



## Genotype Tissue Expression (GTEx) Project Community Meeting

**Tuesday June 18th, 2013**

The Broad Institute  
7 Cambridge Center  
Cambridge, MA 02142

### AGENDA

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- 7:30 a.m. ***Registration and Breakfast***
- 8:00 a.m. Welcome – GTEx LDACC
- 8:05 a.m. NIH introduction to GTEx – program presentation.  
***Simona Volpi***
- 8:30 a.m. GTEx LDACC: Project overview, Pilot data, and scale up.  
***Kristin Ardlie***
- 9:00 a.m. GTEx LDACC: Overview of analysis pipeline, data QC, processing and release.  
***David DeLuca***
- 9:30 a.m. Expression QTLs (eQTLs) in the multi-tissue GTEx data  
***Emmanouil Dermitzakis***
- 10:00 a.m. The human transcriptome across tissues and individuals.  
***Roderic Guigo***
- 10:30 a.m. ***Coffee Break and Poster viewing (Lobby)***
- 11:00 a.m. The impact of polymorphisms within probe sequence on expression QTL studies.  
***Michael Weale***
- 11:20 a.m. Replication of cis- and trans-eQTLs across cell types.  
***Barbara Englehardt***
- 11:40 a.m. Whole Genome Survey of Expression Short Tandem Repeats.  
***Yaniv Erlich***
- 12:10 a.m. Prediction of individual level genotypes based solely on GTEx gene expression.  
***João Fadista***

- 12:30 p.m. ***Lunch and Poster viewing (Lobby)***
- 1:30 p.m. High resolution allele-specific expression across multiple tissue transcriptomes.  
***Stephen Montgomery***
- 1:50 p.m. Allele-specific expression in GTEx data: quantifying regulatory variation in personalized transcriptomes.  
***Tuuli Lappalainen***
- 2:10 p.m. Transcriptome analysis of the functional impact of putative loss of function variants.  
***Manuel Rivas***
- 2:30 p.m. Sherlock: A Comprehensive Approach to Discovering Gene-Disease Associations in GWAS Using eQTL.  
***Chris Fuller***
- 2:50 p.m. GTEx: Expanding on Genome-Wide Association Studies.  
***Eric Gamazon***
- 3:10 p.m. ***Coffee Break and Poster viewing (Lobby)***
- 3:40 p.m. Chasing causal loci: Genome engineering of a non-coding region of 9p21 to identify mechanisms of diabetes predisposition.  
***Jason Wright***
- 4:00 p.m. Using GTEx data to prioritize candidate mutations in severe Mendelian diseases.  
***Daniel MacArthur***
- 4:20 p.m. Systematic annotation of GTEx eQTLs using ENCODE and Roadmap data.  
***Luke Ward***
- 4:40 p.m. Open Discussion (What data should be available; Long term plans for GTEx; What else is needed; Integration with other NIH initiatives and programs).  
***GTEx & NIH panel***
- 5:15p.m. Closing – Wrap up and Goodbye.  
***Gad Getz***
- 5:30 p.m. ***Adjourn***