Conference Program

Friday, May 17

6:00 p.m.-6:30 p.m. **Opening Remarks**
Grand Ballroom E-K

From naive simplicity to the reality of harvesting patient benefits: Some lessons we should have expected
Stephen H. Friend, Sage Bionetworks, Seattle, WA

6:30 p.m.-8:00 p.m. **Opening Plenary Session 1:**
Genome Scale Synthetic Lethal Screens in Model Organisms
Grand Ballroom E-K
Session Chairperson: William C. Hahn, Dana-Farber Cancer Institute, Boston, MA

The genetic landscape of a cell
Charlie Boone, University of Toronto, Toronto, ON, Canada

A synthetic genetic interaction approach to find novel anticancer therapeutic targets
Rodney Rothstein, Columbia University Irving Comprehensive Cancer Center, New York, NY

Synthetic lethal screens in *Drosophila*
Norbert Perrimon, Harvard Medical School, Boston, MA

8:00 p.m.-9:30 p.m. **Welcome Reception**
Grand Ballroom A-D

Saturday, May 18

7:00 a.m.-8:00 a.m. **Continental Breakfast**
Grand Ballroom Foyer

8:00 a.m.-10:00 a.m.   **Plenary Session 2:**
Systematic Functional Genomics I
Grand Ballroom E-K
Session Chairperson: Louis M. Staudt, National Cancer Institute, Bethesda, MD

Functional genomics and synthetic lethality
William C. Hahn, Dana-Farber Cancer Institute, Boston, MA

Non-oncogene addiction in multiple myeloma
Louis M. Staudt

Chromosome instability and synthetic lethality in yeast and cancer
Philip Hieter, University of British Columbia, Vancouver, BC, Canada

Functional characterization of breast cancer using pooled lentivirus shRNA screens*
Richard Marcotte, Ontario Cancer Institute, University Health Network, Toronto, ON, Canada

Targeting altered SWI/SNF function through synthetic lethal RNAi screening*
Andrew R. Conery, Constellation Pharmaceuticals, Inc., Cambridge, MA

10:00 a.m.-10:30 a.m.   **Break**

10:30 a.m.-12:30 p.m.   **Plenary Session 3:**
New Technology and Bioinformatics I
Grand Ballroom E-K
Session Chairperson: Sebastian Nijman, Research Center for Molecular Medicine-CeMM, Vienna, Austria

Haploid genetic screens in human cells
Thijn Brummelkamp, Netherlands Cancer Institute, Amsterdam, The Netherlands

Systematic mapping of cancer drug resistance mechanisms through high-density genetic interaction maps
Jonathan Weissman, University of California, San Francisco, CA

Targeting intratumoral genetic heterogeneity through rationally designed combination therapy
Douglas A. Lauffenburger, Massachusetts Institute of Technology, Cambridge, MA

Genome-wide screens for Wnt signaling in human haploid cells*
Andres Lebensohn, Stanford University, Stanford, CA

A network-based approach for drug synergy prediction from gene expression data*
Mariano J. Alvarez, Columbia University, New York, NY

*Short talks from proffered papers

| 12:30 p.m.-3:00 p.m. | **Poster Session A with Lunch** |
| | Grand Ballroom A-D |

3:00 p.m.-5:00 p.m.	**Plenary Session 4:**
	Systematic Functional Genomics II
	Grand Ballroom E-K
	Session Chairperson: William C. Hahn, Dana-Farber Cancer Institute, Boston, MA

Identification of therapeutic targets for MYC-driven cancers by functional genomics
Carla Grandori, Fred Hutchinson Cancer Research Center, Seattle, WA

Functional genomics of breast cancer
Benjamin G. Neel, University of Toronto Ontario Cancer Institute, Toronto, ON, Canada

Targeting the dependence of N-Myc on interaction with Aurora-A with small molecules
Martin Eilers, University of Würzburg, Würzburg, Germany

Construction of synthetic lethal networks for p53 tumor suppressor pathways identifies candidate therapeutic targets for metastatic, chemotherapy resistant HNSCC*
Chris Kemp, Fred Hutchinson Cancer Research Center, Seattle, WA

Systematic genetic interaction maps reveal synthetic-lethal vulnerabilities in leukemia and multiple myeloma*
Martin Kampmann, University of California, San Francisco/HHMI, San Francisco, CA

| 5:00 p.m.- | **Evening on Own** |

Sunday, May 19

| 7:00 a.m.-8:00 a.m. | **Continental Breakfast** |
| | Grand Ballroom Foyer |

8:00 a.m.-8:30 a.m.	**A Clinical Perspective**
	Grand Ballroom E-K
	Session Chairperson: Louis M. Staudt, National Cancer Institute, Bethesda, MD

Harnessing genetic dependencies in cancer therapy
Alan Ashworth, Institute of Cancer Research, London, United Kingdom

*Short talks from proffered papers

**8:30 a.m.-10:00 a.m.   Plenary Session 5:
                            New Technology and Bioinformatics II**

Mapping cellular networks by high-dimensional genetic interaction analysis
Michael Boutros, German Cancer Research Center (DKFZ), Heidelberg University, Heidelberg, Germany

Large-scale systematic explorations of single and combined drug responses to suggest anticancer drugs and overcome resistance
Joseph Lehár, Novartis Institutes for BioMedical Research, Cambridge, MA

Synthetic lethal screens in zebrafish*
Samuel Sidi, Mount Sinai School of Medicine, New York, NY

Identifying effectors of WT1 that regulate KRAS-induced senescence and chemoresistance in non-small cell lung cancer *
Ron Chen, Stanford University, Stanford, CA

10:00 a.m.-10:30 a.m.   Break

**10:30 a.m.-12:30 p.m.   Plenary Session 6:
                            Chemical Biology**
Grand Ballroom E-K
Session Chairperson: Sebastian Nijman, Research Center for Molecular Medicine-CeMM, Vienna, Austria

Exploiting the synthetic lethal properties of selective PI3K-ß inhibition in PTEN deficient cells with GSK2636771
Joel Greshock, GlaxoSmithKline, Collegeville, PA

Gene-drug interaction screens in isogenic cell models
Sebastian Nijman

Mapping insights about genetic interactions from yeast to human cells
Chad Myers, University of Minnesota, Minneapolis, MN

Synthetic lethal interaction of combined BCL-XL and MEK inhibition promotes tumor regressions in KRAS-mutant cancer models*
Ryan B. Corcoran, Massachusetts General Hospital Cancer Center, Boston, MA

A cyclic AMP-regulated melanocyte lineage program confers resistance to MAP kinase pathway inhibition*
Cory Johannessen, The Broad Institute of MIT and Harvard, Cambridge, MA

*Short talks from proffered papers

| 12:30 p.m.-3:00 p.m. | **Poster Session B with Lunch** |
| | Grand Ballroom A-D |

3:00 p.m.-5:00 p.m.	**Plenary Session 7:**
	Synergy with Current Cancer Drugs
	Grand Ballroom E-K
	Session Chairperson: William C. Hahn, Dana-Farber Cancer Institute, Boston, MA

Framing therapeutic opportunities in tumor-activated gametogenic programs
Angelique Whitehurst, UNC Lineberger Comprehensive Cancer Center, Chapel Hill, NC

Oncogenomic-dependent vulnerabilities in lung adenocarcinoma
Michael A. White, UT Southwestern Medical Center, Dallas, TX

From genetic screens to clinical trials: New concepts for copositioning anticancer drugs
Thomas "Trey" F. Westbrook, Baylor College of Medicine, Houston, TX

Characterizing the mechanism and the clinical relevance of the synthetic lethal interaction between STAT3 inhibition and HER2 overexpression in breast cancers*
Ruth Rodriguez-Barrueco, Columbia University, New York, NY

A genome-wide shRNA screen reveals that inhibiting kinases potentiates the anti-breast cancer activity of fluvastatin*
Janice Pong, Ontario Cancer Institute, Toronto, ON, Canada

| 5:00 p.m.- | **Evening on Own** |

Monday, May 20

| 7:00 a.m.-8:00 a.m. | **Continental Breakfast** |
| | Grand Ballroom Foyer |

*Short talks from proffered papers

8:00 a.m.-10:00 a.m.   **Plenary Session 8:**
                                Resistance and Codependencies
                                Grand Ballroom E-K
                                Session Chairperson: Louis M. Staudt, National Cancer Institute,
                                Bethesda, MD

Systematic studies of resistance to targeted anticancer agents
Levi A. Garraway, Dana-Farber Cancer Institute, Boston, MA

Exploiting RAS and RAF for therapeutic gain in melanoma
Richard M. Marais, Paterson Institute for Cancer Research, Manchester, United Kingdom

Collateral lethality
Ronald A. DePinho, The University of Texas MD Anderson Cancer Center, Houston, TX

A critical role of the SUMOylation pathway in KRAS-driven transformation*
Ji Luo, National Cancer Institute, Bethesda, MD

Targeting the GATA2 transcriptional network in K-Ras-driven lung adenocarcinoma*
Madhu S. Kumar, Cancer Research UK London Research Institute, London, United Kingdom

10:00 a.m.-10:15 a.m.   **Break**

10:15 a.m.-10:45 a.m.   **A Systems Biology Perspective**
                                Grand Ballroom E-K
                                Session Chairperson: Sebastian Nijman, Research Center for
                                Molecular Medicine-CeMM, Vienna, Austria

Interrogation of cross-species regulatory networks elucidates synergistic addiction mechanisms in aggressive prostate cancer
Andrea Califano, Columbia University, New York, NY

10:45 a.m.-12:15 p.m.   **Plenary Session 9:**
                                Connection to Therapy

Title to be announced
Judy E. Garber, Dana-Farber Cancer Institute, Boston, MA

Functional screens to uncover treatment response
Roderick L. Beijersbergen, Netherlands Cancer Institute, Amsterdam, The Netherlands

Primary resistance to MAPK inhibition in BRAF-mutant cancer is determined by kinetics of feedback release*
Martin L. Sos, Howard Hughes Medical Institute, University of California, San Francisco, CA

Targeting cancer-specific kinase dependency for precision therapy*
Chandan Kumar-Sinha, University of Michigan, Ann Arbor, MI

*Short talks from proffered papers