Array CGH Analysis for Hematological Malignancies

*See link for Array CGH Testing for Hematological Malignancies Information Sheet*

<table>
<thead>
<tr>
<th>Test</th>
<th>Description</th>
<th>Turn Around Time</th>
<th>CPT codes</th>
<th>Specimen Requirements</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Array CGH for Hematological Malignancies</strong></td>
<td>This test utilizes the Agilent 4x180k aCGH+SNP array, which contains ~110,000 oligo probes for the detection of genomic copy number changes, and ~60,000 SNP probes for the detection of copy-neutral loss of heterozygosity (cn-LOH). This array contains genome-wide coverage with an average probe spacing of ~25 kb. It is designed to detect copy number changes with a minimum size of ~50 kb across the genome. This test will detect genomic copy number changes associated with unbalanced chromosomal rearrangements. It will detect aneuploidies, deletions, duplications, amplifications, and unbalanced translocations/insertions of the regions represented on the array, as well as cn-LOH. It has a greater resolution than both routine chromosome analysis and FISH analysis in detecting submicroscopic aberrations.</td>
<td>~2 weeks</td>
<td>81229x1</td>
<td>Bone marrow (BM) aspirate in a BM transport medium tube (4-5 cc) OR Peripheral blood (PB) in one EDTA (Purple top) tube and one Na Heparin (Green top) tube (4-5 cc per tube) At least 30% involvement of the BM or PB by the malignant process is required</td>
</tr>
</tbody>
</table>