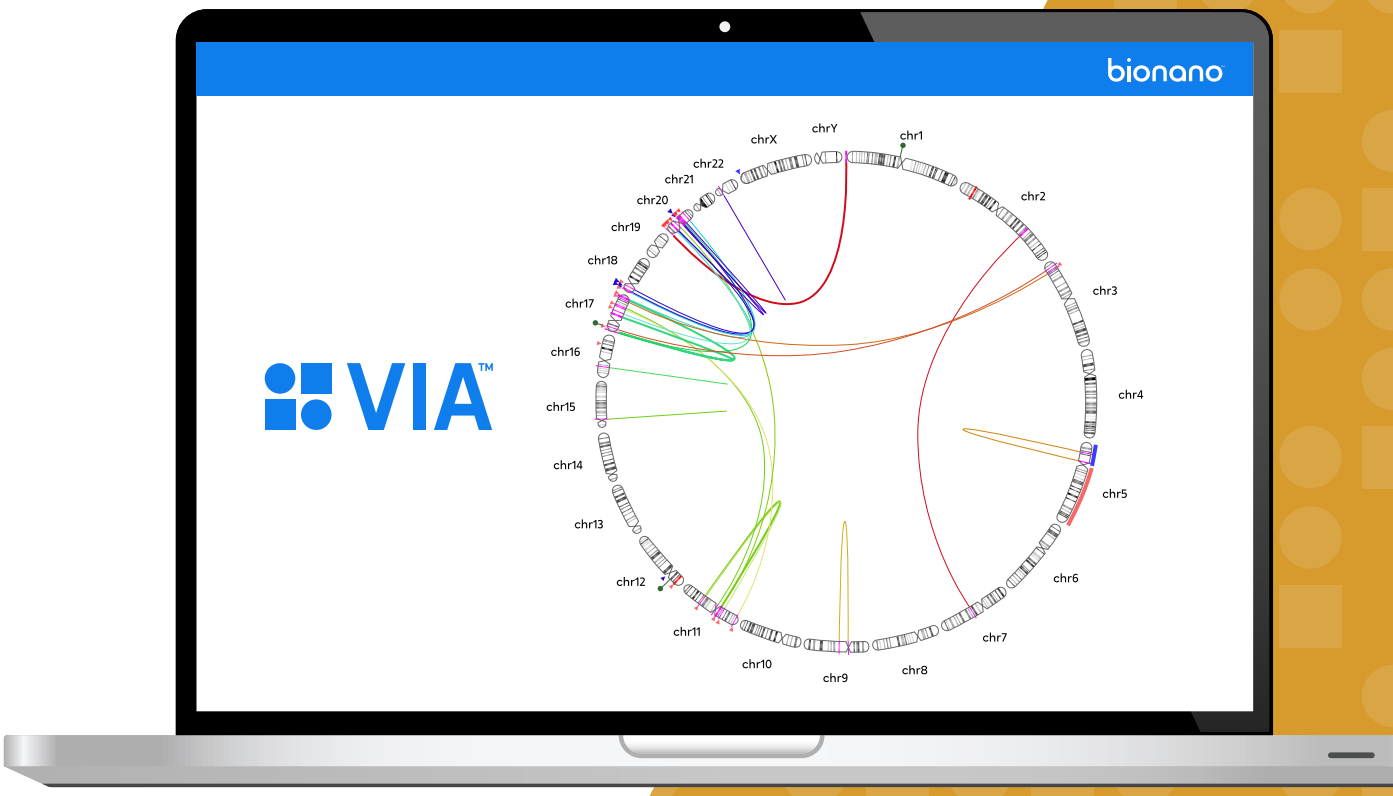
bionano™

Harness the Full Potential of Your Data. VIA™ Software is the Way.



Introducing VIA™ Software

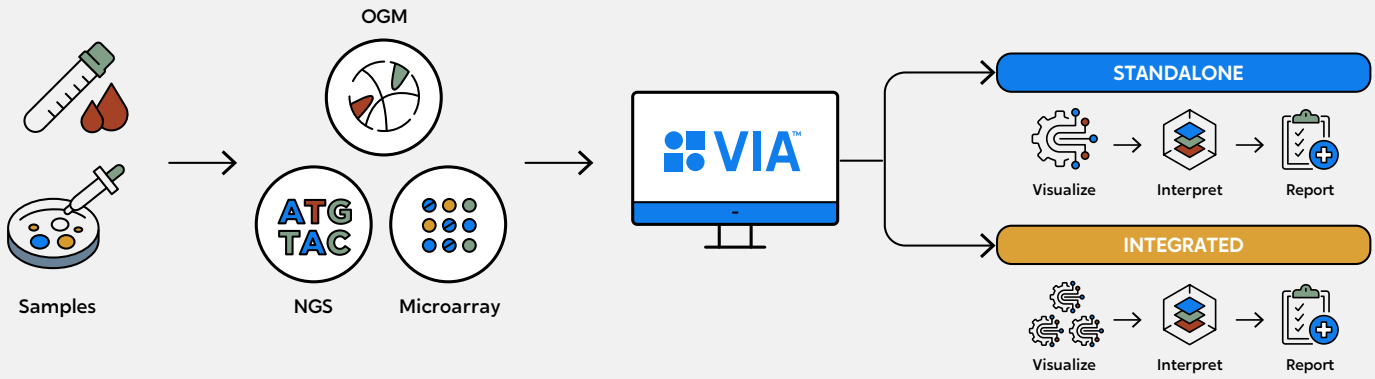
A faster and more complete genomic data analysis platform for clinical research

Existing data analysis solutions for genomics can be laborious, time-consuming and incomplete. You have to manage various systems, navigate complex workflows and spend inordinate amounts of time hunting for annotations and creating data visualizations. Good news: those days are over.

Variant Intelligence Applications™ (VIA) software radically simplifies your sample-to-report workflow and empowers you to deliver more meaningful answers from across technologies faster. VIA software brings various data types into one view and automates variant calling, interpretation and annotation, so you can reduce turnaround times and optimize operations at every step.

How it Works

VIA software is the only analysis software that combines secondary and tertiary analysis, receiving and interpreting data from Optical Genome Mapping (OGM), Next-Generation Sequencing (NGS) and microarrays to contextualize all classes of genomic variation and drive meaningful insights.



Experience the Benefits of VIA Software

VISUALIZE

Generate powerful visualizations for enhanced contextualization across multiple variant types

REPORT

Deliver clear, highly visual reports that support informed decision-making

INTERPRET

Accelerate time to results with intelligent automation for filtering, classifying, annotating and interpreting data across technologies

INTEGRATE

View and fully analyze data from OGM, NGS and microarray into one system for a simplified and integrated workflow

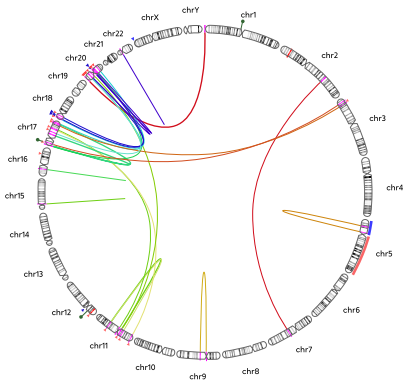
VISUALIZE

Instant Visualization, Zero Hassle. Automate Data Display for Powerful Insights.

VIA software amplifies the story of your data by automatically generating powerful visualizations of different variants independently or simultaneously, so you can see them in the context of other variant types occurring in the same genomic region. VIA allows you to drill down to single chromosome, gene, and nucleotide levels for deeper analysis.

Leverage Multiple Views: Genome Browser, Karyogram, Track View and Circos Plot

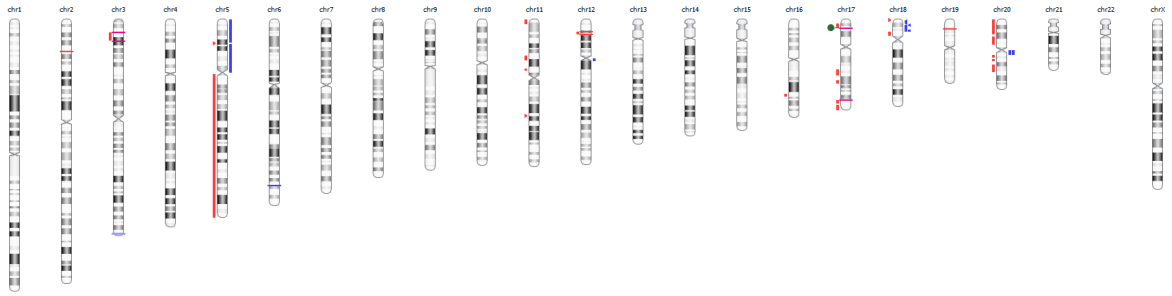
Circos Plot View



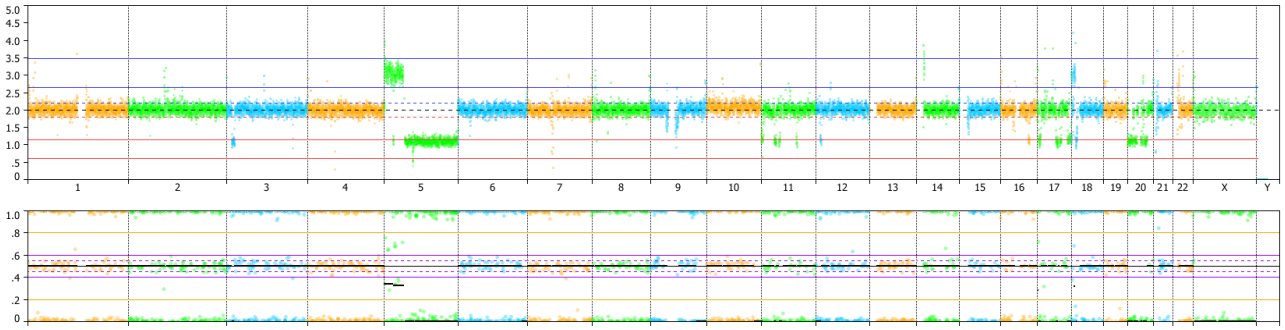
ADDITIONAL VISUALIZATIONS AVAILABLE

- Chromosome browser with multiple tracks displayed
- Variant information details
- Detailed events table

Karyogram View



Whole Genome Representation



Representation of genomic variants in a karyogram and whole genome plots for logR intensity and B-Allele frequency from OGM data provided in VIA software.

Reveal Greater Insights with Powerful Informatics

VIA software provides highly sensitive detection of mosaic and non-mosaic CNV and AOH/LOH events by leveraging a new SNP-FASST3 algorithm. For OGM data, VIA offers a novel capability to extract B-Allele Frequency (BAF) for enhanced visualization and variant calling based on the allelic contribution.

INTERPRET

Put Your Analysis on Autopilot and Get to What Matters Faster

VIA software introduces intelligent automation for filtering, classifying, annotating and interpreting data across technologies, no more hours manually searching through databases. VIA accelerates time to results to drive faster, better classification of variants by pathogenicity while reducing associated costs.

ANNOTATE

Integrate gene/variant annotation from external databases and previously reported variants from historical data.

FILTER

Automatically classify variants using a rules-based engine, dynamically filter against curated datasets and remove irrelevant variants.

INTERPRET

Capture expert interpretation from analysts automatically and implement case signoffs.

External Annotation Databases*

- OMIM
- RefSeq
- DGV
- DECIPHER
- ClinGen
- ClinVar
- CIVIC

Internal Annotation Options

- Build your own central database.
- Input your annotations.
- Look back at past samples and compare them to new sample findings.
- Curate local knowledgebase of expert interpretations
- Link out to Genomenon Mastermind to streamline literature search.

"[VIA software] performs exactly as I was hoping. Standard filters give 89 variants. Applying the AML panel brings it to exactly 3 variants to classify...A great example of how VIA brings the most relevant SVs for classification right to your attention within a few seconds."

Adam Smith, PhD, FCCMG, FACMG, erCLG
Director, Cancer Cytogenetics Laboratory
University Health Network, Toronto

*External resources are curated and updated in the software on a regular cadence.

REPORT

Flexible Reporting that Simplifies Decision Making

Easily create reports with simplicity and clarity thanks to VIA software's comprehensive set of customizable reporting options to clearly communicate results incorporating various society guidelines. Bring the most relevant information to the surface along with visuals and data that support interpretations and capture guideline-based evidence.

VIA software also provides the option for utilizing the new Hematological Malignancy workflow for a streamlined analysis and reporting solution for OGM data. See the Application Spotlight.

Easily Customize Your Reports

Different labs have different needs for their report structures.
VIA software makes it easy to create a report with only the sections you need.

"Bionano software is able to use NGS and microarray data for the assessment of HRD, which is very helpful to overcome things like tumor percentage and we look forward to doing the same analysis with OGM."

Christopher Lum, MD
Medical Director
Molecular Diagnostics Laboratory at Diagnostic Laboratory Services, Inc.

INTEGRATE

A Single Platform for All Your Variant Data. VIA Software is the One.

VIA software eliminates complex data analysis workflows by bringing data types together in one centralized platform, including your historical data from previous cases. You can seamlessly transition between technologies and all classes of genomic variation within VIA.

View and analyze OGM, NGS, and microarray data without switching between systems.

Perform analysis of structural variants, copy-number variants, allelic imbalances, single nucleotide variants and indels for enhanced discovery of causative findings that may be missed if analyzed independently.

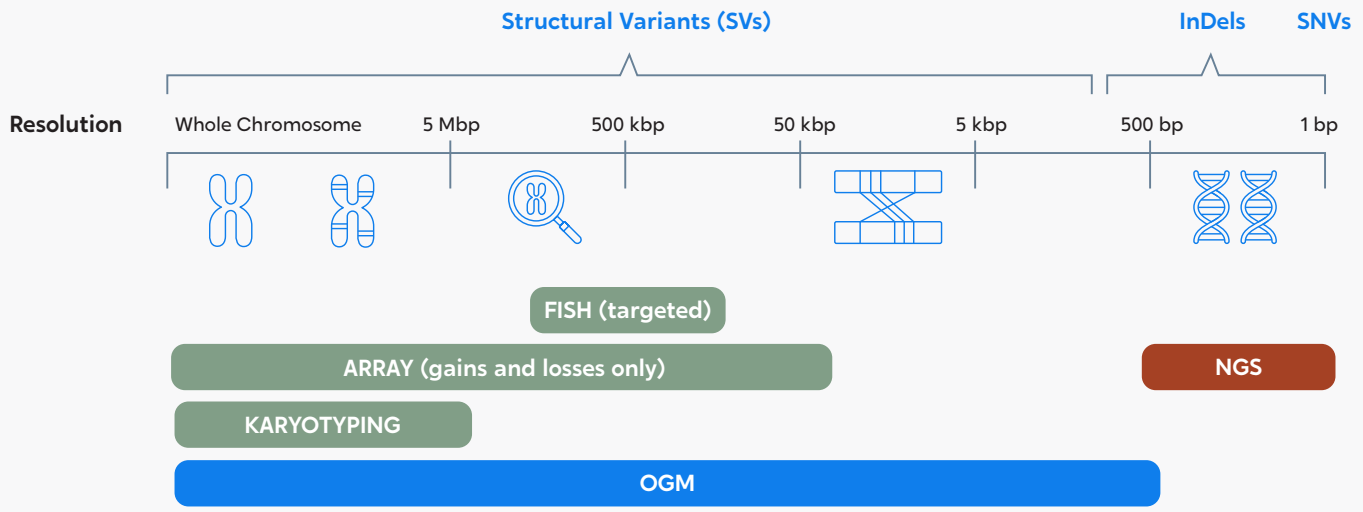
Retain and recall historical case interpretations for faster analyses.

VIA ADAPTS TO YOUR NEEDS

VIA software is configurable to your specific analytical needs, including cancer and constitutional applications employing OGM, NGS or array methodologies.

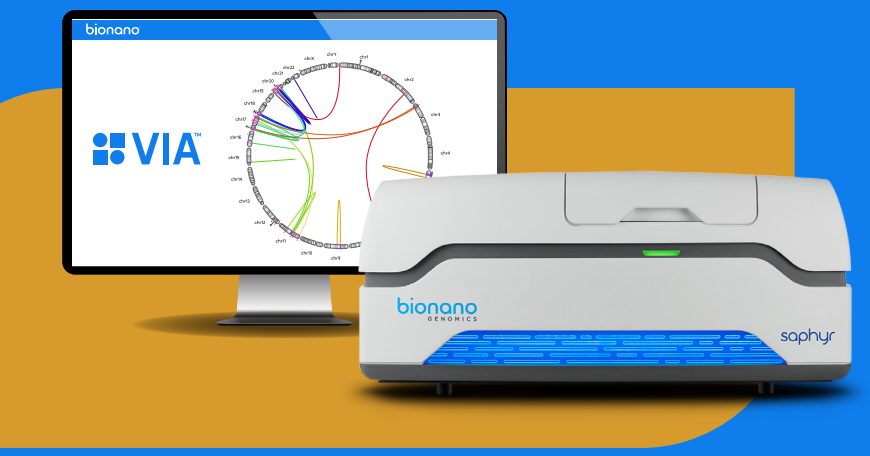
Generate More Meaningful Insights by Combining Genomic Data Types

Combining data from NGS with OGM gives you a very comprehensive view of the genomic variant continuum by detecting SNVs, CNVs and SVs of all classes and sizes. Bringing these two data types is akin to having cytogenetic and molecular genetic lab data in one system for more powerful insights.



Streamline Analysis of Hematological Malignancies with OGM and VIA Software

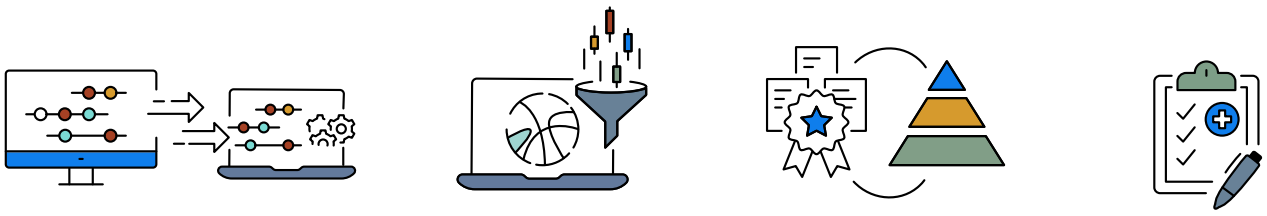
The latest versions of Bionano™ Solve, Bionano Access™ and VIA software combine to deliver a comprehensive and automated workflow for analyzing, interpreting and reporting SVs and CNVs detected by OGM associated with hematological malignancies.



This complete workflow leverages intelligent software automation to reduce the time to result for hematological malignancy sample data from OGM, including curated resources in VIA that represent guideline-based targets applicable to hematological disease. VIA software automatically pre-classifies variants detected with OGM technology using a rules-based engine to classify events based on pathogenicity or variant tiering system.

These oncology workflows are configurable to your site-specific preferences.

OGM & VIA Software Oncology Workflow



1. Connect OGM Data from Bionano Access to VIA software to initiate variant pre-classification using intelligent automation
2. Review variants utilizing curated annotations, advanced visuals, and dynamic filters to assign interpretations
3. Associate Tiered variants to guidelines derived from the WHO, NHS, and US societies for disease-specific or pan-heme workflows
4. Complete case sign-off and generate a configurable report to communicate results

Say Goodbye to Multiple Systems and Simplify Your Workflow with VIA™ Software

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Move Forward with Bionano

NUCLEIC ACID PURIFICATION

GENOME MAPPING SYSTEMS

ANALYSIS SOFTWARE

To schedule a demo or order VIA software, contact your Bionano Regional Business Manager, call or email us.

orders@bionano.com
1.858.888.7600

Learn more at bionano.com/via-software

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