

## Individual Laboratory Report - Lab 3538

FUSION (S) | 2025

### SUMMARY OF YOUR PERFORMANCE IN THIS EQA

Assessment Category	Performance (mean score) <sup>1</sup>
Genotyping	1.60
Interpretation	2.00
Patient Identifiers and Clerical Accuracy	2.00
<b>EQA Result (PASS or POOR)</b>	<b>PASS</b>

### CASE SPECIFIC FEEDBACK

#### Case 1

Assessment Category	Score <sup>2</sup>	Comments (& deductions) <sup>3</sup>
Genotyping	1.60	Exon-level detail /breakpoint genomic coordinates of fusion not provided. Please see comments and/or the scheme report for further information. (0.2) Reference sequence is missing / incorrect / inconsistent (0.2) Reference sequence version / transcript number is missing / incorrect / inconsistent (0) HGNC nomenclature used (0) Reference sequence for CD74 not provided.
Interpretation	2.00	It is not advisable to use specific drug names, drug classes are preferable (0) No/insufficient information about test limitations. No deduction made as a pathogenic variant has been identified (0)
Patient Identifiers and Clerical Accuracy	2.00	All essential patient identifiers present and no significant clerical errors (0)

**Key:** Green (Pass), Red (Poor performance), NRS (no results submitted), WDS (withdrew from scheme)

<sup>2</sup> Maximum score is 2.00

<sup>3</sup> Deductions from the maximum score

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EMQN CIC is an incorporated Community Interest Company registered in England and Wales (registration no: 12020789), which provides external quality assessment schemes for genomic diagnostic testing laboratories. EMQN is a UKAS accredited proficiency testing provider, No. 4367 and our registered address is Third Floor, ICE Building, 3 Exchange Quay, Salford, M5 3ED, United Kingdom.

Email: [office@emqn.org](mailto:office@emqn.org) Web: <https://www.emqn.org/>



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## Case 2

Assessment Category	Score <sup>2</sup>	Comments (& deductions) <sup>3</sup>
Genotyping	1.60	Exon-level detail /breakpoint genomic coordinates of fusion not provided. Please see comments and/or the scheme report for further information. (0.2) Reference sequence is missing / incorrect / inconsistent (0.2) Reference sequence version / transcript number is missing / incorrect / inconsistent (0) HGNC nomenclature used (0) Reference sequence for TPM3 not provided.
Interpretation	2.00	It is not advisable to use specific drug names, drug classes are preferable (0) No/insufficient information about test limitations. No deduction made as a pathogenic variant has been identified (0)
Patient Identifiers and Clerical Accuracy	2.00	All essential patient identifiers present and no significant clerical errors (0)

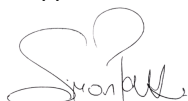
## Case 3

Assessment Category	Score <sup>2</sup>	Comments (& deductions) <sup>3</sup>
Genotyping	1.60	Minor nomenclature error. Please see comments and/or the scheme report for further information. (0.2) Reference sequence is missing / incorrect / inconsistent (0.2) Reference sequence version / transcript number is missing / incorrect / inconsistent (0) HGNC nomenclature used (0) Breakpoints do not match validated breakpoints. Reference sequence for TACC3 not provided.
Interpretation	2.00	It is not advisable to use specific drug names, drug classes are preferable (0) No/insufficient information about test limitations. No deduction made as a pathogenic variant has been identified (0)
Patient Identifiers and Clerical Accuracy	2.00	All essential patient identifiers present and no significant clerical errors (0)

This Individual Laboratory Report should be read in conjunction with scheme summary report.

Thank you for participating in this year's EQA, we look forward to you participating again next year.

Report approved and authorised by Simon Patton (05 May 2026) on behalf of EMQN.



**Dr. Simon Patton (CEO)**

**Key:** Green (Pass), Red (Poor performance), NRS (no results submitted), WDS (withdrew from scheme)

<sup>2</sup> Maximum score is 2.00

<sup>3</sup> Deductions from the maximum score

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