Conference Program

NOTE:

A = Session in the Translation of the Cancer Genome Conference

B = Session in the Computational and Systems Biology of Cancer Conference

A and B = Joint Session

Sunday, February 8

7:00 p.m.-8:00 p.m.   **[JOINT SESSION] Welcome and Keynote address**
Grand Ballroom

Spatial systems biology and cancer
Joe W. Gray, Oregon Health & Science University, Portland, OR

8:00 p.m.-9:30 p.m.   **Reception**
Venetian Room

Monday, February 9

7:00 a.m.-8:00 a.m.   **Breakfast**
Venetian Room

8:00 a.m.-10:00 a.m.   **[JOINT SESSION] Session A6, B1: Patient Stratification: Biomarker/Genomic Approaches**
Grand Ballroom
Session Chairperson: William R. Sellers, Novartis Institutes for BioMedical Research, Cambridge, MA

The application of integrative sequencing for precision oncology
Arul M. Chinnaiyan, University of Michigan, Ann Arbor, MI

Towards the next clinical option: Experience from a precision cancer medicine trial
Mark A. Rubin, Weill Cornell Medical College, New York, NY

Somatic mutations in human lung cancer
Matthew L. Meyerson, Dana-Farber Cancer Institute, Boston, MA

The prognostic landscape of genes and infiltrating immune cells across human cancers*
Andrew Gentles, Stanford University, Stanford, CA

Multiple Pathway Learning accurately predicts gene essentiality in the Cancer Cell Line Encyclopedia*
Vladislav Uzunangelov, University of California, Santa Cruz, CA

10:00 a.m.-10:30 a.m.   **Break**
Grand Ballroom Foyer

*Short talks from proffered papers.

10:30 a.m.-12:15 p.m.   **[JOINT SESSION] Session A7, B2: Big Data in Clinical Applications**
Grand Ballroom
Session Chairperson: Andrea Califano, Columbia University, New York, NY

Modeling signaling systems in breast cancer cell lines
Paul T. Spellman, Oregon Health and Science University, Portland, OR

Network stratification of tumor mutations
Trey Ideker, University of California San Diego, La Jolla, CA

Genomic approaches for risk assessment in acute myeloid leukemia*
Allegra Petti, Washington University, St. Louis, MO

High-throughput gene expression profiling as a generalizable assay for determination of mutation impact on gene function*
Alice H. Berger, Broad Institute of MIT and Harvard, Cambridge, MA

Investigating the importance of low allele frequency mutations for cancer patient management*
Ken Chen, The University of Texas MD Anderson Cancer Center, Houston, TX

12:15 p.m.-1:45 p.m.   **Lunch on Own**

1:45 p.m.-4:00 p.m.   **[JOINT SESSION] Session A8, B3: Network-based Cancer Biology**
Grand Ballroom
Session Chairperson: Peter K. Jackson, Stanford University, Stanford, CA

Using single cell pharmacology to improve drug design
Peter K. Sorger, Harvard Medical School, Boston, MA

Interactome networks and cancer
Marc Vidal, Dana-Farber Cancer Institute, Boston, MA

Systematic elucidation and pharmacological targeting of non-oncogene dependencies in human malignancies
Andrea Califano, Columbia University, New York, NY

Nucleation of transcriptional super-enhancers at tumor oncogenes*
Brian J. Abraham, Whitehead Institute for Biomedical Research, Cambridge, MA

Functional analysis of diverse oncogenic driver mutations using an isogenic cell line library identifies novel drug responses and alterations in metabolism*
Andrei Goga, University of California, San Francisco, CA

New tools for mapping genetic modifiers of cancer risk in the tumor microenvironment*
Michael J. Flister, Medical College of Wisconsin, Milwaukee, WI

*Short talks from proffered papers.

COMPUTATIONAL AND SYSTEMS BIOLOGY OF CANCER

4:15 p.m. -5:00 p.m.   **[JOINT SESSION] Keynote Talk 2**
Grand Ballroom

Cognitive computing for oncology
Eric W. Brown, IBM TJ Watson Research Center, Yorktown Heights, NY

5:00 p.m. -5:15 p.m.   **Closing remarks for the attendees of the AACR Special Conference on Translation of Cancer Genome**

5:15 p.m. -7:45 p.m.   **Poster Session B1 with Reception**
Gold Room/Venetian Room

Tuesday, February 10

7:00 a.m.-8:00 a.m.   **Breakfast**
Venetian Room

8:00 a.m.-10:00 a.m.   **Session B4: Modeling and Interrogating Cancer Regulatory Networks**
Grand Ballroom
Session Chairperson: Cigall Kadoch, Dana-Farber Cancer Institute, Boston, MA

Differential networks and drug networks: A computational approach to drug discovery
Diego di Bernardo, Telethon Institute of Genetics and Medicine, Naples, Italy

Regulatory networks of genetic variants underlying common disease and cancer
Manolis Kellis, Massachusetts Institute of Technology, Cambridge, MA

Lean data integration strategy in cancer systems biology and systems pharmacology
Avi Ma'ayan, Mount Sinai Hospital, New York, NY

Extracellular stiffness cues drive spatial reorganization of the genome to globally constrain RNA abundance*
Russell Bainer, University of California, San Francisco, CA

Oncogenic dysregulations in neuroblastoma are associated with distal large chromosomal aberrations*
Gonzalo Lopez, Columbia University, New York, NY

10:00 a.m.-10:30 a.m.   **Break**
Grand Ballroom Foyer

*Short talks from proffered papers.

10:30 a.m.-12:30 p.m.   **Session B5: Noncoding RNAs in Cancer**
Grand Ballroom
Session Chairperson: Diego di Bernardo, Telethon Institute of Genetics and Medicine, Naples, Italy

Genomic alterations dysregulate cancer genes by modulating microRNA activity
Pavel Sumazin, Baylor College of Medicine, Houston, TX

microRNA-based therapeutics in cancer
Frank J. Slack, Harvard Medical School, Boston, MA

Title to be announced
Pier Paolo Pandolfi, Beth Israel Deaconess Medical Center, Boston, MA

Reference pharmacologic class analysis for Connectivity Map discovery*
Steven M. Corsello, Broad Institute of MIT and Harvard, Cambridge, MA

Noncoding RNA regulation of cancer stem cell division symmetry*
Xiling Shen, Cornell University, Ithaca, NY

12:30 p.m.-3:00 p.m.   **Poster Session B2 with Lunch**
Gold Room/Venetian Room

3:00 p.m.-5:00 p.m.   **Session B6: Cancer Proteomics**
Grand Ballroom
Session Chairperson: Sohail Tavazoie, Rockefeller University, New York, NY

Protein networks linking new and old tumor suppressors
Peter K. Jackson, Stanford University, Stanford, CA

Cross-species computational and functional studies to identify key drivers of Kras-driven oncogenesis in lung cancer
Alejandro Sweet-Cordero, Stanford University, Stanford, CA

Regulation of signaling interactomes in cancer
Anne-Claude Gingras, Lunenfeld-Tanenbaum Research Institute, Toronto, ON, Canada

Systems and structural biology approaches to elucidate new effectors in KRAS mutant tumors*
Joshua E. Broyde, Columbia University, New York, NY

Integrative functional genomics of breast cancer*
Richard Marcotte, Princess Margaret Cancer Centre, Toronto, ON

5:00 p.m.-   **Dinner on Own**

*Short talks from proffered papers.

7:00 a.m.-8:00 a.m.	**Breakfast** Venetian Room

8:00 a.m.-10:15 a.m.   **Session B7: Integrative and Systems Approaches to Elucidating Tumor Progression**
Grand Ballroom
Session Chairperson: Dana Pe'er, Columbia University, New York, NY

Post-transcriptional regulation of metastatic progression
 Sohail Tavazoie, Rockefeller University, New York, NY

Minute-by-minute analysis of BAF-polycomb opposition
Cigall Kadoch, Dana-Farber Cancer Institute, Boston, MA

Targeting chromatin remodeling complexes in cancer
Gerald R. Crabtree, Stanford University, Stanford, CA

Using systems biology of mouse models to identify master regulators of malignancy and drug response
Cory Abate-Shen, Columbia University Irving Comprehensive Cancer Center, New York, NY

Predicting the essentialities of protein-protein interactions in cancer*
Carlos S. Moreno, Emory University, Atlanta, GA

10:15 a.m.-10:30 a.m.   **Break**
Grand Ballroom Foyer

10:30 a.m.-12:15 p.m.   **Session B8: Tumor Heterogeneity and Plasticity**
Grand Ballroom
Session Chairperson: Pavel Sumazin, Baylor College of Medicine, Houston, TX

Computational dissection of phenotypic and functional heterogeneity in cancer
Dana Pe'er, Columbia University, New York, NY

Cancer heterogeneity and drug resistance
Steven Altschuler, University of California, San Francisco, CA

A systems structured view of immunity and cancer
Garry P. Nolan, Stanford University School of Medicine, Stanford, CA

Transcriptional landscape of drug response guides the design of specific and potent drug combinations*
Marc Hafner, Harvard Medical School, Boston, MA

12:15 p.m.-   **Closing Remarks**

*Short talks from proffered papers.