Poster Listing

Even numbered posters will be attended by their authors on Friday, November 8, 2:45pm-3:45pm.

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

GENETICS

G001. Utilization of Rapid Whole Genomic Sequencing (rWGS) Demonstrates Significant Improvement in Clinical Utility and Cost Effectiveness in Neonatal and Pediatric Hospital Intensive Care Units
S. Nahas

G002. Relative Information Content of Comprehensive High-Throughput Single Nucleotide Analyses in *PTEN*
A. Moon

G003. Characterization of Reference Materials for Genetic Testing of Rare *CYP2D6* Alleles: A GeT-RM Collaborative Project
A. Gaedigk

G004. Correlational Study on Altered Epicardial Adipose Tissue as a Stratification Risk Factor for Valve Disease Progression through IL-13 Signaling
M.M. Corsi Romanelli

G005. Prenatal Testing for Hereditary Cancer Risk Variants: Where Are We Now?
L.S. Rosenblum

G006. An Unusual Cause for Coffin-Lowry Syndrome in Three Siblings with a Novel Microduplication in the *RPS6KA3* Gene Affecting mRNA Expression Levels: Implication for Diagnosis
F. Vetrini

G007. Building an Integrated Clinical Noninvasive Prenatal Screening Program in a Large Reference Laboratory Setting: Lessons Learned Using a Single Nucleotide Polymorphism-Based Method
Y. Ji

G008. Germline *RAD51B* Loss-of-Function Variants Confer Susceptibility to Hereditary Breast and Ovarian Cancers and Result in Homologous Recombination Deficient Tumors
D. Mandelker

G009. Use of Synthetic Internal Standards to Measure Very Low Frequency *TP53*, *PIK3CA*, and *BRAF* Somatic Mutations in Normal Airway Epithelial Field of Injury Associated with Lung Cancer Risk
J. Willey

G010. A Method to Missense Madness: Improving Clinical Variant Interpretation with a Pathway-Focused Functional Assay
S.E. Brnich

G011. Clinical and Molecular Profile of *IDH1*-Mutant Cutaneous Melanoma
J.S. Ross

G012. Performance of AmplideX SMN1/2 Assay from Asuragen
L. Mazur

G013. Mitochondrial Genome Sequencing Uncovers a Novel Alteration in MT-TL2 in a Patient with MELAS-Like Phenotype
J.L. Lopes

G014. A Framework of Critical Considerations in Interpretation of NGS-Based Tests for Germline Disorders: On Behalf of CLSI Document Development Committee (DDC) on Nucleic Acid Sequencing (MM09)
J. Buchan

G015. Accurate and Efficient Chimerism Determination Using a SNP-Based Chimeric ID Panel
K.E. Jackson

G016. North Carolina Newborn Exome Sequencing for Universal Screening (NC NEXUS) Detects Molecular Etiologies Underlying Inborn Errors of Metabolism and Hearing Loss
T.S. Roman

G017. Clinical Significance of Reinterpreting Previously Reported Immunologic Disease Genomic Tests
J.A. SoRelle

G018. Alpha-1 Antitrypsin Deficiency Genotype-Phenotype Correlations: Clinical Experience Testing S, Z, F, and I Alleles
K.S. Dhillon

G019. The VeriDose *CYP2D6* CNV Panel: A One-Well Solution for Copy Number and Hybrid Allele Detection of *CYP2D6*
R.E. Everts

G020. The VeriDose Core Panel: Strong Performance When Analyzing Challenging Pharmacogenetic Samples
A. Lois

G021. Target Selector DNA EGFR Kit for Tissue Demonstrates High Sensitivity without the Need for Macro-dissection
V. Alexiadis

G022. A Multiplex PCR/CE CFTR Assay Resolves Zygosity of the 23 ACMG/ACOG-Recommended CFTR Variants and Sizes Poly-T and TG Repeats in a Single Tube
P. Rao

G023. Integrated Germline and Somatic Analysis Identifies Actionable Cancer Predisposing Germline Mutations in 9,734 Patients with Advanced Cancers
G. Jayakumaran

G024. Assessment of Long IVT mRNA Fragments with the Fragment Analyzer System
C. Pocernich

G025. Validation and Diagnostic Utility of Targeted Next-Generation Sequencing Panel in Korean Patients with Retinitis Pigmentosa
C. Seol

G026. CHLA Ocular Disease Focused Exome: Precision Molecular Diagnosis Enabling Precision Therapies for Retinal Dystrophies
R.J. Schmidt

G027. Genetic Characterization of Spinocerebellar Ataxia 12 Patients in an Indian Cohort: KDAH Experience
J.C. Vyas

G028. Clinical Exome Sequencing, an Effective Tool for Detecting Causative Mutations for Rare Diseases: Retrospective Study of the Past Seven Years
C.C. Eno

G029. Therapy-Related Clonal Hematopoiesis and the Risk of Secondary Hematological Malignancies in Patients with Prior Radiation Therapy
H. Jin

G030. Findings from the Global External Quality Assessment of Lung Cancer Liquid Biopsy Testing
J. Fairley

G031. Implementing Physician-Mediated Consumer-Driven Clinical Elective Genome Sequencing: One Laboratory's Experience
M. Leduc

G032. Chromosomal Microarray Complements Traditional Cytogenetics in Acute Myeloid Leukemia
J. Giffin

G033. Expansion of Clinical Carrier Screening in Spinal Muscular Atrophy through DNA Fragment Analysis by Capillary Electrophoresis
S. Turner

G034. HLA Diversity Score as a Predictor of Checkpoint Blockage Immunotherapy Survival
B. Zhang

G035. Development and Validation of an NGS Assay to Detect UGT1A1 and ABCG2 Polymorphisms Associated with Drug Metabolism
M. Fitarelli-Kiehl

G036. Significance Associated with Phenotype (SAP) Score: A Method for Ranking Genes and Genomic Regions Based on Sample Phenotype
J. Ji

G037. ddPCR-Based Differentiation between Constitutional and Acquired inv(11)(q21q23) Rearrangements in Acute Leukemia
C.J. Zepeda Mendoza

G038. Identity Testing of Paired Neoplastic and Non-neoplastic Samples Using a Custom Single-Nucleotide- Polymorphism-Based Next-Generation Sequencing Assay
K.J. Jensen

G039. Analytical Validation of a Circulating Tumor DNA (ctDNA) Genomic Profiling Assay for the Detection of Somatic Sequencing and Structural Variants
R. Snyder

G040. Clinical Relevance of Liquid Biopsies in Metastatic Adenocarcinoma of Non-small Cell Lung Cancer (NSCLC)
A. Chougule

G041. Analysis of Next-Generation Sequencing Data for Disorders of Somatic Mosaicism Reveals the Importance of Reanalysis in the Clinical Setting
M.J. Evenson

G042. Characterization of Complex *Mixed Lineage Leukemia 1* (*MLL1*) Gene Rearrangements in Leukemia
G. Velagaleti

G043. Likely Pathogenic or Likely Benign: Analysis of Deletions of the *MBD5* Gene
J. Schleede

G044. A Rapid Diagnostic and Screening System for Spinal Muscular Atrophy That Reports Copy Number Changes, Single Nucleotide Variants, and Small Indels
H. Zhu

G045. Genomic Characterization of Pediatric Acute Megakaryoblastic Leukemia and the Clinical Impact
E. Lalonde

G046. Expanded Tumor Spectrum in Individuals with Large Germline Deletions Including *CDKN2A* and Additional Genes Including the Interferon Gene Cluster
P.R. Blackburn

G047. Standardization, Optimization, and Quality Management of FFPE Solid Tumor Diagnostic Samples in Next-Generation Sequencing: An Experience in Our Tata Memorial Centre India
A. Chougule

G048. RapiDxFire Thermostable Reverse Transcriptase: A Novel Reverse Transcriptase for Improved High-Temperature RNA Synthesis and Extended Stability
J. Kramer

G049. Using Isotachophoresis as a Novel Method to Improve the Yield and Quality of Nucleic Acid Purification from FFPE Samples
L.A. Marshall

G050. Challenges of Interpreting *DMD* Gene Duplication Variants
M.L. Fulmer

G051. A Multi-Platform Approach to Friedreich Ataxia Molecular Diagnostics
R. Majumdar

G052. Feasibility of a Synthetic Dried Blood Spot Mimic for Use as an External Control for Newborn Screening of Genetic Disorders
A. Parsons

G053. A Multiplexed SNP Panel Using Oligonucleotide Ligation Assays Run on the N-PLEX Platform for the Allelic Assignment of Genetic Risk Factors of Lung Cancer Development
S.B. Harkins

G054. Incidental Cases of NIPT-Associated Maternal Constitutional Aberrations
K.K. Phillips

G055. Methylation-Based NIPT Test on MALDI -TOF for Down's Syndrome Screening
H.H. Tao

HEMATOPATHOLOGY

H001. Integrative Genomic Testing Improves Clinical Management of Hematological Neoplasms: A Focus on Structural Variations
L. Boiocchi

H002. Clinical Validation of an NGS-Based IGHV Somatic Hypermutation Assay
C.C. Ho

H003. Performance of NGS in Evaluating *TP53* Aberrations in Lymphoid Neoplasm
A. Alsuwaidan

H004. The Result of 122 Consecutive NGS-Based Analysis of T-Lymphoblastic Leukemia/Lymphoma and Early T-cell Precursor Leukemia (ETP)
W. Xie

H005. Frequency of *JAK2* Mutations in Patients with Suspected Myeloproliferative Neoplasms
A. Judd

H006. WT1 Mutation Is an Independent Poor Prognostic Factor in Intermediate Risk Acute Myeloid Leukemia (AML): A Case of Relapsed AML with Leukostasis
N. Hakim

H007. Rapid Next-Generation Karyotyping for Clinical Evaluation of Hematologic Malignancies
E. J. Duncavage

H008. Multidisciplinary Quality Improvement Involving the Molecular Pathology Laboratory Expedites Diagnosis of Acute Promyelocytic Leukemia
S.N. Asadbeigi

H009. Feasability of an RNAseq Assay for Detection of Translocations and Immunoglobulin Clonality in Aggressive B-Cell Lymphomas
X. Wang

H010. Evaluation of Intraclonal Heterogeneity in Diffuse Large B-Cell Lymphoma by Next-Generation Sequencing of Immunoglobulin Heavy Chain (IGH) Gene
M. Zhu

H011. Utility of Next-Generation Sequencing in the Workup and Diagnosis of Patients with Myelodysplastic Syndromes and Unexplained Cytopenias: A Single Institution Experience
D. Carr

H012. Cytogenetic Analysis of Adult T-Cell Leukemia/Lymphoma in a Caribbean Cohort: Correlation with Next-Generation Sequencing (NGS) Data, Clinical Features and Survival
X. Zhang

H013. Validation and Implementation of a Comprehensive Genomics Profiling (CGP) Assay for Hematologic Malignancies
S. Turner

H014. Clinically Significant *CUX1* Mutations Detected by a Targeted Next-Generation Sequencing Panel Are Common in Myeloid Disorders with a High Number of Co-mutated Genes and Dysplastic Features
J.K. Dermawan

H015. Mutant-p53 Antibody Stains Cytokeratin-Negative CTCs Enriched and Detected with a "Pan-CTC" Antibody Cocktail
S.H. Hsiao

H016. Non-coding *NOTCH1* Mutations in Chronic Lymphocytic Leukemia
F. Jelloul

H017. Development of Full-Process Quality-Control Material *BCR-ABL1* Panel Traceable to WHO International Standard
L. Liu

H018. Evaluation of Efficiency-Driven Adjustments to the Abbott RealTime *IDH1* and *IDH2* Assays
A.M. Carlin

H019. *GATA2* Variants Detected by Next-Generation Sequencing with Myeloid Comprehensive Panel: Pathogenic or Benign Polymorphism?
D. Morlote

H020. *IDH1* p.S280F Mutation Is Potentially a Novel Mechanism of Resistance to Ivosidenib Therapy in an *IDH1*-Positive Acute Myeloid Leukemia
Z.N. Oltvai

H021. *IGH* Locus Assessment Using Hybrid-Capture: A Proof-of-Concept Study
E. Mahe

H022. Benchmarking High-Resolution Optical Mapping to FISH, Karyotyping and Chromosomal Microarray
T. Mantere

H023. A Rapid, Capture-Based Enrichment NGS Panel for Assessing Myeloid Malignancies
A. Barry

H024. *JAK2* Exons 12, 13, 14, and 15 Mutation Analysis
L. Cai

H025. When Do FISH and Next-Generation Sequencing Add Diagnostic or Prognostic Value in the Initial Marrow Evaluation of MDS?
P.C. Tsang

H026. Single-Step, Multiplex and Automated Droplet Digital PCR of p190 *BCR-ABL1* Fusion Transcript for Minimal Residual Disease Quantification in B Lymphoblastic Leukemia
R.J. Martinez

H027. Convergence on Genomic Abrogation of the DNA Damage Response Pathway in CLL Is Observed in Patients with Loss of 18p
W. Wong

H028. *CEBPA* Mutation Phasing Using Pacific Biosciences Circular Consensus Sequencing
L. Cai

H029. Nanopore "Flongle" Sequencing for Fusion Detection as a Rapid, Single Specimen Clinical Test
W. Jeck

H030. A Comparative Study of *FLT3*-ITD Allelic Ratio Evaluation Using Peak Height versus Peak Area Measurements
M. Mai

H031. Newly Discovered 74-Base Pair Insertion in *CALR* Exon 9 in a Myeloproliferative Neoplasm Patient
P.L. Ollila

H032. Exploring Driver Mutations and Tumor Mutational Burden Load in Enteropathy-Associated T-Cell Lymphoma by Next-Generation Exome Sequencing
J. Kim

H033. Long-Term Monitoring of Hematopathology, Cytogenetic, and Genetic Abnormalities in a Patient with MIRAGE Syndrome
S. Rentas

H034. Identification of Neoplastic Clonal T-Cell Sequences in Unrelated Healthy Individuals: Limitations of High-Throughput TRG Sequencing for Minimal Residual Disease (MRD) Analysis
S. Sen

H035. New Subtype of AML with a Very Poor Prognosis
C.A. Schandl

H036. Comprehensive Genomic Characterization of *ASXL1* and *SRSF2* Co-mutated Acute Myeloid Leukemia
L. Ramkissoon

H037. WITHDRAWN

H038. Performance Characteristics of the First FDA-Cleared Droplet Digital PCR (ddPCR) IVD Assay, the QXD BCR-ABL %IS Kit on the QXD ddPCR System for Monitoring Chronic Myelogenous Leukemia (CML)
N. Sepulveda

H039. Measurable Residual Disease Monitoring for Patients with Acute Myeloid Leukemia Following Hematopoietic Cell Transplantation Using Error-Corrected Hybrid-Capture Next-Generation Sequencing
V. Balagopal

H040. Characterization of a Cryptic *PML/RARA* Fusion by Next-Generation Sequencing in a Newly Diagnosed Case of Acute Promyelocytic Leukemia with Normal FISH and Chromosome Studies
M.J. Schultz

H041. Development and Characterization an NGS Myeloid Panel: A Single-Tube, Multiplex-PCR-Based NGS Assay with 739 Tiled Amplicons
N.J. Lodato

H042. Antigen Receptor Stereotypy in Chronic Lymphocytic Leukemia
F. Jelloul

H043. Utility and Validation of a Comprehensive DNA Panel (523 Genes-TruSight Oncology 500) for Determination of SNVs, Indels, CNVs, TMB, and MSI on an NGS for Hematological

Malignancies
R. Kolhe

H044. Copy Number Variant Detection by Targeted Gene Next-Generation Sequencing
C.E. Myers

H045. Clinical Utility of Chromosome Genomic Array Testing in Assessing TP53 Abnormalities in CLL
M. Fang

H046. Rapid Detection of TP53 Mutations in Hematopoietic Neoplasms
X. Xu

H047. Exploring Whole Exome Sequencing Data for Predisposing Germline Variants in Pediatric Myeloid Neoplasia
C. Soderquist

H048. Monitoring Haematopoietic Stem Cell Transplant Using Whole Blood and Lineage-Specific Chimerism
O. Shetty

INFECTIOUS DISEASES

ID001. Evaluation of the ELITechGroup MGB Alert CRE RUO Kit on the ELITe InGenius at the Indiana State Department of Health
C. Campion

ID002. Validation and Utility of HIV Drug Resistance Mutation (DRM) Analysis by NGS Platform
R. Kolhe

ID003. Microbial Cell-Free DNA Sequencing for Multiplexed Detection and Quantitation of Cytomegalovirus, Epstein-Barr Virus, and BK Virus
T.A. Blauwkamp

ID004. Next-Generation Sequencing-Based Approach to Detect Integration of HPV16 Following Exposure to Chronic Oxidative Stress
Y. Chen Wongworawat

ID005. Can Real-Time PCR Help in Diagnosis of Neglected Tropical Diseases?
V. Gupta

ID006. Development and Evaluation of a Novel, Sample-to-Answer Molecular Assay for the Detection of *Pneumocystis jirovecii* from Bronchoalveolar Lavage Fluid
B. Liu

ID007. Performance of Aptima HIV Quant Assay on Hologic Panther
B.G. Baltagjieva

ID008. Developing a Clinical 16s rRNA Multi-amplicon-Based Metagenomic Sequencing Test for Bacterial Pathogen Detection in Body Fluid and Tissue Specimens
S. Realegeno

ID009. Performance Verification of the COBAS HEV Nucleic Acid Test on the COBAS 6800

Platform for Hepatitis E Virus Screening
C. Chai

ID010. Diagnostic Stewardship: Framework for Development of Best Practices Algorithm for Hepatitis C Testing
M. Andrade

ID011. Performance of Aptima *M. genitalium* IVD Assay on Hologic Panther
L.J. Mazur

ID012. Institutional Positivity Rates and Implications for the Treatment of Group A *Streptococcus* Pharyngitis with Conventional versus Molecular Alere i Strep A2 Nucleic Acid Amplification Testing
E.C. Calvaresi

ID013. Analytical Performance and Estimated Clinical Outcomes of a Molecular Multiplexed Bacterial Identification Blood Culture Panel
S.L. Mitchell

ID014. Evaluation of GeneXpert MTB/RIF Assay for Rapid Diagnosis of Extrapulmonary Tuberculosis in a Low-Prevalence Setting
P.M. Thwe

ID015. Quantification of Viral Load in AcroMetrix HPV 16, 18, and 68 Genotype Controls Using Bio-Rad Droplet Digital PCR System
H. Wang

ID016. Validation of Altona Real-Star Analyte-Specific Reagents for the Quantitative Detection of Epstein-Barr Virus and Human Herpesvirus 6 in Cerebrospinal Fluid
G. Patricia

ID017. Clinical Evaluation of a Robust Custom-Designed Multiplexed qPCR Microarray-Based Assay for Urinary Tract Infection
M. Shanmugam

ID018. Cell-Free RNA Is More Sensitive Than DNA for the Detection of Pediatric Bacterial Sepsis via Shotgun Metagenomic Sequencing
C.E. Dougherty

ID019. *Mycoplasma genitalium* Assay Results from High- and Low-Risk Populations: Implications for Sexually Transmitted Infection Panel Menu
M. Andrade

ID020. Clinical and Histologic Features of Patients Tested Using the BioFire FilmArray Gastrointestinal Panel
J.C. Mowers

ID021. High-Throughput, Cost-Effective Screening for Multi-drug Resistance Markers and Toxigenic *C. difficile* with ChromaCode's HDPCR Multi-drug Resistance Panel RUO
S. Powell

ID022. Performance Validation of PCR/Sequencing Assays for Upper Respiratory Pathogens
A. Pham

ID023. Performance Characterization of a Respiratory Pathogen Panel with an Automated High-Throughput System
C. Knoth

ID024. Clinical Assessment of the Applied BioCode Respiratory Pathogen Panel
X. Zhang

ID025. Arbovirus Surveillance in a Private Brazilian Hospital: A Four-Year Retrospective Study
R. Petroni

ID026. Validation of the QuanDx MeltPro High Risk and Low Risk HPV Genotyping Assays in FFPE Tissue
L.M. Petersen

ID027. Increased Prevalence of Vabomere and Plazomicin Resistance among Carbapenem-Resistant Enterobacteriaceae from a Cancer Center
X. Zhang

ID028. Development of a Multiplex Qualitative Real-Time PCR Panel for Identification of Tick-Borne Pathogens from Whole Blood
L.M. Petersen

ID029. Profiling of Microbe Co-existence in Respiratory Tract Infections
J. Li

ID030. Detection and Monitoring of Adenovirus Infection in Post-HSCT Recipients by PCR with Patient Outcomes
R. Walia

ID031. Performance Evaluation of the Comprehensive Respiratory Tract Microbiota (RTM) Panel Using Clinical Repository Specimen and QCMD Controls
K. Li

ID032. Performance of a Rapid Multiplex Strep Assay on the Fully Automated NeuMoDx Molecular Systems
B. Keusch

ID033. A Novel Highly Sensitive Assay for Quantitative Detection of Human Immunodeficiency Virus-1 in Human Plasma
H. Lee

ID034. Performance Characteristics of a Fully Automated High-Throughput MDx Assay for the Detection of *Bordetella pertussis* and *Bordetella parapertussi*s
B. Eaton

ID035. Development of Synthetic Multiplexed External Controls for Monitoring the Performance of Qualitative Laboratory Nucleic Acid Testing Panels Used for Identification of Lower Respiratory Pathogens
T. Spenlinhauer

ID036. Evaluation of an Automated Coronavirus Assay to Supplement Respiratory Pathogen Panel Testing on Board the Panther Fusion System using the Open Access Functionality
J.H. Moberly

ID037. Verification of the Roche COBAS HIV-1, HCV and HBV Tests on the COBAS 6800 System and Correlation to the COBAS Ampliprep/COBAS TaqMan System
M. Sabato

ID038. Comparative Yield of Culture and a Molecular Panel in the Diagnosis of Meningitis at a Tertiary Care Cancer Center
T. McMillen

ID039. Sensitive Hybridization Capture and Detection of Urine Cell-Free DNA for Tuberculosis Diagnosis
A. Oreskovic

ID040. Direct Detection of Bacterial and Fungal Pathogens Using Next-Generation Sequencing of Lower Respiratory Specimens
L.A. Cooper

ID041. Local Foodborne Disease and Outbreak Detection for *Salmonella javiana* and *Salmonella newport* Patient Samples in South Carolina Using Whole Genome Sequencing: Details of 192 *Salmonella* Cases
L.M. Lane

ID042. WITHDRAWN

ID043. Investigation of Amplicon Sequencing Technology in Diagnosis of Drug-Resistant Tuberculosis by Testing FFPE Specimens
N. Che

INFORMATICS

I001. Development and Validation of a Melanoma Genomic Index (MGI) Focused on CNVs and AOH from Whole-Genome SNP Aiding in Histological Assessments Complex Melanocytic Lesions
V. Agarwal

I002. Validation and Adoption of Somatic Gene-Level CNV Detection from Tumor-Only NGS Panels Identifies Clinically Significant Alterations in Childhood Tumors
R. Chandramohan

I003. Evaluation of Tertiary Analysis Software for Solid Tumor Next-Generation Sequencing
T.R. Sundin

I004. Impact of Next-Generation Sequencing Panel Composition on Tumor Mutation Burden Calculation: *In Silico* Comparison of Frequently Utilized Panels
N. Bevins

I005. Evaluation of the NAVIFY Mutation Profiler for Next-Generation Sequencing Variant Interpretation and Reporting
L. Bonomi

I006. Performance Analysis of Three Bioinformatic Variant Callers Using a Somatic Reference Standard
B. Porath

I007. Tracking of Index Hopping Percent as a Quality Control Metric for Illumina Sequencers with Patterned Flow Cell Technology
Y. Sakai

I008. WITHDRAWN

I009. Amplicon-Based Targeted Sequencing of Single Circulating Tumor Cells
N. Ericson

I010. Using RNA Expression Analysis to Find Non-fusion Translocations
J.R. Gagan

I011. Discovering SNVs and Indels from RNA-Seq: Comparison of Results of Whole Transcriptome Sequencing to Those of Whole Genome Sequencing
J. Lee

I012. Integrated Networks Dissect the Molecular Biology of Estrogen Receptor-Positive Breast Cancers
I. Katsyv

I013. Benchmarks for Difficult-to-Sequence Genes and Structural Variants
J.M. Zook

I014. Variant Detection and Tumor Mutational Burden (TMB) Concordance in Blood and Tumor Tissue Using Next-Generation Sequencing (NGS) in Patients with Non-small Cell Lung Cancer (NSCLC)
J. Baden

I015. Curation of Pediatric Cancer Variants within the Clinical Genome Resource (ClinGen)
A. Roy

I016. Large-Scale Cytogenetic Profiling of Acute Myeloid Leukemia (AML) from the Mitelman Database Using CytoGenetic Pattern Sleuth (CytoGPS)
Z.B. Abrams

I017. Improve PPV without Sacrificing Sensitivity for Germline NGS Tests Using Lithium Software Package
L. Yang

I018. Oncogenic *EGFR* Kinase Domain Duplications Detected through Aberrant Splice Recognition in RNA-Seq
A. Garcia

I019. Assessment of SureSeq Interpret Software on Low-Frequency Variants Using Reference Standards
J. Reid

I020. Mixed Reality for a Precision Medicine Laboratory: The Future Is Now!
A. Sigaras

I021. Datanorm: A User Friendly Tool That Assists in the Validation of Next-Generation Sequencing Assays
V.S. Williamson

I022. Validation of a Novel Tumor Mutation Burden Assay Using a 130 Gene Tumor Only Targeted Sequencing Panel Covering Less Than 0.25 Megabases
R.P. Joshi

I023. Genomic Database for Assessing Specificity of Primers with Mismatches and Single-Base Bulges
Z.L. Dwight

I024. A Deep-Learning Method for High-Throughput *FMR1* Triplet Repeat Screening
L. Ringel

I025. Ultra-rapid and Accurate Data Analysis Solution for TSO500 ctDNA: Enabling Comprehensive Genomic Profiling with a Plasma-Based Assay
T. Jiang

I026. Targeted Informatics for Optimal FLT3-ITD Detection, Characterization, and Quantification across Multiple NGS Platforms
H. Tsai

I027. Identification of Low-Frequency Variants in AML Populations
S. Johnson

I028. Development of a Convolutional Neural Network Algorithm for Detection of Copy Number Loss in Exome Sequencing Data
S. Muthusamy

I029. InferCNV.org: Inferring Regional Copy Number Changes from Discrete Gene-Level Amplification Signals in Clinical Cancer Genomics Reports for Prioritization of Therapeutic Targets
P.A. Kenny

I030. Pratical Informatic Solutions for Molecular Diagnostics Quality Management
L.M. Scicchitano

I031. Platform-Agnostic Deployment of Bioinformatics Pipelines for Clinical NGS Assays Using Containers, Infrastructure Orchestration, and Workflow Manager
S. Kadri

I032. Evaluation of Nanopore Sequencing and Associated Bioinformatics Pipelines for Accurate Pathogen Identification and Antimicrobial Resistance Prediction
L.M. Petersen

I033. A Next-Generation Sequencing-Based Analysis of Clonality across 39 Subjects Treated for Lymphoproliferative Disorders Reveals Matching Clones in the Diverse IGH Locus
A.M. Zlotnicki

I034. Detection of Internal Tandem Duplications in the *FLT3* Gene Using PiVAT Software
S.M. Polvino

I035. Clinical Bioinformatics Pipelines in the Cloud: Considerations and Deployment
S. Kadri

I036. High-Throughput Genetic Variant Classification for Inherited Cancer Gene Panels through an Artificial Intelligence Inference Engine
S. Nohzadeh-Malakshah

I037. Clinical Validation and Informatic Implementation of Targeted NGS for Low-Input and Degraded Specimens
A. Chitturi

I038. Calculation of Tumor Mutational Burden (TMB) Using a Small, Targeted Next-Generation Sequencing (NGS) Panel for Solid Tumor Samples Absent Matched Normal Samples
P.D. Velu

I039. Downstream Third-Party NGS Pipelines in Comparison to In-House Semi-Automated Variant Processing May Demonstrate Limitations on Some Platforms
K. Ikemura

I040. Machine Learning Applications for Patient Testing: Computational Assessment of MSI by NGS in the Clinical Laboratory
G. Omerza

Other *(e.g.*, Education)

OTH001. HLA Typing: Do We Need Secondary Typing Methods in the Era of NGS?
L. Kumer

OTH002. Alignment of Fellowship Training and Job Needs in Molecular Genetic Pathology
K.L. Kaul

OTH003. Development of Tumor-Specific NGS Gene Subpanels Based on a Medium-Sized NGS Panel (TST170) in a Small Hospital-Based Molecular Diagnostics Laboratory
K.C. Behling

OTH004. Single Cell Genomics and Spatial Transcriptomics Enable Novel Approaches to Dissect Tumor Heterogeneity
L.D. Gibbs

OTH005. Reporting Indeterminate Variants from Massively Parallel Sequencing Assays
J.J. Roth

OTH006. Standardized Process for Molecular Laboratory Engagement and Quality Improvement
K. Halverson

OTH007. Laboratory Standards for Interpretation and Reporting of Acquired Copy Number Abnormalities and Copy-Neutral Loss of Heterozygosity in Neoplastic Disorders: A Consensus ACMG/CGC Document
G. Raca

OTH008. Real-Time Outbreak Investigation Informed by Whole Genome Sequencing and Data Mining: Expecting the Unexpected
M.M. Hernandez

OTH009. Whole Exome Sequencing in the Clinical Laboratory: Pre-analytical Challenges and Triumphs
J. Catalano

OTH010. Large Panel NGS Testing: Financial Barriers to Entry
J. Catalano

OTH011. Analysis of CAP Proficiency Testing Responses and Commonly Used Annotation Software Output Shows Substantial Discrepancy in Variant Nomenclature
R.J. Schmidt

SOLID TUMORS

ST001. Comparison of Next-Generation Sequencing Assays for Clinical Use in Solid Tumor Malignancies
T. Sundin

ST002. Development of a DNA/RNA Full Process Run Control for Next-Generation Sequencing Assays
A.E. Shean

ST003. Relevance of Next-Generation Sequencing in Lung Cancer: Data from a Tertiary Lab with Interesting Case Presentations
N. Sabnis

ST004. Quality Impact of Implementing Reflex Clinical Genomic Analysis in Non-Small Cell Lung Cancer
B.F. Smith

ST005. Correlation of MET Exon 14 Skipping and *TP53* Mutation with PD-L1 Expression in Chinese Patients with NSCLC
N. Che

ST006. WITHDRAWN

ST007. Molecular Profiles of Lung Adenocarcinoma (LAC) from Rural Maine: Correlation of Next-Generation Sequencing (NGS) Data with Clinical Features and Outcome
L. Skacel

ST008. Diverse Landscape of Fibroblast Growth Factor Receptor 2 (*FGFR2*) Rearrangement Partners in Intrahepatic Cholangiocarcinoma (iCCA)
I.M. Silverman

ST009. Improved Detection of *MET* Exon 14 Skipping Mutations in Lung Adenocarcinoma with Combined DNA/RNA Testing and Refined Analysis Methods
D.M. Manthei

ST010. Detection of Point Mutations in Paediatric Low Grade Glioma (PLGG) and Diffuse Intrinsic Pontine Glioma (DIPG) Patients: Validation of a Novel Liquid Biopsy Assay
M. Johnson

ST011. Microsatellite Instability Testing Using the Moffitt STAR Next-Generation Sequencing Panel
J.M. Rodriguez

ST012. Implementation and Analysis of Colorectal Cancer NGS Panel at a Brazilian Low Income Cancer Hospital
G.N. Berardinelli

ST013. Cell-Free Plasma miR-149 as a Biomarker for Screening Lung Cancer
W. Mahmud

ST014. CFL1 Promotes Proliferation and Invasiveness and Regulates NF-κB-Mediated Inflammatory Factors in Hepatocellular Carcinoma
C. Zhang

ST015. Clonal Hematopoiesis Mutations in Plasma cfDNA *RAS/BRAF* Genotyping of Metastatic Colorectal Cancer
B. Wang

ST016. Utility of NGS MSI Calling Software in a 0.35 Mb Targeted Panel Utilizing Amplicon-Based Target Enrichment on an Ion Torrent Platform
C.M. Sebastian

ST017. Correlative Analysis Genes Encoding Cholesterol Synthesis with Tumor Character and Clinical Parameters in Colorectal Carcinomas
K. Vaiphei

ST018. Accurate Classification of Salivary Gland Carcinomas Using a Custom AmpliSeq RNAseq Panel
D.M. Manthei

ST019. *IDH* Mutations, *MGMT* Methylation and 1p/19q Status Provides Better Diagnosis and Survival Prediction in an Indian Cohort of Diffuse Gliomas
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