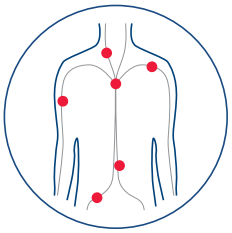
Challenging biomarkers – simplified leukemia testing

Streamline your leukemia workflows

One NGS solution for multiple genomic alterations

Sample to Insight

QIAGEN



Challenges of leukemia profiling

Oncohematology studies focus on profiling of relevant DNA variants and, particularly, RNA fusions, which frequently occur in myeloid and lymphoid hematological malignancies. A critical factor for accurate results is that there is no compromise on performance, especially when profiling challenging regions. Detection, calling and reporting of large InDels, such as CALR type 1 (52 bp del) and FLT3 ITDs, and also full coverage of GC-rich regions, such as CEBPA, requires optimized NGS workflows.

Recent advances in NGS chemistries, platforms and bioinformatics pipelines have empowered users to efficiently interrogate DNA and RNA alterations in biological samples. Current approaches, however, require the use of 2 separate workflows to prepare libraries from separate DNA and RNA isolates. Limitations of such approaches include:

- Precious samples, such as bone marrow, must be split to extract DNA and RNA in separate sample prep protocols
- Large amounts of sample material are required to generate sufficient amounts of input DNA and RNA for multiple workflows
- Workflow has added complexity of deriving integrated insights from results of different technical approaches, each with its own innate bias
- Separate workflows result in inefficient use of resources and long turnaround times

Streamlined, consolidated one-day workflow

To overcome the limitations associated with current approaches, the QIAseq Leukemia Multimodal panel starts with total nucleic acids (or DNA + RNA) and prepares targeted DNA and RNA libraries containing Unique Molecular Indices (UMIs) for Illumina® platforms using a one-day, consolidated workflow (see Figure 1).

The QIAseq Leukemia Multimodal panel delivers:

- The ONLY single consolidated workflow for simultaneous DNA + RNA library prep using total nucleic acids as input
- Operational efficiency with a 50% reduction in user interventions
- Confident detection of low-frequency variants with UMIs allowing detection of JAK2 and KIT at 1% VAF and KIT D816V at 0.4% VAF
- Reduced index hopping with Unique Dual Indices (UDIs)
- Comprehensive coverage of known and novel fusions as well as all relevant alterations
- Detection of large InDels, such as CALR type 1 (52 bp del) and FLT3 ITDs
- Full coverage of GC-rich regions, such as CEBPA
- Calling of homopolymer regions, such as for the ASXL1 homopolymeric p.G646fs*12 variant
- 145 DNA gene targets and 209 RNA fusion gene targets (Tables 1 and 2)

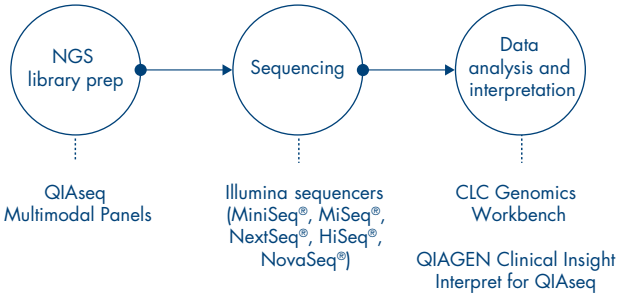


Figure 1. Extract more information, while reducing sample, time and cost with a simple, one-day workflow.* This flexible solution enables the construction of libraries compatible with Illumina platforms from as little as 10 ng total nucleic acid isolated from a wide range of samples. The data analysis pipelines in CLC Genomics Workbench translate raw sequence data in FASTQ format to DNA and RNA variant files (VCFs), which can be further interpreted for biological significance through QCI® Interpret for QIAseq.

Confidently interpret NGS variants

Our software workflow makes it easy to extract, identify the variants of interest and deliver a comprehensive variant interpretation from your raw NGS data. The industry leading genomic analysis and interpretation software solutions, CLC Genomic Workbench and QCI Interpret for QIAseq, provide you with a comprehensive report to support your workflow, including variant classification, details on variant function, literature references, drug labels, drug interactions and relevant clinical trials. Accelerate your clinical research and go from raw NGS data to detailed and trusted insights in minutes – not hours.

Our analysis and interpretation software solutions enable:

- Detection, calling and reporting of large InDels, such as CALR type 1 (52 bp del) and FLT3 ITDs with an identified insertion site (up to 228 bp) (Figures 2 and 3)
- Calling of homopolymer regions, even challenging ASXL1 homopolymeric variants, such as p.G646fs*12 (Figure 4)
- Full coverage of GC-rich regions, such as CEBPA (Figure 5)
- Detectable and reportable sensitivity levels down to 1% VAF for JAK2 and KIT and 0.4% VAF for KIT D816V using a comprehensive tutorial

Key differentiators

- The ONLY single consolidated workflow for DNA + RNA library prep using total nucleic acids as input
- Cuts user interventions by 50%
- Confident detection of low-frequency variants
- Detection of both known and novel fusions
- Increased target coverage of all relevant alterations
- Detection, calling and reporting of large InDels, such as CALR type 1 (52 bp del) and FLT3 ITDs
- Full coverage of GC-rich regions, such as CEBPA
- Calling of homopolymer regions, such as for the ASXL1 homopolymeric p.G646fs*12 variant

* One-day workflow for nucleic acid extraction and library prep.

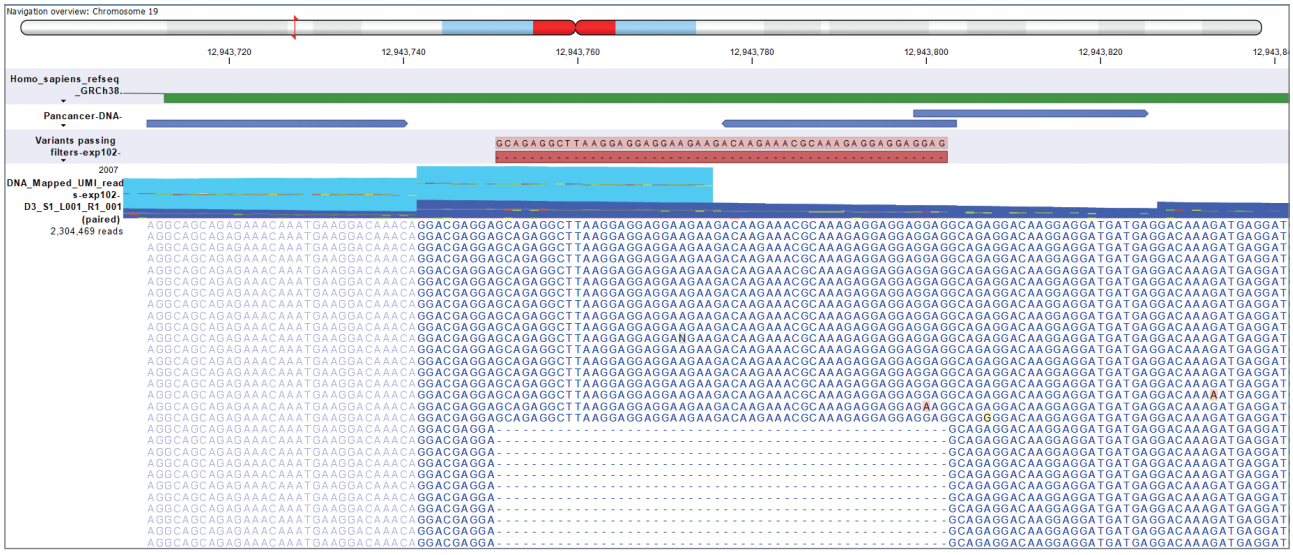


Figure 2. Detection, calling and reporting of large InDels, such as CALR type 1 (52 bp del).

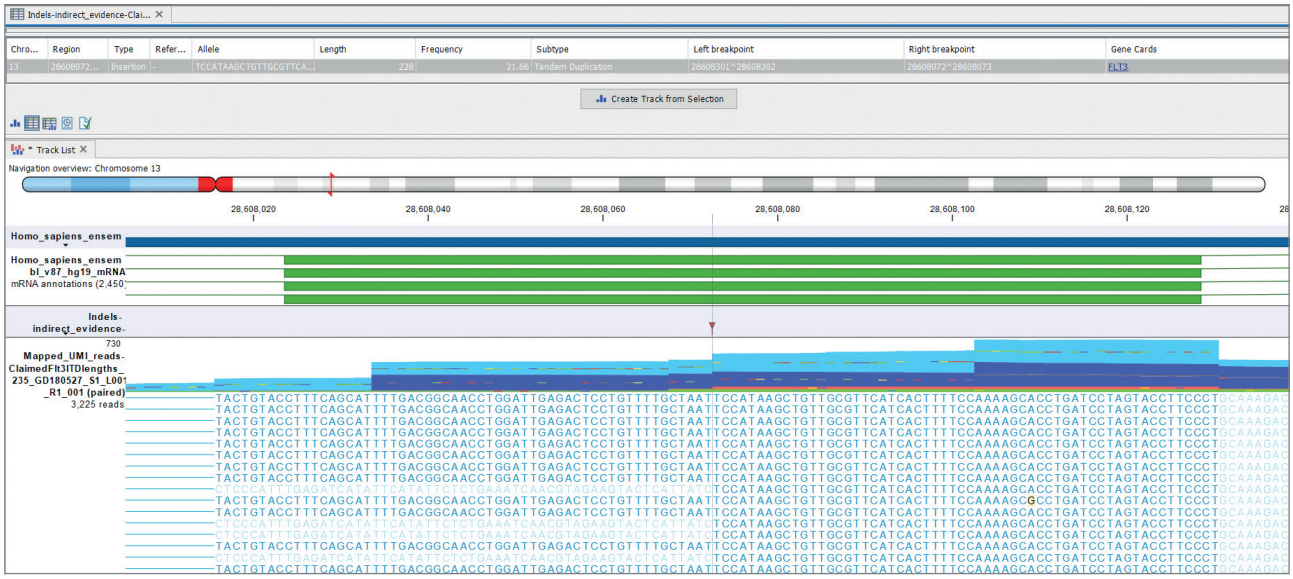


Figure 3. Detection, calling and reporting of FLT3 ITDs with an identified insertion site (up to 228 bp).

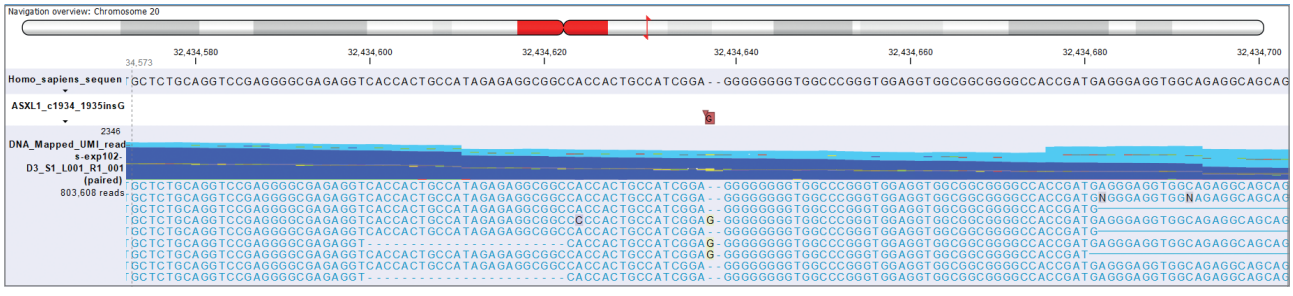


Figure 4. Calling of homopolymer regions, even challenging ASXL1 homopolymeric variants, such as p.G646fs*12.

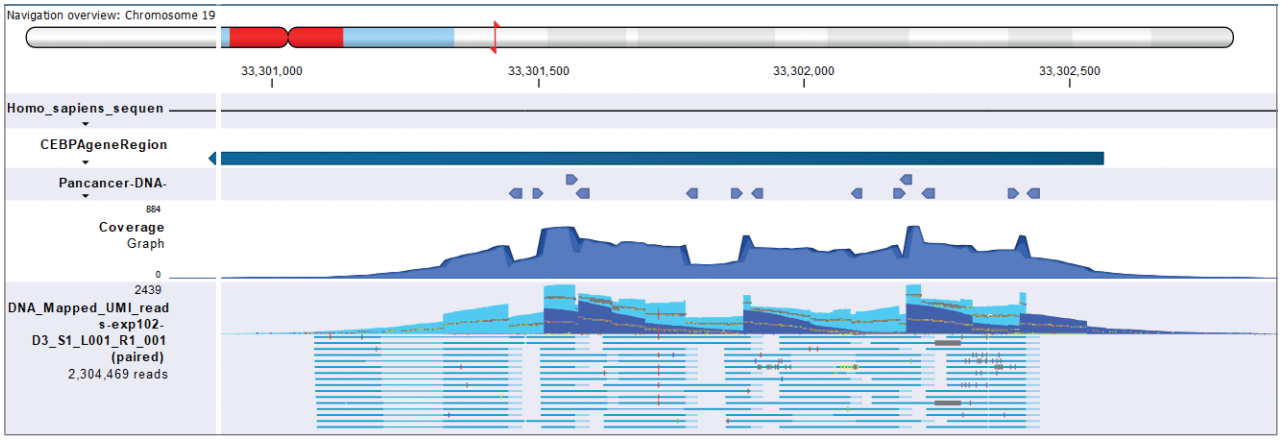


Figure 5. Full coverage of challenging GC-rich regions, such as CEBPA.

Table 1. 145 DNA gene targets

ABL1	*CBLB*	*ETNK1*	*IL7R*	*MPL*	*PHF6*	*SH2D1A*	*WAS*
ADA	*CBLC*	*ETV6*	*JAK1*	*MSH2*	*PML*	*SMARCB1*	*WRN*
ANKRD26	*CDKN2A*	*EZH2*	*JAK2*	*MSH6*	*PMS2*	*SMC1A*	*WT1*
ASXL1	*CEBPA*	*FAM154B*	*JAK3*	*MYC*	*PPM1D*	*SMC3*	*XPO1*
ASXL2	*CHEK2*	*FAM47A*	*KAT6A*	*MYD88*	*PRAMEF2*	*SRP72*	*ZRSR2*
ATM	*CREBBP*	*FAM5C*	*KCNA4*	*NBN*	*PRF1*	*SRSF2*	
ATRX	*CRLF2*	*FAS*	*KCNK13*	*NF1*	*PRPF40B*	*STAG2*	
BCL6	*CSF1R*	*FBXW7*	*KDM6A*	*NOTCH1*	*PRPF8*	*STAT3*	
BCOR	*CSF3R*	*FLRT2*	*KDR*	*NPAT*	*PTEN*	*STXBP2*	
BCORL1	*CTCF*	*FLT3*	*KIT*	*NPM1*	*PTPN11*	*SUZ12*	
BCR	*CUX1*	*GATA1*	*KLHDC8B*	*NRAS*	*RAD21*	*TAL1*	
BIRC3	*DAXX*	*GATA2*	*KLHL6*	*NSD1*	*RB1*	*TERC*	
BLM	*DDX41*	*GJB3*	*KMT2A*	*NTRK3*	*RELN*	*TERT*	
BRAF	*DNM2*	*GNAS*	*KMT2C*	*OR13H1*	*RET*	*TET2*	
BRCA1	*DNMT1*	*HNRNPK*	*KMT2D*	*OR8B12*	*RUNX1*	*TNFRSF13B*	
BRCA2	*DNMT3A*	*HRAS*	*KRAS*	*P2RY2*	*SETBP1*	*TP53*	
C17orf97	*EED*	*IDH1*	*LRRC4*	*PAX5*	*SF1*	*TPMT*	
CALR	*EGFR*	*IDH2*	*LUC7L2*	*PBRM1*	*SF3A1*	*TUBA3C*	
CARD11	*ELANE*	*IKZF1*	*MAP2K1*	*PCDHB1*	*SF3B1*	*U2AF1*	
CBL	*EP300*	*IKZF3*	*MLH1*	*PDGFRA*	*SH2B3*	*U2AF2*	

Table 2. 209 RNA fusion gene targets

ACTN4-KMT2A	*INPP5D-ABL1*	*KMT2A-SEPT2*	*PAX5-ESRRB*
AFF1-KMT2A	*IRF2BP2-RARA*	*KMT2A-SEPT5*	*PAX5-ETV6*
AGGF1-PDGFRB	*JAK2-ETV6*	*KMT2A-SEPT6*	*PAX5-FOXP1*
ATF7IP-PDGFRB	*JAK2-PAX5*	*KMT2A-SEPT9*	*PAX5-JAK2*
ATG16L2-KMT2A	*JAK2-PCM1*	*KMT2A-SH3GL1*	*PAX5-PML*
BCL3-MYC	*KAT6A-CREBBP*	*KMT2A-SORBS2*	*PAX5-ZNF521*
BCOR-RARA	*KAT6A-EP300*	*KMT2A-TET1*	*PBX1-KMT2A*
BCR-ABL1	*KAT6A-NCOA2*	*KMT2A-TNRC18*	*PCM1-JAK2*
BCR-FGFR1	*KMT2A-ABI1*	*KMT2A-TOP3A*	*PICALM-MLLT10*
BCR-JAK2	*KMT2A-ABI2*	*KMT2A-ZFYVE19*	*PML-RARA*
BTG1-MYC	*KMT2A-ACTN4*	*KMT2E-ASNS*	*RABGAP1L-KMT2A*
CBFA2T3-GLIS2	*KMT2A-AFF1*	*LASP1-KMT2A*	*RANBP2-ALK*
CBFB-MYH11	*KMT2A-AFF3*	*LPP-KMT2A*	*RARA-KMT2A*
CCDC88C-PDGFRB	*KMT2A-AFF4*	*MAPRE1-KMT2A*	*RBM15-MKL1*
CHIC2-ETV6	*KMT2A-ARHGAP26*	*MEF2D-BCL9*	*RCSD1-ABL1*
CREBBP-KMT2A	*KMT2A-ARHGEF12*	*MEF2D-CSF1R*	*RCSD1-ABL2*
CREBBP-ZNF384	*KMT2A-BCL9L*	*MEF2D-HNRNPUL1*	*RPN1-MECOM*
CUX1-FGFR1	*KMT2A-BTBD18*	*MLLT10-CEP164*	*RUNX1-CBFA2T3*
DDX3X-MLLT10	*KMT2A-CASC5*	*MLLT10-CLP1*	*RUNX1-ETV6*
DEK-NUP214	*KMT2A-CBL*	*MLLT10-KMT2A*	*RUNX1-MECOM*
DHH-RHEBL1	*KMT2A-CEP170B*	*MLLT10-PICALM*	*RUNX1-PRDM16*
DSCAML1-KMT2A	*KMT2A-CREBBP*	*MLLT10-PPP2R1B*	*RUNX1-RPL22*
EBF1-PDGFRB	*KMT2A-CT45A2*	*MLLT1-KMT2A*	*RUNX1-RUNX1T1*
ELF2-KMT2A	*KMT2A-DAB2IP*	*MN1-ETV6*	*RUNX1-USP42*
EML1-ABL1	*KMT2A-DCP1A*	*MNX1-ETV6*	*SET-NUP214*
EP300-ZNF384	*KMT2A-ELL*	*MYB-GATA1*	*SFPQ-ABL1*
EPS15-KMT2A	*KMT2A-EP300*	*NAP1L1-MLLT10*	*SSBP2-CSF1R*
ETV6-ABL1	*KMT2A-EPS15*	*NDE1-PDGFRB*	*SSBP2-JAK2*
ETV6-ABL2	*KMT2A-FLNA*	*NF1-LRRC37B*	*STAT5B-RARA*
ETV6-ACSL6	*KMT2A-FNBP1*	*NFKB1-KMT2A*	*STIL-TAL1*
ETV6-ANLN	*KMT2A-FOXO3*	*NOTCH1-NOTCH1*	*STMN1-SPI1*
ETV6-JAK2	*KMT2A-FOXO4*	*NPM1-HAUS1*	*TAF15-ZNF384*
ETV6-LYN	*KMT2A-FRYL*	*NPM1-MLF1*	*TCF3-HLF*
ETV6-MN1	*KMT2A-GAS7*	*NPM1-RARA*	*TCF3-PBX1*
ETV6-NCOA2	*KMT2A-GPHN*	*NUMA1-RARA*	*TCF3-ZNF384*
ETV6-NTRK3	*KMT2A-KIAA0284*	*NUP214-ABL1*	*TCF7-SPI1*
ETV6-PDGFRB	*KMT2A-KIAA1524*	*NUP98-DDX10*	*TFG-GPR128*
ETV6-PTPRR	*KMT2A-LASP1*	*NUP98-HOXA9*	*TNIP1-PDGFRB*
ETV6-RUNX1	*KMT2A-LPP*	*NUP98-HOXC11*	*TOP1-NUP98*
EWSR1-ZNF384	*KMT2A-MAML2*	*NUP98-HOXC13*	*TRA-NOTCH1*
FGFR1-LRRFIP1	*KMT2A-MAPRE1*	*NUP98-HOXD13*	*TRA-SALL2*
FGFR1OP-FGFR1	*KMT2A-MLLT1*	*NUP98-KDM5A*	*TRB-NOTCH1*
FGFR1-RANBP2	*KMT2A-MLLT10*	*NUP98-LNP1*	*TRIP11-PDGFRB*
FIP1L1-PDGFRA	*KMT2A-MLLT11*	*NUP98-NSD1*	*UBA2-WTIP*
FIP1L1-RARA	*KMT2A-MLLT3*	*NUP98-PHF23*	*USP9X-DDX3X*
FUS-ERG	*KMT2A-MLLT4*	*NUP98-PRRX1*	*ZBTB16-ABL1*
FXYD6-KMT2A	*KMT2A-MLLT6*	*NUP98-PSIP1*	*ZBTB16-RARA*
IGH-BCL6	*KMT2A-MYO1F*	*NUP98-RAP1GDS1*	*ZMIZ1-ABL1*
IGH-ETV6	*KMT2A-NCKIPSD*	*NUP98-TOP1*	*ZMYM2-FGFR1*
IGH-MYC	*KMT2A-PDS5A*	*NUP98-WHSC1L1*	*ZMYM2-FLT3*
IGK-MYC	*KMT2A-PICALM*	*P2RY8-CRLF2*	
IGL-BCL6	*KMT2A-SARNP*	*PAX5-AUTS2*	
IGL-MYC	*KMT2A-SEPT11*	*PAX5-ELN*	

Ordering Information

Product	Contents	Number of samples	Panel variant number	Cat. no.
QIAseq Leukemia Multimodal Panel	Kit containing **all** reagents (except indices) for multimodal (DNA and RNA) sequencing	12	UHS-005Z-12	333932
		96	UHS-005Z-96	333935
QIAseq Multimodal Index I (12)	Box containing oligos, enough to process a total of 12 samples, for indexing up to a total of 12 samples for Multimodal panel sequencing on Illumina platforms			333962
QIAseq Multimodal Index I Set A (96)	Box containing oligos, enough to process a total of 48 samples, for indexing up to a total of 48 samples for Multimodal panel sequencing on Illumina platforms; one of two sets required for multiplexing 96 samples			333965
QIAseq Multimodal Index I Set B (96)	Box containing oligos, enough to process a total of 48 samples, for indexing up to a total of 48 samples for Multimodal panel sequencing on Illumina platforms; Two of two sets required for multiplexing 96 samples			333975
CLC Genomics Workbench, Desktop Plus	1 year subscription for a static license to use the software on a single computer. Includes maintenance, upgrade and service.			832021

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Download our comprehensive tutorial for detection of specific low-frequency variants.

The QIAseq Leukemia Multimodal Panel is intended for molecular biology applications. This product is not intended for the diagnosis, prevention, or treatment of a disease.

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