Crystal Digital PCR® Assay

Information Sheet

For Research Use Only. Not for use in diagnostic procedures.

Product Name

TP53 (R248Q, drop-off Y234-N239/G245-R248) Crystal Digital PCR® Assay (R51047)

Description

Detected Targets

Targets	Sample Type	Detection Channels	Multiplex
TP53 R248Q, Drop-off Y234-N239/G245-R248	DNA	Blue/Green/Red	3

TP53 (R248Q, drop-off Y234-N239/G245-R248) Crystal Digital PCR® Assay is a 10X assay designed to detect and quantify the specific mutation R248Q and mutations between Y234-N239 or G245-R248 of the TP53 gene using the Ruby Chip. TP53 is pivotal in regulating cell division, thus an important tumor suppressor gene. This assay is available in 200 and 1000 reaction formats.

Assay configuration

The table below indicates with a “X” which channel(s) are used for each target in the assay:

Targets	Blue	Teal	Green	Yellow	Red	Infra-Red	Long-Shift
Wild-type (WT) TP53	X		X				
TP53 mutations (between Y234 and N239)	X						
TP53 mutations (between G245 and R248)			X				
Mutant (MUT) TP53 R248Q			X		X		

Components

TP53 (R284Q, drop-off Y234-N239/G245-R248) Crystal Digital PCR® Assay comprises two reagents: a pool of the assay specific primers and Crystal Flex Probes and a Positive Control. Please refer to the lot specific Certificate of Conformity for characterized concentration, available upon demand to Stilla's Technical Support team at support-stilla@bio-rad.com.

Component Name	Reference	Concentration	Description
TP53 (R248Q, drop-off Y234-N239/G245-R248) Crystal Digital PCR® Assay	R51047	10X	Detects mutations between codons Y234 and N239 or G245 and R248 in the exon 7 of the TP53 gene
TP53 Positive Control	R51047.PC0	10X	Contains: hgDNA, Synthetic TP53 mutants (C238Y, R248Q, R248W)

Thermocycling Programs

On the Nio Digital PCR:

Step		Ramp rate
Step 1	Partition for Ruby Chip	-
Step 2	Temperature 95°C for 180 seconds	1°C/sec
Step 3	Begin Loop for 40 Iterations	-
Step 3.1	Temperature 95°C for 15 seconds	2°C/sec
Step 3.2	Temperature 60°C for 30 seconds	2°C/sec
Step 4	Temperature 55°C for 600 seconds	1°C/sec
Step 5	Release for Ruby Chip	-

Data Acquisition

Download Nio dedicated technical files from bio-rad.com.

- NioProtocol_3C-40X-60°C-30s+55°C600s.nioprotocol (Nio Digital PCR)
- NioAssay_3C_TP53_R51047.nioassay (Nio Digital PCR)

Data Analysis

The following files are embedded in the dedicated scanning files listed above:

- UniversalCompMatrix_3C_Prism6-Nio.ncm (6-color naica® system, Nio® Digital PCR)
- AnalysisConfiguration_TP53_R51047.nca (all systems)

Consumables Required but Not Provided

- Ruby Chip (C16011)
- naica® PCR MIX 10X (R10106)
- Crystal Universal Reporters 3 (R41401 200 reactions, R41402 1000 reactions)
- Nuclease-free water

Instruction for PCR Mix Preparation

Specific instructions for preparing the PCR mix are given below.

Reagent Name	Initial Concentration	Final Concentration	Volume per reaction (µL)
naica® PCR MIX Buffer A	10x	1x	0.60
naica® PCR MIX Buffer B	100%	4%	0.24
Crystal Digital PCR® Assay	10x	1x	0.60
Crystal Universal Reporter Tube A	40x	1x	0.15
Nuclease-free water	NA	NA	Variable
Template DNA	**NA**	**NA**	**Variable**
or Positive Control	**10x**	**1x**	**0.60**
		Total reaction volume (µL)	***6.0***

DNA Digestion

DNA samples with ≥10 kb average length (e.g., genomic DNA) could be fragmented by restriction digestion before partitioning to ensure even distribution of the DNA template during partitioning. Restriction digestion is not required for highly fragmented DNA (e.g., FFPE DNA or circulating DNA). This step could improve assay performance and should be tested utilizing desired samples.

Care must be taken to use restriction enzymes that do not cut within the amplified sequence or the Crystal Flex Probes.

For a list of restriction enzymes compatible with a given Crystal Digital PCR® assay, contact our Technical Support team (support-stilla@bio-rad.com).

Loading Amount

For optimal performance, it is recommended not to exceed a chamber concentration (DNA concentration in the reaction mix) of 1,000 copies/µL. The performance of the assay at higher concentrations is not guaranteed and must be validated by the user.

Representative Data and Instructions for Analysis

In the menu “Analyze data, Plots & Populations”, view the results in 2D dot plot. Check or manually adjust the position of the polygons for each target population according to the Positive Control. If needed, select “individual per chamber” in the thresholding mode to adjust the polygons for each sample. Examples of results obtained on the Nio®+ are given below.

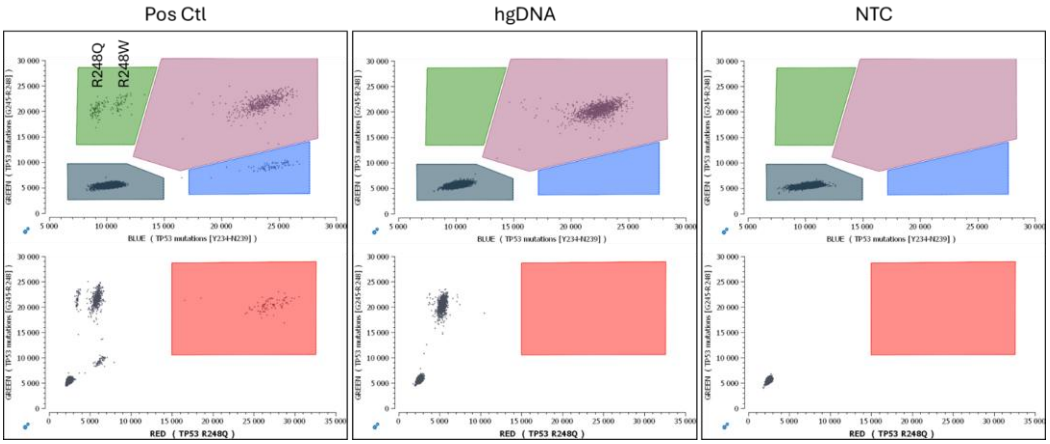
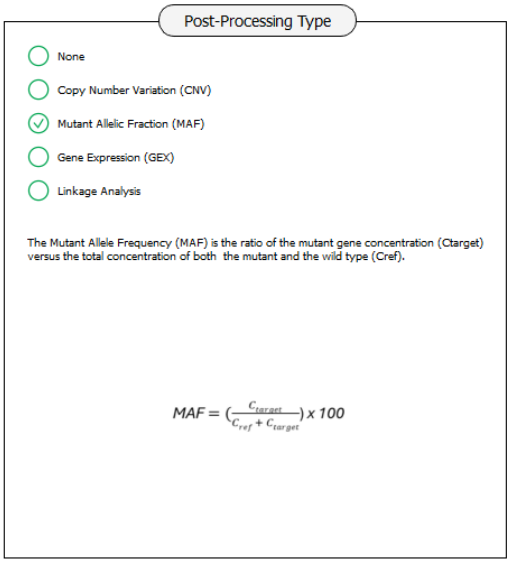
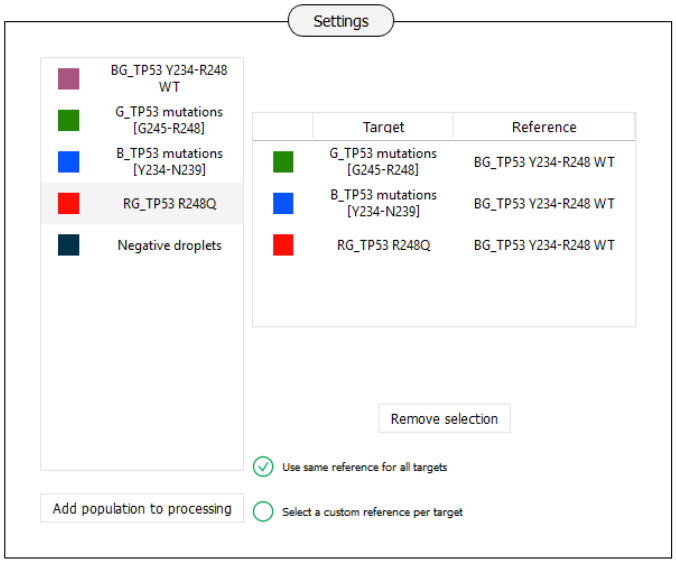


Figure 1: 2D plots obtained during wet lab testing on the Nio®+ system. *The polygons should be adjusted for each target population and for each sample.*

Post-Processing (only available with NioAnalyzer software)

To perform a post-processing analysis of the results, click on “Setup” in the “POST PROCESSING” menu and select the appropriate analysis: **Mutant Allelic Fraction (MAF)**. Follow specific instructions for this assay:





All populations should be added to processing, and “BG_TP53 Y234-R248 WT” selected as reference.

Clicking on apply will launch the calculation. The values will be displayed in the “Results” tab.

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