«TableStart:Samples»

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| --- | --- | --- |
| To: PETER MAC CANCER CENTRE  305 GRATTAN STREET  MELBOURNE  VIC 3000 | **Patient**: «patient»  **URN**: «urn»  **DOB**: «dob»  **SEX**: «sex»  **Location**: «location»  **Requester**: «requester» | Sample: «sample»  Ext Ref: «extref»  Collected: «collect\_date»  Received: «rcvd\_date»  Specimen:  Block ID: |
|  |  |  |

**INTEGRATED MOLECULAR REPORT** «isdraft»

|  |  |
| --- | --- |
| **MUTATIONS DETECTED** | |
| **Gene** | **Mutation** |
| **«TableStart:Variants»«gene»** | «refseq»: «hgvsc»;«hgvsp»  «TableEnd:Variants» |
|  | |
| **SUMMARY** | |
|  | |

**Clinical indication –**

**Sample type –**

**Histological features –**

|  |  |
| --- | --- |
| **ASSAY** | **LYMPHOID NGS PANEL** |
| **Genes** | AKT1 (exon 3), BIRC3 (exon 6-9), BRAF (exon 11, 15), BTK (exon 15), CARD11 (exon 4-9), CXCR4 (exon 2), DNMT3A (exon 23), EZH2 (exon 16, 18), FYN (exon 7), FOXO1 (exon 1), IDH1 (exon 4), IDH2 (exon 4), JAK3 (exon 13, 15), KRAS (exon 2-4), MYD88 (exon 5), NOTCH1 (exon 26-28, 34), NRAS (exon 2-4), PHF6 (exon 7-10), PIK3CA (exon 10, 21), PLCG1 (exon 11), PLCG2 (exon 19, 20, 24), RHOA (exon 2), RUNX1 (exon 4-9), SF3B1 (exon 14-16), STAT3 (exon 21), STAT5B (exon 16), STAT6 (exon 10, 13, 16), TP53 (exon 2-11) |

**Individual Variant Analysis**

«TableStart:Variants»**«gene»:** «mut»«TableEnd:Variants»

**Method**

DNA is analysed using a custom-designed lymphoid amplicon gene panel (Lymphoid v5.4.2). Samples are uniquely indexed, pooled and sequenced on the Illumina MiSeq using MiSeq v2 chemistry at 2x151bp reads. Alignment, variant calling and annotation are performed using an amplicon-optimised pipeline. Only plausible pathogenic variants passing multiple functional and quality filters and that are present in the “*Genes analysed*” list above are reported. Amplicons with less than 100 aligned reads are not analysed. The technology employed here is not suitable for detecting loss of heterozygosity, copy number variations, gross structural rearrangements, or aneuploidies. At 1000x coverage, this assay has a detection limit of approximately 5%.

DNA extraction produced sufficient good quality material for lymphoid amplicon gene panel testing. Sample processing passed all expected QC metrics and high quality sequence with high coverage («ampReads» mean aligned reads/amplicon) and uniformity («ampPct»% amplicons >0.2 mean aligned reads) was obtained.

Please contact the laboratory on 03 8559 8402 if you wish to discuss this report further.

**Reported by: Dr. Piers Blombery (Consultant Haematologist)**

**Authorised by: Ms. Michelle McBean**

**Reported:**

*«TableEnd:Samples»*