Poster Listing

Even numbered ePosters will be attended by their authors on Tuesday, November 17, 1:00pm – 2:00pm Eastern

Odd numbered ePosters will be attended by their authors on Thursday, November 19, 1:00pm – 2:00pm Eastern.

GENETICS

G01. Development and Validation of a High-Throughput Next-Generation Sequencing Assay from Buccal Cell DNA as a Cost-Effective Screening Method for Celiac Genetic Risk
S. Gunn

G02. Copy Number Variant Analysis Improves the Diagnostic Yield in a Cohort of Pediatric Patients with Previously Negative Constitutional Exome Sequencing Results
E. Hahn

G03. A Retrospective Study of Products of Conception with More Than 44,000 Specimens in 27 Years at a National Cytogenetic Reference Laboratory
H. Meng

G04. WITHDRAWN

G05. Reevaluation of Genomic Test Results for Germline Disorders: A Framework of Critical Considerations on Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)
J. Ji

G06. Single Gene Transcript Analysis and 3D Modeling: An Integrated Approach to Variant Assessment
F. Vetrini

G07. Detection of Allelic Dropout in a Mass Array HFE Genotyping Assay
A. Campbell

G08. Result Interpretation for Clinical Exome and Genome Sequencing: On Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)
J. Buchan

G09. Incidental Diagnosis of NR5A1-Related 46,XY Disorder of Testicular Development in Neonate with Mosaic Partial Trisomy 2q
S. Vallee

G10. Optimization and Validation of a Sanger Sequencing Clinical Assay for Germline BRCA1/2 Gene Mutation Detection at King Hussein Cancer Center
W. Naser

G11. Mosaicism in Cancer Susceptibility Genes in Unselected Cancer Patients
D. Mandelker
D. Toledo

G13. Comparison of Universal versus Traditional Genetic Testing Models for Cancer Patients
O. Ceyhan-Birsoy

T. Huard

T. Prior

G16. A Rare Single Nucleotide Variant Causing a False-Negative HTT CAG Repeat Expansion Result in the Evaluation of a Patient for Huntington Disease
F. El-Sharkawy

G17. Amplification-Free Targeted Enrichment Powered by CRISPR-Cas9 and Long-Read Single Molecule Real-Time Sequencing Can Efficiently and Accurately Sequence Challenging Repeat Expansion Disorders
J. Ekholm

G18. A Single-Assay Diagnostic Workflow for Genotyping and Phasing SNPs with Repeat Expansions for Allele-Selective Therapy in Huntington Disease
S. Statt

M. Avenarius

G20. Test Validation and Characterization of Reference Materials for ADH5 Genotyping
A. Otsubo

G21. CYP2D6 Guided Methadone Dosing in a Multi-Ethnic Population: A Pharmacogenomic Screen to Decrease Withdrawal Morbidity
C. Lum

G22. Developing DPYD Genotyping Method for Personalized 5-fluorouracil Therapy
B. Wong

G23. High-Throughput Fetal-Fraction Amplification Increases Analytical Performance of Noninvasive Prenatal Screening
D. Muzzey

G24. A Software Tool That Prevents Incorrect Estimations of Gestational Age and Maternal Age at Estimated Date of Delivery Reported by the College of American Pathologists NIPT Participant Summary
Y. Wang

G25. Genetic Insights and Incidental Findings from Maternal Cell Contamination Testing
N. Kopp

G26. The Relationship between Variant Type and Phenotype among Diseases Screened by the Foresight Expanded Carrier Screen
K. Karimi
G27. **Two-Site Evaluation of a Rapid and Simple CFTR PCR/CE Assay and Software Targeting Mutations across Diverse Ethnic Groups**  
*S. Filipovic-Sadic*

G28. **SMN1 and SMN2 Copy Number Distribution in 733 Clinical Cases of Carrier Screening for Spinal Muscular Atrophy**  
*D. Toledo*

G29. **Proof-of-Concept for Single-Platform Trio Carrier Screening of FMR1, SMN1/2, and CFTR Variants Using PCR and Capillary Electrophoresis with Consolidated Workflows**  
*W. Laosinchai-Wolf*

G30. **The Single-Tube SLIMamp NGS Assay for Detection of Mutations Associated with Thalassemia Is both Rapid and Robust**  
*X. Wu*

G31. **Exploring Mosaic Mutations in Megalencephaly and Other Growth Disorders by Next-Generation Sequencing**  
*N. Madkhali*

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**HEMATOPATHOLOGY**

H01. **Personalized Medicine in Practice: Comprehensive Genomic Profiling of a Lung Adenocarcinoma Leads to Reclassification of a Concurrent Lymphoma**  
*P. Terraf*

H02. **WITHDRAWN**

H03. **Limitation in Confirming Low Allele Frequency Calls from Sensitive Cancer Assays: MSK Experience with the LiquidPlex cfDNA Panel on Hematologic Samples**  
*J. Jeon*

H04. **Somatic Mutation Testing for Pediatric Patients with Known or Suspected Inherited Bone Marrow Failure Syndromes**  
*K. Fisher*

H05. **A Highly Reproducible Single-Day FISH Assay for Detection of t(11;14) in Multiple Myeloma Patient Samples**  
*A. Prokhorova*

H06. **Comparison of Capture-Based Next-Generation Sequencing Designs in a Clinical Myeloid Neoplasm Panel**  
*M. Dina*

H07. **Clinical Utility of a Custom-Designed Next-Generation Sequencing (NGS) Panel for Detection of Gene Fusions, Deletions, and Hotspot Mutations in Myeloid and Lymphoid Neoplasms**  
*R. Starks*

H08. **Genomic Landscape of Primary Breast Lymphoma Diffuse Large B-Cell Lymphoma (PB-DLBCL)**  
*L. Liu*

H09. **Evaluation of the Ion Torrent Oncomine Myeloid Sequencing Panel**  
*B. Houde*
H10. Proteomics-Based Biomarkers in Squamous Cell Carcinoma: A Pilot Study Correlating Proteomic Profiles and Tumor Differentiation
Y. Chen Wongworawat

H11. Detection of Low-Frequency Variants for Minimal Residual Disease (MRD) Monitoring of Acute Myeloid Leukemia
N. Valencia

H12. A Next-Generation DNA Sequencing Assay for Detection of SNVs, Insertions, Deletions, and Copy Number Variants in 25 Lymphoma Genes in Samples
S. Roman

H13. High Throughput TRG Sequencing in a Clinical Laboratory: Analysis of Equivocal Results
V. Smith

H14. CloneRetriever: An Automated Algorithm to Identify Clonal Immunoglobulin Gene Rearrangements by Next-Generation Sequencing
E. Halper-Stromberg

H15. IGH V-Gene Somatic Hypermutation Assessment by Hybrid-Capture
E. Mahe

H16. Comparison of Next-Generation Sequencing-Based TRG and TRB Assays for the Diagnostic Evaluation of T Cell Lymphoid Malignancies
C. Ho

H17. Characterization of the Immunoglobulin Heavy- and Light-Chain Repertoires in a Single Reaction
G. Lowman

H18. Assessment of a High-Throughput Sequencing Assay for Measurable Residual Disease (MRD) Monitoring in Patients with T-Cell Malignancies
J. Tung

H19. Improved Clonality and Somatic Hypermutation Analysis of CLL with a Highly Multiplex IGHV Assay
M. Toro

H20. The Development of an NGS Assay of Immunoglobulin Heavy Variable Gene Somatic Hypermutation in CLL
G. Shi

H21. Validation of MYD88 L265P ddPCR Assay and Application in Assessment of Primary CNS Lymphoproliferative Disorders
M. Cantu

R. Garcia

H23. Precise Detection of PDL1/PDL2 Copy Number Alterations in Classic Hodgkin Lymphoma Using Combined CD30 Immunophenotyping and FISH Analysis
Y. Zhang
   J. Schubert

H25. Novel Fusion of PVT1-RCOR1 in B-Cell Prolymphocytic Leukemia (BCPCLL) Producing False FISH Fusion of MYC-IGH with an Atypical Pattern
   P. Koduru

H26. Identification of Clinical Molecular Targets for Childhood Burkitt Lymphoma
   N. Zeng

H27. Characterization of TP53 Mutations in Myeloid Neoplasms for Targeted Therapy
   A. Mindiola Romero

H28. Chromosome Arm Gain or Loss by Next Generation Sequencing
   M. Dabrowski

H29. Clinical Significance of CEBPA Double Mutants: Challenges in Variant Classification and Subtyping of Acute Myeloid Leukemia
   J. Yoon

H30. Cytogenetic and Molecular Landscape in Hispanic Acute Myeloid Leukemia Patients from Puerto Rico
   P. Deb

H31. Evaluation and Follow-up of JAK2 V617F Positive Patients with Low Allele Burden: A Single-Center Experience
   K. Reddy

H32. Number of Variants and Pathogenic Variants in ASXL1, STAG2, and RUNX1 Correlate with High Ogata Score by Flow Cytometry in Myelodysplastic Syndromes: A National Reference Laboratory Experience
   M. Williams

H33. Clinical Implementation of a Custom Myeloid NGS Assay and Overview of NPM1 and IDH1/IDH2 Mutation Status in a Clinical Cohort
   M. Kluk

H34. Development of FIP1L1-PDGFRα Real-time RT-PCR Assay
   M. Mai

H35. FLT3-ITD Mutant Allelic Ratio: Impact of Using Non-standardized Published Calculations and Potential Correction Based on Marrow Blast Percentage
   J. Reinartz

   R. Yang

H37. Curation of FLT3 Variants in Acute Myeloid Leukemia by Clinical Genome Resource Somatic Hematologic Cancer Taskforce (ClinGen HCT)
   X. Xu

H38. Persistent IDH Mutations in AML Patients in Remission on IDH Inhibitors
   J. Xu
H39. Diagnostic Value of Molecular Markers in the Work-up of Myelodysplastic Syndromes
R. He

H40. Clinical Validation of Mutant IDH1 and IDH2 Detection by Multiplex Digital Droplet PCR
J. Racchumi

H41. Comparison of Targeted Myeloproliferative Subpanel versus Comprehensive Myeloid Panel in the Evaluation of Suspected BCR-ABL1-Negative Myeloproliferative Neoplasms
D. Morlote

H42. Haplotype Phase of CEBPA Mutations in Acute Myeloid Leukemia
S. Harley

H43. Identifying Non-canonical Mutations in Myeloproliferative Neoplasms: Our Experience with JAK2 Sequencing
L. Baugh

H44. Comparison of Whole Genome Sequencing (WGS) with Conventional Cytogenetics in Profiling Genome-Wide Large-Scale Copy Number and Structural Variations in Pediatric and Adolescent AML
L. Wang

H45. Workflow Comparison between Two NCCN Guideline Recommended Myeloproliferative Neoplasms Screening Workup: A Single Institution’s Experience
N. Tabish

INFECTION DISEASES

ID01. Multisite Evaluation of the ARIES MRSA Assay for the Detection of Methicillin-Resistant Staphylococcus aureus (MRSA) from Nasal Swabs
B. Buchan

ID02. Comparison of a Cartridge-Based Host Gene Expression Test to a Manual Method for Use in the Diagnosis of Sepsis
S. Cermelli

ID03. Comparison of Two Multiplex Real-Time PCR Assays for Detection of Tick-Borne Pathogens
T. Uphoff

ID04. Development and Performance of a Multiplex Polymerase Chain Reaction (PCR)-Based Assay for Detection of Bacteria in Sterile Body Fluids
C. Johnson

ID05. Automated Multiplex Real-Time PCR Detection of Anaplasma phagocytophilum and Ehrlichia chaffeensis Using the Panther Fusion Open Access System
K. Stellrecht

ID06. Automated Real-Time PCR Detection of Babesia microti Using the Panther Fusion Open Access System
K. Stellrecht

ID07. Evaluation of an Automated rRNA Quantitation System for Rapid AST in Clinical Lab Diagnostics
D. Liu
ID08. Prospective Evaluation of a Multiplex HDPCR Tick-Borne Pathogen Panel
T. Uphoff

ID09. Development of a 29-mRNA Loop Mediated Isothermal Amplification Assay for the Rapid Diagnosis of Acute Infection and Sepsis
M. Remmel

ID10. In silico Performance of a Rapid Sepsis Test in Patients with Candidemia
D. Sampson

ID11. Development of ViroKey SARS-CoV-2 RT-PCR Test v2.0 for the Sensitive and Accurate Automated Detection of the SARS-CoV-2 Virus
I. Ng

ID12. Comparison of Four Commercial Molecular Diagnostic Kits for Detection of SARS-CoV-2: A Pilot Study
P. Chheda

ID13. Evaluation of Ion AmpliSeq SARS-CoV-2 NGS Research Panel
W. Liu

C. Knox

ID15. SARS-CoV-2 Cycle Number as a Metric for Population Trends in New Hampshire
E. Bradley

ID16. Verification of the Centers for Disease Control and Prevention Real-Time SARS-CoV-2 Assay for Emergency Use Authorization
K. Lancor

ID17. Analytical Validation of a SARS-CoV-2 Whole Genome Sequencing Method by Amplicon-Based NGS
S. Rosenthal

C. Wang

ID19. Comparison of Test Performance of Two Rapid SARS-CoV-2 Viral Assays
R. Abdulbaki

S. Glogowski

ID21. Detecting Signatures of SARS-CoV-2 Using Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)
R. Barney

ID22. A Practical Comparison of Seven Molecular SARS-CoV-2 Methods
C. Gentile

S. Kim
ID24. The Combination Assay for SARS-CoV-2 and Other Respiratory Viruses in Symptomatic Patients and the Statistical Outcome Visualizing Metrics and Trends
S. Lee

ID25. Temporal Spatial Heterogeneity of Immune Response to SARS-CoV-2 Lung Infection
N. Desai

A. Rahman

ID27. Evaluating the Clinical Utility of Next-Generation Sequencing of Nasopharyngeal Specimens for SARS-CoV-2 in the COVID-19 Pandemic
P. Velu

ID28. Validation of Saliva Testing for SARS-CoV-2 on Abbott m2000
S. Amin

ID29. Validation of an Emergency Use Authorization RT-PCR Test for Detecting SARS-CoV-2 in Upper and Lower Respiratory Tract Specimens
L. Cong

M. Steffen

M. Amadei

ID32. Development of a Multiplex Respiratory Panel and a Singleplex SARS-CoV-2 External Control for Use in a Rapid Nucleic Acid Amplification Detection System
J. Salem

ID33. Comparison of Two High-Throughput qPCR Assays for SARS-CoV-2
S. Turner

ID34. Development of a Multiplexed Synthetic Control for Rapid Detection of SARS-CoV-2 and Other Respiratory Pathogens Using a Nucleic Acid Syndromic Testing Panel
T. Schleicher

ID35. Comparison of Nasopharyngeal Swabs and Saliva Samples for the Detection of SARS-CoV-2 RNA
T. McMillen

ID36. Strategy for Analysis of Human ACE2 Putative Variants Linked to Protein Structure and Stability: Implications for ACE2 Receptor Binding to SARS-CoV-2
E. Hughes

ID37. Comparison of Oral Rinses and Nasopharyngeal Swabs for the Detection of SARS-CoV-2 RNA
T. McMillen

ID38. Lung Injury Due to COVID-19 Relative to Influenza and Non-viral ARDS and Normal Controls
A. Borczuk
ID39. Evaluation of Sample Pooling for the Detection of SARS-CoV-2 RNA Using the Cobas SARS-CoV-2 Test  
T. McMillen

ID40. RT-PCR Detection of SARS-CoV-2 Infection in Formalin-Fixed, Paraffin-Embedded Tissue Sections in Autopsy Cases  
D. Berman

ID41. The Evaluation of Oropharyngeal Swabs and Saliva Samples for the Detection of SARS-CoV-2 RNA  
T. McMillen

ID42. Evaluation of a Sample-to-Answer Cartridge-Based SARS-CoV-2 Assay  
J. Lefferts

ID43. Viral Sequencing Suggesting Transmission of SARS-CoV-2 from a Patient with False-Negative Molecular Results to Health Care Providers  
D. Green

ID44. Digital Droplet PCR to Detect Low-Titer SARS-CoV-2 in Nasopharyngeal, Nasal, and Salivary Specimens  
J. Xu

ID45. Leveraging Clinical Metagenomic Testing against SARS-CoV-2  
B. Briggs

ID46. A Systematic Review of the Genomic Diversity of SARS-CoV-2 Virus Detected in Dartmouth-Hitchcock Hospital  
D. Green

ID47. Evaluation of Saliva as an Alternative Sample Type for SARS-CoV-2 Detection Using the Hologic Panther Aptima EUA Assay  
W. Rehrauer

ID48. Automated, High-Throughput Testing Using the RealTime SARS-CoV-2 Assay  
M. Johnston

ID49. The Utility of Repeat Testing for Severe Acute Respiratory Syndrome-Coronavirus-2 by Reverse Transcriptase-Polymerase Chain Reaction in Improving Diagnostic Accuracy  
S. Fathima

ID50. Clinical Performance of GenMark ePlex SARS-CoV-2 Test Compared to a Laboratory Developed Procedure  
J. Laudadio

ID51. Evaluation of the SARS-CoV-2 Chromacode EUA Assay  
L. Thompson

ID52. Design and Optimization of Novel ITS2-28s rRNA Gene Primers for Fungal Species Detection from Formalin-Fixed, Paraffin-Embedded Tissues with a Targeted Next-Generation Sequencing Assay  
G. Wang

ID53. Non-invasive Microbial Cell-Free DNA Sequencing Detects Invasive Mold Infections in Immunocompromised Patients with Pneumonia  
T. Blauwkamp
ID54. A Comparative Study of qPCR to a NGS Metagenomics Assay to Detect and Quantify DNA Viruses in Pediatric Bone Marrow Transplant Patients  
L. Cooper

ID55. Investigating Targeted Next-Generation Sequencing of 16S RNA as a Tool for Detecting Shiga Toxin-Producing *E. coli* and *Salmonella* in Ground Beef  
J. Au-Young

ID56. Subtyping of Human Papillomavirus (HPV) Using Next-Generation Sequencing (NGS) Data in Cervical Cancer: A Feasibility Study with Comparison to Conventional Clinical Assays  
J. Chen

ID57. Analytical Performance Characteristics of Galileo ONE: An End-to-End Metagenomics Assay for the Unbiased Sequencing and Bioinformatics Analysis of Microbial DNA and RNA Directly from EDTA Plasma  
M. Carpenter

ID58. Application of Whole-Genome Sequencing for Bacterial Strain Typing in Investigating Hospital Infections  
K. Park

ID59. Validation of ddPCR-Quantified Standards for Use in Viral Load Measurements by NGS  
D. Hoerres

ID60. Performance Evaluation of Abbott Alinity m System to Detect HBV, HCV, and HIV-1 Infections: Comparison with Hologic Panther Aptima System  
J. Han

H. Wang

ID62. WITHDRAWN

ID63. Evaluation of a Novel VZV Molecular Assay for Detection of VZV from CSF and Swabs  
A. Cruz

ID64. A Multi-Lab Collaboration for Quantitative BK Virus Test Development on the Fully Automated Cobas 6800/8800 OMNI Utility Channel  
K. Lebel

ID65. Utilization of Digital PCR Assay for the Detection of HPV-16 in Cell-Free DNA in Patients with Head and Neck Cancer at an Oncology Center  
T. McMillen

ID66. Detection of Adenovirus Serotype 7 in a Cancer Patient Population  
R. Sumner

ID67. Retrospective Review of Seasonality of Human Parainfluenza Virus Subtypes at an Oncology Center  
T. McMillen

ID68. Validation of the RealStar Adenovirus Reagents on Plasma and Stool Samples and Comparison to a Laboratory-Developed Test Using the MultiCode Adenovirus Reagents  
C. Lee
INFORMATICS

I01. Assessment of RAS Dependency for BRAF Mutations Using Real-World Evidence Databases
G. Zheng

I02. CarrierSeq, an Expanded Carrier Screening Product Using Next-Generation Sequencing Technology
T. Fahland

I03. Evaluation of Roche NAVIFY Mutation Profiler for NGS Variant Annotation and Reporting
P. Ward

I04. Optimizing the Detection of Insertions and Deletions Using Next-Generation Sequencing in the Clinical Laboratory
K. Craven

I05. Optimizing Reference Mixture Samples for Bioinformatics Pipeline Assessment on Variant Calling Detection for Cancer Diagnostics and Treatment
C. Laing

I06. Use and Feasibility of Multi-Algorithmic Consensus-Based Bioinformatics Pipelines in the Detection of Fusions in FFPE Treated Samples
V. Williamson

I07. Highly Scalable and Automated Approach to Gut Microbiome Profiling and Quantification Using a New Ion Torrent Next-Generation Sequencing Assay
S. Sarda

I08. Microhaplotype Locus-Based Workflow for Sample Contamination Detection in Multiplexed Next-Generation Sequencing (NGS) Assays
J. Balan

I09. Prediction of DDR and Other Mutation Signatures Using Panel-Based Sequencing
A. Chellappan

I10. Accurate Detection and Quantification of FLT3 Internal Tandem Duplications in Clinical Hybrid Capture Next-Generation Sequencing Data
J. Tung

I11. Identification of Large Deletions Affecting CTNNB1 Exon 3 in Solid Tumors
Z. Zhang

I12. Development of a Clinical Bioinformatics Pipeline for the Comprehensive Genomic Profiling of Patient-Derived Xenograft Tumors
S. Turner

I13. Comprehensive Single-Nucleotide, Indel, Structural, and Copy-Number Variant Detection in Human Genomes with PacBio HiFi Reads
W. Rowell

I14. Look before You Leap: A Toolkit for Moving Clinical Panels to GRCh38
A. Skol
I15. A Novel Machine Learning Approach to Characterize Cancer Signatures for Improved Clinical Reporting  
S. Shams

I16. Pindel as a Back-up INDEL Caller to a GATK4 Mutect2-Based in-House Developed Somatic Secondary Analysis Bioinformatics Pipeline for a Custom Clinical Cancer NGS Panel  
S. Harada

I17. Classification Methods for Germline and Somatic Single Nucleotide Variant (SNV) in Circulating Tumor DNA (ctDNA) of Small Cell (SCLC) and Non-small Cell Lung Cancer (NSCLC)  
C. Wöstmann

I18. Evaluating Machine Learning Methods for Accurate Variant Calling Detection on Acute Myeloid Mutation Analysis  
C. Laing

C. Laing

I20. Clinical Cancer Genomics: Artificial Intelligence Assisted Data Re-analysis to Improve Detection of Potentially Actionable Mutations  
C. Fischer

I21. Capturing and Visualizing Cancer Genomic Data with Category Variants in the JAX Clinical Knowledgebase (JAX-CKB)  
T. Yin

I22. MPath STAR-QC: Automated Quality Control Application for Contamination and Sample Swap Detection Using Short Tandem Repeat Testing  
S. Lachhander

I23. Many NGS-Based Assays, One Platform: Ensuring a High-Quality Case Review and Sign-out Process with NGS Reporter (NGSR)  
A. Sboner

I24. Database for Managing Results of High-Throughput Sequencing Clonality Assays in Clinical Laboratories  
C. Ho

I25. MPath Lab QC: A Centralized Assay Agnostic Approach to Store, Review, and Finalize Laboratory QC for NGS-Based Genomic Clinical Tests  
A. Agarunov

I26. MPath Results PCR: An Integrated Approach to Programmatically Load, Curate and Report Non-NGS Germline Results  
R. Murray

I27. mrLab: Leveraging Mixed Reality in a Precision Medicine Laboratory to Increase Safety and Productivity of Healthcare Workers during the COVID-19 Pandemic  
A. Sigaras

I28. Building a Comprehensive Teaching Repository of Whole Slide Images  
E. Iriabho
OTHER (e.g., Education)

OTH01. Effect of Implementation of a Medium-Sized NGS Panel and Organ-Specific Subpanels on Send-out Testing: Experiences of a Small, Hospital-Based Molecular Diagnostics Lab
R. Kumar

OTH02. Establishment of a Multidisciplinary Precision Medicine Lymphoma Tumor Board Incorporating Results of Massively Parallel Sequencing
N. Gupta

OTH03. Educating in a Pandemic: Rapid Changes to Molecular Genetic Pathology Graduate Medical Education Training during COVID-19
F. El-Sharkawy Navarro

OTH04. Economic, Operational, and Clinical Considerations in Deploying Rapid NGS for Lung Cancer
C. Sande

OTH05. Study of the Critical Role Denials, Appeals, and Patient Engagement Play in the Financial Health of Pathology Practices and Molecular Laboratories
D. Richard

SOLID TUMORS

ST01. Clinical Application of oncoMonitor: A Simple ctDNA Assay for Liquid Biopsy Monitoring of Treatment and Assessment of Therapy in Colorectal and Lung Cancers
M. Minarik

ST02. Validation and Performance of Fusion Gene Panel for MiT Family Translocation Renal Cell Carcinomas: Quality of RNA is Important for Fusion Detection
S. Harada

ST03. Testing for CDKN2A Loss in Infiltrating Gliomas Using Targeted Amplicon-Based Sequencing
E. Hissong

ST04. Long Mononucleotide Repeat Markers Improve Detection of Microsatellite Instability in Non-colorectal Cancers
J. Lin

ST05. Comprehensive Coverage of Lung Cancer Somatic Mutations by IntelliPlex Lung Cancer Panel
L. Felicioni

ST06. Assessment of Microsatellite Instability on a Multi-Racial Cohort of High Grade Prostate Cancer Using Idylla MSI Test
M. Rodriguez Pena

ST07. CANTRK: A Canadian Multi-Centre NTRK Gene Fusion Testing Validation in Solid Tumors Project
S. Martins-Filho

ST08. De-stained Cytology Smears Can Be Used for Detection of KRAS Mutations Using the Biocartis Idylla PCR-Based Molecular Diagnostic Assay
Q. Wei
ST09. A Next-Generation Sequencing Assay for Comprehensive Genomic Profiling and Identification of Microbial Signatures in Tumor Samples  
M. Yee

ST10. Assessment of PD-L1 Expression in Gastric Tumor Samples  
P. Scorer

ST11. Targeted Mutational Analysis of Predictive and Prognostic Biomarkers in Colorectal Carcinoma  
G. Huang

ST12. Simultaneous Detection of Genetic and Copy-Number Variations in BRCA1/2 Genes  
L. Georgieva

S. Verma

H. Jung

ST15. Validation of a Comprehensive, Targeted Next-Generation Sequencing Panel for Solid Tumors  
E. Barrie

ST16. MammaPrint and BluePrint Next-Generation Sequencing (NGS) Results Are Robust and Accurate for Patients with Early Stage Breast Cancer  
D. Kingma

ST17. Evaluation of Three RNA Quantification Methods for Next-Generation Sequencing of Formalin-Fixed, Paraffin-Embedded Tumor Samples  
D. Chan

ST18. An Exome- and Transcriptome-Based NeXT Dx Test Enables Therapy Selection for Cancer Patients and Offers Insight into Emerging Composite Biomarkers for Immunotherapy  
J. Saldivar

ST19. A Comprehensive Approach for Detection of Known and Novel Gene Fusions with RNA Sequencing  
A. Marcovitz

ST20. Cancer-Testis Antigen Detection by Targeted RNA Sequencing  
J. Conroy

ST21. WITHDRAWN

ST22. FGFR Gene Mutation Analysis in Urothelial Cancer Using the therascreen FGFR RGQ Assay in FFPE Specimen Type  
L. Cai

ST23. Development and Validation of the OncoScreen RNA Panel for the Detection of Gene Fusions and Splice Variants in Tumors  
B. Li
ST24. **Benefits of Rapid Genotyping of KRAS Mutations versus NGS in Pancreatic Cyst Fluids**
A. Farahani

ST25. **PIK3CA Gene Mutation Analysis in Breast Cancer Using the therascreen PIK3CA RGQ Assay in FFPE Specimen Type**
L. Cai

ST26. **Detection of Microsatellite Instability Using Anchored Multiplex PCR and Next-Generation Sequencing**
R. Rogge

ST27. **Clinical and Analytical Validation of the ONCO/Reveal Dx Lung and Colon Cancer Assay (O/RRdX-LCCA)**
N. Lodato

ST28. **Noninvasive Genomic Profiling of 113 Patients with Advanced Renal Cell Carcinoma**
E. Gedvilaite

ST29. **Utilization of a Targeted Next-Generation Sequencing Assay for Assessment of Tumor Cellularity, and Genome-Wide and Gene-Specific Loss of Heterozygosity (LOH)**
M. Gupta

ST30. **Highly Sensitive and Specific Analysis of PIK3CA Mutations in Formalin-Fixed, Paraffin-Embedded (FFPE) Samples Using MALDI-TOF Mass Spectrometry**
A. Sartori

ST31. **Internal Validation and Performance Characteristics Using the Oncomine Precision Assay to Detect Multiple Variant Types from Solid and Liquid Biopsy Samples**
J. Schageman

ST32. **Somatic Variant Analysis Using a Pan-Solid Tumor Expanded Gene Panel**
S. Deharvengt

ST33. **Evaluation of a Mass Spectrometry-Based PIK3CA Mutation Assay for Predictive Breast Cancer Therapeutic Decision Making**
A. Box

ST34. **Single-Cell RNA Sequencing of Childhood Medulloblastoma**
N. Willard

ST35. **Identifying Prognostic and Predictive Gene Alterations in Metastatic Prostate Cancer**
E. Goyette

ST36. **Validation of an NGS Panel for Pancreatic Cyst Fluid Analysis**
J. Huang

ST37. **Clinical Validation of an Automated 170 Gene Panel Workflow in a CAP/CLIA Laboratory for Solid Tumors**
S. Deharvengt

ST38. **An RNA Sequencing Panel for Detection of Fusions and Splice Site Variants in Solid Tumors**
D. Green
ST39. Uncovering Subsets of Non-small Cell Lung Cancer (NSCLC) Enriched in Mutations in Cytoskeletal Dynamics and DNA Repair Genes: Additive Value of Large Gene Panels for Clinical Tumor Profiling
H. Tu

ST40. Rapid qPCR Testing in the NGS Era Enables Same-Day Resulting of EGFR Mutant NSCLC
N. Z. Georgantas

ST41. Rapid Assessment of Microsatellite Instability across a Spectrum of Tumor Types Using the Idylla System
A. Momeni-Boroujeni

ST42. DNA Methylome Profiling of DNA Extracted from Archived Stained Tissue Slides for Central Nervous System Tumor Diagnostics
Z. Abdullaev

ST43. WITHDRAWN

ST44. IDH1 and IDH2 Mutations in Colorectal Cancers
M. Lin

ST45. Detection of Renal Cell Carcinoma with TFEB Amplification Using Archer FusionPlex RNASeq Gene Expression Data
S. Harada

ST46. Identification of Novel Genomic Alterations in Pineal Parenchymal Tumors
R. Ondrasik

ST47. Assessment of NTRK Alterations and TRK Inhibitor Therapy: A Single Center Experience
A. Reddy

ST48. Tumor Microbiome in Colorectal Carcinoma: Bacterial Enrichment Is Associated with Oncogenic Variants within Specific Signaling Pathways
C. Beech

ST49. NKX2-1 Gene Variants in Solid Tumors: The Spectrum and Potential Impact in Surgical Pathology Diagnosis
F. El-Sharkawy Navarro

ST50. Comprehensive Genomic Profiling of Different Subsets of Merkel Cell Carcinoma: Insights on Pathogenetic Pathways
R. DeCoste

ST51. Correlation between MMR IHC and MSI Testing for Detection of MSI-High Solid Tumors
M. Shirazi

ST52. Circulating Tumor DNA Genomic and Methylation Profiling in Advanced Non-small Cell Lung Cancer Patients
J. Qin

Y. Lo

J. Chen
ST55. Comprehensive Genomic Profiling in Patients with Advanced Cancer in a Large US Healthcare System
  B. Piening

ST56. Development of Quality Control Reference Materials for Microsatellite Instability (MSI) Testing
  C. Huang

ST57. Mutated Allele Frequency and NRAS Mutational Status Are Significantly Associated with High-Risk Prognosis by 31-Gene Expression Profile
  F. Monzon

ST58. Genomic Profiling Uncovers Mutation Signatures That Differentiate Pediatric Rhabdomyosarcoma (RMS) Subgroups and Predict Clinical Outcomes
  F. Lin

ST59. Detection of Actionable Alterations in Breast and Ovarian Tumor Tissues by Testing with a 50-gene NGS Panel
  C. Ma

ST60. Microsatellite Instability Testing for Lynch Syndrome Screening in Colorectal Adenomas
  A. Javanbakht

ST61. Detection and Interpretation of Canonical and Cryptic Splice Sites in Solid Tumors and Their Relevance to FDA Approved Therapies and Clinical Trials
  E. Bogdanova

ST62. Co-occurrence of PTEN and TERT Mutations Predicts Poor Prognosis in Glioblastomas
  H. Chen

ST63. Gene Expression Profile of Sex Cord Stromal Cell Tumors and Their Relevance to Prognosis
  P. Bhattacharyya

ST64. Expression Profiling Reveals Novel Molecular Signature in Pleomorphic Lobular Carcinoma in situ
  E. Makhoul

ST65. Aberrant PAX3 (Paired Box Gene 3) RNA Splicing Is a Potential Marker for Diagnosis of Melanoma
  I. Kasago

ST66. Biomarker Testing for Patients with Advanced/Metastatic Non-small Cell Lung Cancer (NSCLC) in Academic and Community-Based Practices in the United States (US)
  L. Hess

ST67. Initial Tertiary Reporting Results from Personalize My Treatment (PMT): A Pan-Canadian Initiative Integrating Precision Oncology across Canada: PMT-001 Pilot Project
  M. Marques

ST68. Neurotrophic Tyrosine Receptor Kinase (NTRK) Gene Fusion Testing in Clinical Trials of Larotrectinib
  E. Rudzinski
ST69. Biomarker Testing and Overall Survival among Patients Diagnosed with Advanced or Metastatic Non-small Cell Lung Cancer
L. Hess

ST70. A Predictive Model of the Diagnostic Value of Next-Generation Sequencing-Based Genomics Testing in Patients with Advanced or Metastatic Non-small Cell Lung Cancer in the United States
P. Quon

ST71. Clinical Characteristics of RET- and NTRK-Rearranged Tumors in a Single Tertiary Cancer Center
T. Vougiouklakis

ST72. Incidence of T790M Mutation by ddPCR in Patients Progressing on First- and Second-Generation TKIs and Clinical Outcomes on Osimertinib
S. Nathany

ST73. Frequency of EGFR Mutations and ALK Expression in NSCLC in the North of México
B. Montaña Miyagui

ST74. Tissue Requirements of a Novel 27-Gene Immuno-Oncology Algorithm Measuring Tumor Microenvironment to Predict Response to Immunotherapies
T. Nielsen

ST75. Pan-Cancer Liquid Biopsy Assay for Mutation Profiling in 61 Genes by Low-Depth Sequencing
P. Hao

ST76. WITHDRAWN

ST77. Spatially Resolved Gene Expression Profiles in Human Glioblastoma
A. Hartnett

ST78. Spatially Resolved Molecular Interrogation of Triple Negative Breast Cancer
S. Williams

ST79. Quantitative Assessment of Functional Activity of Multiple Signaling Pathways in Recurrent Breast Cancer with Low to Intermediate 21 Gene Recurrence Score
L. Lin

ST80. Prospective Study Using Virtual Enrollment to Assess an RNA-FIT Assay for Non-invasive Detection of Colorectal Cancer, Advanced Adenomas, and Other Precancerous Adenomas
E. Barnell

ST81. NAB2-STAT6 Gene Fusions to Identify Primary/Metastasis Hemangiopericytoma/Solitary Fibrous Tumors
N. Singh

ST82. Development and Performance of Formalin Compromised FFPE Reference Materials
O. Clement

ST83. CNV Detection from a Multi-Cancer NGS Panel: A Single-Tube, Multiplex-PCR Based NGS with 309 Tiled Amplicons
A. LaBonte
ST84. Rapid Isolation of High-Quality Ultra-High Molecular Weight Genomic DNA from Blood, Bone Marrow Aspirates, and Fresh Frozen Human Tumors
H. Sadowski

ST85. Novel Amplicon-Based NGS Library Preparation Protocols Compared and Evaluated across Two Sequencing Technologies
E. Petrilli

ST86. Chromosomal Microarray Analysis of Benign Mesenchymal Tumors with RB1 Deletion
A. Dusenbery

ST87. A Novel Nanoparticle-Based Approach to Improve Extraction of Circulating Tumor DNA (ctDNA)
E. Williams

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TT01. Dimensionality Reduction for Noise Filtering of Big Data Sets
E. Mahe

TT02. Molecular Profiling in Challenging Oncology Research Samples Using a Novel Library Preparation Chemistry
H. Huang

TT03. Droplet Digital-PCR (ddPCR) as Confirmatory Method for Low Allelic Frequency Variants Detected by Manual Review of Data in Clinical NGS Testing
W. Song

TT04. Performance Validation of Magnis BR: A Full-Automatic Capture-Based Library Preparation Platform for Next-Generation Sequencing (NGS)
X. Wang

TT05. From Plasma to Variants: A Fully Automated Workflow Solution for Low-Frequency Variant Detection in Cell-Free DNA
T. Barnes

TT06. Concordance of Variant Detection between the MoCha ctDNA Assay and Matched Tissue Biopsy in Non-small Cell Lung Cancer
C. Karlovich

TT07. Reproducibility of Allelic Fractions of Genomic Variants from Colorectal and Lung Cancer Tissue Downstream of DNA Extraction
M. Javey

TT08. Flexible and Complete Exome Next-Generation Sequencing (NGS) Solution for Variants Detection with Improved Human Exome Panel
M. Hong

TT09. DNA Samples with Low Concentration Can Benefit from Speed Vacuum Concentration in NGS Testing
W. Song
L. Zhang

TT11. Workflow Evaluation: Impact of Specimen Storage and Transport on ccfRNA Multiplex Analysis in Dedicated Blood Collection Tubes
T. Voss

TT12. Reference Materials for Measurable Residual Disease (MRD) Monitoring in Circulating Cell-Free DNA (ccfDNA)
Y. Königshofer

TT13. Automation of Fluorescence *in situ* Hybridization Processing and Digital Analysis
M. Azim

TT14. A Modified Vendor Extraction Protocol Better Preserves the Structural Integrity of Genomic DNA Extracted from FFPE Tissue
C. Artymiuk

TT15. WITHDRAWN

TT16. Detection of the Mutational Status in Colorectal Cancer from Formalin-Fixed, Paraffin-Embedded (FFPE) Tissue
E. Haenssler

TT17. Centrifugation and RBC Lysis-Free Preparation of Blood Samples in less than 30 Minutes
C. Barr

TT18. A Complete Yet Flexible Workflow for Library Preparation and Analysis with Enhanced Error Correction for Low Input FFPE Tissue Biopsy and Circulating Tumor DNA Samples
S. Lee

TT19. Next-Day Analysis from Specimen to Variant Calling with the Genexus System
J. Gioia

TT20. Pushing the Limits of Cancer Research: An Integrated and Automatic Workflow on Ion Torrent Genexus System from Nucleic Acid Extraction to Next-Generation Sequencing
R. Cao

TT21. Analytical Performance Testing of the MoCha Circulating Tumor DNA Assay
R. Harrington

TT22. Digital PCR Paired with High-Speed AFM for Quantitation and Length Analysis of DNA Length Polymorphisms
S. Koebley

TT23. Focused-Ultrasonication Driven High-Quality DNA and RNA Extraction and Purification from FFPE Samples
K. Amirault

TT24. Evaluating Effects of PCR Instruments and Temperature Ramp Rates to Base-Composition Bias in TruSight Oncology 500 (TSO500) Panel
W. Song
TT25. Evaluation of the Biocartis Idylla ctEGFR Mutation Assay on Samples with DNA Concentrations Insufficient for Next-Generation Sequencing (NGS)  
W. Keegan

TT26. Analysis of Simple and Complex Variants and Biomarkers for Comprehensive Genomic Profiling (CGP) of Solid Tumors and Hematologic Malignancies Using a Single NGS Workflow from FFPE and cfDNA Samples  
R. Samara

Y. Lu

TT28. Archival FFPE and DNA Quality: Optimal Storage Time and Predictive Metrics for Next-Generation Sequencing  
V. Parimi (Parini)

TT29. Confirmation of Fusions Detected with Sequencing  
D. Jones

TT30. Development of a Universal Probe System for Droplet Digital PCR  
D. Jones

TT31. Targeting Clinically Significant “Dark” Regions of the Human Genome with High-Accuracy Long-Read Sequencing  
C. Heiner

TT32. Performance of GeoMx CTA and WTA, High-Plex, Spatial Gene Expression Profiling Tools  
K. Sorg

TT33. Standardizing Plasma ctDNA Measurements Using SNAQ-SEQ ONCO1LB Internal Controls  
S. Deharvengt

TT34. Optical Mapping Enables High-Throughput Analysis of Pathogenic Repeats  
E. Lam