ihg Institute for Human Genetics

IHG PRESENCE @ ASHG 2016

SESSIONS MODERATED by IHG Faculty @ ASHG

WEDNESDAY, October 19

11:00am—1:00pm

Chun Jimmie Ye

Session 17: ***CRISPR: A New Paradigm for Forward Human Genetics***

Concurrent Invited Session I • Ballroom A

THURSDAY, October 20

9:00—10:30am

Anne Slavotinek

Session 33: ***Insights into the Genetic Basis of Eye Syndromes***

Concurrent Platform Session B • Room 221

Noah Zaitlen

Session 34: ***Methods for Genome- and Transcriptome-Wide Association Studies***

Concurrent Platform Session B • Room 302

11:00am—1:00pm

Joseph Shieh

Session 42: ***Craniofacial and Ocular Malformations***

Concurrent Platform Session C • Room 221

PLATFORM PRESENTATIONS by IHG Faculty & Trainees @ ASHG

WEDNESDAY, October 19

10:15am

Michela Traglia (Postdoc, Weiss Lab)

Maternal and fetal genetic control of mid-gestational and neonatal levels of markers of immune function (Abstract #34)

[Session 10: *Advances in Characterizing the Genetic Basis of Autism*]

Concurrent Platform Session A • Room 119

THURSDAY, October 20

10:15am

Ryan Hernandez (Faculty)

Human evolutionary history has increased the role of rare variants in complex phenotypes (Abstract #92)

[Session 30: *Methods for Studying Rare Variants*]

Concurrent Platform Session B • Room 119

11:00am

Serghei Mangul (Postdoc, Zaitlen Lab)

Comprehensive analysis of RNA-sequencing to find the source of every last read across 544 individuals from 53 tissues (Abstract #165)

[Session 41: *Interpreting the Transcriptome in Health and Disease*]

Concurrent Platform Session C • Room 221

11:45am

Pui Kwok (Faculty)

Structural variation landscape across 26 human populations reveals population specific variation patterns in complex genomic regions (Abstract #152)

[Session 39: *Digging Deep into Structural Variation*]

Concurrent Platform Session C • Room 119

12:00pm

Tom Hoffmann (Faculty)

A large genome-wide study of age-related hearing impairment using electronic health records (Abstract #129)

[Session 36: *Insights from Large Cohorts: Part 2*]

Concurrent Platform Session C • Ballroom B

12:15pm

Anne Slavotinek (Faculty)

Biallelic sequence variants in INTS1 in patients with developmental delays, cataracts and craniofacial anomalies (Abstract #178)

[Session 42: *Craniofacial and Ocular Malformations*]

Concurrent Platform Session C • Room 221

FRIDAY, October 21

10:00am

Joshua Hoffman (Postdoc, Witte Lab) **Finalist for Epstein Award**

Assessing pleiotrophy among common cancers in the UK Biobank (Abstract #193)

[Session 98: *Mapping Cancer Susceptibility Alleles*]

Concurrent Platform Session D • Ballroom A

10:15am

Rachel Gate (Graduate student, Ye Lab) **Semifinalist for Epstein Award**

Genetic determinants of chromatin accessibility predict variation in T cell activation and autoimmunity across human individuals (Abstract #206)

[Session 50: *Chromatin Architecture, Fine Mapping, and Disease*]

Concurrent Platform Session D • Ballroom C

Meena Subramaniam (Graduate student, Ye & Zaitlen Labs)

Leveraging the diploid genome to increase power in *QTL studies (Abstract #230)

[Session 54: *Novel Methods for Analyzing GWAS and Sequencing Data*]

Concurrent Platform Session D • Room 221

SATURDAY, October 22

9:15am

Danny Park (Graduate Student, Zaitlen Lab)

Partitioning phenotype-ancestry correlations (Abstract #252)

[Session 72: *From Phenotypes to Gene Discovery*]

Concurrent Platform Session E • Ballroom B

10:30am

Yulia Mostovoy (Postdoc, Kwok Lab)

A hybrid approach for de novo human genome sequence assembly, phasing and detection of complex structural variation (Abstract #314)

[Session 86: *Methods for Variant Calling*]

Concurrent Platform Session F • Room 211

12:00pm

Aashish Adhikari (Postdoc, Brenner Lab)

Exome sequencing of infant dried blood spots identifies threequarters of metabolic disorders found by newborn screening, indicating limits to exomes in both newborn screening and diagnostic testing (Abstract #3400)

[Session 89: *ASHG Closing Plenary Symposium*]

Ballroom B, West Building

POSTER Presentations at ASHG 2016 by IHG Faculty & Trainees

TUESDAY, October 18

7:00—9:00pm

Anne Biton (Postdoc, Zaitlen Lab)

A novel sgRNA tagging technology identifies and addresses heritable clonal heterogeneity in CRISPR screens (Abstract #3175)

Poster Talks: New for 2016 • Room 119

WEDNESDAY, October 19 — Exhibit Hall B, West Building, Convention Centre

2:00—3:00pm

Sergio Baranzini (Faculty)

Cell specific, network-based pathway analysis of GWAS data provide further insights into pathogenesis of multiple sclerosis (Abstract #1675)

Rivka Sukenik Halevy (Clinical Fellow, Ahituv Lab)

Novel mutations in the fourth β-propeller domain of LRP4 are associated with isolated syndactyly with fusion of the third and fourth fingers (Abstract #2353)

Arunabha Majumdar (Postdoc, Witte Lab)

Bayesian meta-analysis for cross-phenotype genetic association study (Abstract #571)

Shaila Musharoff (Postdoc, Zaitlen Lab)
Modeling ancestry-dependent phenotypic variance reduces bias and increases power in genetic association studies (Abstract #553)

Sasha Targ (Graduate Student, Ye Lab)
Genetic architect: Discovering genomic structure using learned neural architectures (Abstract #1873)

Raul Torres (Postdoc, Hernandez Lab)
Background selection in the human genome explains FST better than recombination rate along (Abstract #1171)

Marquitta White (Postdoc or student, Burchard & Ziv)
Whole genome sequence analysis of a multi-ethnic population of children with asthma reveals novel pharmacogenetic associations (Abstract #1621)

3:00—4:00pm

Steven Brenner (Faculty)
Findings from the fourth critical assessment of genome interpretation (CAGI), a community experiment to evaluate phenotype prediction (Abstract #1822)

Brieana Fregeau (Research Staff, Sherr Lab)
De Novo Mutations of RERE Cause a Genetic Syndrome with Features that Overlap Those Associated with Proximal 1p36 Deletions (Abstract #2392)

Kevin Hartman (Postdoc, Hernandez Lab)
Partitioning heritability of complex human disease by minor allele frequency (Abstract #1768)

Sherman Jia (Clinical Fellow, Risch Lab)
Whole-exome sequencing in bipolar disorder identifies rare variants associated with Parkinson disease and other neuropsychiatric diseases (Abstract #1438)

Angel Mak (Burchard & Ziv Labs)
Whole genome sequencing study on bronchodilator drug response in ethnically diverse children with asthma (Abstract #1660)

THURSDAY, October 20 — Exhibit Hall B, West Building, Convention Centre

2:00—3:00pm

Elena Flowers (Faculty)
Morning Fatigue in Cancer Patients Receiving Chemotherapy is Associated with Differential Expression and Methylation of Regions Associated with Immune Function/Inflammation and Energy Metabolism (Abstract #2711)

Brielin Brown (Graduate Student, Zaitlen Lab)
Poster Award ***Transethnic genetics: Implications for precision medicine and the study of complex traits across diverse populations*** (Abstract #3107)

Galen Joseph (presented by Flavia Chen, Barbara Koenig, Pui Kwok, Jennifer Puck)
Clinician views of public health newborn screening using next generation sequencing technologies: Implications for policy (Abstract #3113)

Melissa Spear (Postdoc, Hernandez Lab)
Admixture inference of African Americans and Latinos in the United States through time (Abstract #1079)

3:00—4:00pm

Nima Emami (Graduate Student, Witte Lab)
Novel Rare variants underpin prostate cancer susceptibility genome-wide (Abstract #2744)

Stephen Francis (Postdoc, Wiemels Lab)
HERVnGoSeq: Identifying and mapping unfixed HERV elements in the genome and application in cancer genomics (Abstract #2798)

Mark Kvale (IHG Scientific Programmer)
Association between telomere length and SNP array probe intensities in a cohort of 100,000 subjects (Abstract #1808)

Dmytro Lituiev (Postdoc, Ye Lab)
Joint prediction of gene expression using multimodal functional genomic readouts (Abstract #362)

Joel Mefford (Graduate Student, Zaitlen & Witte Labs)
Cross-Validated BLUPs: A novel and powerful summary statistic opens new doors to multi-phenotype analyses (Abstract #1892)

Florence Petit (UCSF Visiting Scholar, Ahituv Lab)
Unraveling the TBX5 regulatory landscape (Abstract #2174)

Sara Rashkin (Postdoc, Witte Lab)
A genetic analysis of longitudinal prostate-specific antigen concentrations (Abstract #2780)

Sarah Sawyer (Ziv Lab)
Genetic ancestry affects the predictive power of PRS in Latinas (Abstract #2804)

FRIDAY, October 21 — Exhibit Hall B, West Building, Convention Centre

2:00—3:00pm

Richard Ahn (Postdoc, Liao Lab)
Large-scale imputation of KIR genes in psoriasis case-control cohorts (Abstract #1245)

Yun-Fai Chris Lau (Faculty)
The Y-located TSPY and its X-homologue are co-activator and co-repressor respectively for androgen receptor functions in human cancers and diseases (Abstract #2955)

Dominic Tong (Postdoc, Hernandez Lab)
The impact of genotype imputation on the statistical power of rare variant association studies (Abstract #525)

John Witte (Faculty)
Variants associated with telomere length give rise to multiple cancer associations (Abstract #2787)

Clint Cario (Graduate Student, Witte Lab)
Machine learning to prioritize cancer variants for screening of cell free DNA (cfDNA) (Abstract #2856)

Maria Contreras (Graduate Student, Burchard Lab)
Exploring the Latino asthma paradox: Significant interactions between genetic ancestry, psycho-social stressors, and environmental exposures on asthma susceptibility in Puerto Rican and Mexican children (Abstract #450)

Page Goddard (Graduate Student, Burchard Lab)
Novel genetic variants associated with asthma exacerbations in African American youth (Abstract #1302)

Adam de Smith (Wiemels Lab)
Somatic and germline mutational heterogeneity in high hyperdiploid acute lymphoblastic leukemia (Abstract #2706)

Ludmila Pawlikowska (Faculty)
Origin of the KRIT1 common Hispanic founder mutation causing cerebral cavernous malformation type 1 (Abstract #606)

Joseph Shieh (Faculty)
Identification of novel Ras superfamily nucleotide-binding protein alterations in individuals with brain malformation using Missense-Depleted Regions (MDRs) in population exomes (Abstract #3150)

Caroline Tai (Graduate Student, Witte Lab)
Heritability of aggressive prostate cancer (Abstract #2784)

Yaqiong Wang (Postdoc, Brenner Lab)
Impact of annotation parameter choice on exome sequence analysis pipeline output for application to metabolic disorders in newborn screening (Abstract #1773)