



Saturday, November 2

| | | |
|----------------|--|------------------------|
| 12:00pm-6:00pm | Registration | Crystal Foyer |
| 5:00pm-6:30pm | Embassy Suites Evening Reception Join colleagues at the Embassy Suites hotel reception! Complimentary for hotel guests. | 4th Floor Lobby |

Sunday, November 3

IGES Annual Meeting-Day 1

| | | |
|----------------------|--|-----------------------------|
| 7:00am-5:30pm | Registration | Crystal Foyer |
| 7:00am-10:30am | Hotel Breakfast Buffet Open for Embassy Hotel Guests | 4th Floor Lobby |
| 8:15am-8:55am | Opening Session | Crystal Ballroom |
| 8:15am-8:25am | Welcome | John Witte |
| 8:25am-8:55am | Presidential Address | Elizabeth Gillanders |
| 8:55am-9:55am | Session 1 - Williams Awards Chair: John Witte | Crystal Ballroom |

| | Presentation | Abstract | Author |
|-----------------|---|----------|--------------------------|
| 8:55am-9:10am | Co-expression-Wide Association Studies Implicate Protein-Protein Interactions in Complex Disease Risk | 65 | Mykhaylo Malakhov |
| 9:10am-9:25am | The Problem with Proteins: What Mendelian Randomization Can (and can't) Reveal | 38 | Emma Hazelwood |
| 9:25am-9:40am | Multi-ancestry Proteome-wide Mendelian Randomization Offers a Comprehensive Protein-disease Atlas and Potential Therapeutic Targets | 103 | Chen-Yang Su |
| 9:40am-9:55am | Multi-FISHNET: Finding Significant Hits in Networks | 1 | Sandeep Acharya |
| 9:55am-10:00am | ELSI Activity | | Marie-Pierre Dubé |
| 10:00am-10:20am | Refreshment Break | | Crystal Foyer |
| 10:20am-11:50am | Session 2 - Neel Awards Chair: Lisa Strug | | Crystal Ballroom |

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|-----------------|--|--|---------------------|
| 10:20am-10:50am | Keynote Presentation: Population Genetics in an Era of Genomic Health | | Eimear Kenny |
|-----------------|--|--|---------------------|

| | Presentation | Abstract | Author |
|-----------------|--|----------|-----------------|
| 10:50am-11:05am | Robust Fine-Mapping in the Presence of Linkage Disequilibrium Mismatch | 130 | Wenmin Zhang |
| 11:05am-11:20am | A Novel Polygenic Risk Scoring Framework Integrating Common and Rare Variants for Enhanced Genetic Prediction Across Ancestries | 114 | Jacob Williams |
| 11:20am-11:35am | A Novel Multivariable Mendelian Randomization Framework to Disentangle Highly Correlated Exposures with Application to Metabolomics | 13 | Lap Sum Chan |
| 11:35am-11:50am | Multi-Trait Inference of Full Genome-Wide Associations of Type 2 Diabetes Subtypes Informs Distinctive Biology and Putatively Causal Genes | 125 | Satoshi Yoshiji |

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| 11:50pm-1:20pm | Lunch on Your Own | | |
| 11:50am-1:20pm | IGES Board Meeting | | Minturn (2nd Floor) |
| 11:50am-1:20pm | Committee Meetings (meeting rooms located on the 3rd floor) | | |
| | Publications Committee | | Aspen A |
| | Communications Committee | | Redstone |
| | Young Investigators Committee | | Leadville |
| | Program Committee | | Aspen B |
| | Education Committee | | Rexford |
| | ELSI | | Cripple Creek |

Sunday, November 3

| | | | |
|----------------|---|---|-----------------------|
| 1:20pm-2:50pm | Session 3 - Machine Learning | Crystal Ballroom | |
| | Chair: Xiaofeng Zhu | | |
| 1:20pm-1:50pm | Keynote Presentation: Genetic Architecture of Human Organs through Imaging Genetics: Challenges and Opportunities | Hongtu Zhu | |
| | Presentation | Abstract | Author |
| 1:50pm-2:05pm | Bridging Histology to Spatial Transcriptomics: A Pathology Foundation Model-driven Contrast Learning for Predicting Spatial Transcriptomic Profiles from Histology Images | 43 | Pingzhao Hu |
| 2:05pm-2:20pm | scPrediXcan: A Method for Transcriptome-Wide Association Studies at Cell-Type Level Using Deep Learning | 131 | Yichao Zhou |
| 2:20pm-2:35pm | Biobank-Scale Genetically Regulated Expression Is Predictive of 3D Chromatin Contact Frequency | 7 | Michael Betti |
| 2:35pm-2:50pm | Quantile IV Relaxes Parametric Assumptions and Enables Conditional Average Treatment Effect Estimation in Mendelian Randomization | 53 | Marc-André Legault |
| 2:50pm-3:05pm | Poster Highlights | | |
| | Poster | Abstract | Author |
| | A Multi-phenotype Colocalization Framework in <i>LocusFocus</i> | 59 | Hua Lu |
| | Mendelian Randomization of Sex-Dependent Traits | 87 | Eric Sanders |
| | A New Multi-trait Fine-mapping Method Using a Non-local Prior, with Applications in Circulating Metabolic Biomarker Level Analysis | 49 | Ville Karhunen |
| | Subtle Stories in GWAS Data: Multiomics Implicate GPX3 at the <i>TNIP1</i> Locus in Alzheimer's Disease | 75 | Daniel Panyard |
| | Cross-omic Characterization of the Molecular Profile of TD2 in Hispanic/Latinos | 28 | Elizabeth Frankel |
| | Pleiotropic Effects of Pathway-Partitioned Genetic Risk Scores for Asthma in UK Biobank | 88 | Matthew Saward |
| 3:05pm-4:05pm | Poster Session 1 & Refreshments | Crestone Ballroom | |
| 4:05pm-5:35pm | Session 4 - OMICS | Crystal Ballroom | |
| | Chair: David Conti | | |
| | Presentation | Abstract | Author |
| 4:05pm-4:20pm | Learning Sparse Gaussian Graphical Models from Correlated Data | 127 | Zeyuan Song |
| 4:20pm-4:35pm | Integrative Proteogenomic Analyses Reveal Insights into Subtype-specific Glioma Risk | 71 | Taishi Nakase |
| 4:35pm-4:50pm | Enhancing Non-linear TWAS Performance Via Trait Imputation with Applications to Alzheimer's Disease | 74 | Wei Pan |
| 4:50pm-5:05pm | Human Protein-Small Molecule Interaction Networks Reveal the Cross-Talks Between Genomic Components and Metabolome Across Complex Metabolic Traits | 69 | Vaha Akbary Moghaddam |
| 5:05pm-5:20pm | Multi-ancestry Proteome-wide Association Studies Leveraging Both cis-and trans-pQTL and Protein-protein Interaction Networks | 106 | Lang Wu |
| 5:20pm-5:35pm | FunColoc: A Generalized Functional Regression Model for Genetic Colocalization Analysis of microRNA Counts and Disease-related Outcomes | 12 | Myriam Brossard |
| 7:00pm-10:00pm | Annual Banquet & Networking Entertainment by Ojo de Luna | Cripple Creek Ballroom (2nd floor) | |



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People inspired.

RGIC[®]

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Monday, November 4

IGES Annual Meeting-Day 2

| | | | |
|----------------|--|--|-------------------------|
| 7:00am-5:30pm | Registration | | Crystal Foyer |
| 6:30am-9:30am | Hotel Breakfast Buffet Open for Embassy Hotel Guests | | 4th Floor Lobby |
| 8:30am-10:00am | Session 5 - Robert Elston Award for Best Paper and Complex Traits | | Crystal Ballroom |

Chair: Hae Kyung Im

| | | | |
|-----------------|---|-----------------|----------------------------|
| 8:30 | Best Paper Presentation | | |
| | Presentation | Abstract | Author |
| 9:00am-9:15am | Maternal Health in Pregnancy and Autism Risk - Genetic and Non-genetic Mechanisms | 50 | Magdalena Janecka |
| 9:15am-9:30am | Enhanced Mapping of Gene-Environment Interactions for Vitamin D through Variability Quantitative Trait Loci | 60 | Tianyuan Lu |
| 9:30am-9:45am | The Polygenic Architecture of Hidradenitis Suppurativa and its Clinical Implications | 77 | Lynn Petukhova |
| 9:45am-10:00am | Epigenome-Wide Mediation Analysis of the Relationship between Psychosocial Stress and Cardiometabolic Risk Factors in the Health and Retirement Study | 85 | Lauren Opsasnick Rogers |
| 10:00am-10:05am | Regeneron Presentation | | Timothy A. Thornton |
| 10:05am-10:20am | Poster Highlights | | |

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|--|--|-----------------|------------------------------|
| | Poster | Abstract | Author |
| | Multi-Ancestry Analysis Identifies Susceptibility Variants and Improves Polygenic Risk Scores for Breast Cancer Subtypes | 129 | Haoyu Zhang |
| | Accounting for Heterogeneity Due to Ancestry and Environment Improves the Resolution of Multi-Ancestry Fine-Mapping | 110 | Siru Wang |
| | Genome-wide Association Study of Protein-altering and Regulatory Variants with Resistance to <i>Mycobacterium Tuberculosis</i> Infection | 18 | Clement Conil |
| | Genome-wide Association Study of Multiple Neuropathology Endophenotypes Identifies Novel Risk Loci and Provides Insights into Genetic Risk of Dementia | 25 | David Fardo |
| | Multi-ancestral Maternal GWAS Meta-analysis of Longitudinal Trajectory of Fetal Growth | 113 | Prabhavi Wijesiriwardhana |
| | The Multiethnic Cohort: A Resource for the Study of Genetic and Non-genetic Cancer Risk Across Populations | 10 | David Bogumil |

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|-----------------|--|--|--------------------------|
| 10:20am-11:20am | Poster Session 2 & Refreshments | | Crestone Ballroom |
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|-----------------|--|--|-------------------------|
| 11:20am-12:50pm | Session 6 - Population Biobanks | | Crystal Ballroom |
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Chair: Linda Kachuri

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|-----------------|--|--|----------------------|
| 11:20am-11:50am | Keynote Presentation: Deciphering Complex Genetic Architectures to Understand Disease Risk Variants In African Ancestry Populations | | Neil Hanchard |
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|--|---------------------|-----------------|---------------|
| | Presentation | Abstract | Author |
|--|---------------------|-----------------|---------------|

| | | | |
|-----------------|--|-----|---------------------------------------|
| 11:50pm-12:05pm | A Framework to Maximise Genetic Diversity in Genome-Wide Association Study Meta-Analyses | 123 | Chuan Fu |
| 12:05pm-12:20pm | Genome-wide Association Studies in a Large Korean Cohort Identify Novel Loci for 36 Quantitative Traits and Illuminate Their Genetic Architectures | 44 | Yon Ho Jee |
| 12:20pm-12:35pm | Accounting for Heterogeneity due to Environmental Sources in Meta-analysis of Genome-wide Association Studies | 72 | Oyesola Ojewunmi |
| 12:35pm-12:50pm | Dissecting Ancestry-aware Molecular Causal Effects for Type 2 Diabetes | 9 | Ozvan Bocher |
| 12:50pm-2:15pm | Lunch on Your Own | | |
| 12:50pm-2:15pm | Young Investigators Mentoring Lunch Advance sign-up required. | | Silverton Ballroom (2nd floor) |

Monday, November 4

IGES Annual Meeting-Day 2

| | | | |
|---------------|--|-------------------------|-----------------|
| 2:15pm-3:45pm | Session 7 - Clinical Biobanks | Crystal Ballroom | |
| | Chair: Marie-Pierre Dubé | | |
| 2:15pm-2:45pm | Keynote Presentation: Why Genetics of Disease Progression Matters | Andrea Ganna | |
| | Presentation | Abstract | Author |
| 2:45pm-3:00pm | Leveraging Genetic Similarity to Investigate Understudied Genetic Variation Associated with EHR-derived Phenotypes in Diverse Patient Biobanks | 128 | David Zhang |
| 3:00pm-3:15pm | Analysis of Follow-Up Data in Large Biobank Cohorts: A Review of Methodology | 62 | Merli Mändul |
| 3:15pm-3:30pm | Polygenic Scores of Blood Cell Profiles Predict Gastrointestinal Adverse Events in Non-small Cell Lung Cancer Patients Treated with Immune Checkpoint Inhibitors | 68 | Pooja Middha |
| 3:30pm-3:45pm | Statistical Considerations for Cross-fitting Two-sample Mendelian Randomization Across Biobank Datasets Using Summary Statistics | 52 | Nicholas Larson |
| 3:45pm-4:00pm | Refreshment Break | Crystal Foyer | |
| 4:00pm-5:30pm | Business Meeting and Awards | Crystal Ballroom | |

Tuesday November 5

Educational Workshop

| | | |
|-----------------|--|-------------------------|
| 7:00am-11:00am | Registration | Crystal Foyer |
| 6:30am-9:30am | Hotel Breakfast Buffet Open for Embassy Hotel Guests | 4th Floor Lobby |
| 8:00am-11:00am | Education Workshop | Crystal Ballroom |
| 9:00am | Introduction & Welcome | |
| 9:05am-9:50am | Session 1: High Level Overview (PRS, ELSI considerations) <i>Chris Gignoux, Leslie Lange, Amke Caliebe</i> | |
| 9:50am-10:10am | Session 2: Genetic Effects and Polygenic Weights <i>Chris Arehart, Iain Konigsberg</i> | |
| 10:10am-10:50am | Hands-on Tutorial: P-value thresholding approach for estimating PRS weights from GWAS data <i>Chris Arehart, Iain Konigsberg</i> | |
| 10:50am-11:00am | Refreshment Break | Crystal Foyer |
| 11:00am-11:30am | Session 3: Score Calculations, Applications, and Considerations <i>Meng Lin, Maizy Brasher</i> | |
| 11:30am-12:00pm | Hands-on Tutorial | |
| 12:00pm | Wrap up: Key takeaways | |

Join our meeting sponsors as they participate in the 2024 Annual Meeting



Regeneron Genetics Center

Regeneron will be doing a short presentation Monday, at 10:00am right before the Poster Highlights



Canssi will have an exhibit table located in the Crystal Foyer near registration though-out the meeting

<https://iges.memberclicks.net>

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IGES: @geneticepi

Young Investigators: @igesYI

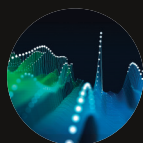


CANSSI ONTARIO

Our mission is to strengthen and enhance research and training in statistical science by developing programs that promote interdisciplinary research and enable multidisciplinary collaborations.



Funding & Training Opportunities



POSTDOCTORAL FELLOWSHIP IN STATISTICS

For postdoctoral fellows undertaking full-time research projects on theoretical or other areas of statistical sciences at a CANSSI Ontario partner university or at their affiliated research institutes. Details [here](#).

Postdoc Recruitment: NOV 2024-JAN 2025



POSTDOCTORAL FELLOWSHIP IN GENOME DATA SCIENCE

To support early-career investigators at CANSSI Ontario partner universities or their affiliated research institutes who are focused on genomics and data science with an emphasis in new genomic technologies or multi-omic integration. Details [here](#).

Deadline: JAN 20, 2025



JOB BOARD

Looking for exciting career opportunities in statistical genetics and genetic epidemiology? Our specialized [job board](#) connects you with roles in these fields. Whether you're an experienced or budding researcher, our platform offers a curated selection of positions from research institutions and universities.

STAGE TRAINING PROGRAM

Come to Ontario for world-class training with leading faculty mentors! CANSSI Ontario STAGE offers top-tier training in genetic epidemiology and statistical genetics for PhD students and postdoctoral fellows.

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- Trainee-Speaker Group Meetings
- Journal Club
- Monthly Seminars (ISSS)

INTERNATIONAL SPEAKER SEMINAR SERIES (ISSS)

The ISSS focuses on statistical genetics and genetic epidemiology research, offering trainees exposure to cutting-edge international research, fostering interdisciplinary collaborations, and building new networks for future research partnerships.



Funding opportunities are generously supported by the University of Toronto Faculty of Arts & Science as part of their commitment to CANSSI Ontario.

MAILING LIST

Be the First to Know What's New!

Scan the QR code to sign up for updates about funding and job opportunities, events, seminars, and community news.



Sunday, November 3

| 3:30pm-4:30pm Poster Session 1 with *Poster Highlights | | |
|--|--------|--|
| Presenter | Poster | Title |
| *Elizabeth Frankel | 28 | Cross-omic Characterization of the Molecular Profile of TD2 in Hispanic/Latinos |
| *Ville Karhunen | 49 | A New Multi-trait Fine-mapping Method Using a Non-local Prior, with Applications in Circulating Metabolic Biomarker Level Analysis |
| *Hua Lu | 59 | A Multi-phenotype Colocalization Framework in <i>LocusFocus</i> |
| *Daniel Panyard | 75 | Subtle Stories in GWAS Data: Multiomics Implicate GPX3 at the <i>TNIP1</i> Locus in Alzheimer's Disease |
| *Eric Sanders | 87 | Mendelian Randomization of Sex-Dependent Traits |
| *Matthew Saward | 88 | Pleiotropic Effects of Pathway-Partitioned Genetic Risk Scores for Asthma in UK Biobank |
| Sandeep Acharya | 2 | A Methodology for Gene Level Omics-WAS Integration Identifies Genes Influencing Traits Associated with Cardiovascular Risks: The Long Life Family Study |
| Raghav Awasthi | 4 | DNA Large Language Models (DNA-LLMs) for Predicting Individual-Level Gene Expression from DNA Sequences |
| Anastasia Leschyk | 5 | Association Between Alzheimer's Disease Polygenic Protective Score (AD PPS) and Cognitive Function in Centenarians |
| Celia Greenwood | 8 | Evaluation of the Impact of Selection Bias in Canada's Nationwide Host Genome Sequencing Initiative (HostSeq) with Application to a Thromboembolism-informed HD-GWAS of COVID-19 Severe Outcomes |
| Raphaël Vernet | 11 | GWAS of IgG Responses to RV and RSV Genome-wide Association Study of Rhinovirus and Respiratory Syncytial Virus IgG Responses in Children and Adults |
| Jerome Choi | 16 | Multi-omics Data Integration for Phenotype Prediction Using Machine Learning Identifies Novel Alzheimer's Disease Risk Factors |
| Zinhle Cindi | 17 | Polygenic Risk Scores and Risk of Drug-induced Liver Injury Following Initiation of Antiretroviral Therapy in People Living with HIV |
| Rebecca Darlay | 19 | Genome-wide Association Study on Metabolic Dysfunction-associated Steatotic Liver Disease (MASLD) |
| Mulong Du | 21 | Deciphering the Genetic Architecture of Lung Cancer Survival: GWAS Meta-analysis with 10K Patients and Integrative Multi-omics Study |
| Ellyn Dunbar | 22 | Trans-ancestry Meta-regression Analysis MR-MEGA Replicates European IBD Loci Using Multiple Ancestries |
| Wei Pan | 24 | Univariate and Multivariate Proteome-wide Association Studies to Identify Causal Proteins for Alzheimer's Disease in the Presence of Invalid Instruments with GWAS Summary Data |
| Anne Florentine Goemans | 30 | Use of Genome-wide Polygenic Risk Scores for Specific Organ Impairment in Coronavirus Disease 2019 (COVID-19) Non-recovery |
| Jinko Graham | 31 | Statistics to Prioritize Rare Variants in Family-based Sequencing Studies with Disease Subtypes |
| Catherine Greene | 32 | Examining the Shared Genetic Architecture of Keloid Scars and Uterine Fibroids |
| Tesfa Dejenie Habtewold | 34 | Epigenome-wide Association Study of Placental DNA Methylation and Cumulative Maternal Glycemic Levels Throughout Pregnancy |
| Sihao Han | 37 | Proteome-wide Mendelian Randomization Identifies Potential Causal Circulating Proteins for Colorectal Cancer Risk |
| Lisa Strug | 39 | Detecting Phase Effects Using Long-read Sequencing Data |
| Mary Horton | 41 | Metabolomic Analysis Indicates Adenine, Oleic Acid, and Glutamic Acid are Associated with Flare Remission, DNA Methylation Changes, and Clinical Subtypes in Systemic Lupus Erythematosus |
| Jian Huang | 42 | Genomic Co-localisation, Child Proteomics and Brain Imaging Support a Link Between Obesity-associated Genotype and Child Language Development |
| Jing-Rong Jhuang | 45 | Rare Variant Intensity Estimation for Genetic Mapping of Complex Traits |

| 3:30pm-4:30pm Poster Session 1 continued | | |
|--|--------|--|
| Presenter | Poster | Title |
| Anastasia Leshchyk | 55 | A Community of Networks Approach for Multi-Omics Integration |
| Wei Pan | 56 | Inferring Causal Direction Between Two Traits Using R2 with Application to Transcriptome-wide Association Studies |
| Anna Lorenz | 58 | The Effect of Alzheimer's Disease Risk Genes on Limbic White Matter Microstructure |
| Brooke Morris | 70 | Decoding the Genetic Basis of Autoimmune Gastritis and Pernicious Anemia |
| Inti Pagnuco | 73 | Transferability of a Single- and Cross-Tissue Transcriptome Imputation Models across Ancestry Groups |
| Gina Parcesepe | 76 | New Genetic Discovery for Diseases with Shared Pathology but Low Genome-Wide Genetic Correlation |
| Dillon Pruett | 78 | Leveraging Biobank-linked Electronic Health Records for Drug-Induced Stuttering Discovery |
| Andreas Ziegler | 82 | Comprehensive Analysis of the Genetic Variation in the LPA Gene from Short-read Sequencing |
| Hannah M. Seagle | 90 | Prioritization of Icosapent Ethyl for Potential Reversal of Metabolic Dysfunction Associated Fatty Liver Disease |
| Mark Seielstad | 91 | Shared Genetic Associations in Chronic Viral Infection and Vaccine Failure |
| Sebastian Sendel | 92 | Developing a Polygenic Score for Idiopathic Parkinson's Disease: Insights into Mutation Penetrance |
| Jayati Sharma | 95 | Predictive Performance of a Multi-Ancestry Polygenic Risk Score for LDL with Gene-Environment Interactions of Smoking and Air Pollution in Diverse Groups: Results from the PAGE Study |
| David Conti | 97 | Applications and Evaluations of Polygenic Risk Scores in Cancer Outcomes: Context Matters |
| Heejong Sung | 104 | Copy Number Variants in Familial Bipolar Disorder Ascertained from Anabaptist Founder Populations |
| Raphaél Vernet | 107 | Genetic Clusters of Childhood Asthma Identification of Genetic Clusters Underlying Endotypes of Childhood-onset Asthma |
| Mengyao Wang | 108 | Association Analysis of Mitochondrial Heteroplasmy with RNA-seq in the Framingham Heart Study |
| Xiang Shu | 112 | Polygenic Risk of Coronary Artery Disease for Long-Term Survivors of Breast Cancer |
| Hsin-Chou Yang | 119 | Revolutionizing Precision Health for T2D: AI Integration of Multimodal Medical Imaging and Genome-Wide SNP Data in a Large-Scale Biobank |
| Hsin-Chou Yang | 120 | Revolutionizing Precision Health in Type 2 Diabetes: Unveiling the Synergy of Medical Imaging and Genetic Data Integration through Artificial Intelligence in a Large-scale Biobank |
| Yihe Yang | 121 | Investigation of the bias from using marginal effect sizes of instrumental variables in Mendelian Randomization |
| Celia Greenwood | 126 | DKLasso: Bridging Complexity and Interpretability in Genetic Epidemiology through Deep Kernel Learning with Feature Sparsity |
| Cristian Riccio | 133 | Rare Variant Analysis Pipelines: A Systematic Review |
| Pamela N. Romero Villela | 135 | Loci on Chromosome 20 Interact with rs16969968 to Influence Cigarettes per Day in European Ancestry Individuals |

| 10:20am-11:20am Poster Session 2 with *Poster Highlights | | |
|--|--------|--|
| Presenter | Poster | Title |
| *David Bogumil | 10 | The Multiethnic Cohort: A Resource for the study of Genetic and non-Genetic Cancer Risk Across Populations |
| *Clemént Conil | 18 | Genome-wide Association Study of Protein-altering and Regulatory Variants with Resistance to <i>Mycobacterium Tuberculosis</i> Infection |
| *David Fardo | 25 | Genome-wide Association Study of Multiple Neuropathology Endophenotypes Identifies Novel Risk Loci and Provides Insights into Genetic Risk of Dementia |
| *Siru Wang | 110 | Accounting for Heterogeneity Due to Ancestry and Environment Improves the Resolution of Multi-Ancestry Fine-Mapping |
| *Prabhavi Wijesiriwardhana | 113 | Multi-ancestral Maternal GWAS Meta-analysis of Longitudinal Trajectory of Fetal Growth |
| *Haoyu Zhang | 129 | Multi-Ancestry Analysis Identifies Susceptibility Variants and Improves Polygenic Risk Scores for Breast Cancer Subtypes |
| Ozvan Bocher | 3 | Dissecting the Biological Mechanisms Behind Type 2 Diabetes Causal Effects on Non-cardiometabolic Comorbidities |
| James Baker | 6 | Two Complementary Identity-by-Descent Based Methods for Use Within Biobanks |
| Han Chen | 14 | StocSum: A Reference-panel-free Summary Statistics Framework for Diverse Populations |
| Uchechukwu Chimeh | 15 | Exploring Aryl Hydrocarbon Receptor (AHR) Variant Effects in the UK Biobank and Interactions with Diesel Exposure in the Personalized Environment and Genes Study (PEGS) |
| Huaying Fang | 23 | gmmcoda: Graphical Model for the Mixture of Compositional Data and Absolute Abundance Data with Applications to Microbiome Studies |
| Abiodun Fatoba | 26 | Exploring the Potential Causal Association of Gut Microbiota on Panic and Conduct Disorder: A Two-sample Mendelian Randomization Approach |
| Krista Fischer | 27 | One Population-Based Biobank, Two Cohorts: Selection Effects in Biobank Cohorts from the Estonian Perspective |
| Harriett Fuller | 29 | The Role of Pre-Diagnostic Circulating Metabolites in Prostate Cancer Risk: A Cross-Population Meta-Analysis of Untargeted Metabolomic Studies |
| Boya Guo | 33 | Populations and Methods Used to Define Prostate Cancer Polygenic Risk Score Categories Impact the Interpretation of Risk |
| Gideon Hallum | 35 | Cell Type Prediction in Spatial Transcriptomics by Projection of Validated Single-Cell RNA Reference Datasets in Seurat |
| Sarah Hanks | 36 | Methods for Accurately Estimating Hereditary Cancer Prevalence in Diverse U.S. Biobanks in the Presence of Participation Bias |
| Anthony Herzig | 40 | 100,000 Genomes of Europe: Unlocking Genetic Variability Across Europe for Science and Health |
| Ebrima Joof | 46 | Genetic Analysis of Fibrotic Multi-morbidity |
| Rachit Kumar | 51 | Rapid Long-Range Linkage Disequilibrium Calculations at Biobank Scale using GPU Acceleration |
| Rebecca Lelievre | 54 | Effect Modification by Sex of Genetic Associations with Vitamin C Related Metabolites in the Canadian Longitudinal Study on Aging |
| Jonathan Lifferth | 57 | Genetic Ancestry-specific eQTL in Healthy Lung Tissue |
| Sharon Lutz | 61 | A Statistical Cautionary Tale: Estimating Correlations When Inferring the Causal Direction Between Two Traits in Genetic Association Studies |
| Louis Macias | 63 | Blood Metabolome and Transcriptome Integration in Bullous Pemphigoid: A Case-Control and Case-only Cohort Study |
| Christina Magyar | 64 | The Impact of Genetic Ancestry on Survival Outcomes in Pediatric Rhabdomyosarcoma: A Report from the Children's Oncology Group |
| Tongzhu Meng | 66 | A Genome-Wide Association Study of Preferences for 18 Bitter-tasting Foods and Beverages in the UK Biobank |
| Mengxuan Li | 67 | Identifying Frequently Pleiotropic SNPs in Mendelian Randomization using MRBEE |

Monday, November 4

| 10:20am-11:20am | | Poster Session 2 continued |
|-------------------------|--------|--|
| Presenter | Poster | Title |
| Bryan Queme | 80 | Impact of Bias in Variance Analysis: From SNPs to Pathways |
| Marie-Hélène Roy-Gagnon | 81 | Hybrid Design of Case-Parent Trio and Control Parents Under Mating Asymmetry |
| Debashree Ray | 83 | A Novel Statistical Test of Pleiotropy Between Traits Using GWAS Summary Statistics |
| Natalia Rivera | 84 | Exploring the Genetic Link Between Diabetes Mellitus and Sarcoidosis |
| Rashedeh Roshani | 86 | Evaluating Kidney Size as a Marker for Renal and Hepatic Health |
| Alyssa Scartozzi | 89 | Candidate Gene-based Rare Variant Analysis of Developmental Stuttering |
| Alyssa Manning | 93 | Population Descriptors Variation in Plasma Proteomic and Metabolomic Profiles and Their Association with Type 2 Diabetes Risk |
| Ruhollah Shemirani | 96 | Accounting for the Effects of Recent Population Structure on Heritability Estimation in Biobank Studies |
| Nick Shrine | 98 | Alternative Genetic Models for Discovery and Characterisation of Genetic Associations with Lung Function in UK Biobank |
| Yeunjoo E. Song | 100 | Mosaic Chromosomal Alterations in Peripheral Blood Cells from Whole-Genome Sequencing and Alzheimer's Disease in the Amish |
| Josey Sorenson | 101 | Survival-Associated Tumor Expression Quantitative Trait Loci (eQTLs) in Pediatric Hepatoblastoma |
| Katharina Stahl | 102 | Simulation Study: Aggregating SNPs to Spikes Enables Better Preservation of True Positive Associations in Filtering for Imputation Quality |
| Emily Tran | 105 | Association Between Eye Disease and Cognitive Function Modified by a KIBRA (WWC1) Genetic Variant |
| Phyo Wei Win | 115 | Integration of Mitochondrial DNA Variation Calling with Nuclear Omic Profiles in a Longitudinal Cohort |
| Jessica LG Winters | 116 | Gestational Diabetes Mellitus Shares Genetic Risk Factors With Type 1 and Type 2 Diabetes and Is Predicted by Diabetes Polygenic Scores |
| Xueyao Wu | 117 | Investigating the Relationship between Breast Cancer Risk Factors and Mammographic AI-generated Texture Feature |
| Yao Tu | 122 | Sex-specific Genetic Risk Factors of Coronary Heart Disease in Hispanic/Latino Populations |
| Toni-Ann Yapp | 124 | Validation of Multi-Ancestry Polygenic Scores for Lipid Levels in 3,119 Participants from Samoa and American Samoa |
| Wanying Zhu | 132 | Genetically Regulated Prediction Modeling in Lipidomics and Transcriptomics in a Hispanic Cohort |
| Julie-Alexia Dias | 136 | Evaluating Methods for Genome-Wide Associations Studies in Diverse Ancestral Populations |
| Mara Delesa-Velina | 137 | NMR Metabolomics Data as a Powerful Predictor of Mortality and Biological Age in Estonian Biobank |
| Elizabeth Blue | 138 | Multi-Ancestry Meta-Analysis Identifies Genetic Modifiers of Age-at-Onset of Alzheimer's Disease at Known and Novel Loci |
| Jessica Dennis | 139 | Genetic Factors Associated with Depression and Cognitive Decline |



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Denver, Colorado USA

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**INTERNATIONAL GENETIC
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August 31-September 2, 2025
Education Workshop and Annual Meeting
Pullman Hotel
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