

Pacific time

**08:00 – 08:15 Welcome & Overview**

Ting Wang (Washington University School of Medicine, USA)

*Why A Pangenome?*

David Haussler (UC Santa Cruz Genomics Institute, USA)

**08:15 – 08:55 Data Production & Technology***HPRC Data Production Center: Progress Report and Future Deliverables*

Karen Miga (UC Santa Cruz Genomics Institute, USA)

*Production & Technology Techniques, Developments, & Standards Towards High-Quality Reference Genomes*

Bob Fulton (Washington University School of Medicine, USA)

**08:55 – 09:40 Data Analysis & Pangenomes***Current State Of GRCh38, The Linear Reference Assembly*

Valerie Schneider (NCBI/NLM/NIH, USA)

*The HPRC Genome Assembly Bakeoff: Evaluating & Comparing State-Of-The-Art Assembly Strategies*

Kerstin Howe (Wellcome Sanger Institute, UK) &amp;

Erich Jarvis (The Rockefeller University, USA)

**09:40 – 10:00 Short break****10:00 – 10:45 Genome Representation Presentations***Pangenomics With VG*

Benedict Paten (UC Santa Cruz, USA)

*Pangenome tools*i. *K-Mer Analytics For Annotation Of Pangenome Features*

Hanlee Ji (Stanford University, USA)

ii. *Characterizing Variable-Number Tandem Repeats With Repeat-Pangenome Graphs*

Mark Chaisson (University of Southern California, USA)

iii. *The Construction & Utility Of Pangenome Graphs*

Heng Li (DFCI, USA)

**10:50 – 11:10 Panel Discussion****11:10 – 11:30 Short break**

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**11:30 – 12:00****Samples & Representation***Shaping A Policy To Inform Engagement & Outreach In HPRC*  
Eimear Kenny (Icahn School of Medicine at Mount Sinai, USA)*Establishment Of The Human Pangenome Cell Bank*  
Alissa Resch (Coriell Institute, USA)*Representing Human Diversity In The Reference Genome: Good Science Demands An “Embedded Ethics” Approach*  
Barbara Koenig (UC San Francisco, USA)**12:05 – 12:25****Panel Discussion****12:25 – 12:45****Short break****12:45 – 13:15****Future Perspectives***The Importance Of Expanding Human Diversity*  
Evan Eichler (University of Washington & HHMI, USA)*The HPRC Freeze1 Resource, & Beyond*  
Ira Hall (Yale University, USA)*Dissemination & Adoption Of The Pangenome Reference*  
Paul Flicek (EMBL-EBI, UK)**13:20 – 14:00****Meeting Recap***Brainstorming & Open Scientific Discussion With NHGRI, SAB, & HPRC Leaders*Karen Miga (UC Santa Cruz Genomics Institute, USA) &  
Ting Wang (Washington University School of Medicine, USA)**14:05 – 14:35****Breakout***Breakout 1: SAB/NHGRI Private Discussion**Breakout 2: Networking & Activity***14:40 – 15:05****SAB Comments****15:05 – 15:15****Wrap up & Close**

Ting Wang (Washington University School of Medicine, USA)

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**08:00 – 08:20 Welcome & Opening remarks**

Karen Miga (UC Santa Cruz Genomics Institute, USA)

*A 2020 Strategic Vision For Improving Human Health  
At The Forefront Of Genomics*

Eric Green (NHGRI, USA)

**08:20 – 08:45 Keynote Address***The Human Genome: Finishing The Job*

Robert H. Waterston (University of Washington, USA)

**08:50 – 09:15 Keynote Address***Finishing The Complete Sequence Of A Human Genome*

Adam Phillippy (NHGRI, USA)

**09:15 – 09:35 Short break****09:35 – 10:55 Sequence Technology & Innovation***High-Fidelity Long Reads, Can You Have Your Cake & Eat It Too?*

Sergey Koren (NIH/NHGRI, USA)

*Leveraging PacBio HiFi & ONT Data To Resolve**Entire Human Chromosomes*

Glenn Logsdon (University of Washington, USA)

*Custom Assembly Pipeline For CHM13 T2T Reconstruction*

Sergey Nurk (NIH/NHGRI, USA)

*Resolving Large Segmental Duplications With HiFi & Ultralong ONT Reads*

Mikko Rautiainen (Max-Planck-Institut für Informatik, Germany)

**11:00 – 11:30 GRCh38: Looking Forward To The Human Pan-Genome**

Valerie Schneider (NCBI/NLM/NIH, USA)

&amp; Tina Graves-Lindsay (Washington University School of Medicine, USA)

**11:35 – 11:55 Short break****11:55 – 12:55 Finishing & Assembly Quality Assessment***Chasing Perfection: Validating & Improving A**Telomere-To-Telomere Assembly*

Arang Rhie (NIH, USA)

*Assembling & Analyzing Centromeres*

Pavel Pevzner (UC San Diego, USA)

*T2T-Variants: How The T2T Assembly Can Help Call Variants**In Hard To Measure Regions*

Justin Zook (National Institute of Standards &amp; Technology, USA)

**13:00 – 13:20 Short break**

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**13:20 – 14:40 New Insights Into Genome Biology & Structure***A Complete View Of Segmental Duplications & Their Evolution*

Mitchell R. Vollger (University of Washington, USA)

*Genetic & Epigenetic Maps Of Human Centromeric Regions*

Karen Miga (UC Santa Cruz Genomics Institute, USA)

*Gene Annotation Of The T2T Assembly*

Mark Diekhans (UC Santa Cruz, USA)

*Into The Unknown: Epigenetics Of Repetitive DNA*

Ariel Gershman (Johns Hopkins University, USA)

**14:45 – 15:05 Short break****15:05 – 15:50 The Future Of T2T Genomics***The Vertebrate Genomes Project: Producing High-Quality Genomes**Of All Vertebrate Species For A New Age Of Biology*

Erich Jarvis (The Rockefeller University, USA)

*The Future: HPRC Diploid T2T Assemblies*

Evan Eichler (University of Washington &amp; HHMI, USA)

**15:50 – 16:00 Wrap Up & Close**

Karen Miga (UC Santa Cruz Genomics Institute, USA) &amp;

Adam Phillippy (NIH/NHGRI, USA)

**16:00 – 17:00 Posters & Lightning Talks**

TOWARDS A  
COMPLETE  
REFERENCE OF  
HUMAN GENOME  
DIVERSITY



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**08:00 – 08:10 Welcome & Opening Remarks**

Ting Wang (Washington University School of Medicine, USA) & Adam Felsenfeld (NIH/NHGRI, USA)

**08:10 – 08:35 HGP Historical Perspective**

*A Genome Story*  
David Haussler (UC Santa Cruz Genomics Institute, USA)

**08:35 – 09:00 Keynote Address**

*The Transformative Impact Of The H3Africa Initiative Across Africa & Globally*  
Charles N. Rotimi (NIH, USA)

**09:05 – 09:25 Short break**

**09:25 – 10:45 Sample Representation & Diversity**

*Population Sampling & Representation For The Human Pangenome Reference Consortium*

Eimear Kenny (Icahn School of Medicine at Mount Sinai, USA)

*Lifelong Relations: Community Engagement & Representation In Genomic Research*

Katrina Claw (University of Colorado, USA)

*Australian National Centre for Indigenous Genomics*

Simon Easteal (Australian National University, Australia)

*Expanding Sequencing, Phenotyping, Interpretation, & Biobanking At The Personal Genome Project*

Alexander (Sasha) Wait Zaranek (Curii Corporation, USA)

**10:50 – 11:10 Upgrading The Human Reference Genome: Where Does Ethics Fit In?**

Barbara Koenig (UC San Francisco, USA), Erich Jarvis (The Rockefeller University, USA) & Charles N. Rotimi (NIH, USA)

**11:15 – 11:35 Short break**

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**11:35 – 12:35 Genome Technology & Production**

*How To Make Great Assemblies Even Better*  
Kerstin Howe (Wellcome Sanger Institute, UK)

*Production & Technology Techniques, Developments, & Standards Towards High-Quality Reference Genomes*

Bob Fulton (Washington University School of Medicine, USA)

*Streamlining Accessibility & Computability Of Large-Scale Genomic Datasets With The NHGRI Genome Data Science Analysis, Visualization, & Informatics Lab-Space (AnVIL)*

Michael Schatz (Johns Hopkins University, USA)

**12:40 – 13:00 Short break**

**13:00 – 14:45 Graph Genomes & Variant Calling**

*Update From The Human Genome Structural Variation Consortium (HGSVC)*  
Jan Korbel (EMBL-Heidelberg, Germany)

*The Human Pangenome Resource: HPRC Freeze1*

Ira Hall (Yale University, USA)

*The Construction & Utility Of Pangenome Graphs*

Heng Li (DFCI, USA)

*Personalized & Graph Genomes Reveal Missing Signal In Epigenomic Data*

Guillaume Bourque (McGill University, Canada)

*Expanding Variant Studies To Hard To Measure Regions Of The Genome*

Karen Miga (UC Santa Cruz Genomics Institute, USA)

**14:45 – 14:50 Wrap Up & Close**

Ting Wang (Washington University School of Medicine, USA)

**14:50 – 15:50 Posters & Lightning Talks**