April 2026

BRAF Pyro® Kit Handbook

For quantitative measurement of mutations in codons 600 and 464–469 of the human *BRAF* gene using PyroMark® Q24, PyroMark Q24 Advanced, and PyroMark Q48 Autoprep

Sample to Insight

Table of Contents

Kit Contents

BRAF Pyro Kit Catalog no. Number of reactions	(24) 1065142 24
Seq Primer BRAF 600	2 × 24 µL
Seq Primer BRAF 464–469	2 × 24 µL
PCR Primer BRAF 600	24 µL
PCR Primer BRAF 464–469	24 µL
PyroMark PCR Master Mix, 2×	850 µL
CoralLoad® Concentrate, 10×	1.2 mL
H_2O	3 × 1.9 mL
Unmethylated Control DNA, 10 ng/µL	100 µL

Controls

Unmethylated Control DNA is included in the kit as a positive control for PCR and sequencing reactions. This control DNA has a wild-type genotype in the regions sequenced using this kit and is required for adequate result interpretation. Include a sample containing Unmethylated Control DNA for each assay in every Pyrosequencing® run. In addition, include a negative control (no template DNA) in every PCR setup for at least one assay.

Shipping and Storage

The BRAF Pyro Kit is shipped on dry ice. PyroMark PCR Master Mix, CoralLoad Concentrate, Unmethylated Control DNA, and all primers should be stored at –30°C to –15°C upon arrival.

The BRAF Pyro Kit is stable until the kit expiration date when stored under these conditions.

Intended Use

The BRAF Pyro Kit is intended for molecular biology applications. This product is not intended for the diagnosis, prevention, or treatment of a disease.

All due care and attention should be exercised in the handling of the products. We recommend all users of QIAGEN® products to adhere to the NIH guidelines that have been developed for recombinant DNA experiments, or to other applicable guidelines.

Safety Information

When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, please consult the appropriate safety data sheets (SDSs). These are available online in convenient and compact PDF format at **www.qiagen.com/safety**, where you can find, view, and print the SDS for each QIAGEN kit and components.

CAUTION

Always wear safety glasses, gloves, and a lab coat. The responsible body (e.g., laboratory manager) must take the necessary precautions to ensure that the surrounding workplace is safe and that the instrument operators are not exposed to hazardous levels of toxic substances (chemical or biological) as defined in the applicable Safety Data Sheets (SDSs) or OSHA,* ACGIH,† or COSHH‡ documents. Venting for fumes and disposal of waste must be in accordance with all national, state, and local health and safety regulations and laws.

* OSHA: Occupational Safety and Health Administration (United States of America).
† ACGIH: American Conference of Government Industrial Hygienists (United States of America).
‡ COSHH: Control of Substances Hazardous to Health (United Kingdom).

Quality Control

In accordance with QIAGEN's ISO-certified Quality Management System, each lot of the BRAF Pyro Kit is tested against predetermined specifications to ensure consistent product quality.

Introduction

Principle and procedure

The BRAF Pyro Kit is used for quantitative measurement of mutations in codon 600 in exon 15 and codons 464–469 in exon 11 of the human *BRAF* gene (**Ensembl ID**: ENSG00000157764). The kit consists of two assays: one for detecting mutations in codon 600 and one for detecting mutations in codons 464–469 (Figure 1). The two regions are amplified separately by PCR and sequenced through the defined regions. Sequences surrounding the defined positions serve as normalization and reference peaks for quantification and quality assessment of the analysis.

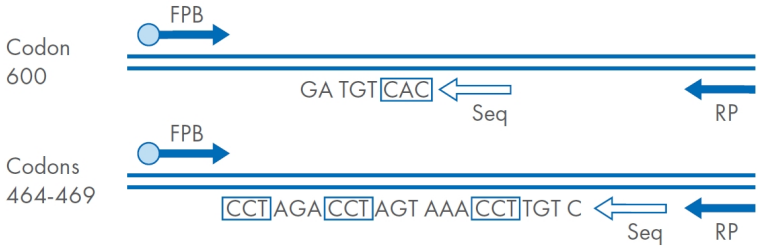

Figure 1. Illustration of the *BRAF* assay. The indicated sequence is the analyzed sequence for a wild-type sample. **FPB**, forward PCR primers (B indicates biotinylation); **RP**, reverse PCR primers; **Seq**, sequencing primers.

Both assays are sequenced in the reverse direction.

The product consists of a PCR primer mix and a sequencing primer for each assay. The primers are supplied in solution. Each vial contains 24 µL of each primer or primer mix.

Equipment and Reagents to be Supplied by User

When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, consult the appropriate safety data sheets (SDSs), available from the product supplier.

- DNA preparation reagents
- For further information on required equipment and reagents, refer to the user manual of the instrument being used:
    - PyroMark Q24: See Section 5.3, "Sample Preparation," in the *PyroMark Q24 User Manual* (**www.qiagen.com/HB-0240**).
    - PyroMark Q24 Advanced: See Section 5.3, "Sample and Reagent Preparation," in the *PyroMark Q24 Advanced User Manual* (**www.qiagen.com/HB-1341**).
    - PyroMark Q48 Autoprep: See the "Preparing Templates and Reagents" section in the *PyroMark Q48 Autoprep User Manual* (**www.qiagen.com/HB-1971**).

Important Notes

- Create an Assay Setup as described below. This must only be done once, before running the *BRAF* Pyro assay for the first time (see "Protocol: Assay and Run Setup", page 15).
- Ensure that the reactions are thoroughly mixed and prepared and incubated at the recommended temperatures.
- The Sequencing Primer stock solution has a concentration of 10 µM.
    - **PyroMark Q24**: Mix 0.8 µL of undiluted Sequencing Primer stock solution (10 µM) with 24.2 µL Annealing Buffer to prepare 25 µL of a Sequencing Primer solution at a final concentration of 0.32 µM.
    - **PyroMark Q24 Advanced**: Mix 0.75 µL of undiluted Sequencing Primer stock solution (10 µM) with 19.25 µL Advanced Annealing Buffer to prepare 20 µL of a Sequencing Primer solution at a final concentration of 0.375 µM.
    - **PyroMark Q48 Autoprep**: Dilute the Sequencing Primer stock solution (10 µM) to a final concentration of 4 µM by mixing 0.8 µL Sequencing Primer stock solution with 1.2 µL Advanced Annealing Buffer for one reaction.
        - For manual sequencing primer loading, pipet 2 µL of diluted Sequencing Primer (4 µM) into each well.

          Important: Wait until the software prompts you to add the Sequencing Primer (4 µM). Do not pipet the Sequencing Primer (4 µM) into the wells in the beginning of the run. For more information, see *PyroMark Q48 Autoprep User Manual* (**www.qiagen.com/HB-1971**).
        - For automatic sequence primer loading, prepare higher volumes of diluted Sequencing Primer (4 µM), as required.

Description of protocols

The first step is to amplify the target DNA by PCR, as described in "Protocol: PCR Using the PyroMark PCR Kit", page 12. The *BRAF* Pyro Assay and Run should be set up while the PCR is running, following the instructions in "Protocol: Assay and Run Setup," page 15. After amplification, follow the protocols according to the respective instrument user manual to prepare the sequencing templates for Pyrosequencing analysis:

- *PyroMark Q24 User Manual* (**www.qiagen.com/HB-0240**): See Section 5.3, "Sample preparation," continuing from Section 5.3.3 "Immobilizing the PCR products to beads," and Section 5.4 "Preparation of PyroMark Gold Q24 Reagents."
- *PyroMark Q24 Advanced User Manual* (**www.qiagen.com/HB-1341**): See Section 5.3, "Sample and reagent preparation," continuing from Section 5.3.3, "Immobilizing the PCR products to beads."
- *PyroMark Q48 Autoprep User Manual* (**www.qiagen.com/HB-1971**): See "Preparing templates and reagents," continuing from Section 6.1.5, "Absorber strip".

Finally, perform the Pyrosequencing run and analyze the data according to the relevant instrument user manual:

- *PyroMark Q24 User Manual* (**www.qiagen.com/HB-0240**): See Section 5.5, "Processing a run on the PyroMark Q24 Instrument."
- *PyroMark Q24 Advanced User Manual* (**www.qiagen.com/HB-1341**): See Section 5.4, "Processing a run on the PyroMark Q24 Advanced."
- *PyroMark Q48 Autoprep User Manual* (**www.qiagen.com/HB-1971**): See "Starting a run" and Section 7, "PyroMark Q48 Autoprep Software".

Protocol: PCR Using the PyroMark PCR Kit

This protocol describes the setup and cycling conditions for the amplification of DNA using the PyroMark PCR Master Mix (included in kit). The PCR products are subsequently used for detection of mutations in of the *BRAF* gene by Pyrosequencing analysis.

Important points before starting

- See the *PyroMark PCR Kit Handbook* (**www.qiagen.com/HB-3794**) for more detailed information.
- HotStarTaq® DNA Polymerase requires an activation step of 15 min at 95°C (step 5 of the protocol).
- Set up all reaction mixtures in an area separate from areas used for DNA preparation or PCR product analysis.
- Use disposable tips containing hydrophobic filters to minimize cross-contamination.
- Before opening the tubes containing PCR primers, spin briefly to collect contents at the bottom of the tubes.
- Adjust the concentration of the control and sample DNA, if necessary, to 0.4–2 ng/µL.

Procedure

1. Thaw the PyroMark PCR Master Mix, CoralLoad Concentrate, and primer solutions.

   Important: Mix the solutions before use to avoid localized concentrations of salt.

2. Prepare a reaction mix for each PCR primer set according to Table 1.

Table 1. Preparation of reaction mix for each PCR primer mix

Component of reaction mix	Volume (µL) per reaction
PyroMark PCR Master Mix, 2	12.5
CoralLoad Concentrate, 10×	2.5
PCR Primer *BRAF* codon 600 or PCR Primer *BRAF* codons 464–469	1
RNase-free water	4
Total volume	**20**

3. Gently pipet the reaction mixture up and down to mix thoroughly, and dispense 20 µL into each PCR tube. It is not necessary to keep PCR tubes on ice, as HotStarTaq DNA Polymerase is inactive at room temperature.

4. Add 5 µL template DNA (2–10 ng of genomic DNA) to the individual PCR tubes, and mix thoroughly.

   Note: Include a negative control sample (without template DNA) in every PCR setup for at least one assay. In addition, include a sample containing Unmethylated Control DNA for each assay in every Pyrosequencing run (see "Controls," page 3).

5. Program the thermal cycler according to Table 2.

Table 2. Optimized cycling protocol for PyroMark PCR Master Mix

	Time	Temperature (°C)	Notes
Initial PCR activation step	15 min	95	HotStarTaq DNA Polymerase is activated by this heating step
3-step cycling			
Denaturation	20 s	95	
Annealing	30 s	53	
Extension	20 s	72	
Number of cycles			**42**
Final extension	5 min	72	
Hold	∞	4	

6. Place the PCR tubes in the thermal cycler and start the cycling program.

   Note: After amplification, samples can be stored overnight at 2–8°C. For longer storage store at –30°C to –15°C.

7. Use 10 µL of PCR product for subsequent Pyrosequencing analysis. We recommend checking the PCR product before Pyrosequencing analysis, for example, by rapid analysis on the QIAxcel® system or by agarose gel analysis. See the *PyroMark PCR Kit Handbook* (**www.qiagen.com/HB-3794**) for details. The amplicon lengths are 115 bp for codon 600 and 93 bp for codons 464–469.

8. Proceed to "Protocol: Assay and Run Setup," next page.

Protocol: Assay and Run Setup

These protocols are for setting up the assay parameters and creating a Run Setup for mutation analysis in *BRAF*.

Use default settings in the software for all assay setups if not otherwise stated.

Procedure

1. Set up the *BRAF* assay by selecting **New AQ** Assay in the PyroMark Q24, PyroMark Q24 Advanced, or PyroMark Q48 Autoprep Software.
2. Table 3 shows the "Sequence to Analyze" for both *BRAF* assays. Type the assay-specific sequence in the "Sequence to Analyze" field of the software.

   Note: The "Sequence to Analyze" can also be modified after the run (if not locked) to analyze for mutations at different positions in codons 464–469 and codon 600. To reanalyze and target additional mutations, go to **Analysis Setup** and change the default "Sequence to Analyze" to one of the additional "Sequence to Analyze" listed in Table 4. Click **Apply**, and then click **To All** when the Apply Analysis Setup window appears.

   Note: We strongly recommend reanalyzing all samples with no mutation detected using the standard "Sequence to Analyze", as well as samples that received a "Check" or "Failed" quality assessment or show peaks that do not match the height of the histogram bars. "Check" and "Failed" quality assessments may indicate a mutation that is not addressed by the standard "Sequence to Analyze", resulting in peak height deviations.
3. Manually enter the assay-specific "Dispensation Order" from Table 3.

   Note: Do not use the **Generate Dispensation Order** button. Both "Sequence to Analyze" and "Dispensation Order" must be entered in manually.

4. Click the toolbar, and save the assay as *BRAF codon 600* or *BRAF codons 464–469*.

   Note: The complex mutations in *BRAF* codon 600 and codons 464–469 cannot be analyzed using the PyroMark AQ analysis. As a result, mutation frequencies cannot be reliably calculated. Even if a value is displayed, the true mutation frequency must be determined manually (see Table 4). If a complex mutation is suspected, compare the pyrogram with the histograms presented in Figure 6–Figure 10 to enable accurate identification of the corresponding mutation.

Table 3. Assay setup: "Sequence to analyze" and "Dispensation order" for the two *BRAF* Pyro assays

Assay	Sequence to analyze	Dispensation order
BRAF 600	CWCTGTAGC	TCGTATCTGTAG
BRAF 464–469	CTGTTNCAAATGATHCAGATHCA	AGCTCGTAGCATGCATACGAGCATAC

Table 4. Common mutations in the human *BRAF* gene detected by the BRAF Pyro Kit with respective "Sequence to analyze"

Nucleic acid substitution	Amino acid substitution	Cosmic ID	Sequence to analyze
Codon 600 (GTG)			
1799T>A*	V600E	476	CWCTGTAGC
1799T>G	V600G	6137	CVCTGTAGC
1799T>C	V600A	18443	CVCTGTAGC
1798G>A*	V600M	1130	CAYTGTAGC
1799_1800TG>AA*	V600E complex	475	CWCTGTAGC • Deselect T1, C7, and T8 as reference peak • Calculation of mutation frequency: analyze peak height ratio for T4 (mut):C7 (wt)

Table 4. Common mutations in the human BRAF gene detected by the BRAF Pyro Kit with respective "Sequence to analyze" (continued)

Nucleic acid substitution	Amino acid substitution	Cosmic ID	Sequence to analyze
1799_1800TG>AT	V600D	477	MACTGTAGC • Deselect C2 and T6 as reference peak • Calculation of mutation frequency: analyze peak height ratio for T6 (mut):C2 (wt)
1798_1799GT>AA*	V600K	473	CWCTGTAGC • Deselect T4, A5, C7, and T8 as reference peak • Calculation of mutation frequency: analyze peak height ratio for $\frac{T4}{3}$ (mut):C7 (wt)
1798_1799GT>AG	V600R	474	CWCTGTAGC • Deselect C2, T4, A5, C7 and T8 as reference peak • Calculation of mutation frequency: analyze peak height ratio for $\frac{T4}{3}$ (mut):C7 (wt)
Codon 469 (GGA)			
1406G>C*	G469A	460	CTGTTNCAAATGATHCAGATHCA
1406G>T*	G469V	459	CTGTTNCAAATGATHCAGATHCA
1406G>A	G469E	461	CTGTTNCAAATGATHCAGATHCA

Table 4. Common mutations in the human BRAF gene detected by the BRAF Pyro Kit with respective "Sequence to analyze" (continued)

Nucleic acid substitution	Amino acid substitution	Cosmic ID	Sequence to analyze
1405_1406GG>TC	G469S	458	CTGTTNCAAATGATHCAGATHCA • Calculation of mutation frequency: analyze peak height ratio for G9 (mut): $\frac{C10}{2}$ (wt)
Codon 466 (GGA)			
1397G>T*	G466V	451	CTGTTNCAAATGATHCAGATHCA
1397G>A	G466E	453	CTGTTNCAAATGATHCAGATHCA
Codon 464 (GGA)			
1391G>A*	G464E	449	CTGTTNCAAATGATHCAGATHCA
1391G>T	G464V	450	CTGTTNCAAATGATHCAGATHCA

* For these mutations, the ability to detect different mutation frequencies on the PyroMark Q48 Autoprep was validated.

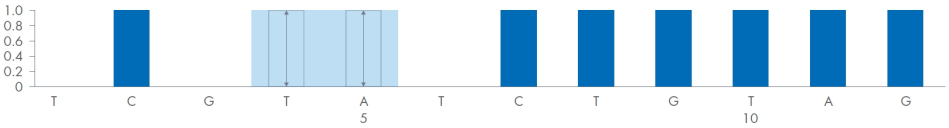

Figure 2. Histogram for codon 600 (nucleotide 1799) with the "Sequence to Analyze" CWCTGTAGC.

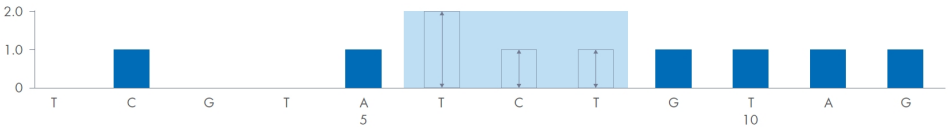

Figure 3. Histogram for codon 600 (nucleotide 1798) with the "Sequence to Analyze" CAYTGTAGC.

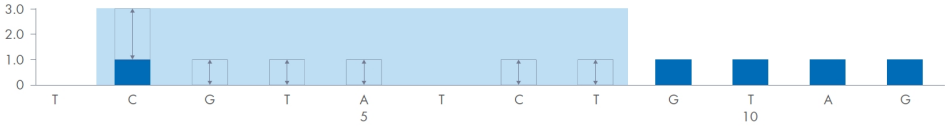

Figure 4. Histogram for codon 600 (nucleotide 1799) with the "Sequence to Analyze" CVCTGTAGC.

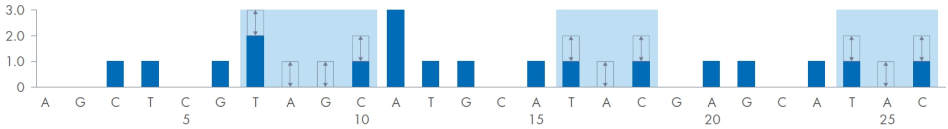

Figure 5. Histogram for codons 464–469 (nucleotide 1391 [codon 464], 1397 [codon 466], and 1406 [codon 469]).

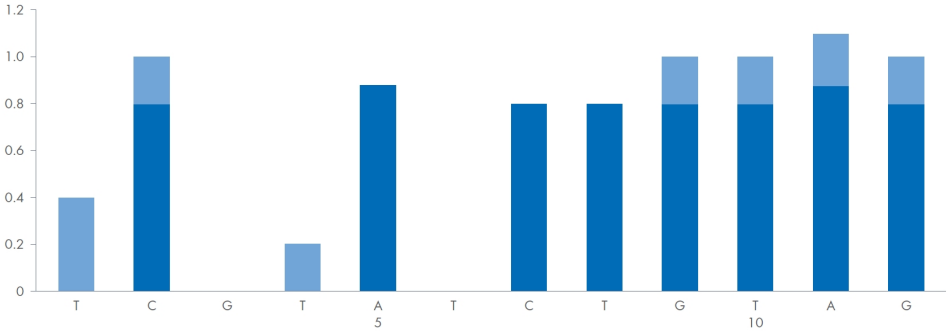

Figure 6. Schematic histogram for mutation 1799_1800TG>AA in codon 600 (mutation frequency: 20%).

Example calculation

$$\text{Peak height at T4 (peak of mutated alleles)} = 20\ \text{RLU}$$

$$\text{Peak height at C7 (peak of wild-type alleles)} = 80\ \text{RLU}$$

Calculated mutation frequency

$$\frac{20\ \text{RLU}}{20\ \text{RLU}+80\ \text{RLU}} = 0.2$$

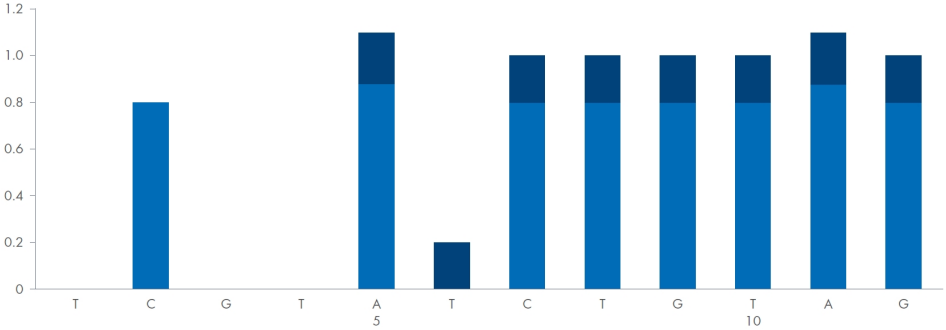

Figure 7. Schematic histogram for the mutation 1799_1800TG>AT in codon 600 (mutation frequency: 20%).

Example calculation

$$\text{Peak height at T6 (peak of mutated alleles)} = 20\ \text{RLU}$$

$$\text{Peak height at C2 (peak of wild-type alleles)} = 80\ \text{RLU}$$

Calculated mutation frequency

$$\frac{20\ \text{RLU}}{20\ \text{RLU}+80\ \text{RLU}} = 0.2$$

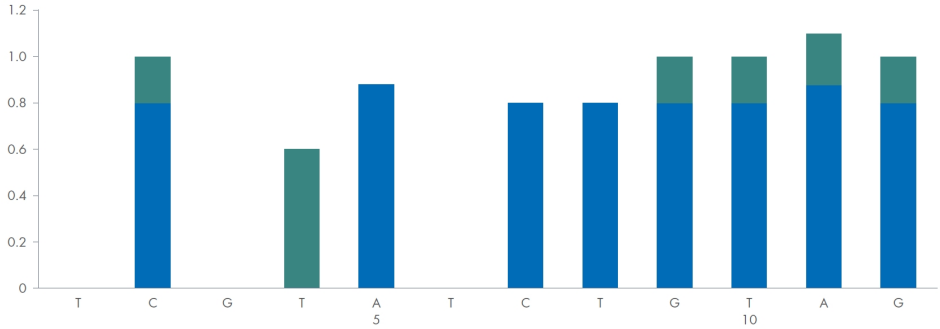

Figure 8. Schematic histogram for the mutation 1798_1799GT>AA in codon 600 (mutation frequency: 20%).

Example calculation

$$\text{Peak height at T4 (peak of 3 nucleotides of mutated alleles)} = 60\ \text{RLU}$$

$$\text{Peak height at C7 (peak of wild-type alleles)} = 80\ \text{RLU}$$

Calculated mutation frequency

$$\frac{\left(\frac{60\ \text{RLU}}{3}\right)}{\left[\left(\frac{60\ \text{RLU}}{3}\right)+80\ \text{RLU}\right]} = \frac{20\ \text{RLU}}{(20\ \text{RLU}+80\ \text{RLU})} = \frac{20\ \text{RLU}}{100\ \text{RLU}} = 0.2$$

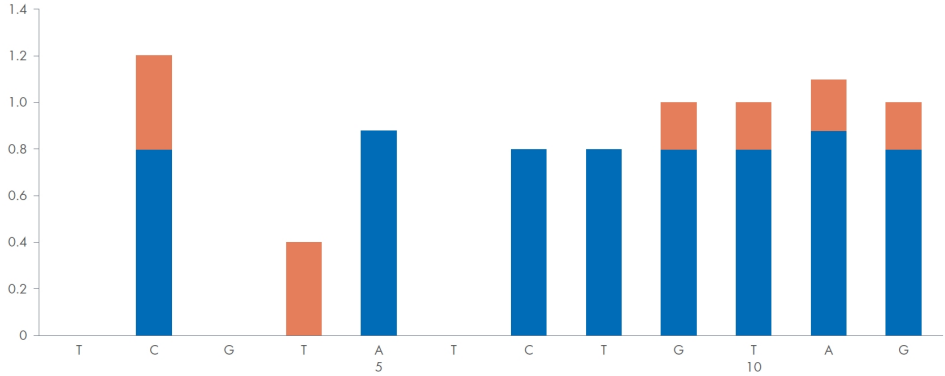

Figure 9. Schematic histogram for mutation 1798_1799GT>AG in codon 600 (mutation frequency: 20%).

Example calculation

$$\text{Peak height at T4 (peak of 2 nucleotides of mutated alleles)} = 40\ \text{RLU}$$

$$\text{Peak height at C7 (peak of wild-type alleles)} = 80\ \text{RLU}$$

Calculated mutation frequency

$$\frac{\left(\frac{40\ \text{RLU}}{2}\right)}{\left[\left(\frac{40\ \text{RLU}}{2}\right)+80\ \text{RLU}\right]} = \frac{20\ \text{RLU}}{(20\ \text{RLU}+80\ \text{RLU})} = \frac{20\ \text{RLU}}{100\ \text{RLU}} = 0.2$$

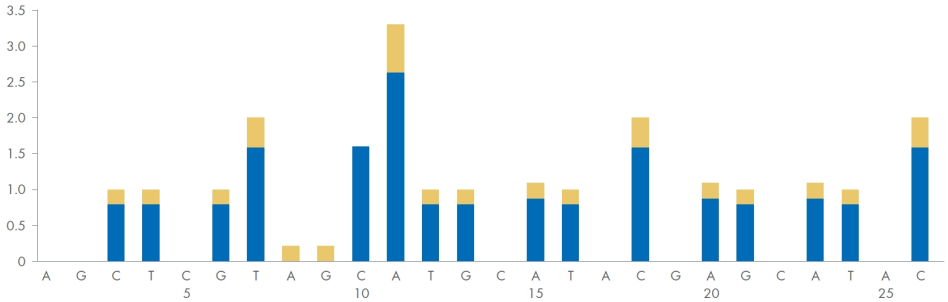

Figure 10. Schematic histogram for mutation 1405_1406GG>TC in codon 469 (mutation frequency: 20%).

Example calculation

$$\text{Peak height at G9 (peak of mutated alleles)} = 20\ \text{RLU}$$

$$\text{Peak height at C10 (peak of 2 nucleotides of wild-type alleles)} = 160\ \text{RLU}$$

Calculated mutation frequency

$$\frac{20\ \text{RLU}}{\left[20\ \text{RLU}+\left(\frac{160\ \text{RLU}}{2}\right)\right]} = \frac{20\ \text{RLU}}{(20\ \text{RLU}+80\ \text{RLU})} = \frac{20\ \text{RLU}}{100\ \text{RLU}} = 0.2$$

Run setup

1. Create a new run file by select **New Run**.
2. Setup the plate by adding the *BRAF* assays to selected wells.
3. Proceed with the Run Setup, preparation of samples and run according to the instructions in *PyroMark Q24 User Manual*, *PyroMark Q24 Advanced User Manual*, or *PyroMark Q48 Autoprep User Manual*.

Troubleshooting Guide

This troubleshooting guide may be helpful in solving any problems that may arise. For more information, see also the Frequently Asked Questions page at our Technical Support Center: **www.qiagen.com/FAQ/FAQList.aspx** (for contact information, visit **www.qiagen.com**).

Refer to the user manual for the PyroMark instrument which is used.

- When using PyroMark Q24, see Section 7, "Troubleshooting Guide," in the *PyroMark Q24 User Manual*.
- When using PyroMark Q24 Advanced, see Section 7, "Troubleshooting Guide," in the *PyroMark Q24 Advanced User Manual*.
- When using PyroMark Q48 Autoprep, see Section 9, "Troubleshooting Guide," in the *PyroMark Q48 Autoprep User Manual*.
- For an assay-specific Troubleshooting Guide, see "Troubleshooting Guide," in the *BRAF Pyro Handbook* for PyroMark Q24 (**www.qiagen.com**).

Assay-specific troubleshooting

"Check" or "failed" result	Comments and suggestions
Warning message "High peak height deviation" for dispensation 6 with the codon 600 assay and "Sequence to Analyze" CAYCTGTAGC	The Pyrogram should be carefully compared with the histogram, which can be displayed by right-clicking in the Pyrogram window. If background noise at dispensation T6 is below the expected level and the remaining measured peaks match the height of the histogram bars, the warning and the "Check" or "Failed" quality assessment can be disregarded.
Warning message "High peak height deviation" for dispensation 3 or 4 with the codon 600 assay and "Sequence to Analyze" CVCTGTAGC	The Pyrogram should be carefully compared with the histogram, which can be displayed by right-clicking in the Pyrogram window. If background noise at dispensation G3 or T4 is below the expected level and the remaining measured peaks match the height of the histogram bars, the warning and the "Check" or "Failed" quality assessment can be disregarded.
Warning message "The sequence contains less reference peaks than required" for the codon 600 assay with "Sequence to Analyze" CVCTGTAGC	If the measured peaks match the height of the histogram bars, the warning and the "Check" quality assessment can be disregarded.

Contact Information

For technical assistance and more information, please see our Technical Support Center at **support.qiagen.com** or contact one of the QIAGEN Technical Service Departments or local distributors (visit **support.qiagen.com**).

Ordering Information

Product	Contents	Cat. no.
Assays & Controls		
BRAF Pyro Kit	For 24 reactions: Forward primer, Reverse primer, and Sequencing primer for the mutation analysis of *BRAF* using the PyroMark Q24, PyroMark Q24 Advanced, or PyroMark Q48 Autoprep	970470 1065142
PyroMark Control Oligo	For installation check of the system	979203
PyroMark Q24		
PyroMark Q24	Instrument, for laboratory use only	9001514
PyroMark Q24 Software	Analysis software, for laboratory use only	9019062
PyroMark Q24 Advanced		
PyroMark Q24 Advanced CpG Reagents (4 × 24)	For 4 × 24 samples for use on the PyroMark Q24 Advanced: Enzyme Mixture, Substrate Mixture, Buffers, and Nucleotides for CpG and long-read sequencing runs	970922
PyroMark Q24 Advanced	Instrument, software, and installation for advanced Pyrosequencing analysis of 24 samples in parallel	9002270
PyroMark Q48 Autoprep		
PyroMark Q48 Autoprep	Instrument, software, and pipette	9002470
PyroMark Q48 Discs (50)	50 discs for running PyroMark Q48 Autoprep reactions	974901
PyroMark Q48 Absorber Strips (100)	100 absorber strips for running PyroMark Q48 Autoprep reactions	974912
PyroMark Q48 Autoprep Starter Kit	PyroMark Q48 Magnetic Beads (300), PyroMark Q48 Advanced CpG Reagents (4 × 48), PyroMark Control Oligo, PyroMark Q48 Discs (50) and PyroMark Q48 Absorber Strips (100)	974230
PyroMark Q48 Advanced Reagents (4 × 48)	Reagents for 4 × 48 PyroMark Q48 Autoprep standard reactions	974002
PyroMark Q48 Advanced CpG Reagents (4 × 48)	Reagents for 4 × 48 PyroMark Q48 Autoprep CpG and long-read reactions	974022
PyroMark Q48 Magnetic Beads (300)	Magnetic streptavidin-coated Sepharose beads for running 300 PyroMark Q48 Autoprep reactions	974203

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at **www.qiagen.com** or can be requested from QIAGEN Technical Support or your local distributor.

Document Revision History

Date	Description
04/2026	Initial release

Limited License Agreement for BRAF Pyro Kit

Use of this product signifies the agreement of any purchaser or user of the product to the following terms:

1. The product may be used solely in accordance with the protocols provided with the product and this Instructions for Use and for use with components contained in the kit only. QIAGEN grants no license under any of its intellectual property to use or incorporate the enclosed components of this panel with any components not included within this panel except as described in the protocols provided with the product, this Instructions for Use, and additional protocols available at **www.qiagen.com**. Some of these additional protocols have been provided by QIAGEN users for QIAGEN users. These protocols have not been thoroughly tested or optimized by QIAGEN. QIAGEN neither guarantees them nor warrants that they do not infringe the rights of third-parties.
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