Saturday, February 7

1:00 p.m.-3:00 p.m.  Session A1: Cancer Genomics and Epigenomics  
Grand Ballroom  
Session Chairperson: Levi A. Garraway, Dana-Farber Cancer Institute, Boston, MA

**Genomic heterogeneity in localized lung cancer**  
Andrew Futreal, The University of Texas MD Anderson Cancer Center, Houston, TX

**Cancer genomics: Translational challenges**  
Elaine R. Mardis, Washington University, St. Louis, MO

**The Pediatric Cancer Genome Project: Lessons learned**  
James R. Downing, St. Jude Children’s Research Hospital, Memphis, TN

**Identifying clinically important somatic mutations through a knowledge-based approach**  
Benjamin J. Ainscough, Washington University in St. Louis School of Medicine, St. Louis, MO

**Aneuploidy as a driver of liver cancer**  
Lee Albacker, Harvard Medical School, Boston, MA

3:00 p.m.-3:30 p.m.  Break  
Grand Ballroom Foyer

3:30 p.m.-5:30 p.m.  Session A2: Clinical Applications of Cancer Genomics  
Grand Ballroom  
Session Chairperson: Elaine R. Mardis, Washington University, St. Louis, MO

**Clinical decision support in the era of genome-informed cancer medicine**  
Mia A. Levy, Vanderbilt University, Nashville, TN

**Guiding principles of resistance to targeted therapeutics**  
Levi A. Garraway, Dana-Farber Cancer Institute, Boston, MA

**Genomic medicine: Transforming cancer research and care**  
Lynda Chin, The University of Texas MD Anderson Cancer Center, Houston, TX

**Pan-cancer analysis of the etiology and consequences of intratumor heterogeneity**  
Noemi Andor, Stanford University School of Medicine, Stanford, CA

**Cancer drug response networks built for comparative cancer pharmacogenomics identifies combination therapies for repositioning**  
Gurkan Bebek, Case Western Reserve University, Cleveland, OH

*Short talks from proffered papers.*
**Sunday, February 8**

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

**8:00 a.m.-10:00 a.m.**  Session A3: Genomics and Target Discovery  
Grand Ballroom  
*Session Chairperson: Todd R. Golub, Broad Institute of MIT and Harvard, Cambridge, MA*

- **Globally monitoring translation one codon at a time through ribosome profiling**  
  Jonathan Weissman, University of California San Francisco, San Francisco, CA

- **Functional genomics to identify cancer targets**  
  William C. Hahn, Dana-Farber Cancer Institute, Boston, MA

- **Therapy of lymphoma inspired by functional and structural genomics**  
  Louis M. Staudt, National Cancer Institute, Bethesda, MD

- **Personalized medicine**  
  René Bernards, Netherlands Cancer Institute, Amsterdam, The Netherlands

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

**10:30 a.m.-12:30 p.m.**  Session A4: Genomics and Drug Discovery  
Grand Ballroom  
*Session Chairperson: Wendy Winckler, Novartis Institutes for BioMedical Research, Cambridge, MA*

- **Tools for genomic approaches to drug discovery: PRISM and Connectivity Map**  
  Todd R. Golub, Broad Institute of MIT and Harvard, Cambridge, MA

- **Functional genomic approaches to find the best cancer targets**  
  Frank Stegmeier, Novartis, Cambridge, MA

- **Deconvoluting the molecular circuitry of cancerous cells with high-throughput experimentation**  
  Lawrence Lum, UT Southwestern Medical Center, Dallas, TX

- **Using genome-scale CRISPR-mediated loss-of-function and gain-of-function screens to analyze gene-drug interactions in cancer**  
  Martin Kampmann, Howard Hughes Medical Institute, University of California, San Francisco, CA

- **Functional prioritization of rare gene aberration drivers of cancer**  
  Kenneth L. Scott, Baylor College of Medicine, Houston, TX

*Short talks from proffered papers.*
12:30 p.m.-3:00 p.m.  Poster Session A2 with Lunch
Gold Room/Venetian Room

3:00 p.m.-5:00 p.m.  Session A5: Genomics and Diagnostics
Grand Ballroom
Session Chairperson: Louis M. Staudt, National Cancer Institute, Bethesda, MD

Single-cell sequencing in cancer genomics
Christopher Love, Massachusetts Institute of Technology, Cambridge, MA

Next-generation diagnostics for precision cancer medicine
Wendy Winckler, Novartis Institute for Biomedical Research, Cambridge, MA

Circulating tumor DNA
Luis A. Diaz, Johns Hopkins Kimmel Comprehensive Cancer Center, Baltimore, MD

Towards precision functional genomics via next-generation functional mapping of cancer variants*
Jesse S. Boehm, Broad Institute of Harvard and MIT, Cambridge, MA

In silico dissection of bulk tumors reveals immune subsets that predict cancer clinical outcomes*
Aaron M. Newman, Stanford University, Stanford, CA

5:00 p.m.-7:00 p.m.  Dinner on Own

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

*Short talks from proffered papers.
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

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

*Short talks from proffered papers.
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

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 the Cancer Genome

*Short talks from proffered papers.