



Advances in Genome Biology and Technology
2024 General Meeting
Orlando, Florida

Sunday, Feb. 4, 2024

1:00 p.m. - 8:00 p.m. Transfers from Orlando International Airport (MCO)

12:00 p.m. - 8:00 p.m. **Meeting Registration / Hospitality Desk**
Palms Registration

Monday, Feb. 5, 2024

7:00 a.m. - 4:00 p.m. Transfers from Orlando International Airport (MCO)

8:00 a.m. - 8:00 p.m. **Meeting Registration / Hospitality Desk**
Palms Registration

Scientific Program

Plenary Session: **Genomics I (Eric Green, National Human Genome Research Institute, Chair)**
Palms Ballroom II & III

5:00 p.m. - 5:10 p.m. **Opening Remarks**

5:10 p.m. - 5:40 p.m. **Stephanie Hicks, Johns Hopkins**
"Scalable computational methods and software for single-cell and spatial data science"

5:40 p.m. - 6:10 p.m. **Anshul Kundaje, Stanford University**
"Debugging, denoising, debiasing and interpreting the causal sequence syntax of regulatory profiling experiments with efficient deep learning models"

6:10 p.m. - 6:40 p.m. **Angela Brooks, University of California, Santa Cruz**
"Systematic assessment of long-read RNA-seq methods for transcript identification"

6:40 p.m. - 7:00 p.m. **Sadie VanHorn, (Abstract Selected) Washington University, St. Louis**
"High-resolution single-cell lineage tracing at scale reveals reprogramming dynamics"

7:00 p.m. - 10:00 p.m. **Welcome Reception**

Poolside

Tuesday, Feb. 6, 2024

(Morning)

7:30 a.m. - 9:00 a.m.

Breakfast
The Grove

7:30 a.m. - 9:30 p.m.

Meeting Registration / Hospitality Desk
Palms Registration

Plenary Session:

Evolutionary Genomics (Beth Shapiro, University of California, Santa Cruz, Chair)
Palms Ballroom II & III

9:00 a.m. - 9:30 a.m.

Kirsten Bos, Max Planck Institute
"Genomic reconstructions of ancient pathogens"

9:30 a.m. - 10:00 a.m.

Bridgett vonHoldt, Princeton University
"Ghost wolves: Reviving an endangered canid species"

10:00 a.m. - 10:30 a.m.

Sean Eddy, Harvard University
"Computational analysis of RNA structure and function"

10:30 a.m. - 11:00 a.m.

Coffee Break
Sponsor Promenade

11:05 a.m. - 11:25 a.m.

Julian Hess, (Abstract Selected) Broad Institute of MIT and Harvard
"High accuracy somatic variant calling on Ultima Genomics facilitates detailed phylogenetic reconstruction across 303 metastatic tumor samples"

11:25 a.m. - 11:45 a.m.

Poster Flash Talks

Tuesday, Feb. 6, 2024

(Afternoon)

12:00 p.m. - 1:30 p.m.

Gold Sponsor Workshop & Lunch – Ultima Genomics
Grand Sierra Ballroom D & E
Gilad Almogy, Ph.D., Chief Executive Officer, Ultima Genomics
Mirna Jarosz, Ph.D., Head of Product, Ultima Genomics
Stacey Gabriel, Ph.D., Executive Vice President of Platforms and Scientific Execution, Institute Scientist, Broad Institute of MIT and Harvard
Aziz Al'Khafaji, Ph.D., Associate Director, Technology Development - Genomics Platform, Broad Institute of MIT and Harvard
Dan Landau, M.D., Ph.D., Professor of Physiology and Biophysics, Weill Cornell Medical College
Rahul Satija, D.Phil., Core Faculty Member, New York Genome Center
Will Salerno, Ph.D., Executive Director of Genome Informatics & Data Engineering, Regeneron Pharmaceuticals

"Genomics unleashed: the \$100 genome and beyond"

12:00 p.m. - 1:30 p.m.	AGBT Lunch The Grove
1:30 p.m. - 3:30 p.m.	Poster Session with Coffee & Dessert Palms Ballroom I
Plenary Session:	Biology (Penelope Bonnen, Baylor College of Medicine, Chair) Palms Ballroom II & III
3:30 p.m. - 4:00 p.m.	Mark Blaxter, Wellcome Sanger Institute “Sequence locally, think globally: biodiversity genomics across the tree of life”
4:00 p.m. - 4:20 p.m.	Sarah Bates, (Abstract Selected) National Human Genome Research Institute/NIH “The power and importance of inclusive, fact-driven communications in human genomics”
4:20 p.m. - 4:40 p.m.	Jiwoon Park, (Abstract Selected) Weill Cornell Medicine “The Spatial Atlas of Human Anatomy (SAHA) project: unveiling cellular landscapes and orchestrating a new paradigm in precision medicine”
4:40 p.m. - 5:00 p.m.	Meredith Wright, (Abstract Selected) Rady Children’s Institute for Genomic Medicine “Leveraging population databases and machine learning models to scale whole genome newborn sequencing”
Tuesday, Feb. 6, 2024	(Evening)
5:15 p.m. - 7:15 p.m.	Dinner On Your Own
5:15 p.m - 7:15 p.m.	Women’s Networking Event-Featuring Astronaut Kathleen “Kate” Rubins Sun Deck
Concurrent Session:	
7:30 p.m. - 9:30 p.m.	Cancer (John McPherson, University of California, Davis, Chair) Grand Sierra Ballroom D & E
7:30 p.m. - 7:50 p.m.	Ruli Gao, Northwestern University “Studying isoforms and adaptive evolution of brain metastasis with long read single cell RNA sequencing”
7:50 p.m. - 8:10 p.m.	Cynthia Lawley, Olink “Next gen proteomics combined with genomics identifies potential therapeutic targets for breast cancer”
8:10 p.m. - 8:30 p.m.	Jessica Nordlund, SciLifeLab, Uppsala University “Mapping ex vivo drug responses in single cells”

- 8:30 p.m. - 8:50 p.m. **Brian Haas, Broad Institute, Methods Development Laboratory**
 “High Accuracy Fusion Transcript Detection from Long-Read Isoform Sequencing using CTAT-LR-Fusion”
- 8:50 p.m. - 9:10 p.m. **Holger Heyn, Centro Nacional de Análisis Genómico (CNAG)**
 “Spatio-temporal dissection of colorectal cancer initiation using whole transcriptome imaging”
- 9:10 p.m. - 9:30 p.m. **Hanghui Ye, The University of Texas MD Anderson Cancer Center**
 “A pan-cancer single-cell analysis of intratumoral copy number diversity and evolution”

Concurrent Session:

- 7:30 p.m. - 9:30 p.m. **Computational Biology (Mike Zody, New York Genome Center, Chair)**
 Palms Ballroom II & III
- 7:30 p.m. - 7:50 p.m. **Ana Conesa, Spanish National Research Council**
 “Quantifying isoform expression and transcriptome complexity by high-throughput single-molecule sequencing”
- 7:50 p.m. - 8:10 p.m. **Javan Okendo, National Institute of Health**
 “Telomere-to-telomere genome assemblies for commonly used zebrafish lab strains”
- 8:10 p.m. - 8:30 p.m. **Maria Sierra, Weill Cornell Medicine**
 “Detection of human herpesviruses in Alzheimer's brains and implications for neurodegenerative diseases”
- 8:30 p.m. - 8:50 p.m. **Yueyao Gao, Broad Institute of MIT and Harvard**
 “T2T-ACE: A novel approach for accurate CNV evaluation using Telomere-to-Telomere assemblies”
- 8:50 p.m. - 9:10 p.m. **Alexander Hoischen, Radboud University Medical Center**
 “Assessing HiFi genome sequencing as first-tier test in rare disease genetics”
- 9:10 p.m. - 9:30 p.m. **Koen van Gassen, University Medical Center, Utrecht**
 “Replacing karyotyping and FISH with Hi-C chromosome conformation capture”
- Starting at 9:30 p.m. **Sponsor’s Social (Connect, Collaborate, and Chill)**
 Sponsor Promenade

Wednesday, Feb. 7, 2024 (Morning)

- 7:30 a.m. - 9:00 a.m. **Breakfast**
 The Grove
- 7:30 a.m. - 8:00 p.m. **Hospitality Desk**
 Palms Registration

Plenary Session:	Genetics (Stephen Montgomery, Stanford University School of Medicine, Chair) Palms Ballroom II & III
9:00 a.m. - 9:30 a.m.	Melissa Boneta Davis, Weill Cornell Medicine "Ancestry in genomics of cancer disparities"
9:30 a.m. - 10:00 a.m.	Melina Claussnitzer, Broad Institute, Massachusetts General Hospital, Harvard Medical School "From metabolic disease maps to mechanism to medicines"
10:00 a.m. - 10:30 a.m.	Federica Di Palma, Genome British Columbia "Harnessing responsible genomics for biodiversity: Protecting Colombia's natural wealth"
10:30 a.m. - 11:00 a.m.	Coffee Break Sponsor Promenade
11:00 a.m. - 11:20 a.m.	Konrad Karczewski, (Abstract Selected) Massachusetts General Hospital "All by All of Us: common and rare variant association testing in 250,000 whole genomes across diverse ancestry groups"
11:20 a.m. - 11:40 a.m.	Next Gen Leadership Awards (Eric Green, NHGRI, Elinor Karlsson, Broad Institute, MIT and Harvard, Beth Shapiro, University California, Santa Cruz, Co-Chairs)
Wednesday, Feb. 7, 2024	(Afternoon)
12:00 p.m. - 2:15 p.m.	Silver Sponsor Workshops and Lunch Grand Sierra Ballroom D & E
12:05 p.m. - 1:05 p.m.	Silver 1 Sponsor Workshop and Lunch – Element Biosciences Molly He, Element Biosciences "ABC and AVITI: Opening a gateway to the next evolution of sequencing"
1:10 p.m. - 2:10 p.m.	Silver 2 Sponsor Workshop and Lunch – 10X Genomics Sarah Taylor, Ben Hindson, Mike Schnall-Levin and Patrick Marks "Mind blowing science enabled by industry-leading single cell & spatial technologies"
12:00 p.m. - 2:10 p.m.	AGBT Lunch The Grove
2:15 p.m. - 4:44 p.m.	Bronze Sponsor Workshops (Kim Doheny, Johns Hopkins University, Chair) Palms Ballroom II & III
2:20 p.m. - 2:40 p.m.	Bronze 1 Sponsor - Scale BioSciences Giovanna Prout, CEO

- "The single cell era, scaled"
- 2:40 p.m. - 3:00 p.m. **Bronze 2 Sponsor - BioSkryb Genomics**
Jay West
"The next generation of single-cell technology – resolve more with BioSkryb"
- 3:00 p.m. - 3:20 p.m. **Bronze 3 Sponsor - Twist Bioscience**
Emily Leproust, Ph.D. CEO & co-founder of Twist Bioscience
"Unveiling next-gen solutions for precision diagnostics and beyond"
- 3:20 p.m. - 3:35 p.m. **Bronze 4 Sponsor - New England Biolabs**
Keerthana Krishnan, Ph.D., Development Group Leader, Next Generation Sequencing
"NEBNext product development: streamlining workflows and addressing new applications"
- 3:35 p.m. - 3:50 p.m. **Bronze 5 Sponsor - NanoString**
Joseph Beechem, Ph.D, Chief Scientific Officer and Senior Vice President of Research and Development, NanoString
"NanoString spatial biology roadmap: the holy grail of spatial is here"
- 3:50 p.m. - 4:05 p.m. **Bronze 6 Sponsor - Singular Genomics**
Eli Glezer PhD, CSO and Co-Founder
"In-situ sequencing: enabling spatial biology at scale"
- 4:05 p.m. - 4:20 p.m. **Bronze 7 Sponsor - Watchmaker Genomics**
Travis Sanders
"Flipping the script on DNA methylation sequencing: A positive readout to enable multimodal analyses"
- 4:20 p.m. - 4:32 p.m. **Bronze 8 Sponsor – PacBio**
Isabelle Thiffault, MSc, PhD, FACMGG, FABMGG. Director of Translational Genetics - Clinical Lab. Genomic Medicine Center, Children's Mercy Research Institute, Children's Mercy Hospitals and Clinics
"Empowering precision medicine research: the potential paradigm shift of HiFi genome sequencing in first-line clinical tests"
- 4:32 p.m. - 4:44 p.m. **Bronze 9 Sponsor - N6**
Dr. Pranav Patel, PhD (USF Health)
"iconPCR: A universal method for up to a 99% improvement in NGS library prep workflows and sequencing quality"
- 4:45 p.m. - 6:10 p.m. **Poster Session and Wine & Cheese Reception**
Palms I Ballroom
- Wednesday, Feb. 7, 2024 (Evening)**
- 6:10 p.m. - 7:25 p.m. **AGBT Dinner**
The Grove

- 7:30 p.m. - 9:30 p.m. **Concurrent Session: Technology (Elinor Karlsson, Broad Institute of MIT and Harvard, Chair)**
Palms II & III
- 7:30 p.m. - 7:50 p.m. **Dawn Chen, Broad Institute of MIT and Harvard**
“Long-range continuous mutagenesis of endogenous genomes”
- 7:50 p.m. - 8:10 p.m. **Andrew Adey, Oregon Health & Science University**
“Atlas-scale single-cell DNA methylation”
- 8:10 p.m. - 8:30 p.m. **Elizabeth Neuman, University of California, Davis**
“Using MS based ISH Approaches to understand gene expression and its relation to metabolomics”
- 8:30 p.m. - 8:50 p.m. **Hadas Keren Shaul, Weizmann Institute of Science**
“Genomics sandbox: a playground for genomics research and science innovation”
- 8:50 p.m. - 9:10 p.m. **Joshua Levin, Broad Institute of MIT and Harvard**
“Development of experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data”
- 9:10 p.m. - 9:30 p.m. **Huan Wang, Broad Institute of MIT and Harvard**
“Systematic benchmarking of imaging spatial transcriptomics platforms in Formalin-Fixed Paraffin-Embedded samples across healthy and cancerous tissues”
- 7:30 p.m. - 9:30 p.m. **Concurrent Session: Biology (Federica Di Palma, Genome British Columbia, Chair)**
Grand Sierra Ballroom D & E
- 7:30 p.m. - 7:50 p.m. **Massimo DelleDonne, University of Verona**
“Adaptive gene loss shapes the evolution of the *Phaseolus vulgaris* pan-genome during species range expansion and dual domestications”
- 7:50 p.m. - 8:10 p.m. **Darrell Dinwiddie, University of New Mexico HSC**
“Sequencing of museum biospecimens for the discovery and genomic characterization of orthohantaviruses”
- 8:10 p.m. - 8:30 p.m. **Shruti Iyer, Cold Spring Harbor Laboratory**
“Using targeted long-read sequencing to identify genetic and epigenetic changes across different stages of colorectal cancer”
- 8:30 p.m. - 8:50 p.m. **Brenda Murdoch, University of Idaho**
“Centromere content and organization in cattle and sheep Y chromosomes are considerably different than in the human Y chromosome”
- 8:50 p.m. - 9:10 p.m. **Miranda Orr, Wake Forest University School of Medicine**
“Ultra-high plex single-cell spatial multi-omic imaging of tau neuropathology in human brain sections”
- 9:10 p.m. - 9:30 p.m. **Alexander Urban, Stanford University**

“Machine learning analysis of deep whole-genome sequencing data in a large cohort of human brains reveals common presence of somatic, mosaic LINE-1 insertions”

Thursday, Feb 8, 2024

(Morning)

7:30 a.m. - 9:00 a.m.

Breakfast
The Grove

7:30 a.m. - 6:00 p.m.

Hospitality Desk
Palms Registration

Plenary Session:

Genomics II (Stacey Gabriel, Broad Institute of MIT and Harvard, Chair)
Palms Ballroom II & III

9:00 a.m. - 9:30 a.m.

Kristin Laidre, University of Washington
"A new population of the world's largest land carnivore and why it matters"

9:30 a.m. - 10:00 a.m.

Michael Schatz, Johns Hopkins University
"BioDIGS: bioDiversity and informatics for genomics scholars"

10:00 a.m. - 10:20 a.m.

Yichen Si, (Abstract Selected) University of Michigan
“FIGURE: Segmentation-free factor analysis for sub-micron resolution spatial transcriptomics”

10:20 a.m. - 11:00 a.m.

Coffee Break
Sponsor Promenade

11:05 a.m. - 11:25 a.m.

Thomas Gingeras, (Abstract Selected) Cold Spring Harbor Laboratory
“The EN-TEEx resource of multi-tissue personal epigenomes & variant-impact models”

11:25 a.m. - 11:45 a.m.

Sek Won Kong, (Abstract Selected) Boston Children’s Hospital
“Discordance between a deep learning model and clinical-grade variant pathogenicity classification in a rare disease cohort”

12:00 p.m. - 1:00 p.m.

Silver 3 Sponsor Workshop & Lunch – Complete Genomics
Grand Sierra Ballroom D & E

Rade Drmanac, Ph.D., Chief Scientific Officer, Complete Genomics

"Advancing sequencing capacities: exploring DNBSEQ™ technology and complete WGS"

Christopher E. Mason, Ph.D., Professor, Department of Physiology and Biophysics, Weill Cornell Medicine

"Spatial oncology maps and space biology maps"

Ioannis Ragoussis, Ph.D., Professor, Department of Human Genetics - Head of Genome Sciences, McGill Genome Centre

"A cost-effective whole genome sequencing method identifies clinically relevant germline variants in patients recruited in a breast cancer clinic"

12:00 p.m. - 1:30 p.m.

AGBT Lunch
The Grove

Thursday, Feb. 8, 2024

(Afternoon)

Plenary Session:

Technology (Chris Mason, Weill Cornell Medicine, Chair)
Palms Ballroom II & III

1:30 p.m. - 2:00 p.m.

Kathleen Rubins, NASA

2:00 p.m. - 2:20 p.m.

Jagadish Sankaran, (Abstract Selected) Genome Institute of Singapore

"Holistic identification of morphogenomic phenotypes using morphology and expression data optimal clustering (MEDOC)"

2:20 p.m. - 2:40 p.m.

Xin Jin, (Abstract Selected) Scripps Research

"Massively parallel in vivo Perturb-seq reveals cell type-specific transcriptional networks in cortical development"

2:40 p.m. - 3:00 p.m.

Billy Lau, (Abstract Selected) Stanford University

"Joint single-molecule fragmentomic and methylation signatures of cell-free DNA for multi-omic cancer detection using nanopore sequencing"

3:00 p.m. - 3:20 p.m.

Dennis Yuan, (Abstract Selected) New York Genome Center

"High-throughput miniaturized-automated workflow for joint high-depth whole genome and whole transcriptome sequencing of thousands of human primary cells"

3:20 p.m. - 3:40 p.m.

Daniel Turner, (Abstract Selected) Enhanc3D Genomics

"Interrogating 3-dimensional genomic architecture to reveal novel disease biology"

3:40 p.m. - 4:00 p.m.

Closing Comments, Meeting Feedback and AGBT '25 Anniversary Announcement

7:00 p.m. - Midnight

Farewell Dinner – Mardi Gras
The Grove

