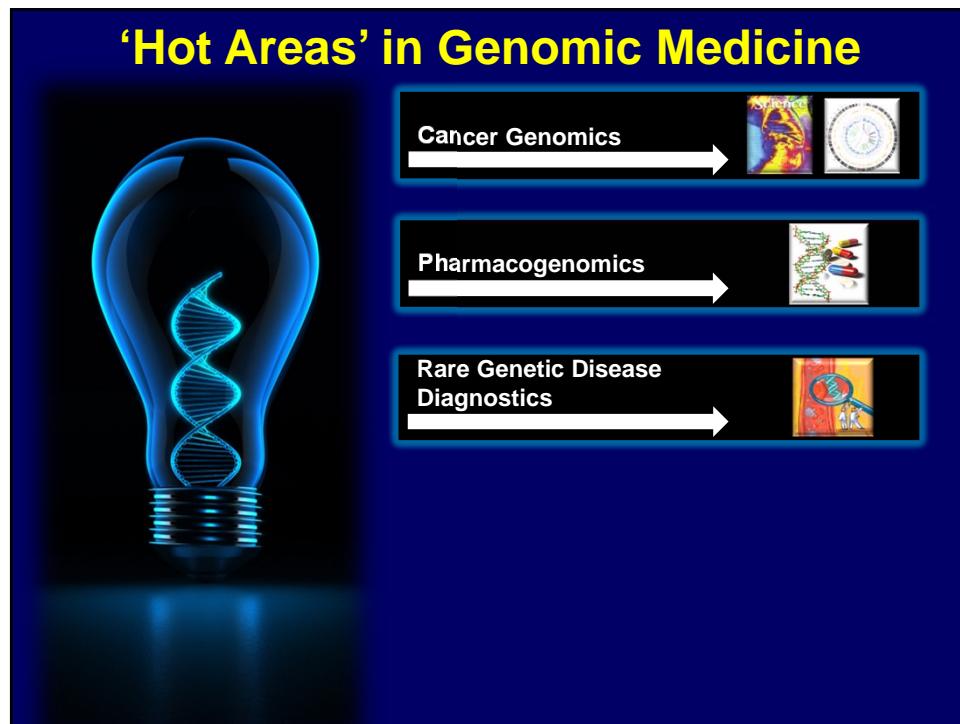
All of these work.

Just not for everyone.

Perlegen may be able to help you sort out which medicine helps which patient. Working with you, we can comprehensively analyze the DNA from thousands of patients taking your drug. Out of the millions of genetic variations between patients, we may be able to help you identify the ones that are associated with strong efficacy, poor efficacy, or side effects. Perlegen's exceptional coverage of the genome and experienced team of analysts could help you get clinically relevant answers, not just data, in a matter of months. We partner with the top pharmaceutical companies around the world. We also license late-stage drugs. If you have a drug that can benefit from our approach, please contact us.

COURTESY OF PERLEGEN





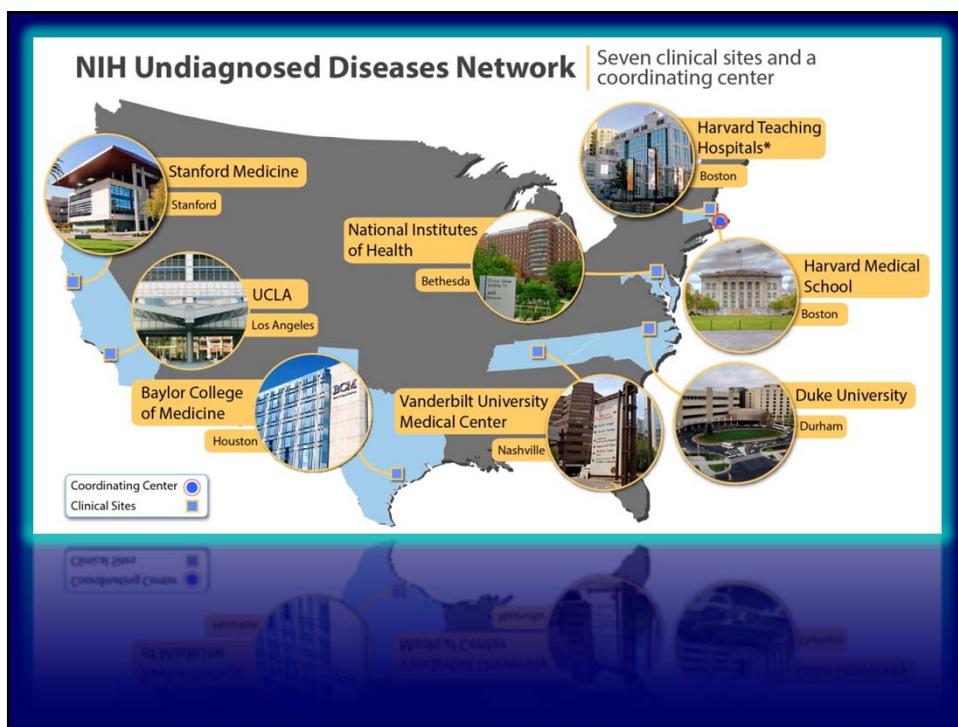
**TECHNOLOGY FEATURE**

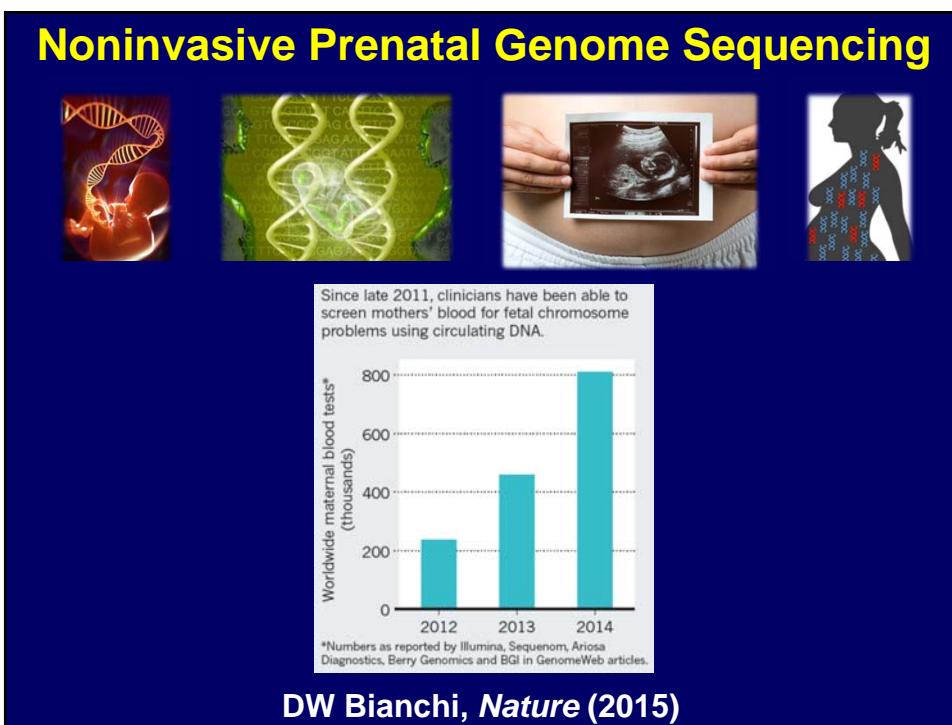
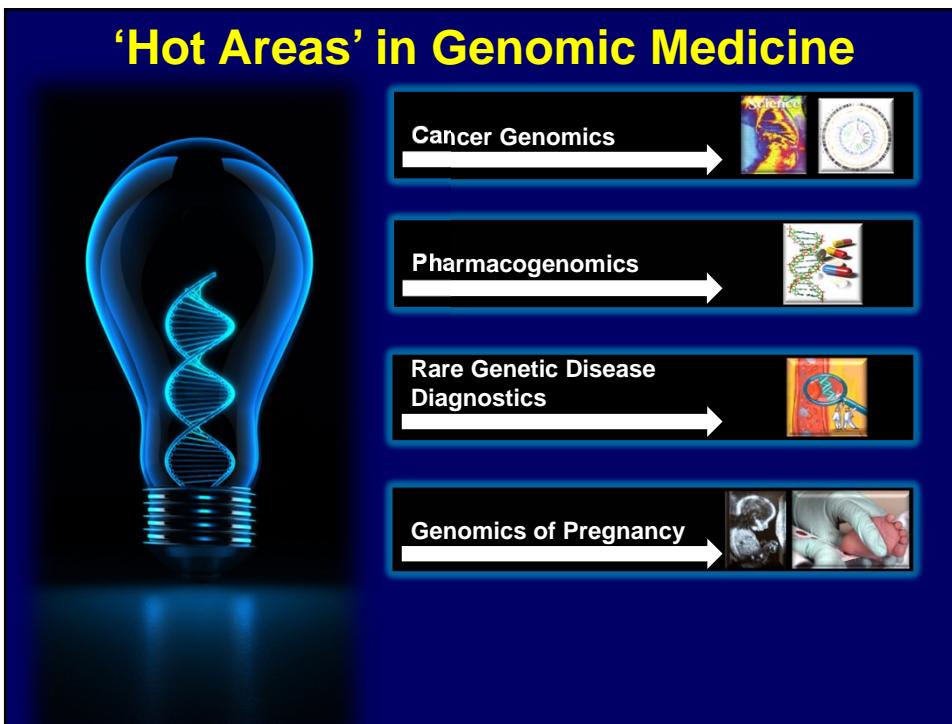
## WHEN DISEASE STRIKES FROM NOWHERE

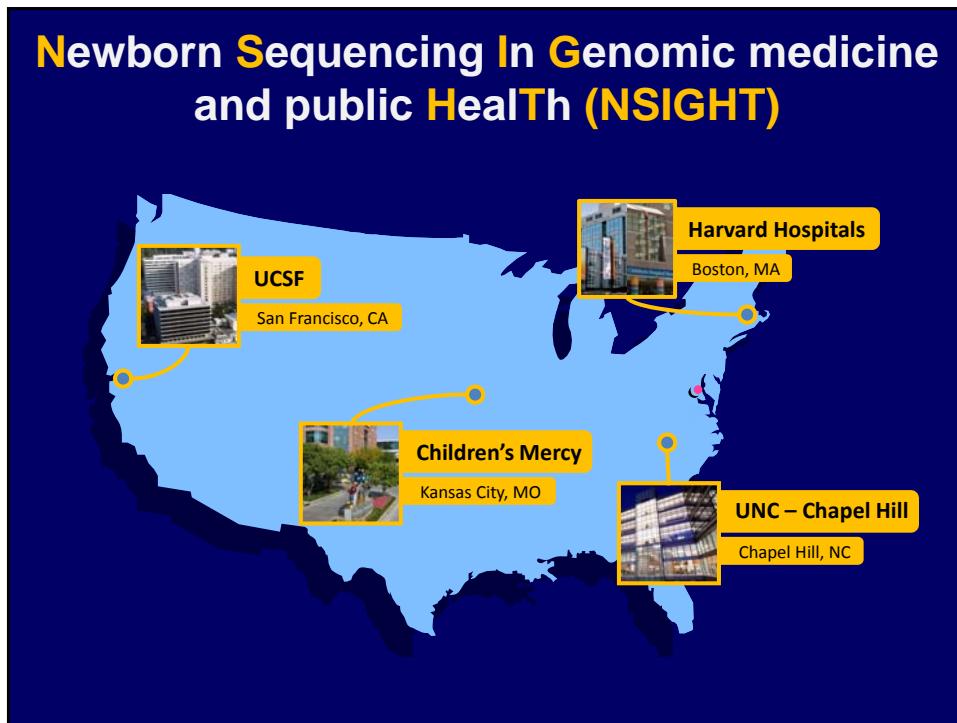
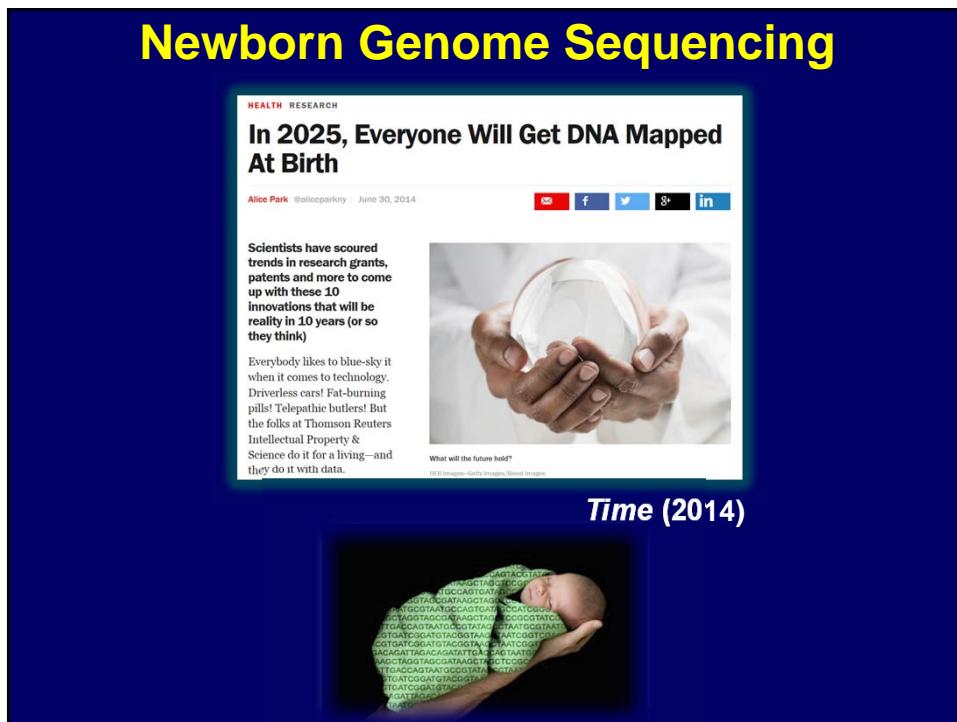
When healthy parents have a child with a genetic disorder, the cause is sometimes a new mutation. Tools are emerging to meet the challenge of finding such changes.

“ ...disorders not readily explained by standard tests can sometimes be diagnosed through genome sequencing and analysis.”

*Nature* (2014)







## Genome Sequencing of Acutely Sick Newborns



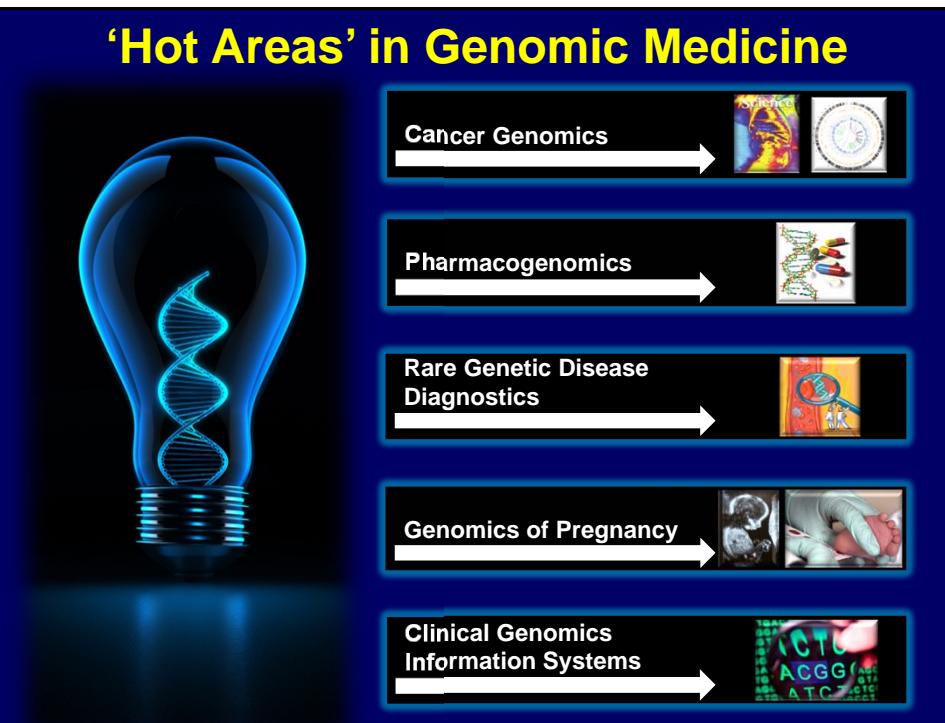
The genomes of ill newborns can be sequenced in less than 24 hours to give clinicians a rapid diagnosis.

**GENOMICS**

### Fast sequencing saves newborns

Rapid analysis of infant genomes is aiding diagnosis and treatment of inexplicably ill babies.

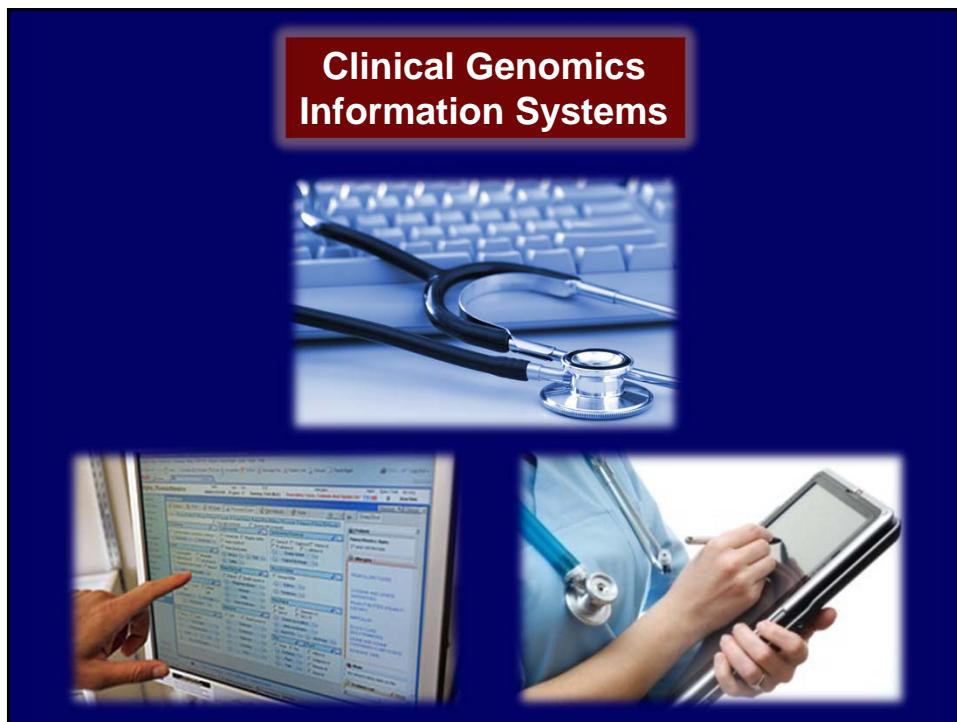
**Nature (2014)**



## Generating a Human Genome Sequence is (Almost) Trivial

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TGAAACCCATTGGCACGATGCTCCGTGAGGAAACTTGAACACCATTGGGTGAGGAAACTTGAACAC  
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CACGATGCTCCGTGAGGAAACTTGAACACCATTGGCACGATGCTCCGTGAGGAAACTTGAACACC  
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GGCACGATGCTCCGTGAGGAAACTTGAACACCATTGGGTGAGGAAACTTGAACAC





**Clinical Genome Resource (ClinGen)**

[clinicalgenome.org](http://clinicalgenome.org)

**ClinGen — The Clinical Genome Resource**

Heidi L. Rehm, Ph.D., Jonathan S. Berg, M.D., Ph.D., Lisa D. Brooks, Ph.D.,  
Carlos D. Bustamante, Ph.D., James P. Evans, M.D., Ph.D., Melissa J. Landrum, Ph.D.,  
David H. Ledbetter, Ph.D., Donna R. Maglott, Ph.D., Christa Lese Martin, Ph.D.,  
Robert L. Nussbaum, M.D., Sharon E. Plon, M.D., Ph.D., Erin M. Ramos, Ph.D.,  
Stephen T. Sherry, Ph.D., and Michael S. Watson, Ph.D., for ClinGen

**NEJM (2015)**

# The Genomic Medicine Ecosystem

# *Healthcare Delivery*

# The Genomic Medicine Ecosystem

## ***Education & Genomic Literacy***



# The Genomic Medicine Ecosystem

## *Regulatory Oversight*



## Understanding the Structure of Genomes

## Understanding the Biology of Genomes

## Understanding the Biology of Disease

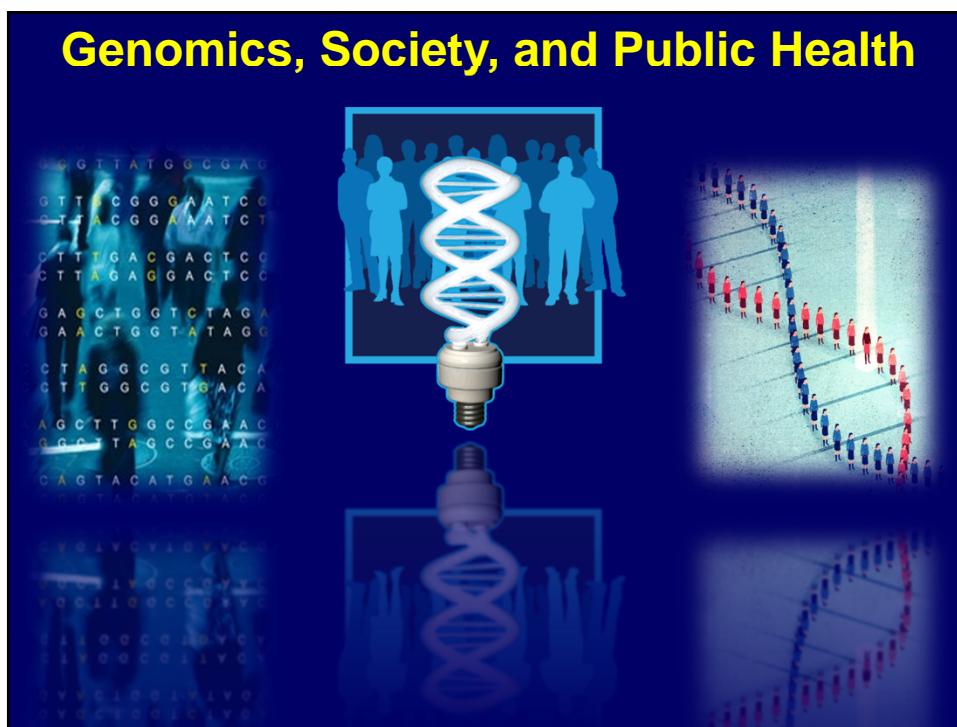
Advancing  
the Science of  
Medicine

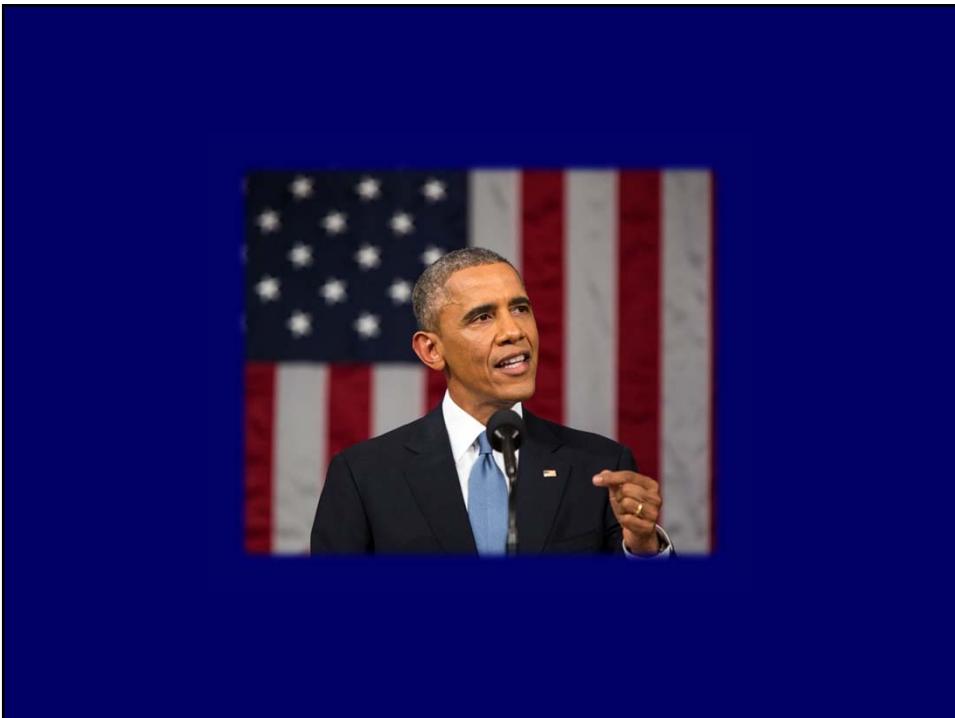
## Improving the Effectiveness of Healthcare



**A pessimist sees the difficulty in every opportunity.  
An optimist sees the opportunity in every difficulty.**

--Winston Churchill





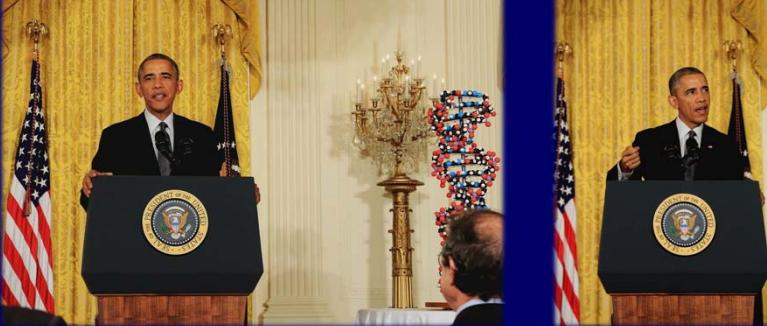
## Precision Medicine

- Today: most medical care based on expected response of the average patient
- Tomorrow: medical care based on individual genomic, environmental, and lifestyle differences that enable more precise ways to prevent and treat disease



How do we get from today to tomorrow?





“...[the] new Precision Medicine Initiative [will bring] America closer to curing diseases like cancer and diabetes, and gives all of us access, potentially, to the personalized information that we need to keep ourselves and our families healthier.”

President Barack Obama  
January 30, 2015



The NEW ENGLAND JOURNAL of MEDICINE

January 30, 2015

## Perspective

A New Initiative on Precision Medicine

Francis S. Collins, M.D., Ph.D., and Harold Varmus, M.D.

“Tonight, I’m launching a new Precision Medicine Initiative to bring us closer to curing diseases like cancer and diabetes — and to give all of us access to the personalized information we need to keep ourselves and our families healthier.”

— President Barack Obama, State of the Union Address, January 20, 2015

The proposed initiative has two main components: a near-term focus on cancers and a longer-term aim to generate knowledge applicable to the whole range of health and disease. Both components are now within our reach because of advances in basic research, including molecular biology, genomics, and bioinformatics. Furthermore, the initiative

## U.S. National Research Cohort



- >1 million U.S. volunteers
- Participants to share genomic data, lifestyle information, biological samples – all linked to their EHRs
- Forge new model for ‘doing science’ that emphasizes:
  - Engaged participants
  - Open, responsible data sharing
  - Strong privacy protections

## Everything Old is New Again

### insight commentary

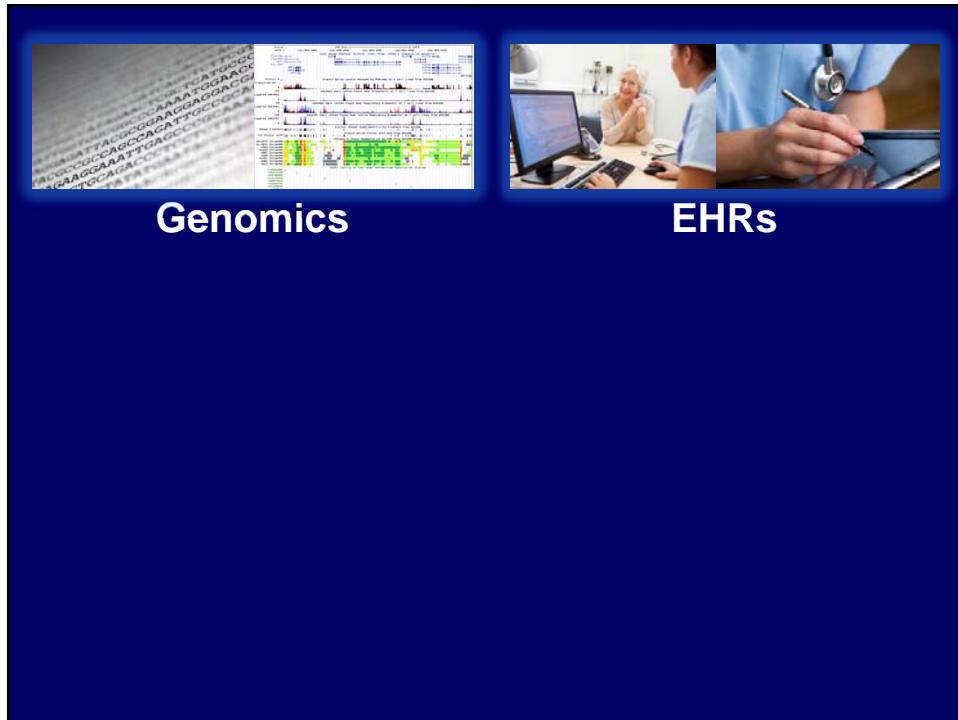
## The case for a US prospective cohort study of genes and environment

Francis S. Collins

National Human Genome Research Institute, National Institutes of Health, Building 31, Room 4B09, MSC 2152, 31 Center Drive, Bethesda, Maryland 20892-2152, USA (e-mail: fc23a@nih.gov)

Information from the Human Genome Project will be vital for defining the genetic and environmental factors that contribute to health and disease. Well-designed case-control studies of people with and without a particular disease are essential for this, but rigorous and unbiased conclusions about the causes of diseases and their population-wide impact will require a representative population to be monitored over time (a prospective cohort study). The time is right for the United States to consider such a project.

***Nature* (2004)**



**Electronic Medical Records and Genomics (eMERGE) Network**

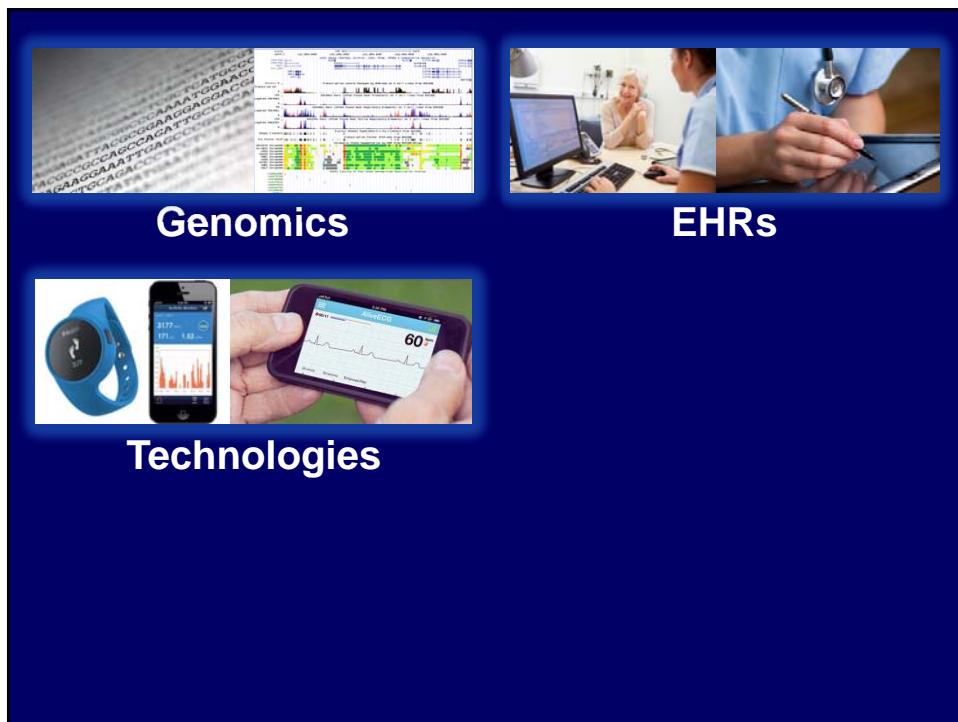
[LOGIN TO EMERGE](#)

eMERGE network  
ELECTRONIC MEDICAL RECORDS AND GENOMICS

451      47      55,028

Number of network publications      Number of phenotypes developed      Number of participants in the Network Cohort

[emerge.mc.vanderbilt.edu](http://emerge.mc.vanderbilt.edu)



**THE BODY ELECTRIC**

**RESEARCHERS WANT TO WIRE THE HUMAN BODY WITH SENSORS THAT COULD HARVEST REAMS OF DATA — AND TRANSFORM HEALTH CARE.**

BY ELIZABETH GIBNEY

**Nature (2015)**

**WIRED FOR LIFE** Sensors woven into the body could alert people to medical problems before they become seriously ill — if the devices can overcome some daunting challenges.

Sensors mounted on the skin are easy to apply and remove, and can obtain high-quality data on breathing, heart rate, blood pressure and other vital signs. But they must be flexible and stretchy enough to follow the natural movement of the body.

Sensors injected under the skin can access the trove of information carried in the blood by chemical signals called biomarkers. The devices must be long-lived and biocompatible, so that they don't trigger an immune response.

Devices implanted into the heart, brain or other deep tissues can gather data directly from the source and deliver drugs or stimulation exactly where needed. But they must have ways to get power in and data out — without resorting to wires.

The diagram shows a hand with a sensor patch, a cross-section of skin layers with sensors embedded, and a human figure with internal implants. Labels include: Epidermis, Dermis, Subcutaneous tissue, Carbon-nanotube-based sensors, Flexible brain sensor, Flexible heart pacemaker, and Spine-implanted ion pump.





**Report on Precision Medicine Initiative Cohort Program**



The Precision Medicine Initiative Cohort Program – Building a Research Foundation for 21<sup>st</sup> Century Medicine

Precision Medicine Initiative (PMI) Working Group Report to the Advisory Committee to the Director, NIH

September 17, 2015

For Immediate Release: Thursday, September 17, 2015

NIH framework points the way forward for building national, large-scale research cohort, a key component of the President's Precision Medicine Initiative

The National Institutes of Health Advisory Committee to the Director (ACD) today presented to NIH Director Francis S. Collins, M.D., Ph.D., a detailed design framework for building a national research participant group, called a cohort, of 1 million or more Americans to expand our knowledge and practice of precision medicine. Dr. Collins embraced the design recommendations made by the ACD, noting the need to remain nimble and adaptable as the initiative progresses. He also thanked the Committee for their recommendations on policy issues and welcomed the opportunity to review them. NIH plans to move quickly to build the infrastructure so that participants can begin enrolling in the cohort in 2016, with a goal of enrolling at least 1 million participants in three to four years.

## Precision Medicine Initiative

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### PRECISION MEDICINE INITIATIVE

Precision Medicine Initiative

Near-term Goals Longer-term Goals Scale and Scope Participation PMI Working Group Events Announcements PMI in the News Multimedia

Faces of the Precision Medicine Initiative – Dr. Russ Altman NIH Director's blog: Read precision medicine-related blogs by the NIH Director.

**ABOUT THE PRECISION MEDICINE INITIATIVE**

Too many diseases do not have a proven means of prevention or effective treatments. We must gain better insights into the biology of these diseases to make a difference for the millions of Americans who suffer from them. Precision medicine is an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle for each person. While significant advances in precision medicine have been made for select cancers, the practice is not currently in use for most diseases. Many efforts are underway to help make precision medicine the norm rather than the exception. To accelerate the pace, President Obama unveiled the Precision Medicine Initiative (PMI) – a bold new enterprise to revolutionize medicine and generate the scientific evidence needed to move the concept of precision medicine into every day clinical practice.

Email Updates

To sign up for updates please enter your e-mail address.

Submit

Related Links

NEJM Perspective: A New Initiative on Precision Medicine  
White House Precision Medicine Web Page  
White House Fact Sheet: President Obama's Precision Medicine Initiative  
Precision Medicine Initiative and Cancer Research  
Storify: #PMINetwork Twitter Chat  
Storify: The Precision Medicine Initiative Announcement  
Precision Medicine Initiative YouTube Channel

[www.nih.gov/precisionmedicine](http://www.nih.gov/precisionmedicine)

## Déjà Vu, All Over Again?



**Human Genome Project**  
*Circa Winter 1990*

**Precision Medicine Initiative**  
*Circa Winter 2015*

The Genomics Landscape  
A monthly newsletter from the NHGRI Director

October 6, 2015

This month brought a historic 'odometer moment' for the field of genomics – October 1, 2015, marked the 25<sup>th</sup> anniversary of the launch of the Human Genome Project. I, for one, cannot believe a quarter-century has now passed since many of us started working on the Project. At the same time, it is truly incredible to think about how far genomics has progressed since that time. I thought the significance of this anniversary warranted making this topic the lead story in this month's *The Genomics Landscape*; in addition, I reflect on this important anniversary in a recent video interview now available on the NHGRI web site.

To subscribe, follow link from:  
[genome.gov/Director](http://genome.gov/Director)

