

## 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 down to 1% VAF

#### 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 heterogenous group of diseases, associated with a wide variety of variants ranging from mutations to structural variations. The hybridisation-based SureSeq Pan-Myeloid Panel is able to consistently detect clinically relevant variants down to 1% variant allele frequency (VAF) in 70 key genes implicated in myeloid malignancies.

### 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<sup>1,2</sup>. 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).

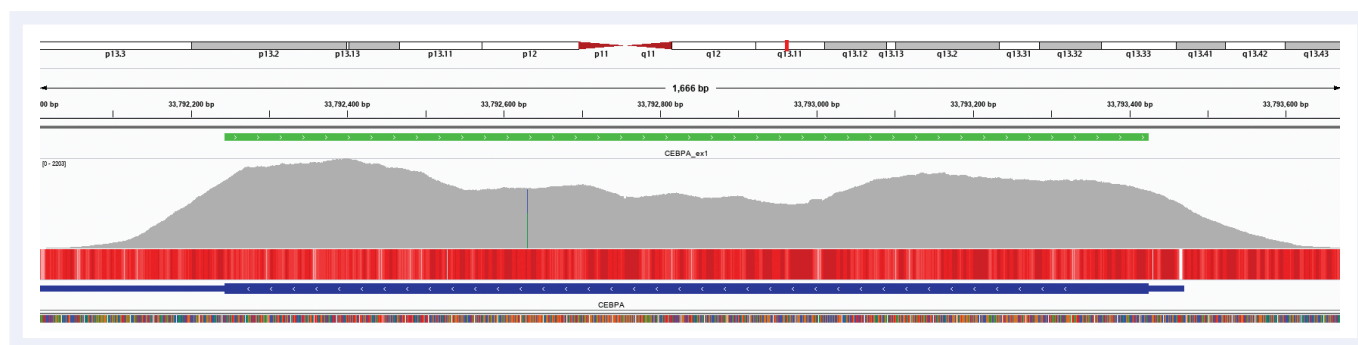


Figure 1: Illustration of the excellent coverage uniformity of the *CEBPA* gene. Depth of coverage per base (grey). Targeted region (green). Gene coding region as defined by RefSeq (blue). GC percentage (red).

*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).

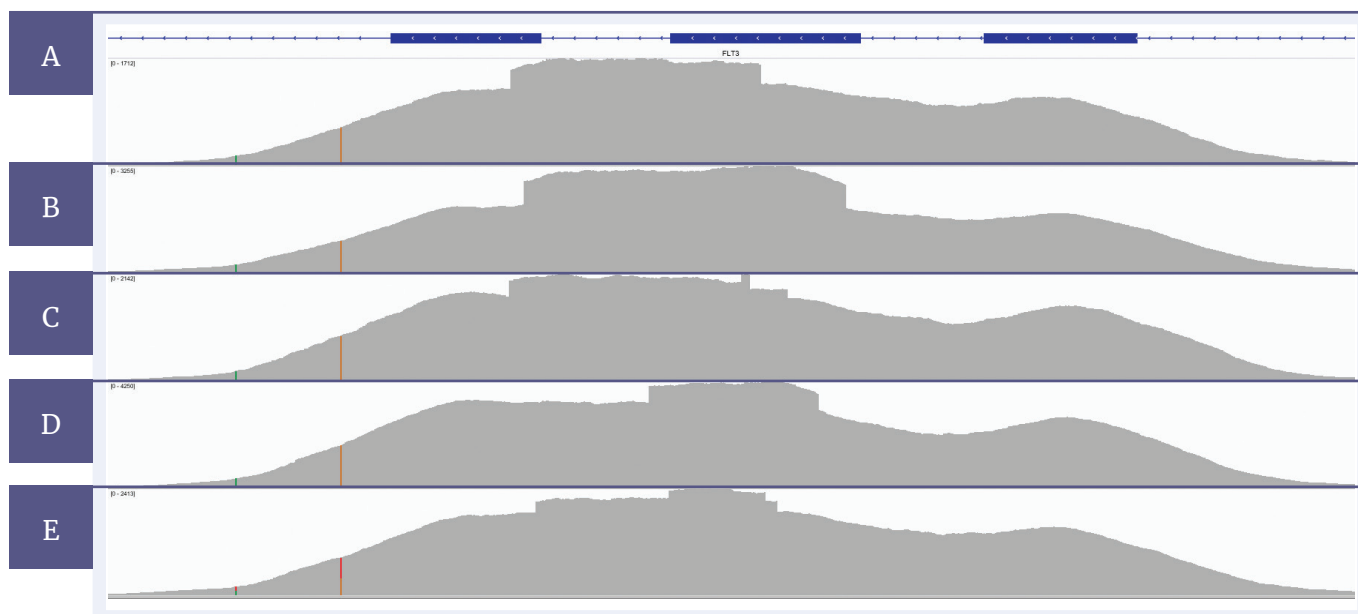


Figure 2: *FLT3*-ITDs of various sizes and even regions containing multiple ITDs can be confidently detected. ITD sizes are **A** 174 bp, **B** 225 bp, **C** 195 bp with additional 6 bp, **D** 120 bp and **E** 168 bp with additional 69 bp.

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).

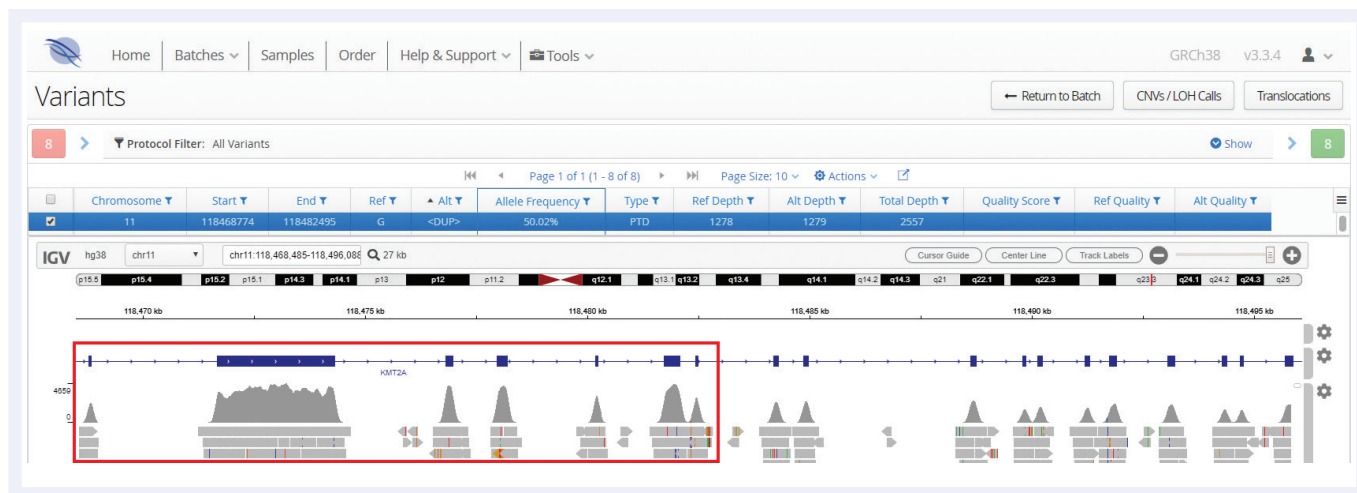


Figure 3: PTD detected spanning exons 2-8 of *KMT2A* by OGT's Interpret NGS analysis software.

### 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.

### 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 myPanel Custom Myeloid Panel - 49 gene plus, or our disease-specific content, such as our SureSeq myPanel NGS Custom AML panels.

Feature	Specification
Number of genes	70
Panel size	221 kb
Mean target coverage	>1000x
Coverage uniformity	>99% of bases at >20% of mean target coverage
DNA input recommended	>500ng high quality DNA
Limit of detection	SNVs/ indels: 1% VAF
Samples per MiSeq® v2 run*	12 samples / run

\*Metrics calculated with 1000 ng DNA using Covaris and Speedvac options in the protocol. Contact support for specific information based on your laboratory workflow.

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

### References

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

### Ordering information

UK +44 (0) 1865 856800

US +1 914 467 5285

contact@ogt.com

ogt.com

Product	Contents	Cat. No.
SureSeq Pan-Myeloid Panel (16 reactions)	Enrichment baits sufficient for 16 samples; Interpret Software	602024-16
SureSeq Pan-Myeloid Panel (96 reactions)	Enrichment baits sufficient for 96 samples; Interpret Software	602024-96
SureSeq Core MPN Panel (16)	Enrichment baits sufficient for 16 samples; Interpret Software	602002
SureSeq Core MPN Panel (96)	Enrichment baits sufficient for 96 samples; Interpret Software	602001
SureSeq Myeloid Panel (16 reactions)	Enrichment baits sufficient for 16 samples; Interpret Software	600075
SureSeq Myeloid Panel (96 reactions)	Enrichment baits sufficient for 96 samples; Interpret Software	700076
SureSeq myPanel Custom Myeloid Panel - 49 gene plus (16 reactions)	Enrichment baits sufficient for 16 samples; Interpret Software	602017-16
SureSeq myPanel Custom Myeloid Panel - 49 gene plus (96 reactions)	Enrichment baits sufficient for 96 samples; Interpret Software	602017-96
SureSeq myPanel NGS Custom AML Panels	Enrichment baits; Interpret Software	Various
SureSeq NGS Library Preparation Complete Solution (16)	Bundle of 1x SureSeq NGS Library Preparation Kit (16), containing adaptors, PCR primers and enzymes, 1x SureSeq NGS Index Kit – Collection A, 1x SureSeq NGS Hyb & Wash Kit (16), 1x Dynabeads M270 Streptavidin (2ml) and 1x AMPure XP beads (10ml). Sufficient for 16 samples	500084
SureSeq NGS Library Preparation Complete Solution (48)	Bundle of 1x SureSeq NGS Library Preparation Kit (48), containing adaptors, PCR primers and enzymes, 1x SureSeq NGS Index Kit – Collection B, 3x SureSeq NGS Hyb & Wash Kit (16), 3x Dynabeads M270 Streptavidin (2ml) and 3x AMPure XP beads (10ml). Sufficient for 48 samples	500085



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**What binds us,  
makes us.**

Oxford Gene Technology Ltd., Begbroke Science Park, Woodstock Road, Begbroke, Oxfordshire, OX5 1PF, UK

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