|  |
| --- |
| **Name: {{ patient\_info.Patient }}**  URN: {{ patient\_info.URN }}  DOB: {{ patient\_info.DOB }}  Sex: {{ patient\_info.Sex }} |

|  |
| --- |
| **TEST DETAILS** |
| Lab No: {{ patient\_info.Lab\_No }}  Ext Ref: {{ patient\_info.Ext\_Ref }}  Collected: {{ patient\_info.Collected }}  Received: {{ patient\_info.Received }}  Specimen: {{ patient\_info.Specimen }} |
| **TEST ORDERED BY** |
| Requester: {{ patient\_info.Requester }}  Referral Lab: {{ patient\_info.Referral\_Lab }} |

|  |  |
| --- | --- |
| ***Clinical Indication*** | {{ other\_info.Clinical\_Indication }} |
| ***Correlative Morphology*** | {{ other\_info.Correlative\_Morphology }} |

|  |
| --- |
| **HAEMATOLOGICAL MALIGNANCY GENE PANEL REPORT** |

|  |  |
| --- | --- |
| ***Test Description*** | {{ report\_title.Test\_Description}} |

|  |  |
| --- | --- |
| ***Result Summary:*** | **{{ report\_title.Result\_Summary}}** |
| |  |  | | --- | --- | | ***Test Results*** | | | |  |  |  |  |  | | --- | --- | --- | --- | --- | | **ASSUMED ORIGIN** | **GENE** | **VARIANT** | **VRF (%)** | **CLINICAL SIGNIFICANCE IN AML** | | **{%tr for gene in reportable\_variants %}** |  |  |  |  | | **{{ gene.ASSUMED\_ORIGIN }}** | **{{ gene.GENE }}** | **{{ gene.VARIANT }}** | **{{ gene.VRF }}** | **{{gene.CLINICAL\_SIGNIFICANCE\_IN\_AML }}** | | **{%tr endfor %}** |  |  |  |  |   VRF – variant read frequency | | | ***Clinical Interpretation*** | {{ report\_title.Clinical\_Interpretation }} | | ***FLT3-ITD Analysis*** | FLT3-ITD DETECTED BY SEPARATE ASSAY (see Reportable Variants table for details) | | ***Reportable Variants*** | {{ report\_title. reportable\_variants\_description }} | | |

## *Test Methodology*

## {{ Test\_Methodology }}

## *Test Limitations*

## {{ Test\_Limitations }}

## *Panel Summary*

{{ Panel\_Summary.Summary }}

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Transcript** | **Targeted exons** | **Coverage at >500x**  **(%)** | **Gene** | **Transcript** | **Targeted exons** | **Coverage at >500x**  **(%)** | **Gene** | **Transcript** | **Targeted exons** | **Coverage at >500x**  **(%)** |
| ABL1 | NM\_005157.4 | 4-10 | 100 | FLT3\* | NM\_004119.2 | 14-15,17,20 | 100 | PHF6 | NM\_001015877.1 | 7-10 | 95 |
| ARAF | NM\_001654.4 | 7,10,15 | 100 | FYN | NM\_002037.5 | 7 | 100 | PIGA | NM\_002641.3 | All coding | 100 |
| ASXL1 | NM\_015338.5 | 10-12 | 100 | GATA1 | NM\_002049.3 | 2-6 | 100 | PLCG1 | NM\_002660.2 | 11 | 100 |
| BCL2 | NM\_000633.2 | All coding | 100 | GATA2 | NM\_032638.4 | All coding | 100 | PLCG2 | NM\_002661.3 | 16,19-20,24 | 100 |
| BIRC3 | NM\_001165.4 | 6-9 | 100 | ID3 | NM\_002167.4 | All coding | 100 | RHOA | NM\_001664.2 | 2 | 100 |
| BRAF | NM\_004333.4 | 15 | 100 | IDH1 | NM\_005896.2 | 4,7 | 100 | RUNX1 | NM\_001754.4 | All coding | 100 |
| BTK | NM\_000061.2 | 11,15-16 | 100 | IDH2 | NM\_002168.2 | 4,7 | 100 | SETBP1 | NM\_015559.2 | 4 | 100 |
| CALR | NM\_004343.3 | 9 | 100 | IRF8 | NM\_002163.2 | 3 | 100 | SF3B1 | NM\_012433.2 | 14-16 | 100 |
| CARD11 | NM\_032415.4 | 4-9,15,20 | 100 | JAK2 | NM\_004972.3 | 12-14,16 | 100 | SH2B3 | NM\_005475.2 | All coding | 98.6 |
| CBL | NM\_005188.3 | 8-9 | 100 | JAK3 | NM\_000215.3 | 11,13,15 | 94.9 | SRSF2 | NM\_003016.4 | 1 | 100 |
| CD274 | NM\_014143.3 | All coding,3'UTR | 100 | KIT | NM\_000222.2 | 8,10-11,17 | 100 | STAT3 | NM\_139276.2 | 6,13,15,18-21 | 100 |
| CD79B | NM\_000626.2 | 5,6 | 100 | KRAS | NM\_033360.2 | 2-4 | 100 | STAT5B | NM\_012448.3 | 16 | 100 |
| CEBPA | NM\_004364.3 | All coding | 100 | MAP2K1 | NM\_002755.3 | 2-3 | 100 | STAT6 | NM\_001178078.1 | 10,13,16 | 100 |
| CSF3R | NM\_156039.3 | 14,17 | 100 | MPL | NM\_005373.2 | 1-11 | 100 | TCF3 | NM\_001136139.2 | 17 | 100 |
| CXCR4 | NM\_003467.2 | 2^ | 100 | MYD88 | NM\_002468.4 | 4-5 | 100 | TET2 | NM\_001127208.2 | All coding | 100 |
| DDX41 | NM\_016222.2 | All coding | 100 | NOTCH1 | NM\_017617.3 | 26-28,34,3'UTR^ | 100 | TP53 | NM\_000546.5 | All coding | 100 |
| DNMT3A | NM\_022552.4 | All coding | 100 | NPM1 | NM\_002520.6 | 11 | 100 | U2AF1 | NM\_006758.2 | 2,6 | 100 |
| ETNK1 | NM\_018638.4 | 3 | 100 | NRAS | NM\_002524.4 | 2-4 | 97.4 | XPO1 | NM\_003400.3 | 15-16 | 100 |
| EZH2 | NM\_004456.4 | All coding | 100 | PDCD1LG2 | NM\_025239.3 | All coding,3'UTR | 100 | ZRSR2 | NM\_005089.3 | All coding | 100 |

\* Please note FLT3-ITDs are not detected with this assay. A separate assay may have been performed, result included in Test Results if sample tested.   
^ Partial coverage of region

Please note variants may not be optimally detected in genes with less than 100% coverage. The gene coverage above is considered acceptable given the available information about the clinical context, however please contact the laboratory for further advice should specific genes covered at less than 100% require full coverage. A list of regions with suboptimal coverage is available upon request.

Please contact the laboratory on 03 8559 7284 if you wish to discuss this report further.

## Reported by {{ Panel\_Summary.Reported­\_by }}

**Authorised by {{ Panel\_Summary. Authorized\_by }}**

## Reported {{ Panel\_Summary.Reported }}

**References**

1. {{ References }}