Analyzing 13 genes associated with hereditary colon cancer

What is the ColoTrue® Test?

- ColoTrue® is a 13-gene hereditary cancer panel designed for individuals and families with features suggestive of hereditary colon cancer. Testing includes full sequencing analysis of 13 genes. In addition, this test also offers site-specific analysis of the MDM2–SNP309 allele.

Why choose ColoTrue®?

- 3 week turnaround time
- Buccal swab, saliva and blood specimens accepted
- Reflex testing available

Colon Cancer Fast Facts

- Colorectal cancer is the second leading cause of cancer-related deaths in the U.S. It is estimated that 132,700 people will be diagnosed in 2015.
- Approximately five percent of all colon cancer cases are due to a inherited predisposition to develop cancer

Interested in learning more about Pathway Hereditary Cancer testing? Visit www.pathway.com today!

Who Should Consider Testing?

- History of early onset colorectal or endometrial cancer (<50 yrs)
- History of ≥ 10 adenomas or polyps
- History of two or more associated cancers*
- Two or more relatives with associated cancers,* with one diagnosed <50yrs
- Three or more relatives with related cancers* at any age
- Abnormal MSI and/or IHC testing

*Associated cancers are listed in the table below.

Benefits of Testing

- Better define future cancer risks
- More personalized surgical and ongoing surveillance plans
- Informed treatment decisions
- Identify at-risk family members

ColoTrue® Genes and Associated Cancer Types

<table>
<thead>
<tr>
<th>Associated Cancers</th>
<th>APC</th>
<th>BMPR1A</th>
<th>CDH1</th>
<th>CHEK2</th>
<th>MLH1</th>
<th>MSH2</th>
<th>MSH6</th>
<th>MUTYH</th>
<th>PMS2</th>
<th>PTEN</th>
<th>SMAD4</th>
<th>STK11</th>
<th>TPS3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colon</td>
<td></td>
<td>⬤</td>
<td></td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td>⬤</td>
<td></td>
</tr>
<tr>
<td>Endometrial</td>
<td></td>
<td></td>
<td>⬤</td>
<td></td>
<td>⬤</td>
<td></td>
<td></td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td>⬤</td>
<td></td>
</tr>
<tr>
<td>Gastric</td>
<td></td>
<td>⬤</td>
<td></td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td></td>
</tr>
<tr>
<td>Ovarian</td>
<td></td>
<td>⬤</td>
<td></td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>⬤</td>
<td></td>
</tr>
<tr>
<td>Breast</td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Melanoma</td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Prostate</td>
<td>⬤</td>
<td>⬤</td>
<td></td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pancreatic</td>
<td></td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td>⬤</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Cancer types associated with pathological variants in each of the respective genes on ColoTrue®. In the figure above, represents a well-defined increased cancer risk, while represents a mildly increased cancer risk, or potentially increased cancer risks that are not yet well defined. Please note that additional cancers are also associated with pathological variants in these genes as denoted by the row marked other. These additional cancer types are described in the Pathway Genomics’ ColoTrue Technical Bulletin. The marker *SNP309T>G in the MDM2 gene has been associated with an earlier age of cancer onset in patients with Li-Fraumeni syndrome.

Test Specifications: ColoTrue® analyzes the coding and flanking regions (+/- 20 bp) of 13 genes associated with hereditary colorectal cancer (APC, BMPR1A, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, SMAD4, STK11, TP53) by next-generation sequencing-based (NGS) and Sanger confirmation of reported gene variants. Additionally, site-specific analysis is performed to test for the variant defined as SNP309T>G in the MDM2 gene. Sanger fill-in is used for all genes in areas of low coverage, which is defined as a read depth of less than 25x.