



Precipio, Inc.

Instructions for Use

**BRAF Exon 15 Mutation Analysis using ICE COLD-PCR for
Detection with Real-Time PCR Analysis**

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Manufacturer

This Kit was manufactured by Precipio, Inc. at 8813 F Street, Omaha, NE 68127, USA.
USA Telephone 1-203-787-7888

Reagent Preparation

All reagents supplied with this kit are ready to use. Some components will need to be thawed, vortexed and/or spun in a microcentrifuge before use; check details in Assay Procedure below. Reagents do need to be combined to produce Master Mixes and reaction mixtures; full details are given in the procedure below.

Kit Components and Storage Conditions

The BRAF Exon 15 Kit contains the components to perform ICE COLD-PCR amplification for mutation enrichment as well as Real-Time PCR Detection for 27 total samples with controls. Recommended storage conditions are listed in [Table 1](#).

Table 1: Kit components with recommended storage conditions.

| Reagent, ICE COLD-PCR | Lid Color | Color of Label | Volume Total (µL) | Storage (°C) |
|--------------------------|-----------|----------------|-------------------|--------------|
| PCR Primers/RS-Oligo Mix | Clear | Blue | 180 | -20 |
| 2X Polymerase Master Mix | Clear | Green | 900 | -20 |
| Wild Type Control | Clear | White | 18 | -20 |
| 1% V600E Control | Clear | Red | 18 | -20 |
| 1% V600K Control | Clear | Red | 18 | -20 |
| Reagent, TaqMan | Lid Color | Color of Label | Volume Total (µL) | Storage (°C) |
| Taqman Assay – V600E | Orange | White | 40 | -20 |
| Taqman Assay – V600K | Orange | White | 40 | -20 |
| 2X GTXpress Master Mix | Green | White | 900 | 4 |

The kit contains enough reagents to perform 32 total analyses. For optimal usage of the kit, it is suggested that 27 samples are run/batch along with 1 set of controls.

This kit was designed specifically to enrich the following mutations:

1. c.1799T>A; p.V600E
2. c.1798_1799GT>AA; p.V600K

Reagents Required but not Supplied

1. Molecular Biology Grade Water: Thermo Fisher Catalog # AM9937

Primary Sample Collection, Handling and Storage

This Kit can be used with the following:

- DNA extracted from formalin-fixed paraffin-embedded tumor samples (FFPE slides & blocks) or fine needle aspirations (FNAs)
- Circulating free DNA (cfDNA) from plasma or serum
- DNA isolated from other body fluids

For optimal DNA extraction from FFPE, the tissue should be fixed in neutral buffered formalin for 14–24 hours, placed in ethanol and then embedded in paraffin following standard histological practices. Tumor biopsies are a heterogeneous mixture of tumor cells and non-tumor cells. In addition **the tumor itself is a heterogeneous mixture of tumor cells with mutations and tumor cells without mutations**. Because these somatic mutations may not be evenly distributed throughout the tumor, the resultant mutational analysis of different sections from the same tumor may be different. To increase the probability of detecting a mutation, DNA from the tumor region of the tissue should be isolated by scraping only the tumor area from the glass slide using a fresh, sterile scalpel for each new slide. It is recommended that at least two independent analyses are performed for each sample.

Notes for this Assay

- The ICE COLD-PCR assay has been optimized using the **Bio-Rad C1000** thermal cycler.
- A single sequencing primer is provided for uni-directional sequencing.
- Due to heterogeneity associated with tumors, biopsy samples may contain normal cells as well as Wild-Type and mutant tumor cells.
- The Limit of Detection (LOD) of any mutations present in the sample DNA following ICE COLD-PCR is dependent on the sensitivity of the downstream sequence detection platform used.
- Only the DNA Polymerases supplied with this kit should be used as indicated for the ICE COLD-PCR assays.
- This is a mutation enrichment assay. Any mutation or mismatch covered by the RS-Oligo will be enriched during the ICE COLD-PCR process. There are two possible sources of false positive results related to this assay:
 - Polymerase errors. While the polymerase included in the kit is a high-fidelity enzyme, there is the possibility of a polymerase-induced error.
 - The formalin-fixation process used in preparing FFPE tumor biopsy samples may result in deamination of cytosines. Deamination converts cytosine to uracil. The polymerase will recognize this uracil as a thymine and incorporate an adenine in the copied strands. The correct allele G is then replaced with an A causing an artifact mutation due to the fixation process and not a true somatic mutation.
 - It is highly suggested that an extraction protocol which incorporates Uracil-N-Glycosylase be used for FFPE Extractions.
 - These mutations do not repeat upon re-analysis. Therefore, it is recommended that any such mutation be confirmed by duplicate analysis using the same extracted genomic DNA.
- Some TaqMan SNP genotyping assays could potentially exhibit cross reactivity with non-target single nucleotide polymorphisms (SNP) at the same nucleotide positions as the target SNP. This is caused by mismatch base-pairing by the allele-specific probe. When TaqMan SNP genotyping assays were used to

detect ICP-enriched mutant alleles, cross reactivity was observed for the V600E assay. Experiments were conducted to investigate and establish cross reactivity patterns for the following assays:

- BRAF V600E (c.1799T>A) assay was tested with BRAF V600K (c.1798_1799GT>AA) mutation; Minor cross reactivity was observed.
 - BRAF V600K (c.1798_1799GT>AA) assay was tested with BRAF V600E (c.1799T>A) mutation; No significant cross reactivity was detected.
- When it is necessary to differentiate the target mutation from non-target mutations with cross reactivity, a second nucleotide sequence detection technique, such as Sanger sequencing, can be applied.

ICE COLD-PCR Protocol

IMPORTANT! Use dedicated hood/room for ICE COLD-PCR reaction setup to avoid contamination from post-PCR products.

IMPORTANT! The following procedures are optional but highly recommended prior to PCR setup:

- Turn on UV light inside hood or a UV crosslinker.
 - Prior to preparing Master Mixes, UV crosslink all empty Master Mix tubes. Also UV crosslink 1.7 mL tubes containing appropriate volume of Molecular Biology Grade Water needed for Master Mix preparation. These tubes should be UV irradiated for 10 min.
 - Make sure all work areas are prepared for analysis of low level mutations. This includes correct use of the PCR Workstation, dedicated pipettes, tips, 10% bleach solution and/or DNA Away™ solutions.
1. Remove controls, PCR Primer/RS-Oligo Mix and 2X Polymerase Master Mix from freezer and thaw on ice.
 2. Once thawed, vortex all kit components ~3-5 sec to mix thoroughly. Briefly centrifuge 5 sec to ensure no liquid remains on tube lids and place on ice.
 3. **Experiment layout:** Follow [Table 2](#) for layout to simplify later steps of the procedure. The following three controls are required for each setup: **NTC** (No Template Control) and the control DNAs provided by the kits, including **WT** (BRAF wild type), **V600E_1per** (1% BRAF-V600E), and **V600K_1per** (1% BRAF-V600K).

NOTE: Additional controls may be added in place of test samples.

Table 2: Proposed experimental layout for the ICE COLD-PCR for 32 reactions (27 samples plus controls).

| | 1 | 2 | 3 | 4 |
|----------|-------|-------|-------|--------------|
| A | SMP01 | SMP09 | SMP17 | SMP25 |
| B | SMP02 | SMP10 | SMP18 | SMP26 |
| C | SMP03 | SMP11 | SMP19 | SMP27 |
| D | SMP04 | SMP12 | SMP20 | WT |
| E | SMP05 | SMP13 | SMP21 | V600E_1per |
| F | SMP06 | SMP14 | SMP22 | V600K_1per |
| G | SMP07 | SMP15 | SMP23 | NTC1 |
| H | SMP08 | SMP16 | SMP24 | *Leave Empty |

* This well will be used for No Template Control #2 (NTC2) in later steps.

4. Use **Table 3** as a guide for calculating and preparing the ICE COLD-PCR Master Mix assuming a DNA volume of 15 μL at 3.3 $\text{ng}/\mu\text{L}$. Please note that less total DNA can be added to the reaction.
 - a. If the extracted DNA concentration is $> 3.3 \text{ ng}/\mu\text{L}$, dilute to a working concentration of 3.3 $\text{ng}/\mu\text{L}$ and use 15 μL of the diluted DNA for analysis.
 - b. If the extracted DNA concentration is $\leq 3.3 \text{ ng}/\mu\text{L}$, add 15 μL of extracted DNA for analysis.

Table 3: Calculations for Master Mix preparation:

| Reagent | 1X reaction* |
|--|--------------|
| UV-treated Molecular Biology Grade Water (μL) | 5 |
| 2X Polymerase Master Mix (μL) | 25 |
| Primer/RS-Oligo Mix (μL) | 5 |
| Total Volume PCR Master Mix for 1 reaction (μL) | 35 |
| Volume DNA added to reaction (μL) | 15 |

**Multiply volumes in this table by the number of samples being tested.*

NOTE: A Master Mix volume slightly greater than this calculation will be required to allow for losses during pipetting.

NOTE: Amount of UV-treated Molecular Biology Grade Water and volume of DNA can be adjusted accordingly.

NOTE: We suggest **fifty** ng of DNA should be used for each PCR reaction in order to potentially detect $\geq 0.1\%$ mutation present in the starting material (minimum 18 ng). The assay has been shown to be robust for DNA input amounts between 1 and 300 ng (using high quality DNA). Up to 20 μL DNA can be used in each PCR reaction with adjustment of volume of water used.

NOTE: If DNA contains contaminants (ethanol carryover, EDTA, etc.), increasing DNA volume may decrease PCR efficiency.

5. Label a 1.7 mL-centrifuge tube for PCR Master Mix preparation.
6. Add required volume of molecular biology grade water to Master Mix tube.
7. Add required volume of 2X Polymerase Master Mix to Master Mix tube.
8. Add required volume of Primer/RS-Oligo Mix to Master Mix tube.
9. Cap Master Mix tube, vortex for $\sim 3\text{-}5$ sec, briefly centrifuge and store on ice until use.
10. Label a 96-well plate with appropriate sample information.
11. Pipette appropriate volume of ICE COLD-PCR Master Mix into applicable wells. If using a repeat pipettor, ensure that there is no spillage or splashing from well to well.
12. To appropriate wells, add required volume of each DNA sample, control, or water (NTC). Use separate pipette tips for each sample and avoid cross-contamination of the samples by splashing. Securely cap all wells containing DNA samples, controls, and NTC with 8-cap strips.

NOTE: Addition of the kit controls last lessens the chance of contaminating any test sample wells.

13. Vortex (1/2 speed) for $\sim 3\text{-}5$ sec. Centrifuge for ~ 5 sec to ensure all solutions are collected at the bottom of wells or tubes. If not, repeat centrifugation.

Thermal Cycler Program for ICE COLD-PCR

1. Use the thermal cycler protocol in [Table 4](#) for ICE COLD-PCR.

IMPORTANT! Ensure that the following ramp rates are used depending on the thermal cycler:

- BioRad C1000 Touch: 1.5°C/sec
- BioRad Tetrad II: default (3.0°C/sec)
- Applied Biosystems Veriti: 100%

Table 4: Thermal cycler conditions for ICE COLD-PCR.

| Step | Temperature | Time | Cycles |
|---------------------------------|-------------|--------|--------|
| Initial Denaturation | 98 °C | 30 sec | 1 |
| Main ICE COLD-PCR Amplification | 98 °C | 10 sec | 45 |
| | 69 °C | 30 sec | |
| | 74 °C | 30 sec | |
| | 63 °C | 30 sec | |
| | 72 °C | 20 sec | |
| Amplification | 98 °C | 10 sec | 5 |
| | 63 °C | 10 sec | |
| | 72 °C | 20 sec | |
| Final Extension | 72 °C | 5 min | 1 |
| Hold | 12 °C | ∞ | |

NOTE: Samples can be stored at -20 °C post amplification.

Quality Control of ICE COLD-PCR Products (OPTIONAL)

1. Analyze an aliquot of ICE COLD-PCR product alongside an aliquot of 100-bp DNA mass ladder on a 2% agarose gel to verify amplification of DNA.
2. Only a single band corresponding to the main ICE COLD-PCR product should be observed (~125-170 bp).
3. If multiple smaller bands (<80 bp) are present check quality of input DNA.
4. If no product is observed, ensure quality of input template DNA was sufficient.
5. No ICE COLD-PCR products should be visible in No Template Control sample.
 - a. If DNA products of the expected product size are visible in No Template Control sample, contamination is likely and sample should not be taken to sequence analysis.

Real-Time PCR Step-by-Step Instructions using the ABI 7900HT System

IMPORTANT! To avoid cross contamination, set up real-time PCR reactions in an area or room that is separated from DNA extraction and the designated pre-PCR areas. Good laboratory practices, especially cleaning the bench and pipettes after reaction setup, are also required to avoid contamination.

IMPORTANT! Taqman assays need to be diluted to a 20X working solution in Low TE prior to performing the real-time PCR assay.

1. Preparation of Template DNA for Real-time PCR Analysis
 - a. Make a 1:200 dilution by adding 199 μL water into the wells of a clean, labelled 96-well plate. Add 1 μL of ICE COLD-PCR product from the ICE COLD-PCR plate to the water in the corresponding wells. Maintain the original plate layout. Cap the wells and mix well by vortexing for ~ 10 sec. Spin down briefly.
2. Real-time PCR after ICE COLD-PCR
 - a. Remove the Taqman assay from freezer, thaw on ice, vortex each for 10 sec, and spin the tubes briefly.
 - b. Remove the GTXpress Master Mix from fridge, mix by inverting the tube and briefly spin it down. Keep it on ice.

NOTE: Keep Taqman reagents in the dark until ready to use. Add them last to reaction mixtures. Once added, keep the plate in the dark until the plate is disposed of following run on the ABI 7900HT. Minimize freeze-thaw cycles.

- c. Prepare reaction mix for each target, using [Table 5](#) as a guide.

Table 5: Master Mix calculations for each Taqman assay.

| Components | 1X Reaction* |
|--|--------------|
| Molecular Biology Grade Water (μL) | 6.25 |
| 2X Real-Time PCR Polymerase Master Mix (μL) | 12.50 |
| Assay Mix, 20X (μL) | 1.25 |
| Total Volume real-time PCR Master Mix for 1 reaction (μL) | 20.00 |
| Volume DNA added to reaction | 5.00 |

**Multiply volumes in this table by the number of samples being tested.*

NOTE: See [Table 6](#) for recommended plate layout. Following this layout will allow simplification of real-time PCR program setup on ABI 7900HT.

NOTE: A Master Mix volume slightly greater than this calculation will be required to allow for losses during pipetting.

- d. Mix the reaction mix tube by pulse vortexing on low and spin the tube briefly.

- e. Aliquot 20 μ L of the reaction mix to the relevant wells of a MicroAmp Optical 96-well Reaction Plate. See **Table 6** for plate layout.

Table 6: Example template for running 27 samples with controls.

| | 1 | 2 | 3 | 4 |
|---|-------|-------|-------|------------|
| A | SMP01 | SMP09 | SMP17 | SMP25 |
| B | SMP02 | SMP10 | SMP18 | SMP26 |
| C | SMP03 | SMP11 | SMP19 | SMP27 |
| D | SMP04 | SMP12 | SMP20 | WT |
| E | SMP05 | SMP13 | SMP21 | V600E_1per |
| F | SMP06 | SMP14 | SMP22 | V600K_1per |
| G | SMP07 | SMP15 | SMP23 | NTC1 |
| H | SMP08 | SMP16 | SMP24 | NTC2 |

- f. To appropriate wells, add 5 μ L of diluted ICE COLD-PCR product from Step 1a, or water (NTC2). See **Table 6** for plate layout. Pipette-mix to ensure sample is well mixed into reaction mixture.
 - g. Place MicroAmp Optical Film over plate and seal. Spin the plate briefly to eliminate any air bubbles from the solution.
 - h. Use the MicroAmp Optical Film Compression Pad over the reaction plate while on the 7900HT instrument. Remember the reaction mix is light sensitive so keep the plate in the dark until loaded onto ABI 7900HT.
3. Set up of the ABI 7900HT to perform an Allelic Discrimination Pre-Read Run

IMPORTANT! AD_Setup-Table file and AQ_Setup-Table file are available for download at www.precipiodx.com to facilitate .sds file setup on ABI 7900HT System. It is recommended to use the files and track the user sample names with relevant setup table file sample names.

- a. System Set Up
 - i. Power on the 7900HT instrument.
 - ii. Power on the computer.
 - iii. Launch the SDS 2.4 software from the icon on the desktop
- b. If AD_Setup-Table file and AQ_Setup-Table file are to be used:
 - i. Make a copy of the downloaded Setup-Table file. Open the copied file in Microsoft Excel. On the "Sample List" sheet, fill in or copy/paste the sample names in the highlighted "Assigned Sample Name" column. Check the resulted plate layout on the right to make sure it is as expected. Save the "AD_Setup-Table" sheet and "AQ_Setup-Table" sheet separately as Text (Tab delimited, .txt) files. Use these .txt files as AD_Setup-Table file and AQ_Setup-Table later in Step 3 and Step 4, respectively.

- c. If this is the first time to run the assays, create new markers and new detectors listed in **Table 7**. **IMPORTANT!** Follow **Table 7** exactly to simplify later steps. If these markers and detectors have previously been created, skip to step 3c.

Table 7: Creating the markers and detectors for the BRAF Exon 15 real-time PCR assay.

| Marker Name | Allele X Detector | | | | Allele Y Detector | | | |
|-------------------|-----------------------------|--------------|----------|--------------------|-----------------------------|--------------|----------|--------------------|
| | Allele/ Detector Name | Base Name | Reporter | Quencher | Allele/ Detector Name | Base Name | Reporter | Quencher |
| BRAF-V600E | V600E-WT | T | VIC | Non Fluorescent | V600E | A | FAM | Non Fluorescent |
| BRAF-V600K | V600E-WT | GT | VIC | Non Fluorescent | V600E | AA | FAM | Non Fluorescent |

- i. To create a new detector, select **Tools**, click on **Detector Manager**. The Detector Manager window opens. Click on **New...** Then type in the name (See **Table 7** for detector information), choose a reporter, the type of quencher, and then select a color to represent the detector (optional). Next, click **Ok**. Repeat the above to create all 6 detectors in **Table 7**. Click **Done**.
- ii. To create a new marker, select **Tools**, click on **Marker Manager**. The Marker Manager window opens. Click on **New...** Enter marker name (See **Table 7** for maker information). Leave the Assay ID field blank. Click on the **color** box and choose a color to represent the marker (optional). Next, click on Allele X **Browse** button to open the Detector Manager. Click on the relevant detector. Make Allele X the wild type detector and Allele Y the mutant detector to make sample comparison easier (See **Table 7**). Next, click on the **Base** drop down list and choose the base that represents allele X and allele Y. Then click **Ok**. Repeat the above to create all markers in **Table 7**. Click **Done**.
- d. Open a new plate document, select **File, New Plate Wizard**.
- e. Click on **Allelic Discrimination (AD)** and then click on **Next**.
- f. Choose the plate type that is being used (e.g. 96 Wells Clear Plate). Then click on **Blank Document**. If the AD_Setup-Table file is used to set up the AD program and the reaction plate layout strictly followed **Table 6**, click on **Setup File**, and then **Browse** button to select the AD Setup Table file. Click on **Next**.
- NOTE:** If the AD_Setup-Table file is used to set up the program, then all samples, markers and detectors have been input into the program, so click **Next** and go to Step 3m.
- g. Enter the samples names by double-clicking in the sample field to activate the cursor. Then type in the sample name. After typing in the name, press **Enter** and a new row will appear. Make sure to press **Enter** after the very last sample row. If a same set of samples was used in an existing plate, click **Existing Plate** to import the existing sample names.
- h. Click on **Marker Manager** and select all necessary markers for the assay(s) and then click on **Copy to Plate Document**. Select **OK** in the pop-up window, then click **Done**.
- i. Once the marker has been added to the plate, click on **Next**.
- j. Assign samples and markers to the appropriate wells. From the plate layout drop-down list, select **Individual Wells**.

- k. Select the well(s) that contain the first sample and then select the **Add Samples and Markers** tab. Then select the appropriate sample and marker that corresponds to that well. In the Task field drop-down list, click on NTC for the NTC1 and NTC2 and Unknown for the controls and samples.
 - l. Repeat for all samples.
 - m. Select the **Well Inspector** tab to check that all the wells are correctly assigned. Click on **Finish**.
 - n. Export the setup table of the file by clicking on **File > Export**. From the Export drop-down list, select Setup table. Then click Save.
 - o. **IMPORTANT!** Save the new plate document by clicking on **File > Save**. Save the document as the plate label + _AD (for allelic discrimination) making sure it is a SDS 7900HT Document (*.sds) file. Then click **Save**.
 - p. Performing the Pre-Read Run
 - i. Click on **Instrument > Plate Read > Connect > Open/Close**. Then load the plate onto the instrument tray with the compression pad on top of the plate. Then click on **Open/Close** again followed by **Pre Read**. After the pre-read is finished, click ok. Click **File > Save** to save the data.
4. Perform a Standard Curve Amplification Run.
- a. Open a new plate document select **File > New Plate Wizard**.
 - b. Click on **Standard Curve (AQ)** and then click on **Next**.
 - c. Select the plate type that is being used (eg. 96 Wells Clear Plate) and then click on **Setup File**. Click **Browse** button to select a Setup Table file. Click on **Next**.

NOTE: If the **AQ_Setup-Table** file is selected here, click on **Next** and skip to Step 4h. If the **Setup Table** file saved in Step 3n is selected, go to next step.

- d. All relevant samples and detectors have been imported in this window. Click on **Next**.
- e. Samples have been automatically assigned to the wells. Now assign markers to the wells. From the plate layout drop-down list, ensure **Individual Wells** is selected.
- f. In the **Add Samples and Detectors** tab, choose the appropriate detectors that pertain to the selected well(s). In the Task field drop-down list, click on NTC for the Non-Template controls and Unknown for the controls and samples.
- g. Repeat as necessary until all wells have been assigned appropriate detectors and tasks.
- h. Select the **Well Inspector** tab to check that all the wells are correctly assigned. Click on **Finish**.
- i. **IMPORTANT!** Save the new plate document by clicking on **File > Save**. Save the document using appropriate identifying information, making sure it is a SDS 7900HT Document (*.sds) file. Then click **Save**.

- j. Performing an Amplification Run:
 - i. In the Standard Curve (AQ) plate document that was created, click **Setup**.
 - ii. Verify that the Passive Reference setting is **ROX** dye.
 - iii. Select the **Instrument > Thermal Cycler** tabs.
 - iv. Select **Standard** mode.
 - v. Enter 25 µL as the sample volume, if 96-well reaction plate is used.
 - vi. Select the **Thermal Profile** tab.
 - vii. The following thermal cycler conditions should be used (**Table 8**).

Table 8: Thermal cycler program to be used for the Taqman assay.

| | Temperature | Time | Cycles |
|-----------------------|-------------|--------|--------|
| Polymerase Activation | 95 °C | 20 sec | 1 |
| PCR Amplification | 95 °C | 3 sec | 40 |
| | 60 °C | 20 sec | |

- viii. Select **Real-time** tab.
 - ix. Select **Connect to Instrument**.
 - x. Select **Start Run**.
 - xi. Once the reaction is completed, select **File > Save** and close the plate document.
 - k. Performing the Post-Read
 - i. Select **File > Open**. Find the previously saved Allelic discrimination (AD) plate document and open it.
 - ii. Click on **Instrument > Plate Read > Connect > Post Read**.
 - iii. After the run, the status values and buttons are grayed-out, the Analysis button is enabled, and a message indicates whether or not the run was successful. When the run is complete click on **Open/Close** to eject the reaction plate.
 - iv. Select **File > Close** to save the raw data; or, go directly to the next step to analyze the run.
5. Data Analysis using TaqMan Genotyper Software (V. 1.3)

NOTE: This software is available for download via ThermoFisher Scientific at:

<https://www.thermofisher.com/us/en/home/technical-resources/software-downloads/taqman-genotyper-software.html>

- a. Create a study
 - i. Click **Create Study** in the home window of the software.
 - 1. Enter the study properties
 - a. In the Properties dialog box, enter a study name, select an instrument type, then select “Endpoint+pre-PCR read” as the genotyping experiment type
- OPTIONAL:** Enter a description of the study and/or enter comments.
- ii. Import experiments into the study
 - 1. In the Workflow Menu pane, select **Experiments** to open the Experiments screen.

2. Click **Import**, browse to and select the Allelic Discrimination experiment(s) of interest, then click **Import**.
- iii. Set the analysis settings
 1. In the toolbar, click **Analysis Settings** to open the Analysis Settings dialog box.
 2. Select the **Call Settings** tab, select **Autocalling** as the call method. Uncheck “Use Reference Panels for Autocalling”. Uncheck “Use Hardy-Weinberg for Analysis”.
 3. Select the **Control Identifiers** tab, select **Override Control Settings from Experiments**, then type in “NTC1, NTC2” for **NTC (for all Assays)** and “WT” for the **Positive Controls VIC/VIC**. A drop down list with sample names will be created when names are typed in. It can be used to select relevant controls.
 4. Click **QC Settings** tab. Uncheck “Assay Call Rate Low”. Uncheck “Experiment Call Rate Low”. Uncheck “Sample Call Rate Low”. These QC flags are not relevant to the study.
 5. Click **OK** to save the changes and close the dialog box.
- b. View and analyze the data
 - i. In the Workflow Menu pane, select **Analysis** to open the Results screen.
 - ii. View the data in the scatter plot. In the **Assays** panel, select specific assay to be viewed. The blue and green dots indicate samples with mutations targeted by the assay. Red dots indicate samples that are wild type at the nucleotide targeted by the assay.
 - iii. View the data in the **Results** table. If needed, you can bookmark wells, omit wells, and/or enter comments about the wells.

NOTE: Since the real-time PCR analysis is done on ICE COLD-PCR amplified DNA samples with enriched variant(s), the heterozygosity/homozygosity analysis is not an accurate representation of the original mutant frequency. Consider both VIC/FAM and FAM/FAM calls as a positive variant call.

 - iv. Click **Save**.
 - v. View the data in the Quality Control screen
 1. In the Workflow Menu pane, select **Quality Control** to open the Quality Control screen.
 2. Select the **Flags Summary** tab. Look for any flags that were generated by the analysis. **Table 9** shows a list of flag descriptions and recommended actions.
 3. Any wells with quality concerns can be bookmarked. To bookmark a sample, highlight the sample in the **Samples** panel, then highlight the relevant assay in the **Results** panel and click **Bookmarks > Set Bookmarks**. The bookmarks are now associated with the sample in other screens too.

Table 9: Flag descriptions and recommended actions when using the Genotyper Software.

| QC Flag | Description | Action |
|-------------------------|--|--|
| Failed Control | A Failed Control flag can be raised for any data point that is identified as a control: NTC, or Positive Control. If the user-assigned control identifier for a data point is inconsistent with the call that would be assigned by the software algorithm to an Unknown with the same FAM™ and VIC® dye intensities, a flag is raised. | Review the flagged data point. Note: This may be an indication of wrongly assigned controls or cross-contamination of the controls, including NTC or Positive Control. Track this for further troubleshooting. |
| Genotype Quality Low | A Genotype Quality Low flag can be raised for any data point that is identified or tasked as an Unknown. If the quality value assigned by the software algorithm for a data point is below the threshold, a flag will be raised. | Review the flagged data point and determine if the data point is an outlier or located in acceptable coordinates. You can manually assign a call or modify the quality value threshold to include the data point. |
| Low ROX™ Intensity | A Low ROX™ Intensity flag can be raised for any data point. If the ROX™ dye intensity determined by the software for a data point is below the threshold, a flag will be raised. | No action should be taken for these data points. If the ROX dye intensity is below the default threshold, the data point does not meet the minimum conditions for assigning a call. This may be a reaction issue. |
| NTC FAM™ Intensity High | An NTC FAM™ Intensity High flag can be raised for any data point that is identified or tasked as an NTC. If the FAM™ dye signal intensity for a data point tasked as NTC is greater than the threshold, a flag will be raised. | Review the flagged data point and determine if the high signal is acceptable or not. Note: If the coordinates of the NTC data point are located next to Unknown data points, this could indicate experiment cross-contamination, or an amplifying NTC. Track this for further troubleshooting. |
| NTC VIC® Intensity High | An NTC VIC® Intensity High flag can be raised for any data point that is identified or tasked as an NTC. If the VIC® dye signal intensity for a data point tasked as NTC is greater than the threshold, a flag will be raised. | Review the flagged data point and determine if the high signal is acceptable or not. Note: If the coordinates of the NTC data point are located next to Unknown data points, this could indicate experiment cross-contamination, or an amplifying NTC. Track this for further troubleshooting. |

Refer to the [TaqMan® Genotyper Software Getting Started Guide \(PN 4448637\)](#) for any other operations such as data export and transfer.

Technical Support/Questions

For any questions regarding the kit or IFU, please contact us at Techsupport@preciiodx.com or call 1.203.787.788 ext. 509.