Belfast Health and Social Care Trust

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UKAS MEDICAL 8952

Regional Molecular Diagnostics Laboratory
Belfast City Hospital

Laboratory Number: **S2502116**

Patient Name: [redacted]

Lab No: **S2502116**
Forename: [redacted]
Surname:
Address:

[redacted]
Consultant Pathologist
Antrim Area Hospital
45 Bush Road
Antrim
Co. Antrim
BT41 2RL

NHS Referrer: [redacted]
Hospital: **Antrim Area Hospital**
Sample ID: **G2516908**
Sample Type: **FFPE Tissue**

Ped No:
Receipt Date: **11/07/2025**

DOB: [redacted]
Patient ID: [redacted]
Hospital No:
Collection Date:

Sex: **Female**
Request Date: **11/07/2025**

REFERRAL

Laboratory ID: S2502116
Referral Specimen ID: 25N20001050-A1
Sample type: FFPE tissue
Procedure: Cytology
Site of tumour: Lymph node
Clinical Indication: M4 NSCLC
Clinical/Referral Details: Squamous cell carcinoma, lymph node fine needle aspirate

TEST RESULTS

The macro-dissected area of this specimen contains approximately 10% neoplastic nuclei and is of very low cellularity. DNA sequencing has yielded 504x mean unique coverage depth, making it suboptimal for analysis.

Sequence variants

Gene	Result*	VAF**	Comments
EGFR	No variant Detected		
KRAS	No variant Detected		
BRAF	No variant Detected		
MET	No variant Detected		
ERBB2	No variant Detected		

Structural variants

Gene	Result	Comments
ALK	No rearrangement detected	
ROS1	No rearrangement detected	
RET	No rearrangement detected	
NTRK†	No rearrangement detected	

Copy number variants

Gene	Result‡	Comments
MET	No amplification detected	

PD-L1 immunohistochemistry

Clone	Result (category)^	Comments
SP263	Inadequate	

CLINICAL REPORT

No actionable variants were detected in the genes analysed. These results do not support the use of licenced targeted therapies specific to these markers.

Unfortunately, there was insufficient tumour cells present (<100 tumour cells) in the sections submitted for PD-L1 IHC testing and therefore a valid analysis could not be performed. Please submit repeat material from an alternative block if available

TEST DETAILS

DNA was extracted from FFPE samples using the Maxwell 16 FFPE Plus LEV Kit (Promega). DNA libraries were prepared using the KAPA Hyper Plus Kit (Kapa Biosystems) and sequenced using the 'small Pan-Cancer' NGS assay (PMC) covering common mutations and structural variations in 83 cancer genes. Alignment, de-duplication and variant calling was performed using the 'small Pan-Cancer' NGS bioinformatics pipeline v1.9 (PMC). This assay is designed to detect >98% of SNVs/indels with limit of detection (LOD) >4% VAF and >95% of structural variants with LOD >5% in the regions analysed. Reference Sequences: EGFR: NM_005228.5, KRAS: NM_004985.4, BRAF: NM_004333.4, MET: NM_000245.4, ERBB2: NM_004448.4, ALK: NM_004304.5, ROS1: NM_002944.3, RET: NM_020975.6, NTRK1: NM_002529.4, NTRK3: NM_002530.4. This assay has been validated to detect amplifications in MET at >5 copies in samples with >20% tumour. *This laboratory does not report known polymorphic variants unless clinically actionable. Additional somatic variants may have been identified in this specimen, however only those with clinical relevance at the time of authorisation have been reported, please contact the laboratory if more details are required. **VAF: Variant Allele Frequency. †NTRK fusion detection with this assay is limited to NTRK1 fusions and ETV6::NTRK3 fusion, with an estimated combined sensitivity of >80% and specificity of >99%. ‡LogR: logarithmic ratio of normalised read depth for the relevant gene. PD-L1 IHC: PD-L1 protein expression tested using (SP263 clone) from Ventana; the minimum number of cells required for PD-L1 testing is 100. ^This assay guides immunotherapy decisions in non-small cell lung carcinoma (NSCLC) patients eligible for treatment with Pembrolizumab (KEYTRUDA®), Durvalumab (IMFINZITM), Nivolumab (OPDIVO®), Atezolizumab (TECENTRIQ®) and Cemiplimab (LIBTAYO®) only, using the tumour proportion scoring (TPS) system.