Sunday, August 31

Education Workshop: Navigating Biobank Data: Advanced Strategies for Genetic Epidemiology Research

10:00am-5:00pm	Registration	**Ballsaal Foyer, Ground Level**
12:00pm-1:00pm	Workshop Lunch	Ballsal Foyer
1:00pm-6:00pm	**Education Workshop**	Ballsaal AB
1:00pm	Introduction & Welcome	
1:10pm-2:10pm	**Session 1: Biobank Design – From Phenotype to Omics Integration** *Natalia Rivera, Callie Zaborenko*	
2:10pm-3:40pm	**Session 2: Methodological Advances for Biobank-Based Genetic Epidemiology** *Reedik Mägi, Krista Fischer*	
3:40pm-4:00pm	Coffee Break	
4:00pm-4:45pm	**Session 3: Scalable Computational Approaches for Cross-Biobank Analysis** *Xihao Li, Jacob Williams*	
4:45pm-5:30pm	**Session 4: Practical Tutorial – A Walkthrough of Cross-Biobank Analysis** *Jacob Williams, Xihao Li*	
5:30pm-6:00pm	**Panel Discussion + Q&A: Future Directions in Biobank-Based Research**	
5:00pm-6:30pm	**IGES Board of Directors Meeting**	Brasserie e.l.f., Ground Floor

Monday, September 1 — IGES Annual Meeting-Day 1

7:00am-5:30pm	Registration	**Ballsaal Foyer**
7:00am-8:00am	Breakfast	Hotel Restaurant d*light, Ground Level
8:15am-8:55am	**Opening Session**	**Ballsaal AB**
8:15am-8:25am	**Welcome: Elizabeth Gillanders**	
8:25am-8:55am	**Presidential Address: Hae Kyung Im**	
8:55am-9:00am	**CANSSI** Presentation	
9:00am-10:00am	**Session 1 - Williams Awards**	**Ballsaal A**

Chair: Elizabeth Gillanders

	Presentation	Abstract	Author
9:00am-9:15am	Biological Group-Guided Mediation Analysis	97	Yixin Zhang
9:15am-9:30am	Influence of Heritable Covariates on Genetic Studies of the Human Gut Microbiome	18	Alec McKinlay
9:30am-9:45am	Polygenic Scores in Proteomic Risk Prediction	43	Jakob Woerner
9:45am-10:00am	Characterisation of Diverse Global Ancestries Within Participants of the UK Biobank	58	Fiona Pantring
10:00am-10:20am	Refreshment Break		Ballsaal Foyer

10:20am-11:50am **Session 2 - Neel Awards** — **Ballsaal AB**

Chair: Sanjay Shete

10:20pm-10:50am **Keynote Presentation:**

Multiomic Insights into Diverse Human Diseases — **Claudia Langenberg**

	Presentation	Abstract	Author
10:50am-11:05am	Parent-of-Origin Effects on Complex Traits: Evidence from 265,000 Individuals	26	Robin Hofmeister
11:05am-11:20am	Heterogeneity Due to Ancestry and Environment Improves the Resolution of Multi-Ancestry Fine-Mapping	69	Siru Wang
11:20am-11:35am	covImpute: Leveraging Genetic Correlations to Impute Missing EHR Phenotypes	21	Hyunkyu Lee
11:35am-11:50am	Bayesian Inference Model to Prioritise Rare Variants from Family-Based Whole Genome Sequencing Data	28	Cathal Ormond

11:50am-1:20pm Lunch-open to all attendees or explore Cologne — Ballsaal Foyer

11:50am-1:20pm **Committee Meetings and Lunch** (rooms located on level 2)

- Publications Committee — Magnus 1
- Program Committee — Magnus 2
- Young Investigators Committee — Severinus 1

1:25pm-2:55pm **Session 3 - Diversity** — **Ballsaal AB**

Chair: Thomas Winkler

1:25pm-1:55pm **Keynote Presentation:**

Translational Genomics of Complex Disease — **Eleftheria Zeggini**

	Presentation	Abstract	Author
1:55pm-2:10pm	Estimating Gene Conversion Rates	15	Brian L. Browning
2:10pm-2:25pm	WGS-Based HLA Allele Imputation Quantifies Pleiotropic Associations with Disease-Related Traits	110	Peyton McClelland
2:25pm-2:40pm	High Consanguinity, Underrepresented Populations, and Genome Sequencing for Rare Variant Discoveries	109	Mohamad Saad
2:40pm-2:55pm	Multi-Ancestral GWAS of GDM and Glycemic Traits During Pregnancy	57	Valentina Rukins

2:55pm-3:15pm **Poster Highlights 1**

Chair: Han Chen

Poster	Abstract	Author
A Multi-Trait GWAS to Disentangle Kidney Trait Genetics	38	Hannah Cathrin de Hesselle
Fantasio: A Case-Control Approach to Detect Rare Recessive Variants in Multifactorial Diseases	114	Sidonie Foulon
Selection Bias in Genetic Risk Estimates: HostSeq Simulation and GWAS of COVID-19 Severe Outcomes	92	Ohanna C. Bezerra
Fine-Scale Pharmacogenetic Diversity in Europe	79	Marc Gros-La-Faige
Multi-Ancestry Polygenic Risk Scores for Chronic Obstructive Pulmonary Disease Improve Transferability Across Diverse Populations	65	Jing Chen
The Role of Stress Sensitivity in the Genetics of Juvenile Myoclonic Epilepsy	96	Eric Sanders

3:15pm-4:15pm **Poster Session 1 & Refreshments** — **Ballsaal CD**


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Monday, September 1 — IGES Annual Meeting-Day 1

4:15pm-5:45pm **Session 4 - Statistical Modeling** — **Ballsaal AB**

Chair: Xiaofeng Zhu

	Presentation	Abstract	Author
4:15pm-4:30pm	Leveraging a Multi-Population Likelihood Framework for Bayesian Model Uncertainty in PRS Construction	113	Gillian King
4:30pm-4:45pm	TrACES of Time: A Targeted mRNA Sequencing Approach for Estimating Time-of-Day of Bloodstain Deposition in Forensic Casework	86	Sebastian Sendel
4:45pm-5:00pm	Why Meta-Analysis Fine-Mapping Can Be Confidently Wrong and How to Fix It	27	Chris Wallace
5:00pm-5:15pm	Framework for Allelic Effect Heterogeneity Assessment in Genome-Wide Association Study Meta-Analyses	45	Chuan Fu Yap
5:15pm-5:30pm	Uncovering Genetic Pathways in Type 2 Diabetes Using Genomic Structural Equation Modeling	85	Merli Koitmäe
5:30pm-5:45pm	Penalized Generalized Linear Mixed Models for Longitudinal Outcomes in Genetic Association Studies	60	Julien St-Pierre

6:30pm-10:30pm **Chocolate tasting, dinner and museum tour** — The Chocolate Museum
Am Schokoladenmuseum 1a
Click here for walking directions. Allow 20-30 minutes for walking. Please wear your badge.
Reception from 6:30-7:30pm, dinner will follow at 7:30pm.
Tour the museum from 8:30 -9:30pm and enjoy dessert afterwards.

Tuesday, September 2 — IGES Annual Meeting-Day 2

7:00am-5:30pm Registration — **Ballsaal Foyer**

7:00am-9:00am Breakfast — Hotel Restaurant d*light

8:30am-10:00am **Session 5 - Robert Elston Award for Best Paper and Machine Learning** — **Ballsaal AB**

Chair: Silke Szymczak

8:30am-8:35am **Regeneron** Presentation — Andrey Ziyatdinov

8:35am-9:05am Special Presentation: Best Paper 2024

	Presentation	Abstract	Author
9:05am-9:20am	IBD Mapping Identifies Associations for Brain Imaging Phenotypes	107	Han Chen
9:20am-9:35am	Deep Learning Based Multivariable Instrumental Variable Regression for Nonlinear TWAS	135	Wei Pan
9:35am-9:50am	Robust Rare Variant Association Tests for Machine-Learning Derived Phenotypes	115	Andrey Ziyatdinov
9:50am-10:05am	Improving Epigenetic Age Estimation by Combining Epigenetic Clocks	122	Denitsa Vasileva

10:05am-10:25am **Poster Highlights 2**

Chair: Ohanna Cavalcanti

Poster	Abstract	Author
Improving Association Analysis of Mitochondrial DNA Heteroplasmy and Pancreatic Cancer by Hierarchical Testing	103	Brahim Aboulmaouahib
LLM-Driven Single-Cell Analysis Enhances Prediction of Breast Cancer Therapy Response	121	Pingzhao Hu
Supervised Admixture Sensitive to Relative Sample Size	127	Anthony Herzig
Familial Hypercholesterolemia: Is it Prime Time for Population-Wide Screening in Germany?	6	Cristian Riccio
Identifying Multi-Allelic Quantitative Trait Loci Using Empirical Haplotypes	128	Katelyn McInerney
PRS Convex Combinations for Two-Phase Re-sequencing Studies	31	Osvaldo Espin Garcia

10:25am-11:25am **Poster Session 2 & Refreshments** — **Ballsaal CD**

11:25am-12:55pm	**Session 6 - Causal Inference**		**Ballsaal AB**
	Chair: Mohamad Saad		
11:25pm-11:55am	**Keynote Presentation:**		
	Advances in Statistical Fine-Mapping of Putative Causal Variants and Genes from GWAS		**Xiang Zhou**
	Presentation	Abstract	Author
11:55am-12:10pm	Exploring the Lifecourse Impact of Childhood Adiposity on the Human Plasma Proteome	47	Phoebe Dickson
12:10pm-12:25pm	Multi-Ancestry Mendelian Randomization with Transfer Learning	146	Xiaofeng Zhu
12:25pm-12:40pm	Negative Controls and Selection Bias in MR	10	Apostolos Gkatzionis
12:40pm-12:55pm	Multi-Omics Analysis Identifies New Risk Loci for Differentiated Thyroid Carcinoma	20	See Hyun Park
12:55pm-2:25pm	Lunch-open to all attendees or explore Cologne		Ballsaal Foyer
	Young Investigators Mentoring Lunch (advanced sign-up required)	Hotel Restaurant	d*light, Ground Level
	Committee Meetings and Lunch (rooms located on level 2)		
	Communications Committee		Magnus 1
	Education Committee		Magnus 2
	ELSI Committee		Severinus 1
2:30pm-4:00pm	**Session 7 - Multi-Omics**		**Ballsaal AB**
	Chair: Hae Kyung Im		
2:30pm-3:00pm	**Keynote Presentation:**		
	Critical Challenges in Multi-Omic Data Analysis		**Michael Wu**
	Presentation	Abstract	Author
3:00pm-3:15pm	A Fast Hierarchical Bayesian Model with Functional Annotation for Accurate Cross-Ancestry Prediction	124	Zhonghe Shao
3:15pm-3:30pm	Mind the Colocalisation Gap in Immune-Mediated Diseases	66	Elena Vigorito
3:30pm-3:45pm	Genetic Regulation of Protein Expression in Prediabetes and Type 2 Diabetes	133	Archit Singh
3:45pm-4:00pm	Genetic Dysregulation of Protein Expression in Aging and Neurodegeneration	119	Mykhaylo M. Malakhov
4:00pm-4:15pm	Refreshment Break		**Ballsaal Foyer**
4:15pm-5:45pm	**Business Meeting and Awards**		**Ballsaal AB**

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Abstracts: Invited Speakers

Monday September 1
Session 2

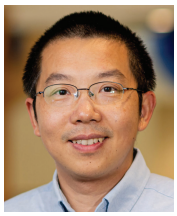
Multiomic Insights Into Diverse Human Disease
Claudia Langenberg

Application of different omic technologies is now feasible at population scale. This talk will present examples of how the integration of different omics in large patient and population studies can help to predict disease risk, understand mechanisms, and reveal shared connections between rare and common diseases. Studies include different metabolomic and proteomic technologies and an investigation how these can be combined and how their complementarity can be employed for synergistic insights into human health.

Session 3
Translational Genomics of Complex Disease
Eleftheria Zeggini

In this talk, I will give an overview of how we have used translational genomics approaches to enhance our understanding of complex diseases like osteoarthritis and type 2 diabetes, shed novel biological insights, and provide a stepping stone for bridging the gap between basic discovery and translation.

Tuesday, September 2



Session 6
Advances in Statistical Fine-Mapping of Putative Causal Variants and Genes from GWAS
Xiang Zhou

Genome-wide association studies (GWAS) have identified many SNPs associated with common diseases and complex traits. However, the underlying causal variants and biological mechanisms driving these associations remain largely elusive. In this talk, I will present several recent statistical methods developed by our group aimed at fine-mapping putative causal SNPs and genes from GWAS data. First, I will introduce MESuSiE, a probabilistic multi-ancestry fine-mapping method that enhances accuracy and resolution by integrating association signals across diverse ancestries. Next, I will discuss PMR, a probabilistic Mendelian randomization framework that unifies various TWAS and MR approaches. PMR accommodates multiple correlated instruments and enables robust testing for gene-to-trait causal effects, even in the presence of horizontal pleiotropy. Finally, I will present GIFT, a frequentist approach for conditional TWAS analysis that fine-maps causal genes by controlling for nearby genes in a locus. GIFT accounts for gene expression correlation, cis-SNP linkage disequilibrium, and the uncertainty in gene expression prediction models. Together, these methods offer new tools for advancing our understanding of complex trait biology and for more precisely identifying causal genes and variants in the post-GWAS era.

Session 7
Critical Challenges in Multi-Omic Data Analysis
Michael Wu

Progress in high-throughput biotechnologies has culminated in a wide range of -omic sciences that each offer a unique window into biological processes underlying complex traits and conditions. Contemporary studies are now simultaneously considering multiple omics data types with the promise of comprehensively addressing scientific questions that have eluded researchers for decades. However, despite the promise of multi-omic data integration, critical challenges remain. In this presentation, we review current progress and central challenges with multi-omics data analysis, not least of which is understanding analytic objectives. To this end, we characterize different types of study objectives, illustrating them with our specific methods integrating microbiome and other omics. We further consider tools to aid others in formalizing analytic frameworks.

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Monday, September 1

3:15pm-4:15pm		Poster Session 1 with *Poster Highlights
Presenter	Poster	Title
*Hannah Cathrin de Hesselle	**38**	A Multi-Trait GWAS to Disentangle Kidney Trait Genetics
*Jing Chen	**65**	Multi-Ancestry Polygenic Risk Scores for Chronic Obstructive Pulmonary Disease Improve Transferability Across Diverse Populations
* Marc Gros-La-Faige	**79**	Fine-Scale Pharmacogenetic Diversity in Europe
*Ohanna C. Bezerra	**92**	Selection Bias in Genetic Risk Estimates: HostSeq Simulation and GWAS of COVID-19 Severe Outcomes
*Eric Sanders	**96**	The Role of Stress Sensitivity in the Genetics of Juvenile Myoclonic Epilepsy
*Sidonie Foulon	**114**	Fantasio: A Case-Control Approach to Detect Rare Recessive Variants in Multifactorial Diseases
Dhanya Ramachandran	**4**	Genomic Determinants of Cervical Cancer Risk
Anat Reiner-Benaim	**5**	Improved Methods for Analyzing Small Samples in High Dimensions With Application to Genome-Wide Association Studies of Rare Diseases
Samuel O. Antwi	**9**	Spatial Genomics Profiling of Metabolic Dysfunction-Associated Steatohepatitis Biopsy Tissues for Liver Cancer Risk Prediction
Winfred Gatua	**12**	Negative Controls to Evaluate the Sensitivity of Mendelian Randomization Estimates to Sample Selection Bias
Geetha Chittoor	**13**	Phenome-Wide Association Study of Coronary Heart Disease Susceptibility Loci
Jieyu Ge	**14**	A Mixture Model Approach for Correcting Systematic Measurement Errors in Sitting Height Data from UK Biobank
Soumeen Jin	**16**	Genetic Architecture of Time to Reach EDSS 6 in Multiple Sclerosis
Yung-Han Chang	**17**	Formal Statistical Replication Analysis in Lung Cancer Genome-Wide Association Studies
Katherine Fawcett	**19**	The role of the *ADRB2* Thr164Ile Variant in Lung Function Determination, Plasma Proteome Variability and Other Phenotypes in UK Biobank
Hanna Julienne	**22**	Multi-Trait GWAS Across 52 Infectious Diseases: Mapping Common Variants Associated With the Immune Response
Sarah E Orr	**23**	Mapping the Epigenetic Mechanisms Underlying Musculoskeletal Disease Across the LifeCourse
Gang Chen	**25**	Cross-Ancestry Genome-Wide Association Study of Creatine Kinase Reveals Novel Genetic Loci and Insights into Muscle Injury
Yuriko Katsumata	**32**	Multiallelic Genetic Architecture Underlying AD and ADRD Proteinopathy
Federico Murgia	**33**	Expanding Insights into the Genetic Architecture of Coronary Artery Disease: A Multi-Ancestry and Multi-Trait Genome-Wide Meta-Analysis Among ~2 Million Individuals
Katie Watts	**34**	Genetic Comparative Analyses of Atopic Dermatitis and Psoriasis
Tessel E. Galesloot	**35**	Body Size and Non-Muscle Invasive Bladder Cancer Outcome: What Do the Genes Say?
Janina Marie Herold	**36**	Age-Informative Polygenic Score for Quantitative Traits: An Approach and Its Chances and Challenges to Predict Kidney Function and Kidney Function Decline
Amra Dhabalia Ashok	**37**	Design and Development of a Results Relational Database for Cardiovascular Phenotypes
Yu-Ming Lee	**39**	Genomic Prediction of Actinic Keratosis Risk Using GWAS-Derived Polygenic Scores and Machine Learning Approaches

Monday, September 1

3:15pm-4:15pm		Poster Session 1 continued
Presenter	Poster	Title
Andrew Paterson	**40**	Incorporating Large-Scale Genetic Association Results into Clinical Genetics Consortium (ClinGen) Sequence Variant Classification
Bowei Xiao	**41**	A Multivariate Approach to Identify CpGs in Peripheral Blood Where DNA Methylation is Associated with Cerebrospinal Fluid Biomarkers of Alzheimer Disease
Yan Sun	**42**	Epigenetic Factors Predict Incident Heart Failure and Clinical Subtypes
Tanja K. Rausch	**46**	Comparison of Classic Polygenic Scores with Machine Learning Algorithms to Predict Hypertension
Lam Opal Huang	**48**	Neurodevelopmental Disorders Copy Number Variants and Risk of Internalising and Cardiometabolic Disorders
Morteza Vaez	**49**	Recurrent Copy Number Variants and Polygenic Scores Jointly Influence the Risk of Psychiatric Disorders in the iPSYCH2015 Case-Cohort Sample
Sandra Freitag-Wolf	**50**	Genetic and Geographic Influence on Phenotypic Variation in European Sarcoidosis Patients
Marina Bleskina	**51**	Comparison of Meta-Learners for Late-Stage Prediction Modeling for Multi-Omics Data
Andrés Ingason	**52**	Re-Evaluating the Association Between 22q11 Deletion Syndrome and Schizophrenia
Soha Hamid Sabtiy	**53**	The Neurodevelopmental Risk Associated With Congenital Heart Disease and Recurrent Copy Number Variants
Victor Vera Frazão	**54**	Large-Scale Genotype-Phenotype Simulations for Genomic Studies
Catherine John	**55**	Collection of Multi-Omics Data for the Investigation of Long-Term Conditions in EXCEED (Extended Cohort for E-health, Environment and DNA)
Yaxin Luo	**56**	The Relationship Between Maternal Migraine During Pregnancy and Offspring ADHD Traits
Iona Collins	**59**	A Genome-Wide Association Study Using the Bacillus Calmette-Guérin Scar to Elucidate the Genetic Basis of Scarring in a European Population
Dominic Sayers	**62**	Identifying Shared Genetic Associations in Fibrosis: A Multi-Organ Rare Variant Analysis
Stefan Böhringer	**63**	Back-in-Time Reconstruction of Population Structure Using Reconstructed Haplotypes
Nick Shrine	**64**	Single Variant and Gene-based Collapsing Association of Rare Variants With Lung Function to Refine Mapping of Causal Genes and Biological Pathways
Vivian Link	**67**	Roadmap to a Successful Rare Variant Association Study - A Topic Review
Inti Anabela Pagnuco	**68**	Transcriptome-Wide Association Analysis of Age-Related Macular Degeneration Across Two Retinal Layers
Yi-Qian Sun	**70**	Association Between Pace of Aging Estimated Using Blood Dna Methylation and All-Cause Mortality: The Hunt Study
Yeliz Eski	**71**	The Effect of Genetic Profiles on Physical Activity and Sedentary Behavior in Children - The GECKO Drenthe Cohort
Daniel Stow	**72**	Evaluating Transferable Polygenic Risk Scores for Internalising and Cardiometabolic Multimorbidity
Alexander T Williams	**74**	Genome-Wide Association Study of Eye Protrusion

Tuesday, September 2

10:20am-11:20am		Poster Session 2 with *Poster Highlights
Presenter	Poster	Title
*Cristian Riccio	**6**	Familial Hypercholesterolemia: Is It Prime Time for Population-Wide Screening in Germany?
*Osvaldo Espin-Garcia	**31**	PRS Convex Combinations for Two-Phase Re-Sequencing Studies
*Brahim Aboulmaouahib	**103**	Improving Association Analysis of Mitochondrial DNA Heteroplasmy and Pancreatic Cancer by Hierarchical Testing
*Pingzhao Hu	**121**	LLM-Driven Single-Cell Analysis Enhances Prediction of Breast Cancer Therapy Response
*Anthony Herzig	**127**	Supervised Admixture Sensitive to Relative Sample Size
*Katelyn McInerney	**128**	Identifying Multi-Allelic Quantitative Trait Loci Using Empirical Haplotypes
Lisa-Marie Nuxoll	**75**	Genetic Prediction of Blood Glucose Variability in Preterm Infants: A Polygenic Score Approach
Brandon Lim	**76**	Using Mendelian Randomization to Identify Mass Spectrometry Quantified Proteins Causally Associated with Lung Function
Stephanie Sheir	**77**	Revisiting the Association Between BMI and Depression Using Phenome-Wide Association Clustering of MR Instruments (PWC-MR)
Haibo Huang	**78**	Genetic Correlations Between Asthma Subtypes and Neuropsychiatric Disorders
Ghestem Florence	**80**	Knowledge Graph to Dissect Genotype-Phenotype Associations.
Bryony Hayes	**81**	Assessing the Role of Insomnia in Breast Cancer Risk Across Multiple Ancestries Within the “All of Us” Research Program
Emmanuelle Génin	**82**	Mapping French Genetic Diversity: From Regions to Europe for Genomic Medicine
Marc Gros-La-Faige	**83**	Evaluation of Star Allele Annotation Tools and the Influence of Imputation and Population Origin
Kayesha Coley	**84**	Association of Polygenic Scores for ACE Inhibitor-Induced Cough Across Cohorts, Ancestries and Phenotypes
Anne E. Justice	**87**	Multi-Population GWAS of Waist-To-Hip Ratio Reveals Heterogeneous Pathways to Central Obesity
Shu-Hsien Cho	**88**	VACANT-M: An Annotation-Enhanced Variant-Set Association Test Accounting for Genetic Relatedness and Population Structure
Matthew Boyton	**89**	Integrative Heritability-Informed Mendelian Randomization Identifies Divergent Roles for IL6 and TNF in Asthma and Lung Cancer
Anna Lorenz	**90**	Alzheimer’s Disease Genetic Risk Variants Influence Age Trajectories of Circulating Peripheral Proteins
Felix Reichelt	**91**	Heritability and Shared Genetics Among Stress Exposures and With Personality: Insights from the Multigenerational Lifelines Cohort Study
Richard Packer	**93**	Enabling Metanalysis Across Multiple Biobank Studies for Phenome Wide Association Studies with DeepPheWAS
Aida Eslami	**94**	Comparison of Statistical Methods for Identifying X Chromosome Inactivation Patterns - Application in Asthma
Ruby Tsang	**95**	Polygenic Liability to Internalising and Cardiometabolic Multimorbidity and Health Trajectories Across Early Life
Kristel Van Steen	**100**	Challenges and Innovations in Constructing and Validating Individual-Specific Networks for Precision Medicine
Kavya Singh	**101**	Advances in Individual-Specific Networks for Patient Subtyping in Precision Medicine
François Cornélis	**104**	HLA Genotype Combinations Impact Allele Association With Multiple Sclerosis Risk

Tuesday, September 2

10:20am-11:20am		Poster Session 2 continued
Presenter	Poster	Title
Kari E. North	**105**	Uncovering the Genetic Nexus of Obesity and Addiction: Pleiotropic Loci from Large-Scale GWAS Reveal Shared Neurobehavioral Risk
Janne Pott	**106**	Proprotein Convertase Subtilisin/Kexin Type 9 and Breast Cancer Survival: A Mendelian Randomization Study
Mark Lamin	**108**	Comparison of Linear and Non-Linear Approaches to Ancestry Estimation in Highly-Admixed Populations
Lap Sum Chan	**112**	DrFARM: Identification of Pleiotropic Genetic Variants in Genome-Wide Association Studies
Heather M Highland	**116**	Glycemic Traits are Associated With Insulin Signaling and Hormone Metabolism in a High- Risk Hispanic/Latino Population on the US/Mexico Border
Wenyu Huang	**118**	Mendelian Randomization Provides No Evidence for the Associations of Genetically Predicted Heart Rate Variability with Seven Psychiatric Diseases
Shelley B Bull	**120**	Effects of Trait Ascertainment and Selection on Polygenic Scores in Family-Based Study Designs for Genetic Association Analysis of Rare Variants
Roxana Moslehi	**123**	Multidimensional Analyses of Pedigree, Epidemiologic, Proteomics, and Transcriptomics Data Provide Etiologic Clues for Myalgic Encephalomyelitis/Chronic Fatigue Syndrome
Mael Guivarch	**126**	Assessing Clustering Performance and Impact on Allele Frequency Estimation Across Sampling Schemes in Fine-scale Genetic Simulations
Devleena Ray	**129**	Mendelian Randomization Study of the On-Target Effects of Long-Term Aromatase Inhibitor Use
Magdalena Janecka	**132**	Direct and Indirect Genetic Effects in the Associations Between Maternal Health and Autism: A Novel, Family-Based Method
Wei Pan	**134**	An Alternative Analysis Method for Transcriptome-Wide Association Studies
Jennifer Below	**136**	Class-Specific Lipid Dysregulation and Cardiometabolic Risk in Severe Obesity
Jessica Martinez	**137**	Univariate and Multivariate Genome Wide Association Studies Reveal New Variants Associated With Cytokine Levels in Asthmatic Families
Takiy-Eddine Berrandou	**139**	Multi-Trait Genome-Wide and Gene-Based Analyses Implicate Coagulation and Vascular Smooth-Muscle Pathways in Spontaneous Coronary Artery Dissection
James Alexander Temple	**141**	Using Kolmogorov-Arnold Networks, an Explainable AI Method, to Integrate Multiomics and Interpret the Relationships Underpinning Complex Traits
Chrstelle Ngueda Kemda	**143**	1-NN Imputation of Missing DNA-Methylation Values
Anne-Kathrin Ruß	**144**	Genome-Wide Association Study of Post COVID-19 Syndrome in a Population-based Cohort in Germany
Paolo Dalena	**145**	Polygenic Risk Scores and Arrhythmic Risk in Dilated Cardiomyopathy: Insights From Common Variant Associations and Prognostic Modeling
Anna D Argoty-Pantoja	**147**	Genome-Wide Association Meta-Analysis on Type D Personality
Cheryl D. Cropp	**149**	Genomics Education Reframed: Race, Ancestry, Ethnicity, and Culture in the Classroom
Lindsay Fernandez-Rhodes	**151**	The Metabolic Subtype of Polycystic Ovary Syndrome: A Gene by Lifestyle Interaction Study in Hispanic/Latinas

POSTER SESSIONS

*Poster Highlights

Session 1 - Monday, September 1
3:15pm-4:15pm

Session 2 - Tuesday, September 2
10:20am-11:20am