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Easy® KRAS

User manual – version 2017/07

The "**Easy® KRAS**" Kit detects mutations of the *KRAS* codons 12, 13, 59, 61, 117 and 146 by Real-Time PCR.

For *in vitro* diagnostic use

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Changes made since the previous version 2016/02:

- Substitution of **Water (diluent)** with **Water**
- Update of section “Materials required but not provided”. – Amplification, Materials
- Validation of the kit on **ABI 7500 Fast**.

For further details contact the technical support of the Diatech Pharmacogenetics (support@diatechpharmacogenetics.com).

INTENDED USE

The *in vitro* diagnostic "**Easy® KRAS**" kit is intended for the qualitative detection by Real-Time PCR of *KRAS* somatic mutations in the genomic DNA isolated from fresh, frozen or formalin fixed paraffin-embedded (FFPE) tumor tissue.

The "**Easy® KRAS**" Kit is validated on the following instruments:

- **CFX96** - Bio-Rad (software v. 3.1)
- **ABI 7300**- Applied Biosystems (software v. 1.4.1)
- **ABI 7500, 7500 Fast** - Applied Biosystems (software v.2.0.5)
- **Stratagene Mx3000P**, **Mx3005P** - Agilent Technologies (software v. 4.10 - Build 389)
- **Rotor-Gene Q** - Qiagen (software v. 1.7 - Build 87)
- **Rotor-Gene 6000** - Corbett (software v. 1.7 - Build 87)

List of detectable mutations:

KRAS codon 12 ▪ G12R (34G>C) ▪ G12S (34G>A) ▪ G12C (34G>T) ▪ G12A (35G>C) ▪ G12D (35G>A) ▪ G12V (35G>T)
KRAS codon 13 ▪ G13D (38G>A)
KRAS codon 59 (not distinguishable between them) ▪ A59T (175G>A) ▪ A59E (176C>A) ▪ A59G (176C>G)
KRAS codon 61 (not distinguishable between them) ▪ Q61K (181C>A) ▪ Q61L (182A>T) ▪ Q61R (182A>G) ▪ Q61H (183A>C) ▪ Q61H (183A>T)
KRAS codon 117 (not distinguishable between them) ▪ K117E (349A>G) ▪ K117R (350A>G) ▪ K117N (351A>T) ▪ K117N (351A>C)
KRAS codon 146 (not distinguishable between them) ▪ A146T (436G>A) ▪ A146P (436G>C) ▪ A146V (437C>T)

PRINCIPLE OF THE ASSAY

The "**Easy® KRAS**" kit is designed to selectively amplify mutant specific sequences in samples that contain a mixture of wild-type and mutated DNA. The detection is achieved using fluorescent probes labelled with FAM and HEX.

The "**Easy® KRAS**" kit is composed of 11 assays for the detection of the *KRAS* mutations and a control assay for the assessment of DNA content in the sample.
Each assay contains primers and probes for the detection of the target (FAM) as well as an endogenous control gene (HEX).
The amplification of the endogenous control gene enables to verify the amplification procedure and the possible presence of inhibitors, which may cause false negative results.

1. **KRAS G12A**: the assay detects the G12A (35G>C) mutation
2. **KRAS G12D**: the assay detects the G12D (35G>A) mutation
3. **KRAS G12V**: the assay detects the G12V (35G>T) mutation
4. **KRAS G12R**: the assay detects the G12R (34G>C) mutation
5. **KRAS G12S**: the assay detects the G12S (34G>A) mutation
6. **KRAS G12C**: the assay detects the G12C (34G>T) mutation
7. **KRAS G13D**: the assay detects the G13D (38G>A) mutation
8. **KRAS A59x**: the assay detects the A59T (175G>A), A59E (176C>A), A59G (176C>G) mutations but does not distinguish between them
9. **KRAS Q61x**: the assay detects the Q61K (181C>A), Q61L (182A>T), Q61R (182A>G), Q61H (183A>C), Q61H (183A>T) mutations but does not distinguish between them
10. **KRAS K117x**: the assay detects the K117E (349A>G), K117R (350A>G), K117N (351A>T), K117N (351A>C) mutations but does not distinguish between them
11. **KRAS A146x**: the assay detects the A146T (436G>A), A146P (436G>C), A146V (437C>T) mutations but does not distinguish between them
12. **KRAS ctrl**: the assay detects a *KRAS* region without any known polymorphism/mutation

The "**Easy® KRAS**" kit includes a DNA reference standard **Horizon KRAS G12V 1%** containing a defined ratio between wild-type and mutant DNA to check the analytical process and the assay performances.

KIT CONTENTS

The kit contains sufficient reagents to carry out 24 tests for each assay for a maximum of 3 runs on ABI 7300, ABI 7500, ABI 7500 Fast, CFX96 and Mx3000P/3005P (6 samples and two controls per run) and of 4 runs on Rotor-Gene (4 samples and two controls per run).

COMP		QUAN	Color	
KRAS G12A mix (1)		3 x 10 µl	BLUE	Mixture of specific primers and probes targeting both KRAS G12A mutation and the internal control.
KRAS G12D mix (2)		3 x 10 µl	GREEN	Mixture of specific primers and probes targeting both KRAS G12D mutation and the internal control.
KRAS G12V mix (3)		3 x 10 µl	PINK	Mixture of specific primers and probes targeting both KRAS G12V mutation and the internal control.
KRAS G12R mix (4)		3 x 10 µl	RED	Mixture of specific primers and probes targeting both KRAS G12R mutation and the internal control.
KRAS G12S mix (5)		3 x 10 µl	WHITE	Mixture of specific primers and probes targeting both KRAS G12R mutation and the internal control.
KRAS G12C mix (6)		3 x 10 µl	ORANGE	Mixture of specific primers and probes targeting both KRAS G12C mutation and the internal control.
KRAS G13D mix (7)		3 x 10 µl	YELLOW	Mixture of specific primers and probes targeting both KRAS G13D mutation and the internal control.
KRAS A59x mix (8)		3 x 10 µl	BROWN	Mixture of specific primers and probes targeting both KRAS A59T, A59E, A59G and the internal control.
KRAS Q61x mix (9)		3 x 10 µl	TRANSPARENT	Mixture of specific primers and probes targeting both KRAS Q61K, Q61L, Q61R, Q61H (183A>C), Q61H (183A>T) and the internal control.
KRAS K117x mix (10)		3 x 10 µl	PURPLE	Mixture of specific primers and probes targeting both KRAS K117E, K117R, K117N (351A>T), K117N (351A>C) and the internal control.
KRAS A146x mix (11)		3 x 10 µl	BLACK	Mixture of specific primers and probes targeting both KRAS A146T, A146P, A146V and the internal control.
KRAS ctrl mix (12)		6 x 10 µl	GREY	Mixture of specific primers and probes targeting both region of the KRAS gene free from any known polymorphism/mutation and the internal control.
Easy KRAS pos ctrl	CONTROL +	3 x 200 µl		Positive control DNA containing a mixture of synthetic DNA sequences that correspond to each mutation detected by this kit in a background of wild-type genomic DNA.
Horizon KRAS G12V 1%		1 x 12 µl		Horizon DNA reference standard KRAS G12V 1% to check the analytical process.
WATER	CONTROL -	3 x 1.5 ml		DNase-, RNase-free water, 2 aliquot to be used exclusively for the preparation of the PCR mix and as negative control, and 1 aliquot to be used exclusively as samples diluent
Taq Premix 920		4 x 920 µl		Solution containing hot start Taq DNA polymerase, reaction buffer, Mg2+ and dNTP Mixture.
Dye R-I		4 x 40 µl		Inert fluorophore to be used for the amplification on the ABI 7300 instrument.
Dye R-II		4 x 40 µl		Inert fluorophore to be used for the amplification on the ABI 7500 and ABI 7500 Fast instrument.
12 strip tubes & caps		1 x 5 strips		0.2 ml 12-tube strip DNase-, RNase-free to be used for the preparation of reaction mixture.

DOCUMENTS AVAILABLE ON-LINE

Easy® KRAS User Manual and Safety Data Sheet (SDS) are available at www.diatechpharmacogenetics.com/en/reserved-area**.**

For any clarification contact the Diatech Pharmacogenetics technical support (support@diatechpharmacogenetics.com)

MATERIALS REQUIRED BUT NOT PROVIDED

Genomic DNA extraction

The "**Easy® KRAS**" kit does not contain reagents for DNA extraction.

Recommended kits:

- "QIAamp® DNA FFPE Tissue kit" (cod. 56404, Qiagen)
- "QIAamp® DNA Mini kit" (cod. 51304, Qiagen)
- "Genomic DNA FFPE One-Step Kit" (cod. MGF-03, RBC); to use with MagCore Automated Nucleic Acid Extractor (RBC Bioscience) automatic systems
- "Genomic DNA Tissue Kit" (cod. MGT-02, RBC); to use with MagCore Automated Nucleic Acid Extractor (RBC Bioscience) automatic systems
- In case you are using FFPE tissues, you will also need:
    - Xilene (e.g:. "Xylenes, histological grade" – cod. 534056, Sigma Aldrich)
    - Absolute Ethanol (quality of analytical degree)

ⓘ In case you employ kits which are different from those recommended, it is the user's responsibility to use standardized samples (e.g,: VEQ – EQAS quality schemes, Horizon Diagnostics samples) to verify that this does not imply a reduction of the performance of the system under analysis.

Amplification

Real-Time PCR Instruments:

- **CFX96** - Bio-Rad (software v. 3.1)
- **ABI 7300**- Applied Biosystems (software v. 1.4.1)
- **ABI 7500, 7500 Fast** - Applied Biosystems (software v.2.0.5)
- **Stratagene Mx3000P**, **Mx3005P** - Agilent Technologies (software v. 4.10 - Build 389)
- **Rotor-Gene Q** - Qiagen (software v. 1.7 - Build 87)
- **Rotor-Gene 6000** - Corbett (software v. 1.7 - Build 87)

Detection channels for FAM and HEX fluorescence. Range of environmental temperature: 15-30°C.

Materials:

- 1,5 ml polypropylene twist-lock tubes (DNase-, RNase-, DNA-, PCR inhibitor-free)
- Micropipettes (volumes from 1 to 1.000 µl)
- Sterile filter tips DNase-, RNase-free (volumes from 1 to 1.000 µl)
- 96 well plates and foil or caps compatibles with the thermal-cycler used (check the compatibility in the user manual of the instrument) for instance:
    1. **Bio-Rad CFX96**: **Hard Shell PCR plates 96-well WHT/CLR** cod. HSP 9601; **MICROSEAL B SEALS** cod. MSB 1001
    2. **ABI 7300/ ABI 7500: MICROAMP OPTICAL 96 WELL RNX PLATE** cod. N8010560; **OPTICAL ADHESIVE COVERS** cod. 4360954
    3. **ABI 7500 Fast: MICROAMP FAST OPTICAL 96 WELL RNX PLATE** cod. 4346907; **OPTICAL ADHESIVE COVERS** cod. 4360954
    4. **Stratagene Mx3000P/Mx3005P: Optical caps** (8x strip) cod. 401425; **QPCR 96-Well Plates, Non-Skirted** cod. 401333
- DNase-and RNase-free, thin-wall, PCR tubes with flat cap or 0.1 ml tubes in strip, suitable for use on Rotor-Gene, for instance:
    - **PCR tubes 0.1 (1000)** – cod. DIA-PL1, Diatech Pharmacogenetics
    - **Strip tubes and caps, 0.1 ml (250)** – cod. 981103, Qiagen
- Powder-free disposable gloves

STABILITY AND STORAGE

Store all the reagents according to the instructions on the packages, in particular:

- Store all the reagents at -35/-20°C in the original package immediately upon receipt.
- After thawing, store **Taq PreMix 920** at +2/+8°C and use it within 6 months or within the expiration date.
- Avoid thawing and re-freezing the reagents more than twice, as this could lead to poor performance.
- Protect all mixes containing probes from light to avoid degradation of the fluorescent dyes.
- If properly stored, the reagents remain stable until the expiration date displayed on the individual label.

SYMBOLS

REF	Catalog number (product code)	CONTROL +	Positive control
GTIN	Global Trade Item Number	CONTROL -	Negative control
LOT	Lot number		Consult the instruction
	Content sufficient for <n> tests		User manual (handbook)
IVD	For *in vitro* diagnostic use		Expiration date
CONT	Content		Storage conditions
COMP	Components		Manufactured by
NUM	Number of aliquots		Important Note
QUAN	Quantity per aliquot		

PRODUCT USE LIMITATIONS

- The "**Easy® KRAS** kit can only be used by specialized personnel, properly instructed and trained.
- It is necessary to operate in compliance with the general guidelines of Good Laboratory Practice (GLP) and the instructions contained in this manual.
- Do not use expired or incorrectly stored reagents.
- The "**Easy® KRAS**" kit is designed to be used with the instruments "**Rotor-Gene Q**" (Qiagen), "**Rotor-Gene™ 6000**" (Corbett Research), **CFX96** (Bio-Rad), **ABI 7300/ABI 7500/ABI 7500 Fast** (Applied Biosystems) and Stratagene **Mx3000P/Mx3005P** (Agilent Technologies).
- The reliability of the results also depends on the procedures carried out in the pre-amplification stages, including the selection of starting biological speciments, the preservation of the samples and DNA extraction.
- Any diagnostic results generated by this procedure must be interpreted with reference to other clinical or laboratory findings.
- "**Easy® KRAS"** is a CE-IVD marked product under the European Directive 98/79/EC on IVD medical devices only into those countries which are accepting the handbook translated in the languages listed at www.diatechpharmacogenetics.com/area-riservata
- Diatech Pharmacogenetics does not respond to the quality of the result obtained using accessories other than those recommended in this manual

QUALITY ASSURANCE

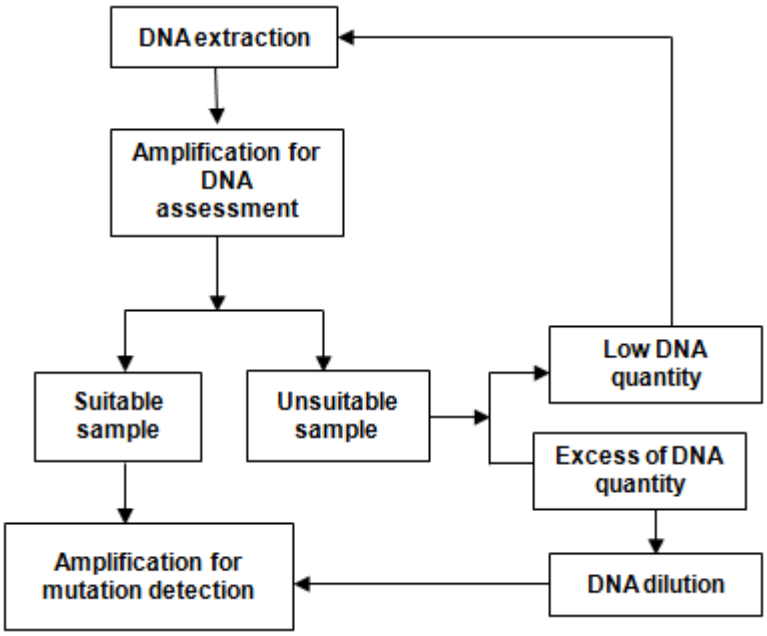
- The "**Easy® KRAS**" Kit was designed, developed and validated in accordance with the Directive 98/79/EC on in vitro diagnostic medical devices, transposed at national level with the D.Lgs n. 332/2000 and the subsequent legislative changes, and in accordance with the company system of full quality assurance certified in accordance to the European standards EN ISO 9001 and ISO 13485
- The consistent product quality of the "**Easy® KRAS**" kit is guaranteed by the application of a tight quality control process on operating procedures for the realization of the product and subsequent managment to the customer. The quality of each lot is attested in the Certficate of Analysis available upon request to the Customer Service (support@diatechphamaracogenetics.com)

WARNINGS AND PRECAUTIONS

1. The kit may only be used by specialist personnel, properly instructed and trained to perform *in vitro* laboratory techniques.
2. Carefully read this User Manual.
3. Check that the version of this User Manual corresponds to the one described on the "**Easy® KRAS**" kit box label.
4. Handle all samples as potentially infectious material inside a laminar flow hood (class II biological safety cabinet or higher).
5. Follow the laboratory safety procedures described in "Biosafety in Microbiological and Biomedical Laboratories" (Richmond, JY and McKinney, RW (eds) - 5th edition (2009) and in the NCCLS (National Committee for Clinical Laboratory Standards) Document M29-T. Protection of Laboratory Workers from Infectious Disease Transmitted by Blood, Body Fluids and Tissue. Tentative guidelines. – Villanova, PA:NCCLS, 1989).

6. Do not eat, drink or smoke in the laboratory. When handling biological samples, disposable gloves, gowns and goggles or face masks should be worn to protect against biological agents.
7. Constantly check that the gloves are free from contamination by the biological material being treated. If not, replace them immediately to avoid the possibility of cross-contamination between samples and contamination of the workplace. Wash hands thoroughly after handling samples and reagents.
8. The Safety Data Sheet (SDS) is available in the reserved area of the web-site Diatech Pharmacogenetics www.diatechpharmacogenetics.com.
9. Perform the procedure in accordance with Good Laboratory Practice (GLP) general guidelines.
10. It is recommended to ensure that the laboratory workflow proceeds in a unidirectional manner, preparing, if possible, two separate work areas for:
    a. extraction of nucleic acids;
    b. amplification reaction;
11. Organize the laboratory so that dedicated pipettes, tips and materials are used for each activity.
12. Use sterile filter tips. Avoid aerosols.
13. Use tubes with twist-lock caps during the extraction of nucleic acids in order to avoid the leakage of the samples and potential contamination.
14. During the procedures for nucleic acid extraction and amplification, avoid contamination of reagents with airborne microbes by only opening the reagents within the hood.
15. Change the pipette tip before each extraction of reagents and every time you move from one sample to another in any stage of the procedure.
16. The precision pipettes used should have an accuracy within 3% of the set volume.
17. Periodically check the calibration status of the dispensing instruments.
18. Do not use reagents after the expiration date shown on each container.
19. All reagents supplied in the "**Easy® KRAS**" kit are intended to be used solely with the other reagents in the same "**Easy® KRAS**" kit. Do not substitute or mix reagents in the kit from different batches, in order to maintain optimal performance.
20. Only use the **Taq PreMix 920** that is provided in the kit. Do not substitute with **Taq PreMix 920** from other kits or with similar reagents from other suppliers.
21. Discard unused reagents and the expired kit and waste in accordance with current national laws and local regulations.
22. Extraction area: at the end of the procedure, decontaminate the pipettes and the laboratory surfaces on which work has been carried out, by cleaning with appropriate products (e.g. FD 322, Dürr Dental, Germany) and UV irradiate the work surface of the biological cabinet where the pipettes should be carefully placed after decontamination.
23. Amplification area: at the end of the procedure, decontaminate the pipettes and the laboratory surfaces on which work has been carried out, by cleaning with appropriate products to eliminate nucleic acids and amplicons (e.g. "DNA Cleaner" - code DC001, Diatech Pharmacogenetics) and subsequent UV irradiation, if available.
24. Avoid contamination of samples and reagents.
25. Store reagents and samples separately.
26. In order to avoid possible contamination from carry-over, do not open the reaction tubes after amplification.
27. Before use all reagents need to be thawed at room temperature, mixed by inverting 10 times and centrifuged briefly.
28. All reagents contained in the kit are ready-to-use and don't need to be diluted. The reagent dilution may result in a loss of performance.
29. Include in each run at least 1 negative control (**WATER**) and 1 positive control (**Easy KRAS pos ctrl**).
30. In order to avoid any mixing up of samples pay particular attention to samples dispensation, placement of tubes into the instrument, editing the sample name in the software.
31. The right to contest the kit before the expiration date becomes void if the product is used in violation of GLP guidelines and the manufacturer's recommendations.
32. The registered names and trademarks indicated in this document are to be considered protected by law, even when not explicitly stated.

ANALYTICAL PROCEDURE



DNA EXTRACTION

ⓘ Perform this step in the area dedicated to DNA isolation and dilution, using dedicated materials and instruments.

- The "**Easy® KRAS**" kit does not include the reagents for DNA extraction.
- The quantity of biological material required for the DNA extraction depends on protocols.
- Refer also to the extraction kit manual for selection and treatment of FFPE slides.
- Commercial kits working with silica filters or magnetic beads are recommended. Avoid methods that use phenol or boiling in basic solution without purification.
- Perform the DNA extraction following the instructions of the extraction kit in use.
- If the extraction protocol involves the use of wash buffers containing ethanol, it is advisable to perform a further centrifugation before final elution to remove any possible traces of ethanol. This will prevent iInhibition of the reaction by the ethanol.
- After the extraction, proceed immediately with the quali-quantitative evaluation of the DNA and the amplification reaction, or store the extracted DNA at ≤-20°C, divided into aliquots in order to maintain the experimental conditions constant in case of repetition.
- Just as an indication, for non-paraffin embedded samples like fresh/frozen tissue, plasma, blood, the recommended DNA amount in each test tube is 5-10 ng; for paraffin embedded samples, the recommended DNA amount in each reaction tube is 15-20 ng.

ⓘ As absorbance reading cannot distinguish between fragmented and not fragmented DNA and therefore it can overestimate the concentration of template, DNA assessment should be based on the **KRAS ctrl mix**. The evaluation of quality and quantity of the DNA in the samples with the **KRAS ctrl mix** before the mutation analysis is highly recommended. DNA assessment based on the **KRAS ctrl mix** may differ from spectrophotometric quantification.

ⓘ All assays in the "**Easy® KRAS**" kit amplify short DNA sequences. However heavily fragmented DNA can generate no amplification product.

AMPLIFICATION

General recommendations for amplification *(valid for all instruments)*

ⓘ Perform this step in the area dedicated to amplification mixes preparation, using dedicated materials and instruments. Before starting decontaminate pipettes, benches and hood in order to degrade any trace of DNA and possibly radiate with UV light for at least 30 minutes.

- Switch on the instrument and the software at least 20-30 minutes before starting the reaction to allow the heating of the lamps where necessary.
- Thaw all necessary reagents before use.
- Thoroughly mix the reagents in a vortex, or inverting each tube ten times, and spin them briefly before use.
- Prepare and mark an appropriate number of tubes or wells of the plate to use.
- Each run must include at least one amplification negative control (**WATER**) and one amplification positive control (**Easy KRAS pos ctrl**) for each mix.

INSTRUMENT SETUP

Rotor-Gene Q, Rotor-Gene 6000

- Follow the instructions reported in the user manual of the instrument to set up the following fluorescence acquisition channels and thermal profile:
- "Green": source 470 nm – detector 510 nm – Gain 8
- "Yellow": source 530 nm – detector 555 nm – Gain 10
- "Green 2": source 470 nm – detector 510 nm –- "Gain Optimisation" 58°C Before 1st acquisition, "Tube Position":51 (**KRAS A146x mix**), "Target Sample Range" 20-30 Fl
- "Yellow 2": source 530 nm – detector 555 nm – "Gain Optimisation" 58°C Before 1st acquisition, "Tube Position":51 (**KRAS A146x mix**), "Target Sample Range" 20-30 Fl

Thermal Profile	
Hold	95°C for 2 minutes
40 cycles	95°C for 10 seconds / 58°C for 60 seconds (acquire fluorescense in channels "Green", "Green 2", "Yellow", Yellow 2")

- Reaction volume: 20 µl.

Stratagene Mx3000P, Mx3005P

- Select "New" – "Quantitative PCR (Multiple standards)", then "OK".
- Check for the presence of the message "Lamp – Warm-up".
- Follow the instructions reported in the user manual of the instrument to set up the following fluorescence acquisition channels and thermal profile:
  - "FAM": source 492 nm – detector 516 nm – Filter gain factor x8
  - "HEX": source 535 nm – detector 555 nm – Filter gain factor x8

Thermal Profile	
Hold	95°C for 2 minutes
40 cycles	95°C for 10 seconds / 58°C for 60 seconds (acquire fluorescence in channels "FAM" and "HEX" setting up END 1)

- Reaction volume: 20 µl.

CFX96

- Follow the instructions reported in the user manual of the instrument to set up the following fluorescence acquisition channels and thermal profile:

Thermal Profile	
Step	
1	95°C for 2 minutes
2	95°C for 10 seconds
3	58°C for 60 seconds (Plate read – All Channels)
4	GO TO 2 39 more times

- Reaction volume: 20 µl.

ⓘ Select the options "All Channels" to acquire the signal in both FAM and HEX.

ABI 7300

- Select "Create new document" – On Assay: "Standard Curve (Absolute Quantitation)", then "Next".
- Follow the instructions reported in the user manual of the instrument to set up the following fluorescence acquisition channels and thermal profile:

Thermal Profile	
Hold	95°C for 2 minutes
40 cycles	95°C for 10 seconds / 58°C for 60 seconds (acquire fluorescence in channels FAM, JOE; Quencer – None; Passive Reference Dye - ROX)

- Reaction volume: 20 µl.

ABI 7500, ABI 7500 Fast

- Select "New Experiment" then "7500 (96 Wells)", "Quantitation – Standard Curve", "TaqMan® Reagents", "Standard (~2 hours to complete a run)".
- Follow the instructions reported in the user manual of the instrument to set up the following fluorescence acquisition channels and thermal profile:

Thermal Profile	
Hold	95°C for 2 minutes
40 cicli	95°C for 10 seconds / 58°C for 60 seconds (acquire fluorescence in channels FAM, JOE; Quencer – None; Passive Reference Dye - ROX)

- Reaction volume: 20 µl.

DNA ASSESSMENT

- For each sample and control prepare an amplification mixture (**Amp-Mix**), according to the following table, where N is the total number of samples and controls to be tested:

Rotor-Gene, Stratagene, CFX96		
Amp-Mix	**Reagent volume for 1 reaction (µl)**	**Reagent volume for N reactions +1 (µl)**
Taq Premix 920	10	
WATER CONTROL -	4	
KRAS ctrl mix (12)	1	
Total Volume	15	

ABI 7300		
Amp-Mix	**Reagent volume for 1 reaction (µl)**	**Reagent volume for N reactions +1 (µl)**
Taq Premix 920	10	
Dye R-I	0.4	
WATER CONTROL -	3.6	
KRAS ctrl mix (12)	1	
Total Volume	15	

ABI 7500, ABI 7500 Fast		
Amp-Mix	**Reagent volume for 1 reaction (µl)**	**Reagent volume for N reactions +1 (µl)**
Taq Premix 920	10	
Dye R-II	0.2	
WATER CONTROL -	3.8	
KRAS ctrl mix (12)	1	
Total Volume	15	

- Mix the **Amp-Mix** thoroughly by repeated pipetting or rapid vortexing, then centrifuge briefly.
- Pipette 15 µl of the **Amp-Mix** in all the marked reaction test tubes or wells.
- Add to the respective test tubes or wells:

negative control	5 µl **WATER**	CONTROL -
samples	5 µl DNA	
positive control	5 µl **Easy KRAS pos ctrl**	CONTROL +

- Final volume: 20 µl.
- Briefly centrifuge the plate.
- Check that the thermal profile is setted up correctly and start the run.

ⓘ Before starting the run, please pay attention to the plate orientation (well A1 on the upper left position) or to the Rotor-Gene 0.1ml strips of tubes orientation (mark the first tube of each strip).

ⓘ Proceed with the analysis following the instructions of the section “Data analysis”.

MUTATION DETECTION

ⓘ Only samples that after DNA assessment are suitable can be analyzed for mutations detection.

ⓘ Each sample must be amplified with 12 different mixes: **KRAS G12A (1)**, **KRAS G12D (2)**, **KRAS G12V (3)**, **KRAS G12R (4)**, **KRAS G12S (5)**, **KRAS G12C (6)**, **KRAS G13D (7)**, **KRAS A59x (8)**, **KRAS Q61x (9)**, **KRAS K117x (10)**, **KRAS A146x (11)**, **KRAS ctrl (12)**.

ⓘ The DNA reference standard **Horizon KRAS G12V 1%** must be amplified only with the mixes **KRAS G12V (3)** and **KRAS ctrl (12)**.

ⓘ The kit content is optimized to analyze six clinical samples and two controls **Easy KRAS pos ctrl** and **WATER** in each run performed on CFX96, ABI7300/7500/7500 Fast, Stratagene and four clinical samples and two controls **Easy KRAS pos ctrl** and **WATER** in each run performed on Rotor-Gene:

Mx3000P/3005P, ABI 7300/7500/7500 Fast, CFX96 (RT001 sample grid A)

	1	2	3	4	5	6	7	8	9	10	11	12
A	DNA1	DNA1	DNA1	DNA1	DNA1	DNA1	DNA1	DNA1	DNA1	DNA1	DNA1	DNA1
B	DNA2	DNA2	DNA2	DNA2	DNA2	DNA2	DNA2	DNA2	DNA2	DNA2	DNA2	DNA2
C	DNA3	DNA3	DNA3	DNA3	DNA3	DNA3	DNA3	DNA3	DNA3	DNA3	DNA3	DNA3
D	DNA4	DNA4	DNA4	DNA4	DNA4	DNA4	DNA4	DNA4	DNA4	DNA4	DNA4	DNA4
E	DNA5	DNA5	DNA5	DNA5	DNA5	DNA5	DNA5	DNA5	DNA5	DNA5	DNA5	DNA5
F	DNA6	DNA6	DNA6	DNA6	DNA6	DNA6	DNA6	DNA6	DNA6	DNA6	DNA6	DNA6
G	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL	POS CTRL
H	WATER	WATER	WATER	WATER	WATER	WATER	WATER	WATER	WATER	WATER	WATER	WATER

1	G12A mix (1)
2	G12D mix (2)
3	G12V mix (3)
4	G12R mix (4)
5	G12S mix (5)
6	G12C mix (6)
7	G13D mix (7)
8	A59x mix (8)
9	Q61x mix (9)
10	K117x mix (10)
11	A146x mix (11)
12	ctrl mix (12)

Rotor-Gene (RT001 sample grid B)

DNA1		DNA2		DNA3		DNA4		POS CTRL		WATER		DNA1		DNA3		POS CTRL	
1	•	9	•	17	•	25	•	33	•	41	•	49	•	57	•	65	•
2	•	10	•	18	•	26	•	34	•	42	•	50	•	58	•	66	•
3	•	11	•	19	•	27	•	35	•	43	•	51	•	59	•	67	•
4	•	12	•	20	•	28	•	36	•	44	•	52	•	60	•	68	•
DNA1		**DNA2**		**DNA3**		**DNA4**		**POS CTRL**		**WATER**		**DNA2**		**DNA4**		**WATER**	
5	•	13	•	21	•	29	•	37	•	45	•	53	•	61	•	69	•
6	•	14	•	22	•	30	•	38	•	46	•	54	•	62	•	70	•
7	•	15	•	23	•	31	•	39	•	47	•	55	•	63	•	71	•
8	•	16	•	24	•	32	•	40	•	48	•	56	•	64	•	72	•

- Prepare, for each sample and control, 12 different amplification mixtures (**Amp-Mix**), one for each assay, as indicated in the following scheme, where N is the numer of samples and controls to be tested.

ⓘ If you are working with a 96 well plate, it is possible to prepare the **Amp-Mix** in the strip provided with the kit, so you can dispense the all **Amp-Mix** with a multichannel pipette.

Rotor-Gene, Stratagene, CFX96		
Amp-Mix	**Reagent volume for 1 reaction (µl)**	**Reagent volume for N reactions +1 (µl)**
Taq Premix 920	10	
WATER CONTROL -	4	
KRAS G12A mix (1) or **KRAS G12D mix (2)** or **KRAS G12V mix (3)** or **KRAS G12R mix (4)** or **KRAS G12S mix (5)** or **KRAS G12C mix (6)** or **KRAS G13D mix (7)** or **KRAS A59x mix (8)** or **KRAS Q61x mix (9)** or **KRAS K117x mix (10)** or **KRAS A146x mix (11)** or **KRAS ctrl mix (12)**	1	
Total Volume	15	

ABI 7300		
Amp-Mix	**Reagent volume for 1 reaction (µl)**	**Reagent volume for N reactions +1 (µl)**
Taq Premix 920	10	
Dye R-I	0.4	
WATER CONTROL -	3.6	
KRAS G12A mix (1) or **KRAS G12D mix (2)** or **KRAS G12V mix (3)** or **KRAS G12R mix (4)** or **KRAS G12S mix (5)** or **KRAS G12C mix (6)** or **KRAS G13D mix (7)** or **KRAS A59x mix (8)** or **KRAS Q61x mix (9)** or **KRAS K117x mix (10)** or **KRAS A146x mix (11)** or **KRAS ctrl mix (12)**	1	
Total Volume	15	

ABI 7500, ABI 7500 Fast		
Amp-Mix	**Reagent volume for 1 reaction (µl)**	**Reagent volume for N reactions +1 (µl)**
Taq Premix 920	10	
Dye R-II	0.2	
WATER CONTROL -	3.8	
KRAS G12A mix (1) or **KRAS G12D mix (2)** or **KRAS G12V mix (3)** or **KRAS G12R mix (4)** or **KRAS G12S mix (5)** or **KRAS G12C mix (6)** or **KRAS G13D mix (7)** or **KRAS A59x mix (8)** or **KRAS Q61x mix (9)** or **KRAS K117x mix (10)** or **KRAS A146x mix (11)** or **KRAS ctrl mix (12)**	1	
Total Volume	15	

- Mix all **Amp-Mix** thoroughly by repeated pipetting or rapid vortexing, then centrifuge briefly.
- Pipette 15 µl of each **Amp-Mix** in all the tubes/wells previously marked.
- Add to the respective tubes/wells for each of the twelve assays:

negative control	5 µl **WATER**	CONTROL –
sample	5 µl DNA	
positive control	5 µl **Easy KRAS pos ctrl**	CONTROL +

- Reaction volume: 20 µl.
- Briefly centrifuge the plate.
- Check that the thermal profile is setted up correctly and start the run.

ⓘ Before starting the run, please pay attention to the plate orientation (well A1 on the upper left position) or to the Rotor-Gene 0.1ml strips of tubes orientation (mark the first tube of each strip).

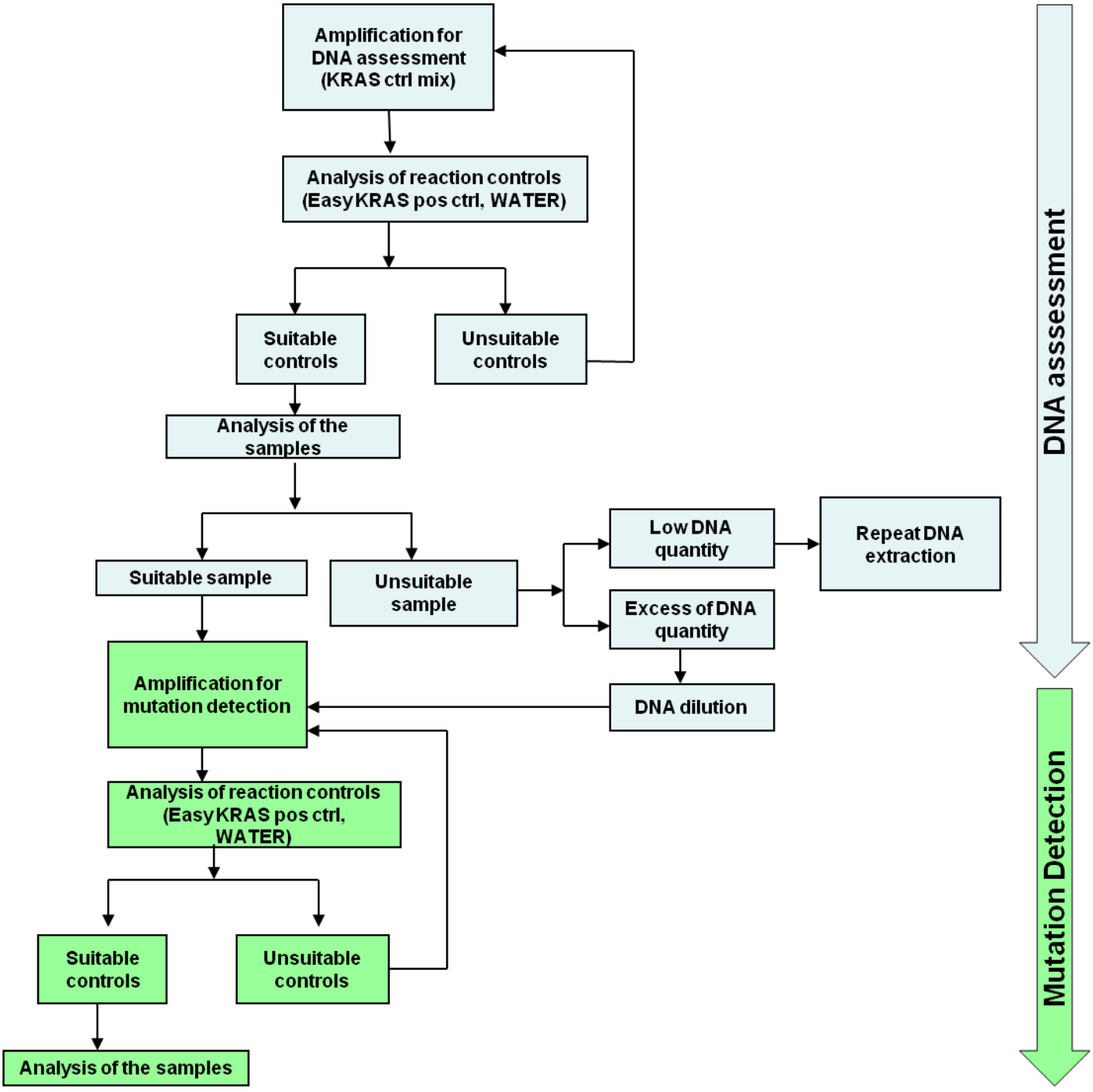
ⓘ Proceed with the analysis following the instructions of the section “Data analysis”.

DATA ANALYSIS

General reccomandations pertain to all the instruments

- Analyze first the negative control **WATER** and the positive control **Easy KRAS pos ctrl**. If they are in the range of expected values, proceed with the analysis of the samples, otherwise the session should be considered invalid and the results of the samples should be rejected.
- It is necessary to verify that the Ct values obtained are generated from a real amplification reaction (sigmoidal fluorescense curve) and not from an artifact (linear fluorescence curve), checking the normalized fluorescence graphs.
- Only the samples that after the DNA assessment reaction (**KRAS ctrl mix)** are suitable can be analyzed for the presence of mutations.

Proceed with the analysis as indicated by the following scheme:



Rotor-Gene

- At the end of the run, click Analysis and select Quantitation.
- Highlight Dynamic tube and Slope correct for all the channels.
- Set Threshold 0.04 for the Green and Yellow channels.

ⓘ If it is not possible to perform the analysis in the Green and/or Yellow channel because of the fluorescence level is too high, see Troubleshooting section.

1. Analysis of the reaction controls

	KRAS ctrl mix	G12A, G12D, G12V, G12R, G12S, G12C, G13D, A59x, Q61x, A117x, A146x mix	All mixes	
	Green	Green	Yellow	Results
WATER	Ct > 35	Ct > 35	Ct > 32	Proceed with analysis of the samples.
	Ct ≤ 35	Ct ≤ 35	Ct ≤ 32	Possible contamination: it is not possible to analyze the samples (see Troubleshooting).
Easy KRAS pos ctrl	23.5 ≤ Ct ≤ 26.5	15≤ Ct ≤ 21	19 ≤ Ct ≤ 24	Proceed with analysis of the samples.
	Ct<23.5 or Ct >26.5	Ct<15 or Ct >21	Ct<19 or Ct >24	Possible error in the set up of the reaction/run: it is not possible to analyze the samples (see Troubleshooting).

2. Analysis of **KRAS ctrl mix** for the DNA assessment

KRAS ctrl mix	Green	Yellow	Results
DNA samples	21≤ Ct ≤ 30	18≤ Ct ≤30	Suitable sample. Proceed with the mutation analysis[1].
	Ct<21	Ct <18	Excess of DNA. Samples must be diluted with **Water** (aliquot to be used for sample dilution) so that Ct fall in the ranges indicated above. Consider that the dilution 1:2 of the DNA increases the Ct of 1 unit.
	Ct >30	Ct >30	Suboptimal amount of starting DNA or PCR inhibition; YOU CAN NOT CONTINUE WITH THE ANALYSIS OF MUTATION: ▪ If it is possible, amplify a DNA volume > 5µl (max 9µl) or proceed with a new DNA extraction to obtain an higher concentration of template and/or a DNA of higher quality. ▪ If the presence of inhibitors is suspected, dilute the sample with **Water** (aliquot to be used for sample dilution). Consider that the dilution reduces the presence of inhibitor, but also decreases the concentration of the target DNA.

1. If the results of the Yellow channel are not in the expected range, consider only the Green channel results to value the sample suitability.

3. Analysis of the mutation assays

ⓘ Only samples that following the assessment of DNA are suitable can be analyzed to search for mutations.

- Compare ΔCt values of the samples with those reported in the following table. The specified values are in the range and include extremes. The ΔCt values should be calculated with the following formula, taking care that the Ct value in Green for the mutation and the equivalent for the control assay belong to the same sample:

ΔCt = Ct Green Mutation – Ct Green KRAS ctrl mix

Assay	**Amplification of Internal Control (Yellow)**	**ΔCt**	**Results**
G12A	OK (similar Ct value for all the mixes)	≤ 10.6	G12A positive
G12D		≤ 7.0	G12D positive
G12V		≤ 9.5	G12V positive
G12R		≤ 9.2	G12R positive
G12S		≤ 6.8	G12S positive
G12C		≤ 9.4	G12C positive
G13D		≤ 7.0	G13D positive
A59x		≤ 4.3	A59x positive
Q61x		≤ 5.0	Q61x positive
K117x		≤ 10	K117x positive
A146x		≤ 5.0	A146x positive
G12A	OK (similar Ct value for all the mixes)	> 10.6	Wild-type sample or beneath the LOD[1]
G12D		> 7.0	
G12V		> 9.5	
G12R		> 9.2	
G12S		> 6.8	
G12C		> 9.4	
G13D		> 7.0	
A59x		> 4.3	
Q61x		> 5.0	
K117x		> 10	
A146x		> 5.0	
G12A	NO	\	Failed: not sufficient template/PCR inhibition / mistake during samples dispensation
G12D		\	
G12V		\	
G12R		\	
G12S		\	
G12C		\	
G13D		\	
A59x		\	
Q61x		\	
K117x		\	
A146x		\	

1. LOD = Limit Of Detection.
\ Any value

ⓘ If multiple assays show a ΔCt equal to or below the cut-off value, the signal giving the higher ΔCt is probably due to cross-reactivity. Although double mutants have been observed, these are rare. In this case the sample should be considered positive only for the mutation with the lowest ΔCt.

Stratagene Mx3000P, Mx3005P

- At the end of the run click Set-up, Plate Setup, and enter the sample names.
- In the section Analysis, Analysis Selection/Setup, deselect the function Amplification-based threshold and select only the reactions controls **WATER** and **Easy KRAS pos ctrl.**
- In the section Analysis, Results, click on the lock icon in the box Threshold Fluorescence (in this way the automatically selected values cannot be modified).
- Go back to the section Analysis, Analysis Selection/Setup, and select all the samples.
- In the section Analysis, Results, select Text report to see the results in both channels with their respective threshold and Ct values.
- Click save.

1. Analysis of reaction control

	KRAS ctrl mix	**G12A, G12D, G12V, G12R, G12S, G12C, G13D, A59x, Q61x, A117x, A146x mix**	**All mixes**	
	FAM	**FAM**	**HEX**	**Results**
WATER	Ct > 35	Ct > 35	Ct > 32	Proceed with analysis of the samples.
	Ct ≤ 35	Ct ≤ 35	Ct ≤ 32	Possible contamination: it is not possible to analyze the samples (see Troubleshooting).
Easy KRAS pos ctrl	23 ≤ Ct ≤ 28	15≤ Ct ≤ 22	19 ≤ Ct ≤ 25	Proceed with analysis of the samples.
	Ct<23 or Ct >28	Ct<15 or Ct >22	Ct<19 or Ct >25	Possible error in the set up of the reaction/run: it is not possible to analyze the samples (see Troubleshooting).

2. Analysis of **KRAS ctrl mix** for the DNA assessment

KRAS ctrl mix	**FAM** [1]	**HEX** [1]	**Results**
DNA samples	(x-2.5) ≤ Ct ≤ (x+5.5)	(x-2.5) ≤ Ct ≤ (x+5.5)	Suitable sample. Proceed with the mutation analysis [2].
	Ct<(x-2.5)	Ct<(x-2.5)	Excess of DNA. Samples must be diluted with **Water** (aliquot to be used for sample dilution) so that Ct fall in the ranges indicated above. Consider that the dilution 1:2 of the DNA increases the Ct of 1 unit.
	Ct > (x+5.5)	Ct > (x+5.5)	Suboptimal amount of starting DNA or PCR inhibition; YOU CAN NOT CONTINUE WITH THE ANALYSIS OF MUTATION: ▪ If it is possible, amplify a DNA volume > 5µl (max 9µl) or proceed with a new DNA extraction to obtain an higher concentration of template and/or a DNA of higher quality. ▪ If the presence of inhibitors is suspected, dilute the sample with **Water** (aliquot to be used for sample dilution). Consider that the dilution reduces the presence of inhibitor, but also decreases the concentration of the target DNA

1. x = Ct **Easy KRAS pos ctrl**
2. If the results of the HEX channel are not in the expected range, consider only the FAM channel results to value the sample suitability.

3. Analysis of the mutation assays

ⓘ Only samples that following the assessment of DNA are suitable can be analyzed to search for mutations.

- Compare ΔCt values of the samples with those reported in the following table. The specified values are in the range and include extremes. The ΔCt values should be calculated with the following formula, taking care that the Ct value in FAM for the mutation and the equivalent for the control assay belong to the same sample:

ΔCt = Ct FAM Mutation – Ct FAM KRAS ctrl mix

Assay	**Amplification of Internal Control (HEX)**	**ΔCt**	**Results**
G12A	OK (similar Ct value for all the mixes)	≤ 9.0	G12A positive
G12D		≤ 7.5	G12D positive
G12V		≤ 9.0	G12V positive
G12R		≤ 9.0	G12R positive
G12S		≤ 6.0	G12S positive
G12C		≤ 8.4	G12C positive
G13D		≤ 6.0	G13D positive
A59x		≤ 3.0	A59x positive
Q61x		≤ 3.5	Q61x positive
K117x		≤ 6.0	K117x positive
A146x		≤ 4.5	A146x positive
G12A	OK (similar Ct value for all the mixes)	> 9.0	Wild type sample or beneath the LOD[1]
G12D		> 7.5	
G12V		> 9.0	
G12R		> 9.0	
G12S		> 6.0	
G12C		> 8.4	
G13D		> 6.0	
A59x		> 3.0	
Q61x		> 3.5	
K117x		> 6.0	
A146x		> 4.5	
G12A	NO	\	Failed: not sufficient template/PCR inhibition / mistake during samples dispensation
G12D		\	
G12V		\	
G12R		\	
G12S		\	
G12C		\	
G13D		\	
A59x		\	
Q61x		\	
K117x		\	
A146x		\	

1. LOD = Limit Of Detection.
\ Any value

ⓘ If multiple assays show a ΔCt equal to or below the cut-off value, the signal giving the higher ΔCt is probably due to cross-reactivity. Although double mutants have been observed, these are rare. In this case the sample should be considered positive only for the mutation with the lowest ΔCt.

CFX96

- At the end of the run, click Plate Setup – View/Edit Plate, select the wells used, pick the FAM and HEX fluorophores and enter samples name.
- In the section Settings set up the following analysis criteria as default:
  - Cq determination mode: Single Threshold
  - Baseline settings: Baseline Subtracted Curve fit
  - Analysis Mode: Fluorophore
  - Baseline Threshold: Auto Calculated for every channel
- In the page Quantification data, the results are displayed for both channels with the corresponding values of Cq.
- Click Save.

1. Analysis of reaction controls

	KRAS ctrl mix	G12A, G12D, G12V, G12R, G12S, G12C, G13D, A59x, Q61x, A117x, A146x mix	All mixes	
	FAM	**FAM**	**HEX**	**Results**
WATER	Cq > 35	Cq > 35	Cq > 32	Proceed with analysis of the samples.
	Cq ≤ 35	Cq ≤ 35	Cq ≤ 32	Possible contamination: it is not possible to analyze the samples (see Troubleshooting).
Easy KRAS pos ctrl	23 ≤ Cq ≤ 28	15≤ Cq ≤ 21	19 ≤ Cq ≤ 25	Proceed with analysis of the samples.
	Cq <23 or Cq >28	Cq <15 or Cq >21	Cq <19 or Cq >25	Possible error in the set up of the reaction/run: it is not possible to analyze the samples (see Troubleshooting).

2. Analysis of **KRAS ctrl mix** for the DNA assessment

KRAS ctrl mix	FAM [1]	HEX [1]	Results
DNA samples	(x-2.5) ≤ Cq ≤ (x+5.5)	(x-2.5) ≤ Cq ≤ (x+5.5)	Suitable sample. Proceed with the mutation analysis [2].
	Cq <(x-2.5)	Cq <(x-2.5)	Excess of DNA. Samples must be diluted with **Water** (aliquot to be used for sample dilution) so that Ct fall in the ranges indicated above. Consider that the dilution 1:2 of the DNA increases the Cq of 1 unit.
	Cq > (x+5.5)	Cq > (x+5.5)	Suboptimal amount of starting DNA or PCR inhibition; YOU CAN NOT CONTINUE WITH THE ANALYSIS OF MUTATION: ▪ If it is possible, amplify a DNA volume > 5µl (max 9µl) or proceed with a new DNA extraction to obtain an higher concentration of template and/or a DNA of higher quality. ▪ If the presence of inhibitors is suspected, dilute the sample with **Water** (aliquot to be used for sample dilution). Consider that the dilution reduces the presence of inhibitor, but also decreases the concentration of the target DNA.

1. x = Cq **Easy KRAS pos ctrl**
2. If the results of the HEX channel are not in the expected range, consider only the FAM channel results to value the sample suitability.

3. Analysis of the mutation assays

ⓘ Only samples that following the assessment of DNA are suitable can be analyzed to search for mutations.

- Compare ΔCq values of the samples with those reported in the following table. The specified values are in the range and include extremes. The ΔCq values should be calculated with the following formula, taking care that the Cq value in FAM for the mutation and the equivalent for the control assay belong to the same sample:

ΔCq = Cq FAM Mutations – Cq FAM KRAS ctrl mix

Assay	**Amplification of Internal Control (HEX)**	**ΔCq**	**Results**
G12A	OK (similar Ct value for all the mixes)	≤ 10.6	G12A positive
G12D		≤ 6.5	G12D positive
G12V		≤ 9.0	G12V positive
G12R		≤ 9.0	G12R positive
G12S		≤ 5.5	G12S positive
G12C		≤ 8.0	G12C positive
G13D		≤ 7.5	G13D positive
A59x		≤ 3.5	A59x positive
Q61x		≤ 3.5	Q61x positive
K117x		≤ 8.5	K117x positive
A146x		≤ 3.5	A146x positive
G12A	OK (similar Ct value for all the mixes)	> 10.6	Wild type sample or beneath the LOD[1]
G12D		> 6.5	
G12V		> 9.0	
G12R		> 9.0	
G12S		> 5.5	
G12C		> 8.0	
G13D		> 7.5	
A59X		> 3.5	
Q61x		> 3.5	
K117x		> 8.5	
A146x		> 3.5	
G12A	NO	\	Failed: not sufficient template/PCR inhibition / mistake during samples dispensation
G12D		\	
G12V		\	
G12R		\	
G12S		\	
G12C		\	
G13D		\	
A59x		\	
Q61x		\	
K117x		\	
A146x		\	

1. LOD = Limit Of Detection
\ Any value

ⓘ If multiple assays show a ΔCq equal to or below the cut-off value, the signal giving the higher ΔCq is probably due to cross-reactivity. Although double mutants have been observed, these are rare. In this case the sample should be considered positive only for the mutation with the lowest ΔCq.

ABI 7300

- At the end of the run, click Results - Plate and enter samples name.
- In the page Results – Amplifcation plot select all the samples and controls.
- Select Detector – All.
- In Analysis settings select Auto Ct then Analyze.
- Select Manual Ct, Manual baseline Start cycle 3, End cycle 15 then Analyze.
- In the page Report Ct values are visualized for both channels.
- Click Save.

1. Analysis of reaction controls

	KRAS ctrl mix	G12A, G12D, G12V, G12R, G12S, G12C, G13D, A59x, Q61x, A117x, A146x mix	All mixes	
	FAM	**FAM**	**JOE**	**Results**
WATER	Ct > 35	Ct > 35	Ct > 32	Proceed with analysis of the samples.
	Ct ≤ 35	Ct ≤ 35	Ct ≤ 32	Possible contamination: it is not possible to analyze the samples (see Troubleshooting).
Easy KRAS pos ctrl	23 ≤ Ct ≤ 28	15≤ Ct ≤ 21	21 ≤ Ct ≤ 27	Proceed with analysis of the samples.
	Ct<23 or Ct >28	Ct<15 or Ct >21	Ct<21 or Ct >27	Possible error in the set up of the reaction/run: it is not possible to analyze the samples (see Troubleshooting).

2. Analysis of **KRAS ctrl mix** for the DNA assessment

KRAS ctrl mix	FAM [1]	JOE [1]	Results
DNA samples	(x-2.5) ≤ Ct ≤ (x+5.5)	(x-2.5) ≤ Ct ≤ (x+5.5)	Suitable sample. Proceed with the mutation analysis [2].
	Ct<(x-2.5)	Ct<(x-2.5)	Excess of DNA. Samples must be diluted with **Water** (aliquot to be used for sample dilution) so that Ct fall in the ranges indicated above. Consider that the dilution 1:2 of the DNA increases the Ct of 1 unit.
	Ct > (x+5.5)	Ct > (x+5.5)	Suboptimal amount of starting DNA or PCR inhibition; YOU CAN NOT CONTINUE WITH THE ANALYSIS OF MUTATION: ▪ If it is possible, amplify a DNA volume > 5µl (max 9µl) or proceed with a new DNA extraction to obtain an higher concentration of template and/or a DNA of higher quality. ▪ If the presence of inhibitors is suspected, dilute the sample with **Water** (aliquot to be used for sample dilution). Consider that the dilution reduces the presence of inhibitor, but also decreases the concentration of the target DNA.

1. x = Ct **Easy KRAS pos ctrl**
2. If the results of the JOE channel are not in the expected range, consider only the FAM channel results to value the sample suitability.

3. Analysis of the mutations assays

ⓘ Only samples that following the assessment of DNA are suitable can be analyzed to search for mutations.

- Compare ΔCt values of the samples with those reported in the following table. The specified values are in the range and include extremes. The ΔCt values should be calculated with the following formula, taking care that the Ct value in FAM for the mutation and the equivalent for the control assay belong to the same sample:

ΔCt = Ct FAM Mutation – Ct FAM KRAS ctrl mix

Assay	**Amplification of Internal Control (JOE)**	**ΔCt**	**Results**
G12A	OK (similar Ct value for all the mixes)	≤ 10.6	G12A positive
G12D		≤ 6.0	G12D positive
G12V		≤ 9.5	G12V positive
G12R		≤ 9.0	G12R positive
G12S		≤ 6.0	G12S positive
G12C		≤ 8.0	G12C positive
G13D		≤ 6.5	G13D positive
A59x		≤ 3.5	A59x positive
Q61x		≤ 4.0	Q61x positive
K117x		≤ 9.0	K117x positive
A146x		≤ 4.0	A146x positive
G12A	OK (similar Ct value for all the mixes)	> 10.6	Wild type sample or beneath the LOD[1]
G12D		> 6.0	
G12V		> 9.5	
G12R		> 9.0	
G12S		> 6.0	
G12C		> 8.0	
G13D		> 6.5	
A59x		> 3.5	
Q61x		> 4.0	
K117x		> 9.0	
A146x		> 4.0	
G12A	NO	\	Failed: not sufficient template/PCR inhibition / mistake during samples dispensation
G12D		\	
G12V		\	
G12R		\	
G12S		\	
G12C		\	
G13D		\	
A59x		\	
Q61x		\	
K117x		\	
A146x		\	

1. LOD = Limit Of Detection
\ Any value

ⓘ If multiple assays show a ΔCt equal to or below the cut-off value, the signal giving the higher ΔCt is probably due to cross-reactivity. Although double mutants have been observed, these are rare. In this case the sample should be considered positive only for the mutation with the lowest ΔCt.

ABI 7500, ABI 7500 Fast

- At the end of the run, click Setup – Plate setup – Assign Targets and Samples and enter samples name.
- In the section Analysis – Amplification plot in the page View Plate layout select all the samples and controls and omit all empty wells.
- Select Reanalyse.
- In Analysis settings, for each channel, deselect Use Default Settings, Automatic Threshold and Automatic Baseline.
- Click on Apply Analysis Settings and then Reanalyse.
- In the page View Well Table Ct values are visualized for both channels.
- Click Save.

1. Analysis of reaction controls

	KRAS ctrl mix	**G12A, G12D, G12V, G12R, G12S, G12C, G13D, A59x, Q61x, A117x, A146x mix**	**All mixes**	
	FAM	**FAM**	**JOE**	**Results**
WATER	Ct > 35	Ct > 35	Ct > 32	Proceed with analysis of the samples.
	Ct ≤ 35	Ct ≤ 35	Ct ≤ 32	Possible contamination: it is not possible to analyze the samples (see Troubleshooting).
Easy KRAS pos ctrl	23 ≤ Ct ≤ 29	14≤ Ct ≤ 20	20 ≤ Ct ≤ 26	Proceed with analysis of the samples.
	Ct<23 o Ct >29	Ct<14 o Ct >20	Ct<20 o Ct >26	Possible error in the set up of the reaction/run: it is not possible to analyze the samples (see Troubleshooting).

2. Analysis of **KRAS ctrl mix** for the DNA assessment

KRAS ctrl mix	**FAM** [1]	**JOE** [1]	**Results**
DNA samples	(x-2.5) ≤ Ct ≤ (x+5.5)	(x-2.5) ≤ Ct ≤ (x+5.5)	Suitable sample. Proceed with the mutation analysis [2].
	Ct<(x-2.5)	Ct<(x-2.5)	Excess of DNA. Samples must be diluted with **Water (diluent)** so that Ct fall in the ranges indicated above. Consider that the dilution 1:2 of the DNA increases the Ct of 1 unit.
	Ct > (x+5.5)	Ct > (x+5.5)	Suboptimal amount of starting DNA or PCR inhibition; YOU CAN NOT CONTINUE WITH THE ANALYSIS OF MUTATION: ▪ If it is possible, amplify a DNA volume > 5µl (max 9µl) or proceed with a new DNA extraction to obtain an higher concentration of template and/or a DNA of higher quality. ▪ If the presence of inhibitors is suspected, dilute the sample with **Water (diluent)**. Consider that the dilution reduces the presence of inhibitor, but also decreases the concentration of the target DNA.

1. x = Ct **Easy KRAS pos ctrl**
2. If the results of the JOE channel are not in the expected range, consider only the FAM channel results to value the sample suitability.

3. Analysis of the mutations assays

ⓘ Only samples that following the assessment of DNA are suitable can be analyzed to search for mutations.

- Compare ΔCt values of the samples with those reported in the following table. The specified values are in the range and include extremes. The ΔCt values should be calculated with the following formula, taking care that the Ct value in FAM for the mutation and the equivalent for the control assay belong to the same sample:

ΔCt = Ct FAM Mutation – Ct FAM KRAS ctrl mix

Assay	**Amplification of Internal Control (JOE)**	**ΔCt**	**Results**
G12A	OK (similar Ct value for all the mixes)	≤ 11.0	G12A positive
G12D		≤ 8.0	G12D positive
G12V		≤ 12.0	G12V positive
G12R		≤ 10.5	G12R positive
G12S		≤ 8.5	G12S positive
G12C		≤ 9.5	G12C positive
G13D		≤ 8.5	G13D positive
A59x		≤ 4.0	A59x positive
Q61x		≤ 5.8	Q61x positive
K117x		≤ 12.5	K117x positive
A146x		≤ 6.5	A146x positive
G12A	OK (similar Ct value for all the mixes)	> 11.0	Wild type sample or beneath the LOD[1]
G12D		> 8.0	
G12V		> 12.0	
G12R		> 10.5	
G12S		> 8.5	
G12C		> 9.5	
G13D		> 8.5	
A59x		> 4.0	
Q61x		> 5.8	
K117x		> 12.5	
A146x		> 6.5	
G12A	NO	\	Failed: not sufficient template/PCR inhibition / mistake during samples dispensation
G12D		\	
G12V		\	
G12R		\	
G12S		\	
G12C		\	
G13D		\	
A59x		\	
Q61x		\	
K117x		\	
A146x		\	

2. LOD = Limit Of Detection
\ Any value

ⓘ If multiple assays show a ΔCt equal to or below the cut-off value, the signal giving the higher ΔCt is probably due to cross-reactivity. Although double mutants have been observed, these are rare. In this case the sample should be considered positive only for the mutation with the lowest ΔCt.

TROUBLESHOOTING

Problem	Possible reason	Recommendation
Low or absent amplification signal in the channel “Green/FAM” and/or in the channel “Yellow/HEX” for both **Easy KRAS pos ctrl** and samples.	Incorrect selection of the fluorescence acquisition channels.	▪ Check the fluorescence acquisition channels and repeat amplification with the settings described in this manual.
	Incorrect selection of the Gain on the Rotor-Gene.	▪ Repeat amplification of Rotor-Gene setting the gain properly, as described in this manual.
	Incorrect setting of the thermal-profile.	▪ Check the temperature profile and repeat amplification with the settings described in this manual.
	Incorrect dispensation or manipulation of the reagents.	▪ Mix reagents by vortexing or inverting the tubes ten times and briefly spin before use. ▪ Keep reagents on ice or refrigerated blocks during the preparation of the **Amp-Mix**.
	Reagents improperly stored or expired.	▪ Protect all mixes from light. ▪ Store all reagents at -35/-20°C and avoid thawing and refreezing more than twice. ▪ Do not store the mixes containing primers and probes at +2/+8°C for more than 5 hours. ▪ Do not store the **Taq Premix 920** at +2/+ 8°C for more than 6 months. ▪ Do not use expired reagents.
No amplification signal in both "Green / FAM" and "Yellow / HEX" channels for all assays. **Easy KRAS pos ctrl** is within the expected values.	Insufficient amount of input DNA and / or presence of PCR inhibitors.	▪ Check the quantity and quality of the extracted DNA and, if appropriate, repeate the extraction faithfully following the instructions of the extraction kit. ▪ If the extraction protocol involves the use of washing buffers containing ethanol, it is advisable to carry out a further centrifugation prior to final elution to remove any possible trace of alcohol. ▪ If it is assumed that the amount of input DNA is insufficient, repeat the reaction amplifying > 5ul DNA (max volume 9 ul), reducing the corresponding volume of **WATER** in the **Amp-Mix**. Otherwise repeat the DNA extraction by reducing the volume of elution. ▪ If you suspect the presence of inhibitors, repeat the amplification diluting sample 1:5 or 1:10 with **Water**.
	Incorrect or no dispensation of the samples.	▪ Repeat the amplification dispensing the correct volume of DNA and including positive and negative controls.
Amplification signal weak or absent in "Green / FAM" and "Yellow / HEX" only for the positive control **Easy KRAS pos ctrl**.	Degradation of the **Easy KRAS pos ctrl**.	▪ Repeat the amplification testing a new aliquot of **Easy KRAS pos ctrl**.
	Incorrect or failure in the dispensation of the **Easy KRAS pos ctrl**.	▪ Repeat the amplification by pipetting the appropriate volume of **Easy KRAS pos ctrl**.
You can not perform the analysis on Rotor-Gene in Cycling A. Green and/or Cycling A. Yellow because of a fluorescence intensity too high or out of scale for one or more than one assay.	Rotor-Gene gain too high.	▪ Perform analysis on Rotor-Gene selecting the channel Green 2 and/or Yellow 2 and the threshold value at 0.04.The ΔCt values should be calculated with the following formula: ΔCt = Ct Green 2 Mutation – Ct Green 2 KRAS ctrl mix.
The positive control **Easy KRAS pos ctrl** shows no amplification signal in the channel "Green / FAM" for assays of mutations or the signal is detectable only for some mixes; while one or more samples show an amplification signal in all assays of mutations.	Wrong tubes identification.	▪ Repeat the amplification after marking unambiguously the reaction tubes for samples and controls.
	Incorrect dispensing of the samples.	▪ Repeat the amplification paying attention to the dispensation of the DNA and the **Easy KRAS pos ctrl** in reaction tubes/wells.
	Incorrect samples names set-up in the software.	▪ Check samples names set-up.
One sample shows HEX/Yellow Ct values different from each other for the assays.	DNA dispensation error	▪ Repeat the amplification paying attention to the dispensation of the DNA in reaction tubes/wells.
The negative control **WATER**, shows an amplification signal in both FAM/Green and HEX/Yellow channels.	Contamination.	▪ The results should be rejected and samples must be reamplified using new reagents. ▪ Prepare **Amp Mix** in a dedicated area. Carefully decontaminate benches, pipettes and instruments.
Fluorescence intensity variable.	Cutaneous fat on the reaction tube.	▪ Wear gloves.
If the problems persist despite the implementation of the recommendations given and for any other questions or problems, please contact technical support of Diatech Pharmacogenetics: ▪ e-mail support@diatechpharmacogenetics.com ▪ telephone +39 0731 213243 ▪ fax +39 0731 213239		

PERFORMANCE VALIDATION

The performance validation has been performed using all the reagents supplied with the Kit.

The experiments have been performed according to the instructions reported in this user manual on the following real-time instruments:

- **CFX96** - Bio-Rad (software v. 3.1)
- **ABI 7300**- Applied Biosystems (software v. 1.4.1)
- **ABI 7500, ABI 7500 Fast** - Applied Biosystems (software v. 2.0.5)
- **Stratagene Mx3000P**, **Mx3005P** - Agilent Technologies (software v. 4.10 - Build 389)
- **Rotor-Gene Q** - Qiagen (software v. 1.7 - Build 87)
- **Rotor-Gene 6000** - Corbett (software v. 1.7 - Build 87)

Clinical specificity

In order to evaluate the Kit specificity DNA samples isolated from FFPE tumor tissue have been tested. Samples were suitable in terms of starting DNA amount and for the presence of mutations detected by the Kit, and have been already genotyped through pyrosequencing technology (kit "**Anti-EGFR MoAb response® (KRAS status)**", cod. UP032 Diatech Pharmacogenetics), or with Mass Spectrometry using MassArray® platform ("**Myriapod® Cancer Status**" cod. SQ020; "**Myriapod® Colon Status**" cod. SQ010, "**Myriapod® Lung Status**" cod. SQ011, Diatech Pharmacogenetics), or with direct sequencing. If no FFPE samples were available, Horizon Diagnostics standards, cell lines or plasmids have been tested.

	Rotor-Gene		Stratagene Mx3000P, Mx30005P		CFX96		ABI 7300		ABI 7500/ABI7500 Fast	
	N° samples tested	N° samples correctly genotyped	N° samples tested	N° samples correctly genotyped	N° samples tested	N° samples correctly genotyped	N° samples tested	N° samples correctly genotyped	N° samples tested	N° samples correctly genotyped
KRAS G12A	8	8/8	4	4/4	*	*	*	*	1	1/1
KRAS G12D	11	11/11	8	8/8	4	4/4	4	4/4	1	1/1
KRAS G12V	12	12/12	5	5/5	3	3/3	3	3/3	4	4/4
KRAS G12R	2	2/2	2	2/2	*	*	*	*	*	*
KRAS G12S	4	4/4	2	2/2	*	*	*	*	*	*
KRAS G12C	12	12/12	6	6/6	2	2/2	2	2/2	*	*
KRAS G13D	8	8/8	2	2/2	2	2/2	2	2/2	1	1/1
KRAS A59X	*	*	*	*	1	1/1	*	*	*	*
KRAS Q61X	9	9/9	9	9/9	6	6/6	8	8/8	1	1/1
KRAS K117X	2	2/2	2	2/2	2	2/2	2	2/2	*	*
KRAS A146X	4	4/4	4	4/4	4	4/4	4	4/4	*	*
KRAS wild-type	41	41/41	23	23/23	10	9/10(1)	10	9/10(1)	13	13/13
Total	113	113/113	67	67/67	34	33/34	35	34/35	21	21/21

* FFPE sample not available: Horizon Diagnostics standard, cell lines or plasmids have been tested.

1. Sample genotyped as wild-type with a different method, is positive for KRAS G12D on different real-time instruments. This can be due to an higher sensitivity of the real-time assay.

Limit of detection (LOD)

The LOD of the Kit is defined as the lowest amount of mutant DNA in a background of wild-type DNA at which a mutant sample will provide mutation-positive results in 95% of tests.
To determine the LOD, samples with different percentage of mutation and a medium input DNA concentration have been tested.
For each real-time instrument (Rotor-Gene, Mx3000P/Mx3005P, ABI 7300, ABI 7500, ABI 7500 Fast, CFX96) three independent experiments have been performed. In each experiment mutated samples have been tested in duplicates.
If available Horizon Diagnostics standards have been tested to determinate the LOD, otherwise cell lines or plasmids have been used.
The LOD of the "**Easy® KRAS**" Kit, considering all the instruments tested is:

Assay	LOD C_{95} (at medium DNA input concentration)
G12A	0.5-1%
G12D	1-5%
G12V	0.5%
G12R	0.5%
G12S	2-5%
G12C	0.5-1%
G13D	1-5%
A59x	5-7.5%
Q61x	5-7.5%
K117x	2-5%
A146x	5%

Reproducibility

System reproducibility (*inter-assay* variability) has been evaluated analyzing the data deriving from three independent runs with standard DNA samples. Results were reproducible in terms of genotyping for all assays and samples analyzed.

Repeatability

System repeatability (*intra-assay* variability) has been evaluated analyzing the data deriving from three independent runs with standard DNA samples. Results were reproducible in terms of genotyping for all assays and samples analyzed.

Robustness

Lot to lot consistency
Different batches of Taq PreMix have been tested with the same DNA samples. Results from the different lots are comparable.
Two different batches of primers and probes have been tested with the same DNA samples. Results from the different lots are comparable.

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APPENDIX A - RT001 96 well plate sample grid A – Easy® KRAS

DATE		RUN NAME	

	1	2	3	4	5	6	7	8	9	10	11	12
A												
B												
C												
D												
E												
F												
G												
H												
	G12A mix (1)	G12D mix (2)	G12V mix (3)	G12R mix (4)	G12S mix (5)	G12C mix (6)	G13D mix (7)	A59x mix (8)	Q61x mix (9)	K117x mix (10)	A146x mix (11)	ctrl mix (12)

INSTRUMENT n.				USER MANUAL version	
CODE		LOT		EXPIRY DATE	
NOTES					
OPERATOR				SIGN	

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APPENDIX B - RT001 Rotor-Gene sample grid B – Easy® KRAS

DATE		RUN NAME	

1	•	9	•	17	•	25	•	33	•	41	•	49	•	57	•	65	•
2	•	10	•	18	•	26	•	34	•	42	•	50	•	58	•	66	•
3	•	11	•	19	•	27	•	35	•	43	•	51	•	59	•	67	•
4	•	12	•	20	•	28	•	36	•	44	•	52	•	60	•	68	•
5	•	13	•	21	•	29	•	37	•	45	•	53	•	61	•	69	•
6	•	14	•	22	•	30	•	38	•	46	•	54	•	62	•	70	•
7	•	15	•	23	•	31	•	39	•	47	•	55	•	63	•	71	•
8	•	16	•	24	•	32	•	40	•	48	•	56	•	64	•	72	•

G12A mix (1)	G12D mix (2)	G12V mix (3)	G12R mix (4)	G12S mix (5)	G12C mix (6)	G13D mix (7)	A59x mix (8)	Q61x mix (9)	K117x mix (10)	A146x mix (11)	ctrl mix (12)

INSTRUMENT n.				USER MANUAL version	
CODE		LOT		EXPIRY DATE	
NOTES					
OPERATOR				SIGN	

OPERATOR NOTES

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