# Input Recommendation for selected Protocol

<table>
<thead>
<tr>
<th>Protocol</th>
<th>Illumina TruSight Tumor 15</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input Material</td>
<td>DNA</td>
</tr>
<tr>
<td>Minimum Input</td>
<td>25,0 ng</td>
</tr>
<tr>
<td>Standard Input</td>
<td>25,0 ng</td>
</tr>
<tr>
<td>Maximum Volume</td>
<td>12,5 µL</td>
</tr>
<tr>
<td>Minimal Concentration</td>
<td>2,00 ng/µL</td>
</tr>
<tr>
<td>Standard Concentration</td>
<td>2,00 ng/µL</td>
</tr>
</tbody>
</table>

Extraction derived from **Non-FFPE**

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For more Information please visit the manufacturers homepage


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The CMTD is not responsible for the consequences/results, if an ordering work group wants to sequence RNA/DNA samples that failed the predefined quality parameters for sequencing!

Possible, risks which can occur are for example bad sequencing quality, no sequencing possible due to failure in library generation, introducing false signals of gene expression or allele frequency.