



National Institutes
of Health

All
of Us

RESEARCH PROGRAM

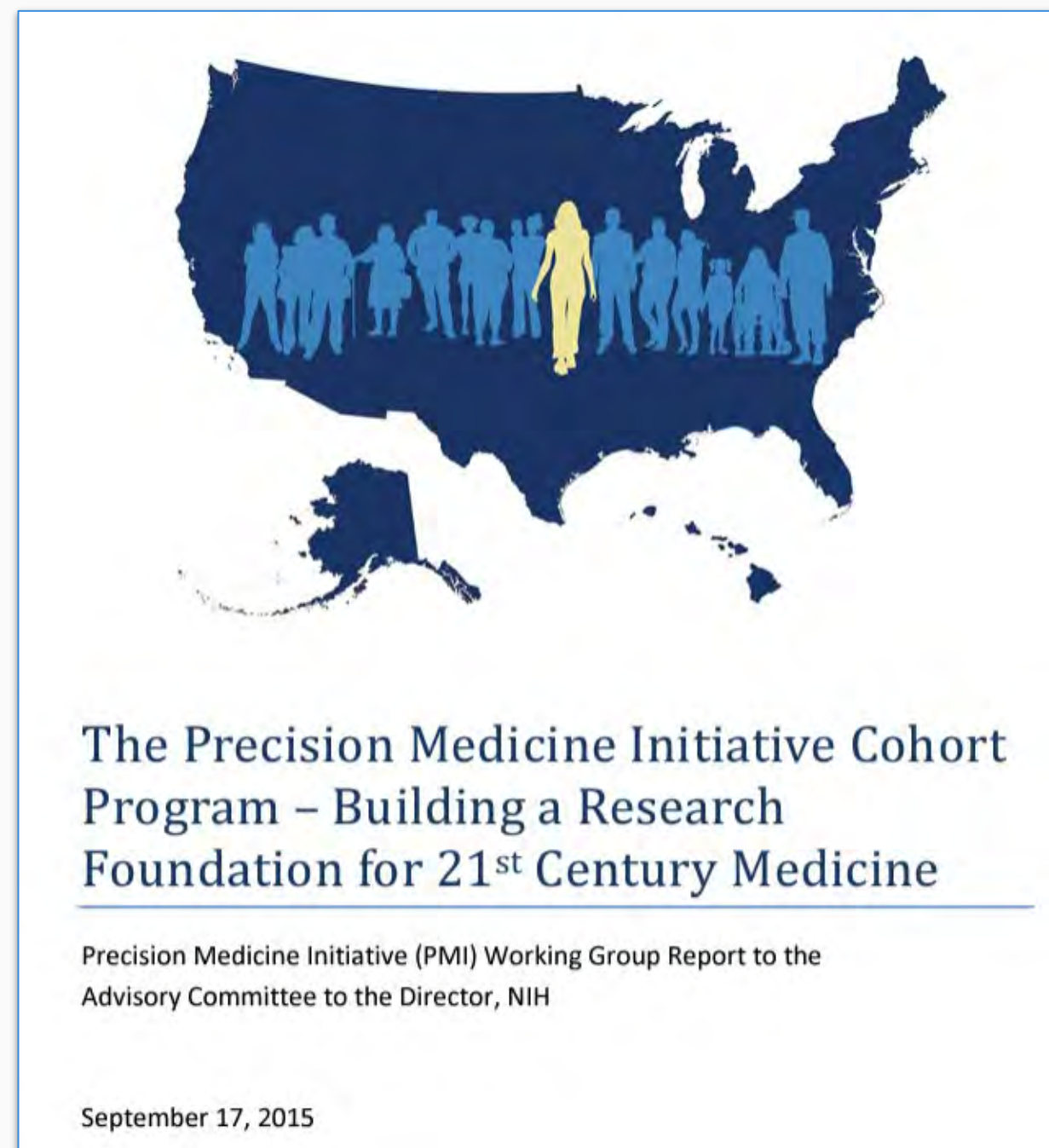
All of Us Research Program

Josh Denny, M.D., M.S.
Chief Executive Officer



What is the NIH *All of Us* Research Program?

The *All of Us* Research Program is a historic, longitudinal effort to **gather data from one million or more people** living in the United States **to accelerate research and improve health**. By taking into account individual differences **in lifestyle, socioeconomic, environment, and biology**, we hope that researchers will one day uncover paths toward delivering **precision medicine – or individualized prevention, treatment, and care – for all of us**.

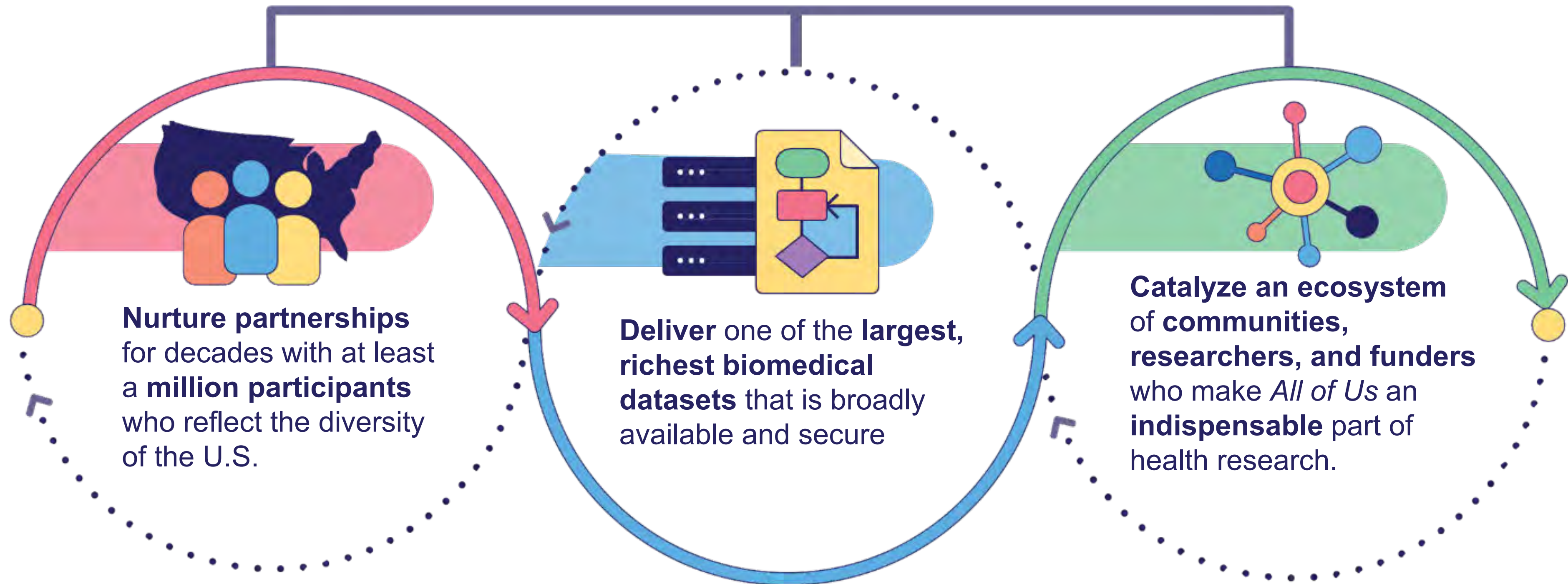


“*All of Us* is among the most ambitious research efforts that our nation has undertaken!”

NIH Director Francis Collins, M.D., Ph.D.

The *All of Us* Research Program Mission

Accelerate health research and medical breakthroughs,
enabling individualized prevention, treatment, and care for all of us.



Made possible by a team that maintains a culture built around the program's core values

All of Us Research Program Core Values

Participation is **open** to all.

Participants reflect the rich **diversity** of the U.S.

Participants are **partners**.

Trust will be earned through **transparency**.

Participants have **access** to their information.

Data will be accessed **broadly** for research purposes.

Security and privacy will be of highest importance.

The program will be a catalyst for **positive change** in research.

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Consented 740K+ Participants With Continued Growth

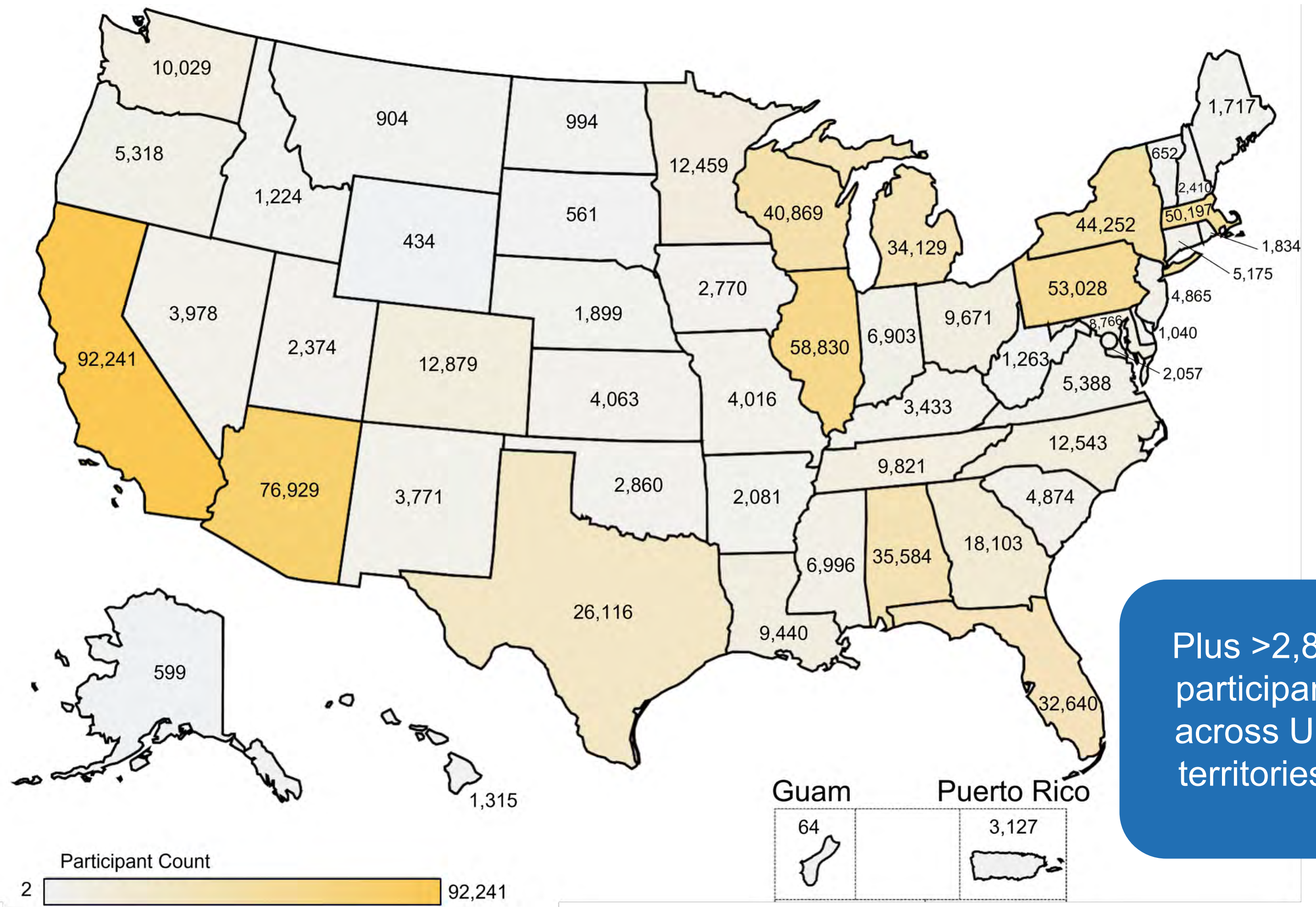
Map of Consented Participants

740,000+
Participants

507,000+
Participants who
have completed initial
steps of the program

409,000+
Electronic
Health Records

525,000+
Biosamples

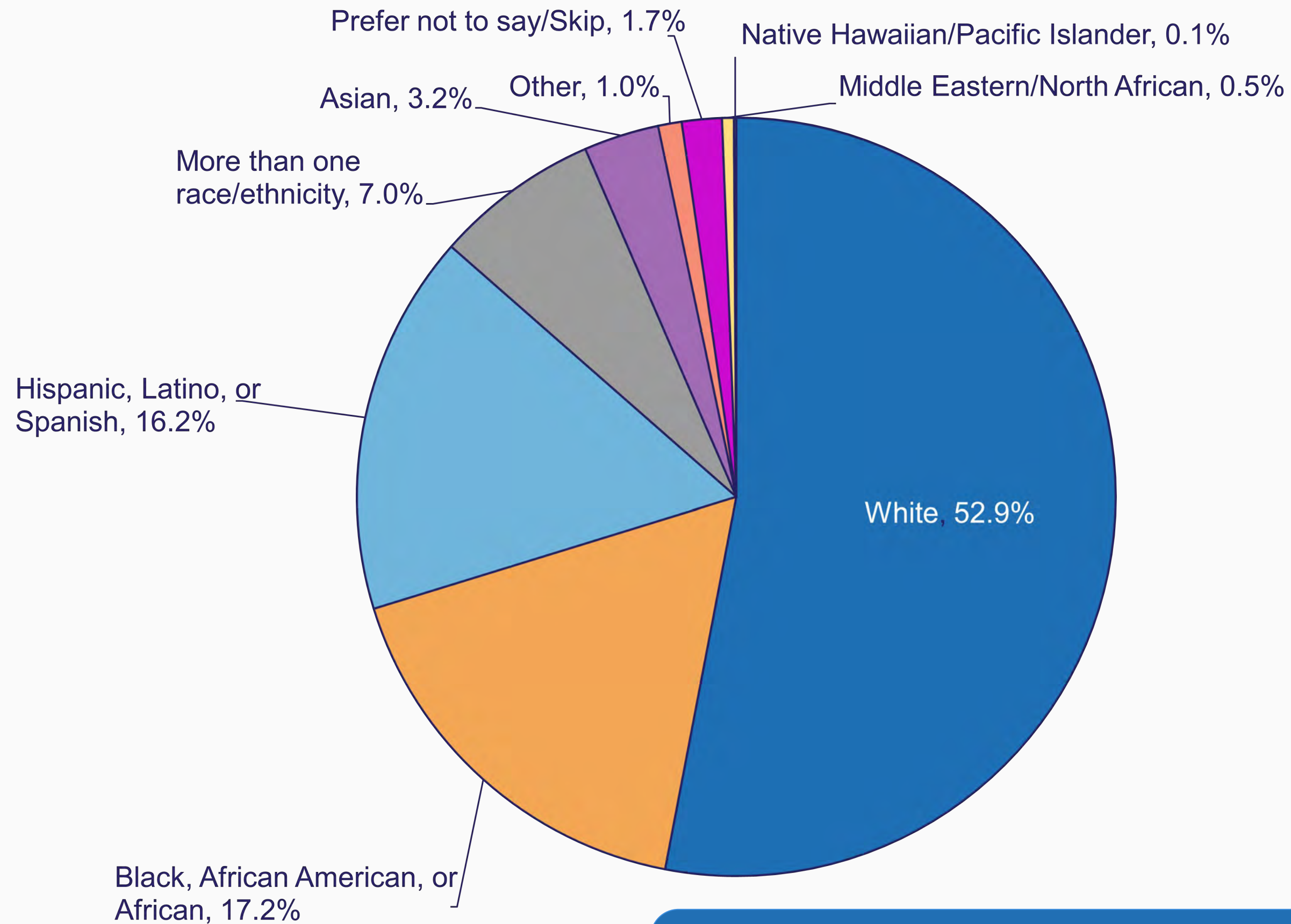


Plus >2,800
participants
across U.S.
territories

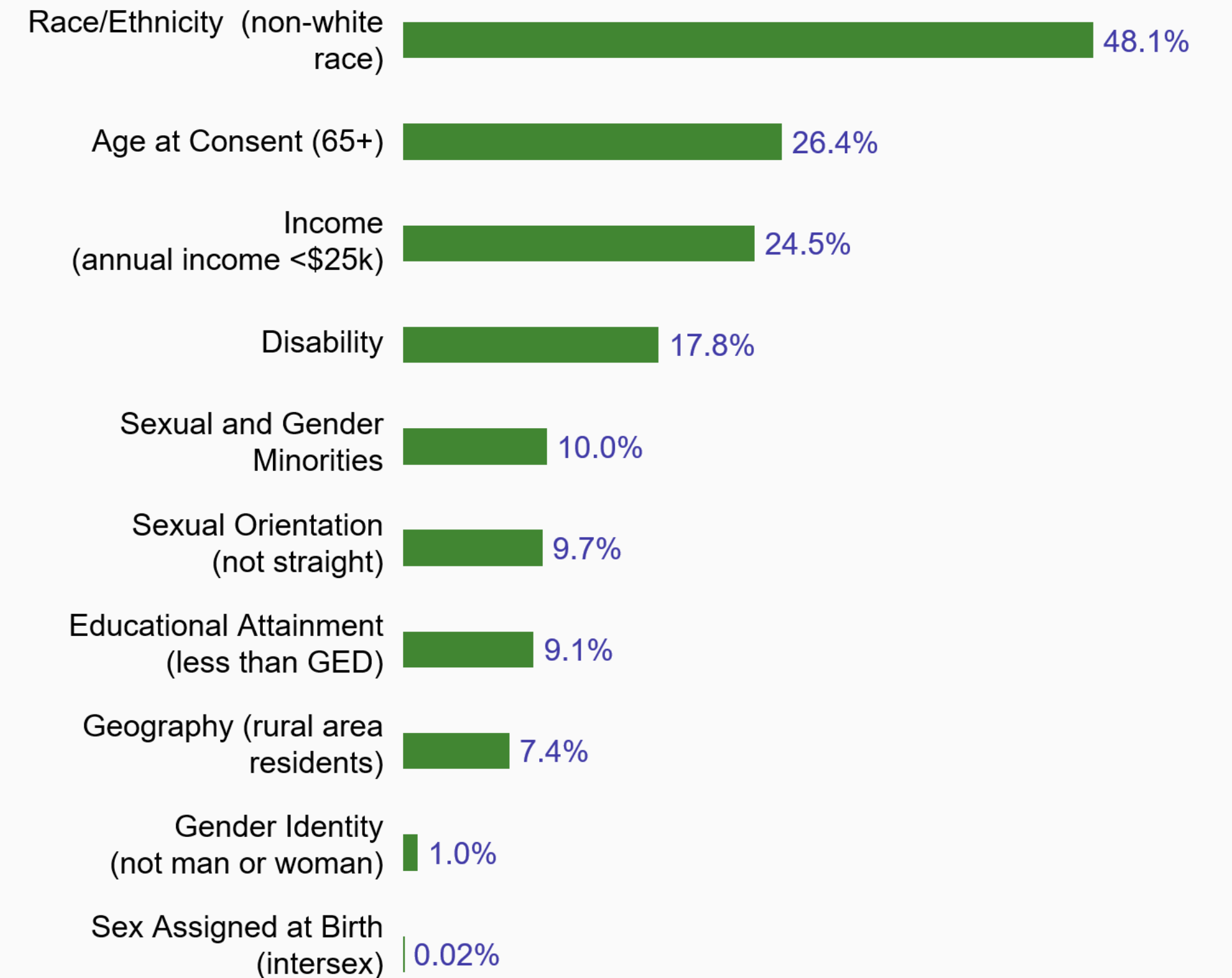
Numbers current as of November 29, 2023

Participant Diversity

Race & Ethnicity of Participants



UBR Category



Over 80% of *All of Us* participants are underrepresented in biomedical research

Numbers current as of November 29, 2023

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All of Us Consortium Members (as of November 2023)

The Participant Center



Communications & Engagement



<h3>HPO Network</h3> <p>(Health Care Provider Organizations)</p>	<h3>Illinois Precision Medicine Consortium</h3>	<h3>All of Us New England</h3>	<h3>Trans America Consortium</h3>	<h3>New York City Consortium</h3>	<h3>All of Us Southern Network</h3>	<h3>All of Us Southeast Enrollment Center</h3>	<h3>Heartland Consortium</h3>
<h3>All of Us California</h3>							
<h3>All of Us Wisconsin</h3>	<h3>All of Us Pennsylvania</h3>	<h3>University of Arizona and Banner Health</h3>	<h3>FQHCs</h3>	<h3>VA Medical Centers</h3>	<h3>Nutrition for Precision Health (NPH)</h3>	<h3>All of Us Puerto Rico</h3>	

<h3>Participant Technology Systems Center (PTSC)</h3>	<h3>Center for Linkages and Acquisition of Data (CLAD)</h3>	<h3>Biobank</h3>	<h3>Data & Research Center (DRC)</h3>	<h3>Genomics Partners</h3>
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Note: These are not approved lockups and should not be repurposed on assets.

All of Us Community and Provider Partner Network (as of April 2023)



Note: These are not approved lockups and should not be repurposed on assets.

All of Us Engagement Ecosystem



Today, the program includes **35 Participant Ambassadors** and **10 Participant Partners** who serve on the Steering Committee, the Executive Committee, and the Advisory Panel.



All of Us Tribal Engagement



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Data Collected and Return of Value to *All of Us* Participants



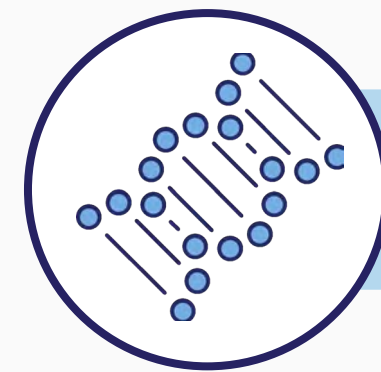
Consent and Electronic Health Records



Participant Surveys



Physical Measurements



Biosamples

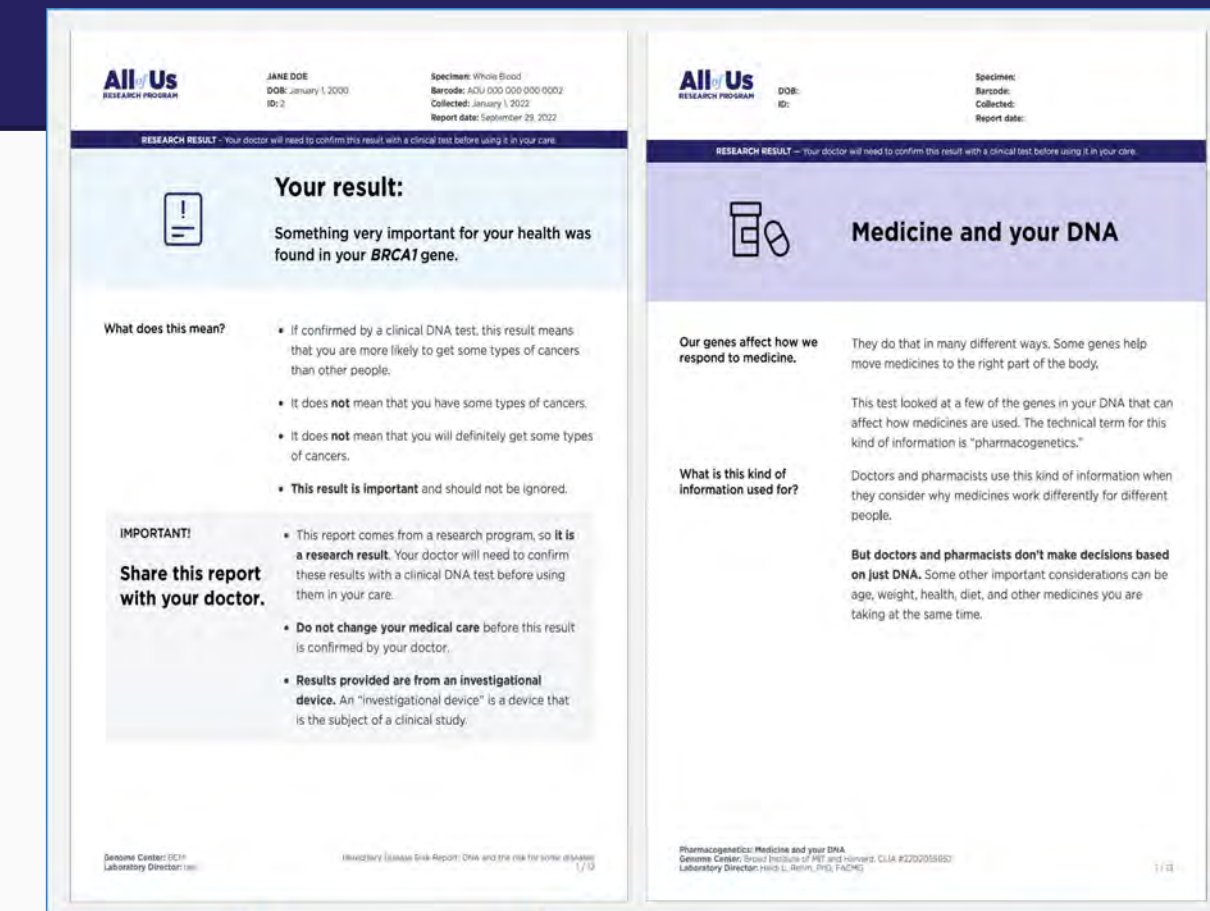


Mobile/Wearable Tech

Return of Value for Participants

Participants may receive:

- **Genetic information**
- Survey data (comparative)
- EHR and claims data
- Ongoing study updates
- Aggregate results
- Scientific findings
- Opportunities to be contacted for other research opportunities



Participants Can Receive Four Types of Genetic Research Results

Engaging insights

Genetic ancestry and traits results



7 regions (20 subregions) and 4 traits

- Sub-Saharan Africa
- Europe
- Oceania
- Southern Asia
- Eastern and northern Asia
- The Middle East and North Africa
- The Americas
- Ear wax
- Bitter taste perception
- Cilantro preference
- Lactose intolerance

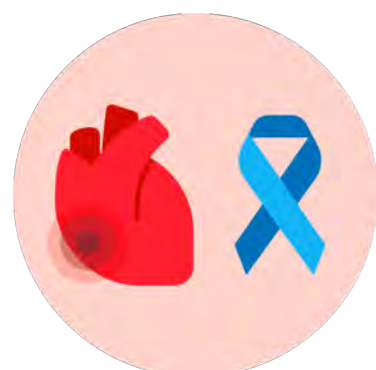
Medicine and your DNA Report



7 pharmacogenomics (PGx) genes and 50+ medications

- *CYP2C19*
- *DPYD*
- *G6PD*
- *SLCO1B1*
- *NUDT15*
- *TPMT*
- *UGT1A1*

Hereditary Disease Risk (HDR) Report

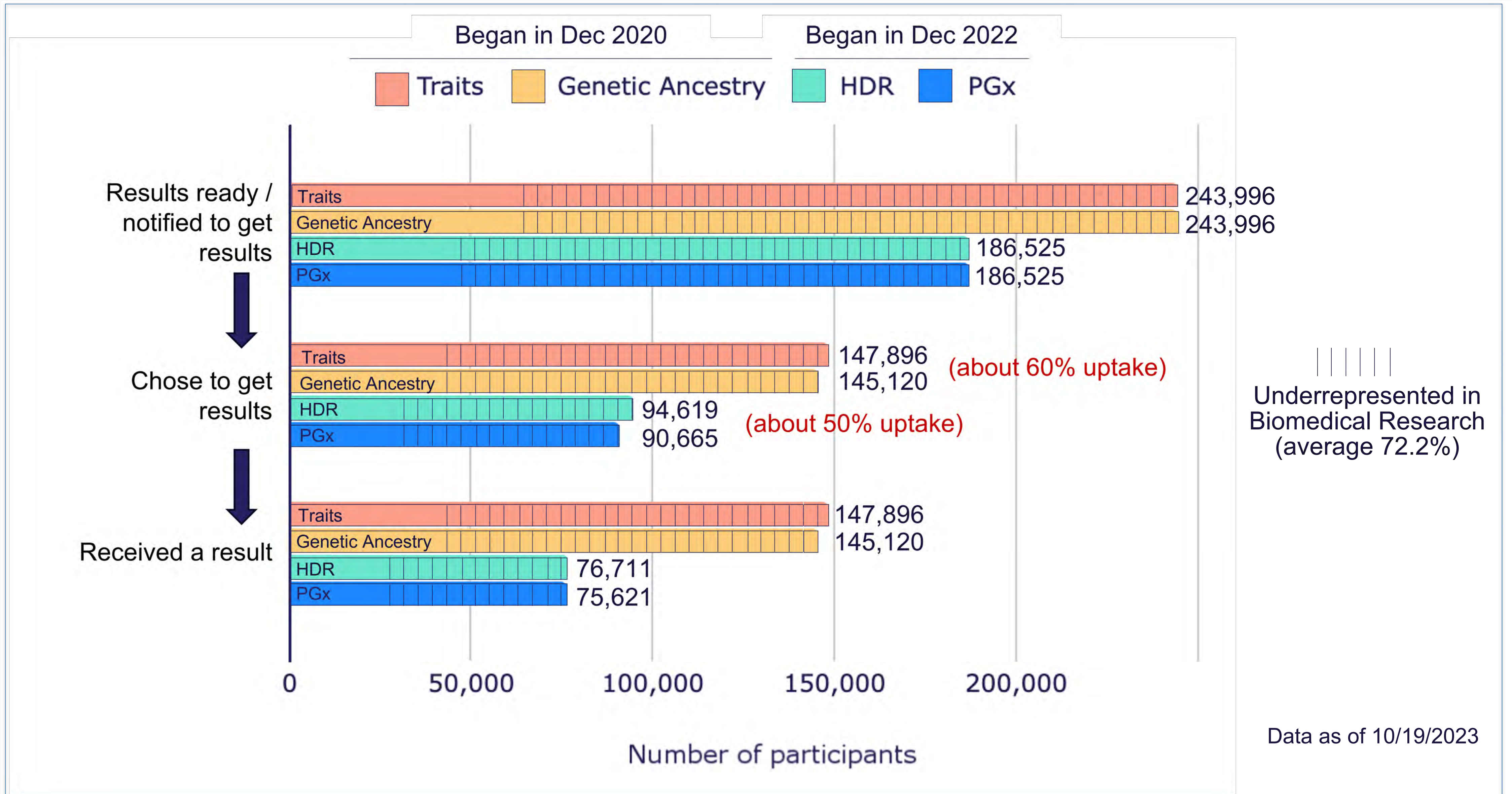


59 genes (SNVs + indels)

- Breast cancer
- Ovarian cancer
- Uterine cancer
- Colorectal cancer
- Prostate cancer
- Melanoma
- Brain cancer
- Pancreatic cancer
- Stomach cancer
- Familial hypercholesterolemia
- Cardiomyopathies
- Arrhythmias
- Arteriopathies

Health results

240,000+ Participants are Currently Eligible to Receive Genetic Results



Returning Genetic Ancestry and Traits (as of November 29, 2023)

DNA Results

You'll see all of your DNA results here when they're ready. See [options for your DNA results](#).

Genetic ancestry and trait results

5 results



Genetic ancestry

Genetic ancestry can be very interesting, but you may also learn information you didn't know. [Learn more](#)



Bitter taste perception

Learn what your genes can tell you about how you taste bitter things.



Cilantro preference

Your genes play a role in whether you love cilantro or think it tastes like soap.



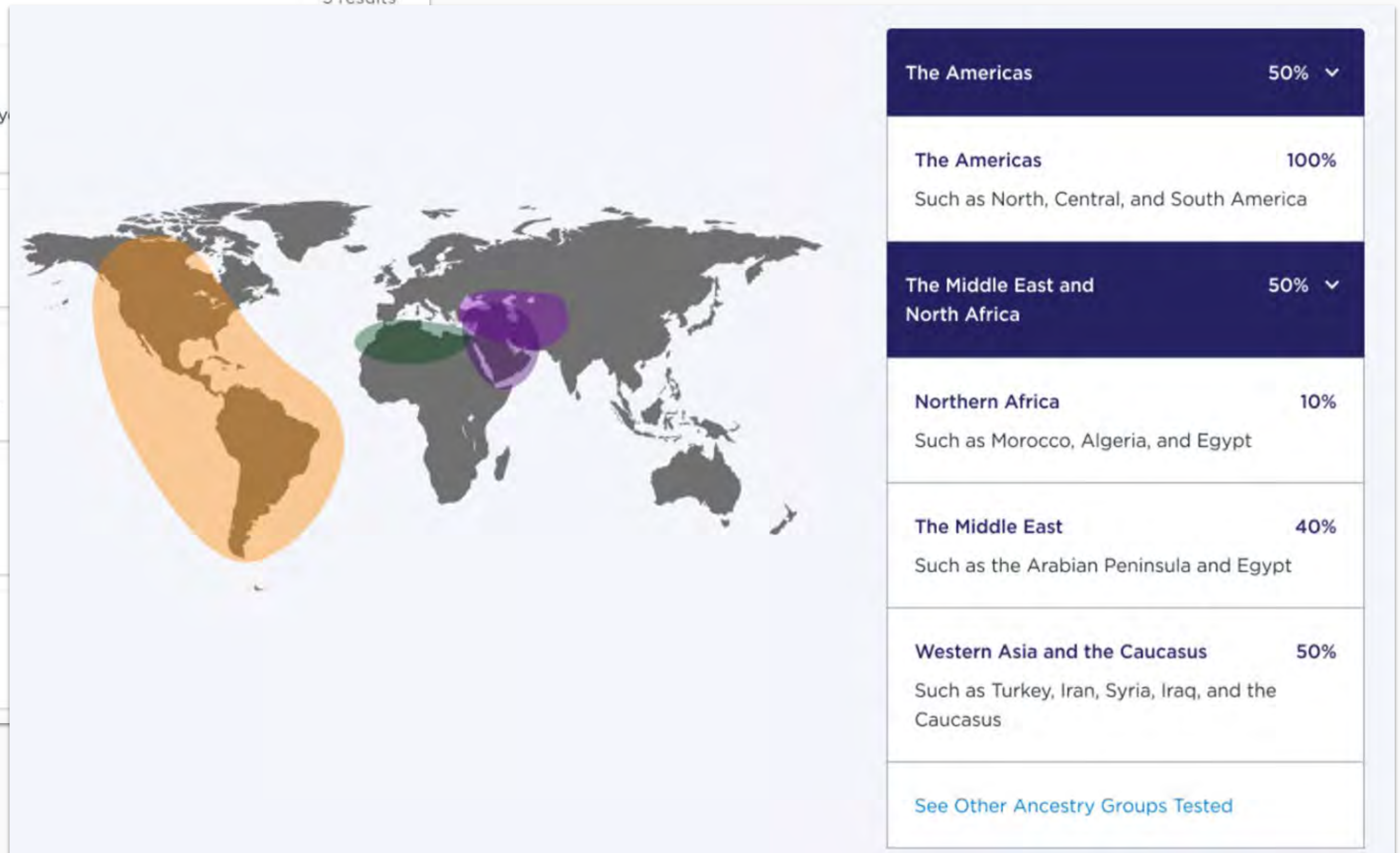
Earwax type

Flaky or sticky? Earwax type is in your genes.

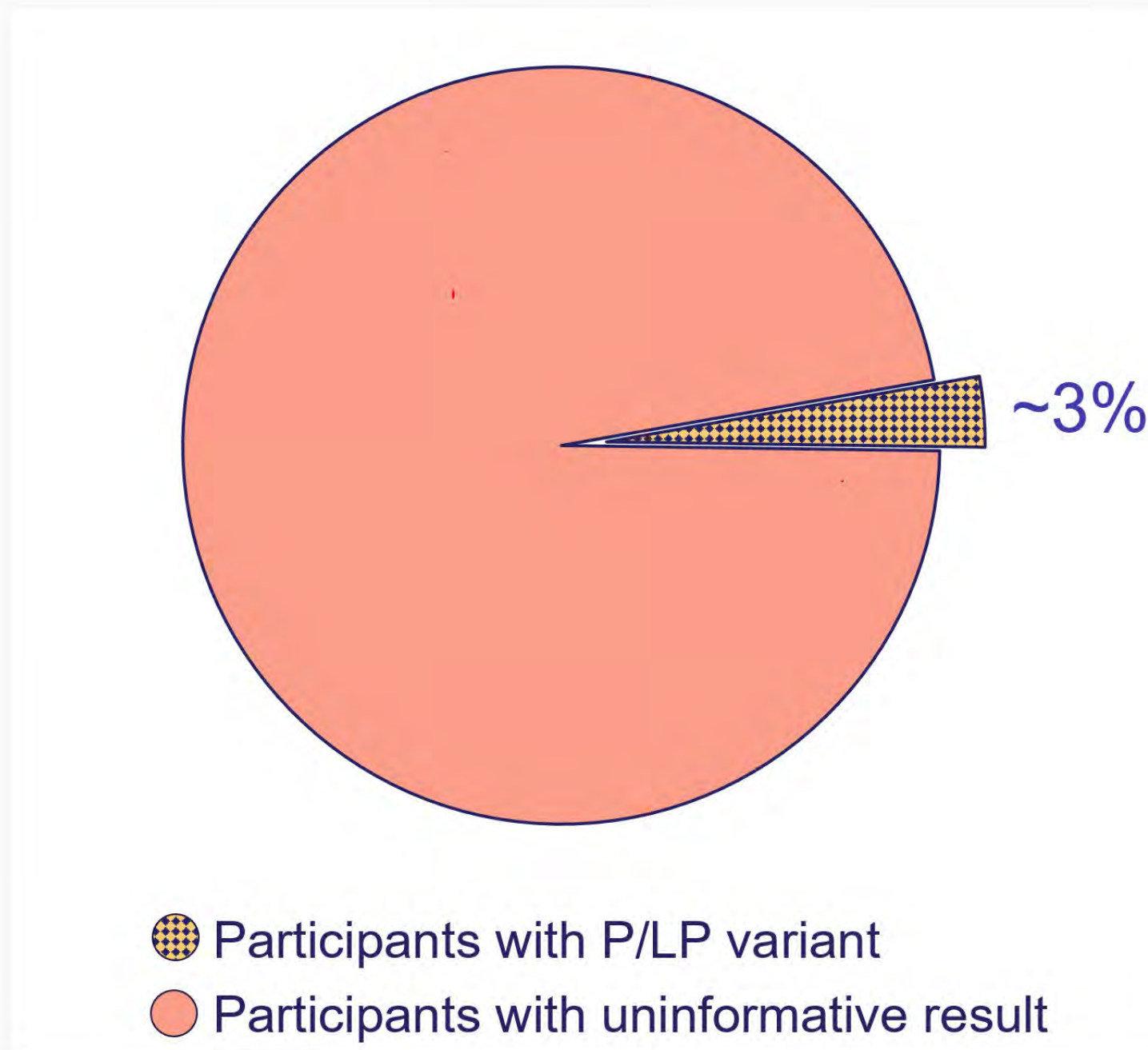


Lactose intolerance

Your genes have a say in how well you digest lactose products like milk.



Returned 76,000+ Hereditary Disease Risk (HDR) Results; Identified 2,200+ Participants with P/LP Variants



All of Us Log Out

My Data > DNA Results > Hereditary Disease Risk Results

Hereditary disease risk results

Actions

Your results Next steps Risk with *BRCA1* Discuss results

RESEARCH RESULT - Your doctor will need to confirm this result with a clinical test before using it in your care.

YOUR RESULT:

Something very important for your health was found in your *BRCA1* gene.

What does this mean?

If confirmed by a clinical DNA test, this result means that you are more likely to get some types of cancers than other people.

It does **not** mean that you have some types of cancers. It does **not** mean that you will definitely get some types of cancers. **This result is important.**

Risk if your sex assigned at birth was female

[Why does this matter?](#)

If this result is confirmed by a clinical DNA test, it means:

- You have a higher chance of developing breast cancer, ovarian cancer, and pancreatic cancer.

This chart shows the risk for people assigned female at birth with this result in the *BRCA1* gene compared to the general population. *

Breast cancer

Risk by age 80

↑ Risk with a confirmed *BRCA1* result ¹: 59-78%

👤 Average risk in the U.S. ²: 13%

Ovarian cancer

Risk by age 80

↑ Risk with a confirmed *BRCA1* result ¹: 44-65%

👤 Average risk in the U.S. ²: 1.1%

Pancreatic cancer

Risk by age 80

↑ Risk with a confirmed *BRCA1* result ^{3,4}: 3-5%

👤 Average risk in the U.S. ²: 1.7%

Risk if your sex assigned at birth was male

[Why does this matter?](#)

If this result is confirmed by a clinical DNA test, it means:

- You have a higher chance of developing breast cancer, pancreatic cancer, and prostate cancer.

This chart shows the risk for people assigned male at birth with this result in the *BRCA1* gene compared to the general population. *

Breast cancer

Risk by age 80

↑ Risk with a confirmed *BRCA1* result ^{3,6}: 1.8%

👤 Average risk in the U.S. ²: <1%

Pancreatic cancer

Risk by age 80

↑ Risk with a confirmed *BRCA1* result ^{3,4}: 3-6%

👤 Average risk in the U.S. ²: 1.7%

Prostate cancer

Risk by age 80

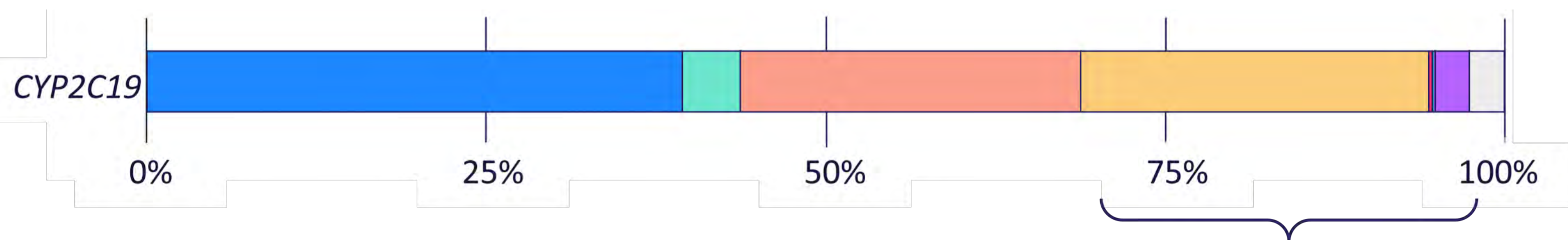
↑ Risk with a confirmed *BRCA1* result ^{6,7}: Higher than average

👤 Average risk in the U.S. ²: 13%

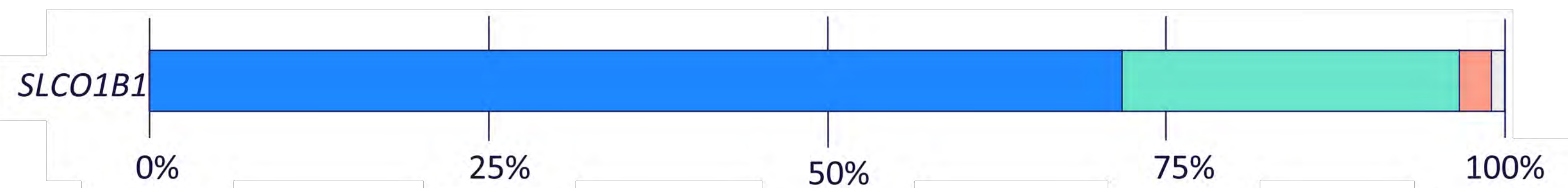
* This data comes from research primarily from one population, and may not represent your exact risk(s). This data may change over time based on new research and information. We recommend speaking to your doctor or health care provider about your risk based on genetic and non-genetic factors.

Returned 75,000+ PGx Results, with 68,000+ (>90%) Participants with a Result That Could Impact How the Body Processes Certain Medications

Distributions of two PGx Results in 75,000+ participants



Intermediate or poor metabolizers



Decreased or poor function

Data as of 10/19/2023



This table points out some medicines that may be affected by your genetic results.

If you are taking one of these medicines, talk with your doctor or pharmacist about whether ordering a clinical pharmacogenetic test is right for you.

These medicines MAY BE impacted by your genetics.

In some cases, pharmacogenetic information may help doctors and pharmacists choose medicines and doses.

Gene

CYP2C19

- brivaracetam (Briviact®)
- clobazam (Onfi®)
- clopidogrel (Plavix®)

Gene

SLCO1B1

- simvastatin (Zocor®)

Just because a medicine is listed here doesn't mean that you should or should not be taking it. Some people with these genetic results still process these medicines normally.

New Surveys on Mental Health and Well-Being Launched July 2023

Emotional Health History and Well-Being

Emotional Health History and Well-Being

8 minutes



Start

Topics Assessed:

- Generalized and lifetime anxiety
- Present and past depression
- Suicidal behavior
- Childhood and adult adversity/trauma
- General well-being

Behavioral Health and Personality

Behavioral Health and Personality

5 minutes



Start

Topics Assessed:

- Adult ADHD
- Bipolar disorder
- Psychosis
- Panic disorder
- Obsessive compulsive disorder
- Social phobia and agoraphobia
- Personality

Over 100,000 participants have completed both surveys to date

What do your responses say about your personality?

The "Big 5" is a model of personality that includes five key traits. The Big 5 personality model has been very well studied and confirmed as valid. The five key traits include:

- **Openness to experience:** How you feel about new experiences and ideas.
- **Conscientiousness:** How organized you are and if you prefer structure and rules.
- **Extraversion:** How social and energetic you are around others.
- **Agreeableness:** How much you consider the needs and feelings of others in relation to your own needs.
- **Emotional resilience:** How you may respond to stressful experiences or negative emotions, like anxiety or sadness. The Big 5 Inventory calls this trait "neuroticism."

Each of the traits really falls on a spectrum or a scale. For example, the extraversion trait has introversion on one end of the scale and introversion on the other end. Most people fit somewhere in between these.

These results report on only five personality traits, so they do not fully reflect who you are. Your traits indicate how you may respond in different situations. How you actually respond will depend on more than just your traits.

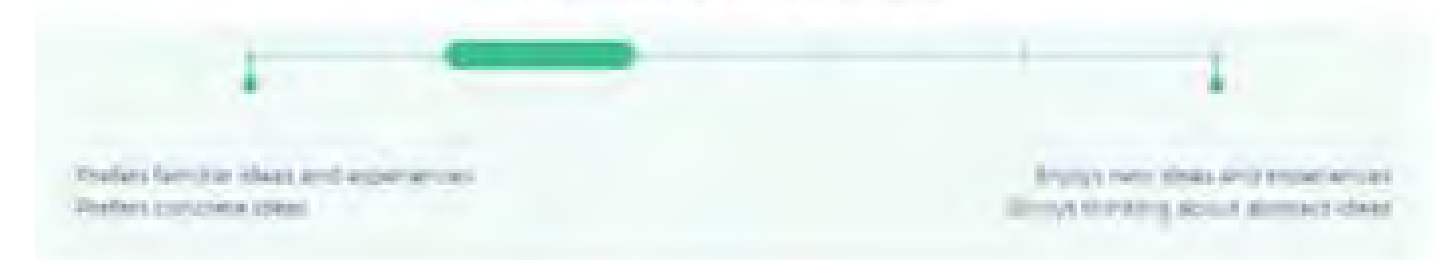
Several different survey tools measure the Big 5 personality traits. The expert group assigned to develop the Mental Health and Well-Being survey chose this tool for several reasons:

- The survey is a validated tool
- The survey covers all five personality traits
- The survey includes only 15 questions



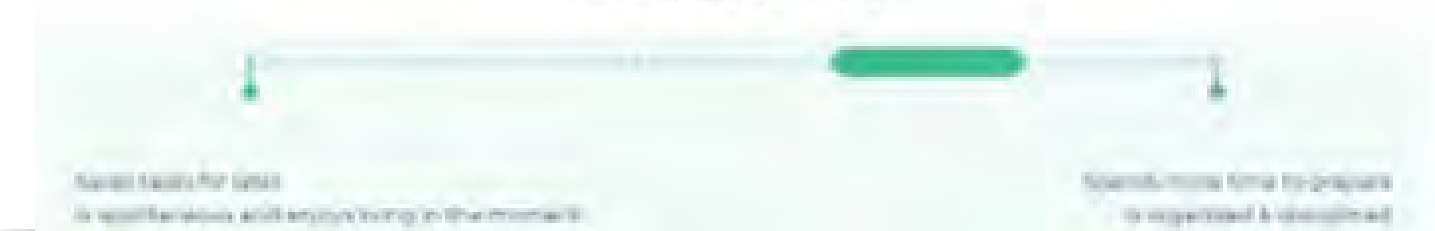
Openness

This is how someone feels about new experiences and ideas.
Your answers show that you **usually** prefer familiar ideas and experiences, rather than new ones.



Conscientiousness

This is how organized someone is and if they prefer structure and rules.
Your answers show that you are **usually** organized and like to know structure and rules.



Participants receive personality trait report at the end

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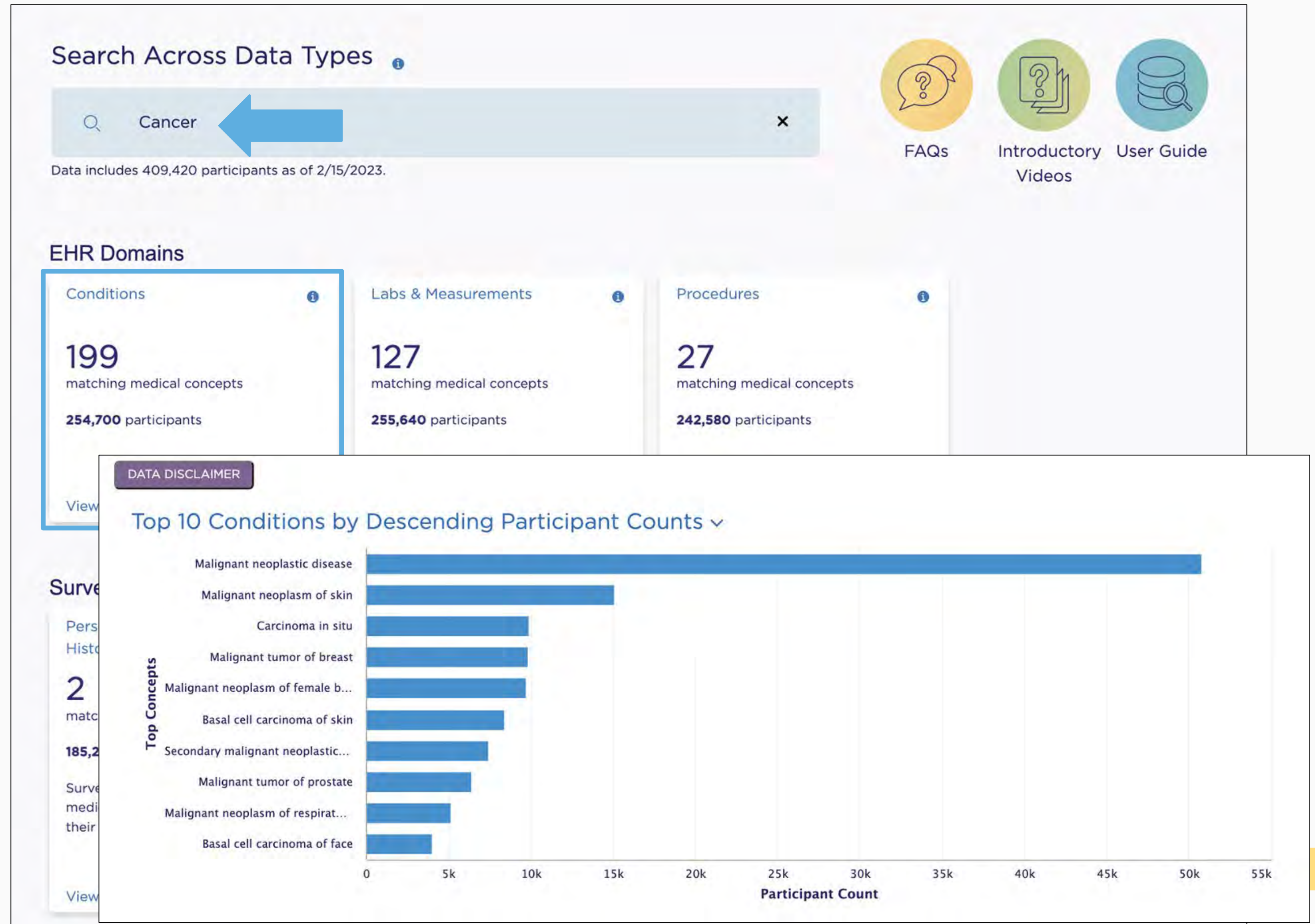
The program will be a catalyst for **positive change** in research.

All of Us Research Hub: Public Data Browser

Summary statistics of:

- EHR Data (Conditions, Drug Exposures, Lab & Measurements, Procedures)
- Genomic Variants
- Survey Questions (including COVID-19 surveys)
- Physical Measurements
- **Open Access (no login required)**

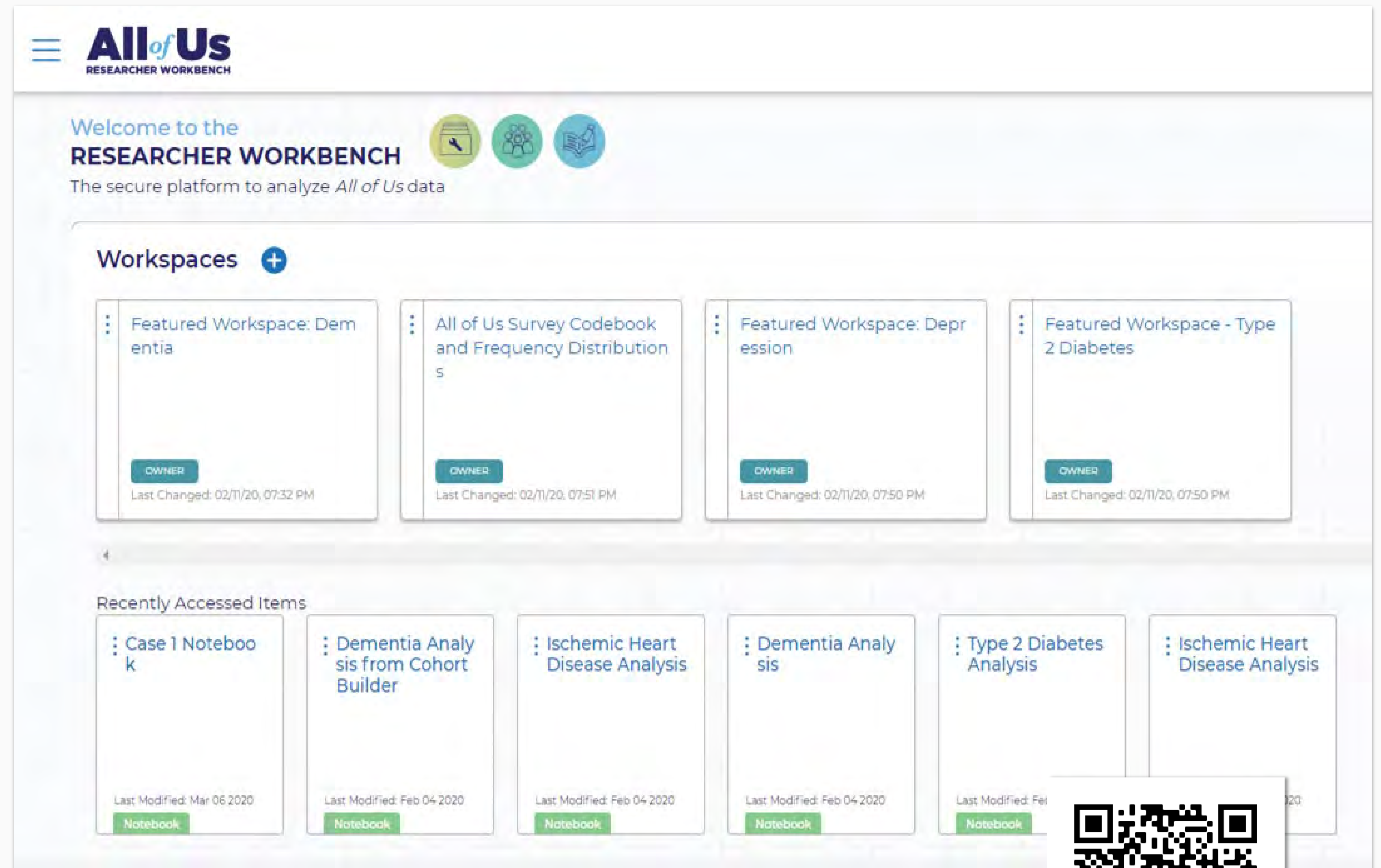
Data Browser



All of Us Researcher Workbench: Access to Row-Level Data for Analysis

Researcher Workbench

- Cloud-based central resource for broad data accessibility
- R and Python, soon SAS will be available also
- **Passport access model for approved researchers** - just create, describe your workspace, and get to work! **No separate IRB approval needed.**
- Currently open to academic, health care and not-for-profit organizations



The screenshot displays the All of Us Researcher Workbench interface. At the top, the logo "All of Us RESEARCHER WORKBENCH" is visible. Below the logo, a welcome message reads "Welcome to the RESEARCHER WORKBENCH" and "The secure platform to analyze All of Us data". The main content area is divided into two sections: "Workspaces" and "Recently Accessed Items".

Workspaces: This section contains four workspace cards, each with a "OWNER" button and a "Last Changed" timestamp:

- Featured Workspace: Dementia (Last Changed: 02/11/20, 07:32 PM)
- All of Us Survey Codebook and Frequency Distributions (Last Changed: 02/11/20, 07:51 PM)
- Featured Workspace: Depression (Last Changed: 02/11/20, 07:50 PM)
- Featured Workspace - Type 2 Diabetes (Last Changed: 02/11/20, 07:50 PM)

Recently Accessed Items: This section contains six notebook cards, each with a "Notebook" button and a "Last Modified" timestamp:

- Case 1 Notebook (Last Modified: Mar 06 2020)
- Dementia Analysis from Cohort Builder (Last Modified: Feb 04 2020)
- Ischemic Heart Disease Analysis (Last Modified: Feb 04 2020)
- Dementia Analysis (Last Modified: Feb 04 2020)
- Type 2 Diabetes Analysis (Last Modified: Feb 04 2020)
- Ischemic Heart Disease Analysis (Last Modified: Feb 04 2020)

ResearchAllofUs.org/Data-Tools/Workbench/



Nearly 250,000 Whole Genome Sequences Available to Advance Precision Medicine



413,350+
Survey Responses



337,500+
Physical Measurements



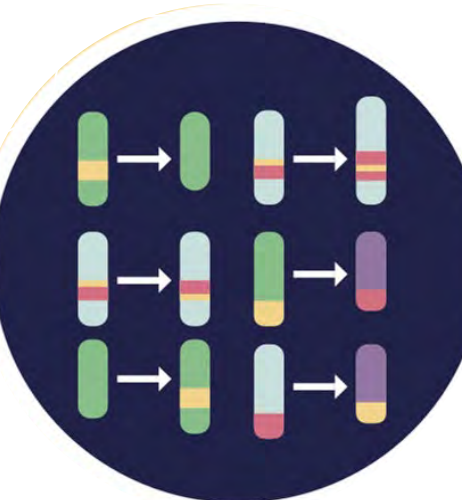
312,900+
Genotyping Arrays



287,000+
Electronic Health Records



245,350+
Whole Genome Sequences



11,350+
Structural Variants

NEW! In 2023



1,000+
Long-Read Sequences


NEW! In 2023



15,600+
Fitbit Records

NEW! Sleep Data

The whole genome sequence dataset includes variation at more than **1 billion** locations, which is nearly **one-third** of the entire human genome

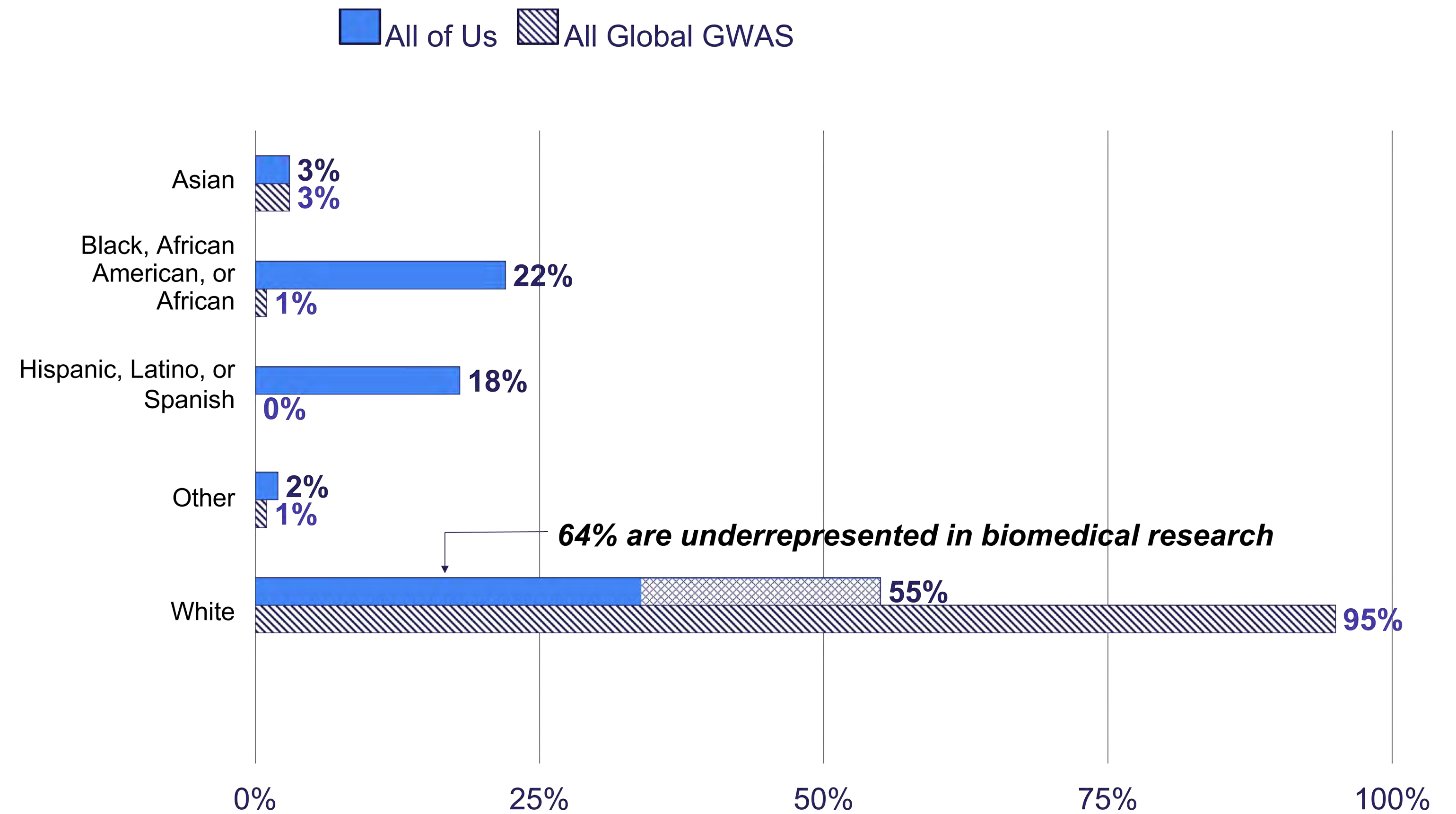


All of Us is Enhancing Diversity of Genomic Studies

Updated genomic data set

~45% diverse by race/ethnicity

77% underrepresented in biomedical research



All Global GWAS values from www.gwasdiversitymonitor.com. Values current as of November 2023

Researcher Workbench Usage and Diversity (data as of November 29, 2023)

Our Researchers

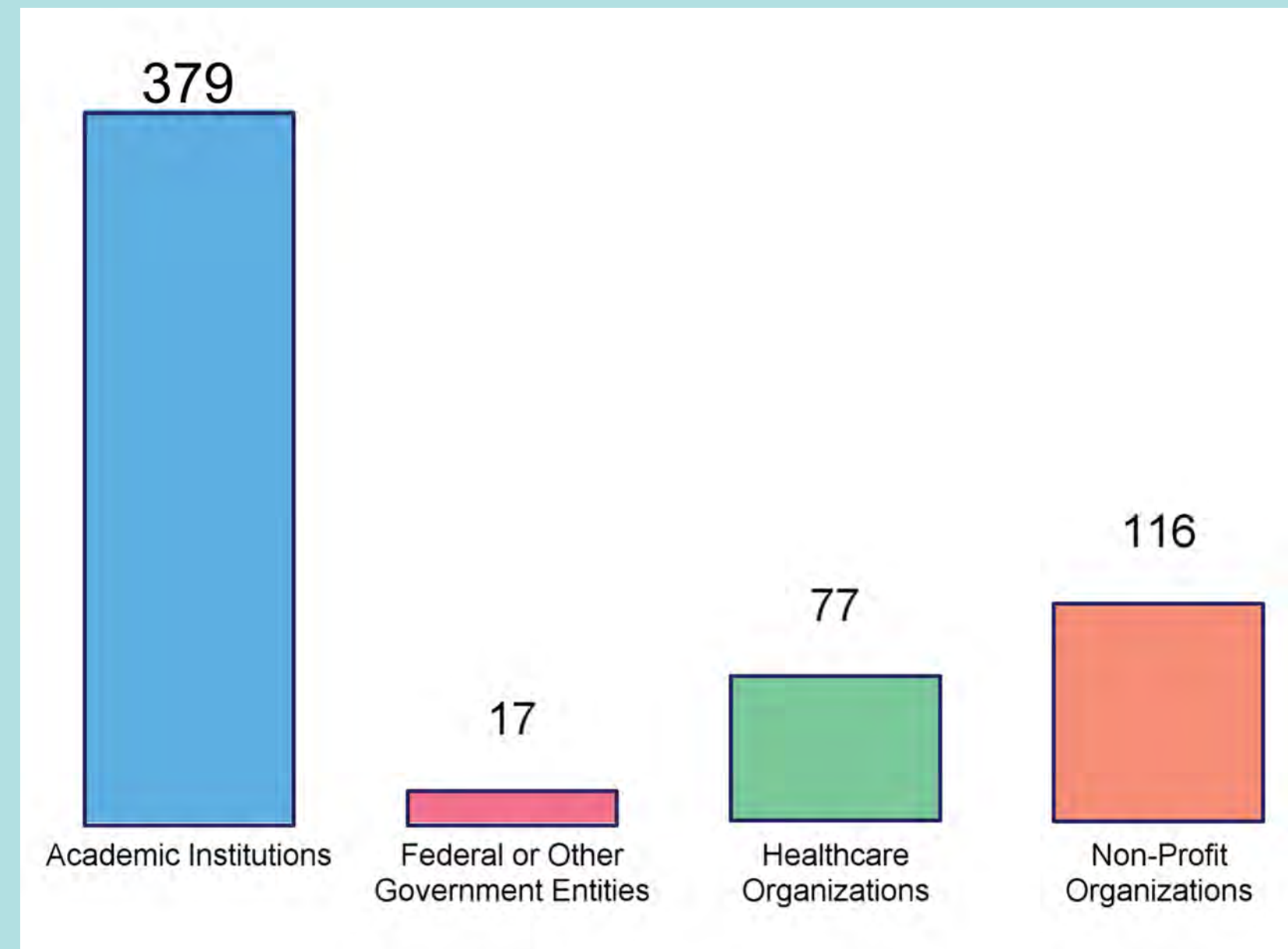


8,120+
Registered
Researchers



620+
Institutions

Over 74% of our researchers are underrepresented in the biomedical workforce — including over 33% diverse by race and ethnicity (other than Non-Hispanic White or Asian)



620+ Organizations:

- 40 Historically Black Colleges & Universities
- 61 Hispanic Serving Institutions

**Research
Currently
Underway**



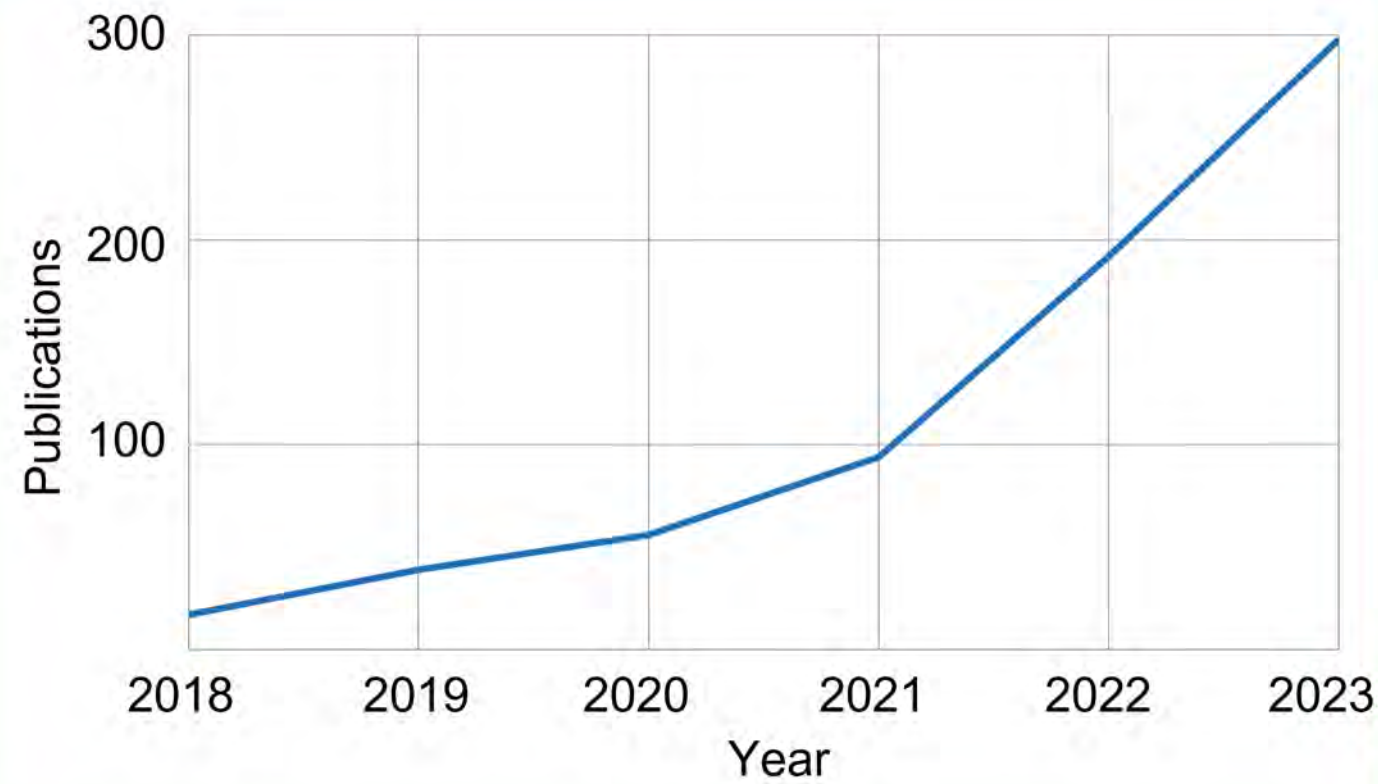
8,100+
Active projects



Top conditions being studied

- Cardiovascular disease
- Hypertension
- Mental Health
- Cancer
- Diabetes

Publications are Growing



Otolaryngology—Head and Neck Surgery



Hearing Loss and Sociodemographic Barriers to Health Care Access Using the *All of Us* Research Program

Luis E. Cortina BS, Andrew Amini BS, Jalen Benson BS, Victoria W. Huang MD, James G. Naples MD

First published: 20 July 2023 | <https://doi.org/10.1002/ohn.431>

International Journal of Dermatology

The association of cutaneous squamous cell carcinoma and basal cell carcinoma with solid organ transplantation: a cross-sectional study of the *All of Us* Research Program

Annika Belzer BS, Audrey C. Leasure MD, MHS, Jeffrey M. Cohen MD, Sara H. Perkins MD

First published: 05 May 2023 | <https://doi.org/10.1111/ijd.16700>

PLOS ONE

Family and personal history of cancer in the *All of Us* research program for precision medicine

Lauryn Keeler Bruce, Paulina Paul, Katherine K. Kim, Jihoon Kim, Theresa H. M. Keegan, Robert A. Hiatt, Lucila Ohno-Machado, On behalf of the *All of Us* Research Program Investigators

Published: July 17, 2023 • <https://doi.org/10.1371/journal.pone.0288496>

medRxiv

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CSH Cold Spring Harbor Laboratories | BMJ | Yale

Pre-Print

Multi-ancestry genome-wide study in >2.5 million individuals reveals heterogeneity in mechanistic pathways of type 2 diabetes and complications

Ken Suzuki, Konstantinos Hatzikotoulas, Lorraine Southam, Henry J. Taylor, Xianyong Yin, Kim M. Lorenz, Ravi Mandla, Alicia Huerta-Chagoya, Nigel W. Rayner, Ozvan Bocher, S.V. Arruda Ana Luiza de, Kyuto Sonehara, Shinichi Namba, Simon S. K. Lee, Michael H. Preuss, Lauren E. Petty, Philip Schroeder, Brett Vanderwerff, Mart Kals.

Research article | [Open Access](#) | [Published: 11 June 2023](#)

Using machine learning to develop a clinical prediction model for SSRI-associated bleeding: a feasibility study

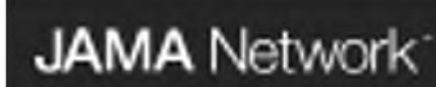
Jatin Goyal, Ding Quan Ng, Kevin Zhang, Alexandre Chan, Joyce Lee, Kai Zheng, Keri Hurley-Kim, Lee Nguyen, Lu He, Megan Nguyen, Sarah McBane, Wei Li & Christine Luu Cadiz

BMC Medical Informatics and Decision Making 23, Article number: 105 (2023) | [Cite this article](#)

894 Accesses | [Metrics](#)

Original Investigation | Oncology

August 10, 2023



Alcohol Consumption Among Adults With a Cancer Diagnosis in the *All of Us* Research Program

Mengyao Shi, MBBS, MPH¹; Chongliang Luo, PhD¹; Oluseye K. Oduyale, MD¹; et al

Higher Hospital Frailty Risk Score Is Associated With Increased Risk of Stroke: Observational and Genetic Analyses

Daniela Renedo, Julián N. Acosta, Andrew B. Koo, Cyprien Rivier, Nanthiya Sujjantararat, Adam de Havenon, Richa Sharma, Thomas M. Gill, Kevin N. Sheth, Guido J. Falcone and Charles C. Matouk

Originally published 22 May 2023 | <https://doi.org/10.1161/STROKEAHA.122.041891> | *Stroke*. 2023;54:1538–1547

Article | [Open Access](#) | [Published: 10 October 2022](#)

Association of step counts over time with the risk of chronic disease in the *All of Us* Research Program

Hiral Master, Jeffrey Annis, Shi Huang, Joshua A. Beckman, Francis Ratsimbazafy, Kayla Marginean, Robert Carroll, Karthik Natarajan, Frank E. Harrell, Dan M. Roden, Paul Harris & Evan L. Brittain

Nature Medicine 28, 2301–2308 (2022) | [Cite this article](#)



AJHG

ASHG75 Supports open access

ARTICLE | VOLUME 110, ISSUE 2, P228-239, FEBRUARY 02, 2023 | [Download Full Issue](#)

Functional interpretation, cataloging, and analysis of 1,341 glucose-6-phosphate dehydrogenase variants

Renee C. Geck • Nicholas R. Powell • Maitreya J. Dunham

[Open Access](#) • Published: January 20, 2023 • DOI: <https://doi.org/10.1186/s13075-023-03000-0>

Original Investigation | Equity, Diversity, and Inclusion

July 31, 2023

Prevalence of 12 Common Health Conditions in Sexual and Gender Minority Participants in the *All of Us* Research Program

Nguyen K. Tran, PhD, MPH^{1,2}; Mitchell R. Lunn, MD, MAS^{1,2,3}; Claire E. Schulkey, PhD⁴; Samantha Tesfaye, BA; Siddhartha Nambiar, PhD⁵; Snigdhasu Chatterjee, PhD⁶; Dawn Kozlowski, MEd⁷; Paula Lozano, PhD^{8,9}; Fornessa T. Randal, MCRP^{8,9}; Yick Lun Mo, MSW^{8,9}; Siya Qi, MS^{8,9}; Eli Hundertmark, BS^{1,10}; Chloe Eastburn, BA^{1,11}; Anthony T. Pho, PhD^{1,2}; Zubin Dastur, MS, MPH^{1,10}; Micah E. Lubensky, PhD^{1,12}; Annesa Flentje, PhD^{1,12,13}; Juno Obedin-Maliver, MD, MPH, MAS^{1,3,10}

Nuclear genetic control of mtDNA copy number and heteroplasmy in humans

Rahul Gupta, Masahiro Kanai, Timothy J. Durham, Kristin Tsuo, Jason G. McCoy, Anna V. Kotrys, Wei Zhou, Patrick F. Chinnery, Konrad J. Karczewski, Sarah E. Calvo, Benjamin M. Neale & Vamsi K. Mootha

Nature 620, 839–848 (2023) | [Cite this article](#)



[Open Access](#) | [Article](#)

Race, Ethnicity, and Pharmacogenomic Variation in the United States and the United Kingdom

by Shivam Sharma^{1,2}, Leonardo Mariño-Ramírez² and I. King Jordan^{1,*}

Pharmaceutics 2023, 15(7), 1923; <https://doi.org/10.3390/pharmaceutics15071923>

Received: 12 June 2023 / Revised: 30 June 2023 / Accepted: 5 July 2023 / Published: 11 July 2023



Search preprints

Brief Communication

Quantifying physical activity needed to mitigate genetic risk for obesity

Ide Han, Jeffrey Annis, Hiral Master, Andrew Hughes, Dan Roden, and 3 more

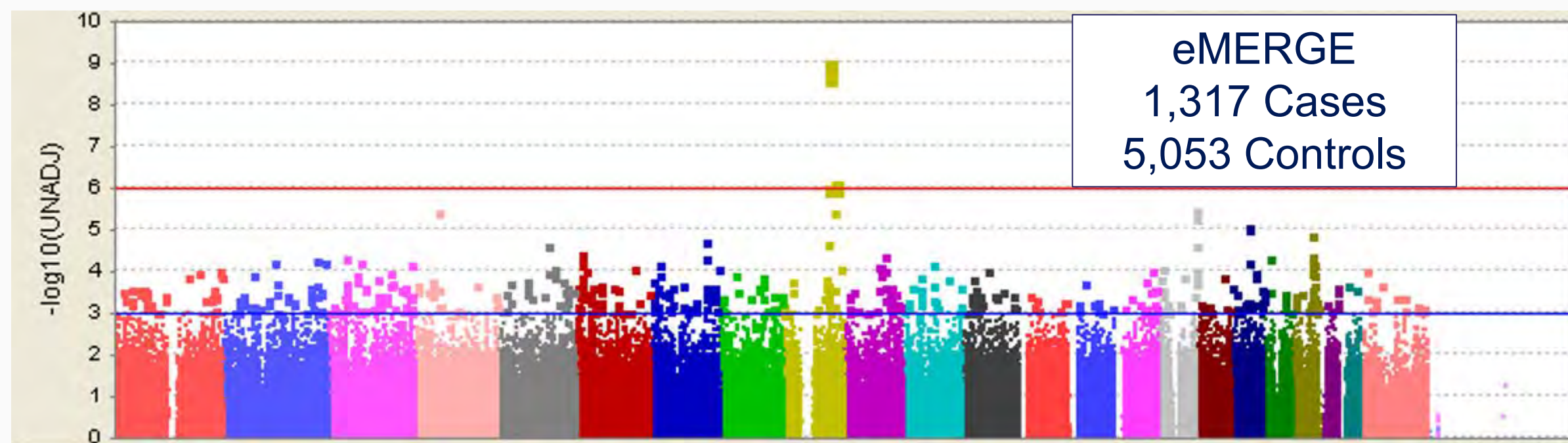
Pre-Print

One example of GWAS in *All of Us*

The Genetic Basis of Primary Hypothyroidism

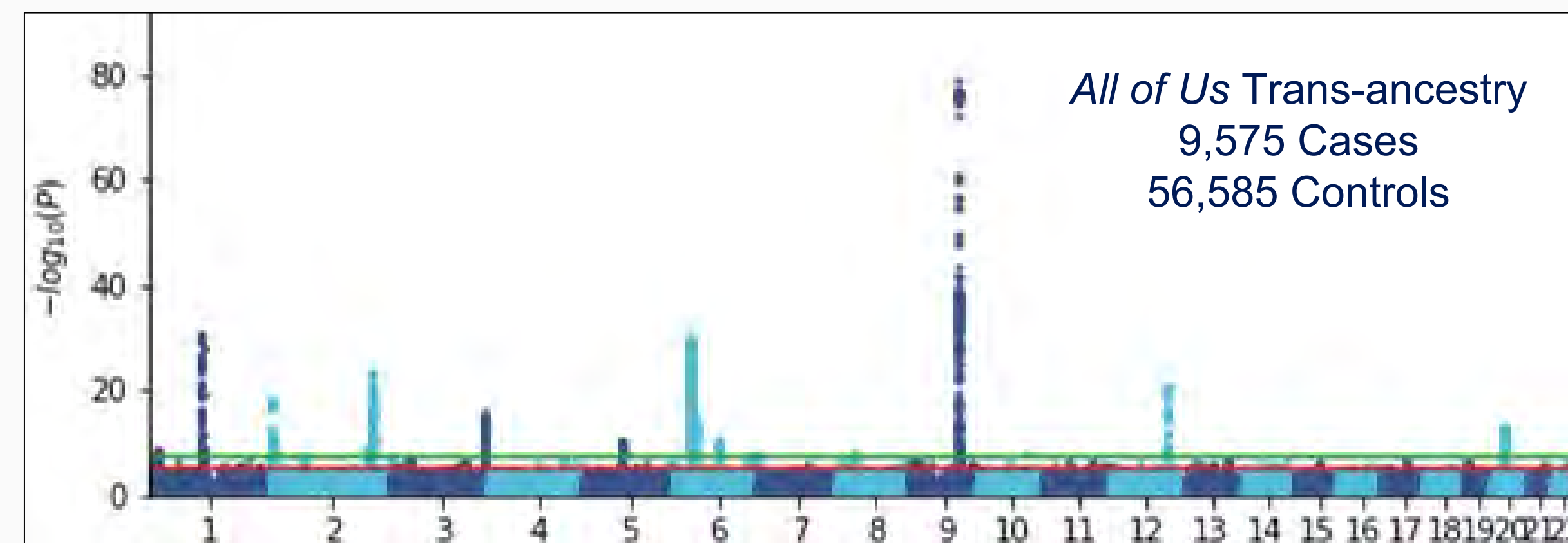
2011 - eMERGE Network analysis

- 5 sites worked together to find autoimmune hypothyroidism in EHRs
- Discovered one genetic loci in European ancestry individuals
- Took ~2.5 years and ~40 people

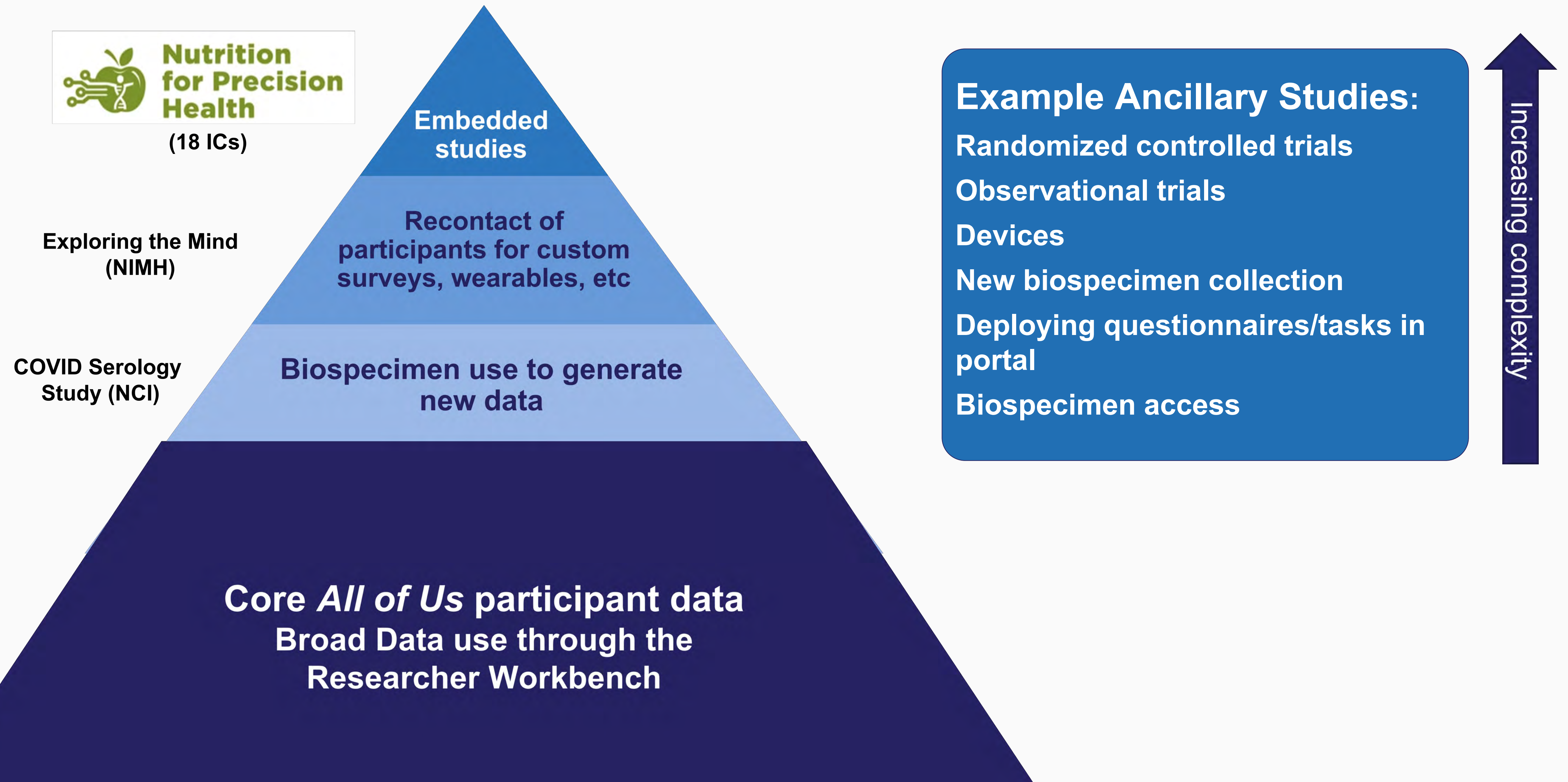


2023

- *All of Us* Researcher Workbench
- >10 genetic loci in diverse population
- Took one postbaccalaureate student about 6 weeks for initial analysis



Ancillary Studies Will Have a Positive Impact on Increasing Access to a Research-Ready, Diverse National Cohort

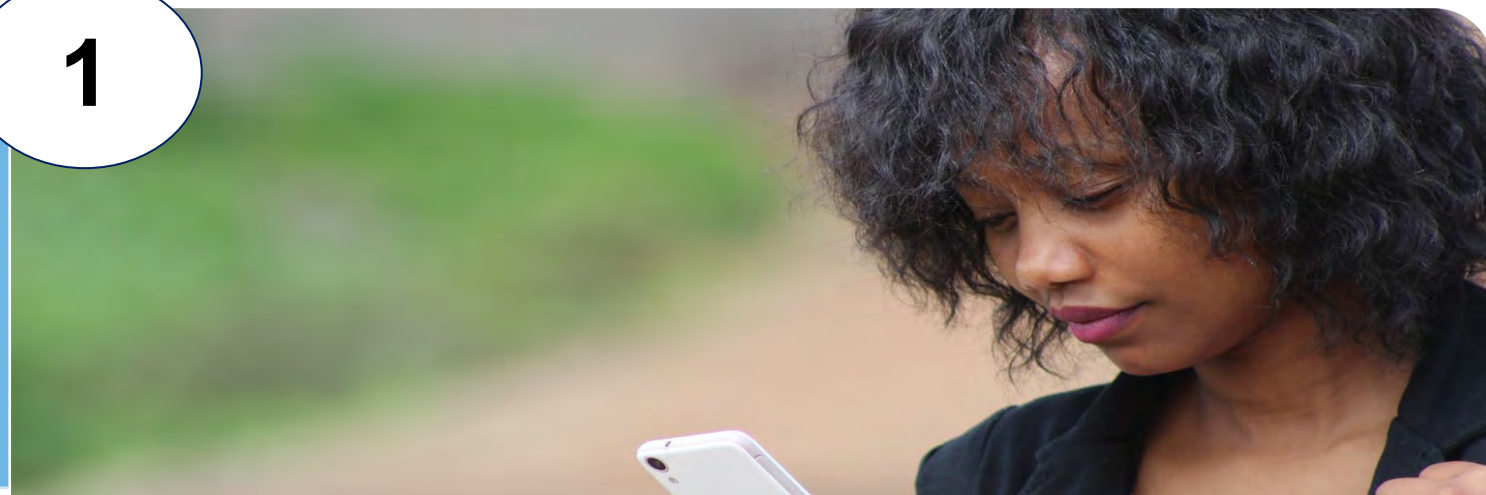


Nutrition for Precision Health

Powered by the *All of Us* Research Program

Goal: To develop algorithms to predict individual responses to foods and dietary patterns

1



Examine baseline diet and physiological responses to meal challenges

10,000 *All of Us* participants

2



Examine responses to 3 short-term intervention diets in free-living controlled feeding studies

1,500-2,000 Module 1 participants

3



Examine responses to 3 short-term intervention diets in domiciled controlled feeding studies

500-1,000 Module 1 participants

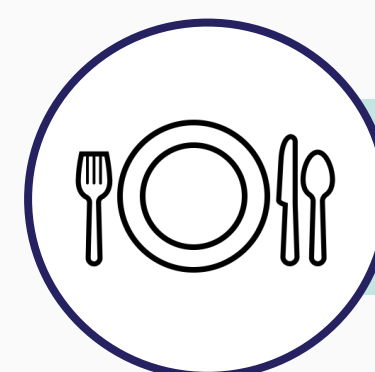


Ancillary Studies: Nutrition for Precision Health

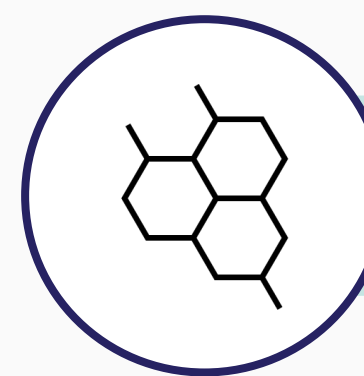
New Data from Nutrition for Precision Health



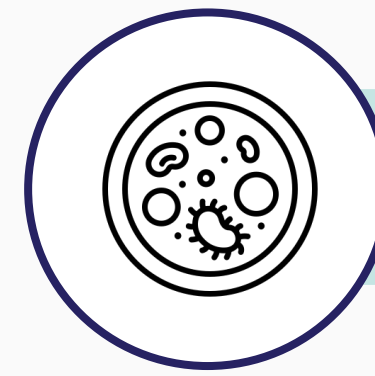
Lifestyle/Behavioral Data



Diet



Physiometabolic Data



Microbiome

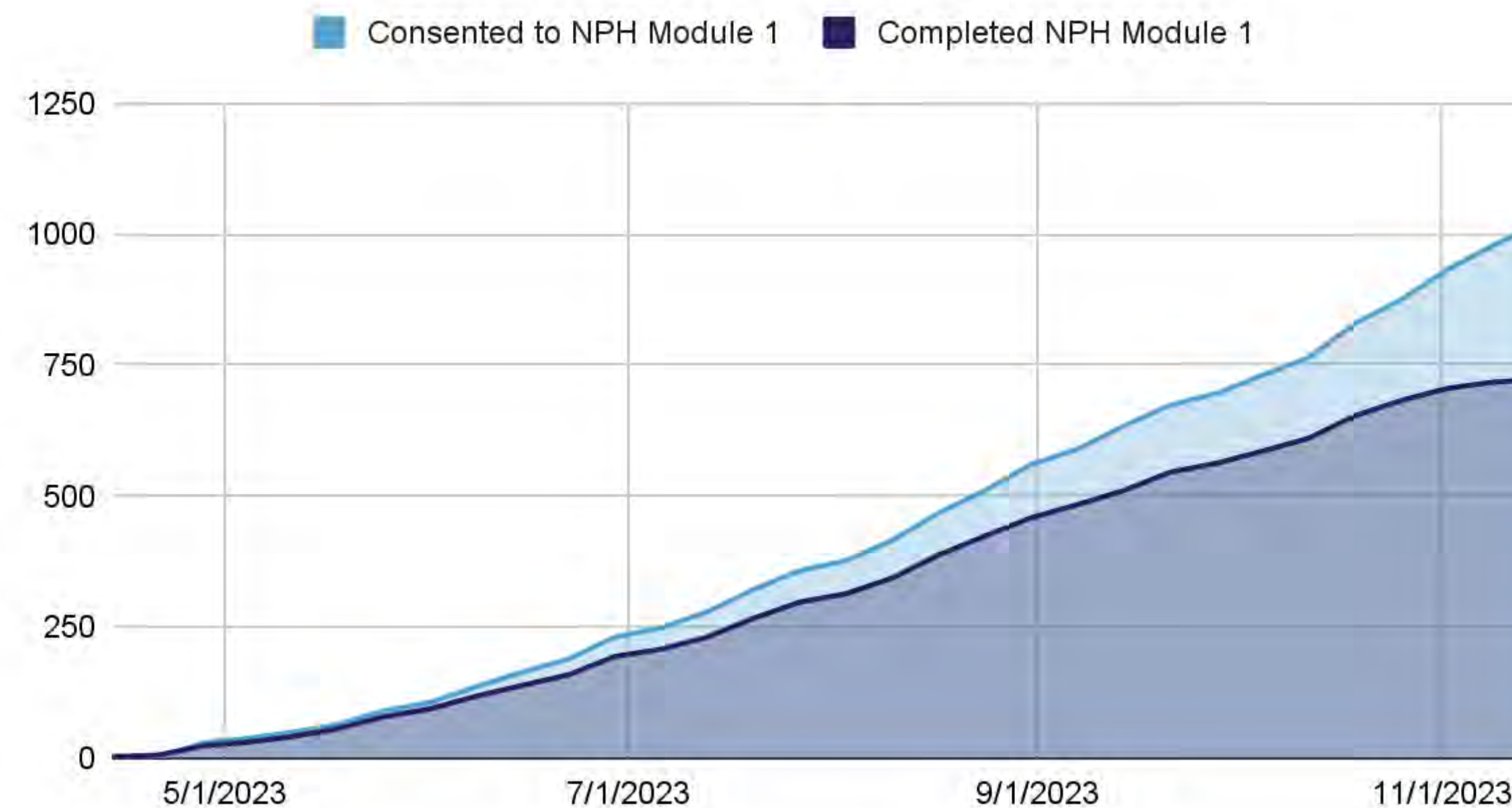


Physical Measurements



Environmental Data

NPH Enrollment Over Time



Recent *All of Us* Funding Announcements

Program Announcements



NIH Awards \$9.7 Million to Advance the Use of All of Us Research Program Dataset

- *All of Us* and 10 partner ICOs are funding 26 research projects using *All of Us* data.
- Funding for awards provided by *All of Us*, NEI, NHLBI, NHGRI, NIAMS, NIDA, NIMH, NIMHD, NLM, OBSSR, and ODSS



All of Us Awards \$1.5 Million to Institutions Collaborating with Tribal Communities

- Funding will support outreach and engagement with Tribal and Indigenous communities, strengthen the research infrastructure supporting AI/AN researchers, and broaden the base of researchers conducting cultural and ethical research with Tribal communities
- Awardees are the University of Arizona, Marshfield Clinic, American Indian Science and Engineering Society



All of Us Establishes New Center for Linkage and Acquisition of Data (CLAD)

- Awarded \$30 million to the University of Colorado Anschutz Medical Campus and its partners.
- CLAD will connect new types of information to *All of Us* participant data to help researchers better understand the drivers of health and disease (e.g., health care claims, mortality data, environmental data).



Changing the Health Landscape: Bringing the NIH Close to Home



“By Participating in the *All of Us* Research Program, I am helping to shape health research. By providing my health information to *All of Us*, I am learning things about myself, like how my body responds to certain medications. This information empowers me to work with my doctor to find the right dose. Health research hasn’t always included people like me, but *All of Us* is changing that. I’m ready for it.”

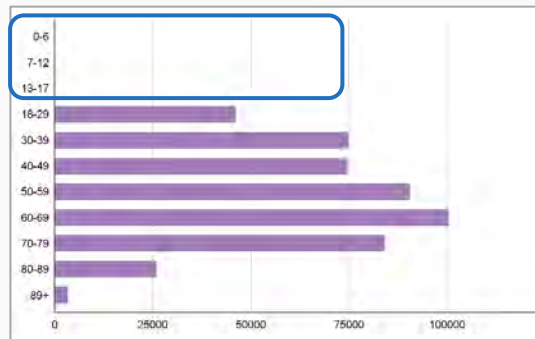
— Michelle Anderson, Former *All of Us* Participant Ambassador

Learn More: [USA Today Article](#)

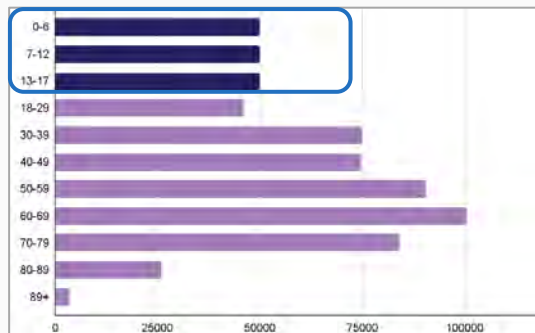


Supporting Health Research Across the Lifespan

Age at Enrollment: Current State



Age at Enrollment: Future State



Phased Approach

Enroll: Birth to age 4

Phase 1: Participation from birth to 6

Enroll: Birth to age 10

Phase 2: Participation from birth to 12

Enroll: All ages

Phase 3: Participation from birth to age of majority



[All of Us.NIH.gov](https://allofus.nih.gov)

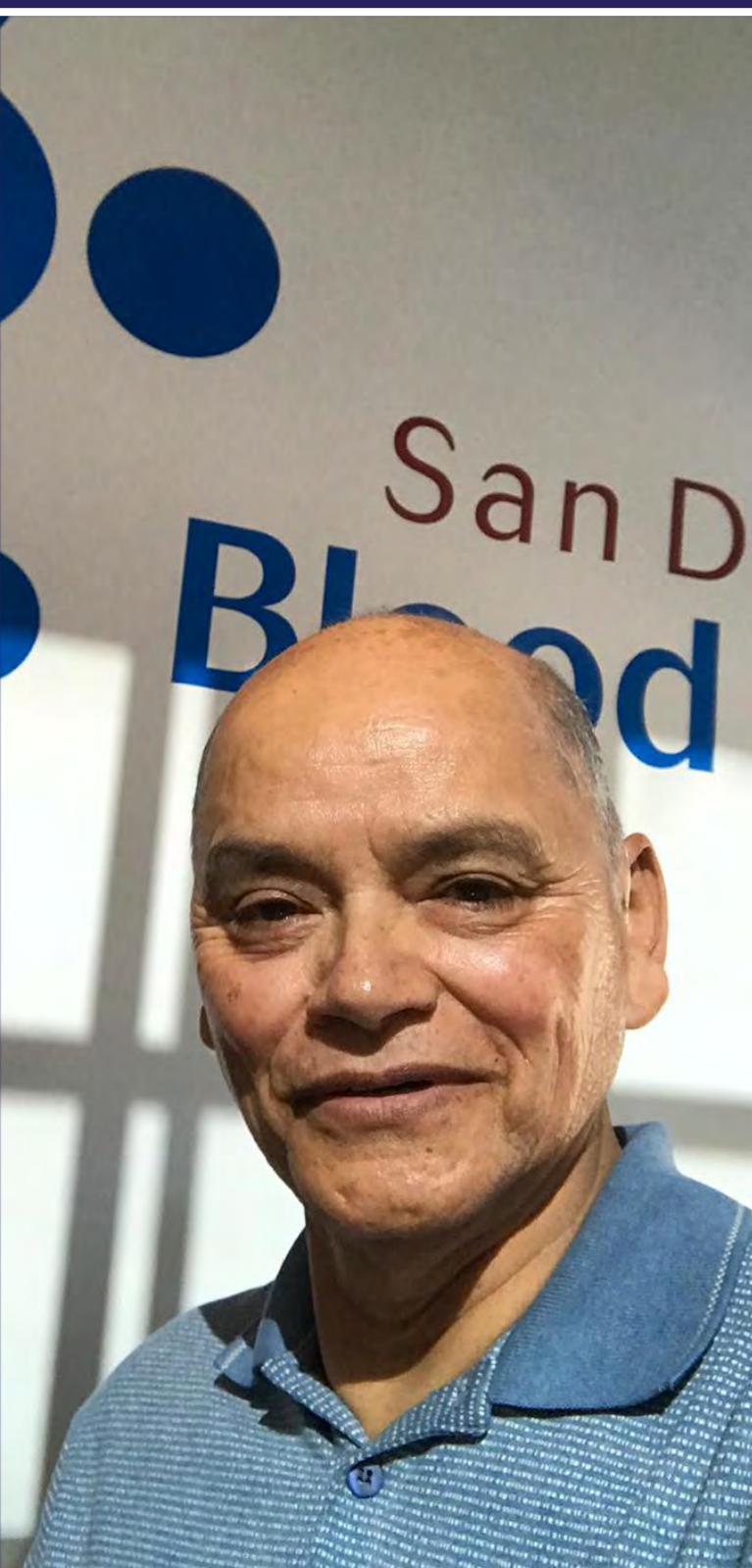
JoinAllofus.org

ResearchAllofus.org

Thank you!

@AllofusResearch
@AllofusCEO
#JoinAllofus



Thank you to our 740,000+ participants!