

# Swift Sensitive Surveillance

## Because Cure Matters

**HemeMARK™** is a comprehensive next-generation sequencing (NGS) assay for ultrasensitive biomarker detection in haematological malignancies.

HemeMARK™ examines 72 genes (*including CEBPA*), 20 RNA fusions, 8 CNVs and 6 MSI.

### How HemeMARK™ Helps

#### Initial Diagnosis

- Informs Diagnosis
- Identifies Treatment Targets
- Provides Prognosis

#### Treatment

- Monitoring of Treatment Response
- Minimal Residual Disease (MRD) detection

#### Post- Treatment

- Minimal Residual Disease (MRD) surveillance
- Resistance Mutation Profiling

### Method

Ultra-deep mirror barcode amplicon-based NGS

### Sample Requirement

2 Streck tubes of peripheral whole blood or  
1 EDTA tube of Bone marrow aspirate

### Turnaround time

2 Calendar weeks

## SNVs/ Indels

<i>ABL1</i>	<i>CCR4</i>	<i>FBXW7</i>	<i>JAK3</i>	<i>PPM1D</i>	<i>TCF3</i>
<i>ANKRD26</i>	<i>CD79B</i>	<i>FGFR3</i>	<i>KIT</i>	<i>PTPN11</i>	<i>TERT</i>
<i>ASXL1</i>	<i>CDKN2A</i>	<i>FLT3</i>	<i>KRAS</i>	<i>RAD21</i>	<i>TET2</i>
<i>ATM</i>	<i>CDKN2B</i>	<i>FOXO1</i>	<i>MAP2K1</i>	<i>RHOA</i>	<i>TP53</i>
<i>B2M</i>	<i>CEBPA</i>	<i>GATA1</i>	<i>MPL</i>	<i>RIT1</i>	<i>U2AF1</i>
<i>BRAF</i>	<i>CREBBP</i>	<i>GATA2</i>	<i>MYC</i>	<i>RUNX1</i>	<i>WT1</i>
<i>BTG1</i>	<i>CSF3R</i>	<i>HRAS</i>	<i>MYD88</i>	<i>SETBP1</i>	<i>XPO1</i>
<i>BTG2</i>	<i>CXCR4</i>	<i>ID3</i>	<i>NOTCH1</i>	<i>SF3B1</i>	
<i>BTK</i>	<i>DDX41</i>	<i>IDH1</i>	<i>NOTCH2</i>	<i>SGK1</i>	
<i>CALR</i>	<i>DNMT3A</i>	<i>IDH2</i>	<i>NPM1</i>	<i>SOCS1</i>	
<i>CBL</i>	<i>ERG</i>	<i>IKZF1</i>	<i>NRAS</i>	<i>SRSF2</i>	
<i>CCND1</i>	<i>ETV6</i>	<i>IKZF3</i>	<i>PHF6</i>	<i>STAG2</i>	
<i>CCND3</i>	<i>EZH2</i>	<i>JAK2</i>	<i>PLCG1</i>	<i>STAT3</i>	

## CNV

<i>CDKN2A</i>	<i>CDKN2B</i>	<i>FLT3</i>	<i>IKZF1</i>	<i>MYC</i>	<i>NRAS</i>
<i>TET2</i>	<i>TP53</i>				

## RNA Fusions

<i>ABL1</i> <sup>#</sup>	<i>ETV6</i>	<i>KMT2A</i>	<i>NUP214</i>	<i>RARA</i>
<i>BCR-RET</i>	<i>FGFR1</i>	<i>NTRK1</i>	<i>PDGFRA</i>	<i>RUNX1</i>
<i>CBFB-MYH11</i>	<i>JAK2</i>	<i>NTRK2</i>	<i>PDGFRB</i>	<i>STIL-TAL1</i>
<i>CUX1</i>	<i>KAT6A</i>	<i>NTRK3</i>	<i>PICALM-MLLT10</i>	<i>TCF3</i>

## MSI

BAT25	BAT26	NR21	NR24	NR27	MONO27
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\*Targeted regions are selected for sequencing to maximise detections of known hotspot mutations. List available on request.

#Detecting major isoforms of *BCR-ABL1* fusions, including p190, p210 and p230.

	LOD Mutant Allele Frequency	Sensitivity	Specificity
Single Nucleotide Variants (SNVs)	> 0.05 %	> 92 %	> 99 %
Insertions/ Deletions (Indels)	> 0.05 %	> 91 %	> 99 %
RNA Fusions	10 copies	> 97 %	> 99 %