

BROAD INSTITUTE | ASHG 2018

BOOTH 1634 | WEDNESDAY OCTOBER 17TH

San Diego Convention Center, San Diego, CA

Expo Hall Booth #1634

10:00 AM - 4:30 PM

Genomic Sequencing Services

Jane Wilkinson & Andy Hollinger

2:00 PM - 3:00 PM

Q & A with Daniel MacArthur

Daniel MacArthur

10:00 AM - 4:30 PM

Broad Institute Recruiting

Andrea Petrosino

2:00 PM - 4:00 PM

**Broad Institute Strategic Alliances
and Partnering**

Nate Kurtis

10:00 AM - 12:00 PM

FireCloud Workshop Q&A

Geraldine Van De Auwera

3:30 PM - 4:30 PM

Poster Q & A - SC Genetics

Yen-Chen Feng

10:30 AM - 12:00 PM

Diabetes Knowledge Portal

Maria Costanzo

Sessions

9:00 AM - 9:15 AM

PgmNr 17: Mosaic chromosomal alterations increase proliferative loads from rare coding variants and common polygenic risk.

Room 6A - Upper Level

Po-Ru Loh

9:00 AM - 9:15 AM

PgmNr 21: Genetic studies of accelerometer-based sleep measures in 85,670 individuals yield new insights into the biology of human sleep behaviour.

Room 6B - Upper Level

Samuel Jones

9:00 AM - 9:15 AM

PgmNr 5: Variation across 141,456 human exomes and genomes reveals the spectrum of loss-of-function intolerance in human genes.

Ballroom 20A - Upper Level

Konrad Karczewski

9:15 AM - 9:30 AM

PgmNr 14: Rheumatoid arthritis heritability is concentrated in regulatory elements with CD4+ T cell-state-specific transcription factor binding chromatin signatures.

Ballroom 20D - Upper Level

Tiffany Amariuta

9:45 AM - 10:00 AM

PgmNr 20: Leveraging single-cell RNA-seq to infer cell type-specific somatic mutations and mosaicism in Alzheimer's disease.

Room 6A - Upper Level

Carles Boix

9:45 AM - 10:00 AM

PgmNr 8: Assessment of penetrance of 10 Mendelian disease states in 46,980 exomes.

Ballroom 20A - Upper Level

Julia Goodrich

5:00 PM - 5:15 PM

PgmNr 62: Polygenic localization of disease heritability using functional annotations.

Room 6A - Upper Level

Omer Weissbrod

6:00 PM - 6:15 PM

PgmNr 95: Refining the map of genomic disorder loci and associated driver genes by integrating microarray data from 102,257 genomes and exome sequencing of 37,269 individuals.

Ballroom 20A - Upper Level

Ryan Collins

6:15 PM - 6:30 PM

PgmNr 120: Analyzing the world's largest public human variation resources in less than a day: Massively scalable software for genomic analysis.

Room 6D - Upper Level

Timothy Poterba