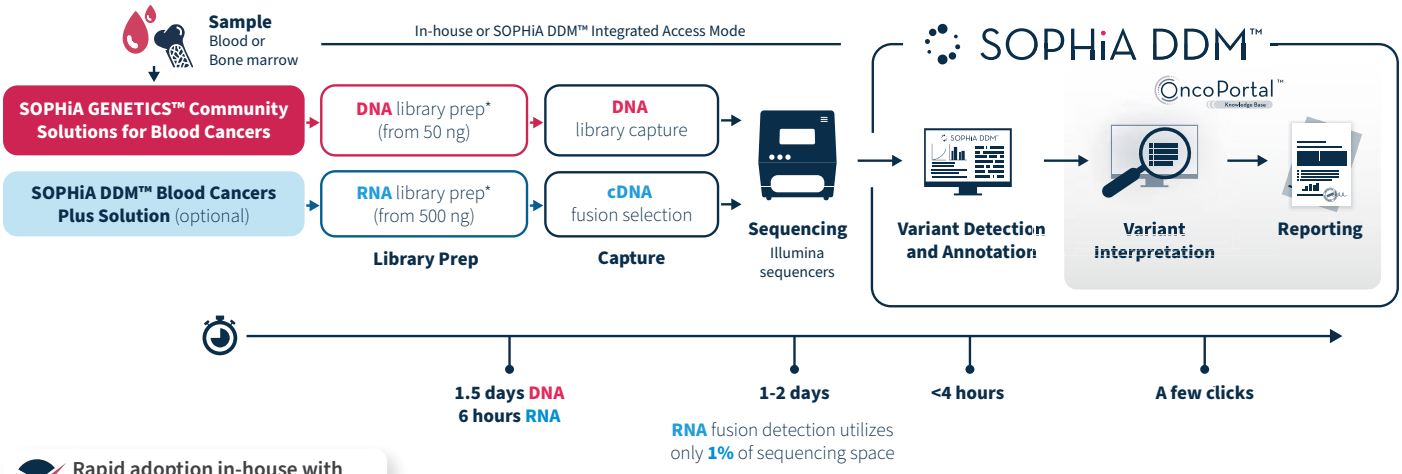
SOPHiA GENETICS™

SOPHiA GENETICS™ Community Solutions for Blood Cancers

Accelerate discovery with expert-designed applications

SOPHiA GENETICS™ Community Solutions for Blood Cancers are **expert-designed**, customizable, and **capture-based**, minimizing setup time and accelerating research. Tailored for hematological malignancies, these solutions, combined with the analytical power of the SOPHiA DDM™ Platform, deliver fast, accurate, and cost-effective insights from targeted regions of interest.

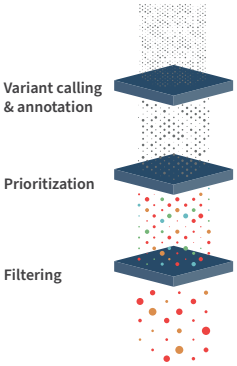
STREAMLINED SAMPLE-TO-REPORT WORKFLOW



RNA fusion detection utilizes only **1%** of sequencing space

Rapid adoption in-house with SOPHiA DDM™ MaxCare Program

RELIABLE VARIANT DETECTION WITH OPTIONAL FUSION CALLING



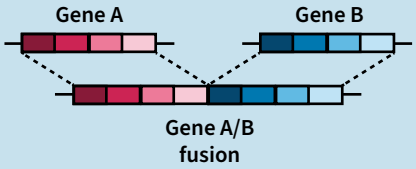
Detect **SNVs**, **CNVs**, **Indels**, and **known fusions** in a single workflow, with comprehensive and reliable **annotation**

Pre-classify variant pathogenicity based on recent guidelines and machine learning

Leverage **virtual panels** to focus interpretation on specific gene subsets, with **cascading filters** to refine analysis to the most relevant alterations

ADD-ON

SOPHiA DDM™ Blood Cancer Plus Solution



Detect **118** fusion pairs from **RNA** samples

Our fusion detection technology is designed to minimize false positives and allow the accurate detection of fusions even in degraded samples.

BENEFITS OF SOPHiA GENETICS™ COMMUNITY SOLUTIONS FOR BLOOD CANCERS

- Uniform coverage of target regions
- High-quality probe design to optimize on-target rate
- Gene content curated by experts in hematological malignancies
- Simple and reliable data analysis and interpretation

OFFICIAL INDIA CHANNEL PARTNER Genique Lifesciences™

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contact@genique.co +91 124-426-3051 www.genique.co

1. Currently readily available for some solutions. For others, the Plus add-on is available on-demand.

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TARGETED APPLICATIONS FOR MYELOID MALIGNANCIES

Solution name Reference	Genes covered & additional variants called[1]	Sequencer/Flowcell/ Samples per run[2]	Product codes
SOPHiA DDM™ Community Myeloid Solution 35 genes (CMYS-35)* CMYS_B_v1	**35 genes:** *ABL1, ASXL1, BCOR, BRAF, CALR, CBL, CEBPA, CSF3R, DNMT3A, ETV6, EZH2, FLT3, HRAS, IDH1, IDH2, JAK2, KIT, KRAS, MPL, MYD88, NOTCH1, NPM1, NRAS, PPM1D, PTPN11, RUNX1, SETBP1, SF3B1, SRSF2, STAG2, TET2, TP53, U2AF1, WT1, ZRSR2*	**Reads/sample:** 2.9-3.8 million[3] **MiSeq v2/v3:** 32 / 48 **NextSeq 500/550 MO/HO:** 180 / 540 **NextSeq 1000/2000 P1/P2:** 136 / 540	CS2111ILLRSMY10-048 **CMYS-35+ (DNA&RNA):** CS2542ILLRSMY10-48
SOPHiA DDM™ Community Myeloid Solution 51 genes (CMYS-51)* CMYS_R_v1	**51 genes:** *ABL1, ANKRD26, ASXL1, BCOR, BCORL1, BRAF, CALR, CBL, CEBPA, CSF3R, DDX41, DHX15, DNMT3A, ETNK1, ETV6, EZH2, FLT3, GATA1, GATA2, GNB1, HRAS, IDH1, IDH2, JAK2, KIT, KMT2A, KRAS, MPL, NF1, NFE2, NPM1, NRAS, PHF6, PPM1D, PRPF8, PTPN11, RAD21, RUNX1, SETBP1, SF3B1, SMC1A, SMC3, SRSF2, STAG2, TET2, THPO, TP53, U2AF1, UBA1, WT1, ZRSR2*	**Reads/sample:** 5-6.7 million[3] **MiniSeq HO:** 8 **MiSeq v2/v3:** 4-8 / 8-12 **NextSeq 500/550 MO/HO:** 40 / 120 **NextSeq 1000/2000 P1/P2:** 30-32 / 120	CS2520ILLRSMY10-16 CS2520ILLRSMY10-32 CS2520ILLRSMY10-48 **CMYS-51+ (DNA&RNA):** CS2556ILLRSMY10-16 CS2556ILLRSMY10-32 CS2556ILLRSMY10-48
SOPHiA DDM™ Community Myeloid Solution 65 genes (CMYS-65)* CMYS_F_v3	**65 genes:** *ANKRD26, ASXL1, ASXL2, ATM, BCOR, BCORL1, BRAF, CALR, CBL, CCND3, CEBPA, CSF3R, CSNK1A1, DDX41, DNMT3A, EIF6, EP300, EPOR, ETNK1, ETV6, EZH2, FLT3, GATA1, GATA2, HRAS, IDH1, IDH2, JAK2, KIT , KRAS, MPL, NF1, NFE2, NPM1, NRAS, PHF6, PPM1D, PRPF8, PTPN11, RAD21, RBBP6, RPL23, RUNX1, SBDS, SETBP1, SF3B1, SH2B3, SMC1A, SMC3, SRP68, SRP72, SRSF2, STAG1, STAG2, TERC, TERT , TET2, TET3, THPO, TP53, U2AF1, U2AF2, UBA1, WT1, ZRSR2*	**Reads/sample:** 6.1-8.2 million[3] **MiSeq v3:** 8	CS2463ILLRSMY10-32 CS2463ILLRSMY10-48 **CMYS-65+ (DNA&RNA):** CS2604ILLRSMY10-48
SOPHiA DDM™ Community Myeloid Solution v2 (MYS2) ExtMYS_v2_FD_hg38	**94 genes:** *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, BCL9, BCR, CBFB, DEK, EP300, ETV6, FGFR1, FIP1L1, JAK2, KAT6A, KMT2A, MEF2D, MYH11, NUP214, NUP98, PCM1, PDGFRA, PDGFRB, PICALM, PML, RARA, RUNX1, RUNX1T1, SET, TAL1, TCF3, ZNF384* **Additional variants:** *FLT3* ITDs, *KMT2A* PTDs, Chromosomal aberrations, partner-agnostic fusions, LoH[5]	**Reads/sample:** 25 million[4] **NextSeq 500/550 MO/HO:** 8-12 / 32 **NextSeq 1000/2000 P1/P2:** 8-12 / 32	CS2598ILLRSMY13-16 CS2598ILLRSMY13-32 CS2598ILLRSMY13-48

TARGETED APPLICATIONS FOR LYMPHOID MALIGNANCIES

Solution name Reference	Genes covered & additional variants called[1]	Sequencer/Flowcell/ Samples per run[2]	Product codes
SOPHiA DDM™ Community CLL Clonality Solution (CLL) CCLL_A_v3	**23 genes:** *ATF1, ATM, BCL2, BIRC3, BTK, CDK4, CUL4A, CXCR4, DLEU1, EGR2, FBXW7, KLF5, KRAS, MYD88, NFKBIE, NOTCH1, PLCG2, POT1, PROZ, RB1, SF3B1, TP53, XPO1* **Additional variants:** IGH locus rearrangements	**Reads/sample:** 2.5-3.4 million[3] **MiSeq v2/v3:** 12 / 16-24 **NextSeq 500/550 MO/HO:** 96 / 320 **NextSeq 1000/2000 P1/P2:** 60 / 320	CS2462ILLRSMY10-16 CS2462ILLRSMY10-32 CS2462ILLRSMY10-48
SOPHiA DDM™ Community Lymphoid Solution 33 genes (CLYMP-33) CLYMP_B_v1	**33 genes:** *ARID1A, B2M, BCL2, BIRC3, BRAF, BTK, CARD11, CCND1, CD79A, CD79B, CDKN2A, CREBBP , CXCR4, EP300, EZH2, FOXO1, ID3, KLF2, MEF2B, MYC, MYD88, NFKBIE, NOTCH1, NOTCH2, PLCG2, PTPRD, SF3B1, STAT6, TCF3, TNFAIP3, TP53, TRAF2, XPO1*	**Reads/sample:** 2.3-3.1 million[3] **MiSeq v3:** 16	CS2291ILLRSMY10-32
SOPHiA DDM™ Community Multiple Myeloma Solution 43 genes (CMM-43) CMM_A_v1	**43 genes:** *ACTG1, ATM, BIRC2, BRAF, CCND1, CDKN1B, CDKN2C, CKS1B, CRBN, CYLD, DIS3, DUSP2, EGR1, FAT3, FGFR3, FMN2, HIST1H1E, HUWE1, IRF4, KLHL6, KRAS, L TB, MAF, MAX, MYC, NF1, NFKB2, NRAS, PPM1D, PRDM1, PRKD2, PTPN11, RASA2, RB1, ROBO1, SP140, TENT5C, TP53, TRAF2, TRAF3, UBR5, ZFHX4, ZNF292*	**Reads/sample:** 6.6-8.8 million[3] **MiSeq v3/v2:** 4 / 8 **NextSeq 500/550 MO/HO:** 30 / 96 **NextSeq 1000/2000 P1/P2:** 24 / 96	CS2221ILLRSMY10-016
SOPHiA DDM™ Community Lymphoid Solution 73 genes (CLYMP-73) LYMP_CLSO_v3	**73 genes:** *ARID1A, ATM, B2M, BCL2, BCL6, BCOR, BIRC3, BRAF, BTG1, BTK, CARD11, CCND1, CCND3, CD28, CD58, CD79A, CD79B, CDKN2A, CDKN2B, CIITA, CREBBP , CXCR4, DDX3X, DNMT3A, EP300, ETV6, EZH2, FAT1, FBXW7, FOXO1, GNA13, HIST1H1E, ID3, IDH2, INPP5D, IRF4, ITPKB, JAK3, KLF2, KMT2D, KRAS, MAP2K1, MEF2B, MFHAS1, MYC, MYD88, NFKBIE, NOTCH1, NOTCH2, NRAS, PIM1, PLCG1, PLCG2, PRDM1, PTEN, PTPRD, RHOA, SETD2, SF3B1, SOCS1,STAT3, STAT5B, STAT6, TBL1XR1, TCF3, TET2, TNFAIP3, TNFRSF14, TP53, TP63, TRAF2, TRAF3, XPO1*	**Reads/sample:** 4.5 million[6] **NextSeq 500/550 MO/HO:** 24 / 72 **NextSeq 1000/2000 P1/P2:** 16-24 / 72	CS2456ILLRSM10-32 CS2456ILLRSMY10-48

CLL, Chronic Lymphocytic Leukemia; HO, High-Output Kit; IDTs, Internal Tandem Duplications; IGH, Immunoglobulin Heavy Locus; LoH, Loss of Heterozygosity; MO, Mid-Output Kit; PTDs, Partial Tandem Duplications.
*Fusion detection with SOPHiA DDM™ Blood Cancers Plus Solution currently available. For other Community Solutions, the Plus add-on module is available on-demand.
1. Variants called in addition to SNVs, CNVs, and Indels. 2. Sequencing recommendations and pipelines for other sequencing kits and instruments are available upon request. The number of samples per run is recommended for 1000x coverage depth. Illumina NextSeq instruments require 2×150 bp sequencing on compatible flow cells. 3. Reads per sample ranges recommended for blood samples for Illumina MiSeq® instruments for 2x300bp and 2x150bp read length. 4. Reads per sample recommendations based on blood samples in Illumina NextSeq™ instruments. 5. The application enables client inference on LoH; future developments are planned to optimize clients' LoH analysis. 6. Reads per sample recommended for FFPE samples in Illumina NextSeq™ instruments.

COMPREHENSIVE & HEREDITARY APPLICATIONS FOR BLOOD CANCERS

Solution name Reference	Genes covered	Sequencer/Flowcell/ Samples per run[2]	Product codes
SOPHiA DDM™ Comprehensive Blood Cancer Solution 59 genes (CBS-59) CHEMA_B_v1	**59 genes:** *AKT1, ATM, BCL11B, BRAF, CCND3, CNOT3, CREBBP , CTCF, DNM2, EED, EP300, ETV6, EZH2, FAT1, FAT3, FBXW7, FL T3, GATA3, GLI1, GLI2, GLI3, IKZF1, IL2RB, IL7R, JAK1, JAK3, KDM6A, KMT2D, KRAS, LEF1, LMO1, LMO2, MED12, MYB, NF1, NOTCH1, NRAS, NT5C2, PHF6, PIK3CD, PIK3R1, PTCH1, PTEN, RELN, RPL10, RPL22, RPL5, RUNX1, SETD2, SH2B3, SMARCA4, SMO, STAT5B, SUZ12, TP53, TYK2, USP7, USP9X, WT1*	**Reads/sample:** 12 million[2] **MiSeq v3:** 5	CS2450ILLRSMY10-32
SOPHiA DDM™ Comprehensive Blood Cancer Solution 109 genes (CBS-109)* CHMLS_B_v1	**109 genes:** *ABL1, ANKRD26, ARID1A, ASXL1, ASXL2, ATM, ATRX, B2M, BCL2, BCL6, BCOR, BCORL1, BIRC3, BRAF, BTK, CALR, CARD11, CBL, CBLB, CBLC, CCND1, CCND2, CCND3, CD58, CD79A, CD79B, CDKN2A, CDKN2B, CEBPA, CREBBP , CRLF2, CSF3R, CUX1, CXCR4, DDX41, DNMT3A, EP300, ETNK1, ETV6, EZH2, FBXW7, FL T3, FOXO1, GATA1, GATA2, GNA13, GNAS, HRAS, ID3, IDH1, IDH2, IKZF1, IL7R, JAK1, JAK2, JAK3, KDM6A, KIT , KLF2, KMT2A, KMT2D, KRAS, MAP2K1, MEF2B, MPL, MYC, MYD88, NF1, NFKBIE, NOTCH1, NOTCH2, NPM1, NRAS, PAX5, PDGFRA, PHF6, PIM1, PLCG2, POT1, PPM1D, PRDM1, PTEN, PTPN11, RAD21, RB1, RHOA, RUNX1, SETBP1, SETD2, SF3B1, SH2B3, SMC1A, SMC3, SOCS1, SRP72, SRSF2, STAG2, STAT3, STAT5B, STAT6, TCF3, TET2, TNFAIP3, TNFRSF14, TP53, U2AF1, WT1, XPO1, ZRSR2*	**Reads/sample:** 15.3 million[2] **NextSeq 500/550 MO/HO:** 16 / 48 **NextSeq 1000/2000 P1/P2:** 12 / 48	CS2445ILLRSMY10-16 CS2445ILLRSMY10-32 CS2445ILLRSMY10-48 **CBS-109+ (DNA&RNA):** CS2446ILLRSCY10-16 CS2446ILLRSCY10-32 CS2446ILLRSCY10-48
SOPHiA DDM™ Hereditary Blood Cancers Solution 160 genes (CHBS-160) CHHS_A_v1	**160 genes:** *ACD, ACKR1, ADA2, ADAR, AIRE, AK2, ANKRD26, AP3B1, ASXL1, ATG2B, ATM, BLM, BLOC1S6, CARD11, CASP10, CASP8, CBL, CD19, CD27, CD40, CD40LG, CD70, CD79B, CEBPA, CLPB, CSF3R, CTC1, CTLA4, CTPS1, CXCR2, CXCR4, DCLRE1C, DDX3X, DDX41, DKC1, DNAJC21, DNM2, EFL1, EIF2AK3, ELANE, EOMES, ERAP1, ERCC6L2, ETV6, FADD, FAS, FASLG, FOXP3, G6PC3, GATA1, GATA2, GATA3, GBA, GFI1, GORASP1, GSKIP , HAX1, IKBKG, IKZF1, IL10, IL10RA, IL10RB, IL13, IL2RA, ITK, JAGN1, KRAS, LAMTOR2, LIG4, LRBA, LYST , MAGT1, MECOM, MPL, MRTFA, MS4A1, MYD88, MYSM1, NAF1, NBN, NCKAP1L, NFKB1, NHEJ1, NHP2, NOP10, NPM1, NRAS, PARN, PIK3CB, PIK3CD, PIK3R1, POT1, PRF1, PRKCD, PVT1, RAB27A, RAC2, RAG1, RAG2, RASGRP1, RBBP6, REL, RMRP, RPL11, RPL15, RPL26, RPL27, RPL35A, RPL5, RPS10, RPS14, RPS17, RPS19, RPS24, RPS26, RPS27, RPS28, RPS29, RPS7, RTEL1, RUNX1, SAMD9, SAMD9L, SBDS, SEC61A1, SH2D1A, SLC37A4, SLC7A7, SMARCAL1, SMARCD2, SOCS1, SRP54, SRP72, STAT1, STAT3, STAT5B, STK4, STN1, STX11, STXBP2, TAZ, TCF3,TCIRG1, TCN2, TERC, TERT , TINF2, TLR8, TNFRSF13B, TNFRSF13C, TP53, TSR2, UNC13D, USB1, VPS13B, VPS45, WAS, WIPF1, WRAP53, XIAP*	**Reads/sample:** 3.6-4.8 million[3] **MiSeq v3:** 12 **NextSeq 500/550 MO:** 48	CS2396ILLRGMY10-48

FUSION PAIRS INTERROGATED BY THE SOPHiA DDM™ BLOOD CANCERS PLUS SOLUTION

Fusion partner 1	Fusion partner 2
ATF7IP(13)	*JAK2(9,11,13,15,17,18,19)*
BCR(1,4,6,7,12,13,14,19)	*ABL1(2,3,4), FGFR1(11), JAK2(9,11,13,15,17,18,19), PDGFRA(12)*
BMP2K(14,15)	*ZNF384(2,3,4,7)*
CMFA2T3(10, 11)	*GLIS2(4,5)*
CBFB(4,5)	*MYH11(29,30,31,32,33,34,35)*
CCDC6(1,7)	*PDGFRB(9,11)*
CHIC2(3)	*ETV6(2,3)*
CNTRL(38)	*FGFR1(11)*
CREBBP(4,5,6,7)	*ZNF384(2,3,4,7)*
CUX1(11)	*FGFR1(11)*
DEK(9)	*NUP214(17,18)*
EBF1(10,13,14,15)	*JAK2(9,11,13,15,17,18,19), PDGFRB(9,11)*
EML1(18)	*ABL1(2,3,4)*
EP300(6)	*ZNF384(2,3,4,7)*
ETV6(4,5,6,7)	*ABL1(2,3,4), ARNT(3), JAK2(9,11,13,15,17,18,19), NTRK3(14), NTRK3(15), PDGFRB(9,11), RUNX1(1), RUNX1(3)*
FGFR1OP(5,6,7)	*FGFR1(11)*
FIP1L1(12)	*PDGFRA(12)*
FOXP1(19)	*ABL1(2,3,4)*
INPP5D(8)	*ABL1(2,3,4)*
KAT6A(16)	*CREBBP(2,3)*
KMT2A(8,9,10,11)	*AFDN(2), AFF1(4,5,6,11), AFF3(7,8,12), AFF4(4,5,6), ARHGAP26(19), ARHGEF12(11,12,13), ARHGEF17(2,3,4,5), C2CD3(13,14,15,17), CBL(10), CIP2A(17), CREBBP(2,3), DCPS(2), ELL(2,3,6), EPS15(2,6), FOXO3(2), KMT2A(2), KNL1(12), MAML2(2,3), MAPRE1(2,4,6), MLLT1(2,4,5,6,7), MLLT10(5,7,10,12,17), MLLT11(2), MLLT3(4,5,6,9,10), MLLT6(8,9,12), NRIP3(2), RARA(2), SEP5(2), SEPT6(2), SEPT9(2), TET1(9)*
MEF2D(7)	*CSF1R(12)*
MN1(1)	*ETV6(2,3)*
MNX1(1)	*ETV6(2,3)*
MYB(8)	*GATA1(5)*
NCOR1(35)	*LYN(8)*
NDE1(6)	*PDGFRB(9,11)*
NPM1(4,6)	*MLF1(3), RARA(2)*
NUP214(23,26,28,29,30,31,32,34)	*ABL1(2,3,4)*
NUP98(10,11,12,13,14)	*DDX10(6,7), HOXA9(1,2), KDM5A(27), NSD1(6), RAP1GDS1(2,3), TOP1(8)*

Fusion partner 1	Fusion partner 2
OFD1(21)	*JAK2(9,11,13,15,17,18,19)*
P2RY8(1)	*CRLF2(1)*
PAG1(8)	*ABL2(3,5)*
PAX5(4)	*ETV6(2,3), JAK2(9,11,13,15,17,18,19)*
PAX5(5)	*ETV6(2,3), JAK2(9,11,13,15,17,18,19)*
PCM1(26,36)	*JAK2(9,11,13,15,17,18,19)*
PDE4DIP(16)	*PDGFRB(9,11)*
PICALM(17,18,19)	*MLLT10(5,7,10,12,17)*
PML(3,6)	*RARA(2)*
RANBP2(18)	*ABL1(2,3,4)*
RBM15(1)	*MKL1(4,5)*
RCSD1(2)	*ABL1(2,3,4)*
RCSD1(3)	*ABL1(2,3,4)*
RUNX1(3)	*RUNX1T1(6)*
SET(7)	*NUP214(17,18)*
SFPQ(9)	*ABL1(2,3,4)*
SNX2(3)	*ABL1(2,3,4)*
SPAG9(26)	*JAK2(9,11,13,15,17,18,19)*
SPTBN1(4)	*FLT3(14), PDGFRB(9,11)*
SSBP2(5,6,8,10,16)	*CSF1R(12), JAK2(9,11,13,15,17,18,19)*
STAT5B(15,16)	*RARA(2)*
STIL(1)	*TAL1(3,4,6)*
STRN(6)	*PDGFRA(12)*
STRN3(8,9)	*JAK2(9,11,13,15,17,18,19)*
TAF15(6,9)	*ZNF384(2,3,4,7)*
TCF3(11,13,15,16,17)	*HLF(4), PBX1(3)*
TERF2(8)	*JAK2(9,11,13,15,17,18,19)*
TPM3(8)	*PDGFRB(9,11)*
TPR(22,39)	*FGFR1(11)*
TRIM24(9,10,11)	*FGFR1(11)*
ZBTB16(3,4)	*ABL1(2,3,4), RARA(2)*
ZC3HAV1(12)	*ABL2(3,5)*
ZEB2(9)	*PDGFRB(9,11)*
ZMIZ1(18)	*ABL1(2,3,4)*
ZMYM2(17)	*FGFR1(11)*

1. Sequencing recommendations and pipelines for other sequencing kits and instruments are available upon request. The number of samples per run is recommended for 1000x coverage depth. Illumina NextSeq instruments require 2×150 bp sequencing on compatible flow cells. 2. Reads per sample recommendations based on blood samples in Illumina NextSeq™ instruments. 3. Reads per sample ranges recommended for blood samples for Illumina MiSeq® instruments for 2x300bp and 2x150bp read length.

WANT TO KNOW MORE?

Contact us at info@sophiagenetics.com

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