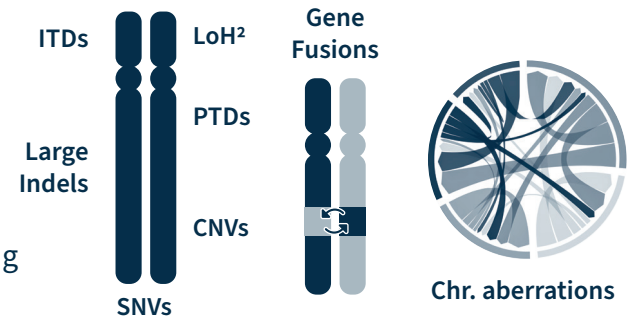
SOPHiA GENETICS™

SOPHiA DDM™ Community Myeloid Solution v2

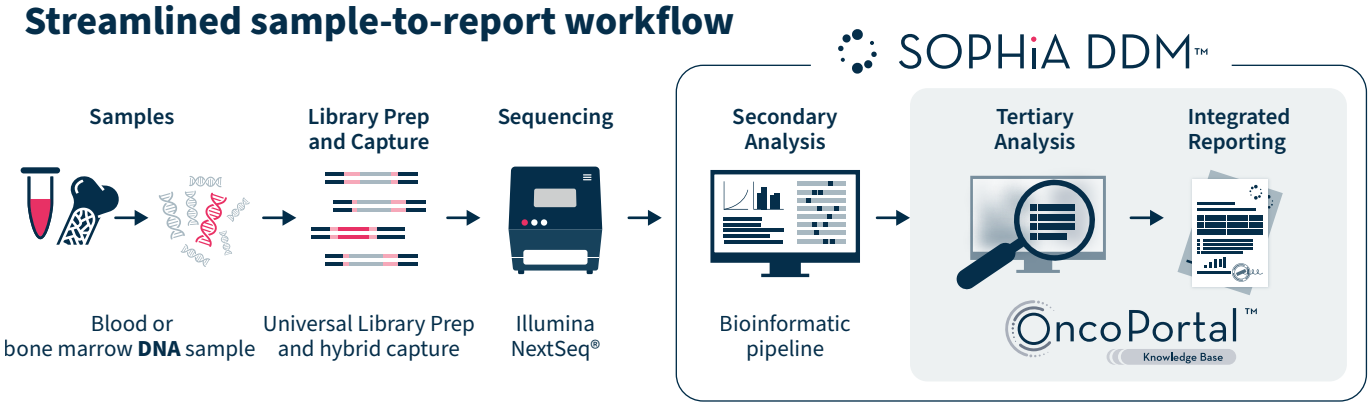
Built to magnify myeloid discovery

Optimize lab efficiency with a comprehensive workflow designed to detect a wide range of genomic alterations associated with myeloid malignancies in just **3.5 days**[1].

This end-to-end solution reflects the latest **guidelines** and reduces hands-on time, accelerating time-to-insights for informed decision-making.



Streamlined sample-to-report workflow



Ready-to-sequence libraries in **only 1.5 days** • **Automation scripts** available • High sample **multiplexing capability** • **3.5-day** turnaround[1]

Benefits of the SOPHiA DDM™ Community Myeloid Solution v2

COMPREHENSIVE

Consolidate **SNVs, Indels, CNVs, partner-agnostic gene fusions, structural changes**, and LoH² detection into a simplified **DNA**-only workflow.

CURATED

The expert-curated content reflects the latest **ELN** and **NCCN** guidelines, ensuring comprehensive coverage of key genes.

EFFICIENT

Leverage a comprehensive workflow powered by Universal Library Prep and automation (validated for Hamilton NGS STAR & STARlet) to **enhance productivity.**

1. For indicative purposes only; actual duration may be subject to change depending on the number of samples, server load, and other technical limitations.
2. The application enables client inference on LoH; future developments are planned to optimize clients' LoH analysis.

CNVs, copy number variants; Indels, insertions/deletions; SNVs, single nucleotide variants; ITDs, internal tandem duplications; PTDs, partial tandem duplications; LoH, loss of heterozygosity.

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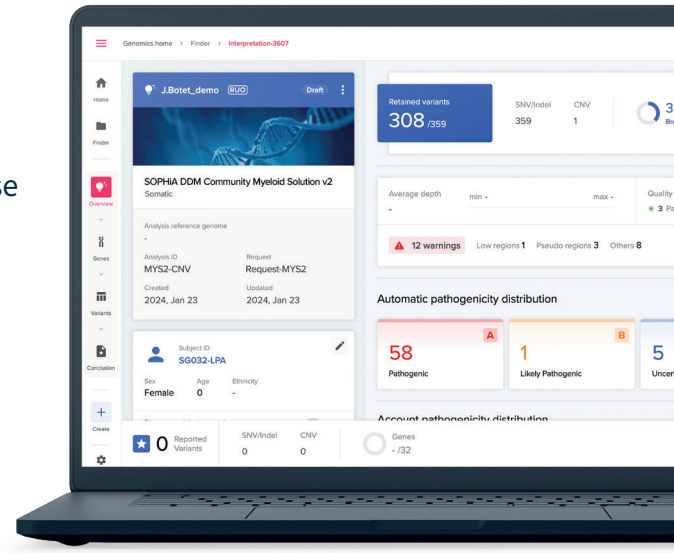
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Confident decision-making with the new generation of SOPHiA DDM™ Platform[1]

Advanced secondary analysis leveraging on proprietary algorithms to distinguish signal from noise

Enhanced variant annotation with point-based ACMG classification, zygosity annotation, extended catalogs (including splicing predictors), and cross-application variant frequency

Intuitive interface for seamless interpretation and comprehensive **visualization of large-scale genomic alterations**



Advanced analytical performance[2]

99.7% Sensitivity

100% Specificity

Accurate CNV detection with MUSKAT™ technology

DNA agnostic-fusion detection with CARDAMOM technology

1,000x coverage in >99% of the target regions

Sensitive detection of variants at low allele frequencies (down to 2% VAF) with CUMIN molecular barcoding technology

[a] The values have been calculated based on 72 samples processed on Illumina NextSeq® 1000/2000

Our comprehensive Myeloid Solution

	SOPHiA DDM™ Community Myeloid Solution v2
Genes	**94 genes (full CDS):** *ABL1, ANKRD26, ASXL1, ASXL2, ATM, ATRX, BCOR, BCORL1, BLM, BRAF, CALR, CBL, CBLB, CBLC, CCND2, CDKN2A, CEBPA, CHEK2, CREBBP, CSF3R, CSNK1A1, CTCF, CUX1, DDX41, DHX15, DNMT3A, ELANE, ETNK1, ETV6, EZH2, FBXW7, FLT3, GATA1, GATA2, GNAS, GNB1, HRAS, IDH1, IDH2, IKZF1, IL7R, JAK1, JAK2, JAK3, KDM6A, KIT, KMT2A, KMT2D, KRAS, LUC7L2, MPL, MSH2, MYC, MYD88, NF1, NOTCH1, NOTCH2, NPM1, NRAS, PAX5, PDGFRA, PHF6, PIGA, PML, PPM1D, PRPF8, PTEN, PTPN11, RAD21, RB1, RBBP6, RUNX1, SAMD9, SAMD9L, SBDS, SETBP1, SF3B1, SH2B3, SMC1A, SMC3, SRP72, SRSF2, STAG1, STAG2, STAT3, STAT5B, TERT, TET2, TP53, U2AF1, U2AF2, UBA1, WT1, ZRSR2* **Partner-agnostic fusion calling in 28 genes:** *ABL1* (1, 2, 3), *BCL9* (8, 9), *BCR* (1, 13, 14, 15, 19), *CBFB* (5), *DEK* (2, 9), *EP300* (6), *ETV6* (4, 5), *FGFR1* (7, 8, 9, 10), *FIP1L1* (10, 11, 12, 13), *JAK2* (8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19), *KAT6A* (15, 16), *KMT2A* (6, 7, 8, 9, 10, 11, 12, 21, 22, 23), *MEF2D* (5, 6, 7), *MYH11* (28, 29, 30, 31, 32), *NUP214* (6, 16, 17), *NUP98* (10, 11, 12, 13), *PCM1* (24, 25, 26, 28, 36), *PDGFRA* (11, 12) **[12]**, *PDGFRB* (9, 10, 11), *PICALM* (16, 17, 18), *PML* (3, 5, 6) **[6]**, *RARA* (2), *RUNX1* (6), *RUNX1T1* (1), *SET* (7), *TAL1* (1, 2, 3), *TCF3* (13, 14, 15, 16, 17), *ZNF384* (2)[3]
Chromosomal aberrations	*+8, +9, +19, -5, -7, -13, del(5q), del(7q), del(11q), del(12p), del(13q), del(17p), del(20q)*
Variants detected	SNVs · Indels · CNVs · *FLT3* ITDs · *KMT2A* PTDs · Chr. aberrations · LoH[4] · Partner-agnostic fusions
Sample type	Blood or bone marrow
Starting material	From 50 ng DNA
Reads per sample	25 million
Multiplexing guidelines for 1,000x depth (2x150bp)	Illumina NextSeq® 1000/2000 P1: **8-12 samples** Illumina NextSeq® 1000/2000 P2: **32 samples** Illumina NextSeq® 500/550 Mid-Output v2: **8 samples**[5] Illumina NextSeq® 500/550 High-Output v2: **32 samples**
Product codes	CS2598ILLRSMY13-16; CS2598ILLRSMY13-32; CS2598ILLRSMY13-48

1. Launching in May 2025. 2. Data on File. 3. List of genomic breakpoint fusions in (intronic) and [exonic] regions. 4. The application enables client inference on LoH; future developments are planned to optimize clients' LoH analysis. 5. Certain target regions may not reach 1,000x coverage depth due to technical limitations.

Want to know more?
contact us at: info@sophiagenetics.com

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