ABN 42 100 504 883

|  |  |  |
| --- | --- | --- |
| **Patient** {{ patient\_info.Patient }}  **URN** {{ patient\_info.URN }}  **DOB** {{ patient\_info.DOB }}  **Sex** {{ patient\_info.Sex }} | Lab No  Ext Ref  Collected  Received  Specimen | Requester  Referral Lab |

Clinical Indication

Correlative Morphology

HAEMATOLOGICAL MALIGNANCY GENE PANEL REPORT

Test Description

Result Summary

Clinical Interpretation

Test Results

FLT3-ITD Analysis

Reportable Variants

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 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

Test Methodology

DNA is analysed by targeted gene sequencing of coding regions and flanking splice sites (within 2 bp) of the genes listed below. Libraries are prepared using a custom QIAGEN QIAseq single primer extension-based panel (Peter MacCallum Cancer Centre AllHaem v1) and sequenced on an Illumina NextSeq500 with 150 bp paired end reads. A customised CLC bioinformatics pipeline including QIAGEN CLC enterprise solutions is used to generate aligned reads and call variants (single nucleotide variants and short insertions or deletions) against the hg19 human reference genome. Variants are analysed using PathOS software (Peter Mac) and described according to HGVS nomenclature version 19.01 (http://varnomen.hgvs.org/) with minor differences in accordance with Peter MacCallum Cancer Centre Molecular Pathology departmental policy. The following population variation and cancer or genetic disease databases are commonly used in addition to literature review to assist with variant interpretation: the Genome Aggregation Database (gnomAD; gnomad.broadinstitute.org), the Catalogue of Somatic Mutations in Cancer