Crystal Digital PCR® Assay

Information Sheet

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

Product Name

EGFR (T790, T790M, C797S) Crystal Digital PCR® Assay (R51039)

Description

Detected Targets

Targets	Sample Type	Detection Channels	Multiplex
EGFR T790, T790M, C797S	DNA	Blue/Green/Red	3

The EGFR (T790, T790M, C797S) Crystal Digital PCR® Assay is a 10X assay designed to detect and quantify mutations in exon 10 of the EGFR gene using the Ruby Chip. EGFR is essential for regulating multiple cellular processes through the PI3K/AKT/mTOR signaling pathway including cell growth, proliferation, survival, and metabolism.

Assay Configuration

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

Targets	Base changes	Blue	Teal	Green	Yellow	Red	Infra-Red	Long-Shift
Wild-type EGFR T790	N/A	X						
EGFR T790M	c.2369C>T			X				
EGFR C797S	c.2389T>A c.2390G>C	X				X		

Components

EGFR (T790, T790M, C797S) 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
EGFR (T790, T790M, C797S) Crystal Digital PCR® Assay	R51039	10X	Detects EGFR wild-type T790, the mutations T790M and C797S (T>A, G>C).
EGFR Positive Control	R51039.PC0	10X	Contains: hgDNA, Synthetic EGFR mutants (T790M, C797S T>A, C797S G>C)

Thermocycling Programs

On the naica system:

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 60 Iterations	-
Step 3.1	Temperature 95°C for 15 seconds	1°C/sec
Step 3.2	Temperature 58°C for 30 seconds	1°C/sec
Step 4	Release for Ruby Chip	-

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 60 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 58°C for 300 seconds	1°C/sec
Step 5	Release for Ruby Chip	-

Data Acquisition

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

- NioProtocol_3C-60X-60°C-30s+58°C300s.nioprotocol (Nio Digital PCR)
- NioAssay_3C_EGFR_R51039.nioassay (Nio Digital PCR)

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

- ScanningTemplate_Prism3_EGFR_R51039.ncx (3-color naica system)
- ScanningTemplate_Prism6_EGFR_R51039.ncx (6-color naica system)

Data Analysis

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

- MeanCompMatrix_Prism3_EGFR_R51039.ncm (3-color naica system)
- UniversalCompMatrix_3C_Prism6-Nio.ncm (6-color naica system, Nio Digital PCR)

- AnalysisConfiguration_EGFR_R51039.nca (all systems)

Consumables Required but Not Provided

- Ruby Chip (C16011)
- naica® PCR MIX 10X (R10106)
- 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

Set thresholds for separating positive and negative populations on the 1D plots. To optimize the analysis, the thresholds should be set at approximately equal distance from the positive and negative clusters. Examples of results obtained on the Nio+ are given below.

Remark: The threshold can be adjusted on each individual chamber to optimize its placement.

Wet lab testing was carried out using genomic hgDNA as a negative control and a positive control consisting of hgDNA and synthetic EGFR mutants (E746-A750del, L858R, L861Q, T790M, C797S). Synthetic EGFR mutants were also tested individually (T790M, C797S T>A, C797S G>C).

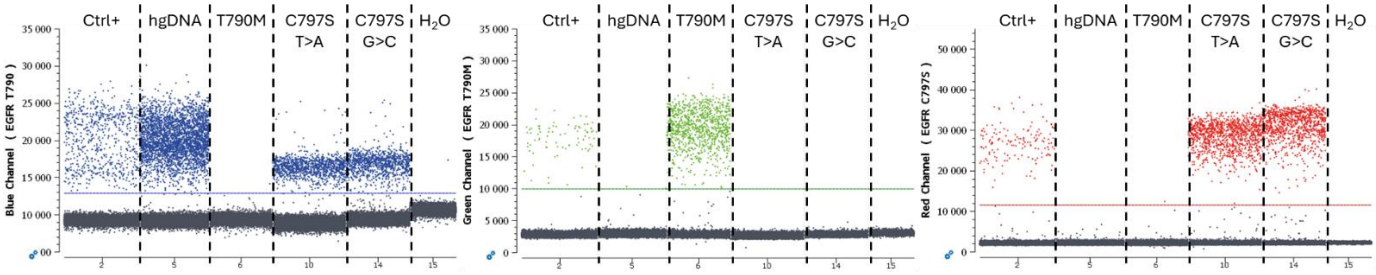

Figure 1: 1D plots obtained during wet lab testing on the Nio™+. *The thresholds are set at approximately equal distance from the positive and negative clusters.*

Calculation of Mutant Allelic Fraction (MAF)

The Mutant Allelic Fraction of each target can be calculated as follows:

$$\textbf{MAF T790M (\%)} = \frac{[EGFR\ T790M]}{[EGFR\ T790M]+[EGFR\ T790WT]} * 100$$

- [EGFR T790M] = measured EGFR T790M concentration
- [EGFR T790WT] = measured EGFR T790WT concentration

$$\textbf{MAF C797S (\%)} = \frac{[EGFR\ C797S]}{[EGFR\ T790M]+[EGFR\ T790WT]} * 100$$

- [EGFR C797S] = measured EGFR C797S concentration
- [EGFR T790M] = measured EGFR T790M concentration
- [EGFR T790WT] = measured EGFR T790WT concentration

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