SureSeq

A Sysmex Group Company

Myeloid Fusion Panel

Features

Developed in partnership with myeloid cancer experts to the latest WHO guidance

- Combining expert-led panel design with hybridization-based enrichment for unparalleled uniformity and depth of coverage

RNA-based, partner gene agnostic panel

- Detect 30 common myeloid fusions plus novel fusion partners in a single cost-efficient assay

Full assay and software solution

- Streamlined library prep and intuitive, complimentary data analysis software — all backed up by OGT's expert support

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Introduction

Fusion genes, hybrid genes formed from two previously independent genes, are implicated in a wide range of cancers — particularly myeloid cancers. Research has revealed the presence of fusion genes in ~41% of acute myeloid leukaemia (AML) and 29% of acute lymphoblastic leukaemia (ALL) cases[1,2].

Traditional methods to detect fusion genes include fluorescence *in situ* hybridization (FISH) and reverse transcription polymerase chain reaction (RT-PCR). More recently, next-generation sequencing (NGS) has emerged as a key method for fusion gene identification and characterisation. This technique, unlike FISH, can simultaneously detect multiple fusion genes in a single assay. Furthermore, hybridization-based NGS assays, such as the SureSeq™ Myeloid Fusion Panel, can identify novel fusion partners — providing more comprehensive and informative analyzes than possible using PCR-driven methods.

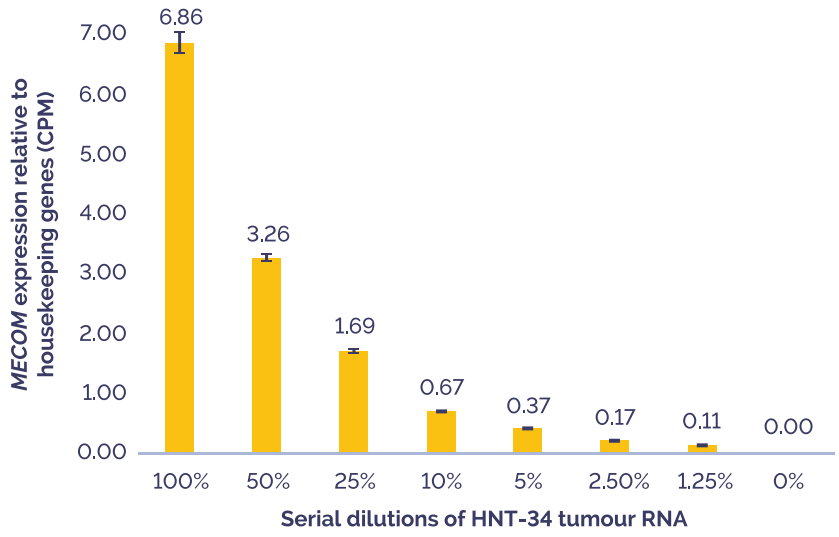
Expert-led, evidence-based content

The RNA-based SureSeq Myeloid Fusion Panel has been designed in collaboration with leading myeloid cancer experts and has been informed by the latest WHO guidance to include clinically relevant fusions in AML[3]. The panel further enables the identification of gene expression changes in *MECOM*, supporting the identification of *GATA2::MECOM* (inv(3)(q21.3q26.2)) and *RPN1::MECOM* (inv(3)(q21q26)).

SureSeq Myeloid Fusion Panel			
RBM15::*MKL1* t(1;22)(p13.3;q13.3)	***KMT2A***::*ELL* t(11;19)(q23;p13.1)	***FUS***::*ERG* t(16;21)(p11.2;q22.2)	***FGFR1***::*ZMYM2* t(8;13)(p11;q12)
GATA2::***MECOM*** (*GATA2::EVI1*) inv(3)(q21.3q26.2) **via *MECOM* overexpression**	***KMT2A***::*MLLT1* (*ENL*) t(11;19)(q23;p13.3)	***CBFB***::*MYH11* inv(16)(p13.1q22)	*FIP1L1*::***PDGFRA*** del(4)(q12q12)
RPN1::***MECOM*** (*RPN1::EVI1*) inv(3)(q21q26) **via *MECOM* overexpression**	***KMT2A***::*AFDN (KMT2A::AF6; KMT2A::MLLT4)* *t(6;11)(q27;q23)*	***RUNX1***::*RUNX1T1* (*AML1::ETO*) t(8;21)(q22;q22.1)	***PDGFRB***::*EBF1* del(5)(q32q33)
DEK::***NUP214*** (*DEK::CAN*) t(6;9)(p23;q34.1)	***KMT2A***::*MLLT11* t(1;11)(q21;q23)	*ETV6*::***RUNX1*** (*TEL::AML1*) t(12;21)(p13;q22)	***PDGFRB***::*TNIP1* t(5;5)(q32;q33)
NUP98::*NSD1* t(5;11)(q35.2;p15.4)	***KMT2A***::*NEBL* t(10;11)(p12;q23)	***RUNX1***::***MECOM*** (*AML1::EVI1*) t(3;21)(q26.2;q22)	***PDGFRB***::*ATF7IP* t(5;12)(q33;p13)
NUP98::*HOXA9* t(7;11)(p15.4;p15.2)	***PML***::*RARα* t(15;17)(q24;q21)	***BCR***::*ABL1* t(9;22)(q34.1;q11.2)	***PDGFRB***::*ETV6* t(5;12)(q33;p13)
PICALM::*MLLT10* t(10;11)(p12.3;q14.2)	*KAT6A*::***CREBBP*** t(8;16)(p11.2;p13.3)	*NPM1*::***MLF1*** t(3;5)(q25.1;q35.1)	
KMT2A::*MLLT3* (*KMT2A::AF9*) t(9;11)(p21.3;q23.3)	*PCM1*::***JAK2*** t(8;9)(p22;p24)	***FGFR1***::***BCR*** t(8;22)(p11;q11)	

Table 1: The SureSeq Myeloid Fusion Panel allows identification of 30 of the most clinically-relevant fusions implicated in AML. Specific gene targeting (bold text) allows accurate partner gene agnostic identification of fusion genes.

A



B

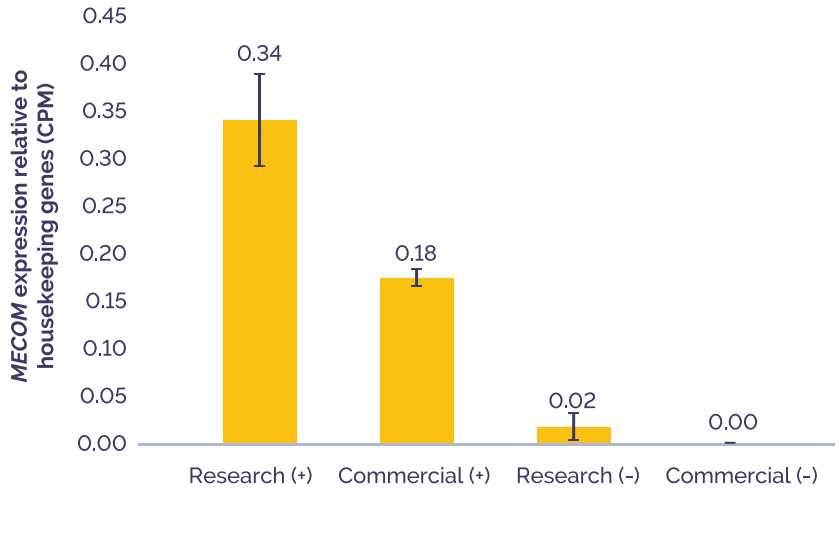


Figure 1: Consistent and confident detection of *MECOM* overexpression in A serial dilutions of HNT-34 cell line as well as B research and commercial samples, including positive and negative controls. *MECOM* expression is normalised to the expression of housekeeping genes and expression values are calculated as counts per million (CPM). 'Research (+)' refers to research sample containing *GATA2::MECOM* (inv(3)(q21.3q26.2)). 'Commercial (+)' refers to Universal Human Reference RNA (UHRR) used as positive control. 'Research (-)' refers to blood extracted RNA with no *GATA2::MECOM* (inv(3)(q21.3q26.2)). 'Commercial (-)' refers to normal human lymphocyte RNA used as negative control. Error bars represent standard deviation.

SureSeq

Myeloid Fusion Panel

Partner gene-agnostic fusion detection

By harnessing RNA-based partner gene agnostic technology you can simultaneously interrogate baited target fusions, including driver genes with multiple fusion partners (i.e. *KMT2A*). Together, with the ability to identify novel and/or rare fusions, this panel fully supports your research into myeloid cancer classification and progression. This unique approach further serves to minimize the panel size, lowering sequencing costs and enabling increased depth of coverage for more sensitive results.

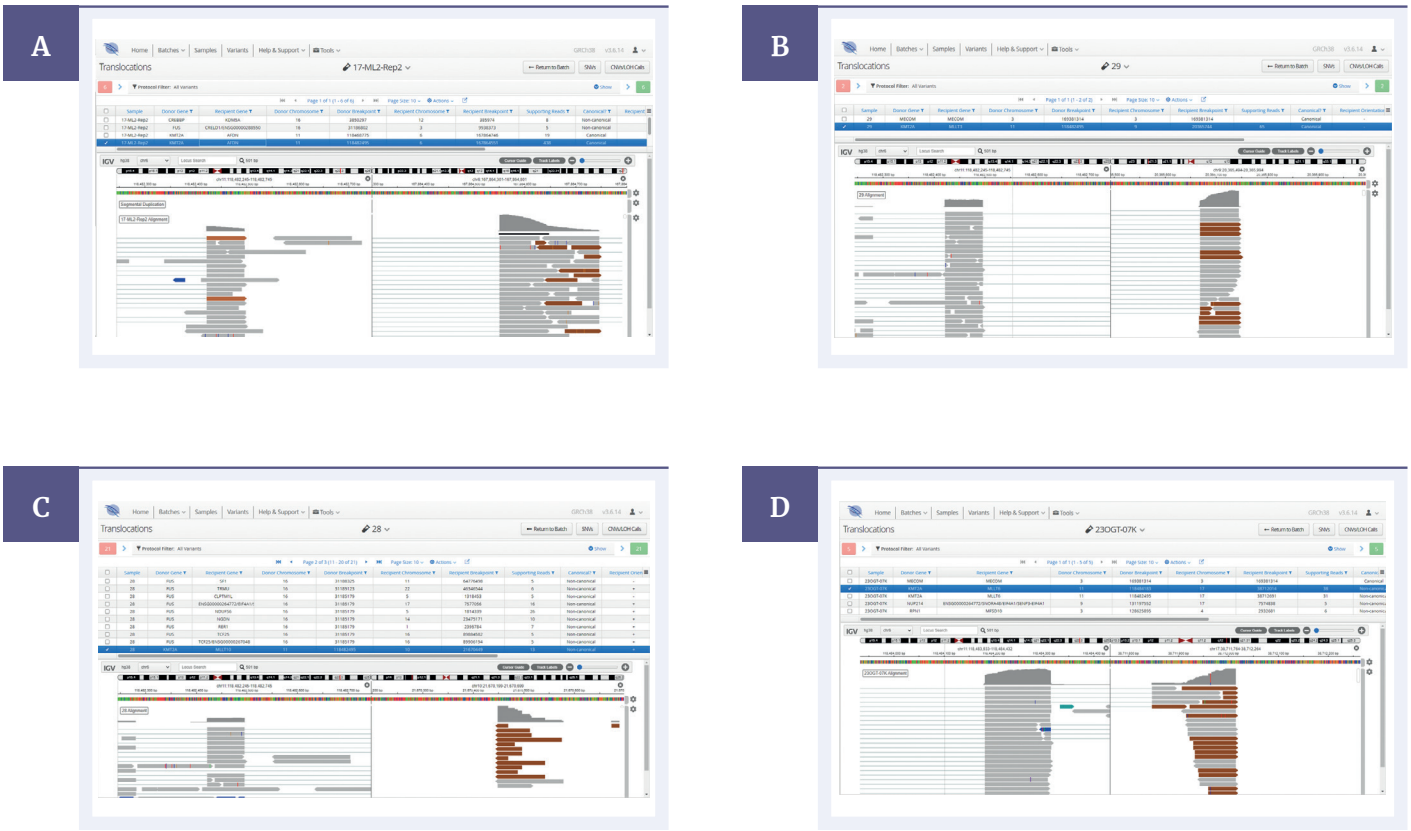


Figure 2: Interpret, OGT's complementary analysis software, enables identification of (A B) canonical fusions such as *KMT2A::AFDN (KMT2A::AF6; KMT2A::MLLT4)* and *KMT2A::MLLT3 (KMT2A::AF9)* as well as (C D) novel fusions such as *KMT2A::MLLT10* and *KMT2A::MLLT6* emphasising the partner gene agnostic capability for fusion detection.

A streamlined solution

The SureSeq Myeloid Fusion Complete NGS Workflow Solution V2 is an RNA-based assay, which allows sensitive and more cost-efficient identification of fusion genes than alternative DNA-based panel designs. Only transcriptionally expressed and therefore more clinically relevant gene fusions are analyzed.

All SureSeq panels utilise hybridization-based enrichment, which, when combined with OGT's intelligent probe design, offers highly uniform coverage for sensitive and reliable results.

Two kit sizes are available, offering the facility to analyze either 24 or 96 samples, with multiplexing of up to 24 samples in a single MiSeq® sequencing run. The streamlined workflow, which utilises the industry-standard Universal NGS Workflow Solution, incorporates Unique Dual Indexes (UDI) prior to sample amplification to support accurate sample demultiplexing for highly robust and reliable results (Figure 3).

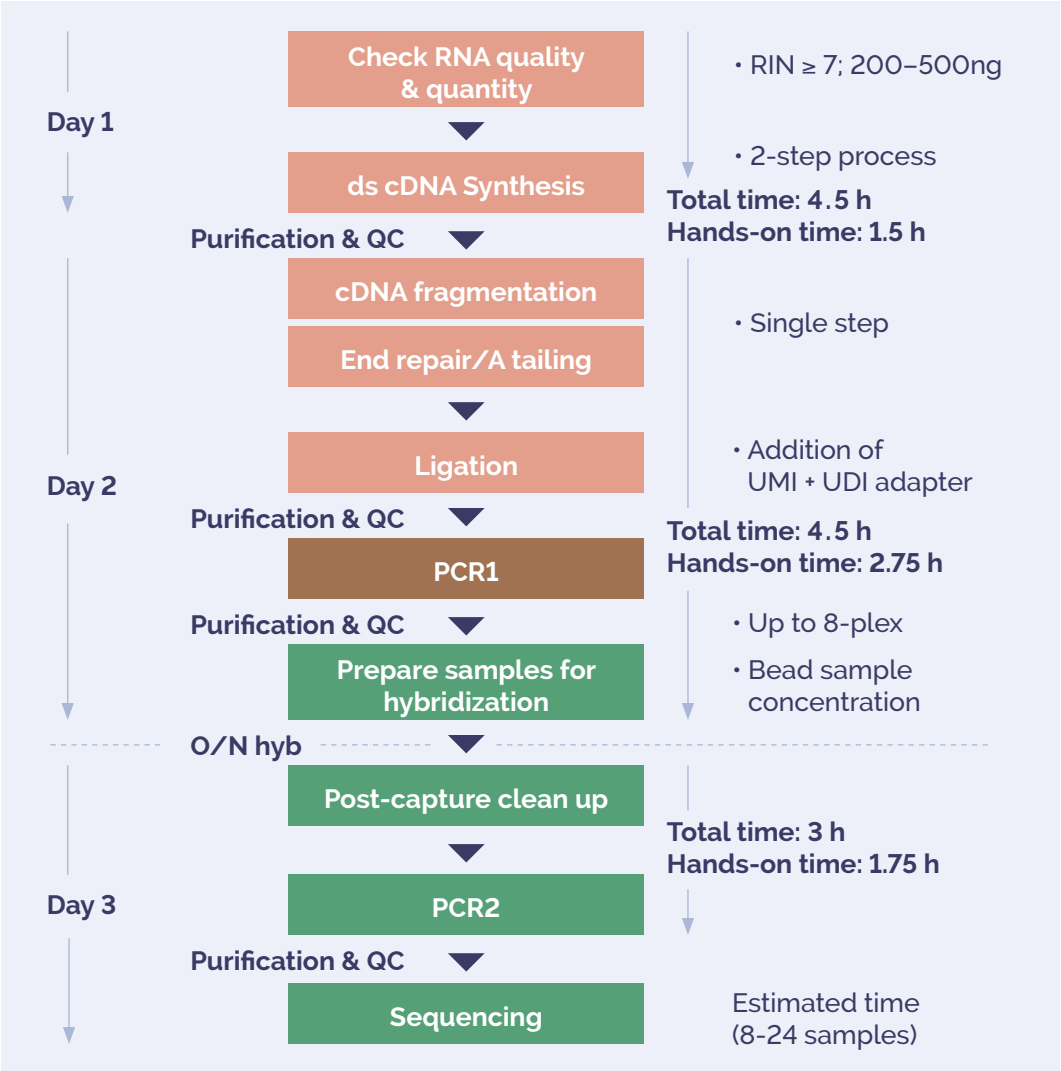


Figure 3: The fully optimized SureSeq Myeloid Fusion Complete NGS Workflow Solution V2 minimises hands-on time and provides all the reagents required to go from purified RNA to sequence-ready libraries.

Complimentary analysis software

Included as standard with all SureSeq panels, Interpret NGS Analysis Software, OGT's powerful and easy-to-use NGS data analysis solution, delivers comprehensive identification of fusion genes, including novel fusions (Figure 4). The software allows you to easily visualize fusion genes detected, focus in on breakpoints, the number of reads spanning each breakpoint and alignment of sequence reads at nucleotide resolution — for complete confidence in results. In addition, the software reports normalised gene expression levels related to *MECOM* rearrangements, plus all data files are available for further downstream analysis.

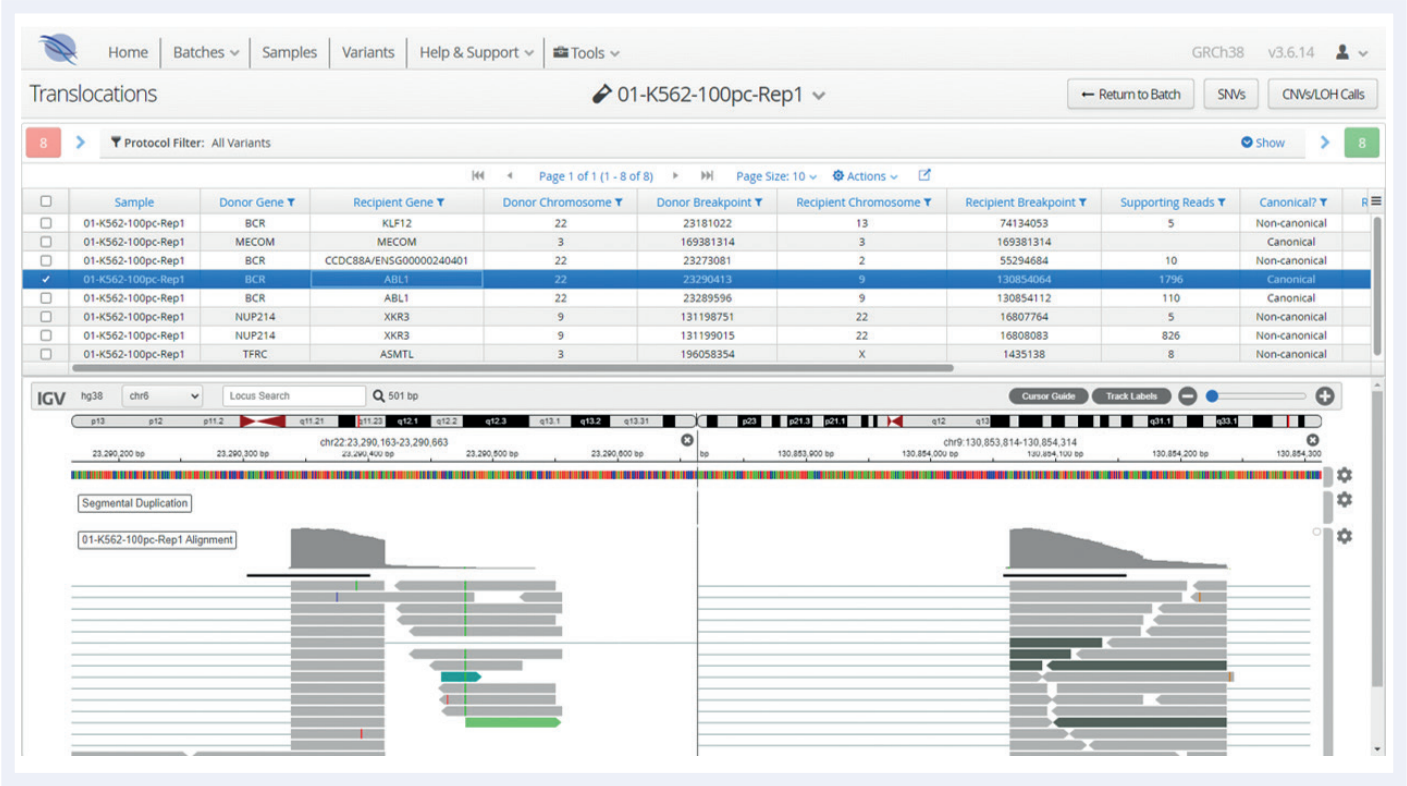


Figure 4: Interpret, OGT's complimentary analysis software, enables identification of canonical fusions such as *BCR::ABL1* in K562 cell line.

Our range of innovative NGS myeloid malignancy solutions

Browse our full range of myeloid panels, including the focused three-gene SureSeq Core MPN Panel and the SureSeq Pan-Myeloid Panel, incorporating key variants in 70 genes implicated in a wide range of myeloid disorders. In addition, the SureSeq Myeloid MRD Plus NGS Panel enables detection of of low-frequency variants as low as 0.01% VAF with confidence, even in challenging biomarkers.

SureSeq Myeloid Fusion Panel: technical information

Feature	Specification
Capabilities	Fusion and *MECOM* expression detection
Number of Fusions	30
Panel Size	61 kb
RNA input recommended	200–500 ng good quality RNA (RIN ≥7)
Sample Source	Whole blood, bone marrow extracted RNA

Request a quote at www.ogt.com or contact one of our experts at contact@ogt.com.

Ordering information

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US +1 914 467 5285

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ogt.com

Product	Contents	Cat. No.
SureSeq Myeloid Fusion Complete NGS Workflow Solution V2 (24)	Enrichment baits sufficient for 3 x 8-sample pools. Bundle of 1 x Double-Stranded cDNA Synthesis Kit (24). 1 x Universal Library Preparation Kit (24) containing PCR primers and enzymes. 1 x Universal Hybridization & Wash Kit V2 (24). 1 x Pre-PCR Universal Bead Kit (24). 1 x Post-PCR Universal Bead Kit (24). 1 x Universal Index Adapter Kit (24). Interpret NGS Analysis Software	890001-24
SureSeq Myeloid Fusion Complete NGS Workflow Solution V2 (96)	Enrichment baits sufficient for 12 x 8-sample pools. Bundle of 1 x Double-Stranded cDNA Synthesis Kit (96). 1 x Universal Library Preparation Kit (96) containing PCR primers and enzymes. 1 x Universal Hybridization & Wash Kit V2 (96). 1 x Pre-PCR Universal Bead Kit (96). 1 x Post-PCR Universal Bead Kit (96). 1 x Universal Index Adapter Kit (96). Interpret NGS Analysis Software	890001-96
SureSeq Myeloid Fusion Panel (24)	Enrichment baits sufficient for 3 x 8-sample pools. Interpret NGS Analysis Software	880001-24
SureSeq Myeloid Fusion Panel (96)	Enrichment baits sufficient for 12 x 8-sample pools. Interpret NGS Analysis Software	880001-96
SureSeq Double-Stranded cDNA Synthesis Kit (24)	Kit for conversion of 24 RNA samples to cDNA samples	880500-24
SureSeq Double-Stranded cDNA Synthesis Kit (96)	Kit for conversion of 96 RNA samples to cDNA samples	880500-96
Universal NGS Workflow Solution V2 (24)	Bundle of 1 x Universal Library Preparation Kit (24) containing, PCR primers and enzymes, 1 x Universal Hybridization & Wash Kit V2 (24). Pre-PCR Universal Bead Kit (24). Post-PCR Universal Bead Kit (24). 1 x Universal Index Adapter Kit (24)	770510-24
Universal NGS Workflow Solution V2 (96)	Bundle of 1 x Universal Library Preparation Kit (96) containing, PCR primers and enzymes, 1 x Universal Hybridization & Wash Kit V2 (96). Pre-PCR Universal Bead Kit (96). Post-PCR Universal Bead Kit (96). 1 x Universal Index Adapter Kit (96)	770510-96

References

1. Chen *et al.* Leuk Res. 2018;72:99-104.
2. Chen *et al.* Leuk Lymphoma 2019;60:1071-8.
3. Khoury *et al.* Leuk 2022;36:1703-19.

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What binds us, makes us.

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