



Sessions and Posters at ASHG 2024

Tuesday, November 5, 2024

Time	Location	Session information	Presenter(s)
10:00 a.m.– 12:00 p.m.	Room 711	<p>All of Us Workshop</p> <p>Presentation title: Getting Started with Biomedical and Genomic Data in the <i>All of Us</i> Researcher Workbench</p>	<p>Julie Coleman, Baylor College of Medicine</p> <p>Shamika Ketkar, Baylor College of Medicine</p> <p>Jinyoung Byun, University of New Mexico</p>

Wednesday, November 6, 2024

Time	Location	Session information	Presenter(s)
8:00 a.m.– 9:30 a.m.	Mile High Ballroom 2 & 3	<p>Presentation in panel, “Biobank Scale Genetic Data Resources for Studying Complex and Rare Human Diseases”</p> <p>Presentation Title: Structural variant discovery with GATK-SV in 97,940 short-read whole genomes from the <i>All of Us</i> Research Program (8:30 a.m.–8:45 a.m.)</p>	<p>Emma Pierce-Hoffman, Broad Institute</p>
10:15 a.m.– 11:45 a.m.	Room 405	<p>Presentation in panel, “Creative Community Engagement: Gathering Data for Better Participatory Research”</p> <p>Presentation title: Co-Creating a story-based video collection to engage LGBTQIA+ community members with the <i>All of Us</i> Research Program: An engagement marketing and human-centered design approach (10:30 a.m.–10:45 a.m.)</p>	<p>Jennifer Uhrig, Research Triangle Institute (RTI)</p>

Wednesday, November 6, 2024

Time	Location	Session information	Presenter(s)
10:15 a.m.– 11:45 a.m.	Room 401	<p>Presentation in panel, “Moving Polygenic Risk Scores Closer to Clinical Implementation”</p> <p>Presentation title: <i>All of Us</i> diversity and scale improve polygenic prediction contextually with greatest improvements for under-represented populations (10:30 a.m.–10:45 a.m.)</p>	Ying Wang, Massachusetts General Hospital
10:15 a.m.– 11:45 a.m.	Room 401	<p>Presentation in panel, “Moving Polygenic Risk Scores Closer to Clinical Implementation”</p> <p>Presentation title: Performance of contemporary polygenic risk scores for atherosclerotic cardiovascular disease in the <i>All of Us</i> Workbench (11:15 a.m.–11:30 a.m.)</p>	Johanna Smith, Mayo Clinic
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	<p>Poster: Engaging high school students in exploring big data via the All of Us Data Browser</p> <p>Board No. 7068W</p>	Louisa Stark, University of Utah
		<p>Poster: The <i>All of Us</i> Researcher Academy Internship Program: An Experiential Learning Opportunity Designed to Support Research Skills Development of Diverse Early-Stage Researchers</p> <p>Board No. 1090W</p>	Sula Hood, RTI
		<p>Poster: SGLT2 Inhibitors Attenuate Risk of APOL1-mediated Chronic Kidney Disease</p> <p>Board No. 5154W</p>	Ariel Williams, National Human Genome Research Institute (NHGRI)
		<p>Poster: Genomic Return of Results for The United States’ <i>All of Us</i> Research Program</p> <p>Board No. 1068W</p>	Hannah Hoban, Color Health
		<p>Poster: Deciphering fine-scale population structure in the U.S. to uncover population-specific disease risks for health equity</p> <p>Board No. 1057W</p>	Mariko Isshiki, Albert Einstein College of Medicine

Wednesday, November 6, 2024

Time	Location	Session information	Presenter(s)
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	<p>Poster: Assessing the impact of social exposomes on genetic liability for bipolar disorder</p> <p>Board No. 4017W</p>	Rachel Sharp, University of North Carolina at Chapel Hill
		<p>Poster: A methodology to assess concordance of last prescribed treatment with CPIC guideline recommendations: A case study application in a diverse <i>All of Us</i> research cohort</p> <p>Board No. 7002W</p>	Iliia Rattsev, Johns Hopkins University
		<p>Poster: A novel, scalable, and efficient blockLASSO PGS method in <i>All of Us</i> and the UK Biobank</p> <p>Board No. 4004W</p>	Timothy Raben, Michigan State University
		<p>Poster: Association analysis of rare genetic variants in circulatory and respiratory phenotypes among participants from the <i>All of Us</i> Research Program</p> <p>Board No. 4019W</p>	Jingwen Zhang, Boston University
		<p>Poster: Phenome-wide association studies of Mucins in <i>All of Us</i> data reveal tandem repeat-associated phenotypic traits</p> <p>Board No. 3026W</p>	Evangelos Nizamis, University of Washington
		<p>Poster: Population Descriptors in Genomic Legacy Data: Reflections and Recommendations for Future Research Directions from a Trans-NIH Workshop</p> <p>Board No. 7081W</p>	Lucia Hindorff, NHGRI
		<p>Poster: Measuring the accuracy of electronic health record-based phenotyping in the <i>All of Us</i> Research Program using pathogenic BRCA1 and BRCA2 carrier frequencies in putative ovarian cancer cases</p> <p>Board No. 1077W</p>	John Baierl, Cedars-Sinai Medical Center

Wednesday, November 6, 2024

Time	Location	Session information	Presenter(s)
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	Poster: Phenome-wide association study of MTHFR variant in UK Biobank and <i>All of Us</i> Board No. 1086W	Anas Awan, NHGRI
		Poster: Multi-Ancestry Genome Wide Association Study (GWAS) in the <i>All of Us</i> Cohort for Primary Open Angle Glaucoma Board No. 5124W	Kiana Tavakoli, University of California San Diego
		Poster: Genome wide association study investigating increased risk of postpartum depression among women affected by immune-mediated inflammatory conditions Board No. 5075W	Alyks Linerud, Brigham Young University

Thursday, November 7, 2024

Time	Location	Session information	Presenter(s)
8:00 a.m.– 9:30 a.m.	Four Seasons Ballroom 4	Presentation in panel, “Contributions of Tandem Repeats to Human Variation, Traits, and Disease” Presentation title: Tandem repeats make widespread contributions to complex traits (8:50 a.m.–9:05 a.m.)	Helyaneh Ziaei Jam, University of California San Diego
10:15 a.m.– 11:45 a.m.	Four Seasons Ballroom 1	Presentation in panel, “Disease Insights from Omic-Wide Approaches” Presentation title: All by <i>All of Us</i> : common and rare variant association testing in 245,000 whole genomes across diverse ancestry groups (11:00 a.m.–11:15 p.m.)	Konrad Karczewski, Massachusetts General Hospital
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	Poster: Genetic architecture and comprehensive phenotypic assessment of alcohol use disorder and related outcomes in <i>All of Us</i> Board No. 5078T	Bradley Webb, RTI
		Poster: Utilizing large-scale whole genome sequencing data from the <i>All of Us</i> research program to discover novel genes and endogenous retroviral loci associated with female infertility and recurrent pregnancy loss Board No. 6091T	Erik Stricker, Baylor College of Medicine

Thursday, November 7, 2024

Time	Location	Session information	Presenter(s)
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	<p>Poster: Severe COVID-19 enriched in participants with G6PD deficiency in the <i>All of Us</i> Research Program dataset</p> <p>Board No. 5155T</p>	Eric Venner, Baylor College of Medicine,
		<p>Poster: Underdiagnosis and Health Disparities in Hereditary Hemorrhagic Telangiectasia</p> <p>Board No. 1096T</p>	Nicholas Singh-Miller, NHGRI
		<p>Poster: Hidden Population Structure in the <i>All of Us</i> Research Project</p> <p>Board No. 3022T</p>	Ruhollah Shemirani, Icahn School of Medicine at Mount Sinai
		<p>Poster: Characterizing Genetic Diversity in the <i>All of Us</i> Research Program in the Context of Genetic Association Studies</p> <p>Board No. 4030T</p>	Sophia Gunn, New York Genome Center
		<p>Poster: Genetic correlates of treatment-resistant depression: Insights from polygenic scores across cognitive, temperamental, and sleep traits in the <i>All of Us</i> cohort</p> <p>Board No. 5080T</p>	Bohan Xu, Laureate Institute for Brain Research
		<p>Poster: Genome-wide Association Study of Long COVID by Predictive Phenotyping of EHR Data using Deep Learning: Transferring Trained Model from National COVID Cohort Collaborative to <i>All of Us</i> Research Platform Enables Genetic Discovery</p> <p>Board No. 5093T</p>	Ardalan Naseri, University of Texas Health Science Center
		<p>Poster: Leveraging EHR Phenotyping and Genome-Wide Association Studies to Identify Genetic Predisposition Factors for Systemic Lupus Erythematosus Within <i>All of Us</i> Research Program</p> <p>Board No. 5123T</p>	Dayo Shittu, NHGRI

Friday, November 8, 2024

Time	Location	Session information	Presenter(s)
8:00 a.m.– 9:30 a.m.	Room 505	<p>Presentation in panel, “Aging, Clonal Hematopoiesis, and Our Health”</p> <p>Presentation title: Clonal expansion: leveraging biobank scale data to identify molecular mechanisms and non-oncologic disease consequences (8:15 a.m.–8:30 a.m.)</p>	Alex Bick, Vanderbilt University Medical Center
8:00 a.m.– 9:30 a.m.	Room 505	<p>Presentation in panel, “Aging, Clonal Hematopoiesis, and Our Health”</p> <p>Presentation title: Determinates of Clonal Hematopoiesis Progression to Hematologic Malignancy (8:45 a.m.–9:00 a.m.)</p>	Kelly Bolton, Washington University in St. Louis
10:15 a.m.– 11:45 a.m.	Room 401	<p>Presentation in panel, “Translating Genetics into Screening Programs”</p> <p>Presentation title: Biobank-scale genotype-to-phenotype analyses reveal the challenges in using exome sequencing for population screening (11:30 a.m.–11:45 a.m.)</p>	David Blair, University of California, San Francisco
1:15 p.m.– 2:15 p.m.	Four Seasons Ballroom 2&3	<p>Presentation in panel, “Rare Variants and Admixture Modeling in Diverse Population”</p> <p>Presentation title: Large-scale admixture mapping in the <i>All of Us</i> Research Program improves the characterization of cross-population phenotypic differences (1:15 p.m.–1:30 p.m.)</p>	Ravi Mandla, University of California, Los Angeles
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	<p>Poster: Functional components of heritability in admixed African-ancestry <i>All of Us</i> whole-genome sequencing data</p> <p>Board No. 4063F</p>	Jordan Rossen, Broad Institute
		<p>Poster: Genome-Wide Meta-Analysis of Single Variant Associations in Uterine Fibroid Samples</p> <p>Board No. 7035F</p>	James Jaworski, Vanderbilt University Medical Center
		<p>Poster: Empowering Researchers: A Cost-Effective and Versatile PRS Calculator for the <i>All of Us</i> Program</p> <p>Board No. 4046F</p>	Ahmed Khattab, Scripps Research Translational Institute

Friday, November 8, 2024

Time	Location	Session information	Presenter(s)
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	<p>Poster: Systematic Evaluation of Polygenic Score Performance Across Diverse Population Characteristics in the <i>All of Us</i> Research Program</p> <p>Board No. 1090F</p>	Jack Staples, University of Colorado Anschutz Medical Campus
		<p>Poster: The Long Road to Long Reads: Challenges to Implementing a Long Read Sequencing Service</p> <p>Board No. 1175F</p>	Michelle Kokosinski, Johns Hopkins University
		<p>Poster: Variability in Self-reported Race Among Individuals with Middle Eastern Inferred Genetic Ancestry in the UK Biobank, <i>All of Us</i> and MGB Biobank</p> <p>Board No. 6092F</p>	Yang Sui, Broad Institute
		<p>Poster: Leveraging the <i>All of Us</i> Research Program to better understand the genetic architecture of opioid use disorder spectrum behaviors</p> <p>Board No. 5116F</p>	Amy Moore, RTI
		<p>Poster: Novel genetic loci associated with knee osteoarthritis in 284,184 cases and controls in the Million Veteran Program and the <i>All of Us</i> Research Network</p> <p>Board No. 5132F</p>	Chelsea Nguyen, University of Alabama Birmingham
		<p>Poster: Insights into causes and consequences of repeat expansions from biobank sequencing data</p> <p>Board No. 5093F</p>	Margaux Hujoel, Brigham and Women's Hospital and Harvard Medical School and Broad Institute
		<p>Poster: Insights into copy-number evolution and polygenic score transferability from LPA</p> <p>Board No. 3022F</p>	Ronen Mukamel, Harvard Medical School
		<p>Poster: Association of orofacial cleft risk loci with elevated risk of prostate cancer</p> <p>Board No. 4021F</p>	John Shaffer, University of Pittsburgh

Friday, November 8, 2024

Time	Location	Session information	Presenter(s)
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	<p>Poster: Leveraging the <i>All of Us</i> platform to enable rapid genomic analysis of primary autoimmune hypothyroidism in diverse populations</p> <p>Board No. 1079F</p>	Anav Babbar, NHGRI
		<p>Poster: Efficient large scale PheWAS analysis with PheTK</p> <p>Board No. 4043F</p>	Tam Tran, NHGRI
		<p>Poster: High-throughput genotype-phenotype association data aid variant classification in a diverse cohort</p> <p>Board No. 6043F</p>	Chenjie Zeng, NHGRI
		<p>Poster: Exploring allelic variation at structurally variant and medically relevant loci in the <i>All of Us</i> Research Program long-read genomes</p> <p>Board No. 7006F</p>	Julie Wertz, University of Washington
		<p>Poster: Evaluating Genetic Diversity in the <i>All of Us</i> Research Program</p> <p>Board No. 3011F</p>	Mateus Henrique Gouveia, NHGRI
		<p>Poster: Exploring Uterine Fibroid Disparities among Black and Hispanic Women: Insights from the <i>All of Us</i> Workbench</p> <p>Board No. 7063F</p>	Lynette Hammond Gerido, Case Western Reserve University
		<p>Poster: Ancestry-aware genome-wide association study of African American multiple sclerosis patients in <i>All of Us</i> (poster)</p> <p>Board No. 4017F</p>	Steven Brugger, Brigham Young University
		<p>Poster: Cross-population replication analysis of STR-trait associations in the <i>All of Us</i> dataset</p> <p>Board No. 1057F</p>	Nichole Ma, University of California San Diego

Friday, November 8, 2024

Time	Location	Session information	Presenter(s)
2:30 p.m.– 4:30 p.m.	Exhibit & Poster Hall/Upper Level	<p>Poster: Pharmacogenomic genome-wide association study of LDL response to statins using high-throughput electronic health records analysis</p> <p>Board No. 4113F</p>	Slavina Goleva, NHGRI
		<p>Poster: Genome-Wide Meta-Analysis of Single Variant Associations in Uterine Fibroid Samples</p> <p>Board No. 7035F</p>	J. Jaworski, Vanderbilt University Medical Center
		<p>Poster: Type 2 Diabetes protective effects of rare loss of function variants in African Americans: an <i>All of Us</i> cohort study</p> <p>Board No. 5172F</p>	Shivam Sharma, Georgia Institute of Technology
		<p>Poster: Using <i>All of Us</i> to investigate genetic factors influencing the measles vaccine response</p> <p>Board No. 6089F</p>	Alireza Majd, University of California, San Francisco
		<p>Poster: Enhancing polygenic scores prediction across multiple ancestries with S4-Multi model</p> <p>Board No. 4048F</p>	Ping-Hung Lai, Cedars Sinai Medical Center
		<p>Poster: Investigating sex-specific genetic susceptibility in autoimmune diseases</p> <p>Board No. 5105F</p>	Peter Sauer, NHGRI
		<p>Poster: Establishing prevalence and phenotypic spectrum of purine and pyrimidine disorders using genotype-first approach to mining electronic health record biobanks</p> <p>Board No. 2030F</p>	Katharine Chailett, NHGRI
		<p>Poster: TERTp.K1050N: A founder variant in Ashkenazi Jewish populations associated with telomere biology disorders</p> <p>Board No. 8052F</p>	Kelvin Cesar De Andrade, National Cancer Institute

Saturday, November 9, 2024

Time	Location	Session information	Presenter(s)
9:30 a.m.– 10:30 a.m.	Room 405	Presentation in panel, “Technology for Translation” Presentation title: The <i>All of Us</i> Research Program data release 2024 (CDR v8): Powering genomic research through <i>All of Us</i> (10:15 a.m.–10:30 a.m.)	Anjene (Anji) Musick, <i>All of Us</i> Research Program
9:30 a.m.– 10:30 a.m.	Four Seasons Ballroom 2 & 3	Presentation in panel, “Phenomenal PheWAS” Presentation title: Phenome-Wide Association of APOE Alleles in the <i>All of Us</i> Research Program (10:15 a.m.–10:30 a.m.)	Jason H. Karnes, University of Arizona

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