### Variant Classification and Interpretation

- Test your variant interpretation
- Varying genotypes included
- 8-12 weeks to submit results
- All EQA samples validated
- Detailed instructions provided
- Results assessed by expert panel
- Marking criteria based on professional guidelines

<table>
<thead>
<tr>
<th>EQA</th>
<th>Type of EQA</th>
<th>Sample Type</th>
<th>Technique</th>
<th>Testing</th>
<th>ISO17043 Accredited</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathogenicity of germline Sequence Variants (Classification only)</td>
<td>Variant Classification</td>
<td>N/A</td>
<td>N/A</td>
<td>Classification of variants. Submit classification results on a <em>proforma</em>.</td>
<td>✓</td>
</tr>
<tr>
<td>Pathogenicity of germline Sequence Variants (Classification and Interpretation)</td>
<td>Variant Classification and Interpretation</td>
<td>N/A</td>
<td>N/A</td>
<td>Classification and clinical interpretation of variants. Submit a diagnostic report including clinical interpretation of the variants.</td>
<td>✓</td>
</tr>
<tr>
<td>Pathogenicity of somatic Sequence Variants (Classification only) (pilot) <em>NEW</em></td>
<td>Variant Classification</td>
<td>N/A</td>
<td>N/A</td>
<td>Classification of variants. Submit classification results on a <em>proforma</em>.</td>
<td>×</td>
</tr>
<tr>
<td>Variant Validation</td>
<td>Technical, Genotyping and Interpretation</td>
<td>DNA</td>
<td>Any molecular technique</td>
<td>Validation and interpretation of sequence variant(s) detected on a research basis and family follow-up studies</td>
<td>✓</td>
</tr>
</tbody>
</table>

For further information on these EQAs contact us at info@genqa.org

Please see overleaf for more EQA information

Email: info@genqa.org
Receive validated EQA material plus clinical questions

Education/Internal review/Quality improvement

Compare laboratory performance (benchmark)

Expert evaluation of submissions

Analyze material/variants using routine procedures

Upload results

For further information, please contact us at info@genqa.org