Even numbered posters will be attended by their authors on Friday, November 17, 2:30pm – 3:30pm.

Odd numbered posters will be attended by their authors on Saturday, November 18, 9:45am – 10:45am.

GENE	Validation of the Ion S5 and Ion Chef for Cystic Fibrosis Mutation Analysis T.R. Sundin	G10.	Validation of A Cystic Fibrosis 55 Mutation Screening Assay on the QuantStudio 12K Flex Open Array System <i>M.M. Moradian</i>
602.	Reinterpreting Previously Reported Genetic Variants is Clinically	G11.	Linked-Read Sequencing for Molecular Cytogenetics S. Garcia
	Significant J.A. SoRelle	G12.	High Throughput Linked-Read Sequencing for Improved Variant
603.	Hypertrophic Epicardial Adipose Tissue is a Source of EPAC Proteins Directly Associated to ST2		Detection A.N. Fehr
	Production and Heart Dilation and may be a Potential Index of Heart Remodeling in CVDs Patients <i>M.M. Corsi Romanelli</i>	G13.	GALC Deletion/Duplication Detection by Droplet Digital PCR for Krabbe Disease Confirmation in a Single Dried Blood Spot Punch <i>R. Majumdar</i>
04.	Discovery of a Novel, Accurate Tagging SNP for HLA-B*15:02 Screening Before Carbamazepine Therapy in the Multiethnic United States Population <i>H. Fang</i>	G14.	Pericentromeric Regions of Homozygosity on the X Chromosome are Likely Benign Population Variation <i>E.S. Barrie</i>
05.	Spectrum of Mutations in Hbb Gene among Thalassemia Major Patients in a Cohort of Nepalese Population <i>S. Thapa</i>	G15.	Clinical Utility of Next Generation Sequencing (NGS) studies in Neurological Disease – Our Experience at Kokilaben Dhirubhai Ambani Hospital, India
06.	Custom NGS Panels from Optimized Gene Sets for Inherited		J.C. Vyas
	Disease Research M. Andersen	G16.	Clinical Impact of Characterizing Genomic Alterations Using Whole- Genome Mate Pair Sequencing
07.	WITHDRAWN		J. Blommel
08.	Comprehensive Carrier Testing of 9,785 Chinese Couples for Common Severe Recessive Disorders	G17.	Comparison of Specimen Collection Methods for Pharmacogenetic Testing <i>H. Katzov-Eckert</i>
	S. Zhao	G18.	Using the GeneReader NGS System
09.	Exome Re-Analysis and Complementary Testing Identify Novel Mutations for Rare Mendelian Disorders <i>C. Wei</i>		to Identify Mutations in BRCA 1/2, PTEN and TP53 <i>N. Dennison</i>

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G19.	Detecting Pharmacogenomic Variants Using Long- and Short- Read Next Generation Sequencing Platforms <i>C.A. Schumacher</i>	G2'
G20.	Microdeletion in SNRPN May Lead to False Positive Results for Angelman Syndrome Using Methylation Analysis <i>B.M. Zhang</i>	G3
G21.	BRCA1 Mutation Detection Using QIAGEN GeneReader NGS System in a Case with RET Codon 634 Mutation <i>B. Sarkadi</i>	G3
G22.	Colorectal Cancer Predisposition and its Genetic Characterization of Korean Patients K. Park	G3
G23.	Tumor Mutations Can Help Classify Germline Variants: Learning from Mismatch Repair Deficiency <i>B.H. Shirts</i>	G3
G24.	Discovery of Unique Disease- and Gene-Specific Peripheral Blood DNA Methylation Signatures Allows Molecular Diagnosis and VUS Classification in Hereditary Genetic Syndromes " <i>B. Sadikovic</i>	G3
G25.	Analytical Validation of the Advanta Immuno-Oncology Gene Expression Assay for Profiling of Immunobiology and the Development of Predictive Gene Signatures for Response to Immunotherapies <i>P. Chen</i>	G3 G3
G26.	Genome Sequencing Reveals Variants in Non-Coding Regions Cause Hereditary Hemorrhagic Telangiectasia G. Akay Tayfun	G3
G27.	Genetic Testing of Noonan Syndrome Using Targeted Next- Generation Sequencing Panel <i>C. Seol</i>	G3
G28.	Short Tandem Repeat Analysis Reveals a High Rate of Partial Hydatidiform Moles in Triploid Conceptions Identified by Prenatal Chromosome Microarray <i>X. Wu</i>	G3

G29.	Comparison of EUROArray HLA- DQ2/DQ8-h Direct and Olerup SSP for the Determination of Celiac Disease Associated Risk Factors HLA-DQ2.2, -DQ2.5 and -DQ8 <i>N. Miron</i>
G30.	Improved Screening for Cancer Predisposition Mutations in Patients with Advanced Solid Tumors Enabled by Tumor-Normal Sequencing <i>D. Mandelker</i>
G31.	Importance of Whole Exome Sequencing in Solving Complex Phenotypes: A Case Report <i>R.M. Minillo</i>
G32.	Automated Reanalysis of Genomic Data: Challenges and the Promise of Novel Diagnoses J. Murrell
G33.	Chromosome Anomalies Involving the APC Gene Lead to an Increased Risk for FAP and Developmental Delays B.A. Hilton
G34.	Analysis of Cell Pellets Using the Cytoscan Dx Chromosomal Microarray <i>C.J. Broehm</i>
G35.	Interindividual Variability of Delta-9-Tetrahydrocannabinol Metabolism by CYP2C9 Polymorphism and Possible CYP3A Inhibitors <i>M. Nakano</i>
G36.	An Atypical Presentation of a Homozygous Delta-F508 Mutation <i>O. Rouhi</i>
G37.	Expert Review of NGS Results Removes Need for Routine Sanger Sequencing Confirmation <i>D. Muzzey</i>
G38.	High Prevalence of Alpha-1 Antitrypsin Z Alleles in Formalin- Fixed Paraffin-Embedded Liver Explant Tissue with PAS-D Globules <i>L. Pac</i>
G39.	Clinically Relevant Findings from Pharmacogenomic Testing in >36k Patients Across Multiple Diagnoses <i>J.P. Jarvis</i>



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G40.	Analytical and Clinical Validation	HEMATOPATHOLOGY		
	of Variants Identified by Exome Sequencing through Secondary			
	Review and Sanger Confirmation in a CLIA-Certified Molecular Laboratory N.T. Strande	H01.	Diffuse Large B-Cell Lymphoma Gene Expression Profiling for Cell-of-Origin Determination (Lymph2Cx Testing) Using FFPE Tissue Sections in a Clinical	
G41.	The Mother of all Confounders: Strategies to Avoid False Positives Caused by Maternal Copy Number		Molecular Diagnostics Laboratory R.S. Robetorye	
	Variants in Noninvasive Prenatal Screening K.E. Kaseniit	H02.	Performance Evaluation of a T-cell Receptor Gamma Gene Rearrangement (TRG) Next Generation Sequencing (NGS)	
G42.	The Analysis of Oral Microbiome in CytoScan Assay Performance <i>D. Lizarraga</i>	_	Assay for Clinical Practice V. Borodin	
G43.	Second Specimen Testing for TP53 Variants J. Bissonnette	Н03.	Minimal Recipient Chimerism Detection by qPCR Method for the Post-Transplant Patients Who Achieved Complete Donor Chimerism by STR Method	
G44.	Runs of Homozygosity (ROH) Reveal that Segmental-UPD Occurs		L. Kumer	
	as a Result of Recombination Mediated Repair of Genomic Imbalance <i>A.L. Penton</i>	H04.	Frequency and Pattern of BCR-ABL Kinase Domain Mutation in Chronic Myeloid Leukemia-An Indian Perspective <i>R. Katara</i>	
G45.	Comparison between Different Activity Score Models for CYP2D6 Phenotype and Frequencies of Actionable Combined Genotypes of CYP2D6 and CYP2C19 <i>M. Nakano</i>	H05.	Clinical Validation of a Highly Sensitive and Highly Reproducible BCR-ABL1 Quantification Assay for CML Monitoring <i>M. Alikhan</i>	
G46.	Mutation Spectrum of the <i>KCNQ1,</i> <i>KCNH2</i> , and <i>SCN5A</i> Genes for the Long QT Syndrome in Korea <i>M. Kim</i>	H06.	Comparison of Clonality Testing on B Plus Fixed Versus Formalin Fixed Tissue <i>E. Castro-Echeverry</i>	
G47.	Spectrum of <i>MNX1</i> Mutations in Korean Patients with Currarino Syndrome S. <i>Lee</i>	H07.	Detection of Fusion Transcripts in Hematologic Malignancies by RNA-Seq <i>P. Szankasi</i>	
G48.	WITHDRAWN	H08.	Development and Validation	
G49.	Genetics Insights into Hereditary Cancer Risk in the Latin American Population <i>A. Leon</i>		of a Multiplex Droplet Digital PCR Assay for the Detection and Quantification of BCR/ABL1 Fusion Transcripts <i>R.Y. Walder</i>	
G50.	Comprehensive Detection of <i>CFTR</i> Variants Using Anchored Multiplex PCR and Next-Generation Sequencing <i>M.T. Hardison</i>	H09.	Evaluation of the QIAGEN CALR RGQ PCR Kit for the Detection of CALR Mutations in Suspected Myeloproliferative Neoplasms L.J. Doyle	

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H10.	Comparison of FLT3-ITD Allelic Ratio by PCR Analysis and Next Generation Sequencing <i>E. Castro-Echeverry</i>	H19.	Genetic Heterogeneity and Stratification of AML Samples with NPM1 Mutation Detected by the MyAML NGS Test S. Gramatikova
H11.	Differential Mutation Patterns of the Calreticulin Gene in 14,064 Patients: Distribution of Deletions, and Insertions in a Clinical Population J. Sebastian	H20.	Impact of Molecular Sequencing Information as Related to 2008 and 2016 WHO Classification of Acute Myeloid Leukemia and Myelodysplasia <i>L.N. Toth</i>
H12.	Impact of <i>MYC</i> Abnormalities, Trisomy of Chromosome 8 and Estimated Tumor Progression Values in Plasma Cell Myeloma <i>R. Garcia</i>	H21.	Validation of a Next Generation Sequencing-Based Assay to Detect Recurrent Translocations in Ph-Like Acute Lymphoblastic Leukemia D. Duose
H13.	One Children's Oncology Group Cytogenetics Laboratories' Experience With Single Nucleotide Polymorphism Chromosome Microarray Analysis of Pediatric	H22.	Isocitrate Dehydrogenase 1 and 2 Mutations in Myeloid Neoplasms <i>L.N. Toth</i>
H14.	Acute Leukemia's <i>M. Micale</i> Use of an NGS Based Custom	H23.	RNA-Based Immune Repertoire Sequencing for Characterizing B-Cell Lineage Malignancy Clonality and IGHV Mutation Status
1114.	Myeloid Gene Panel for Sequencing of Formalin-Fixed Paraffin		J. Haimes
	Embedded Bone Marrow Clot Sections and Air-Dried Smears in Acute Myeloid Leukemia <i>A.N. Huho</i>	H24.	Utilization of Peripheral Blood for Diagnostic Testing for MDS/MPN Patients: Efficacy and Benefits of a SNP Microarray Analysis S. Schwartz
H15.	A Prolonged Low Level JAK2 V617F Is Significant In Clinically Suspicious Myeloproliferative Neoplasms (MPN) <i>E. Vail</i>	H25.	Clinical and Genetic Characteristics of MYC Gene Aberration in Multiple Myeloma S. Min
H16.	Clinical Validation and Implementation of a Targeted Sequencing Panel for Myeloid Neoplasms D. Steiner	H26.	Clinical Validation of a Molecular Barcoded Amplicon-based Next Generation Sequencing Test for Mutation Profiling of Myeloid Neoplasms <i>T. Yang</i>
H17.	Lack of Racial Differences in Primary Cytogenetic Abnormalities in Multiple Myeloma J. Richter	H27.	Performance of ACL LDT CALR Exon 9 Assay L.J. Mazur
H18.	Distinct Patterns of PML-RARA Fusion Gene Formation in High Risk Acute Promyelocytic Leukemia	H28.	Haplotype Counting for Sensitive AML Relapse Detection <i>M. Debeljak</i>
	Revealed by Whole Genome Sequencing Y. Cho	H29.	Evaluation of Fragment Analysis Assay for Detection of <i>CALR</i> Exon 9 Insertion and Deletion Mutation in Myeloproliferative Neoplasms



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H30.	Hematopoietic Tumor Contamination in Human Fingernail Clippings Used as a Germline Comparator in an NGS- based Myeloid Panel <i>D. Olson</i>	H39.	Multi-Year Review of Cytogenetic Abnormalities in Patients with Multiple Myeloma from a Single Institution and a Proposed Testing Algorithm <i>P. Paulraj</i>
H31.	Successful Coverage of Difficult to Sequence Genes (CALR, CEBPA, and FLT3) Associated with Myeloid Disorders Using a Hybridisation- Based Enrichment Approach Prior to Next-Generation Sequencing	H40.	ALL-ICP, a Simple and Comprehensive Method to Detect Chromosome Abnormalities in Acute Lymphocytic Leukemia <i>R. Babu</i>
	(NGS). L. Georgieva	H41.	Multi-Platform-Based Comprehensive Molecular Analysis of Hematological Malignancies for
H32.	Commonly Mutated Genes across Myeloid Malignancies Using a Targeted NGS Panel: A Single Institution Experience J. Yan		Somatic Mutations, Copy Number Changes, and Translocations for Routine Clinical Testing <i>R. Kanagal-Shamanna</i>
H33.	Targeted Sequencing of Recurrently Mutated Genes in Myeloid Neoplasms Using the Raindance Thunderstorm-Illumina Miseq Platform: My Heme (Myeloid	H42.	Correlation between Calreticulin (<i>CALR</i>) Mutations as Detected by PCR and CAL2 Antigen Expression by Immunohistochemistry <i>E. Wolak</i>
	Hematologic Malignancy) Panel S. Cheng	H43.	Validation of a Low-input, Amplicon-Based Dual-Strand Assay to Detect DNA Variants in
H34.	Implementation Considerations: Designing and Medically Vetting a Targeted Gene Panel for Hematologic Malignancies		Lymphomas by Next-Generation Sequencing (NGS) <i>A. Oran</i>
	N. Sidiropoulos	H44.	HDAC6 Regulates MicroRNA-27b that Suppresses Proliferation,
H35.	Development of a Targeted Next Generation Sequencing Panel for Multiple Myeloma <i>M. Mai</i>		Promotes Apoptosis and Target C-MET in Diffuse Large B-Cell Lymphoma Y. Jia
H36.	Comparison of a MALDI-TOF-based SNP Panel with STR Analysis for Chimerism Testing Y. Linnik	H45.	Clonality Detection Using Next- Generation Sequencing and Capillary Electrophoresis Methods in Suspect Lymphoproliferative Samples
H37.	Performance Evaluation of a Novel, Rapid, Multiplexed, One-Step		Y. Huang
	RT-PCR Assay for Simultaneous Detection of Common Leukemia- Associated Translocations S.S. Talwalkar	H46.	NGS Based Identification of FLT3 ITD Mutations Using Unique Molecular Indexes <i>B.A. Parikh</i>
H38.	Development of a Droplet Digital PCR Assay for Detection and Quantification of BCR-ABL1 e1a2 Fusion Transcripts in Acute B Lymphoblastic Leukemia <i>P. Mroz</i>	H47.	Clinical Utility of Semiconductor- Based Next Generation Sequencing for Evaluation of IgVH Somatic Hypermutation Status in Chronic Lymphocytic Leukemia / Small Lymphocytic Lymphoma (CLL/SLL) <i>B. Tandon</i>



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H48.	Unusual Cases of MDS/MPN-RS-T Without Overt Anemia Share Molecular Signatures Classic for MDS and MPN Overlap Syndromes <i>P. Li</i>	ł
H49.	Sensitive CXCR4 Sequencing Using Bridged Nucleic Acid (BNA) PCR Clamp Technology <i>K.E. Halverson</i>	H
H50.	Del(7)(q22) Resulting From an Unbalanced der(7)t(3;7)(q26;q21) Generating a CDK6-MECOM Fusion and FLT3 Alterations in Pediatric Acute Myeloid Leukemia with Myelodysplasia-Related Changes <i>E.M. Azzato</i>	H
H51.	Going Beyond MMR to the Analysis of Deep Molecular Response K. Drafahl	H
H52.	Comprehensive Assessment for Structural Rearrangements Using a Customized Anchored Multiplex PCR-Based Next-Generation Sequencing Assay Targeting 199 Genes A.K. Dupuy	E
H53.	Validation of the LeukoStrat CDx FLT3 Mutation Assay to Detect Internal Tandem Duplication (ITD) and Tyrosine Kinase Domain (TKD) Mutations in 1058 Patients with AML and Response to Midostaurin A. Osgood	E
H54.	Clinical Validation of the Lymph2Cx Assay to Determine the Cell of Origin of DLBCL D. Abdel Azim	H
H55.	BCR-ABL1 Minor Breakpoint (e1a2) Monitoring Using an Analytically Validated Multiplex Assay <i>M. Dodge</i>	
H56.	Droplet Digital PCR Method for Absolute BCR-ABL1 Major and Minor Transcript Quantification C.A. Schandl	H
H57.	Method Based Validation of 94 Genes Next Generation Sequencing (NGS)-Based Hematologic Malignancy Panel and Confirmation of Variants Using Sanger Sequencing <i>C.S. Sears</i>	F

H58.	Multiple Highly Concordant Assays Facilitate Clinical Analyses of Samples at Different Scales and Sensitivities <i>L.M. Chamberlain</i>
H59.	Detection of Rare Variant <i>NPM1</i> Transcripts Using an Allele Specific Real-Time qPCR Assay Targeting Mutation Types A, B, and D J.A. Schumacher
H60.	Comparison of Clinical Digital Karyotyping by Comprehensive Next Generation Sequencing with Standard Cytogenetic Analysis in Pediatric Leukemia <i>E.M. Azzato</i>
H61.	Sequential NGS-Based Multi-Gene Mutational Analysis in <i>de novo</i> Acute Myeloid Leukemia with <i>RUNX1</i> Mutation <i>R. Luthra</i>
H62.	A Case Report of Donor- Derived Clonal Hematopoiesis After Allogeneic Stem Cell Transplantation J. Smith
H63.	Acute Promyelocytic Leukemia with Atypical Karyotype and <i>FLT3</i> ITD Mutation is Associated with Inferior Clinical Outcome <i>A. Idrees</i>
H64.	High Frequency of <i>MYD88</i> L265P Mutation in Ocular Adnexal Marginal Zone Lymphomas and Its Clinical Correlates <i>A. Behdad</i>
H65.	A Balanced Formulation of Dimethyl Sulfoxide and Bovine Serum Albumin Provides Highly Uniform Coverage of CEBPA in a Droplet PCR-Based NGS Panel S. Mallampati
H66.	Next Generation Sequencing-Based Heme Panel Testing for Myeloid Neoplasms at a Tertiary Care Hospital and Cancer Center K. Shah
H67.	Subclonal <i>CEBPA</i> Mutations Identified by Deep Sequencing Using a Clinically Validated Deep Sequencing Assay in Acute Myeloid Leukemia <i>S. Png</i>



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H68.	Diagnostic Yield of Somatic Mutation Detection in Hematologic Malignancies Does Not Increase with Additional Mutation Analysis, and Supports More Focused	ID02.	Pathogen Detection by Metagenomic Next Generation Sequencing of Purulent Body Fluids <i>W. Gu</i>
	Disease-Specific Testing Models S. Szelinger	ID03.	Utilization of a Cost-effective High- Throughput Sequencing Approach for Comprehensive Metagenomic
H69.	The Utility of SNP-Array Analysis in the Detection of 1p36 Abnormality in t(14;18)-Negative Follicular Lymphoma		Surveillance of Viral Pathogens in Respiratory Specimens S. Png
	L. Wang	ID04.	Analytical Validation of an Analyte Specific Reagent (ASR) for
H70.	Next Generation Sequencing Targeting IGH Demonstrates Clinical Utility in Detection of B-Cell Clonality in Non-Hodgkin		Mycoplasma genitalium Detection and Point Prevalence Assessment S. McClellan
	Lymphomas B. Tandon	ID05.	Evaluation of RealStar Pneumocystis Jirovecii PCR Kit 1.0 for Qualitative Detection of
H71.	JAK2-Negative Refractory Anemia with Ring Sideroblasts Associated with Marked Thrombocytosis (RARS-T) Occurs More Commonly in Women		Pneumocystis jirovecii Pneumonia (PCP) Specific DNA in Respiratory Sample Types K. Rottengatter
	M. Hussaini	ID06.	Evaluation of RealStar Bordetella pertussis PCR Kit 1.0 for Qualitative
H72.	Next Generation Sequencing Studies in Early Myeloid Neoplasms C. Soderquist		Detection and Differentiation of Bordetella pertussis and Bordetella parapertussis Specific DNA in Respiratory Samples
H73.	Correlation of Mutational Burden Detected by Targeted Next-		K. Rottengatter
	Generation Sequencing with Pathological Disease Burden in Hematological Malignancies. S.L. Kang	ID07.	Development of a Quantitative BK Virus PCR Assay on the Luminex ARIES Molecular Diagnostics Platform T. Her
H74.	Unique 9q34 Rearrangements in T-ALL: Elucidation and	ID08.	Development of a Panfungal Next
	Characterization by Microarray Analysis, RNA Sequencing and FISH J. Tepperberg	1000.	Generation Sequencing Assay K.D. Tardif
H75.	Comparative Study of the Panel Based Validation with Method Based Validation in Myeloid Panel	ID09.	Next Generation Nucleic Acid Extraction System: NucliSens eMAG A.M. McClernon
	R. Wu	ID10.	HPV: The Use of Full Process Controls to Monitor Extraction
INFE	CTIOUS DISEASES		Variation A. Ricketts
ID01.	Evaluation of Cepheid Xpert HIV-1 Qual Assay in Whole Blood for Diagnosis of HIV-1 Infection S. Lim	ID11.	Detection of <i>Borrelia burgdorferi</i> DNA by Loop Mediated Isothermal Amplification (LAMP) in Pediatric Synovial Fluids <i>R.V. Ponaka</i>



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ID12.	ITS1 (Internal Transcribed Spacer) Primer Binding Site Polymorphism in Clinical Fungal Isolates <i>J.F. Mele</i>
ID13.	The Film Array Global Fever Panel: Goal of Quick Diagnosis of Infectious Diseases Presenting with Acute Febrile Illness <i>C. Toxopeus</i>
ID14.	Evaluation of Two Molecular Diagnostic Assays for <i>Clostridium</i> <i>difficile</i> Infection <i>G.A. Capraro</i>
ID15.	Molecular-Based HPV Screening in Resource Limited Countries A. Atkinson
ID16.	Association of <i>Clostridium difficile</i> Molecular Typing with Colonization and Development of <i>Clostridium</i> <i>difficile</i> Infection (CDI) <i>T. Theparee</i>
ID17.	Detection of Gram-Negative Bacteria and Antimicrobial Resistance Markers Using the iCubate iC-GN Assay <i>M.S. Conover</i>
ID18.	Real-time Gastrointestinal Illness Surveillance Through Cloud Based Epidemiology Network of Clinical Laboratories J.M. Ruzante
ID19.	WITHDRAWN
ID20.	Testing High-Risk Human Papillomavirus on Head and Neck Tumor Tissue Squamous Cell Carcinoma Using a Modified Commercial PCR Assay A.N. Huho
ID21.	Investigation of Differences in Gene Expression by Kanamycin Stress in Multidrug-Resistant <i>Mycobacterium</i> <i>tuberculosis</i> with / without <i>rrs</i> Mutation Using RNA-Seq <i>Y. Kim</i>
ID22.	Evaluation of a Molecular Point of Care System for the Detection of <i>Clostridium difficile</i> <i>I.O. Op den Buijs</i>

ID23.	Dermatomycosis – a Novel and Rapid Detection of Causative Fungal Agents with a DNA- Based Microarray (EUROArray Dermatomycosis) S. Kosanke
ID24.	Performance Comparison of the DiaSorin Simplexa <i>C. difficile</i> Direct Assay with the Illumigene <i>C.</i> <i>difficile</i> DNA Amplification Assay in Unformed Stool Samples <i>B.C. Sutton</i>
ID25.	Comparison of the Accula Influenza A/B PCR Assay and Alere i Influenza A/B Isothermal Nucleic Amplification Assay for the Detection of Influenza in Adult and Pediatric Populations S. Young
ID26.	Developing High Throughput Urinary Tract Microbiota Profiling Using TaqMan and OpenArray Technologies <i>K. Li</i>
ID27.	Rapid Detection of <i>Clostridium</i> <i>difficile</i> with the GenePOC CDiff Assay <i>A. Zumoberhaus</i>
ID28.	Multicenter Evaluation of Cobas HBV Real-Time PCR Assay on the Roche Cobas 4800 System in Comparison with COBAS AmpliPrep/COBAS TaqMan HBV Test: Leading Circle for Cobas 4800 Virology (LCCV) Project <i>H. Kim</i>
ID29.	A Model for Detection of Novel Influenza Incidence in the United States J.D. Jones
ID30.	Comparative Evaluation of ARIES Flu A/B & RSV and Xpert Flu/RSV XC for Simultaneous Detection and Identification of Influenza Viruses A, B and Respiratory Syncytial Virus in Cancer Patients L. Ling
ID31.	Rapid Diagnosis of Bloodstream Infections Through Identification of Pathogens and Resistance Markers Directly from Whole Human Blood at 1 CFU/mI <i>N. Casali</i>

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ID32.	A Clinical Performance Evaluation of QPLEX STI Detection Kit S. Cho	ID43.	Direct Detection of VZV from Cutaneous, Mucocutaneous and CSF Specimens Using the Simplexa VZV Direct Assay on the DiaSorin	
ID33.	Rapid Detection of Respiratory Pathogens with GenMark's ePlex RP Panel		LIAISON MDX System E. Eleazar	
	K. Henthorn	ID44.	Validation of Human Papilloma Virus Detection in Anal Cytology	
ID34.	34. Challenges Associated with Developing Rapid Molecular Diagnostics for Detection of Antibiotic Resistance		Specimens on the Cobas 4800 System <i>L. Helander</i>	
ID35.	M. Stonebraker Quantitative Detection of HCV	ID45.	Multicenter Evaluation of Cobas HCV Real-Time PCR Assay on	
	and HBV on NeuMoDx Molecular System C. Couture		the Roche Cobas 4800 System in Comparison with COBAS AmpliPrep/COBAS TaqMan HCV Test: Leading Circle for Cobas 4800 Virology (LCCV) Project	
ID36.	Validation and Performance of Sequencing-Based Reference		W. Lee	
	Assays for Biocode Gi Pathogen Panel <i>A. Pham</i>	ID46.	Comparison of Cobas HCV GT Against Versant HCV Genotype 2.0 Assays with Confirmation by Sequencing	
ID37.	Development of a Respiratory Pathogen Panel with an Automated		T. Png	
_	High-Throughput System S. Mi	ID47.	A Multi-Center Clinical Evaluation of a Sample to Answer Real-Time PCR Assay for Toxigenic <i>C. difficile</i> ir Symptomatic Subjects <i>S. Young</i>	
ID38.	Comparison of Luminex ARIES Vaginosis Panel and BD AFFIRM VPIII for the Detection of <i>Candida</i>			
	spp., Gardnerella vaginalis, and Trichomonas vaginalis J. Barry	ID48.	Evaluation of the Focus Diagnostic Simplexa HSV 1 & 2 Direct for Detection and Differentiation of Herpes Simplex Virus 1 and 2 in Neonatal Swab Specimens <i>K. Gvozdjan</i>	
ID39.	Clinical Evaluation of the xMAP MultiFLEX ZIKA RNA Assay A. Walden			
ID40.	Evaluation of ELITech Group's MGB Alert HSV-1 and HSV-2 ASRs on the Abbott m2000sp/rt Platform	ID49.	Performance of NxTag RPP Assay from Luminex <i>L. Mazur</i>	
ID41.	K. Stepaniants Comprehensive Women's Health	ID50.	Evaluation of the Anyplex MTB/ NTM Real-Time Detection (V2.0)	
1041.	Diagnostic Testing Using Innovative Multiplex PCR Assays <i>W. Hauser</i>		for Detection of Nontuberculous Mycobacteria in Respiratory Specimens <i>H. Kim</i>	
ID42.	Sensitive Detection of Bacterial Targets on the NeuMoDx Molecular System J. Zhu	ID51.	Direct Detection of mRNA in Whole Blood Samples for Transcriptomic Profiling <i>A. Khine</i>	



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ID52.	Comparison Between BD Maxwell VP and ACL LDT SwabOne Assay <i>L.J. Mazur</i>	ID62.	Rapid and Sensitive Isothermal Molecular Amplification of Group A Streptococcus (GAS) with Alere i Molecular Platform	
ID53.	Performance Evaluation of the Abbott RealTime CMV IUO Assay on the m2000 Platform Compared to the Roche COBAS AmpliPrep/ TaqMan CMV Assay in Transplant and Immunocompromised Individuals <i>P.M. Kulling</i>	ID63.	N. Moore Improved Cost and Turnaround Time Using an Extraction-Free Amplification and Detection Method for Respiratory Viruses in Clinical Specimens M. Elkan	
ID54.	Molecular Analysis of Fungal Populations in Patients with Onychomycosis Using Next Generation Sequencing (NGS) and Real-Time PCR <i>E. Gustafson</i>	ID64.	Optimization of Metatranscriptomic Method for Rapid and Unbiased Detection of Microbial Pathogens in Bronchoalveolar Lavage Specimens <i>C. Yin</i>	
ID55.	Mosquito Surveillance and Testing for Local Zika Virus in New York City 2016 <i>J. Rakeman</i>	ID65.	Development and Validation of the Alert MGB ASR for BK Virus Quantitative Viral Load Testing on the ELITEe InGenius Sample-to- Answer System	
ID56.	Monitor Vaginal Microbiota with One Swab: Copan ESwab as Convenient Collection and Transport Device for Cross Platform Molecular Tests of Women's Health <i>Z. Huang</i>	ID66.	D. Banerjee Using Independent Run Controls to Monitor Relative Amplification Efficiency in a STI Assay J. Yundt-Pacheco	
ID57.	Multicenter Clinical Evaluation of a Real-Time PCR Assay for <i>Bordetella</i> <i>pertussis</i> T.S. Uphoff	ID67.	A Two-Step RT-LAMP Provides Improved Sensitivity for Point of Care Detection of Arboviruses J. Benzine	
ID58.	A Novel Approach for Sensitive Detection of ZIKV RNA in Whole Blood and Urine Samples Y. Chen	ID68.	Early Detection of Fungi and Yeast Using Species Specific Dual Amplification PCR (MycoDART) for Clinical Diagnosis. S.S. Sutton	
ID59.	Using Independent Run Controls to Monitor Relative Amplification Efficiency of a HAI Assay J.C. Yundt-Pacheco	ID69.	Detection of Group B Streptococcus Using the Simplexa GBS Direct Assay B. Martin	
ID60.	Extreme One-Step RT-PCR: Potential for Point-of-Care Viral Detection. J.A. Houskeeper	ID70. ID71.	WITHDRAWN	
ID61.	Performance Evaluation of Commercial Multianalyte Control Materials Calibrated Against the 1st WHO International Standards for Quantification of CMV, EBV and BKV in Transplant Patients <i>F. Sabato</i>	ID72.	Evaluation of the Abbott Real-Time RT-PCR EBV Assay for EBV Detection and Quantification <i>M. Yoon</i>	





ID73.	Concordance of <i>C. difficile</i>	INFO	RMATICS
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	Diagnostic Assay T. Hall	101.	An End-to-End Bioinformatics Pipeline Optimized for Somatic Variant Analysis Returns Clinically
ID74.	Detection of Resistance-Associated Substitutions in the Hepatitis C Viral Genome Using the Sentosa SQ Hepatitis C Virus Genotyping Next-		Actionable Results with a Rapid Turnaround Time <i>R. Kamal</i>
	Generation Sequencing Assay M. Campan	102.	Informatics to Illuminate Real- World Genetic Test Ordering Practices at a Large Academic
ID75.	Comparative Evaluation of the Omniplex-HPV and RFMP HPV PapilloTyper for the Detecting of		Institution V.A. Arboleda
	Human Papillomavirus Genotypes in Cervical Specimen Y. Yoon, Y. Choi	103.	Real-Time Thermodynamics and Local Variant Display for Primer Selection Z.L. Dwight
ID76.	A Clinical Performance Evaluation of QPLEX STI Detection Kit S. Cho	104.	Cloud-Based Somatic Pipeline Development and Validation for
ID77.	Comparison of the Hologic Panther Fusion Respiratory Assays to BioFire FilmArray Respiratory Panel for Detection of Respiratory Viruses in		Clinical Somatic Variant Detection, Including Large Indels, from Targeted Panels <i>A. Bolia</i>
	Children A. Lebe	105.	A Computational Framework for Large-Scale Analysis of TCRβ Immune Repertoire Sequencing
ID78.	Stability of Zika Virus and Recombinant Zika Controls H. Greiss		Data on Cloud-Based Infrastructure
ID79.	Evaluation of Cross Reactivity and Inhibitory Effects of Sexually Transmitted and Mosquito Borne	106.	A New Allele-Centric VCF File for Variants in ClinVar <i>M.J. Landrum</i>
	Pathogens on Zika Testing Using Aptima Zika Virus Assay on the Fully Automated Panther System <i>H. Greiss</i>	107.	Custom-Built Heuristic Approach to Variant Calling Tools Development <i>D. Thakral</i>
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ID81.	Performance of the Hologic GBS Assay on the Fully Automated Panther Fusion System <i>C. Hentzen</i>	109.	Repository of Quality Control and Metrics: A Web-Browser Based Application for Review and Approval of Clinical NGS Quality Metrics <i>L.M. Peterson</i>
ID82.	HPV Genotypes in Precancerous Lesions and Cervical Cancer of Korean Women <i>E. Lee</i>	110.	Improving Quality Control of Gene Amplification (GA) Detection in an Amplicon-Based Next-Generation Sequencing (NGS) Cancer Gene Panel by Implementing Gene-Level Segment Visualizations



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112.	Comparison of an Automated Approach to Mining the Genomic Literature Against COSMIC, a Manually Curated Database <i>M. Kiel</i>	122.	HLA on FHIR in the Cloud to Facilitate Entry in Electronic Medical Records <i>Y.S. Wang</i>
113.	Overlapping Variants Can Lead to Potential for Missed Calls in Custom Next Generation Sequencing Bioinformatics Pipeline <i>C. Vanderbilt</i>	123.	High-Throughput, Low-Pass Whole- Genome Sequencing (LP-WGS) Method for Single-Cell Copy- Number (CN) Profiling on Ampli1 Whole-Genome Amplification (WGA) Products for Illumina Platform
114.	Evaluation of Structural Variant Callers from a Clinical Perspective C.P. Johnson	124.	N. Manaresi Breaking the Turnaround Time
115.	Transmission of North American Association of Central Cancer Registries (NAACCR) Data Using the Lung Biomarker Template from the College of American Pathologists (CAP)		Barrier in Next Generation Sequencing-Based Clinical Mutation Profiling Using an Integrated Workflow and Informatics Approach <i>R. Ruiz-Cordero</i>
_	K.I. Hulkower	125.	Vetting Targeted Capture Probe Design with a Computational
116.	Homopolymer Compression Improves Reference-Free, Kmer Based Whole Genome Strain Comparison for Ion Torrent Data		Strategy Combining KmerSniper and BLAT <i>A.E. Kellogg</i>
117.	K.E. Simmon Bioinformatics Assay Design for Development of Multiplex PCR- Based Next Generation Sequencing Panels D. Wang	126.	A Novel Automated Approach to Identifying Disease-Gene-Variant Associations from the Medical Literature to Inform Gene Panel Design <i>M. Kiel</i>
118.	An Open Software Ecosystem for High Throughput Clinical Diagnostics <i>K.D. Doig</i>	127.	Creating Custom Gene Panels for Next-Generation Sequencing: Optimization of 5000 Gene Assays, Selection by Disease Research Area and Integrated Analysis for
l19.	NeGeSel – An All-Purpose Decision Support Tool for the Clinical		Variant Prioritization F. Hyland
	Nanagement of Next Generation Sequencing Assays in the Clinical Laboratory V. Williamson	128.	An Interlaboratory Assessment of Complex Variant Detection Using Multiplexed Positive Controls <i>S. Lincoln</i>
120.	Redesigning the Molecular Pathology Clinical Report for the Next-Generation Genomic Era: The MSKCC Experience with the MSK- IMPACT Assay A. Syed	129.	Estimating Mutation Load from Tumor Research Sample Using Targeted Next-Generation Sequencing Assay at ≥5% Allelic Frequency <i>R. Chaudhary</i>

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130.	Improvement of Indel Detection Power by Revising Default Parameter Settings in Vendor Supplied Next Generation Sequencing Analysis Software <i>W. Zhang</i>	I41. I42.	Engraftment Assessment by Next Generation Sequencing Using Single Nucleotide Polymorphism (SNP) Fingerprinting A. Mohanty ClonoTracker: A Computational
131.	Dynamic Levels of Evidence Tiering to Support Evolving Guidelines in Variant Assessment <i>X.S. Li</i>	172.	Framework and Clinical Tool for NGS-Based Clonality and MRD Analysis J. Nakitandwe
132.	Evaluation of the Open-Source Variant Caller Platypus in the Clinical Laboratory for Detecting Somatic Variants in Tumors <i>J. Reuther</i>	143.	Clinical Next Generation Sequencing Leveraging Unique Molecular Barcodes in Somatic Mutation Calling Absent a Matched-Normal <i>A. Bigdeli</i>
133.	Monitoring Germline SNPs to Control for Sample Cross- Contamination in the Ion AmpliSeq Cancer Hotspot Panel Next- Generation Sequencing Assay <i>P.A. Kenny</i>	144.	Evaluation of Copy Number Variation Detection Methods for Amplicon Sequencing Assays A. Bigdeli
134.	Breaking the NGS Noise Barrier to Accurately Detect Variants Below 1% Allele Frequency S.K. Sandhu	145.	GIMP: Genomic <i>In-silico</i> Mutator Program for Bioinformatics Validation of Clinical Next Generation Sequencing Assays <i>I. Mujacic</i>
I35. I36.	Genome in a Bottle: You've Sequenced a Genome, How Well Did You Do? <i>J.M. Zook</i> Rapid RNASeq: Rapid and Hugely	146.	Discrepancies between the Human Reference Genome (GRCh37) and Transcriptome (RefSeq) Complicate Variant Detection and Interpretation for Clinical Exome
150.	Scalable Fusion Gene Detection in the Cloud		and Genome Sequencing B. Yoo
137.	S. Newman Building the Enterprise Omics Repository for an Integrated Healthcare System G.B. Christensen	147.	The Quality Sequencing Metric (QSM) a Concise, Transparent Notation of NGS Data Quality for Clinical Testing <i>S. Yost</i>
138.	Descriptive Analytics Decision Support for Clinical Genomics E. Dominguez Meneses	148.	+STAR-SEQR: Accurate Detection and Quantification of RNA Fusions Using NGS Data J.S. Jasper
139.	Analysis of Therapy and Trial Recommendations Based on Gene Panel Size O.G. Miller	149.	Pediatric Gut Microbiome Characterization as a Companion Diagnostic in the Clinical Evaluation of Gastrointestinal Symptoms <i>R. Luna</i>
140.	Automated Cancer Risk Scoring Using FHIR Genomics Profiles and Secure Web Services <i>M. Harney</i>	150.	Identification of Distinctive Cell Signaling Patterns in Renal Cell Carcinoma Gene Expression TCGA Data Sets <i>K. Volyanskyy</i>



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151.	Proficiency Testing for Next- Generation Sequencing: Multi- Institutional <i>in-silico</i> FASTQ File Exchange Ensures Robust and Reproducible Bioinformatics Workflows for Reporting Complex Mutations <i>T. Schneider</i>
152.	Analysis of Individual Genes Identifies the Impact of Physiological Functions on AlloMap Gene Expression Profiling <i>R.N. Woodward</i>
153.	Genotype Matching of Serially Collected Clinical Samples Using Next Generation Sequencing Can Identify Sample Handling Errors <i>M. Grskovic</i>
154.	Using Replication to Break the NGS Noise Floor for Liquid Biopsy Variant Detection <i>C. Ionescu-Zanetti</i>
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OTH02.	Good or Bad Sequencing Data? Setting a Benchmark for the Quality of Diagnostic NGS in the Lab <i>W. Gutowska-Ding</i>
ОТН03.	Liquid Biopsy Based Monitoring of PD-L1 Expression in Non-Small Cell Lung Cancer (NSCLC) Patients for Immunotherapy G. Singh
OTH04.	Improved Polymer Enhanced Detection of Nucleic and Amino Acid Targets <i>J. Klonoski</i>
OTH05.	A NGS Library Preparation Training Module Facilitating Rapid Orientation and Productivity of New Employees in a Clinical NGS

OTH06.	Interactive Online Lymphoma
01100.	Unknown Conference: An Instructive Platform for Ordering Flow Cytometry and Molecular Studies S.E. Harley
ОТН07.	Long QT Syndrome: Integrating Genetic Testing into a Diagnostic Work Flow: A Process to Identify Opportunities and Gaps <i>E.R. Lockhart</i>
OTH08.	The Northern New England Genomics Consortium <i>N. Sidiropoulos</i>
ОТН09.	Time-Resource Analysis for Right-Sizing an NGS Laboratory: Exercising Restraint, Building Responsibly J.R. Milano
OTH10.	Characterization of BCR-ABL Laboratory Ordering for Quality Improvement <i>W. Zheng</i>
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	Improvement in Diagnostic Laboratory Performance by Participation in External Quality Assessment for Molecular Pathology: Lessons Learned and the Need for Continued Quality Improvement
ST01.	Improvement in Diagnostic Laboratory Performance by Participation in External Quality Assessment for Molecular Pathology: Lessons Learned and the Need for Continued Quality Improvement <i>M.H. Cheetham</i> <i>APC</i> and <i>KRAS</i> Genetic Variants Associated with Colorectal Cancer Histology Grade and Tumor Staging
ST01. ST02.	Improvement in Diagnostic Laboratory Performance by Participation in External Quality Assessment for Molecular Pathology: Lessons Learned and the Need for Continued Quality Improvement <i>M.H. Cheetham</i> <i>APC</i> and <i>KRAS</i> Genetic Variants Associated with Colorectal Cancer Histology Grade and Tumor Staging <i>W. Zhang</i>



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ST07.	A Verification Study of the GeneReader NGS System in a Routine Laboratory Setting		Small Cell Lung Cancer (NSCLC) W. Mahmud	
ST08.	A. Boesl Detection of <i>MLH1</i> Promoter Methylation by MassARRAY MALDI- TOF <i>A.A. Hall</i>	ST17.	Comparing Pyrosequencing and MALDI-TOF Mass Spectrometry to Methylation-Specific qPCR for Quantifying MGMT Promoter Methylation <i>R.L. Margraf</i>	
ST09.	Molecular and Clinicopathologic Features Associated with PD-L1 Expression in Lung Adenocarcinoma <i>S. Yang</i>	ST18.	Implementation of Rapid Blood- Based Mutation Testing for Patients with Lung Cancer <i>T.A. Boyle</i>	
ST10.	Evaluation of NGS Based Methods to Detect the Recurrent Gene Arrangements in Lung Cancer <i>A. Tilak</i>	ST19.	A Comparison of Mutation Frequencies Observed in Non- Small Cell Lung Cancer (NSCLC) Patients by Two Different Methods: SNaPshot and Polymerase Chain Reaction (PCR) Versus Next-	
ST11.	Assessment of UltraSEEK Colon Cancer Panel for Detection of Low Frequency Somatic Mutations in Blood	ST20.	Generation Sequencing (NGS) <i>M. Goudie</i> Comparison of the Clinical Utility of	
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ST13.	Performance Comparison of Two AR-V7 Detection Methods Confirms That Unexpected Responses to Abiraterone/Enzalutamide in AR-V7 Positive Patients are Not Due to	ST21.	Development and Evaluation of a Pan-Sarcoma Fusion Gene Detection Assay Using the NanoString nCounter Platform <i>K.T. Chang</i>	
ST14.	Assay Differences C. Bernemann Spectrum of Mutations in	ST22.	Genome-Wide Copy Number Variation and Targeted Next- Generation Sequencing Studies of	
5114.	Metastatic Chondrosarcomas Identified by Clinical Targeted Next-		Merkel Cell Carcinoma M. Carter	
	Generation Sequencing P.J. Lee	ST23.	Study of TMPRSS2-ERG Molecular Translocation in Prostate Cancer and its Correlation with Clinical and	
ST15.	Intratumoral Heterogeneity is the Single Source of Assay Variability During Laboratory Verification of		Histopathological Parameters S. Desai	
	the Prosigna Assay A. Nelson	ST24.	A Rare Case of HER2 Amplified Invasive Ductal Breast Carcinoma with Pericentric Deletion of Chromosome 17 <i>B.S. Karir</i>	

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ST25.	Biallelic TP53 Gain of Function Mutations in Rapid Progressing Solid Tumors and Correlating Immunohistochemistry <i>C.M. Sande</i>
ST26.	1p Deletion, The Most Common Subtype of Leiomyomas Encountered in NIPT? <i>M. Van Ness</i>
ST27.	A Novel Non-Invasive Bladder Cancer Recurrence Surveillance Test Using Urine Sample <i>P. Piatti</i>
ST28.	Ultra-Sensitive Tag Sequencing for Detection of Low Level Somatic Alterations in Plasma Cell Free DNA of Metastatic Colorectal Tumors on Ion S5XL Platform <i>M. Mehrotra</i>
ST29.	Effect of Blood Collection Tubes on Circulating Tumor DNA (ctDNA) Yield and Specificity <i>D. Murray</i>
ST30.	Successful Lung Cancer EGFR Sequencing from DNA Extracted from TTF-1 Immunohistochemistry Slides: A New Means to Extend Insufficient Tissue <i>G. Deftereos</i>
ST31.	Testing for Segmental Chromosomal Aberrations of Multiple Genes Using Multiplex Ligation-Dependent Probe Amplification (MLPA) Technique in Children with Neuroblastoma. <i>M. Ramadwar</i>
ST32.	Multiple Mutations in <i>TP53</i> : Tumor-Specific Patterns and Their Implications for Breast Cancer Pathogenesis and Variant Annotation <i>J. Coleman</i>
ST33.	Low Cost Liquid Biopsy Combining Hotspot Mutant DNA Enrichment with Cost Effective Duplex Sequencing <i>D. Broemeling</i>
ST34.	Anaplastic Lymphoma Kinase (<i>ALK</i>) Mutation Testing for Pediatric Neuroblastic Tumors: A Single Institution Experience <i>T. Qdaisat</i>

ST35.	EGFR Amplification as a Biomarker of Shorter Overall Survival in Grade III Gliomas <i>T. Bale</i>
ST36.	Papillary Renal Cell Carcinoma Associated with Bi-Allelic SDHA Mutations <i>C.R. McEvoy</i>
ST37.	Molecular Profiling with ALK, ROS1 and MET Genes FISH Panel in Non-Small Cell Lung Cancers: Indian Tertiary Cancer Institutional Experience O.A. Shetty
ST38.	Real Time PCR Assessment of Actionable Mutations in Non-Small Cell Lung Cancer A. Atkinson
ST39.	Integrated Genomic Profiling in Pediatric Solid Tumors: An Institutional Experience <i>L.F. Surrey</i>
ST40.	Factors that Predict the Success of RNA Seq Analysis on Solid and Hematologic Tumor Specimens <i>R.N. Wehrs</i>
ST41.	HPV Genotyping of Solid Tumors Using Real-Time PCR and Multi- Color Melt Curve AnalysisHPV Genotyping of Solid Tumors Using Real-Time PCR and Multi-Color Melt Curve Analysis A. Atkinson
ST42.	Validation of a Low DNA Input Hotspot Solid Tumor Assay on the Agena Bioscience MassARRAY System Utilizing Reference Standards and FFPE-Derived Clinical Samples <i>T. Neuwerth</i>
ST43.	Validation of an Anchored Multiplex PCR-Based Next Generation Sequencing Assay for the Detection of <i>MET</i> Exon 14 Skipping <i>K.D. Davies</i>
ST44.	<i>TERT</i> Promoter Mutation Status in Morphological Variants of Urothelial Carcinoma <i>D. Pradhan</i>



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ST46.	Targeted Mutational Analysis of Predictive and Prognostic Biomarkers in Colorectal Carcinoma <i>A.M. Olofson</i>	ST55.	Early Evaluation Site Experience with a Liquid Biopsy Kit Designed for Next Generation Sequencing of Circulating Tumor DNA S. Gunn
ST47.	Evaluation of Targeted Next Generation Sequencing of Circulating Cell-Free Tumor DNA for Clinical Diagnosis Using Archer Reveal ctDNA Assay <i>A.A. Stence</i>	ST56.	Clinical Utility of Large Scale Genomic Sequencing of Solid Tumors at a Large Academic Medical Center <i>N.A. Brown</i>
ST48.	Cell Free DNA in Patients with Pancreatic Adenocarcinoma: Evaluation of a Commercial Assay and Clinicopathologic Correlations <i>T. Theparee</i>	ST57.	Epi proColon, Septin 9 Gene Methylation Detection Assay as a Screening Tool for Colorectal Cancer L. Cai
ST49.	Improved Detection of Low Abundance Somatic Mutations of <i>KRAS</i> , <i>BRAF</i> , <i>NRAS</i> and <i>PIK3CA</i> in Melanoma Using iPLEX HS, a New Highly Sensitive Assay for	ST58.	Application of the GeneReader NGS System in Testing of Actionable Mutations in Tumor and Blood Samples <i>C. Mayo de las Casas</i>
CTEO	MassARRAY B.C. Sutton	ST59.	Rare <i>BRAF</i> Inactivating Mutation G466E and Literature Review <i>M. Kruzel</i>
ST50.	Low Level METex14 Skipping Is Observed at Low Frequencies in Patients with Solid Tumors from the NCI-MATCH Clinical Trial V. Datta	ST60.	lon Torrent Next Generation Sequencing: Detect 0.1% Low Frequency Somatic Variants and Copy Number Variations Simultaneously in Cell-Free DNA
ST51. ST52.	Assessing Sensitivity of NGS RNA Fusion Assays Using a Multiplexed and Well Characterized Linearity Panel C. Huang Clinical Cancer Whole Exome	ST61.	Y. Li Investigation of Mutational Burden in Urothelial Tumors Using a Targeted NGS Panel W. Zhang
5152.	and Transcriptome Sequencing of Pediatric Tumors at Columbia University Medical Center: Laboratory Perspective at Three Years	ST62.	Integrated Molecular Diagnostic Call Criteria for <i>MET</i> Exon 14 Skipping in Lung Cancer <i>R.J. Schmidt</i>
ST53.	S.J. Hsiao Pre-Designed Gene Content Enables Rapid Deployment of High- Quality Customized Enrichment Panels A.J. Barry	ST63.	Gene Expression Profiling of Traditional Immunohistochemical Tumor Biomarkers Using Nuclease Protection Coupled with Targeted Next-Generation Sequencing <i>M. Reinholz</i>

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ST64.	Spectrum of Variants Detected In a Large Cohort of Lung Adenocarcinomas at New York- Presbyterian Hospital <i>G. Ramrattan</i>
ST65.	Development of a Targeted NGS Cancer Gene Panel Using Multiplex PCR-Based Enrichment in an Integrated Fluidic Circuit <i>H. Gong</i>
ST66.	Assessment of Tumor Mutational Burden and Microsatellite Instability with Illumina's TruSight Tumor 170 Panel S. Zhang
ST67.	Mutational Spectrum in a Multi-Gene Panel of Germline and Somatic Ovarian Cancer in Singapore S. Ho
ST68.	A Droplet Digital PCR Assay for Detection of Methylated BCAT1 and IKZF1 in Circulating Tumor DNA <i>N. Boulter</i>
ST69.	Validation of CD274/PD-L1 FISH as a Predictive Biomarker for the Use of Immune Check Point Therapies in Undifferentiated Malignancies <i>K. Devereaux</i>
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ST71.	Molecular Characterization of a Series of Solitary Fibrous Tumors, Tested for NATB2-STAT6 Fusion Transcripts Using Reverse Transcriptase(RT)–Polymerase Chain Reaction(PCR) Technique: an Indian Experience <i>B. Rekhi</i>
ST72.	Prospective Analysis of the Clinical Impact of Expanded Genomic Tumor Testing on Management and Outcomes of Adult Oncology Patients at a Large Academic Medical Center A. Sireci

ST73.	RNA Sequencing Using Non-Cell Block Cytology Slides and FFPE Specimens Augments a DNA-Based Next Generation Sequencing Panel for Non-Small Cell Lung Cancer K.J. Hampel
ST74.	The Importance of Tumor-Normal Sequencing For Accurate Somatic Variant Determination in Genomic Cancer Testing <i>T. McDaniel</i>
ST75.	Added Value of Non-Cell Block Cytology Slides Compared to Formalin-Fixed Paraffin-Embedded (FFPE) Specimens for Targeted Genomic Profiling of Solid Tumors K. Hampel
ST76.	The Assessment by Next- Generation Sequencing of FFPE Derived Tumor DNA Using an Ovarian Cancer and a Custom Solid Tumor Hybridisation-Based Enrichment Panel Approach J. Chan
ST77.	A Comparison of EGFR Mutation Detection between Targeted Next-Generation Sequencing and Real-Time PCR Assay in Non-Small Cell Lung Cancer Y. Cheng
ST78.	Analysis of Active Oncogenic Signal Transduction Pathways in Ovarian Cancer <i>P.v. Wiel</i>
ST79.	Circulating Cell Free DNA (cfDNA) Isolated and Amplified from the Plasma of Pancreatic Cancer Patients as Reference Material for ctDNA Assays Y. Konigshofer
ST80.	Performance Comparison of Commercially Available Gene Fusion Next Generation Sequencing Panels <i>K.E. Bartow</i>
ST81.	Tumor in Normal or Normal in Tumor: What to Do When Somatic Mutations Are Detected in "Normal" Germline Control Used for NGS- Based Targeted Somatic Mutation Testing A. Yemelyanova



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5105.	Fusions Detected by Targeted Next Generation Sequencing and Their Impact on Clinical Management V.A. Paulson	ST94.	An Integrated Genomic and Proteomic Analysis of Human Tumors Enables Epitope Prediction for Cancer Immunotherapy <i>M. Davis</i>
ST84.	Head to Head Comparison of Archer VariantPlex/FusionPlex Solid Tumor and the Illumina TruSight Tumor 170 Assays O. Rouhi	ST95.	Development of Real-Time PCR Assay for Relative Expression of Total EGFR mRNA and Detection of EGFRvIII mRNA in Glioblastoma Multiforme Tumors
ST85.	Use of Synthetic Mutation Standards to Bolster Validation		R. Kular
	of DNA Based NGS Panels for Detection of Translocation and Large Indels <i>P.M. Rindle</i>	ST96.	Validation of a Single-Gene Next- Generation Sequencing Assay for TP53 Mutation Detection in Solid Tumor FFPE Samples in CLIA Laboratory Using Illumina MiSeq
ST86.	Characterization of Copy Number Alterations in Circulating Tumor		B.A. Barkoh
	Cells from Metastatic Prostate Cancers Using a Novel Enrichment Platform and Genome Wide Next- Generation Sequencing <i>G. Morrison</i>	ST97.	Molecular Profiling of Gallbladder Cancer Tumors of New Mexico Populations <i>R. Gullapalli</i>
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	V. Avadhani	ST100.	Utilizing a Comprehensive Next-
ST89.	Performance Evaluation of the Ion Torrent S5 XL for Targeted Next- Generation Sequencing (NGS) for Clinical Oncology <i>F. Sabato</i>		Generation Sequencing Panel to Improve Clinical Outcomes in Patients with Non-Small Cell Lung Cancer S. Springborn
ST90.	Analysis of Immune Response Gene Expression and Tumor Associated Macrophages in Triple Negative Breast Carcinoma K. Walker	ST101.	MET Amplification Predicts Primary Resistance to EGFR-TKIs in Advanced Non–Small Cell Lung Cancer Patients with Sensitive EGFR Mutation L. Fang
ST91.	Specimen Identification and Tracking from DNA Extraction to NGS Results Through the Addition of Barcoded Synthetic DNA <i>R. Bastien</i>	ST102.	Validation of a Clinical Targeted CNS Next Generation Sequencing Panel for Detection of SNPs, Indels and 1p/19q Co-Deletion <i>S. Rosati</i>



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ST105.	Correlation Between PD-L1 22C3 Expression and Oncogene Driver Mutations in <i>EGFR</i> , <i>ALK</i> , <i>KRAS</i> and BRAF in Non-Small Cell Lung Cancer <i>C. Nicka</i>	ST114.	Identification of Germline Variants in Tumor Genomic Sequencing Assays: Usefulness of Variant Allele Fraction and Population Variant Databases <i>N.D. Montgomery</i>
ST106.	Development of a Comprehensive Solid Tumor Next-Generation Sequencing Assay to Support Both Clinical Diagnostics and Immunotherapy Cancer Research in	ST115.	An Efficient and Ultrasensitive Next-Generation Sequencing Solution for Profiling Circulating Tumor DNA <i>B.C. Haynes</i>
ST107.	a Large Healthcare System J. Welle Improved Detection of Low Abundance Somatic Mutations	ST116.	Validation of Whole Exome and Whole Transcriptome Sequencing of FFPE Derivatives on Illumina Platforms S.A. Shurtleff
	of KRAS, BRAF, NRAS and PIK3CA in Melanoma using iPLEX HS, a New Highly Sensitive Assay for MassARRAY B.C. Sutton	ST117.	Increased Incidence of PIK3CA Variants in Triple Negative Breast Carcinomas with Apocrine Features Identified by Targeted NGS <i>J.E. Baum</i>
ST108.	Routine Use of the FusionPlex Solid Tumor Panel in Identifying Clinically Actionable Gene Rearrangements in Lung Adenocarcinomas <i>C. Nicka</i>	ST118.	Molecular Analysis of Lymphoepithelioma-Like carcinoma (LELCA) of the Thymus S. Rosati
ST109.	A Modular Next-Generation Sequencing Technology that Couples the Detection of RNA Structural Variants and DNA Mutations in Lung Cancer	ST119.	Clinical Utility of Fusion Genes in Solid Tumors - A Single Center Experience <i>P. Selvam</i>
ST110.	R. Blidner in silico Long-Read Sequencing from FFPE Solid Tumor Tissue for	ST120.	Using Liquid Biopsies for Low Frequency Variant Detection and Tissue-of-Origin Exploration <i>A. McUsic</i>
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ST111.	Evaluation of a Custom-Design Targeted Next-Generation Sequencing (NGS) Panel for Clinical Screening of Mutations, Copy Number Alterations, and Gene Fusions in Primary CNS Tumors <i>L. Xi</i>	ST122.	<i>S.F. Sarabia</i> Enhanced Genome-Wide Copy Number Variation Detection Using a SNP-Focused Targeted NGS Panel for Tumor Analysis <i>J. Wang</i>



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ST123.	BRCA1 and BRCA2 Somatic Mutational Spectrum of Metastatic Cancer Revealed from Prospective Clinical Sequencing of 16,000 Patients <i>K. Nafa</i>	ST132.	Performance of Traditional Ampliseq Based NGS Panel for Genotyping of Circulating Cell Free DNA from plasma of Metastatic Colorectal Cancer Patients <i>X. Shi</i>
ST124.	A Study of Ovarian High Grade Serous Carcinoma with IHC p53 Positive and Negative Patterns by Targeted NGS <i>S. Zomorrodian</i>	ST133.	Evaluation of a 170 Gene NGS Panel for the Detection of RNA and DNA Based Variants in FFPE Solid Tumor Samples <i>F. De Abreu</i>
ST125.	Analytic Validation and Application of Comprehensive Genomic Testing for Somatic Mutations and Microsatellite Instability in Rare Cancers <i>M.R. Wing</i>	ST134.	Analytical Validation of a Circulating Tumor Methylated-DNA Assay for Detection of Colorectal Cancer Recurrence in a CLIA Licensed Clinical Laboratory J.P. Alsobrook
ST126.	Concordance of Genomic Alterations by Next Generation Sequencing (NGS) in Tumor Tissue versus Cell-Free DNA in Stage I-IV NSCLC Y. Jiang	ST135.	Analytical and Clinical Validation of a Liquid Biopsy NGS Assay for the Detection of SNVs, Indels, Copy Number Variations and Gene Fusions in Patients with Non-Small Cell Lung Adenocarcinomas <i>C. Raymond</i>
ST127.	Digital Spatial Profiling Platform Allows for Spatially-Resolved, Multiplexed Measurement of Protein and RNA Distribution and Abundance in FFPE Tissue Sections <i>C. Merritt</i>	ST136.	Genes with Clonal Mutations and Their Pathway Associations for Breast Cancer Subtypes Y. Cheung
ST128.	Discordance Among Biomarkers for Anti-PD1 Therapy Response: Tumor Mutational Burden and Anti-PD-L1 Staining P.R. Hess	ST137.	Detection of Tumor Mutations with Cell-Free DNA in Plasma by Targeted Next Generation Sequencing J. Cheng
ST129.	Beyond PD-L1: Challenges in Implementing Tumor Mutational Burden (TMB) to Predict Patient Response to Immuno-Oncology (IO) Therapies	ST138.	"Unburdening" Variant Review for High Tumor Mutation Burden (TMB) Cases in a Clinical Next-Generation Sequencing (NGS) Assay <i>C.R. Orr</i>
	P.M. Krein	ST139.	Library Complexity Estimation from Amplicon-Enriched, Low Input DNA
ST130.	Evaluation of Seraseq FFPE Tumor Fusion RNA Reference Material for Use in Routine Clinical NGS Testing <i>F.B. De Abreu</i>	_	Samples using Unique Molecular Identifiers <i>E.J. Duncavage</i>
ST131.	Evaluation of the Pillar NGS SLIMamp Cancer Hotspot Panel <i>F.B. De Abreu</i>	ST140.	SNP Chromosomal Microarray as a Diagnostic Aid in the Diagnosis of a Rare Renal Neoplasm <i>R.A. Henne</i>
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ST142.	PRKACA Amplification as Novel Genomic Driver in Fibrolamellar Carcinoma <i>R. Graham</i>
ST143.	Comprehensive Detection of BRCA1/2 Pathogenic Variants by Anchored Multiplex PCR and Next- Generation Sequencing <i>A.T. Garnett</i>
ST144.	Detection of MET Exon 14 Skipping in Non-Small Cell Lung Cancer (NSCLC) via RNA Anchored Multiplexed PCR and DNA Next- Generation Sequencing <i>C. Paolillo</i>
ST145.	Distinct Genome Abnormalities that Distinguish Enchondroma from Chondrosarcoma: Clinical Utility of SNP Cytogenomic Microarray Analysis Y. Liu
ST146.	Molecular Progression of Superficial Papillary Urothelial Carcinoma of the Renal Pelvis to a Metastatic Lesion <i>M. Pepper</i>
ST147.	Comprehensive Detection of MET Mutations, Including Novel Gene Fusions, by Anchored Multiplex PCR and Next-Generation Sequencing J. Haimes
ST148.	Clinicopathological and Molecular Characterization of FGFR3/TACC3 Gliomas S. El Hallani
ST149.	OncoKids: A Comprehensive NGS Panel for the Full Spectrum of Pediatric Malignancies <i>M. Hiemenz</i>
ST150.	Comparison of the APTIMA Assay and mRNA In-Situ Hybridization for Detection of Human Papilloma Virus (HPV) in Oropharyngeal Carcinomas <i>S.S. Talwalkar</i>
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ТТ02.	Comparison of Bone Marrow Biopsies with Marrow-Derived Cell Suspensions for Next-Generation Genomic Sequencing <i>R.M. Rattray</i>
ТТ03.	Comparison of Exome Sequencing Analytical Performance Between Cell Lines, Peripheral Blood and Buccal Swab as Tissue Types L. Johnstone
TT04.	Evaluation of Two Methods for Generating Circulating Cell-Free DNA Reference Materials <i>L. Liu</i>
TT05.	High Speed Melting Analysis for Microfluidic Genotyping <i>R.J. Pryor</i>
TT06.	Highly Multiplexed FISH for <i>in situ</i> Genomics <i>M.L. Onozato</i>
TT07.	A Robust and Reproducible ctDNA Assay Utilizing the Illumina TruSight Tumor 170 Panel A.C. Jager
ТТ08.	Next Generation Sequencing Tissue Workflow Offers a Limited ctDNA Evaluation with Minimal Modification <i>M.P. Greenwood</i>
TT09.	Multiplexing Method for Significantly Increasing the Bandwidth of qPCR Instrumentation A. Rajagopal
TT10.	Transition of a LDT to the Fully Automated Cobas 6800/8800 Systems Using the Cobas Omni Utility Channel <i>R. Hein</i>
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TT14.	Influence of Blood Collection Tube Types on cfDNA Yields and Quantification Comparison <i>S. Katz</i>	TT25.	Implementation of Laboratory Developed Tests on the NeuMoDx Molecular System <i>M. Mastronardi</i>
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	in PIK3CA-Related Segmental Overgrowth Disorders Using Targeted Sanger Sequencing and a Next-Generation Sequencing Cancer Hotspot Panel <i>K.L. Sumner</i>	TT28.	Creation of a Custom Indexing Strategy and Cross-Reactivity Testing in a Clinical Next Generation Sequencing Core Laboratory <i>M.A. Dina</i>
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TT18.	Performance Evaluation of Collection/Stabilization/Purification Systems for Liquid Biopsy Cancer Biomarker Applications D. Groelz	TT30.	Validation Study of Clinically Relevant AML Variants Using Multiple Detection Methods for Next-Generation Sequencing on Illumina MiniSeq
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TT34.	Novel Predictive Biomarker for Monitoring Adverse Reactions to Radiation Therapy J. Du
TT35.	Reliable Interpretation of NGS Data Using Well-Established, Highly Multiplexed Reference Materials <i>C. Hendrickson</i>
TT36.	Discovering Novel FFPE MicroRNA Biomarkers with a Highly- controlled qPCR Workflow <i>H. Cheng</i>
TT37.	A Novel Non-Control Based Homologous Recombination Deficiency (HRD) Algorithm for Predicting PARP Inhibitor Response in Breast and Ovarian Cancer Patients Z. Liu
TT38.	An Improved Method for RNA Extraction from FFPE Tissue Samples Yields Less Degraded RNA for Gene Expression Analysis <i>P. Chen</i>
TT39.	A Suite of Information Technology Tools to Manage the Production, Interpretation, and Communication of Clinical Genomic Test Results in the Precision Oncology Era D.L. Cooper
TT40.	A Novel Circulating Tumor DNA (ctDNA) Reference Material Compared on Next Generation Sequencing (NGS) to Digital PCR (dPCR) Assays <i>F.L. Tomson</i>
TT41.	A Highly Efficient and Reliable Transcriptome Profiling Method for Single-Cell or Low Input RNA Y. Bei
TT42.	Comparison of Manual and Automated Surepath Pre-Analytic Preparation for Roche Cobas 4800 HPV Testing <i>R.D. Byrd</i>

TT43.	Automating Low Input Library Preparation for Next Generation Sequencing J.A. Raney
TT44.	Improved Methods for Next Generation Sequencing Library Cleanup and Size Selection <i>C. Knox</i>
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TT46.	Customizable All-In-One Cancer Panels and Cnv/Tl Algorithms to Simultaneously Detect Mutation, Gene Copy Number Variation and DNA Rearrangement by Targeted Next-Generation Sequencing <i>H. Tao</i>
TT47.	Making the Most of Small Samples: Optimization of Tissue Allocation for Clinical Care and Research <i>A. Church</i>
TT48.	Validation of a Next-Generation Sequencing-Based Assay to Detect Extended RAS Mutations in FFPE Samples for Identification of Metastatic Colorectal Cancer Patients Eligible for Treatment with Panitumumab <i>N. Udar</i>
TT49.	Development and Analytic Validation of an Automated Circulating RNA Extraction System Using a Laboratory Validated ddPCR Test Process <i>L. Jackson</i>
ТТ50.	Visual Adequacy Scale: A Method to Optimize Adequacy Assessment of Non-Cell Block Cytology Samples for Successful Downstream Molecular Diagnostics J. Armstrong
TT51.	Evaluation of Intraoperative Sampling for Genomic Analysis of Central Nervous System (CNS) Tumors by Next-Generation Sequencing (NGS). <i>R.T. Sussman</i>





TT52.	Plasma DNA Extraction Optimization for Cell Free DNA Sequencing <i>C.J. Trennepohl</i>	TT61.	Multiplexed High-Definition PCR: A Novel Chemistry and Signal Detection Approach Applied to Respiratory Virus Panel Testing as a Proof of Concept
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TT54.	Accurate Detection of Ultra-Low Frequency Mutations Using a Highly Efficient Dual-Stranded		Preparation Method K.R. Duggan
	Molecular Tagging Strategy J. Wang	TT64.	Targeted Next Generation Sequencing: Process Improvements Resulting in Reduced Turnaround
TT55.	Lyophilization-compatible qPCR mix for low-copy number target detection		Time E.P. Garcia
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TT56.	Enhancing Signal-to-Noise in Next Generation Sequencing Detection of Fusion Oncogenes with CRISPR- Cas9		PCR and High-Resolution Melting Analysis <i>L. Zhou</i>
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	Throughput Sample Preparation Workflows A. Cheng	TT68.	Cold Fusion: A Rapid RNAseq Paradigm Using Nanopore Sequencing <i>W. Jeck</i>
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TT73.	A Method to Improve NGS Library Loading Consistency Z. Zheng
TT74.	Analytical Validation of a Digital Molecular Analysis Assay to Detect an Inhibitor-Sensitive Alternative ALK Transcript (ALK-ATI) in Formalin-Fixed, Paraffin-Embedded Melanoma <i>R.A. Jackson</i>
TT75.	How to Evaluate the Sensitivity of a NGS RNA Fusion Gene Assay D. Qin
ΤΤ76.	Engineering of Isogenic Cell Lines Using the CRISPR/Cas9 Technology and Precise Characterization of Low Allelic Frequency FFPE Cell Line Blocks for Use as Molecular Reference Standards <i>S. Saddar</i>
TT77.	A Strand-Specific, Low-Bias Library Preparation Method for Transcriptome Profiling of Low Input and Low Quality RNA <i>D.N. Rodriguez</i>
TT78.	Application of Roche Enzymes for Improved FFPE NGS Performance <i>M. Loyzer</i>
TT79.	High Sensitivity Sanger Sequencing for Minor Indel Detection and Characterization <i>H. Leong</i>

TT80.	In-depth Assessment Reveals Powerful Performance and Flexibility of AVENIO ctDNA Analysis Kits <i>A.F. Lovejoy</i>
TT81.	Linear Amplification Coupled Exponential (LACE) PCR: A Novel Approach to Improve the Performance of Molecular Barcoded Next-Generation Sequencing Technology S. Mallampati
TT82.	High Performance Detection of Cancer Mutations from Circulating DNA Using Single Color Digital PCR <i>B.T. Lau</i>
TT83.	The Binding and Nucleotide Incorporation Kinetics of DNA Polymerase <i>A.M. Zuiter</i>
TT84.	An Engineered DNA Ligase for Efficient Conversion of Input DNA during NGS Library Preparation <i>M. Miller</i>
TT85.	Comparison of Liquid Biopsy Blood Collection Tubes <i>C.D. Browne</i>
TT86.	An Efficient NGS Workflow for Liquid Biopsy Research Using a Comprehensive Assay Panel to Assess Cell-Free Total Nucleic Acid <i>R. Chien</i>
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TT92.	Successful Extraction of RNA from Archived Bone Marrow Aspirate Smears for Use in Targeted RNA Sequencing <i>T. Restrepo</i>		O. Sala-Torra



