
Sunday 05 November 2017

11:15 - 13:15	Arrival / Registration with light refreshments ATC Reception and Foyer	
13:15 - 13:30	Opening remarks ATC Auditorium	
13:30 - 16:15	Session 1: Structural genomics and cancer Chairs: Peter Lichter and Peter Campbell	
13:30 - 14:00	Advancing the field of mutational signatures: Insights into mutational mechanisms and clinical applications Serena Nik-Zainal <i>Wellcome Trust Sanger Institute, United Kingdom</i>	1
14:00 - 14:15	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours Bernardo Rodríguez-Martín <i>CINBIO, University of Vigo, Spain</i>	2
14:15 - 14:30	Genomic footprints of activated telomere maintenance mechanisms in cancer Lina Sieverling <i>German Cancer Research Center, Germany</i>	3
14:30 - 15:00	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes Jan Korbel <i>EMBL Heidelberg, Germany</i>	4
15:00 - 15:30	Coffee Break ATC Foyer	
15:30 - 15:45	Inherited determinants of early recurrent somatic mutations in prostate cancer Alessandro Romanel <i>University of Trento, Italy</i>	5

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- 15:45 - 16:00 **Validating the concept of mutational signatures with isogenic cell models** 6
Xueqing 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** 7
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** 8
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 <i>Hopp Children's Comprehensive Cancer Center at the NCT Heidelberg (KITZ), German Cancer Research Center (DKFZ), Heidelberg University Hospital, Germany</i>	9
09:30 - 09:45	Pan-cancer driver discovery in more than 2,500 whole cancer genomes Jakob Skou Pedersen <i>Aarhus University Hospital, Denmark</i>	10
09:45 - 10:00	Identification and characterization of oncogenic SOS1 mutations in lung adenocarcinoma Diana Cai <i>Harvard University, United States of America</i>	11
10:00 - 10:30	To be presented onsite Nuria Lopez-Bigas <i>ICREA, Institute for Research in Biomedicine, Spain</i>	12
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 <i>Ontario Institute for Cancer Research, Canada</i>	13
11:15 - 11:30	The evolutionary history of 2,658 cancers Peter Van Loo <i>The Francis Crick Institute, United Kingdom</i>	14

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11:30 - 11:45	Pervasive intra-tumour heterogeneity and subclonal selection across cancer types	15
	Kerstin Haase <i>The Francis Crick Institute, United Kingdom</i>	
11:45 - 12:00	Identification of non-neutral tumour evolution across human cancer types	16
	Maxime Tarabichi <i>The Francis Crick Institute, United Kingdom</i>	
12:00 - 12:15	Elucidating the effects of SNPs in genotype-phenotype mappings of carcinogenesis	17
	Jimmie Haellman <i>University of Sheffield, United Kingdom</i>	
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	18
	David Tamborero <i>Universitat Pompeu Fabra; Institute for Research in Biomedicine, Spain</i>	
16:00 - 16:30	A novel mechanism of cancer immune evasion vis 3'-UTR disruption of PD-L1	19
	Seishi Ogawa <i>Kyoto University, Japan</i>	

- 16:30 - 16:45 **Analysis of allele specific HLA loss in lung cancer evolution** 20
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** 21
Alexander van Oudenaarden
Hubrecht Institute, The Netherlands
- 18:30 - 20:00 **Dinner**
EMBL Canteen
- 20:00 - 21:30 **After-dinner drinks**
ATC Rooftop Lounge

Tuesday 07 November 2017

09:00 - 12:00	Session 4: Cancer genome and epigenome Chairs: Matthew Meyerson and Elizabeth Murchison	
09:00 - 09:30	Clarifying the impact of genetic defects in prostate cancer through epigenetics Mathieu Lupien <i>Princess Margaret Cancer Centre, University Health Network, Canada</i>	22
09:30 - 09:45	A pan-cancer analysis of promoter activity highlights the regulatory role of alternative transcription start sites and their association with noncoding mutations Jonathan Goeke <i>Genome Institute of Singapore, Singapore</i>	23
09:45 - 10:00	Mutation accumulation during human foetal development Francis Blokzijl <i>UMC Utrecht, The Netherlands</i>	24
10:00 - 10:30	Genomic instability triggered by chromosome gains Zuzana Storchova <i>TU Kaiserslautern, Germany</i>	25
10:30 - 11:00	Coffee Break ATC Foyer	
11:00 - 11:30	Mutations and their interactions in individuals Ben Lehner <i>Centre for Genomic Regulation (CRG), Spain</i>	26
11:30 - 11:45	Identification and characterization of recurrent deletions in the human genome promoted by expression of transposase-derived gene across different tumor types Elias Rodriguez-Fos <i>Barcelona Supercomputing Center (BSC), Spain</i>	27

11:45 - 12:00	Pan-cancer analysis of DNA replication strand asymmetry in mutational signatures	28
	Marketa Tomkova <i>University of Oxford, United Kingdom</i>	
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	29
	Lynda Chin <i>Institute for Health Transformation, University of Texas System, United States of America</i>	
16:00 - 16:15	The TARGET pilot study of a comprehensive precision medicine platform for children with high-risk cancer	30
	Emily Mould <i>Children's Cancer Institute, Australia</i>	
16:15 - 16:45	Integrative Literature Mining and Knowledge Networks for Kinase Cancer Drug Analytics	31
	Cathy Wu <i>University of Delaware, United States of America</i>	
16:45 - 17:30	Coffee Break & Meet the Speakers ATC Foyer	
17:30 - 17:45	Establishment and characterization of an ovarian cancer organoid biobank	32
	Jose Espejo Valle-Inclan <i>University Medical Center Utrecht, The Netherlands</i>	
17:45 - 18:00	Mapping the evolution of carboplatin resistance in ovarian cancer with single cell sequencing	33
	Olivier Harismendy <i>University of California, San Diego, United States of America</i>	

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18:00 - 18:30	To be presented onsite Jessica Zucman-Rossi <i>Inserm, France</i>	34
18:30 - 20:30	Banquet Dinner EMBL Canteen	
20:30 - 00:00	Conference Party with DJ ATC Foyer	

Wednesday 08 November 2017

09:00 - 12:00	Session 6: The future of cancer genomics Chair: Zuzana Storchova and Jan Korbel	
09:00 - 09:30	Interrogating the architecture of cancer genomes Peter Campbell <i>Wellcome Trust Sanger Institute, United Kingdom</i>	35
09:30 - 09:45	Copy number signatures across primary tumours Tauanne Amarante <i>Wellcome Trust Sanger Institute, United Kingdom</i>	36
09:45 - 10:15	Two transmissible cancers in Tasmanian devils Elizabeth Murchison <i>University of Cambridge, United Kingdom</i>	37
10:15 - 10:30	Somatic variation and mutagenesis in a canine transmissible cancer Adrian Baez-Ortega <i>University of Cambridge, United Kingdom</i>	38
10:30 - 11:00	Coffee Break & Meet the Speakers ATC Foyer	
11:00 - 11:15	Tumor heterogeneity over time in zebrafish using single-cell RNA-Seq Itai Yanai <i>New York University Langone Health, United States of America</i>	39
11:15 - 11:30	High density of cancer mutations in normal oesophagus Inigo Martincorena <i>Wellcome Trust Sanger Institute, United Kingdom</i>	40
11:30 - 12:00	Genomic analysis of human cancers Matthew Meyerson <i>Dana-Farber Cancer Institute and Harvard Medical School, United States of America</i>	41

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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.