REVOLUTIONIZING CYTOGENOMICS

Consolidate traditional cytogenetic assays into a single workflow with Optical Genome Mapping (OGM) and the Bionano Saphyr® System

10,000x
greater resolution
compared to karyotyping

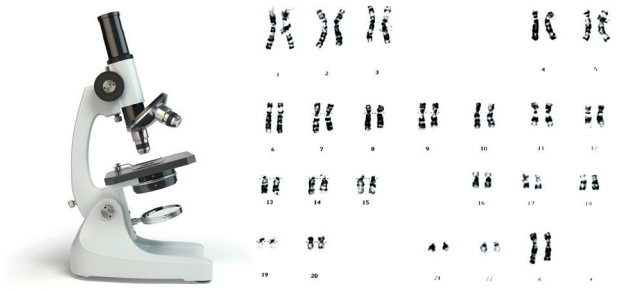
In spite of the revolution sequencing technologies have brought about for genomics research and diagnostics, it has barely modified the way cytogenomic labs look at chromosomal aberrations. While NGS identifies single-nucleotide variants along with small insertions and deletions (<150 bp), it fails to identify most large insertions, deletions, and copy-number variations in repetitive regions of the genome. NGS does not reliably detect balanced SVs such as inversions and translocations. Moreover, NGS relies on short-read sequences that are mapped to a reference human genome, which introduces bias while calling structural variants. Long-read sequencing is still limited in its resolution.

These limitations make direct visualization of the DNA the most reliable approach for the identification of structural variants to date. Unsurprisingly, the way structural variants are detected in clinical samples has minimally evolved over the past decades, and mainly relies on traditional cytogenetic methods such as karyotyping, Fluorescent in situ Hybridization (FISH) and array-based technologies. None of these methods alone can address complex cases due to technical limitations and need to be combined and complemented with molecular methods such as MLPA, qPCR, RNA-seq to provide a complete therapeutic and prognostic assessment of the patient or tumor genome.

OGM transforms traditional cytogenetics techniques by delivering an improved visualization of the genome by going from microscope to a fully digital, high-resolution chromosomal analysis. Only here, we apply 500,000 such bands to a genome, and the imaging is performed in an extremely high-throughput, automated manner in nanochannel arrays that linearize megabase-size molecules. This allows us to see events at 10,000x greater resolution than by karyotyping: insertions and deletions at 500 bp, vs ~5 Mbp by chromosome banding analysis.

CYTOGENETICISTS

Visualize patterns on intact DNA molecules to detect structural variation



SAPHYR®

Automates the imaging of 1000x more label patterns on intact DNA molecules to detect structural variation in massively parallel nanochannel arrays

bionanogenomics.com/cytogenomics

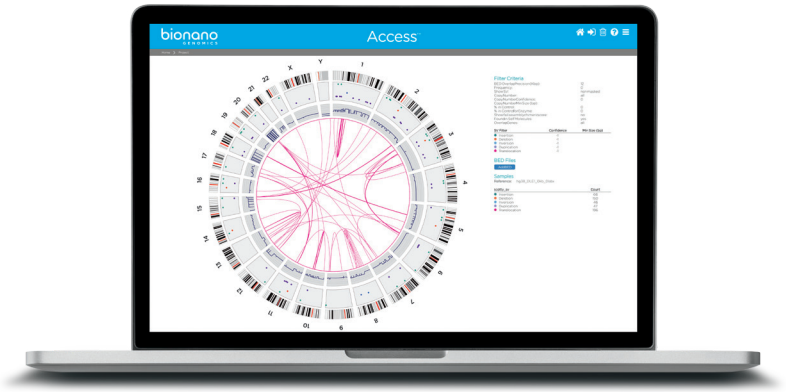
OGM PROVIDES HIGHLY SENSITIVE DETECTION OF ALL CLASSES OF STRUCTURAL VARIANTS

Validation studies around the world are confirming OGM's performance. OGM finds the clinically relevant variants detected by karyotyping, FISH and microarray combined, and reveals many that are missed.

OGM demonstrated 100% concordance with karyotyping, FISH, and chromosomal microarray in constitutional disorders in two studies appearing in the July 2021 issue of the American Journal of Human Genetics (AJHG).

The authors in these back-to-back AJHG publications describe OGM as a better alternative to traditional cytogenetics assays for both inherited genetic disease and hematologic malignancy applications since it consolidates multiple antiquated methods requiring manual integration for interpretation into a single workflow with higher resolution for detection of all classes of structural variants.[1]

Publication of a study of 76 subjects by authors at The University of Texas MD Anderson Cancer Center evaluated the utility of OGM as an alternative to traditional cytogenomic methods for the characterization of structural variation in myelodysplastic syndrome (MDS). The study was published in Blood, the journal of the American Society of Hematology (ASH), and presented at the 2021 ASH annual conference.[2]



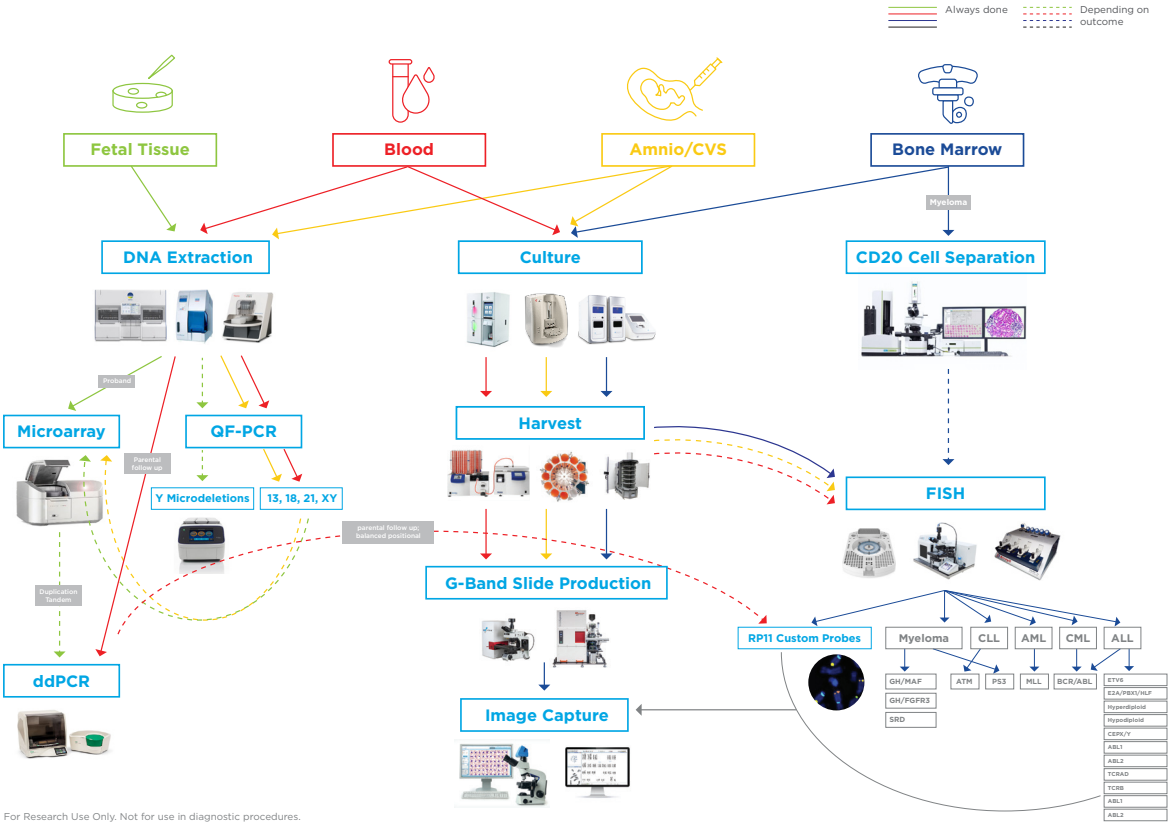
Method	Resolution	
Karyotyping	~5 - 10 Mbp	Extensive training required for interpretation. Slow, labor-intensive data collection and analysis. Cell culture required.[4]
FISH	~100 kbp	Targeted, extremely limited approach; only shows handful of variants. Slow, labor-intensive data collection. Requires validation of every lot of probes utilized.[4]
Array-based techniques	~50 kbp	Cannot detect balanced rearrangements. Cannot resolve nature of a structural aberration.[4]
OGM	**As low as 500 bp**	**Fully automated detection of: CNVs, repeat expansions, FSHD1-related repeat contractions, unbalanced events from single exon level to aneuploidies, balanced events, inversions, translocations, gene fusions, and AOH.**

OGM CONSOLIDATES THE TRADITIONAL CYTOGENETIC ASSAYS INTO A SINGLE WORKFLOW

OGM is the ONLY technology that allows for the highly sensitive detection of all structural variant types, even those present at low allele fraction in heterogenous cancer samples, in an unbiased genome-wide manner.

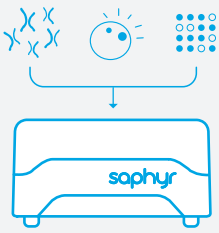
By providing a complete and unambiguous picture of the genome structure, OGM identifies prognostic markers not currently monitored, and enables a complete characterization of the cancer or subject's genome, **replacing multiple cytogenetic tests that make up the gold standard**.

Current Cyto Lab Workflow

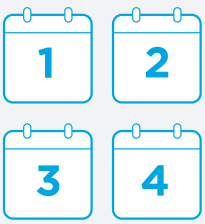


For Research Use Only. Not for use in diagnostic procedures.

EXPERIENCE THE ADVANTAGES OF OGM AND SAPHYR



One streamlined workflow



Sample to result in as few as 4 days[5]

Variant allele fraction detection

Coverage per sample

3 WAYS TO GET BIONANO DATA

GET THE SERVICE

BIONANO DATA SERVICES

Submit your samples to Bionano Data Services and receive an appropriately filtered set of structural variant calls. SV data is presented using the Bionano Access® visualization software. Files can be exported in the format of your choice.

The Bionano Support team will work with you on experiment design and analysis training. Full analysis is available as an option.

Sample Types Accepted – Frozen, Mammalian Preferred

- Tissue Biopsies
- Blood
- Cultured Cells
- Bone Marrow Aspirates

Pricing available upon request.

- Diploid/Genetic disease samples collected at 120x
- Mosaic/Cancer samples collected at 400x
- Low-frequency variant samples collected up to 1600x

GET THE CONSUMABLES

REAGENT RENTAL AGREEMENT

Run samples in-house with a Saphyr® Instrument free of charge for the duration of your project. The Bionano Support team will install the Saphyr System and provide training on sample preparation, instrument operation, and data analysis.

Please contact Bionano to request a reagent rental quote.

- Pricing is based on total genome commitment during a 6-month period
- Per-genome pricing includes DNA isolation, labeling, chips, and Bionano Compute On Demand
- Installation and training included

GET THE SAPHYR SYSTEM

SYSTEM AND CONSUMABLES PURCHASE

Purchase the Saphyr System for your institution without any reagent commitment. The Bionano Support team will install the Saphyr System and provide training on sample preparation, instrument operation, and data analysis.

Saphyr System Components

- Saphyr Instrument
- Saphyr Chips
- Bionano Prep Kits
- Bionano Access Server
- Bionano Access Software
- Bionano Compute On Demand (optional)

Please contact Bionano for a detailed quote. Pricing may vary, depending on region, availability, and secondary hardware needs.

- Saphyr System includes installation and training
- Volume-based, per-genome consumable pricing
- Consumables include DNA isolation, labeling, chips, and Bionano Compute On Demand

To see all cytogenomics case studies, presentations, and additional materials, visit bionanogenomics.com/cytogenomics

References: 1. Levy B, Baughn LB, Chartrand S, et al. A national multicenter evaluation of the clinical utility of optical genome mapping for assessment of genomic aberrations in acute myeloid leukemia. medRxiv 2020.11.07.20227728. doi.org/10.1101/2020.11.07.20227728 2. Hui Yang, Guillermo Garcia-Manero, Guillermo Montalban-Bravo, et al. High-Throughput Characterization of Cytogenomic Heterogeneity of MDS Using High-Resolution Optical Genome Mapping. Blood 2021; 138 (Supplement 1): 105. doi: https://doi.org/10.1182/blood-2021-154005 3. Neveling K, Mantere T, Vermeulen S, et al. Next-generation cytogenetics: Comprehensive assessment of 52 hematological malignancy genomes by optical genome mapping. Am J Hum Genet. 2021;108(8):1423-1435. doi:10.1016/j.ajhg.2021.06.001 4. Silva M, de Leeuw N, Mann K, et al. European guidelines for constitutional cytogenomic analysis. Eur J Hum Genet. 2019;27(1):1-16. doi:10.1038/s41431-018-0244-x 5. For human samples collected at 100x and analyzed through the de novo assembly pipeline.

Contact your Bionano Regional Business Manager to get started.

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30368_Rev.C_Cytogenetics Vignette Effective: 05/06/2022