



Non-Coding Variation

**Fairmont Waterfront Hotel
Vancouver, BC, Canada**

18th October 2016

7:30 – 8:20 Registration

8:20 - 8:30 **Introduction**
Steven Brenner

Session 1 Moderator: Steven Brenner

8.30 – 9:00 **Functional Characterisation of Gene Regulatory Elements**
Nadav Ahituv
Dept. of Bioengineering and Therapeutic Sciences, Univ. California San Francisco, CA, USA

9:00 – 9:30 **The Genomics of Human Physiological Adaptation**
Rasmus Nielsen
Univ. California Berkeley, CA, USA

9:30 – 9:45 **The Contribution of de novo Mutations in Enhancers and conserved Non-Coding Elements to Severe Developmental Disorders in 8000 Children**
Patrick Short
Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK.

9:45 - 10:00 **Tissue-Specific Functional Effect Prediction of Genetic Variation and Applications to Complex Trait Genetics**
Iuliana Ionita-Laza
Department of Biostatistics, Columbia University, New York, NY

10:00 – 10:15	Rapid Fire Poster Presentations
	<ul style="list-style-type: none"> • Simon Fishilevich • Marc Greenblatt • Ping Liang • Graham Taylor
10:15 – 11:00	Coffee Break & Poster Session
Session 2	Moderator: Bruce Gottlieb
11:00 – 11:30	Local and Distant Regulatory Effects of Genetic Variation in 44 Human Tissues in the GTEx Project Barbara Engelhardt <i>Princeton Univ., NJ, USA</i>
11:30 – 12:00	Genetic Variations in the Regulation of Alternative Splicing Grace Xiao <i>Dept. Integrative Biology and Physiology, Univ. California Los Angeles, CA, USA</i>
12:00 – 12:20	HGVS Nomenclature update Reece Hart
12:20– 13:30	Lunch and HGVS Annual General Meeting
Session 3	BRCA Share Session Moderator: Sean Mooney
13:30 – 13:40	Introduction The Landscape of Organisations Dealing with BRCA
13:40 – 13:50	Origin of BRCA Share Christophe Beroud <i>INSERM UMR_S910, Faculté de Médecine La Timone, 4ème étage, Marseille, France</i>
13:50 – 14:15	Functional Assays as a Tool for Clinical Annotation of BRCA1 VUS Nicholas Woods <i>Univ. California Berkeley, CA, USA</i>
14:15 – 14:40	Massively Parallel Functional Analysis of Missense Mutations in BRCA1 for Interpreting Variants of Uncertain Significance Lea Starita <i>Univ. Washington, WA, USA</i>
Session 4	Moderator: Rachel Karchin

- 14:40 – 14:55** **Computational method to identify non-coding cancer drivers**
Ekta Khurana
Weill Cornell Medical College, New York, New York 10065, USA.
- 14:55 - 15:10** **Integrative analysis of epigenomes reveals roles of noncoding regions and variants in differentiation and diseases of blood cells**
Ross Hardison
Departments of Biochemistry and Molecular Biology and of Statistics, Pennsylvania State University, University Park, PA
- 15:10 – 15:40** **Title Not available at time of printing**
Olga Troyanskaya
Lewis Sigler Institute of Integrative Genomics, Princeton Univ., NJ, USA
- 15:40 – 15:45** Closing Remarks
- 15:45** **MEETING END IN TIME FOR ASHG PLENARY SESSION**