
Sunday 29 September 2019

- 11:30 - 13:00 **Registration**
ATC Registration Desk
- 13:00 - 13:15 **Opening Remarks**
ATC Auditorium
- 13:15 - 14:15 **Keynote Lecture**
ATC Auditorium
- Systematic genetic perturbation screens to map biological networks** 1
Brenda Andrews
University of Toronto, Canada
- 14:15 - 17:15 **Session 1**
Chair: Patricia Wittkopp
ATC Auditorium
- 14:15 - 14:45 **Analysis of context-specific genetic effects using single-cell RNA-sequencing of differentiation iPS cells** 2
Oliver Stegle
EMBL Heidelberg and German Cancer Research Center, Germany
- 14:45 - 15:00 **Cross-species analysis of melanoma enhancer logic** 3
Liesbeth Minnoye
KU Leuven - VIB, Belgium
- 15:00 - 15:30 **Coffee Break and Meet the Speakers**
ATC Auditorium Foyer
- 15:30 - 16:00 **New technologies to read, write, edit (and heal) genomes** 4
Lars Steinmetz
EMBL Heidelberg, Germany
- 16:00 - 16:15 **Comparative analysis of yeast species reveals transcriptional rewiring in cis and in trans** 5
Gat Krieger
Weizmann Institute of Science, Israel

- 16:15 - 16:30 **Cell-to-cell protein expression variability in the human immune system is a heritable and polygenic trait** 6
Michael Morgan
Wellcome Sanger Institute, United Kingdom
- 16:30 - 16:45 **Identifying signs of polygenic adaptation using polygenic scores** 7
Olivier Bakker
University Medical Centre Groningen, The Netherlands
- 16:45 - 17:15 **High throughput functional characterization of natural alleles in *S. cerevisiae*** 8
Maitreya Dunham
University of Washington, United States of America
- 17:15 - 18:30 **Speed Networking Session**
ATC Auditorium Foyer
- 18:30 - 20:00 **Dinner**
EMBL Canteen
- 20:00 - 22:00 **Welcome Reception**
ATC Rooftop Lounge

Monday 30 September 2019

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|---------------|--|----|
| 09:00 - 12:00 | Session 2 Chair: Marcelo Nobrega ATC Auditorium | |
| 09:00 - 09:30 | Towards predicting gene expression from DNA sequence Jussi Taipale <i>University of Cambridge, United Kingdom</i> | 9 |
| 09:30 - 09:45 | Defining the architecture of complex traits to understand the emergent properties of genomes Chris Jakobson <i>Stanford University School of Medicine, United States of America</i> | 10 |
| 09:45 - 10:15 | The genomic aetiology of osteoarthritis Eleftheria Zeggini <i>Helmholtz Zentrum München, Germany</i> | 11 |
| 10:15 - 10:45 | Coffee Break and Meet the Speakers ATC Auditorium Foyer | |
| 10:45 - 11:00 | The genetic interaction landscape of human membrane transporters Enrico Girardi <i>CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria</i> | 71 |
| 11:00 - 11:30 | Exploring genomics and phenomics with machine learning toward an improved understanding of complex traits Marylyn Ritchie <i>University of Pennsylvania, United States of America</i> | 13 |
| 11:30 - 11:45 | Integration of transcriptome, proteome and phosphoproteome data elucidates the genetic control of molecular networks Andreas Beyer <i>University of Cologne, Germany</i> | 14 |

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| 11:45 - 12:00 | Context-sensitive analysis of genomic insulator function Matt Maurano <i>New York University School of Medicine, United States of America</i> | 15 |
| 12:00 - 13:30 | Lunch ATC Auditorium Foyer | |
| 13:30 - 17:00 | Session 3 Chair: Maitreya Dunham ATC Auditorium | |
| 13:30 - 14:00 | From epigenetic variation across individuals to insights into disease and ageing Judith Zaugg <i>EMBL Heidelberg, Germany</i> | 16 |
| 14:00 - 14:15 | Single and combinatorial CRISPR gene perturbations with 3Cs gRNAs Manuel Kaulich <i>Goethe University Frankfurt, Germany</i> | 79 |
| 14:15 - 14:30 | Exploring the omnigenic model Neel Prabh <i>Max Planck Institute for Evolutionary Biology, Germany</i> | 95 |
| 14:30 - 15:00 | Single cells collectively reveal non-deterministic effects of genetic variants Gaël Yvert <i>CNRS and École Normale Supérieure de Lyon, France</i> | 18 |
| 15:00 - 15:30 | Coffee Break and Meet the Speakers ATC Auditorium Foyer | |
| 15:30 - 16:30 | Panel discussion: Open science and opportunities in systems genetics ATC Auditorium | |
| 16:30 - 17:00 | Flash Talks Session 1 Abstract #47, 53, 56, 57, 59, 83, 87, 115 ATC Auditorium | |

Programme

17:00 - 19:00 **Poster Session 1 (odd numbers)**

ATC Helix B

19:00 - 20:30 **Dinner**

EMBL Canteen

20:30 - 22:30 **After Dinner Drinks**

ATC Rooftop Lounge

Tuesday 1 October 2019

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| 09:00 - 12:00 | Session 4 Chair: Brenda Andrews ATC Auditorium | |
| 09:00 - 09:30 | Using single-cell genomics to investigate transcriptional dynamics Rickard Sandberg <i>Karolinska Institutet, Sweden</i> | 19 |
| 09:30 - 09:45 | Dynamic control of transcription at different chromosome positions Siqi Zhao <i>Washington University in St. Louis, United States of America</i> | 20 |
| 09:45 - 10:00 | Single cell RNA-seq identifies the origins of heterogeneity in efficient cell transdifferentiation and reprogramming Mirko Francesconi <i>LBMC and École Normale Supérieure de Lyon, France</i> | 21 |
| 10:00 - 10:15 | Quantitative phenotyping of <i>C. elegans</i> drug responses Andy Fraser <i>University of Toronto, Canada</i> | 22 |
| 10:15 - 10:45 | Coffee Break and Meet the Speakers ATC Auditorium Foyer | |
| 10:45 - 11:15 | Using single cell genomics to understand cell fate decisions in early development John Marioni <i>EMBL-EBI Hinxton and University of Cambridge, United Kingdom</i> | 23 |
| 11:15 - 11:30 | Curating an atlas of human gene function from CRISPR-Cas9 fitness screens Joshua Pan <i>Broad Institute, United States of America</i> | 24 |

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| 11:30 - 12:00 | Impacts of mutations on regulatory networks Patricia Wittkopp <i>University of Michigan, United States of America</i> | 25 |
| 12:00 - 13:30 | Lunch ATC Auditorium Foyer | |
| 13:30 - 17:00 | Session 5 Chair: Gaël Yvert ATC Auditorium | |
| 13:30 - 14:00 | Solving protein structures and understanding genetic interactions using deep mutagenesis Ben Lehner <i>Centre for Genomic Regulation, Spain</i> | 26 |
| 14:00 - 14:15 | Sequencing the BXD family, a cohort for experimental systems genetics and precision medicine David Ashbrook <i>The University of Tennessee Health Science Center, United States of America</i> | 27 |
| 14:15 - 14:30 | Characterizing cell type specificity of eQTLs from estimated cell type abundances across GTEx tissues Sarah Kim-Hellmuth <i>New York Genome Center, United States of America</i> | 28 |
| 14:30 - 15:00 | Humans and their bugs: The role of host-microbiome interactions in health and diseases Alexandra Zhernakova <i>University Medical Center Groningen, The Netherlands</i> | 29 |
| 15:00 - 15:30 | Coffee Break and Meet the Speakers ATC Auditorium Foyer | |

- 15:30 - 16:00 **Dissecting the genetic and molecular basis of organismal phenotypes in the Drosophila Genetic Reference Panel** 30
Bart Deplancke
École Polytechnique Fédérale de Lausanne, Switzerland
- 16:00 - 16:15 **Disentangling genetic and environmental effects on the proteotypes of individuals** 31
Natalie Romanov
EMBL Heidelberg, Germany
- 16:15 - 16:30 **Fission yeast transcriptional heterogeneity surveyed by single cell RNA sequencing** 32
Samuel Marguerat
MRC London Institute of Medical Sciences and Imperial College London, United Kingdom
- 16:30 - 17:00 **Flash Talks Session 2**
Abstract #50, 62, 64, 68, 70, 82, 88, 106
ATC Auditorium
- 17:00 - 19:00 **Poster Session 2 (even numbers)**
ATC Helix B
- 19:00 - 21:00 **Conference Dinner**
EMBL Canteen
- 21:00 - 00:00 **Conference Party**
ATC Auditorium Foyer

Wednesday 2 October 2019

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| 09:00 - 12:45 | Session 6 Chair: Rickard Sandberg ATC Auditorium | |
| 09:00 - 09:30 | The GTEx Consortium atlas of genetic regulatory effects across human tissues Tuuli Lappalainen <i>New York Genome Center and Columbia University, United States of America</i> | 33 |
| 09:30 - 09:45 | A high-resolution genetic map of the metazoan cell generated by image-based profiling of co-perturbations Florian Heigwer <i>German Cancer Research Center and Heidelberg University, Germany</i> | 34 |
| 09:45 - 10:00 | Adaptation is shaped by genetic architecture and genotype Rob Jelier <i>KU Leuven, Belgium</i> | 35 |
| 10:00 - 10:30 | Functionally dissecting the genetic landscape of complex human traits Marcelo Nobrega <i>University of Chicago, United States of America</i> | 36 |
| 10:30 - 11:00 | Coffee Break and Meet the Speakers ATC Auditorium Foyer | |
| 11:00 - 11:30 | Variation of gene essentiality in yeast and human Leopold Parts <i>Wellcome Trust Sanger Institute, United Kingdom</i> | 37 |
| 11:30 - 11:45 | Simultaneous quantification of mRNA and protein in single cells reveals trans-acting genetic variation Frank Albert <i>University of Minnesota, United States of America</i> | 38 |
| 11:45 - 12:45 | Keynote Lecture ATC Auditorium | |

Big data and health

Michael Snyder

Stanford University, United States of America

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12:45 - 13:00 **Closing Remarks and Poster Prize**

ATC Auditorium

13:00 **Packed Lunch and Departure**

ATC Auditorium Foyer

Poster removal: Please remember to collect your poster. Posters which have not been collected will be disposed of after the meeting.

Feedback questionnaire: Check your inbox when the meeting ends. You will find an email with the link to the online feedback questionnaire. Please take time to complete it.