

# 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 |
|-------|-------|------|------|------|--------|

\*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 %      |