Wednesday, 22 February 2023

Time	Auditorium 1
09h00 - 16h00	H3A Bionet: Celebrating 10 Years of Advancing Bioinformatics Research and Capacity Building in Africa (Hall 8, CTICC 2)
09h00 - 14h00	Pre-congress workshop: Genomics in Paediatric Care (hosted by Illumina) (Meeting Block 2.60, Level 2)
09h00 - 13h00	IFHGS EXCO Meeting (Meeting Block 2.44, Level 2)
12h00 - 19h00	Registration Open (Registration Foyer, Ground Floor)
16:30 - 18:30	**Opening Ceremony (Ballroom, Level 1)** **Chair: Raj Ramesar** 16h30 - 16h50 Welcome Address *(Raj Ramesar & Charles Rotimi, Co-Chairs of the Local Organising Committee)* 16h50 - 16h55 Welcome from the President of the African Society of Human Genetics *(Ambroise Wonkam)* 16h55 - 17h00 Welcome from the President of the Southern African Society of Human Genetics *(Collet Dandara)* 17h00 - 17h10 Welcome from IFHGS President and Programme Introduction *(Michele Ramsay, Chair of International Scientific Programme Committee)* 17h10 - 17h20 Naledi Pandor (South African Minister of International Relations and Cooperation) 17h20 - 18h20 Opening Address: **"The Rise of Genomics in Africa"** *(Francis Collins, Former director, National Institutes of Health, USA)* 18h20 - 18h30 Acknowledgements & Declare Congress Open *(Raj Ramesar & Charles Rotimi)*
18:30 - 20:00	**Welcome Reception and Official Opening of Exhibition (Exhibition Hall 1 & 2)**

Thursday, 23 February 2023

07:30 - 17:00	**Registration (Registration Foyer - Ground Level)**								
09:00 - 16:00	**Exhibition (Hall 1 & 2 - Ground Level)**								
07:30 - 08:45	**Meet the Professor**								
09:00 - 10:30	**Plenary 1 - Genomics and anthropology - insights on the peopling of Africa** Venue: Ballroom (Level 1) Chairs: Michele Ramsay and Charles Rotimi								
09:00 - 09:45	"The genetic history of Africa based on modern and ancient DNA " - Carina Schlebusch, Sweden								
09:45 - 10:30	"Academic and Social Consequences of Past Classifications of African Peoples" - Shomarka Keita, USA								
10:30 - 11:00	**Tea / Coffee Break**								
11:00 - 12:30	**INVITED SESSIONS**	**Session 1 - Genetic and Epigenetic Links Between Early Life and Later Life Health Outcomes** Chair: Fasil Tekola-Ayele, USA (Venue: Ballroom East, Level 1)	**Session 2 - Global Perspectives on Return of Individual Research Results to Participants** Chair: Johanna Maria Catharina Blom, Italy (Venue: Meeting Block 1,61 - 1,62 Level 2)	**Session 3 - Hemoglobinopathies: Challenges and Perspectives** Chair: Martine de Rycke, Belgium (Venue: Meeting Block 1.41 - 1,42: Level 1)	**Session 4 - Vascular Anomalies: from Somatic Mutations towards Targeted Therapies** Chair: Miikka Vikkula, Belgium (Venue: Meeting Block 1.43 - 1,44: Level 1)	**Session 5 - The Contribution of African Genomics Research to Innovation in Psychiatry** Chairs: Shareefa Dalvie, South Africa & Nastassja Koen, South Africa (Venue: Meeting Block 1,63-1,64, Level 1)	**Session 6 -The future of Genomics (ClinGen and ClinVar)** Chair: Erin Rooney Riggs, USA (Venue: Meeting Block 2.6, Level 2)	**Session 7 - Cancer Genetics** Chair: Raj Ramesar, South Africa (Venue: Meeting Block 2.44-2.46, Level 2)	**Session 8 - Susceptibility to Infectious Disease - from genetics to exposome** Chairs: Inga Prokopenko, UK & Brent Richards, Canada (Venue: Meeting Block 2.41 - 2.43, Level 2)
		Genetic and epigenetic regulation of fetal growth and links with adult cardiometabolic diseases: Fasil Tekola-Ayele, USA	Return of Results in a Healthy Cohort: The CHRIS Policy: Deborah Mascalzoni, Sweden/Italy	Perspectives in Genomics and Sickle Cell Disease Care in Africa: Ambroise Wonkam, USA/South Africa	Vascular Malformations: Genetic Discoveries on Pathophysiology: Miikka Vikkula, Belgium	An overview of NeuroGAP, including the rationale for launching the initiative and primary findings from this large-scale African genomic study: Lukoye Atwoli, Kenya	Panel: Nadia Carstens, South Africa; Melissa Nel, South Africa; Joao Bosco de Oliveira Filho, Brazil (precorded)	GWAS of Cancers in African Populations: Chris Mathew, South Africa/UK	Understanding how obesity causes severe COVID-19: Brent Richards, Canada
		Genetic links between birthweight and type 2 diabetes in adulthood:Rachel Freathy, USA	Ethical Framework of the Hong Kong Genome Project on Return of Individual Research Results as Benefit Sharing: Calvin Ho, China	Hemoglobinopathies: Molecular genetics, diagnostic applications, challenges and future perspectives: Jan Traeger-Synodinos, Greece (pre-recorded)	Vascular Malformations: Lessons Learned from Preclinical Models: Taija Mäkinen, Sweden	`	ClinVar: Perspectives from Global Users/Submitters: João Bosco de Oliveira Filho, Brazil	Genomic Landscape of African Cancers: Sandeep Dave, USA	Applied genetic epidemiology and infectious disease: an emerging story: Fergus Hamilton, UK (pre-recorded)
		Genetic and epigenetic modifiers and mediators of perinatal environmental exposures and offspring cardiovascular health: Daniel Enquobahrie, USA	Communitarian Ethics and the Return of Genetic Results in Africa: Nchangwi Syntia Munung, South Africa	Preimplantation Genetic Testing for hemoglobinopathies and HLA typing: Martine De Rycke, Belgium	Vascular Malformations: Towards Precision Therapies: Laurence M. Boon, Belgium	Population genomic resources to empower the PUMAS Project: Lerato Majara, South Africa	The Clinical Genome Resource (ClinGen): An Overview: Erin Rooney Riggs, USA	Affordable prevention of hereditary colon cancer: Sir John Burn, UK	Genetic Mechanisms of Critical Illness in Covid-19: James F Wilson, UK
		Using electronic health records to identify pleiotropy and shared genetic architectures of complex diseases: Tesfaye Mersha, USA	The FACILITATE ethical framework on the return of data to patients in clinical trials: Ciara Staunton, Italy				Utilizing ClinGen Resources: Danielle Azzariti, USA		
12:30 - 14:00	**Lunch Break**								
13:00 - 14:00	**Lunch Symposia / Workshops**	**Proposing a network of Genomic Centres of Excellence in Africa (GenCoE) (Ballroom East, Level 1)**	**Lunchtime Symposium 2**	**Rare Diseases Celebration Day (Meeting Block 1.41 & 1.42, Level 1)**	**H3Africa AGenDA Meeting: 14h15 - 14h45, Meeting Block 1.43 & 1.44, Level 1**	**Workshops / Focus Groups 3**	**Workshops / Focus Groups 4**	**Workshops / Focus Groups 5**	**Workshops / Focus Groups 6**
14:00 - 15:00	**POSTER SESSION** (Venue: Exhibition Hall - Hall 1 & 2, Ground Level)								
15:00 - 15:30	**Tea / Coffee Break**								
		MEETING ROOM : Ballroom East	**MEETING ROOM : Room 1,61 - 1,62**	**MEETING ROOM : Room 2,6**	**MEETING ROOM: 1,43 - 1,44**	**MEETING ROOM:1,63 -1,64**	**MEETING ROOM: 2,41 - 2,43**	**MEETING ROOM: 2,44 - 2,46**	**MEETING ROOM: 1,41 - 1,42**
	Session Chairs	**Karen Fieggen and Tjitske Kleefstra**	**Gerome Breen and Magdalena Mroczek**	**Eimear Kenny and Noemi Piga**	**Georgia Chenevix-Trench and Lindie Lamola**	**Amy Bentley and Tinashe Chikowore**	**Danielle Azzariti and Syntia Munung**	**Aime Lumaka and Candice Feben**	**Cesar Augusto Fortes Lima and Dhriti Segup**
15:30 - 16:00	**Invited Keynote Speakers**	Keynote 1 - Mendelian Phenotypes through the lens of OMIM: Ada Hamosh, USA	Keynote 2 - The genetics of major depression in diverse populations: Karoline Kuchenbaecker, UK	Keynote 3 - Multivariate methods and their applications in complex trait genetics: Inga Prokopenko, UK	Keynote 4 - Genomes and Genomics of Breast Cancers in Asian Patients: Soo-Hwang Teo, Malaysia	Keynote 5 - Leveraging multi-omics for understanding mechanisms of hypertension: Patricia Munroe, UK	Keynote 6 - Implementing Equitable Genomic Medicine: Challenges and Opportunities: Cathy Wicklund, USA	Keynote 7 - New therapies for skeletal dysplasia (dwarfism): Ravi Savarinrayan, Australia	Keynote 8 - Connecting Population Genetics to Human Diseases: Special Referecne to Asia and the Indian Subcontinent: Analabha Basu, India
	Oral Presentations								
16:00 -16:15		**OP001**. The utility of clinical exome sequencing as a first-tier diagnostic tool in critically ill infants in South Africa: *Lisa Campbell, South Africa*	**OP007**. Polygenic risk scores for lifespan, BMI, and chronic pain predict a medication-based Rx-Risk Comorbidity Index in the Australian Genetics of Depression Study: *Penelope Lind, Australia*	**OP013**. Multi-omics study highlights several metabolites and gene expression levels as predictors of weight loss maintenance: *Tingyu Guo, UK*	**OP019**. CRISPR screens of candidate breast cancer risk genes using multiple assays to identify genes involved in proliferation, tumorigenicity, DNA damage response and immune-surveillance: *Georgia Chenevix-trench, Australia*	**OP025**. Detailing the Inflammatory Cascade of Severe Malaria through Transcriptomic, Proteomic, and Metabolomic Analyses: *Rafal Sobota, USA*	**OP031**. Whole genome sequencing (WGS) partnership program: a risk-sharing agreement to implement WGS as a first line test in paediatric monogenic disease: *Ben Lundie, Australia*	**OP037**. Development of a polygenic score to predict cisplatin-induced ototoxicity: *Deanne Nixie Miao, Canada*	**OP043**. Core Investigation of Exonic Variations in Olfactory Receptor Genes (ORGs) in Indigenous Populations from Southeast Asia: *Sze Mei Lee. Malaysia*
16:15 - 16:30		**OP002**. Exome Sequencing in Childhood-Onset Essential Hypertension Implicates Monogenic Disruption of Vascular Integrity in Disease Pathogenesis: *Edmond Wonkam Tingang, USA*	**OP008**. Rare-variant analysis of whole-genome sequence data obtained from multi-ancestry families identifies new genes associated with late-onset Alzheimer's disease: *Suzanne Leal, USA*	**OP014**. Circulating cytokines and their role in type 2 diabetes among Africans: A Mendelian randomization study: *Karlijn Meeks, USA*	**OP020**. Targeted delivery of miR-218 via decorated hyperbranched polyamidoamine for liver cancer regression: *Mahmoud Elhefnawi, Egypt*	**OP026**. Investigating the impacts of age at menarche on cognitive function based on a Mendelian randomization approach using a nationwide cohort from the Taiwan Biobank: *Meng-Che Tsai, Taiwan*	**OP032**. What are patient perspectives on privacy and trust in digital genomic tools? A qualitative study: *Vedika Jha, Canada*	**OP038**. Large cardiac arrythmia gene panel genetic testing as prognostic tool for Brugada syndrome: *Sonia Van Dooren, Belgium*	**OP044**. Evidence of recent positive selection in the innate immune system and ion homeostasis among populations of diverse ancestries in mainland India: *Chandrika Bhattacharyya, India*
16:30 - 16:45		**OP003**. Comprehensive cytogenetic study of a large cohort of Egyptian referral patients with Disorders of Sex Development (DSD): *Mona Mekkawy*	**OP009**. Characterizing the shared genetic influences between schizophrenia and reaction time variability: *Olivia Wootton, South Africa*	**OP015**. GWAS meta-analysis in SCAD, a women predominant ischemic heart disease, reveals common variants and genes related to artery integrity and tissue-mediated coagulation: *Takiy Berrandou, France*	**OP021**. Mismatch Repair variant classification with ACMG/AMP criteria and comparison with Bayesian probability framework: *Finlay Macrae, Australia*	**OP027**. Acceptability of Dried Blood Spot collection by Primary Caregivers of Filipino patients with Maple Syrup Urine Disease and Phenylketonuria: A Philippine's experience on Long Term Management for Newborn Screening patients:*Roxanne Janica Merencilla, Phillipines*	**OP033**. Navigating Layers of Uncertainty: Perspectives from South African Genetic Counselling Interactions: *Meagan Scott, South Africa*	**OP039**. Developing an integrated risk score for cardiovascular diseases in African populations: *Michelle Kamp, South Africa and UK*	**OP045**. Global Proteomic Analyses of Type 2 Diabetes and Obesity in West Africans*: Adebowale Adeyemo, USA*

16:45 - 17:00		**OP004**. Deciphering Developmental Disorders in Africa (DDD-Africa) – Clinical lessons learnt following whole exome sequencing in an African setting: *Amanda Krause, South Africa*	**OP010**. Variant-to-gene mapping paired with cross-species validation reveals novel effector genes for insomnia: *Amber Zimmerman, USA*	**OP016**. Non-additive polygenic score: *Rikifumi Ota, Japan*	**OP022.** Novel biological insights into the genetic architecture of bipolar disorder form multi-ancestry genome-wide association studies: *Kevin O'Connell*	**OP028**. Novel Copy Number Variants associated to venous thromboembolism (VTE) and warfarin dose requirement in African Americans: *Carolina Clark OBO Minoli Perera, USA*	**OP034**. Engaging with Local Communities in Botswana: Understanding impact of Cultural Values, Norms and Beliefs on Gene-Editing Research: *Setlhomo Koloi-Keaikitse*	**OP040.** Pleiotropic association of rare variation with the plasma lipidome and type 2 diabetes: *Joanne E Curran, United States*	**OP046**. Genome-wide association study of oesophageal cancer identifies trans-ethnic risk variants in African and Chinese populations: *Wenlong Chen, South Africa*
17:00 - 17:15		**OP005**. Molecular diagnosis of RASopathy patients using a next generation sequencing multi-gene targeted panel and multiplex ligation-dependent probe amplification analysis: *Maria Mudau, South Africa*	**OP011**. The incorporation of novel audiogram classification strategies to identify genes and pathways involved in age-related hearing loss: *Samah Ahmed, Canada*	**OP017**. BridgePRS: A powerful trans-ancestry Polygenic Risk Score method: *Paul O'Reilly, USA*	**OP023**. Investigating the role of polygenic background in neurodevelopmental disorders: *Qinqin Huang*	**OP029**. Discovery of the first two genome-wide significant loci for ectopic pregnancy highlights MUC1 as a potential candidate gene and identifies genetic and phenotypic relationships across traits: *Natàlia Pujol Gualdo, Estonia*	**OP035**. Personal values versus professional role: healthcare professionals experiences with offering termination of pregnancy for fetal abnormalities: *Malebo Malope, South Africa*	**OP041**. Genetic relationships and causality between overall and central adiposity and breast, prostate, lung and colorectal cancer: *Jared Maina, France*	**OP047**. Evidence of potential natural selection in African American individuals post admixture: *James Jaworski, USA*
17:15 - 17:30		**OP006**. Loss-of-function of AMFR causes autosomal recessive hereditary spastic paraplegia by altering lipid metabolism: *Stefan Barakat, Netherlands*	**OP012**. Genome-wide association study of breast density among women of African Ancestry: *Shefali Verma, USA*	**OP018**. Recessive effects of protein-coding variants in a cohort of 44,000 British Pakistanis and Bangladeshis: *Teng Hiang Heng, UK*	**OP024**. The Genetics of Extreme Birthweight and its Relationship with Cardiometabolic Disease: *Gunn-Helen Moen, Australia*	**OP030**. Genomic spectrum of non-syndromic hearing impairment in Senegal: *Rokhaya Ndiaye, Senegal*	**OP036**. Genetic risk prediction of high-risk human papillomavirus infection and cervical cancer: *Triin Laisk, Estonia*	**OP042**. An assessment of the copy number variation landscape in Sub-Saharan African populations: *Laura Cottino, South Africa*	**Blank**
18:00 - 19:30	Southern African Society of Human Genetics (SASHG) - BGM (Meeting Block 1.41 & 1.42) Workshop: It's more than just training: Capacity building in context. (Hosted by Wellcome Connecting Science) (Meeting Block 1.43 & 1.44)								
19:30 - late	**President's Dinner (by invitation only)**								

Friday, 24 February 2023

07:30 - 17:00	**Registration open** (entrance to Hall 1, Ground Level)								
09:00 - 16:00	**Exhibition open** (Hall 1 & 2, Ground Level)								
07:30 - 08:45									
09:00 - 10:30	**Plenary 2 - Translational Genomics and Implementation Science** Chairs: David Amor and Kelly Ormond Venue: Ballroom, Level 1								
09:00 - 09:45	"Non-Invasive Prenatal Testing as an Archtype of Translational Genomics" - Dennis Lo, Hong Kong (pre-recorded)								
09:45 - 10:30	"Genomics and the Future of Medicine" - Mayana Zatz, Brazil (pre-recorded)								
10:30 - 11:00	**Tea / Coffee Break**								
11:00 - 12:30	**INVITED SESSIONS**	**Session 9 - Diversity for the Future of Precision Medicine & Health Population Screening** Chair: Vicky Nembaware, South Africa (Venue: Ballroom East, Level 1)	**Session 10 -Global Initiatives in Genomic Medicine Workforce Development: Ensuring Best Practice in Genomic Education** Chairs: Tina-Marie Wessels, South Africa & Sylvia Metcalfe, Australia (Venue: Meeting Block 1,61 - 1,62 , Level 1)	**Session 11 -Therapeutic Approaches to Genetic Disorders - Before, During and After** Chairs: Jennifer Posey, USA & Careni Spencer, South Africa (Venue: Meeting Block 1.41 - 1,42, Level 1)	**Session 12- Advances in Genetics and Gene Directed Therapies for Inherited Retinal Diseases** Chair: Alison Hardcastle, UK (Venue: Meeting Block 1,43 - 1,44 Level1)	**Session 13 - Methodology and Considerations for Analyses in Diverse Populations** Chairs: Marika Kaakinen, UK & Krista Fischer, Estonia (Venue: Meeting Block 1.63 - 1,64, Level 1)	**Session 14 - AI-driven next-generation phenotyping: impact on the clinical diagnostic process** Chairs: Shahida Moosa, South Africa & Thomy de Ravel, Belgium (Venue: Meeting Block 2.41 - 2.43, Level 2)	**Session 15 - Multi-Omics** Chair: Ayse Demirkan, UK & Inga Prokopenko, UK (Venue: Meeting Block 2.44 - 2.46, Level 2)	**Session 16 - Sustainable Development Goals (SDG 2030) For Genetic and Genomic Disorders** Chair: Meow-Keong Thong, Malaysia (Venue: Meeting Block 2.6 Level 2)
		Lack of Diversity Remains an Unsolved Problem for Precision Medicine but Hopefully Not for Long: Janina Jeff, USA	Ensuring Best Practice in Genomics Education and Evaluation: The Australian Genomics Workforce and Education Research Program: Amy Nisselle, Australia	Novel Therapies: Achondroplasia as a Model: Melita Irving, UK	Advances in Defining the Inherited Retinal Disease Genome: Alison Hardcastle, UK	The Power of Diverse Populations for Discovery and Translation of Genome-Wide Association Studies: Andrew Morris, UK	Face2Gene: a toolbox for AI-based dysmorphism evaluation: Nicole Fleischer, USA	The use of multi-omics in African American Genomic Medicine: Minoli Perera, USA	Achieving Sustainable Development Goals for Congenital Disorders: Challenges and Opportunities: Meow Keong Thong, Malaysia
		Novel and Known Genes associated with Cardiovascular Disease Risks in African Populations: Palwendé Boua, Burkina Faso	Supporting The Implementation of a National Genomics Medicine Service In England: Michelle Bishop, UK	Genetic Biobanks, Registries, Patient Organisations: Towards Therapies for FOP: Luca Sangiorgi, Italy (pre-recorded)	Modelling Inherited Retinal Diseases with Stem Cells: Michael Cheetham, UK	Diversity in Genetic Studies aids Locus Discovery, Fine-Mapping, Gene Prioritisation, and Causal Inference: Karoline Kuchenbaecker, Genomics England	GestaltMatcher and DeepGestalt : powerful engines for clinical and molecular diagnostic : Peter M Krawitz, Germany	Single Cell Transcriptomics: Peter Kharchenko, USA (pre-recorded	Newborn Screening: Way Forward for SDGS From Global Perspective: Carmencita Padilla, Philippines
		Importance of Building up Local Infrastructure to Provide Whole-Genome Sequencing for Rapid Response, for Critically Ill Patients: Ahmad Abou Tayoun, United Arab Emirates	The African Genomic Medicine Training (AGMT) Initiative: Nicola Mulder, South Africa	Therapeutic approaches for genetic conditions: Ethical and social considerations: Nchangwi Syntia Munung, South Africa	Genetic Therapies for Inherited Retinal Diseases: From Fiction to Fact: Bart Leroy, Belgium	Incorporating Local Ancestry in the Construction of Polygenic Risk Scores: Yun Li, USA (pre-recorded)	Objective evaluation of dysmorphism by automated analysis of facial photographs in African individuals: Aimé Lumaka, DR Congo	Gut microbiome: Alexandra Zhernakova, Netherlands	Next Generation Sequencing Technology: Levelling the Playing Field For SDGS in Genomic Medicine: Lai Poh San, Singapore
			Educating the Genomics Community on Updated ACMG/Clingen Technical Standards for Interpretation and Reporting of Constitutional Copy Number Variants: Erin Rooney Riggs, USA						
			Panel discussion with all presenters: Lessons Learned from International Workforce Development Initiatives: Looking Back to Move Forward						
12:30 - 14:00	**Lunch Break**								
13:00 - 14:00	**LUNCHTIME SYMPOSIA / WORKSHOPS**	**Lunchtime Symposium 5**	**Lunchtime Symposium 6**	**Lunchtime Symposium 7**	**Lunchtime Symposium 8**	**Africa Population Cohorts Consortium (CE-APCC) (Meeting Block 1.60, Level 1)**	**Workshop / Focus Group 10**	**Workshop / Focus Group 11**	**Workshop / Focus Group 12**
14:00 - 15:00	**POSTER SESSION** (Venue: Exhibition Hall - Hall 1 & 2, Ground Level)								
15:00 - 15:30	**Tea / Coffee Break**								
th		**MEETING ROOM : Ballroom East**	**MEETING ROOM : Room 1,61 - 1,62**	**MEETING ROOM : Room 1,41 - 1,42**	**MEETING ROOM: 1,43 - 1,44**	**MEETING ROOM:1,63 - 1,64**	**MEETING ROOM: 2,6**	**MEETING ROOM: 2,44 - 2,46**	**MEETING ROOM: 2,41 - 2,43**
	Session Chairs	**Jozef Gecz and Maria Mudau**	**Souad Rahmouni and Juliana Miranda Cerqueira**	**Deborah Morris-Rosendahl and Khuthala Mnika**	**MK Thong and Ileana-Delia Sabau**	**Melanie Newport and Mridul Johari**	**Leon Mutesa and Rhys Dore**	**Margaret Pericak-Vance and Nadia Carstens**	**Pilar Carvallo and Rita Matos**
15:30 - 16:00	**Invited Keynote Speakers**	Keynote 9 - From Chromosomal Microarray Analysis to a Complete Genome Scan: the ever-evolving lessons from Prenatal Diagnosis: Richard Choy, China	Keynote 10 - How digital tools are changing equity & quality of genomic medicine: Evidence, preferences & policy: Yvonne Bombard, Canada	Keynote 11 - Consanguinity and genetic diseases in North Africa: are we ready for precision medicine? Cherine Charfeddine, Tunisia	Keynote 12 - Genomics Equity for Health in Latin America: Claudia Gonzaga-Jauregui, Mexico	Keynote 13 - Using Zebrafish Larvae to Characterize Candidate Genes for Cardiometabolic Health: Marcel den Hoed, Sweden	Keynote 14 -Using Epigenomics to Understand Human Disease: John Greally, USA	Keynote 15 - Establishing an African-relevant roadmap for prostate cancer precision medicine: lessons from whole genome profiling within the Southern African Prostate Cancer Study (SAPCS): Vanessa Hayes, Australia	Keynote 16 - Rare variants and common traits: Alex Reymond, Switzerland
	Oral Presentations								
16:00 - 16:15		**OP049**. Diagnosing rare genetic disorders in LMICs using WES and automated deep phenotyping and its implications on public health: *Alexej Knaus, Germany*	**OP055**. Large-scale single-cell RNA sequencing of healthy and inflamed terminal ileal samples yields insights into Crohn's disease biology: *Monika Krzak, UK*	**OP061**. WHO and Partners present a revision of the burden of birth defects: *Kathleen Strong, Switzerland*	**OP067**. Maximizing Participation in Genomics Research; Feedback from the Community: *Daniel Sekwo, Ghana*	**OP073**. Characterizing 99 cardiometabolic candidate genes for a role in NAFLD using CRISPR/Cas9, in vivo imaging and deep learning in zebrafish larvae: *Endrina Mujica, Sweden*	**OP079**. Epigenetic age acceleration in the emerging burden of cardiometabolic diseases among migrant and non-migrant African populations: the population based cross-sectional RODAM study: *Felix Chilunga, Netherlands*	**OP085**. Heterogeneous genetic architectures of prostate cancer in African populations: *Joseph Lachance, USA*	**OP091**. A multi-omics classifier for prediction of Androgen treatment response In prostate cancer patients: *Itunuoluwa Isewon, Nigeria*
16:15 - 16:30		**OP050**. Diagnostic yield of massive parallel sequencing in postmortem genetic analyses of sudden unexplained deaths in the young Kazakhstani individuals: *Ainur Akilzhanova, Kazakhstan*	**OP056**. PheWAS-based clustering of Mendelian Randomization instruments reveals distinct mechanism-specific causal effects between obesity and educational attainment: *Liza Darrous, Switzerland*	**OP062**. Breast cancer patients from Inkosi Albert Luthuli Central Hospital in South Africa: comparison of clinical and molecular characteristics between triple-negative and luminal-like disease: *Herculaas MvE Combrink OBO Jaco Oosthuizen, South Africa*	**OP068**. A staged approach to developing the genomics workforce while implementing genomic medicine: *Amy Nisselle, Australia*	**OP074**. Large-scale analysis of retinal vascular parameters from UK BioBank colour fundus images reveals their phenotypic and genotypic correlations, as well as genes and pathways associated with vascular pathomechanics and diseases: *Sven Bergmann, Switzerland*	**OP080**. Genomewide longitudinal DNA methylation profiling of pregnant women and its association with preterm birth outcome – a GARBH-Inl study: *Jagyashila Das, India*	**OP086**. Rare, risk-associated variants in DNA damage repair genes identified through germline sequencing in two hereditary prostate cancer cohorts: *Georgea Foley, Australia*	**OP092**. Application of Machine Learning to predict prostate cancer aggressiveness – using clinical and genomic datasets: *Shakuntala Baichoo, Mauritius*
16:30 - 16:45		**OP051**. Rapid and comprehensive diagnostic method for repeat expansion diseases using nanopore sequencing: *Naomichi Matsumoto, Japan*	**OP057**. Assessment of 3D genomic features across multiple cell types reveals novel insights into the pathogenesis of childhood obesity: *Khanh B. Trang, USA*	**OP063**. Genome-wide association study identifies common variants associated with breast cancer in South African black women: *Mahtaab Hayat, South Africa*	**OP069**. The Common Infrastructure for National Cohorts in Europe, Canada, and Africa (CINECA) Project: *Thomas Keane, UK*	**OP075**. The Genetic Architecture of the Corpus Callosum and its Subregions: *Megan Loraine Campbell, South Africa*	**OP081**. Epigenome-wide association study reveals CpG sites associated with thyroid function and regulatory effects on KLF9: *Alexander Teumer, Germany*	**OP087**. The role of genetics in colorectal carcinogenesis; Does race matter?: *Hassan Ashktorab, USA*	**OP093**. Benchmarking of univariate pleiotropy detection methods: *Michael Nothnagel*
16:45 - 17:00		**OP052**. Combination of glass-needle-based chromosome microdissection and bisulfite sequencing to assess allele-specific DNA methylation data in unbalanced X-autosome translocations: *Bianca Favilla, Brazil*	**OP058**. Development of a pathology-supported genetic testing service at the intersection of research and oncology practice: Translating population risk into personal utility using point-of-care genomics and next generation sequencing: *Maritha Kotze, South Africa*	**OP064**. Impact of DNA repair genes on reproduction and cancer predisposition: *Svetlana Yatsenko, USA*	**OP070**. The GIRDA project: promoting precision ophthalmology in Africa: *Lisa Roberts, South Africa*	**OP076**. The Genetic Architecture of Amygdala Nuclei: *Mary Mufford, South Africa*	**OP082**. cis-eQTL mapping of TB-T2D comorbidity elucidates the involvement of African ancestry in TB susceptibility: *Yolandi Swart, South Africa*	**OP088**. Genetic ancestry correlates of the somatic mutational landscape from tumor profiling data of 100,000 cancer patients: Francisco De La Vega, USA	**OP094**. Identifying genes involved in hip osteoarthritis and describing the cells in which they are differentially expressed: *Kaitlyn Flynn, Australia*
17:00 - 17:15		**OP053**. Stepwise ABC system for classification of any type of genetic variant: Experience so far and suggested updates: *Gunnar Douzgos Houge, Norway*	**OP059**. The influence of autozygosity on disease across the phenotypic spectrum: *Hilary Martin OBO Daniel Malawsky, UK*	**OP065**. Confined placental mosaicism and clinical impact, a retrospective cohort analysis: *Diane Van Opstal, Netherlands*	**OP071**. Development and evaluation of a decision aid for BRCA1/2 genetic testing in high-risk Malaysian families with varying degrees of health literacy: A mixed-methods study: *Bettina Meiser, Australia*	**OP077**. Understanding genetic contributions to the brain building blocks of musical rhythm traits: *Reyna Gordon, USA*	**OP083**. 3D genome architecture in frontal cortex suggests novel mechanisms for ancestry-specific genetic risk for Alzheimer's Disease: *Liyong Wang, USA*	**OP089**. ancMETA: Bayesian Framework for Gene/Subnetwork-Specific Meta-Analysis: *Joel Defo, South Africa*	**OP095**. Neurobiological Pathways Underlying Opioid Addiction Identified by Systems Biology Multi-omic Gene Integration: *Daniel Jacobson, USA*
17:15 - 17:30		**OP054**. Clinical Genomics in Southern Africa: Lessons from the Undiagnosed Disease Programme: *Shahida Moosa, South Africa*	**OP060**. Novel genetic associations underlying symptom severity and infection susceptibility to SARS-CoV-2: *Mattia Cordioli, Finland*	**OP066**. Novel gene discovery for Parkinson's disease in a South African family: *Katelyn Cuttler, South Africa*	**OP072**. The Baylor College of Medicine Genomic Research to Elucidate the Genetics of Rare (BCM-GREGoR) Disease Program: Annotating Gene Function to Provide Insights into Human Biology and Disease Across Worldwide Populations: *Jennifer Posey, USA*	**OP078**. Replication of Suggestive GWAS Signals Identified Novel Loci for Non-syndromic Orofacial Clefts in the African Population: *Azeez Alade, USA*	**OP084**. Exploring temporal gene expression dynamics during postnatal human brain maturation: a single nucleus RNA sequencing study of the paediatric and adult human brain: *Christina Steyn, South Africa*	**OP090**. Using a population-specific reference panel improves genotype imputation accuracy in individuals of African ancestry: *Richard Mayanja*	**OP096**. Copy number variant identification from exome sequencing data – a possible approach for African developmental disorder datasets?: *Nadja Louw, South Africa*

	HUGO Gathering Event (Meeting Block 1.60)
18:00 - 19:30	GenQA Dinner Symposium: How to deliver a high quality genomic diagnostic testing service - reporting results, standardising nomenclature and quality assurance. (Meeting Block 2.60)

Saturday, 25 February 2023

07:30 - 17:00	**Registration open** (entrance to Hall 1, Ground Level)								
09:00 - 16:00	**Exhibition open** (Hall 1 & 2, Ground Level)								
07:30 - 08:45	**Meet the Professor / Meet the Expert / Workshops / Focus Groups / Breakfast Symposia** Non Profit Organisations, Academic Institutions and Individuals applications (closing date: 30 November 2022): https://www.ichg2023.com/workshops-satellite-meetings-2/) Sponsor and Exhibitor Applications (apply for a workshop / symposium sponsorship: https://www.ichg2023.com/sponsorship/)								
09:00 - 10:30	**Plenary 3 - Mechanisms of Disease: The Functional Genome** Chairs: Poh San Lai and Inga Prokopenko Venue: Ballroom, Level 1								
09:00 - 09:45	"Autozygome as a Tool to Enhance the Clinical Annotation of the Human Genome" - Fowzan Alkuraya, Saudi Arabia								
09:45 - 10:30	Genetics and epigenetics of pediatric epilepsy: moving from etiology to precision therapy - Heather Mefford, USA								
10:30 - 11:00	**Tea / Coffee Break**								
11:00 - 12:30	**INVITED SESSIONS**	**Session 17 - Predicting Phenotypes for Polygenic Traits in Diverse Populations** Chair: Ricardo Vrdugo, Chile (Venue: Meeting Block 2,41 - 2,43 , Level 2)	**Session 18 - The Role of Patient Advocacy - The Example of Rare Disease** Chairs: Helen Malherbe, South Africa & Mariela Larrandaburu, Uruguay (Venue: Meeting Block 1,61 -1,62 , Level 1)	**Session 19 - Long read genomics** Chair: Naomichi Matsumoto, Japan (Venue: Meeting Block 2,6, Level 2)	**Session 20 - Inherited Errors of Immune Deficiency: Primary Immune Deficits** Chairs: Craig Kinnear, South Africa (Venue: Meeting Block 1.43 - 1,44, Level 1)	**Session 21 - Overcoming Barriers to Capturing Diversity in Global Genetics Research** Chair: Athena Starlard-Davenport, USA (Venue: Meeting Block 1,63 - 1,64, Level 1)	**Session 22 - Shaping the Global Landscape and Developing a Common Language and Standards for Human Genetics and Genomics** Chair: Michele Ramsay, South Africa (Venue: Ballroom East, Level 1)	**Session 23 - Artificial Intelligence to Enable Clinical Genomics Around the World** Chair: Francisco De La Vega, USA & Karen Eliback, USA (Venue: Meeting Block 2.44 - 2,46 Level 2)	**Session 24 - Reproductive Carrier Screening - Meeting the Challenges** Chair: Edwin Kirk, Australia (Venue: Meeting Block 1.41 - 1.42, Level 2)
		Assessment of the Predictive Power of Polygenic Risk Scores in an Admixed Population from South America for Nine Common Diseases: Ricardo A. Verdugo, Chile	Orphanet and hospital-based programs as tools to address undiagnosed and rare diseases: Francesc Palau, Spain	A catalogue of human structural variations: Shinichi Morishita, Japan	NGS and Infectious Diseases - A Journey of Discoveries: Anne Puel, France (prerecorded)	Diversity in Genetics and Genomic Studies: Adebowale A. Adeyemo, USA	HUGO, The Human Genome Organization, Working to Ensure that the Human Genome Includes and Benefits All: Ada Hamosh, USA	Identifying facial phenotypes of genetic disorders using deep learning: Peter Krawitz, Germany	Ethical aspects of population-scale reproductive genetic carrier screening: Ainsley Newson, Australia
		Developing Effective Polygenic Risk Scores for Cancer for Latin American Populations: Luis Carvajal-Carmona, USA	The importance of collaboration between the lay support communities and research groups for rare disease research: Colleen Aldous, South Africa	Long-read genomics to unravel undiagnosed rare diseases: Alexander Hoischen, The Netherlands	WES and WGS in South Africa for Inherited Errors of Immunity – Facts, Fallacies and VUS: Brigitte Glanzmann, South Africa	Beyond Inclusion: Empowering Indigenous Genomic Data Equity in Health: Krystal Tsosie, USA	Developing Technical Standards and Policy Frameworks to Accelerate Responsible Sharing of Genomic and Related Health Data: Peter C Goodhand, Canada	Artificial intelligence for near instant diagnosis of rare genetic disease from whole-genome and deep phenotype data: Martin Reese, USA	Turning the tide on autosomal recessive diseases: The double edged sword of consanguinity: Fowzan Alkuraya, Saudi Arabia
		Developing Effective Polygenic Risk Scores for Multi-Ethnic Populations in Africa: Eimear Kenny, USA	The strength of the associative movement in rare diseases in Ibero-America: ENSERIO LATAM study, future challenges: Juan Carrion, Spain	Strategy detecting abnormal repeats in human diseases: Naomichi Matsumoto, Japan	IEI & Genetics: Clinical illustrations of the Southern African challenges' Andre van Niekerk, South Africa	Building capacity in African Genomics: perspectives from an early career researcher: Lerato Majara, USA	Realizing the Full Potential of Longitudinal Populations Studies and Health Systems to Advance Global Health: Geoffrey S Ginsburg, USA	Histogenomics: Prediction of cancer somatic mutations, tumor mutational burden, and molecular subtypes from histopathological images by deep learning: Francisco De La Vega, USA	Design, implementation and outcomes of The Australian Reproductive Genetic Carrier Screening Project ("Mackenzie's Mission") – screening > 9,000 couples for 1,281 genes to pave the way for a national screening program: Edwin Kirk, Australia
			The Power of Advocacy: Marianne Gomes, South Africa						
12:30 - 14:00	**Lunch Break**								
13:00 - 14:00	**LUNCHTIME SYMPOSIA / WORKSHOPS**	**Lunchtime Symposium 5**	**Lunchtime Symposium 6**	**Lunchtime Symposium 7**	**Lunchtime Symposium 8**	**Workshop / Focus Group 9**	**Workshop / Focus Group 10**	**Workshop / Focus Group 11**	**Workshop / Focus Group 12**
14:00 - 15:00	**POSTER SESSION** (Venue: Exhibition Hall - Hall 1 & 2, Ground Level)								
15:00 - 15:30	**Tea / Coffee Break**								
		MEETING ROOM: Meeting Room 1,63 - 1,64	**MEETING ROOM : Room 1,61 - 1,62**	**MEETING ROOM : Room 1,41 - 1,42**	**MEETING ROOM: 2,6**	**MEETING ROOM: Ballroom East**	**MEETING ROOM: 2,41 - 2,43**	**MEETING ROOM: 2,44 - 2,46**	**MEETING ROOM: 1,43 - 1,44**
	Session chairs	**Zane Lombard and Mohamed Alimohamed**	**Cairna Schlebusch and James Wilson**	**Hugues Abriel and Jennifer Posey**	**Colleen Aldous and Elena Avram**	**Andrew Morris and Yosuke Tanigawa**	**Collet Dandara and Oppah Kuguya**	**Philip Awadalla and Wisdom Akurugu**	**ed**
15:30 - 16:00	**Invited Keynote Speakers**	Keynote 17 - Hetrotaxy:the Evo-Devo of Left-Right patterning across vertebrates: Bruno Reversade, Singapore	Keynote 18 - Populations genetics and evolution - A Mexican cohort: Mashaal Sohail, Mexico	Keynote 19 - Genetic bases of severe childhood speech disorders: Angela Morgan, Australia	Keynote 20 - Enabling the ethical return of genomic research results: a global perspective: Danya Vears, Australia	Keynote 21 - Challenges in biobank-based personalized risk prediction and communication: Krista Fischer, Estonia	Keynote 22 - Ethical challenges of cutting-edge technologies: Ursula Matte, Brazil	Keynote 23 - Bioinformatics for Personalized Medicine in Estonian Biobank: Reedik Magi - Estonia	Keynote 24 - Recent progress in the genetics of complex traits with special reference to human twinning: Nick Martin, Australia
	Oral Presentations								
16:00 - 16:15		**OP097**. Deciphering Developmental Disorders in Africa (DDD-Africa): clinical characterization in a Central African setting: *Prince Makay, DRC (Congo)*	**OP103**. Expansion of pastoralism across the African continent from a genomic perspective: *Cesar Fortes-Lima, Sweden*	**OP109**. Age Estimate of GJB2-p.(Arg143Trp) Founder Variant in Hearing Impairment in Ghana, Suggests Multiple Independent Origins across Populations: *Elvis Twumasi Aboagye, Ghana*	**OP115**. Trustworthy health data governance and the social license for precision medicine: Outcomes from mixed methods research in Singapore (2018-2021): *Tamra Lysaght, Singapore*	**OP121**. Use of exome sequence data from 200,000 UK Biobank subjects to elucidate the rare variant contribution to common phenotypes: *David Curtis, UK*	**OP127**. Building an African-specific pangenome based on short-read whole genome sequence data: *Shaun Aron, South Africa*	**OP133**. Transcriptome signature of sodium intake in and links to cardiovascular traits: *Amadou Gaye, USA*	**OP139**. Trans-ancestry GWAS meta-analysis of random glucose provides insights into diabetes pathophysiology, complications, and treatment stratification: *Marika Kaakinen, UK*
16:15 - 16:30		**OP098**. Recurrent variants in subunits of the Human Mediator complex affect brain development and lead to severe neurodegenerative diseases: *Elisa Cali, United Kingdom*	**OP104**. Precolonial sex-biased admixture in Indigenous Americans living on the eastern slopes of the Andes: *Victor Borda, USA*	**OP110**. Long-read sequencing and profiling of RNA-binding proteins reveals the pathogenic mechanism of aberrant splicing of an SCN1A poison exon in individuals with epilepsy: *Hannah Happ, USA*	**OP116**. Democratizing sickle cell disease gene therapy knowledge: A community based model for stakeholder engagement: *Vence Bonham, USA*	**OP122**. 300 Billion Associations: Genetic architecture of >2000 phenotypes in 658,000 individuals of diverse ancestries in the VA Million Veteran Program: *Anurag Verma, USA*	**OP128**. Individuals of African ancestry at the APOE ε4 gene have a lower risk effect for Alzheimer disease potentially due to gene expression and chromatin accessibility profiles: *Katrina Celis, USA*	**OP134**. Non-Mendelian inheritance patterns and extreme deviation rates of CGG short tandem repeats in autism: *Dale Annear, Belgium*	**OP140**. Multi-ancestry genome-wide association study in >2.5 million individuals reveals distinct biological pathways driving type 2 diabetes susceptibility with heterogeneous effects across diverse population groups: *Eleftheria Zeggini, Germany*
16:30 - 16:45		**OP099**. Spliceosome malfunction causes neurodevelopmental disorders with autistic features: *Dong Li USA*	**OP105**. Genetic diversity in immune receptor genes in African populations: *Yasmina Jaufeerally-Fakim, Mauritius*	**OP111**. Genetic, molecular and mouse model investigations of broad neurodevelopmental impact of deleterious variants of the TREX mRNA export complex subunits: *Jozef Gecz, Australua*	**OP117**. Consanguinity and rare recessive variants involved in multifactorial traits in non-European descent individuals from UK Biobank: *Anne-louise Leutenegger, France*	**OP123**. Subcontinental admixture in Europeans and European Americans: Implications for genetic epidemiology studies: *Amy Bently OBO Mateus Gouveia, USA*	**OP129**. Characterisation of pharmacogene haplotype variation in African populations: *David Twesigomwe, South Africa*	**OP135**. A meta-analysis algorithm called Meta-Analysis by Information Content algorithm is used to prioritise SNPs associated with susceptibility to COVID-19: *Bo Wang, UK*	**OP141**. Genetics of metabolic dysfunction through lenses of insulin resistance using GWIS: *Inga Prokopenko OBO Liudmila Zudina, UK*
16:45 - 17:00		**OP100**. DHX9, the gene encoding the DExH-box helicase DHX9, underlies neurodevelopmental disorders and Charcot-Marie-Tooth disease: *Daniel Calame, USA*	**OP106**. Structure and origin of genetic diversity in Tuvans revealed by genome-wide SNPs and Y-chromosomal haplogroups: *Vadim Stepanov, Russian Federation*	**OP112**. Selection acting on somatic structural variation in blood impacts molecular function and cancer risk among humans: *Kimberly Skead, Canada*	**OP118**. Adaptation and Implementation of Cancer Genetics Testing and Counseling in Africa: *Achille Van Christ Manirakiza, Rwanda*	**OP124**. Indigenous American ancestry composition of reference panel causes different imputation performance in two distinct Latin American cohorts: *Jennifer French-Kwawu, UK*	**OP130**. Pharmacogenomics of Warfarin: Black Africans Portray Unique Profiles Important for an African-Specific Dosing Algorithm: *Arinao Ndadza, South Africa*	**OP136**. Elucidating a molecular mechanism linking infectious disease exposure and psychosis using multi-omic schizophrenia datasets: *Conrad Iyegbe, USA*	**OP142**. Integrating transcriptomics and methylomics with genome wide association analyses reveal novel insights into obesity in Africans: *Guanjie Chen, USA*

17:00 - 17:15		**OP101**. Genomic characteristics of Rett syndrome modifier genes: *Alana Slike, Canada*	**OP107**. Genome-wide association study identifies novel candidate malaria resistance genes in Cameroon: *Kevin Esoh, South Africa*	**OP113**. Monogenic causes of Premature Ovarian Insufficiency are likely rare and mostly recessive: *Saleh Shekari, UK*	**OP119**. Feedback of individual research results in neurodevelopmental disorders in South-Africa: Challenges encountered when bridging the research-diagnostic gap: *Zandre Bruwer, South Africa*	**OP125**. The effect of family history and polygenic risk scores on obesity in the Lifelines Cohort Study: *Rujia Wang, Netherlands*	**OP131**. GSTM1 and GSTP1 polymorphisms as pharmacogenetic markers for relapse and peripheral neuropathy among African cervical cancer patients on cisplatin treatment: *Oppah Kuguyo, Zimbabwe*	**OP137**. Tuberculosis (TB) surveillance in wastewater using the metatranscriptomic approach: *Hlengiwe Nombuso Mtetwa, South Africa*	**OP143**. Anthropometric and cardiometabolic traits in Southern African populations are strongly impacted by Khoe-San ancestry and its interaction with lifestyle factors: *Dhriti Sengupta, South Africa*
17:15 - 17:30		**OP102**. Identification of episignatures in overgrowth disorders with intellectual disability: A novel approach for genomic diagnostic confirmation: *Jair Antonio Tenorio Castaño, Spain*	**OP108**. Characterizing mosaic chromosomal alterations in an African cohort: *Jonathan Evans, South Africa*	**OP114**. Combating Obesity by Modulating Lipid Accumulation: In Search of Novel Molecular Regulators of Adipogenesis: *Melvin Ambele, South Africa*	**OP120**. Shingles infection and recurrent miscarriage – using genetics to dissect shared genetic susceptibility and causal relationships: *Yevheniya Sharhorodska, Ukraine*	**OP126**. African-specific genetic loci determine iron status in African children: *John Muriuki, Kenya*	**OP132**. Ex vivo studies of a rare TP53 germline variant (NM_001126114.2, c.1018A>G, p.N340D): Peripheral blood mononuclear cells completely resist cell death induced by the anthracycline, doxorubicin: *Claudia Christowitz, South Africa*	**OP138**. The dark side of short-read whole genome sequencing: exploring camouflaged gene regions in African genomes: *Melissa Nel, South Africa*	**OP144**. Discovery and fine-mapping of kidney function loci in 80 000 African ancestry individuals: *Christopher Kintu, Uganda*
18h30 - 22h30	**Conference Dinner at GOLD Restaurant (A true African experience)** Ticketed event: R1,150 per person Limited to 350 places								

Sunday, 26 February 2023

07:30 - 17:00	**Registration open** (entrance to Hall 1, Ground Level)								
09:00 - 16:00	**Exhibition open** (Hall 1 & 2, Ground Level)								
07:30 - 08:45									
09:00 - 10:30	**Plenary 4 - The future of genetics and genomics** Chairs: Ambroise Wonkam and Adebowale Adeyemo (TBC) Venue: Ballroom, Level 1								
09:00 - 09:45	"Interpreting Genomic Variation in Cancer " - Mathieu Lupien, Canada								
09:45 - 10:30	"The Next Frontier in Personal Genomics" - Eric Topol, USA (pre-recorded)								
10:30 - 11:00	**Tea / Coffee Break**								
11:00 - 12:30	**INVITED SESSIONS**	**Session 25 - International Genetic Epidemiology Society: Genomics for Global Precision Medicine** Chair: Eleftheria Zeggini, Germany (Venue: Meeting Block 2,6 Level 2)	**Session 26 - Global Globin Network (GGN): (Public Health Issues in Haemoglobinopathies)** Chair: Ghada El-Kamah, Egypt (Venue: Meeting Block 1,61 - 1,62, Level 1)	**Session 27 - Resolving Unresolved Neurodevelopmental Disabilities** Chairs: Jozef Gecz, Australia & Heather Mefford, USA **(Venue: Meeting Block 1.41 - 1,42 Level 1)**	**Session 28 - Southern African Population Structure, Admixture and Adaptation** **Chair: Carina Schlebusch, Sweden** **(Venue: Meeting Block 143 - 1,44 Level 1)**	**Session 29 - Polygenic Risk Scores In Practice: Laboratory, Clinical, And Ethical Perspectives** Chair: Jason Vassy, USA (Venue: Ballroom East, Level 1)	**Session 30 -Precision Molecular Cytogenetics: A Time to Sequence** Chair: Richard Kwong Wai Choy, China (Venue: Meeting Block 2.41 - 2,43, Level 2)	**Session 31: Showcasing H3Africa research** Chair: Zane Lombard, South Africa (Venue: Meeting Block 2.44 - 2.46, Level 2)	**Session 32 - Privacy, consent and data sharing in the international genetics community** Chairs: Francesca Forzano, UK & Kelly Ormond, Switzerland/USA (Venue: Meeting Block 1,63 - 1,64, Level 1)
		Genomics of Metabolic Disease in Diverse Populations: Inês Barroso, UK	Genetic diversity of thalassaemia in Southeast Asia: Ezalia Esa, Malaysia	Current day clinical genetics in neurodevelopmental disorderss: Tjitske Kleefstra, Netherlands.	The Complexity of Population Movements and Admixture Patterns during the Bantu Expansion: Sandra Beleza, UK	Polygenic Risk Scores in the Clinical Laboratory: Matthew Lebo, USA (pre-recorded)	Mate-Pair Sequencing and the Road towards Comprehensive Identification and Interpretation of Pathogenic Structural Variation: Cynthia C Morton, USA	Intergenerational and epigenetic effects of trauma and PTSD following exposure to the 1994 genocide against the Tutsi in Rwanda: Leon Mutesa, Rwanda	Genomic data sharing in Africa with perspectives from H3Africa and the South African Protection of Personal Information Act: Michele Ramsay, South Africa
		Polygenic risk scores across diverse populations: Alisa Manning, USA	Modern therapeutics approaches in Beta Thalassemia: Ghada El-Kamah, Egypt	DNA Methylation Episignatures as Clinical Diagnostic Biomarkers for Rare Diseases: Bekim Sadikovic, Canada	Khoisan Gene Flow in Southern Africa and Implications for Genetic Studies: Ananyo Choudhury, South Africa	Polygenic Risk Scores in Medical Practice: Jason Vassy, USA	Implementation Of Genome Sequencing: Experience in a Genetic Diagnostic Laboratory: Zirui (Elvis) Dong, China (pre recorded)	Neurogenetics study in Mali: new discoveries and perspectives: Guida Landoure, Mali	The Brazilian Initiative on Precision Medicine (BIPMed): experiences on sharing genomic information in Brazil and Latin America for the past seven years: Iscia Lopes-Cendes, Brazil
		Using Genomics for the Treatment and Prevention of Breast Cancer: Olufunmilayo Olopade, USA	Human Genetics and Health: Gene Therapy for Sickle Cell Disease in Africa: Julie Makani, Tanzania (pre-recorded)	Rare and Common Variant Contributions to NDD: Hilary Martin, UK	The Evolution of Skin Pigmentation in Southern Africa: Dana Al-Hindi, USA	Ethical Considerations of Polygenic Risk Scores in the Clinic: Anna C.F. Lewis, USA	Diagnostic Management of Apparently Balanced Structural Variants: Matthew Chau.USA	Ten years of AWI-Gen: insights from genomic studies and the way forward: Dhriti Sengupta, South Africa	Research and Policy initiatives in Australia regarding genomic data sharing: Ainsley Newson, Australia
									Round Table discussion
12:30 - 13:30	**Closing Ceremony** Chairs: Chrales Rotimi, Raj Ramesar and Michele Ramsay (Venue: Ballroom, Level 1) - Awards - Best Oral - Awards - Best Poster - Awards - Lifetime Achievement - Handover to next host country and the next President of the IFHGS								