All of Us Research Program: Key Updates Including New Data Release





September 12, 2024

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







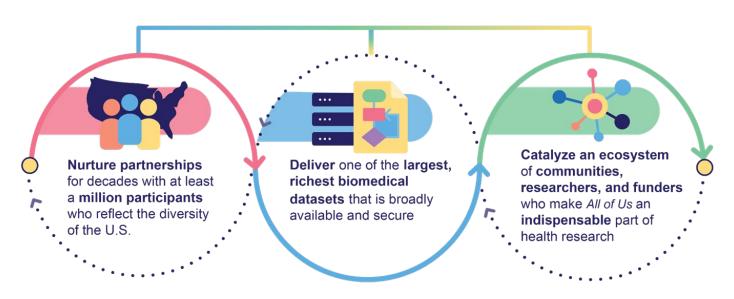






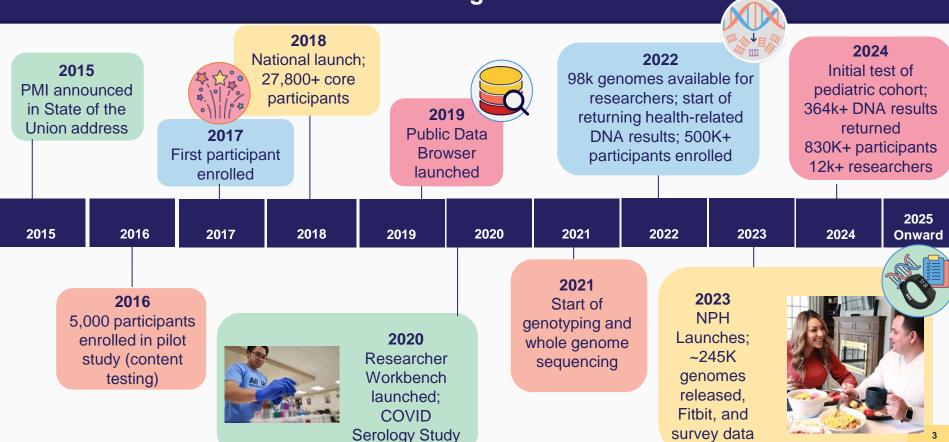
The All of Us Research Program Mission

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

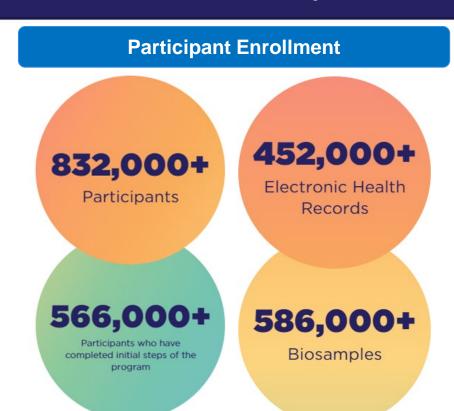


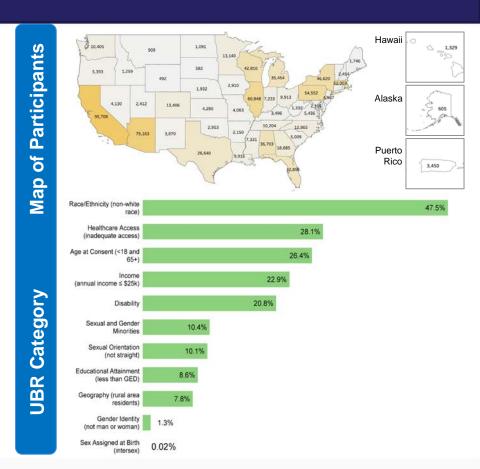
Made possible by a team that maintains a culture built around the program's core values

Timeline of the All of Us Research Program



Status of *All of Us* Participants





Numbers as of August 24, 2024

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





Delivering Clinically Impactful Individual Health Results

Hereditary Disease Risk



124k *All of Us* Participants have viewed this report, which looks for genetic variants in 59 genes associated with serious health conditions, including:

- Breast cancer
- Ovarian cancer
- Uterine cancer
- Colorectal cancer
- Prostate cancer

- Melanoma
- Brain cancer
- Pancreatic cancer
- Stomach cancer

- Familial hypercholesterolemia
- Cardiomyopathies
- Arrhythmias
- Arteriopathies
- Neurofibromatosis type 2

~3% (>3,300 to date) of participants who receive their hereditary disease risk report will have a potentially life-changing genetic variant.

Medicine and Your DNA



143.2k *All of Us* Participants have viewed this report, which analyzes seven genes that can affect how bodies process medicine and impacts which medication or what dosage you take. This report includes 50+ different medicines that may be impacted by your genetics, including:

- Citalopram (Celexa®)
- Clopidogrel (Plavix®)
- Escitalopram (Lexapro®)
- Sertraline (Zoloft®)
- Lidocaine
- Glimepiride (Amaryl®)
- Sulfamethoxazole/ trimethoprim (Bactrim®)
- Simvastatin (Zocor®)
- Amitriptyline (Elavil®)

~90% (>106,000) of participants who received this report have a result that could impact how their body processes a medication within this report.

Retrospective research using *All of Us* data suggests that ~20% of participants will be exposed to a drug with an actionable pharmacogenetic result.

Data Tiered Access Levels Enable Discovery



Available to **Anyone**



Available to Registered Researchers

PUBLIC TIER

Public resources include:

- Data Snapshots: Aggregated, public-facing overviews of participant characteristics and data types
- Data Browser: Interactive preview into the All of Us dataset through public-facing aggregate data
 - Currently includes participant-provided survey responses, physical measurements, data from EHRs and wearables, and genomic data
- Survey Explorer: Details the questions included in each of the surveys
- Research Projects Directory: Descriptions of each research project within the Researcher Workbench

RESEARCHER WORKBENCH

REGISTERED TIER

Registered researchers can access in-depth data and a variety of research tools to conduct a wide range of studies.



Electronic

Health

Records





Wearables

CONTROLLED TIER

Registered researchers with amended institutional agreements can access all of the data in the Registered Tier plus additional and expanded data types, including genomic data, real dates of health events, ICD codes, granular demographic data, and more.

Genomics

Health and

Lifestyle surveys

Data Currently in the All of Us Researcher Workbench



Participant Surveys 1,958,520+ Surveys Completed



Mobile/Wearable Tech 15,600+Fitbit Records



Electronic Health Records 287,000+ EHRs



As says 1,500,000+ Structural Variants



Physical Measurements 337,500+ Physical Measures



Omics

312,900+ Genotyping Arrays 245,350+ Whole Genome Sequences 1,000+ Long-Read Sequences The All of Us Researcher
Workbench contains the one of the
largest sets of whole genome
sequences widely available for
research.

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





Biospecimens 14,000,000+ Aliquots (DNA, RNA, serum, plasma, cfDNA, RNA, urine)

All of Us Research Program's Commitment to Researcher Diversity

(as of August 26, 2024)



12,475+ Registered Researchers



865+ Organizations 44 HBCUs and 73 HSIs



610+ Publications using All of Us data

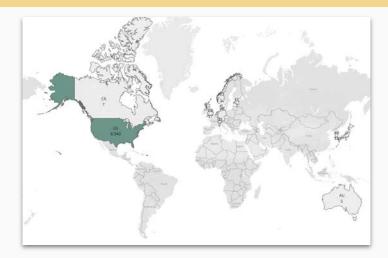




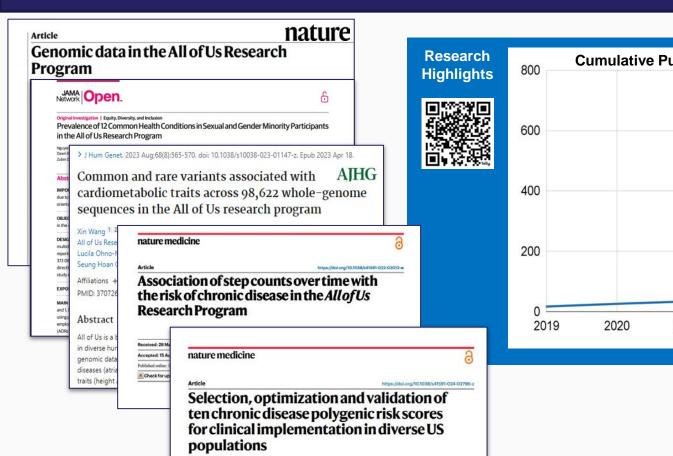


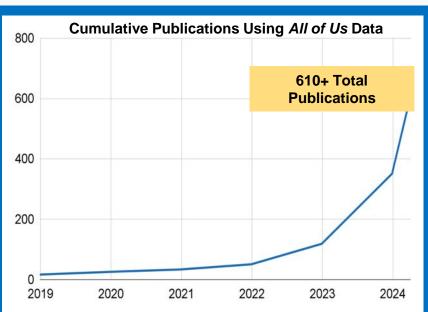
Over 78% of our researchers are underrepresented in the biomedical workforce, including more than 34% who are underrepresented by race and ethnicity (non-White and non-Asian researchers).

All of Us is open to national and international researchers at academic, not-for-profit, commercial, and health care institutions.



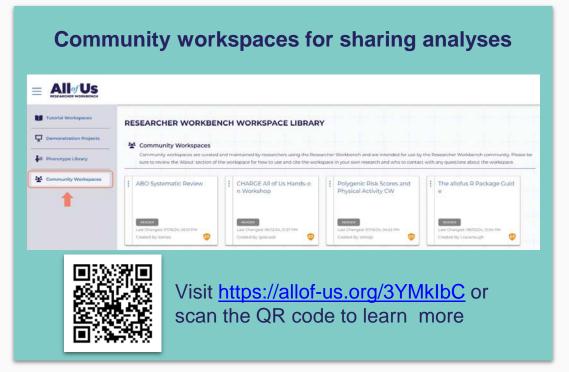
The Exponential Growth of All of Us-Enabled Discoveries





Researcher Workbench Supports Powerful Analyses and Collaboration





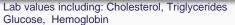
"All by All" Analyses Uncovering ~500 Billion Gene-Phenotype Associations Results in Workbench; Public Website Coming in November

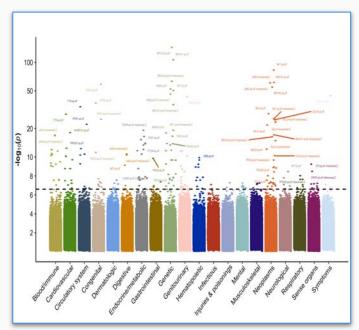
Phenotypes with number of participants > 200 per group

All by All: Common and rare variant association testing in 250,000 whole genomes across diverse ancestry groups

Genetic ancestry group	Num. individuals	Num. variants
AFR	56,913	383,702,267
AMR	45,035	334,390,971
EAS	5,706	122,729,124
EUR	133,581	628,935,579
MID	942	41,842,694
SAS	3,217	83,584,317
	245,394	1,116,593,592

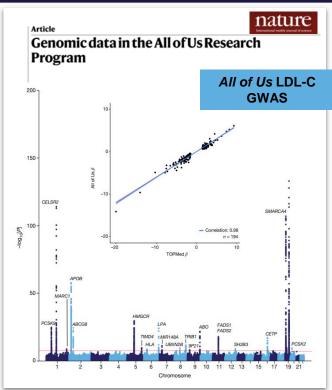
Category	AFR	AMR	EAS	EUR		SAS
Lab measurements	12	12	12	12	12	12
Random phenotypes	30	30	30	30	30	30
mcc2 phecode	573	477	45	1000	1	20
mcc2 phecodeX	869	776	80	1361	0	42
r drug	758	715	357	857	42	288
pfhh survey	20	17	0	78	0	0
hysical measurements	10	10	10	10	10	10
Total: 8,688	2,272	2,037	534	3,348		402

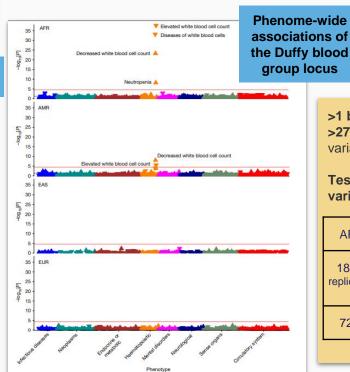




Associations across > 5K phecodes

Using a Diverse Dataset to Discover Novel Genomic Variants





>1 billion genetic variants
>275 million previously unreported genetic variants

Tested for replications of 3,724 genetic variants associated with 117 diseases:

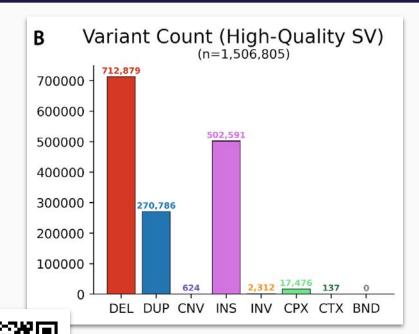
AFR	AMR	EAS	EUR	SAS
18/25 replicated	13/13 replicated	7/15 replicated	1,064/1,421 replicated	1/1 replicated
72%	100%	46.6%	74.9%	100%

Pioneering Genomic Research: Over 1.5 Million Structural Variants Ready for Discovery

All of Us greatly expanded the structural variant (SV) data available in the Researcher Workbench's Controlled Tier this summer.

Now, there are more than 1.5 million SVs from nearly 98,000 participants with linked phenotype information. This makes *All of Us* one of the largest and most widely available catalogs of SV data.

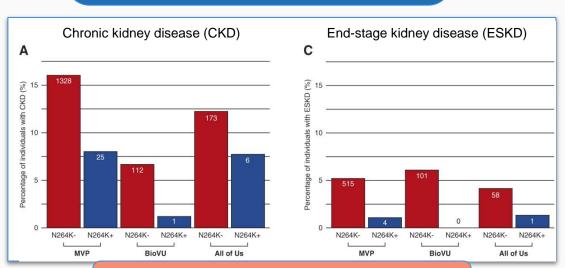
This release represents a huge step toward our goal of expanding the breadth and depth of genomic data: https://allof-us.org/SVData.



Using Large, Diverse Datasets to Understand Disease Risk of APOL1 Variants

Variants in the *APOL1* gene are associated with end stage kidney disease (ESKD) in people of African ancestry

70% of excess ESKD risk in African Americans is thought to be related to *APOL1*



Significance:

- All of Us data from v5 with 98k WGS (v7 has 245k WGS — almost 2.5x increase!)
- Potential drug target for treating APOL1 ESKD



Hung et al. (2023). Journal of the American Society of Nephrology: JASN 15

All of Us Ancillary Studies



Embedded studies



Recontact of participants for custom surveys, wearables, etc

COVID Serology Study Biospecimen use to generate new data

Ancillary studies:

- Address important scientific questions and deliver insights into health and disease.
- Expand the All of Us dataset by adding new data and/or engaging unique participant communities.
- **3. Enable research across boundaries** with novel analyses of lifestyle, environmental, and biologic data.

23 NIH Institutes, Centers and Offices are involved in 9 completed, ongoing, and proposed ancillary studies.

Core All of Us participant data
Broad Data use through the
Researcher Workbench

Largest Precision Nutrition Research Effort of its Kind

Nutrition for Precision Health



Module 1: The Usual Diet Study

Examine baseline diet and physiological responses to meal challenges



Module 2: The Provided Diet Study

Examine responses to 3 shortterm intervention diets in freeliving controlled feeding studies



Module 3: The Live-in Diet Study

Examine responses to 3 shortterm intervention diets in domiciled controlled feeding studies

Q Newsletter

Researching how nutrition can be tailored to each person's genes, culture, and environment to improve health

Involving at least **8,000** *All of Us* participants



WELLNESS - May 3, 2024

Becky Worley on what it's like to join a research study

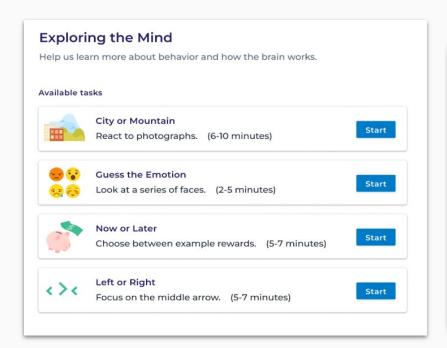
ABC News' Becky Worley took part in a study being performed by the National Institutes of Health that could be a game-changer for health research.



Watch the Video

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All of Us x NIMH: Cognitive Leaps with 10x More Data from 50K Minds in 6 Months



All of Us collected 10x more task completions in ~6 months than the Many Brains project collected in >10 years.



Over 73,000 participants have completed tasks and their responses overlap with other biomedical data types in *All of Us*:

- 94% have provided physical measurements
- 93% donated biospecimens
- 89% completed both mental health and well-being surveys
- 60% have EHR data

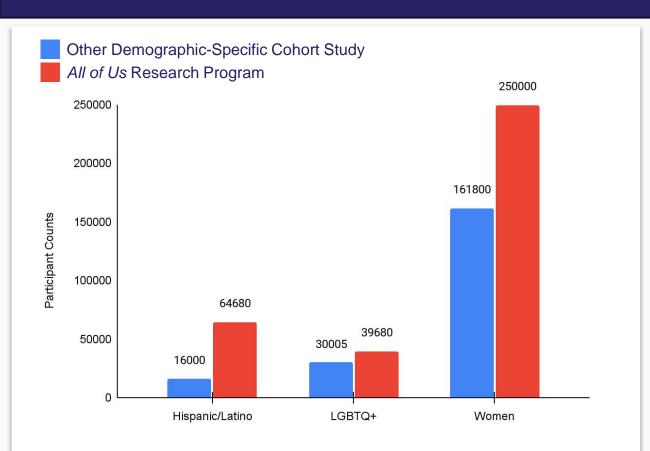
Exposome Ancillary Study on Environmental Health Launched in July

National Institute of Environmental Health Sciences (NIEHS) and *All of Us* launched a new ancillary study to assess **environmental exposures** and their interactions with genomic and behavioral health factors. Initial investigation is for participants with Type 2 diabetes (incident since joining *All of Us*). These data will become available to all approved *All of Us* researchers.



By leveraging *All of Us* as a platform for this research, NIEHS was able to begin data collection <1 year after submitting their initial proposal and reduced the cost of this study by 75%.

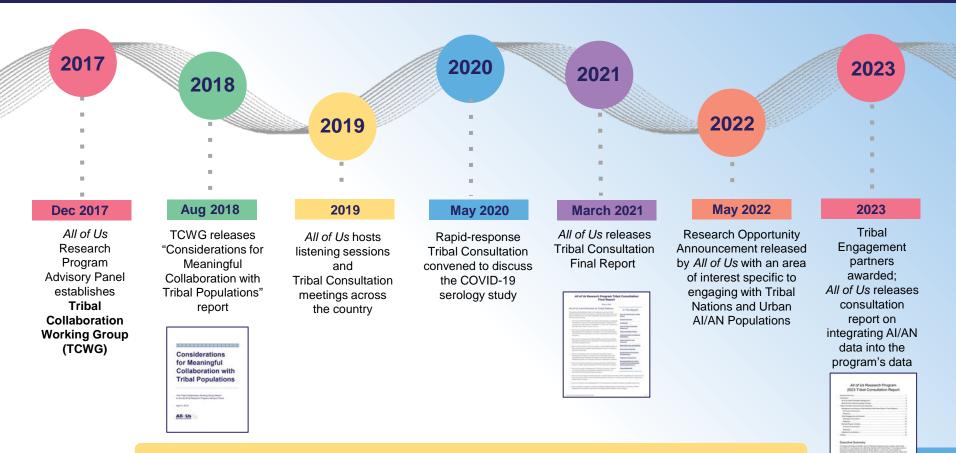
Inclusion in All of Us Compared to Other Community-Specific Cohorts



All of Us has unprecedented representation compared to other major studies including:

- Hispanic Community
 Health Study/Study of
 Latinos
- PRIDEnet
- Women's Health Initiative
- RURAL Cohort Study

Brief Milestones of All of Us Consultation & Tribal Engagement



Data from self-identified Al/AN participants coming in Sep 2024

Intentional and Thoughtful Outreach Driven by Foundational Commitments



Visit https://allof-us.org/TribalEngagement or scan the QR code to learn more

- We will respect Tribal sovereignty by engaging Tribal Nations to ensure that research using the program's biospecimens and data from Tribal members is done in a way that is respectful and transparent.
- We will not recruit on Tribal lands or share information about participants' Tribal affiliation without first getting approval from the Tribe.
- We will support the development of educational materials for researchers and participants, work with AI/AN researchers in partnership with AI/AN communities, and promote community-based participatory research.
- We will work to ensure representation of Al/AN populations throughout all aspects of program governance.

Indigenous-led Demonstration Projects for In-Depth First Look at Al/AN Data



All of Us awarded the American Indian Science and Engineering Society (AISES) to create and promote the "We Are All Scientists" campaign, focused on Indigenous workforce diversity.

Phenotypic/Survey Project

Purpose: To analyze and compare non-genomic data in comparison to the NHLBI Strong Heart Study

Genotypic Project

Purpose: To compare data to reference populations and associations with elevated disease risk and prevalence factors

Goal: To publish these findings, along with a marker paper describing the program's Tribal engagement and outreach efforts to date

Communications About Al/AN Data Update

To date, data from self-identified AI/AN participants has not been included in the data available to registered researchers or in the Public Data Browser.

Through the years, we have conducted an extensive series of Tribal consultations and engagement activities to work towards the inclusion of data from self-identified AI/AN participants in the *All of Us* Researcher Workbench.

When this time comes, communications about this data update will be shared through a comprehensive notification plan including:

- Advance notifications to NIH and HHS Tribal advisory groups and collaborators
- Message to Al/AN participants
- Updates to All of Us websites
- Information for investigators, including All of Us' new policy "Respectful Research Involving American Indian and Alaska Native Populations" and a research guide coming soon



Coming in September: Incredible New Data on the Researcher Workbench

Total participants will increase from 413k to 633k (+53%)



429,000+

With genotyping arrays

(+37%)



633,000+
With survey responses

(+53%)



400,000+

With whole genome sequences (WGS)

(+63%)



2,700+

Long-Read Sequences

(+170%)



59,000+ With Fitbit records (+278%) 6.3 TB!

633,000+

Racial and Ethnic Subcategories

(+53%)



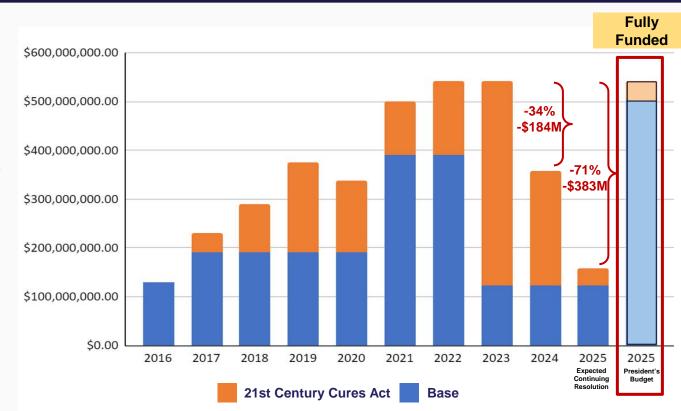
Self-Identified Al/AN Participant Data

Budget Background and FY25 Budget Requirements



Senate FY25 Labor-HHS bill **restored funding** for the program to the FY23 enacted level of \$541M.

If the base allocation stays flat, when the Cures Act funding drops, the program's budget will be cut an additional 56%.



*During the Aug. 1st FY25 L-HHS markup, Subcommittee Chair Tammy Baldwin (D-WI) and Ranking Member Shelley Moore Capito (R-WV) strongly supported advancing precision medicine by restoring full funding to *All of Us*.

Pediatrics: Limited Launch Now; Ready to Expand when Funding Permits

Now Enrolling Ages 0-4 at Five Clinical Sites



"Data from children and parents will allow researchers to elucidate the biological, social, and environmental influences that impact our health over time."



Read the Press Release







SanD













@AllofUsResearch @AllofUsCEO #JoinAllofUs









Thank you to our 832,000+ participants!