**USEFUL FOR**
- Evaluation of acute myeloid Leukemia (AML) at the time of diagnosis, to assist in appropriate classification and prognosis
- This test can be used at the time of AML relapse to determine if a different gene mutation profile is present

**CLINICAL INFORMATION**
Next-generation sequencing (NGS) is a rapidly evolving and complex methodology that can interrogate multiple regions of genomic tumor DNA in a single assay. Many hematologic neoplasms, including acute myeloid leukemia (AML), are characterized by morphologic or phenotypic similarities, but can have characteristic somatic mutations in many genes. In addition, many cases of AML lack a clonal cytogenetic finding at diagnosis (normal karyotype) and can be better classified according to gene mutation profile. The presence and pattern of gene mutations in AML can provide critical prognostic information and may help in guiding therapeutic management decisions by physicians.

**GENETICS INFORMATION**
Targeted Genes Interrogated by Next Generation Sequencing, Acute Myeloid Leukemia, 8-Gene Panel

<table>
<thead>
<tr>
<th>GENE</th>
<th>EXONS</th>
<th>GENE</th>
<th>EXONS</th>
</tr>
</thead>
<tbody>
<tr>
<td>CEBPA</td>
<td>1</td>
<td>KRAS</td>
<td>2-3</td>
</tr>
<tr>
<td>FLT3</td>
<td>14-20</td>
<td>NPM1</td>
<td>9, 11, and 12</td>
</tr>
<tr>
<td>IDH1</td>
<td>4</td>
<td>NRAS</td>
<td>2-3</td>
</tr>
<tr>
<td>IDH2</td>
<td>4</td>
<td>TP53</td>
<td>4-9</td>
</tr>
</tbody>
</table>

**INTERPRETATION**
Mutations (gene alterations) identified, if present. An interpretive report will be provided.
**INCIDENCE OF TARGETED GENE MUTATIONS and FUNCTIONAL PATHWAYS**

**SIGNAL TRANSDUCTION**
- FLT3 (20%)
- KRAS (5%)
- NRAS (5%)

**TRANSCRIPTION FACTOR**
- CEBPA (10%)

**DNA DAMAGE / REPAIR**
- NPM1 (45%)

**EPIGENETIC**
- IDH1/2 (10%)

**TUMOR SUPPRESSOR**
- TP53 (5%)

**CLINICAL REFERENCE**