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# **ORIGINAL ARTICLE**

# Clinical Laboratory Validation and Implementation of Quantitative, Real-Time PCR-based Detection of NPM1 Type A Mutation

### Joelle Racchumi, Wayne Tam, Michael J. Kluk

Weill Cornell Medicine, Department of Pathology & Laboratory Medicine, New York, NY, USA

#### SUMMARY

*Background: NPM1* mutations have prognostic significance in acute myeloid leukemia (AML) and monitoring mutant *NPM1* levels during and after therapy has been described to predict relapse and survival. Despite the published significance of this molecular biomarker, routine monitoring for mutant *NPM1* levels has not been widely adopted in academic clinical laboratories. Therefore, our objective was to validate a quantitative, reverse transcription-PCR assay for the detection of NPM1 Type A mutant transcripts for use in the clinical laboratory.

*Methods:* A quantitative, real-time, reverse-transcription PCR-based method for the detection of *NPM1* Type A mutant transcripts was validated for use in routine clinical practice. Results from this assay were compared to results from orthogonal methods, including next generation sequencing and digital droplet PCR.

*Results:* This real-time, reverse-transcription PCR-based method is sensitive (limit of detection: 0.0150% NCN and reproducible ( $\leq 0.5 \log_{10}$ -fold variation). We summarize the rigorous validation results and share observations that will help other clinical laboratories that may wish to implement this testing. We show the superior sensitivity of this assay compared to other assays (e.g., 45 gene Myeloid Next Generation Sequencing panel) and present a representative case which highlights the assay's utility in the pathologic assessment of cases with borderline morphologic or flow cytometric findings.

*Conclusions:* As molecular testing for residual disease in AML continues to expand, this sensitive and reproducible method will be an appropriate testing option for the detection of *NPM1* Type A mutant transcripts in clinical practice.

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#### **Correspondence:**

Michael J. Kluk, MD, PhD Weill Cornell Medicine New York-Presbyterian Hospital Associate Professor of Clinical Pathology and Laboratory Medicine Department of Pathology and Laboratory Medicine Box 69 1300 York Ave. Office: K509 New York, NY, 10065 USA +1 212-746-3972 Phone: +1 212-746-8173 Fax mik9095@med.cornell.edu Email:

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# Supplementary Tables and Figures

Table 1	. Analytic	sensitivity.	Cell line.

Sample; RNA dilution (% Pos. control RNA)	NPM Type A Mutant, number of copies	ABL, number of copies	% NCN, NPM1 Type A mutant/ABL	Mean, % NCN	SD
Cell lines dilution (% pos. control RNA)					
OCI-AML3_100%	449,078.875	74,524.29	602.594	603.331	1.042
OCI-AML3_100%	453,850.406	75,132.38	604.068		
OCI-AML3+MV411_10%	31,229.891	48,039.60	65.009	57.588	10.495
OCI-AML3+MV411_10%	26,652.297	53,127.45	50.167		
OCI-AML3+MV411_1%	3,235.177	46,716.25	6.925	6.738	0.264
OCI-AML3+MV411_1%	3,376.028	51,527.98	6.552		
OCI-AML3+MV411_10-1%	330.779	47,363.50	0.698	0.671	0.039
OCI-AML3+MV411_10-1%	322.527	50,119.39	0.644		
OCI-AML3+MV411_10-2%	32.126	56,495.57	0.057	0.071	0.020
OCI-AML3+MV411_10-2%	43.579	51,327.15	0.085		
OCI-AML3+MV411_10-3%	<u>3.231</u>	<u>54,812.52</u>	<u>0.006</u>	<u>0.006</u>	<u>0.000</u>
OCI-AML3+MV411_10-3%	<u>3.091</u>	<u>55,290.85</u>	<u>0.006</u>		
OCI-AML3+MV411_10-4%	1.817	68,993.86	0.003	0.002	0.002
OCI-AML3+MV411_10-4%	0.366	73,434.43	0.000		
OCI-AML3+MV411_10-5%	0.009	79,998.87	0.000	0.000	0.000
OCI-AML3+MV411_10-5%	0.000	74,978.66	0.000		
MV-4-11	0.001	70,750.01	0.000	0.000	0.000
MV-4-11	0.000	69,508.93	0.000		

# Table 2. Probit analysis for Limit of Detection (LOD).

% NCN, NPM1 Type A Mutant/ABL	Samples	Detected
62	10	10
6.3	10	10
0.67	10	10
0.07	10	10
0.007	10	9
0.0007	10	5
0.00007	10	3
0.000007	10	0

## Table 3. Real Time PCR vs. ddPCR.

Sample	Real Time PCR, % NCN, (NPM1 Type A Mutant/ABL)	dd PCR, % NCN, (NPM1 Type A Mutant/ABL)	
P11_100%	355.5253	255.9524	
P11_10% RNA dilution	51.9009	36.5452	
P11_1% RNA dilution	5.6104	2.7967	
P11_10-1% RNA dilution	0.8219	0.4374	
P11_10-2% RNA dilution	0.0995	0.0593	
P11_10-3% RNA dilution	0.0128	0.0085	
Sample	Real Time PCR, % NCN, (NPM1 Type A Mutant/ABL)	dd PCR, % NCN, (NPM1 Type A Mutant/ABL)	
P1_RNA dilution_run1	0.2765	0.3099	
P1_RNA dilution_run2	0.2769	0.4058	
P11_RNA dilution_run1	0.0961	0.0719	
P11_RNA dilution_run2	0.106	0.0807	
P16_RNA dilution_run1	0.0651	0.1411	
P16_RNA dilution_run2	0.0879	0.1216	
P_sample A_run1	0.043	0.027	
P_sample A_run2	0.052	0.025	



### Figure 1.

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Figure 2.



Figure 3.



Figure 4.