The 16th International Meeting on Human Genome Variation and Complex Genome Analysis (HGV2015)

November 11-13, 2015
Mission Bay Conference Center, San Francisco, California, USA

PROGRAM

Wednesday, November 11, 2015

12:00 – 1:00	**Registration**	**Fisher Atrium Foyer – 1st Floor**
1:00 – 1:15	**Welcome and Overview**	**Robertson Auditorium – 2nd Floor**
1:15 – 3:15	**Session 1 – Chair: Ada Hamosh "Are We There Yet? Be Patient With Genomics"**	**Robertson Auditorium – 2nd Floor**
1:15 – 1:40	Lessons learned from implementing clinical exome sequencing in the care of childhood cancer patients.	**Sharon Plon**, MD, PhD, Baylor College of Medicine
1:40 – 2:05	The Effect of Variant Representation and Annotation on Clinical Interpretation.	**Sarah Garcia**, PhD, Personalis, Inc.
2:05 – 2:30	Challenges and opportunities in applying molecular genetic testing to diagnosis and prevention.	**Robert Nussbaum**, MD, Invitae Corporation
2:30 – 2:55	Unraveling the Mystery of Autism: Mining the EHR-enabled Genome, Microbiome, Exposome, Socialome, and Phenome.	**John Mattison**, MD, Kaiser Permanente
2:55 – 3:15	From DNA to Home Village in 3 seconds: A novel biogeographical tool can empower personalized medicine.	**Eran Elhaik**, PhD, University of Sheffield
3:15 – 3:45	**Coffee and Exhibit Viewing**	**Conference Center – 2nd Floor Foyer**
3:45 – 6:00	**Session 2 – Chair: Steven Brenner "The Cancer Genome, Lights, Camera, Actionability"**	**Robertson Auditorium – 2nd Floor**
3:45 – 4:10	Abundant contribution of short tandem repeats to gene expression variation in humans.	**Yaniv Erlich**, PhD, Columbia University
4:10 – 4:30	Clinical validity and actionability of multigene NGS-based tests for hereditary cancers in a large multi-center study.	**Stephen Lincoln**, Invitae Corporation
4:30 – 4:50	Familial colorectal cancer gene variant interpretation: the InSiGHT initiative.	**Bryony Thompson**, PhD, University of Utah
4:50 – 5:10	Large-Scale Genome-wide Association Study of Prostate Specific Antigen Identifies Numerous Novel Loci that Allow for Personalized Prostate Cancer Screening.	**John Witte**, PhD, University of California, San Francisco
5:10 – 5:35	NCI Genomic Data Commons and Cloud Pilots – supporting FAIR – Findable, Accessible, Interoperable, Reusable.	**Warren A. Kibbe**, PhD, National Cancer Institute
5:35 – 6:00	Advances in Cancer Genomics.	**Richard Wilson**, PhD, Washington University School of Medicine
6:00 – 6:30	**Posting of posters**	**Robertson Auditorium – 2nd Floor**
6:30 – 8:30	**Welcome Reception/Dinner (sponsored by Illumina)**	**Fisher Banquet Room – 1st Floor**

Thursday, November 12, 2015

7:00 – 8:15	**Breakfast**	**Conference Center – 2nd Floor Foyer**
8:15 – 10:05	**Session 3 – Chair: Anthony Brookes** **"The Yin and Yang of Genomic Complexity"**	**Robertson Auditorium – 2nd Floor**
8:15 – 8:35	Reproducible and Shareable Quantifications of Pathogenicity.	**Arjun K Manrai**, PhD, Harvard University
8:35 – 8:55	Systematic pan-cancer analysis of tumor purity.	**Dvir Aran**, PhD, University of California, San Francisco
8:55 – 9:15	ClinVar: Registry of human genomic variation in relation to human health.	**Jennifer Lee,** PhD, National Center for Biotechnology Information
9:15 – 9:40	What we have learned about Genetic Susceptibility to Cancer in the GWAS Era.	**Stephen Chanock**, MD, National Cancer Institute
9:40 – 10:05	Clinical interpretation of individuals and populations presenting with whole genome sequences.	**Atul Butte**, MD, PhD, University of California, San Francisco
10:05 – 10:30	**Coffee, Posters and Exhibit Viewing**	**Conference Center – 2nd Floor Foyer**
10:30 – 12:10	**Session 4 – Chair: Mark Lawler** **"It Is About Time We Get Personal With Genomics"**	**Robertson Auditorium – 2nd Floor**
10:30 – 10:55	International efforts to identify new Mendelian disease genes: Progress and Promise.	**Ada Hamosh**, MD, MPH, Johns Hopkins University
10:55 – 11:20	Translatable genomics of GWAS discoveries: first we find a genetic marker, next we find a novel gene and its clinical applications.	**Ludmila Prokunina-Olsson**, PhD, National Cancer Institute
11:20 – 11:45	Looking Ahead: Transitioning to Self-directed Testing.	**Susanne Haga**, PhD, Duke University
11:45 – 12:10	The electronic health record as a tool for genome science: what we have learned, and where we might be going.	**Dan Roden**, MD, Vanderbilt University
12:10 – 1:30	**Lunch and Exhibit Viewing**	**Fisher Banquet Room – 1st Floor**
1:30 – 3:35	**Session 5 – Chair: Stephen Chanock** **"I'll Show You Mine If You Show Me Yours"**	**Robertson Auditorium – 2nd Floor**
1:30 – 1:55	Free the data: unlocking genomic silos through the Global Alliance for Genomics and Health.	**Mark Lawler**, PhD, Queen's University Belfast
1:55 – 2:20	Discovering Data Discovery.	**Anthony Brookes**, PhD, University of Leicester
2:20 – 2:45	Caring about Data Sharing.	**David Glazer**, Google Genomics
2:45 – 3:10	Impediments to interoperability: why can't we all just get along?	**Knox Carey**, PhD, Genecloud
3:10 – 3:35	Challenges and opportunities for genomic data sharing and preserving individual privacy.	**Carlos Bustamante**, PhD, Stanford University
3:35 – 5:45	**Coffee, Posters and Exhibit Viewing**	**Robertson Auditorium – 2nd Floor**
6:00 Sharp	**Board Buses for Conference Dinner Cruise**	**Conference Center – Entrance**
6:30 – 9:15	**Hornblower Bay Dinner Cruise** **(Sponsored by Affymetrix)**	**Pier 3, Embarcadero**
9:30	**Buses to Union Square or Mission Bay Conference Center**	

Friday, November 13, 2015

7:00 – 8:15	**Breakfast**	**Conference Center – 2nd Floor Foyer**
8:15 – 10:30	**Session 6 – Chair: Pui-Yan Kwok** **"Let's Go Techno...Unraveling Genetic Complexity"**	**Robertson Auditorium – 2nd Floor**
8:15 – 8:40	Single-cell genomics to study the biology of cellular heterogeneity in health and disease.	**Thierry Voet**, PhD, University of Leuven and Wellcome Trust Sanger Institute
8:40 – 9:00	Visualizing structural variation at the single cell level to explore human genome heterogeneity.	**Ashley Sanders**, British Columbia Cancer Agency
9:00 – 9:20	Ancestry Matched Genome-wide Association Study Identifies Variants Associated with Spontaneous Preterm Birth.	**Marina Sirota**, PhD, University of California, San Francisco
9:20 – 9:40	Leveraging Gene-Mapping by Environmental Risk: Initial GxE Findings from the CONVERGE Study of Major Depression.	**Roseann Peterson**, PhD, Virginia Commonwealth University
9:40 – 10:05	Genomic signatures of human ageing.	**James Timmons**, PhD, King's College London
10:05 – 10:30	Integrative analytic Methods Facilitate Rapid Discovery in Biobanks.	**Nancy Cox**, PhD, Vanderbilt University
10:30 – 12:15	**Coffee, Poster and Exhibit Viewing**	**Robertson Auditorium – 2nd Floor**
12:15 – 1:30	**Lunch**	**Fisher Banquet Room – 1st Floor**
1:30 – 3:30	**Session 7 – Chair: Lisa Brooks** **"Too Many Facets Of DNA Mutations"**	**Robertson Auditorium – 2nd Floor**
1:30 – 1:55	Genomics in Context: A Social Justice Perspective.	**Wylie Burke**, MD, PhD, University of Washington
1:55 – 2:15	Chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome.	**Mitchell Machiela**, ScD, National Cancer Institute
2:15 – 2:40	Diagnostic Role of Exome Sequencing in Immune Deficiency Disorders.	**Steven Brenner**, PhD, University of California, Berkeley
2:40 – 3:05	Highly parallel measurement of the impact of mutations in proteins.	**Doug Fowler**, PhD, University of Washington
3:05 – 3:30	Genome sequence assembly for complete variation analysis.	**Pui-Yan Kwok**, MD, PhD, University of California, San Francisco
3:30 – 4:00	**Coffee**	**Conference Center – 2nd Floor Foyer**
4:00 – 4:45	**Panel Discussion: Moderator: Rick Wilson** **"Technologies for *De Novo* Genome Sequence Assembly for Variation Detection"**	**Robertson Auditorium – 2nd Floor** Han Cao (BioNano) Meredith Ashby (PacBio) Mike Schnall-Levin (10X Genomics) Nik Putnam (Dovetail), Hugo Lam (Bina)
4:45 – 5:00	**Poster Awards and Closing Remarks**	
5:00	**Close of meeting**	