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| **Patient** **PATIENT\_IN**  **URN** URN\_IN  **DOB** DOB\_IN  **Sex** SEX\_IN | **Lab No** LAB\_NO\_IN  **Ext Ref** EXT\_REF\_IN  **Collected** COLLECTED\_IN  **Received** RECEIVED\_IN  **Specimen** SPECIMEN\_IN | **Requester** REQUESTER\_IN  **Referral Lab** REFERRAL\_LAB\_IN |

**Clinical Indication** CLINICAL\_INDICATION\_IN

**Specimen Details** SPECIMEN\_DETAILS\_IN

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| **HAEMATOLOGICAL MALIGNANCY GENE PANEL REPORT** |

**Test Description** Somatic variant analysis of 56 genes with clinical significance in haematological malignancy. Refer to Panel Summary for gene list.

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| **Result Summary Failed assay due to suboptimal DNA quantity/quality.** See comment below regarding the test limitations of cell free DNA analysis. |

**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).

**Test Limitations**

Please note the quantity of tumour derived cell free DNA within this sample is unknown. In addition, the profile of mutations present within the cell free DNA compartment may differ from that in any given individually assessed tumour sample. Therefore a negative result, or the absence of detection of a particular mutation does not imply its absence from all tumour sites in the patient1. In addition, the sensitivity of this assay for variant detection is not appropriate for monitoring or minimal residual detection but rather for determining mutation profile at diagnosis/relapse.

**Panel Summary**

\* Please note FLT3-ITDs are not detected with this assay ^ Partial coverage of region

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

**Reported by REPORTED\_BY1\_IN**

**REPORTED\_BY2\_IN**

**Authorised by AUTHORISED\_BY\_IN**

**Reported 10-Jan-2023**

**References**

1. Blombery PA, Ryland GL, Markham J, et al. Detection of clinically relevant early genomic lesions in B-cell malignancies from circulating tumour DNA using a single hybridisation-based next generation sequencing assay. *Br J Haematol* 2018; **183**(1): 146-9.