WEDNESDAY, JUNE 24TH, 2015
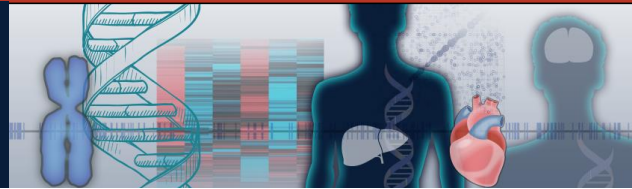Ida Noyes Hall at the University of Chicago
1212 East 59th Street, Chicago, IL 60637

8:00 a.m. – 4:00 p.m.
MAIN AGENDA
(Cinema)

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***