June 2016

ipsogen® JAK2 Muta*Screen* Kit Handbook

Σ 10 (catalog no. 673022)

Σ 24 (catalog no. 673023)

Version 1

IVD

Quantitative in vitro diagnostics

For use with Rotor-Gene® Q, Applied Biosystems®, ABI PRISM®, and LightCycler® instruments

CE

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Contents

Intended Use

The *ipsogen* JAK2 Muta*Screen* Kits are intended for the detection of the JAK2 V617F/G1849T mutation in genomic DNA from subjects with suspected myeloproliferative neoplasm. The absence of JAK2 V617F/G1849T does not exclude the presence of other JAK2 mutations. The test can report false negative results in case of additional mutations located in codons 615 to 619 (1).

Note: The kit should be used following the instructions given in this manual, in combination with validated reagents and instruments. Any off-label use of this product and/or modification of the components will void QIAGEN's liability.

Summary and Explanation

A recurrent somatic mutation, V617F, affecting the Janus tyrosine kinase 2 (JAK2) gene, has been identified in 2005 (2–5), leading to a major breakthrough in the understanding, classification, and diagnosis of myeloproliferative neoplasms (MPN). JAK2 is a critical intracellular signaling molecule for a number of cytokines, including erythropoietin.

The JAK2 V617F mutation is detected in >95% of patients with polycythemia vera (PV), 50–60% of patients with essential thrombocythemia (ET), and in 50% of patients with primary myelofibrosis (PMF). JAK2 V617F has been also detected in some rare cases of chronic myelomonocytic leukemia, myelodysplastic syndrome, systemic mastocytosis, and chronic neutrophilic leukemia, but in 0% of CML (6).

The mutation corresponds to a single-nucleotide change of JAK2 nucleotide 1849 in exon 14, resulting in a unique valine (V) to phenylalanine (F) substitution at position 617 of the protein (JH2 domain). It leads to constitutive activation of JAK2, hematopoietic transformation in vitro, and erythropoietin-independent erythroid colony (EEC) growth in all patients with PV and a large proportion of ET and PMF patients (7). JAK2 V617F represents a key driver in the transformation of hematopoietic cells in MPN, but the exact pathological mechanisms leading, with the same unique mutation, to such different clinical and biological entities remain to be fully elucidated.

Traditionally, the diagnosis of MPNs was based on clinical, bone marrow histology and cytogenetic criteria. The discovery of a disease-specific molecular marker resulted in both simplification of the process and increased diagnostic accuracy. Detection of the JAK2 V617F mutation is now part of the reference WHO 2008 criteria for the diagnosis of BCR-ABL negative MPN (Table 1), and presence of this mutation is a major criterion for diagnostic confirmation.

Table 1. WHO criteria for the diagnosis of MPN (adapted from reference 8)

Criteria for a diagnosis of polycythemia vera (PV)	
Major	1. Hemoglobin (Hgb) >18.5 $g.dl^{-1}$ (men) or >16.5 $g.dl^{-1}$ (women) or Hgb or hematocrit (Hct) >99th percentile of reference range for age, sex, or altitude of residence or Hgb >17 $g.dl^{-1}$ (men) or >15 $g.dl^{-1}$ (women) if associated with sustained increase of ≥2 $g.dl^{-1}$ from baseline that cannot be attributed to correction of iron deficiency or Elevated red cell mass >25% above mean normal predicted value 2. Presence of *JAK2V617F* or similar mutation
Minor	1. Bone marrow trilineage myeloproliferation 2. Subnormal serum erythropoietin level 3. Endogenous erythroid colony (EEC) growth
Criteria for a diagnosis of essential thrombocythemia (ET)	
Major	1. Platelet count ≥450 x 10^9 l^{-1} 2. Megakaryocyte proliferation with large and mature morphology. No or little granulocyte or erythroid proliferation 3. Not meeting WHO criteria for chronic myeloid leukemia (CML), PV, primary myelofibrosis (PMF), myelodysplastic syndrome (MDS), or other myeloid neoplasm 4. Demonstration of *JAK2V617F* or other clonal marker or No evidence of reactive thrombocytosis
Minor	-
Criteria for a diagnosis of primary myelofibrosis (PMF)	
Major	1. Megakaryocyte proliferation and atypia accompanied by either reticulin and/or collagen fibrosis or In the absence of reticulin fibrosis, the megakaryocyte changes must be accompanied by increased marrow cellularity, granulocytic proliferation and often decreased erythropoiesis (i.e. prefibrotic PMF) 2. Not meeting WHO criteria for (CML), PV, MDS, or other myeloid neoplasm 3. Demonstration of *JAK2V617F* or other clonal marker or No evidence of reactive marrow fibrosis
Minor	1. Leukoerythroblastosis 2. Increased serum lactate dehydrogenase (LDH) 3. Anemia 4. Palpable splenomegaly

Recently, international experts have proposed criteria for therapeutic trials in PV and ET. Based on data on allograft, alpha-interferon, or hydroxyurea, JAK2V617F quantification has been incorporated as a potentially useful tool to monitor treatment response (9). A decrease in JAK2 V617F burden has been observed in response to some of the new anti-JAK2 targeted drugs in clinical development (10).

Principle of the Procedure

In an allelic discrimination assay, two TaqMan® probes are used in a multiplexed assay. One is a perfect match to the allele 2 sequence (e.g., the wild-type allele), and the other one is a perfect match to the allele 1 sequence (e.g., the allele with a mutation). Each probe is labeled with a distinctive fluorescent dye at its 5' end, the reporter, such as FAM™ or VIC®, and contains a non-fluorescent quencher at the 3' end. The probes also contain a minor grove binder (MGB™) permitting the use of shorter probes with greater stability and thereby a more accurate allelic discrimination.

During the extension phase of the PCR, the perfectly matched probe is cleaved by the 5'→3' exonuclease activity of *Taq* DNA polymerase, separating the reporter dye from the quencher and thus releasing detectable fluorescence. The probe not perfectly matched will be displaced rather than cleaved by the *Taq* DNA polymerase and no reporter dye is released. The fluorescence signal (VIC or FAM) generated is collected at the end of the PCR (end-point) and immediately indicates the presence of the targeted sequence(s) in the sample (wild-type allele, mutated allele or both) without the requirement of long and laborious post-PCR steps, which also increase the contamination risk. The actual quantity of target sequence is not determined.

The *ipsogen* JAK2 Muta*Screen* Kit uses this technology as illustrated (see Figure 1).

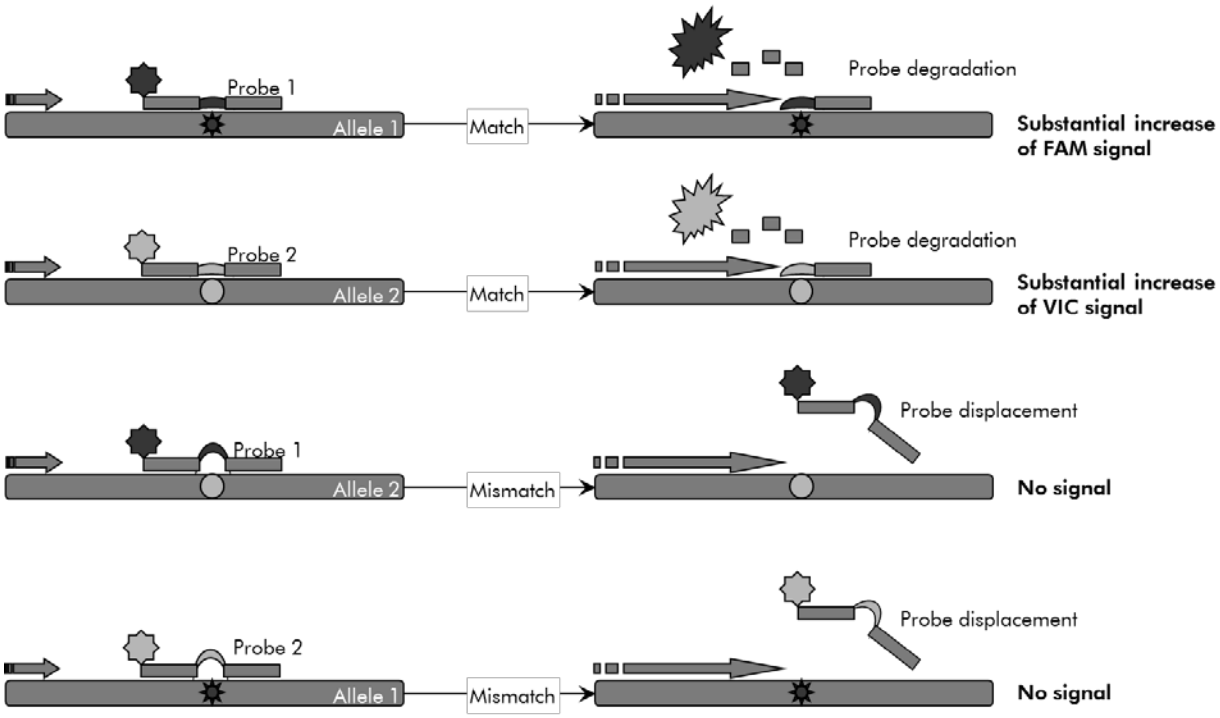


Figure 1. TaqMan probe multiplex assay. The *ipsogen* JAK2 Muta*Screen* Kit uses this technology for allelic discrimination.

Materials Provided

Kit contents

***ipsogen* JAK2 Muta*Screen* Kit**		**(10)**	**(24)**
Catalog no.		**673022**	**673023**
Number of reactions		**24**	**10**
V617F Positive Control*	PC-VF	30 µl	30 µl
V617F Negative Control†	NC-VF	30 µl	30 µl
Cut-Off Sample	COS-VF	30 µl	30 µl
Primers and probes mix JAK2 V617F‡	PPM-VF 10x	70 µl	145 µl
ipsogen *JAK2 Muta*Screen *Kit Handbook* (English)		1	1

* Positive control: 100% V617F DNA.

† Negative control: 100% wild type DNA; 0% V617F.

‡ Mix of specific reverse and forward primers for the *JAK2* gene, specific V617F FAM probe and wild type VIC probe.

Note: Briefly centrifuge tubes before use.

Note: Analyzing unknown samples with the *ipsogen* JAK2 Muta*Screen* Kit requires the extraction of genomic DNA. Reagents needed to perform DNA extraction (e.g., QIAGEN® QIAamp® DNA Mini Kit, cat. no. 51304) are not provided and must be validated in combination with the kit.

Materials Required but Not Provided

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.

Reagents

- Nuclease-free PCR grade water
- Nuclease-free 1x TE buffer, pH 8.0 (e.g., Thermo Fisher Scientific Inc., cat. no. 12090015)
- Buffer and *Taq* DNA polymerase: The validated reagents are TaqMan Universal PCR Master Mix (Master Mix PCR 2x) (Thermo Fisher Scientific Inc., cat. no. 4304437) and LightCycler TaqMan Master (Master Mix PCR 5x) (Roche, cat. no. 04535286001)
- Reagents for 0.8–1% agarose gel in 0.5x TBE electrophoresis buffer

Consumables

- Nuclease-free aerosol-resistant sterile PCR pipet tips with hydrophobic filters
- 0.5 ml or 0.2 ml RNase- and DNase-free PCR tubes
- Ice

Equipment

- Pipets* dedicated for PCR (1–10 µl; 10–100 µl; 100–1000 µl)
- Benchtop centrifuge* with rotor for 0.2 ml/0.5 ml reaction tubes (capable of attaining 10,000 rpm)
- Spectrophotometer* for DNA quantitation
- Real-time PCR instrument:* Rotor-Gene Q 5plex HRM or other Rotor-Gene instrument; LightCycler 2.0, or 480; Applied Biosystems 7300 Real-Time PCR System, Applied Biosystems 7500 Real-Time PCR System, ABI PRISM 7000 SDS, ABI PRISM 7700 SDS, or ABI PRISM 7900HT SDS; and associated specific material
- Equipment* for pulsed-field gel electrophoresis

* Ensure that instruments have been checked and calibrated according to the manufacturer's recommendations.

Warnings and Precautions

For in vitro diagnostic use

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 kit component.

Discard sample and assay waste according to your local safety regulations.

General precautions

qPCR tests require good laboratory practices, including equipment maintenance, that are dedicated to molecular biology and compliant with applicable regulations and relevant standards.

This kit is intended for in vitro diagnostic use. Reagents and instructions supplied in this kit have been validated for optimal performance. Further dilution of the reagents or alteration of incubation times and temperatures may result in erroneous or discordant data. PPM-VF reagent may be altered if exposed to light. All reagents are formulated specifically for use with this test. For optimal performance of the test, no substitutions should be made.

Use extreme caution to prevent:

- DNase contamination which might cause degradation of the template DNA
- DNA or PCR carryover contamination resulting in false positive signal

We therefore recommend the following.

- Use nuclease-free labware (e.g., pipets, pipet tips, reaction vials) and wear gloves when performing the assay.
- Use fresh aerosol-resistant pipet tips for all pipetting steps to avoid cross-contamination of the samples and reagents.
- Prepare pre-PCR master mix with dedicated material (pipets, tips, etc.) in a dedicated area where no DNA matrices (DNA, plasmid) are introduced. Add template in a separate zone (preferably in a separate room) with specific material (pipets, tips, etc.).

Reagent Storage and Handling

The kits are shipped on dry ice and must be stored at –30°C to –15°C upon receipt.

- Minimize exposure to light of the primers and probes mixes (PPM-VF tube).
- Gently mix and centrifuge the tubes before opening.
- Store all kit components in original containers.

These storage conditions apply to both opened and unopened components. Components stored under conditions other than those stated on the labels may not perform properly and may adversely affect the assay results.

Expiration dates for each reagent are indicated on the individual component labels. Under correct storage conditions, the product will maintain performance until the expiration date printed on the label.

There are no obvious signs to indicate instability of this product. However, positive and negative controls should be run simultaneously with unknown specimens.

Procedure

Sample DNA preparation

Genomic DNA should be obtained either from whole blood, purified peripheral blood lymphocytes, polynuclear cells, or granulocytes. To be able to compare results, we recommend adopting the same cellular fraction and DNA extraction method. DNA extraction should be performed by any home brew or commercial method.

DNA quantity is determined by measuring optical density at 260 nm. DNA quality should be assessed by spectrophotometry or gel electrophoresis.

The A_{260}/A_{280} ratio should be 1.7–1.9. Smaller ratios usually indicate contamination by protein or organic chemicals. Electrophoretic analysis on a 0.8–1% agarose gel should allow visualization of the isolated DNA as a distinct band of about 20 kb. A slight smear is acceptable.

The resultant DNA is diluted to 5 ng/µl in TE buffer. The qPCR reaction is optimized for 25 ng of purified genomic DNA.

Storing nucleic acids

For short-term storage of up to 24 hours, we recommend storing purified nucleic acids at 2–8°C. For long-term storage of over 24 hours, we recommend storage at –20°C.

Protocol: qPCR on Rotor Gene Q instruments with 72-tube rotor

Using this instrument, we recommend performing all measurements in duplicate, as indicated in Table 2.

Table 2. Number of reactions for Rotor Gene Q MDx 5plex HRM or Rotor Gene Q 5plex HRM instruments with 72-tube rotor

Samples	Reactions
JAK2 V617F primers and probes mix (PPM-VF) (56 reactions)	
24 DNA samples	24 x 2 reactions
3 DNA controls	3 x 2 reactions (PC-VF, NC-VF, and COS-VF, each one tested in duplicate)
Water control	2 reactions

Sample processing on Rotor-Gene Q instruments with 72-tube rotor

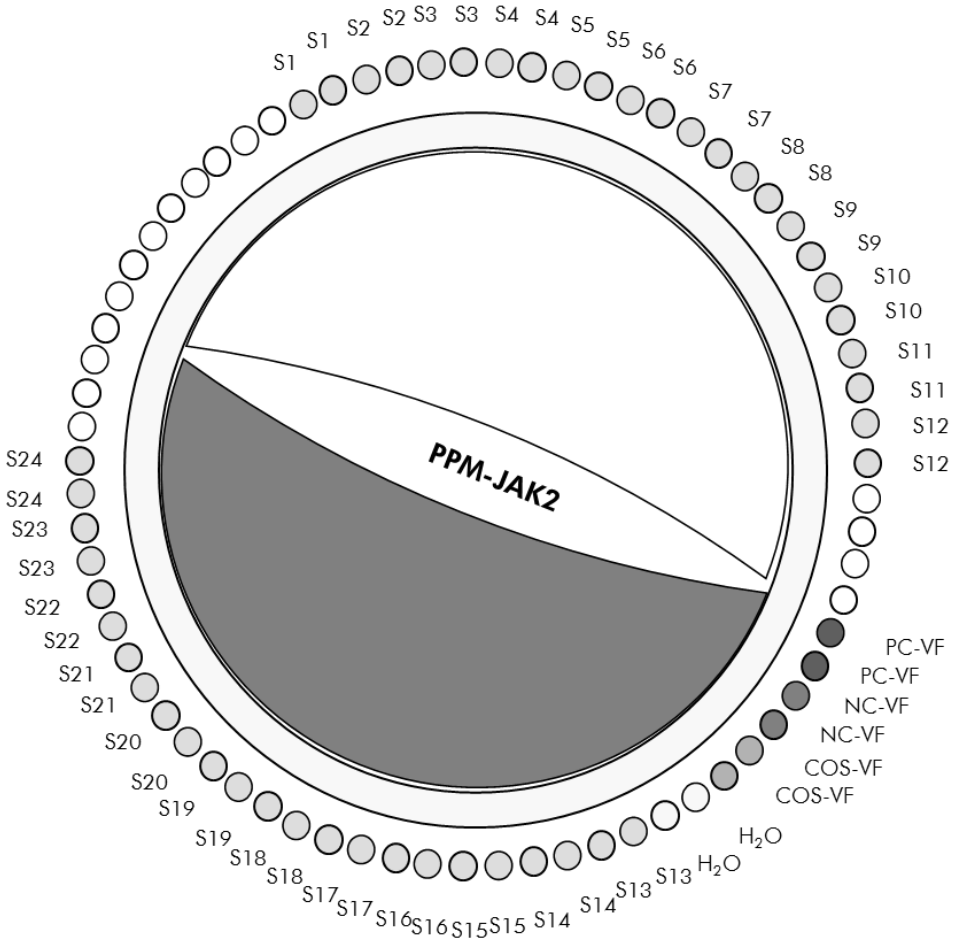


Figure 2. Suggested rotor setup for an experiment with the *ipsogen* JAK2 Muta*Screen* Kit. PC-VF: positive control; **NC-VF**: negative control; **COS-VF**: cut-off sample; **S**: DNA sample; **H_2O**: water control.

Note: Take care to always place a sample to be tested in position 1 of the rotor. Otherwise, during the calibration step, the instrument will not perform calibration, and incorrect fluorescence data will be acquired.

Fill all other positions with empty tubes.

qPCR on Rotor-Gene Q instruments with 72-tube rotor

Note: Perform all steps on ice.

Procedure

1. **Thaw all necessary components and place them on ice.**
   Components should be taken out of the freezer approximately 10 min before starting the procedure.
2. **Vortex and briefly centrifuge all the tubes (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**

3. Prepare the following qPCR mix according to the number of samples being processed.

All concentrations are for the final volume of the reaction.

Table 3 describes the pipetting scheme for the preparation of one reagent mix, calculated to achieve a final reaction volume of 25 µl. A pre-mix can be prepared, according to the number of reactions, using the same primer and probe mix. Extra volumes are included to compensate for pipetting error.

On Rotor-Gene instruments, the *ipsogen* JAK2 Muta*Screen* Kit can be used for analysis of 24 samples in duplicate in one experiment (Figure 2), 20 samples in duplicate in two experiments, or 15 samples in duplicate in three experiments.

Table 3. Preparation of qPCR mix

	Number of reactions (µl)				
Component	**1**	**56+1***	**28+1†**	**18+1‡**	**Final concentration**
TaqMan Universal PCR Master Mix, 2x	12.5	712.5	362.5	237.5	1x
Primers and probes mix, 10x	2.5	142.5	72.5	47.5	1x
Nuclease-free PCR grade water	5	285	145	95	–
Sample (to be added at step 5)	5	5 each	5 each	5 each	–
Total volume	25	25 each	25 each	25 each	–

* 24 samples; one experiment/kit.

† 10 samples; two experiments/kit.

‡ 5 samples; three experiments/kit.

4. **Vortex and briefly centrifuge the qPCR mix (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**
5. **Dispense 20 µl of the qPCR pre-mix per tube.**
6. **Add 5 µl of the sample DNA material or controls in the corresponding tube (total volume 25 µl).**
7. **Mix gently, by pipetting up and down.**
8. **Close the PCR tubes. Place the tubes in the 72-tube rotor according to the manufacturer's recommendations. Fill all other positions with empty tubes.**
9. **Make sure that the locking ring (accessory of the Rotor-Gene Instrument) is placed on top of the rotor to prevent accidental opening of the tubes during the run. Place the rotor in the Rotor-Gene Q instrument according to the manufacturer's recommendations.**
10. **For the detection of JAK2 DNA, create a temperature profile according to the following steps.**

Setting the general assay parameters	**Figures 3, 4**
Amplification of the DNA	**Figure 5**
Adjusting the fluorescence channel sensitivity	**Figure 6**

Further information on programming Rotor-Gene Instruments can be found in the instrument user manual. In the illustrations, the software settings are framed in bold black. Illustrations are included for Rotor-Gene Q Instruments.

11. **Start the Rotor-Gene Software. In the "New Run" dialog box, click "New".**

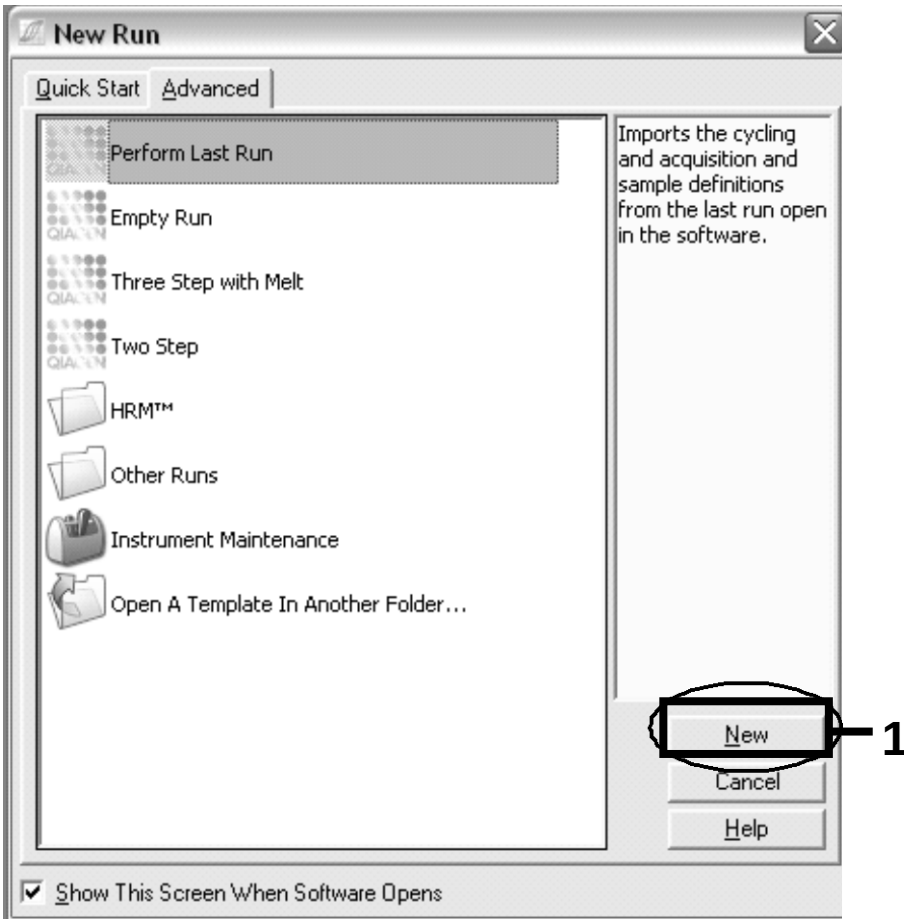


Figure 3. The "New Run" dialog box.

12. In the "New Run Wizard", set the volume to 25 µl and click "Next".

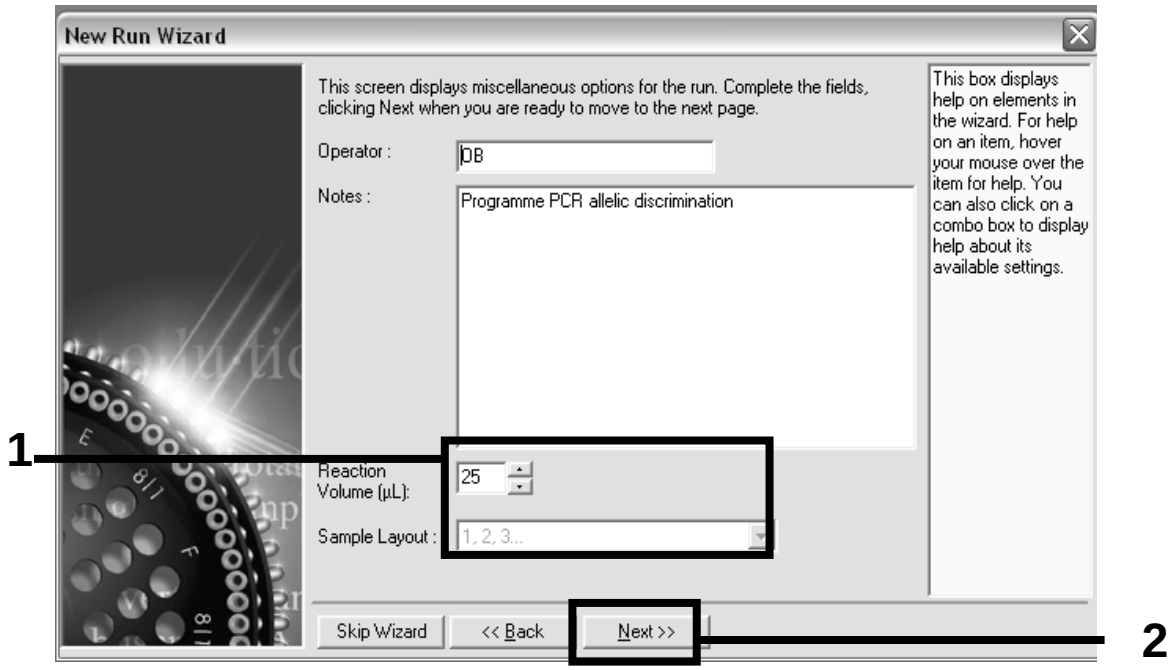


Figure 4. Setting the general assay parameters.

13. **Click the "Edit Profile" button in the next "New Run Wizard" dialog box, and program the temperature profile as shown in Table 4 and Figure 5. Be sure to add the last acquiring step at 60°C, at each cycle, for both channels Green (FAM) and Yellow (VIC).**

Table 4. Temperature profile

Hold	Temperature: 50°C Time: 2 min
Hold 2	Temperature: 95°C Time: 10 min
Cycling	50 times 92°C for 15 s 60°C for 1 min; single Acquisition of FAM fluorescence in channel Cycling A Green Acquisition of VIC fluorescence in channel Cycling A Yellow

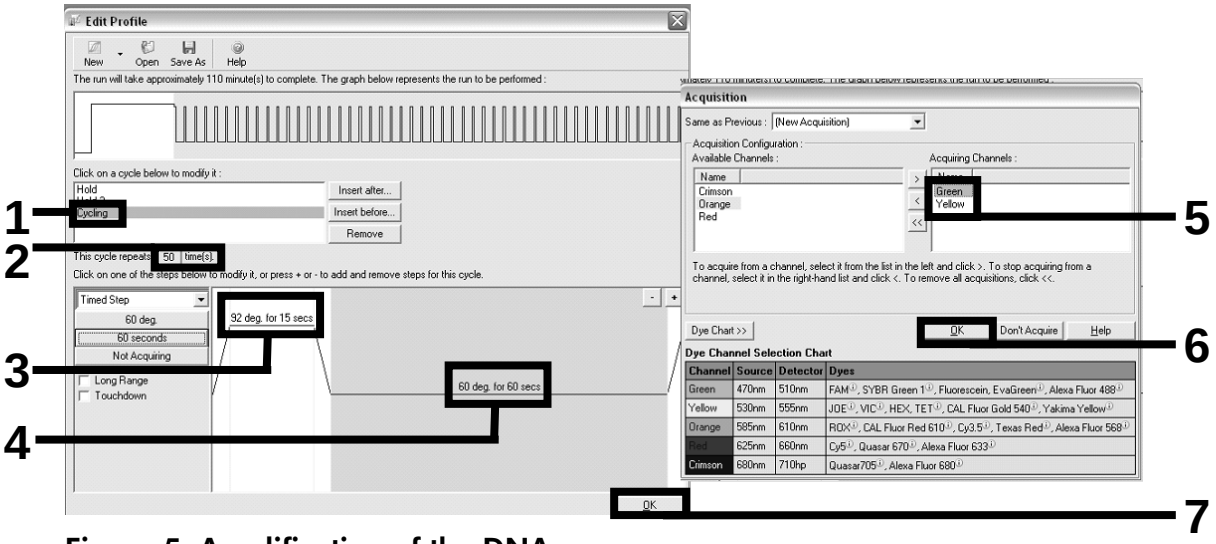


Figure 5. Amplification of the DNA.

14. **The detection range of the fluorescence channels has to be determined according to the fluorescence intensities in the PCR tubes. Click "Gain Optimisation" in the "New Run Wizard" dialog box to open the "Auto-Gain Optimisation Setup" dialog box. Click "Optimise Acquiring" (Figure 6), and then click "OK" in the "Auto-Gain Optimisation Channel Settings" dialog boxes for each channel (Green and Yellow,**

Figure 6). Make sure that the "Perform Optimisation Before 1st Acquisition" box is checked for each channel (Figure 6).

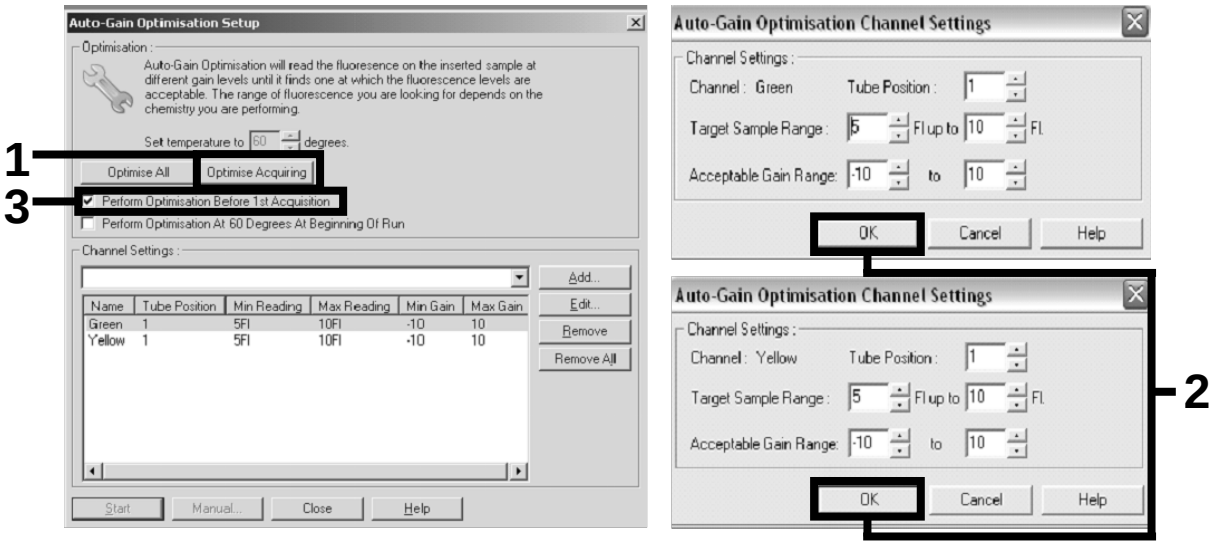


Figure 6. Adjusting the fluorescence channel sensitivity.

15. **The gain values determined by the channel calibration are saved automatically and are listed in the last menu window of the programming procedure. Click "Start Run" to run the program.**
16. **Enter the rotor setup in the Rotor-Gene software (Figure 7).**

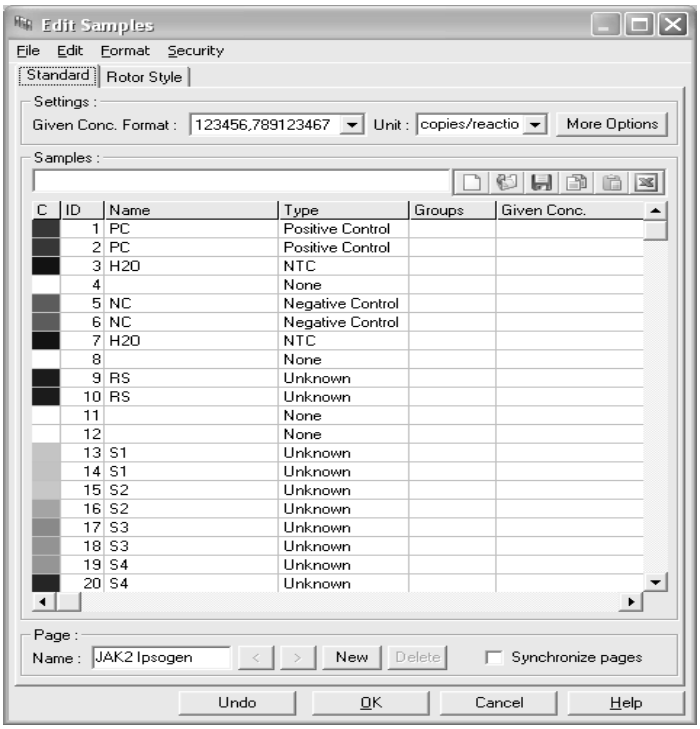


Figure 7. Rotor-Gene setup: "Edit Samples".

End point analysis procedure for Rotor-Gene Q 5plex HRM instrument setting

17. After the PCR program has ended, click "Analysis" in the toolbar (Figure 8).

Figure 8. Analysis.

18. In the "Analysis" dialog box (Figure 9), double-click "Cycling A Green", and then "OK". Repeat for Cycling A yellow.

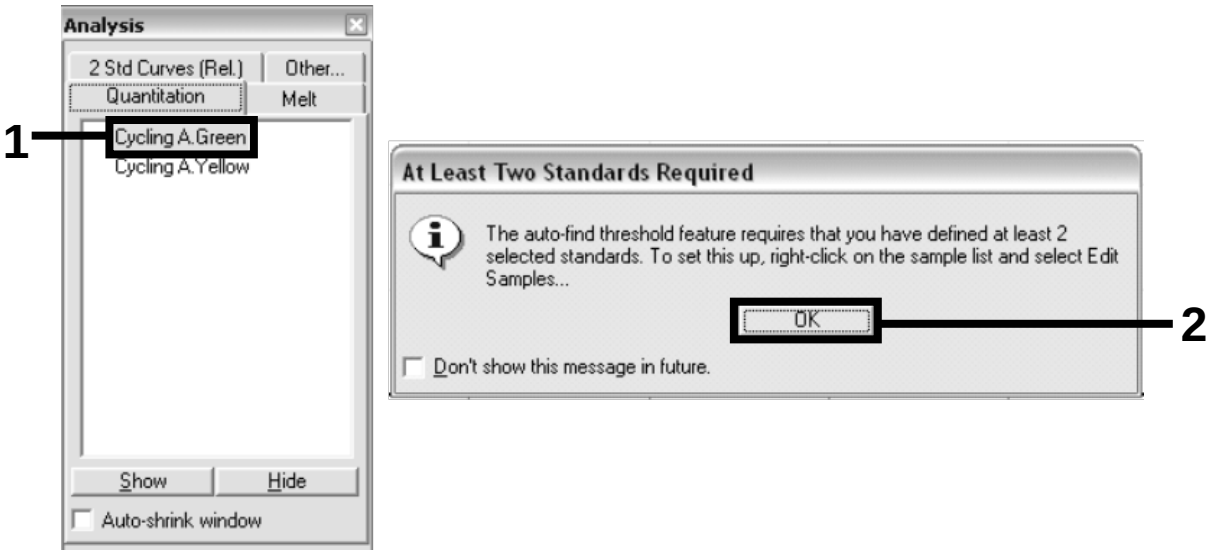


Figure 9. Quantitation: "Cycling A. Green".

19. A new window appears (Figure 10). Click "Slope Correct" in both panels, as shown in Figure 10.

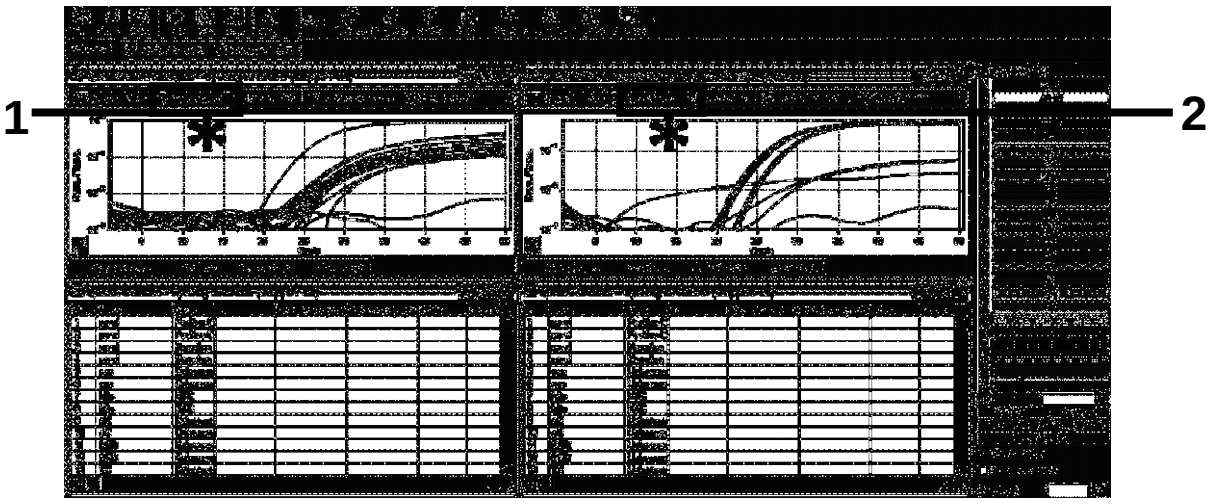


Figure 10. Setting "Slope Correct".

20. **To export data, save as an Excel® data sheet. Click "OK", give a name to the export file, and save the text file (*.txt).**
21. **Open the text file in Excel and select column A. Click "Data", then "Convert", and "Next". Select "Comma" and then click "End". The results will appear as shown in Figure 11.**

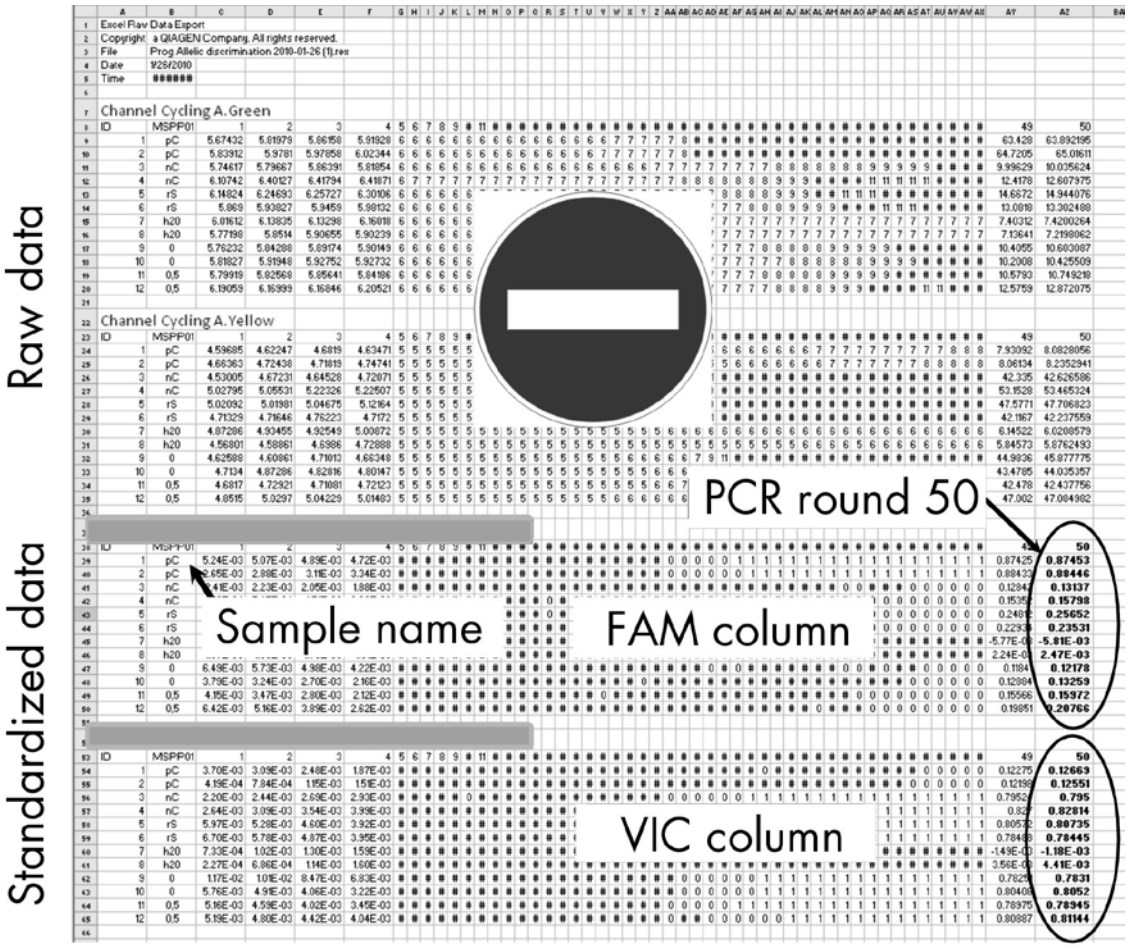


Figure 11. Example of results, shown in Excel file.

Note: The file contains both raw data and standardized data. Only standardized data must be considered.

These data are given in the Quantitative analysis of channel Cycling A Green and Quantitative analysis of channel Cycling A Yellow sections of the table. The data intended for interpretation are those acquired at PCR cycle 50 (in circles on the right).

Protocol: qPCR on Applied Biosystems and ABI PRISM instruments

Using 96 wells plate qPCR equipment, we recommend performing all measurements in duplicate as indicated in Table 5.

Table 5. Number of reactions for Applied Biosystems 7300 and 7500, ABI PRISM 7000, ABI PRISM 7700, or ABI PRISM 7900HT instruments

Samples	Reactions
JAK2 V617F primers and probes mix (PPM-VF) (56 reactions)	
24 DNA samples	24 x 2 reactions
3 DNA controls	3 x 2 reactions (PC-VF, NC-VF, and COS-VF, each one tested in duplicate)
Water control	2 reactions

Sample processing on Applied Biosystems 7300 and 7500, ABI PRISM 7000, ABI PRISM 7700, or ABI PRISM 7900HT instruments

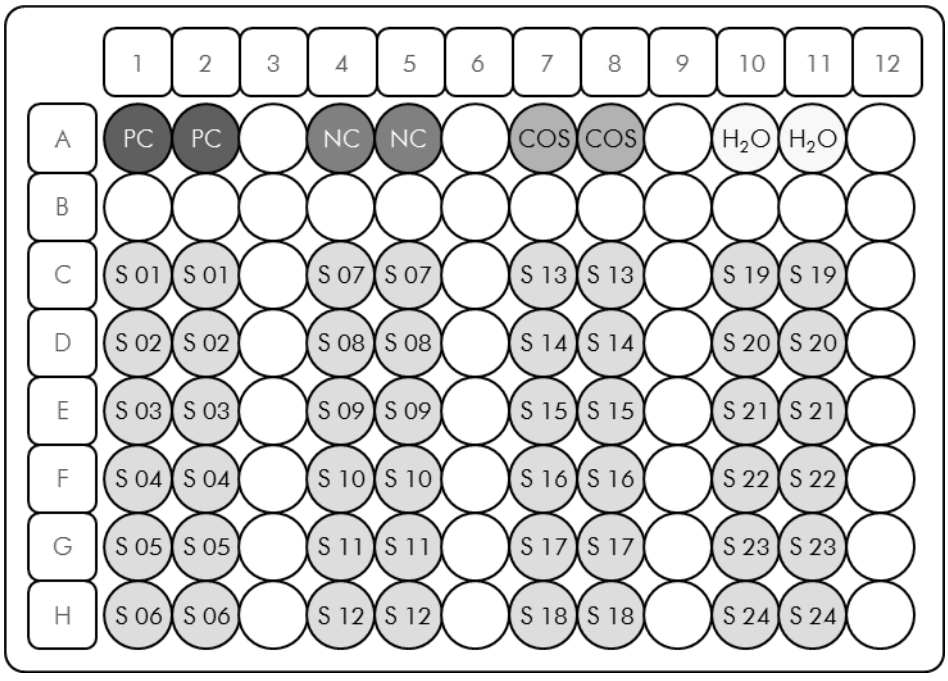


Figure 12. Suggested plate setup for an experiment with the *ipsogen* JAK2 MutaScreen Kit. PC: positive control; **NC**: negative control; **COS**: cut-off sample; **S**: DNA sample; **H_2O**: water control.

qPCR on Applied Biosystems 7300 and 7500, ABI PRISM 7000, ABI PRISM 7700, or ABI PRISM 7900HT instruments

Note: Perform all steps on ice.

Procedure

1. **Thaw all necessary components and place them on ice.**
   Components should be taken out of the freezer approximately 10 min before starting the procedure.
2. **Vortex and briefly centrifuge all the tubes (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**
3. **Prepare the following qPCR mix according to the number of samples being processed.**
   All concentrations are for the final volume of the reaction.

   Table 6 describes the pipetting scheme for the preparation of one reagent mix, calculated to achieve a final reaction volume of 25 µl. A pre-mix can be prepared, according to the number of reactions, using the same primer and probe mix. Extra volumes are included to compensate for pipetting error.

   On the Applied Biosystems 7300 and 7500, ABI PRISM 7000, ABI PRISM 7700, or ABI PRISM 7900HT instruments, the *ipsogen* JAK2 Muta*Screen* Kit can be used for analysis of 24 samples in duplicate in one experiment (Figure 12), 20 samples in duplicate in two experiments, or 15 samples in duplicate in three experiments.

Table 6. Preparation of qPCR mix

Component	Number of reactions (µl)				Final concentration
	1	56+1*	28+1†	18+1‡	
TaqMan Universal PCR Master Mix, 2x	12.5	712.5	362.5	237.5	1x
Primers and probes mix, 10x	2.5	142.5	72.5	47.5	1x
Nuclease-free PCR grade water	5	285	145	95	–
Sample (to be added at step 4)	5	5 each	5 each	5 each	–
Total volume	25	25 each	25 each	25 each	–

* 24 samples; one experiment/kit.

† 10 samples; two experiments/kit.

‡ 5 samples; three experiments/kit.

4. **Vortex and briefly centrifuge the qPCR mix (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**
5. **Dispense 20 µl of the qPCR pre-mix per well.**
6. **Add 5 µl of the sample DNA material or controls in the corresponding well (total volume 25 µl).**
7. **Mix gently, by pipetting up and down.**
8. **Close the plate and briefly centrifuge (300 x *g*, approximately 10 s).**
9. **Place the plate in the thermal cycler according to the manufacturer's recommendations.**
10. **Program the thermal cycler with the thermal cycling program as indicated in Table 7, and start the run.**

Table 7. Temperature profile for Applied Biosystems and ABI PRISM instruments

Hold	Temperature: 50°C Time: 2 min
Hold 2	Temperature: 95°C Time: 10 min
Cycling	50 times 92°C for 15 s 60°C for 1 min

Post-read run analysis procedure for Applied Biosystems and ABI PRISM instruments

For programming details of the Applied Biosystems 7300 and 7500, ABI PRISM 7000, ABI PRISM 7700, or ABI PRISM 7900HT instruments, refer to the instrument user guide. For a better overview, the software settings are framed in bold black.

11. **After the run is finished, select "Start/Program", and then select "File/New".**
12. **In the "New Document Wizard" dialog box, click the "Assay" drop-down list, and select "Allelic Discrimination" (Figure 13).**
13. **Accept the default settings for the "Container" and "Template" fields ("96-Well Clear" and "Blank Document", Figure 13). In the "Plate Name" field, type *AD Post-read* (Figure 13), and then click "Next>" to access the "Select Markers" dialog box.**

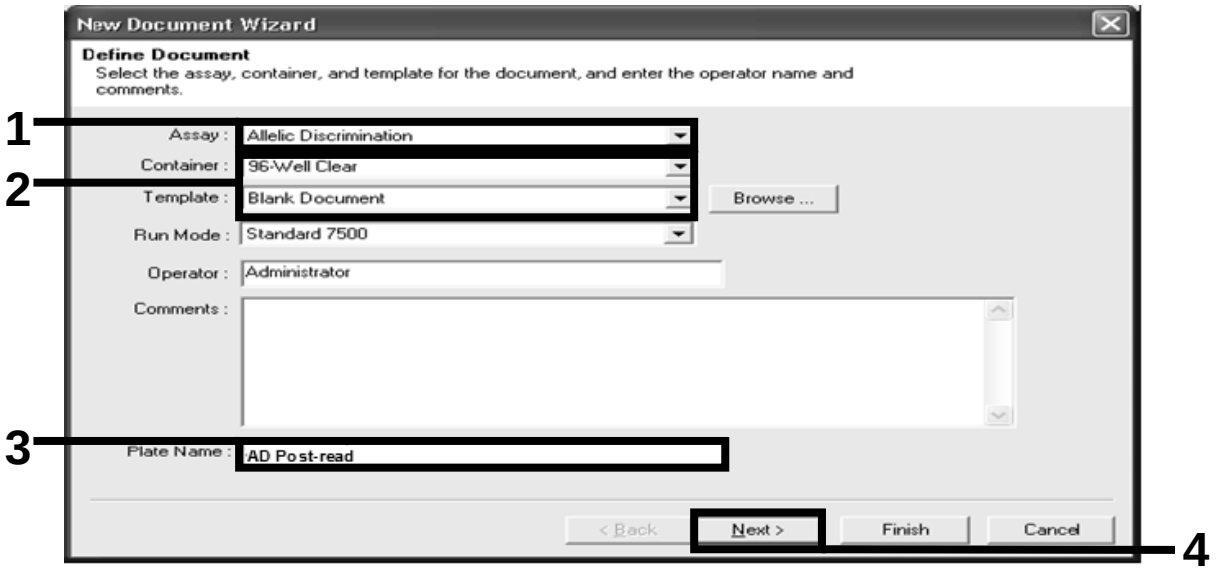


Figure 13. Pre-settings for creating a new post-read run (New Document Wizard).

14. **If the "Markers in Document" panel in the "Select Markers" dialog box contains a suitable marker for your application, proceed with step 18. If not, then continue with step 15.**
15. **Create detectors and markers as follows. Click "New Detector" (Figure 14).**

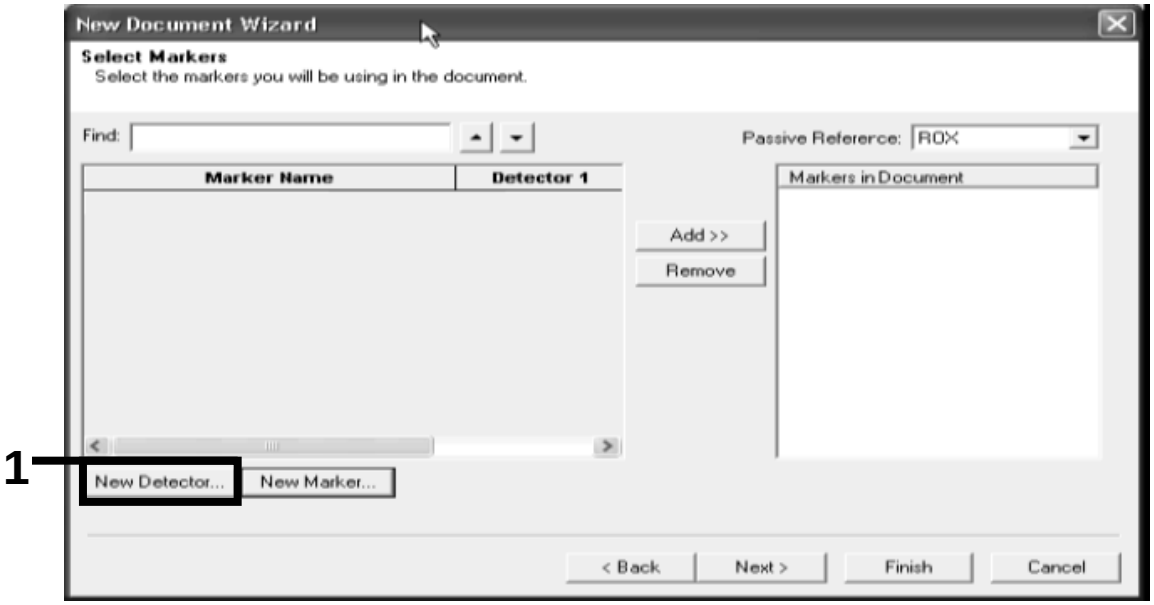


Figure 14. The "Markers in Document" panel does not contain a suitable marker for your application.

16. **In the "New Detector" dialog box, type *Allele A* in the "Name" field (Figure 15). Leave the "Reporter Dye" set to "FAM". Click the "Color" button, select a color, and then click "OK" (Figure 15). Click "Create Another" (Figure 15).**

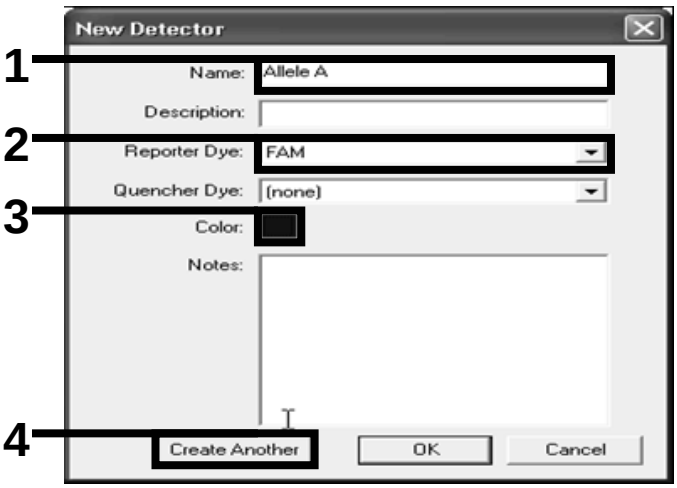


Figure 15. Creating detectors.

17. **In the next "New Detector" dialog box, type *Allele B* in the "Name" field. Select "VIC" in the "Reporter Dye" field. Click the "Color" button, select a color, and then click "OK".**
18. **Click "New Marker" in the "Select Markers" dialog box (see Figure 14).**
19. **In the "New Marker" dialog box, type *JAK2* in the "New Marker Name" field (Figure 16). Select the "Allele A" and "Allele B" detectors as created in steps 16 and 17 (or already defined), and click "OK" (Figure 16).**

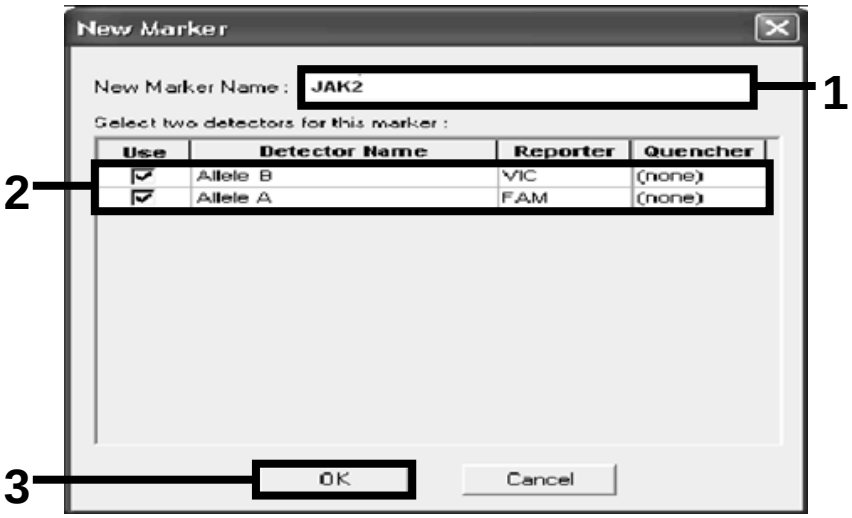


Figure 16. Creating markers.

20. **In the "Select Markers" dialog box, select "JAK2", as created above, or a suitable predefined marker, and then click "Add>>" (Figure 17).**

    Note: To remove a marker, select it and then click "Remove".

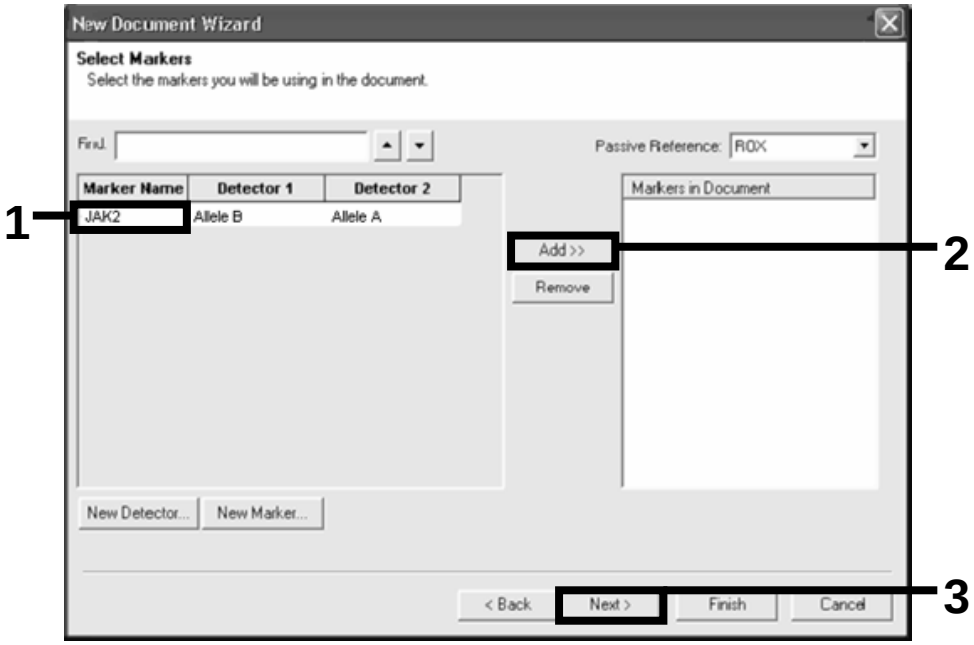


Figure 17. Selecting markers.

21. **Click "Next>".**
22. **In the "Setup Sample Plate" dialog box, click and drag to select the marker for wells that contain samples. Click "Finish".**
23. **Select the "Instrument" tab, and change the sample volume to *25 µl*.**
24. **Select "File/Save" and then click "Save" to retain the name you assigned when you created the plate.**
25. **Load the reaction plate into the instrument according to the manufacturer's recommendations**

26. Start the post-read run. Click "Post-Read".

The instrument will perform a run of 1 cycle for 60 s at 60°C. During this run, the instrument collects FAM and VIC fluorescence in each well (Figure 18).

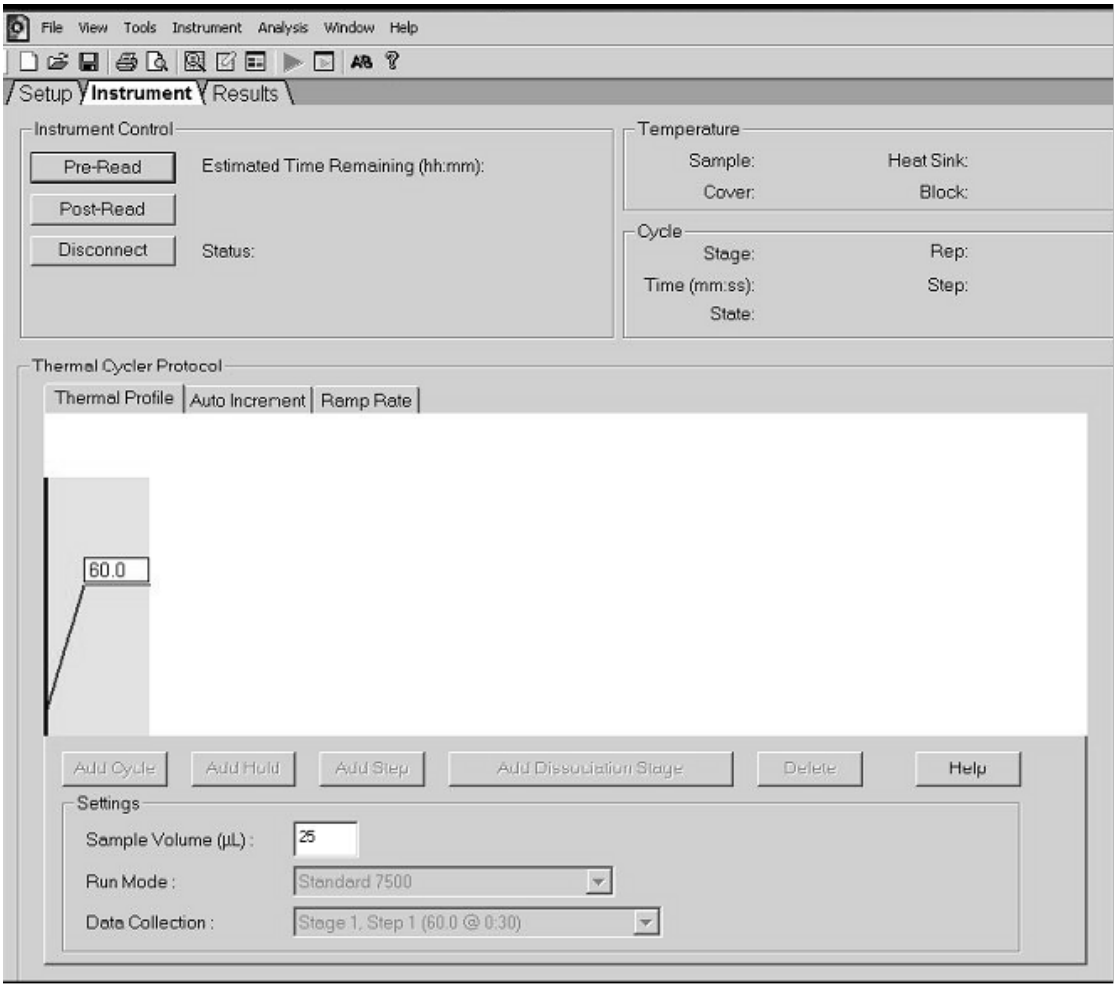
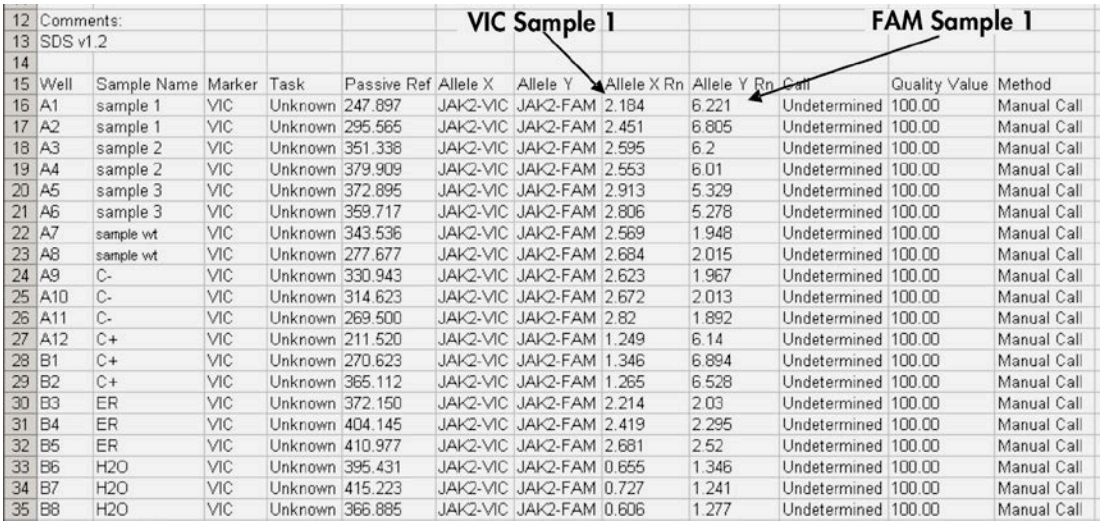


Figure 18. Post-read run.

27. **Select "File/Export" and then click "Results" to export the results to an Excel file. The results will appear as shown in Figure 19.**



12	Comments:										
13	SDS v1.2										
14											
15	Well	Sample Name	Marker	Task	Passive Ref	Allele X	Allele Y	Allele X Rn	Allele Y Rn	Call	Quality Value	Method
16	A1	sample 1	VIC	Unknown	247.897	JAK2-VIC	JAK2-FAM	2.184	6.221	Undetermined	100.00	Manual Call
17	A2	sample 1	VIC	Unknown	295.565	JAK2-VIC	JAK2-FAM	2.451	6.805	Undetermined	100.00	Manual Call
18	A3	sample 2	VIC	Unknown	351.338	JAK2-VIC	JAK2-FAM	2.595	6.2	Undetermined	100.00	Manual Call
19	A4	sample 2	VIC	Unknown	379.909	JAK2-VIC	JAK2-FAM	2.553	6.01	Undetermined	100.00	Manual Call
20	A5	sample 3	VIC	Unknown	372.895	JAK2-VIC	JAK2-FAM	2.913	5.329	Undetermined	100.00	Manual Call
21	A6	sample 3	VIC	Unknown	359.717	JAK2-VIC	JAK2-FAM	2.806	5.278	Undetermined	100.00	Manual Call
22	A7	sample wt	VIC	Unknown	343.536	JAK2-VIC	JAK2-FAM	2.569	1.948	Undetermined	100.00	Manual Call
23	A8	sample wt	VIC	Unknown	277.677	JAK2-VIC	JAK2-FAM	2.684	2.015	Undetermined	100.00	Manual Call
24	A9	C-	VIC	Unknown	330.943	JAK2-VIC	JAK2-FAM	2.623	1.967	Undetermined	100.00	Manual Call
25	A10	C-	VIC	Unknown	314.623	JAK2-VIC	JAK2-FAM	2.672	2.013	Undetermined	100.00	Manual Call
26	A11	C-	VIC	Unknown	269.500	JAK2-VIC	JAK2-FAM	2.82	1.892	Undetermined	100.00	Manual Call
27	A12	C+	VIC	Unknown	211.520	JAK2-VIC	JAK2-FAM	1.249	6.14	Undetermined	100.00	Manual Call
28	B1	C+	VIC	Unknown	270.623	JAK2-VIC	JAK2-FAM	1.346	6.894	Undetermined	100.00	Manual Call
29	B2	C+	VIC	Unknown	365.112	JAK2-VIC	JAK2-FAM	1.265	6.528	Undetermined	100.00	Manual Call
30	B3	ER	VIC	Unknown	372.150	JAK2-VIC	JAK2-FAM	2.214	2.03	Undetermined	100.00	Manual Call
31	B4	ER	VIC	Unknown	404.145	JAK2-VIC	JAK2-FAM	2.419	2.295	Undetermined	100.00	Manual Call
32	B5	ER	VIC	Unknown	410.977	JAK2-VIC	JAK2-FAM	2.681	2.52	Undetermined	100.00	Manual Call
33	B6	H2O	VIC	Unknown	395.431	JAK2-VIC	JAK2-FAM	0.655	1.346	Undetermined	100.00	Manual Call
34	B7	H2O	VIC	Unknown	415.223	JAK2-VIC	JAK2-FAM	0.727	1.241	Undetermined	100.00	Manual Call
35	B8	H2O	VIC	Unknown	366.885	JAK2-VIC	JAK2-FAM	0.606	1.277	Undetermined	100.00	Manual Call

Figure 19. Example of results, shown in an Excel file.

Protocol: qPCR on the LightCycler 480 instrument

Using 96-well plate qPCR equipment, we recommend performing all measurements in duplicate as indicated in Table 8.

Table 8. Number of reactions for the LightCycler 480 instrument

Samples	Reactions
With the JAK2 V617F primers and probes mix (PPM-JAK2)	
24 DNA samples	24 x 2 reactions
3 DNA controls	3 x 2 reactions (PC-VF, NC-VF, and COS-VF, each one tested in duplicate)
Water control	2 reactions

Sample processing on the LightCycler 480 instrument

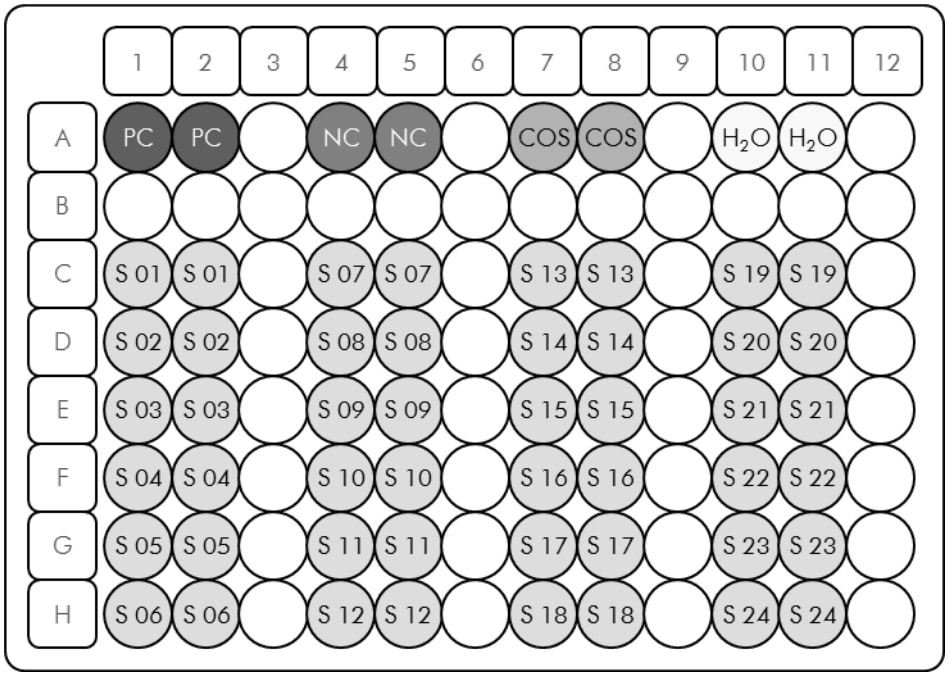


Figure 20. Suggested plate setup for an experiment with the *ipsogen* JAK2 *MutaScreen* Kit. PC: positive control; **NC**: negative control; **COS**: cut-off sample; **S**: DNA sample; **H_2O**: water control.

qPCR on the LightCycler 480 instrument

Note: Perform all steps on ice.

Procedure

1. **Thaw all necessary components and place them on ice.**

   Components should be taken out of the freezer approximately 10 min before starting the procedure.

2. **Vortex and briefly centrifuge all the tubes (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**

3. **Prepare the following qPCR mix according to the number of samples being processed.**

   All concentrations are for the final volume of the reaction.

   Table 9 describes the pipetting scheme for the preparation of one reagent mix, calculated to achieve a final reaction volume of 25 µl. A pre-mix can be prepared, according to the number of reactions, using the same primer and probe mix. Extra volumes are included to compensate for pipetting error.

   On the LightCycler 480 instrument, the *ipsogen* JAK2 Muta*Screen* Kit can be used for analysis of 24 samples in duplicate in one experiment (Figure 20), 20 samples in duplicate in two experiments, or 15 samples in duplicate in three experiments.

Table 9. Preparation of qPCR mix

Component	Number of reactions (µl) 1	56+1*	28+1†	18+1‡	Final concentration
TaqMan Universal PCR Master Mix, 2x	12.5	712.5	362.5	237.5	1x
Primers and probes mix, 10x	2.5	142.5	72.5	47.5	1x
Nuclease-free PCR grade water	5	285	145	95	–
Sample (to be added at step 6)	5	5 each	5 each	5 each	–
Total volume	25	25 each	25 each	25 each	–

* 24 samples; one experiment/kit.

† 10 samples; two experiments/kit.

‡ 5 samples; three experiments/kit.

4. **Vortex and briefly centrifuge the qPCR mix (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**
5. **Dispense 20 µl of the qPCR pre-mix per well.**
6. **Add 5 µl of the sample DNA material or controls in the corresponding well (total volume 25 µl).**
7. **Mix gently, by pipetting up and down.**
8. **Close the plate and briefly centrifuge (300 x *g*, approximately 10 s).**
9. **Place the plate in the thermal cycler according to the manufacturer's recommendations.**
10. **On the home page, select "New Experiment".**

11. For the LightCycler 480 I, follow step 11a. For the LightCycler 480 II, follow step 11b.

For programming details of the LightCycler 480 instrument, refer to the instrument user guide. For a better overview, the software settings are framed in bold black.

11a. LightCycler 480 I: Select "Multi Color Hydrolysis Probe", click "Customize", and then check that the channels "FAM (483–533)" and "Hex (533–568)" (i.e., VIC) are selected (Figure 21). Set the reaction volume to "25" µl (Figure 21) and proceed with step 12.

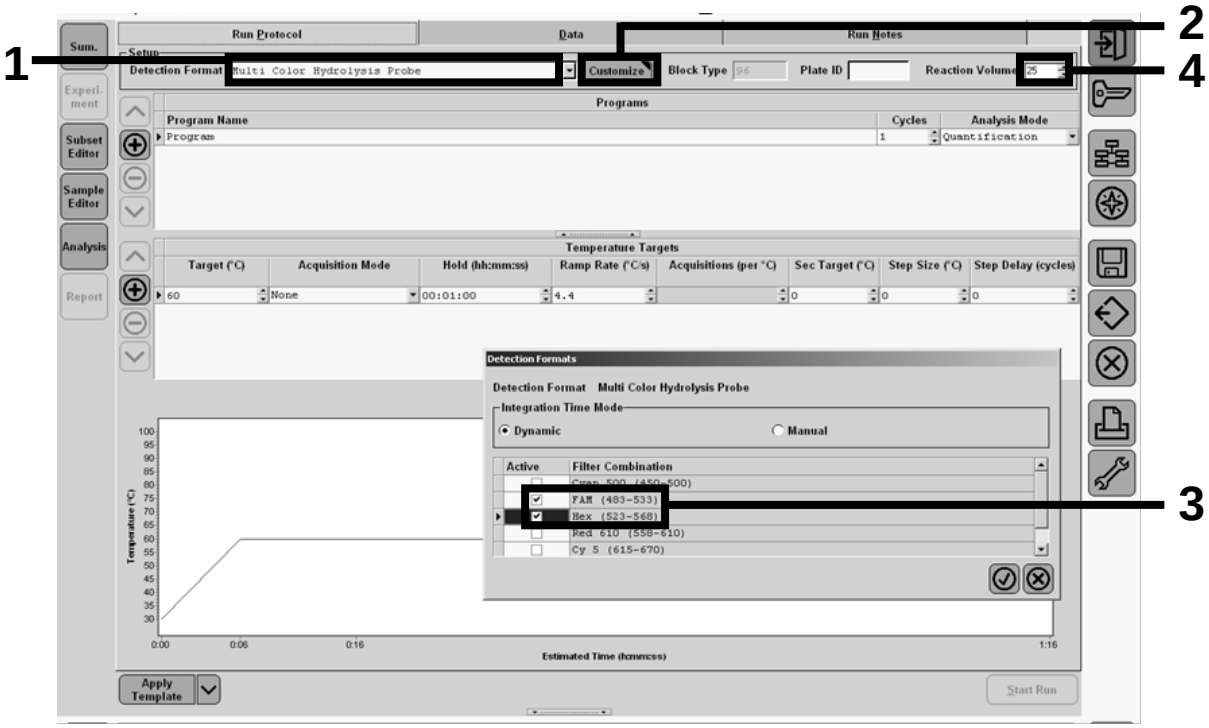


Figure 21. LightCycler 480 I: Setting the detection format.

11b. LightCycler 480 II: Select "Dual Color Hydrolysis Probe", click "Customize", and then check that the channels "FAM (465–510)" and "VIC / HEX / (533–580)" are selected (Figure 22). Set the reaction volume to "25" µl (Figure 22) and proceed with step 12.

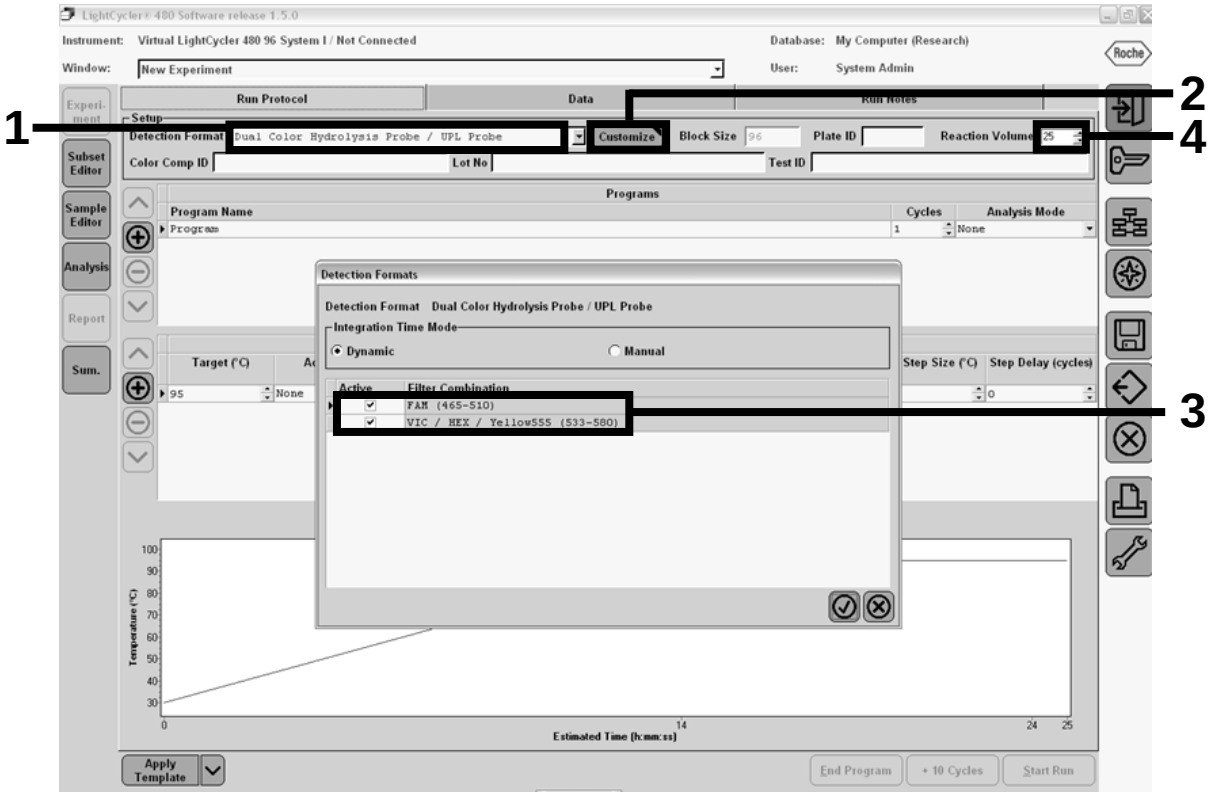


Figure 22. LightCycler 480 II: Setting the detection format.

12. **Program the thermal cycler with the thermal cycling program as indicated in Table 10, and start the run.**

    Note: When describing the plate setup on the instrument, select "Endpt Geno" in the "Step 1 : select workflow" section.

Table 10. Temperature profile for the LightCycler 480 instrument

Hold	Temperature: 50°C Time: 2 min
Hold 2	Temperature: 95°C Time: 10 min
Cycling	50 times 92°C for 15 s; single 60°C for 1 min; single
Hold 3	60°C for 1 min; single

End-point analysis procedure for the LightCycler 480 instrument

13. **After the run is finished, click "Analysis".**
14. **In the "Create New Analysis" dialog box, select "Endpoint Genotyping", and then select the subset to analyze in the "Subset" menu (Figure 23).**

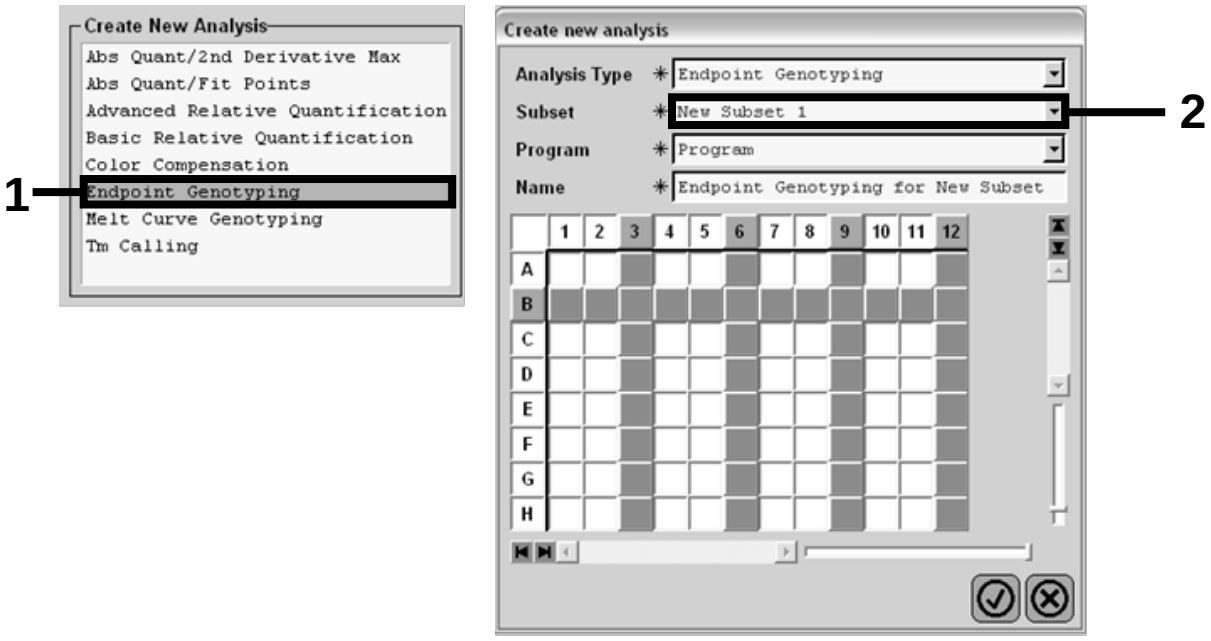


Figure 23. Selecting analysis type and subset to analyze.

15. In the next window, select “Hex” (i.e., VIC) fluorescence for “Allele X” and “FAM” fluorescence for “Allele Y” (Figure 24).

Figure 24. Selecting fluorescence for “Allele X” and “Allele Y”.

16. The next window (Figure 25) shows plate setup (1, upper left), fluorescence results for each sample (2, bottom left), and the scatter plot with allelic discrimination (3, right; FAM and VIC fluorescence measured at the 50th PCR cycle).

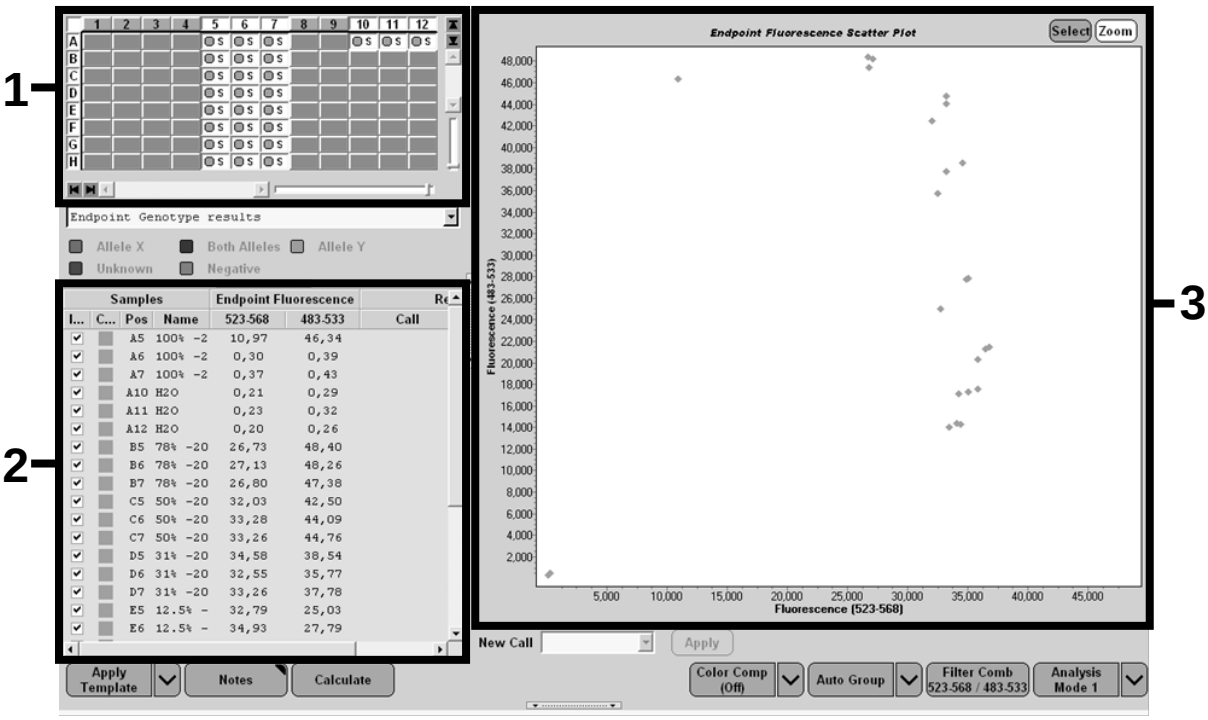
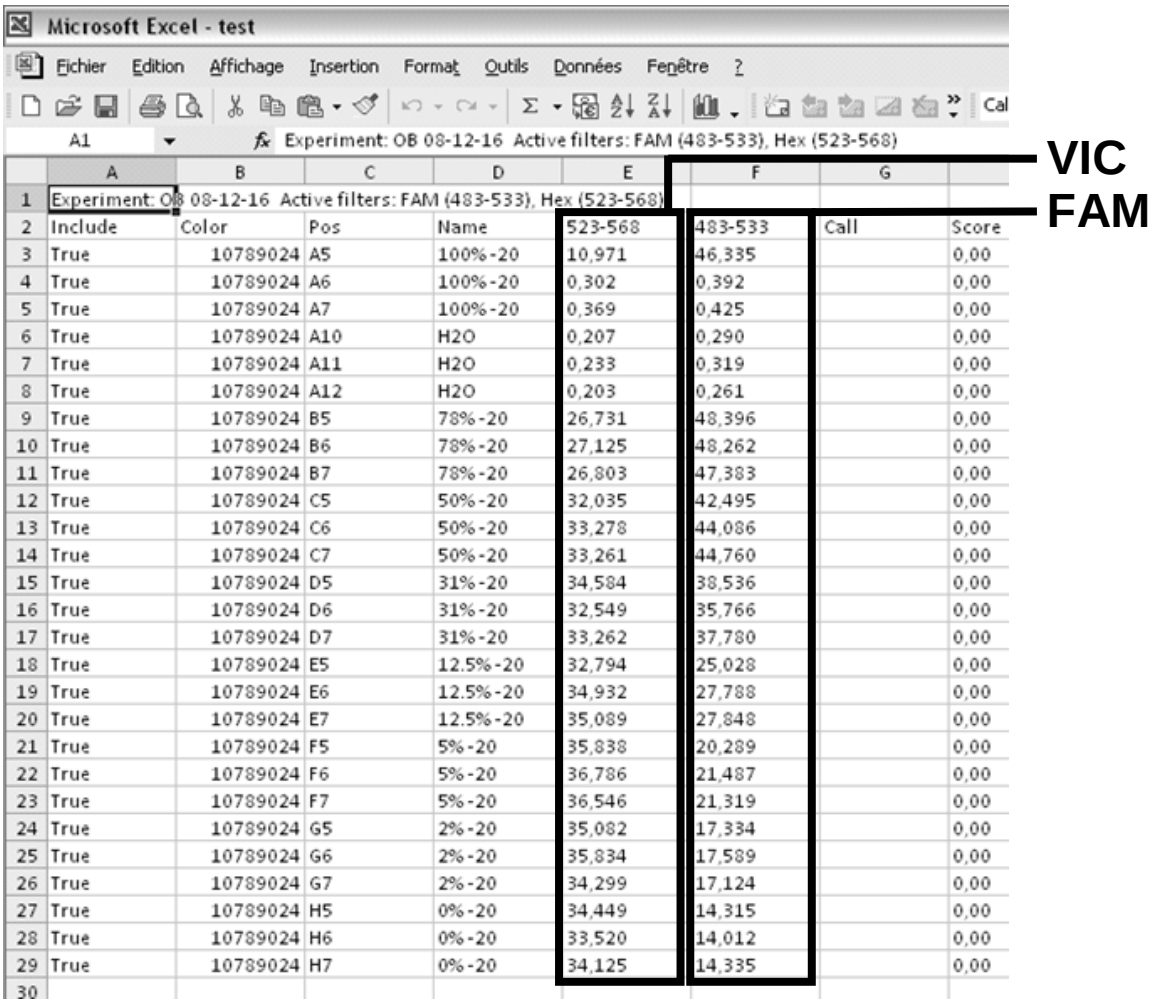


Figure 25. Data summary.

17. To export data, right-click on the sample results template, and then select “Export Table”. The file will be saved in a text (.txt) file format.

18. **To view and analyze results, open the file using Excel. The results will appear as shown in Figure 26.**



	A	B	C	D	E	F	G	
1	Experiment: OB 08-12-16 Active filters: FAM (483-533), Hex (523-568)							
2	Include	Color	Pos	Name	523-568	483-533	Call	Score
3	True	10789024	A5	100%-20	10,971	46,335		0,00
4	True	10789024	A6	100%-20	0,302	0,392		0,00
5	True	10789024	A7	100%-20	0,369	0,425		0,00
6	True	10789024	A10	H2O	0,207	0,290		0,00
7	True	10789024	A11	H2O	0,233	0,319		0,00
8	True	10789024	A12	H2O	0,203	0,261		0,00
9	True	10789024	B5	78%-20	26,731	48,396		0,00
10	True	10789024	B6	78%-20	27,125	48,262		0,00
11	True	10789024	B7	78%-20	26,803	47,383		0,00
12	True	10789024	C5	50%-20	32,035	42,495		0,00
13	True	10789024	C6	50%-20	33,278	44,086		0,00
14	True	10789024	C7	50%-20	33,261	44,760		0,00
15	True	10789024	D5	31%-20	34,584	38,536		0,00
16	True	10789024	D6	31%-20	32,549	35,766		0,00
17	True	10789024	D7	31%-20	33,262	37,780		0,00
18	True	10789024	E5	12.5%-20	32,794	25,028		0,00
19	True	10789024	E6	12.5%-20	34,932	27,788		0,00
20	True	10789024	E7	12.5%-20	35,089	27,848		0,00
21	True	10789024	F5	5%-20	35,838	20,289		0,00
22	True	10789024	F6	5%-20	36,786	21,487		0,00
23	True	10789024	F7	5%-20	36,546	21,319		0,00
24	True	10789024	G5	2%-20	35,082	17,334		0,00
25	True	10789024	G6	2%-20	35,834	17,589		0,00
26	True	10789024	G7	2%-20	34,299	17,124		0,00
27	True	10789024	H5	0%-20	34,449	14,315		0,00
28	True	10789024	H6	0%-20	33,520	14,012		0,00
29	True	10789024	H7	0%-20	34,125	14,335		0,00
30								

Figure 26. Example of results, shown in an Excel file.

Protocol: qPCR on LightCycler 2.0 instrument

Note: Because of particular technological requirements, LightCycler 2.0 experiments must be performed using specific reagents. We recommend the use of the LightCycler TaqMan Master. Follow the manufacturer's instructions to prepare the Master Mix 5x.

Using a 32-capillary rotor, we recommend performing all measurements in duplicate as indicated in Table 11.

Table 11. Number of reactions for LightCycler 2.0 instrument

Samples	Reactions
JAK2 V617F primers and probes mix (PPM-VF) (32 reactions)	
12 DNA samples	12 x 2 reactions
3 DNA controls	3 x 2 reactions (PC-VF, NC-VF, and COS-VF, each one tested in duplicate)
Water control	2 reactions

Sample processing on LightCycler 2.0 instrument

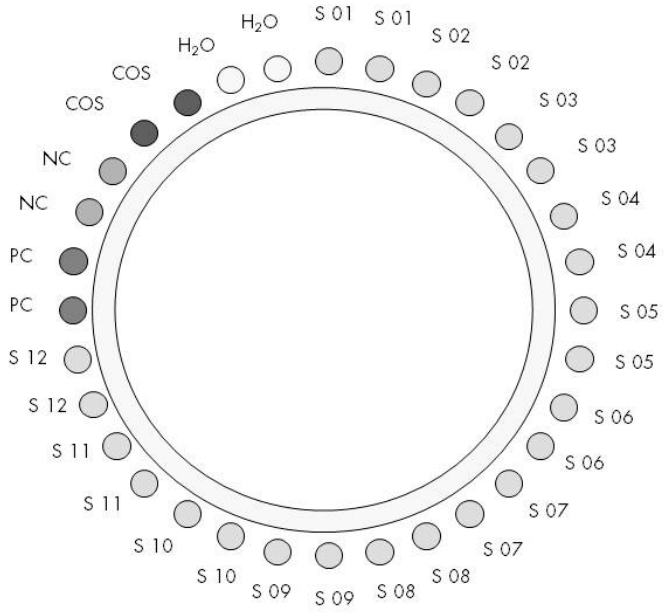


Figure 27. Suggested rotor setup for an experiment with the *ipsogen* JAK2 *MutaScreen* Kit. PC: positive control; **NC**: negative control; **COS**: cut-off sample; **S**: DNA sample; **H_2O**: water control.

qPCR on LightCycler 2.0 instrument

Note: Perform all steps on ice.

Procedure

1. **Thaw all necessary components and place them on ice.**
   Components should be taken out of the freezer approximately 10 min before starting the procedure.
2. **Vortex and briefly centrifuge all the tubes (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**
3. **Prepare the following qPCR mix according to the number of samples being processed.**
   All concentrations are for the final volume of the reaction.

   Table 12 describes the pipetting scheme for the preparation of one reagent mix, calculated to achieve a final reaction volume of 20 µl. A pre-mix can be prepared, according to the number of reactions, using the same primer and probe mix. Extra volumes are included to compensate for pipetting error.

   On the LightCycler 2.0 instrument, the *ipsogen* JAK2 Muta*Screen* Kit can be used for analysis of 12 samples in duplicate in one experiment (Figure 27).

Table 12. Preparation of qPCR mix for LightCycler 2.0 instrument

	Number of reactions (µl)		
Component	**1**	**32+1**	**Final concentration**
LightCycler TaqMan Master Mix, 5x	4	132	1x
Primers and probes mix, 10x	2	66	1x
Nuclease-free PCR grade water	9	297	–
Sample (to be added at step 4)	5	5 each	–
Total volume	20	20 each	–

4. **Vortex and briefly centrifuge the qPCR mix (approximately 10 s, 10,000 rpm, to collect the liquid in the bottom of the tube).**
5. **Dispense 15 µl of the qPCR pre-mix per capillary.**
6. **Add 5 µl of the sample DNA material or controls in the corresponding capillary (total volume 20 µl).**
7. **Mix gently, by pipetting up and down.**
8. **Place the capillaries in the adapter provided with the instrument and briefly centrifuge (700 x *g*, approximately 10 s).**
9. **Load the samples in the thermal cycler according to the manufacturer's recommendations.**
10. **Program the thermal cycler (Figure 28) with the program as indicated in Table 13.**

    For programming details of the LightCycler 2.0 instrument, refer to the instrument user guide. For a better overview, the software settings are framed in bold black.

    Note: Make sure that the setting is for Quantification and single acquisition of FAM fluorescence and single acquisition of VIC fluorescence in both the amplification/cycling step and the final hold at 60°C.

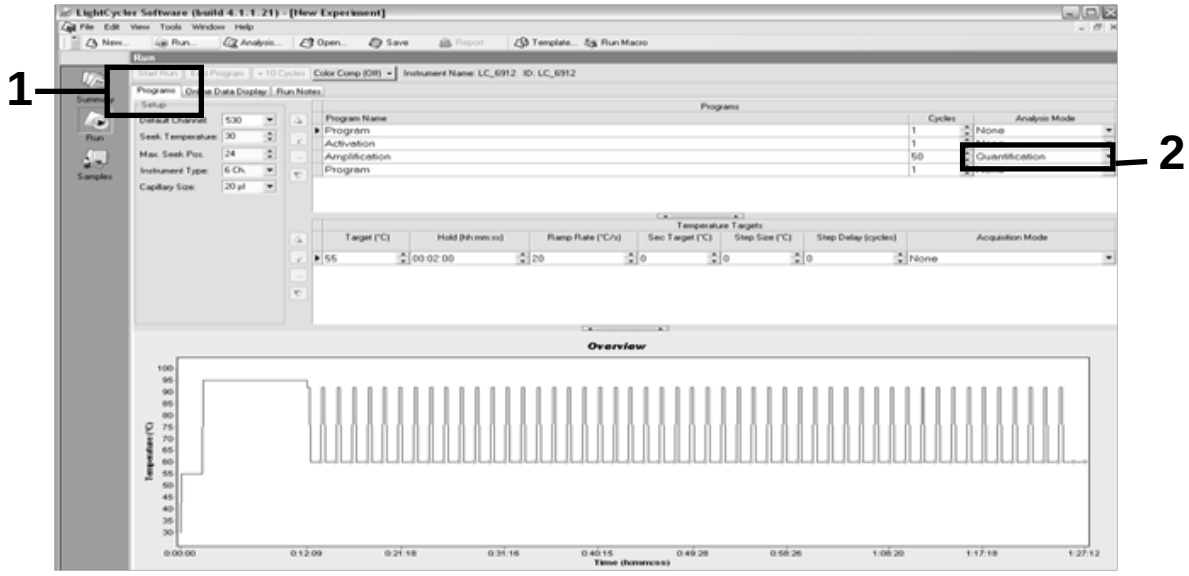


Figure 28. Programming screen for LightCycler 2.0.

Table 13. Temperature profile for LightCycler 2.0 instrument

Hold	Temperature: 55°C Time: 2 min Ramp: 20
Hold 2	Temperature: 95°C Time: 10 min Ramp: 20
Cycling	50 times 92°C for 15 s; ramp: 20 60°C for 1 min; ramp 20
Hold 3	60°C for 1 min; ramp 20

End-point analysis procedure for LightCycler 2.0 instrument

11. At the end of the amplification run, click the tab for "Online Data Display" (Figure 29). Open the display menu on the top left of the "Current Fluorescence" window, then write *51* in "Acquisition no." .

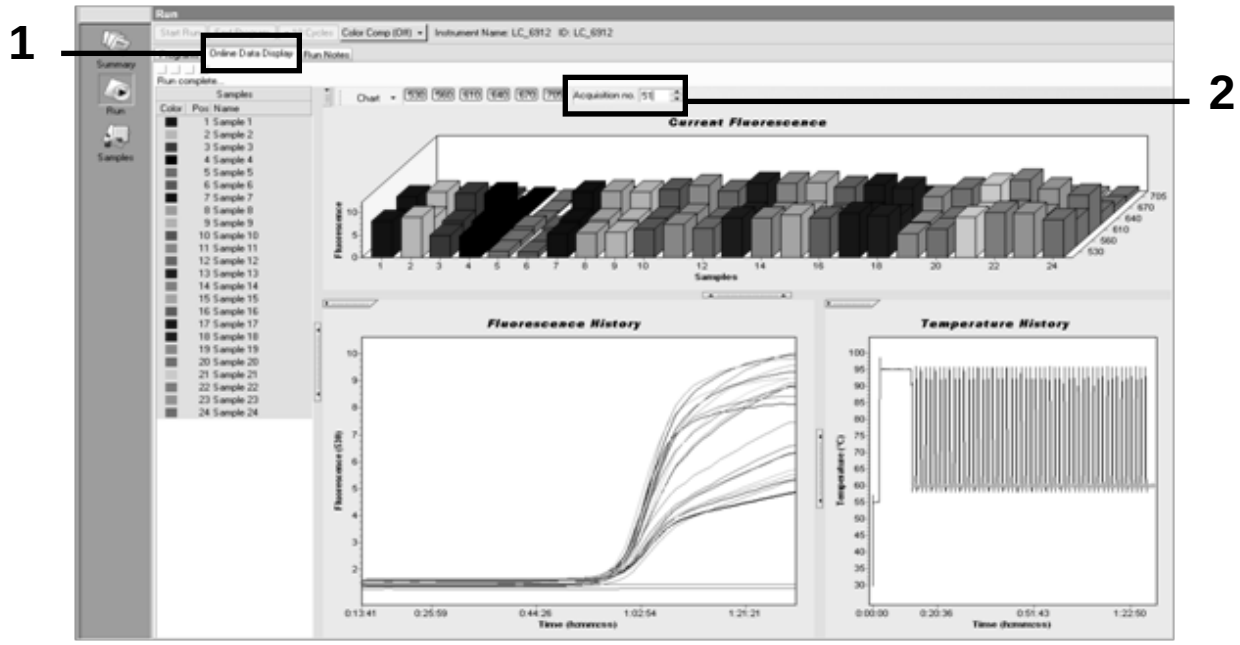


Figure 29. Results and history in Online Data Display.

12. Right-click near the "Current Fluorescence" graph and select "Export".

13. **Click the "Excel" box on the "Export chart" dialog box (Figure 30). Enter a name in the "Filename" dialog field. Select an export destination for the result file with the ... button. Click "Export".**

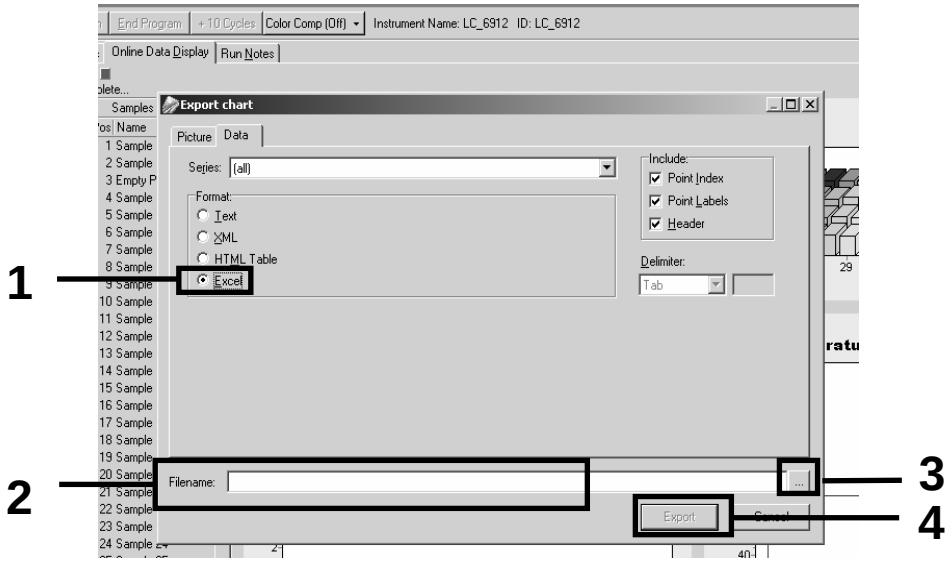


Figure 30. Selecting the export format and data file destination.

14. **To view and analyze results, open the file in Excel. The results for LightCycler 2.0 will appear as shown.**

Position

I	J	K	L	M	N	O	P	Q	R	S	T	U
X	Bar	Text	X	Bar	Text	X	Bar	Text	X	Bar		
1	2,9709	1: Sample 1 (610)	1	8,2734	1: Sample 1 (560)	1	6,6361	1: Sample 1 (530)	1	4,9943		
2	3,0182	2: Sample 2 (610)	2	8,4428	2: Sample 2 (560)	2	6,7659	2: Sample 2 (530)	2	5,0767		
3	2,9496	3: Sample 3 (610)			3: Sample 3 (560)	3	6,5568	3: Sample 3 (530)	3	4,9699		
4	2,9526	4: Sample 4 (610)	4	8,2887	4: Sample 4 (560)	4	6,6163	4: Sample 4 (530)	4	4,9119		
5	2,9450	5: Sample 5 (610)	5	8,2689	5: Sample 5 (560)	5	6,6209	5: Sample 5 (530)	5	4,9638		
6	2,9969	6: Sample 6 (610)	6	8,4184	6: Sample 6 (560)	6	6,7674	6: Sample 6 (530)	6	5,1209		
7	3,0045	7: Sample 7 (610)	7	8,4520	7: Sample 7 (560)	7	6,7506	7: Sample 7 (530)	7	5,0507		
8	3,2822	8: Sample 8 (610)	8	9,1936	8: Sample 8 (560)	8	7,3960	8: Sample 8 (530)	8	5,5314		
9	3,0274	9: Sample 9 (610)	9	8,5557	9: Sample 9 (560)	9	6,8437	9: Sample 9 (530)	9	5,0843		
10	2,8336	10: Sample 10 (610)	10	7,9713	10: Sample 10 (560)	10	6,3905	10: Sample 10 (530)	10	4,7883		
11	2,8275	11: Sample 11 (610)	11	7,9774	11: Sample 11 (560)	11	6,3874	11: Sample 11 (530)	11	4,7669		
12	2,8351	12: Sample 12 (610)	12	8,0171	12: Sample 12 (560)	12	6,4118	12: Sample 12 (530)	12	4,7944		
13	2,9511	13: Sample 13 (610)	13	8,3726	13: Sample 13 (560)	13	6,6957	13: Sample 13 (530)	13	4,9699		
14	2,8367	14: Sample 14 (610)	14	8,0217	14: Sample 14 (560)	14	6,4439	14: Sample 14 (530)	14	4,7654		
15	2,9908	15: Sample 15 (610)	15	8,4337	15: Sample 15 (560)	15	6,7445	15: Sample 15 (530)	15	5,0523		
16	2,8885	16: Sample 16 (610)	16	8,1498	16: Sample 16 (560)	16	6,5568	16: Sample 16 (530)	16	4,9577		
17	3,0152	17: Sample 17 (610)	17	8,4901	17: Sample 17 (560)	17	6,8193	17: Sample 17 (530)	17	5,1225		
							VIC			FAM		

Figure 31. Example of LightCycler 2.0 results, shown in an Excel file.

Interpretation of Results

Obtain a file suitable to extract exported data for all instruments: Rotor-Gene Q MDx 5plex HRM or other Rotor-Gene instrument, LightCycler 2.0, or 480; Applied Biosystems 7300 or 7500 Real-Time PCR System, ABI PRISM 7000 SDS, 7700 SDS, or 7900HT SDS, and check the fluorescence levels (these must be consistent between duplicates).

Prepare a graphical representation (scatter plot) of fluorescence data. The x axis is VIC fluorescence; the y axis is FAM fluorescence.

Graphical representation and quality control criteria

An example of a scatter plot is shown in Figure 32.

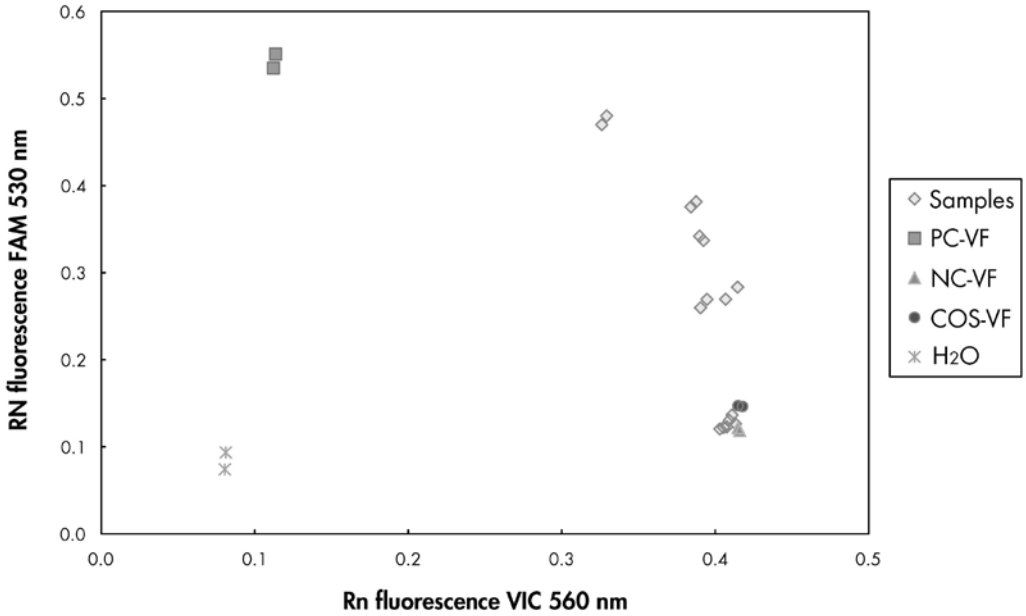


Figure 32. Scatter plot of a representative allelic discrimination experiment.
Instruments: Rotor-Gene Q, Applied Biosystems, ABI PRISM, and LightCycler 480.

Samples should be located on the arc connecting the negative controls (NC) to the positive controls (PC).

Improper positioning of any control may indicate an experimental error.

- Positive controls should be located in the upper left.
- Negative controls should be located in the bottom right.
  - Poor positioning of a negative control may indicate contamination.
- The cut-off sample should appear above the negative controls.

- Water controls should be located at the bottom left.
  - Poor positioning of a water control (higher than NC for FAM measurement or higher than PC for VIC) may indicate contamination.

Note: Positioning of the controls may be different on analysis of LightCycler 2.0 instrument data (see Figure 33). The water controls should still be located at the bottom left.

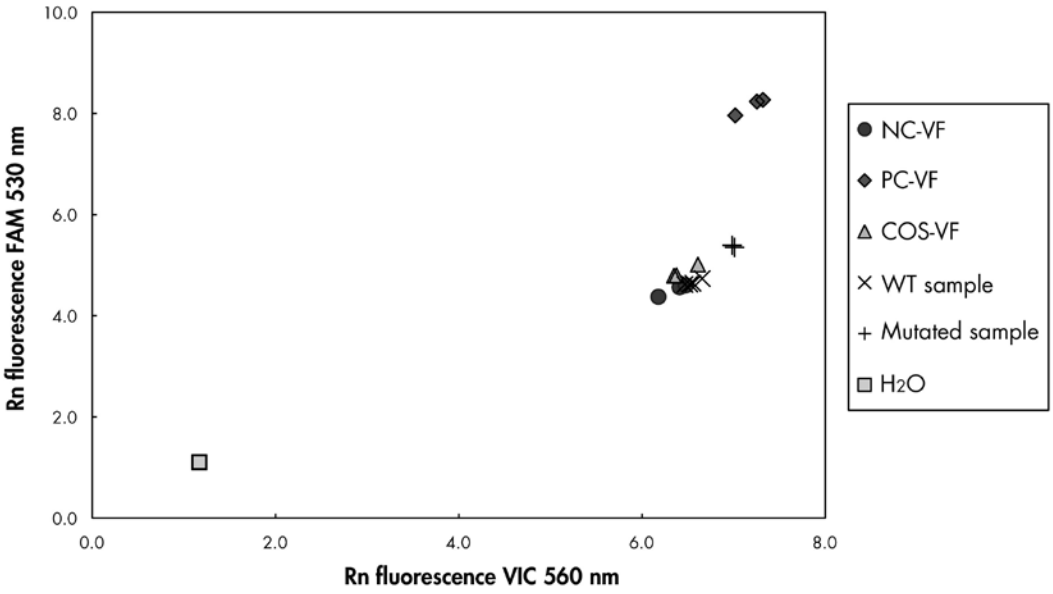


Figure 33. Scatter plot of a representative allelic discrimination experiment. Instrument: LightCycler 2.0.

Calculation of normalized FAM/VIC ratio and genotyping

Calculate the FAM/VIC ratios for all the samples. Calculate the FAM/VIC ratios for the positive control (PC), the cut-off sample (COS), and the negative control (NC). The ratios must be consistent between duplicates. Calculate the average ratio of all duplicates.

Calculate the normalized ratio (NRatio) for the cut-off sample (COS) and for all the samples:

$$NRatio_{Sample} = \frac{Ratio_{Sample}}{Ratio_{NC}}$$

Note: The gray zone (GZ) of a test is defined as an area of values where the discriminatory performance is insufficiently accurate. A value in the gray zone indicates that the target marker cannot be scored as either present or absent. The gray zone must be calculated for each experiment.

Calculate the gray zone, or the incertitude area, around the normalized ratio of the COS ($NRatio_{COS}$):

GZ: [($NRatio_{COS}$ x 0.94); ($NRatio_{COS}$ x1.06)]

Compare the normalized ratio of each sample to the $NRatio_{COS}$ GZ. Interpretation of results is outlined in Table 14 and an example of data calculation and interpretation is given in Table 15.

Table 14. Interpretation of genotyping results using normalized ratios

Results	Interpretation
$NRatio_{Sample} > NRatio_{COS}$ x 1.06	JAK2 V617F is detected
$NRatio_{Sample} < NRatio_{COS}$ x 0.94	JAK2 V617F is not detected
$NRatio_{Sample}$ within $NRatio_{COS}$ GZ	Result inconclusive

Table 15. An example of fluorescence data calculation and interpretation

Sample	VIC	FAM	Ratio	Mean ratio	NRatio	Interpretation
NC	2.415	1.782	0.738	0.747	1.000	Mutation not detected
NC	2.46	1.861	0.757			
PC	1.241	5.606	4.517	4.672	6.253	Mutation detected
PC	1.182	5.706	4.827			
COS	1.91	1.832	0.959	0.958	1.282	Cut-off sample
COS	2.035	1.946	0.956			
S 1	2.311	1.783	0.772	0.742	0.992	Mutation not detected
S 1	2.555	1.818	0.712			
S 2	1.097	5.745	5.237	4.276	5.723	Mutation detected
S 2	1.437	4.764	3.315			
S 3	2.265	2.149	0.949	0.927	1.241	Inconclusive result
S 3	2.435	2.206	0.906			
S 4	2.385	2.063	0.865	0.904	1.210	Inconclusive result
S 4	2.322	2.191	0.944			
GZ	**1.205**	**1.359**				

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**. The scientists in QIAGEN Technical Services are always happy to answer any questions you may have about either the information and protocols in this handbook or sample and assay technologies (for contact information, see "Contact Information", page 56).

	Comments and suggestions
Positive control signal negative	
a) Pipetting error	Check pipetting scheme and the setup of the reaction. Repeat the PCR run.
b) Inappropriate storage of kit components	Store the *ipsogen* JAK2 Muta*Screen* Kit at –30 to –15°C and keep primers and probes mix (PPM) protected from light. See "Reagent Storage and Handling", page 10. Avoid repeated freezing and thawing. Aliquot reagents for storage.
Negative controls are positive	
Cross-contamination	Replace all critical reagents. Repeat the experiment with new aliquots of all reagents. Always handle samples, kit components, and consumables in accordance with commonly accepted practices to prevent carry-over contamination.
No signal, even in positive controls	
a) Pipetting error or omitted reagents	Check pipetting scheme and the setup of the reaction. Repeat the PCR run.
b) Inhibitory effects of the sample material, caused by insufficient purification	Repeat the DNA preparation.

	Comments and suggestions
c) LightCycler: Incorrect detection channel chosen	Set Channel Setting to F1/F2 or 530 nm/640 nm.
d) LightCycler: No data acquisition programmed	Check the cycle programs. Select acquisition mode "single" at the end of each annealing segment of the PCR program.
Absent or low signal in samples but positive controls okay	
Poor DNA quality or low concentration	Always check the DNA quality and concentration before starting.
LightCycler: Fluorescence intensity too low	
a) Inappropriate storage of kit components	Store the *ipsogen* JAK2 Muta*Screen* Kit at –30 to –15°C and keep primers and probes mix (PPM) protected from light. See "Reagent Storage and Handling", page 10. Avoid repeated freezing and thawing. Aliquot reagents for storage.
b) Very low initial amount of target DNA	Increase the amount of sample DNA. **Note**: Depending of the chosen method of DNA preparation, inhibitory effects may occur.
LightCycler: Fluorescence intensity varies	
a) Pipetting error	Variability caused by so-called "pipetting error" can be reduced by analyzing data in the F1/F2 or 530 nm/640 nm mode.
b) Insufficient centrifugation of the capillaries	The prepared PCR mix may still be in the upper vessel of the capillary, or an air bubble could be trapped in the capillary tip. Always centrifuge capillaries loaded with the reaction mix as described in the specific operating manual of the apparatus.
c) Outer surface of the capillary tip dirty	Always wear gloves when handling the capillaries.

Quality Control

In accordance with QIAGEN's ISO-certified Quality Management System, each lot of *ipsogen* JAK2 Muta*Screen* Kit is tested against predetermined specifications to ensure consistent product quality Certificates of Analysis are available upon request at **www.qiagen.com/support/**.

Limitations

The users must be trained and familiar with this technology prior to the use of this device. This kit should be used following the instructions given in this manual, in combination with a validated instrument mentioned in "Materials Required but Not Provided", page 8.

Any diagnostic results that are generated must be interpreted in conjunction with other clinical or laboratory findings. It is the user's responsibility to validate system performance for any procedures used in their laboratory which are not covered by the QIAGEN performance studies.

Attention should be paid to expiration dates printed on the box and labels of all components. Do not use expired components.

Performance Characteristics

Nonclinical studies

Nonclinical studies were conducted to establish the analytical performance of the *ipsogen* JAK2 Muta*Screen* Kit.

Precision

Three dilution levels of genomic DNA from cell lines harboring the JAK2 V617F mutation in wild type DNA were tested with the *ipsogen* JAK2 Muta*Screen* Kit. The dilutions corresponded to mutation loads of 1%, 2%, and 3%. Independent dilution batches were obtained for each level, and replicates of these dilutions were tested in 3 independent experiments. Ratios obtained for each DNA sample ($Ratio_{Sample}$) were compared with the negative control ratio (JAK2 100% wild type DNA, $Ratio_{NC}$). Results are summarized in Table 16.

Table 16. Precision data for nonclinical studies

Mutation level	$Ratio_{Sample} > Ratio_{NC}$	%CV (ratio)
1% V617F DNA	100% (n = 183)	6.8
2% V617F DNA	100% (n = 72)	4.5
3% V617F DNA	100% (n = 135)	5.1

Interlaboratory analytical data

A multi-center study was performed involving 13 laboratories. Analytical data were collected on dilutions of genomic DNA harboring JAK2 V617F mutation in wild type DNA. Three experiments were performed in each laboratory. For each experiment, the following DNA samples were tested from cell lines:

- 1 negative control (NC) 0% V617F
- 1 positive control (PC) 100% V617F
- 1 cut-off sample (COS) 2% V617F
- 3 samples harboring intermediate mutation loads (20%, 50%, and 80%)

The experiments were performed on seven different instrument models:

- ABI PRISM 7000 SDS
- Applied Biosystems 7300 Real-Time PCR System
- Applied Biosystems 7500 Real-Time PCR System
- ABI PRISM 7700 SDS
- ABI PRISM 7900 SDS
- LightCycler 2.0
- iCycler®

Results are summarized in Table 17.

Table 17. Interlaboratory analytical data obtained from dilutions of genomic DNA from cell lines harboring the JAK2 V617F mutation in wild type DNA

Sample detection	Positive samples	Negative samples
JAK2 V617F	177*	0
JAK2 wild type	0	36

* Positive samples included 36 positive controls (PC-VF), 36 cut-off samples (COS-VF; 2% V617F), 34 samples harboring 20% JAK2 V617F, 35 samples harboring 50% JAK2 V617F, and 36 samples harboring 80% JAK2 V617F.

Clinical studies

Comparison between *ipsogen* JAK2 Muta*Screen* Kit and ARMS® method

DNA samples from 141 patients with suspected MPN were tested in parallel with the *ipsogen* JAK2 Muta*Screen* Kit and a qPCR assay based on the amplification refractory mutation system (ARMS) principle (11). Results of the comparison are shown in Table 18 (2 x 3 contingency table) and Table 19 (percentage agreement).

Table 18. Comparison between methods: *ipsogen* JAK2 Muta*Screen* Kit and ARMS

		Results of ARMS testing method		
		JAK2 V617F >2%	**JAK2 wild type (JAK2 V617F <2%)**	**Total**
Results of *ipsogen* JAK2 Muta*Screen* testing method	**JAK2 V617F Mutation detected**	91	0	**91**
	Inconclusive result	1	2	**3**
	JAK2 WT Mutation not detected	1	46	**47**
Total		**93**	**48**	**n = 141**

Table 19. Comparison between methods: *ipsogen* JAK2 Muta*Screen* Kit and ARMS

	Agreement (%)	**95% CI* (%)**
Positive data Agreement between *ipsogen* JAK2 Muta*Screen* Kit and ARMS	**98.9**	94.1–99.8
Negative data Agreement between *ipsogen* JAK2 Muta*Screen* Kit and ARMS	**100**	92.3–100
Total agreement	**99.3**	**96.0–99.9**

* Confidence intervals were calculated according to CLSI EP12-A "User Protocol for Evaluation of Qualitative Test Performance; Approved Guideline".

Comparison between *ipsogen* JAK2 Muta*Screen* Kit and sequencing

DNA samples from 51 patients with suspected MPN were tested in parallel with the *ipsogen* JAK2 Muta*Screen* Kit and the reference technique ("gold standard"), direct sequencing. One sample could not be interpreted due to sequencing failure. Comparisons of results obtained from the 50 interpretable samples are summarized in Table 20 (2 x 3 contingency table) and Table 21 (percentage agreement).

Table 20. Comparison between methods: *ipsogen* JAK2 Muta*Screen* Kit and sequencing

		Results of direct sequencing		
		JAK2 V617F >2%	**JAK2 wild type (JAK2 V617F <2%)**	**Total**
Results of *ipsogen* JAK2 Muta*Screen* testing method	**JAK2 V617F Mutation detected**	26	1	**27**
	Inconclusive result	0	1	**1**
	JAK2 WT Mutation not detected	2	20	**22**
Total		**28**	**22**	**n = 50**

Table 21. Comparison between methods: *ipsogen* JAK2 Muta*Screen* Kit and sequencing

	Agreement (%)	**95% CI* (%)**
Positive data Agreement between *ipsogen* JAK2 Muta*Screen* Kit and sequencing	**92.9**	77.4–98.0
Negative data Agreement between *ipsogen* JAK2 Muta*Screen* Kit and sequencing	**95.2**	77.3–99.2
Total agreement	**93.9**	**83.5–97.9**

* Confidence intervals were calculated according to CLSI EP12-A "User Protocol for Evaluation of Qualitative Test Performance; Approved Guideline".

Multicenter study on 228 patient samples

DNA samples from patients were analyzed with home brew techniques in 13 laboratories contributing to an interlaboratory study. In each laboratory, 3 experiments were performed, using DNA from cell lines as described for the nonclinical precision data (see above), and with DNA from 10 patients available in the laboratory.

The 228 samples with a known JAK2 genotype were tested in parallel with the *ipsogen* JAK2 Muta*Screen* Kit and by home brew methods, including qualitative PCR, allele specific PCR, fluorescence energy resonance transfer (FRET), sequencing, allele specific oligonucleotide PCR, RFLP, and allelic discrimination. Results of the comparisons are shown in Table 22 (2 x 3 contingency table) and Table 23 (percentage agreement).

Table 22. Comparison between methods: *ipsogen* JAK2 Muta*Screen* Kit and home brew methods

		Results of home brew testing		
		Mutation detected JAK2 V617F	**Mutation not detected JAK2 wild type**	**Total**
Results of *ipsogen* JAK2 Muta*Screen* testing method	**JAK2 V617F Mutation detected**	139	3	**142**
	Inconclusive result	5	17	**22**
	JAK2 WT No mutation detected	3	61	**64**
Total		**147**	**81**	**n = 228**

Table 23. Comparison between methods: *ipsogen* JAK2 MutaScreen Kit and home brew methods

	Agreement (%)	95% CI* (%)
Positive data Agreement between *ipsogen* JAK2 MutaScreen Kit and home brew	**97.9**	94.0–99.3
Negative data Agreement between *ipsogen* JAK2 MutaScreen Kit and home brew	**95.3**	87.1–98.4
Total agreement	**97.1**	**93.8–98.7**

* Confidence intervals were calculated according to CLSI EP12-A "User Protocol for Evaluation of Qualitative Test Performance; Approved Guideline".

Robustness: testing of samples from healthy donors

DNA samples from103 healthy blood-donors were analyzed with the *ipsogen* JAK2 MutaScreen RS Kit. All of the samples were detected as JAK2 wild-type. Analysis of 38 samples with the LightCycler 480 instrument is shown in Figure 34.

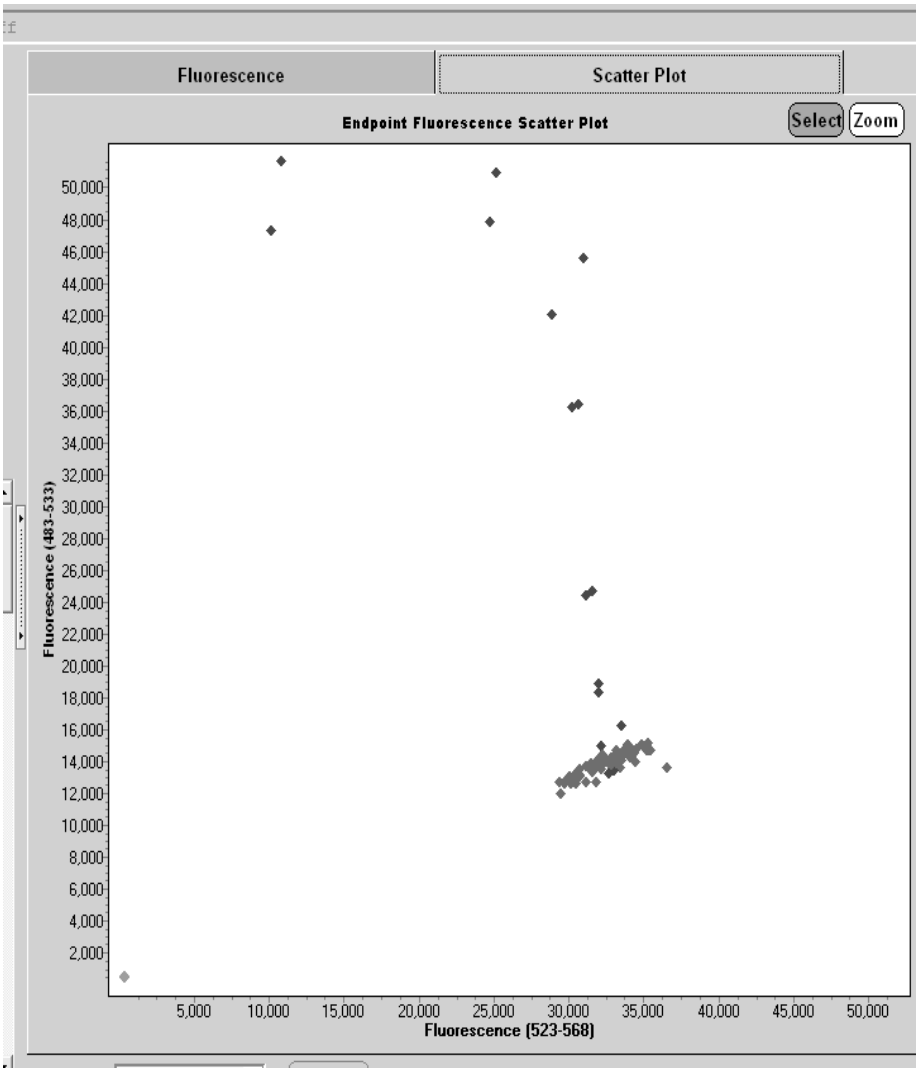


Figure 34. Analysis of healthy donors. LightCycler 480 analysis of 38 healthy donors (◆) with the *ipsogen* JAK2 Muta*Screen* RS Kit (cat. no. 673123). Positive results in duplicate (◆) correspond to a reference scale supplied with the kit. VIC fluorescence values are plotted on the x axis and FAM values are plotted on the y axis.

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Symbols

The following symbols may appear on the packaging and labeling:

	Contains reagents sufficient for <N> reactions
	Use by
	In vitro diagnostic medical device
	Catalog number
	Lot number
	Material number
	Global Trade Item Number
	Temperature limitation
	Manufacturer
	Consult instructions for use

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Ordering Information

Product	Contents	Cat. no.
ipsogen JAK2 MutaScreen Kit (10)	For 10 reactions: V617F Positive Control, V617F Negative Control, V617F Cut-Off Sample, Primers and Probes Mix JAK2 wild type and JAK2 V617F	673022
ipsogen JAK2 MutaScreen Kit (24)	For 24 reactions: V617F Positive Control, V617F Negative Control, V617F Cut-Off Sample, Primers and Probes Mix JAK2 wild type and JAK2 V617F	673023
Rotor-Gene Q MDx — for IVD-validated real-time PCR analysis in clinical applications		
Rotor-Gene Q MDx 5plex HRM Platform	Real-time PCR cycler and High Resolution Melt analyzer with 5 channels (green, yellow, orange, red, crimson) plus HRM channel, laptop computer, software, accessories, 1-year warranty on parts and labor, installation and training not included	9002032
Rotor-Gene Q MDx 5plex HRM System	Real-time PCR cycler and High Resolution Melt analyzer with 5 channels (green, yellow, orange, red, crimson) plus HRM channel, laptop computer, software, accessories, 1-year warranty on parts and labor, installation and training	9002033

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