«TableStart:Samples»

Sample: «sample» Name: «patient» DOB: «dob» URN: «urn»

**SPECIMEN**

Block ID:block\_id, Tumour site: «site» Histology/Morphology: «morphology», Tumour cell content: «tumour\_pct» % tumour estimated in marked area

**INDICATION**

**Enter clinical details from request form including reason for testing**

**TARGETED CANCER PANEL** «isdraft»

**RESULT SUMMARY**

**This test did not identify any abnormalities in the tumour sample.**

**RESULT**

**NO MUTATIONS DETECTED**

**CLINICAL INTERPRETATION**

A negative result reflects the limited sensitivity of the Targeted Cancer Panel for rarer genomic changes underlying many cancer types.

**CLINICAL RECOMMENDATIONS**

Suggest more extensive genomic analysis such as the Comprehensive Cancer Panel.

**METHODOLOGY**

Tumour DNA was tested for mutations in 41 cancer related genes using a custom designed dual-stranded amplicon assay and Illumina TruSeq Amplicon Low Input chemistry. Target sequencing depth on Illumina MiSeq or NextSeq was 1000x. Alignment, variant calling and annotation were performed using a custom designed amplicon-optimised pipeline. Benign variants and variants of uncertain clinical effect are not reported.

**LIMITATIONS**

Only variants within target regions can be detected. Contact the laboratory for target region details. The assay has a limit of detection of approximately 5% minor allele frequency at 1000x coverage. This test is not suitable for detecting loss of heterozygosity, structural rearrangements or anueploidies. The test is unable to discriminate between somatic and inherited variants. Suspected germline variants should be confirmed on a separate sample.

**DISCLAIMERS**

While we make every effort to report accurate information, our recommendations may be based on evidence from third party data sources which draw on incomplete medical literature. Recommendations should be interpreted in the context of other clinical and laboratory findings, including tumour stage, purity, and histopathological classification.

This panel is classified as a Class 1–3 in-house IVD by NPAAC. Currently, not all targets in this gene panel can be fully validated to the current NPAAC requirements because control materials permitting determination of assay performance are not available for all genes on the panel. Results should be interpreted accordingly. For further information please contact the Laboratory.

*«TableEnd:Samples»*