

Date: March 03, 2026

From: Stephen Yip, MD, PhD, FRCPC  
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RE: **Optical Genome Mapping as the First-Tier Test for Myeloid Malignancies**

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The Cancer Genetics and Genomics Laboratory (CGL) at BC Cancer - Vancouver will begin using Optical Genome Mapping (OGM) on the Bionano platform as the first-tier test for myeloid malignancies, replacing karyotype as the initial test. OGM provides higher resolution, whole genome analysis and, in a one-year pilot where karyotype and OGM were performed in parallel, identified additional prognostic abnormalities not detected by conventional karyotyping.

As OGM has a higher resolution, more abnormalities may be reported than those identified by karyotype analysis. Similar to the past year, copy number variants (CNVs) > 5Mb will be reported within all areas of the genome, while smaller CNVs will be reported within a panel of genes relevant to the disease (see [CGL website](#) for more information). All variants will be interpreted and tiered using the same classification system as our Myeloid Panel. Important details regarding this testing are outlined below.

### How has testing changed?

OGM analysis will be performed as the first-tier test for myeloid malignancies. Karyotype analysis will be the second-tier test and will only be activated when OGM fails or when a bone marrow (BM) in EDTA is not received. It is important that the BM in media continue to be collected in addition to the BM in EDTA required for OGM, to allow for possible FISH or karyotype testing if needed.

**Note:** As OGM analysis has a longer turnaround time, for acute leukemia patients, a preliminary karyotype report will be issued within 2-4 days after receipt in CGL. The final genome analysis will be by OGM, with a final report issued within two weeks after receipt in CGL.

### What is detected by OGM?

OGM will detect most balanced rearrangements, with the exception of whole arm translocations, and copy number variants down to an allele fraction of 15%, although this is dependent on the genomic region and may be higher in different regions of the genome. CGL will report CNVs larger than 5 Mb across the whole genome and will report smaller CNVs in genes relevant to the disease in question.

### Who qualifies for testing?

Any patient who would qualify for a karyotype would qualify for OGM as the first-tier test (see [CGL website](#)).

## How is the test ordered?

Test is ordered on the CGL Myeloid Requisition [link](#).

## What sample is required?

All specimens below are required for most optimal testing:

### New:

- Bone marrow (OGM): 1 x 0.5ml in EDTA tube

### Unchanged from previous:

- Bone marrow (DNA): 1 x 0.5ml in EDTA tube
- Bone marrow (RNA): 1 x 5ml in EDTA tube
- Bone marrow (cytogenetics): 2 x 1.0ml in transport media tube

**Note:** Bone core specimens are *not* validated for OGM. Karyotype analysis will therefore continue to be the first-tier test for this specimen type.

## Where and how does the sample get sent?

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: 3 days.

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

## How will the test be reported?

Every attempt will be made to describe abnormalities similar to karyotype following the International System for Human Cytogenomic Nomenclature (ISCN) for OGM results (Moore et al PMID: 38071973). Historically, cytogenetics reports have provided a prognosis based on the whole karyotype, however, for consistency, OGM abnormalities will be interpreted and reported similar to our myeloid panel, using a modified version of published recommendations for OGM (Levy et al Am J Hematol. 2024 Apr;99(4):642- 661. PMID: 38164980) and are as follows:

### **TIER I - VARIANTS OF STRONG CLINICAL SIGNIFICANCE**

Variants in this tier have known clinical implications according to professional guidelines and can be acted upon using standard of care practices. These variants:

- Define a specific entity in the WHO and/or ICC classification.

- Are included in professional clinical practice guidelines as clinically significant variants (e.g., NCCN, Children’s Oncology Group (COG), Myelodysplastic Syndromes (MDS) International Prognostic Scoring System, International Myeloma Working Group Criteria).
- Have high quality evidence (level 1 CEBM evidence) in the literature showing association with a specific neoplasm, prognosis, or treatment response. This includes well-powered studies in the form of randomized controlled clinical trials, systematic review and meta-analysis of these studies, and cohort studies with consensus from experts in the field.
  - Can be treated by an approved targeted therapy.

## **TIER II - VARIANTS OF POTENTIAL CLINICAL SIGNIFICANCE**

Variants in this tier include acquired variants or a specific pattern of acquired variants with existing but limited evidence supporting their diagnostic, prognostic, and/or therapeutic clinical significance. These variants:

- Have good quality evidence (level 2 CEBM evidence) in the literature showing association with a specific neoplasm, prognosis, or treatment response. This includes multiple (at least two) smaller clinical studies in the form of cohort or case–control studies that have been confirmed and reproduced by different independent groups.
- Have been observed in different neoplasms but not specific to a particular tumor type; these variants usually affect genes associated with cancer and are included in the Catalogue of Somatic Mutations in Cancer (COSMIC) census cancer genes(s).

## **TIER IIIA –VARIANTS OF UNCERTAIN CLINICAL SIGNIFICANCE**

Variants in this tier are known or presumed to alter normal function of the gene product, however no convincing published evidence of a predictive, prognostic or diagnostic association was found or evidence is sufficiently conflicting that a conclusion cannot be reached.

## **TIER IIIB – VARIANTS OF UNCERTAIN FUNCTION**

Variants are not observed at a significant allele frequency in the population at large, are not identified in pan-cancer or tumour-specific variant databases, and their effect on normal gene function cannot be confidently predicted. No convincing published evidence of a predictive, prognostic or diagnostic association was found or evidence is sufficiently conflicting that a conclusion cannot be reached.

## **TIER IV – BENIGN AND LIKELY BENIGN VARIANTS** [NOTE: Tier IV variants are not routinely reported.]

Variants are known or presumed to not disrupt normal function of the gene product, and/or are found at a significant frequency (>1%) within the population, and/or are cataloged in the

Database of Genomic Variants (DGV). Note that these generally do not encompass COSMIC cancer gene(s).

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

The anticipated TAT for OGM testing is  $\leq 21$  days from receipt of a bone marrow report for MPN and MDS and  $\leq 14$  days for acute leukemia. Note that for acute leukemia, a preliminary karyotype report will be issued within 2-4 days.

### 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: <https://cancergeneticslab.ca/>

## References

1. Levy et al. A framework for the clinical implementation of optical genome mapping in hematologic malignancies. *Am J Hematol.* 2024 Apr;99(4):642-661. PMID: 38164980.
2. Moore et al. ISCN Standing Committee. Genome Mapping Nomenclature. *Cytogenet Genome Res.* 2023;163(5-6):236-246 PMID: 38071973.
3. Levy et al. Optical genome mapping in acute myeloid leukemia: a multicenter evaluation. *Blood Adv.* 2023 Apr 11;7(7):1297-1307. PMID: 36417763.

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