

Agenda (only eligible sessions listed)

Please note as you are planning your agenda for the meeting, there is no partial credit for sessions. You may only claim credit for one full session per time block. Credits will not be available for on-demand content post-meeting. Thank you for your understanding.

Time	Session Type	Session Title	CME Credit Hours	NSGC Contact Hours	P.A.C.E.® Contact Hours
Tuesday, October 25					
1:00 – 1:30 pm	Plenary	Presidential Welcome and Address: One Human Race: Billions of Genomes	0.50	0.50	0.50
2:15 – 4:00 pm	Plenary	Featured Plenary Abstract Session I	1.75	1.75	1.50
4:30 – 6:00 pm	Invited	COVID-19 in the post-pandemic era: Long COVID, vaccine response, and beyond	1.50	1.50	1.50
		Demographic history, natural selection, and disease risk in diverse global biobanks			
		Genome mapping technologies – Enabling next-generation cytogenetics			
		Genomic perspectives on biological sex			
		Mosaicism, vascular anomalies, and emerging therapeutics: Models for using the rare to understand the common			
New advances in computational genome interpretation: From prediction to the clinic					
Wednesday, October 26					
7:00 – 8:30 am	Workshop	Genomic research in the All of Us Researcher Workbench: Advancing precision medicine for all	1.50	1.50	1.50
		Investigating public variant datasets with the UCSC Genome Browser			
8:30 – 10:00 am	Platform	A collection of cardiovascular and metabolic disease conundrums	1.50	1.50	1.50
		Applying Mendelian randomization to complex traits			
		Considering ancestry in study populations			
		Genetic and functional advances in inherited neuromuscular disease			
		Genetic impacts on the epigenome and beyond			
		Genetics of human immunity, inflammation and infection			
High-throughput characterization of coding variants, from benchtop to desktop					

10:45 am – 12:15 pm	Platform	Averting Alzheimer's as soon as possible	1.50	1.50	1.50
		Epigenomic associations with disease			
		Let's talk about sex and its contributions to disease risk			
		Massively parallel variant characterization			
		Novel statistical genetics methods for complex traits			
		Somatic mosaicism in human health and disease			
1:45 – 2:45 pm	Platform	Ancestry and admixture in diverse populations	1.00	1.00	1.00
		Emerging topics in biobank-scale association analysis			
		Genotypes and phenotypes of Mendelian disorders			
		How do we express ourselves? Examining promoter and enhancer biology			
		Influence of germline variants on somatic genomic features in cancer risk and progression			
		Investigating complex genomic regions			
5:15 – 7:00 pm	Plenary	Featured Plenary Abstract Session II	1.75	1.75	1.50
Thursday, October 27					
8:30 – 10:00 am	Plenary	Presidential Symposium: African Genomics	1.50	1.50	1.50
10:30 am – 12:00 pm	Platform	Navigating the complex genetic landscape of neurodevelopmental disorders	1.50	1.50	1.50
		Polygenic prediction of complex disease			
		Populations evolving: Modeling genetic variation to understand evolutionary processes			
		The methylome and transcriptome of complex traits			
		Using omics to dissect GWAS signals			
1:45 – 2:45 pm	Platform	All of Us for All of You	1.00	1.00	1.00
		Genetics of substance use disorders			
		Novel methods for rare variants			
		Reading between the reads: Getting the most out of sequencing results			
		RNA based mechanisms in neuropsychiatric disorders			
		The current environment for gene-environment interactions			
		Using EHRs to withdraw new insights from biobanks			
5:15 – 7:00 pm	Plenary	Featured Plenary Abstract Session III	1.75	1.75	1.50

Friday, October 28					
8:30 – 10:00 am	Invited	ASHG/ESHG Building Bridges: Complete Genomes Require New Directions to Democratize Data	1.50	1.50	1.50
		Long-read RNA-seq to illuminate splice-driven mechanisms of human genetic diseases			
		Novel preclinical models of Down syndrome elucidate the complex genetic etiology of neurodevelopmental phenotypes			
		The impact of ascertainment, phenotyping, and population structure on human genetic research			
		To report or not to report: The quandary of variants of uncertain significance (VUSs)			
		Upset the set up: Moving from community engagement to community empowerment			
10:30 am – 12:00 pm	Platform	Computational approaches for understanding noncoding variants	1.50	1.50	1.50
		Extended applications of polygenic risk scores			
		Genetics and integrated -omics of diabetes and associated metabolic disorders in diverse populations			
		Hearing and seeing the advancements in auditory and vision genetics			
		New molecular and analytical tools to study Mendelian disorders			
		Population screening: From patient identification to return of results			
		Towards the defeat of neurodegenerative disease			
2:00 – 3:30 pm	Platform	Context matters! Tissue, cell type, and condition-specificity of epigenetics and expression	1.50	1.50	1.50
		Leveraging population genetics to inform diverse cohorts and biobanks			
		Methods and databases: Open, benchmarked and FAIR			
		Molecular investigations into disease mechanisms			
		Structural variation in population and disease			
4:00 – 5:00 pm	Platform	Challenges in everyday clinical genetics	1.00	1.00	1.00
		Gee, What A Session! (GWAS)			
		Genetic architecture of adiposity			
		Genetic variants and cancer risk in diverse populations			
		Let me sleep on it			
		Splicing together the story			
Therapeutic insights leveraged from preclinical models of disease					
5:30 – 6:10 pm	Plenary	Late Breaking Plenary Abstract Session	0.50	0	0.50

Saturday, October 29					
7:30 – 9:00 am	Workshop	How to Use The Human Pangenome Reference in AnVIL	1.50	1.50	1.50
		Using the Ensembl Variant Effect Predictor (VEP) to interrogate coding and non-coding variants			
9:00 – 10:00 am	Platform	A mix of murine models for mechanistic mapping	1.00	1.00	1.00
		Non-coding variation and cancer			
		Novel approaches to increase the diagnostic yield of genetic disorders			
		The many ways to make polygenic risk scores			
		Unwrapping the role of chromatin in neurodevelopmental disorders			
10:30 – 11:30 am	Platform	Detection and effect of CNVs in general populations	1.00	1.00	1.00
		Expanding roles of repeats			
		Genetic and functional underpinnings of epilepsy			
		The past matters for cancer treatment and risk			
		Understanding GWAS signals: From variants to function			
TOTAL CREDIT COUNTS			26.25 CME	25.75 NSGC	25.50 P.A.C.E.®