FISH Analysis – Lymphomas

**CPT Code(s):** 88237, 88275, 88271 (x per probe)

**Service Code (IU Health):** 53101259, 53100707, 53100640

**Ordering Recommendation:** For detection of a neoplastic clone that is observed in patients with lymphoma; to identify and track chromosome abnormalities in patients; and for to evaluate response to therapy.

**Synonyms:** FISH, Hematopoietic malignancy, lymphoma, Hodgkin’s lymphoma, non- Hodgkin’s lymphoma, Burkitt Lymphoma, Burkitt-like Lymphoma, Diffuse Large Cell Lymphoma, Follicular Lymphoma, MALT Lymphoma, Mantle Cell Lymphoma, MYC - 8q24 Rearrangement

**Methodology:** Fluorescence *in situ* hybridization (FISH) analysis.

**Performed:** Monday through Friday

**Reported:** 2-3 days

**Panels:** Lymphoma Panel - t(8;14)(MYC/IGH), MYC, t(14;18) (IGH/BCL2)

**Additional Probes:** t(2;5), BCL6, t(11;14), t(11;18), MALT1

**Specimen Requirements**

**Collect:** Non-diluted bone marrow aspirate in sodium heparin (green top) vacutainer, heparinized syringe or flask with sterile media (provided upon request).

**Specimen Volume:** Preferred: 2 mL for normal WBC (decreased WBC requires more, elevated WBC requires less); 0.5 mL (minimum).

**Storage/Transport:** Room temperature. Do not freeze or expose to extreme temperatures.

**Unacceptable Conditions:** Frozen specimens. Formalin-fixed specimens.

**Stability:** Ambient: 48 hours; Refrigerated: 48 hours; Frozen: Unacceptable
Interpretive Data

Characteristics: When the percent of cells with an abnormality exceeds the normal reference range for any given probe, it is considered an abnormal clone. Absence of an abnormal clone does not rule out the possibility of a neoplastic disorder. The normal range varies with each observed signal pattern and is listed in the table below. A report detailing interpretation of results will be provided.

Reference Range:

<table>
<thead>
<tr>
<th>Probe Name</th>
<th>Normal Range (%)</th>
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<tbody>
<tr>
<td>3q27 (BCL6)</td>
<td>0 – 4.5</td>
</tr>
<tr>
<td>t(8;14) (MYC/IGH)</td>
<td>0 – 6.5</td>
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<tr>
<td>8q24 (MYC)</td>
<td>0 – 4.5</td>
</tr>
<tr>
<td>t(11;14) (CCND1/IGH)</td>
<td>0 – 7.0</td>
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<tr>
<td>t(11;18) (API2/MALT1)</td>
<td>0 – 7.5</td>
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<tr>
<td>14q32 (IGH)</td>
<td>0 – 5.5</td>
</tr>
<tr>
<td>t(14;18) (IGH/BCL2)</td>
<td>0 – 6.5</td>
</tr>
<tr>
<td>18q21 (MALT1)</td>
<td>0 – 2.5</td>
</tr>
</tbody>
</table>

Incidence:  NHL - 19.7/100,000, with median age of 66 years at diagnosis.  
            HL - 2.7/100,000, with median age of 39 years at diagnosis.

Limitations: The probes in this FISH panel detect only specific aberrations. Chromosomal alterations present outside the regions targeted by the probes will not be detected.

References: