7.30 a.m.  
*Registration and Breakfast (Lobby, Library, Lounge)*

**Moderator:** Kristin Ardlie

8.00 a.m.  
Opening welcome.  
*Kristin Ardlie, Gad Getz, Broad Institute.*

8.05 a.m.  
NIH introduction and overview.  
*Simona Volpi, NHGRI, NIH.*

8.20 a.m.  
GTEx LDACC: Project overview, data and analysis update.  
*Kristin Ardlie, Broad Institute.*

8.45 a.m.  
Incidental neoplastic and non-neoplastic histopathologic findings from the GTEx project: an interim report on 800 donors.  
*Philip Branton, BBRB, NCI.*

9.00 a.m.  
Population-scale and single-cell RNA sequencing provide insight into the pattern of X chromosome inactivation across human tissues.  
*Taru Tukiainen, MGH, Broad Institute.*

9.20 a.m.  
Monoallelically expressed autosomal genes exhibit higher expression variance and less CNV-associated pathogenicity.  
*Alexander Gimelbrant, Harvard Medical School, Dana-Farber Cancer Institute.*

9.40 a.m.  
Examining lost reads to survey the microbiome and immune components of the human body across multiple human tissues.  
*Serghei Mangul, University of California, Los Angeles.*

10.00 a.m.  
*Morning break and open poster viewing (Lobby, Library, Lounge)*

**Moderator:** Barbara Stranger

10.20 a.m.  
Replication of cis and trans eQTL in GTEx and other eQTL datasets.  
*Sushila A. Shenoy, Weill Cornell Medical College.*
10.40 a.m. Identifying causal eQTL using resampling methods in a multi-tissue DNA-RNA seq dataset. 
Andrew Brown, University of Geneva.

11.00 a.m. Genetic regulation of whole blood gene expression quantified in large families pedigrees. 
Ana Viñuela, University of Geneva.

11.20 a.m. The role of mendelian genes in complex disease risk. 
Kaanan P. Shah, University of Chicago.

11.40 a.m. "Imputing" the genetics of type 2 diabetes: Testing the association of genetically imputed gene expression with type 2 diabetes. 
Jason Torres, University of Chicago.

12.00 p.m. Lunch break with sponsor presentations (Cinema)

12.10 p.m. 1. Christopher Hopkins, Illumina. "Streamlining the RNA-seq workflow: Advances in library preparation and sequencing workflow."

12.30 p.m. 2. Thomas Briggs, PreAnalytiX. "Advances in stabilization of blood, bone marrow, and tissue for molecular analyses."

Moderator: Gad Getz
1.10 p.m. Integration of GTEx with pharmacogenomic datasets enables identification of tumor-specific isoforms as expression-based biomarkers predictive of drug response. 
Benjamin Haibe-Kains, University of Toronto, Princess Margaret Cancer Centre.

1.30 p.m. GTEx assignment of cancer cell lines by tissue of origin. 
Heather Selby, Boston University, Dana-Farber Cancer Institute.

1.50 p.m. Using big data to define biological variation and guide clinical RNA-seq analysis. 
David T. Mulder, University of Toronto, University Health Network.

2.10 p.m. Afternoon break and open poster viewing (Lobby, Library, Lounge)

Moderator: Matthew Stephens
2.30 p.m. Fast Identification of Significant Associations in eQTL studies using GRAT and Linear Mixed Models. 
Michael Bilow, University of California, Los Angeles.

2.50 p.m. Detection of Allelic Heterogeneity in eQTL studies. 
Farhad Hormozdiari, University of California, Los Angeles.

3.10 p.m. Tissue specific expression analysis of duplicated human genes. 
Osnat Penn, University of Washington, Seattle.

3.30 p.m. Evolution of expression in duplicated genes. 
Xun Lan, Stanford University.

3.50 p.m. Wrap up/closing
Moderators.

4.00 p.m. Adjourn