



The following applies to COMCP / Hereditary Common Cancer Panel. Testing is performed to evaluate for the presence of variants in coding regions and extending to +/- 10 base pairs of adjacent intronic sequence on either side of the coding exons of the genes analyzed. In addition, the analysis will cover select noncoding variants. Next-generation sequencing, multiplex ligation-dependent probe amplification and/or a polymerase chain reaction-based quantitative method is performed to test for the presence of copy number variants (CNV) in the genes analyzed. Polymerase chain reaction and gel electrophoresis is performed to test for the presence of the 10 megabase (Mb) inversion of coding exons 1–7 of the *MSH2* gene. Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

This list is current from November 2021 to the present. This document is intended to highlight additional evaluations for variants of high clinical interest as well as technical limitations. However, this document does not comprehensively reflect all genomic regions covered by this test. For questions regarding transcripts, genes or regions covered, contact the laboratory at 800-533-1710.

Genomic Build: GRCh37 (hg19) unless otherwise specified

Gene	Reference Transcript	Additional Evaluations	Technical Limitations
<i>APC</i>	NM_000038.6	Promoter 1A: c.-172 to c.-19 (variants between c.-565 to c.-173 may be detected) Promoter 1B: c.-30632 to c.-30046	-
<i>ATM</i>	NM_000051.3	-	-
<i>AXIN2</i>	NM_004655.4	-	-
<i>BARD1</i>	NM_000465.4	-	-
<i>BMPR1A</i>	NM_004329.2	-	-
<i>BRCA1</i>	NM_007294.4	+/- 20 base pairs of adjacent intronic sequence on either side of the coding exons	-
<i>BRCA2</i>	NM_000059.3	+/- 20 base pairs of adjacent intronic sequence on either side of the coding exons	-
<i>BRIP1</i>	NM_032043.3	-	-
<i>CDH1</i>	NM_004360.5	-	-
<i>CDK4</i>	NM_000075.4	-	-
<i>CDKN2A</i>	NM_000077.4	-	-
<i>CHEK2</i>	NM_007194.4	-	-
<i>DICER1</i>	NM_177438.2	-	-
<i>EPCAM</i>	NM_002354.3	-	Analysis for sequence variants will not be performed
<i>GREM1</i>	NM_013372.7	-	Analyzed for CNV duplication of upstream enhancer region only; Analyses for sequence variants and additional CNV will not be performed
<i>HOXB13</i>	NM_006361.5	-	-
<i>MEN1</i>	NM_130799.2	-	-
<i>MLH1</i>	NM_000249.3	c.-27C>A (rs587779001) c.454-13A>G (rs267607749) c.1990-16_1990-2del (rs267607881)	-
<i>MSH2</i>	NM_000251.3	10 Mb inversion of exons 1–7	-

# Targeted Genes and Methodology Details for Hereditary Common Cancer Panel (continued)

Gene	Reference Transcript	Additional Evaluations	Technical Limitations
<i>MSH3</i>	NM_002439.5	-	-
<i>MSH6</i>	NM_000179.2	-	-
<i>MUTYH</i>	NM_001128425.1	c.504+19_504+31del (rs781222233)	-
<i>NBN</i>	NM_002485.4	-	CNV in exon 16 will not be detected or reported
<i>NF1</i>	NM_000267.3	-	Analysis for sequence variants beyond coding exons +/- 10 base pairs of adjacent intronic sequence will not be performed
<i>NTHL1</i>	NM_002528.7	-	-
<i>PALB2</i>	NM_024675.4	-	-
<i>PMS2</i>	NM_000535.7	-	-
<i>POLD1</i>	NM_002691.4	-	-
<i>POLE</i>	NM_006231.4	-	-
<i>PTEN</i>	NM_000314.8	Promoter: c.-1302 to c.-589	-
<i>RAD51C</i>	NM_058216.3	-	-
<i>RAD51D</i>	NM_002878.3	-	-
<i>RET</i>	NM_020975.6	-	-
<i>SMAD4</i>	NM_005359.6	-	-
<i>STK11</i>	NM_000455.5	-	-
<i>TP53</i>	NM_000546.5	-	-

Effective Date	Version	Synopsis of Test Change
June 2023	V2	Updated format (additional columns: Additional Evaluations and Technical Limitations)