

HGNC approved gene symbol	Transcript	OMIM gene ID	median depth	% covered >10x	% covered >20x	% covered >30x	% covered >50x
<i>APC</i> **	NM_001127511	611731	360	100	100	100	100
<i>EPCAM</i>	NM_002354, exon 9			MLPA			
<i>MLH1</i> **	NM_000249	120436	144	100	100	100	100
<i>MSH2</i> **	NM_000251	609309	163	100	100	100	100
<i>MSH6</i> **	NM_000179	600678	340	100	100	100	100
<i>MUTYH</i> **	NM_001048171	604933	145	100	100	100	100
<i>NTHL1</i>	NM_002528, exon 2			Sanger sequencing			
<i>PMS2</i> ***	NM_000535	600259	162	100	100	99	98
<i>POLE</i>	NM_006231, exon 9_14	174762		Sanger sequencing			
<i>POLD1</i>	NM_002691, exon 8_12	174761		Sanger sequencing			
<i>PTEN</i> ***	NM_000314	601728	142	100	100	100	100
<i>STK11</i>	NM_000455	602216	125	100	100	100	97

* Colorectal carcinoma

** Core genes

***although the coverage is good, the analysis is less reliable because of the presence of pseudogene(s).

On request, we offer to test the relevant *PMS2* exons with Sanger sequencing.

MLPA for *MLH1*, *MSH2*, *EPCAM* is included in the CRC panel.

Upon request we will perform MLPA for *APC*, *MUTYH* and/or *MSH6*, *PMS2*

