

NPM1 Mutation Status Programme

Distribution - 232401

Participant ID - 43347

Date Issued - 18 July 2023

Closing Date - 25 August 2023

Trial Comments

This trial was issued to 165 participants, of which 158 (95.8%) returned results. Of the non returns, one participant pre-notified us of their intended non return and three requested an extension to result submission.

Sample Comments

Two vials of cell line based lyophilised samples were manufactured and issued by UK NEQAS LI (sample references NPM1 169 and NPM1 170). Both trial samples were formulated to be positive for a NPM1 Type A duplication.

Results and Performance

Your Results

NPM1 Mutation Status	Your Results	Consensus Result
Sample NPM1 169	Mutation Detected	Mutation Detected
Sample NPM1 170	Mutation Detected	Mutation Detected

All Participant Results

	Mutation Detected (Returns)	No Mutation Detected (Returns)
Sample NPM1 169	155	3
Sample NPM1 170	154	4

Your Performance

Performance	Performance Status for this Trial	Performance Status Classification Over 3 Trial Period	
		Satisfactory	Critical
	Satisfactory	2	1

N/A = Not Applicable

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Template

	Returns
DNA	117
cDNA	41

PCR Type

	Returns
Single PCR	84
Real-Time PCR	33
Multiplex PCR	25
Sequencing	8
Melting Curve Analysis	6
Single PCR with Clamping	1

Protocol Type

	Returns
In-house Assay	127
Qiagen NPM1 Mutascreen Kit	14
Qiagen NPM1 mut A, B & D MutaQuant Kits	7
Ion Torrent Oncomine Myeloid Panel	4
Illumina TruSight Myeloid Sequencing Panel	1
Imegen NPM1 Kit	1
Ion AmpliSeq Cancer Hotspot Panel v2	1
Myeloid Solution by Sophia Genetics	1
Oncomine Myeloid Research Assay	1
Qiagen NPM1 mut A MutaQuant Kits	1

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Analysis Type

	Returns
Capillary Electrophoresis	86
Real-Time PCR Fluorescent Detection	34
Sanger Sequencing	7
High Resolution Melt	6
NGS (ThermoFisher Ion Torrent)	6
Next Generation Sequencing (Miseq)	4
Agarose Gel Electrophoresis	3
Digital PCR (Biorad)	3
NGS (Illumina)	3
Illumina NextSeq 500	2
Acrylamide Gel Electrophoresis (PAGE)	1
Illumina MiniSeq	1
Illumina NextSeq 2000	1
Pyrosequencing	1

Journal Reference for Assay

	Returns
Gorello P. et al (2006) Leukemia, 20(6):1103-1108	29
Noguera N. et al (2005) Leukemia, 19(8):1479-1482	17
Falini B. et al (2005) N Engl J Med, 352(3):254-266	13
Falini B. et al (2007) Blood, 109(3):874-885	13
Gale R. et al (2008) Blood, 111(5):2776-2784	12
In-house method (no published reference available)	10
Schnittger S. et al (2005) Blood, 106(12):3733-3739	10
Thiede C. et al (2006) Blood, 107(10):4011-4020	8
Döhner K. et al (2005) Blood, 106(12):3740-3746	7
Huang Q. et al (2008) Br J Haematol, 142:(3)489-492	7
Belgian Molecular Diagnostic Group	5
Lin LI. et al (2006) Leukemia, 20(10):1899-1903	5
Tan AY. et al (2008) J Haematol Oncol, 1, 10	5
Thiede C. et al (2006) Leukemia, 20(10):1897-1899	5
Boissel N. et al (2005) Blood, 106(10):3618-3620	4
Falini B. et al (2006) Blood 108(6):1999-2005	3
Szankasi P. et al (2008) J Mol Diagn, 10(3)236-241	3
Scholl S. et al (2007) Leuk Res, 31(9):1205-1211	2

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Trial Comments

Sample NPM1 169

- In line with sample formulation, 155 of 158 (98.1%) participants returning results identified an *NPM1* variant in sample NPM1 169.
- Of the three participants reporting a false negative result for NPM1 169, all utilised an in-house assay, one with high resolution melt analysis, one utilised Sanger sequencing and one utilised Real-Time fluorescent detection.
- One hundred and eight participants returned information relating to the type of *NPM1* variant detected. In line with sample formulation, 82 (75.9%) identified a change consistent with the Type A¹ duplication of a TCTG tetranucleotide in exon 11 of the *NPM1* gene (approved HGVS nomenclature NM_002520.7(*NPM1*):c.860_863dup, systematic exon numbering of the *NPM1* transcript applied). Of these, 26 participants reported HGVS nomenclature for the *NPM1* variant. Twenty (76.9%) reported c.860_863dup, with six (23.1%) reporting c.860_863dupTCTG.
- A further 24 laboratories (22.2%) reported a 4 bp insertion but did not specify further details. One participant (0.9%) reported an insertion but did not specify the size of the insertion and one laboratory (0.9%) reported the detection of Type A and Type D *NPM1* variants.

Sample NPM1 170

- One hundred and fifty-four out of 158 (97.5%) participants returning results for sample NPM1 170 identified an *NPM1* variant.
- Of the four participants reporting a false negative result for NPM1 170, three also reported a false negative result for NPM1 169. The remaining participant utilised an in-house assay with Sanger sequencing.
- One hundred and six participants returned information relating to the type of *NPM1* variant detected. In line with sample formulation, 80 (75.5%) identified a change consistent with the Type A¹ duplication of a TCTG tetranucleotide in exon 11 of the *NPM1* gene (approved HGVS nomenclature NM_002520.7(*NPM1*):c.860_863dup, systematic exon numbering of the *NPM1* transcript applied). Of these, 25 participants reported HGVS nomenclature for the *NPM1* variant. Twenty (80.0%) reported c.860_863dup, with five (20.0%) reporting c.860_863dupTCTG.
- A further 24 laboratories (22.6%) reported a 4 bp insertion but did not specify further details. One participant (0.9%) reported an insertion but did not specify the size of the insertion and one laboratory (0.9%) reported the detection of Type A and Type D *NPM1* variants.

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The persistent presence of the *NPM1* variant(s) in patients with *NPM1*+ AML has shown that this is a stable marker to determine molecular assessment of measurable residual disease (MRD) at specific clinical time points³. **For participants interested in EQA for MRD assessment using *NPM1* (and other AML markers), UK NEQAS LI have recently developed a new pilot programme, ‘Acute Myeloid Leukaemia Measurable Residual Disease by Molecular Methods’⁴. If participants require further information about this programme, please contact admin@ukneqasli.co.uk.**

References

1. Falini, B. *et al.* Cytoplasmic Nucleophosmin in Acute Myelogenous Leukemia with a Normal Karyotype. *N. Engl. J. Med.* **352**, 254–266 (2005).
2. Human Genome Variation Society (HGVS), <https://varnomen.hgvs.org/> (v20.05).
3. Schuurhuis, G.J. *et al.* Minimal/measurable residual disease in AML: a consensus document from the European LeukemiaNet MRD Working Party. *Blood.* 2018; **131**(12), 1275-1291.
4. Scott, S. *et al.* Assessment of acute myeloid leukemia molecular measurable residual disease testing in an interlaboratory study. *Blood Adv.* 2023; **7**(14): 3686–3694 (2023). doi: <https://doi.org/10.1182/bloodadvances.2022009379>

NPM1 Mutation Status Programme

Information with respect to compliance with standards BS EN ISO/IEC 17043:2010

4.8.2 a) The proficiency testing provider for this programme is:

UK NEQAS for Leucocyte Immunophenotyping
Pegasus House, 4th Floor Suite
463A Glossop Road
Sheffield, S10 2QD
United Kingdom
Tel: +44 (0) 114 267 3600, Fax: +44 (0) 114 267 3601
e-mail: amanda.newbould@ukneqasli.co.uk

4.8.2 b) The coordinators of UK NEQAS LI programmes are Mr Liam Whitby (Director) and Mr Stuart Scott (Centre Manager).

4.8.2 c) Person(s) authorizing this report:

Mr Liam Whitby (Director) or Mr Stuart Scott (Centre Manager) of UK NEQAS LI.

4.8.2 d) No activities in relation to this EQA exercise were subcontracted.

4.8.2 g) The UK NEQAS LI Confidentiality Policy can be found in the Quality Manual which is available by contacting the UK NEQAS LI office. Participant details, their results and their performance data remain confidential unless revealed to the relevant NQAAP when a UK participant is identified as having performance issues.

4.8.2 i) All EQA samples are prepared in accordance with strict Standard Operational Procedures by trained personnel proven to ensure homogeneity and stability. Where appropriate/possible EQA samples are tested prior to issue. Where the sample(s) issued is stabilised blood or platelets, pre and post stability testing will have proved sample suitability prior to issue.

4.8.2 l), n), o), r) & s) Please refer to the UK NEQAS LI website at www.ukneqasli.co.uk for detailed information on each programme including the scoring systems applied to assess performance (for BS EN ISO/IEC 17043:2010 accredited programmes only). Where a scoring system refers to the 'consensus result' this means the result reported by the majority of participants for that trial issue. Advice on the interpretation of statistical analyses and the criteria on which performance is measured is also given. Please note that where different methods/procedures are used by different groups of participants these may be displayed within your report, but the same scoring system is applied to all participants irrespective of method/procedure used.

4.8.2 m) We do not assign values against reference materials or calibrants.

4.8.2 q) Details of the programme designs as authorized by The Steering Committee and Specialist Advisory Group can be found on our website at www.ukneqasli.co.uk. The proposed trial issue schedule for each programme is also available.

4.8.2 t) If you would like to discuss the outcomes of this trial issue, please contact UK NEQAS LI using the contact details provided. Alternatively, if you are unhappy with your performance classification for this trial, please find the appeals procedure at www.ukneqasli.co.uk/contact-us/appeals-and-complaints/

4.8.4) The UK NEQAS LI Policy for the Use of Reports by Individuals and Organisations states that all EQA reports are subject to copyright, and, as such, permission must be sought from UK NEQAS LI for the use of any data and/or reports in any media prior to use. See associated policy on the UK NEQAS LI website: <http://www.ukneqasli.co.uk/eqa-pt-programmes/new-participant-information/>