

# Crystal Digital PCR® Assay

## Information Sheet

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

### Product Name

BRAF/KRAS/NRAS Crystal Digital PCR® Assay (R51006)

### Description

#### Detected Targets

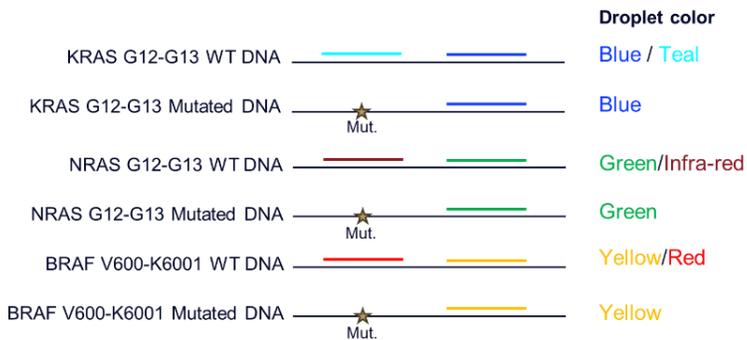
Targets	Sample Type	Detection Channels	Multiplex
<b>BRAF (drop-off V600-K601) / KRAS (drop-off G12-G13) / NRAS (drop-off G12-G13)</b>	DNA	Blue/Teal/Green/ Yellow/Red/Infra-Red	6

The BRAF/KRAS/NRAS Crystal Digital PCR® Assay is a 10X assay designed to detect and quantify mutations in BRAF (codons V600 and K601), KRAS (codons G12 and G13), and NRAS (codons G12 and G13) genes using the Ruby Chip and based on the drop-off detection approach. BRAF, KRAS, and NRAS genes are pivotal in regulating cell signaling pathways implicated in cancer development.

#### 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
<b>Wild-type (WT) KRAS G12-G13</b>	X	X					
<b>Mutant (MUT) KRAS G12-G13</b>	X						
<b>Wild-type (WT) NRAS G12-G13</b>			X			X	
<b>Mutant (MUT) NRAS G12-G13</b>			X				
<b>Wild-type (WT) BRAF V600-K601</b>				X	X		
<b>Mutant (MUT) BRAF V600-K601</b>				X			



**Figure 1: Example of color assignment according to targets.**

## Components

BRAF/KRAS/NRAS 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](mailto:support-stilla@bio-rad.com).

Component Name	Reference	Concentration	Description
<b>BRAF/KRAS/NRAS Crystal Digital PCR® Assay</b>	R51006	10X	Detects mutations in BRAF codons V600 and K601, KRAS codons G12 and G13, and NRAS codons G12 and G13.
<b>BRAF/KRAS/NRAS Positive Control</b>	R51006.PC0	10X	Contains: hgDNA, Synthetic mutants (BRAF V600E, KRAS G12C, NRAS G12D)

## Thermocycling Programs

**On the naica system:**

	Step	Ramp rate
<b>Step 1</b>	Partition for Ruby Chip	-
<b>Step 2</b>	Temperature 95°C for 180 seconds	1°C/sec
<b>Step 3</b>	Begin Loop for 60 Iterations	-
<b>Step 3.1</b>	Temperature 95°C for 15 seconds	1°C/sec
<b>Step 3.2</b>	Temperature 60°C for 60 seconds	1°C/sec
<b>Step 4</b>	Temperature 58°C for 300 seconds	1°C/sec
<b>Step 5</b>	Release for Ruby Chip	-

## On the Nio Digital PCR:

	Step	Ramp rate
<b>Step 1</b>	Partition for Ruby Chip	-
<b>Step 2</b>	Temperature 95°C for 180 seconds	1°C/sec
<b>Step 3</b>	Begin Loop for 60 Iterations	-
<b>Step 3.1</b>	Temperature 95°C for 15 seconds	2°C/sec
<b>Step 3.2</b>	Temperature 62°C for 60 seconds	2°C/sec
<b>Step 4</b>	Temperature 58°C for 300 seconds	1°C/sec
<b>Step 5</b>	Release for Ruby Chip	-

## Data Acquisition

Download Nio dedicated technical files from [bio-rad.com](http://bio-rad.com).

- NioProtocol\_6C-60X-62°C-60s+58°C300s.nioprotocol (Nio Digital PCR)
- NioAssay\_6C\_BRAF-KRAS-NRAS\_R51006.nioassay (Nio Digital PCR)

Download naica dedicated technical files from [bio-rad.com](http://bio-rad.com).

- ScanningTemplate\_Prism6\_BRAF-KRAS-NRAS\_R51006.ncx (6-color naica system)

## Data Analysis

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

- CompensationMatrix\_Prism6\_BRAF-KRAS-NRAS\_R51006.ncm (6-color naica system)
- CompensationMatrix\_Nio\_BRAF-KRAS-NRAS\_R51006.ncm (Nio Digital PCR)
- 2DplotsDefinition\_BRAF-KRAS-NRAS\_R51006.ncp (all systems)
- AnalysisConfiguration\_Prism6\_BRAF-KRAS-NRAS\_R51006\_Polygons.nca (6-color naica system)
- AnalysisConfiguration\_Nio\_BRAF-KRAS-NRAS\_R51006\_Polygons.nca (Nio Digital PCR)

## Consumables Required but Not Provided

- Ruby Chip (C16011)
- naica® PCR MIX 10X (R10106)
- Universal Reporters 7 (R42401 200 reactions, R42402 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
Crystal Universal Reporter Tube B	●	40x	1x	0.15
Nuclease-free water		NA	NA	Variable
Template DNA		<b>NA</b>	<b>NA</b>	<b>Variable</b>
<i>or Positive Control</i>	○	10x	1x	0.60
<i>Total reaction volume (μL)</i>				<i>6.0</i>

## DNA Digestion

DNA samples with  $\geq 10$  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](mailto:support-stilla@bio-rad.com)).

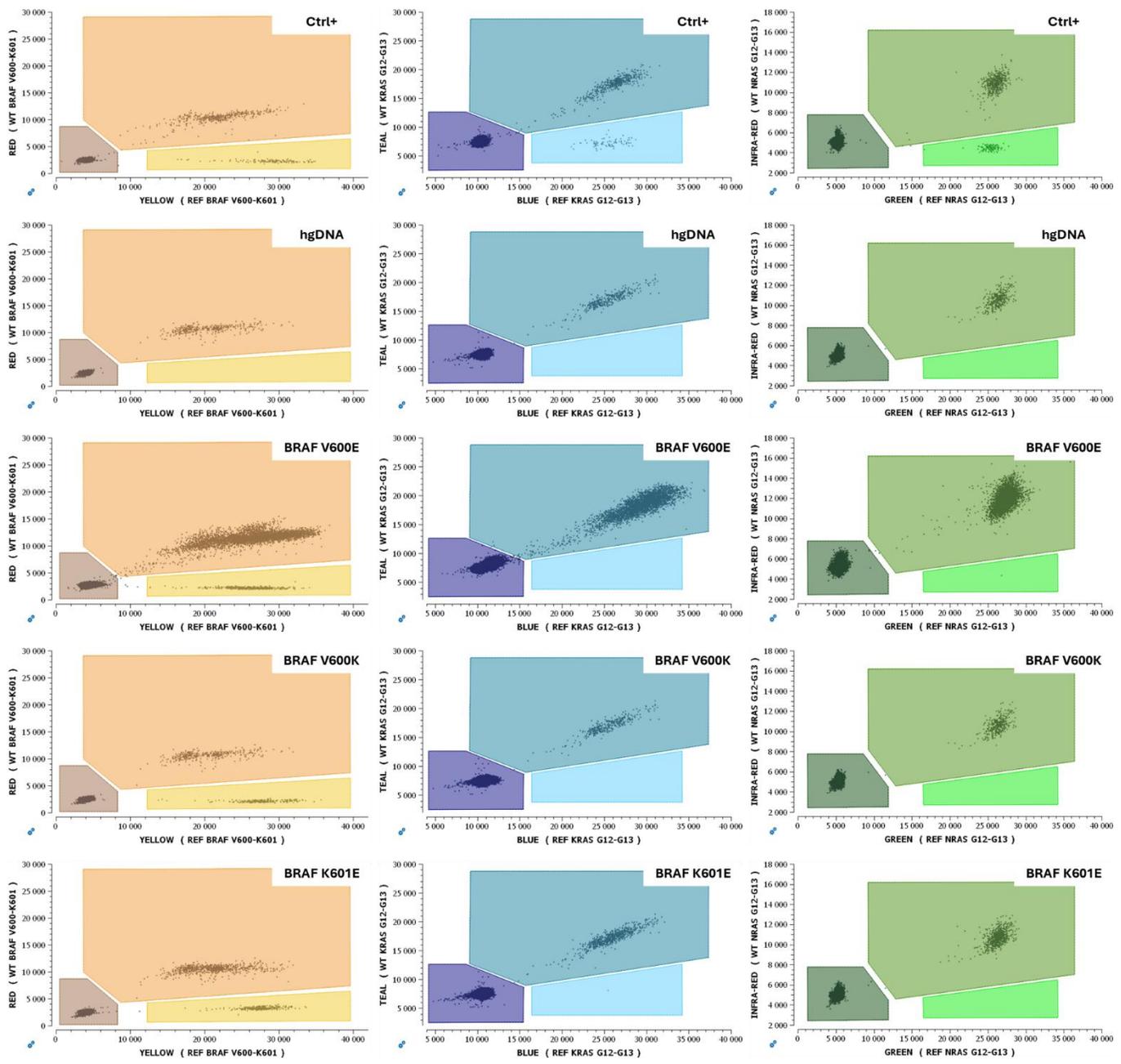
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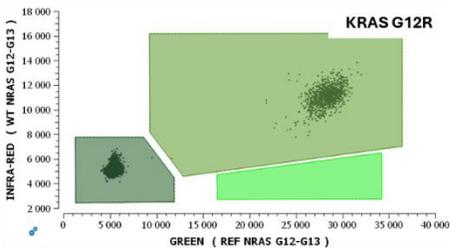
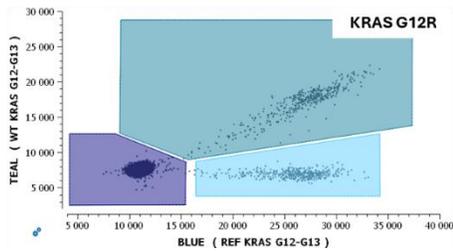
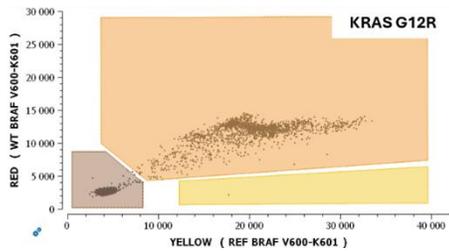
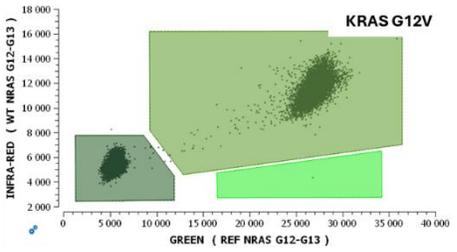
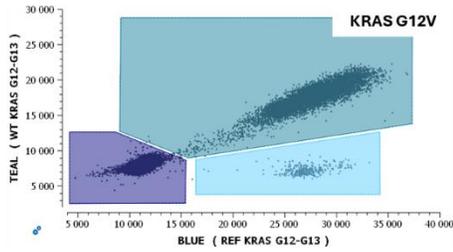
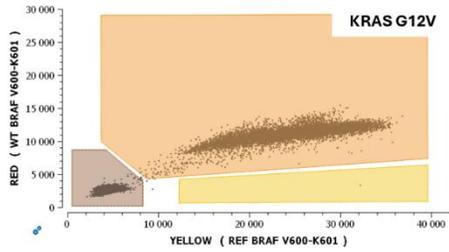
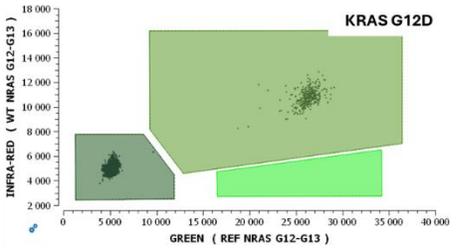
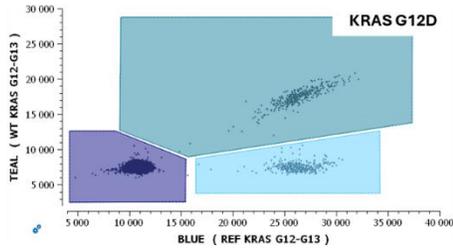
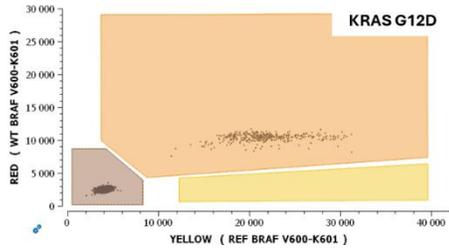
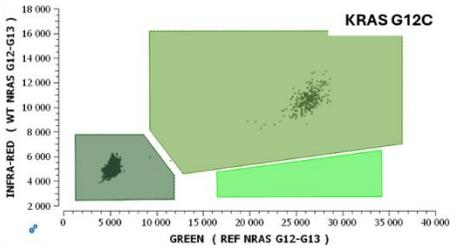
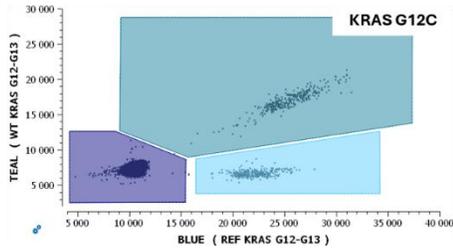
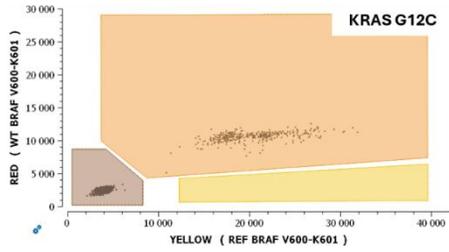
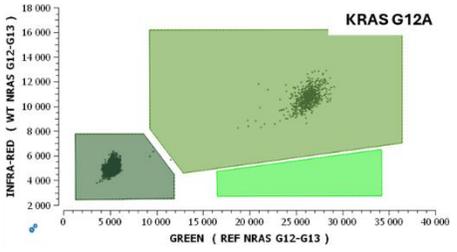
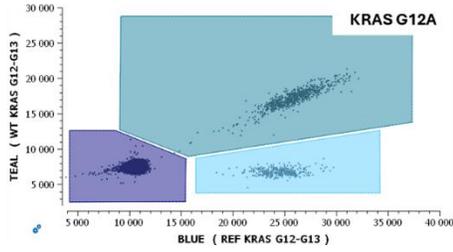
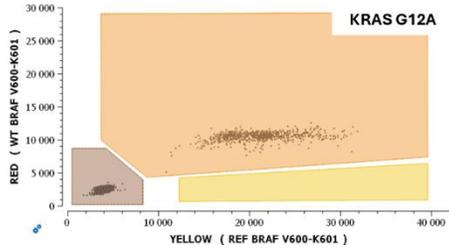
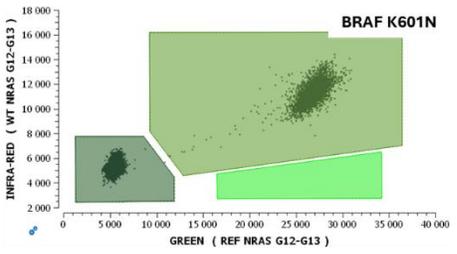
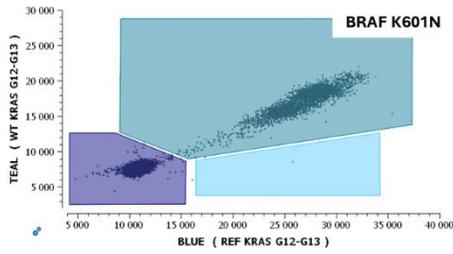
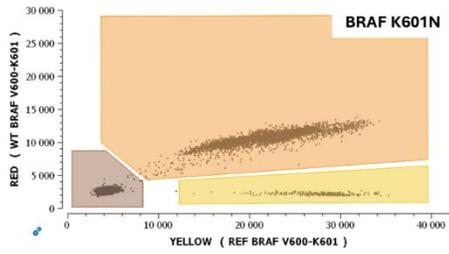
For optimal performance, it is recommended not to exceed a chamber concentration (DNA concentration in the reaction mix) of 1,000 copies/μL. The performance of the assay at higher concentrations is not guaranteed and must be validated by the user.

## 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 6-color naica® system are given below.

Wet lab testing was carried out using genomic hgDNA and H<sub>2</sub>O as negative controls and a positive control consisting of hgDNA and 3 synthetic mutants (BRAF V600E, KRAS G12C and NRAS G12D). Synthetic mutants were also tested individually (BRAF V600E/V600K/K601E/K601N, KRAS G12A/G12C/G12G/G12V, NRAS G12C/G12D/G13R) as well as with Horizon standards composed of 50% mutant DNA (KRAS G12R or KRAS G12S or NRAS G12V) and 50% wild-type DNA.





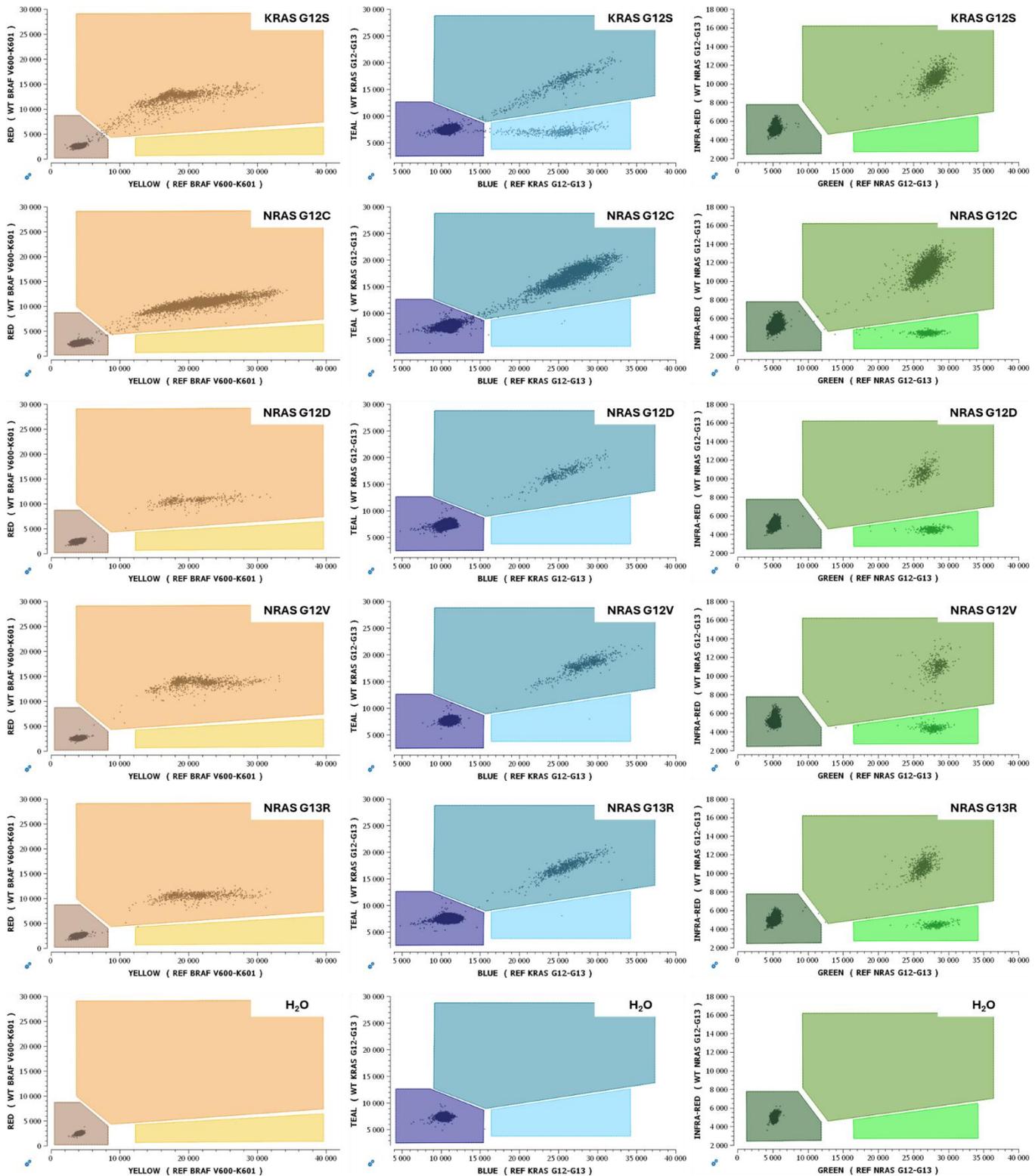


Figure 2: 2D plots obtained during wet lab testing on the 6-color naica® system. The polygons should be adjusted for each target population and for each sample.

## 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:

Post-Processing Type

None

Copy Number Variation (CNV)

Mutant Allelic Fraction (MAF)

Gene Expression (GEX)

Linkage Analysis

The Mutant Allele Frequency (MAF) is the ratio of the mutant gene concentration (C<sub>target</sub>) versus the total concentration of both the mutant and the wild type (C<sub>ref</sub>).

$$MAF = \left( \frac{C_{target}}{C_{ref} + C_{target}} \right) \times 100$$

Settings

<input type="checkbox"/>	BRAF V600-K601 WT
<input type="checkbox"/>	BRAF V600-K601 MUT
<input type="checkbox"/>	KRAS G12-G13 WT
<input type="checkbox"/>	KRAS G12-G13 MUT
<input type="checkbox"/>	NRAS G12-G13 WT
<input type="checkbox"/>	NRAS G12-G13 MUT
<input type="checkbox"/>	BRAF negative drops
<input type="checkbox"/>	KRAS negative drops
<input type="checkbox"/>	NRAS negative drops

	Target	Reference
<input checked="" type="checkbox"/>	BRAF V600-K601 MUT	BRAF V600-K601 WT
<input checked="" type="checkbox"/>	KRAS G12-G13 MUT	KRAS G12-G13 WT
<input checked="" type="checkbox"/>	NRAS G12-G13 MUT	NRAS G12-G13 WT

Use same reference for all targets

Select a custom reference per target

Add all “MUT” populations to processing, and select specific reference for each:

- “BRAF V600-K601 WT” selected as reference for “BRAF V600-K601 MUT” population,
- “KRAS G13-G13 WT” selected as reference for “KRAS G12-G13 MUT” population,
- “NRAS G13-G13 WT” selected as reference for “NRAS G12-G13 MUT” population.

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

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