

Pan-Myeloid Panel

Features

Comprehensive panel content designed by experts

- Investigate key variants in 70 genes implicated in a variety of myeloid malignancies

Unparalleled coverage uniformity, even in difficult regions

- Confidently detect low-frequency SNVs and indels

Robust detection of *FLT3*-ITDs and *KMT2A*-PTDs

- Streamline your laboratory workflow with a single NGS assay

Complimentary Interpret NGS data analysis software

- Easy-to-use analysis solution for accurate detection of all variants in your panel



Introduction

The SureSeq™ Pan-Myeloid Panel has been designed with input from recognised cancer experts to detect key variants in 70 genes implicated in a wide range of myeloid disorders, including acute myeloid leukaemia (AML), myeloproliferative neoplasms (MPNs) and myelodysplastic syndrome (MDS) (Table 1). The SureSeq Pan-Myeloid Panel accurately detects SNVs and indels in genes such as *CEBPA*, *JAK2*, *CALR* and *MPL*, as well as structural variants including *FLT3*-ITDs and *KMT2A*-PTDs, providing researchers with a single NGS workflow delivering a comprehensive picture of the genetic make-up of each myeloid sample.

Gene	Exons	Gene	Exons	Gene	Exons	Gene	Exons	Gene	Exons	Gene	Exons	Gene	Exons
<i>ABL1</i>	All	<i>CEBPA</i>	All	<i>ETNK1</i>	All	<i>IDH1</i>	4	<i>KRAS</i>	2,3	<i>PHF6</i>	All	<i>SRSF2</i>	1
<i>ASXL1</i>	12	<i>CHEK2</i>	All	<i>ETV6</i>	All	<i>IDH2</i>	4,5	<i>MPL</i>	10	<i>PLCG2</i>	19,20,24	<i>STAG2</i>	All
<i>BCOR</i>	All	<i>CREBBP</i>	All	<i>EZH2</i>	All	<i>IKZF1</i>	All	<i>MYD88</i>	3,5	<i>PPM1D</i>	All	<i>STAT3</i>	19-21
<i>BCORL1</i>	All	<i>CSF3R</i>	14-17	<i>FBXW7</i>	9-11	<i>IRF1</i>	All	<i>NF1</i>	All	<i>PTEN</i>	All	<i>STAT5B</i>	16
<i>BIRC3</i>	All	<i>CTNNA1</i>	All	<i>FLT3</i>	13-15,20	<i>JAK1</i>	All	<i>NFE2</i>	All	<i>PTPN11</i>	3,13	<i>TET2</i>	3-11
<i>BRAF</i>	15	<i>CUX1</i>	All	<i>GATA1</i>	All	<i>JAK2</i>	12,14	<i>NOTCH1</i>	26-28, 34,3'UTR	<i>RAD21</i>	All	<i>TP53</i>	All
<i>BTK</i>	15	<i>CXCR4</i>	All	<i>GATA2</i>	2-6	<i>JAK3</i>	All	<i>NPM1</i>	12	<i>RUNX1</i>	All	<i>U2AF1</i>	2,6
<i>CALR</i>	9	<i>DDX41</i>	All	<i>GNAS</i>	8-10	<i>KIT</i>	2,8-11, 13,17	<i>NRAS</i>	2,3	<i>SETBP1</i>	4	<i>WT1</i>	7,9
<i>CBL</i>	8,9	<i>DNMT3A</i>	All	<i>GNB1</i>	5-6	<i>KMT2A</i>	All	<i>PAX5</i>	All	<i>SF3B1</i>	13-16	<i>XPO1</i>	All
<i>CDKN2A</i>	All	<i>EP300</i>	All	<i>HRAS</i>	All	<i>KMT2C</i>	All	<i>PDGFRA</i>	All	<i>SH2B3</i>	All	<i>ZRSR2</i>	All

Table 1: The SureSeq Pan-Myeloid Panel targets 70 genes implicated in a variety of myeloid disorders.

Contains the latest evidence-based content

Myeloid malignancies are a heterogeneous group of diseases, associated with a wide variety of variants ranging from mutations to structural variations. The hybridisation-based SureSeq Pan-Myeloid Panel is capable of detecting clinically relevant variants down to 1% variant allele frequency (VAF) in 70 key genes implicated in myeloid malignancies. Also included are 4 gender marker genes, *AMELY*, *AMELX*, *TGIF2Y* and *TGIF2X*.

Robust detection of *CEBPA* variants, *FLT3*-ITDs and *KMT2A*-PTDs

Mutations in the *CEBPA* gene are among the most common molecular alterations in AML, which itself is the most common type of acute leukaemia in adults^{1,2}. Sequencing of *CEBPA* is challenging due to the presence of repeat regions and the high GC-content of the gene, leading to poor coverage across these regions and potentially missed variants. OGT's expert bait design overcomes these issues and provides exceptional coverage uniformity, enabling reliable detection of variants and eliminating the requirement for supplementary fill-in with Sanger sequencing (Figure 1).

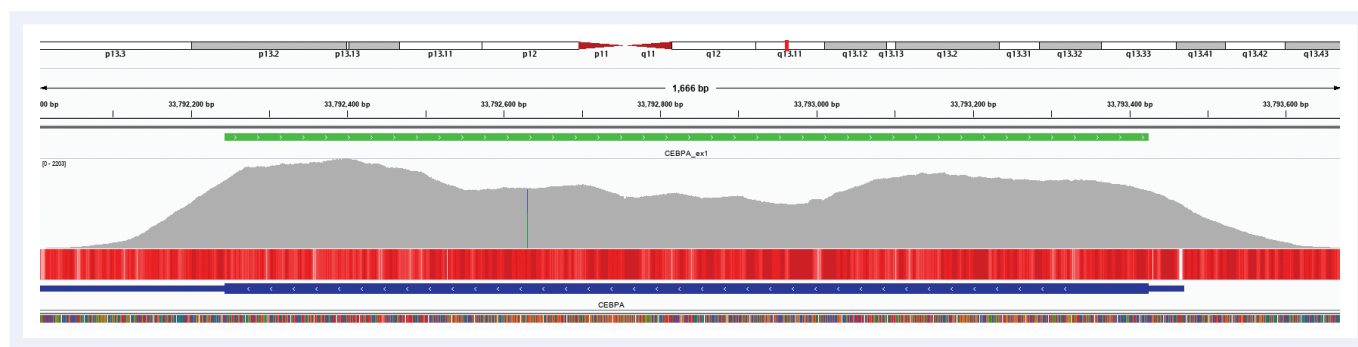


Figure 1: Illustration of the excellent coverage uniformity of the *CEBPA* gene. Depth of coverage per base (grey). Targeted region (green). Gene coding region as defined by RefSeq (blue). GC percentage (red).

FLT3 internal tandem duplications (ITDs) are challenging to target, and subsequently detect, because they are by nature repetitive and can be very long. As a result, *FLT3*-ITDs are generally masked in most panel designs, necessitating additional techniques to obtain a comprehensive genetic picture. OGT employs sophisticated bait designs to generate uniform coverage across, as well as upstream and downstream of the repetitive region. In combination with our complimentary NGS analysis software Interpret, this allows easy detection of *FLT3*-ITDs ranging from a handful of base pairs to >200 bp (Figure 2).

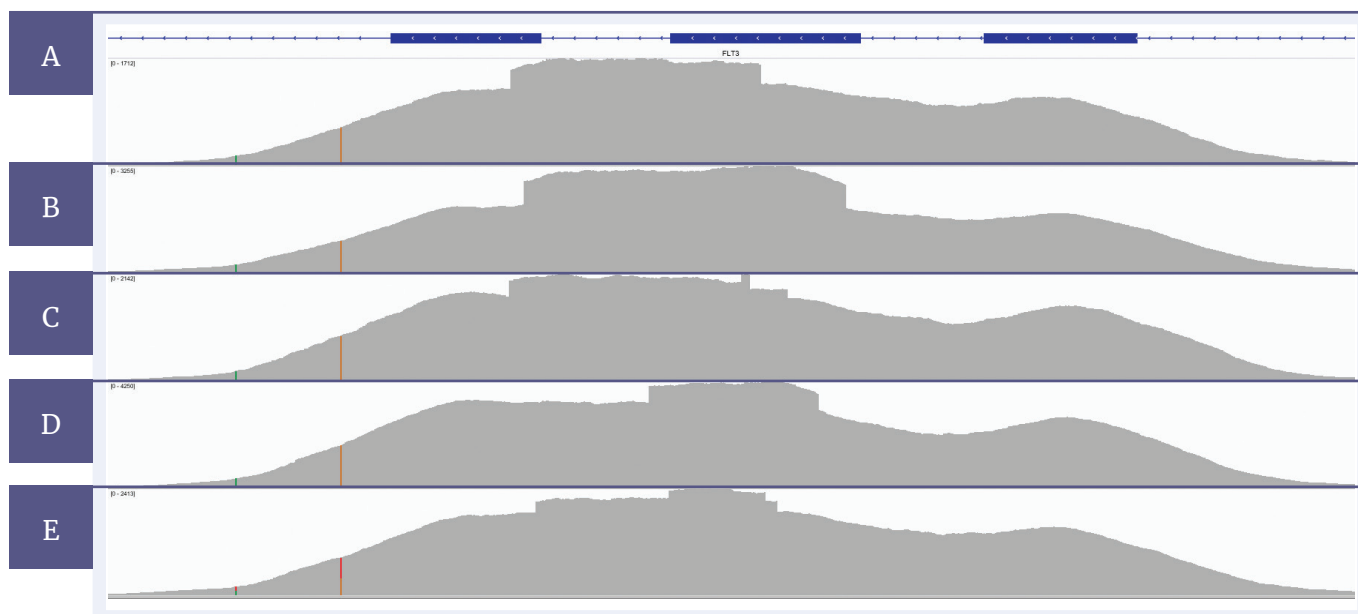


Figure 2: *FLT3*-ITDs of various sizes and even regions containing multiple ITDs can be confidently detected. ITD sizes are **A** 174 bp, **B** 225 bp, **C** 195 bp with additional 6 bp, **D** 120 bp and **E** 168 bp with additional 69 bp.

Other tandem duplications frequently observed in AML are partial tandem duplications (PTDs) in *KMT2A* (MLL). Similar to ITDs, *KMT2A*-PTDs are notoriously difficult to detect due to their size, with duplications spanning multiple exons. With OGT's expertise in hybridisation-based panel design, SureSeq offers robust detection of all sizes of *KMT2A*-PTDs, alleviating the burden of running multiple assays (Figure 3).

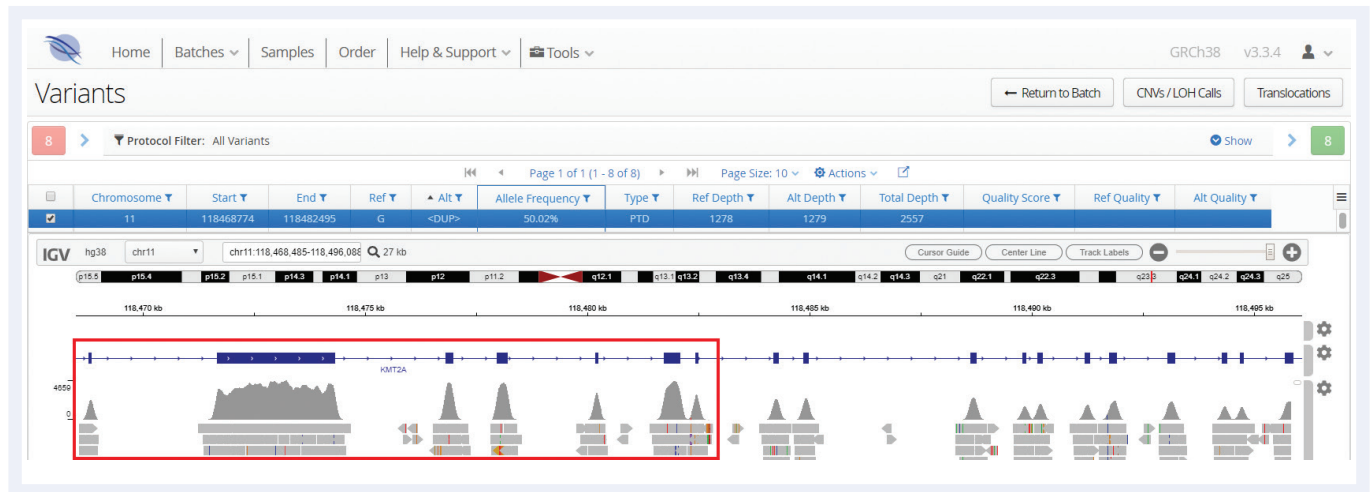


Figure 3: PTD detected spanning exons 2-8 of *KMT2A* by OGT's Interpret NGS analysis software.

Complimentary Interpret NGS analysis software

Interpret is OGT's powerful and easy-to-use NGS analysis solution, facilitating analysis and visualisation of a wide range of somatic variants and structural aberrations. Designed to work seamlessly with all SureSeq panels, Interpret perfectly complements the SureSeq Pan-Myeloid Panel, delivering fast and accurate detection of all SNVs, indels, ITDs and PTDs covered by the panel. Following detection, all variants can be easily visualised in the user-friendly variant browser, for an effortless translation of all your myeloid data into meaningful results.

The OGT Partnership

Behind every sample is a life that can be improved through the right care decisions. The OGT partnership approach is key to providing the highest level of service, working closely with you to understand your unique challenges, customising our approach to meet your exact needs.

Bespoke panel content

You never have to sequence genes you're not interested in and can always modify each panel to what's relevant to your research. If the SureSeq Pan-Myeloid Panel doesn't meet your exact requirements, you can choose from our regularly updated, expert-curated library of pre-optimised cancer content to create your ideal custom SureSeq myPanel™ Myeloid Panel. Alternatively, have a look at the other myeloid panels we have available, including our focused 3-gene SureSeq Core MPN Panel and the SureSeq Myeloid Plus Panel or our disease-specific content, such as our SureSeq myPanel NGS Custom AML panels.

Feature	Specification
Number of genes	70 myeloid genes and 4 gender marker genes
Panel size	221 kb
Mean target coverage	>1000x
Coverage uniformity	>98% of bases at >20% of mean target coverage
DNA input recommended	>500ng high quality DNA
Limit of detection	Capable of detecting SNVs/ indels: 1% VAF
Samples per MiSeq® v2 run	8 samples/run

For more information about the SureSeq Pan-Myeloid Panel, our other myeloid panels or customisation queries, visit ogt.com/PanMyeloid or contact us at contact@ogt.com.

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Product	Contents	Cat. No.
SureSeq Pan-Myeloid Complete NGS Workflow Solution (24)	Bundle of Enrichment baits sufficient for 3 pools of 8 samples; 1x Universal NGS Library Preparation Kit (24), containing PCR primers and enzymes, 1x Universal NGS Index Adapter Kit (24), 1x Universal NGS Hyb & Wash Kit (24), 1x Universal NGS Bead Kit (24)	780003-24
SureSeq Pan-Myeloid Complete NGS Workflow Solution (96)	Bundle of Enrichment baits sufficient for 12 pools of 8 samples; 1x Universal NGS Library Preparation Kit (96), containing PCR primers and enzymes, 1x Universal NGS Index Adapter Kit (96), 1x Universal NGS Hyb & Wash Kit (96), 1x Universal NGS Bead Kit (96)	780003-96
SureSeq Pan-Myeloid Panel (24 reactions)	Enrichment baits sufficient for 3 pools of 8 samples; Interpret Software	770003-24
SureSeq Pan-Myeloid Panel (96 reactions)	Enrichment baits sufficient for 12 pools of 8 samples; Interpret Software	770003-96
Universal NGS Workflow Solution (24)	Bundle of 1x Universal NGS Library Preparation Kit (24), containing PCR primers and enzymes, 1x Universal NGS Index Adapter Kit (24), 1x Universal NGS Hyb & Wash Kit (24), 1x Universal NGS Bead Kit (24)	770500-24
Universal NGS Workflow Solution (96)	Bundle of 1x Universal NGS Library Preparation Kit (96), containing PCR primers and enzymes, 1x Universal NGS Index Adapter Kit (96), 1x Universal NGS Hyb & Wash Kit (96), 1x Universal NGS Bead Kit (96)	770500-96

References

1. Siegel *et al.*, *CA Cancer J Clin* 2015; 65(1):5–29.
2. Pabst *et al.*, *Nat Genet* 2001;27:263–270.



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**What binds us,
makes us.**

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