### Sunday 05 November 2017

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
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<tbody>
<tr>
<td>11:15 - 13:15</td>
<td><strong>Arrival / Registration with light refreshments</strong>&lt;br&gt;ATC Reception and Foyer</td>
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<tr>
<td>13:15 - 13:30</td>
<td><strong>Opening remarks</strong>&lt;br&gt;ATC Auditorium</td>
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<tr>
<td>13:30 - 16:15</td>
<td><strong>Session 1: Structural genomics and cancer</strong>&lt;br&gt;Chair: Peter Lichter and Peter Campbell</td>
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<tr>
<td>13:30 - 14:00</td>
<td><strong>Advancing the field of mutational signatures: Insights into mutational mechanisms and clinical applications</strong>&lt;br&gt;Serena Nik-Zainal&lt;br&gt;<em>Wellcome Trust Sanger Institute, United Kingdom</em></td>
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<tr>
<td>14:00 - 14:15</td>
<td><strong>Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours</strong>&lt;br&gt;Bernardo Rodríguez-Martín&lt;br&gt;<em>CINBIO, University of Vigo, Spain</em></td>
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<tr>
<td>14:15 - 14:30</td>
<td><strong>Genomic footprints of activated telomere maintenance mechanisms in cancer</strong></td>
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<td>14:30 - 15:00</td>
<td><strong>Germline determinants of the somatic mutation landscape in 2,642 cancer genomes</strong></td>
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<td>15:00 - 15:30</td>
<td><strong>Coffee Break</strong>&lt;br&gt;ATC Foyer</td>
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<tr>
<td>15:30 - 15:45</td>
<td><strong>Inherited determinants of early recurrent somatic mutations in prostate cancer</strong></td>
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<td></td>
<td>Alessandro Romanel&lt;br&gt;<em>University of Trento, Italy</em></td>
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15:45 - 16:00 Validating the concept of mutational signatures with isogenic cell models
Xueqin Zou
Wellcome Trust Sanger Institute, United Kingdom

16:00 - 16:15 Canonical fusions in bone and soft tissue cancer are generated by replication-associated genomic catastrophes
Nathaniel Anderson
The Hospital for Sick Children, Canada

16:15 - 17:00 Coffee Break & Meet the Speakers
ATC Foyer

17:00 - 18:00 Keynote lecture: Peter Lichter
ATC Auditorium
Challenges in understanding the biological and clinical behavior of tumors on the basis of structural and functional genomics
Peter Lichter
German Cancer Research Center, Germany

18:00 - 20:30 Welcome reception with light refreshments
ATC Foyer
Monday 06 November 2017

09:00 - 12:15 Session 2: Systems biology and drivers of cancer
Chairs: Núria López-Bigas and Stefan Pfister

09:00 - 09:30 The Genomic Landscape of Childhood Cancers and its Clinical Implications
Stefan M. Pfister
Hopp Children’s Comprehensive Cancer Center at the NCT Heidelberg (KiTZ), German Cancer Research Center (DKFZ), Heidelberg University Hospital, Germany

09:30 - 09:45 Pan-cancer driver discovery in more than 2,500 whole cancer genomes
Jakob Skou Pedersen
Aarhus University Hospital, Denmark

09:45 - 10:00 Identification and characterization of oncogenic SOS1 mutations in lung adenocarcinoma
Diana Cai
Harvard University, United States of America

10:00 - 10:30 To be presented onsite
Nuria Lopez-Bigas
ICREA, Institute for Research in Biomedicine, Spain

10:30 - 11:00 Coffee Break
ATC Foyer

11:00 - 11:15 Non-coding cancer driver mutations in super-enhancers and long-range chromatin interaction networks
Juri Reimand
Ontario Institute for Cancer Research, Canada

11:15 - 11:30 The evolutionary history of 2,658 cancers
Peter Van Loo
The Francis Crick Institute, United Kingdom

11:30 - 12:15 Coffee Break

12:15 - 13:45 Lunch Break
11:30 - 11:45  Pervasive intra-tumour heterogeneity and subclonal selection across cancer types
Kerstin Haase
The Francis Crick Institute, United Kingdom

11:45 - 12:00  Identification of non-neutral tumour evolution across human cancer types
Maxime Tarabichi
The Francis Crick Institute, United Kingdom

12:00 - 12:15  Elucidating the effects of SNPs in genotype-phenotype mappings of carcinogenesis
Jimmie Haellman
University of Sheffield, United Kingdom

12:15 - 13:45  Lunch
ATC Foyer

13:00 - 13:45  Workshop hosted by Thermo Fisher Scientific
Flex Lab A+B

13:45 - 15:45  Poster Session I (odd numbers)
ATC Helix A

15:45 - 16:45  Session 3: Cancer immunogenomics
Chair: Lynda Chin

15:45 - 16:00  The pan-cancer landscape of interactions between solid tumors and infiltrating immune cell populations
David Tamborero
Universitat Pompeu Fabra; Institute for Research in Biomedicine, Spain

16:00 - 16:30  A novel mechanism of cancer immune evasion vis 3'-UTR disruption of PD-L1
Seishi Ogawa
Kyoto University, Japan
16:30 - 16:45  Analysis of allele specific HLA loss in lung cancer evolution
Rachel Rosenthal
*UCL Cancer Institute, United Kingdom*

16:45 - 17:30  Coffee Break & Meet the Speakers
ATC Foyer

17:30 - 18:30  Keynote lecture: Alexander van Oudenaarden,
ATC Auditorium

*Whole-organism clone-tracing using single-cell sequencing*
Alexander van Oudenaarden
*Hubrecht Institute, The Netherlands*

18:30 - 20:00  Dinner
EMBL Canteen

20:00 - 21:30  After-dinner drinks
ATC Rooftop Lounge
<table>
<thead>
<tr>
<th>Time</th>
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<th>Speakers</th>
<th>Institution</th>
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<tr>
<td>09:00 - 12:00</td>
<td><strong>Session 4: Cancer genome and epigenome</strong></td>
<td>Chairs: Matthew Meyerson and Elizabeth Murchison</td>
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<td>09:00 - 09:30</td>
<td><em>Clarifying the impact of genetic defects in prostate cancer through epigenetics</em></td>
<td>Mathieu Lupien</td>
<td><em>Princess Margaret Cancer Centre, University Health Network, Canada</em></td>
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<tr>
<td>09:30 - 09:45</td>
<td><em>A pan-cancer analysis of promoter activity highlights the regulatory role of alternative transcription start sites and their association with noncoding mutations</em></td>
<td>Jonathan Goeke</td>
<td><em>Genome Institute of Singapore, Singapore</em></td>
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<td>09:45 - 10:00</td>
<td><em>Mutation accumulation during human foetal development</em></td>
<td>Francis Blokzijl</td>
<td><em>UMC Utrecht, The Netherlands</em></td>
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<tr>
<td>10:00 - 10:30</td>
<td><em>Genomic instability triggered by chromosome gains</em></td>
<td>Zuzana Storchova</td>
<td><em>TU Kaiserslautern, Germany</em></td>
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<td>10:30 - 11:00</td>
<td><strong>Coffee Break</strong></td>
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<td>11:00 - 11:30</td>
<td><em>Mutations and their interactions in individuals</em></td>
<td>Ben Lehner</td>
<td><em>Centre for Genomic Regulation (CRG), Spain</em></td>
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<td>11:30 - 11:45</td>
<td><em>Identification and characterization of recurrent deletions in the human genome promoted by expression of transposase-derived gene across different tumor types</em></td>
<td>Elias Rodriguez-Fos</td>
<td><em>Barcelona Supercomputing Center (BSC), Spain</em></td>
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11:45 - 12:00  Pan-cancer analysis of DNA replication strand asymmetry in mutational signatures
Marketa Tomkova
University of Oxford, United Kingdom

12:00 - 13:30  Lunch
ATC Foyer

13:30 - 15:30  Poster Session II (even numbers)
ATC Helix A

15:30 - 18:30  Session 5: Cancer genome medicine
Chair: Mathieu Lupien

15:30 - 16:00  To be presented onsite
Lynda Chin
Institute for Health Transformation, University of Texas System, United States of America

16:00 - 16:15  The TARGET pilot study of a comprehensive precision medicine platform for children with high-risk cancer
Emily Mould
Children’s Cancer Institute, Australia

16:15 - 16:45  Integrative Literature Mining and Knowledge Networks for Kinase Cancer Drug Analytics
Cathy Wu
University of Delaware, United States of America

16:45 - 17:30  Coffee Break & Meet the Speakers
ATC Foyer

17:30 - 17:45  Establishment and characterization of an ovarian cancer organoid biobank
Jose Espejo Valle-Inclan
University Medical Center Utrecht, The Netherlands

17:45 - 18:00  Mapping the evolution of carboplatin resistance in ovarian cancer with single cell sequencing
Olivier Harismendy
University of California, San Diego, United States of America
EMBL Conference: Cancer Genomics

18:00 - 18:30  To be presented onsite  
Jessica Zucman-Rossi  
_Inserm, France_

18:30 - 20:30  Banquet Dinner  
EMBL Canteen

20:30 - 00:00  Conference Party with DJ  
ATC Foyer
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<td>Session 6: The future of cancer genomics</td>
<td>Chair: Zuzana Storchova and Jan Korbel</td>
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<td>09:00 - 09:30</td>
<td>Interrogating the architecture of cancer genomes</td>
<td>Peter Campbell, <em>Wellcome Trust Sanger Institute, UK</em></td>
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<td>09:30 - 09:45</td>
<td>Copy number signatures across primary tumours</td>
<td>Tuanne Amarante, <em>Wellcome Trust Sanger Institute, UK</em></td>
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<td>09:45 - 10:15</td>
<td>Two transmissible cancers in Tasmanian devils</td>
<td>Elizabeth Murchison, <em>University of Cambridge, UK</em></td>
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<td>10:15 - 10:30</td>
<td>Somatic variation and mutagenesis in a canine transmissible cancer</td>
<td>Adrian Baez-Ortega, <em>University of Cambridge, UK</em></td>
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<td>10:30 - 11:00</td>
<td>Coffee Break &amp; Meet the Speakers</td>
<td>ATC Foyer</td>
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<td>Tumor heterogeneity over time in zebrafish using single-cell RNA-Seq</td>
<td>Itai Yanai, <em>New York University Langone Health, USA</em></td>
</tr>
<tr>
<td>11:15 - 11:30</td>
<td>High density of cancer mutations in normal oesophagus</td>
<td>Inigo Martincorena, <em>Wellcome Trust Sanger Institute, UK</em></td>
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<td>11:30 - 12:00</td>
<td>Genomic analysis of human cancers</td>
<td>Matthew Meyerson, <em>Dana-Farber Cancer Institute and Harvard Medical School, USA</em></td>
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12:00 - 12:10  **Closing remarks**  
ATC Auditorium

12:10 - 12:30  **Packed lunch & Departures**

Please remember to collect your poster. Posters that have not been collected will be disposed of after the meeting.

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.