

GTEX PROJECT COMMUNITY MEETING



MONDAY, JULY 11TH, 2016

**Stanford University
Frances C. Arrillaga Alumni Center
326 Galvez Street, Stanford, CA 94305**

MAIN AGENDA

*The main meeting is located in McCaw Hall.
Posters and catering are located in Ford Gardens.*

8.00 a.m. ***Registration and Breakfast***

Moderator: Kristin Ardlie

8.30 a.m. Opening welcome.

8.35 a.m. NIH overview.
Simona Volpi, NHGRI, NIH.

8.50 a.m. GTEX LDACC: Project overview, data production update.
Kristin Ardlie, Broad Institute.

9.00 a.m. GTEX LDACC: Summary of the V7 data release
Francois Aguet, Broad Institute.

9.15 a.m. Is the tumor-adjacent normal tissue really normal?
Dvir Aran, University of California, San Francisco.

9.35 a.m. Identifying causal eQTL using resampling methods in a multi-tissue DNA-RNAseq dataset.
Idit Kostin, University of California, San Francisco.

9.55 a.m. Genetic predictors of gene expression associated with risk of Colorectal Cancer.
Stephanie Bien, Fred Hutchinson Cancer Research Center, Division of Public Health Sciences.

10.15 a.m. Using GTEX data and sample to identify novel non-cancer fusion RNAs.
Hui Li, University of Virginia.

10.35 a.m. ***Morning break and open poster viewing (Ford Gardens)***

Moderator: Stephen Montgomery

- 10.55 a.m. Network-based approaches to decipher the molecular basis of hereditary diseases.
Esti Yeger-Lotem, Ben-Gurion University & Radcliffe Institute.
- 11.15 a.m. Matrix adaptive shrinkage: a general approach for estimating effects among multiple datasets applied to GTEx.
Matthew Stephens, University of Chicago.
- 11.35 a.m. LeafCutter: Annotation-free quantification of RNA splicing.
David Knowles, Stanford University.
- 11.55 a.m. Complex Sources of Genetic Variation in Tissue Expression Data: Analysis of the Genotype-Tissue Expression (GTEx) Lung Transcriptome.
Matthew McCall, University of Rochester.
- 12.15 p.m. The impact of rare variants on gene expression across tissues.
Joe Davis, Stanford University.
- 12.35 p.m. ***Lunch break with sponsor presentations (McCaw Hall)***
- 12.50 p.m. **1. Validating Drug Discovery Using Reference Body Atlas Data and BaseSpace® Correlation Engine.**
Joe Delaney, Illumina.
- 1:05 p.m. **2. New Technology and Workflow for Integrated Collection, Stabilization and Purification of Circulating Cell-free DNA**
Sean Houshmandi, PreAnalytiX.
- 1:20 p.m. **3. Opening-up the Genome for Personalized Genomics.**
Sarah Garcia, 10x Genomics.

Moderator: Manolis Dermitzakis

- 1.45 p.m. The effects of trans-eQTLs across many human tissues.
Barbara Engelhardt, Princeton University.
- 2.05 p.m. Faster than We Thought: Translational Interfaces for GTEx.
Nancy Cox, Vanderbilt University.
- 2.25 p.m. Integrating eQTLs and tissue-specificity across multiple normal human tissues with genome-wide association data helps uncover causal genes and pathways for common diseases.
Ayellet Segre, Broad Institute.
- 2.45 p.m. Integration of GWAS and eQTL data highlights widespread presence of allelic heterogeneity.
Farhad Hormozdiari, University of California, Los Angeles.
- 3.05 p.m. ***Afternoon break and open poster viewing (Ford Gardens)***

Moderator: Mike Snyder

3.30 p.m. Discovering epigenetic and transcriptomic mediators in common psychiatric disorders using multi-layered quantitative trait models.

Yongjin Park, *Massachusetts Institute of Technology.*

3.50 p.m. Genetic basis of innate immunity in human monocytes.

Sara Kim-Hellmuth, *New York Genome Center.*

4.10 p.m. New insights into obesity pathophysiology through a multi-tissue transcriptome analysis.

Taru Tukiainen, *Institute for Molecular Medicine Finland (FIMM) & Broad Institute.*

4.30 p.m. Impacts of Neanderthal-introgressed sequences on the landscape of human gene expression.

Rajiv McCoy, *University of Washington.*

4.50 p.m. Wrap up/closing

Moderators.

5.00 p.m. ***Adjourn***

***Please join us in Ford Gardens for the Poster Session and reception
5.00 p.m. – 7.00 p.m.***