RUNX1-RUNX1T1 (AML1-ETO) t(8;21) Quantitative

Indications for Ordering
Detect and quantitate RUNX1-RUNX1T1 fusions arising from t(8;21) in acute myeloid leukemia (AML)

Test Description
Quantitative reverse transcription polymerase chain reaction (PCR)
- Whole blood, bone marrow (BM)

Tests to Consider
Primary test
RUNX1-RUNX1T1 (AML1-ETO) t(8;21) Detection, Quantitative 2010138
- Can be used for minimal residual disease monitoring

Related tests
Acute Myeloid Leukemia Panel by FISH 2011132
- Diagnosis, prognosis, and monitoring of AML
- Includes

<table>
<thead>
<tr>
<th>Probe Target</th>
<th>Gene(s)/Unique Sequence</th>
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<tbody>
<tr>
<td>t(15;17)(q24;q21)</td>
<td>PML-RARA</td>
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<tr>
<td>t(8;21)(q22;q22)</td>
<td>RUNX1T1-RUNX1 (ETO-AML1)</td>
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<tr>
<td>inv(16)(p13.3q12)</td>
<td>CBFB</td>
</tr>
<tr>
<td>11q23</td>
<td>KMT2A (MLL)</td>
</tr>
<tr>
<td>inv(3) or t(3;3)</td>
<td>RPN1-MECOM (EVI1)</td>
</tr>
<tr>
<td>del(5)(q31)</td>
<td>EGR1</td>
</tr>
<tr>
<td>del(7)(q31)/-7</td>
<td>D7S486</td>
</tr>
</tbody>
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Chromosome Analysis, Bone Marrow 2002292
- Diagnosis, prognosis, and monitoring of AML

Chromosome Analysis, Bone Marrow with Reflex to Genomic Microarray 2007130
- Diagnosis, prognosis, and monitoring of AML
- If chromosome analysis is “normal” or “no growth,” then genomic microarray testing will be added

Cytogenomic SNP Microarray – Oncology 2006325
- Preferred test for fresh specimens at time of diagnosis for detecting prognostically important genomic abnormalities in leukemias/lymphomas and solid tumors involving
  - Loss/gain of DNA
  - Loss of heterozygosity (LOH)
- Monitor disease progression and response to therapy

Chromosome FISH, Interphase 2002298
- Specific FISH probe for t(8;21) must be requested

Myeloid Malignancies Mutation Panel by Next Generation Sequencing 20111117
- Assess for single gene mutations, including substitutions and insertions and deletions that may have diagnostic, prognostic, and/or therapeutic significance

KIT Mutations in AML by Fragment Analysis and Sequencing 2002437
- Prognostication in core-binding factor-related (CBF) AML (NCCN, 2011)

Disease Overview
Incidence – t(8;21) AML represents 5-7% of de novo adult AMLs and 11-13% of pediatric AMLs

Treatment issues
- Identification of t(8;21) AML may influence therapy and survival
- Use of FISH or PCR for identification of this translocation is important in treatment decisions
  - Quantitative test can be used in monitoring
- KIT mutation testing is also important since the presence of the mutation is associated with a worse outcome

Test Interpretation
Sensitivity/specificity
- Analytical sensitivity – 1 cell with t(8;21) in 1,000 normal cells
- Analytical specificity – 100%

Results
- Detected – RUNX1-RUNX1T1 transcripts identified and quantitated
- Not detected – No RUNX1-RUNX1T1 transcripts detected

Limitations
- “Not detected” does not exclude the possibility of RUNX1-RUNX1T1 transcripts below the test limit of detection
- BM samples preferred for maximum sensitivity
- Poor RNA yield and/or quality due to sample age or hypocellularity will negatively impact the test