



LEUKEMIA/BONE MARROW TRANSPLANT PROGRAM OF BRITISH  
COLUMBIA  
Division of Hematology and  
CANCER GENETICS AND GENOMICS LABORATORY - BC CANCER



Division of Hematology  
2775 Laurel Street, 10<sup>th</sup> Floor  
Vancouver, BC V5Z 1M9  
Phone: 604.875.4863  
Fax: 604.875.4763  
[www.leukemiabmtprogram.com](http://www.leukemiabmtprogram.com)

Supported by:  
BC Cancer  
Vancouver Coastal Health  
University of British Columbia

*Interim Medical Director:*

Kevin W. Song  
MD, FRCPC

*Associate Medical Director:*

Maryse M. Power  
MB, MRCP, FRCPath

*Members:*

Yasser R. Abou Mourad  
MD, FRCPC, FACP

Shanee Chung  
MBChB, FRCAP, FRCPA

Donna L. Forrest  
MD, FRCPC

Kevin A. Hay  
MD, MSc, FRCPC

Florian C. Kuchenbauer  
MD, PhD, FRCPC

Stephen H. Nantel  
MD, FRCPC

Sujaatha Narayanan  
MBBS, MRCP, FRCPath

Thomas J. Nevill  
MD, FRCPC

Judith A. Rodrigo  
MD, FRCPC

Claudie Roy  
MD, FRCPC

David S. Sanford  
MD, FRCPC

Heather J. Sutherland  
MD, PhD, FRCPC

Cynthia L. Toze  
MD, MHSc, FRCPC

Jennifer K. White  
MD, MSc, FRCPC

Date: June 26, 2025  
To: BC Hematologists and Oncologists  
From: Dr. Ryan Stubbins, MD, FRCPC  
Hematologist, Leukemia/BMT Program of BC

Stephen Yip, M.D., Ph.D., FRCPC  
Medical Director – Cancer Genetics & Genomics Laboratory  
Medical Director – Centre for Clinical Genomics

**Re: New Rapid Test for *NPM1* Mutations**

Dear Colleagues,

The Cancer Genetics and Genomics Laboratory (CGL) at BC Cancer - Vancouver is piloting a new rapid mutation test for prevalent *NPM1* mutations in patients with newly diagnosed Acute Myeloid Leukemia (AML). The testing has finite funding and its continuation will be re-evaluated after one year.

**The rapid test for *NPM1* is:**

- Available July 1, 2025 – July 1, 2026 with possible extension
- A targeted droplet digital PCR (ddPCR) that detects >95% of the commonly found 4bp insertions within *NPM1* (including variant types A, B, D, and some rarer variants).
- Only *NPM1* variants detected with a VAF  $\geq$  1% will be reported
- Turnaround time is 6 calendar days (from time of receipt of the sample at CGL to reporting)

**How has testing changed?**

*NPM1* will now be included with the *FLT3* ITD/TKD rapid mutation test for patients with AML. This testing will automatically be performed for all patients undergoing *FLT3* testing. There are no changes to myeloid panel testing.

**What is detected by the Rapid *NPM1* Mutation test?**

Most 4bp insertions of *NPM1* between positions c.863 and c.864 are detected (including *NPM1* Types A, B and D). Other mutations in *NPM1* are not targeted but can be detected by the more comprehensive myeloid panel. The myeloid panel is required to identify the specific type of *NPM1* mutation.

**Who qualifies for testing?**

All newly diagnosed patients with AML will qualify for testing.

**How is the test ordered?**

Rapid AML Mutation panel for *NPM1* mutations can be ordered using the CGL Myeloid Requisition [link](#).

### What sample is required?

There are no changes to the sample requirements for patients eligible for the standard of care AML testing. The same sample submitted for *FLT3* will be used for *NPM1*.

- 2 x 0.5 mL of bone marrow in EDTA (one for MRD testing (RNA) and one for Rapid AML Mutation Panel + Myeloid Panel (DNA))
- 1 x 20 mL of peripheral blood in EDTA (for MRD testing (RNA))
- Bone marrow aspirate in media for karyotype analysis and bone marrow aspirate in EDTA to Optical Genome Mapping (OGM), if available, should continue to be sent to the cytogenetics laboratory in your jurisdiction

### Where and how does the sample get sent?

Further information: <https://cancergeneticslab.ca/guidelines/specimens/#Shipping>

Cancer Genetics and Genomics Laboratory  
BC Cancer - Vancouver  
Room #3307 – 600 West 10th Avenue  
Vancouver, BC  
V5Z 4E6

Ship at room temperature – do not freeze.

Maximum transit time from collection: 7 days (DNA-based test).

Maximum transit time from collection: 48 hours (RNA-based test).

### How will the test be reported?

The *NPM1* results (including allele fraction) are reported along with the rapid *FLT3* ITD/TKD test into one single report. Note that the specific *NPM1* variant will not be identified by this test and will only be reported with the myeloid panel report.

### What is the expected turnaround time (TAT) for results?

The anticipated TAT is ≤ 6 days from receipt of the sample and all required documentation (i.e., completed requisition and flow report confirming AML) in CGL.

### How can I access the clinical report results for my patient?

The clinical report will be:

- Generated using the CGL SHIRE platform which is used for all CGL reporting
- Uploaded electronically to CAIS, CST Cerner and CareConnect
  - For CareConnect information on how to view the report or to request access, [click here](#)
- Mailed as a paper copy via Canada Post unless previously opted out

- To discontinue receipt of the mailed paper copy, [complete this form](#)

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## Questions

Email: [cancergeneticslab@bccancer.bc.ca](mailto:cancergeneticslab@bccancer.bc.ca)

Website: [cancergeneticslab.ca](http://cancergeneticslab.ca)