AACR Virtual Special Conference on
Tumor Heterogeneity: From Single Cells to Clinical Impact
September 17-18, 2020

Presentation Formats:

Opening and Closing Keynotes:	25-minute presentation + 5-minute Q&A
Invited Speaker Presentations:	20-minute presentations + 5-minute Q&A
Short-Talks from Highly Rated Abstracts:	10-minute presentations + 5-minute Q&A

Accepted abstracts/posters: 5-minute presentations, no Q&A.
   ***Abstracts will be released as 5-minute presentations (5 slides) at the beginning of the meeting
   in a single "poster" session.*

Cochairs:
Nicholas E. Navin, The University of Texas MD Anderson Cancer Center, Houston, TX
Kornelia Polyak, Dana-Farber Cancer Institute, Boston, MA
Alex K. Shalek, Massachusetts Institute of Technology, Cambridge, MA
Charles Swanton, The Francis Crick Institute and UCL Cancer Institute, London, England

THURSDAY, SEPTEMBER 17

Welcome and Opening Keynote
9:30 AM - 10:05 AM
Moderator: Alex K. Shalek, Massachusetts Institute of Technology, Cambridge, MA

Welcome and Opening Remarks
Charles Swanton, The Francis Crick Institute and UCL Cancer Institute, London, England

Introduction of Keynote Speaker
Alex K. Shalek, Massachusetts Institute of Technology, Cambridge, MA

Keynote Address:
Single cell analysis of CRISPR T cells
Carl H. June, University of Pennsylvania, Philadelphia, PA

Break
10:05 AM - 10:20 AM

Session 1: Spatial Pathology: Technological Innovations
10:20 AM - 11:50 AM
Moderator: R. Michael Angelo, Stanford University, Palo Alto, CA

Slide-seq: A platform for understanding cellular circuits in tissue
Fei Chen, Broad Institute of MIT and Harvard, Cambridge, MA

Highly multiplexed imaging of tissues with subcellular resolution by imaging mass cytometry

Bernd Bodenmiller, University of Zürich, Zurich, Switzerland

Relating single cell function to tissue structure in human tumors using MIBI-TOF
R. Michael Angelo, Stanford University, Palo Alto, CA

Analysis of spatiotemporal phenotypic heterogeneity in chemoresistant triple negative breast cancer using imaging mass cytometry*
Amanda Rinkenbaugh, MD Anderson Cancer Center, Houston, TX

Break
11:50 AM - 12:05 PM

Session 2: Spatial Pathology: Computational Developments
12:05 PM - 1:10 PM
Moderator: Sylvia K. Plevritis, Stanford University, Stanford, CA

Deciphering the co-evolution of cancer and the microenvironment
Yinyin Yuan, Institute of Cancer Research, London, United Kingdom

Computational modeling of the tumor microenvironment
Sylvia K. Plevritis, Stanford University, Stanford, CA

Inferring the evolutionary dynamics of ductal carcinoma in situ through multi-regional sequencing and mathematical modeling*
Marc D. Ryser, Duke University, Durham, NC

Break
1:10 PM - 1:25 PM

Session 3: Defining and Targeting the Tumor Microenvironment
1:25 PM - 2:55 PM
Moderator: Yardena Samuels, Weizmann Institute of Science, Rehovot, Israel

UVB-induced tumor heterogeneity directs immune response in melanoma
 Yardena Samuels, Weizmann Institute of Science, Rehovot, Israel

Tracking the impact of tumor mutations in the T cell differentiation landscape of lung cancer
Sergio A. Quezada, University College London Cancer Institute, London, United Kingdom

Genetic mechanisms underlying immunotherapy efficacy
Timothy A. Chan, Cleveland Clinic Lerner College of Medicine, Cleveland, OH

Subtype-specific microenvironmental crosstalk and tumor cell plasticity in metastatic pancreatic cancer*
Peter Winter, Massachusetts Institute of Technology, Cambridge, MA

Break
2:55 – 3:10 PM

Session 4: Clinical Insights for Targeting and Monitoring Cellular Heterogeneity
3:10 – 4:40 PM
Moderator: Catherine J. Wu, Dana-Farber Cancer Institute, Boston, MA

Uncovering the ecology of glioblastoma with spatial digital profiling and single cell genotyping
Michalina Janiszewska, The Scripps Research Institute Florida, Jupiter, FL

Detecting and targeting cellular heterogeneity of the lymphoid blood malignancies
Catherine J. Wu, Dana-Farber Cancer Institute, Boston, MA

Single cell multi-omics to define normal and malignant differentiation topologies
Dan-Avi Landau, Weill Cornell Medical College, New York, NY

Understanding tumor clonal evolution by single-cell transcriptomic analysis in liver cancer*
Lichun Ma, National Cancer Institute, Bethesda, MD

FRIDAY, SEPTEMBER 18

Session 5: Prevention and Premalignancies
9:30 AM - 11:00 AM
Moderator: Nicholas E. Navin, UT MD Anderson Cancer Center, Houston, TX

In the light of evolution: Why do we get more cancers in old age?
James V. DeGregori, University of Colorado Anschutz Medical Campus, Aurora, CO

Breast cancer evolution – Insights from single cell genomics
Nicholas E. Navin, UT MD Anderson Cancer Center, Houston, TX

Inflammatory memory and tumorigenesis
Shruti Naik, New York University Langone Medical Center, New York, NY

Mapping the tumor and microenvironmental evolution underlying DCIS progression through multiplexed ion beam imaging*
Tyler Risom, Stanford University, Palo Alto, CA

Break
11:00 AM - 11:15 AM

Session 6: Tumor Progression and Therapeutic Resistance
11:15 AM - 12:45 PM
Moderator: Charles Swanton, The Francis Crick Institute, London, United Kingdom

Cancer evolution, immune evasion and metastasis
Charles Swanton, The Francis Crick Institute, London, United Kingdom

Measuring and modeling cancer evolution with single cell approaches
Sohrab Shah, Memorial Sloan Kettering Cancer Center, New York, NY

Genomic evolution of brain metastases: Implications for precision medicine
Priscilla K. Brastianos, Harvard Medical School/Massachusetts General Hospital, Boston, MA

Stabilising selection causes grossly altered but stable karyotypes in metastatic colorectal cancer*
Salpie Nowinski, Barts Cancer Institute, Queen Mary University London, London, United Kingdom

Break
12:45 PM - 1:00 PM

Session 7: Liquid Tumors and Hematologic Malignancies
1:00 PM - 2:40 PM
Moderator: Alex K. Shalek, Massachusetts Institute of Technology, Cambridge, MA

Clonal heterogeneity and evolution of acute myeloid leukemia
Koichi Takahashi, UT MD Anderson Cancer Center, Houston, TX

Aberrant leukemic developmental hierarchies and MRD-specific targeting informed by single-cell biophysical and molecular profiling
Alex K. Shalek, Massachusetts Institute of Technology, Cambridge, MA

Stem cells play a role in human leukemia from origin to relapse
John E. Dick, University of Toronto, Toronto, ON, Canada

Single cell proteomics to capture human dysplasia and dysfunction
Sean Bendall, Stanford University School of Medicine, Palo Alto, CA

Break
2:40 – 2:55 PM

Session 8: Computational Advances in Tumor Analysis
2:55 – 4:25 PM
Moderator: Peter Vasili Kharchenko, Harvard Medical School, Boston, MA

Impact of metastatic prostate cancer on human bone marrow
Peter Vasili Kharchenko, Harvard Medical School, Boston, MA

Dissecting glioblastoma by single cell RNA-seq
Itay Tirosh, Weizmann Institute of Science, Rehovot, Israel

Spatial characterization of the tumor-immune microenvironment through neoadjuvant HER2-targeted therapy
Christina Curtis, Stanford University, Stanford, CA

A systems biology approach to reprogramming drug-resistant breast cancer stem-like cells*
Jeremy Worley, Columbia University, New York, NY

Break
4:25 PM - 4:40 PM

Keynote Address and Closing Remarks
4:40 PM - 5:20 PM
Moderator: Nicholas E. Navin, The University of Texas MD Anderson Cancer Center, Houston, TX

Introduction of Keynote Speaker
Nicholas E. Navin, The University of Texas MD Anderson Cancer Center, Houston, TX

Keynote Address:
Tumor evolution: From Darwin's finches to breast cancer
Kornelia Polyak, Dana-Farber Cancer Institute, Boston, MA

Closing Remarks
Kornelia Polyak, Dana-Farber Cancer Institute, Boston, MA