Poster Listing

Even numbered posters will be attended by their authors on Friday, November 2, 2:30pm-3:30pm.

Odd numbered posters will be attended by their authors on Saturday, November 3, 9:45am-10:45am.

GENETICS

G001. Genomic DNA Reference Panels for HLA Class I and II Loci: A GeT-RM Collaborative Project
M.P. Bettinotti

G002. Frequency and Diagnostic Yield of Mosaic Variation Identified by Whole Exome Sequencing
C.R. Miller

G003. WITHDRAWN

G004. Performance Evaluation of VCU Health NIPT, a Single-Nucleotide-Polymorphism (SNP) Based Non-invasive Prenatal Testing for Common Aneuploidy
C. Yang

G005. Development of a Clinical CD33 Genotying Assay to Predict Response to Gemtuzumab
B.A. Barkoh

G006. Characterization of Beta Hemoglobinopathy Results in a Large Population Referred for Carrier Testing
C.A. Holland

G007. Pro-fibrotic Cardiac Gene Activation in Diabetic Zucker Rat Model is Directly Associated to the Incremental Visceral Adiposity: The EPACs Proteins Signaling
M.M. Corsi Romanelli

G008. Validation of a Targeted Variant Genotyping Assay for Personalized Antihypertensive and Chronic Kidney Disease Therapy
W.M. Stansberry

G009. Analysis of ARID1A Mutations and Co-occurring Variants in Cancer Biopsies Reveals Significant Associations in Multiple Diseases.
T. Buys

G010. Validation of an Economical, Real Time PCR Genotyping Assay for Detection of ACMG/ACOG Recommended Mutations in the *CFTR* Gene for General Population Screening
S. Beqay

G011. Cre Recombinase-mediated Circularization for Custom Mate Pair Library Preparation
E. Zimmerman Zuckerman

G012. Clinical Laboratory Experience with Different Carrier Screen Panels
H. Zhu

G013. Rapid Molecular Haplotyping of Thiopurine Methyltransferase *3A, *3B, and *3C
M. Leong

G014. Pathogenic Variants in MID1 in Patients with X-linked Opitz G/BBB Syndrome Type 1
L. Fan

G015. Clinical Evaluation of the Luminex ARIES System for Single Nucleotide Polymorphism Analysis of rs6025 (Factor V Leiden), rs1801133 (Methylenetetrahydrofolate Reductase), and rs1799963 (Prothrombin)
M. Leong

G016. **How to Consistently Determine if a Variant is a Polymorphism?**
D. Qin

G017. High-throughput Approach for Multi-omic Testing for Prostate Cancer Research
M. Shannon

G018. Clinically Integrated Molecular Diagnostics in Adenoid Cystic Carcinoma
J.C. Thierauf

G019. Germline BRCA Mutation Studies in a Select Indian Cohort Using Next-generation Sequencing (NGS)
J.C. Vyas

G020. Phylogenetic Analysis of Duffy, Kidd, and Lewis Allele
M. Kim

G021. Brazilian Panorama of Whole Exome: Details of 315 Cases
R.M. Minillo

G022. Clinical Validation of a Multi-gene Panel on Myeloid Malignancies by Next Generation Sequencing
G. Liu

G023. A Recurrent Heterozygous *RPL21* Mutation Responsible for Hereditary Hypotrichosis Simplex in a Chinese Family
Z. Xu

G024. Confirmation of Cis Inheritance of Variants in *ABCB1*, *SHROOM3*, and *SLC28A3* During the Validation of a Targeted Genotyping Assay
W.M. Stansberry

G025. Verification of Very Small Copy Number Variants (Micro CNVs) Detected on Whole Genome CMA Analysis and Implications for Clinical Reporting
U.P. Kappes

G026. Two-site Evaluation of a One-tube PCR/CE Assay that Resolves CAG Length Polymorphisms in Exon 1 of the *HTT* Gene
S.N. Statt

G027. A Streamlined, Single-Tube PCR Assay that Quantifies *SMN1* and *SMN2* Copy Numbers Using Capillary Electrophoresis
W. Laosinchai-Wolf

G028. New Variant-centric XML for ClinVar Data
M. Landrum

G029. Measuring the Economic Value of Sequencing: Why is it Important, Why is it Challenging, and What are Solutions
K.A. Phillips

G030. Newborn Screening, Diagnosis, and Carrier Testing for Spinal Muscular Atrophy by Multiplex Droplet Digital PCR
N. Vidal-Folch

G031. What's in a VUS Rate? Simulated VUS Rate Calculations for Hereditary Cancer Genes Using Population Frequency Data and ClinVar Submissions
K.E. Kaseniit

G032. What Can We Learn From Oncologists? A Survey of Molecular Testing Patterns
J.S. Menezes

G033. A Data-Driven Approach to Determine Disease Content in Expanded Carrier Screening Panels
R. Ben-Shachar

G034. Clinical Impact and Cost Effectiveness of a 176 Condition Expanded Carrier Screen
K.A. Beauchamp

G035. Detection of Copy-Number Variants in Expanded Carrier Screening Maximizes Identification of Cystic Fibrosis Carriers
D. Muzzey

G036. The Algorithm for Estimation of Human T-cell Receptor Repertoire with Single Cell RNA Sequencing
Y. Cho

G037. WITHDRAWN

G038. Pharmacogenomics: *VKORC1* + *CYP2C9* and *TPMT*: Two New, Ready-to-use Real-time PCR Assays
M. Gramegna

G039. Interpretation of Microdeletion Variants Aided by Population Analysis of Copy-number Variation
K.E. Kaseniit

G040. Frequency of Deletion 13q Associated with other Abnormalities Detected by Fluorescence *in situ* Hybridization (FISH) in Multiple Myeloma Patients – an Experience from a Referral High-end Diagnostic Centre
M. Kumar

G041. Molecular Diagnosis of Graft-versus-Host Disease after Liver Transplantation: an Institutional Experience
S.M. Hosseini

G042. Analytical Performance of the Oncomine BRCA1/2 Assay on the Ion Torrent S5
D. Saxena

G043. A Novel Custom Panel Target Sequencing with Molecular Tags for 0.1% Allelic Frequency Detection
X. Peng

G044. Designing and Implementing NGS Tests for Inherited Disorders – a Practical Framework with Step-by-step Guidance for Clinical Laboratories
A.B. Santani

G045. SMA Complete: Addressing SMN Copy Number and Silent Carrier Status with a Single Complete Multi-plex qPCR Assay
R. Daber

G046. Double Splicing Variants in BCR-ABL are Associated with Tyrosine Kinase Inhibitor (TKI) Resistance in Chronic Myelogeneous Leukemia (CML)
D. Dash

G047. Validation of a Neuro-Oncology Next-generation Sequencing 219-Gene Panel
C. Zysk

G048. IGF1 Proteomic Variant Confirmation using Genotyping Assay
A.D. Maus

G049. Adaptation and Validation of a Pan-cancer Somatic Next Generation Sequencing Assay for Detection of Germline Hereditary Cancer Predisposition Variants
D.K. Manning

G050. Expression Analysis of Telomere-related Genes in Solid and Hematologic Tumors Using RNA-Seq
M.A. Atiq

G051. Meta-analysis of AKT1 rs2494732 Genotype and the Risk of Psychotic Adverse Effects by Cannabis Use
M. Nakano

G052. In cis Heterozygous BRCA2 Pathogenic Mutations in a Jordanian Family: Case Report
L. Abu Jamous

G053. Characterization of Novel Aneuploidy Reference Materials for NGS-based Non Invasive Prenatal Screening (NIPT)
F. Sabato

G054. The SureMASTR BRCA Screen Assay Combined with MASTR Reporter Analysis is an Accurate and Precise Workflow for SNV, Indel and CNV Detection in Blood- and FFPE-derived DNA
A. Rotthier

G055. CNV Contribution to Pathogenic Alleles within a Healthy Population: Results from Expanded Carrier Screening of 137,000 Individuals
S.G. Cox

G056. Use of Molecular Identifiers and Targeted NGS to Enable Variant Detection Below 1% Allele Frequencies in Circulating Cell-free DNA
L. Kurihara

G057. WITHDRAWN

G058. Evaluation of a Single-tube, Long-read, Two-mode PCR Technology that Reports the Categorical Range of DMPK CTG Expansions and Resolves up to 2000 Repeats in Myotonic Dystrophy Type 1
B. Hall

G059. ACMG Incidental Findings at the CLIA-certified Colorado Center for Personalized Medicine Biobank: Data from the First 10,000 Subjects
S.J. Wicks

G060. Phenotypic and Genotypic Study of Patients with Hermansky-Pudlak Syndrome
J.A. Majerus

G061. Performance Characteristics of High-resolution Human Leukocyte Antigen (HLA) Typing Using TruSight Next-generation Sequencing (NGS) Technology
A. Budhai

G062. WITHDRAWN

G063. Multiplex Synthetic Reference Material for Monitoring the Analytical Performance of Highly Complex Variant Detection of Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) using Next Generation Sequencing
R. Mihani

G064. Low Input Microfluidic Library Preparation Platform for Targeted CFTR Using Blood, Buccal Swabs and Saliva Samples
N. Ramalingam

G065. Validation of a Next-generation Sequencing Gene Panel for Inherited Platelet Disorders
W. Zhang

G066. Identification of Mutation Signatures in Tumors Using Panel-based Targeted Sequencing
S. Rana

G067. WITHDRAWN

G068. CleanPlex Amplicon-based Next Generation Sequencing Heredity Panels for Determining Genetic Predispositions
L. Lin

HEMATOPATHOLOGY

H001. The Detection of a *BRAF* Mutated Clone in Acute Myeloid Leukemia with Mutated *Npm1* and Extensive Extramedullary Involvement
K. Gvozdjan

H002. Short Tandem Repeat Aberrancies in Hematopoietic Stem Cell Transplant Recipients
K. Gvozdjan

H003. A Strategy for Implementing Sensitivity Controls for qPCR Chimerism Monitoring
J. Tyler

H004. Genetic Profiling of Adult Acute Myeloid and Lymphoid Leukemia Cases in a Major Referral Center in Lebanon
S. Halabi

H005. Clinical Implementation of T-cell Clonality Testing by Next-generation Sequencing: Improved Detection Sensitivity and Reliability in Initial Diagnosis and Minimal Residual Disease Detection of T-cell Malignancies
J. Yao

H006. Performance Evaluation of a Custom DNA/RNA Next-generation Sequencing (NGS) Assay for Hematologic Malignancies
J. Karrs

H007. Evaluation of Performance of Two Commercially Available BCR-ABL Real-time PCR Assays for Deep Molecular Response in International Scale.
B. Das

H008. Fusion Detection by Next-generation Sequencing from Methanol/Acetic Acid Fixed Cell Pellets in the Setting of Acute Lymphoblastic Leukemia Workup
X. Qu

H009. Fluorescence *in situ* Hybridization as a Tool for Minimal Residual Disease Testing in Multiple Myeloma
S. Golem

H010. Reproducibility of Clinical Samples by the Illumina TruSight Myeloid Next-generation Sequencing Panel
L. Commander

H011. Extended Myeloid Mutation Profiling Using NGS in Triple-negative Myeloproliferative Neoplasms: Single Institution Experience at a High Volume National Reference Laboratory
A. Jhuraney

H012. Validation of a Custom, Focused Next-generation Sequencing Panel for Lymphoma
M. Kluk

H013. Identification of *FLT3* ITD Using Next-generation Sequencing (NGS): A Single Institution's Experience
A. Campbell

H014. Mate Pair Sequencing: Ushering Cytogenetics Into the Era of Personalized Medicine
N. Hoppman

H015. Evaluation of *NPM1* Mutation Detection by Droplet Digital PCR for Minimal Residual Disease Detection
R.Y. Walder

H016. Detection of *CRLF2* Rearrangements in B-cell Acute Lymphoblastic Leukemia in Children with Down Syndrome
A. Garcia

H017. Standardization of *FLT3*-ITD Mutation Allelic Ratio Reporting in the Clinical Laboratory Setting
S. Bhattacharyya

H018. A Limited FISH Panel is a Useful Surrogate for Metaphase Analysis to Rapidly Identify Patients with AML-MRC
N.D. Nelson

H019. IntelliGEN Myeloid 50 Gene Panel Validation and Testing Experiences
L. Cai

H020. Mutational Analysis of Myeloid Neoplasms in Paired Peripheral Blood and Bone Marrow by Next-generation Sequencing
P. Michaels

H021. Guideline-adherent, Evidence-based NGS Workflow for Myeloid Leukemia
R. Kohle

H022. Evaluation of Targeted Next-generation Sequencing Panels for Myeloid Malignancies-Focusing on *CEBPA* and *FLT3* Genes
R. Akabari

H023. Novel *PML-SYK* Fusion in Acute Myeloid Leukemia Constitutively Activates Targetable Pathways
J. Mosquera

H024. Validation of a Low Input Targeted NGS Assay for Lymphoma Across Multiple Specimen Types
A. Oran

H025. Ultradeep Error Corrected Next-generation Sequencing (NGS) of ABL1 Kinase Domain Mutations in BCR-ABL1 Positive Malignancies
N. Patkar

H026. Routine Clinical Monitoring of Disease Status Through NGS Measurement of Clonal Architecture in AML and MDS
P.D. Velu

H027. Peripheral T-cell Lymphoma: Understanding and Characterizing the Phenotypic Behavior Using Molecular Tools
O. Shetty

H028. Myeloseq One: A Cost Effective Integrated Next-generation Sequencing Assay for Myeloid Malignancies
R. Kodgule

H029. Minimal Residual Disease in AML can be Monitored Utilizing Cell-free DNA
L.M. Chamberlain

H030. Rosai-Dorfman Disease Co-existing with Lymphoma in the Same Lymph Node: A Localized Histiocytic Proliferation with MAPK/ERK Pathway-induced Cyclin D1 Upregulation
S. Garces

H031. Clinical Utility of Targeted Next-generation Sequencing in Evaluation of Cytopenias of Undetermined Significance
R. Beck

H032. Myeloid Neoplasms with Ring Sideroblasts without SF3B1 Mutation
S. Bhavsar

H033. Clinical Use of Rapid Transcriptome (R-RNASeq) Analysis for Gene Fusion and Rearrangement Detection in Pediatric Leukemia
E.M. Azzato

H034. Mutational Signatures Differ between Cytogenetic Risk Groups of *de novo* AML
R.T. Sussman

H035. Therapy-related Acute Myeloid Leukemia, Characterized by t(8;16)(p11;p13);*MYST3-CREBBP* and Co-occurring *TET2* and *ASXL1* Mutations
A. Alsuwaidan

H036. Variant Characterization for a Clinical Lymphoma Sequencing Panel
S. Deihimi

H037. Post-remission NGS-based MRD Surveillance is Critical for Early Detection of Impending Relapse in B-ALL
S. Cheng

H038. Clinical Evaluation of the Archer VariantPlex Myeloid Panel for Mutation Profiling in Myeloid Neoplasms
A. Campbell

H039. Donor-derived Clonal Hematopoiesis of Indeterminant Potential Mutations are Detected in Transplant Recipients after Allogeneic Hematopoietic Stem Cell Transplant
J. Liu

H040. Comprehensive Assessment of Variants in *SOCS1*, *JAK2* and *B2M* Using Anchored Multiplex PCR and Next-generation Sequencing
H.E. Robinson

H041. Longitudinal Monitoring of AML Tumors with High-throughput Single-cell DNA Sequencing Reveals Rare Clones Prognostic for Disease Progression and Therapy Response
D.J. Eastburn

H042. Next-generation Sequencing-based Detection of Clinically Significant *IKZF1* Deletions and *KMT2A* Partial Tandem Duplications
K.C. Floyd

H043. Development of Synthetic Secondary Standards for *BCR-ABL1* Quantification on GeneXpert BCR-ABL V2 and Xpert BCR-ABL Ultra Assays
R. Mihani

H044. Validation of a Custom Next-Generation Sequencing (NGS) Panel for Characterizing Mutations in Ph-like ALL Using Anchored Multiplex PCR Technology
A. Guimaraes-Young

H045. Detection of Clonal Rearrangements in Multiple Myeloma Samples Using LymphoTrack Assays
Y. Huang

H046. Pediatric Myeloid Sarcoma: A Single Institution Clinicopathologic and Molecular Analysis
T. Zho

H047. PTPN11 Mutation is Uncommon in Acute Myeloid Leukemia, but Associated with a Complex Karyotype, Co-mutations in *KRAS* or *NRAS* and Poor Prognosis
R. Ruiz-Cordero

H048. Accurate Detection of *FLT3*-ITDs and *CEBPA* Variants in Acute Myeloid Leukemia by Anchored Multiplex PCR and Next-generation Sequencing
N.M. Nair

H049. A Single NGS-based Assay for Simultaneous Identification of *BCR/ABL1* Fusion and *ABL1* Sequencing Detects Resistance Mutation and Subclones
R. Ruiz-Cordero

H050. Clinicopathologic Characterization of Myeloid Neoplasms with Concurrent Spliceosome Mutations and MPN-associated Mutations
Y. Liu

H051. SNP Genotyping-based Stem Cell Engraftment Detection in Targeted NGS Testing
W. Chen

H052. Development of a Reverse Transcriptase Quantitative Polymerase Chain Reaction (RT-qPCR) Assay for Nucleophosmin (NPM1) Minimal Residual Disease (MRD) Monitoring in Acute Myeloid Leukemia
M. Mai

H053. Next-generation Sequencing in Burkitt-like Lymphoma with 11q Aberration: A Clinicopathologic Correlation
A.N. Alsuwaidan

H054. Integrative Analysis of Programmed Death-Ligand 1 DNA, mRNA, and Protein Status and their Clinicopathological Correlation in Diffuse Large B-cell Lymphoma
X. Zhou

H055. Optimizing Diagnostic Algorithms for Pediatric Leukemia: Synergy Between Next-generation Sequencing, Chromosomal Microarray, and Conventional Cytogenetics
M.C. Hiemenz

H056. Variant Allele Frequency does not correlate with Marrow-based Leukemic Blast Proportions in Acute Myeloid Leukemia
L.N. Toth

H057. BCOR Mutations Portend Poor Survival Independent of Concurrent Mutations in Other Epigenetic Modulators in Myelodysplastic Syndrome
I. Badat

H058. Isochromosome 17q in Acute Myeloid Leukemia and Myeloid Neoplasms
M. Kim

H059. Comparison of Interpretive Guidelines for IGH and TCR Clonality by NGS in B and T-cell Cancers
L. Lay

H060. Impact of Single versus Multiple Splicesome Mutations in MDS/CMML
M. Hussaini

INFECTIOUS DISEASES

ID001. Development of a Real-time PCR Assay for the Direct Detection of *Mucorales* Species
K.D. Tardif

ID002. Comparison of the Roche Cobas Ampliprep/Cobas Taqman v2.0 and Cobas 6800 for HIV, HCV, HBV and CMV Viral Load Determination
T.R. Sundin

ID003. Evaluation of a Commercial Sample–to-Answer Assay for the Detection of Varicella-Zoster Virus Directly from Clinical Specimens
M.J. Espy

ID004. Evaluation of a Novel Isothermal Amplification Assay for Detection and Genotyping of Human Papillomavirus in Formalin-fixed Paraffin-embedded Tissue of Oropharyngeal Carcinomas
L. Lozano

ID005. Second Generation Next-generation Sequencing-based System for Detecting Drug Resistance Mutations in HIV-1 Combined with Isothermal Amplification
E.J. Wee

ID006. Comparison of Real-time PCR with Transcription Mediated Amplification for HPV Detection/Genotype and Correlation with Cytological and Histological Results
S. McClellan

ID007. The Diagnostic Yield of Universal Pathogen Detection by Next-generation Sequencing Compared to the Standard of Care in Patients with Pneumonia
B.A. Young

ID008. Spectrum Profile of Respiratory Pathogens Detected by the BIOFIRE Plex Assay: Experience of a Major Tertiary Care Center in Lebanon
S. Halabi

ID009. Evaluation of Cobas HBV, HCV, and HIV-1 Tests on the Cobas 6800 Platform
M.K. Leong

ID010. Performance and Workflow Comparison of Simplexa Bordetella Direct (IUO) with Illumigene Pertussis
E.M. Dault

ID011. Performance Evaluation of Two Commercial Molecular Assays for Genotyping Hepatitis C Virus
S.L. Mitchell

ID012. Comprehensive Solid Tumor Microbiome Profiling via Analysis of Unmapped Reads in Large Panel, Hybridization Capture-based NGS Assay Data
C.M. Vanderbilt

ID013. Evaluation of the DiaSorin Molecular Simplexa Bordetella Real-time Sample-to-Result PCR Test on the LIAISON MDX System
T.E. Schutzbank

ID014. Evaluation of Panther Fusion System for Respiratory Viral Detection in a Pediatric Hospital
A. Rector

ID015. Adjusting the pH of Urine Samples at the Time of Collection May Provide a More Accurate Measurement of Cytomegalovirus (CMV) Viral Load
M. Galdzicka

ID016. Detection of Herpes Simplex Virus (HSV) Types 1 and 2 and Varicella-Zoster Virus (VZV) From Cutaneous and Mucocutaneous Lesions Using the Quidel Solana HSV 1+2/VZV Assay
E. Tam

ID017. Efflux Gene Expression by Ofloxacin Stress in Multidrug-resistant *Mycobacterium tuberculosis* and Extensively Drug-resistant *M. tuberculosis* with/without *gyrA* Mutation using RNA-seq
H. Lee

ID018. Triplex Assay for Zika, Dengue, and Chikungunya Viruses by Sentosa SA Real-time RT-PCR Assay
J. Wong

ID019. A Host Gene Signature for Diagnosis and Risk Stratification of Acute Infection and Sepsis at Hospital Admission: HostDx Sepsis
O. Liesenfeld

ID020. Development and Validation of a Quantitative Multiplex Real-time PCR Assay for Identification of Bacterial Pathogens From Respiratory Specimens
A. Seth

ID021. Evaluation and Time-motion Analysis of the GenePOC Rapid C. difficile Assay Compared to the Meridian Illumigene Assay
H. Webber

ID022. Evaluation of the Galileo Pathogen Solution Next-generation Sequencing Pipeline for the Identification and Quantification of DNA Viruses in Transplant Patients
M.L. Carpenter

ID023. Clinical Implications of the Increased Sensitivity of the FDA Roche 6800 CMV Viral Load Assay
J. Pettersson

ID024. Performance Evaluation of AdvanSure RV-plus Real-time PCR Assays for the Detection of Respiratory Viruses
J. Sohn

ID025. Quantitative Detection of HCV Using the NeuMoDx Molecular Diagnostic System
J. Zhu

ID026. Quantitative Detection of Epstein-Barr Virus (EBV) in Plasma and Whole Blood Matrices
L. Gong

ID027. WITHDRAWN

ID028. Evaluation of the GenMark ePlex Respiratory Pathogen Panel for the Detection of Respiratory Pathogens
A.M. Carlin

ID029. Development of a New Diagnostic System Based on Real-time LAMP PCR for Specific Detection of 10 Species of Arboviruses
E. Choi

ID030. Analytical Validation of a Sample-to-Sequence Pipeline for Non-targeted Pathogen Detection in Clinically Relevant Matrices
K. Parker

ID031. Identification of *M. tuberculosis* and *M. bovis* in Clinical Respiratory Specimens Using the VELA Diagnostics Sentosa SA MTC PCR Assay
H. Webber

ID032. Pre-market Evaluation of Hologic's Group B *Streptococcus* PCR Assay on the Panther Fusion System
F. Zhang

ID033. Multicenter Evaluation of the Sentosa SA HSV1/2 Qualitative PCR Test
D. Kohn

ID034. A Rapid Host Gene Expression Assay to Discriminate Bacterial from Viral Infections
W. Nie

ID035. High Throughput FluA/B/RSV Testing May Complement Existing Methods During the Peak of Flu Season
R. Hein

ID036. WITHDRAWN

ID037. A High Throughput System for Profiling Respiratory Tract Microbiota
J. Li

ID038. WITHDRAWN

ID039. Cost Effectiveness Model Describing Emergency Department Use of a Novel Multi-mRNA Test for Diagnosis and Risk Assessment of Acute Respiratory Tract Infections and Sepsis
I. Stojanovic

ID040. Quantitative Detection of Cytomegalovirus on NeuMoDx Molecular Systems
M. Mastronardi

ID041. Performance Evaluation of Unpreserved Stool and Stool in Transport Medium with a Multiplex Gastrointestinal Pathogen Panel with an Automated, High Throughput System
C. Knoth

ID042. WITHDRAWN

ID043. Development and Evaluation of a High Throughput Multiplex Molecular Panel that Detects 20 Respiratory Pathogens in Clinical Specimens
M. Aye

ID044. Hepatitis C Virus Genotyping by Next-generation Sequencing: An Accurate and Cost-effective Alternative
B.G. Nezami

ID045. Technology to Produce Non-infectious Recombinant Virus as Reference Materials for Unculturable or Highly Dangerous Viral Pathogens
B. Anekella

ID046. Detecting *Helicobacter pylori* and Predicting Antibiotic Resistance from Formalin-fixed Paraffin Embedded Gastric Biopsies Using Targeted Next-generation Sequencing
B.G. Nezami

ID047. Clinical Evaluation of the Aptima *Mycoplasma genitalium* Assay Reveals the Prevalence of *Mycoplasma genitalium* Infection among Patients Tested for other Sexually Transmitted Pathogens in Indiana
R.F. Relich

ID048. Evaluation of DiaSorin Molecular Simplexa Bordetella Direct Kit for the Detection and Differentiation of *Bordetella pertussis* and *Bordetella parapertussis*
T. Ton

ID049. A Cross-sectional Study of Swab versus Tissue Sampling of Wounds for the Detection of Microbes by PCR
E. Baum-Jones

ID050. Evaluation of a Next-generation Sequencing Assay: The Sentosa SQ HIV Genotyping Assay for HIV Genotype and Drug Resistance Mutation Analysis
D. Kohn

ID051. Rapid and Accurate Cross-kingdom Human Pathogen Identification and Detection Using Hyb & Seq Technology
D. Bezdan

ID052. Validation of a Novel Qualitative Real-time PCR Assay Versus Direct Fluorescent Antibody Testing for the Detection of *Pneumocystis jirovecii* Pathogen
A. Spohn

ID053. WITHDRAWN

ID054. Simultaneous Detection of Tick-borne Pathogens Using a High Definition Multiplexed PCR Assay
M.W. Mashock

ID055. Clinical Performance Study Results of the Hologic GBS Assay on the Fully Automated Panther Fusion System
B. Eaton

ID056. Quantification of CMV Using the m2000 RealTime CMV Assay
M.A. Johnston

ID057. High-definition PCR (HDPCR): a Novel, Instrument Agnostic qPCR Multiplexing Technology Applied to Tick-borne Pathogen Testing
B. Amro

ID058. Evaluation of a Completely Automated BKV Viral Load Assay on the Abbott m2000 Platform
F. Nolte

ID059. Validation of Qualitative HIV Detection of HIV in Whole Blood with the Hologic Aptima HIV Assay
K. Tardif

ID060. The Prevalence of Clarithromycin-resistant *Helicobacter pylori* in Utah; a Laboratory-based Survey
K.N. Carter

ID061. Is There a Need for HCV Resistance Testing in Routine Diagnostics and Patient Treatment? Routine HCV Genotyping and Resistance Testing and Performance of the Sentosa SQ HCV Genotyping v2.0 Assay
M. Obermeier

ID062. Evaluation of the ARIES *Bordetella* Assay for Detection and Identification of *Bordetella* pertussis in Nasopharyngeal Swab Specimens
T. McMillen

ID063. A Quantitative, Multiplexed RNA Detection Platform for Rapid Pathogen Identification and Phenotypic Antibiotic Susceptibility Testing (AST) using NanoString Technology
R.P. Bhattacharyya

ID064. The Galileo Pathogen Solution Next-Generation Sequencing Pipeline Detects and Identifies RNA Respiratory Viruses in Haematopoietic Stem Cell Transplant Patients
M.L. Carpenter

ID065. Molecular Screening for *Trichomonas vaginalis* and *Mycoplasma genitalium* in the RADAR Longitudinal Cohort Study of Young Transgender Women and Young Men who Have Sex with Men
E. Munson

ID066. Evaluation of Performance and Workflow using the GenePOC Strep A, C/G Assay for Detection of Group A, C, and G *Streptococcus* from Patients Presenting with Pharyngitis to the Emergency Department
D. Mastandrea

ID067. Evaluation of the BD MAX Vaginal Panel for the Detection of Vaginitis in Women
K. Culbreath

ID068. Evaluation of ELITech HSV 1&2 ELITe MGB for the Detection and Differentiation of Herpes Simplex Virus 1 and 2 from Lesions
V.P. Maceira

ID069. Different CMV Strains for Quality Controls and its Impact on Assay Calibration
J. Boonyaratanakornkit

ID070. Detection of Microorganisms and Antibiotic Resistance Genes in Skin and Soft Tissue Infections by a PCR-based Diagnostic Test
G. Zhu

ID071. Comparison of Three Nucleic Acid Amplification Tests (NAATs) to Culture for Detection of Group B Streptococcus (GBS)
J. Shin

INFORMATICS

I001. Evaluation of a Guideline-adherent Microsatellite Instability (MSI) Module for Calculation of MSI Using a Comprehensive 170 Assay on an NGS Platform.
R. Kolhe

I002. Clinical Implications of the Reference Sequence Used for Diagnostic Interpretation
J.A. SoRelle

I003. CCKB: A High-Performance and Genome-Scale Informatics Portal for Analysis and Multi-Institutional Sharing of Pediatric Cancer Variants
X. Gai

I004. A Machine-Learning Framework for Accurate Classification and Quantification of Oncogenic Variants Using the QuantideX NGS DNA Hotspot 21 Kit
L. Ringel

I005. Improving Variant Call Accuracy by Combining Torrent Variant Caller and PLATYPUS
Z. Siddiqui

I006. Improving the Molecular Pathology Workflow with Machine Learning: Automated Calculation of Tumor Percentages on H&E Digital Whole Slide Images
C.M. Cirelli

I007. Assessment of a Somatic Mutation Detection Pipeline Using a Simulated Tumor Genome
Z. Li, R. Zhang

I008. Interpretation of Mutational Signatures Associated With Smoking from an Amplicon-Based Clinical Oncology Sequencing Panel
J.E. Adler

I009. Personalized Transcriptomic Drug Profiling in Non-small Cell Lung Cancer
Z. Abrams

I010. NeGeSeI-NIPT: A Web Based Tool for the Management of Non-Invasive Prenatal Screening Assays in the Clinical Laboratory
V. Williamson

I011. NeGeSeI–Inheriseq: a scalable informatics solution for the management of assays for hereditary cancer
V. Williamson

I012. A Local Population Allele Frequency Query Tool
M. Leong

I013. Classification of Variants from Myeloid NGS Panel Testing Using a Scalable Evidence Based Variant Classification Workbench (SEBVaC)
W. Chen

I014. A Molecule-Centric Approach to Phasing
M. Debeljak

I015. Using AutoIt to Automatically Enter Molecular LDT Results into the Laboratory Information System
J. Grojean

I016. Fragment Size Characterization of Cell-Free DNA Mutations from Clonal Hematopoiesis
T. Jiang

I017. NGS Panel Analyzer: A Software Tool to Assess NGS Panel Design
S.B. Patel

I018. WITHDRAWN

I019. Database of High-Resolution Melting Publications with Data Mining and Statistical Reporting
Z.L. Dwight

I020. A Clinical Decision Support Tool to Integrate Next-Generation Sequencing and Cytogenetics Assays for Myeloid Cancers
S. Bandla

I021. Development and Analysis of a Machine Learning Variant Caller
D.E. Wood

I022. Evaluation of SOPHiA DDM v4 for NGS Analysis of Ampliseq Cancer Hotspot Panel
D.C. Green

I023. Precision Medicine Requires Molecular Pathologists Have Clinical Decision Support and Automation Found in Agilent Alissa to Analyze and Interpret Large Numbers of Variants from NGS Assays
S. Van Vooren

I024. Identification of Germline Mutations in Tumor DNA Samples Absent a Matched-normal
A. Bigdeli

I025. Identification of Viral Integration Sites in Cancer Genomes Using Unmapped Reads in Targeted Next-generation Sequencing Data
A.S. Bowman

I026. Variant Inspector: A Computational Approach for Somatic Variant Prioritization in Routine Clinical Practice
R.J. Maglantay

I027. Detection of Microsatellite Instability Using a Large Next-generation Sequencing Panel across Diverse Tumor Types
J. Pang

I028. A Rigorous Interlaboratory Examination of the Need to Confirm NGS-Detected Variants by an Orthogonal Method in Clinical Genetic Testing
S.E. Lincoln

I029. Dual-Assay Demultiplexing with Preferential Read Allocation and Unequal Index Size Presents Bioinformatics Challenges
A. Chitturi

I030. Integrating Clinical Genomics into Electronic Health Records to Foster Precision Medicine
A. Sigaras

I031. Standardization of Molecular Diagnostic Testing for Non-small Cell Lung Cancer
A. Karimnezhad

I032. Effects of Probe Regions on Somatic Variant Calling in TruSeq Amplicon Cancer Panel
P.B. Mayigowda

I033. Modern Application Deployment Infrastructure for Supporting Clinical Next- generation Sequencing (NGS) Testing
L. Santana Dos Santos

I034. Assessing Cancer Diagnosis from Clinical Genomics Data Using Machine Learning.
P.R. Hess

OTHER (e.g. Education)

OTH001. Virtual Case Sets for Genomics Education: Thinking Outside the Slide Box
J.N. Rosenbaum

OTH002. Standardized Protocol for Salvaging Quality or Quantity Not Sufficient (QNS) Samples in an Academic NGS Laboratory
S.F. Priore

SOLID TUMORS

ST001. Clinical Utility of Reflex Ordered Testing for Molecular Biomarkers in Stage IV Lung Cancer
T.L. Phung

ST002. Analysis of Urinary Cell-free DNA for Early Detection and Surveillance of Bladder Cancer
J. Dudley

ST003. Utility of a Comprehensive and Cost-effective DNA/RNA Panel (170 Genes) for Single Nucleotide Variants (SNV's), Small Insertions or Deletions (Indels), Copy Number Variations (CNV's) Splice Variations, and Gene Fusions on an NGS in Evaluation of Colon Cancer
R. Kolhe

ST004. Validation of *FFPE* Tissue Punches for Detection of *KRAS* and BRAF Mutations with the Idylla PCR-based Molecular Diagnostics Assay
D. Morlote

ST005. Evaluation of a Guideline-adherent Tumor Mutational Burden (TMB) Module for Calculation of TMB Using a Comprehensive 170 Gene Assay on a NGS Platform.
R. Kolhe

ST006. Comparison of Two DNA Polymerases in Detection of DNA Methylation via Pyrosequencing
C.M. Farrell

ST007. WITHDRAWN

ST008. Analyses of *BRAF* Mutations and MSI Status Frequencies in TKi Non-treatable Lung Adenocarcinoma Patients
G.N. Berardinelli

ST009. Evaluation of Microsatellite Instability Testing and Lynch Syndrome Screening Through Tumor Sequencing Using Illumina TruSight Oncology 500 panel
S. Zhang

ST010. Identification of Different Levels and Spatial Patterns of Methylation of Promoter-Associated CpGs74-78 of the O6-Methylguanine Methyltransferase Gene *(MGMT)* in Gliomas
F. Khan

ST011. Evaluation of Molecular Spectrum of *BRCA* Gene Mutation in Indian Scenario using Next Generation Sequencing (NGS) Approach
B. Das

ST012. Development of a Novel Pan-Cancer Biomarker Panel for Improved Detection of MSI in Tumor and Liquid Biopsies
J. Bacher

ST013. Comparison of Cobas EGFR Mutation Test and PANAMutyper R EGFR Assay in the Detection of *EGFR* Mutations in Plasma from Non-small Cell Lung Cancer Patients
K. Lee

ST014. Comprehensive Genomic Profiling of Thyroid Neoplasm by Next-generation Sequencing of Fine Needle-Aspiration Biopsy Material Preserved in CytoLyt
H.J. Park

ST015. TruSight Oncology 500: Measuring Tumor Mutation Burden with Targeted Sequencing
J. Ju

ST016. Analytical Validation of the Oncomine Comprehensive Assay v3 with FFPE and Cell Line Tumor Specimens in a CAP-accredited and CLIA-certified Clinical Laboratory
A. Yuki

ST017. Nextgen Digital Spatial Molecular Pathology: Digital IHC Coupled to Automated Gene and Protein Expression Profiling Measuring Complex Signatures within the Context of the Tumor Microenvironment
E. Imler

ST018. Clinical Implementation of Precision Medicine in the Classification of Medulloblastomas: Concordance, Conflict, Recurrence, and Reclassification
B. Liechty

ST019. Clinical Validation of a Combined DNA and RNA Target-capture Next Generation Sequencing (NGS) Test for Solid Tumors on FFPE Specimens
S.P. Strom

ST020. Molecular Epidemiology of *CREBBP* and *EP300* Mutations in Solid Tumors
J.P. Solomon

ST021. Prevalence of *EGFR* Mutations in Indian Lung Cancer Patients
R. Katara

ST022. Detection and Quantitation of Human Papilloma Virus Type 16 in Oropharyngeal Squamous Cell Carcinomas
K. Vadlamudi

ST023. Cross-Platform Comparison of NGS and MALDI-TOF for Detecting RAS/RAF Mutations in Circulating Tumor DNA from Metastatic Colorectal Cancer Patient Plasma
W. Guo

ST024. Clinical Implementation of Mutational Signature Analysis
L. Lawrence

ST025. Implementation and Validation of the Moffitt Solid Tumor Actionable Result (STAR) Assay
E.L. Roberts

ST026. A Functional DNA Repair Assay Platform to Stratify Melanoma and Select the Best Therapeutic Option
S. Sauvaigo

ST027. Ultra-Rapid EGFR Mutation Assessment in Lung Adenocarcinoma without Prior DNA Extraction
M.E. Arcila

ST028. Confirmation of Novel Gene Fusions Detected by Next-Generation Sequencing using Enriched RNA Libraries
N.T. Ngo

ST029. Assessment of Significant Components in Multigene Testing for Breast Cancer in Clinical Laboratories
P. Gao

ST030. Culture of Circulating Tumor Cells (CTCs) using Three-dimensional Culture and Conditional Reprogramming Methods
C. Park

ST031. ISO Certification of a Complete Next Generation (NGS) Sequencing Workflow for *BRCA1/2* Analysis
S. Marchini

ST032. Analytical Validation of the Oncomine Breast cfDNA Assay v2
W. Liu

ST033. Assessment of Pre-analytical Effects on RNA Sequencing
A. Beams

ST034. Performance Evaluation of Asuragen QuantideX NGS RNA Lung Cancer Panel by ACL Laboratories
S. Spirtovic

ST035. Performance Evaluation of Illumina TruSight Tumor 15 Panel by ACL Laboratories.
S. Spirtovic

ST036. Comparison of Three Next-generation Sequencing Platforms in Fusion Detection: FusionPlex by Archer, Oncomine by ThermoFisher, and AmpliSeq by Illumina
X. Qu

ST037. WITHDRAWN

ST038. A Turnkey Solution for NGS-based Detection of Somatic Mutations in Cancer
M. Yee

ST039. Clinicopathologic and Molecular Features of Undifferentiated Round Cell Sarcomas of Bone and Soft Tissues, including BCOR-CCNB3 and CIC-DUX4 Test Results
B. Rekhi

ST040. *KRAS* Mutations in Tissue Samples from Cologuard-Positive Patients
K. Murphy

ST041. Evaluation of the Biocartis Idylla Rapid Near-to-Patient EGFR Mutation CE-IVD Marked Tissue Test: Correlation to an FDA Approved Orthogonal Method using 79 Clinical Formalin-Fixed, Paraffin-Embedded Tissue Samples
M. Kohlman

ST042. Clinically Significant Germline Variants Detected by Mutation Profiling of Non-small Cell Lung Cancer in Patients with Multiple Nodules Harboring Different Somatic Mutations
A. Almradi

ST043. Clinical Validation of a Custom-designed Next-generation Sequencing-based FusionPlex Panel for Salivary Gland Tumors
N.V. Guseva

ST044. A Comparison of the Performance Characteristics of the Illumina TruSeq Stranded mRNA Kit and TruSeq RNA Sample Preparation v2 Kit for Gene Fusion Detection
R.N. Wehrs

ST045. Development and Validation of an RNA Sequencing Assay for the Detection of Gene Fusions in Formalin-fixed Paraffin Embedded Tumors
R.A. Jackson

ST046. Multi-institutional Evaluation of the 2017 AMP, ASCO and CAP Standards and Guidelines for Interpretation and Reporting of Sequence Variants in Cancer
D. Sirohi

ST047. Establishing the Impact of *STK11* Canonical Splice Site Variants Identified by NGS Panel Testing in Non-Small Cell Lung Cancers (NSCLC): Prognostic and Therapeutic Implications
D.J. Seward

ST048. Validation of the ArcherDx VariantPlex Solid Tumor Assay for the Molecular Analysis of Clinical Tumor Samples
K.D. Davies

ST049. Clinical Targeted Next-generation Sequencing Panel Testing in Non-small Cell Lung Cancer: Single Institution Experience at a High Scale National Reference Laboratory
K. Barber

ST050. *MLH1/PMS2*-deficient, *BRAF*-mutated, and Calretinin-positive Colorectal Carcinoma Presents at Advanced Stage and is Associated with Poor Differentiation and Poor Prognosis
W. Zhang

ST051. Analytical Validation of a DNA Dual Strand Approach for an FDA-approved NGS based Praxis Extended RAS Panel for FFPE Metastatic Colorectal Cancer Samples
A. Iyer

ST052. Optimization of Testing Methods in Detecting MET Amplification, Expression, and Activation for Targeted MET TKI Treatment in Non-small Cell Lung Cancer Patients
H. Gong

ST053. Personalized ddPCR Mutation Assays Targeting Patient Specific ctDNA: A Tool to Monitor Treatment Responses to Mutation-Specific T-cell Transfer Immunotherapy in Epithelial Cancer Patients
L. Xi

ST054. Importance of Amplicon Size for Detecting Microsatellite Instability in Liquid Biopsies
M. Campan

ST055. DNA Sequencing of Human, Epstein - Barr Virus, and *Helicobacter pylori* Genomes to Classify and Monitor Gastric Adenocarcinoma
K. Greene

ST056. Clinical Utility of Comprehensive Genomic Profiling in Pediatric Brain Tumors
J. Ji

ST057. Validation of Antibody Panels for High-plex Immunohistochemistry Applications
D.A. Hinerfeld

ST058. Novel Liquid Biopsy (ctDNA) Reference Material Development and Characterization using CRISPR/Cas9-engineered Cell Lines
S. Saddar

ST059. Detection of *ALK, RET, ROS1* Rearrangements by NanoString in Brazilian Patients with Non-small Cell Lung Cancer
L. Novaes

ST060. Characterization of the Tumor Microenvironment using a Novel High-plex Protein Imaging Technology
D.A. Hinerfeld

ST061. GNAS Expression Improves Survival Prognostication of SHH Medulloblastoma Molecular Subgroup
L. Leal

ST062. Distinct Genetic Signature of Mucinous Micropapillary Breast Carcinoma from its Invasive Non-mucinous Counterpart
M. Gurav

ST063. Development of a Next Generation Sequencing Panel for Glioma Classification
N. D'Haene

ST064. Mutational Profiling in Advanced Non-small Cell Lung Cancer (NSCLC) Patients: A Tertiary Care Study of 1,052 Cases from Eastern India
P. Gupta

ST065. Optimization of a Next Generation Sequencing Panel to Reduce DNA Input and Neoplastic Content Requirements
M. Soucy

ST066. Genetically Defined Subgrouping of Medulloblastomas; a Comparative Study of Real-time PCR and Nanostring Technology Based Gene Expression
S. Epari

ST067. Microsatellite Instability Testing on Solid Tumors
L.Cai

ST068. Development of whole transcriptome sequencing (RNASeq) for the Detection of Clinically Actionable Gene Fusions from FFPE Solid Tumor Biopsies
D. Bergeron

ST069. Molecular Profiling of Adult Diffuse Gliomas without 1p19q Co-deletion, IDH and TERT Promoter Mutations Reveals Abundance of *TP53* and *NF1* Mutations and Additional Chromosome Rearrangements
C.J. Zepeda Mendoza

ST070. Clinical Validation of a Fusion Transcript Next-generation Sequencing (NGS) Panel for Sarcomas and Solid Tumors with Diagnostic, Prognostic and Therapeutic Value
R. Paolillo

ST071. Precise Characterization of an FFPE Block Developed Using a Mixture of CRISPR/Cas9 Engineered Cell Lines for use as a Molecular Reference Standard
V. Mani

ST072. Detection of IDH Mutations by DNA Sequencing and Immunohistochemistry in Diffuse Gliomas
P. Dileep Menon

ST073. Comprehensive and Sensitive Detection of Somatic Mutations for Monitoring Minimal Residual Disease
S. Sankaran

ST074. Quality Before Input: Validation of a NGS Assay with Respect to Input and Degradation
R. Paolillo

ST075. Molecular Genetic Profiling of Gliomas in Routine Clinical Practice
E. Hughes

ST076. Clinical Validation of *MLH1* Promoter Methylation Testing using the High-throughput MethylationEPIC (850k) Array Platform
J. Benhamida

ST077. Analytic Validation of a Clinical Next-generation Sequencing (NGS) Panel for Somatic Mutations in Uveal Melanoma
K.R. Covington

ST078. Analytic Validation of a Clinical Next-generation Sequencing (NGS) Test for *BRAF* and *NRAS* Mutations in Cutaneous Melanoma
L.E. Meldi-Sholl

Poster Listing

Even numbered posters will be attended by their authors on Friday, November 2, 2:30pm-3:30pm.

Odd numbered posters will be attended by their authors on Saturday, November 3, 9:45am-10:45am.

GENETICS

G001. Genomic DNA Reference Panels for HLA Class I and II Loci: A GeT-RM Collaborative Project
M.P. Bettinotti

G002. Frequency and Diagnostic Yield of Mosaic Variation Identified by Whole Exome Sequencing
C.R. Miller

G003. WITHDRAWN

G004. Performance Evaluation of VCU Health NIPT, a Single-Nucleotide-Polymorphism (SNP) Based Non-invasive Prenatal Testing for Common Aneuploidy
C. Yang

G005. Development of a Clinical CD33 Genotying Assay to Predict Response to Gemtuzumab
B.A. Barkoh

G006. Characterization of Beta Hemoglobinopathy Results in a Large Population Referred for Carrier Testing
C.A. Holland

G007. Pro-fibrotic Cardiac Gene Activation in Diabetic Zucker Rat Model is Directly Associated to the Incremental Visceral Adiposity: The EPACs Proteins Signaling
M.M. Corsi Romanelli

G008. Validation of a Targeted Variant Genotyping Assay for Personalized Antihypertensive and Chronic Kidney Disease Therapy
W.M. Stansberry

G009. Analysis of ARID1A Mutations and Co-occurring Variants in Cancer Biopsies Reveals Significant Associations in Multiple Diseases.
T. Buys

G010. Validation of an Economical, Real Time PCR Genotyping Assay for Detection of ACMG/ACOG Recommended Mutations in the *CFTR* Gene for General Population Screening
S. Beqay

G011. Cre Recombinase-mediated Circularization for Custom Mate Pair Library Preparation
E. Zimmerman Zuckerman

G012. Clinical Laboratory Experience with Different Carrier Screen Panels
H. Zhu

G013. Rapid Molecular Haplotyping of Thiopurine Methyltransferase *3A, *3B, and *3C
M. Leong

G014. Pathogenic Variants in MID1 in Patients with X-linked Opitz G/BBB Syndrome Type 1
L. Fan

G015. Clinical Evaluation of the Luminex ARIES System for Single Nucleotide Polymorphism Analysis of rs6025 (Factor V Leiden), rs1801133 (Methylenetetrahydrofolate Reductase), and rs1799963 (Prothrombin)
M. Leong

G016. **How to Consistently Determine if a Variant is a Polymorphism?**
D. Qin

G017. High-throughput Approach for Multi-omic Testing for Prostate Cancer Research
M. Shannon

G018. Clinically Integrated Molecular Diagnostics in Adenoid Cystic Carcinoma
J.C. Thierauf

G019. Germline BRCA Mutation Studies in a Select Indian Cohort Using Next-generation Sequencing (NGS)
J.C. Vyas

G020. Phylogenetic Analysis of Duffy, Kidd, and Lewis Allele
M. Kim

G021. Brazilian Panorama of Whole Exome: Details of 315 Cases
R.M. Minillo

G022. Clinical Validation of a Multi-gene Panel on Myeloid Malignancies by Next Generation Sequencing
G. Liu

G023. A Recurrent Heterozygous *RPL21* Mutation Responsible for Hereditary Hypotrichosis Simplex in a Chinese Family
Z. Xu

G024. Confirmation of Cis Inheritance of Variants in *ABCB1*, *SHROOM3*, and *SLC28A3* During the Validation of a Targeted Genotyping Assay
W.M. Stansberry

G025. Verification of Very Small Copy Number Variants (Micro CNVs) Detected on Whole Genome CMA Analysis and Implications for Clinical Reporting
U.P. Kappes

G026. Two-site Evaluation of a One-tube PCR/CE Assay that Resolves CAG Length Polymorphisms in Exon 1 of the *HTT* Gene
S.N. Statt

G027. A Streamlined, Single-Tube PCR Assay that Quantifies *SMN1* and *SMN2* Copy Numbers Using Capillary Electrophoresis
W. Laosinchai-Wolf

G028. New Variant-centric XML for ClinVar Data
M. Landrum

G029. Measuring the Economic Value of Sequencing: Why is it Important, Why is it Challenging, and What are Solutions
K.A. Phillips

G030. Newborn Screening, Diagnosis, and Carrier Testing for Spinal Muscular Atrophy by Multiplex Droplet Digital PCR
N. Vidal-Folch

G031. What's in a VUS Rate? Simulated VUS Rate Calculations for Hereditary Cancer Genes Using Population Frequency Data and ClinVar Submissions
K.E. Kaseniit

G032. What Can We Learn From Oncologists? A Survey of Molecular Testing Patterns
J.S. Menezes

G033. A Data-Driven Approach to Determine Disease Content in Expanded Carrier Screening Panels
R. Ben-Shachar

G034. Clinical Impact and Cost Effectiveness of a 176 Condition Expanded Carrier Screen
K.A. Beauchamp

G035. Detection of Copy-Number Variants in Expanded Carrier Screening Maximizes Identification of Cystic Fibrosis Carriers
D. Muzzey

G036. The Algorithm for Estimation of Human T-cell Receptor Repertoire with Single Cell RNA Sequencing
Y. Cho

G037. WITHDRAWN

G038. Pharmacogenomics: *VKORC1* + *CYP2C9* and *TPMT*: Two New, Ready-to-use Real-time PCR Assays
M. Gramegna

G039. Interpretation of Microdeletion Variants Aided by Population Analysis of Copy-number Variation
K.E. Kaseniit

G040. Frequency of Deletion 13q Associated with other Abnormalities Detected by Fluorescence *in situ* Hybridization (FISH) in Multiple Myeloma Patients – an Experience from a Referral High-end Diagnostic Centre
M. Kumar

G041. Molecular Diagnosis of Graft-versus-Host Disease after Liver Transplantation: an Institutional Experience
S.M. Hosseini

G042. Analytical Performance of the Oncomine BRCA1/2 Assay on the Ion Torrent S5
D. Saxena

G043. A Novel Custom Panel Target Sequencing with Molecular Tags for 0.1% Allelic Frequency Detection
X. Peng

G044. Designing and Implementing NGS Tests for Inherited Disorders – a Practical Framework with Step-by-step Guidance for Clinical Laboratories
A.B. Santani

G045. SMA Complete: Addressing SMN Copy Number and Silent Carrier Status with a Single Complete Multi-plex qPCR Assay
R. Daber

G046. Double Splicing Variants in BCR-ABL are Associated with Tyrosine Kinase Inhibitor (TKI) Resistance in Chronic Myelogeneous Leukemia (CML)
D. Dash

G047. Validation of a Neuro-Oncology Next-generation Sequencing 219-Gene Panel
C. Zysk

G048. IGF1 Proteomic Variant Confirmation using Genotyping Assay
A.D. Maus

G049. Adaptation and Validation of a Pan-cancer Somatic Next Generation Sequencing Assay for Detection of Germline Hereditary Cancer Predisposition Variants
D.K. Manning

G050. Expression Analysis of Telomere-related Genes in Solid and Hematologic Tumors Using RNA-Seq
M.A. Atiq

G051. Meta-analysis of AKT1 rs2494732 Genotype and the Risk of Psychotic Adverse Effects by Cannabis Use
M. Nakano

G052. In cis Heterozygous BRCA2 Pathogenic Mutations in a Jordanian Family: Case Report
L. Abu Jamous

G053. Characterization of Novel Aneuploidy Reference Materials for NGS-based Non Invasive Prenatal Screening (NIPT)
F. Sabato

G054. The SureMASTR BRCA Screen Assay Combined with MASTR Reporter Analysis is an Accurate and Precise Workflow for SNV, Indel and CNV Detection in Blood- and FFPE-derived DNA
A. Rotthier

G055. CNV Contribution to Pathogenic Alleles within a Healthy Population: Results from Expanded Carrier Screening of 137,000 Individuals
S.G. Cox

G056. Use of Molecular Identifiers and Targeted NGS to Enable Variant Detection Below 1% Allele Frequencies in Circulating Cell-free DNA
L. Kurihara

G057. WITHDRAWN

G058. Evaluation of a Single-tube, Long-read, Two-mode PCR Technology that Reports the Categorical Range of DMPK CTG Expansions and Resolves up to 2000 Repeats in Myotonic Dystrophy Type 1
B. Hall

G059. ACMG Incidental Findings at the CLIA-certified Colorado Center for Personalized Medicine Biobank: Data from the First 10,000 Subjects
S.J. Wicks

G060. Phenotypic and Genotypic Study of Patients with Hermansky-Pudlak Syndrome
J.A. Majerus

G061. Performance Characteristics of High-resolution Human Leukocyte Antigen (HLA) Typing Using TruSight Next-generation Sequencing (NGS) Technology
A. Budhai

G062. WITHDRAWN

G063. Multiplex Synthetic Reference Material for Monitoring the Analytical Performance of Highly Complex Variant Detection of Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) using Next Generation Sequencing
R. Mihani

G064. Low Input Microfluidic Library Preparation Platform for Targeted CFTR Using Blood, Buccal Swabs and Saliva Samples
N. Ramalingam

G065. Validation of a Next-generation Sequencing Gene Panel for Inherited Platelet Disorders
W. Zhang

G066. Identification of Mutation Signatures in Tumors Using Panel-based Targeted Sequencing
S. Rana

G067. WITHDRAWN

G068. CleanPlex Amplicon-based Next Generation Sequencing Heredity Panels for Determining Genetic Predispositions
L. Lin

HEMATOPATHOLOGY

H001. The Detection of a *BRAF* Mutated Clone in Acute Myeloid Leukemia with Mutated *Npm1* and Extensive Extramedullary Involvement
K. Gvozdjan

H002. Short Tandem Repeat Aberrancies in Hematopoietic Stem Cell Transplant Recipients
K. Gvozdjan

H003. A Strategy for Implementing Sensitivity Controls for qPCR Chimerism Monitoring
J. Tyler

H004. Genetic Profiling of Adult Acute Myeloid and Lymphoid Leukemia Cases in a Major Referral Center in Lebanon
S. Halabi

H005. Clinical Implementation of T-cell Clonality Testing by Next-generation Sequencing: Improved Detection Sensitivity and Reliability in Initial Diagnosis and Minimal Residual Disease Detection of T-cell Malignancies
J. Yao

H006. Performance Evaluation of a Custom DNA/RNA Next-generation Sequencing (NGS) Assay for Hematologic Malignancies
J. Karrs

H007. Evaluation of Performance of Two Commercially Available BCR-ABL Real-time PCR Assays for Deep Molecular Response in International Scale.
B. Das

H008. Fusion Detection by Next-generation Sequencing from Methanol/Acetic Acid Fixed Cell Pellets in the Setting of Acute Lymphoblastic Leukemia Workup
X. Qu

H009. Fluorescence *in situ* Hybridization as a Tool for Minimal Residual Disease Testing in Multiple Myeloma
S. Golem

H010. Reproducibility of Clinical Samples by the Illumina TruSight Myeloid Next-generation Sequencing Panel
L. Commander

H011. Extended Myeloid Mutation Profiling Using NGS in Triple-negative Myeloproliferative Neoplasms: Single Institution Experience at a High Volume National Reference Laboratory
A. Jhuraney

H012. Validation of a Custom, Focused Next-generation Sequencing Panel for Lymphoma
M. Kluk

H013. Identification of *FLT3* ITD Using Next-generation Sequencing (NGS): A Single Institution's Experience
A. Campbell

H014. Mate Pair Sequencing: Ushering Cytogenetics Into the Era of Personalized Medicine
N. Hoppman

H015. Evaluation of *NPM1* Mutation Detection by Droplet Digital PCR for Minimal Residual Disease Detection
R.Y. Walder

H016. Detection of *CRLF2* Rearrangements in B-cell Acute Lymphoblastic Leukemia in Children with Down Syndrome
A. Garcia

H017. Standardization of *FLT3*-ITD Mutation Allelic Ratio Reporting in the Clinical Laboratory Setting
S. Bhattacharyya

H018. A Limited FISH Panel is a Useful Surrogate for Metaphase Analysis to Rapidly Identify Patients with AML-MRC
N.D. Nelson

H019. IntelliGEN Myeloid 50 Gene Panel Validation and Testing Experiences
L. Cai

H020. Mutational Analysis of Myeloid Neoplasms in Paired Peripheral Blood and Bone Marrow by Next-generation Sequencing
P. Michaels

H021. Guideline-adherent, Evidence-based NGS Workflow for Myeloid Leukemia
R. Kohle

H022. Evaluation of Targeted Next-generation Sequencing Panels for Myeloid Malignancies-Focusing on *CEBPA* and *FLT3* Genes
R. Akabari

H023. Novel *PML-SYK* Fusion in Acute Myeloid Leukemia Constitutively Activates Targetable Pathways
J. Mosquera

H024. Validation of a Low Input Targeted NGS Assay for Lymphoma Across Multiple Specimen Types
A. Oran

H025. Ultradeep Error Corrected Next-generation Sequencing (NGS) of ABL1 Kinase Domain Mutations in BCR-ABL1 Positive Malignancies
N. Patkar

H026. Routine Clinical Monitoring of Disease Status Through NGS Measurement of Clonal Architecture in AML and MDS
P.D. Velu

H027. Peripheral T-cell Lymphoma: Understanding and Characterizing the Phenotypic Behavior Using Molecular Tools
O. Shetty

H028. Myeloseq One: A Cost Effective Integrated Next-generation Sequencing Assay for Myeloid Malignancies
R. Kodgule

H029. Minimal Residual Disease in AML can be Monitored Utilizing Cell-free DNA
L.M. Chamberlain

H030. Rosai-Dorfman Disease Co-existing with Lymphoma in the Same Lymph Node: A Localized Histiocytic Proliferation with MAPK/ERK Pathway-induced Cyclin D1 Upregulation
S. Garces

H031. Clinical Utility of Targeted Next-generation Sequencing in Evaluation of Cytopenias of Undetermined Significance
R. Beck

H032. Myeloid Neoplasms with Ring Sideroblasts without SF3B1 Mutation
S. Bhavsar

H033. Clinical Use of Rapid Transcriptome (R-RNASeq) Analysis for Gene Fusion and Rearrangement Detection in Pediatric Leukemia
E.M. Azzato

H034. Mutational Signatures Differ between Cytogenetic Risk Groups of *de novo* AML
R.T. Sussman

H035. Therapy-related Acute Myeloid Leukemia, Characterized by t(8;16)(p11;p13);*MYST3-CREBBP* and Co-occurring *TET2* and *ASXL1* Mutations
A. Alsuwaidan

H036. Variant Characterization for a Clinical Lymphoma Sequencing Panel
S. Deihimi

H037. Post-remission NGS-based MRD Surveillance is Critical for Early Detection of Impending Relapse in B-ALL
S. Cheng

H038. Clinical Evaluation of the Archer VariantPlex Myeloid Panel for Mutation Profiling in Myeloid Neoplasms
A. Campbell

H039. Donor-derived Clonal Hematopoiesis of Indeterminant Potential Mutations are Detected in Transplant Recipients after Allogeneic Hematopoietic Stem Cell Transplant
J. Liu

H040. Comprehensive Assessment of Variants in *SOCS1*, *JAK2* and *B2M* Using Anchored Multiplex PCR and Next-generation Sequencing
H.E. Robinson

H041. Longitudinal Monitoring of AML Tumors with High-throughput Single-cell DNA Sequencing Reveals Rare Clones Prognostic for Disease Progression and Therapy Response
D.J. Eastburn

H042. Next-generation Sequencing-based Detection of Clinically Significant *IKZF1* Deletions and *KMT2A* Partial Tandem Duplications
K.C. Floyd

H043. Development of Synthetic Secondary Standards for *BCR-ABL1* Quantification on GeneXpert BCR-ABL V2 and Xpert BCR-ABL Ultra Assays
R. Mihani

H044. Validation of a Custom Next-Generation Sequencing (NGS) Panel for Characterizing Mutations in Ph-like ALL Using Anchored Multiplex PCR Technology
A. Guimaraes-Young

H045. Detection of Clonal Rearrangements in Multiple Myeloma Samples Using LymphoTrack Assays
Y. Huang

H046. Pediatric Myeloid Sarcoma: A Single Institution Clinicopathologic and Molecular Analysis
T. Zho

H047. PTPN11 Mutation is Uncommon in Acute Myeloid Leukemia, but Associated with a Complex Karyotype, Co-mutations in *KRAS* or *NRAS* and Poor Prognosis
R. Ruiz-Cordero

H048. Accurate Detection of *FLT3*-ITDs and *CEBPA* Variants in Acute Myeloid Leukemia by Anchored Multiplex PCR and Next-generation Sequencing
N.M. Nair

H049. A Single NGS-based Assay for Simultaneous Identification of *BCR/ABL1* Fusion and *ABL1* Sequencing Detects Resistance Mutation and Subclones
R. Ruiz-Cordero

H050. Clinicopathologic Characterization of Myeloid Neoplasms with Concurrent Spliceosome Mutations and MPN-associated Mutations
Y. Liu

H051. SNP Genotyping-based Stem Cell Engraftment Detection in Targeted NGS Testing
W. Chen

H052. Development of a Reverse Transcriptase Quantitative Polymerase Chain Reaction (RT-qPCR) Assay for Nucleophosmin (NPM1) Minimal Residual Disease (MRD) Monitoring in Acute Myeloid Leukemia
M. Mai

H053. Next-generation Sequencing in Burkitt-like Lymphoma with 11q Aberration: A Clinicopathologic Correlation
A.N. Alsuwaidan

H054. Integrative Analysis of Programmed Death-Ligand 1 DNA, mRNA, and Protein Status and their Clinicopathological Correlation in Diffuse Large B-cell Lymphoma
X. Zhou

H055. Optimizing Diagnostic Algorithms for Pediatric Leukemia: Synergy Between Next-generation Sequencing, Chromosomal Microarray, and Conventional Cytogenetics
M.C. Hiemenz

H056. Variant Allele Frequency does not correlate with Marrow-based Leukemic Blast Proportions in Acute Myeloid Leukemia
L.N. Toth

H057. BCOR Mutations Portend Poor Survival Independent of Concurrent Mutations in Other Epigenetic Modulators in Myelodysplastic Syndrome
I. Badat

H058. Isochromosome 17q in Acute Myeloid Leukemia and Myeloid Neoplasms
M. Kim

H059. Comparison of Interpretive Guidelines for IGH and TCR Clonality by NGS in B and T-cell Cancers
L. Lay

H060. Impact of Single versus Multiple Splicesome Mutations in MDS/CMML
M. Hussaini

INFECTIOUS DISEASES

ID001. Development of a Real-time PCR Assay for the Direct Detection of *Mucorales* Species
K.D. Tardif

ID002. Comparison of the Roche Cobas Ampliprep/Cobas Taqman v2.0 and Cobas 6800 for HIV, HCV, HBV and CMV Viral Load Determination
T.R. Sundin

ID003. Evaluation of a Commercial Sample–to-Answer Assay for the Detection of Varicella-Zoster Virus Directly from Clinical Specimens
M.J. Espy

ID004. Evaluation of a Novel Isothermal Amplification Assay for Detection and Genotyping of Human Papillomavirus in Formalin-fixed Paraffin-embedded Tissue of Oropharyngeal Carcinomas
L. Lozano

ID005. Second Generation Next-generation Sequencing-based System for Detecting Drug Resistance Mutations in HIV-1 Combined with Isothermal Amplification
E.J. Wee

ID006. Comparison of Real-time PCR with Transcription Mediated Amplification for HPV Detection/Genotype and Correlation with Cytological and Histological Results
S. McClellan

ID007. The Diagnostic Yield of Universal Pathogen Detection by Next-generation Sequencing Compared to the Standard of Care in Patients with Pneumonia
B.A. Young

ID008. Spectrum Profile of Respiratory Pathogens Detected by the BIOFIRE Plex Assay: Experience of a Major Tertiary Care Center in Lebanon
S. Halabi

ID009. Evaluation of Cobas HBV, HCV, and HIV-1 Tests on the Cobas 6800 Platform
M.K. Leong

ID010. Performance and Workflow Comparison of Simplexa Bordetella Direct (IUO) with Illumigene Pertussis
E.M. Dault

ID011. Performance Evaluation of Two Commercial Molecular Assays for Genotyping Hepatitis C Virus
S.L. Mitchell

ID012. Comprehensive Solid Tumor Microbiome Profiling via Analysis of Unmapped Reads in Large Panel, Hybridization Capture-based NGS Assay Data
C.M. Vanderbilt

ID013. Evaluation of the DiaSorin Molecular Simplexa Bordetella Real-time Sample-to-Result PCR Test on the LIAISON MDX System
T.E. Schutzbank

ID014. Evaluation of Panther Fusion System for Respiratory Viral Detection in a Pediatric Hospital
A. Rector

ID015. Adjusting the pH of Urine Samples at the Time of Collection May Provide a More Accurate Measurement of Cytomegalovirus (CMV) Viral Load
M. Galdzicka

ID016. Detection of Herpes Simplex Virus (HSV) Types 1 and 2 and Varicella-Zoster Virus (VZV) From Cutaneous and Mucocutaneous Lesions Using the Quidel Solana HSV 1+2/VZV Assay
E. Tam

ID017. Efflux Gene Expression by Ofloxacin Stress in Multidrug-resistant *Mycobacterium tuberculosis* and Extensively Drug-resistant *M. tuberculosis* with/without *gyrA* Mutation using RNA-seq
H. Lee

ID018. Triplex Assay for Zika, Dengue, and Chikungunya Viruses by Sentosa SA Real-time RT-PCR Assay
J. Wong

ID019. A Host Gene Signature for Diagnosis and Risk Stratification of Acute Infection and Sepsis at Hospital Admission: HostDx Sepsis
O. Liesenfeld

ID020. Development and Validation of a Quantitative Multiplex Real-time PCR Assay for Identification of Bacterial Pathogens From Respiratory Specimens
A. Seth

ID021. Evaluation and Time-motion Analysis of the GenePOC Rapid C. difficile Assay Compared to the Meridian Illumigene Assay
H. Webber

ID022. Evaluation of the Galileo Pathogen Solution Next-generation Sequencing Pipeline for the Identification and Quantification of DNA Viruses in Transplant Patients
M.L. Carpenter

ID023. Clinical Implications of the Increased Sensitivity of the FDA Roche 6800 CMV Viral Load Assay
J. Pettersson

ID024. Performance Evaluation of AdvanSure RV-plus Real-time PCR Assays for the Detection of Respiratory Viruses
J. Sohn

ID025. Quantitative Detection of HCV Using the NeuMoDx Molecular Diagnostic System
J. Zhu

ID026. Quantitative Detection of Epstein-Barr Virus (EBV) in Plasma and Whole Blood Matrices
L. Gong

ID027. WITHDRAWN

ID028. Evaluation of the GenMark ePlex Respiratory Pathogen Panel for the Detection of Respiratory Pathogens
A.M. Carlin

ID029. Development of a New Diagnostic System Based on Real-time LAMP PCR for Specific Detection of 10 Species of Arboviruses
E. Choi

ID030. Analytical Validation of a Sample-to-Sequence Pipeline for Non-targeted Pathogen Detection in Clinically Relevant Matrices
K. Parker

ID031. Identification of *M. tuberculosis* and *M. bovis* in Clinical Respiratory Specimens Using the VELA Diagnostics Sentosa SA MTC PCR Assay
H. Webber

ID032. Pre-market Evaluation of Hologic's Group B *Streptococcus* PCR Assay on the Panther Fusion System
F. Zhang

ID033. Multicenter Evaluation of the Sentosa SA HSV1/2 Qualitative PCR Test
D. Kohn

ID034. A Rapid Host Gene Expression Assay to Discriminate Bacterial from Viral Infections
W. Nie

ID035. High Throughput FluA/B/RSV Testing May Complement Existing Methods During the Peak of Flu Season
R. Hein

ID036. WITHDRAWN

ID037. A High Throughput System for Profiling Respiratory Tract Microbiota
J. Li

ID038. WITHDRAWN

ID039. Cost Effectiveness Model Describing Emergency Department Use of a Novel Multi-mRNA Test for Diagnosis and Risk Assessment of Acute Respiratory Tract Infections and Sepsis
I. Stojanovic

ID040. Quantitative Detection of Cytomegalovirus on NeuMoDx Molecular Systems
M. Mastronardi

ID041. Performance Evaluation of Unpreserved Stool and Stool in Transport Medium with a Multiplex Gastrointestinal Pathogen Panel with an Automated, High Throughput System
C. Knoth

ID042. WITHDRAWN

ID043. Development and Evaluation of a High Throughput Multiplex Molecular Panel that Detects 20 Respiratory Pathogens in Clinical Specimens
M. Aye

ID044. Hepatitis C Virus Genotyping by Next-generation Sequencing: An Accurate and Cost-effective Alternative
B.G. Nezami

ID045. Technology to Produce Non-infectious Recombinant Virus as Reference Materials for Unculturable or Highly Dangerous Viral Pathogens
B. Anekella

ID046. Detecting *Helicobacter pylori* and Predicting Antibiotic Resistance from Formalin-fixed Paraffin Embedded Gastric Biopsies Using Targeted Next-generation Sequencing
B.G. Nezami

ID047. Clinical Evaluation of the Aptima *Mycoplasma genitalium* Assay Reveals the Prevalence of *Mycoplasma genitalium* Infection among Patients Tested for other Sexually Transmitted Pathogens in Indiana
R.F. Relich

ID048. Evaluation of DiaSorin Molecular Simplexa Bordetella Direct Kit for the Detection and Differentiation of *Bordetella pertussis* and *Bordetella parapertussis*
T. Ton

ID049. A Cross-sectional Study of Swab versus Tissue Sampling of Wounds for the Detection of Microbes by PCR
E. Baum-Jones

ID050. Evaluation of a Next-generation Sequencing Assay: The Sentosa SQ HIV Genotyping Assay for HIV Genotype and Drug Resistance Mutation Analysis
D. Kohn

ID051. Rapid and Accurate Cross-kingdom Human Pathogen Identification and Detection Using Hyb & Seq Technology
D. Bezdan

ID052. Validation of a Novel Qualitative Real-time PCR Assay Versus Direct Fluorescent Antibody Testing for the Detection of *Pneumocystis jirovecii* Pathogen
A. Spohn

ID053. WITHDRAWN

ID054. Simultaneous Detection of Tick-borne Pathogens Using a High Definition Multiplexed PCR Assay
M.W. Mashock

ID055. Clinical Performance Study Results of the Hologic GBS Assay on the Fully Automated Panther Fusion System
B. Eaton

ID056. Quantification of CMV Using the m2000 RealTime CMV Assay
M.A. Johnston

ID057. High-definition PCR (HDPCR): a Novel, Instrument Agnostic qPCR Multiplexing Technology Applied to Tick-borne Pathogen Testing
B. Amro

ID058. Evaluation of a Completely Automated BKV Viral Load Assay on the Abbott m2000 Platform
F. Nolte

ID059. Validation of Qualitative HIV Detection of HIV in Whole Blood with the Hologic Aptima HIV Assay
K. Tardif

ID060. The Prevalence of Clarithromycin-resistant *Helicobacter pylori* in Utah; a Laboratory-based Survey
K.N. Carter

ID061. Is There a Need for HCV Resistance Testing in Routine Diagnostics and Patient Treatment? Routine HCV Genotyping and Resistance Testing and Performance of the Sentosa SQ HCV Genotyping v2.0 Assay
M. Obermeier

ID062. Evaluation of the ARIES *Bordetella* Assay for Detection and Identification of *Bordetella* pertussis in Nasopharyngeal Swab Specimens
T. McMillen

ID063. A Quantitative, Multiplexed RNA Detection Platform for Rapid Pathogen Identification and Phenotypic Antibiotic Susceptibility Testing (AST) using NanoString Technology
R.P. Bhattacharyya

ID064. The Galileo Pathogen Solution Next-Generation Sequencing Pipeline Detects and Identifies RNA Respiratory Viruses in Haematopoietic Stem Cell Transplant Patients
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ID065. Molecular Screening for *Trichomonas vaginalis* and *Mycoplasma genitalium* in the RADAR Longitudinal Cohort Study of Young Transgender Women and Young Men who Have Sex with Men
E. Munson

ID066. Evaluation of Performance and Workflow using the GenePOC Strep A, C/G Assay for Detection of Group A, C, and G *Streptococcus* from Patients Presenting with Pharyngitis to the Emergency Department
D. Mastandrea

ID067. Evaluation of the BD MAX Vaginal Panel for the Detection of Vaginitis in Women
K. Culbreath

ID068. Evaluation of ELITech HSV 1&2 ELITe MGB for the Detection and Differentiation of Herpes Simplex Virus 1 and 2 from Lesions
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ID069. Different CMV Strains for Quality Controls and its Impact on Assay Calibration
J. Boonyaratanakornkit

ID070. Detection of Microorganisms and Antibiotic Resistance Genes in Skin and Soft Tissue Infections by a PCR-based Diagnostic Test
G. Zhu

ID071. Comparison of Three Nucleic Acid Amplification Tests (NAATs) to Culture for Detection of Group B Streptococcus (GBS)
J. Shin

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I002. Clinical Implications of the Reference Sequence Used for Diagnostic Interpretation
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I003. CCKB: A High-Performance and Genome-Scale Informatics Portal for Analysis and Multi-Institutional Sharing of Pediatric Cancer Variants
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I004. A Machine-Learning Framework for Accurate Classification and Quantification of Oncogenic Variants Using the QuantideX NGS DNA Hotspot 21 Kit
L. Ringel

I005. Improving Variant Call Accuracy by Combining Torrent Variant Caller and PLATYPUS
Z. Siddiqui

I006. Improving the Molecular Pathology Workflow with Machine Learning: Automated Calculation of Tumor Percentages on H&E Digital Whole Slide Images
C.M. Cirelli

I007. Assessment of a Somatic Mutation Detection Pipeline Using a Simulated Tumor Genome
Z. Li, R. Zhang

I008. Interpretation of Mutational Signatures Associated With Smoking from an Amplicon-Based Clinical Oncology Sequencing Panel
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I009. Personalized Transcriptomic Drug Profiling in Non-small Cell Lung Cancer
Z. Abrams

I010. NeGeSeI-NIPT: A Web Based Tool for the Management of Non-Invasive Prenatal Screening Assays in the Clinical Laboratory
V. Williamson

I011. NeGeSeI–Inheriseq: a scalable informatics solution for the management of assays for hereditary cancer
V. Williamson

I012. A Local Population Allele Frequency Query Tool
M. Leong

I013. Classification of Variants from Myeloid NGS Panel Testing Using a Scalable Evidence Based Variant Classification Workbench (SEBVaC)
W. Chen

I014. A Molecule-Centric Approach to Phasing
M. Debeljak

I015. Using AutoIt to Automatically Enter Molecular LDT Results into the Laboratory Information System
J. Grojean

I016. Fragment Size Characterization of Cell-Free DNA Mutations from Clonal Hematopoiesis
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I017. NGS Panel Analyzer: A Software Tool to Assess NGS Panel Design
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I019. Database of High-Resolution Melting Publications with Data Mining and Statistical Reporting
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I021. Development and Analysis of a Machine Learning Variant Caller
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I022. Evaluation of SOPHiA DDM v4 for NGS Analysis of Ampliseq Cancer Hotspot Panel
D.C. Green

I023. Precision Medicine Requires Molecular Pathologists Have Clinical Decision Support and Automation Found in Agilent Alissa to Analyze and Interpret Large Numbers of Variants from NGS Assays
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I024. Identification of Germline Mutations in Tumor DNA Samples Absent a Matched-normal
A. Bigdeli

I025. Identification of Viral Integration Sites in Cancer Genomes Using Unmapped Reads in Targeted Next-generation Sequencing Data
A.S. Bowman

I026. Variant Inspector: A Computational Approach for Somatic Variant Prioritization in Routine Clinical Practice
R.J. Maglantay

I027. Detection of Microsatellite Instability Using a Large Next-generation Sequencing Panel across Diverse Tumor Types
J. Pang

I028. A Rigorous Interlaboratory Examination of the Need to Confirm NGS-Detected Variants by an Orthogonal Method in Clinical Genetic Testing
S.E. Lincoln

I029. Dual-Assay Demultiplexing with Preferential Read Allocation and Unequal Index Size Presents Bioinformatics Challenges
A. Chitturi

I030. Integrating Clinical Genomics into Electronic Health Records to Foster Precision Medicine
A. Sigaras

I031. Standardization of Molecular Diagnostic Testing for Non-small Cell Lung Cancer
A. Karimnezhad

I032. Effects of Probe Regions on Somatic Variant Calling in TruSeq Amplicon Cancer Panel
P.B. Mayigowda

I033. Modern Application Deployment Infrastructure for Supporting Clinical Next- generation Sequencing (NGS) Testing
L. Santana Dos Santos

I034. Assessing Cancer Diagnosis from Clinical Genomics Data Using Machine Learning.
P.R. Hess

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OTH001. Virtual Case Sets for Genomics Education: Thinking Outside the Slide Box
J.N. Rosenbaum

OTH002. Standardized Protocol for Salvaging Quality or Quantity Not Sufficient (QNS) Samples in an Academic NGS Laboratory
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ST002. Analysis of Urinary Cell-free DNA for Early Detection and Surveillance of Bladder Cancer
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ST003. Utility of a Comprehensive and Cost-effective DNA/RNA Panel (170 Genes) for Single Nucleotide Variants (SNV's), Small Insertions or Deletions (Indels), Copy Number Variations (CNV's) Splice Variations, and Gene Fusions on an NGS in Evaluation of Colon Cancer
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ST005. Evaluation of a Guideline-adherent Tumor Mutational Burden (TMB) Module for Calculation of TMB Using a Comprehensive 170 Gene Assay on a NGS Platform.
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ST008. Analyses of *BRAF* Mutations and MSI Status Frequencies in TKi Non-treatable Lung Adenocarcinoma Patients
G.N. Berardinelli

ST009. Evaluation of Microsatellite Instability Testing and Lynch Syndrome Screening Through Tumor Sequencing Using Illumina TruSight Oncology 500 panel
S. Zhang

ST010. Identification of Different Levels and Spatial Patterns of Methylation of Promoter-Associated CpGs74-78 of the O6-Methylguanine Methyltransferase Gene *(MGMT)* in Gliomas
F. Khan

ST011. Evaluation of Molecular Spectrum of *BRCA* Gene Mutation in Indian Scenario using Next Generation Sequencing (NGS) Approach
B. Das

ST012. Development of a Novel Pan-Cancer Biomarker Panel for Improved Detection of MSI in Tumor and Liquid Biopsies
J. Bacher

ST013. Comparison of Cobas EGFR Mutation Test and PANAMutyper R EGFR Assay in the Detection of *EGFR* Mutations in Plasma from Non-small Cell Lung Cancer Patients
K. Lee

ST014. Comprehensive Genomic Profiling of Thyroid Neoplasm by Next-generation Sequencing of Fine Needle-Aspiration Biopsy Material Preserved in CytoLyt
H.J. Park

ST015. TruSight Oncology 500: Measuring Tumor Mutation Burden with Targeted Sequencing
J. Ju

ST016. Analytical Validation of the Oncomine Comprehensive Assay v3 with FFPE and Cell Line Tumor Specimens in a CAP-accredited and CLIA-certified Clinical Laboratory
A. Yuki

ST017. Nextgen Digital Spatial Molecular Pathology: Digital IHC Coupled to Automated Gene and Protein Expression Profiling Measuring Complex Signatures within the Context of the Tumor Microenvironment
E. Imler

ST018. Clinical Implementation of Precision Medicine in the Classification of Medulloblastomas: Concordance, Conflict, Recurrence, and Reclassification
B. Liechty

ST019. Clinical Validation of a Combined DNA and RNA Target-capture Next Generation Sequencing (NGS) Test for Solid Tumors on FFPE Specimens
S.P. Strom

ST020. Molecular Epidemiology of *CREBBP* and *EP300* Mutations in Solid Tumors
J.P. Solomon

ST021. Prevalence of *EGFR* Mutations in Indian Lung Cancer Patients
R. Katara

ST022. Detection and Quantitation of Human Papilloma Virus Type 16 in Oropharyngeal Squamous Cell Carcinomas
K. Vadlamudi

ST023. Cross-Platform Comparison of NGS and MALDI-TOF for Detecting RAS/RAF Mutations in Circulating Tumor DNA from Metastatic Colorectal Cancer Patient Plasma
W. Guo

ST024. Clinical Implementation of Mutational Signature Analysis
L. Lawrence

ST025. Implementation and Validation of the Moffitt Solid Tumor Actionable Result (STAR) Assay
E.L. Roberts

ST026. A Functional DNA Repair Assay Platform to Stratify Melanoma and Select the Best Therapeutic Option
S. Sauvaigo

ST027. Ultra-Rapid EGFR Mutation Assessment in Lung Adenocarcinoma without Prior DNA Extraction
M.E. Arcila

ST028. Confirmation of Novel Gene Fusions Detected by Next-Generation Sequencing using Enriched RNA Libraries
N.T. Ngo

ST029. Assessment of Significant Components in Multigene Testing for Breast Cancer in Clinical Laboratories
P. Gao

ST030. Culture of Circulating Tumor Cells (CTCs) using Three-dimensional Culture and Conditional Reprogramming Methods
C. Park

ST031. ISO Certification of a Complete Next Generation (NGS) Sequencing Workflow for *BRCA1/2* Analysis
S. Marchini

ST032. Analytical Validation of the Oncomine Breast cfDNA Assay v2
W. Liu

ST033. Assessment of Pre-analytical Effects on RNA Sequencing
A. Beams

ST034. Performance Evaluation of Asuragen QuantideX NGS RNA Lung Cancer Panel by ACL Laboratories
S. Spirtovic

ST035. Performance Evaluation of Illumina TruSight Tumor 15 Panel by ACL Laboratories.
S. Spirtovic

ST036. Comparison of Three Next-generation Sequencing Platforms in Fusion Detection: FusionPlex by Archer, Oncomine by ThermoFisher, and AmpliSeq by Illumina
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ST038. A Turnkey Solution for NGS-based Detection of Somatic Mutations in Cancer
M. Yee

ST039. Clinicopathologic and Molecular Features of Undifferentiated Round Cell Sarcomas of Bone and Soft Tissues, including BCOR-CCNB3 and CIC-DUX4 Test Results
B. Rekhi

ST040. *KRAS* Mutations in Tissue Samples from Cologuard-Positive Patients
K. Murphy

ST041. Evaluation of the Biocartis Idylla Rapid Near-to-Patient EGFR Mutation CE-IVD Marked Tissue Test: Correlation to an FDA Approved Orthogonal Method using 79 Clinical Formalin-Fixed, Paraffin-Embedded Tissue Samples
M. Kohlman

ST042. Clinically Significant Germline Variants Detected by Mutation Profiling of Non-small Cell Lung Cancer in Patients with Multiple Nodules Harboring Different Somatic Mutations
A. Almradi

ST043. Clinical Validation of a Custom-designed Next-generation Sequencing-based FusionPlex Panel for Salivary Gland Tumors
N.V. Guseva

ST044. A Comparison of the Performance Characteristics of the Illumina TruSeq Stranded mRNA Kit and TruSeq RNA Sample Preparation v2 Kit for Gene Fusion Detection
R.N. Wehrs

ST045. Development and Validation of an RNA Sequencing Assay for the Detection of Gene Fusions in Formalin-fixed Paraffin Embedded Tumors
R.A. Jackson

ST046. Multi-institutional Evaluation of the 2017 AMP, ASCO and CAP Standards and Guidelines for Interpretation and Reporting of Sequence Variants in Cancer
D. Sirohi

ST047. Establishing the Impact of *STK11* Canonical Splice Site Variants Identified by NGS Panel Testing in Non-Small Cell Lung Cancers (NSCLC): Prognostic and Therapeutic Implications
D.J. Seward

ST048. Validation of the ArcherDx VariantPlex Solid Tumor Assay for the Molecular Analysis of Clinical Tumor Samples
K.D. Davies

ST049. Clinical Targeted Next-generation Sequencing Panel Testing in Non-small Cell Lung Cancer: Single Institution Experience at a High Scale National Reference Laboratory
K. Barber

ST050. *MLH1/PMS2*-deficient, *BRAF*-mutated, and Calretinin-positive Colorectal Carcinoma Presents at Advanced Stage and is Associated with Poor Differentiation and Poor Prognosis
W. Zhang

ST051. Analytical Validation of a DNA Dual Strand Approach for an FDA-approved NGS based Praxis Extended RAS Panel for FFPE Metastatic Colorectal Cancer Samples
A. Iyer

ST052. Optimization of Testing Methods in Detecting MET Amplification, Expression, and Activation for Targeted MET TKI Treatment in Non-small Cell Lung Cancer Patients
H. Gong

ST053. Personalized ddPCR Mutation Assays Targeting Patient Specific ctDNA: A Tool to Monitor Treatment Responses to Mutation-Specific T-cell Transfer Immunotherapy in Epithelial Cancer Patients
L. Xi

ST054. Importance of Amplicon Size for Detecting Microsatellite Instability in Liquid Biopsies
M. Campan

ST055. DNA Sequencing of Human, Epstein - Barr Virus, and *Helicobacter pylori* Genomes to Classify and Monitor Gastric Adenocarcinoma
K. Greene

ST056. Clinical Utility of Comprehensive Genomic Profiling in Pediatric Brain Tumors
J. Ji

ST057. Validation of Antibody Panels for High-plex Immunohistochemistry Applications
D.A. Hinerfeld

ST058. Novel Liquid Biopsy (ctDNA) Reference Material Development and Characterization using CRISPR/Cas9-engineered Cell Lines
S. Saddar

ST059. Detection of *ALK, RET, ROS1* Rearrangements by NanoString in Brazilian Patients with Non-small Cell Lung Cancer
L. Novaes

ST060. Characterization of the Tumor Microenvironment using a Novel High-plex Protein Imaging Technology
D.A. Hinerfeld

ST061. GNAS Expression Improves Survival Prognostication of SHH Medulloblastoma Molecular Subgroup
L. Leal

ST062. Distinct Genetic Signature of Mucinous Micropapillary Breast Carcinoma from its Invasive Non-mucinous Counterpart
M. Gurav

ST063. Development of a Next Generation Sequencing Panel for Glioma Classification
N. D'Haene

ST064. Mutational Profiling in Advanced Non-small Cell Lung Cancer (NSCLC) Patients: A Tertiary Care Study of 1,052 Cases from Eastern India
P. Gupta

ST065. Optimization of a Next Generation Sequencing Panel to Reduce DNA Input and Neoplastic Content Requirements
M. Soucy

ST066. Genetically Defined Subgrouping of Medulloblastomas; a Comparative Study of Real-time PCR and Nanostring Technology Based Gene Expression
S. Epari

ST067. Microsatellite Instability Testing on Solid Tumors
L.Cai

ST068. Development of whole transcriptome sequencing (RNASeq) for the Detection of Clinically Actionable Gene Fusions from FFPE Solid Tumor Biopsies
D. Bergeron

ST069. Molecular Profiling of Adult Diffuse Gliomas without 1p19q Co-deletion, IDH and TERT Promoter Mutations Reveals Abundance of *TP53* and *NF1* Mutations and Additional Chromosome Rearrangements
C.J. Zepeda Mendoza

ST070. Clinical Validation of a Fusion Transcript Next-generation Sequencing (NGS) Panel for Sarcomas and Solid Tumors with Diagnostic, Prognostic and Therapeutic Value
R. Paolillo

ST071. Precise Characterization of an FFPE Block Developed Using a Mixture of CRISPR/Cas9 Engineered Cell Lines for use as a Molecular Reference Standard
V. Mani

ST072. Detection of IDH Mutations by DNA Sequencing and Immunohistochemistry in Diffuse Gliomas
P. Dileep Menon

ST073. Comprehensive and Sensitive Detection of Somatic Mutations for Monitoring Minimal Residual Disease
S. Sankaran

ST074. Quality Before Input: Validation of a NGS Assay with Respect to Input and Degradation
R. Paolillo

ST075. Molecular Genetic Profiling of Gliomas in Routine Clinical Practice
E. Hughes

ST076. Clinical Validation of *MLH1* Promoter Methylation Testing using the High-throughput MethylationEPIC (850k) Array Platform
J. Benhamida

ST077. Analytic Validation of a Clinical Next-generation Sequencing (NGS) Panel for Somatic Mutations in Uveal Melanoma
K.R. Covington

ST078. Analytic Validation of a Clinical Next-generation Sequencing (NGS) Test for *BRAF* and *NRAS* Mutations in Cutaneous Melanoma
L.E. Meldi-Sholl

ST079. Validation of Cobas HR-HPV Genotyping Assay Head and Neck Squamous Cell Carcinoma FFPE Specimens
W. Zhou

ST080. Clinical Grade Semi-automated Platform to Annotate Somatic Variants in Solid Tumors per AMP Guidelines
D. Weeraratne

ST081. MSI Status in Primary Pancreatic Carcinoma: A Pilot Study of a New England Cohort
A.M. Strait

ST082. Clinical Implications of "Indeterminate" UroVysion Fluorescence in situ Hybridization Results: An Institutional Retrospective Study of Over 1,200 Patients
J. Xu

ST083. Development and Characterization of *EML4-ALK* and *KIF5B-ALK* Gene Fusion NSCLC Cell Line using CRISPR/Cas9 Technology as a Reference Material for use with Next-Generation Sequencing Platforms
Q. Zheng

ST084. Evaluating Double-equivocal *HER2* Invasive Breast Cancer Cases and Potential Solutions
R.A. Allen

ST085. Large-scale Hybrid Capture-based RNA Sequencing for Clinical Detection of Gene Fusions and Broad Transcriptomic Assessments of Solid Tumors
V. Balagopal

ST086. Sanger Sequencing Method for the Detection of Extended *RAS* and *BRAF* with an LOD of 10% VAF
D.R. Pringle

ST087. Enabling Standardized Testing of Liquid Biopsy Assays Detecting EGFR Mutations using Bespoke Reference Materials
S. Deans

ST088. Novel *BCOR* and *CREBBP* Fusion Events in High Grade Infiltrating Glioma
D.J. Pisapia

ST089. Utility of GlioSeq Next-generation Sequencing Test for Classification of Ependymomas
A. Wald

ST090. Role of Genomic Profiling in Staging of Patients with Multifocal Lung Carcinomas
S. Jiwani

ST091. Reduced Sensitivity of Break-apart FISH for *ALK* Gene Rearrangements in *EML4-ALK* Fusion Positive Lung Cancer Samples Detected by NGS
S. Knight

ST092. Optimization Studies for the Development of Highly Multiplexed Reference Materials in FFPE Format for Solid Tumor Profiling
B. Anekella

ST093. NEBNext Direct Custom Ready Panels Overcome Challenges Associated with Targeted Re-sequencing
A.J. Barry

ST094. Loss of Heterozygosity in Uterine Serous Carcinoma: Prognostic and Therapeutic Implications
E. Abdulfatah

ST095. Identification of Rare Clinically Actionable Variants in *KRAS, EGFR*, and *BRAF* Using a Comprehensive Gene Panel
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ST096. A Novel and Accurate Real-time PCR Approach for Simultaneous Detection of Multiple Driver Gene Mutations in Non-small Cell Lung Cancer
G. Zhu

ST097. Clinicopathological and Molecular Characterization of *KIT* and *PDGFRA* Mutations in Advanced Gastrointestinal Stromal Tumors
A. Alsuwaidan

ST098. Prediction of Tumor Mutation Burden in Lung Adenocarcinoma using a 130 Gene Targeted Sequencing Panel Covering 0.23 Megabases
R.P. Joshi

ST099. An Analysis of the Level of Supporting Evidence used to Guide Treatment Decisions for Off-label Therapy in Cancer Precision Medicine
C.M. Statz

ST100. Bigger Nets Catch More Fish: Expanded Fusion Analysis Identifies Potential Novel Targets in Pediatric Brain Tumors
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ST101. Association of Microsatellite Instability and Tumor Mutation Burden
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ST102. Histomorphometric Features of Nuclei Architecture and Morphology in Digitized H&E Images Correlate with Mutations in *EGFR* and *KRAS* in Early-stage Non-small Cell Lung Cancer
P.D. Velu

ST103. Clinical Implementation of Targeted RNA Sequencing for Detecting Fusions in Solid Tumors
J. Reuther

ST104. Development and Analytical Validation of Colorectal Cancer Specific Next-generation Sequencing Gene Panel for Cell-free DNA (cfDNA) Based Molecular Testing of Disease Progression
S. Zalles

ST105. Inhibitory Effects of Toluidine Blue on RNA Sequencing Library Preparation
K.J. Hampel

ST106. Single-Vial Amplification Based NGS with Rapid Turn-Around-Time for Interrogation of Variants in Tumors with Limited Diagnostic Material
S. Barua

ST107. Clinical Validation of MSK-ACCESS: An Ultrasensitive Next-generation Sequencing Assay for Liquid Biopsies in the Clinic
A. Brannon

ST108. Suboptimal Somatic Mutation Detection for *EGFR* by the OncoScan CNV Plus Assay
S.C. Smith

ST109. Clinical Experience of a Next-generation Sequencing Assay that Evaluates Common Somatic Mutations and Rearrangements in Patients with Lung Cancer
S. Knight

ST110. Next-generation Sequencing for the Detection of Actionable Genetic Alternations in Advanced Breast Cancer: Should We be Testing and How?
S.E. Abbott

ST111. Validation of the MSI Analysis System, Version 1.2 (Promega) Using the ABI 3130XL Genetic Analyzer System
J. Sen

ST112. Development of a Plasma-based Method for Microsatellite Instability (MSI) Detection using a Next-generation Sequencing Panel
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ST113. Concomitant PD-L1 Expression and Driver Oncogenes in Non-small Cell Lung Cancer
N. McNeill

ST114. HOXB13 IHC Expression and Mutational Profile in Ductal Adenocarcinoma of the Prostate
S. Zomorrodian

ST115. Novel Solvent-Free Deparaffinization Method for FFPE Sample Prep Enabling a More Convenient Workflow
A. Cheng

ST116. Optimization of ctDNA Quantification Methods for Longitudinal Disease Monitoring in Lung Adenocarcinoma
X. Max

ST117. Clinically Validated Fusion Transcript Panel Identifies TERT Fusions
C.R. Orr

ST118. A Robust End-to-end Next-generation Sequencing Solution for Cancer Genome Profiling of Tumor Tissue Samples
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ST119. Rapid Assessment of Microsatellite Instability Status using the Idylla MSI Test
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J. Brock

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B. Wei

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S.J. Deharvengt

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TT008. Evaluation of a Novel Formalin/Methanol-free FNA Fixative for Study of Lung Cancer
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Y. Li

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TT012. Synthetic Serial Dilution Samples Derived from Normal Plasma as a Specimen for Analytical Validation of a Commercial ctDNA Kit
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TT018. An Automated Solution for DNA Extraction and Bisulfite Conversion of High Volume Liquid Biopsy Specimens – Application to Colorectal Cancer Detection Using Methylated *SEPT9*
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K. Curless

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