Pan-Tumour Fusions [FFPE] Pilot EQA 2025

Summary scheme report

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05 May 2026

Dear Colleague,

This pilot external quality assessment (EQA), Pan-Tumour Fusions pilot 2025 is run by EMQN CIC. The EQA assessment included the scoring of genotype, interpretation and clerical accuracy. This EQA summary scheme report includes assessment data using harmonised marking criteria. EMQN CIC is responsible for this EQA, and all correspondence related to it should be directed to us.

The assessment is now complete and your individual laboratory scores have been agreed by the assessors. Please go to your EMQN CIC website account to download your Individual Laboratory Report (ILR):

- EMQN CIC (www.emqn.org): select the 2025 "FUSION(S)" EQA.

EQA design and purpose

This EQA scheme was designed to test the entire routine diagnostic workflow of a laboratory, from nucleic acid extraction and sample processing to data analysis and variant reporting. Three mock clinical referrals and corresponding formalin-fixed paraffin embedded (FFPE) tissue samples were supplied to participants for testing via their routine diagnostic pipeline.

The aim was to assess the ability of participating laboratories to undertake fusion gene testing in FFPE tissue, for a range of clinically significant fusion variants, involving the following genes: *ALK*, *ROS1*, *RET*, *NTRK1*, *NTRK2*, *NTRK3*, *FGFR1*, *FGFR2*, or *FGFR3*. This included an assessment of testing accuracy and an evaluation of the standard of clinical reporting against three categories: genotyping, interpretation, and clerical accuracy, with the objective of helping laboratories to standardise and improve their reporting. Each category was assessed using a set of pre-defined comments (Appendix 4, Table 3), as agreed by the working group. Feedback from the assessment is provided in the form of both individual laboratory reports (ILRs) and this EQA Summary Report.

The EQA design meets these objectives by assessing the ability of the participating laboratories to:

- Genotype sections from artificial FFPE samples accurately and to identify which variants are relevant to the clinical referral,
- Interpret the results in response to the clinical referral in a clear and concise format,
- Correctly use internationally accepted standard nomenclature, and
- Provide appropriate and accurate patient and sample information and identifiers.

This scheme report contains information from the cohort of participants including geographical spread, methodologies employed, common errors, learning points and scheme statistics to allow participants to benchmark their results.

Summary report on behalf of the assessment team

General

- A total of 91 laboratories registered to participate in the EQA scheme with 86 laboratories submitting results. Three laboratories withdrew from participation; 1 laboratory did not submit any results and 1 laboratory submitted results in a language not accepted for this EQA.

All Cases

Genotyping

- There were 16 critical genotyping errors reported by 14 participating laboratories, the genotyping error rate was 16/258 (6.2%) (Appendix, Table 6). Please see feedback on individual cases for further information. The mean genotyping score was 1.74 out of a possible score of 2.0. This is a decline on the overall average score of 1.83 achieved in the previous pilot round.

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- Participants were instructed to report fusion genes in accordance with nomenclature guidelines from a reputable source such as Human Genome Variation Society (HGVS)[1], the Hugo Gene Nomenclature Committee (HGNC)[2] or the Variant Interpretation for Cancer Consortium (VICC)[3]. Whilst many laboratories (64%) chose to report results using the most simplistic form of nomenclature (i.e. following guidelines from HGNC, which does not include exon-level detail or allow for referencing gene transcript accessions), it was apparent from our assessment that a proportion of laboratories (17%) reported nomenclature that did not conform with the guidelines of any of these organisations.
- Reports submitted by 17 laboratories (17/87, 19.5%) did not include exon-level detail or breakpoint genomic coordinates of the detected fusion event, even though the chemistry used for testing would allow for reporting this level of information.
- Thirty-three laboratories (33/87, 40%) did not include reference transcript accessions or failed to include the version numbers in their reported fusion gene nomenclature. We recommend the use of MANE given its transcripts[4]. However, we recognize transcript reporting may be limited by the assay used for testing. Nevertheless, the fusion nomenclature must be correct according to which transcript the genotype is reported against.
- Therefore, we would like to reiterate our advice from the 2024 Pan Fusion Tumour Pilot EQA round to a wider cohort of participants: Use of a **standardised** form of nomenclature is **crucial** to avoid ambiguity and facilitate data sharing. The assessment team recognise that there is wide variation in the complexity of nomenclature recommended for reporting fusion genes. Although more detailed forms (such as those proposed by HGVS) offer a higher level of detail on the fusion detected (and therefore less ambiguity), we recognise that these complicated forms of nomenclature may be difficult for a non-expert in genetics to understand. Whilst HGNC recommendations for describing fusion genes is clear and concise, we strongly recommend providing exon level detail where testing chemistry allows the provision of such information, as this enables a full biological interpretation of the result and accurate determination of clinical actionability. This is especially important following the detection of novel fusions where it is important to understand the protein domains implicated in the fusion and to corroborate potential oncogenicity based on the known function of those domains.
- The assessment team recommend the use of fusion nomenclature following VICC guidelines since the descriptions are concise, informative and readable; it includes exon level information and transcript accessions. Please see the VICC Gene Fusion Specification Guidelines for further information.
- During the assessment, we noted that 6 laboratories (6/87, 7%) reported fusion breakpoints using genomic coordinates but did not reference the version of the human genome that the coordinates corresponded to. The genome version is crucial to understand the location of the reported coordinates so should always be included even if alternative nomenclature detailing transcript accessions with version numbers is present in the report.
- Ideally, laboratories would report on whether the detected fusion is in-frame or out-of-frame to allow full interpretation of the potential pathogenicity of the aberration, but we appreciate that this is not always feasible and depends on the kit/chemistry used for testing. The report should not strongly state infer that the fusion is in-frame/out-of-frame if this unknown and there should be recommendations for further testing to confirm this.
- The assessment team recommended not to report a fusion based upon expression imbalance testing alone, confirmation with another method is required.
- Several laboratories reported multiple isoforms of the fusions. Identifying the dominant isoform is important for accrate diagnosis and therapy as some isoforms can have different prognostic outcomes, with specific variants associated with more aggressive disease or higher recurrence rates.

Interpretation

- Of the 261 reports assessed for this category, 247 (95.0%) provided an interpretation of the genotype result, which is excellent.
- The average interpretation score across all three cases was 1.92 (out of 2.00), which is very good.
- Where local/national policy allows, a biological and clinical interpretation of the result in the context of the clinical referral, should always be provided in a diagnostic test report.

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This enables the report receiver to understand the significance of the variant detected, and how it relates to the clinical presentation in the patient, if at all. However, if the detected fusion is associated with an approved targeted therapy, a statement reflecting this information would be acceptable as an interpretive comment.

- Across all three cases, there was only one critical interpretation error awarded.
- Ninety-two reports (92/261, 35%) included mention of specific drug names in the interpretation of the fusion gene result. It is preferable to report the class of drugs a patient is eligible for (e.g.- tyrosine kinase inhibitors) to capture all approved drug therapies with the same mechanism of action, and to avoid naming specific brands of drugs which may inadvertently result in excluding patients from newer, equally effective or better tolerated agents. This also allows clinicians to choose the most appropriate treatment option for their patient (i.e.- taking in to account central nervous system penetration if relevant, toxicity profiles, or the presence of resistance mutations)[5]. It is equally important to note that drug availability varies by country and the market evolves quickly.
- Of the 261 reports assessed for interpretation, 29 were evaluated as having no or insufficient information about test limitations. Information such as scope of testing (e.g. genes included), analytical sensitivity and specificity, should be clearly stated on the report to allow the report receiver to make a full and informed interpretation of the result, in the context of the testing performed. This year, because the samples used in each case contained an oncogenic fusion, no marking deduction was applied for this error.
- Across all three cases, only 3 reports (3/261, 1.1%) did not contain information about the assay/testing method used and/or the scope of testing performed. This information is essential for understanding test accuracy, interpretability and informing clinical decision-making, and should always be included on a clinical report.
- It was apparent during the assessment of reports submitted to this EQA round that reporting on quality metrics from fusion gene testing varies hugely and that laboratories require some guidance in this area to improve standardisation, clinical validity and safety of reporting. Ideally, reports should include information on:
    - Technical characteristics, for example: analytical sensitivity (limit of detection; LOD); analytical specificity (i.e.- the test's ability to detect only the intended targets, avoiding false positives from background "noise" or non-specific amplification); reproducibility and precision; and accuracy.
    - Clinical performance, for example: clinical sensitivity and specificity (i.e. the proportion of true positive or true negative results correctly identified); positive/negative predictive value (i.e. likelihood that the positive/negative result is true); and details about the population used for validation (i.e. cohort description, cancer types, fusion events, sample numbers).
    - Test quality metrics, for example: read depth/coverage, on-target rate, mapping quality metrics, internal/quality controls.
    - Test/reporting limitations, for example: regions/fusions not covered, assay limitations, and potential sources of false positives/negatives (e.g.- pseudogenes, low/high complexity regions).

- Whilst the presence of multiple isoforms is biologically plausible due to alternative splicing or the generation of multiple breakpoints during a chromosomal rearrangement (that leads to the formation of a fusion gene), few if any of the laboratories that reported this offered an explanation as to the biological or clinical relevance of multiple isoforms, which could leave the reader confused or open to making their own judgement. This is important because not all alternative isoforms may be oncogenic, it depends which domains the product contains, or they may confer different levels of oncogenic activity. Whilst the presence of alternative isoforms can explain differences in drug sensitivity, drug resistance or prognosis, evidence of the impact of specific isoforms in the presence of others is generally lacking. Multiple isoforms may also arise as an artifact of testing or bioinformatics analysis. Therefore, they should be reported in the context of available evidence and preferably only after confirmation by an alternative method.

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Clerical Accuracy

- Generally, the level of clerical accuracy reporting was high with an average score of 1.82. However, the following observations were made.
- Off the 261 reports assessed, 20 reports failed to state patient identifiers on all pages of the report. Clear and accurate identification of the patient undergoing testing is a crucial element of the reporting process. It is recommended that this information is included on each page of a multi-page report in case the pages become separated[6].
- Only a small number of reports failed to specify the patient' sex. However, this is important for quality control (e.g.- identification of sample swaps), and establishing gender-specific pathogenicity (for example, related gender specific risks, as well as differences in fusion gene expression across genders due to tissue specificity7.
- The full reason for referral was not restated in 49 of the 261 clinical reports assessed (49/261, 1838%). It may contain important clinical information and gives context to the reader.
- Twenty-four reports (24/261, 9.1%) did not include dates of sample receipt/testing/reporting, or the type of sample tested (i.e.- solid tumour FFPE). Reports should also detail the block ID and section number of the specimen tested as a mean of providing a unique identifier for the sample of which testing was performed.
- Sixteen reports (16/261, 6.0%) had incorrect or missing pagination. All pages of a report should include correct pagination, in a format which includes the total number of pages (i.e.: 1 of 2; 2 of 2) such that the reader understands how many pages make up the report in its' entirety, and whether any pages are missing.
- Twenty (20/261, 7.0%) reports did not include a signature indicating the report has been authorised. Every report should include two signatories: one from the individual who interpreted the data and prepared the report, and a second from an appropriately qualified individual who served to check the information, thereby authorising its content and conclusions[6,8].

Case 1

Genotyping

- Case 1 had *CD74::ROS1* fusion.
- The average score was 1.82 and of the 86 laboratories that participated in this case, 43 received full marks for genotyping.
- Two critical genotyping errors were rewarded in case 1.
- Sixteen laboratories (16/87, 18.4%) did not provide exon-level detail or genomic coordinates of the reported fusion, even though the technology they used for testing would have allowed.
- Two laboratories reported multiple isoforms for this fusion. Please see recommendations and clinical implications when reporting isoforms in the section "All cases".

Interpretation

- There were no critical interpretation errors reported in case 1 and the mean score was 1.93.
- of the 77 laboratories assessed for interpretation in this case, 69 (90%) received full marks, which is excellent.
- Seven laboratories did not provide a clinical interpretation due to their laboratory standard practice. No deductions were made.

Case 2

Genotyping

- The sample provided with this case had an *TPM3::NTRK1* fusion.

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- The average score in this case was 1.78. Of the 86 laboratories that participated in this case, 41 (47.7%) received full marks for genotyping.
- Three critical genotyping errors were reported in this case.
- Fifteen laboratories (15/87, 17.2%) did not provide exon-level detail or genomic coordinates of the reported fusion, even though the technology they used for testing would have allowed.
- Four laboratories reported multiple isoforms for this fusion. Please see recommendations and clinical implications when reporting isoforms in the section "All cases".

Interpretation

- There was 1 critical interpretation error awarded in case 2 and the mean score was 1.92.
- Of the 76 laboratories assessed for interpretation in this case, 69 (91%) received full marks, which is excellent.
- Seven laboratories did not provide a clinical interpretation due to their laboratory standard practice. No deductions were made.

Case 3

Genotyping

- The sample provided with this case had a *FGFR3::TACC3* fusion.
- The average score for genotyping was 1.61; of the 86 laboratories that participated, 35 (41%) received full marks in this category.
- Eleven critical genotyping errors were awarded in this case. See (Appendix, Table 7). Please see feedback on individual cases for further information.
- Seven laboratories did not provide a clinical interpretation due to their laboratory standard practice. No deductions were made.

Interpretation

- There were no critical interpretation errors reported in case 3.
- The mean score in the interpretation category was 1.92. Of the 66 laboratories assessed in this category, 59 received full marks.

Professional standards

Laboratories are assessed against the guidelines and relevant peer reviewed literature currently available references. Other guidelines against which laboratory reports are assessed may include the international nomenclature HGVS[1], HGNC[2], VICC[3] and ISO standards (ISO15189)[8].

Assessment team

The assessment of participants' submissions was undertaken by a team of independent, expert assessors.

Table 1: Assessment Team

Assessors	Location	Role
James Beasley	United Kingdom	Scheme assessor
Pauline Rehal	United Kingdom	Scheme assessor
Deniz Ucanok	United Kingdom	Scheme assessor
Arfa Maqsood	United Kingdom	Scheme organiser
Victoria Williams	United Kingdom	Scheme organiser

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Appeals

The marking is not subject to appeal as this is a pilot EQA scheme with no associated poor performance. However, if you wish to comment on your report or contact the relevant EQA provider, you can do this by email (office@emqn.org). Please include your laboratory account number, the name and year of the EQA scheme and details of the case on which you wish to comment/enquire.

Confidentiality

Details of our confidentiality policies can be found here: https://www.emqn.org/terms-conditions/ in section 4.6 Performance evaluation.

Subcontracted activities

Your EQA provider does not subcontract activities such as EQA planning, evaluation of performance or the authorization of reports. However, some activities are subcontracted, for example the preparation of materials may be performed by suitably accredited providers. Validation of EQA materials and technical advice for setting case scenarios and assessment of results is provided by the EQA team and expert centres.

If your laboratory has subcontracted part of the analytical process to another organisation / third party, this should be clearly stated on your clinical reports (ISO15189 REQ 6.8.2 and REQ 7.4.1.7)[8].

Final comments

The assessment team would like to thank all participants for their hard work, prompt return of results and their co-operation during this exercise.

The purpose of the EQA service is to educate and facilitate the raising of standards. Assessors volunteer considerable time and effort to mark the submissions and to provide assistance to laboratories that may require improvement.

We look forward to your participation in the 2026 EQA

Thank you for participating in this EQA scheme and we hope you have found it a useful EQA exercise.

Kind regards,

Arfa Maqsood

Scheme Organiser

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APPENDICES

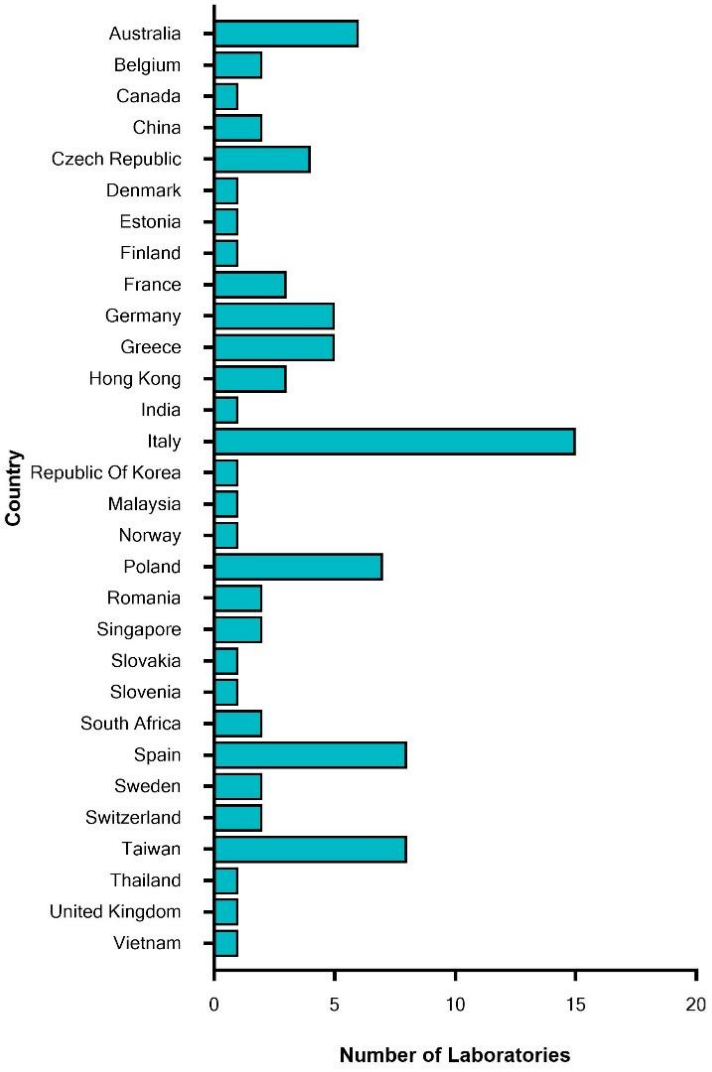
Participation

Table 2: Participation data

Participation Details	Number
Number of registrations	91
Number of withdrawals	3
Number of laboratories that did not submit results	1
Total number of participating laboratories	86*

*Reports were not assessed for one laboratory that submitted results in a language not accepted for this EQA

Figure 1: Participating countries



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Samples Provided and Validated Results

Scheme participants were provided with formalin-fixed paraffin embedded (FFPE) samples for pan fusion gene testing via their routine analytical pipeline(s). FFPE embedded cell lines, purchased from a commercial manufacturer (GeneWell, China), were used as reference materials for this EQA.

Table 3: EQA Sample details and validated results

Case	Name	Sex	Date of Birth (dob)	Referral Reasons	Validated Result
1	Issy SHASHI	F	02/12/1970	A 55-year-old female with a history of light smoking, having quit 20 years ago, was diagnosed with stage IV lung adenocarcinoma, confirmed via pleural effusion cytology. Following chemotherapy, imaging has revealed liver metastases. Genomic profiling did not identify any oncogenic alterations in driver genes such as *EGFR*, *KRAS*, *ERBB2*, *MET* and *BRAF*. Further molecular testing for oncogenic fusion genes is requested to guide targeted therapy.	HGNC: CD74::ROS1 VICC:NM_001025159.3(CD74):e.6::NM_001378902.1(ROS1):e.35 HGVS:NM_001025159.3:r.-161_625:: NM_001378902.1:r.5540_*1139
2	Emery BELLAMY	F	27/04/1980	Emery was found to have a palpable 3cm nodule in the right thyroid lobe with no signs of thyrotoxicosis and hypothyroidism. Fine Needle Aspiration cytology revealed Bethesda VI Papillary thyroid carcinoma. Thyroidectomy was performed to reduce disease burden. Metastases have been confirmed following Radioactive iodine therapy. Initial molecular testing revealed the patient is *BRAF* V600E negative. Patient was also negative for *RET* and *RAS*. Patient is now being referred for oncogenic fusion gene testing to guide targeted therapy.	HGNC: TPM3::NTRK1 VICC: NM_152263.4(TPM3):e.8::NM_002529.4(NTRK1):e.10 HGVS: NM_152263.4:r.-82_775::NM_002529.4:r.1196_*208
3	Bobby CARSON	M	13/09/1968	57-year-old man with a history of heavy smoking presented with gross hematuria and clots in his urine, underwent cystoscopy that revealed a mass in the posterior wall. Histopathology revealed high grade urothelial carcinoma of the bladder. Biopsy and transurethral resection of the bladder tumor was performed and as part of the standard of care patient received 3 cycles of chemotherapy. Six months later, patient demonstrated recurrent of disease. Fusion gene testing has been requested to inform clinical management.	HGNC: FGFR3::TACC3 VICC: NM_000142.5(FGFR3):e.17::NM_006342.3(TACC3):e.4 HGVS: NM_000142.5:r.-275_2274::NM_006342.3:r.575_*158

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Evaluation criteria of the reports

The assessment assigned marks to the genotyping accuracy and the interpretation of the results the laboratories provided in their reports. Patient details and clerical accuracy were also assessed. The full score for each category was 2.00. The assessors considered the accuracy, clarity and clinical relevance of the report issued to the referring clinician, with reference to available professional standards and publications.

Table 4: EQA Marking Criteria

Category	Category	Criterion	Deduction
All Cases	Genotyping	• Correct result reported	0.0
		• Correct result within limitations of test	0.0
		• Critical genotyping error	2.0
		• Major nomenclature error (i.e. Genotype mis-positioned or mis-called)	0.5
		• Minor nomenclature error. Please see comments and/or the scheme report for further information	0.2
		• Exon-level detail /breakpoint genomic coordinates of fusion not provided. Please see comments and/or the scheme report for further information.	0.2
		• Genomic descriptions should reference the genome version	0.2
		• Transcript missing / incorrect / inconsistent	0.2
		• Transcript version number missing/incorrect/inconsistent	0.0
		• Use of MANE transcripts is preferred- see Scheme Summary Report	0.0
		• HGNC nomenclature used	0.0
		• HGVS nomenclature used	0.0
		• VICC nomenclature used	0.0
		• No nomenclature guidelines followed	0.0
		• Fusion partner not characterised when technology permits	0.5
		• Fusion partner not characterised due to test limitations	0.0
		• Comment with deduction	0.2
		• Comment with deduction	0.5
		• Comment with deduction	1.0
		• Comment only	0.0
		• Not tested	0.0
		• Test failed	0.0
		• Not marked	0.0
		• Withdrawn from scheme	0.0
	Interpretation	• Clinical interpretation provided	0.0
		• No clinical interpretation	1.5
		• Critical interpretation error	2.0
		• Failure to mention therapeutic options	1.0
		• It is not advisable to use specific drug names; drug classes are preferable	0.0
		• Report should state that no fusions detected that are related to known therapy for clinical presentation	0.5
		• No/insufficient information about the methodology performed .No deduction made as a pathogenic variant has been identified	0.0
		• No statement about the assay/testing method used and/or scope of testing performed	0.0
		• Comment only	0.0
		• Comment with deduction	0.2
		• Comment with deduction	0.5

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		• Comment with deduction	1.0
		• Not marked	0.0
		• Not marked (due to critical genotyping error)	0.0
		• Withdrawn from scheme	0.0
	Clerical Accuracy	• All essential patient identifiers present and no significant clerical errors	0.0
		• No restatement of the reason for patient referral	1.0
		• Date of birth (dob) incorrect/missing	1.0
		• Patient name has a spelling error	0.5
		• Patient gender is not specified on the report. Whilst not essential, this is another additional identifier of the patient, and we recommend its inclusion on your report	0.0
		• The title of your report is misleading / absent	0.0
		• Failure to provide patient identifiers on each page of the report	0.2
		• Clerical error(s) causing potential for patient harm e.g. incorrect or inconsistent use of patient name in the body of the report	0.5
		• Failure to provide the dates of sample receipt/testing or reporting	0.2
		• Failure to provide the sample type	0.5
		• The sample type is incorrect	0.5
		• Neoplastic cell incorrect or missing	0.5
		• No block ID provided	0.2
		• Section ID is missing	0.2
		• Failure to indicate an authorising signature	0.0
		• Incorrect pagination (use if states Page 2 of 1, for example)	0.2
		• Failure to provide correct pagination e.g. pagination missing or only states Page 1 instead of Page 1 of 1 etc.	0.2
		• Failure to provide a clear presentation of results	0.0
		• Long report, a one- or two-page document with the essential information is preferred	0.0
		• Comment with deduction	0.2
		• Clear and concise report	0.0
		• Not marked	0.0
		• Not marked (due to critical genotyping error)	0.0
		• Withdrawn from scheme	0.0
Case 3	Genotyping	• Using OFA for testing	0.0

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Results: Summary statistics

The mean scores for genotyping/analytical, interpretation, clerical accuracy and the total mean and median score for all participating laboratories are given below in Table 5. A summary of the number of critical errors per case is provided in Tables 6 & 7.

Non-participating laboratories were not marked nor included in this data.

Table 5: Mean Scores

Category		Case 1	Case 2	Case 3
Genotyping	Mean (SD)	1.82	1.78	1.61
	Median (SD)	2.0	2.0	2.0
Interpretation	Mean (SD)	1.93	1.92	1.92
	Median (SD)	2.0	2.0	2.0
Patient Identifiers & Clerical Accuracy	Mean (SD)	1.81	1.83	1.83
	Median (SD)	2.0	2.0	2.0

There were 16 critical genotyping errors reported by 14 laboratories for this EQA (14/86, 16.3%) (see Table 6). Twelve laboratories reported 1 error, and 2 laboratories reported errors in two cases. One (1/86, 1.2%) critical interpretation error was reported by 1 laboratory. Therefore, 72 laboratories (72/86, 84%) achieved a satisfactory result.

Table 6: Critical Genotyping Errors

Category	Case 1	Case 2	Case 3	Total
Number of cases completed	86	86	86	258
Number of laboratories with full marks	43	41	35	119
Number of critical errors	2	3	11	16
Error rate (%)	2.33	3.49	12.79	6.2

Table 7: Critical Interpretation Errors

Category	Case 1	Case 2	Case 3	Total
Number of cases assessed	77	76	66	219
Number of laboratories with full marks	69	69	59	197
Number of critical errors	0	1	0	1
Error rate (%)	0	1.32	0	0.46

Results: Critical Genotyping Errors Summary

Table 8 below shows a breakdown of the critical genotyping errors made by laboratories that participated in this EQA scheme.

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Table 8: Summary of critical genotyping errors made in this EQA scheme

Case	Error	Description	Number of laboratories
1	False positive	Reported the presence of CD74::RET and FGFR3::TACC3 Using RNA-Panel of the Oncomine Comprehensive Plus Assay (Thermo Fisher)	1
1	Sample swap	Potential sample swap with case 2	1
2	False negative	Failed to report the TP53::NTRK1 gene fusion Using SureSelect XT HS Low Input technology (Agilent) and NGS Action ST OncoKit hybridization probe panel (Health in Code)	1
		Failed to report the TP53::NTRK1 gene fusion Using the Illumina Trusight RNA Pan-Cancer Panel	1
2	Sample swap	Potential sample swap with case 1	1
3	False negative	Failed to report the FGFR3::TACC3 gene fusion Using the HANDLE Classic NGS Panel (AmoyDx)	2
		Failed to report the FGFR3::TACC3 gene fusion Using the OncoRNA (LDT)	1
		Failed to report the FGFR3::TACC3 gene fusion Using the QIAseq RNA Fusion XP Solid Tumor from (Qiagen)	1
		Failed to report the FGFR3::TACC3 gene fusion Using Myriapod NGS Cancer probe PLUS (Diatech Pharmacogenetics)	3
		Failed to report the FGFR3::TACC3 gene fusion Using Anchored Multiplex PCR (AMP) (ArcherDX)	1
		Failed to report the FGFR3::TACC3 gene fusion Using Oncomine Precision Assay GX (Thermo Fisher)	1
3	False positive	Reported a MET exon 14 skipping Using the Oncomine Comprehensive Plus Assay (ThermoFisher)	1

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Results: Methodology used

Methodology	Count
NGS	**83**
Agilent	**2**
Agilent SureSelect XYHS2 custom design	1
Agilent SureSelect XT HS Low Input	1
AmoyDX	**2**
AmoyDx HANDLE Classic NGS Panel	2
ArcherDX	**13**
Archer FusionPlex Aarhus Brain Panel (custom panel)	1
Archer FusionPlex Expanded Lung	1
Archer FusionPlex kit lung v2	3
Archer FusionPlex Lung v3 Panel	1
Archer FusionPlex Sarcoma v.2 Archer	1
ArcherDX Anchored Multiplex PCR (AMP)	1
Archer™/IDT various	5
AVENIO	**2**
AVENIO Tumor Tissue CGP Kit V2	1
AVENIO Tumor Tissue Expanded Kit	1
Diatech Pharmacogenetics	**4**
Myriapod NGS cancer probe PLUS	3
Myriapod NGS Cancer panel RNA	1
Dvyser	**1**
OncoDEEP RNA NGS (CE-IVD)	1
GenePlus	**1**
Oncology Multi-Gene Variant Assay	1
Geneseeq	**1**
Geneseeq Prime Assay	1
Hedera Dx	**1**
HederaDX Prime 2	1
Illumina	**15**
Ampliseq for Illumina RNA Fusion Lung Cancer Research Panel	1
Illumina TruSight Oncology	8
Illumina TruSight RNA Pan-Cancer Panel	3
Illumina® Stranded Total RNA Prep, Ligation with Ribo-Zero Plus	1
Illumina TruSeq RNA Library Prep Kit	1
Nextera rapid capture custom enrichment kit	1
In house design	**4**
New England Biolabs	**1**
NEBNext Ultra II FS DNA Lib prep with IDT capture probes	1
Thermo Fisher Scientific	**27**
Ion AmpliSeq™ Library kit	3
Oncomine Comprehensive assay V3	6
Oncomine DX Express Test IVD	1
Oncomine Focus Assay	1
Oncomine Tumor Specific RNA Fusion Panel	1
Oncomine™ Precision Assay GX	15
Pillar Biosciences	**1**
Multi-Cancer Solid Tumor Gene Testing Kit	1
Qiagen	**2**
Qiagen Qiaseq Multimodal Lung	1
Qiagen QIAseq RNA Fusion XP Solid Tumor	1
Roche Diagnostics	**3**
Roche RNA HyperPrep, custom design of probes	1
Roche KAPA HyperChoice Custom Design panel	1
SOPHiA Genetics	**1**
SOPHiA DDM™ RNAtarget Oncology Solution	2
VHIO	**1**
VHIO Epsilon test (LDT)	1
Real-Time/ Quantitative-PCR	**4**
Biocartis	**4**
Idylla Biocartis GENEFUSION Assay	**4**

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Amendments to this Summary Scheme Report

Version	Page	Section	Change	Published
1	-	-	None	5th May 2026
2				
3				

Authorisation

This document has been authorised/approved on behalf of EMQN CIC by:

Dr. Simon Patton on 5th May 2026

CEO