



GTEX Analysis Working Group (AWG) Jamboree

WEDNESDAY, DECEMBER 3, 2014

The Washington Hilton | 1919 Connecticut Avenue NW
 Washington, DC 20009
 202-483-3000

AGENDA

**Main session will be held in the Georgetown Room.
 Breakout session will be held in the Kalorama Room.**

7:30 a.m. – 8:00 a.m.	Registration (<i>outside Georgetown Room</i>)	
8:00 a.m.	<i>Welcome, opening remarks, and announcements</i> (Georgetown Room)	Kristin Ardlie
8:15 a.m.	<i>Single tissue eQTL pipeline – final updates</i>	David DeLuca
8:30 a.m.	<i>Transcript quantifications: detection of splice QTLs and impact of quantification method</i>	Roderic Guigo
8:45 a.m.	<i>Isoform quantification and expression</i>	Francois Aguet
9:00 a.m.	<i>Impact of structural variants on gene expression</i>	Don Conrad
9:15 a.m.	<i>eQTLs across 44 tissues and associations with complex disease, with focused example in cancer</i>	Ayellet Segre
9:30 a.m.	<i>eQTLs and GWAS</i>	Eric Gamazon
9:45 a.m. (*Flash)	<i>Applying mediation analysis to eQTL data</i>	Brandon Pierce
9:52 a.m. (*Flash)	<i>Phenotypes</i>	Kristin (for Taylor)
10:00 a.m. – 10:30 a.m.	Break	
10:30 a.m.	<i>X chromosome inactivation</i>	Taru Tukiainen
10:45 a.m.	<i>Gender eQTLs</i>	Kim Kurkurba
11:00 a.m. (*Flash)	<i>Sex specific eQTLs in the GTEx pilot data</i>	Barbara Stranger
11:07 a.m. (*Flash)	<i>RNA editing analysis</i>	Pouya Kheradpour
11:15 a.m.	<i>Identifying RNA editing trans-regulators using GTEx data</i>	Jin Billy Li
11:30 a.m.	<i>Mapping chromatin variation across 70+ individuals, and mapping of chromatin QTLs</i>	Mike Snyder
11:45 a.m.	<i>Protein variation across 90 HapMap cell lines, Ribo-Seq profiling, mapping translation efficiency QTLs</i>	Can Cenik (Snyder)
12:00 p.m.	<i>Multiple eQTLs per gene; mapping chromatin marks</i>	Manolis Dermitzakis

12:15 p.m. – 1.15 p.m. **Lunch on own**

1:15 p.m. – 3:15 p.m. **eGTEX separate breakout session (Kalorama Room)**

1:15 p.m.	<i>Clustering methods for RNA-seq data</i>	Kushal Dey (Stephens)
1:30 p.m.	<i>Statistical issues in identifying heterogeneity in eQTL effects when sharing levels are high</i>	Sarah Urbut (Stephens)
1:45 p.m.	<i>Multi-tissue eQTL analysis for large numbers of tissues</i>	Matthew Stephens
2:00 p.m. (30 min)	<i>A comparative analysis of multi-tissue eQTL results for the pilot vs new data</i>	Nobel/Wright group
2:30 p.m.	<i>Cis/trans architecture of gene expression traits</i>	Hae Kyung Im
2:45 p.m.	<i>Identifying multiple causal variants underlying cis-eQTL loci using statistical fine mapping</i>	Eleazar Eskin
3:00 p.m.	<i>Imputing the transcriptome of inaccessible tissues in and beyond the GTEx project</i>	Lin Chen

3:15 p.m. – 3.45 p.m. **Break**

3:45 p.m.	<i>Publication policy going forward</i>	Simona, Kristin, All
4:15 p.m.	<i>GTEx renewal introduction</i>	Simona Volpi
4:25 p.m.	<i>GTEx renewal AWG discussion and summary of AWG discussions to date</i>	Kristin, Manolis D., All
5:10 p.m.	<i>Closing, wrap-up, action items</i>	

5:15 p.m. **Adjourn**

6:00 p.m. – 8.00 p.m. Dinner at local restaurant for those interested (please let Casandra know for headcount)

Upcoming GTEx Meetings:

AWG Jamboree and Investigator Steering Committee Meeting

Tentative dates: June 15th-16th, 2015 or June 22nd-23rd, 2015

Tentative location: Chicago, IL (at UChicago) or Boston, MA (at the Broad)

GTEx 3rd Community Scientific Meeting

Tentative dates: June 17th, 2015 or June 24th, 2015

Tentative location: Chicago, IL (at UChicago) or Boston, MA (at the Broad)

AWG Jamboree (at ASHG)

Final: October 5th, 2015 in Baltimore, MD

Investigator Steering Committee Meeting with AWG Jamboree & ESP Meeting

Tentative dates: December 2nd-3rd, 2015 in Washington, D.C.