Poster Program

Poster Session 1
Friday, September 28, 2018 - 13:30-15:00
Room – Regency A

Poster Session 2
Saturday, September 29, 2018 - 13:30-15:00
Room - Regency A

Poster teasers from PT.01 to PT.04 and all posters with an odd number (P.001, P.003, P.005...) will be presented from 13:30-15:00, Friday, September 28, 2018.

Poster teasers from PT.05 to PT.08 and all posters with an even number (P.002, P.004, P.006...) will be presented from 13:30-15:00, Saturday, September 29, 2018.

[PT.01] Analysis of 7,815 cancer exomes from The Cancer Genome Atlas (TCGA) reveals novel associations between mutational processes and somatic driver mutations
R.C. Poulos†1, 2, Y.T. Wong†, R. Ryan†, J.W.H. Wong† 3, 1University of New South Wales, Australia, 2University of Sydney, Australia, 3University of Hong Kong, Australia

[PT.02] TCGA multi-omic data provides the selective advantage that each mutation confers to cancer cells
V.L. Cannataro, S.G. Gaffney, J.P. Townsend*, Yale University, USA

[PT.03] Metabolic portraits of tumors
E. Reznik†1, A. Luna2, J. Xu1, C.J. Creighton3, A.A. Hakimi1, C. Sander2, 1Memorial Sloan Kettering Cancer Center, USA, 2Dana Farber Cancer Institute, USA, 3Baylor College of Medicine, USA

[PT.04] Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing
I. Cortes Ciriano†1, 2, J.K. Lee1, R. Xi1, D. Jain1, L. Yang1, D. Gordenin1, L. Klimczak5, C.Z. Zhang1 6, D. Pellman1 4, P.J. Park1, 1Harvard Medical School, USA, 2University of Cambridge, UK, 3Peking University, China, 4University of Chicago, USA, 5US National Institutes of Health, USA, 6Dana-Farber Cancer Institute, USA

[PT.05] Beyond BRCA: Discovery of novel drivers of homologous recombination deficiencies
D. McGrail†1, Y. Li1, B. Feng2, L. Hu1, G. Mills1, S. Yi1, S. Lin1, N. Sahni1, 4, 1The University of Texas MD Anderson Cancer Center, USA, 2TESARO Inc, USA, 3Dell Medical School, USA, 4Baylor College of Medicine, USA

[PT.06] Rare Cancers: Characterization and assessment of progress and resources
R. Barajas, S. Nelson*, S. Fagan, L. Gallicchio, M. Rotunno, D. Daee, N. Shelburne, D. Carrick, L. Mechanic, National Cancer Institute, USA

[PT.07] Using TCGA data to identify novel RAS-driven immune modulators in LUAD
S. de Carné*, P. East, C. Moore, J. Downward, The Francis Crick Institute, UK

[PT.08] Single-cell characterization of the tumor microenvironment in advanced, oncogene-driven non-small cell lung cancer
C.E. McCoach†1, J. Rotow1, A. Maynard2, D. Naeger1, Y. Gesthalter1, K. Kolli1, J.S. Weissman1, C.M. Blakely1, S. Dormanis2, T.G. Bivona1, 1University of California, San Francisco, USA, 2Chan-Zuckerberg Biohub, USA

[P.001] A comprehensive pan-cancer molecular study of gynecologic and breast cancers
A.C. Berger†1, A. Korkut1, R.S. Kanchi1, A.M. Hegde1, W. Lenoir1, T.C.G.A. Research Network3, J.N. Weinstein1, G.B. Mills1, D.A. Levine4, R. Akbani5, 1University of Texas MD Anderson Cancer Center, USA, 2The Eli and Edythe L. Broad Institute of Massachusetts Institute of Technology and Harvard University, USA, 3National Cancer Institute, USA, 4New York University, USA

[P.002] A pan-cancer analysis reveals high-frequency genetic alterations in mediators of signaling by the TGF-β superfamily
A. Korkut1, S. Zaidi1, R.S. Kanchi1, S. Rao2, N.R. Gough2, A. Schultz1, T.C.G.A. Research Network3, J.N. Weinstein1, L. Mishra2, R. Akbani5, 1University of Texas MD Anderson Cancer Center, USA, 2George Washington University, USA, 3National Cancer Institute, USA

[P.003] Dose response analysis in cell line models for cancer pharmacogenomics
F. Akhtari†1, T. Havener2, G. Small2, J. Jack1, K. Roell1, D. Rotroff1, H. McLeod3, T. Wiltshire2, A.
[P.004] In silico identification of a gene expression signature for patients with IDH-WT glioma having a better prognosis
A. Allaire*, H.D. Nguyen, M. Bisaillon, M.S. Scott, M. Richer, Université de Sherbrooke, Canada

[P.005] Multi-omics data integration reveals miRNA mediated gene regulation in triple-negative breast cancer (TNBC)
S. Verma1, P. Panigrahi1, I. Subramanian1, S. Kumar1, V. Singh1, S. Dixit2, A. Jere1, K. Anamika*1, 1Persistent Systems, India, 2Orchids Breast Health Center in Association with Prashanti Cancer Care Mission, India

[P.006] Pooled shRNA screen identifies SEL1L, an ERAD component, as a crucial mediator of temozolomide resistance in glioblastoma
A. Arora1, V.S. Tomar1, S. Thomas1, V. Patil1, J.D. Hoheisel2, K. Somasundaram1, 1Indian Institute of Science, India, 2Functional Genome Analysis, Deutsches Krebsforschungszentrum, Germany

[P.007] An outcome weighted learning approach for identifying clinically relevant patient subgroups from large-scale sequencing data
A. Arora*, A. Olszen2, V. Seshan1, R. Shen1, 1Memorial Sloan-Kettering Cancer Center, USA, 2University of California, San Francisco, USA

[P.008] Deep sequencing of 3 cancer cell lines on Illumina HiSeqX and Novaseq
K. Arora*, M. Shah, M. Johnson, K. Nagulapalli, R. Sanghvi, J. Shelton, New York Genome Center, USA

[P.009] DNA mutation assessment reveals RNA allelic imbalance in TCGA data
S.T. Bailey*, J. Lund, J.R. Gulcher, WuXi NextCODE Genomics, Inc., USA

[P.010] Convergent pan-cancer de-differentiation to a small cell neuroendocrine phenotype with shared susceptibilities
N. Balanis*, K. Sheu, F. Esedebe, S. Patel, B. Smith, J.W. Park, B. Gomperts, O. Witte, T. Graeber, University of California Los Angeles, USA

[P.011] Identification of breast cancer biomarkers by systems biology
F. Wang1, B. Ljubic1, 2, O. Perez1, C.A. Barrero*1, 1Temple University School of Pharmacy, USA, 2Data Analytics and Biomedical Informatics Center, Temple University, USA

[P.012] The identification of patient-specific cancer genes directs patient stratification in esophageal adenocarcinoma
L. Benedetti*1, 2, T. Mourikis1, 2, E. Foxall1, J. Pemer1, M. Cereda1, J. Lagergren1, M. Howell1, C. Yau1, R. Fitzgerald1, D. Ciccarelli1, 1Francis Crick Institute, UK, 2King’s College London, UK, 3University of Cambridge, UK, 4Italian Institute for Genomic Medicine, Italy, 5University of Birmingham, UK

[P.013] Accessible pipeline for translational research using TCGA: Tristetraprolin as an example relating gene mechanism to a disease specific outcomes
A. Berglund*, R. Putney, J. Creed, G. Aden-Buie, T. Gerke, R. Rounbehler, H. Lee Moffitt Cancer Center & Research Institute, USA

[P.014] Exploration of immune cell infiltrates in brain cancer patients
K. Bhuvaneshwar*, S. Madhavan, Y. Gusev, Georgetown University, USA

[P.015] Impact of gene regulation in the cross-talk between the immune system and melanoma tumors
N. Jorge, P. Possik, M. Boroni*, Brazilian National Cancer Institute, Brazil

[P.016] Applying MethylMix to identify epigenetically deregulated microRNAs in cancer
K. Brennan1, M. Prunello2, G. Robertson2, T. Knijnenburg3, S.JM Jones2, C. Van Waes1, O. Gevaert1, 1Stanford University, USA, 2Canada’s Michael Smith Genome Sciences Centre, Canada, 3National Institute on Deafness and Other Communication Disorders, USA, 4Institute for Systems Biology, USA, 5National University of Rosario, Argentina

[P.017] Next-generation clustered heat maps for the interactive exploration of TCGA data
B.M. Broom1, M.C. Ryan2, C.W. Wakefield1, R. Brown2, F. Ikeda2, M. Stucky2, R. Akbani1, J. Melott1, H. Liang1, J.N. Weinstein1, 1University of Texas MD Anderson Cancer Center, USA, 2In Silico Solutions, USA

[P.018] Cancer CellNet: a resource to evaluate the transcriptomic similarities of cancer models to natural tumors
E. Lo1, B. Issacs1, P. Kumar1, E. de Rocha2, K. DiNapoli1, P. Cahan*, 1Johns Hopkins University, USA, 2Harvard Medical School, USA

[P.019] Understanding the ancestral contribution to cancer risks using TCGA samples
J. Carrot-Zhang*, O.B.O. GDAN Ancestry Informative Markers AWG1, 1Broad Institute, USA, 2NCI, USA
The genomic and epigenomic landscape of mammalian SWI/SNF complex perturbations in cancer
S. Cassel\textsuperscript{1,2}, C. Olsen\textsuperscript{1}, \textsuperscript{1}Harvard Medical School, USA, \textsuperscript{2}Dana Farber Cancer Institute, USA

Prognostic long non-coding RNAs in low grade glioma patients
A. Chattrath\textsuperscript{a}, M. Kiran, A. Ratan, P. Kumar, A. Dutta, \textsuperscript{1}University of Virginia, USA

The landscape of genomic alterations across childhood cancers
S. Gröbner\textsuperscript{2,3}, B. Wost\textsuperscript{2,4}, L. Chavez\textsuperscript{1,3}, M. Zapatka\textsuperscript{3}, S. Pfister\textsuperscript{2,4}, \textsuperscript{1}UC San Diego, USA, \textsuperscript{2}Hopp-Children’s Cancer Center at the NCT Heidelberg (KiTZ), Germany, \textsuperscript{3}German Cancer Research Center (DKFZ), Germany, \textsuperscript{4}Heidelberg University Hospital, Germany

ELMER v.2: An R/Bioconductor package to reconstruct gene regulatory networks from DNA methylation and transcriptome profile
T. Chedraoui Silva\textsuperscript{a, b}, N. Gul\textsuperscript{d}, D. Lin\textsuperscript{e}, B.P. Berman\textsuperscript{a}, \textsuperscript{1}University of São Paulo, Brazil, \textsuperscript{2}Cedars-Sinai Medical Center, USA

Novel cancer drivers identified by joint DNA/RNA analysis of differential allelic cis-regulatory effects (DACRE) in clinical tumors
F. Wang\textsuperscript{1}, S. Zhang\textsuperscript{1}, T-B. Kim\textsuperscript{1}, K. Sircar\textsuperscript{1}, J. Karam\textsuperscript{1}, F. Meric-Bernstam\textsuperscript{1}, J.W. Weinstein\textsuperscript{1}, L. Ding\textsuperscript{2}, G. B. Mills\textsuperscript{1}, K. Chen\textsuperscript{a,1}, \textsuperscript{1}The University of Texas MD Anderson Cancer Center, USA, \textsuperscript{2}Washington University School of Medicine, USA

Recurrent copy number alterations in head and neck cancer deregulate the transcriptome and key signaling networks in cell lines and tumors with worse prognosis
H. Cheng\textsuperscript{a, b}, X. Yang\textsuperscript{1}, H. Si\textsuperscript{c}, A.D. Saleih\textsuperscript{1}, W. Xiao\textsuperscript{1}, J. Coupar\textsuperscript{1}, S.M. Gollin\textsuperscript{3}, R.L. Ferris\textsuperscript{3}, W.G. Yarbrough\textsuperscript{3}, M.E. Prince\textsuperscript{4}, \textsuperscript{1}National Institute on Deafness and Other Communication Disorders, USA, \textsuperscript{2}Emory University, USA, \textsuperscript{3}University of Pittsburgh, USA, \textsuperscript{4}University of Michigan, USA, \textsuperscript{5}Yale University, USA, \textsuperscript{6}Food and Drug Administration, USA

Genomic and functional approaches to understanding cancer aneuploidy
A. Taylor\textsuperscript{1,2}, J. Shih\textsuperscript{2}, G. Ha\textsuperscript{1,2}, G. Gao\textsuperscript{2,3}, X. Zhang\textsuperscript{1,2}, A. Berger\textsuperscript{2}, A. Cherniack\textsuperscript{a, b,1,2}, \textsuperscript{1}Dana-Farber Cancer Institute, USA, \textsuperscript{2}Broad Institute, USA, \textsuperscript{3}Mayo Clinic College of Medicine, USA, \textsuperscript{4}Chan Soon-Shiong Institute of Medicine at Windber, USA, \textsuperscript{5}University of Texas MD Anderson Cancer Center, USA

New molecular subtypes of hepatocellular carcinoma and cholangiocarcinoma
A.D. Cherniack\textsuperscript{a,1}, O.B.O. GDAN Tumor Molecular Pathology AWG\textsuperscript{2}, \textsuperscript{1}The Broad Institute of Harvard and MIT, USA, \textsuperscript{2}NCI, USA

Ensemble computational intelligence reveals novel molecular signatures of cancer biology and pan-cancer survival
P. Yang\textsuperscript{1,2}, N.A. Cilfone\textsuperscript{3,1}, C. Liu\textsuperscript{1,2}, C. Yandava\textsuperscript{1,2}, J.A. White\textsuperscript{1,2}, J. Cui\textsuperscript{1,2}, S. Gujja\textsuperscript{1,2}, S. Bajaj\textsuperscript{1,2}, T.W. Chittenden\textsuperscript{1,4}, \textsuperscript{1}Wuxi NextCODE, USA, \textsuperscript{2}Complex Biological Systems Alliance, USA, \textsuperscript{3}Bioscience Advising, USA, \textsuperscript{4}University of Tennessee Health Science Center, USA, \textsuperscript{5}University of Oxford, UK, \textsuperscript{6}Harvard Medical School, USA

Scissor: Shape changes in selecting sample outliers in RNA-seq
H.Y. Choi\textsuperscript{a,1}, J.S. Marron\textsuperscript{1}, H. Jo\textsuperscript{2}, D.N. Hayes\textsuperscript{1,2}, \textsuperscript{1}University of North Carolina at Chapel Hill, USA, \textsuperscript{2}University of Tennessee, USA

Advances in liquid biopsy sequencing at broad genomics
C. Cibulskis\textsuperscript{1}, M. DeFelice, B. Blumenstiel, J. Grimsby, V. Adalsteinsson, M. Fleharty, M. Duran, S. Gabriel, N. Lennon, Broad Institute, USA

Tumor suppressor genes may promote tumorigenesis through allele specific expression
E.A. Clayton\textsuperscript{a,1}, S. Khairul\textsuperscript{1}, L. Wang\textsuperscript{1}, I.K. Jordan\textsuperscript{1,2}, J.F. McDonald\textsuperscript{1}, \textsuperscript{1}Georgia Institute of Technology, USA, \textsuperscript{2}PanAmerican Bioinformatics Institute, Colombia

Leveraging TCGA gene expression data to build predictive models for cancer drug response
E.A. Clayton\textsuperscript{1}, T.A. Pujo\textsuperscript{1}, J.F. McDonald\textsuperscript{1}, P. Qi\textsuperscript{1}, \textsuperscript{1}Georgia Institute of Technology, USA, \textsuperscript{2}Emory University, USA

Predicting the driver transcription factors in all TCGA cancer types
V. Amin\textsuperscript{1,2}, M.C. Cobanoglu\textsuperscript{a,1}, \textsuperscript{1}University of Texas Southwestern Medical Center, USA, \textsuperscript{2}Baebies Inc, USA

Moonlight: A tool for biological interpretation and driver genes discovery
A. Calaprico\textsuperscript{1,2}, C. Olsen\textsuperscript{1}, C. Caron\textsuperscript{2,3}, T. Tergelsen\textsuperscript{4}, M.H. Bailey\textsuperscript{5}, T.C. Silva\textsuperscript{6}, A.V. Olsen\textsuperscript{4}, L. Cantini\textsuperscript{7}, G. Bertoli\textsuperscript{8}, A. Zinovyev\textsuperscript{9,7}, \textsuperscript{1}Université libre de Bruxelles (ULB), Belgium, \textsuperscript{2}University of Miami, USA, \textsuperscript{3}Institute of Molecular Bioimaging and Physiology of the National Research Council (IBFM-CNR), Italy, \textsuperscript{4}Danish Cancer Society Research Center, Denmark, \textsuperscript{5}Washington University in St. Louis, USA, \textsuperscript{6}University of Sao Paulo, Brazil, \textsuperscript{7}Institut Curie, France, \textsuperscript{8}INSERM, France, \textsuperscript{9}Henry Ford Health System, USA

Molecular natural history of breast cancer: Leveraging transcriptomics to predict breast cancer progression and aggressiveness
Hierarchical organization endows the kinase domain with regulatory plasticity
P. Creixell*1, J. Pandey2, A. Palmeri3, M. Bhattacharyya4, M. Santa-Olalla1, R. Ranganathan5, D. Pincus2, M. Yaffe1, 1Massachusetts Institute of Technology (MIT), USA, 2Whitehead Institute for Biomedical Research, USA, 3Celgene Institute for Translational Research Europe (CITRE), Spain, 4University of California Berkeley, USA, 5University of Texas Southwestern Medical School, USA

Molecular patterns of transdifferentiation define a distinct subset of cholangiocarcinoma-like hepatocellular carcinomas
J. Damrauer1,2, M. Love1,3, J. Parker1,2, K. Hoadley1,2, 1University of North Carolina at Chapel Hill, USA, 2Lineberger Comprehensive Cancer Center, USA, 3Genentech, USA

Oncology model fidelity score differentiates human from mouse
D. Datta*, T. Goldstein, A. Butte, University of California San Francisco, USA

Expression of microRNA isoforms (isomiRs) conveys improved sample classification across TCGA, disclosing a potentially novel functional panorama via targetome shifting
R. Distefano*, L. Tomasello, D. Veneziano, G. Nigita, C. Croce, The Ohio State University, USA

Novel stratification of RAS-driven tumours in TCGA patients
P. East*, S. de Carné, J. Downward, The Francis Crick Institute, UK

The UCSC Xena platform for cancer genomics data visualization and interpretation
M. Goldman*, B. Craft1, J. Zhu1, E. Collison2, S. Lewis5, D. Haussler1, 1UC Santa Cruz Genomics
[P.051] **RNAExplorer: Bayesian inference of cancer-specific miRNA–mRNA regulatory modules**
M. Gönen1,2,1, Koç University, Turkey, 2Oregon Health & Science University, USA

[P.052] **Detecting the mutational signature of homologous recombination deficiency from clinical samples**

[P.053] **Regulatory networks involving long non-coding RNAs (LncRNAs) and estrogen receptor (ER) in pan-gynecologic tumors**
P. Gunaratne1,2, P. Sumazin2, C. Coarfa1, P. Mestagh3, S. Lefever3, C. Williams4, K. Mackenzie5, A. Sood6, University of Houston, USA, 2Baylor College of Medicine, USA, 3Ghent University, USA, 4Karolinska Institutet, Sweden, 5University of New South Wales (UNSW), Australia, 6UT MD Anderson Cancer Center, USA

[P.054] **Comprehensive characterization of alternative polyadenylation in human cancer**
Y. Xiang1, Y. Ye1, G.B. Mills1, L. Han1, 1University of Texas Health Science Center at Houston, USA, 2M.D. Anderson Cancer Center, USA

[P.055] **Genomic determinants of lineage**
L. Happ*, S. Dave, Duke University, USA

[P.056] **Rapid hypothesis generation: The power of high-level interactions with big data**
D.J. Heiman*, M.S. Noble1, H. Zhang1, S. Meier1, K. Hadley1, K. Huang1, J. Kim1, N. Gehlenborg2, L. Chin4, G. Getz1,2, 1Broad Institute of MIT and Harvard, USA, 2Massachusetts General Hospital, USA, 3Harvard Medical School, USA, 4The University of Texas System, USA

[P.057] **A multi-omics strategy to decipher the protein synthesis code of the tumor microenvironment**
J.J.D. Ho*, N.C. Balukoff1, P.R. Theodoridis1, M. Wang1, J.R. Krieger2, S. Lee1, 1University of Miami, USA, 2The Hospital for Sick Children, Canada

[P.058] **Characterizing genome-wide germline correlates of the epigenetic landscape of prostate cancer**
K.E. Houlanan1,2, Y. Shah1, C.Q. Yao1, M. Fraser1, H. He2,3, R.G. Bristow2,3, P.C. Boutros1,2, 1Ontario Institute for Cancer Research, Canada, 2University of Toronto, Canada, 3University Health Network, Canada

[P.059] **Resolving conflicts among the experimental conclusions using TCGA and other public database: A case study of Prrs14/ST14 in breast cancers**
S. Jeon*, K. Kim, M. Kim, Inha University, Republic of Korea

[P.060] **Network optimization technique for finding metabolic insights from publicly available omics data**
A. Jha, S. Luthra*, S. Jatav, S. George, S. Pathak, Elucidata, USA

[P.061] **Mutational landscape in cirrhosis suggests clonal expansion during chronic liver disease**
H. Zhu1, T. Wang, Y. Jia*, M. Zhu, T. Lu, X. Luo, UT Southwestern, USA

[P.062] **QIAseq multimodal technology: An innovative NGS workflow for simultaneous DNA and RNA library construction from a total nucleic acid sample**

[P.063] **Context dependent empirical transcriptome**
H. Jo*, H. Choi, K. Hoadley, J.S. Marron, D.N. Hayes, UNC Lineberger Comprehensive Cancer Center, USA

[P.064] **Breast cancer quantitative proteome and proteogenomic landscape**
H.J. Johansson1, F. Socciarelil, N.M. Vacantii, M.H. Haugenii, Y. Zhu1, I. Siavelis1, A. Fernandez1, M.R. Aure2, B. Sennblad3, M. Vesterlund1, 1Karolinska Institutet, Sweden, 2Oslo University Hospital, Norway, 3Stockholm University, Sweden, 4Akershus University Hospital, Norway, 5The University of Texas MD Anderson Cancer Center, USA, 6KTH Royal Institute of Technology, Sweden, 7The Norwegian University of Science and Technology – NTNU, Norway, 8Oslo Breast Cancer Research Consortium (OSBREAC), Norway

[P.065] **TCGA gene co-expression module analysis reveals gene sets predictive of pathological complete response for HER2+ breast cancer in the NeoSPHERE trial**
R.M. Johnson11, A. Jambusaria4, P. Mazrooei5, G. Bianchini2, A. Daemen1, R. Bourgon1, L. Gianni2, S. de Haas3, A. Kiermaier1,3, A. Udyavari1, Genentech, USA, 2IRCCS Ospedale San Raffaele, Italy, 3F. Hoffmann-La Roche Ltd, Switzerland, 4University of Illinois, USA, 5University of Toronto, Canada

[P.066] **Immune signatures derived from TCGA: Association with disease prognosis in high-grade serous ovarian cancer**
W. Jones*, M. Ganapathi1, R. Ganapathi2, 1Q2Solutions - EA Genomics, USA, 2Levine Cancer Institute, USA
[P.067] Mutational signature and transcriptomic classification analyses as the decisive diagnostic tools for a cancer of unknown primary
R. Olofsson Bagge, A. Demir, J. Karlsson, University of Gothenburg, Sweden

[P.068] Impact of crosstalk between miRNA and DNA methylation on isoform expression signatures in bladder cancer
M. Shivakumar1, S. Han2, Y. Lee2, D. Kim1, 1Geisinger Health System, USA, 2University of Utah, USA

[P.069] A prognostic signature for gliomas based on expression of long noncoding RNAs
M. Kiran*, D. Keenan, A. Dutta, University of Virginia, USA

[P.070] An investigation into the mutational spectrum and sub-types of TNBCs in Indians compared to TCGA; A population with high proportion of TNBCs
A. Korlimarla*, J. Prabhu, S. Rajarajan, H. Shankaranarayana, N. Sahasrabudhe, S. Mukherjee, T. Sridhar, St John’s Research Institute, India

[P.071] Genetic variant calling from RNAseq data
R. Kositsky*, S. Dave, Duke University, USA

[P.072] Patient selection for a developmental therapeutics program using multi-omics
J.-M. Lavoie1, T. Mitchell1, S.-E. Lee1, B. Deol1, S. Jones2, M. Marra2, J. Laskin1, D. Renouf1, 1BC Cancer Agency, Canada, 2Michael Smith Genome Sciences Centre, Canada

[P.073] Pan cancer master regulatory network of cancer stem-like cells (CSCs)
S. Le*, C. Deng, A. Riva, D. Nguyen, V. Patel, J. Amedee, D. Tran, University of Florida, USA

[P.074] Predictive genomic signature for immunotherapy tested in gastric cancer and TCGA pan-cancer data
Y. Jeong, J. Shin, J.-S. Lee*, UT MD Anderson Cancer Ctr., USA

[P.075] Complex genomic rearrangements in the initiation and evolution of lung adenocarcinoma
J.-K. Lee1, 2, S. Park2, H. Park2, K. Yi2, Y. An2, J. Youk2, T.M. Kim3, P. Park2, Y.S. Ju2, Y.T. Kim3, 1Harvard Medical School, USA, 2Korea Advanced Institute of Science and Technology, Republic of Korea, 3Seoul National University Hospital, Republic of Korea

[P.076] Immune signatures correlate with L1 retrotransposition in gastrointestinal cancers
E.A. Lee1, 2, H. Jung3, J.K. Choi3, 1Boston Children’s Hospital, USA, 2Harvard Medical School, USA, 3KAIST, Republic of Korea

[P.077] A Picture of the Pipeline: Biospecimen processing at the Biospecimen Core Resource (BCR) for The Cancer Genome Atlas Project (TCGA)
K. Leraas, Nationwide Children's Hospital, USA

[P.078] The role of enhancers in cancer development: From evolutionary origin to immunotherapy
H. Liang, University of Texas MD Anderson Cancer Center, USA

[P.079] An integrated TCGA pan-cancer clinical data resource (TCGA-CDR) to drive high quality survival outcome analytics
J. Liu1, T. Lichtenberg2, K. Hoadley3, L. Poisson4, A. Lazar5, A. Cherniack6, A. Kovatich7, C. Benz8, D. Levine9, A. Lee10, 1Chan Soon-Shiong Institute of Molecular Medicine at Windber, USA, 2Nationwide Children’s Hospital, USA, 3University of North Carolina at Chapel Hill, USA, 4Henry Ford Health System, USA, 5The University of Texas, USA, 6Broad Institute of MIT and Harvard, USA, 7Uniformed Services University/Walter Reed National Military Medical Center, USA, 8Buck Institute for Research on Aging, USA, 9NYU Langone Medical Center, USA, 10University of Pittsburgh, USA, 11Sage Bionetworks, USA, 12University of California, San Francisco, USA, 13Institute for Systems Biology, USA

[P.080] Favorable outcome of patients with lung adenocarcinoma harboring POLE mutations and expressing high PD-L1
L. Liu1, J. Rui1, S. O’Neill1, S. Grant1, W. Petty1, M. Yang1, 2, K. Chen2, U. Topaloglu1, B. Pasche1, W. Zhang1, 1Wake Forest Baptist Comprehensive Cancer Center, USA, 2Tianjin Medical University Cancer Institute and Hospital, China

[P.081] MAL2 is a tumor suppressor despite its frequent co-amplification with c-Myc on chromosome 8q24.12-21 in various human cancers
A. López-Coral*, G. Del Vecchio, L. Unsworth, P. Tuma, The Catholic University of America, USA

[P.082] Normal to cancer progression using multi-omics data and pattern mining from multidimensional TCGA omics data
A. Jha1, 2, R. Sahay1, 1National University of Ireland, Ireland, 2Harvard University, USA

[P.083] Dissecting the expression landscape of cytochromes P450 in hepatocellular carcinoma: towards novel molecular biomarkers
C. Martenon Brodeur*, M. Bisaillon, Université de Sherbrooke, Canada

[P.084] Precision Trial Drawer (PTD), a computational tool to assist planning of genomics-driven trials in oncology leveraging TCGA information

[P.085] Studying effects of disease associated polymorphism on a transcriptional pathway: A case study in renal cell cancer
V. Schmid1, J.L. Platt1, J.A. Smythies1, H. Chourdhy3, J. Schoedel2, P.J. Ratcliffe1, D.R. Mole*1, 1University of Oxford, UK, 2Harvard Medical School, USA, 3Institut Curie, France, 4Alleanza Contro il Cancro, Italy

[P.086] NET-CAGE: A novel method to map genome-wide enhancers at nucleotide resolution in cancer genomics studies
S. Hirabayashi1, 2, S. Bhagat1, 3, Y. Matsuki4, 4, Y. Hayashizaki1, S. Katayama3, J. Kere3, H. Kawaji4, Y. Murakawa4, 1RIKEN, Japan, 2Kyoto University, Japan, 3Karolinska Institutet, Sweden, 4KK DNAFORM, Japan

[P.087] Migration rather than proliferation transcriptomic signatures are strongly associated with breast cancer patient survival
N.U. Nair*1, A. Das2, 1National Institutes of Health, USA, 2Harvard Medical School, USA

[P.088] GAME-ON/OncoArray: A resource for cancer risk genomics
S. Nelson*, E. Hoover, D. Daee, K. Kortokrax, E. Gillanders, National Cancer Institute, USA

[P.089] Target-directed miRNA degradation in human cancer: A multomic approach
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[P.090] The Firehouse of TCGA in The Era of Extreme Scale Collaborative Analysis
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[P.091] Pan-cancer analysis of transposable element expression
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[P.092] Transforming the oncogene overexpression and pervasive RNA editing in thymoma
S. Park*1, J. Lee1, H. Park1, K. Yi1, J-K. Lee1, Y. An1, J. Youk1, S-Y. Cho1, T-M. Kim1, Y.S. Ju1, 1Graduate School of Medical Science and Engineering, Korea Advanced Institute of Science and Technology, Republic of Korea, 2Ewha Womans University, Republic of Korea, 3Korea Advanced Institute of Science and Technology, Republic of Korea, 4Seoul National University Hospital, Republic of Korea

[P.093] Somatic mutational landscape of splicing factor genes and their functional consequences across 33 cancer types
M. Seiler, S. Peng*, A.A. Agrawal, J. Palacino, T. Teng, P. Zhu, S. Buonamici, L. Yu, H3 Biomedicine Inc., USA

[P.094] Modeling the regulatory networks that govern mRNA stability and their implication in cancer
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[P.096] The ISB cancer genomics cloud
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[P.097] Discovering relationships between cancer modules via integrated analysis of mutual exclusivity, co-occurrence and functional interactions
P. Diao1, Y-A. Kim1, D. Wojtowicz4, S. Madan2, R. Sharan3, T.M. Przytycka*, 1NCBI/NLM/NIH, USA, 2UMD, USA, 3Tel Aviv University, Israel

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[P.099] Iterative FAM50 coupled with principal component analysis improves consistency between intrinsic and clinical subtyping of breast cancer
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S.M. Roth1, A. Wellstein, Georgetown University, USA

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N. Saini1, L. Klimczak1, J. Li1, D. Fargo1, R. Bai1, K. Gerrish1, J. Korbel1, S. Waszak2, S. Roberts3, D. Gordenin1, 1National Institute of Environmental Health Sciences, USA, 2The European Molecular Biology Laboratory, Heidelberg, Germany, 3Washington State University, USA

**P.106** The molecular landscape of oncogenic signaling pathways in metastatic cancer
F. Sanchez-Vega1, C.J. Fong, W.K. Chatila, H. Kantheti, S. Nandakumar, A. Penson, Y. Zheng, J. Gao, B.S. Taylor, N. Schultz, Memorial Sloan Kettering Cancer Center, USA

**P.107** Efficient algorithms to discover alterations with complementary functional association in cancer
R. Sarto Basso1, D. Hochbaum1, Y. Kim2, T. Przytycka3, F. Vandin2, 1University of California, Berkeley, USA, 2University of Padova, Italy, 3National Institute of Health, USA

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J. Lawson, F. Garrett-Bakelman, S. Bekiranov, N. Sheffield*, University of Virginia, USA

**P.110** Identification of novel biomarkers for glioblastoma recurrence using TCGA multi-omic databases
R. Varghese1,2, K. Pridham1,2, Z. Sheng1,2, 1Virginia Tech Carilion Research Institute, USA, 2Virginia Tech Carilion School of Medicine, USA

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**P.113** The HOX genes expression landscape and their cancer-associated targets
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Regulation of expression of TERT and ETS factors by BRAFV600E in Papillary Thyroid Cancer with coexistent BRAFV600E and TERT promoter mutations
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Pan-cancer analysis of IncRNA regulation supports their targeting of cancer genes and pathways in each tumor context
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Systematic identification of non-coding pharmacogenomic landscape in cancer
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Molecular subtyping of gastro-oesophageal junction and gastric adenocarcinomas from American Hispanic/Latino patients
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Machine learning detects pan-cancer ras pathway activation in the cancer genome atlas
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Quality-control: A critical first step in any analysis of TCGA data
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Tissue differences (TIFF), a web-application to examine differences in gene expression, DNA copy number, and mutation status of two groups of tumor and normal samples
A. Wernitznig*, D. Gerlach, T. Zichner, M. Bauer, A. Schlattl, C. Haslinger, N. Kraut, Boehringer Ingelheim, Austria

Multi-omic analysis of TP53 pathway extends the role and function of the most commonly mutated tumor suppressor gene
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Machine learning identifies stemness features associated with dnecogenic dedifferentiation
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HLA DQB1*02:01-DRB1*03:01 Haplotype confers head and neck cancer risk
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Genomic profiling of adenocarcinoma of gastroesophageal junction in Chinese Han population
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Genomic and molecular landscape of DNA damage repair (DDR) deficiency across The Cancer Genome Atlas (TCGA)
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Fast deconvolution tool for purifying signals from mixed tumor genomic data

Y. Ye*, Y. Xiang, J.S. Takahashi, G.B. Mills, S. Yoo, L. Han, The University of Texas, USA

Recurrent mutations at TF binding sites alter chromatin topology and distal gene expression in breast cancer

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Functional genomic studies reveal the transcriptome landscape cross activating the classical and alternative NF-kB pathways in head and neck cancers of differing HPV status

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Integration of proteogenomic profiling and targeted proteomic assay identifies proteogenomic variants associated with prostate cancer aggressiveness

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The genomic landscape and pharmacogenomic interactions of clock genes in cancer chronotherapy

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Combinatorial and recurrent patterns of associations between molecular alterations across cancer types in TCGA data

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Comprehensive transcriptomic analysis of cell lines as models of primary tumor samples across 20 tumor types

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Intratumor heterogeneity and clonal expansion cascade in papillary renal cell carcinoma

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A pathway-based multi-omics integration model for cancer prognosis prediction

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Inferred miRNA activities as cancer biomarker models and therapeutic targets

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Integrating clinical and multiple omics data for prognostic assessment across human cancers

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In-silico, in-vitro and toxicological evaluation of some indolin-2-one derivatives as potential VEGFR-2 inhibitors

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