|  |  |  |
| --- | --- | --- |
| **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 |

**COMMENT\_IN**

**Clinical Indication** CLINICAL\_INDICATION\_IN

**Correlative Morphology** CORRELATIVE\_MORPHOLOGY\_IN

**Specimen Details** SPECIMEN\_DETAILS\_IN

|  |
| --- |
| **HAEMATOLOGICAL MALIGNANCY RNA FUSION PANEL REPORT** |

**Test Description** Identification of clinically significant fusion transcripts in haematological malignancy. Refer to Panel Summary for gene list.

|  |
| --- |
| **Result Summary Failed assay due to suboptimal RNA quantity/quality.** RESULTS\_SUMMARY\_IN |

**Test Methodology**

RNA is analysed by targeted RNA fusion sequencing of the genes listed below. Libraries are prepared using a custom QIAGEN QIAseq RNA Fusion XP single primer extension-based panel (Peter MacCallum Cancer Centre AllHaem RNA v1) and sequenced on an Illumina NextSeq500. A customised CLC bioinformatics pipeline including QIAGEN CLC enterprise solutions is used to identify candidate fusion genes against the hg19 human reference genome. Please note candidate fusion genes may involve gene partners that are not targeted by this assay. Candidate fusion genes are analysed using PathOS software (Peter Mac).

**Test Limitations**

The detection limit of this assay is approximately 5%-10% of ABL1 equivalent. This assay is qualitative and is not suitable for the monitoring of measurable residual disease (MRD). Complex gene fusions involving novel boundaries, intronic sequences, or gene rearrangements not resulting in the expression of an abnormal transcript may not be reliably detected by this assay or accurately described. Gene expression and structural variants such as tandem duplications are not assessed. Gene fusions are analysed using the reference transcripts listed below unless otherwise stated. The performance of sample types other than peripheral blood, bone marrow and FFPE tissue have not been validated for testing using this assay. Please note Peter Mac assumes sample identification and clinical diagnoses are as stated on the request. Our clinical recommendations may be based on evidence from third-party data sources and should be interpreted in the context of all other clinical and laboratory information for this patient.

**Panel Summary**

Selected regions of the following genes are targeted by this assay.

| **Gene** | **Preferred Transcript** | **Gene** | **Preferred Transcript** | **Gene** | **Preferred Transcript** | **Gene** | **Preferred Transcript** | **Gene** | **Preferred Transcript** | **Gene** | **Preferred Transcript** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ABL1 | NM\_005157.5 | CRLF2 | NM\_022148.3 | GLIS2 | NM\_032575.2 | MLLT3 | NM\_004529.3 | NUTM1 | NM\_175741.2 | RBM15 | NM\_022768.4 |
| ABL2 | NM\_007314.3 | CSF1R | NM\_005211.3 | HLF | NM\_002126.4 | MNX1 | NM\_005515.3 | PAX5 | NM\_016734.2 | RET | NM\_020975.4 |
| AFDN | NM\_001040000.2 | DEK | NM\_003472.3 | IL2RB | NM\_000878.4 | MRTFA | NM\_020831.4 | PBX1 | NM\_002585.3 | RUNX1 | NM\_001754.4 |
| AFF1 | NM\_001166693 | ELL | NM\_006532.3 | JAK2 | NM\_004972.3 | MYB | NM\_001130173.1 | PCM1 | NM\_006197.3 | RUNX1T1 | NM\_175635.2 |
| ALK | NM\_004304.4 | EPOR | NM\_000121.3 | KAT6A | NM\_006766.4 | MYC | NM\_002467.4 | PDCD1LG2 | NM\_025239.3 | TCF3 | NM\_003200.3 |
| BCL11B | NM\_138576.3 | ERG | NM\_001136154.1 | KMT2A | NM\_001197104.1 | MYH11 | NM\_001040113.1 | PDGFRA | NM\_006206.5 | TSLP | NM\_033035.4 |
| BCR | NM\_004327.3 | ETV6 | NM\_001987.4 | MECOM | NM\_004991.3 | NPM1 | NM\_002520.6 | PDGFRB | NM\_002609.3 | TYK2 | NM\_003331.4 |
| BRAF | NM\_004333.4 | FGFR1 | NM\_023110.2 | MEF2D | NM\_005920.3 | NTRK1 | NM\_002529.3 | PICALM | NM\_007166.3 | UBTF | NM\_014233.3 |
| CBFA2T3 | NM\_005187.5 | FGFR3 | NM\_000142.4 | MLF1 | NM\_022443.4 | NTRK2 | NM\_006180.4 | PML | NM\_033238.2 | USP2 | NM\_004205.4 |
| CBFB | NM\_022845.2 | FIP1L1 | NM\_030917.3 | MLLT1 | NM\_005934.3 | NTRK3 | NM\_001012338.2 | PTK2B | NM\_004103.4 | ZMYM2 | NM\_003453.4 |
| CPSF6 | NM\_007007.2 | FLT3 | NM\_004119.2 | MLLT10 | NM\_001195626.1 | NUP214 | NM\_005085.3 | RARA | NM\_000964.3 | ZNF384 | NM\_133476.4 |
| CREBBP | NM\_004380.2 | FUS | NM\_004960.3 | MLLT11 | NM\_006818.3 | NUP98 | NM\_016320.4 | RARG | NM\_000966.5 |  |  |

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

**Reported by REPORTED\_BY\_IN**

**Authorised by AUTHORISED\_BY\_IN**

**Reported 15-Jul-2024**