Molecular Pathology Laboratory Network Inc. now offers testing for IgVH somatic hypermutation by next generation sequencing in CLL/SLL.

CLL/SLL is the most common leukemia diagnosed among adults in Western countries and is associated with heterogeneous clinical outcomes. IgVH somatic hypermutation (SHM) status is a primary component of the CLL International Prognostic Index (CLL-IPI) working group formulation for disease risk stratification. Un-mutated IgVH has been established as a strong and independent predictor of adverse clinical prognosis and reduced overall survival.

**MPLN approach to IgVH SHM testing**

Using a next generation sequencing-based approach to IgVH SHM detection, the MPLN methodology utilizes patient DNA as a sample starting material, eliminating many of the challenges related to RNA-based testing. Laboratory workflow is streamlined and automated to result in non-subjective data output that includes percentage homology of clonal reads to germline IGH reference sequences, VDJ gene utilization, and frequencies of IGH gene sequences.

**NGS testing for IgVH SHM is superior to traditional methodologies:**

- Utilizes patient DNA instead of RNA as sample starting material
- Minimal sample requirements: 1ml blood or bone marrow aspirate, or 0.01 µg DNA
- Non-subjective data output includes percentage homology to germline IGH sequences, clonal IGH sequences abundance, and VDJ gene utilization.
- Demonstrates improved sensitivity in detection of clonal populations

**Ordering Requirements**

<table>
<thead>
<tr>
<th>Order Test Code</th>
<th>M IGVH</th>
</tr>
</thead>
<tbody>
<tr>
<td>Turnaround Time</td>
<td>10-14 days</td>
</tr>
<tr>
<td>Specimen Requirements</td>
<td>Whole Blood or Bone Marrow in EDTA</td>
</tr>
<tr>
<td>Storage and Handling</td>
<td>Transport at ambient temperature (18-25°C)</td>
</tr>
</tbody>
</table>

**References**