

GTEX PROJECT COMMUNITY MEETING



WEDNESDAY, JUNE 28TH, 2017

Hilton Washington, DC/Rockville Hotel & Executive Center
1750 Rockville Pike, Rockville, MD 20852.

MAIN AGENDA

*The main meeting is located in the Plaza Ballroom.
Breakfast items and coffee/snack breaks are located in the foyer of the Plaza Ballroom.
Posters and lunch are located in the Atrium.*

7.45 a.m. ***Registration and breakfast (Foyer of the Plaza Ballroom).***

Moderator: Kristin Ardlie

8.25 a.m. Opening.

8.30 a.m. Welcome.
Eric Green, Director, NHGRI, NIH.

8.40 a.m. Opening remarks.
Jim Anderson, Director, Common Fund, NIH.

8.50 a.m. GTEX Program overview.
Simona Volpi, NHGRI, NIH.

9.05 a.m. Overview of GTEX Biospecimen Collections
Abhi Rao & Helen Moore, BBRB, NCI.

9.20 a.m. Overview of GTEX data, analyses, and impact.
Kristin Ardlie, Broad Institute & Manolis Dermitzakis, University of Geneva, Health 2030 Genome Center.

9.45 a.m. Overview of GTEX Ethical, Legal, and Social Issues Study.
Laura Siminoff, Temple University.

10.15 a.m. ***Morning coffee/snack break (Foyer of the Plaza Ballroom).***

Moderator: Alexis Battle

10.45 a.m. Joint effects of regulatory and coding variants shape human genetic variation and disease risk.
Stephane Castel, Columbia University, New York Genome Center.

11.05 a.m. The impact of rare variation on alternative splicing.
Benjamin Strober, Johns Hopkins University.

- 11.25 a.m. Identification and analysis of splicing quantitative trait loci.
Diego Garrido-Martín, Centre for Genomic Regulation.
- 11.45 a.m. Assessing the phenome-wide consequences of gene expression variation using UK Biobank.
Milton Pividori, University of Chicago.
- 12.05 p.m. Leveraging the GTEx histological data: phenotype extraction.
Manuel Muñoz Aguirre, Centre for Genomic Regulation.
- 12.25 p.m. **Lunch break (Atrium).**
- Moderator: Tuuli Lappalainen*
- 1.40 p.m. Regulatory variation quantified from allelic expression in GTEx: genetic architecture and disease applications.
Pejman Mohammadi, Columbia University, New York Genome Center.
- 2.00 p.m. RNAseq analysis of eQTL in bronchial epithelial cells compared with GTEx lung tissue to identify COPD associated genes and SNPs.
James Willey, University of Toledo, Accugenomics, Inc
- 2.20 p.m. eGTEx Mass Spec Proteomics.
Shin Lin, Stanford University, University of Washington.
- 2.40 p.m. Neuronal brain region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric disease heritability.
Peter Hickey, Johns Hopkins School of Public Health.
- 3.00 p.m. **Afternoon coffee/snack break (Foyer of the Plaza Ballroom).**
- Moderator: Gad Getz*
- 3.30 p.m. Identifying cancer-related processes in normal tissues via RNA sequencing.
Keren Yizhak, Broad Institute.
- 3.50 p.m. Landscapes and Dynamics of Fusion Transcripts in Healthy Human Tissues.
Degen Zhuo, Splicingcodes.com, Biotailor, Inc.
- 4.10 p.m. Prediction of Cancer of Unknown Primary Site (CUP) Using Tissue-Specific Molecular Signatures from GTEx and TCGA Data.
Leming Shi, Fudan University, Shanghai Cancer Center.
- 4.30 p.m. A cell-specific microRNAome to deconvolute complex tissue samples.
Marc Halushka, Johns Hopkins University.
- 4.50 p.m. Wrap up/closing.
- 5.00 p.m. **Adjourn.**

**Please join us in the Atrium for the poster session and reception.
5.00 p.m. – 7.00 p.m.**