Green Park Collaborative
A partnership for innovation and effectiveness

CAP ACCREDITATION STANDARDS AND PROFICIENCY TESTING FOR DIAGNOSTIC NEXT GENERATION SEQUENCING

Thursday, March 23, 2017
INTRODUCTION

Donna A. Messner, PhD
Senior Vice President
Center for Medical Technology Policy
Program Director
Green Park Collaborative
PLEASE NOTE

- This call is being recorded

- All attendees will be MUTED upon entering the webinar

- Utilize ReadyTalk’s CHAT FEATURE (to the left of the screen) to communicate directly with the presenters and ask questions
GPC MDX METHODS & POLICY WORK

2013
• **PUBLISHED:** Evaluation of Clinical Validity and Utility of Actionable Molecular Diagnostic Tests in Adult Oncology EGD

2014
• **MEETING:** Multi-stakeholder meeting to discuss methods and standards for evaluation of the clinical utility of NGS

2015
• **PUBLISHED:** Initial Medical Policy and Model Coverage Guidelines for Clinical NGS in Oncology
• **WEBINAR:** Policies for NGS In Oncology, stakeholder perspectives on GPC Published Guidelines

2016
• **MEETING:** GPC Forum on New Genomic Technologies in Clinical Medicine
Karl V. Voelkerding, MD

Professor of Pathology
University of Utah
Medical Director for Genomics and Bioinformatics
ARUP Laboratories

voelkek@aruplab.com
Develop NGS Laboratory Accreditation Requirements

Develop NGS Proficiency Testing

Evolve to Meet Growing Diversity of NGS Applications
Guiding Principle – Find the Right Regulatory Balance

• Foster Innovation and Adoption of NGS Clinical Testing
  • Assure Patient Safety
CAP NGS Accreditation Requirements First Published in 2012
Revised Yearly as NGS Clinical Testing Has Advanced
Wet Bench Process
- Sample Handling
- Library Preparation
- Sequence Generation

FASTQ File

Bioinformatics “Dry Bench” Process
- Sequence Alignment to Reference
- Variant Identification
- Variant Annotation (eg CFTR p.Arg205Lys)

CAP Definition of a NGS Test
Wet Bench Process
- Sample Handling
- Library Preparation
- Sequence Generation

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FASTQ File

Annotated Variants

Data Interpretation and Reporting

Analytical Laboratory Processes

Medical Practice

CAP Definition of a NGS Test
Current CAP NGS Laboratory Accreditation Requirements - 2016

Primary/Referring Laboratory
- NGS Reference Lab Policy
- NGS Confirmatory Testing Policy
- NGS Sample Provenance Tracking

General
- Exception Log/Record
- Data Storage Local/Cloud
- Data Transfer Confidentiality

Wet Bench
- NGS Wet Bench Process Documentation
- NGS Wet Bench Process Validation
- Quality Management Plan
- Laboratory Records
- Monitoring of Upgrades

Bioinformatics
- NGS Bioinformatics Pipeline Documentation
- NGS Bioinformatics Pipeline Validation
- Quality Management Plan
- Pipeline Version Traceability
- Monitoring of Upgrades

Interpretation
- Sequence Variants Interpretation and Reporting
- Reporting of Incidental Genetic Findings
Example Format of a CAP Accreditation Requirement

MOL.36135 Bioinformatics Process/Pipeline - Updates

Phase I

The laboratory has a procedure for monitoring, recording, and implementing patch-releases, upgrades, and other updates to the bioinformatics pipeline.

NOTE: NGS bioinformatics pipelines are comprised of multiple components - open source or commercial software packages, additional scripts, and databases for managing content and aspects of analysis and reporting. Due to the ongoing evolution of the field, laboratories need to establish a procedure for regular monitoring of updates, patch-releases, and other upgrades for each component of the pipeline. Congruent with that procedure, the laboratory must demonstrate that acceptable performance specifications are met when a change to the bioinformatics pipeline is implemented. The extent of revalidation and/or confirmation is modification dependent. Revalidation/confirmation may cover all or a subset of steps in bioinformatics pipeline depending on the type of upgrade implemented (see MOL.36115). This procedure must designate specific monitoring intervals and address when such updates will be implemented.

Evidence of Compliance:
✓ Procedure for monitoring patch-releases, upgrades and updates AND
✓ Records of monitoring activities AND
✓ Records of revalidation/confirmation data including the type of upgrade, metrics, and quality control (QC) parameters monitored to assess analytical run performance AND
✓ Approval of revalidation/confirmation data by the laboratory director AND
✓ Dates of implementation
Current CAP NGS Laboratory Accreditation Requirements - 2016

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Interpretation
- Sequence Variants Interpretation and Reporting
- Reporting of Incidental Genetic Findings
Majority of Laboratories Perform NGS Testing In One Physical Primary Laboratory

- Wet Bench Process: Sequencing
- Bioinformatics Process
- Interpretation and Reporting

Single CLIA License
Some Laboratories Outsource Individual Process Steps

Primary Laboratory

Primary Lab Receives Patient Sample

Wet Bench Process Sequencing

Interpretation Reporting

Reference Laboratory

Outsource

Bioinformatics Process
Some Laboratories Outsource Individual Process Steps

“Distributive” Testing Model Under CLIA

Primary Laboratory

Reference Laboratory

Primary Lab Receives Patient Sample

Wet Bench Process
Sequencing

Outsource

Bioinformatics Process

Interpretation Reporting
Some Laboratories Outsource Individual Process Steps

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Reference Laboratory

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Interpretation
- Sequence Variants Interpretation and Reporting
- Reporting of Incidental Genetic Findings

Flow Chart Adapted from R Nagarajan
NGS Testing – Validation – CAP Requires an Integrated Approach

Wet Bench Process
- Sample Handling
- Library Preparation
- Sequence Generation

FASTQ File

Bioinformatics “Dry Bench” Process
- Sequence Alignment to Reference
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Annotated Variants

Data Interpretation and Reporting

Integrated Methods Based Validation
NGS Testing – Validation – CAP Requires an Integrated Approach

**Wet Bench Process**
- Sample Handling
- Library Preparation
- Sequence Generation

→ **FASTQ File**

**Bioinformatics “Dry Bench” Process**
- Sequence Alignment to Reference
- Variant Identification
- Variant Annotation (e.g., CFTR p.Arg205Lys)

→ **Annotated Variants**

**Data Interpretation and Reporting**

**Integrated Methods Based Validation**

**Validation Specimens Contain a Representative Spectrum of Variant Types**
**Test is Designed to Detect**
NGS Testing – Validation – CAP Requires an Integrated Approach

Wet Bench Process
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Annotated Variants

Data Interpretation and Reporting

Integrated Methods Based Validation

Validation Specimens Contain a Representative Spectrum of Variant Types
Test is Designed to Detect

Establish Assay Performance
NGS Test Validation – Choice of Specimens

Validation Specimens Contain a Representative Spectrum of Variant Types Test is Designed to Detect

For Gene Panels Include Specimens that Contain Common Mutations (e.g. Cancer Hot Spots, CFTR p.Phe508del)

Methods Based

Gene or Analyte Based

Hybrid

NEW

Additions to 2016 NGS Accreditation Requirements
Additions to 2016 NGS Accreditation Requirements

NGS Test Validation – Choice of Specimens

Validation Specimens Contain a Representative Spectrum of Variant Types Test is Designed to Detect

For Gene Panels Include Specimens that Contain Common Mutations (e.g. Cancer Hot Spots, CFTR p.Phe508del)

Add Extra Specimens that Contain Variants That are Technically Difficult to Detect

Methods Based

Hybrid

Gene or Analyte Based

NEW
Requiring Evidence for Genes in a NGS Test

The Genes in a NGS Test Analyzed and Interpreted Should Be Evidence Based

What is the Strength of Gene-Disease Relationship?
Additions to 2016 NGS Accreditation Requirements

Requiring Evidence for Genes in a NGS Test

ClinGen Initiative – Criteria for Gene Inclusion
https://clinicalgenome.org/knowledge-curation/gene-curation

Evidence Spectrum for Gene-Disease Association

None  Limited  Moderate  Definitive
Proposed Changes to 2017 NGS Accreditation Requirements

Addition of Topic Specific Requirements

Molecular Microbiology
- Methods Based Validation
- Metagenomics

Molecular Oncology
- Further Emphasize Validating Lower Limit of Detection
Addition of Topic Specific Requirements

Proposed Changes to 2017 NGS Accreditation Requirements

Next steps...

Molecular Genomics
- Causal Gene Identification Validation
- Exome and Genome Sequencing For Undiagnosed Disorders
Develop
NGS Proficiency Testing
The Clinical Laboratory Amendments of 1988 (CLIA)

Requires CLIA Certified Labs to Participate in Proficiency Testing (PT)
PT is an External Performance Indicator of Laboratory Quality

The College of American Pathologists (CAP)

Has Deemed Status Through the Centers for Medicare and Medicaid Services (CMS)
To Accredit Clinical Laboratories and Administer Proficiency Testing
Critical Challenge --- How to Provide Proficiency Testing For the Growing Diversity of Clinical NGS Applications

- Multi-Gene Diagnostics
  - Germline Variants
  - Inherited Disorders

- Exome
  - Germline Variants
  - Inherited Disorders

- Whole Genome
  - Germline Variants
  - Inherited Disorders

On the Horizon

- Somatic Variants
- Solid Tumors
- Hematologic Malignancies
Leverage Concept of Methods Based PT for NGS

Assess Laboratory’s Ability to Detect Spectrum of Germline or Somatic Variants In Clinically Relevant Genes

Reflects Primary Analytical Goal of Panel, Exome and Genome NGS Testing
Leverage Concept of Methods Based PT for NGS

Assess Laboratory’s Ability to Detect Spectrum of Germline or Somatic Variants In Clinically Relevant Genes

Reflects Primary Analytical Goal of Panel, Exome and Genome NGS Testing

Auto-Inflammatory Syndromes
- Autism
- Cardiomyopathies
- Congenital Hearing Loss
- Glycosylation Disorders
- Hereditary Predisposition to Cancer
- Immune Deficiencies
- Intellectual Disability
- Mitochondrial Disorders
- Neuropathies
- Renal Disorders
- Retinopathies

NGS Panels
- 10-100s Genes Tested

CAP First NGS
PT Program
Germline Variant Detection
Development of NGS Methods Based PT Germline Variants

Source CAP Genome Sequence With Multiple Technologies

Select Germline Variants For PT

Conduct Pilot PT Volunteer Laboratories

Conduct 2015 Educational PT A and B Mailings

Launch Graded 2016 PT A and B Mailings

Generate Consensus Variants
Next-Generation Sequencing

Analytes/procedures in **bold** type are regulated for proficiency testing by the Centers for Medicare & Medicaid Services (CMS).

<table>
<thead>
<tr>
<th>Procedure</th>
<th>Program Code</th>
<th>Challenges/Shipment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Next-generation sequencing</td>
<td>NGS</td>
<td>1</td>
</tr>
</tbody>
</table>

**Program Information**
- One 10.0-μg extracted DNA specimen
- Methods-based challenge for germline variants for laboratories using gene panels, exome, and whole genome sequencing
- Results for this program must be submitted online through e-LAB Solutions Suite
- Two shipments per year

**Additional Information**
Laboratories will have the ability to test up to 200 preselected chromosomal positions within various genes; for a full list of genes in this program, please go to cap.org. Under the Laboratory Improvement tab, click on Catalog and Ordering Information. The list is located under the PT Order Supplements header.

200 Chromosomal Positions or Intervals
Chosen in Genes Involved in Inherited Disorders
Included Reference (Wild Type) Positions, SNVs and Indels
## Laboratory Enrollment in NGS MBPT Germline Surveys

<table>
<thead>
<tr>
<th>Participant Laboratory Data</th>
<th>2015 A Mailing</th>
<th>2015 B Mailing</th>
<th>2016 A Mailing</th>
<th>2016 B Mailing</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Labs Enrolled</td>
<td>139</td>
<td>160</td>
<td>130</td>
<td>142</td>
</tr>
<tr>
<td>Number of Labs Returning Results*</td>
<td>101 (73%)</td>
<td>143 (89%)</td>
<td>125 (91%)</td>
<td>128 (90%)</td>
</tr>
</tbody>
</table>

*Number and (Percentage) of Labs Returning Results At Time of Data Summarization*
## Assays Performed in NGS MBPT Germline Surveys

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Multi-Gene Panels</td>
<td>71</td>
<td>102</td>
<td>72</td>
<td>71</td>
</tr>
<tr>
<td>Exome</td>
<td>20</td>
<td>28</td>
<td>42</td>
<td>47</td>
</tr>
<tr>
<td>Whole Genome</td>
<td>5</td>
<td>7</td>
<td>5</td>
<td>6</td>
</tr>
</tbody>
</table>

*Multiple Responses per Laboratory Allowed
Not All Laboratories Responded
## Platform Usage in NGS MBPT Germline Surveys

<table>
<thead>
<tr>
<th>Platform</th>
<th>2016 A Mailing Responses from 115 Labs</th>
<th>2016 B Mailing Responses from 115 Labs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Illumina MiSeq</td>
<td>33</td>
<td>34</td>
</tr>
<tr>
<td>Illumina HiSeq 2500</td>
<td>37</td>
<td>35</td>
</tr>
<tr>
<td>Illumina NextSeq 500</td>
<td>22</td>
<td>24</td>
</tr>
<tr>
<td>Ion Torrent PGM</td>
<td>9</td>
<td>8</td>
</tr>
<tr>
<td>Illumina HiSeq 3000/4000</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>Ion Torrent Proton</td>
<td>6</td>
<td>5</td>
</tr>
<tr>
<td>Illumina HiSeq 2000</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Illumina MiSeqDx</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Ion Torrent S5/S5 XL</td>
<td>2</td>
<td>3</td>
</tr>
<tr>
<td>Illumina HiSeq X Five/Ten</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>Pacific Biosciences RS/RS II</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Roche 454 GS Junior/FLX+</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

*Multiple Responses per Laboratory Allowed
Not All Laboratories Responded
Preliminary Performance Data Summary
2016 NGS MBPT Germline Graded Surveys
Types of Chromosomal Positions in 2016 A and B Mailing Surveys

<table>
<thead>
<tr>
<th>Chromosomal Position Type</th>
<th>2016 A Mailing</th>
<th>2016 B Mailing</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reference</td>
<td>140 (1)*</td>
<td>90</td>
</tr>
<tr>
<td>Single Nucleotide Variant (SNV)</td>
<td>57 (7)</td>
<td>109 (1)</td>
</tr>
<tr>
<td>Insertion</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Deletion</td>
<td>2</td>
<td>1 (1)</td>
</tr>
</tbody>
</table>

(1)* Position is Non-Coding and Omitted from Data Analysis

Red Parentheses are Non-Graded Positions
Discordance Between Genomic and Transcript Reference Sequences
### Reference Position Analysis for 2016 A and B Mailing Surveys

<table>
<thead>
<tr>
<th></th>
<th>Number of Labs Analyzing Each of the Reference Positions</th>
<th>Range</th>
<th>Mean/Median</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>2016 A Mailing</strong></td>
<td>Number of Labs Analyzing Each of the <strong>139</strong> Graded Reference Positions Data from Table 1</td>
<td>Range 12-68</td>
<td>Mean 26, Median 24</td>
</tr>
<tr>
<td><strong>2016 B Mailing</strong></td>
<td>Number of Labs Analyzing Each of the <strong>90</strong> Graded Reference Positions Data from Table 1</td>
<td>Range 16-59</td>
<td>Mean 31, Median 26</td>
</tr>
</tbody>
</table>
## Reference Position Analysis for 2016 A and B Mailing Surveys

<table>
<thead>
<tr>
<th></th>
<th><strong>2016 A Mailing</strong></th>
<th><strong>2016 B Mailing</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>Analysis Responses for All 139 Graded Reference Positions Data from Table 1</td>
<td>% No Variant Detected</td>
<td>% Variant Detected</td>
</tr>
<tr>
<td></td>
<td>Mean 97.8%</td>
<td>Mean 1.5%</td>
</tr>
<tr>
<td></td>
<td>Median 100%</td>
<td>Median 0.0%</td>
</tr>
<tr>
<td></td>
<td>Range 81.8-100%</td>
<td>Range 0.0-9.5%</td>
</tr>
<tr>
<td>Analysis Responses for All 90 Graded Reference Positions Data from Table 1</td>
<td>% No Variant Detected</td>
<td>% Variant Detected</td>
</tr>
<tr>
<td></td>
<td>Mean 95.4%</td>
<td>Mean 0.0%</td>
</tr>
<tr>
<td></td>
<td>Median 95.8%</td>
<td>Median 0.0%</td>
</tr>
<tr>
<td></td>
<td>Range 80.0-98.3%</td>
<td>Range 0.0-0.0%</td>
</tr>
</tbody>
</table>

**Correct Response**
# Single Nucleotide Variant Analysis for 2016 A and B Mailing Surveys

## 2016 A Mailing

<table>
<thead>
<tr>
<th>Number of Labs Analyzing Each of the 50 Graded SNV Positions Data from Table 1</th>
<th>Range</th>
<th>Mean 43 Median 47</th>
</tr>
</thead>
</table>

## 2016 B Mailing

<table>
<thead>
<tr>
<th>Number of Labs Analyzing Each of the 108 Graded SNV Positions Data from Table 1</th>
<th>Range</th>
<th>Mean 30 Median 24</th>
</tr>
</thead>
</table>
### Single Nucleotide Variant Analysis for 2016 A and B Mailing Surveys

#### Analysis Responses for All 50 Graded SNV Positions* Data from Table 1

<table>
<thead>
<tr>
<th></th>
<th>% Variant Detected</th>
<th>% Not Detected</th>
<th>% Cannot Evaluate</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean 92.4%</td>
<td>Mean 5.5%</td>
<td>Mean 2.1%</td>
</tr>
<tr>
<td></td>
<td>Median 92.3%</td>
<td>Median 5.4%</td>
<td>Median 2.0%</td>
</tr>
<tr>
<td></td>
<td>Range 82.3-100%</td>
<td>Range 0.0-16.2%</td>
<td>Range 0.0-8.7%</td>
</tr>
</tbody>
</table>

#### Analysis Responses for All 108 Graded SNV Positions* Data from Table 1

<table>
<thead>
<tr>
<th></th>
<th>% Variant Detected</th>
<th>% Not Detected</th>
<th>% Cannot Evaluate</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean 94.0%</td>
<td>Mean 1.8%</td>
<td>Mean 4.2%</td>
</tr>
<tr>
<td></td>
<td>Median 95.2%</td>
<td>Median 0.0%</td>
<td>Median 4.3%</td>
</tr>
<tr>
<td></td>
<td>Range 84.0-96.3%</td>
<td>Range 0.0-7.1%</td>
<td>Range 0.0-15%</td>
</tr>
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</table>
## Insertion and Deletion Analysis for 2016 A Mailing Survey

<table>
<thead>
<tr>
<th>Analysis Responses Table 1</th>
<th><strong>AP3B1 Deletion</strong></th>
<th><strong>EYS Deletion</strong></th>
<th><strong>TPM2 Insertion</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Heterozygous</td>
<td>Homozygous</td>
<td>Heterozygous</td>
</tr>
<tr>
<td></td>
<td>c.2409_2411delGAA</td>
<td>c.6079-4_6079-3delTC</td>
<td>c.773_3dupC</td>
</tr>
<tr>
<td></td>
<td>p.Lys804del</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Number of Labs Providing Responses</th>
<th>52</th>
<th>46</th>
<th>45</th>
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<tbody>
<tr>
<td>Variant Detected No. Labs (Percentage)</td>
<td>44 (84.6%)</td>
<td>37 (80.4%)</td>
<td>35 (77.8%)</td>
</tr>
<tr>
<td>Variant Not Detected No. Labs (Percentage)</td>
<td>4 (7.7%)</td>
<td>5 (10.9%)</td>
<td>5 (11.1%)</td>
</tr>
<tr>
<td>Cannot Evaluate</td>
<td>4 (7.7%)</td>
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<td></td>
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</tr>
<tr>
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<td></td>
<td></td>
</tr>
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<td>4 (8.7%)</td>
<td>5 (11.1%)</td>
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Preliminary Performance Data Summary
2016 NGS MBPT Germline Graded Surveys

Observations

- Laboratory Evaluation of Reference Positions and SNVs was Solid
- Detection of Indels is an Area for Improvement
Preliminary Performance Data Summary
2016 NGS MBPT Germline Graded Surveys

Observations

- Laboratory Evaluation of Reference Positions and SNVs was Solid
- Detection of Indels is an Area for Improvement

Participating Laboratories
Not Required to Sanger Confirm NGS Results Before Answering Survey
Critical Challenge --- How to Provide Proficiency Testing For the Growing Diversity of Clinical NGS Applications

- Multi-Gene Diagnostics
  - Germline Variants
  - Inherited Disorders

- Exome
  - Germline Variants
  - Inherited Disorders

- Whole Genome
  - Germline Variants
  - Inherited Disorders

- Somatic Variants
  - Solid Tumors
  - Hematologic Malignancies

On the Horizon
Next-Generation Sequencing—Solid Tumors

**Program Information**
- Three 1.0-μg DNA (50 ng/μL) specimens
- Two shipments per year

<table>
<thead>
<tr>
<th>Procedure</th>
<th>Program Code</th>
<th>Challenges/Shipments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Next-generation sequencing</td>
<td>NGSST</td>
<td>3</td>
</tr>
</tbody>
</table>

**Additional Information**
This is a methods-based proficiency challenge for laboratories performing targeted next-generation sequencing of cancer genes or mutation hotspots in solid tumors. Laboratories will be asked to identify somatic single nucleotide variants and small insertions or deletions in the following genes: AKT1, ALK, APC, ATM, BRAF, CDH1, CTNNB1, EGFR, ERBB2, FBXW7, FGFR2, GNAQ, GNAS, HRAS, IDH1, KIT, KRAS, MET, NRAS, PDGFRα, PIK3CA, PTEN, SMAD4, SMARCB1, SMO, SRC, STK11, TP53.

<table>
<thead>
<tr>
<th>2016 A Mailing Enrollment</th>
<th>2016 B Mailing Enrollment</th>
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</thead>
<tbody>
<tr>
<td>135 Labs</td>
<td>140 Labs</td>
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</table>
**Next-Generation Sequencing—Hematologic Malignancies NGSHM**

<table>
<thead>
<tr>
<th>Procedure</th>
<th>Program Code</th>
<th>Challenges/Shipments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Next-generation sequencing</td>
<td>NGSHM</td>
<td>3</td>
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</tbody>
</table>

**Additional Information**

This is a methods-based proficiency challenge for laboratories performing targeted next-generation sequencing of genes or mutation hotspots in hematologic malignancies. Laboratories will be asked to identify somatic single nucleotide variants and small insertions or deletions in the following genes: ASXL1, ATM, BRAF, CALR, CEBPA, CREBBP, CSF3R, DNMT3A, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KMT2D, MPL, MYD88, NOTCH1, NPM1, SF3B1, SRSF2, TET2, TP53, U2AF1.

**Program Information**

- Three 1.0-μg DNA (50 ng/μL) specimens
- Two shipments per year

<table>
<thead>
<tr>
<th>2016 A Mailing Enrollment</th>
<th>2016 B Mailing Enrollment</th>
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</thead>
<tbody>
<tr>
<td>70 Labs</td>
<td>76 Labs</td>
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</table>
### Next-Generation Sequencing Bioinformatics

<table>
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<tr>
<th>Procedure</th>
<th>Program Code</th>
<th>Challenges/Shipments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Illumina TruSeq Amplicon Cancer Panel</td>
<td>NGSB1</td>
<td></td>
</tr>
<tr>
<td>Ion Torrent AmpliSeq Cancer Hotspot v2</td>
<td>NGSB2</td>
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</tr>
</tbody>
</table>

**Additional Information:**
- This in silico program augments wet bench NGS proficiency testing programs by testing a greater number of variants, at a greater range of variant frequencies.
- The BAM and/or FASTQ files are platform-specific and may not be compatible with other instruments/software.
- For a full list of genes in this program, please go to cap.org. Under the Laboratory Improvement tab, click on Catalog and Ordering Information. The list is located under the PT Order Supplements header.

**Program Information**
- Somatic gene-based sequencing files to be downloaded into your laboratory bioinformatics pipeline; file sizes range from 100MB to 1GB.
- NGSB1 - FASTQ file format for the Illumina TruSeq Amplicon Cancer Panel.
- NGSB2 - BAM and FASTQ file formats for the Ion Torrent AmpliSeq Cancer Hotspot v2 Panel.
- This is an online only program, delivered two times a year; your CAP shipping contact will be notified via email when the activity is available.

**2016 A Mailing Enrollment** | **2016 B Mailing Enrollment**
---|---
43/34 Labs | 34/29 Labs
Questions?

voelkek@aruplab.com
DISCUSSION / Q&A