

GTEX PROJECT COMMUNITY MEETING



WEDNESDAY, JUNE 18, 2014
The Broad Institute | 7 Cambridge Center
Cambridge, MA 02142

AGENDA

7.30 a.m. ***Registration and Breakfast (Lobby)***

Moderator: Kristin Ardlie

8.00 a.m. Welcome – GTEX LDACC

8.05 a.m. NIH introduction – GTEX program updates
Simona Volpi

8.20 a.m. GTEX LDACC: Project overview, data and analysis updates
Kristin Ardlie

8.45 a.m. GTEX LDACC: Data production pipeline – Raw data to portal
Gad Getz

9.00 a.m. Using eQTLs from a range of normal human tissues to provide insights into the biological causes of common genetic diseases
Ayellet Segrè

9.20 a.m. Accurate and fast multiple testing correction to identify eGenes in eQTL studies
Jae Hoon Sul

9.40 a.m. Sparse Bayesian latent factor decompositions for identifying *trans*-eQTLs
Victoria Hore

10.00 a.m. An empirical Bayes approach for multiple tissue eQTL analysis
Gen Li

10.20 a.m. ***Coffee Break and Open Poster Viewing (Lobby)***

Moderator: Barbara Engelhardt

10.50 a.m. The multi-tissue *cis*-eQTL landscape in coronary artery bypass grafting patients: the STokholm Atherogenesis and Gene Expression (STAGE) study
Khanh-Dung 'KD' H. Nguyen

11.10 a.m. Identification of long intergenic non-coding RNA QTLs in four tissue types reveals association with metabolic phenotypes
Barbara Engelhardt

- 11.30 a.m. Sources of somatic mosaicism in the human body
Donald Conrad
- 11.50 a.m. The contribution of STRs to the genetic architecture of gene expression
Melissa Gymrek
- 12.10 p.m. Genetic control of chromatin in a human population
Olivier Delaneau
- 12.30 p.m. **Lunch Break. Open Poster Viewing and Workshops**
Workshops run from 12.45 p.m. – 1.30 p.m.

1. RNA-Seq: eQTLs, Transcriptome Variation, ASE, and other Analysis Methods (Main Auditorium)
2. GTEx Data: Data types, availability, and how and where to access it (Yellowstone Room)
3. Pristine to FFPE: Assessing RNA quality and library prep methods for optimal RNA sequencing (Galapagos Room)

Moderator: Gad Getz

- 1.40 p.m. GTEx and Cancer – Overview of integrated analyses
Gad Getz
- 1.55 p.m. GTEx and Cancer – Single cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma
Itay Tirosh
- 2.15 p.m. PathSeq analysis of microbial sequences detectable in GTEx data
Chandra Sekhar Pedamallu
- 2.35 p.m. GTEx, ENCODE & Roadmap Epigenomics – Fine-mapping, networks and disease
Manolis Kellis
- 2.55 p.m. GTEx and ENCODE – Preliminary transcriptome analyses
Roderic Guigo
- 3.05 p.m. **Coffee Break and Open Poster Viewing**

Moderator: Tuuli Lappalainen

- 3.35p.m. Tissue-specific patterns of imprinting revealed by analysis of monoallelic expression in human populations
Tuuli Lappalainen
- 3.55 p.m. Bayesian regression models for inferring allelic imbalanced expression from RNA-seq data
Daniel Fernandez
- 4.15 p.m. Impact of protein-coding loss-of-function variants on the human transcriptome
Manuel Rivas
- 4.35 p.m. Integrative mining of GTEx data for drug discovery
Simon Xi
- 4.55 p.m. Wrap-up and closing
Kristin Ardlie, Gad Getz
- 5.10 p.m. **Adjourn**