National Human Genome Research Institute

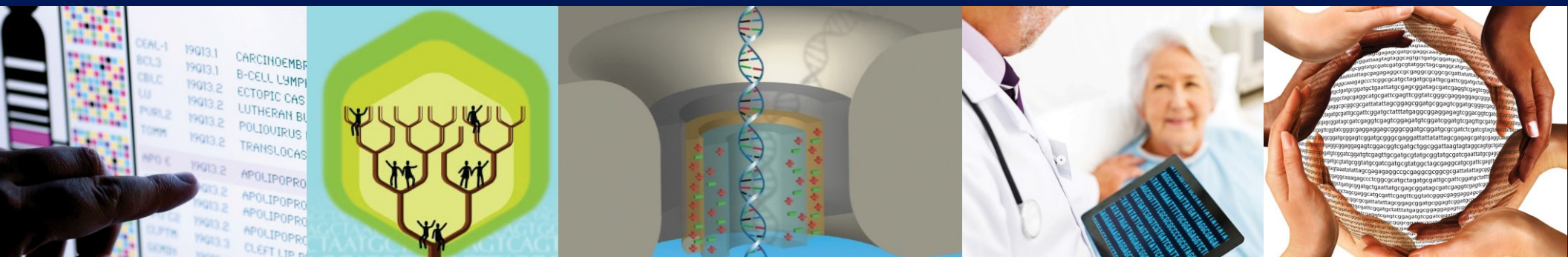
The Forefront of Genomics®

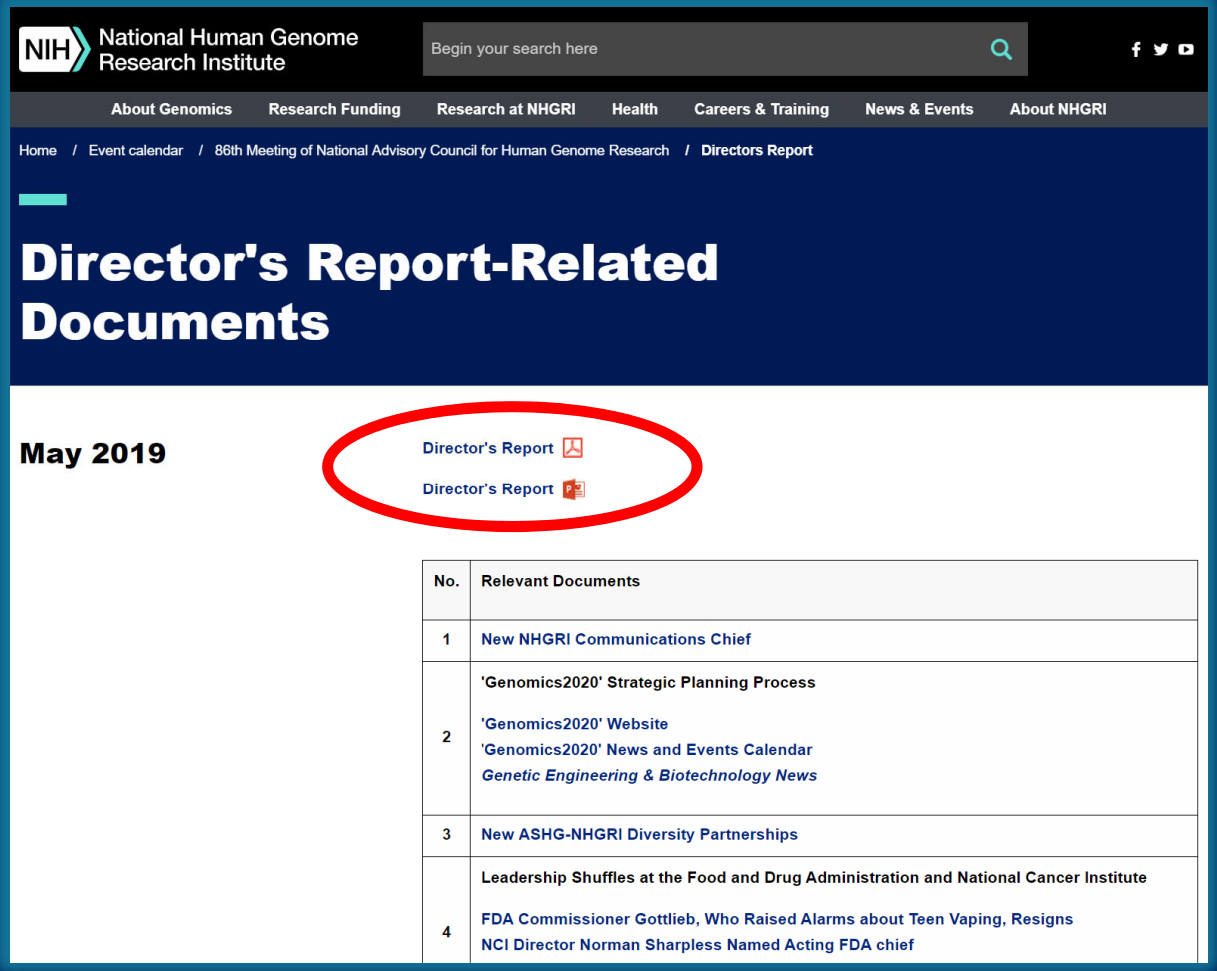
DIRECTOR'S REPORT

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

Director, NHGRI

May 2019





genome.gov/DirectorsReport

Document #

Open Session Presentations

- **Report: ENCODE Project Update**
  Brenton Graveley

- **Concept Clearance: Diversity Action Plan Renewal**
  Tina Gatlin

- **Report: NHGRI Strategic Planning Workshop "From Genome to Phenotype – Genomic Variation Identification, Association, and Function in Human Health and Disease"**
  Sharon Plon

Director's Report Outline

I. General NHGRI Updates

II. General NIH Updates

III. General Genomics Updates

IV. NHGRI Extramural Research Program

V. NIH Common Fund/Trans-NIH

VI. NHGRI Division of Policy, Communications, and Education

VII. NHGRI Intramural Research Program

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Departure of NHGRI Communications Chief

John Ohab, Ph.D.

New NHGRI Communications Chief

Sarah Bates, M.S.

Retirement of Extramural Program Director

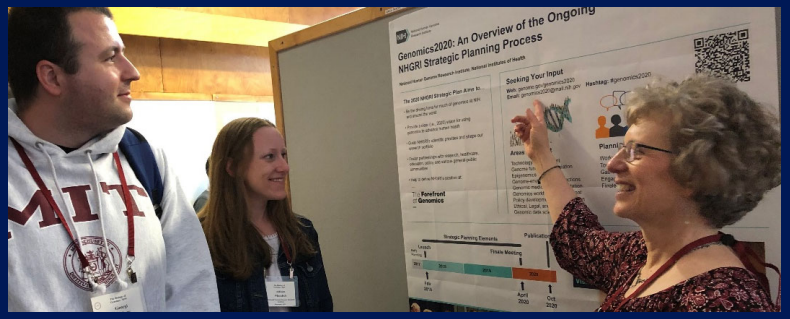
Lisa Brooks, Ph.D.

New Extramural Program Director

Shurjo Sen, Ph.D.

‘Genomics2020’ Strategic Planning Process

- NHGRI Research Training and Career Development Annual Meeting (St. Louis, MO)
- American Medical Informatics Association 2019 Informatics Summit Meeting (San Francisco, CA)
- Grand Challenges in Genomics: An NHGRI and Wellcome Trust Strategy Meeting (London, England)
- Cold Spring Harbor Laboratory Biology of Genomes Meeting



Document 2

‘Genomics2020’ Strategic Planning Process

Genomics' "Green" Future

By Julianna LeMieux, PhD

NHGRI director lays out institutes strategic plan, a "2020 vision for genomics"

The National Human Genome Research Institute (NHGRI) is nearing the halfway point of a major strategic planning process, one that aims to publish a "2020 vision for genomics" in late 2020. The new plan will "detail the most exciting opportunities for genomics research and its application to human health and disease at the dawn of the new decade." In this exclusive interview, Eric D. Green, MD, PhD, the director of the NHGRI, discusses the process and some of the early takeaways from the planning effort.

GEN: How is the development of this plan the same as or different from that of previous strategic plans?

Eric Green: It is helpful to consider the history of our institute. We were created 30 years ago by the U.S. Congress to lead the U.S.'s contribution to the Human Genome Project, but that project was completed 16 years ago. Therefore, our core mission had to change. Beginning 16 years ago, the institute has pivoted beyond the Human Genome Project and focused on enabling the use of genomics for understanding disease and improving the practice of medicine.

One way to assess the NHGRI's success involves looking at the uptake of genomics by other parts of the biomedical research ecosystem. I'll give you some numbers because it frames a really important aspect of our strategic planning process.

When the Human Genome Project ended and we published our 2003 strategic plan, over 95% of human genomics research being supported by the National Institutes of Health (NIH) was directly funded by the NHGRI.

When our next strategic plan came out in 2011, that number had fallen to just below 50%. So, while our 2011 strategic plan nicely summarized the important areas for the NHGRI to fund, there was already a large fraction of human genomic research being supported by other NIH institutes and centers.

What about now? Well, the NHGRI is funding only 15% of the human genomics research being supported by all of the NIH. This requires us to then really focus on the areas of genomics that are really at the forefront of the field—and thus the institute's new mantra: The Forefront of Genomics.

In short, the biggest difference between this round of strategic planning and previous rounds is that now, genomics is disseminated in all the nooks and crannies of biomedical research. If we tried to do strategic planning for every area of genomics, it would just be too much. So, our efforts are now heavily focused on the cutting-edge "forefront" areas, especially those that will enable others in their use of genomics.

GEN: What is one of the most challenging aspects of the current round of strategic planning?

Eric Green: We have to engage many more groups. The field of genomics now extends far and wide—from establishing a basic understanding about how the human genome works to determining how genomic variation plays a role in human disease, and extending to how to use genomic information in the practice of medicine. Understanding the most compelling research questions in each of those areas requires engaging with many different groups, including patients. It gets more complicated because we're touching medicine. The second you touch medicine, you touch patients, and therefore you're touching society.

Another challenge relates to our emphasis on the Forefront of Genomics. For us to understand that forefront, we need to be talking to people whose work we want to enable over the next 10 years. So, we need to be talking to that hematologist searching for genomic variants to understand the basis of hematologic disease. And we want to know what are the tools and approaches that will enable that hematologist to do their science better.

While their work will likely be funded by the National Heart, Lung, and Blood Institute, we want to know what genomic tools and approaches they need to accomplish their goals. If we could design and develop the general toolkit for genomics, the work of many would benefit. Identifying those forefront challenges requires extensive engagement.

Eric D. Green, MD, PhD
Director, NHGRI

GEN Genetic Engineering & Biotechnology News

GEN 39: 15-16, 2019

Document 2

New ASHG-NHGRI Diversity Partnerships

Developing Country Awards Program

Human Genetics Scholars Initiative

Document 3

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Leadership Shuffles at the Food and Drug Administration and National Cancer Institute

Scott Gottlieb, M.D.

Ned Sharpless, M.D.

Doug Lowy, M.D.

Document 4

New Director, NIH Center for Scientific Review

Noni Byrnes, Ph.D.

National Institutes of Health

Document 5

New Director, National Institute on Deafness and Other Communication Disorders

Debara L. Tucci, M.D.

NIH NIDCD

Document 6

Fiscal Year 2020 Appropriations Process

	Fiscal Year 2019 Labor-HHS Appropriation	Fiscal Year 2020 House Labor-HHS Subcommittee Appropriation	$ Increase	% Increase
NIH	$39.1 B	$41.1 B	**~$2.0 B**	**~5.1%**
NHGRI	$575 M	$603 M	**~$28 M**	**~4.9%**

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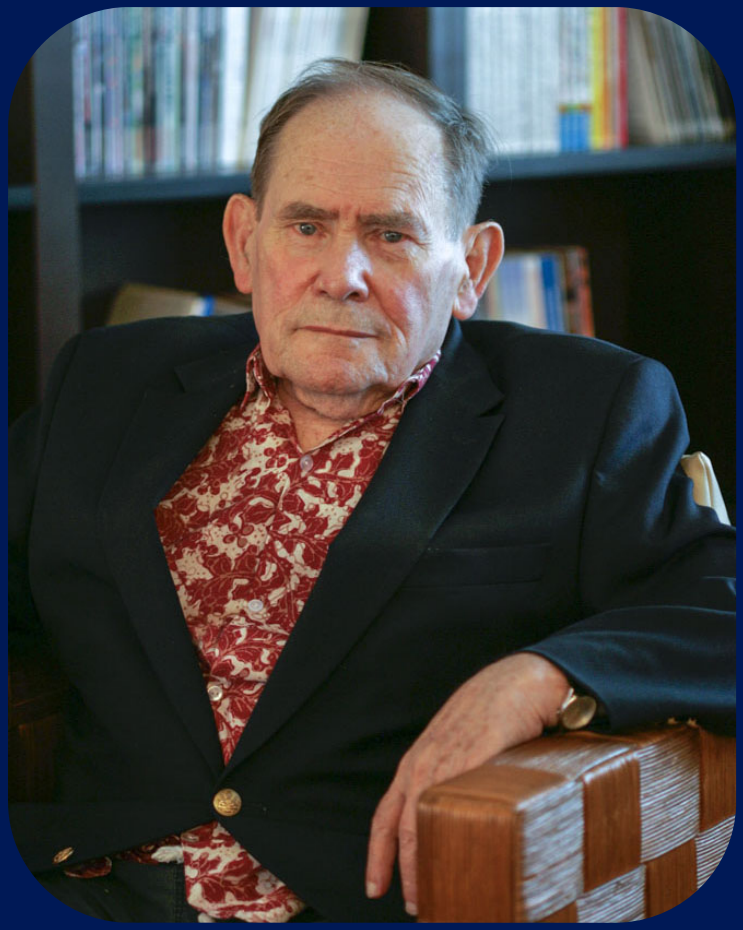
Mourning the Loss of Sydney Brenner



Document 8

Elected to National Academy of Sciences

Jennifer Graves

Mike Lenardo

Timothy Ley

Elaine Ostrander

Aviv Regev

Kári Stefánsson

David Williams

NATIONAL ACADEMY
OF SCIENCES

Document 9

National Academy of Sciences Awards

ASHG Position Statement: Responsibility to Recontact

ASHG POSITION STATEMENT

The Responsibility to Recontact Research Participants after Reinterpretation of Genetic and Genomic Research Results

Yvonne Bombard,[1,2,3,*] Kyle B. Brothers,[1,4] Sara Fitzgerald-Butt,[5,6] Nanibaa' A. Garrison,[1,7,8] Leila Jamal,[1,5,9] Cynthia A. James,[5,10] Gail P. Jarvik,[11,12] Jennifer B. McCormick,[1,13] Tanya N. Nelson,[14,15,16,17,18] Kelly E. Ormond,[1,19] Heidi L. Rehm,[20,21,22] Julie Richer,[14,23,24] Emmanuelle Souzeau,[25,26] Jason L. Vassy,[20,27,28] Jennifer K. Wagner,[1,29] and Howard P. Levy[1,30,31]

- 12 recommendations and a pathway for considering the responsibility to recontact research participants
- Recommendations fill a gap in guidance for when and how to recontact research participants with updated variant knowledge
- Provide principles for use by IRBs when determining whether and how to recontact research participants

Document 11

Genomics In The News…

RESEARCH ARTICLE

The NASA Twins Study: A multidimensional analysis of a year-long human spaceflight

Francine E. Garrett-Bakelman[1,2,*], Manjula Darshi[3,*], Stefan J. Green[4,*], Ruben C. Gur[5,*], Ling Lin[6,*], Brandon R. Macias[7,*], …
+ See all authors and affiliations

Science 12 Apr 2019:
Vol. 364, Issue 6436, eaau8650
DOI: 10.1126/science.aau8650

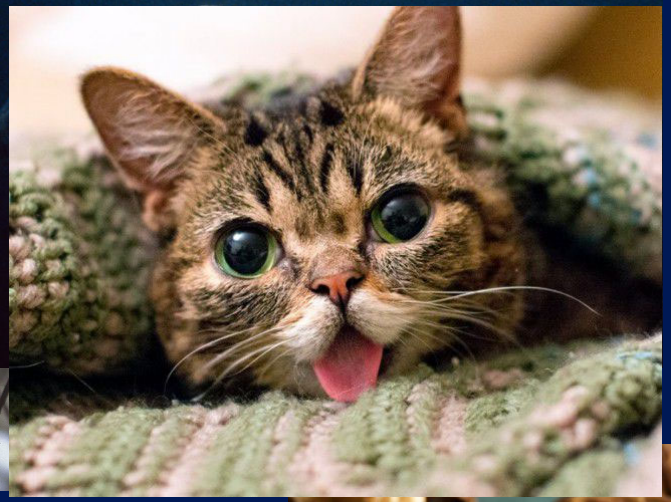
nature
International journal of science

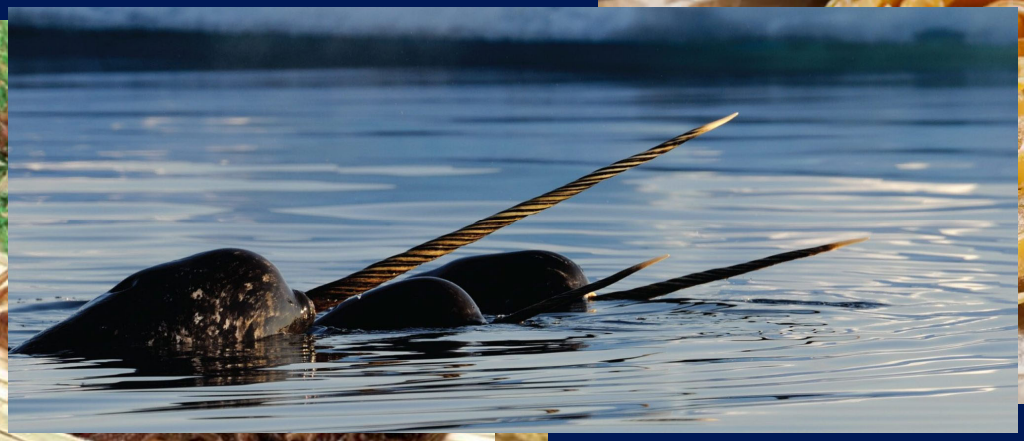
CORRESPONDENCE · 13 MARCH 2019

NIH supports call for moratorium on clinical uses of germline gene editing

Carrie D. Wolinetz & Francis S. Collins

Genomes In The News…





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Genome Sequencing Program

Centers for Common Disease Genomics

Disease Category	Sequence Type	Samples Sequenced	Samples Projected
Cardiovascular	Genomes	51,425	95,000
	Exomes	38,115	172,000
Immune-Mediated	Genomes	9,749	12,000
	Exomes	13,535	37,000
Neuropsychiatric	Genomes	19,335	30,000
	Exomes	29,071	44,000
TOTAL GENOMES		**~80,000**	**~140,000**
TOTAL EXOMES		**~81,000**	**~250,000**

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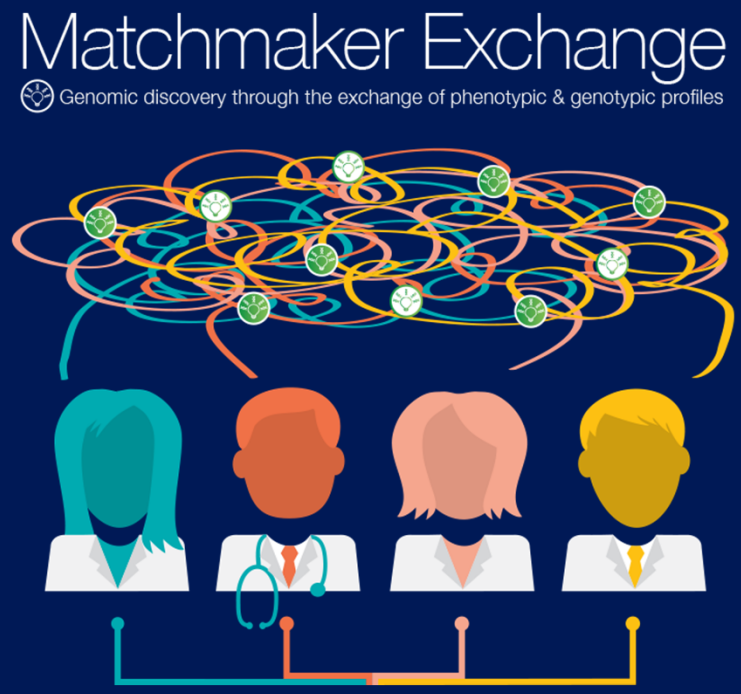
Genome Sequencing Program

Centers for Mendelian Genomics

Recruitment	Number
Samples	61,286
Families	22,742
Collaborators	3,928
Countries	80

Gene Discoveries	Number
Tier 1 Novel	616
Tier 2 Novel	1,101
Tier 1 Phen. Expansion	356
Tier 2 Phen. Expansion	114



ClinVar
Clinically relevant variation

Geno2MP

Genome Sequencing Program Publications

ACAT: A Fast and Powerful p Value Combination Method for Rare-Variant Analysis in Sequencing Studies

rison,[2] Eric Boerwinkle,[2,3] and Xihong Lin[1,*]

Genetics inMedicine | REVIEW ARTICLE

Insights into genetics, human biology and disease gleaned from family based genomic studies

Jennifer E. Posey, MD, PhD[1], Anne H. O'Donnell-Luria, MD, PhD[2,3,4], Jessica X. Chong, PhD[5], Tamar Harel, MD, PhD[6], Shalini N. Jhangiani, MS[7], Zeynep H. Coban Akdemir, PhD[1], Steven Buyske, PhD[8,9], Davut Pehlivan, MD[1], Claudia M. B. Carvalho, PhD[1], Samantha Baxter, MS, CGC[3], Nara Sobreira, MD, PhD[10], Pengfei Liu, PhD[1,11], Nan Wu, MD[1,12], Jill A. Rosenfeld, MS, CGC[1], Sushant Kumar, PhD[13], Di
Janson J. White, PhD[1,5], Kimberly F. Doheny, PhD[1
Corinne Boehm, MS, CGC[10], V. Reid Sutton, MD[1], Donna M.
Murat Günel, MD[16,17], Deborah A. Nickerson, Ph
Daniel G. MacArthur, PhD[2,3], Richard A. Gibbs, I
Richard P. Lifton, MD, PhD[16,20,21], Tara C. Matise, PhD[8], Heid
Michael J. Bamshad, MD[5,18], David V
James R. Lupski, MD, PhD, DSc (hon)[1,7,22,23] Cent

Cell

Genomic Analysis in the Age of Human Genome Sequencing

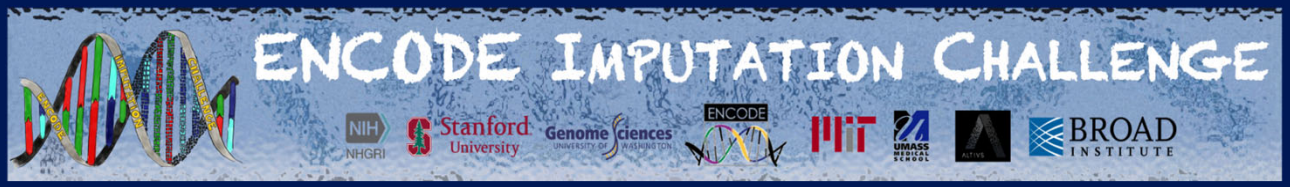
Tuuli Lappalainen,[1,2,*] Alexandra J. Scott,[3,4,5] Margot Brandt,[1,2] and Ira M. Hall[3,4,5,*]

Document 14

Technology Development Program

- **Novel Nucleic Acid Sequencing Technology Development**
  - RFA-HG-18-001 (R01, also linked R21 and R43/44)
  - Next due date: June 27, 2019
- **Advanced Genomic Technology Development Meeting at Northeastern University**
  - Grantee meeting: May 29-30, 2019
  - Public meeting: May 31, 2019

ENCyclopedia Of DNA Elements (ENCODE)

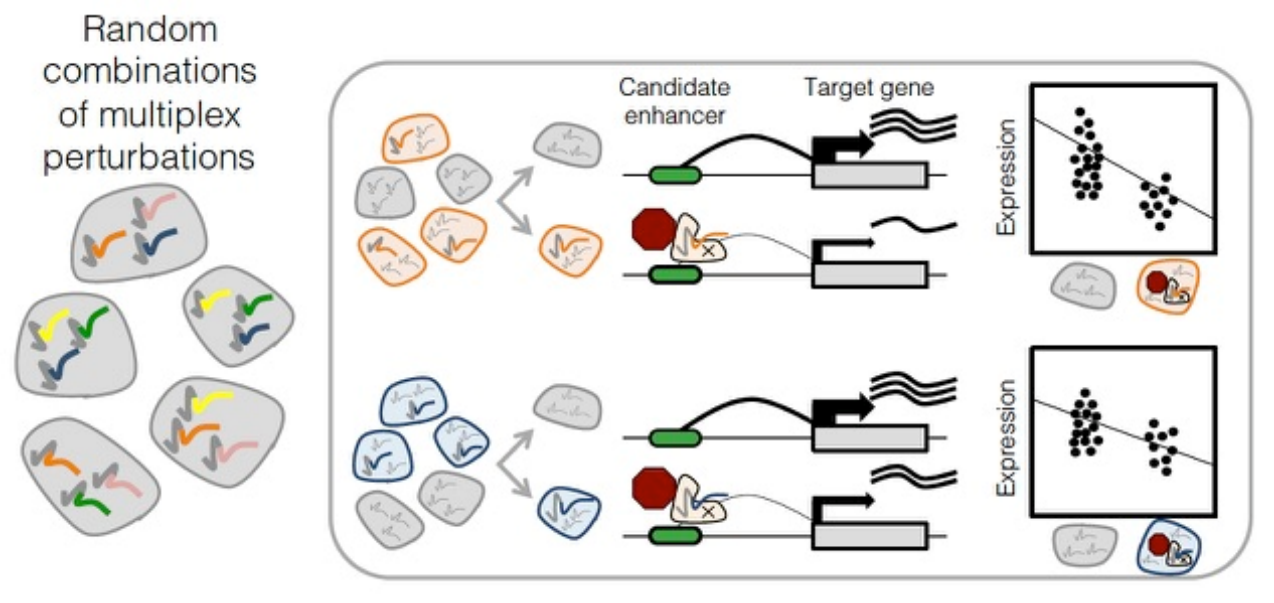


- Multiple competitive rounds
- Research and Applications Users Meeting (July 8-11, 2019 in Seattle)
- ENCODE data are now as an Amazon Web Services Public Data Set

ENCyclopedia Of DNA Elements (ENCODE)

A Genome-wide Framework for Mapping Gene Regulation via Cellular Genetic Screens

Molly Gasperini,[1,*] Andrew J. Hill,[1] José L. McFaline-Figueroa,[1] Beth Martin,[1] Seungsoo Kim,[1] Melissa D. Zhang,[1] Dana Jackson,[1] Anh Leith,[1] Jacob Schreiber,[2] William S. Noble,[1,2] Cole Trapnell,[1,3] Nadav Ahituv,[4] and Jay Shendure[1,3,5,6,*]



Document 16

Phenotypes and Exposures (PhenX) Toolkit

- Pediatric Development
- Cancer Outcomes and Survivorship
- Genomic Medicine Implementation
- Social Determinants of Health

NIH National Institute on Minority Health and Health Disparities

NHGRI-EBI GWAS Catalog

- >100,000 curated SNP-trait associations
- Now accepting summary statistics

The Missing Diversity in Human Genetic Studies

Giorgio Sirugo,[1,2,6,*] Scott M. Williams,[5,6,*] and Sarah A. Tishkoff[3,4,6,*]
[1]Department of Systems Pharmacology and Translational Therapeutics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA
[2]Division of Translational Medicine and Human Genetics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA
[3]Department of Genetics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA
[4]Department of Biology, School of Arts and Sciences, University of Pennsylvania, Philadelphia, PA 19104, USA
[5]Departments of Population and Quantitative Health Sciences, and Genetics and Genome Sciences, Cleveland Institute for Computational Biology, Case Western Reserve University, Cleveland, OH 44106, USA

- Justification for diverse populations in human genetics research
- Majority (52%) of GWAS studies conducted in European populations
- Need to include ancestrally diverse populations

eMERGE network

ELECTRONIC MEDICAL RECORDS AND GENOMICS

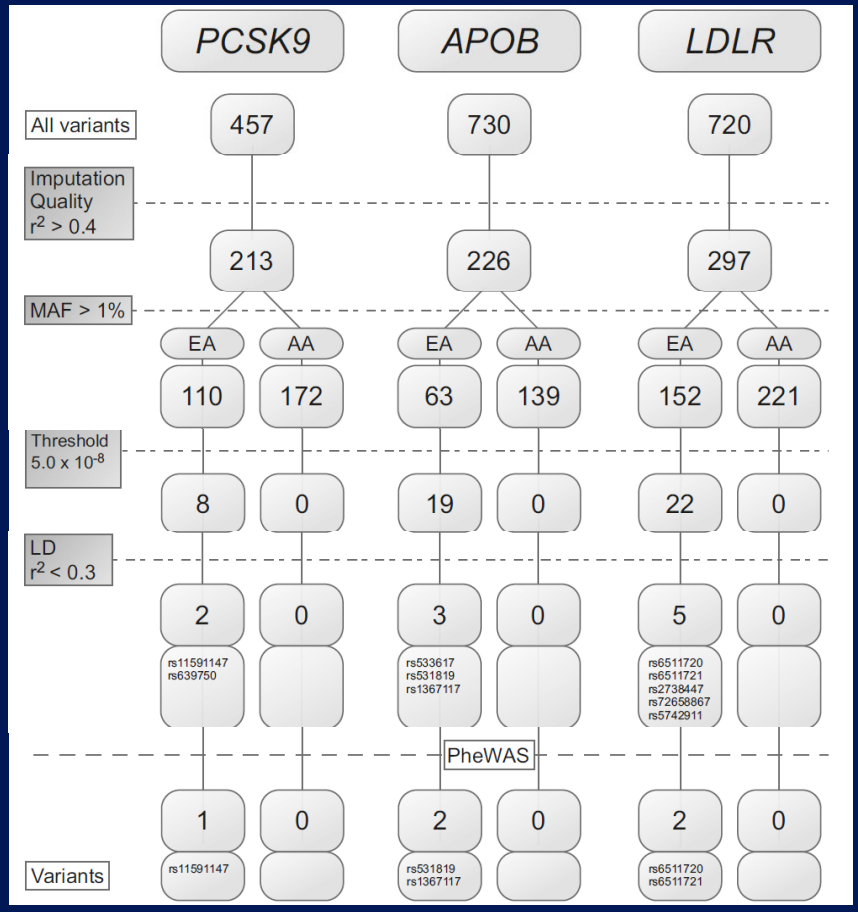
ARTICLE OPEN

A phenome-wide association study to discover pleiotropic effects of *PCSK9*, *APOB*, and *LDLR*

Maya S. Safarova[1], Benjamin A. Satterfield[1], Xiao Fan[1], Erin E. Austin[1], Zhan Ye[2], Lisa Bastarache[3], Neil Zheng[3], Marylyn D. Ritchie[4], Kenneth M. Borthwick[5], Marc S. Williams[6], Eric B. Larson[7], Aaron Scrol[7], Gail P. Jarvik[8], David R. Crosslin[8,9], Kathleen Leppig[10], Laura J. Rasmussen-Torvik[11], Sarah A. Pendergrass[5], Amy C. Sturm[6], Bahram Namjou[12], Amy Sanghavi Shah[13], Robert J. Carroll[3], Wendy K. Chung[14,15], Wei-Qi Wei[3], QiPing Feng[16], C. Michael Stein[16], Dan M. Roden[17], Teri A. Manolio[18], Daniel J. Schaid[19], Joshua C. Denny[3], Scott J. Hebbring[20], Mariza de Andrade[19] and Iftikhar J. Kullo[1]

We conducted an electronic health record (EHR)-based phenome-wide association study (PheWAS) to discover pleiotropic effects of variants in three lipoprotein metabolism genes *PCSK9*, *APOB*, and *LDLR*. Using high-density genotype data, we tested the associations of variants in the three genes with 1232 EHR-derived binary phecodes in 51,700 European-ancestry (EA) individuals and 585 phecodes in 10,276 African-ancestry (AA) individuals; 457 *PCSK9*, 730 *APOB*, and 720 *LDLR* variants were filtered by imputation quality ($r^2 > 0.4$), minor allele frequency (>1%), linkage disequilibrium ($r^2 < 0.3$), and association with LDL-C levels, yielding a set of two *PCSK9*, three *APOB*, and five *LDLR* variants in EA but no variants in AA. Cases and controls were defined for each phecode using the PheWAS package in R. Logistic regression assuming an additive genetic model was used with adjustment for age, sex, and the first two principal components. Significant associations were tested in additional cohorts from Vanderbilt University ($n = 29,713$), the Marshfield Clinic Personalized Medicine Research Project ($n = 9562$), and UK Biobank ($n = 408,455$). We identified one *PCSK9*, two *APOB*, and two *LDLR* variants significantly associated with an examined phecode. Only one of the variants was associated with a non-lipid disease phecode, ("myopia") but this association was not significant in the replication cohorts. In this large-scale PheWAS we did not find LDL-C-related variants in *PCSK9*, *APOB*, and *LDLR* to be associated with non-lipid-related phenotypes including diabetes, neurocognitive disorders, or cataracts.

npj Genomic Medicine (2019)4:3 ; https://doi.org/10.1038/s41525-019-0078-7



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Clinical Genome Resource (ClinGen)

ARTICLE | Genetics inMedicine

ClinGen expert clinical validity curation of 164 hearing loss gene–disease pairs

Marina T. DiStefano, PhD[1,2], Sarah E. Hemphill, BA[1], Andrea M. Oza, MS, CGC[1,3], Rebecca K. Siegert, BS[2], Andrew R. Grant, BA[2], Madeline Y. Hughes, BA[2], Brandon J. Cushman, BA[1], Hela Azaiez, PhD[4], Kevin T. Booth, BS[4,5], Alex Chapin, PhD[6], Hatice Duzkale, MD, MPH[7], Tatsuo Matsunaga, MD, PhD[8,9], Jun Shen, PhD[1,10], Wenying Zhang, MD, PhD[11], Margaret Kenna, MD, MPH[3,10], Lisa A. Schimmenti, MD[12], Mustafa Tekin, MD[13], Heidi L. Rehm, PhD[1,2], Ahmad N. Abou Tayoun, PhD[14] and Sami S. Amr, PhD[1,10] on behalf of the ClinGen Hearing Loss Clinical Domain Working Group

Circulation: Genomic and Precision Medicine

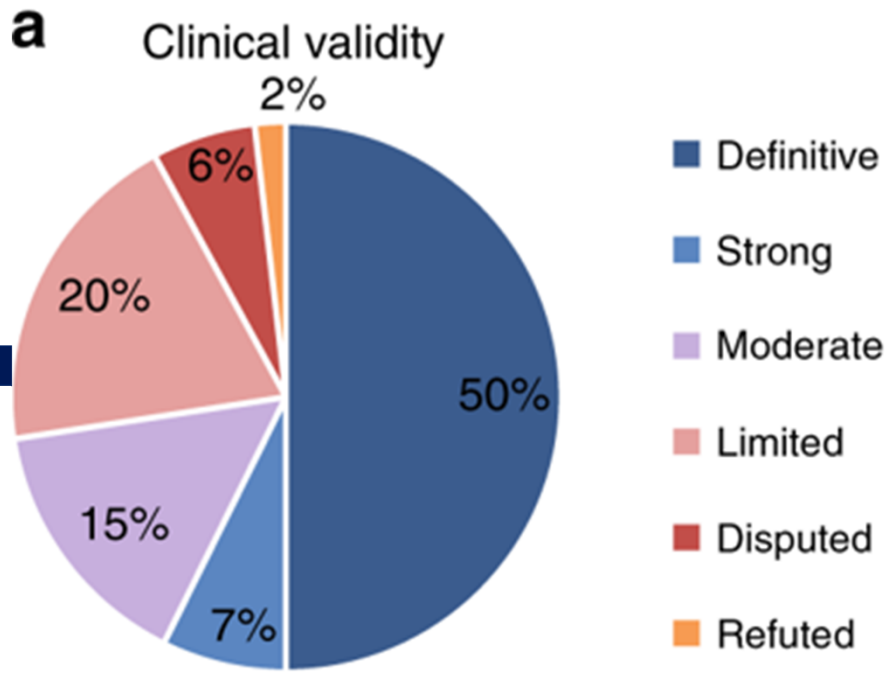
ORIGINAL ARTICLE

Evaluating the Clinical Validity of Hypertrophic Cardiomyopathy Genes

BACKGROUND: Genetic testing for families with hypertrophic cardiomyopathy (HCM) provides a significant opportunity to improve care. Recent trends to increase gene panel sizes often mean variants in genes with questionable association are reported to patients. Classification of

Jodie Ingles, GradDip-GenCouns, PhD, MPH et al

ARTICLE | Genetics inMedicine



Kristy Lee, MS[1], Bryce A. Seifert, PhD[1], Hermela Shimelis, PhD[1], Rajarshi Ghosh, PhD[1], Stephanie B. Crowley, PhD[1], Natalie J. Carter, MS[4], Kurston Doonanco, MS[4], A. Katherine Foreman, MS[1], Deborah I. Ritter, PhD[3], Sharisse Jimenez, BS[1], Mackenzie Trapp, BS[1], Kenneth Offit, MD, MPH[5], Sharon E. Plon, MD, PhD[3] and Fergus J. Couch, PhD[2]

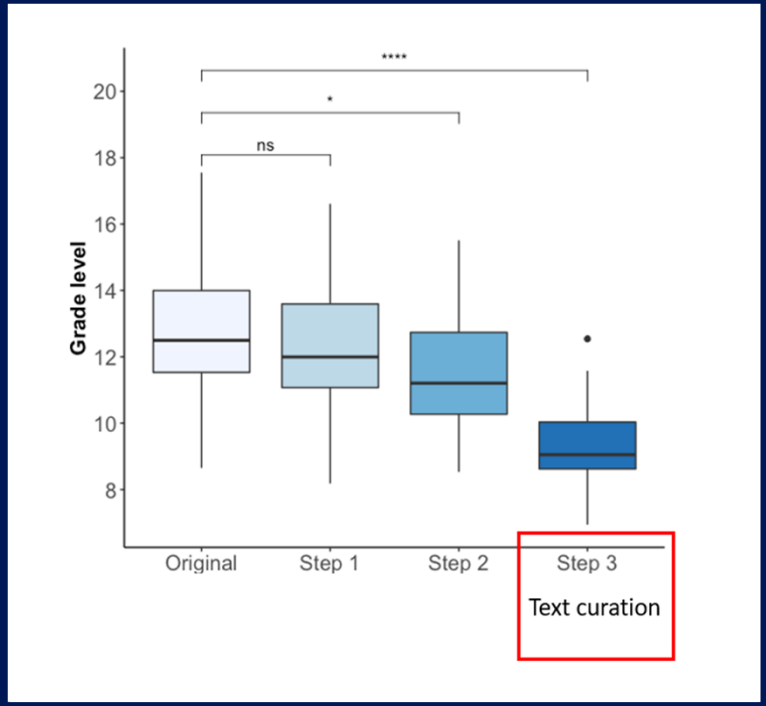
Clinical Sequencing Evidence-Generating Research Program

ACMG 2019 Meeting:

Featured Workshop: Addressing Literacy and Language to Equitably Deliver on the Promise of Precision Medicine

1 platform & 15 poster presentations

Simplifying Readibility for the Genetics Home Reference:



Figures courtesy of the J. Shieh lab

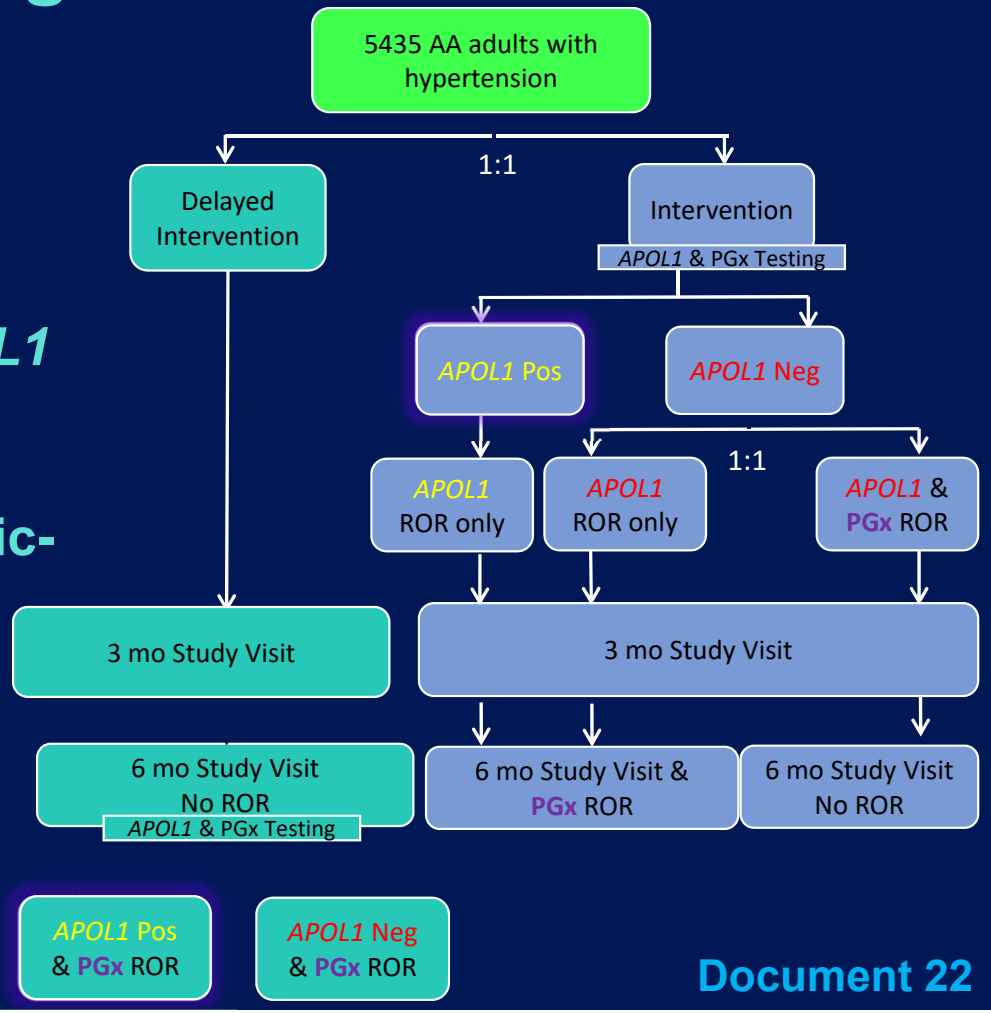
Implementing GeNomics In pracTicE (IGNITE) II: Pragmatic Clinical Trials

- First IGNITE trial to launch:
  Genetic Testing to Understand Renal Disease Disparities in the U.S.

  Aim: Effect of knowing positive *APOL1* status in treating systolic blood pressure (SBP)
  Sub-Study: Effect of Pharmacogenetic-guided therapy on SBP
  Primary Outcome: SBP at 3 months

- Largest NHGRI PCT in an entirely minority population

  ADOPT PGx trial coming soon



Newborn Sequencing In Genomic medicine and public HealTh (NSIGHT)

NSIGHT Public Webinar – June 24, 2019

- For disorders currently screened for in newborns, how can genomic sequencing replicate or augment known newborn screening results?
- What knowledge could genomic sequencing provide about conditions not currently screened for in newborns?
- What additional clinical information could be learned from genomic sequencing relevant to the clinical care of newborns?

International 100K+ Cohort Consortium (IHCC)

Selection of Cohorts:

- 100K+ participants
- Available biospecimens
- Disease-agnostic
- Longitudinal follow-up

International 100K+ Cohort Consortium (IHCC)

IHCC's 1st International Cohorts Summit (2018)

IHCC's 2nd International Cohorts Summit (2019)

- Identify cross-cohort research projects and identify international collaborators to organize and participate in them
- Develop an IHCC scientific agenda to bring forward to research funders

President of Iceland
Guðni Thorlacius Jóhannesson

Computational Genomics and Data Science Program

Analysis, Visualization, and Informatics Lab-space (AnVIL)

- Approved NIH-Designated Data Repository
- Established External Consultant Committee
- Public launch at the end of 2019

ELSI Research Program

CEER Annual Meeting

GSWG Annual Meeting

SBIR/STTR Programs

SBIR Grantees Win Product Awards

Genomenon "Mastermind" Genomic Search Engine wins Best in Show at Bio-IT World for insight into diseases, genes, and genomic variants

Duality Technologies wins 2nd place in Innovation Sandbox at RSAC 2019 for SecurePlus encryption for GWAS

Training and Career Development

2019 Meeting (St. Louis)

2020 Meeting: March 30-April 1 @ UPenn

Training and Career Development

- Mentored Clinical Scientist Research Career Development Awards (K08)
- NHGRI focus: Genomic Medicine
- Awardees to date:

Jennifer Posey, MD, PhD
Baylor College of Medicine

Amit Khera, MD
Massachusetts General Hospital

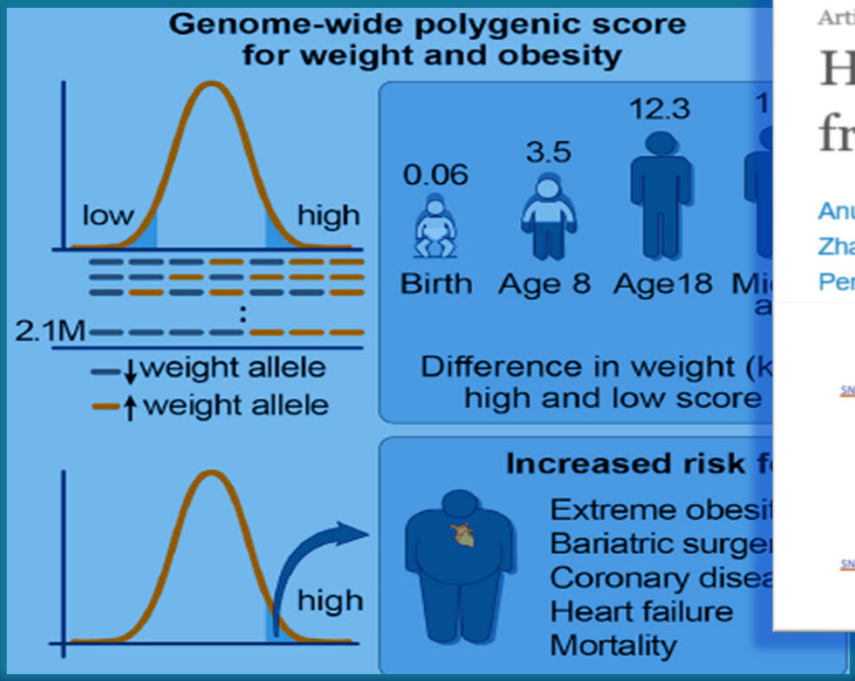
Anandi Krishnan, PhD
Stanford University

Dustin Baldridge, MD, PhD
Washington University, St. Louis

Extramural Investigator-Initiated Highlights

Polygenic Prediction of Weight and Obesity Trajectories from Birth to Ad

Amit V. Khera,[1,2,3,4,15,*] Mark Chaffin,[3,15] Kaitlin H. Wade,[5,6,7] Sohail Zahid,[3,4] Joseph Br
Marina Distefano,[10,11,12] Ozlem Senol-Cosar,[10,11,12] Mary E. Haas,[3] Alexander Bick,[1,3,4]
Eric S. Lander,[3,13,14] George Davey Smith,[5,6] Heather Mason-Suares,[10,11,12] Myriam For
Nicholas J. Timpson,[5,6,7] Lee M. Kaplan,[4,8] and Sekar Kathiresan[1,2,3,4,16,*]



AJHG

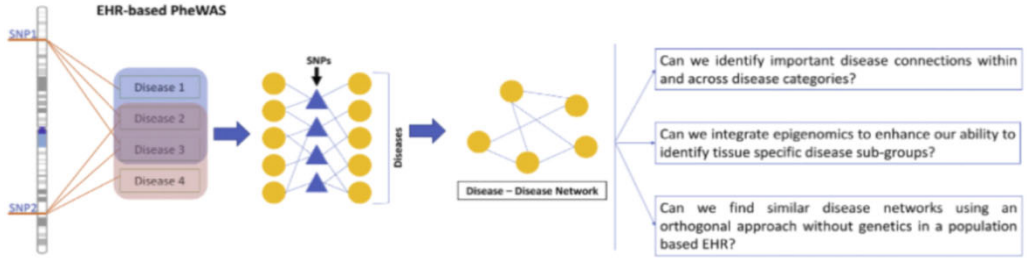
Volume 104, Issue 1, 3 January 2019, Pages 55-64

Cell PRESS

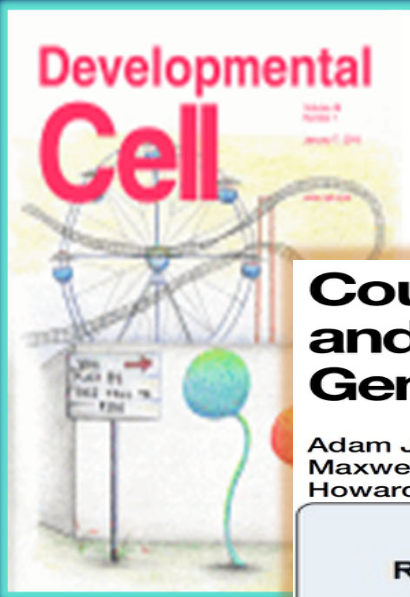
Article

Human-Disease Phenotype Map Derived from PheWAS across 38,682 Individuals

Anurag Verma [1, 2], Lisa Bang [3], Jason E. Miller [1], Yanfei Zhang [4], Ming Ta Michael Lee [4], Yu Zhang [5], Marta Byrska-Bishop [3, 7], David J. Carey [6], Marylyn D. Ritchie [1, 2], Sarah A. Pendergrass [3], Dokyoon Kim [2, 3]



Extramural Investigator-Initiated Highlights

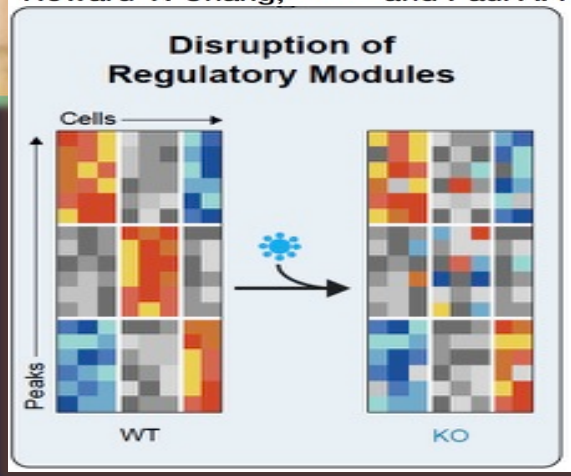


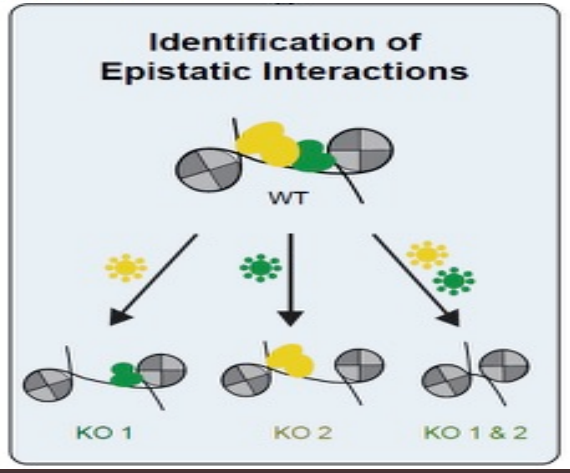
Developmental Cell
Article

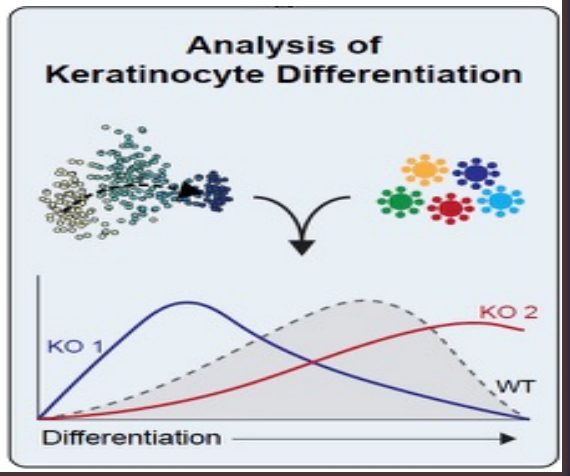
CellPress

Coupled Single-Cell CRISPR Screening and Epigenomic Profiling Reveals Causal Gene Regulatory Networks

Adam J. Rubin,[1,9] Kevin R. Parker,[1,2,9] Ansuman T. Satpathy,[1,3,9] Yanyan Qi,[1] Beijing Wu,[1] Alvin J. Ong,[1,2] Maxwell R. Mumbach,[1,2,4] Andrew L. Ji,[1] Daniel S. Kim,[1] Seung Woo Cho,[1,2] Brian J. Zarnegar,[1] William J. Greenleaf,[4,5,6] Howard Y. Chang,[1,2,4,7,*] and Paul A. Khavari[1,8,10,*]







Extramural Investigator-Initiated Highlights

Genetics inMedicine
Official Journal of the American College of Medical Genetics and Genomics

Disability inclusion in precision medicine research: a first national survey

Maya Sabatello, LLB, PhD[1], Ying Chen, MD, MS[2], Yuan Zhang, MS, MA[3] and Paul S. Appelbaum, MD[1]

Demographic variables	N[b]	%
Primary disability/condition ($n = 1294$)		
Blindness or low vision	271	21
Deafness or hard of hearing	267	21
Physical disability	273	21
Autism	104	8
Intellectual or developmental disability	128	10
Learning disability	136	11
Mental health or psychosocial disability	115	9
Multiple disabilities/conditions ($n = 1294$)	323	25

Director's Report Outline

I. General NHGRI Updates

II. General NIH Updates

III. General Genomics Updates

IV. NHGRI Extramural Research Program

V. NIH Common Fund/Trans-NIH

VI. NHGRI Division of Policy, Communications, and Education

VII. NHGRI Intramural Research Program

Human Microbiome Project (HMP)

NIH Human Microbiome Portfolio Analysis Team* *Microbiome* (2019) 7:31
https://doi.org/10.1186/s40168-019-0620-y

Microbiome

REVIEW Open Access

A review of 10 years of human microbiome research activities at the US National Institutes of Health, Fiscal Years 2007-2016

NIH Human Microbiome Portfolio Analysis Team*

The 2017 NIH-wide microbiome workshop writing team *Microbiome* (2019) 7:32
https://doi.org/10.1186/s40168-019-0627-4

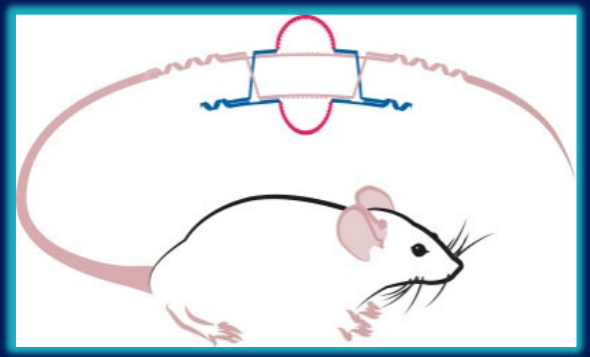
Microbiome

MEETING REPORT Open Access

2017 NIH-wide workshop report on "The Human Microbiome: Emerging Themes at the Horizon of the 21st Century"

The 2017 NIH-wide microbiome workshop writing team[1]

Knockout Mouse Phenotyping Project (KOMP2)



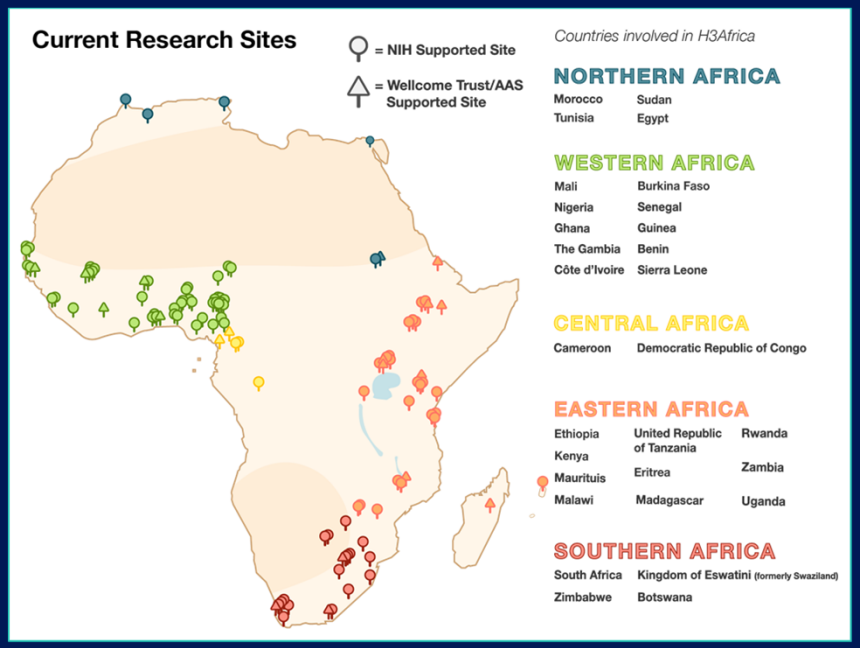
IMPC
International Mouse Phenotyping Consortium

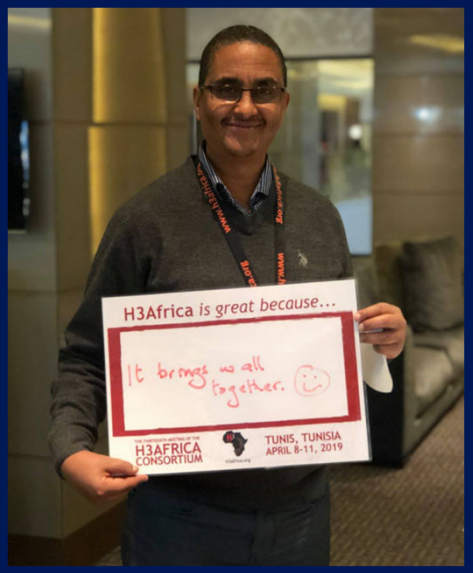
- **INFRAFRONTIER – IMPC Meeting: Helsinki (June 3-5)**

  Genomic Variation, Big Data, and Aging

- **KOMP2 Community Workshop: Bethesda (June 27)**

Human Heredity and Health in Africa (H3Africa)





- H3Africa supports 48 projects across 34 African countries
- 13th Consortium Meeting in Tunisia

Human Heredity and Health in Africa (H3Africa)

H3Africa announced as a driver project for the Global Alliance for Genomics and Health

Christian Happi

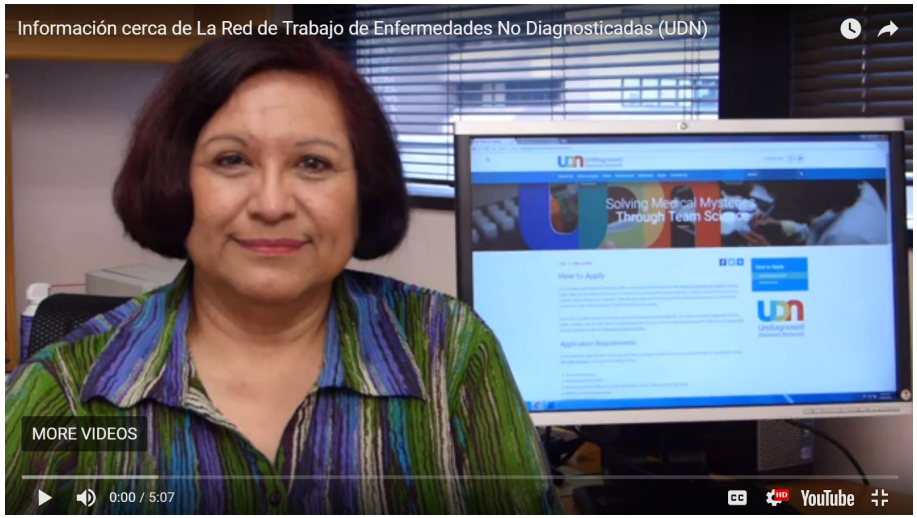
Guida Landoure

Jantina De Vries

Several H3Africa members received recent recognitions

Undiagnosed Diseases Network (UDN)

The UDN website now has information in Spanish!



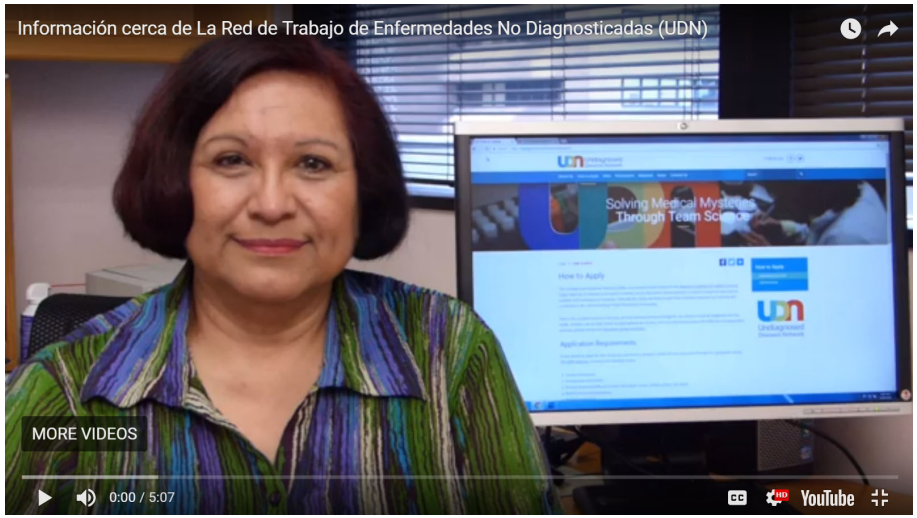
Undiagnosed Diseases Network

- How to apply
- Frequently asked questions
- Video
- Download the application

You can call or email the Helpdesk at the UDN Coordinating Center to find out more. We speak Spanish.

La Red de Trabajo de Enfermedades No Diagnosticadas

¡El sitio web de la UDN ya tiene información en español!



Undiagnosed Diseases Network

- Forma de hacer un solicitud
- Preguntas frecuentes
- Video
- Descargar la solicitud

Usted puede llamar o mandar un correo electrónico al Centro de Coordinación de la UDN para conocer más. Se habla español.

All of Us
RESEARCH PROGRAM

- Information on *All of Us* program data and tools:
  - Data Snapshots
  - Data Browser
  - Survey Explorer

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NHGRI Redesigns genome.gov

The new
genome.gov
is **here!**

G T A C G T A

C G T A C G T

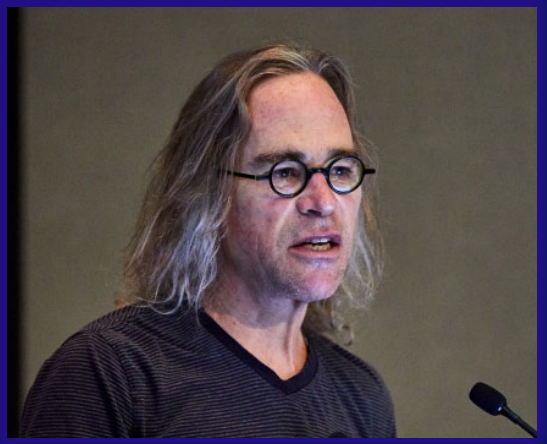
G T A C G T A

C G T A C G T

NHGRI History of Genomics Program

JHB Special Issue

Oral Histories



Speaker Series

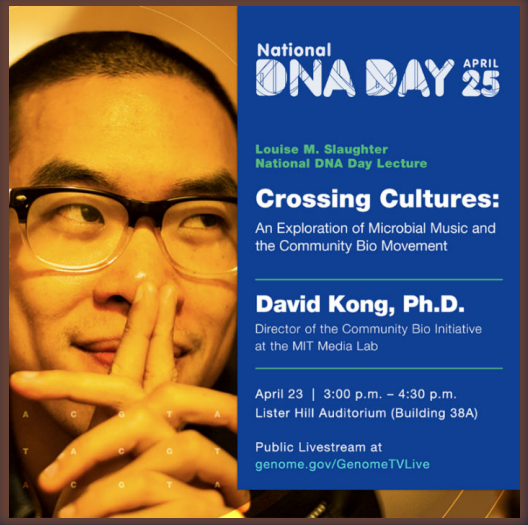
Perspectives on the Human Genome Project and Genomics

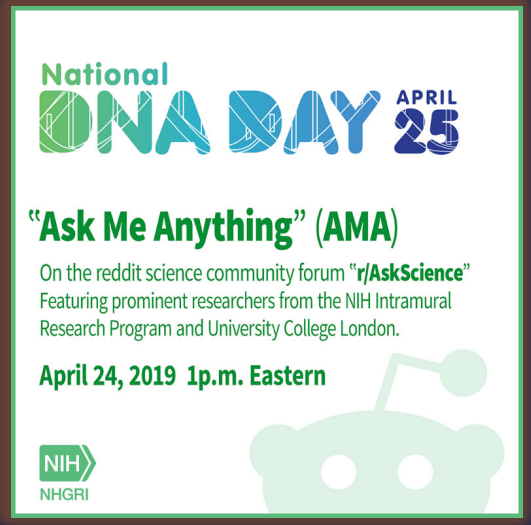
Document 36

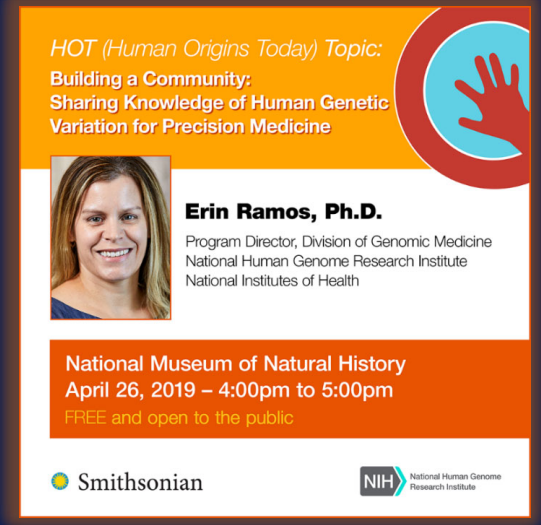
American Sign Language Film: Genetic Testing for Breast Cancer

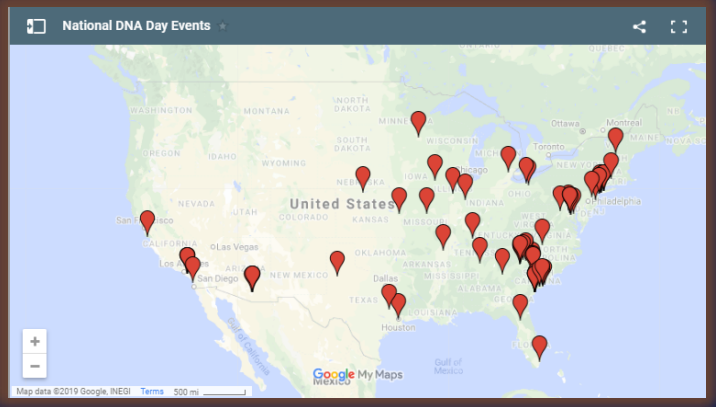
Document 37

2019 National DNA Day



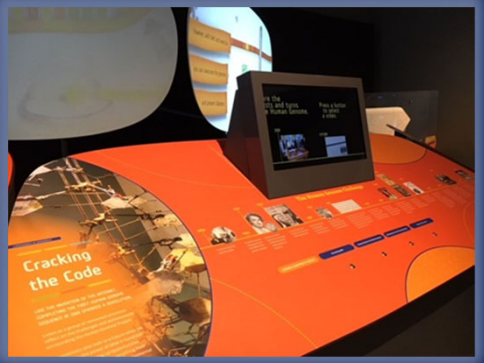






Document 38

Genome: Unlocking Life's Code Exhibition
Travel Schedule



GENOME
UNLOCKING
LIFE'S
CODE

- **September 12 – January 2, 2020**

  Turtle Bay Exploration Park, Redding, CA

- **January 17 – April 12, 2020**

  Museum of Science & History, Jacksonville, FL

Inter-Society Coordinating Committee for Practitioner Education in Genomics (ISCC)

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Elected to National Academy of Sciences

Elaine Ostrander, Ph.D.

Document 41

Health and Human Services Career Achievement Award

Dan Kastner, M.D., Ph.D.

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NHGRI Intramural Research Highlights

nature COMMUNICATIONS

Researchers create the largest global catalog of variations in the dog genome

nature genetics

Researchers uncover gene regions that affect cholesterol levels in smokers

Molecular Psychiatry

Linking genes to ADHD by mapping connections in the brain

The Genomics Landscape

Email Updates

Sign up to receive National Human Genome Research Institute (NHGRI) updates and stay informed about our latest science, research, news, upcoming events and website content.

Email Address

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National Human Genome Research Institute

Thanks!

Special Thanks!


The Forefront
of Genomics®