CANCER SYSTEMS GENETICS
Systematic Functional Annotation of Cancer Variants

The conference will be centered on the translation of basic research into clinical oncology. Current cancer genomics efforts are generating extensive catalogs of previously unrecognized somatic mutations of unknown functional relevance, presenting challenges and opportunities for the translation of genetic information into clinical practice. The aim of the conference is to assess the current state of the art for approaches to gain functional understanding of cancer variants. The meeting will feature sessions on targeting the vulnerabilities of cancer cells, new technologies such as high-throughput CRISPR and RNAi screens, automated phenotyping, and chemical genetics, as well as bioinformatics approaches for functional genomics.

INVITED SPEAKERS

Brenda ANDREWS, University of Toronto
Frank BUCHHOLZ, Technical University Dresden
Martin EILERS, University of Würzburg
William HAHN, Dana-Farber Cancer Institute, Boston
Nuria LOPEZ-BIGAS, Univ. Pompeu Fabra, Barcelona
Ultan MCDERMOTT, Sanger Institute, Cambridge, UK
Jussi TAIPAILE, Karolinska Institute, Stockholm
Krister WENNERBERG, Inst. Mol. Medicine Finland, Helsinki

VENUE ADDRESS
German Cancer Research Center (DKFZ)
Communication Center, Lecture Hall and Foyer
Im Neuenheimer Feld 280
69120 Heidelberg, Germany

ORGANIZERS
Michael Boutros, DKFZ
Claudia Scholl, NCT/DKFZ
Stefan Fröhling, NCT/HUMS
Wolfgang Huber, EMBL

CONTACT
Sarah Zimmermann
Phone: +49 (0)6221/42-2651
E-mail: sa.zimmermann@dkfz.de
**THURSDAY, MAY 19**

13:30 Arrival, Registration & Media Check-in

14:30 Welcome Remarks
   **Michael Boutros**, DKFZ, Heidelberg

14:45 **Krister Wennerberg**, Institute for Molecular Medicine Finland, Helsinki
   Targeting individual cancers with chemical systems medicine

15:20 **Aylin Camgoz**, Technical University Dresden
   UCN-01-induced cell death predominantly results from STK3 inhibition in AML cells

15:40 **Mikolaj Slabicki**, National Center for Tumor Diseases Heidelberg and DKFZ, Heidelberg
   Dissection of CD20 regulation in lymphoma using RNAi

16:00 Coffee Break

16:45 **Maximilian Billmann**, DKFZ, Heidelberg
   Widespread rewiring of genetic networks upon cancer signaling pathway activation

17:05 **William Hahn**, Dana-Farber Cancer Institute, Boston
   KEYNOTE LECTURE: Towards a cancer dependencies map

18:00 Welcome Reception (Foyer)

19:30 Speakers Dinner (by invitation only)

**FRIDAY, MAY 20**

09:00 **Ultran McDermott**, Sanger Institute, Cambridge, UK
   A landscape of pharmacogenomic interactions in cancer

09:35 **Marc Raab**, Heidelberg University Hospital and DKFZ, Heidelberg
   Molecular signaling in multiple myeloma: association of RAS/RAF mutations and MAPK pathway activation

09:55 **Priya Chudasama**, National Center for Tumor Diseases Heidelberg and DKFZ, Heidelberg
   Targeting FGFR1 for treatment of soft-tissue sarcoma

10:15 Coffee Break

10:45 **Martin Eilers**, University of Würzburg
   Complexes of N-MYC and MYC with Aurora-A: a possible inroad to targeting MYC function for tumor therapy

11:20 **Stefanie Böhm**, University of Cologne
   Identification of lineage-dependent synthetic lethal targets in MYC-deregulated cancer cell lines

11:40 **Florian Heigwer**, DKFZ, Heidelberg
   CRISPR library designer (CLD): software for multispecies design of sgRNA libraries

12:00 Lunch

13:15 **Nuria Lopez-Bigas**, University Pompeu Fabra, Barcelona
   Tumor genomes shed light into mutational processes and cancer vulnerabilities

13:50 **Bernd Fischer**, DKFZ, Heidelberg
   Inferring directional genetic interactions from high-content, combinatorial RNAi screens

14:10 **Lars Feuerbach**, DKFZ, Heidelberg
   On the implications of cohort-based variation analysis as a new paradigm in cancer genomics

14:30 Poster Session (with coffee and cake)

16:45 **Michael Böttcher**, University of California, San Francisco
   Illuminating genetic regulatory networks by means of CRISPR-mediated gene activation

17:05 **Shantanu Singh**, Broad Institute, Cambridge, USA
   Functional annotation of cancer-associated genes and alleles using Cell Painting

17:25 Poster and Best Abstract Awards

17:35 **Brenda Andrews**, University of Toronto
   KEYNOTE LECTURE: Genetic networks

19:30 Speakers Dinner (by invitation only)

**SATURDAY, MAY 21**

09:00 **Jussi Taipale**, Karolinska Institute, Stockholm
   Systems biology of cancer

09:35 **Colm J. Ryan**, University College Dublin
   BEST ABSTRACT: The systematic interpretation of genetic dependencies in cancer cell lines

09:55 **Frank Buchholz**, Technical University Dresden
   Functional profiling of AML cells

10:30 Coffee Break

10:45 Panel Discussion
   Comprehensive genomic analyses uncover numerous genomic regions affected by mutations or other structural rearrangements. However, the biological relevance of most of these events remains unclear since functional data are lacking. How can systematic experimental strategies be employed to address this problem for the successful translation of cancer genome data into clinical application?

12:15 Snack and Departure