**To: Dartmouth Health Providers**

**From:** Nidhi D. Shah, MD; Wahab A. Khan, PhD; Joel A. Lefferts, PhD; Parth S. Shah, MD; Laura J. Tafe, MD

**Date:** 7/3/25

**Re:       DH Hereditary Pan-Cancer Panel go-live**

The Laboratory for Clinical Genomics and Advanced Technologies (CGAT) in the Department of Pathology and Laboratory Medicine at DHMC will be offering the Hereditary Pan-Cancer Panel, beginning 7/7/25. The panel analyzes the protein-coding regions of 79 genes to identify germline variants implicated in hereditary cancer risk/predisposition.

Gene Content

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| AIP | CEBPA | MBD4 | PMS2^ | SDHB |
| ALK | CHEK2 | MEN1 | POLD1 | SDHC |
| APC | CTNNA1 | MET | POLE | SDHD |
| ATM | DDX41 | MITF^ | POT1 | SMAD4 |
| AXIN2 | DICER1 | MLH1 | PRKAR1A | SMARCA4 |
| BAP1 | EGFR | MSH2 | PTCH1 | SMARCB1 |
| BARD1 | EPCAM^ | MSH3^ | PTEN | SMARCE1 |
| BMPR1A | ETV6 | MSH6^ | RAD51C | STK11 |
| BRCA1 | FH | MUTYH | RAD51D | SUFU |
| BRCA2 | FLCN | NBN | RB1 | TMEM127 |
| BRIP1 | GATA2 | NF1 | RECQL | TP53 |
| CDC73 | GREM1/SCG5^ | NF2 | RET | TSC1 |
| CDH1 | HOXB13 | NTHL1 | RPS20 | TSC2 |
| CDK4 | KIT | PALB2 | RUNX1 | VHL |
| CDKN1B | LZTR1 | PDGFRA | SDHA | WT1 |
| CDKN2A | MAX | PHOX2B^ | SDHAF2 |  |

^Note that there are special analytical considerations in specific regions of these genes. See specific considerations below.

**Turnaround time:** Results will typically be available within 4 weeks for the hereditary pan-cancer panel.

**Specimen details:** The preferred specimen is EDTA anticoagulated peripheral whole blood. Buccal swab samples can also be accommodated.

- Blood Collection tube: Purple top tube with EDTA for whole blood; volume: 3-5 mL (minimum acceptable: 0.5-1 mL)

- Buccal Collection tube: ORAcollect (OCR-100) from DNA Genotek Inc. (provided by lab)

- Storage (blood and buccal): Ambient temperature for transport within 24 hours to CGAT lab or refrigerated over weekend

**Test ordering details: LAB2332**

**Analytical Range Special Considerations:**

EPCAM: only copy-number alterations affecting the 3' end of the gene will be assessed.

GREM1: Only duplications affecting the upstream regulatory region of GREM1, including exons 3-6 of SCG5, are analyzed or reported.

MITF: only SNVs are analyzed (only the c.952G>A p.E318K variant has thus far been associated with cancer risk)

MSH6: Copy number events affecting MSH6 exon 1 may not be detected.

MSH3 and PHOX2B: the polyalanine repeat regions are excluded from analysis.

PMS2: Due to pseudogene interference, variants will not be detected in exons 11-15 of PMS2.

**For questions or additional information, please contact:** Nidhi Shah, Wahab Khan, Joel Lefferts, Parth Shah, Heather Steinmetz (CGAT manager) or Samantha Allen (CGAT supervisor) in the Department of Pathology and Laboratory Medicine.