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QIAxcel Advanced User Manual

For use with QIAxcel ScreenGel Software v1.6



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Safety information

Before using the QIAxcel Advanced, it is essential that you read this user manual carefully and pay particular attention to the safety information. The instructions and safety information in the user manual must be followed to ensure safe operation of the instrument and to maintain the instrument in a safe condition.

The following types of safety information appear throughout this manual:

WARNING 	The term WARNING is used to inform you about situations that could result in personal injury to you or other persons. Details about these circumstances are given in a box like this one.
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CAUTION 	The term CAUTION is used to inform you about situations that could result in damage to the instrument or other equipment. Details about these circumstances are given in a box like this one.
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The advice given in this manual is intended to supplement, not supersede, the normal safety requirements prevailing in the user's country.

Proper use

WARNING/ CAUTION 	Risk of personal injury and material damage [W1] Improper use of the QIAxcel Advanced may cause personal injuries or damage to the instrument. The QIAxcel Advanced must only be operated by qualified personnel who have been appropriately trained. Servicing of the QIAxcel Advanced must only be performed by QIAGEN Field Service Specialists.
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Perform the maintenance as described in the [Maintenance Procedures](#) section. QIAGEN charges for repairs that are required due to incorrect maintenance.

<p>WARNING/ CAUTION</p> 	<p>Risk of personal injury and material damage [W2]</p> <p>The QIAxcel Advanced is too heavy to be lifted by one person. To avoid personal injury or damage to the instrument, do not lift the instrument alone.</p>
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In case of emergency, switch off the QIAxcel Advanced at the power switch at the rear of the instrument and unplug the power cord from the power outlet.

<p>CAUTION</p> 	<p>Damage to the instrument [C1]</p> <p>If the Pressure 1 status is Low, increase system pressure before performing the unlatch command. Removing the cartridge and unlatching with reduced pressure may damage the instrument.</p>
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<p>CAUTION</p> 	<p>Damage to the instrument [C2]</p> <p>Do not use bleach, solvents, or reagents containing acids, alkalis, or abrasives to clean the QIAxcel Advanced.</p>
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Electrical safety

Disconnect the line power cord from the power outlet before servicing.

<p>WARNING</p> 	<p>Electrical hazard [W3]</p> <p>Any interruption of the protective conductor (earth/ground lead) inside or outside the instrument or disconnection of the protective conductor terminal is likely to make the instrument dangerous.</p> <p>Intentional interruption is prohibited.</p> <p>Lethal voltages inside the instrument</p> <p>When the instrument is connected to line power, terminals may be live, and opening covers or removing parts is likely to expose live parts.</p>
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To ensure satisfactory and safe operation of the QIAxcel Advanced, follow the advice below:

- The line power cord must be connected to a line power outlet that has a protective conductor (earth/ground).

- Do not adjust or replace internal parts of the instrument.
- Do not operate the instrument with any covers or parts removed.
- If liquid has spilled inside the instrument, switch off the instrument, disconnect it from the power outlet, and contact QIAGEN Technical Services.
- When replacing the main fuse, replace only with the type and current rating specified on the rating label.

If the instrument becomes electrically unsafe, prevent other personnel from operating it, and contact QIAGEN Technical Services. The instrument may be electrically unsafe when:

- The line power cord appears to be damaged.
- It has been stored under unfavorable conditions for a prolonged period.
- It has been subjected to severe transport stresses.

Environment

Operating conditions

<p>WARNING</p> 	<p>Explosive atmosphere [W4]</p> <p>The QIAxcel Advanced is not designed for use in an explosive atmosphere.</p>
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<p>WARNING</p> 	<p>Risk of explosion [W5]</p> <p>The QIAxcel Advanced is intended for use with reagents and substances supplied with the QIAGEN QIAxcel Kits. Use of other reagents and substances may lead to fire or explosion.</p>
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<p>CAUTION</p> 	<p>Damage to the instrument [C3]</p> <p>Direct sunlight may bleach parts of the instrument and cause damage to plastic parts.</p> <p>The QIAxcel Advanced must be located out of direct sunlight.</p>
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<p>CAUTION</p> 	<p>Damage to the cartridge [C4]</p> <p>When in use, the gel cartridge should not be left out of the Wash park position of the buffer tray for more than 15 minutes. Failure to do so will cause the capillary tips to dry out, affecting correct function of the cartridge. Dry tips will void the warranty.</p> <p>The capillary tips are made of glass and are very fragile. Take care not to knock the tips on any hard surfaces. Failure to do so will cause the capillary tips to break, affecting correct function of the cartridge. Broken tips will void the warranty.</p>
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<p>CAUTION</p> 	<p>Damage to the cartridge [C5]</p> <p>If less than 12 samples are processed, fill the empty sample wells with the QX DNA Dilution Buffer or QX RNA Dilution buffer. Failure to do so may cause damage to the capillary channels.</p>
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Chemicals

<p>WARNING</p> 	<p>Hazardous chemicals [W6]</p> <p>Some chemicals used with this instrument may be hazardous or may become hazardous after completion of the protocol run.</p> <p>Always wear safety glasses, gloves, and a lab coat.</p> <p>The responsible body (e.g., laboratory manager) must take the necessary precautions to ensure that the surrounding workplace is safe and that the instrument operators are not exposed to hazardous levels of toxic substances (chemical or biological) as defined in the applicable Safety Data Sheets (SDSs) or OSHA[*], ACGIH[†] or COSHH[‡] documents.</p> <p>Venting for fumes and disposal of wastes must be in accordance with all national, state, and local health and safety regulations and laws.</p>
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* OSHA: Occupational Safety and Health Administration (United States of America).

† ACGIH: American Conference of Government Industrial Hygienists (United States of America).

‡ COSHH: Control of Substances Hazardous to Health (United Kingdom).

<p>WARNING</p> 	<p>Risk of fire [W7]</p> <p>When cleaning the QIAxcel Advanced with alcohol-based disinfectant, leave the QIAxcel Advanced doors open to allow flammable vapors to disperse.</p>
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Waste disposal

Used labware and containers may contain hazardous chemicals. Such wastes must be collected and disposed of properly according to local safety regulations.

For information on how to dispose of the QIAxcel Advanced, see [Appendix A](#).

Mechanical hazards

The cartridge door and sample door of the QIAxcel Advanced must remain closed during operation of the instrument.

<p>WARNING</p> 	<p>Moving parts [W8]</p> <p>To avoid contact with moving parts during operation of the QIAxcel Advanced, the instrument must be operated with the cartridge door and sample door closed.</p> <p>If the door sensors are not functioning correctly, contact QIAGEN Technical Services.</p>
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Symbols on the QIAxcel Advanced

Symbol	Location	Description
	Type plate on the back of the instrument	CE mark for European Conformity
	Type plate on the back of the instrument	CSA listing mark for Canada and the USA
	Type plate on the back of the instrument	Legal manufacturer
	Type plate on the back of the instrument	Waste Electrical and Electronic Equipment (WEEE)
	Type plate on the back of the instrument	FCC mark of the United States Federal Communications Commission
	Type plate on the back of the instrument	RCM mark for Australia and New Zealand

Introduction

Thank you for choosing the QIAxcel Advanced. We are confident it will become an integral part of your laboratory.

Before using the QIAxcel Advanced, it is essential that you read this user manual carefully and pay particular attention to the safety information. The instructions and safety information in the user manual must be followed to ensure safe operation of the instrument and to maintain the instrument in a safe condition.

About this user manual

This user manual provides information about the QIAxcel Advanced in the following sections:

- [Safety information](#)
- [Introduction](#)
- [General description](#)
- [Installation procedures](#)
- [Operating procedures](#)
- [QIAxcel ScreenGel Software](#)
- [Maintenance procedures](#)
- [Troubleshooting](#)
- [Glossary](#)
- [Appendices](#)

The appendices include the following:

- Technical data
- QIAxcel Advanced methods and accessories
- Data analysis algorithm descriptions
- Warranty liability clause

General information

Technical assistance

At QIAGEN, we pride ourselves on the quality and availability of our technical support. Our Technical Services Departments are staffed by experienced scientists with extensive practical and theoretical expertise in sample and assay technologies and the use of QIAGEN products. If you have any questions or experience any difficulties regarding the QIAxcel Advanced or QIAGEN products in general, do not hesitate to contact us.

QIAGEN customers are a major source of information regarding advanced or specialized uses of our products. This information is helpful to other scientists as well as to the researchers at QIAGEN. We therefore encourage you to contact us if you have any suggestions about product performance or new applications and techniques.

For technical assistance and more information, please see our Technical Support Center at www.qiagen.com/goto/TechSupportCenter or call one of the QIAGEN Technical Service Departments or local distributors (see back cover or visit www.qiagen.com).

For up-to-date information about the QIAxcel Advanced system, visit www.qiagen.com/p/QIAxcel.

Policy statement

It is the policy of QIAGEN to improve products as new techniques and components become available. QIAGEN reserves the right to change specifications at any time.

In an effort to produce useful and appropriate documentation, we would appreciate your comments on this user manual. Please contact QIAGEN Technical Services.

Version management

This document is the *QIAxcel Advanced User Manual*, version 7.0. Updated versions can be found at www.qiagen.com/p/QIAxcel.

Intended use of the QIAxcel Advanced

The QIAxcel Advanced is a multicapillary electrophoresis instrument, designed to perform fast and fully automated DNA fragment analysis, or qualitative and quantitative RNA analysis.

The QIAxcel Advanced instrument is intended to be used only in combination with QIAxcel Kits for applications described in the respective QIAxcel Kit handbooks.

The QIAxcel Advanced instrument is intended for use by professional users, such as technicians and physicians trained in molecular biological techniques and the operation of the QIAxcel Advanced instrument.

Requirements for QIAxcel Advanced users

This table covers the general level of competence and training necessary for transportation, installation, use, maintenance, and servicing of the QIAxcel Advanced.

Task	Personnel	Training and experience
Transportation	No special requirements	No special requirements
Installation	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Instrument administration	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Routine use (running profiles)	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Analyzing data	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Instrument maintenance	Laboratory technicians or equivalent	Appropriately trained and experienced personnel familiar with use of computers and automation in general
Servicing	QIAGEN Field Service Specialists only	

General description

The QIAxcel Advanced system performs fully automated separation of DNA and RNA fragments according to their molecular weight and can process up to 96 samples without user intervention. The QIAxcel Advanced system consists of the QIAxcel Advanced instrument, a QIAxcel Kit (containing a QIAxcel gel cartridge and reagents), a computer, and QIAxcel ScreenGel Software, which have been optimized to work together across a wide variety of applications and provide unmatched resolution, speed, and throughput for DNA fragment and RNA analysis.

The QIAxcel ScreenGel Software supplied with the QIAxcel Advanced provides both electropherograms and gel images of the nucleic acid separation and can be used to perform the following types of analysis:

- Determination of the size and concentration of DNA fragments
- Determination of the 28S/18S ratio, concentration, and quality of total RNA, and the quality of cRNA/cDNA and fragmented RNA/DNA

Note: We do not recommend determining nucleic acid concentration with the QIAxcel DNA Fast Analysis Kit.

QIAxcel Advanced principle

The QIAxcel Advanced uses capillary electrophoresis to enable high resolution and sensitive separation of DNA and RNA samples. This 12-channel capillary electrophoresis instrument uses disposable, multiple-use cartridges for cost-effective analysis of up to 96 samples in as little as 25 minutes.

1. The QIAxcel Advanced is set up with a gel cartridge, running buffer and wash buffer, and calibrated using intensity markers.
2. The samples for analysis (in a 96-well plate or 12-tube strips) are placed onto the sample plate holder.
3. Required data collection settings are selected and the samples pass through the capillaries of the QIAxcel gel cartridge.
4. Data is analyzed using the QIAxcel ScreenGel Software.

External features of the QIAxcel Advanced



External features of the QIAxcel Advanced.

- | | | | |
|---|---|----|---|
| 1 | Sample door | 8 | N ₂ door |
| 2 | Cartridge door | 9 | Transport lock and buffer tray location |
| 3 | Service door | 10 | Sample plate holder |
| 4 | Power connection for AC connection | 11 | Cartridge bay |
| 5 | Tube fitting for external N ₂ supply | 12 | Slot for smart key |
| 6 | RS232 connection | 13 | Digital pressure display |
| 7 | N ₂ regulator and cylinder | 14 | Purge filter |

Note: If using an external N₂ source, the output pressure must not exceed 75 psi. The QIAxcel Advanced is equipped with an internal regulator that will regulate the pressure provided by the external N₂ source to approximately 40 psi (37–45 psi), which is the instrument's operating pressure.

Gel cartridges

The QIAxcel Advanced can be operated using any of the QIAxcel Kits listed in the table below. Each kit contains a gel cartridge that has been specifically developed for particular applications. Each gel cartridge consists of a gel matrix with a proprietary linear polymer with ethidium bromide intercalating dye.

Kit	Application
QIAxcel DNA High Resolution Kit (1200)	Analysis of DNA 15 bp – 10 kb in size. 96 samples can be analyzed in <1.5 hours.
QIAxcel DNA Screening Kit (2400)	Fast analysis of DNA 15 bp – 5 kb in size. 96 samples can be analyzed in just 40 minutes.
QIAxcel DNA Fast Analysis Kit (3000)	Routine evaluation of DNA fragments in qualitative single or multiplex PCR applications. 96 samples can be analyzed in approximately 25 minutes.
QIAxcel RNA QC Kit v2.0 (1200)	Analysis of RNA quality and quantity. 96 samples can be analyzed in <1.5 hours

Each QIAxcel Kit contains the following additional reagents that are required for use of the QIAxcel Advanced:

- QX Intensity Calibration Marker – calibrates the signal intensity for each new gel cartridge
- QX DNA or RNA Separation Buffer (QIAxcel DNA or RNA Kits) – enables separation of DNA or RNA molecules
- QX FA DNA Separation Buffer (QIAxcel DNA Fast Analysis Kit) – enables separation of DNA molecules (only for use with the QIAxcel DNA Fast Analysis Cartridge)
- QX Wash Buffer – for washing the capillary tips to prevent cross-contamination
- QX DNA or RNA Dilution Buffer – for optimization of sample concentration
- QX Mineral Oil – for covering solutions and/or samples to prevent evaporation
- QX Alignment Marker – used in every run to equalize the migration time variation across all channels (included in the QIAxcel RNA QC Kit v2.0 and QIAxcel Fast Analysis Kit only; for all other kits, see ordering information, [Appendix C](#))

Note: QIAxcel DNA Size Marker is required for use with QIAxcel DNA Kits only. This enables creation of a reference marker table allowing DNA size and concentration to be determined (not included in kit; see ordering information, [Appendix C](#)). QIAxcel RNA Size Marker is provided with the QIAxcel RNA QC Kit v2.0.

Computer and software

The QIAxcel Advanced is shipped with the QIAxcel ScreenGel Software.

A computer with the correct specifications for operation of the QIAxcel Advanced instrument and QIAxcel ScreenGel Software is supplied as part of the QIAxcel Advanced system. However, if a different computer is used to operate the QIAxcel Advanced instrument or run the QIAxcel ScreenGel Software, then the following requirements are necessary:

Computer specifications:

- At least 2.3 GHz CPU
- Minimum 80 GB free hard drive capacity, NTFS formatted
- At least 2 GB RAM (recommended 4 GB RAM)
- 1024 x 768 screen resolution or higher
- 9-PIN Serial Port or I/O card (not provided, contact QIAGEN Technical Services for more information).
- DVD/CD-ROM
- Pointer device (mouse or similar)
- Windows® 7 Professional (32 or 64 bit) with service pack 1 or higher; Windows 10 (64 bit) with minimum required version 1607
- Adobe® Reader® Software 8.2 or higher (for reading PDF reports)

To view reports in PDF format, a PDF reader must be installed on the computer. Adobe Reader can be downloaded at www.adobe.com.

Additional configuration steps:

- Turn off all automatic processes or services, such as indexing or similar, which could produce a high workload, especially when connecting to the QIAxcel Advanced instrument.
- Ensure that energy saving options and hibernation are deactivated during the operation of the QIAxcel Advanced.
- For Windows 10 only – if UEFI Boot is used, the Secure Boot option must be disabled. Otherwise, the Device Driver Installation of the QIAxcel Advanced device driver will fail during installation of the QIAxcel ScreenGel Software.

Note: In case of any concern regarding the Windows configuration, please contact your local IT support.

If connecting the computer to a network, be sure to consider the following:

-
- Ensure that update processes are scheduled to download and install only outside the operating times of the QIAxcel Advanced.
 - Turn off auto-restart after an installation of Windows security patches to prevent automatic computer restart during the operating times of the QIAxcel Advanced.

Note: In order to complete a security update installation, perform a manual restart later.

If virus protection software is required, ensure that the following tasks are scheduled to run outside the operating times of the QIAxcel Advanced:

- Scans (also ensure that files that are created by the QIAxcel ScreenGel are not scanned during creation or on access)
- All kind of updates (download and installation)

Note: The QIAxcel ScreenGel is tested by QIAGEN using the original image supplied with your laptop without connecting the laptop to the Internet. Updates on your operating system might lead to unexpected behavior of the QIAxcel ScreenGel. In such cases, please contact your local IT support.

Note: The minimal screen resolution can be used in combination with small fonts. However, medium size fonts can be used in combination with an improved resolution (e.g., the medium font size (125%) setting in Windows 7 requires a minimum screen resolution of 1400 x 1050). Larger font sizes are not supported.

Installation procedures

This section provides instructions on unpacking and installing the QIAxcel Advanced.

Requirements

This section of the *QIAxcel Advanced User Manual* specifies the requirements for operating the QIAxcel Advanced.

Site

The QIAxcel Advanced must be located out of direct sunlight, away from heat sources, and away from sources of vibration and electrical interference. Refer to [Appendix A](#) for the operating conditions (temperature and humidity). The site of installation should be free of excessive drafts, excessive moisture, excessive dust, and not subject to large temperature fluctuations.

Use a level workbench that is large enough to accommodate the QIAxcel Advanced and computer. Refer to Appendix A for the weight and dimensions of the QIAxcel Advanced.

Ensure that the workbench is dry, clean, vibration-proof, and has additional space for accessories. Approximately 72 cm (28 in.) clearance above the workbench is recommended to allow cartridge loading.

The QIAxcel Advanced must be placed within approximately 1.5 m (4.92 ft.) of a properly grounded (earthed) AC power outlet. The power line to the instrument should be voltage regulated and surge protected.

Ensure that the switch and the main power input socket at the rear of the instrument are easily reachable. Maintain sufficient clearance at the rear to unplug the power line from the main power input socket.

Note: We recommend plugging the instrument directly into its own wall socket and not to share the socket with other lab equipment. To achieve proper capillary electrophoresis separation, do not place the QIAxcel Advanced on a vibrating surface or near vibrating objects.

<p>WARNING</p> 	<p>Explosive atmosphere [W9]</p> <p>The QIAxcel Advanced is not designed for use in an explosive atmosphere.</p>
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<p>WARNING</p> 	<p>Risk of overheating [W10]</p> <p>To ensure proper ventilation, maintain a minimum clearance of 10 cm (3.94 in.) at the sides and rear of the QIAxcel Advanced.</p> <p>Slits and openings that ensure the ventilation of the QIAxcel Advanced must not be covered.</p>
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Power requirements

The QIAxcel Advanced operates at 100–240 V AC, 50–60 Hz, 360 VA.

Ensure that the voltage rating of the QIAxcel Advanced is compatible with the AC voltage available at the installation site. Main supply voltage fluctuations are not to exceed 10% of nominal supply voltages.

Grounding requirements

To protect operating personnel, the instrument is equipped with a 3-conductor AC power cord. To preserve this protection feature, do not operate the instrument from an AC power outlet that has no ground (earth) connection.

For replacement of the 3-conductor AC power cord, contact QIAGEN Technical Services for an authorized spare part.

Unpacking the QIAxcel Advanced

Before unpacking the QIAxcel Advanced, move the package to the site of installation and check that the arrows on the package point upward. In addition, check whether the package is damaged. In case of damage, contact the transporter of the package.

When lifting up the QIAxcel Advanced, slide your fingers under both sides of the instrument and keep your back straight.

<p>WARNING/ CAUTION</p> 	<p>Risk of personal injury and material damage [W2]</p> <p>The QIAxcel Advanced is too heavy to be lifted by one person. To avoid personal injury or damage to the instrument, do not lift the instrument alone.</p>
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After unpacking the QIAxcel Advanced, check that the following documents are supplied:

- Packing list
- Warranty registration form
- Quick-start guide

Read the packing list to check that you have received all items. If anything is missing, contact QIAGEN Technical Services.

The *QIAxcel Advanced User Manual* is available on the software CD in PDF format.

Check that the QIAxcel Advanced is not damaged and that there are no loose parts. If anything is damaged, contact QIAGEN Technical Services. Make sure that the QIAxcel Advanced has equilibrated to ambient temperature before operating it.

Retain the package in case you need to transport or ship the QIAxcel Advanced in the future. Instructions for packing the QIAxcel Advanced are given in section [Packing the QIAxcel Advanced](#). Using the original package minimizes damage during transportation of the QIAxcel Advanced.

Carefully place the QIAxcel Advanced onto the workbench where it will be used. For site requirements, please refer to section [Requirements](#).

Installing the QIAxcel Advanced

Before operating the QIAxcel Advanced:

- The transport lock must be removed
- The power cord must be installed
- The N₂ cylinder or an external N₂ supply must be installed

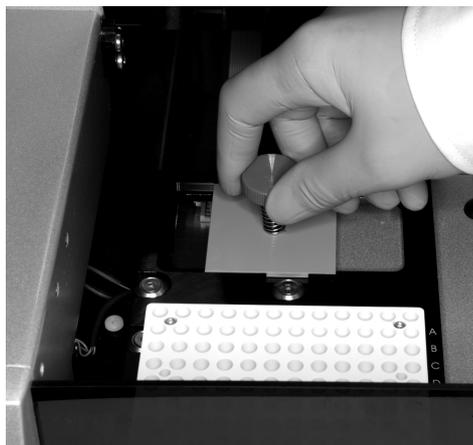
Releasing the transport lock

The QIAxcel Advanced is delivered with a transport lock that secures the tray/transport mechanism during shipment. This transport lock must be removed before the QIAxcel Advanced can be operated.

Note: Please reinstall the transport lock whenever shipping the instrument.

Remove the transport lock as follows:

1. Open the sample door.
2. Release the transport lock securing the buffer tray/sample plate holder.
3. Keep the transport lock in case you need to transport the QIAxcel Advanced in the future.



Removing the transport lock.

Instrument setup

Set up the QIAxcel Advanced as follows:

1. Set up the computer and monitor as described in the computer installation instructions provided with the computer.
2. Connect the RS232 serial cable from the instrument to the computer.

Installation of AC power cord

Connect the QIAxcel Advanced to the power outlet as follows:

1. Ensure that the power switch of the QIAxcel Advanced is set to the off position.
2. Check that the voltage rating on the label at the back of the QIAxcel Advanced matches the voltage available at the installation site.
3. Plug the power cord into the power cord socket at the rear of the instrument.
4. Plug the power cord into a grounded power outlet.

Installation of the N₂ cylinder

Important: Use only N₂ cylinders provided by QIAGEN (cat. no. 929705).

1. Ensure that the power switch of the QIAxcel Advanced is set to the off position.
2. Open the N₂ door and gently pull up on the N₂ cylinder port. Do not pull past the detent hole.
3. Screw the N₂ cylinder into the port clockwise.
4. Turn until the needle inside the port punctures the N₂ cylinder. Do not overtighten; the cylinder should only be finger tight.
5. Gently push down on the N₂ cylinder until it is in its stowed (down) position.
6. Close the N₂ door.

Alternatively, use an external N₂ supply and attach to the rear of the instrument.

Installation of the QIAxcel ScreenGel Software

The QIAxcel ScreenGel version 1.6 is the first version supporting Windows 10 (64 bit). The QIAxcel ScreenGel must be installed before the QIAxcel Advanced is connected to the computer for the first time. A user with Windows administrator privileges is required to install the QIAxcel ScreenGel, but such privileges are required for software installation only.

For computer system requirements, see section [Computer and software](#).

1. Set up the computer as described in the computer installation instructions provided with the computer.
2. Before installing the QIAxcel ScreenGel, shut down all other software and make sure that the QIAxcel Advanced is not connected to the computer.
3. If a previous version of the QIAxcel ScreenGel Software is already installed on the computer, refer to [Updating the QIAxcel ScreenGel Software](#). A dedicated update package is available to update the software. In this case it is not possible to install the QIAxcel ScreenGel software from a CD. If the software shall be installed for the first time, follow the instructions in [First-time installation from a CD](#). A first-time installation is possible from a CD, only. If you have previously installed any version of the QIAxcel ScreenGel Software and need to install it again from a CD, follow the [re-installation](#) procedure.

Note: Default settings are recommended where appropriate for all installation steps.

We recommend having no other software installed on the computer that controls the QIAxcel Advanced other than the QIAxcel ScreenGel. In particular, the BioCalculator Software should not be installed.

However, if it is needed to have both software installed on the same computer for a period of time, consider the following:

- Ensure that you open only one software at a time.
- If switching between QIAxcel ScreenGel and BioCalculator Software to run the QIAxcel Advanced, close the open software, turn the QIAxcel Advanced off at the power switch, wait for 20 seconds and then turn it on again before launching the other software. A computer restart might be necessary if the connection to the instrument isn't working.

First-time installation from a CD

To install the QIAxcel ScreenGel Software from a CD for the first time, follow the steps below.

If a previous version of the software is already installed on the computer, it is not possible to install the QIAxcel ScreenGel Software from a CD. Refer to section [Installation of the QIAxcel ScreenGel Software](#).

Things to do before starting:

1. Ensure that the computer meets the minimum requirements (see [Computer and software](#)).
2. Use a Windows account with administrator privileges.

Note: Windows administrator privileges are required for software installation only.

3. Close any programs running on the computer and make sure that the QIAxcel Advanced is not connected to the computer (i.e., unplug the cable from the computer).

To install the software for the first time from CD:

4. Place the CD in the computer's CD-ROM drive.
5. The setup wizard will automatically start installing the QIAxcel ScreenGel Software and will guide you through the setup process. Select the language from the drop-down box.

Important: If the setup wizard does not start automatically, double-click on My Computer and double-click on the CD-ROM drive. Launch the setup.exe program. This will start the QIAxcel ScreenGel Software installation.

Note: Default settings are recommended where appropriate for all installation steps.

Note: It is possible to switch the language of the installed software later using the **File** menu.

6. Select the option Install QIAxcel ScreenGel Software to start the actual installation procedure.

Note: Select the option **User Manual** to read the user manual in the selected language.

7. The Microsoft Visual C++ 2010 x 86 Redistributable will be installed if it is not already present. In this case, another dialog opens. Accept the license agreement and click **Install**. Click **Finish** to complete the installation of this package. If you cancel or close the dialog before, the QIAxcel ScreenGel will not be able to operate.
8. The appropriate version of the Microsoft .NET Framework will be installed at the beginning of the QIAxcel ScreenGel Software setup, if it is not already present. In this case, another dialog opens. Click **Install** to install the Microsoft .NET Framework. This may take some time. If you cancel or close the dialog, the QIAxcel ScreenGel will not be able to operate.
9. A Microsoft .NET Framework software update will be installed, if it is not already present. In this case, another dialog opens. Click Next to start the installation of this package. Accept the license agreement and click **Next**. Click **Finish** to complete the installation of this package. If you cancel or close the dialog before, the QIAxcel ScreenGel will not be able to operate.
10. Depending on the installed software packages from steps 8–10, a computer restart might be required before proceeding with the setup. After the reboot, the installation procedure is resumed automatically.
11. The QIAxcel ScreenGel setup wizard opens. Click **Next**.
12. Accept the license agreement and click **Next**.
13. Select the program installation path. The default path is C:\Program Files\QIAGEN\QIAxcel\ScreenGel. Click **Next**.
14. Select the data path for acquired data and all other application data. The default path is C:\ProgramData\QIAGEN\QIAxcel\ScreenGel. Click **Next**.

Note: If C:\Program Files\QIAGEN\QIAxcel\ScreenGel is selected on a Windows 64 bit system, the installation will appear in C:\Program Files\x86\QIAGEN\QIAxcel\ScreenGel.

Note: It is not possible to choose C:\Program Files\QIAGEN\QIAxcel\ScreenGel also as the data path. It is also not possible to choose the system root path (e.g., C:\Windows) as the data path.

Note: All paths in this manual refer to the data path as %DATA_DIR%.

Note: The %DATA_DIR% directory and its subdirectories can be opened in the Windows Explorer directly from QIAxcel ScreenGel Software using the menu item **File/Open Data Directory**.

15. Click Install to begin the installation. This may take some time.
16. The QIAGEN QIAxcel Advanced Driver Installer dialog opens, if the driver is not already present on the computer. Click Next. The driver installs. Click Finish to complete the driver installation.
17. Click Finish to complete the QIAxcel ScreenGel setup wizard.
18. Click Exit to close the installation window.
19. Connect the QIAxcel Advanced to the computer.
20. After the installation, the QIAxcel ScreenGel Software can be started either from the Windows start menu under **QIAGEN/QIAxcel** or from the desktop icon. The user manual can be accessed in the available languages from the Windows start menu.

Updating the QIAxcel ScreenGel Software

To update the QIAxcel ScreenGel Software, a previous version of the software must already be installed on the computer and an upgrade package must be used. The upgrade package is available under Product Resources at www.qiagen.com/p/QIAxcel. Before updating, read the information provided on the web page. Experiments and user settings will be retained.

The upgrade can be done from any previous version of the QIAxcel ScreenGel Software directly to the latest version. Furthermore, it is possible to upgrade from a previous English version to another available language version (and vice versa).

Note: The installers for software versions below 1.4 allowed the software to be installed for the current user or for all users of the computer. If the currently installed version had been installed with an option selected for the current user, a direct upgrade cannot be performed. In this case, [uninstall the software](#) first (all experiments, reports, user-created profiles are retained). Then re-install any available version of QIAxcel ScreenGel from a CD, making sure to install this version for all users of the computer. Follow the instructions in section [Re-installation from a CD](#). After installing the older version from a CD, do not launch the software. Continue directly with the update procedure below to a higher software version using the update package. It is not possible to launch the intermediate installation if the software version is below the one that was initially installed on the computer.

Things to do before starting:

1. Ensure that the computer meets the minimum requirements (see [Computer and software](#)).
2. Use a Windows account with administrator privileges.

Note: Windows administrator privileges are required for software installation only.

3. Close any programs running on the computer and make sure that the QIAxcel Advanced is not connected to the computer (i.e., unplug the cable from the computer).

To update the software from web download:

4. Download the update package for the latest version from the QIAGEN website onto your computer. It is available under Product Resources at www.qiagen.com/p/QIAXcel.
5. Unzip the update package.
6. Launch the setup.exe program. This will start the QIAXcel ScreenGel Software installation.
7. Select the language in which the QIAXcel ScreenGel Software shall be installed from the drop-down box.

Note: It is possible to switch the language of the installed software later using the **File** menu.

8. Select the option Install QIAXcel ScreenGel Software to start the actual installation procedure.
9. The Microsoft Visual C++ 2010 x 86 Redistributable will be installed if it is not already present. In this case, another dialog opens. Accept the license agreement and click Install. Click **Finish** to complete the installation of this package. If you cancel or close the dialog before, the QIAXcel ScreenGel will not be able to operate.
10. The appropriate version of the Microsoft .NET Framework will be installed at the beginning of the QIAXcel ScreenGel Software setup, if it is not already present. In this case, another dialog opens. Click **Install** to install the Microsoft .NET Framework. This may take some time. If you cancel or close the dialog, the QIAXcel ScreenGel will not be able to operate.
11. A Microsoft .NET Framework software update will be installed, if it is not already present. In this case, another dialog opens. Click Next to start the installation of this package. Accept the license agreement and click **Next**. Click **Finish** to complete the installation of this package. If you cancel or close the dialog before, the QIAXcel ScreenGel will not be able to operate.
12. Depending on the installed software packages from steps 8–10, a computer restart might be required before proceeding with the setup. After the reboot, launch the setup.exe program again and select Install QIAXcel ScreenGel Software.
13. The QIAXcel ScreenGel setup wizard opens. Click **Next**.
14. Accept the license agreement and click **Next**.
15. Select the program installation path. The default path is C:\Program Files\QIAGEN\QIAXcel\ScreenGel. Click **Next**.

Note: If C:\Program Files\QIAGEN\QIAXcel\ScreenGel is selected on a Windows 64 bit system, the installation will appear in C:\Program Files\x86\QIAGEN\QIAXcel\ScreenGel.

16. Select the data path for acquired data and all other application data. Use the same data path as the installed software version. The default path is C:\ProgramData\QIAGEN\QIAXcel\ScreenGel. Click **Next**.

Note: It is not possible to choose C:\Program Files\QIAGEN\QIAXcel\ScreenGel also as the data path. It is also not possible to choose the system root path (e.g., C:\Windows) as the data path.

Note: All paths in this manual refer to the data path as %DATA_DIR%.

Note: The %DATA_DIR% directory and its subdirectories can be opened in the Windows Explorer directly from QIAXcel ScreenGel Software using the menu item File/Open Data Directory.

17. Click Install to begin the installation. This may take some time.

Note: Reference markers that were created with versions 1.0.0 or 1.0.2 of the QIAxcel ScreenGel Software will be removed during installation. If needed, create the reference markers again from the appropriate size marker runs.

18. The QIAGEN QIAxcel Advanced Driver Installer dialog opens, if the driver is not already present on the computer. Click Next. The driver installs. Click Finish to complete the driver installation.

19. Click **Finish** to complete the QIAxcel ScreenGel setup wizard. Click **Exit** to close the installation window.

20. Connect the QIAxcel Advanced to the computer.

21. After the installation, the QIAxcel ScreenGel Software can be started either from the Windows start menu under **QIAGEN/QIAxcel** or from the desktop icon. The user manual can be accessed in the available languages from the Windows start menu.

22. Use one of the previously created user IDs for login.

Note: It is not possible to update from the BioCalculator Software to the QIAxcel ScreenGel Software. However, run files of the Biocalculator Software can be imported. Refer to section [Importing BioCalculator Data](#) for more information. It is not possible to import the run setup or method files created for the BioCalculator Software.

Re-installation from a CD

Note: The installers for software versions below 1.4 allow the software to be installed for the current user or for all users of the computer. Always use the option for all users of the computer.

Note: Downgrading (i.e., replacing a newer version with an older version of the software) the QIAxcel ScreenGel Software is not recommended. Experiments and profiles created with the newer version cannot be used with the older version. However, it may be necessary to re-install an older version of the software from a CD to perform an upgrade. In this case, do not launch the software after re-installing it from a CD. Continue instead directly with the update procedure described above. It is not possible to launch the intermediate installation if the software version is below that which was initially installed on the computer.

If you have installed any version of the QIAxcel ScreenGel Software before and need to install the QIAxcel ScreenGel Software again from a CD, follow the steps below.

Things to do before starting:

1. Ensure that the computer meets the minimum requirements (see [Computer and software](#)).
2. Use a Windows account with administrator privileges.

Note: Windows administrator privileges are required for software installation only.

3. Close any programs running on the computer and make sure that the QIAxcel Advanced is not connected to the computer (i.e., unplug the cable from the computer).

To reinstall from CD:

4. Ensure that you know the data path of the installed QIAxcel ScreenGel Software. Alternatively, launch the installed QIAxcel ScreenGel Software and login. Select **Open Data Directory** in the **File** menu. Keep open the launched Windows Explorer and close the software.

5. [Uninstall](#) the existing installation of the QIAxcel ScreenGel Software through the Windows Control Panel.
6. If downgrading the QIAxcel ScreenGel Software, rename or move the data directory of the existing version.
7. Place the CD in the computer's CD-ROM drive.
8. The setup wizard will automatically start installation of the QIAxcel ScreenGel Software and will guide you through the setup process. It supports the installation of the QIAxcel ScreenGel Software. Select the language from the drop-down box.

Important: If the setup wizard does not start automatically, double-click on "My Computer" and double-click on the CD-ROM drive. Launch the setup.exe program. This will start the QIAxcel ScreenGel Software installation.

Note: It is possible to switch the language of the installed software later using the **File** menu.

9. QIAxcel ScreenGel uses several software packages provided by Microsoft. If they are not installed on the system, these software packages are automatically installed at the beginning of the QIAxcel ScreenGel Software setup. When the respective dialog is displayed, click the Install button to install these required software packages. Depending on the installed software packages, a reboot of the system may be required before proceeding with the setup. After the reboot, the installation procedure is resumed automatically.
10. Select the option Install QIAxcel ScreenGel Software to start the actual installation procedure.
11. The installers for software versions below 1.4 allow the software to be installed for the current user or for all users of the computer. Always use the option for all users of the computer.
12. Accept the license agreement.
13. Select the program installation path. The default path is C:\Program Files\QIAGEN\QIAxcel\ScreenGel.
14. Select the data path for acquired data and all other application data. The default path is:
 - C:\Documents and Settings\All Users\Application Data\QIAGEN\QIAxcel\ScreenGel for Microsoft Windows XP Professional
 - C:\ProgramData\QIAGEN\QIAxcel\ScreenGel for Microsoft Windows 7 Professional

If you re-install an older version of the software from a CD, as a prerequisite for an update to the current version, select the path, mentioned in step 4.

If downgrading, it is important that the selected data path does not contain any files of the previously installed version. In particular, do not select the renamed directory from step 6.

Note: It is not possible to choose C:\Program Files\QIAGEN\QIAxcel\ScreenGel also as the data path. It is also not possible to choose the system root path (e.g., C:\Windows) as the data path.

Note: Reference markers that were created with versions 1.0.0 or 1.0.2 of the QIAxcel ScreenGel Software cannot be used with other software versions. If needed, create the reference markers again from the appropriate size marker runs.

Note: All paths in this manual refer to the data path as %DATA_DIR%.

Note: The %DATA_DIR% directory and its subdirectories can be opened in the Windows Explorer directly from QIAxcel ScreenGel Software, through the menu item **File/Open Data Directory**.

15. After the installation finished, click **Exit** to close the installation window.
16. If you re-installed an older version of the software from a CD, as a prerequisite for an update to the current version, do not launch the software. Continue directly with the [update procedure](#). In the update procedure, use the same data path as used in step 14.
17. After the installation, the QIAxcel ScreenGel Software can be started either from the Windows start menu under **QIAGEN/QIAxcel** or from the desktop icon. The user manual can be accessed in the available languages from the Windows start menu.

Note: When downgrading, error messages may appear indicating that one of the packages from Microsoft cannot be installed or that the QIAxcel ScreenGel Software cannot be launched after installation. If the computer is intended to be used only for the QIAxcel ScreenGel Software, access the Windows Control Panel and uninstall the QIAxcel ScreenGel Software, all items starting with "Microsoft Visual C++ 20xx Redistributable - ...," and the "Microsoft.NET Framework" items. Then try to install the QIAxcel ScreenGel Software again. If the problem persists, contact QIAGEN Technical Services. If the computer is not intended to be used only for the QIAxcel ScreenGel Software, exercise care when uninstalling the listed items. These may be used by other software running on the computer. Have the installation package(s) of the other software at hand in case repair is necessary.

Uninstall software

Note: Do not uninstall the software if you want to update the software. Follow the instructions in [Updating the QIAxcel ScreenGel Software](#).

When uninstalling the QIAxcel ScreenGel Software, all data within the data folder is retained.

If you want to uninstall the QIAxcel ScreenGel Software together with all data (experiments, reports) from the %DATA_DIR%, ensure that you know the data path of the installed QIAxcel ScreenGel Software. Alternatively, launch the installed QIAxcel ScreenGel Software and login. Select **Open Data Directory** in the **File** menu. Keep the launched Windows Explorer open.

To uninstall the QIAxcel ScreenGel, follow these steps:

1. Close the QIAxcel ScreenGel Software.
2. Open the **Control Panel** by clicking on the Windows **Start** menu and selecting **Control Panel**.
3. Depending on your layout settings, either click **Programs and Features** or **Add/Uninstall Programs**.
4. Select QIAxcel ScreenGel to be uninstalled and click **Uninstall**.

Note: Depending on the Windows configuration, there may be a pop-up message asking if you want to allow the program to install. Allow the program to install.

5. The installer window opens. Click **Uninstall**.
6. Follow the instructions of the installer to uninstall.
7. Finally, click **Exit** to close the installer window.

If you want to uninstall the QlAxcel ScreenGel Software together with all the data, switch to the Windows Explorer before uninstalling the software. Delete the data from the data folder.

Getting started with the QlAxcel ScreenGel Software

Before using the software, read the [Concepts](#) of QlAxcel ScreenGel. Afterwards, configure the software. This can only be carried out by a user with the **Administrator** role.

1. Launch the QlAxcel ScreenGel Software from the Windows start menu in the **QIAGEN/QlAxcel** folder or from the desktop icon.
2. Log in as **Administrator** and click **OK** (for this first login, no password is required).
3. Provide a valid password for the **Administrator** account. Leave the field for the old password empty, then provide a new valid password and enter it again.

Note: The password must contain one upper-case character, one lower-case character, and one digit. The minimum size of the password is eight characters.

4. The **Configuration** environment is displayed by default. Select the **User Manager** tab.
5. Create user accounts for all relevant users. For more information, refer to [User management](#) and [User roles](#).
6. Configure which **COM** port is to be used for connection to the QlAxcel Advanced system. The default adjustment is COM1. For more detailed information, refer to [Settings](#).
7. Configure the global settings for the QlAxcel ScreenGel Software. For further details, refer to [Settings](#).

Packing the QIAxcel Advanced

<p>WARNING/ CAUTION</p> 	<p>Risk of personal injury and material damage [W2]</p> <p>The QIAxcel Advanced is too heavy to be lifted by one person. To avoid personal injury or damage to the instrument, do not lift the instrument alone.</p>
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If you need to transport the QIAxcel Advanced, pack the instrument as follows:

1. Switch on the QIAxcel Advanced.
2. Switch on the computer and launch the QIAxcel ScreenGel Software.
3. Click  in the [Status Information panel](#) to move the buffer tray to the front of the instrument.
4. Open the sample door and remove the buffer tray.
5. Remove the QIAxcel gel cartridge from the QIAxcel Advanced and store in the QX Cartridge Stand as described in section [Unpacking a QIAxcel Kit](#).
6. Remove the N₂ bottle as described in section [N2 cylinder replacement](#).
7. Close the QIAxcel ScreenGel Software and switch off the QIAxcel Advanced.
8. Disconnect the RS232 serial cable from the instrument to the computer and remove the AC power cord.
9. Reinstall the transport lock holding down the sample plate holder (see section [Installing the QIAxcel Advanced](#)).
10. Place the QIAxcel Advanced into the original packaging it was shipped in.

Operating procedures

This section describes how to operate the QIAxcel Advanced.

Before proceeding, we recommend that you familiarize yourself with the features of the QIAxcel Advanced by referring to the section [General Description](#).

The QIAxcel Advanced cartridge door, sample door, and service door must remain closed during operation of the instrument. Only open the doors when the instrument is not operating or when instructed to do so by the software.

Note: Opening the cartridge door or sample door during operation of the QIAxcel Advanced will cause the system to stop the action it is currently performing. Any sample run in progress cannot be recovered. However, due to the small volume of sample used, a new run can be performed.

<p>WARNING/ CAUTION</p> 	<p>Risk of personal injury and material damage [W2]</p> <p>Do not attempt to move the QIAxcel Advanced during operation.</p>
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<p>WARNING</p> 	<p>Moving parts [W8]</p> <p>To avoid contact with moving parts during operation of the QIAxcel Advanced, the instrument must be operated with the cartridge door and sample door closed.</p> <p>If the door sensors are not functioning correctly, contact QIAGEN Technical Services.</p>
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Unpacking a QIAxcel Kit

1. Carefully read the handbook supplied with the QIAxcel Kit before starting.
2. Remove all buffer bottles from the kit. Refer to the handbook for a detailed description of the kit contents.
3. Add 10 ml QX Wash Buffer to both reservoirs of the QX Cartridge Stand (provided with the QIAxcel instrument) reservoir and cover it with 2 ml mineral oil.
4. Remove the QIAxcel gel cartridge from its packaging and carefully wipe off any soft gel debris from the capillary tips using a soft tissue.

Note: The QIAxcel gel cartridge is provided together with a smart key, which is used for fully automatic cartridge detection. Do not remove the smart key from the cartridge.

5. Remove the purge cap seal from the back of the QIAxcel gel cartridge and place it in the QX Cartridge Stand.

Note: A soft tissue should be used to wipe off any gel that may have leaked from the port.

Note: Ensure that the capillary tips are submerged in QX Wash Buffer.

6. **Important:** New cartridges must be allowed to equilibrate at room temperature for at least 20 minutes prior to use. Place the gel cartridge in the QX Cartridge Stand, protected from light with the QX Cartridge Stand Cover, or store the cartridge latched in the instrument in the Park position with wash buffer in the wash park (WP) position, and allow to stand at room temperature (15–25°C) for at least 20 minutes. Do not equilibrate the gel cartridges inside the kit box or in the black cartridge blister.

Note: Incorrect cartridge handling or shorter equilibration times may cause damage to your QIAxcel instrument and could result in a loss of warranty.



QIAxcel gel cartridge in the QX Cartridge Stand.

Setting up the QIAxcel Advanced

The steps required for correct setup of the QIAxcel Advanced instrument before each use are described in this section.

Preparing the buffer tray

Important points before starting

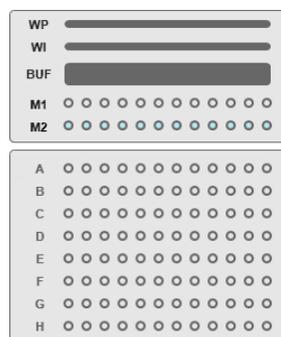
- If using pre-aliquoted alignment marker, the 12-tube strip containing QX Alignment Marker should be equilibrated to room temperature (15–25°C) and centrifuged briefly before use.
- When using QIAxcel DNA Kits, we recommend changing the alignment markers every 50 runs or 3 days, whichever comes first. Additional markers and buffers may need to be purchased (see [Appendix C](#)).
- When using the QIAxcel RNA QC Kit v2.0, we recommend changing the alignment markers every 15–20 runs or 3 days, whichever comes first. Additional markers and buffers may need to be purchased (see [Appendix C](#)).
- When not in use, store the 12-tube strip with QX Alignment Marker at –20°C.
- The volumes of QX Separation Buffer and QX Wash Buffer provided are sufficient for the maximum number of runs stated on the gel cartridge.
- The 12-tube strips should fit loosely in the **MARKER 1** position. Tightly fitting tube strips or tube strips that are too loose may cause injection problems and damage the cartridge capillaries.
- Allow all reagents to equilibrate to room temperature before use.

Procedure

1. Wash the buffer tray in warm water using a mild detergent and rinse thoroughly with deionized or reverse-osmosis water.
2. Fill the positions of the buffer tray as listed below:

Cartridge type	Buffer tray position		
	Wash Park (WP)	Wash Inject (WI)	Buffer (BUF)
DNA High Resolution	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX DNA Separation Buffer
DNA Screening	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX DNA Separation Buffer
DNA Fast Analysis	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX FA DNA Separation Buffer
RNA	8 ml QX Wash Buffer	8 ml QX Wash Buffer	18 ml QX RNA Separation Buffer

3. Add QX Mineral Oil to cover all 3 positions to prevent evaporation. Add 2 ml QX Mineral Oil to positions WP and WI, and add 4 ml QX Mineral Oil to the position BUF.
4. Load 15 µl QX Alignment Marker into each well of a QX 0.2 ml 12-Tube Strip or use a pre-aliquoted strip.
5. Add 1 drop of QX Mineral Oil to each well and insert the strip into the M1 position of the buffer tray.
6. If the cartridge is not calibrated yet, load 15 µl QX Intensity Calibration Marker into each well of a QX Color 0.2 ml 12-Tube Strip. Add a drop of QX Mineral Oil, and insert the strip into the M2 position of the buffer tray.



Buffer tray.

Loading the buffer tray

If not already carried out:

1. Switch on the QIAxcel Advanced at the power switch.
2. Switch on the computer, launch the QIAxcel ScreenGel Software from the Windows start menu under **QIAGEN/QIAxcel** or from the desktop icon.
3. In the QIAxcel ScreenGel software, select a mode (DNA or RNA) and log in (for detailed information, refer to the [User authentication](#) section). The **Process** environment opens and displays the first screen of the process profile of the process wizard.

Note: The  icon indicates that the connection is being established and the  icon shows that the QIAxcel Advanced is connected. In the case that the instrument could not be connected, a message will be shown notifying that the instrument is not available. If you didn't switch on the instrument at the moment, click **Instrument not needed**. If you need the instrument, click **Troubleshoot**.

Follow the instructions in the message. For more detailed instructions, refer to the troubleshooting section [System setup](#). Close the message. To retry to connect to the instrument, click the  icon.

Note: The QIAxcel ScreenGel Software comes with an up-to-date instrument software for the QIAxcel Advanced instruments with serial number 30281 and higher. If the software connects to the instrument for the first time, it checks if the instrument software on the instrument is up-to-date. If not, it updates the instrument software. This process takes a few minutes. A message is shown during that time. Let the update be completed. Do not turn off the instrument or disconnect the cable between the computer and the instrument, and do not close the QIAxcel ScreenGel Software until the update is complete. After a successful update, the QIAxcel ScreenGel Software automatically connects to the instrument.

To load the buffer tray proceed as follows:

1. Close the cartridge door and the sample door.

Note: The QIAxcel Advanced cartridge and sample doors must remain closed during operation of the instrument. Opening either door during operation will cause the system to stop any action it is currently performing.

2. Click  in the [Status Information panel](#) at the left to move the buffer tray holder to the front of the instrument. Wait until the buffer tray holder has reached its stop position.

3. Open the sample door.

4. Carefully place the filled buffer tray into the buffer tray holder. Be careful not to spill any solutions in the instrument or cause any cross-contamination between buffers loaded on the buffer tray.

Note: The 12-tube strips should be positioned towards the front of the instrument with the buffers towards the back.

5. Close the sample door and click  in the [Status Information panel](#) to move the buffer tray holder to the **Wash Park** position.

Note: Leave the sample door open if you want to load your samples immediately afterward.

Note: If you close the sample door, the buffer tray automatically moves to the **Wash Park** position after a period of 5 minutes.

Installing a QIAxcel gel cartridge and smart key

Note: Read section [Unpacking a QIAxcel Kit](#) prior to performing this procedure.

1. Remove the QIAxcel gel cartridge from the QX Cartridge Stand.
2. Open the cartridge door and insert the QIAxcel gel cartridge into the QIAxcel Advanced. The cartridge description label should be facing toward the front and the purge hole should be toward the rear of the instrument.

Note: Ensure the purge cap seal has been removed as described in [Unpacking a QIAxcel Kit](#).

3. Insert the smart key into the smart key socket near the cartridge. The smart key can be inserted in either direction.

Note: The system will not recognize the cartridge and will not operate if the smart key is not inserted.

Note: If the settings option **Latch cartridge automatically** is selected, the cartridge will be automatically latched after the smart key is detected. Therefore, it is important to insert the smart key as soon as the cartridge has been inserted and the cartridge door has been closed. Refer to section [Settings](#) for information about settings.

4. Close the cartridge door. The cartridge ID and cartridge type will be displayed automatically in **Cartridge Status** in the [Status Information panel](#).

▼ Cartridge Status

Cartridge ID
C110414C99

Cartridge Type
RNA Quality Control

Remaining Runs Remaining Cal. Runs
83 3

Expiration Status Calibration Status
Valid OK

▼ Calibration Details

Calibration Date Accepted By
14.04.2011 13:07:10 JohnSmith

Ch.	Area	Cal. Factor	Result
1	0.0053	0.5762	Passed
2	0.0051	0.6114	Passed
3	0.0050	0.9239	Passed
4	0.0053	0.8302	Passed
5	0.0053	0.4594	Passed
6	0.0053	0.9902	Passed
7	0.0050	1.8963	Passed
8	0.0043	0.7028	Passed
9	0.0045	0.5612	Passed
10	0.0053	0.7647	Passed
11	0.0042	0.7104	Passed
12	0.0051	1.2754	Passed

Cartridge status area.

Removing a QIAxcel gel cartridge

To remove a QIAxcel gel cartridge from the QIAxcel Advanced proceed as follows:

1. Prepare the QX Cartridge Stand as described in section [Unpacking a QIAxcel Kit](#).
2. Open the cartridge door.
3. Remove the smart key.

Note: If the settings option **Latch cartridge automatically** is selected, the cartridge will be unlatched automatically after the smart key is removed. Therefore, it is important to remove the smart key first before trying to remove the cartridge. Refer to section [Settings](#) for information about settings.

Note: If the QIAxcel Advanced is switched on and **Latch cartridge automatically** is unchecked, ensure the QIAxcel gel cartridge is unlatched. If latched, unlatch it. See section [Status Information panel](#) for information on how to do this.

4. Remove the QIAxcel gel cartridge.
5. Install the purge cap seal to close the purge port.
6. Place the QIAxcel gel cartridge in the QX Cartridge Stand.

Note: Ensure that the capillary tips are submerged in QX Wash Buffer.

Storing a QIAxcel gel cartridge

Storage of QIAxcel DNA gel cartridges after delivery

All components of the QIAxcel DNA High Resolution Kit, and the QIAxcel DNA Screening Kit, except for the gel cartridge and the QX Intensity Calibration Marker, can be stored dry at room temperature (15–25°C) and are stable until the expiration date under these conditions.

The QIAxcel gel cartridge and the QX Intensity Calibration Marker should be stored at 2–8°C upon arrival and are stable until the expiration date under these conditions.

All components of the QIAxcel DNA Fast Analysis Kit can be stored dry at room temperature, except for the QIAxcel gel cartridge, QX Intensity Calibration Marker, QX DNA Size Marker 50 bp – 1.5 kb, and QX Alignment Marker 15 bp/3 kb. The QIAxcel gel cartridge and the markers should be stored at 2–8°C upon arrival. Components are stable until the expiration date under the indicated conditions.

Storage of the QIAxcel RNA gel cartridge after delivery

QX RNA Size Marker 200–6000 nt should be stored at –20° to –80°C, and is stable until the expiration date under these conditions.

QX RNA Denaturation Buffer should be stored at 2–8°C and is stable until the expiration date under these conditions.

All other components of the QIAxcel RNA QC Kit v2.0, except for the QIAxcel gel cartridge, can be stored dry at room temperature (15–25°C) and are stable until the expiration date under these conditions.

The QIAxcel gel cartridge should be stored at at 2–8°C and is stable until the expiration date under these conditions.

Occasional use

Store QIAxcel DNA and RNA gel cartridges at 2–8°C until the first use. If the QIAxcel gel cartridge is not being used on a daily basis, close the purge port with the purge port seal, return the gel cartridge to the blister package, inserting the capillary tips into the soft gel. Store the QIAxcel DNA or RNA gel cartridge at 2–8°C in an upright position (see orientation label on blister package).

Note: Storing the QIAxcel DNA or RNA gel cartridge below 2°C can severely damage the cartridge.

Prior to use, the QIAxcel gel cartridge should be placed into the QX Cartridge Stand and protected with the cover whenever exposed to light, and allowed to stand for at least 20 minutes at room temperature.

Daily use

If the QIAxcel gel cartridge is being used on a daily basis, store the cartridge latched in the QIAxcel Advanced in the “Park Position.”

Note: The QIAxcel Advanced must be left on if the cartridge is stored in the “Park Position” and the cartridge must be latched. Do not switch the QIAxcel Advanced off.

If more than one QIAxcel gel cartridge is being used on a daily basis, store the second cartridge in the QX Cartridge Stand in the dark or protected with the cover. Make sure that the cartridge stand reservoir is filled with wash buffer and covered with mineral oil (refer to [Unpacking a QIAxcel Kit](#)). Alternatively, close the purge port with the purge port seal, return the QIAxcel gel cartridge to the blister package, inserting the capillary tips into the soft gel, and store the QIAxcel gel cartridge at room temperature in an upright position (see orientation label on blister package).

The QIAxcel gel cartridge can be stored in this manner until expiration date as indicated on the kit label.

Operating the QIAxcel Advanced

Samples are processed using the **Process** environment of the QIAxcel ScreenGel Software.

Depending on the role of the user logged in, the environments behave differently. Users with the **Routine User** role are guided step by step to start a process. Users with the **Advanced User** role will not be guided step by step, they can freely define analysis and process profile parameters when starting a run.

This section describes the operating procedure of the QIAxcel Advanced for the routine user. Advanced features of the QIAxcel ScreenGel Software, which are not available to the routine user, are described in the [Process](#) section.

Things to do before starting

- Carefully read the handbook supplied with the QIAxcel Kit.
- Prepare the reagents and QX Alignment Marker to be used. For instructions about how to do this, see section [Setting up the QIAxcel Advanced](#), or refer to the *QIAxcel Kit handbook*.

Note: Refer to steps 1, 2, 3, 4, 7 and 8 in [Running procedure](#) for information about the alignment marker or size marker. These steps can be skipped later. The alignment marker required is displayed in the software and can now be prepared.

- Prepare your samples. Refer to the handbook supplied with the QIAxcel Kit for instructions about how to do this. For optimal results, the sample solution should be pH 6–9 and should not have an ionic content greater than that of a typical PCR buffer.

Note: If you need to run a size marker side by side with the samples, prepare it in the required position on the sample plate. Refer to the handbook supplied with the QIAxcel Kit for instructions about how to do this.

CAUTION 	Damage to the cartridge [C5] If less than 12 samples are processed, fill the empty sample wells with the QX DNA Dilution Buffer or QX RNA Dilution buffer. Failure to do so may cause damage to the capillary channels.
--	---

Starting a run

Routine users can run predefined process profiles using the process wizard of the QIAxcel ScreenGel Software only (for advanced process options refer to section [Running a process with advanced options](#)). Follow these steps to perform runs as a routine user:

1. Switch on the QIAxcel Advanced at the power switch.
2. Switch on the computer, launch the QIAxcel ScreenGel Software from the Windows start menu under **QIAGEN/QIAxcel** or from the desktop icon.
3. In the QIAxcel ScreenGel software, select a mode (DNA or RNA) and log in (for detailed information, refer to the [User authentication](#) section). The **Process** environment opens and displays the first screen of the process profile of the process wizard.

Note: The  icon indicates that the connection is being established and the  icon shows that the QIAxcel Advanced is connected. In the case that the instrument could not be connected, a message will be shown notifying that the instrument is not available. If you didn't switch on the instrument at the moment, click **Instrument not needed**. If you need the instrument, click **Troubleshoot**.

Follow the instructions in the message. For more detailed instructions, refer to the troubleshooting section [System setup](#). Close the message. To retry to connect to the instrument, click the  icon.

Note: The QIAxcel ScreenGel Software comes with an up-to-date instrument software for the QIAxcel Advanced instruments with serial number 30281 and higher. If the software connects to the instrument for the first time, it checks if the instrument software on the instrument is up-to-date. If not, it updates the instrument software. This process takes a few minutes. A message is shown during that time. Let the update be completed. Do not turn off the instrument or disconnect the cable between the computer and the instrument, and do not close the QIAxcel ScreenGel Software until the update is complete. After a successful update, the QIAxcel ScreenGel Software automatically connects to the instrument.

4. Install the QIAxcel gel cartridge to be used as described in [Installing a QIAxcel Gel Cartridge and smart key](#).

Note: You can inspect the cartridge status in the **Status Information** panel to the left of the **Process** environment. Refer to the [Status Information panel](#) section for detailed information.

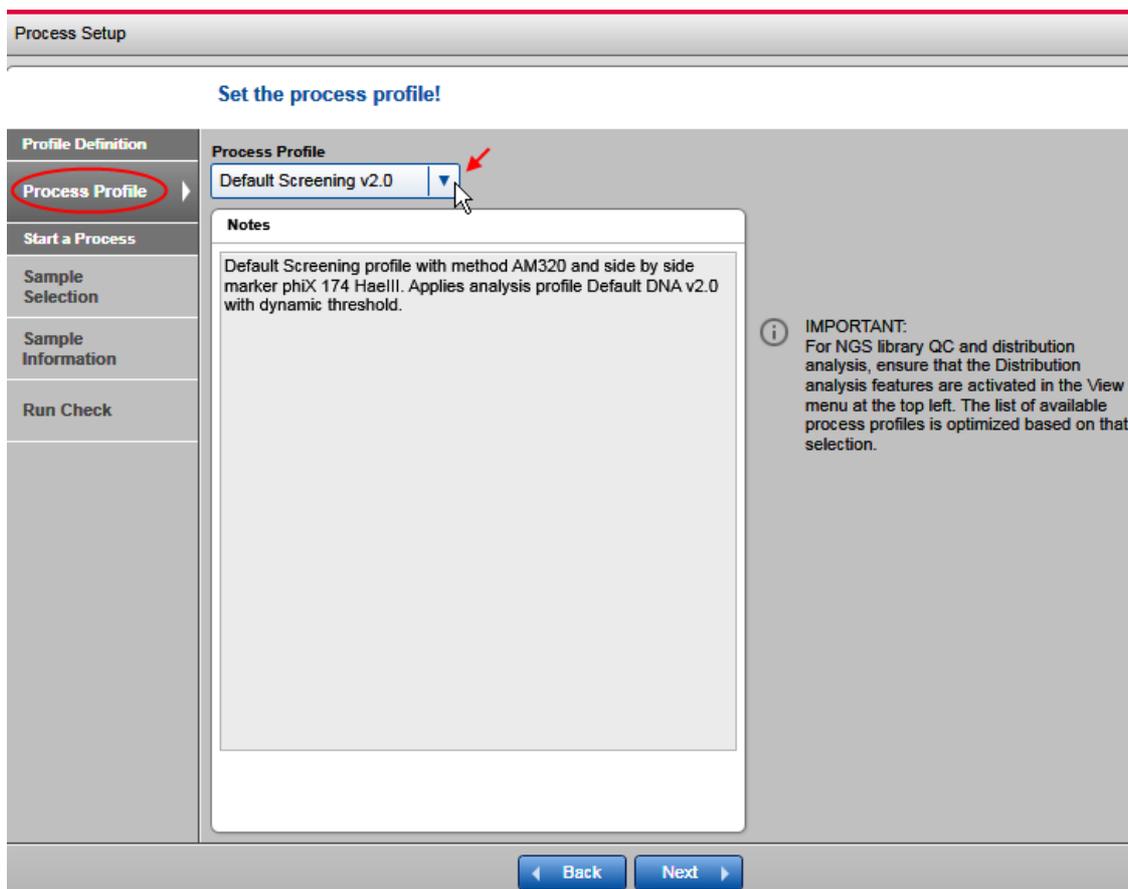
5. Place the buffer tray containing the QX Alignment Marker onto the buffer tray holder as described in [Loading the buffer tray](#).

6. Place the sample strips (in position A) or a 96-well plate onto the sample plate holder.

7. Close the sample door.

Note: If the instrument doors are closed, the buffer tray automatically moves to the **Wash Park** position after a period of 5 minutes.

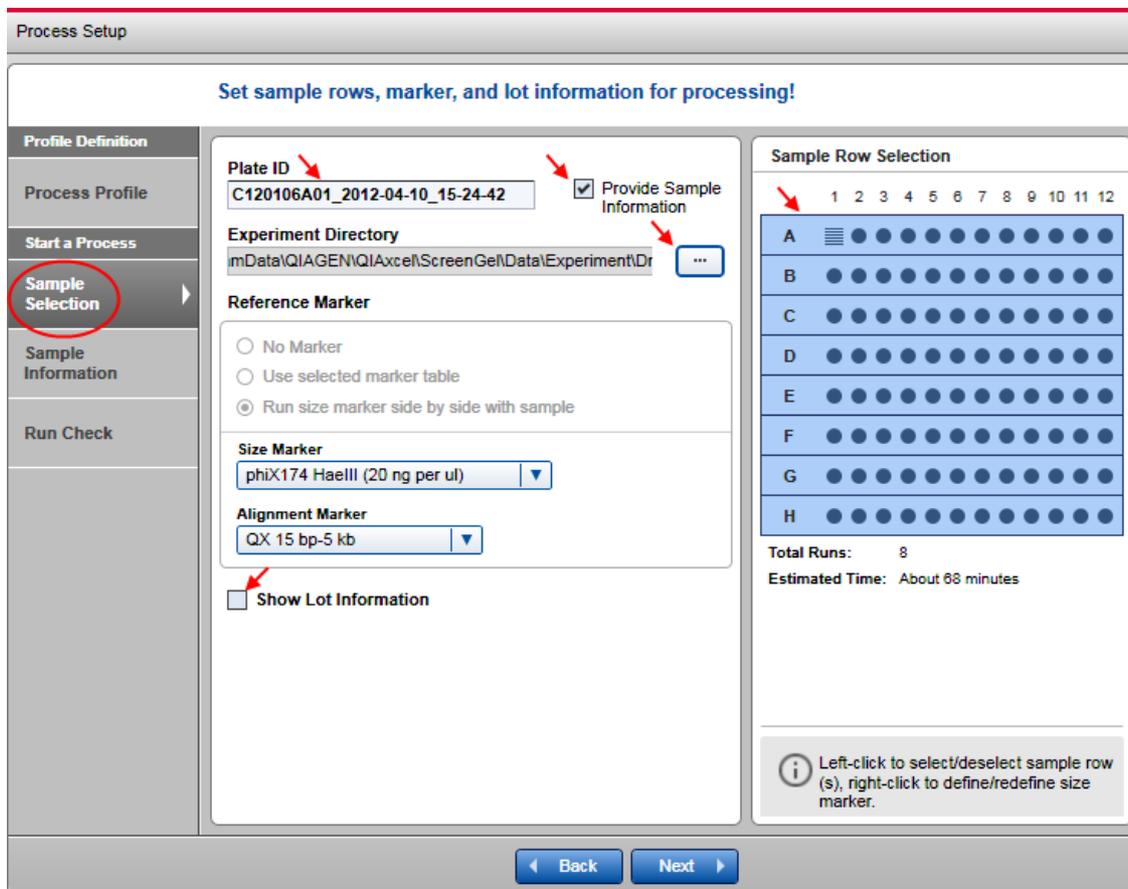
8. In QIAxcel ScreenGel Software, select a predefined process profile in the **Process Profile** screen.



Process Profile screen.

Note: In DNA mode, the **Process Profile** drop-down list does not display profiles that contain peak calling and profiles that contain distribution analysis at the same time. If you miss a profile in the list, activate distribution analysis features for samples containing DNA libraries or genomic DNA and peak calling features for Fast Analysis or standard DNA analysis. To do so, select **Activate Distribution Analysis Features** or **Activate Peak Calling Features** from the **View** menu at the top left. This setting is user specific. It may change automatically, when you open an experiment for review in the **Analysis** environment, that contained peak calling or distribution analysis.

9. Click the **Next** button to proceed to the next screen, **Sample Selection**.



Sample Selection screen.

10. You can optionally change the directory where the experiment will be saved. This can be a local or a network directory.

Note: The directory can only be changed if the process profile used allows it (see [Selecting general process options](#)).

11. Optionally, change the plate ID.

Note: The plate ID will be used to name all the results from this process, for the experiment storing the sample data, as well as for generated report/export files. Therefore, a unique plate ID is required. See [Run parameters and result structure](#) for further information.

Note: For the plate ID, the software allows alpha numeric characters. Special characters such as /&!%\$\$ "' @*+-#=<>|;, etc cannot be used. The software removes blanks at the start and at the end automatically.

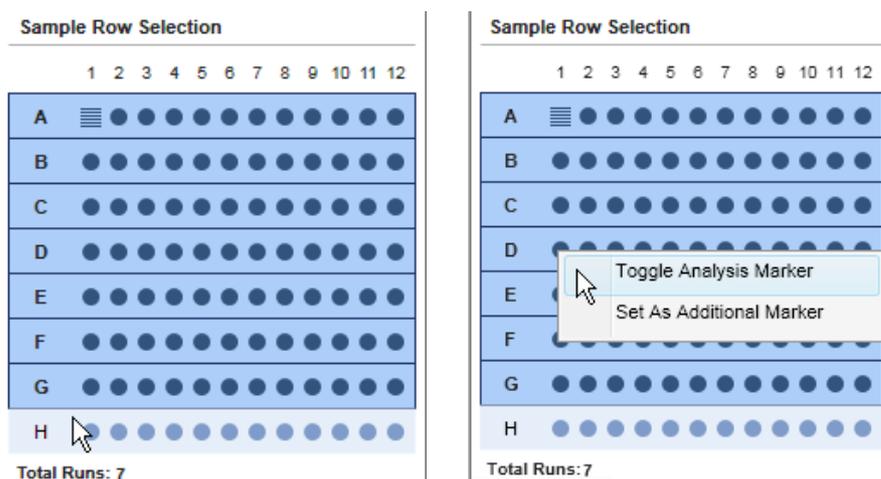
Note: After the process, the plate ID cannot be modified.

Note: If the settings option **Generate plate ID** is selected, the system automatically generates a plate ID following the rules specified in the settings. Refer to section [Settings](#) for more information. However, the plate ID may be modified.

12. You can optionally change selection of sample rows to be processed. Use this option if you want to process less rows than specified in the process profile. Left-click the row to deselect/select.

Note: Changing sample rows is only possible if the process profile used allows it (see [Selecting run parameters](#)).

Note: It is not possible to deselect a row containing the size marker. If you want to do so, proceed to the next step first and then deselect the row.



Sample row H was deselected.

Changing the size marker position to D1.

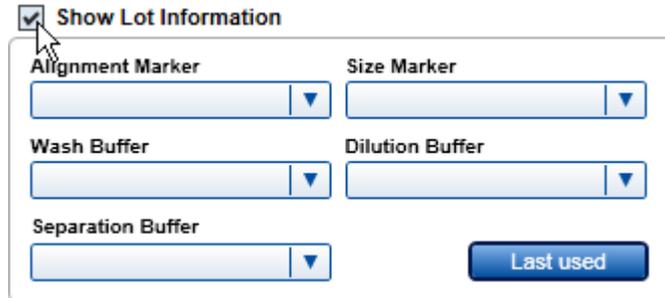
13. You can optionally change the position of the size marker on the plate, by right-clicking the new marker position. Select the option **Toggle Analysis Marker** from the context menu that appears. This size marker will be used for automatic analysis during process, if analysis is included in the process profile.

Note: The size marker position can only be changed if the process profile used allows it (see [Selecting run parameters](#)).

Optional: If you have an additional size marker in the sample plate, right-click the position and select the **Set as Additional Marker** option from the context menu. A rotated ladder symbol appears. Right-click again and select the **Size Marker Name** from the context menu. This information can be used for manual analysis, but will not be used for automatic analysis during the process.

14. If the **No Marker** option is selected, select the prepared alignment marker from the **Alignment Marker** drop-down box. If you leave the **Alignment Marker** drop-down box empty, you have to acknowledge a warning later in the **Run Check** screen.

15. **Optional:** Provide lot information of buffers and markers by checking the **Show Lot Information** box and editing the lot information in the fields displayed.

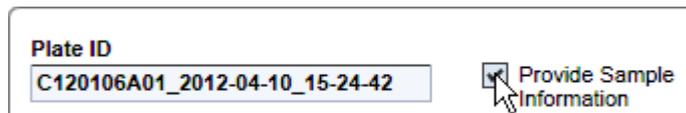


Visible lot information fields.

Note: This is available only if either the settings option **Enable** input fields for **Buffer lot IDs** or **Marker lot IDs** is selected (see [Settings](#)).

Note: The last used lot information values can be selected from drop-down lists. Restore the last used combination of the lot information by clicking on the button **Last used**.

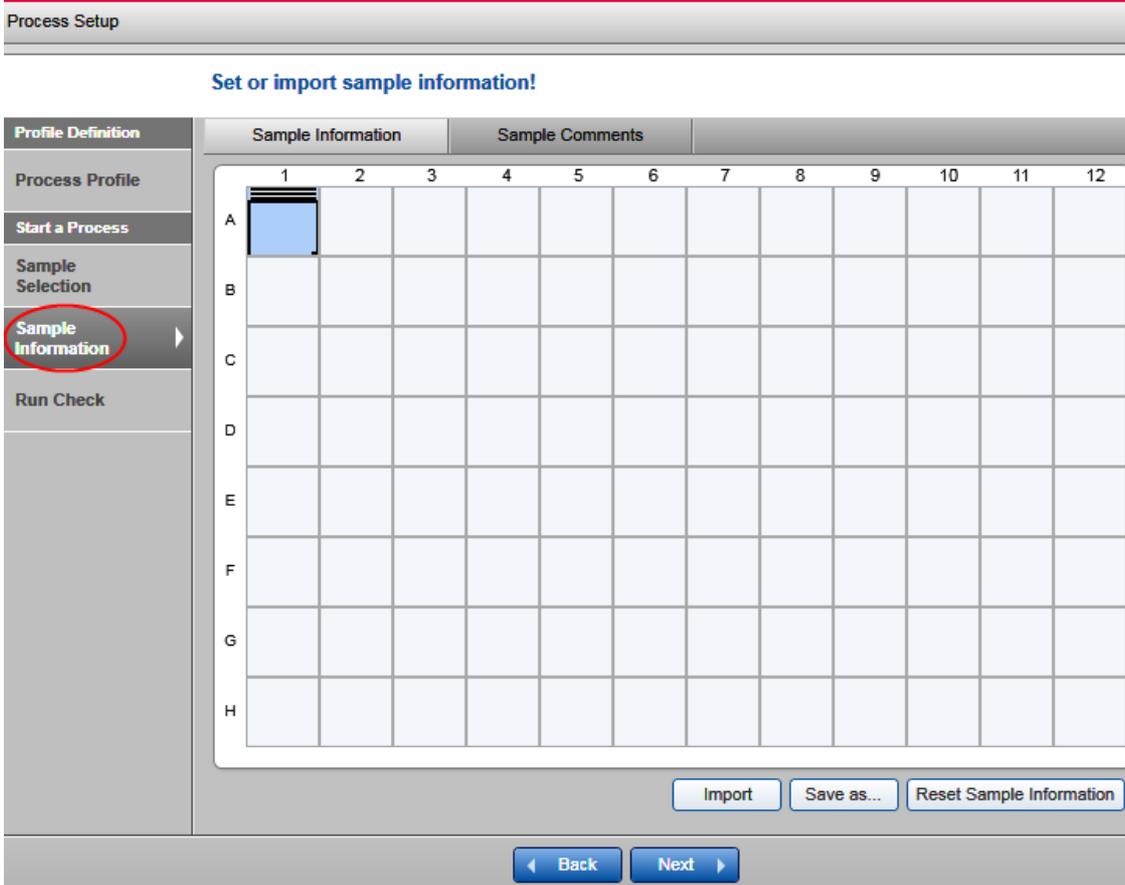
16. **Optional:** Check the **Provide Sample Information** box if you want to provide sample information. If not, proceed to step 19.



Provide Sample Information box checked.

Note: The **Sample Information** screen is enabled only if the check box is checked.

17. Click the **Next** button to proceed to the next screen, **Sample Information**.



Sample Information screen.

18. **Optional:** Provide sample information, entered manually or imported from file.

To provide sample information manually, enter the sample information into the grid. Position A1 is preselected by default. Confirm the information for each position by pressing the **Enter** or the **Tab** key; the next position will be selected automatically for the next input. To provide sample information for a specific position, click the position and enter the sample information.

To save the provided sample information in **rack file** format for later reuse, click the **Save as** button. In the resulting dialog, navigate to the directory where the sample information should be stored, enter a unique file name, and click **OK**.

To import sample information from a file, click the **Import** button. In the lower part of the dialog that appears, select the type of file to be imported. The dialog lists all available files of this type. Alternatively, navigate to the directory where the sample information was stored, select the file and click **OK**. The imported data overwrites all sample information previously provided.

To enter sample comments, click **Sample Comments**. To enter a comment for a specific position, click the relevant cell in the **Sample Comments** tab and enter the text.

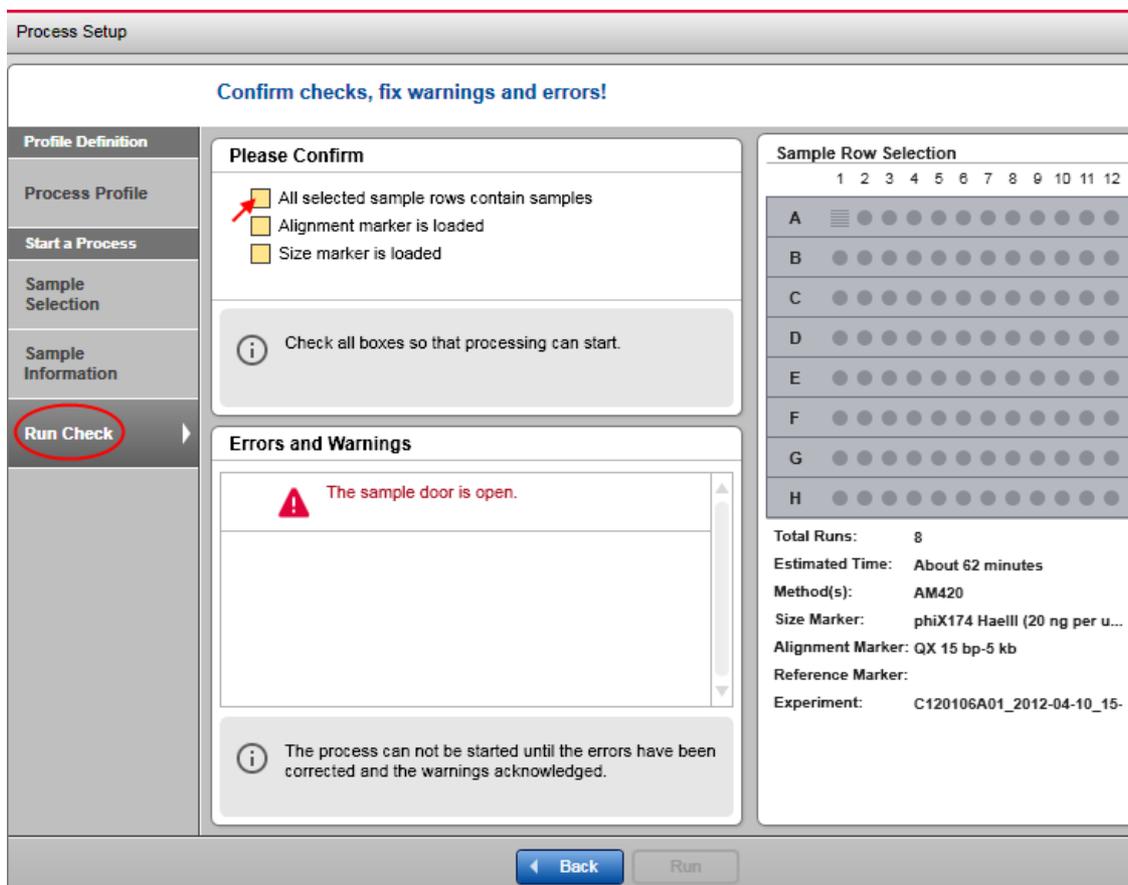
Note: Sample comments can also be imported from a file along with sample information.

For more details, refer to section [Provide Sample Information](#), or click a position in the grid and press the F1 key.

Note: The size marker positions are marked by a "ladder" symbol.

Note: Click the **Reset** button to clear sample information; use the arrow and Tab/Shift+Tab keys to navigate through the positions.

19. Click the **Next** button to proceed to the next screen, **Run Check**.



Run Check screen with "Sample door is open" error.

20. Confirm all check boxes. Resolve the problems indicated by warnings and errors. Use the **Back** and **Next** buttons to navigate.

Note: The process can be started only when all run checks are confirmed and no errors/warnings are shown.

Note: A [handover](#) to an Advanced User may be required.

Note: If the **Run** button is still deactivated, check the [Status Information panel](#) for cartridge and instrument status or refer to the [Troubleshooting](#) section.

Process Setup

Confirm checks, fix warnings and errors!

Profile Definition

Process Profile

Start a Process

Sample Selection

Sample Information

Run Check

Please Confirm

- All selected sample rows contain samples
- Alignment marker is loaded
- Size marker is loaded

Confirmation successful!

Errors and Warnings

No errors or warnings!

Sample Row Selection

	1	2	3	4	5	6	7	8	9	10	11	12
A	☰	●	●	●	●	●	●	●	●	●	●	●
B	●	●	●	●	●	●	●	●	●	●	●	●
C	●	●	●	●	●	●	●	●	●	●	●	●
D	●	●	●	●	●	●	●	●	●	●	●	●
E	●	●	●	●	●	●	●	●	●	●	●	●
F	●	●	●	●	●	●	●	●	●	●	●	●
G	●	●	●	●	●	●	●	●	●	●	●	●
H	●	●	●	●	●	●	●	●	●	●	●	●

Total Runs: 8

Estimated Time: About 62 minutes

Method(s): AM420

Size Marker: phiX174 HaeIII (20 ng per u...

Alignment Marker: QX 15 bp-5 kb

Reference Marker:

Experiment: C120106A01_2012-04-10_15-

Back Run

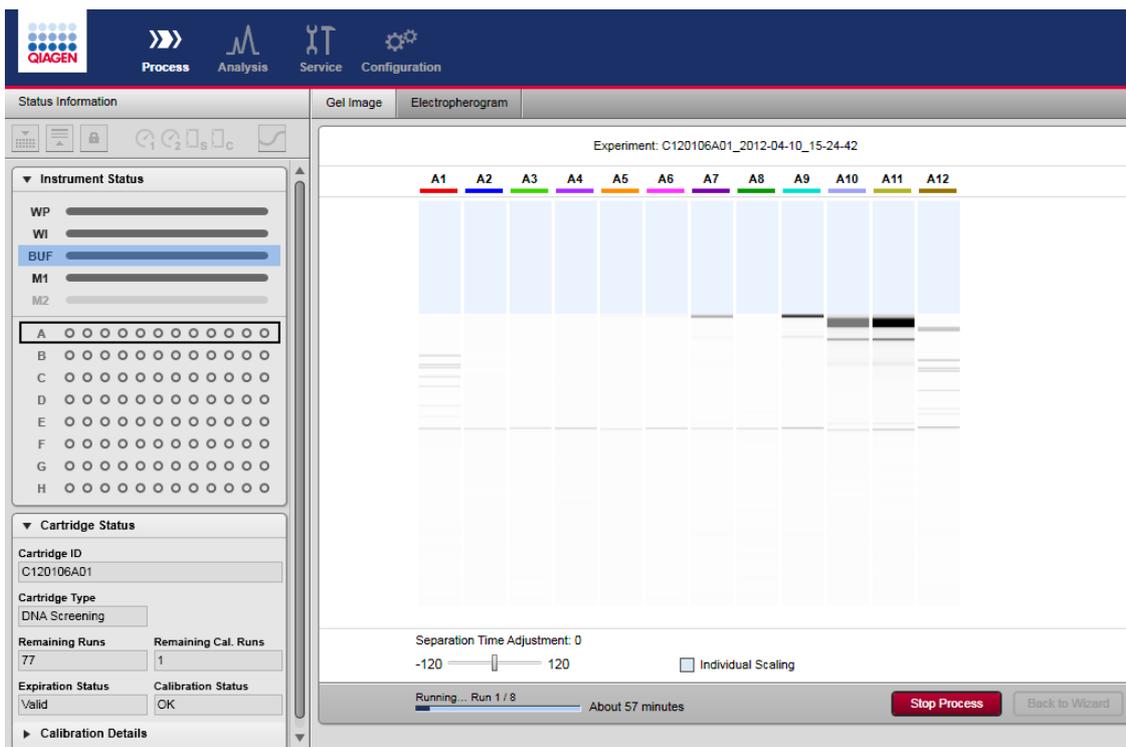
Run Check screen with all confirmation boxes checked and all problems resolved.

21. Start the process by clicking the **Run** button.

The process wizard will be closed and a preview will be shown for each row currently processed. The actions performed by the instrument are shown in the **Instrument Status** panel on the left. A progress bar below the preview shows the progress of the whole process and the estimated remaining process time.

Depending on the report settings the generated report may be displayed.

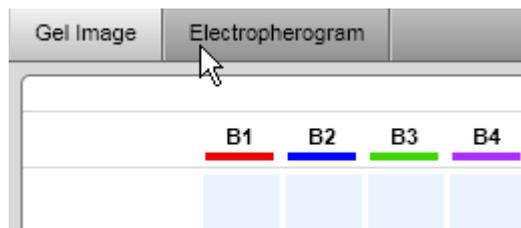
Note: Opening the cartridge door or sample door during operation of the QIAxcel will cause the system to stop the action it is currently performing. The process is stopped and cannot be recovered. No sample data are stored for the row currently processed. Sample data are stored for completed rows only. No analysis, peak calling or report/export is performed. Thus, the stored sample data contain raw data only.



Process currently running row A.

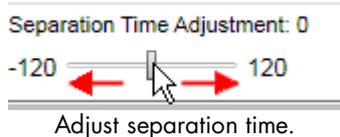
Actions during process run:

- You can switch between the gel and electropherogram preview by clicking on the respective tabs.



Switching from Gel Image to Electropherogram.

- Optionally, adjust the separation time. To do so, move the **Adjust Separation Time** slider below the preview. Moving it to the extreme left position will shorten the separation time by 120 seconds, moving it to the extreme right position will extend the separation time by 120 seconds. Moving the slider takes effect for an actual ongoing separation as well as for all following separations during the process.



Note: When starting the next process by clicking the **Run** button, the slider is automatically reset to the middle position and the separation time will be applied as defined in the method.

- Optionally, switch the check box **Individual Scaling** on/off to adapted colors to the overall maximum signal height of all samples. See [Gel view](#) for more information about individual scaling. The check box **Individual Scaling** is initially set to off.
- The process can be stopped by clicking the **STOP** button below the preview.

Note: If the instrument motors are currently moving, the process will stop after this movement.

Note: No sample data are stored for the row processed. Sample data are stored for completed rows only. No analysis, peak calling, or report/export are performed. Thus, the stored sample data contains raw data only.

Actions after the process has finished:

The screenshot displays the QIAGEN software interface. At the top, there is a navigation bar with icons for Process, Analysis, Service, and Configuration. Below this, the 'Status Information' tab is active, showing 'Instrument Status' and 'Cartridge Status' for Cartridge ID C120106A01. The 'Cartridge Status' section includes fields for Cartridge Type (DNA Screening), Remaining Runs (70), Remaining Cal. Runs (1), Expiration Status (Valid), and Calibration Status (OK). The main area shows an 'Electropherogram' for Experiment: C120106A01_2012-04-10_15-24-42, with lanes labeled H1 through H12. The electropherogram shows a series of peaks across the lanes. At the bottom of the interface, a 'Process finished.' message is displayed, along with a 'Stop Process' button and a 'Back to Wizard' button.

Process has finished.

- The next process can be started by returning to the process wizard by clicking the **Back to Wizard** button below the preview.
- To inspect the sample data, switch to the **Analysis** environment. For information on how to do that, refer to sections [Environments](#), [Handling samples and experiments](#) and [Viewing sample data](#), respectively. Return to the **Process** environment and click the **Back to Wizard** button to start the next process.

QIExcel ScreenGel Software

The user-friendly QIExcel ScreenGel Software has been specifically developed for use with the QIExcel Advanced system. The software offers interactive tools that simplify data analysis, allow fast data interpretation, and provide flexibility in viewing data and results in both electropherogram and gel image formats.

The software provides wizard-based run setup and convenient analysis and template profiles for standardized sample processing, and offers effortless, customizable documentation of results.

The QIExcel ScreenGel Software is based on a unique algorithm, that has been proven to analyze separation data more reproducibly and accurately than other chromatographic analysis packages. It calculates a variety of peak properties, such as peak number, peak height, peak width, and peak area.

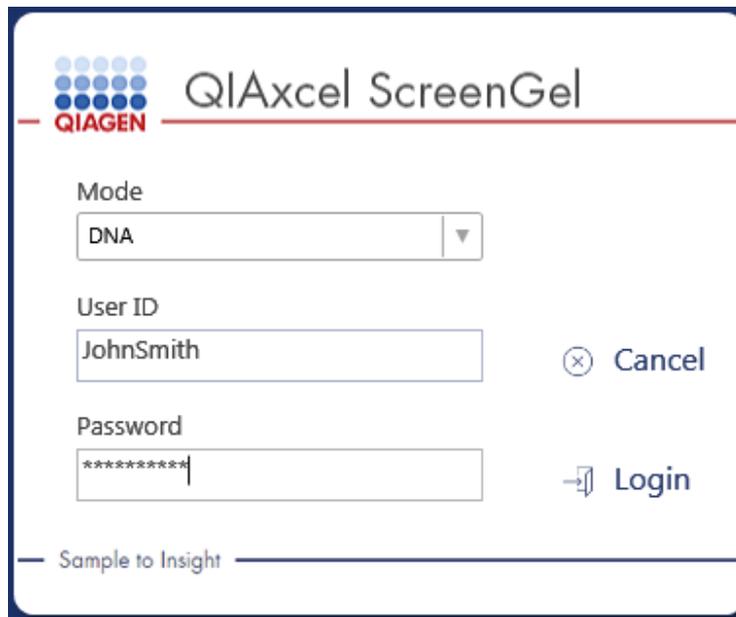
Concepts

This section explains fundamental concepts that each user working with QIExcel ScreenGel Software should become familiar with:

- Modes
- User management
- Environments
- Profiles
- User interface

Modes

The QIAxcel ScreenGel Software has two modes – one for DNA and one for RNA analysis. The main purpose of the modes is to adapt the data analysis algorithms to the properties of the analytes. In addition, the modes ensure that valid cartridge types are used and that only data of the right type can be loaded from files.



The screenshot shows the QIAxcel ScreenGel login dialog box. At the top left is the QIAGEN logo, consisting of a grid of blue dots above the word "QIAGEN" in red. To the right of the logo is the text "QIAxcel ScreenGel" in a large, grey font. Below the header, there are three input fields: "Mode" with a dropdown menu showing "DNA", "User ID" with a text box containing "JohnSmith", and "Password" with a text box containing "*****". To the right of the "User ID" field is a "Cancel" button with a circled 'X' icon. To the right of the "Password" field is a "Login" button with a right-pointing arrow icon. At the bottom left of the dialog box, there is a horizontal line and the text "Sample to Insight".

Mode selection in login dialog box.

User roles

The QIAxcel ScreenGel Software distinguishes four different user roles, which differ in permissions. Each user is assigned one of these four user roles. This section provides a short overview of the use and permissions of each user role:

Role	Used for	Tasks	Access
Administrator	User management Software configuration	Installation of software Configuration of global settings Administration of user accounts	Configuration environment
Routine User	Routine sample processing and data viewing	Sample processing Inspecting samples	All environments (restricted access)
Basic User	Sample processing and analysis of data without the option of modifying profiles	Sample processing Analysis of samples Report/export	All environments (restricted access)
Advanced User	Sample processing Analysis of data with full access to analysis parameters Creation and modification of profiles	Creating/modifying profiles Sample processing Analysis of samples Report/export	All environments (full access)

- **Administrator**

This role is intended for management of settings and users.

Users assigned this role can change the global settings and perform user management, i.e., management of user accounts (rights, user role, etc.). Users do not have access to profiles, the **Process** environment, the **Analysis** environment, or the **Service** environment.

- [Handover](#) to a user with the user role **Administrator** is possible.

- **Advanced User**

This role is intended for experienced users.

Users assigned this role have access to the full functionality of the software, except for user management. Users can create analysis, process, and report profiles and therefore prepare the working base for other users. They can perform advanced analyses, such as comparison of results from different processes (see [Customizing experiments](#)) and modify profile parameters, if required.

- [Handover](#) to a user with the user role **Advanced** is possible.

- **Basic User**

This role ensures the use of predefined profiles, particularly analysis profiles.

Users assigned this role have access to all environments of the software; however, they can not create new or modify predefined profiles, such as analysis and process profiles. While setting up a new process using predefined process profiles, they can modify marker settings and rows that need to be processed. In the analysis environment, they can open existing experiments and perform routine analyses using predefined analysis profiles, but they cannot modify individual analysis parameters. They can perform report and export using predefined report/export profiles with the option to modify the report/export parameters, but without the option to save this changes.

- [Handover](#) to a user with the user role **Basic User** or **Advanced User** role is possible.

- **Routine User**

This role is intended for laboratories that routinely process large numbers of samples. Users are guided by a wizard for efficient process setup.

Users assigned this role are limited to performing processes using predefined process profiles. In the analysis environment, they can open existing experiments for viewing purposes only.

- [Handover](#) to a user with the user role **Routine User**, **Basic User**, or **Advanced User** role is possible.

Note: One person can be assigned several user roles by creating several user accounts with different roles.

Refer to the [User management](#) section for information on how to create user accounts.

Environments

The QIAxcel ScreenGel Software is composed of four environments providing different functionality. Only one environment can be used at a time.



Environment icons with active "Process" environment.

To switch to an environment, click the environment icon. The functionality of the environments is briefly described in the following table:



Environment enabling runs to be performed on the QIAxcel Advanced system.

Supports data acquisition, allowing integrated data analysis and reporting. For detailed information, refer to the [Process](#) section.



Environment that displays and enables analysis of sample data.

Provides advanced visualization and analysis tools for sample data as well as report and export functionality. For detailed information, refer to the [Analysis](#) section.



Environment for maintenance or service of the QIAxcel Advanced system.

Contains all functions for maintenance and troubleshooting of instrument and cartridges. For detailed information, refer to the [Service](#) section.



Environment for administration of users and system configuration.

Provides access to user management, profile management, and software preferences (settings). For detailed information, refer to the [Configuration](#) section.

Profiles

Data acquisition and analysis in the QIAxcel ScreenGel Software are controlled by **Profiles**. Profiles combine settings and parameters and can be conveniently reused for different purposes (see table below).

The standard procedure is to use predefined profiles. The QIAxcel ScreenGel Software will be installed with a set of predefined profiles that cannot be modified. However, if modifications are necessary, experienced users can create new profiles or change profile settings as required. See the following table:

Profile	Description
Process profile	To define settings for data acquisition. Defines all parameters for the electrophoresis run.
Analysis profile	To define the settings for sample data analysis (analysis parameters).
Peak calling instruction	To define search criteria for peaks of interest. Note: In DNA mode, peak calling instructions are available only if peak calling features are active .
Distribution profile	To define criteria for quality assessment of a DNA library, such as the distribution of the library, including quality checks of the molar ratio or height, as well as molarity or concentration. Note: Distribution profiles are available only in DNA mode and only if distribution analysis features are active .
Report/export profile	To define report and export of sample data and analysis results in various formats.

Note: Process profiles can include an **Analysis** profile, a **Peak Calling Instruction** or a **Distribution** profile, and a **Report/Export** profile, which allows fully automated processing including analysis and report.

Note: **Analysis, Distribution and Report/Export** profiles and **Peak Calling Instructions** are included in a process profile by copying the profile name and all profile parameters into the process profile. That means that modifications to the original profiles are not automatically present in the process profile. This prevents process profiles from being changed by mistake and ensures process stability. If the modifications should also be in the process profile, include the modified profile again.

Available profiles and methods are loaded once, upon starting the software.

Profiles created with a previous version of the QlAxcel ScreenGel Software are automatically converted (migrated) to the newest version.

Note: A profile created or saved with a newer version of the QlAxcel ScreenGel Software cannot be opened in previous software versions.

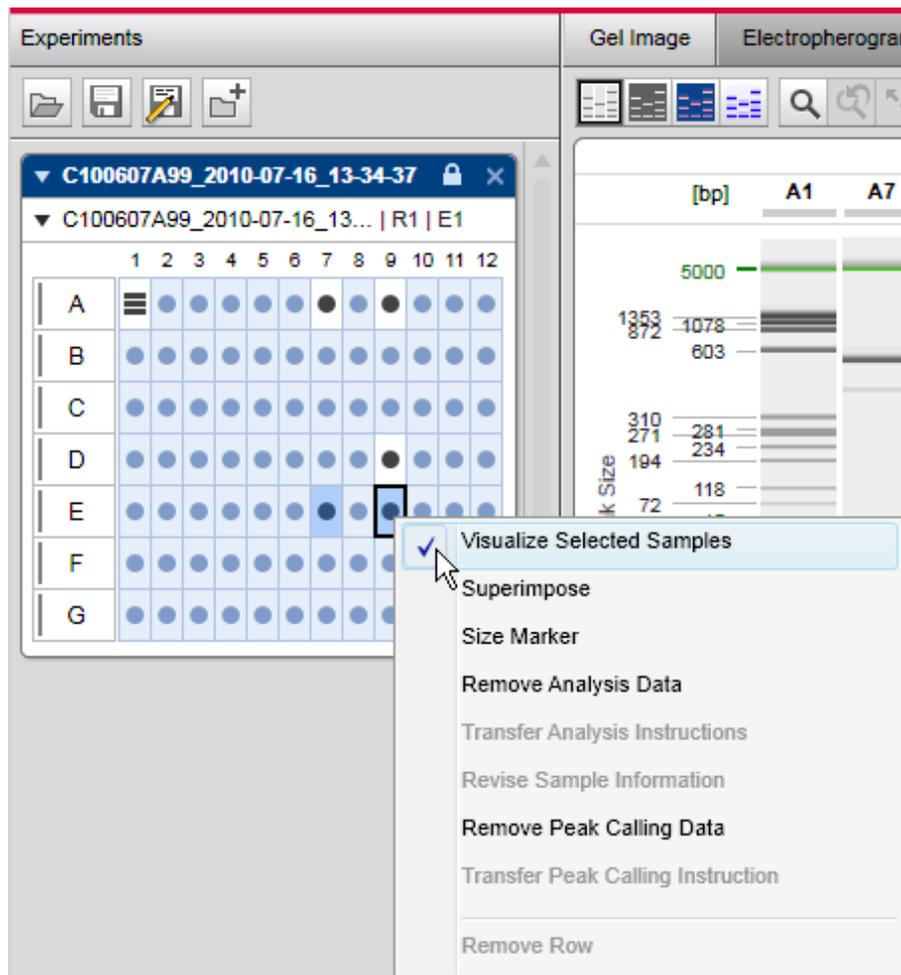
Note: The profile names of the predefined profiles which are installed together with the software are displayed in the selected software language. The profile names of user created profiles are displayed in the language in which the profiles were created. For information how to change the software language, refer to the end of section [Settings](#).

General software usage

QlAxcel ScreenGel Software is a modern software with a state-of-the-art graphical user interface. The controls of the user interface behave in the same way as standard Windows controls. This section explains frequently used terms and several concepts which are specific for the QlAxcel ScreenGel Software user interface.

In the following table, user interface-related terms that are used in this manual are explained.

Left-click	Press the left button of a computer mouse or touchpad.
Right-click	Press the right button of a computer mouse or touchpad.
Double-click	Left-click twice, very quickly.
Drag-and-drop	Move an object (sample, lane) to another place using a computer mouse or touchpad. Left-click to pick up the object. Hold the left mouse button pressed while dragging the object to the new place. Release the mouse button to release the object in its new position. If more than one object was selected, the left-click picks up all selected objects.
Ctrl click	Press and hold the Ctrl key while pressing the left mouse button.
Ctrl+A	Press and hold the Ctrl key while pressing the A key.
Context menu	When right-clicking certain controls, a context-sensitive menu is shown. Not all controls provide a context menu.



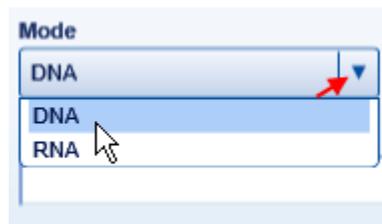
Context menu in the Experiment Explorer.

Tool tip

When the mouse pointer hovers over a control without clicking it, a small text window appears. Not all controls provide a tool tip. Usually a tool tip gives useful information about the functionality of a control, or useful information about possible problems (errors or warnings).

Drop-down box

Drop-down lists allow the selection of one item from a predefined list of items. First, left-click on the triangle to open the list. Then move the mouse down to the correct item. Left-click to select the item.



Drop-down box example.

Toggle button	Left-click the button to toggle. When the button is pressed, the functionality is on. Left-click the button again to toggle the functionality off.
Rubber band function	Span a "rubber band" to define a rectangular region (for zooming into). Left-click to define the starting point, hold the mouse button pressed while dragging. While dragging, a "rubber band" is shown, outlining the rectangular region. Release the mouse button to define the region. The "rubber band" disappears. The system performs the (zooming) functionality based on the defined region.

The status bar (the information line at the bottom of the application window) shows the current user logged in, the date and time, user login name, and application mode (DNA or RNA).



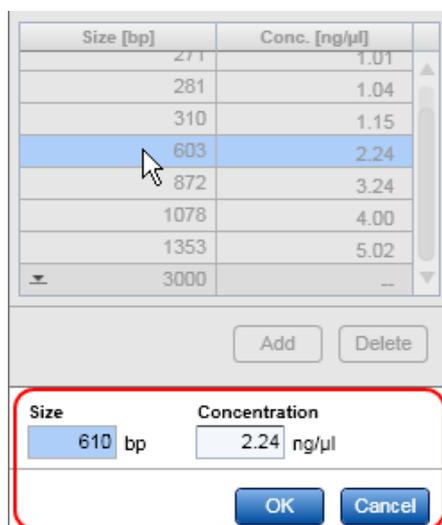
Status bar.

Some areas in the software can be expanded or collapsed; e.g., collapse the **Experiment Explorer** and **Parameters Panel** in the **Analysis** environment by clicking ▼ and expand them again by clicking ►.

Editing data in tables

The graphical user interface of QIAxcel ScreenGel contains many tables. When the table data is editable, this can be performed in a special edit area at the bottom of the table. The table cells themselves are not editable.

An example of an editable table is a **Size Marker** table in the **Process** environment.



Special area for editing table contents.

For example, to change the base pair size from 603 to 610:

1. Highlight the required row by left-clicking it.
2. Click on the **Size** edit field below the table.
3. Enter 610. While editing, only the controls of the edit area are enabled. In this case, the edit fields **Size** and **Concentration** as well as the buttons **OK** and **Cancel** are all enabled.
4. To accept the values into the **Size and Concentration** fields, click **OK**. To cancel editing and discard the changes, click **Cancel**.

Note: The **OK** and **Cancel** buttons are only enabled if the values in the editable fields have been changed and are valid.

Displaying errors and warnings

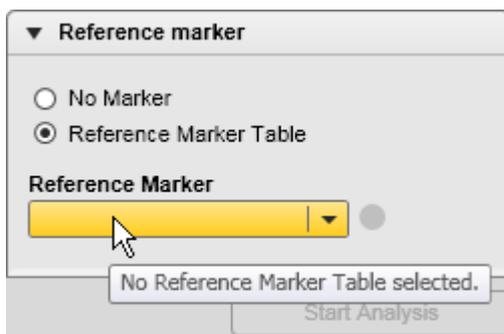
In QIAxcel ScreenGel, yellow controls indicate an error, a warning, or an inconsistency or incompleteness in entered data.

Validation during editing

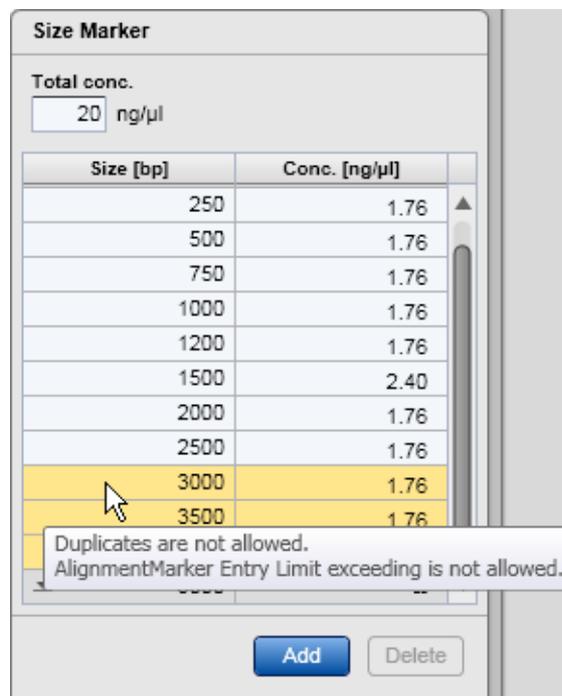
If an incorrect value is entered into an editable field, the background becomes yellow. In addition, a tool tip will be displayed which explains the problem. The following screenshots show examples of errors and the corresponding tool tips.



Negative numbers are not allowed.



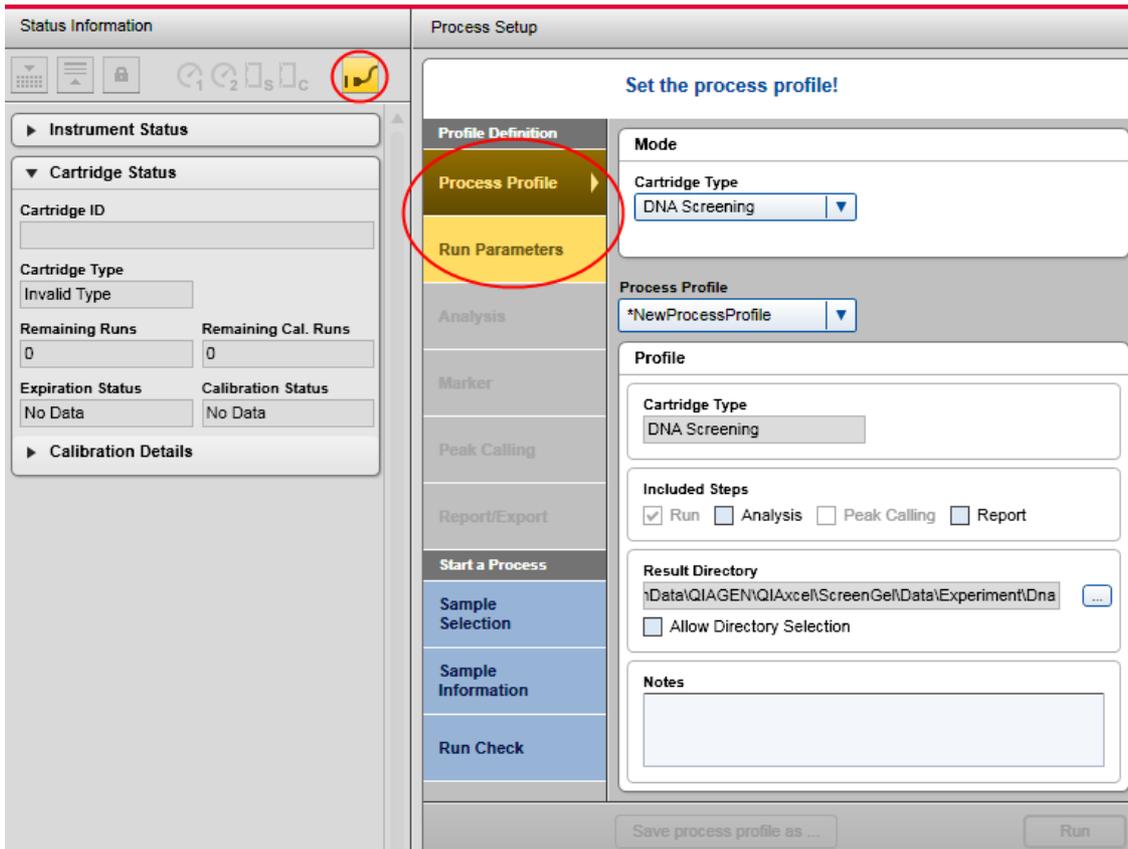
You must select an item.



1. Duplicate entries are not allowed.
2. Exceeding the range of the Alignment Marker is not allowed.

Process screens

If a **Process** wizard screen contains an error or a warning, its screen marker background becomes yellow. You should check the data in this screen and correct the problem.

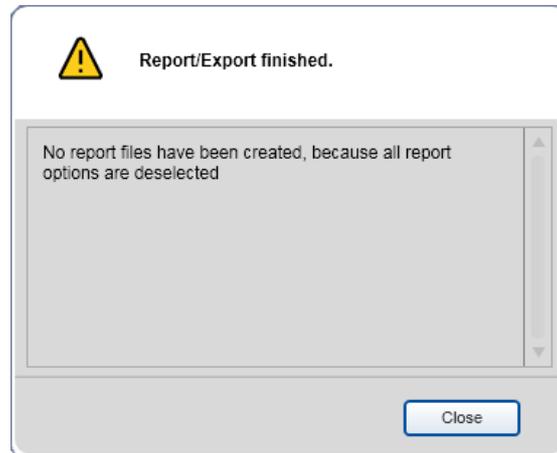


Run Parameters screen is incomplete and therefore the process profile is invalid. Additionally, the instrument is not connected.

Note: The screen marker **Run Check** remains blue (normal state) even if errors/warnings have been detected. To start a process, operate as described in the [Running procedure](#) section for routine users or the [Running a process with advanced options](#) section.

Message boxes

Most problems in QlAxcel ScreenGel are reported using message boxes.

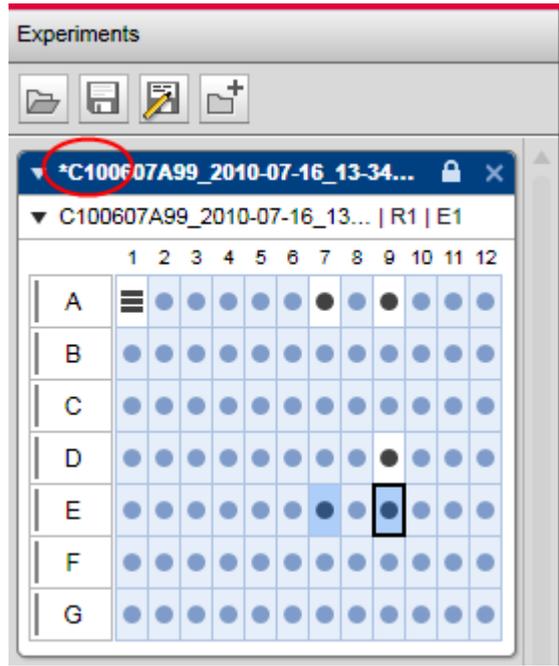


Error message box.

Displaying modifications

The QlAxcel ScreenGel displays modifications in a Windows compliant way, using an asterisk at the left of the name of the modified object. This is demonstrated by a few examples.

Analysis environment/modification of an experiment (apply or remove analysis, change the lane order, etc.). The name of the experiment will be displayed with an asterisk.



Modified experiment.

Note: A changed profile will be shown in the same way.

Process environment/change of any parameter in the Process wizard

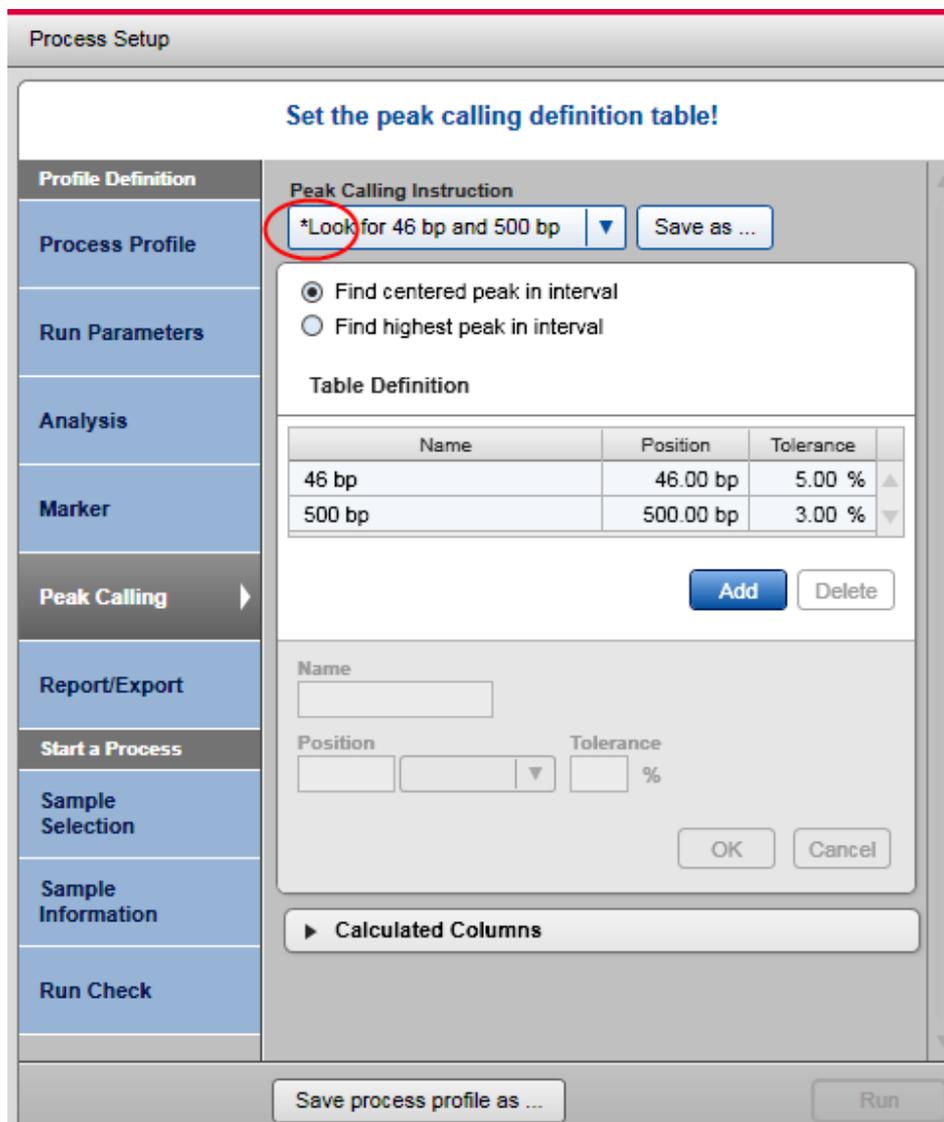
The selected process profile will be displayed with an asterisk.

The screenshot displays the 'Process Setup' window with the 'Process Profile' tab selected. The 'Process Profile' dropdown menu is highlighted with a red circle and shows the selected profile as '*AM320_variant 1'. The 'Profile' section below shows the configuration for this profile, including 'Cartridge Type' (DNA Screening), 'Included Steps' (Run, Analysis, Report), and 'Result Directory' (Data\QIAGEN\QIAxcel\ScreenGel\Data\Experiment\Dna). The 'Notes' section contains the text: 'Default Screening profile with method AM320 and side by side marker phiX 174 HaeIII'. The 'Run' button is visible at the bottom right.

Modified process profile.

Change of parameters in the Peak Calling screen

The selected peak calling instruction in the **Peak Calling Instruction** drop-down list will also be displayed with an asterisk.

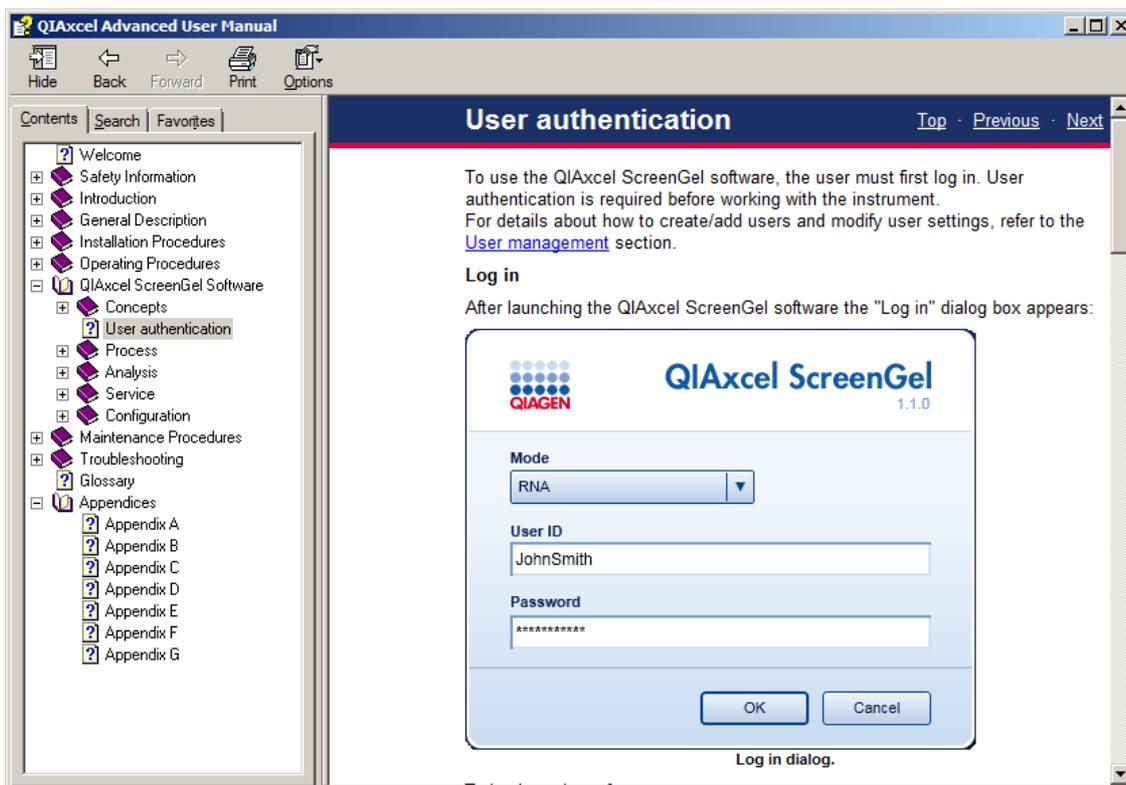


Modified peak calling instruction.

Note: You can start a process or leave the **Process** environment without saving your changes. QIAxcel ScreenGel Software will not remind you to save a process profile as well as the corresponding analysis profile, report/export profile, or peak calling instruction. If you leave the **Process** environment, log out, or exit the application, you should save your changes if they are to be reused.

Getting help

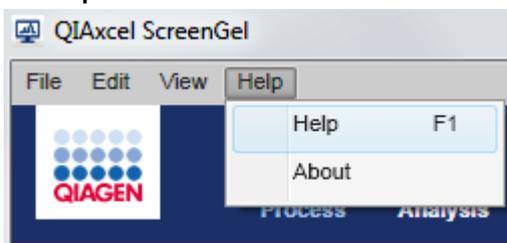
The QIAxcel ScreenGel Software has a context-sensitive help system. After pressing the **F1** key, a context-specific help page is shown. The following image shows the help page corresponding to the login screen:



Help page shown after pressing the F1 key while in the login screen.

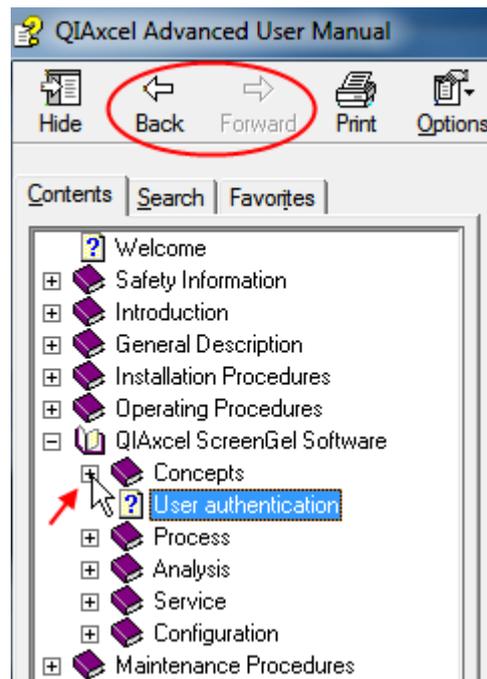
Note: The start menu folder under **QIAGEN/QIAxcel** also contains links to the user manual in **PDF** and **CHM** format.

Alternatively, select **Help** from the **Help** menu.



Access help from the Help menu.

Find a description of the software features in the section [QIAxcel ScreenGel Software](#), organized into sections corresponding to the environments of the software, respectively. Use the content tree on the left-hand side to navigate through the help system.



Click to expand the content tree.

The help system provides several links to other sections. Use the navigation links or buttons of the help system to return to the previous topic.



Click to navigate back.

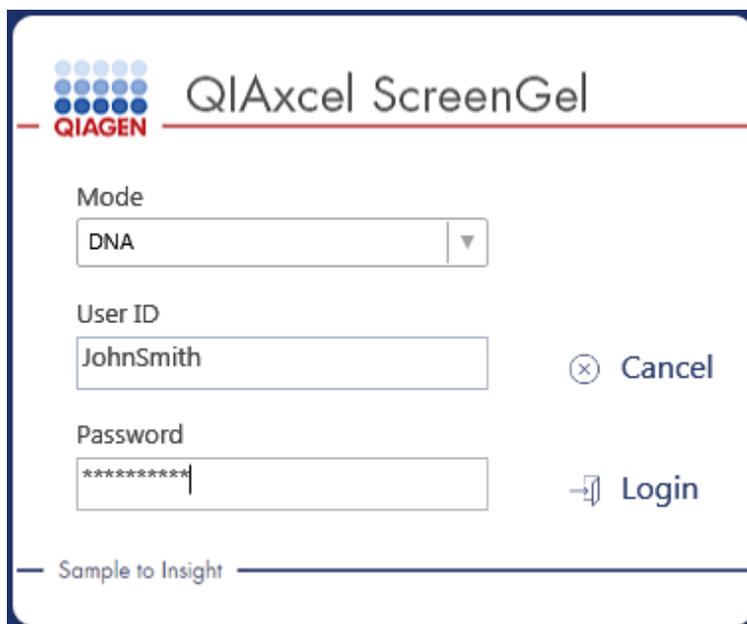
User authentication

To use the QIAxcel ScreenGel Software, the user must first log in. User authentication is required before working with the instrument.

For details about how to create/add users and modify user settings, refer to the [User management](#) section.

Log in

After launching the QIAxcel ScreenGel Software the **Log in** dialog appears:

The image shows a login dialog box for QIAxcel ScreenGel. At the top left is the QIAGEN logo, consisting of a grid of blue dots above the word "QIAGEN" in red. To the right of the logo is the text "QIAxcel ScreenGel" in a large, grey font. Below this is a horizontal red line. The dialog contains three input fields: "Mode" with a dropdown menu showing "DNA", "User ID" with the text "JohnSmith", and "Password" with masked characters "*****". To the right of the User ID field is a "Cancel" button with a close icon (⊗). To the right of the Password field is a "Login" button with a right-pointing arrow icon (→). At the bottom left of the dialog is the slogan "Sample to Insight" in a smaller font.

Log in dialog.

To log in to the software:

1. Select the application mode (DNA or RNA mode).
2. Enter the User ID.
3. Enter the password.
4. Click **Login**.

Note: The mode last used is preselected in the Mode drop-down list.

Note: To change the mode, log out and then log back in again, or restart the application.

Note: If 21 CFR Part 11 support is activated in the [Settings](#) and Maximum number of failed logins is set, the number of failed login attempts is limited. If the limit of failed login attempts is exceeded, the user account is locked. The administrator can unlock the user account in the [user manager](#). If the administrator account is locked, please contact QIAGEN Technical Services.

Note: Refer to the [User management](#) section for information on how to create user accounts.

Note: Refer to the [Getting started with the QIAxcel ScreenGel software](#) section for information about the first login.

Log out

To log out:

1. Select **File/Logout** from the application menu bar.
2. A dialog appears that asks whether you really want to log out. Click the **Yes** the button to confirm the log out.
3. After logging out, the log in dialog appears.

Note: If you want to exit the QIAxcel ScreenGel Software, cancel the log in dialog first.

Hand over

The user can hand over the current session to another user. Hand over is particularly useful as the current working environment, including all open experiments, can be transferred to a different user with equal or extended user rights, e.g., for changing a shift, or advanced analysis, or maintenance.

Note: A handover can only be made to users with an equal or higher [user role](#).

To hand over:

1. Select **File/Handover** from the application menu bar.
2. The **Handover** dialog appears.
3. Enter the **User ID** and **password** and click **Login**.

Changing the user password

To change your password:

1. Select **File/Change Password** from the application menu bar.
2. The **Change password** dialog is displayed.
3. Enter the old password.
4. Enter the new password.

Note: The password must contain one upper-case character, one lower-case character, and one digit. The minimum size of the password is eight characters.

5. Confirm the new password.

6. Click **OK**.

The dialog box features the QIAGEN logo in the top left corner. The title bar reads "Change password for user John Smith." Below the title, there are three text input fields. The first is labeled "Re-enter your old password.", the second is labeled "Enter a new password.", and the third is labeled "Confirm the new password.". At the bottom of the dialog, there are two buttons: "OK" and "Cancel".

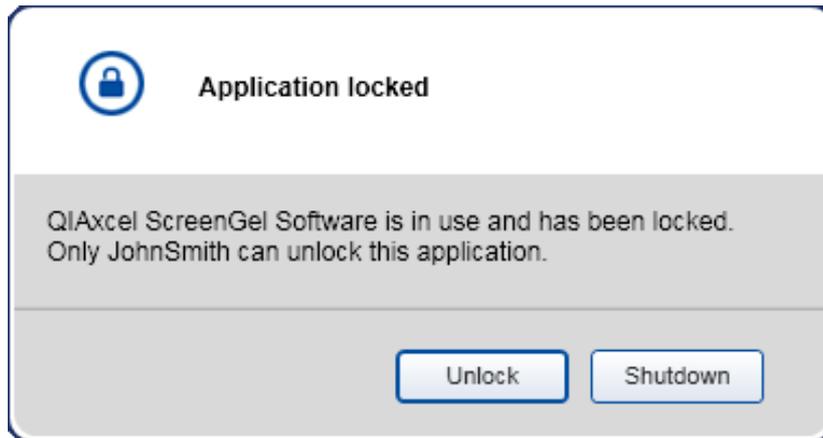
Dialog box that enables the user password to be changed.

Locking the software

The software can be locked to block user access if the computer is left unattended.

To lock the software:

1. Select **File/Lock Application** from the application menu bar.
2. When the application is locked, the following dialog is shown:



Dialog box that enables the application to be unlocked.

Automatic software lock

In order to support 21 CFR Part 11 requirements, the software can be automatically locked after a defined time without user interaction. You can activate 21 CFR Part 11 support and specify the auto-lock time period in the **Settings**. For further details, refer to the [Settings](#) section.

Unlocking the software

To unlock the software:

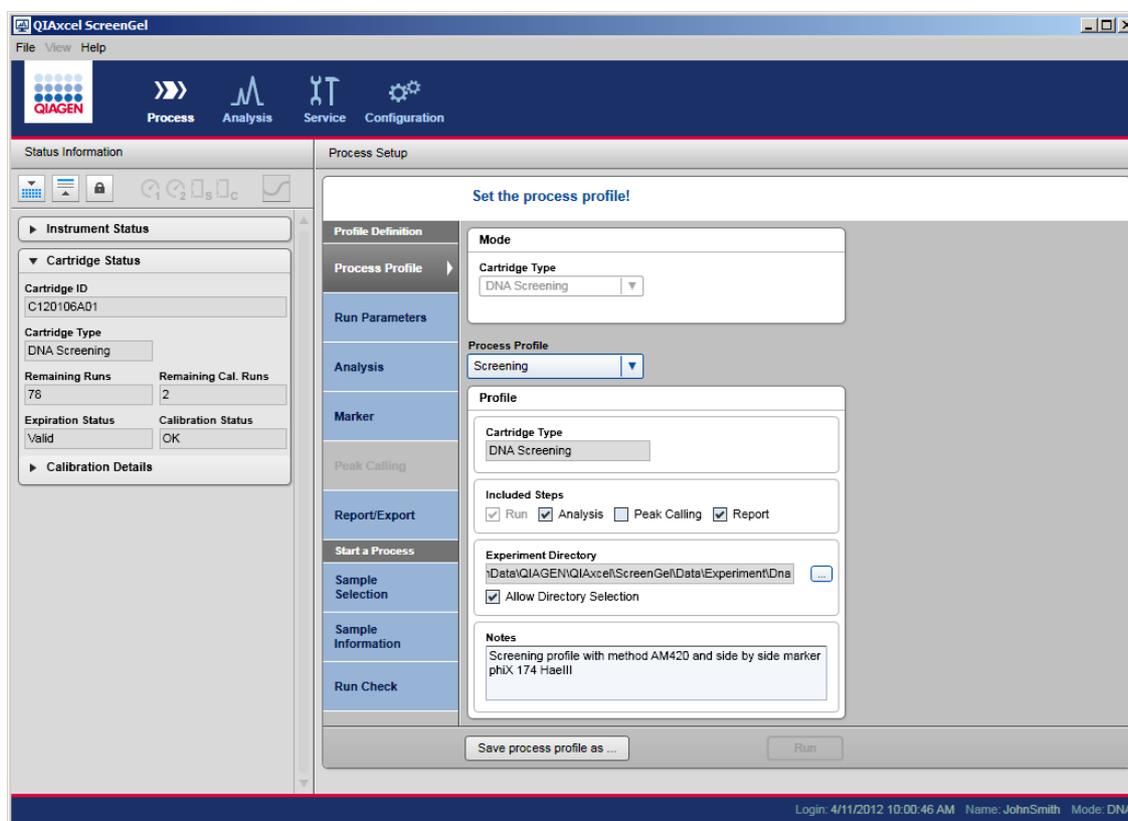
1. Click the **Unlock** button.
2. The **Log in** dialog is displayed.
3. Enter **User ID** and **password**, click **Login**.

Note: Only a user with an equal or higher [user role](#) can unlock the application.

Process

The **Process** environment provides all functionality required for data acquisition:

- Defines process parameters
- Starts the sample process
- Observes the data acquisition process



Process environment with active Process Profile screen and Status Information panel to the left (Advanced User view).

The parameters for the process can be stored for re-use in a process profile.

Refer to the [Starting a run](#) section for information on how to start data acquisition using a predefined process profile. This means that all parameters for data acquisition and also for analysis and report are already defined. The specific sample information has to be entered and the process started. This can be performed by users with the assigned user roles **Routine User**, **Basic User**, or **Advanced User**.

Refer to the [Running a process with advanced options](#) section for detailed information about how to define process parameters and to start a process. This requires the user roles **Basic User** or **Advanced User**; however, there are some limitations for users with the user role **Basic User** with respect to analysis parameters and methods.

To fully automate a process, define a [process profile](#) that optionally includes an **Analysis** profile for analysis parameters and marker information, as well as a peak calling instruction, and a **Report** profile for report/export parameters. Refer to the [Creating a new process profile](#) and [Modifying a process profile](#) sections for information on how to prepare and save process profiles for reuse. This requires the user role **Advanced User**.

The data acquired during processing will be stored in an experiment. Refer to the [Run parameters and result structure](#) and [Handling samples and experiments](#) sections for detailed information.

Running a process with advanced options

Users with the assigned user role **Advanced User** or **Basic User** can modify process profiles, if required. Restrictions apply to users with the role **Basic User** as they can, for example, start a modified process profile, but cannot save it. Restrictions are annotated, where they apply.

Note: For information on how to start a process as a user with the assigned role **Routine User**, refer to section [Starting a run](#).

Follow these steps to perform runs with advanced options:

1. Switch on the QIAxcel Advanced at the power switch.
2. Switch on the computer, launch the QIAxcel ScreenGel Software from the Windows start menu under **QIAGEN/QIAxcel** or from the desktop icon.
3. In the QIAxcel ScreenGel software, select a mode (DNA or RNA) and log in (for detailed information, refer to the [User authentication](#) section). The **Process** environment opens and displays the first screen of the process profile of the process wizard.

Note: The  icon indicates that the connection is being established and the  icon shows that the QIAxcel Advanced is connected. In the case that the instrument could not be connected, a message will be shown notifying that the instrument is not available. If you didn't switch on the instrument at the moment, click **Instrument not needed**. If you need the instrument, click **Troubleshoot**.

Follow the instructions in the message. For more detailed instructions, refer to the troubleshooting section [System setup](#). Close the message. To retry to connect to the instrument, click the  icon.

Note: The QIAxcel ScreenGel Software comes with an up-to-date instrument software for the QIAxcel Advanced instruments with serial number 30281 and higher. If the software connects to the instrument for the first time, it checks if the instrument software on the instrument is up-to-date. If not, it updates the instrument software. This process takes a few minutes. A message is shown during that time. Let the update be completed. Do not turn off the instrument or disconnect the cable between the computer and the instrument, and do not close the QIAxcel ScreenGel Software until the update is complete. After a successful update, the QIAxcel ScreenGel Software automatically connects to the instrument.

4. Install the QIAxcel gel cartridge to be used as described in [Installing a QIAxcel Gel Cartridge and smart key](#).

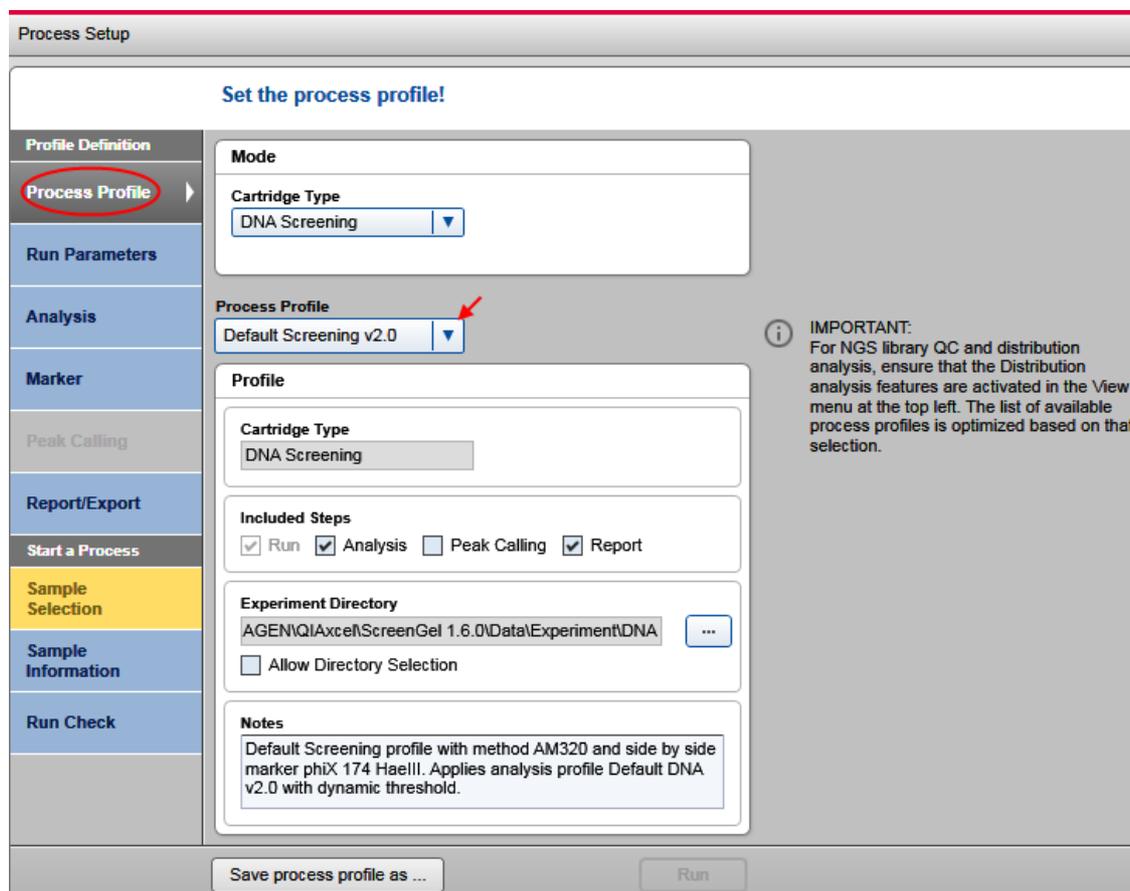
Note: You can inspect the cartridge status in the **Status Information** panel to the left of the **Process** environment. Refer to the [Status Information panel](#) section for detailed information.

5. Place the buffer tray containing the QX Alignment Marker onto the buffer tray holder as described in [Loading the buffer tray](#).

6. Place the sample strips (in position A) or a 96-well plate onto the sample plate holder.
7. Close the sample door.

Note: If the instrument doors are closed, the buffer tray automatically moves to the **Wash Park** position after a period of 5 minutes.

8. In the **Process** environment of QIAxcel ScreenGel, select a process profile in the **Process Profile** screen. The **Process Profile** drop-down lists the available process profiles for the current mode and the cartridge type. The QIAxcel ScreenGel Software comes with a set of predefined process profiles. As a starting point, select the process profile that fits best to your sample type.



Process Profile screen with Screening profile selected.

Note: In DNA mode, the **Process Profile** drop-down list does not display profiles that contain peak calling and distribution analysis in parallel. If you miss a profile in the list, activate distribution analysis features for samples containing **DNA libraries** or **genomic DNA**, and peak calling features for **Fast Analysis** or **standard DNA analysis**. To do so, select **Activate Distribution Analysis Features** or **Activate Peak Calling Features** from the **View** menu at the top left. This setting is user specific. It may change automatically when you open an experiment for analysis in the **Analysis** environment that contained peak calling or distribution analysis.

Note: Select **NewProcessProfile** to create a process profile from scratch. The system will show **NewProcessProfile** after selection. This is only possible for users with the assigned role **Advanced User**. However, it may be easier to select a predefined process profile close to your needs and only modify it slightly.

9. **Optional:** Modify the process profile options if required, as described in the [Process profile options](#) section; restrictions for **Basic Users** are described here.

Note: Experiment directory, markers, and sample rows can be adjusted in the **Sample Selection** screen below, if the process profile allows it. As these adjustments override the options defined in the process profile, modify these options in the process profile only if you want to save them for reuse.

10. **Optional:** Switch to the **Sample Selection** screen.

Sample Selection screen.

11. **Optional:** Change the plate ID.

Note: The plate ID will be used to name all the results from this process, for the experiment storing the sample data, as well as for generated report/export files. Therefore, a unique plate ID is required. See [Run parameters and result structure](#) for further information.

Note: For the plate ID, the software allows alpha numeric characters. Special characters such as /&!%\$\$ "' @*+~#=#<>|;, etc cannot be used. The software removes blanks at the start and at the end automatically.

Note: After the process, the plate ID cannot be modified.

Note: If the settings option **Generate plate ID** is selected, the system automatically generates a plate ID following the rules specified in the settings. Refer to section [Settings](#) for more information. However, the plate ID may be modified.

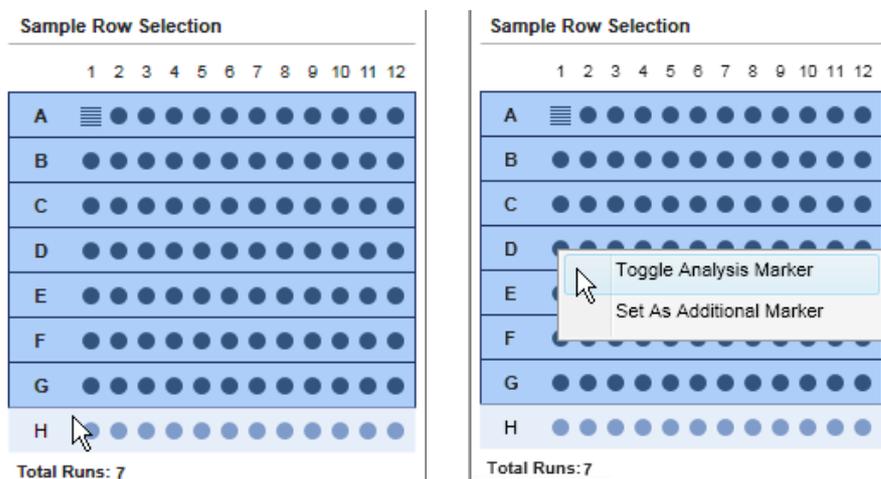
12. **Optional:** Adjust the directory where the experiment will be saved.

Note: This can be a directory on the network. However, during the process, the experiment will be always saved to a local directory first (refer to [Settings](#)), and then copied to the experiment directory defined here, when the process finished.

Note: Changing the experiment directory here is only possible if the process profile allows it (see [Selecting general process options](#)); however, you can switch to the **Process Profile** screen to modify this.

13. **Optional:** Change the selection of sample rows to be processed. Use this option if you want to process less rows than specified in the **Run Parameters** screen. Left-click the row to deselect/select.

Optional: Change the position of the size marker on the plate, by right-clicking the new marker position. Select the option **Toggle Analysis Marker** from the context menu that appears. This size marker will be used for automatic analysis during processing, if analysis is included in the process profile.



Sample row H was deselected.

Changing the size marker position to D1.

Note: Changing sample rows or size marker position here is only possible if the process profile allows it (see [Selecting run parameters](#)); however, you can switch to the **Run Parameters** screen to modify this.

Note: It is not possible to deselect a row containing the size marker.

Optional: If you have an additional size marker in the sample plate, right-click the position and select the **Set As Additional Marker** option from the appearing context menu. A rotated ladder symbol appears. Right-click it again and select the **Size Marker Name** from the context menu. This information can be used for manual analysis, but will not be used for automated analysis during processing.

14. **Optional:** Select the size and alignment marker in the **Size Marker** and **Alignment Marker** drop-down lists as required. This information will be used for automated analysis during the process.

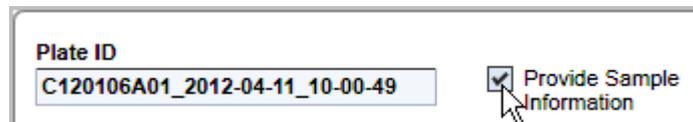
Note: If the **No Marker** option is selected, select the prepared alignment marker. If you do not select an alignment marker in the **Alignment Marker** drop-down list, you will have to acknowledge a warning later in the **Run Check** screen.

15. **Optional:** Provide lot information of buffers and markers by checking the **Show Lot Information** box.

Up to five last-used lot information are stored separately for each lot type. These lastly used values can be selected from drop-down list to use them again. Alternatively, the lot numbers can be typed into the edit field of the combo box. Restore the last used combination of the lot information by clicking on the button **Last used**.

Note: This option is available only if either the option **Enable** input fields for **Buffer lot IDs** or **Marker lot IDs** is selected in the settings (see [Settings](#)).

16. **Optional:** Check the **Provide Sample Information** box if you want to provide sample information. If not, proceed to step 18.

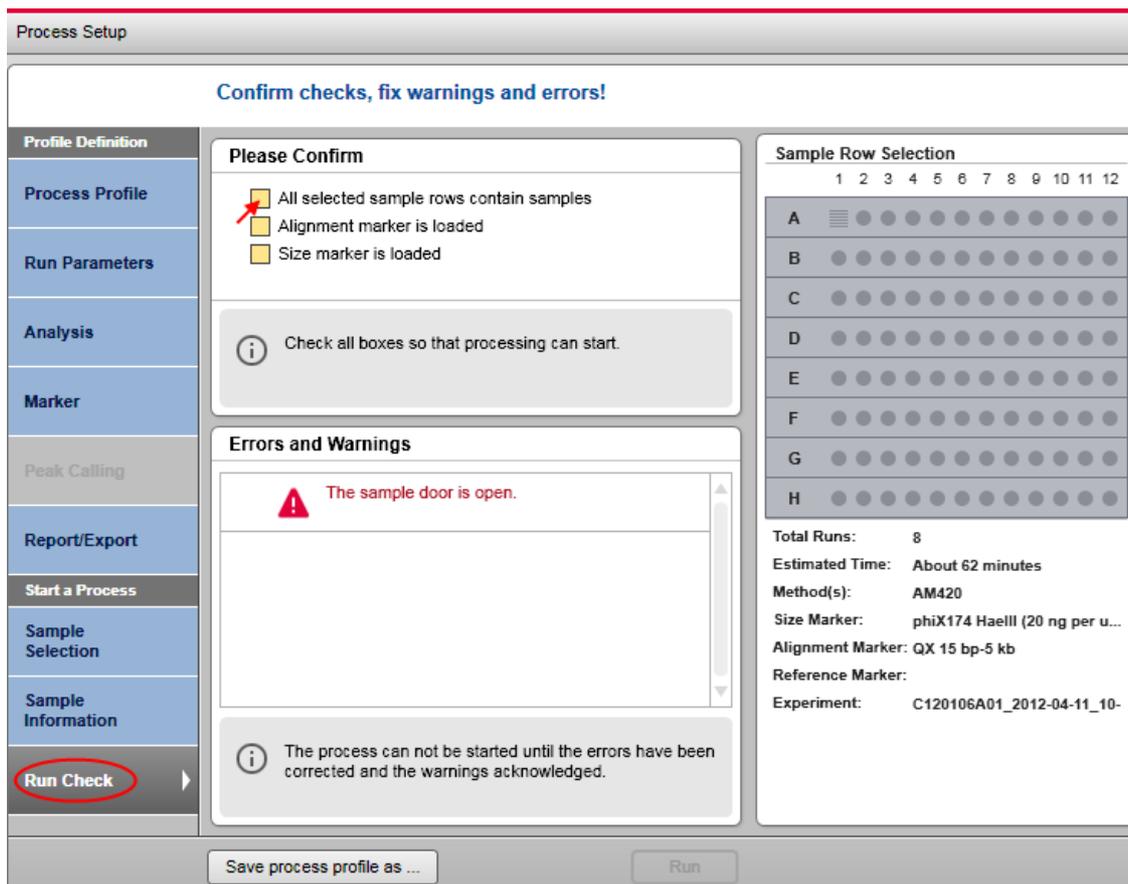
A screenshot of a software interface. On the left, there is a text input field labeled "Plate ID" containing the text "C120106A01_2012-04-11_10-00-49". To the right of this field is a checkbox labeled "Provide Sample Information", which is checked. A mouse cursor is pointing at the checkbox.

Provide Sample Information box checked.

17. **Optional:** Provide sample information in the **Sample Information** screen, entered manually or imported from a file. For detailed information, refer to section [Provide Sample Information](#), or click on one of the positions in the grid and press the **F1** key.

Note: The **Provide Sample Information** box must be checked in the **Sample Selection** screen to access this screen.

18. Switch to the **Run Check** screen. Confirm all check boxes. Resolve the problems indicated by warnings and errors.



Run Check screen with error.

Note: The process can be started only when all run checks are confirmed and no errors are shown. Warnings must be checked as well or removed by eliminating the cause of the warnings.

Note: Advanced Users can acknowledge an uncalibrated cartridge and a red marked reference marker (**Basic Users** can acknowledge a yellow one).

Note: If the run button is still deactivated, check the [Status Information panel](#) for cartridge and instrument status.

19. Start the process by clicking the **Run** button.

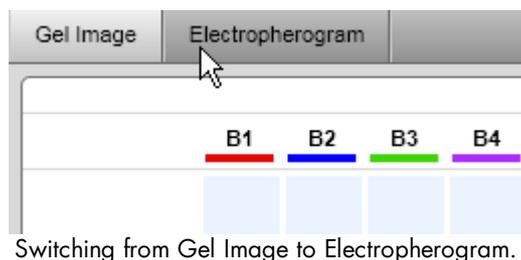
The process wizard will be closed and a preview will be shown for each row currently processed. The actions performed by the instrument are shown in the **Instrument Status** panel on the left. A progress bar below the preview shows the progress of the whole process and the estimated remaining process time.

Depending on the report settings the generated report may be displayed.

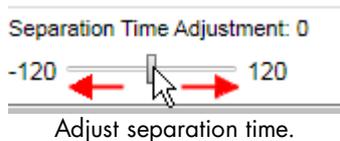
Note: Opening the cartridge door or sample door during operation of the QIAxcel will cause the system to stop the action it is currently performing. The process is stopped and cannot be recovered. No sample data are stored for the row currently processed. Sample data are stored for completed rows only. No analysis, peak calling or report/export is performed. Thus, the stored sample data contain raw data only.

Actions during process run:

- You can switch between the gel and electropherogram preview by clicking on the respective tabs.



- Optionally, adjust the separation time. To do so, move the **Adjust Separation Time** slider below the preview. Moving it to the extreme left position will shorten the separation time by 120 seconds, moving it to the extreme right position will extend the separation time by 120 seconds. Moving the slider takes effect for an actual ongoing separation as well as for all following separations during the process.



Note: When starting the next process by clicking the **Run** button, the slider is automatically reset to the middle position and the separation time will be applied as defined in the method.

- Optionally, switch the check box **Individual Scaling** on/off to adapted colors to the overall maximum signal height of all samples. See [Gel view](#) for more information about individual scaling. The check box **Individual Scaling** is initially set to off.
- The process can be stopped by clicking the **STOP** button below the preview.

Note: If the instrument motors are currently moving, the process will stop after this movement.

Note: No sample data are stored for the row processed. Sample data are stored for completed rows only. No analysis, peak calling, or report/export are performed. Thus, the stored sample data contains raw data only.

Actions after the process has finished:

The screenshot displays the QIAGEN software interface. At the top, there is a navigation bar with icons for Process, Analysis, Service, and Configuration. Below this, the 'Electropherogram' tab is active, showing a gel image for experiment C120106A01_2012-04-10_15-24-42. The gel image has 12 lanes labeled H1 through H12. A left sidebar shows 'Instrument Status' and 'Cartridge Status' for Cartridge ID C120106A01, with 'Remaining Runs' at 70 and 'Remaining Cal. Runs' at 1. The bottom of the interface shows 'Separation Time Adjustment: 0' and 'Process finished.' with a 'Back to Wizard' button.

Process has finished.

- The next process can be started by returning to the process wizard by clicking the **Back to Wizard** button below the preview.
- To inspect the sample data, switch to the **Analysis** environment. For information on how to do that, refer to sections [Environments](#), [Handling samples and experiments](#) and [Viewing sample data](#), respectively. Return to the **Process** environment and click the **Back to Wizard** button to start the next process.

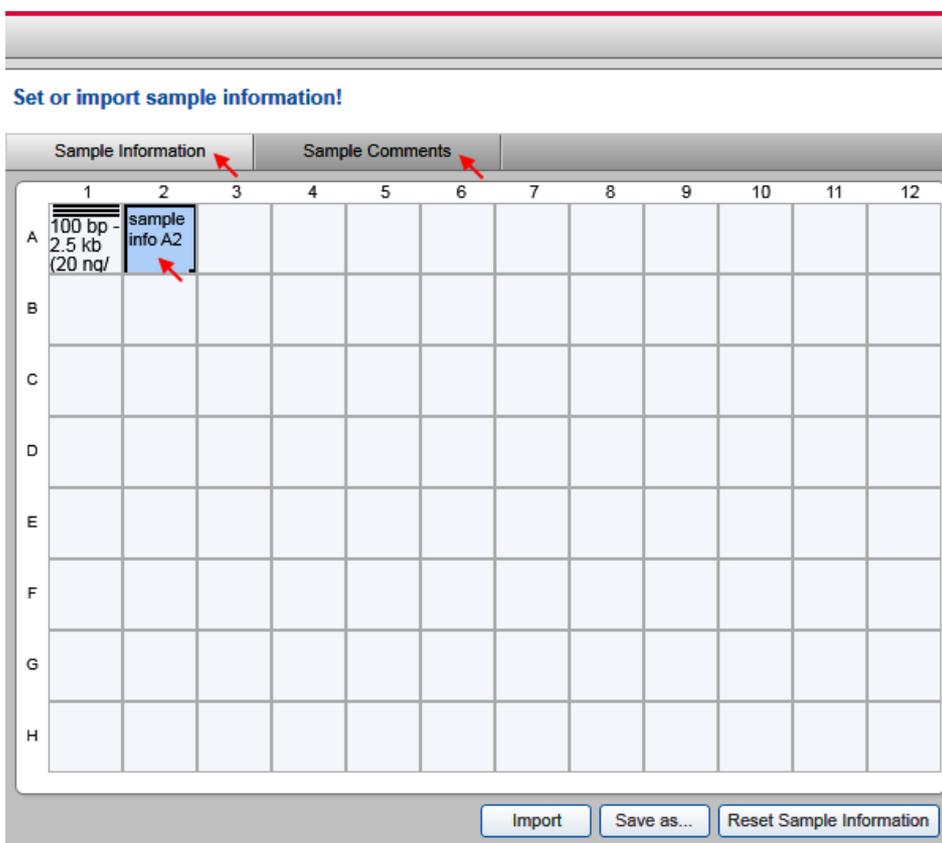
Provide sample information

To access the **Sample Information** screen, the **Provide Sample Information** check box must be checked in the **Sample Selection** screen.

Use the **Sample Information** screen to:

- enter sample information, typically sample IDs
- enter comments
- import sample information and comments for all plate positions from a file
- save sample information (without comments) for later reuse

The sample information grid becomes automatically active upon entering the **Sample Information** step. To switch to sample comments, click the **Sample Comments** tab. To switch back to the sample information grid, click the **Sample Information** tab.



Entering sample information in the Sample Information screen; size marker at A1.

Note: The size marker positions are marked by a "ladder" symbol.

Editing sample information

To provide sample information manually, enter the sample information into the grid. **Position A1** is preselected by default. Confirm the information for each position by pressing the **Enter** or the **Tab** key; the next position will be selected automatically for the next input. To provide sample information for a specific position, click the position and enter the sample information.

The sample information grid supports an auto-increment functionality. **To number sample information texts consecutively:**

1. Write the main sample information in the left uppermost cell.
2. Drag the small black square at the lower right corner of the cell border to extend the selection to all wanted cells.
3. Release the selection square. All selected cells will be filled with the main sample information entered in step 1. The cells will be numbered consecutively, starting with number 1.

To navigate through the sample information grid, use the arrow and **Tab/Shift+Tab** keys (just as in a Microsoft Excel[®] table).

To select multiple cells:

- Starting with one or more selected cells, hold **Ctrl** and left-click cells to add or remove them from the selection.
- Left-click in a cell and, starting in the cell with the cursor, drag to select a rectangular area of cells.

To copy the text of one selected cell into multiple cells:

1. Select the (source) cell.
2. Use the context menu item **Copy** or press the **Ctrl-C** key combination to copy the text into the clipboard.
3. Select the target cells.
4. Right-click one of the selected cells, but not the one with the cursor, and use the context menu item **Paste**. The text will be pasted from the clipboard into all selected cells. In addition, the first selected cell will remain highlighted after the text has been pasted.

To copy a column:

1. Select all cells of the column you want to copy.
2. Use the context menu item **Copy** to copy the text of all selected cells into clipboard.

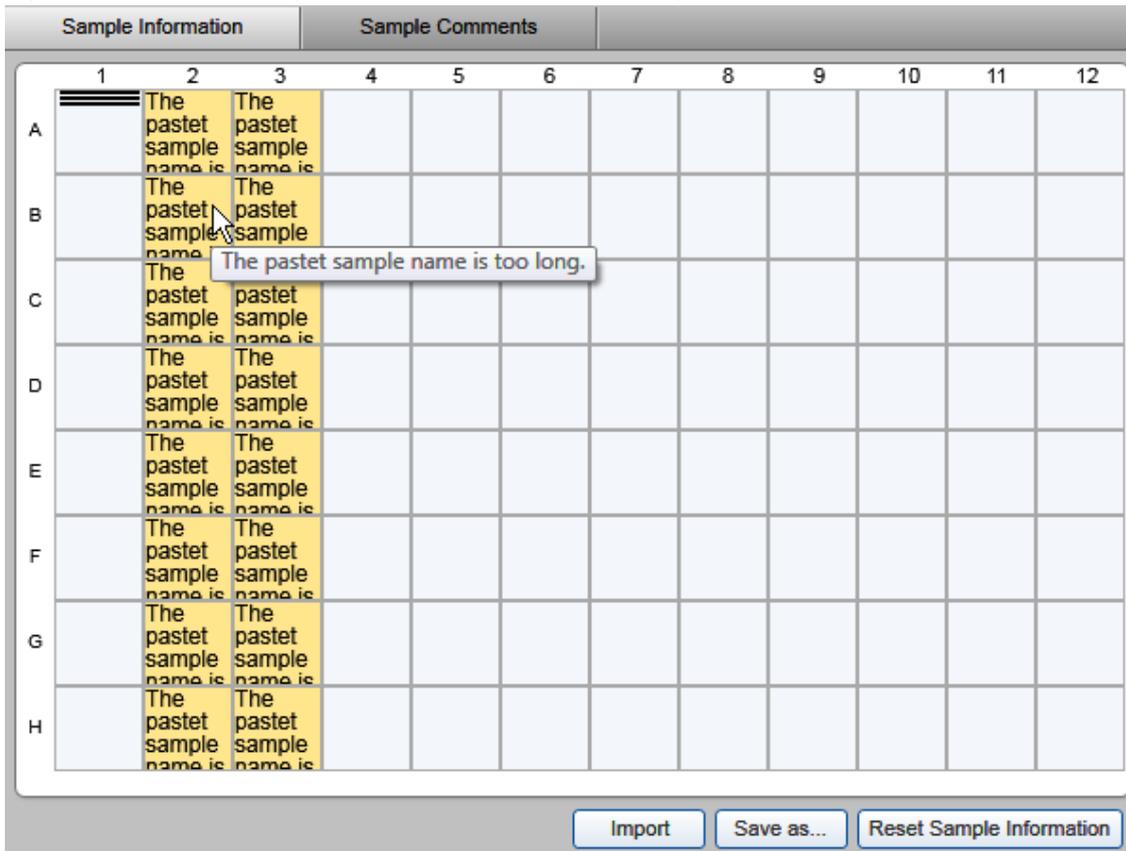
Note: The **Ctrl-C** key combination captures the text of the last selected cell only.

3. Left-click on the first cell of the column from which you want the text to be pasted.
4. Use the context menu item **Paste** or press the **Ctrl-V** key combination. The cells from the clipboard will be pasted to the column starting with the cell selected in the last step.

Note: In the same way, it is possible to copy rows or other selected areas. To start pasting, click the uppermost cell to the left.

To copy multiple cells from a Microsoft Excel table:

1. Copy the cells from the **Microsoft Excel** table into the clipboard.
2. In the **Sample Information** screen, click on the most left cell to paste.
3. Use the context menu item **Paste** or press the **Ctrl-V** key combination. The cells from the clipboard will be pasted to the cells starting with the cell selected in the last step.



Text that is too long (more than 30 characters) that has been pasted into the cells.

Note: If the length of the pasted text exceeds the maximum value (30), the cell background will change.

To clear sample information, click the **Reset Sample Information** button.

Note: Users who are allowed to revise sample information (see [User management](#)) may edit the sample information after the run using the context menu of the **Experiment Explorer**. In the analysis environment, select the sample in the **Experiment Explorer**, right-click the sample, and select the context menu option **Revise Sample Information**, then enter the new sample information.

Editing sample comments

To enter sample comments, click **Sample Comments**. To enter a comment for a specific position, click the relevant cell in the **Sample Comments** tab and enter the text.

To sort the plate positions by row or by column, click the column headers **Row** and **Col**, respectively.

To copy a comment from one cell into another cell:

1. Click the (source) cell.
2. Select the text to be copied using the mouse or by holding down the **Shift** key while using the end, left-arrow or right-arrow key.
3. Select the context menu item **Copy** or press the **Ctrl-C** key combination to copy the text into the clipboard.
4. Click the target cell.
5. Select the context menu item **Paste** or press the **Ctrl-V** key combination. The text will be pasted from the clipboard into the cell.

To clear all sample comments, click the **Reset Sample Comment** button.

Sample comments can also be imported from a file together with the sample information.

Note: Sample comments are restricted to **150 characters**.

Importing sample information

The QIAxcel ScreenGel Software provides the possibility to import sample information, with or without sample comments, from files. Three file types are supported: Microsoft Excel files (Excel 97–2003 Workbook (*.xls), Excel Workbook 2007–2010 (*.xlsx)), QIAGEN rack files, and QIAGEN qdef files, the QIAGEN data exchange format used in both QIASymphony[®] and QIAgility[®] applications.

Note: The **QIAGEN rack file** format does not support sample comments.

To import sample information and/or sample comments from a file, click the **Import** button. In the lower part of the dialog that appears, select the type of file to be imported. The dialog lists all available files of this type. Alternatively, navigate to the directory where the sample information was stored, select the file and click **OK**. The imported data overwrites all sample information and comments previously provided.

Note: Examples of all file types can be found under the **File** menu by selecting **Open Data Directory** and then **Sample Information**.

Note: Imported sample information is read-only if the settings option **Prevent modification of imported sample information** is selected (see [Settings](#)).

For the import of sample information from Microsoft Excel files, the following options are available:

Row-wise	Select this option if the sample list in the Microsoft Excel file follows this order: A1, A2, ..., A12, B1, B2, ..., B12, ..., H1, ..., H12. All samples names must be listed in the first column, starting in the first line of the table. Sample names for all plate positions must be listed in the file. Optional sample comments should be listed in the second column.
Column-wise	Select this option if the sample list in the Microsoft Excel file follows this order: A1, B1, ..., H1, A2, B2, ..., H2, ... , A12, ... H12. All sample names must be listed in the first column, starting in the first line of the table. Sample names for all plate positions must be listed in the file. Optional sample comments should be listed in the second column.

Matrix

Select this option if the sample information in the Microsoft Excel file is written in matrix format spanning cells A1 to L8 in the table. That is: A1, A2, ..., A8 in the first row, and A1, B1, ... ,H1 in the first column.

This option does not support sample comments.

Note: The QIAxcel ScreenGel Software imports sample information from the first worksheet in an alphabetical listing of all worksheets of the Microsoft Excel file. That is, if you rename the worksheets of the Microsoft Excel file, ensure that the relevant sample information is entered in the worksheet that would appear first, when arranged alphabetically by worksheet name.

Saving sample information

To save the provided sample information in rack file format for later reuse, click the **Save as** button. In the resulting dialog, navigate to the directory where the sample information should be stored, enter a unique file name, and click **OK**.

Note: The **Save as** button will be disabled if one or more cells contain more than 30 characters.

Note: The **QIAGEN rack file** format does not support sample comments.

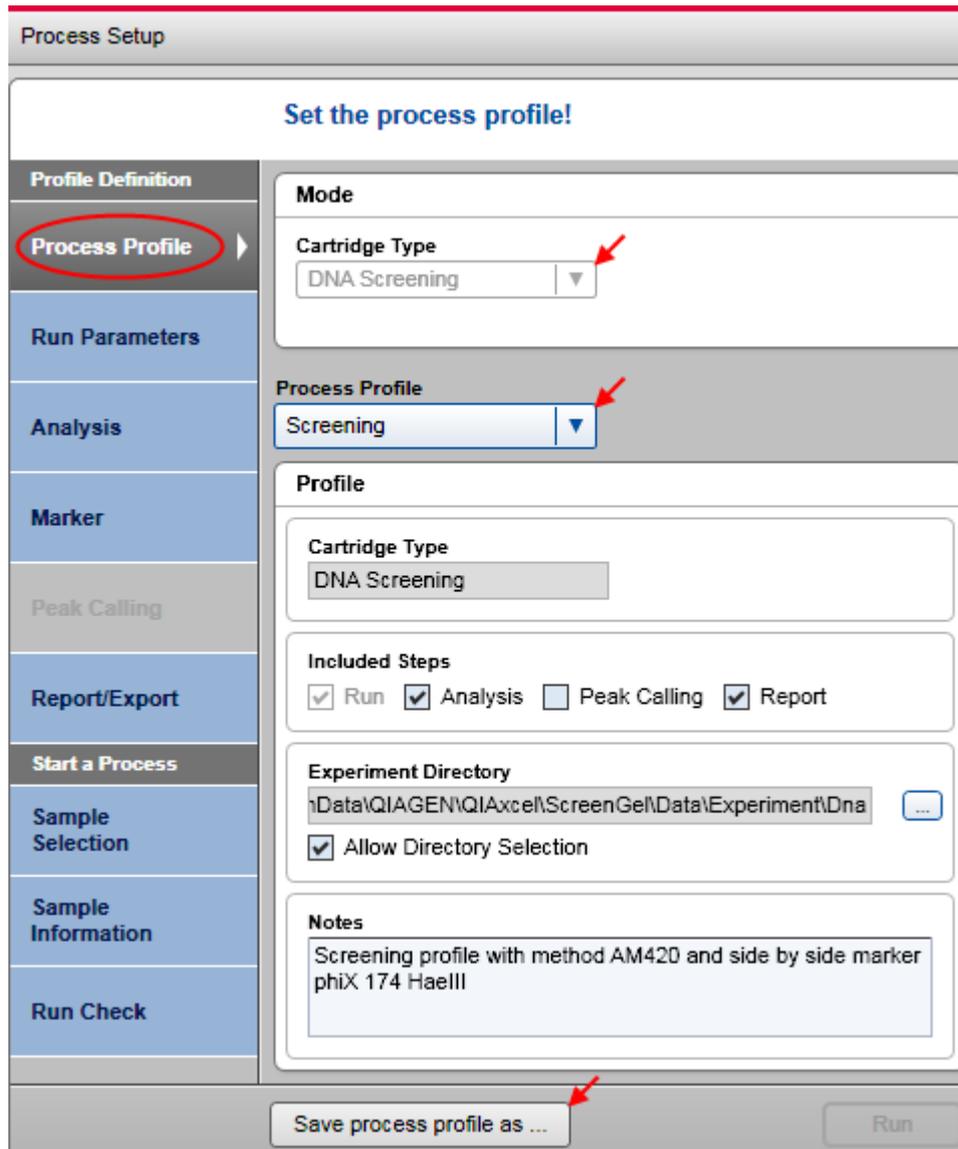
Modifying a process profile

Note: Only users with the assigned role **Advanced User** and **Basic User** can modify process profiles. Restrictions apply to users with the role **Basic User** as they, for example, cannot save the modified process profile. Restrictions are annotated in this manual, where they apply.

To modify a process profile proceed as follows:

1. Launch the **Process** environment.

If not already open, switch to the **Process** environment by clicking the **Process** environment icon. Select the **Process Profile** screen.



Steps to modify a process profile.

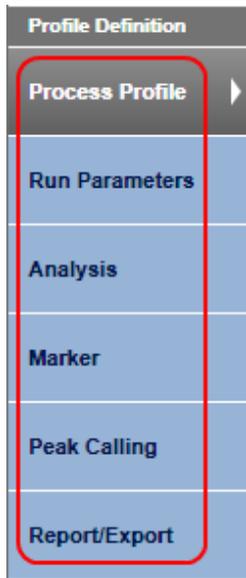
Note: If the last process only just finished, click the **Back to Wizard** button on the right bottom.

2. Select the process profile to be modified.

Use the **Process Profile** drop-down list to select a profile.

Note: Each process profile is related to a certain cartridge type. Therefore, the system can ensure that a process (i.e., data acquisition) can be started only if the correct cartridge type is inserted. If the process profile you want to select is not listed, make sure that the correct cartridge type is selected. If the instrument is connected, the system automatically detects the inserted cartridge type. If you want to modify a process profile to use with another cartridge type, remove the cartridge, or at least the cartridge key. Select the correct cartridge type. The process profile you want to modify should now be listed in the **Process Profile** drop-down list. Select the process profile and proceed.

3. Change the process profile options as required.



Screens for process profile definition.

See the [Process profile options](#) section for detailed information.

4. Save the modified process profile under a new name.

Click the **Save Process Profile** as button below the process setup and enter a new unique profile name in the dialog that appears.

Note: This is possible for users only with the assigned user role **Advanced User**.

Note: If there are process profile screens containing incomplete or inconsistent data highlighted in yellow, the **Save process profile as** button is disabled. Select the marked process profile screens and correct the data. If all data are correct, the **Save process profile as** button becomes enabled and the process profile can be saved.

Note: You can start a process or leave the **Process** environment without saving your changes. QlAxcel ScreenGel Software will not remind you to save a process profile or the embedded analysis profile, report/export profile, or peak calling instruction. If you leave the **Process** environment, log out, or exit the application, you should save your changes if they are to be reused.

Process profile options

The process profile options are grouped into several screens. To specify the complete process profile, follow the screen order as described below. To switch to the **Run Parameters** screen, click the screen name:

The screenshot shows the 'Process Setup' window with the title 'Set the process profile!'. On the left, a sidebar lists navigation options: Profile Definition, Process Profile (highlighted in yellow and circled in red), Run Parameters (highlighted in yellow and circled in red, with a mouse cursor), Analysis, Marker, Peak Calling, Report/Export, Start a Process, Sample Selection, Sample Information, and Run Check. The main content area is divided into sections: Mode (DNA Screening), Cartridge Type (DNA Screening), Process Profile (*NewProcessProfile), Profile (DNA Screening), Included Steps (Run checked, Analysis, Peak Calling, Report), Experiment Directory (\GEN\QIAxcel\ScreenGel Preview\Data\Experiment\DNA), Allow Directory Selection (unchecked), and Notes.

Defining a process profile.

Note: You can return to each screen by clicking the screen name. You can skip screens if modifications are not necessary.

Note: Screens with incomplete or incorrect options are highlighted in yellow. There is no need to correct them straight away, but you cannot save or start an incomplete or incorrect process profile.

The **Process Profile** screen options are described below.

Process Profile	Specifies the process scope. In addition to data acquisition, it is possible to include additional steps such as analysis and report. For detailed information, refer to the Selecting general process options section.
Run Parameters	Specifies the data acquisition details such as method used, rows to be processed, and size marker position. For detailed information, refer to the Selecting run parameters section.
Analysis Parameters	Specifies the analysis parameters for fully automated analysis after data acquisition. For detailed information, refer to the Selecting analysis parameters section. Note: This screen is disabled if analysis is not in the process scope.
Marker	Specifies the markers, alignment marker, and size marker used for analysis. For detailed information, refer to the Selecting marker section. Note: This screen is disabled if analysis is not within the process scope.
Peak Calling	Specifies the parameters for peak calling based on the peak result table. For detailed information, refer to the Selecting peak calling instructions section. Note: This screen is disabled if peak calling is not within the process scope.
Distribution Analysis	Specifies the parameters for distribution analysis based on the smear result table. For detailed information, refer to the Selecting distribution profiles section. Note: This screen is disabled if distribution analysis is not within the process scope.
Report/Export	Specifies the report and/or export parameters for fully automatic report and export as last step during process. For detailed information, refer to the Selecting report/export parameters section. Note: This screen is disabled if report/export is not in the process scope.

Note: In **DNA** mode, the peak calling screen or the distribution analysis screen are available only if the corresponding features (peak calling or the distribution analysis) are active. To activate, select the corresponding option from the **View** menu. Note that only one set of features can be active at a given time.

Selecting general process options

1. Select the **Process Profile** screen.

Refer to the [Process profile options](#) screen for information on how to select the screen.

2. Specify the process scope.

Select the additional steps:

Analysis Includes analysis in the process. This means after data acquisition is complete, the software analyzes the sample data automatically in the background, based on the process options set in the **Analysis** and **Marker** screens (described in the [Selecting analysis parameters](#) and [Selecting marker](#) sections).

The **Analysis Parameters** and **Marker** screens become enabled.

Peak Calling Includes peak calling in the process, based on the analysis peak result table. This means that after analysis, peak calling will be automatically performed, based on the process options set in the **Peak Calling** screen (described in the [Selecting peak calling instructions](#) section).

Note: This step is disabled if **Analysis** is not within the process scope.

Note: In DNA mode, this option is available only if peak calling features are active. To activate peak calling features, select **Activate Peak Calling Features** from the **View** menu.

Distribution Analysis Includes distribution analysis in the process, based on the analysis smear result table. This means that after analysis, distribution analysis will be automatically performed based on the process options set in the **Distribution Analysis** screen (described in the [Selecting distribution profiles](#) section).

Note: This step is disabled if **Analysis** is not within the process scope.

Additionally, the used analysis profile must have the option **Smear Analysis Profile** selected.

Note: In DNA mode, this option is available only if distribution analysis features are active. To activate distribution analysis features, select **Activate Distribution Analysis Features** from the **View** menu.

Report Includes report and/or export as the last step in the process. This means that the software automatically generates report and export.

3. **Optional:** Change the directory where the experiment will be saved.

Note: This can be a directory on the network. However, during the process, the experiment will always be saved to a local directory first (refer to [Settings](#)), and then copied to the experiment directory defined here, when the process finished.

4. **Optional:** Allow directory selection.

Select the option to allow directory selection in the **Sample Selection** screen while preparing a process. Using this option, the run can be customized even by a user with the assigned user role **Routine User**.

5. **Optional:** Edit a note in the process profile.

Use this note field to add a short description about the intended use of the profile. This note is displayed each time the process profile is selected. The note field is limited to maximal 2.000 characters and 25 lines.

Process Setup

Set the process profile!

Process Profile

Mode

Cartridge Type
DNA Screening

Process Profile
Screening

Profile

Cartridge Type
DNA Screening

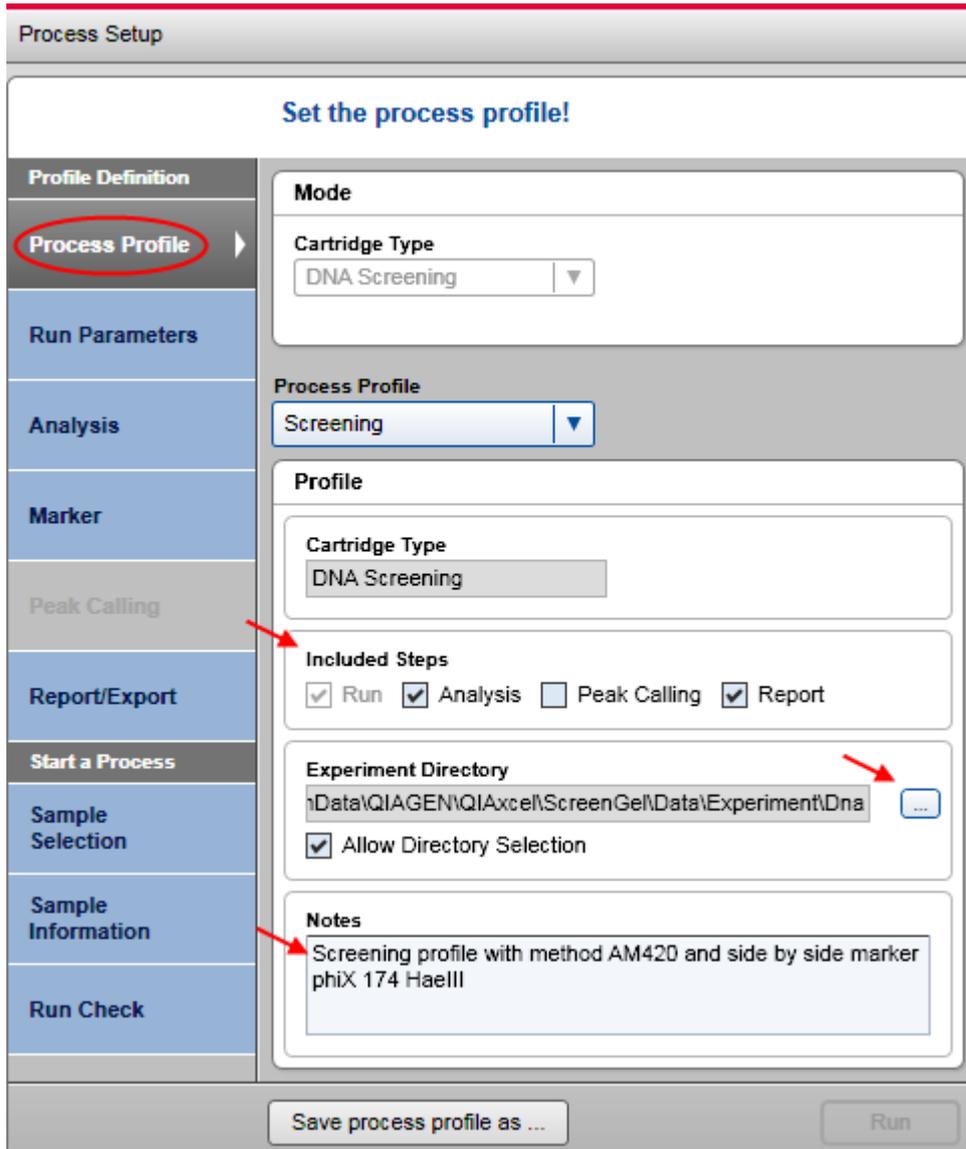
Included Steps
 Run Analysis Peak Calling Report

Experiment Directory
I:\Data\QIAGEN\QIAxcel\ScreenGel\Data\Experiment\Dna ...

Allow Directory Selection

Notes
Screening profile with method AM420 and side by side marker phiX 174 HaeIII

Save process profile as ... Run



Selecting run parameters

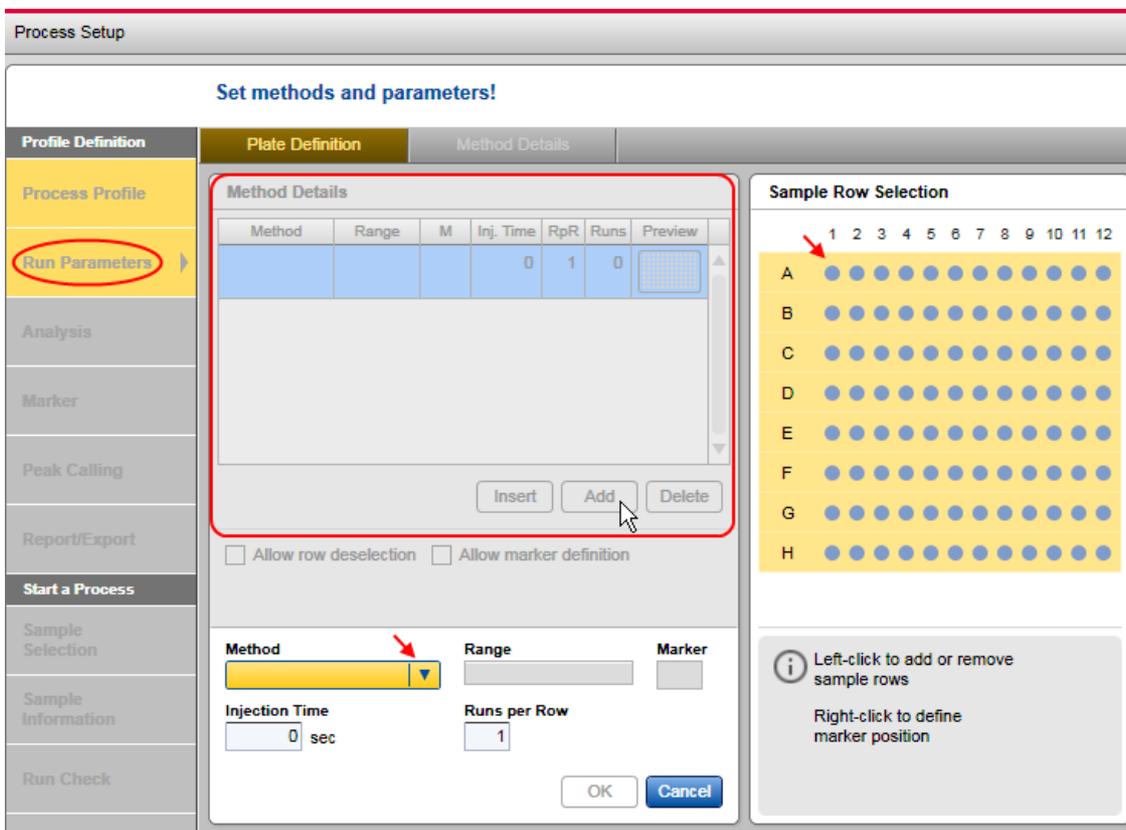
Define the methods and the rows that have to be processed with the methods. Select at least one method. In addition, the position of the size marker can also be specified.

Note: During processing, the list will be processed consecutively. For information about the correlation between run parameters and result structure, refer to the [Run parameters and result structure](#) section.

Proceed as follows:

1a. If the **Method Details** list is empty, click the **Add** button to start the first definition. A new empty entry appears in the **Method Details** list. Proceed with step 2 to specify the entry.

Note: This option is only available for users with the assigned user role **Advanced User**.



Empty Method Details list after the Add button has been clicked.

1b. If the **Method Details** list is not empty you have the following options:

- | | |
|--------|---|
| Add | Click the Add button to add a new entry at the bottom of the list. Proceed with step 2 to specify the entry.
Note: This option is only available for users with the assigned user role Advanced User . |
| Insert | Select an entry by left-clicking and then click the Insert button to insert a new entry before the selected one. Proceed to step 2 to specify the entry.
Note: This option is only available for users with the assigned user role Advanced User . |
| Modify | Select the entry you want to modify. Proceed to step 2 to modify the entry. |
| Delete | Select the entry you want to delete, then click the Delete button. The entry will be deleted from the list. Proceed to step 6.
Note: This option is only available for users with assigned user role Advanced User . |

2. Select the rows to be processed.

In the **Sample Row Selection** view to the right, left-click this view to add or remove a sample row to the plate. The **Range** field shows the row selection you have made.

Note: For **DNA** mode only. If you later refine a process profile that uses **Distribution** analysis, note the following:

- If you reduce the rows to process in the sample row selection in this screen, these rows will be removed automatically also in the **Distribution** analysis screen to ensure a consistent process profile.
- If you add rows later, there's no automatic adaptation in the **Distribution** Analysis screen.

Optional: Define the number of runs per row in the editable field **Runs** per row. The method will be applied as often as you specify here.

3. **Optional:** Define the size marker position.

Note: This position will be used for automatic analysis if the size marker is to be run side by side with the samples.

Right-click to define the position that will contain the size marker. The **Marker** field shows the position of the marker you set.

Note: Only one size marker position can be defined for an entry in the **Method Details** list. If you want to specify the process profile for a plate run containing a size marker at each row, create an entry for each row separately in the **Method Details** list.

4. Select the appropriate method from the **Method** drop-down list.

Note: This option is only available for users with the assigned user role **Advanced User**.

Note: The **Method** drop-down list only contains methods that are allowed for the cartridge type that the process profile is defined for.

Note: A number of default methods are available for each QIAxcel Kit. For a complete list, please refer to [Appendix B](#). Refer to the [Viewing method details](#) section if you want to look at the details of the method you have selected.

If required, change the sample injection time in the **Injection Time** editable field. This time will be applied instead of the sample injection time defined in the method.

The screenshot shows the 'Process Setup' window with the 'Set methods and parameters!' title. The interface is divided into several sections:

- Profile Definition:** Includes tabs for 'Plate Definition' and 'Method Details'.
- Method Details Table:**

Method	Range	M	Inj. Time	RpR	Runs	Preview
AM420	A - C,E,G,H	E7	10	1	6	
AM320	F	F2	10	1	1	
APH600	D	D2	5	3	3	
- Sample row selection:** A grid showing rows A-H and columns 1-12. Row E has a marker icon in column 8.
- Method Parameters:**
 - Method: AM420
 - Range: A - C,E,G,H
 - Marker: E7
 - Injection Time: 20 sec (highlighted with a red arrow and labeled 'Modified value')
 - Runs per Row: 1
- Buttons:** Insert, Add, Delete, OK, Cancel.
- Options:** Allow row deselection, Allow marker definition.
- Instructions:** Left-click to add or remove sample rows; Right-click to define marker position.

Modified sample injection time.

5. Click **OK** to confirm.

Note: The **OK** button becomes enabled as soon as the rows are defined and a method is selected.

The specified parameters appear in the entry created entry in the **Method Details** list.

Note: Click **Cancel** to discard all specifications made during steps 2 to 5. The entry will not be created/the selected entry will not be modified.

Note: The column **Runs** in the **Method Details** list contains the total number of runs specified by this entry: if **Range** is A–C and **RpR** ("Runs per Row") is 2, **Runs** will therefore be $3*2=6$.

6. Define all entries in the **Method Details** list repeating steps 1 to 5.

7. **Optional:** Allow row deselection.

Select the option to allow row deselection in the **Sample Selection** screen while preparing a process. Using this option, the run can be customized even by a user with assigned user role **Routine User**. This option is useful to, for example, prepare the process profile for a complete plate but only run the rows needed.

Note: This option is only available for users with the assigned user role **Advanced User**.

8. **Optional:** Allow marker definition.

Select the option, to allow the size marker position to be redefined in the **Sample Selection** screen while preparing a process. Using this option, the run can be customized even by a user with assigned user role **Routine User**.

Note: This option is only available for users with the assigned user role **Advanced User**.

Selecting analysis parameters

Note: The **Analysis** screen is enabled only if analysis is within the scope of the process profile. For details, refer to the [Selecting general process options](#) section.

Specify the analysis parameters as follows:

1. Select an analysis profile.

Use the **Profile** drop-down list to select the analysis profile. The analysis parameters of the selected profile are shown below the drop-down list.

The screenshot shows the 'Process Setup' dialog box with the 'Analysis' tab selected. The main area is titled 'Set analysis profile and properties!'. It features a 'Profile' dropdown menu with '*NewAnalysisProfile' selected and a 'Save as ...' button. Below this is the 'Analysis Properties' section, which includes a checkbox for 'Smear Analysis Profile' and several tables for filter and integration parameters.

Smoothing Filter	Start	Window
	0.00 min	15 pts

Baseline Filter	Start	Window
	0.00 min	40 sec

Minimum Distance	Start	Value
	0.00 min	0.25 sec

Suspend Integration	Start	End
	0.00 min	0.50 min

Buttons: Add, Delete, OK, Cancel

Selecting an analysis profile to modify.

Note: The analysis profile will be used for fully automatic analysis of all samples.

Note: In order to perform a distribution analysis in the process, the used analysis profile must have the option **Smear Analysis Profile** selected.

Note: Select **NewAnalysisProfile** to define the [analysis parameters](#) from scratch. This is only possible for users with the assigned user role **Advanced User**.

Note: All analysis parameters currently set in the selected analysis profile will be copied to the process profile. Further modifications of the underlying analysis profile do not affect the analysis parameters in this process profile. This prevents the process profile from unwanted changes and ensures process stability. If modifications in the underlying analysis profile are to be included in this process profile as well, include the modified analysis profile again by selecting it from the **Profile** drop-down list.

2. **Optional:** Modify the analysis parameters. You can modify the analysis parameters according to your needs in this screen as described in the [Modifying an analysis profile](#) section.

Note: This is only possible for users with the assigned user role **Advanced User**.

Note: If you define the **Suspend Integration** intervals using relative migration time, make sure that the relative migration times match the marker mode. See [Modifying an analysis profile](#) for details.

Note: The modifications will only be included in this process profile. If the modified parameters are also to be included in the selected analysis profile, save the analysis profile as described below.

3. **Optional:** Save the modified analysis parameters.

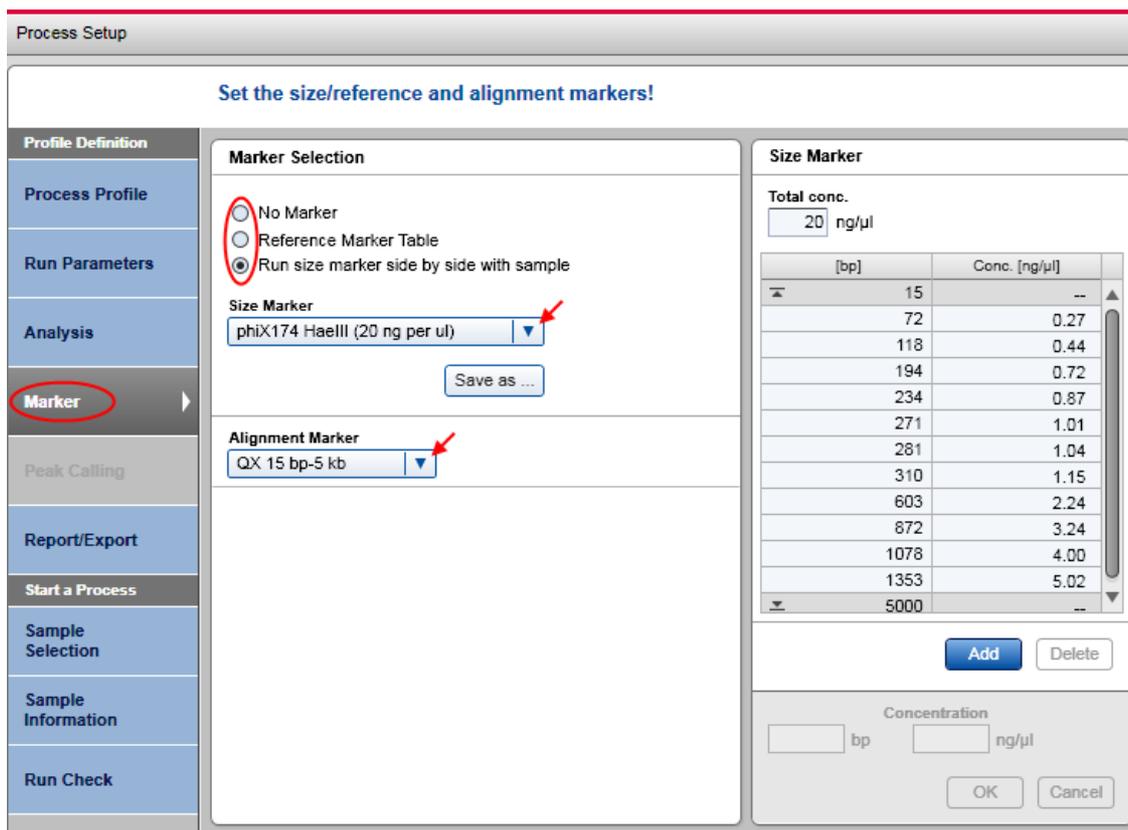
Note: This is only possible for users with the assigned user role **Advanced User**.

The modified analysis parameters can be saved by clicking the **Save as** button. A dialog appears, which includes the name of the selected analysis profile. You have two options:

Click **OK** if you want the modifications to be saved in the selected analysis profile; enter a new unique analysis profile name to save the modified analysis parameters as a new analysis profile, then click **OK**. The name of this new analysis profile and all of its analysis parameters will be included in the process profile.

Selecting marker

Note: The **Marker** screen is only enabled if analysis is within the scope of the process profile. For details, refer to the [Selecting general process options](#) section.



Marker selection.

Define the markers to be used when running this process profile.

1. Select one of the size marker options.
2. Select the correct marker for the selected option.

For information about marker options, see the descriptions below:

No Marker Select this option if automatic analysis is for peak detection only.

Note: No size marker will be used during automatic analysis, therefore determination of size and concentration is not possible.

Reference Marker Table

If analysis of size and/or determination of concentration is to be performed, select this option. The determination of size and/or concentration is based on a previously saved reference marker table.

Select the reference marker table to be used from the **Reference Marker Table** drop-down list.

Note: To ensure compatibility, the drop-down list contains only reference marker tables whose size markers were processed with the same method as defined in this process profile. The drop-down list is marked as invalid and empty if there is no compatible reference marker table. In this case, run a process with size marker side by side with the samples or create a reference marker table from a previous process (refer to the [Creating a reference marker](#) section).

Note: If no cartridge is currently inserted, the system cannot check the compatibility of the selected reference marker table. The drop-down list is marked as invalid and empty, or it contains a previously selected reference marker table only. Insert the cartridge to be processed by the profile and select a reference marker table compatible for this cartridge and method defined in this process profile.

Note: See the table below for explanation of the symbol at the right of the **Reference Marker Table** drop-down box:

●	<p>The selected reference marker table is fully compatible.</p> <p>This means that the size marker used for the reference marker table was processed no more than 90 days (DNA)/60 days (RNA) before with the cartridge that is currently inserted and with the same method as defined in this process profile.</p>
●	<p>The size marker used for the reference marker table was processed more than 90 days (DNA)/60 days (RNA) before with the cartridge that is currently inserted and with the same method as defined in this process profile.</p>
●	<p>The size marker used for the reference marker table was processed with the same method as defined in this process profile, but with a cartridge other than that currently inserted.</p>
●	<p>The reference marker table is not compatible with the method defined in this process profile. This can happen if the method was changed in the Run Parameters screen and the reference marker table was not yet changed correspondingly. Select another reference marker table from the drop-down list that is compatible with the newly selected method.</p>

Run size marker side by side with sample

Select this option if the plate requires a size marker.

Select the size marker to be used from the **Size Marker** drop-down list.

Optional: Change the total concentration of the size marker above the **Size Marker** table to the right, if needed. The individual concentrations of the fragments are then recalculated automatically.

Note: This is only possible for users with the assigned user role **Advanced User**.

In the **Alignment Marker** drop-down list, select the alignment marker to be used in the **MARKER1** position in the buffer tray.

Note: If the **Run** size marker is selected side by side with sample option, but size marker and/or alignment marker is not specified, the **Marker** screen would be considered as invalid.

Note: For **DNA** mode only: Using the correct size marker will increase the accuracy of size and concentration determination. Select the marker containing DNA fragments close to the size of your targeted DNA fragments. The DNA fragments to be analyzed must fall within the smallest and largest fragment size of the size marker.

Note: For **DNA** mode only: In addition, the range of the alignment marker must cover the range of the size marker. If not, the **Size Marker** table to the right shows this discrepancy with rows highlighted in yellow and the **Marker** screen would be considered as invalid.

Note: Refer to the [Selecting run parameters](#) section for information on how to define the position of the size marker.

Selecting peak calling instructions

Note: The **Peak Calling** screen is enabled only if analysis and peak calling are within the scope of the process profile. For details, refer to the [Selecting general process options](#) section.

Refer to the [Peak Calling](#) section for an explanation of the peak calling concept.

Define the instruction for peak calling:

1. Select a peak calling instruction.

Use the **Peak Calling Instruction** drop-down list to select a predefined peak calling instruction. The instruction definition is shown below the drop-down list.

Note: All parameters currently set in the selected peak calling instruction will be copied to the process profile. Further modifications of the underlying peak calling instruction do not affect the peak calling parameters in this process profile. This protects the process profile from unwanted changes and ensures process stability. If modifications in the underlying peak calling instruction are also to be included in this process profile, include the modified peak calling instruction again by selecting it from the **Peak Calling Instruction** drop-down list.

Note: Select **NewPeakCallingInstruction** to create a new instruction (for **Advanced Users** only). The **Peak Calling** screen is highlighted in yellow because the new peak calling instruction is still empty. Proceed to step 2 to define the instruction.

2. Modify the peak calling instruction. The peak calling instruction can be modified as required in this screen as described in the [Modifying a peak calling instruction](#) section.

Note: This can only be carried out by users with the assigned user role **Advanced User**.

Note: If the position of a peak is defined to be found using the relative migration time, make sure that the relative migration times match the marker mode. See [Modifying a peak calling instruction](#) for details.

Note: The modifications will only be included in this process profile. If the modifications are also to be included in the selected peak calling instruction, save the peak calling instruction as described below.

3. Save the modified peak calling instruction.

Note: This can only be carried out by users with the assigned user role **Advanced User**.

The modified peak calling instruction can be stored by clicking the **Save as** button. A dialog appears containing the name of the selected peak calling instruction. You have two options: Click **OK** if the modifications are to be stored in the selected peak calling instruction; enter a new unique peak calling instruction name to save the modifications to a new peak calling instruction, then click **OK**. The name of this new peak calling instruction and all of its parameters will be included to the process profile.

Selecting distribution profiles

Define the distribution profiles to be used in the process and assign the rows to be analyzed with those profiles. Select at least one distribution profile. A sample row can be analyzed with one distribution profile only. Selections made are listed in the **Assignment of Distribution Profiles** list, where each row defines the use of one distribution profile.

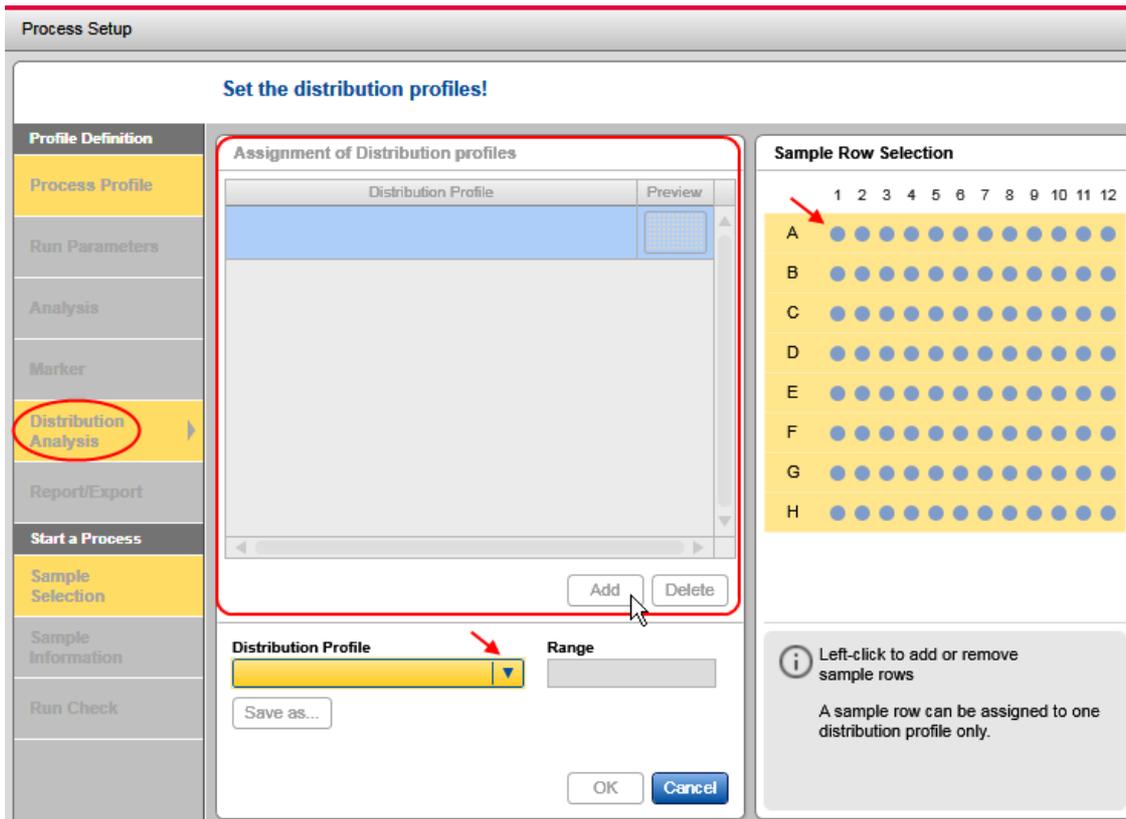
Distribution analysis is performed automatically in the process after smear analysis. Therefore, the **Default Smear DNA** profile should have been selected in the **Analysis** screen, and a size or reference marker must have been selected in the **Marker** screen. For more information, refer to [Distribution analysis](#).

Note: This screen in the **Process Setup** is enabled only if analysis and distribution analysis are within the scope of the process profile. For details, refer to [Selecting general process options](#).

To define the use of distribution profiles:

1a. If the **Assignment of Distribution Profiles** list is empty, click the **Add** button to make the first assignment. An empty entry appears in the assignment list. Proceed with step 2 to specify the entry.

Note: This option is only available for users with the assigned user role **Advanced User**.



Empty Assignment of Distribution Profiles list after the Add button has been clicked.

1b. If the **Assignment of Distribution Profiles** list is not empty, the following options are available:

Add Click the **Add** button to add a new assignment at the bottom of the list. Proceed with step 2 to specify the assignment.

Note: This option is available for users with the assigned user role **Advanced User** only.

Modify Select the assignment to be modify. Proceed to step 2 to modify the assignment.

Delete Select the assignment and click the **Delete** button to remove it from the list. Proceed to step 6.

Note: This option is only available for users with assigned user role **Advanced User**.

2. Select the desired distribution profile from the **Distribution** profile drop-down list.

Note: This option is only available for users with the assigned user role **Advanced User**.

Note: All parameters set in the selected distribution profile are copied to the process profile. Further modifications of the **Distribution** profile in the **Analysis** environment do not affect the distribution parameters in this process profile. This protects the process profile from unwanted changes and ensures process stability. If modifications in the underlying distribution profile are to be included in the process profile, add the modified distribution profile by selecting it from the **Distribution Profile** drop-down list again.

3. Select the sample rows to be analyzed with the distribution profile.

In the **Sample Row Selection** panel, left-click sample rows to select or deselect them. The **Range** field shows the row selection made. It is possible to select only rows to be run in the process, that is, that have already been selected in the **Run Parameters** screen.

Note: A row that has already been assigned to a distribution profile in the assignment list, cannot be selected anymore.

Note: If the rows to be processed have been reduced in the **Run Parameters** screen while refining a process profile, those rows are removed automatically in this screen. If rows have been added in the **Run Parameters** screen, one would need to adapt the row selection in this screen if you would want to use **Distribution** analysis for the added rows as well.

4. Click **OK** to confirm.

Note: The **OK** button becomes enabled as soon as rows are defined and a distribution profile is selected.

The specified parameters appear in the created entry in the **Assignment of Distribution Profiles** list.

Note: Click **Cancel** to discard all entries made during steps 2 and 3. The entry will not be created or the selected entry will not be modified.

5. Repeat steps 1 through 4 to define all assignments in the **Assignment of Distribution Profiles** list.

The parameters of distribution profiles cannot be viewed or edited in this screen. To view or edit the [distribution profile parameters](#), switch to the **Analysis** environment.

If the underlying distribution profile is modified after being selected for the process profile, the name of the distribution profile is preceded with an "*". This indicates that the parameters that will be used by this process profile are not the same those visible in the **Analysis** environment. To view the distribution profile parameters that are defined for the current process profile:

1. Select the row with the distribution profile that is modified.
2. Click the **Save as** button below the **Distribution Profile** drop-down box and save the distribution parameters using a new distribution profile name.

Note: This option is only available for users with the assigned user role **Advanced User**.

3. Switch to the **Analysis** environment to inspect the parameters of the saved distribution profile.

4. You can delete obsolete distribution profiles using the [Profile Manager](#) in the **Configuration** environment.

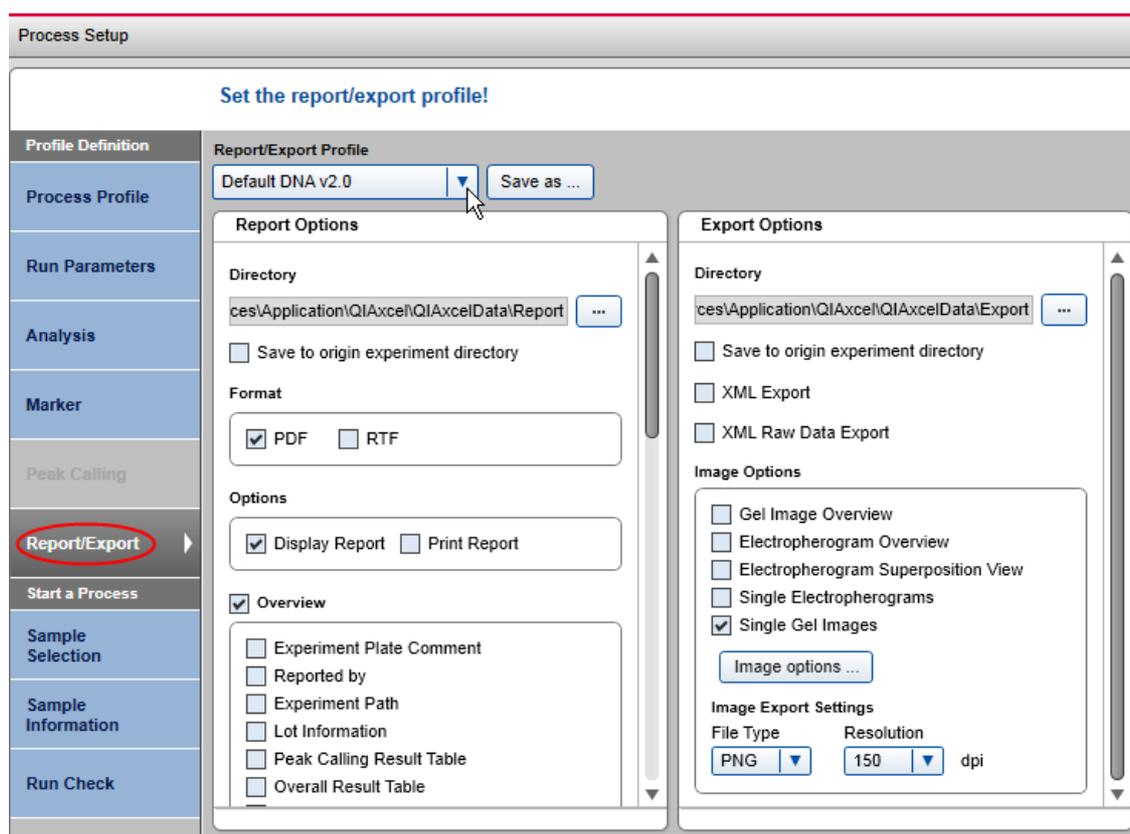
Selecting report/export parameters

Note: The **Report/Export** screen is enabled only if **Report** is within the scope of the process profile. For details, refer to the [Selecting general process options](#) section.

Specify the report and export parameters as follows:

1. Select a report/export profile.

Use the **Report/Export Profile** drop-down list to select the report/export profile. The parameters of the selected profile are shown below the drop-down list.



Selecting a report/export profile.

Note: All report/export parameters currently set in the selected report/export profile will be copied to the process profile. Further modifications of the underlying report/export profile do not affect the report/export parameters in this process profile. This prevents the process profile from unwanted changes and ensures process stability. If modifications in the underlying report/export profile are also to be included in this process profile, include the modified report/export profile by selecting it from the **Report/Export Profile** drop-down list.

Note: Report/export profiles with the option **Use Images as Displayed** selected are not listed in the **Report/Export Profile** drop-down list. This option is available in the analysis environment only. Refer to the [Report/Export options](#) section for more information.

Note: In **DNA** mode, report/export profiles that include selected distribution analysis options are not listed in the **Report/Export Profile** drop-down list if peak calling features are active. Similarly, report/export profiles with selected peak calling options are not listed if distribution analysis features are active.

2. Modify the report/export parameters.

The report/export parameters can be modified as required in this screen. Refer to the [Report/Export options](#) section for more information.

Note: The modifications will only be included in this process profile. If the modified parameters are also to be included in the selected report/export profile, save the report/export profile as described below.

Note: A report/export profile is only applicable if at least one format check box (**PDF** or **RTF**) and one of the content options (**Overview** or **Sample Details**) is selected for report, or if one check box is selected for export. The check boxes and the **Report/Export** screen are highlighted in yellow if no selection is made.

3. Save the modified report/export parameters.

Note: This can only be carried out by users with the assigned user role **Advanced User**.

The modified report/export parameters can be saved by clicking the **Save as** button. A dialog box appears, which includes the name of the selected report/export profile. You have two options: Click **OK** if the modifications are to be stored in the selected report/export profile; enter a new unique report/export profile name to save the modified report/export parameters to a new report/export profile, then click **OK**. The name of this new report/export profile and all of its parameters will be included in the process profile.

Run parameters and result structure

This section provides an example so that the relation between process definition and the structure of the result can be described:

With a **QIAxcel DNA Screening Cartridge**:

- Rows A and B will be run twice with Method AM320, with size marker at position A1
- Rows C and D will be run 3 times with Method AH420, with the same size marker at position C1

The same alignment marker will be used for both methods.

See the **Run Parameters** and **Sample Selection** screens of the process definition:

The screenshot shows the 'Run Parameters' screen with the 'Method Details' tab selected. The table below is a representation of the data shown in the screenshot.

Method	Range	M	Inj. Time	RpR	Runs	Preview
AM320	A,B	A1	10	2	4	
AH420	C,D	C1	20	3	6	

Below the table are three buttons: **Insert**, **Add**, and **Delete**.

There are two checked checkboxes: Allow row selection and Allow marker definition.

At the bottom, there are input fields for: **Method** (AH420), **Range** (C,D), **Marker** (C1), **Injection Time** (20 sec), and **Runs per Row** (3). There are also **OK** and **Cancel** buttons.

Run Parameters screen.

Two entries were defined because of the different methods. The rows and size marker positions were defined for each method, as well as for the runs per row (column **RpR** in the **Method Details** list). In the **Runs** column the total number of runs for each method is listed.

During the process, the software first runs Method AM320 in the order row A and B (first run), and row A and B (second run). It then runs Method AH420 in the order row C and D (first run), row C and D (second run), and row C and D (third run).

The image shows a software interface for sample selection. At the top, there is a field for 'Plate ID' containing the text 'C100520A99_2010-05-18_11-25-21'. Below this is a section titled 'Sample row selection' which displays a grid of 12 columns (numbered 1-12) and 8 rows (labeled A-H). Rows A, B, C, and D are highlighted in blue, indicating they are selected. Each cell in the grid contains a small icon: a horizontal bar for rows A and C, and a circle for rows B, D, E, F, G, and H. Below the grid, the text 'Total Runs: 10' and 'Estimated Time: About 101 minutes' is displayed. There is a checked checkbox labeled 'Provide Sample Information'. At the bottom, there is an information icon and a text box that reads: 'Left-click to select/deselect sample row (s), right-click to define/redefine size marker.'

Sample Selection screen.

The **Plate ID** will be used as the name of the results.

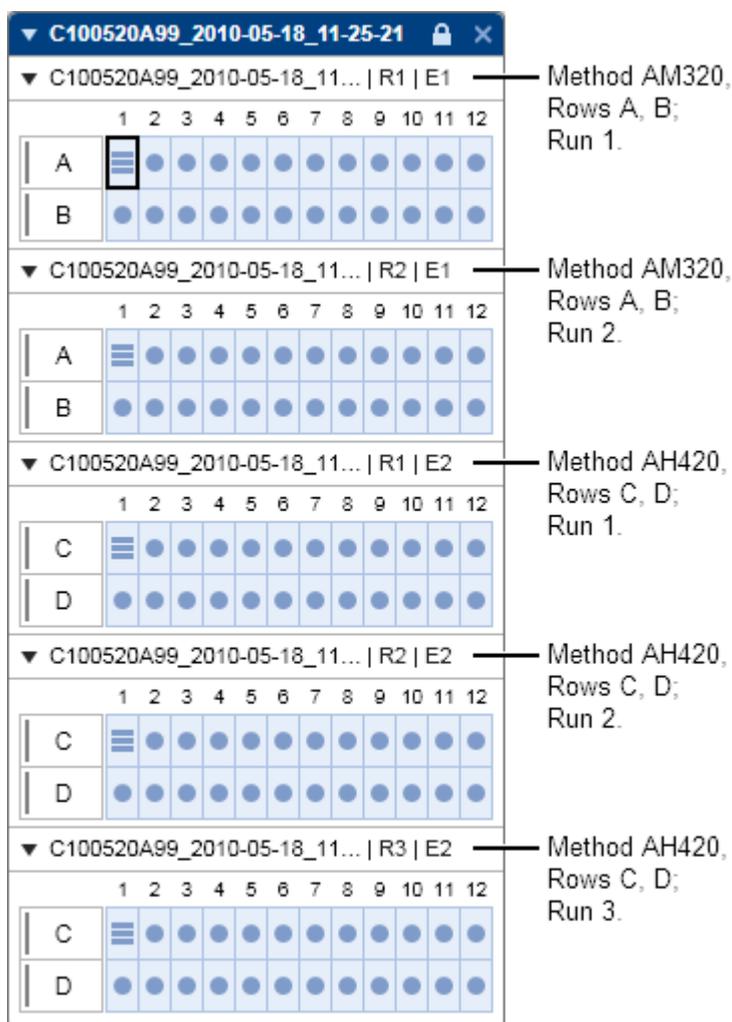
The **Sample** row selection shows a summary of the run definition in the **Run Parameters** screen.

The total number of runs (**Total Runs**) in this example is 10:

2 times A and B = 4 runs for Method AM320

3 times C and D = 6 runs for Method AH420

When the process is finished, the sample data are presented in the **Analysis** environment in the **Experiment Explorer**:



Experiment generated by the process.

All sample data generated by the process are combined into one experiment and named according to the **Plate ID**, which was specified in the **Sample Selection** screen.

All sample data are grouped by so called "**plates**" as they were generated by the process.

The name of the plate identifies the run. It is combined with:

Experiment name The experiment name is created from the **Plate ID** specified in the **Sample Selection** screen.

R# Run number, where "#" represents a number, starting from 1. In this example for method AM320, the run numbers R1 and R2 are generated.

E# Entry number (entry in the **Method Details** list of the **Run Parameters** screen), where "#" represents a number starting from 1. In this example, the entry numbers E1 and E2 are generated, because the **Method Details** list contained 2 entries.

Therefore, the sample data for Method AM320 for rows A and B are listed first and also separately for each run.

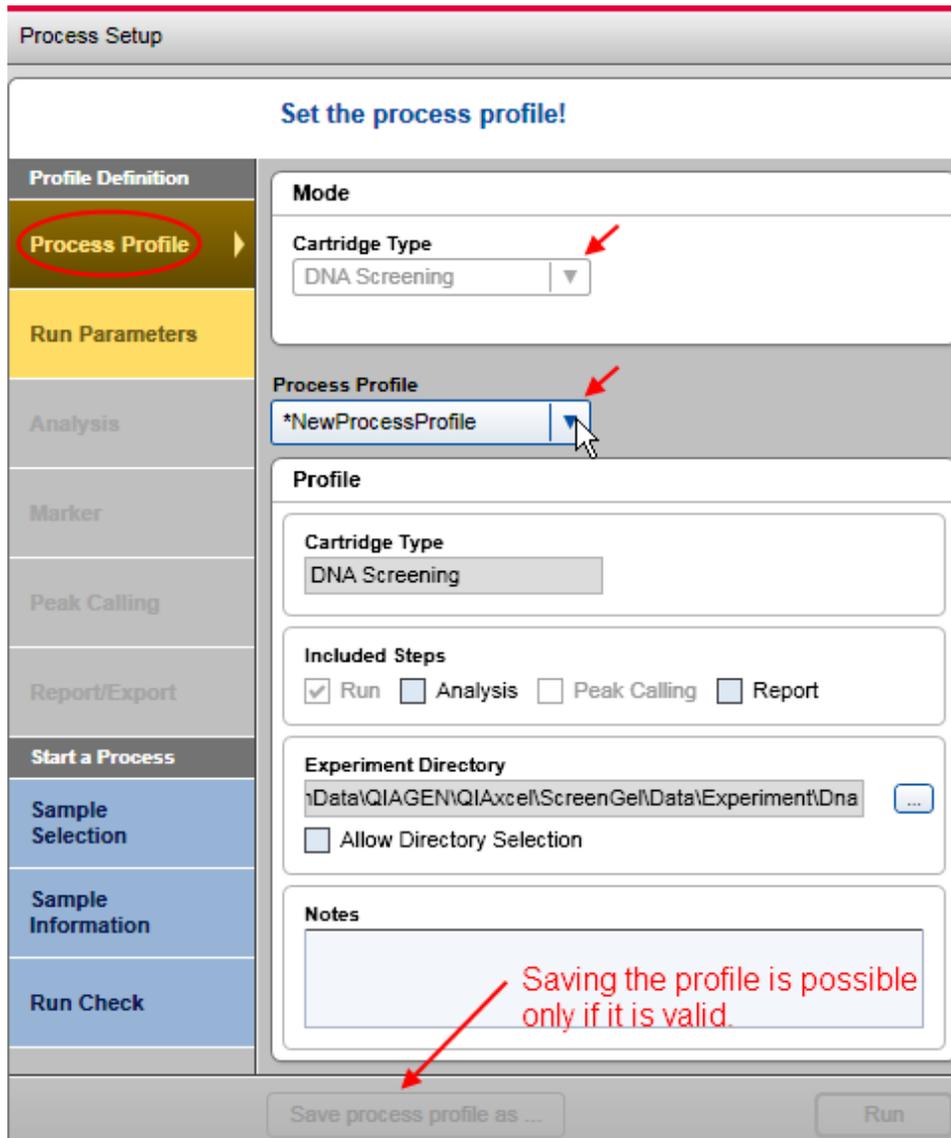
Creating a new process profile

Note: Only users with the assigned role **Advanced User** can create a new process profile.

To create a new process profile, proceed as follows:

1. Open the **Process** environment.

If not open, switch to the Process environment by clicking the **Process** environment icon. Select the **Process Profile** screen.



Main steps for creation of a new process profile.

Note: If the last process was just completed, click the **Back to Wizard** button at the bottom right.

2. Select cartridge type.

Select the cartridge type that is to be used for the new process profile.

Note: Each process profile is related to a certain cartridge type. Therefore, the system can ensure that a process (i.e., data acquisition) can be started only if a cartridge with correct cartridge type is inserted.

Note: If the instrument is connected, the system automatically detects the inserted cartridge and the cartridge type cannot be changed. If you want to create the process profile for another cartridge type, remove the cartridge, or at least the cartridge key, or disconnect from the instrument.

3. Select a process profile.

Use the **Process Profile** drop-down list to select a process profile. The selected profile serves as a template for the creation of the new profile.

Note: Select **NewProcessProfile** to create a process profile from scratch. The system will show * **NewProcessProfile** after selection. This can only be carried out by users with the assigned role **Advanced User**.

3. Set the process profile options according to your needs.

See section [Process profile options](#) for detailed information.

4. Save the modified process profile under a new name.

Click the **Save Process Profile** as button below process setup and enter a new unique profile name in the dialog that appears.

Note: This can only be carried out by users with the assigned user role **Advanced User**.

Note: If there are process profile screens containing incomplete or inconsistent data highlighted in yellow, the **Save** process profile as button is disabled. Select the marked process profile screens and correct the data. If all data are correct, the **Save** process profile as button becomes enabled and the process profile can be saved.

Viewing method details

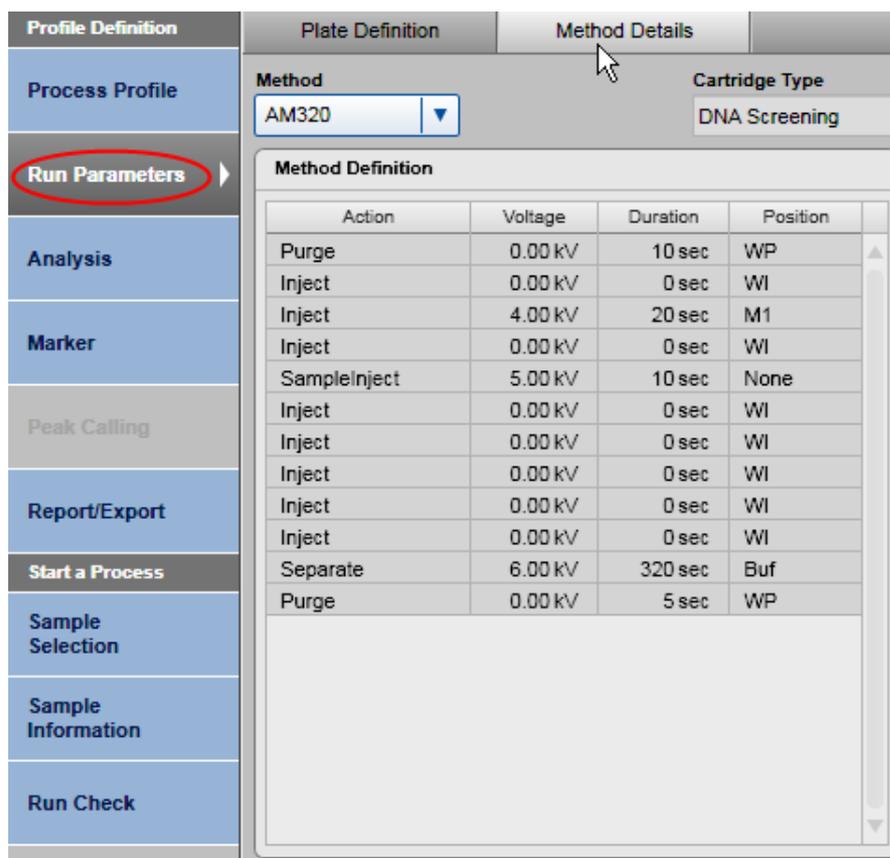
During definition of a process profile, it is possible to view the details of a method.

Note: This function is available for users with the assigned role **Advanced User** and **Basic User** only.

Proceed as follows:

1. Select a process profile in the **Process Profile** screen.
2. Switch to the **Run Parameters** screen. Select the entry containing the method you want to view in the **Plate Definition** tab .
3. Switch to the **Method Details** tab.
4. Select another method to view, if required.

Note: Selecting another method modifies the entry in the **Plate Definition** tab you came from. Ensure you have selected the correct method you want to process.



Method Details screen.

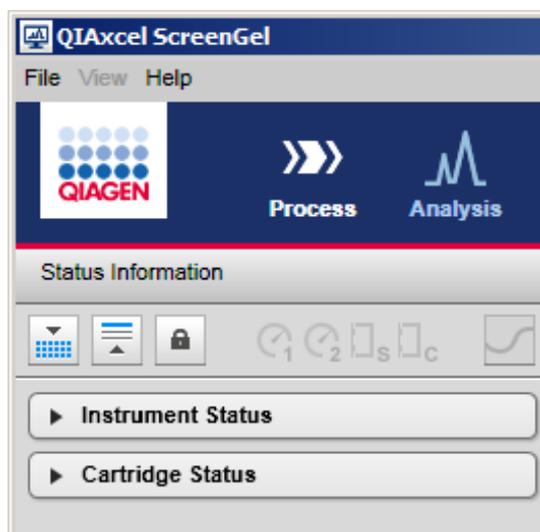
All actions defined in the method are listed. During the run, the actions will be performed sequentially.

For more information about what the position abbreviations mean, see the **Instrument Status** section of the **Status Information** panel to the left of the **Process** environment.

Status information panel

The left panel of the screen in the **Process** environment is called the **Status Information** panel. It is divided into:

- A **toolbar** at the top
- **Instrument Status**
- **Cartridge Status**



Status Information panel.

Instrument Status and **Cartridge Status** can be collapsed and expanded. The **toolbar** buttons and status icons are explained in the following table:



Load Position button. Click the button to move the buffer tray to the front of the instrument to load samples and buffer.

Note: The motors will not move if either the sample door or cartridge door is open.



Wash Park Position button. Click the button to move the cartridge to the wash park position of the buffer tray.

Note: The motors will not move if either the sample door or cartridge door is open.



Indicates that the currently inserted QIAxcel gel cartridge is **latched**. Click the button to unlatch the QIAxcel gel cartridge.

Important: If the **Pressure 1** status is low, increase system pressure before unlatching. Releasing the cartridge latching with reduced pressure may damage the instrument!



Indicates that the currently inserted QIAxcel gel cartridge is **unlatched**. Click the button to latch the QIAxcel gel cartridge.

Important: If the **Pressure 1** status is low, increase system pressure before unlatching. Releasing the cartridge latching with reduced pressure may damage the instrument!



Pressure 1 status: OK/Low. **OK** indicates adequate pressure for the sample run. **LOW** indicates that the N₂ pressure is sufficient for the current sample run; however, the N₂ cylinder should be replaced once the run of the current sample row has finished.



Pressure 2 status: OK/Low. **OK** indicates adequate pressure for the sample run. **LOW** indicates that the N₂ pressure is insufficient for the current sample run and the analysis will not be performed. The N₂ cylinder should be replaced.



Sample door: Closed/Open.



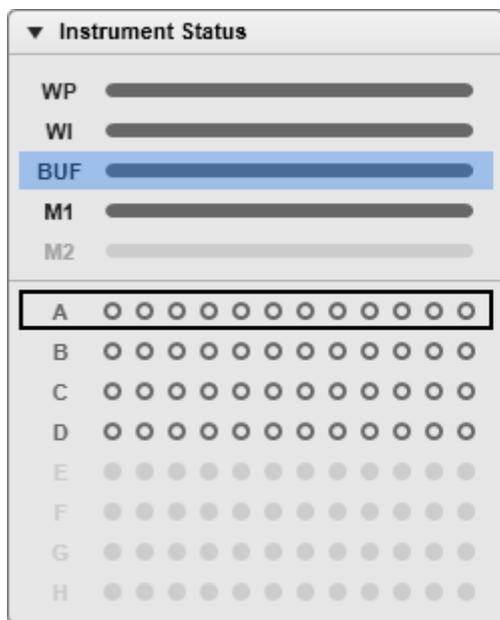
Cartridge door: Closed/Open.



Connection status: Connected, disconnected, and connection is being established with the QIAxcel Advanced instrument.

Note: If disconnected, the icon can be clicked to connect to the instrument.

The **Instrument Status** panel displays the buffer tray and sample plate. The current position of the capillaries of the QIAxcel gel cartridge is highlighted when the process is running. In the example below, the sample rows A–D are processed with the same method.



Position description

- Wash Park
- Wash Inject
- (Separation) Buffer — current capillary position
- Marker 1
- Marker 2
- Sample row A — currently being processed
- Sample row B
- Sample row C
- Sample row D
- Sample row E
- Sample row F
- Sample row G
- Sample row H

Instrument Status panel.

The **Cartridge Status** panel displays information about the QIAxcel gel cartridge currently inserted, such as cartridge ID, cartridge type, remaining number of runs, remaining number of calibration runs, expiration status, and calibration status. When opening the **Calibration Details** expander, additional calibration details are shown.

▼ Cartridge Status			
Cartridge ID			
C110414C99			
Cartridge Type			
RNA Quality Control			
Remaining Runs		Remaining Cal. Runs	
83		3	
Expiration Status		Calibration Status	
Valid		OK	
▼ Calibration Details			
Calibration Date		Accepted By	
14.04.2011 13:07:10		JohnSmith	
Ch.	Area	Cal. Factor	Result
1	0.0053	0.5762	Passed
2	0.0051	0.6114	Passed
3	0.0050	0.9239	Passed
4	0.0053	0.8302	Passed
5	0.0053	0.4594	Passed
6	0.0053	0.9902	Passed
7	0.0050	1.8963	Passed
8	0.0043	0.7028	Passed
9	0.0045	0.5612	Passed
10	0.0053	0.7647	Passed
11	0.0042	0.7104	Passed
12	0.0051	1.2754	Passed

Cartridge Status panel.

Note: Calibration status **NOT OK** means that the cartridge is not calibrated and needs calibration. For information about calibration, refer to the [Calibrating a cartridge](#) section.

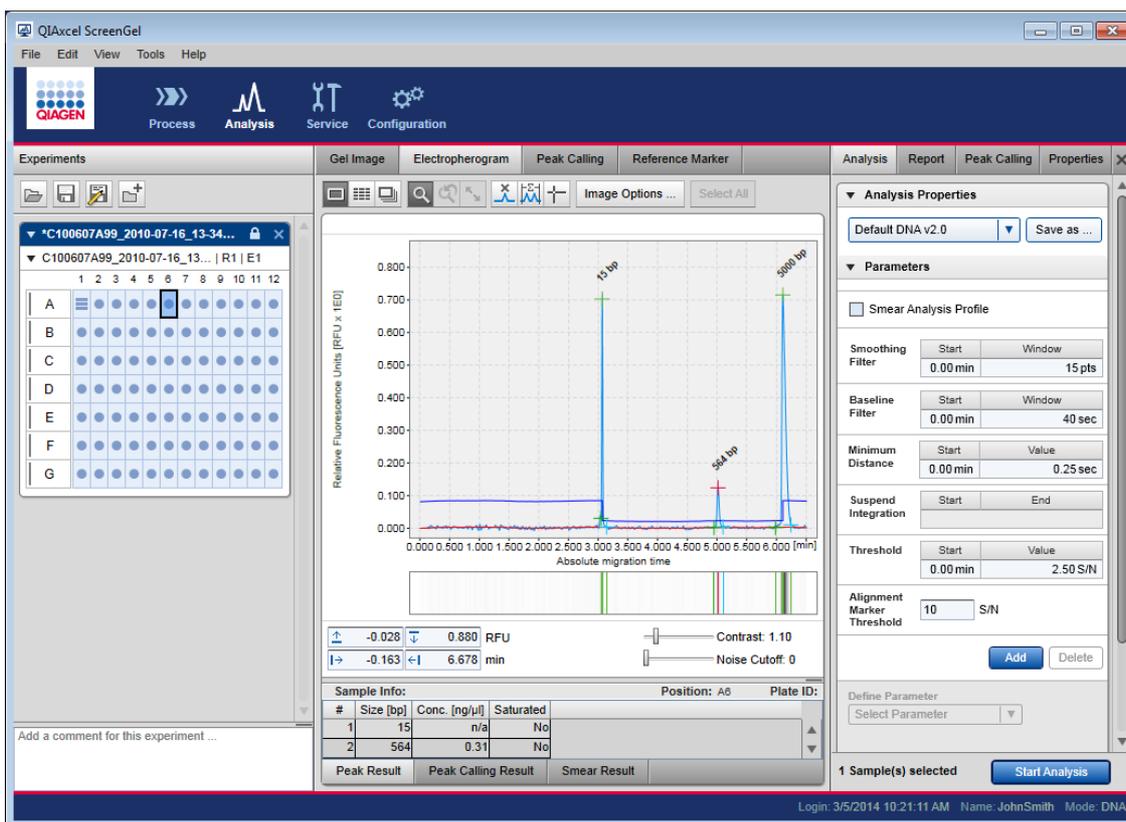
Note: The **Status Information** panel is shown in the **Process** environment and the **Service** environment.

Analysis

The **Analysis** environment provides sophisticated visualizations and analysis algorithms for electropherograms acquired by the QIAxcel Advanced instrument.

The software provides several customizable views for sample raw data, for example, a gel view, a single electropherogram view, and electropherogram superposition view. Electropherogram views also visualize analysis results, enabling fast assessment of the results.

The analysis algorithms provided by the QIAxcel ScreenGel Software automatically determine a variety of peak properties. **Analysis** algorithms can be applied to single samples or collections of samples (called experiments), and can be customized by the user. The size and concentration of analytes can be determined. The **DNA** mode includes functions that enable quality assessment of samples, for example, after a target enrichment step in a workflow. These functions include checking for the presence of certain fragment sizes (peak calling), and determining and assessing the molarity and size distribution of DNA fragments (distribution analysis). The **RNA** mode provides the RNA Integrity Score (RIS) as a tool to objectively assess the quality of eukaryotic RNA samples. In addition, parameters such as 28S/18S ratio and concentration of total RNA can be calculated.



Analysis environment with active Electropherogram screen, Experiment Explorer to the left, and Analysis panel to the right.

The **Experiments** panel on the left displays functions for [Handling samples and experiments](#). The middle panel displays several graphical views and result tables. For more information, refer to [Viewing sample data](#).

On the right is the **Parameters** panel, where analysis parameters and report/export options can be specified.

If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:



Introduction into analysis

Before (re)analysis of samples can start, the experiment must be [loaded](#) in the **Experiment Explorer** on the left and the samples must be [visualized](#) in the middle area. Additionally, the samples that shall be analyzed must be [selected for analysis](#). Refer to [Handling samples and experiments](#) and [Viewing sample data](#) and its sub sections for more details.

The analysis of samples is performed using a two-step approach. First, peaks are detected in the raw data. As a result, the alignment marker peaks are found and the first, very basic peak properties are available, e.g., peak start and peak end, peak apex as a function of time, as well as peak area. After peak detection, the samples can be viewed and aligned according to the alignment marker peaks found in the [Gel view](#) or the [Electropherogram overview](#). Because peak detection is the basis of the analysis, ensure that the peaks and especially the alignment marker peaks have been found correctly. For details, see [Peak detection](#).

In a second step, the peak sizes and peak concentrations are determined by mapping the detected peaks in the sample to peaks of a reference marker which is created based on a size marker that has been used in this or a previous run. To use a size marker from a previous run for analysis, it is important that the same cartridge, method, instrument and alignment marker are used. For size and concentration, see section [Size and Concentration determination](#). The software allows you to combine the first and the second analysis step.

Optionally, a third analysis step is possible. Either [Peak Calling](#) or [Distribution analysis](#) can be used based on peak detection and size determination. These analyses can be used to check whether the samples meet certain defined expectations.

Follow the instructions in [Analysis of DNA samples](#) and [Analysis of RNA samples](#) for step-by-step guidance for your specific samples.

One can benefit from fully automated processing by including analysis steps already into the process of data acquisition. Starting with analysis parameters initially provided by the software, customize the parameters such that the analysis gives good and reliable results for your samples. Save them into [Profiles](#) and use them to create fully automated customized [Process Profiles](#).

Handling samples and experiments

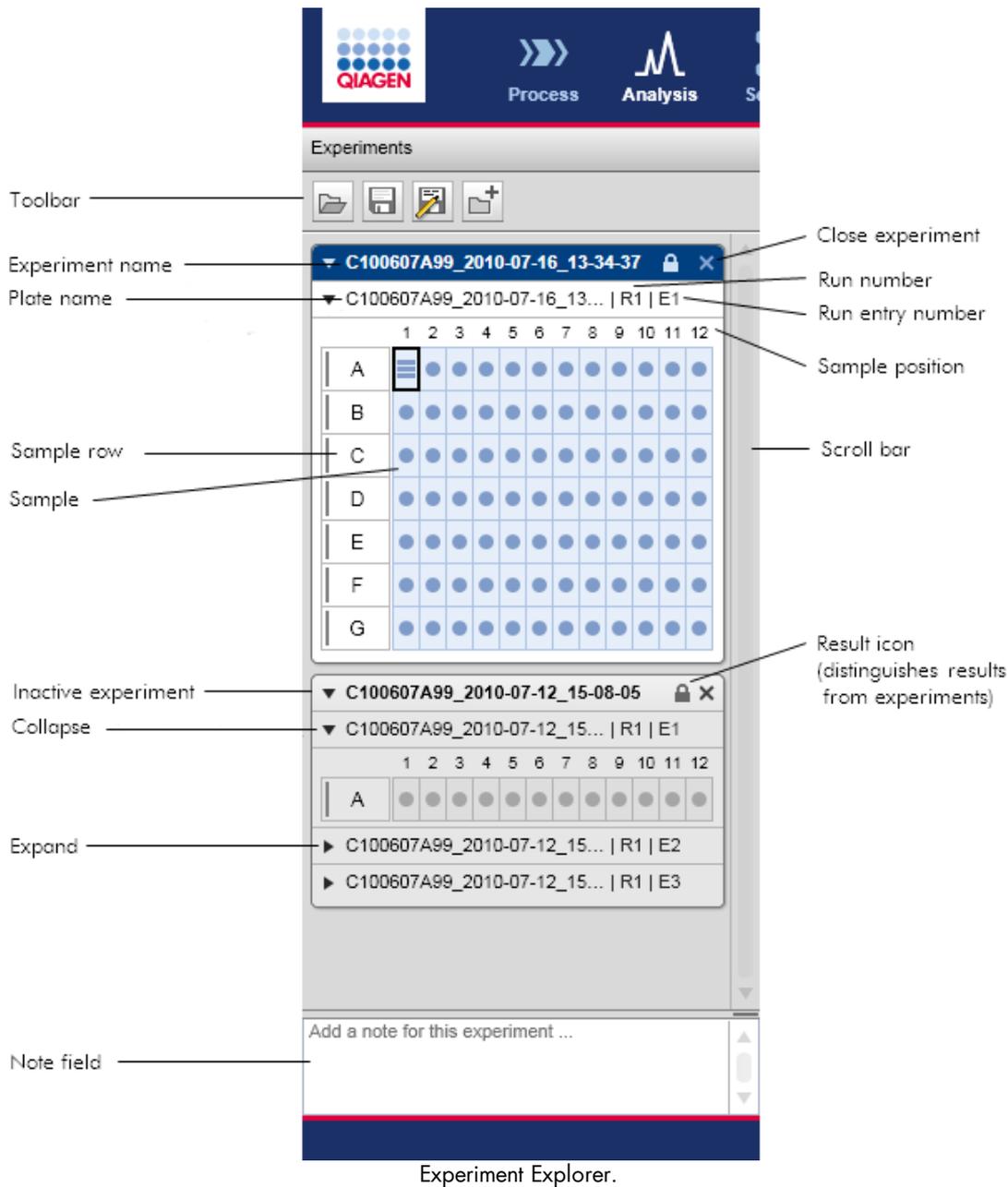
The **Experiment Explorer** in the **Analysis** environment displays samples in a concise manner and provides functionality to load and manage samples.

After a process is completed, the result data are saved in an experiment. If the **Analysis** environment is selected, the experiment is automatically loaded in the experiment explorer.

An experiment groups samples by plates and rows in the order that they were processed. For detailed information, refer to the [Run parameters and result structure](#) section.

Several experiments can be loaded, but only one experiment can be active at a time. The samples in the experiment can be visualized and analyzed. A note for the active experiment can be entered in the note field at the bottom of the explorer.

Customized experiments can be created to combine sample result data from different experiments. Refer to the [Customizing experiments](#) section for detailed information.



Experiment Explorer.

The experiment explorer toolbar has the following buttons:



Load experiment from disk: Refer to the [Loading sample data](#) section for detailed information.



Save: Save the active experiment to disk. Refer to the [Saving an experiment](#) section for detailed information.



Move/rename: Save the active experiment; it allows the name and directory to be changed. Refer to the [Saving an experiment](#) section for detailed information.

Note: This function does not create a copy of the experiment.



Create new experiment: Refer to the [Creating a new experiment](#) section for detailed information.

Meaning of sample icons

In the **Experiment Explorer**, samples are symbolized by a well  and size markers by a ladder .

These symbols vary slightly according to the analysis, visualization, and selection status:

Analyzed	Meaning	Not analyzed
 	Not visualized, not selected.	 
 	Visualized, not selected.	 
 	Not visualized, selected.	 
 	Visualized, selected.	 

The current focus sample has, in addition, a border . This sample is displayed in the single electropherogram view and you can inspect its properties.

The **Size Marker** property  of a sample can be changed by using the sample context menu. Use the **Size Marker** option to toggle.

A reference marker can be created afterward from samples with the **Size Marker** property.

Loading sample data

To load samples from the disk, proceed as follows:

1. Click  at the top of the **Experiment Explorer**.
2. A file dialog appears, showing all experiments that were created in the current run mode (e.g., in DNA mode, you will not see RNA experiments). Navigation starts in the most recently opened directory, or otherwise in the default experiment directory. You can navigate to a different directory.

Note: To open calibration results, select the path ending with "[**Calibration Results**]"

3. Select the experiment from the list by double-clicking it, or clicking it with the mouse and clicking **Load** file.

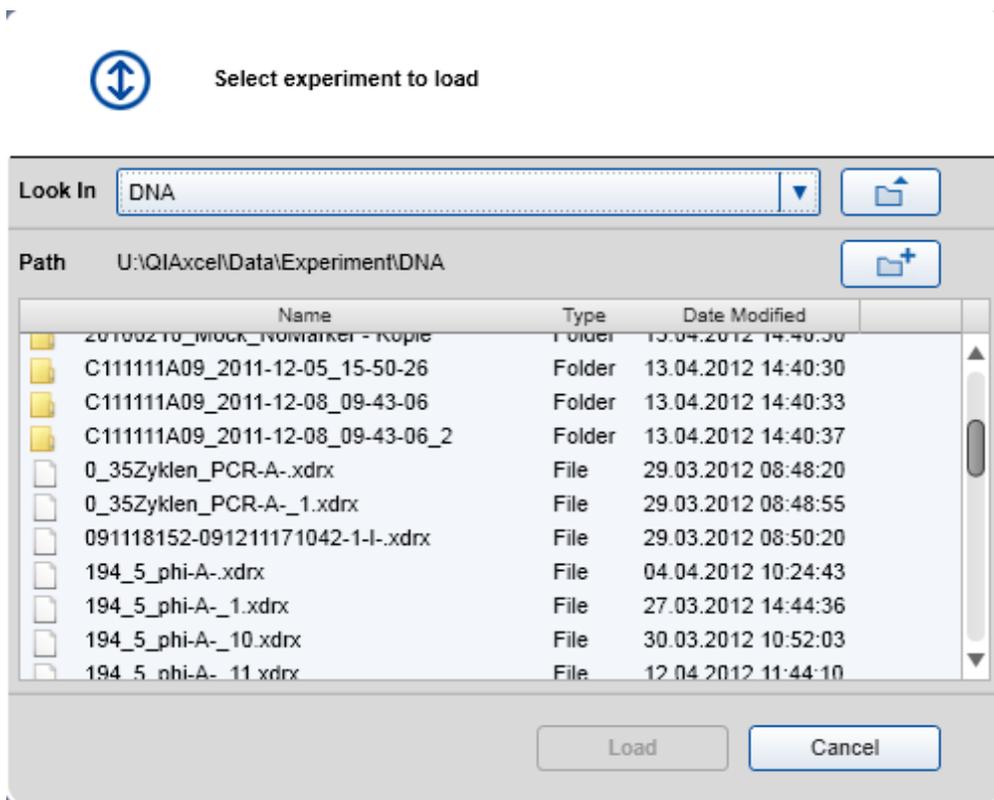
4. The experiment will be loaded and displayed in the **Experiment Explorer**.

Note: If there were experiments already loaded in the **Experiment Explorer**, the experiment just opened will be displayed as the last experiment, at the bottom. The newly loaded experiment automatically becomes active.

Note: In **DNA** mode, loaded experiments that include peak calling or distribution analyses trigger the software to automatically activate peak calling or distribution analysis features, respectively.

Alternatively, you can open one or more experiments via drag and drop from the Windows Explorer. To do so, navigate to the folder where the experiments to be opened are located and drag and drop them into the **Experiment Explorer**. All experiments dragged and dropped into the **Experiment Explorer** that can be opened in the given mode (e.g., in DNA mode, only DNA experiments can be opened) will be loaded and displayed. Files that cannot be opened by the application will be ignored.

Note: Close experiments after analysis and reporting is completed.



The file dialog for loading an experiment.

Representation of an experiment on disk

An experiment is represented on disk as a file with the name of the experiment. The file extension depends on the mode used to create the experiment (.xdrx for DNA, .xrrx for RNA, and for calibration data created during cartridge calibration, .xcdrx, and .xcrrx, respectively).

Loading experiments of previous software versions

To load an experiment that was created with a previous QIAxcel ScreenGel Software version, proceed as described above. The loaded experiments will be automatically converted (migrated) to the newest version.

Note: Experiments which were created by previous software versions in protein mode can no longer be opened.

Note: A migrated experiment cannot be opened by previous software versions any more.

In version 1.0.x of QIAxcel ScreenGel, an experiment was represented on disk as a folder with the name of the experiment. The folder contained a file with the name of the experiment, describing the experiment structure. The extension of this file was dependent on the mode used to create the experiment (.xdr for DNA, .xrr for RNA, .xcr for calibration data created during cartridge calibration). In addition, the folder contained several files, each containing the sample data of a sample row. The file names were extended based on the experiment name.

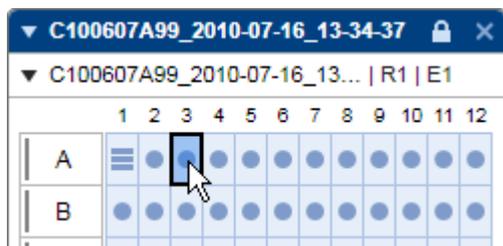
When an experiment created with QIAxcel ScreenGel Software version 1.0.x is loaded to QIAxcel ScreenGel Software versions 1.1 or higher, it is automatically converted (migrated) to the newest version. After saving the experiment, the folder with the experiment and sample files is replaced by a single experiment file with the appropriate new file extension (see above).

When a **RNA** experiment created with QIAxcel ScreenGel Software version 1.0.x is loaded to QIAxcel ScreenGel Software versions 1.1 or higher, the search criteria for the 18S and 28S peak in the reference marker table are automatically converted to a peak calling instruction.

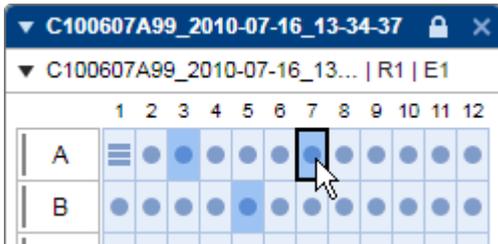
For loading experiments from the BioCalculator Software, refer to the [Importing BioCalculator Data](#) section.

Selecting samples

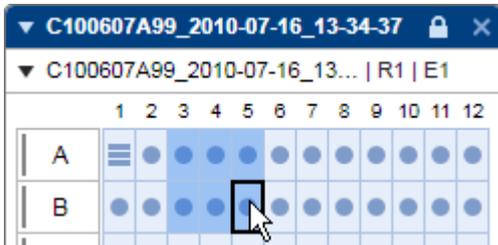
In the **Experiment Explorer** samples inside the active experiment can be selected. For more information about activating an experiment, see the [Activating an experiment](#) section.



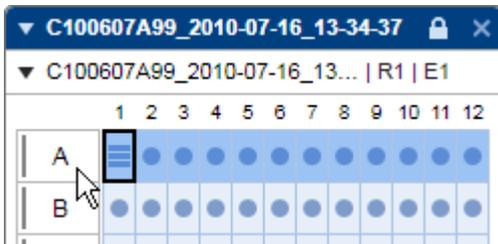
Select an individual sample with a left-click.



To select multiple single samples, simultaneously hold the **Ctrl** key and left-click the samples.

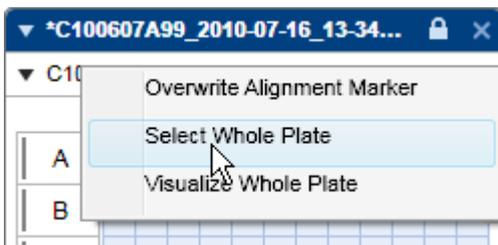


To select multiple samples in a rectangular area, simultaneously hold the **Shift** key and — for this example — left-click the samples A3 and B5.

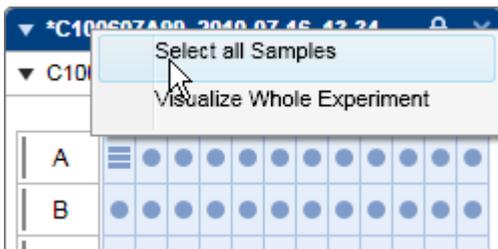


To select all samples in a row, left-click the row letter.

To select multiple rows, hold the **Ctrl** or **Shift** keys simultaneously.



To select all of the samples of a plate, right-click the plate name and select the context menu option **Select Whole Plate**.



To select all of the samples of the experiment, right-click the experiment name and select the context menu option **Select all Samples**.

Switch the focus by left-clicking a sample. During sample selection, the last sample selected has the focus.

If samples from different experiments need to be selected, create a new customized experiment containing these samples. For more information about customized experiments, see the [Customizing experiments](#) section.

Selecting samples for analysis or report

Here, the selection inside the view is relevant — not the selection in the **Experiment Explorer**. The selection of samples depends on the view. Descriptions are provided below:

View	Single sample selection	Multiple sample selection
Gel Image	Select a single sample by clicking the gel lane header of the sample. Selection of a sample for analysis in the Experiment Explorer is not possible in this environment.	Selection of multiple samples can be performed by clicking the gel lane headers using the Shift or Ctrl key (just as in the Windows Explorer). Alternatively, you can select all visualized gel lanes by clicking the Select all key in the tool bar.
Single Electropherogram	Select a single sample in the Experiment Explorer. In this view, the visualized sample will be analyzed.	Not possible in this view.
Electropherogram Overview	Select a single sample by clicking the electropherogram of the sample. Selection of a sample for analysis in the Experiment Explorer is not possible in this environment.	Selection of multiple samples can be performed by clicking the electropherograms using the Shift or Ctrl key (just as in the Windows Explorer). Alternatively, you can select all visualized electropherograms by clicking the Select all key in the tool bar.
Electropherogram Superposition	Not possible in this view.	All samples included in the diagram are selected automatically.

Expanding and collapsing

For a better overview, you can collapse experiments or plates, regardless of whether the experiment is active or not.

To collapse an experiment:

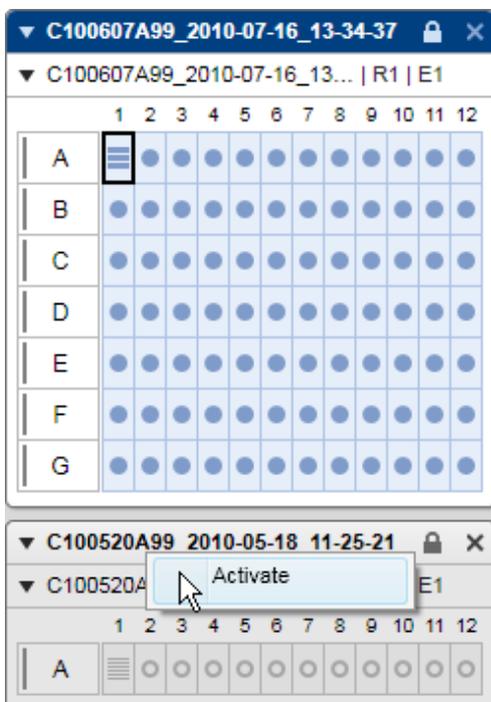
1. Click ▼ to the left of the experiment name. The entire experiment collapses down to the experiment name only.
2. Click ► to expand it again.

Note: You can collapse a single plate inside an experiment by clicking ▼ to the left of the plate name. The plate collapses down to the plate name only. Click ► to expand it again.

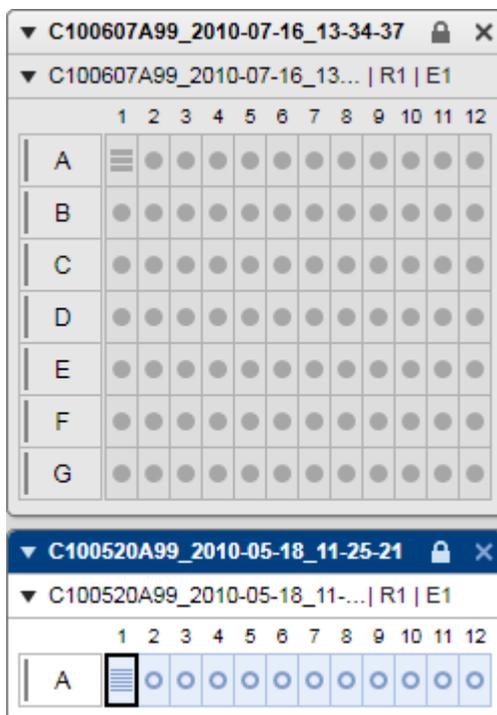
Activating an experiment

Only one experiment can be active at a time. The samples in the active experiment can be visualized and analyzed.

To activate an experiment in the **Experiment Explorer**, right-click the experiment and select **Activate** from the context menu or double-click the experiment header.



Activating an experiment using the context menu.



The experiment is now active.

The previously active experiment will be deactivated automatically. If this experiment was modified, the system asks whether the changes should be saved or not. Click **Yes** to save or **No** to discard the changes. Select **Cancel** to cancel activation. For more information about saving experiments, see the [Saving an experiment](#) section.

Note: Experiments from older software versions cannot be deactivated. Instead, they will be closed if you activate another experiment. Avoid this by saving them in the new format. Note, however, that once saved with the current software version, the experiments can no longer be opened with older software versions.

Note: In DNA mode, activated experiments that include peak calling or distribution analyses trigger the software to automatically activate peak calling or distribution analysis features, respectively.

Saving an experiment

To save the active experiment to the disk, click the **Save** button  at the top of the **Experiment Explorer**.

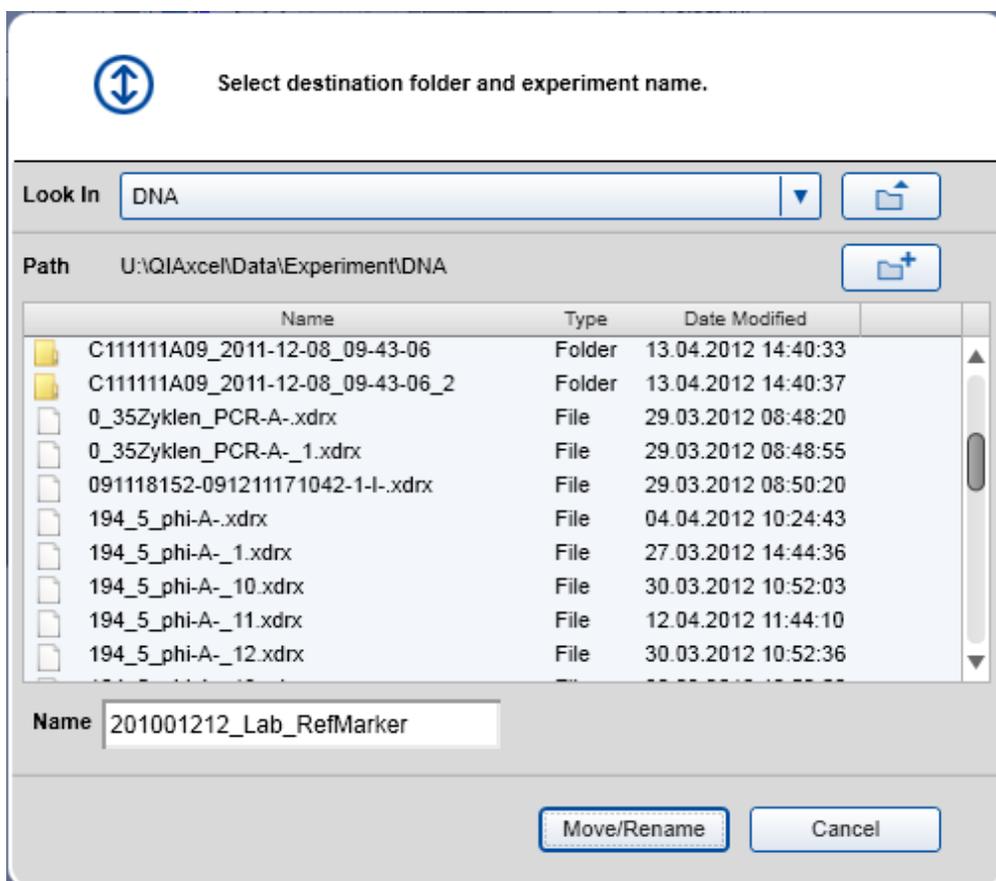
All modifications made to this experiment will be saved, as specified in the settings. This includes analysis results, as well as information about the configuration of the visualization.

Note: Sample data cannot be saved individually.

If you want to save the active experiment to another directory, use the **Move/rename** button . This will open a file dialog for choosing a different directory and experiment name.

Note: To avoid data redundancy, the previous experiment file will be removed.

The same file dialog opens if the experiment was [created](#) in the experiment explorer and has not yet been saved to disk.



The file dialog for saving an experiment.

The file dialog enables navigation to the directories of the disk, creation of a new directory, and allows the user to choose the new name of the experiment. The appropriate file extension will be appended automatically.

Note: The experiment name is restricted to 40 characters.

Information stored in the experiment

The following information is stored in the experiment:

- Experiment structure
- Visualization information: visualization status of the samples (not for superimposition), sample order in the visualization.

The following information is saved in each sample since it can differ from sample to sample:

- **Run information:** all run parameters, including cartridge information, parameters of the method used, sample injection time, and separation time. The run information is stored immediately after the process has finished and will not be changed later.
- **Analysis information,** if the sample has been analyzed: includes analysis parameters, reference marker table used during analysis, and peak calling information.

For more details about samples refer to the [Inspecting sample properties](#) section. For details about settings and directory configuration, refer to the [Settings](#) section.

Closing an experiment

You can close an experiment by clicking **X** to the right of the experiment name, regardless of whether the experiment is active or not.

If the experiment was modified, the system asks you whether to save the changes or not. Click **Yes** to save or **No** to discard the changes. Select **Cancel** to cancel closing.

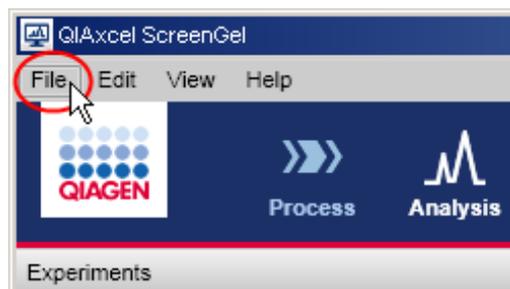
For more details about saving experiments, see the [Saving an experiment](#) section.

Importing BioCalculator Data

Data files from the BioCalculator Software (the QIAxcel Software version prior to QIAxcel ScreenGel Software) can be imported into the QIAxcel ScreenGel Software.

Proceed as follows:

1. Select **Import BioCalculator Data** from the **File** menu.



Opening the File menu.

Note: This menu option is available in the **Analysis** environment only.

2. A dialog appears enabling selection of the BioCalculator data files to be imported. Navigation starts initially with the most recently used BioCalculator import directory or the user's **My Documents** directory. Navigate to the directory that the BioCalculator data files will be imported from. Use the file type to filter.

3. Select the files to be imported from the list and click **Import**.

Note: Only one file of type .hff can be imported at a time. The .hda files referred to by the selected .hff file are expected to be located in the same folder as the .hff file.

Note: Change the file type to **HDA**, to select multiple .hda files.

4. The files will be converted and displayed in the **Experiment Explorer**.

If a .hff file was selected, an experiment will be created containing as many rows and samples as in the .hff file. Repeats will be represented by separate plates.

The experiment will be saved in the default experiment directory, as defined in the user [settings](#).

Note: If there are incomplete rows, the empty sample positions remain empty.

Note: If a sample position is referred to multiple times, separate plates are also generated.

Note: If there were experiments already loaded in the **Experiment Explorer**, the newly opened experiment will be displayed as the last experiment, at the bottom). This experiment automatically becomes active.

Note: If the mode (DNA or RNA) of the selected files is different to the current mode, the files cannot be imported.

5. [Visualize](#) the samples.

Note: To see the imported analysis parameters and reference marker table in the analysis parameters tab, right-click a sample in the experiment explorer and select the context menu option **Transfer Analysis Instructions**.

To load an experiment that was created with the QIAxcel ScreenGel Software, use the **Load** function as described in the [Loading sample data](#) section.

Revising sample information

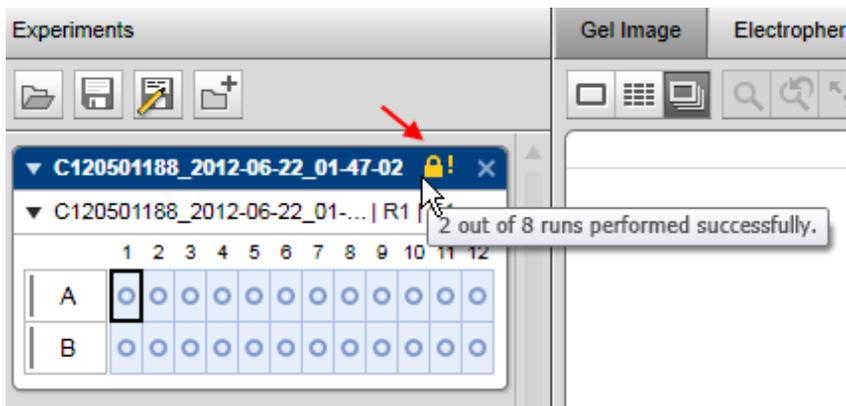
To revise sample information or sample comments after the run, select the sample in the experiment explorer, right-click the sample, and select the context menu option **Revise Sample Information** or **Sample Comment**. Enter the new sample information and/or comment in the dialog that appears.

Note: The context menu option **Revise Sample Information** or **Sample Comment** is enabled only if the user has the right to revise the sample information. The administrator can grant the right in the [User management](#).

Note: The report will indicate that a sample name or comment has been revised.

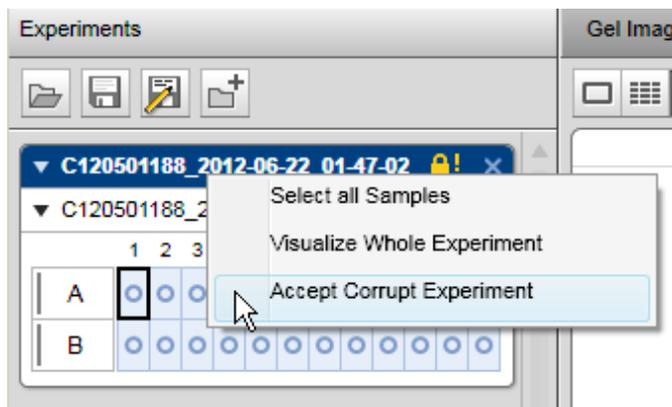
Handling an incomplete experiment

An experiment can be incomplete if the process stopped during data acquisition. This is indicated in the experiment explorer with a yellow lock icon. Hover with the mouse over the lock icon to display a tooltip with further information.



Incomplete experiment.

You can remove this icon from the experiment (for example, because you could successfully reprocess the missing runs). Right-click the experiment name and select the context menu option **Accept Corrupt Experiment**.



Accept an incomplete experiment.

Note: This option is available only for users who have this right (based on their user role). The administrator can grant the right May accept incomplete experiments using the **User Management** system.

The report will contain information about the incomplete process and the acceptance in the report overview section.

Viewing sample data

The **Analysis** environment offers several options for visualization of raw data and analysis results:

- A gel view, which can display several samples — see [Gel view](#).
- A single electropherogram view, which visualizes a single sample along with its analysis results — see [Electropherogram view](#).
- An electropherogram overview, which visualizes several electropherograms in a gallery — see [Electropherogram overview](#).
- An electropherogram superposition view, which visualizes several electropherograms in one plot — see [Electropherogram superposition view](#).

All views allow data exploration by zooming and scaling the data.

Adding samples to views

Note: A maximum of 97 samples can be visualized at a time in the gel view and electropherogram overview. If this limit is reached, visualization of more samples is disabled.

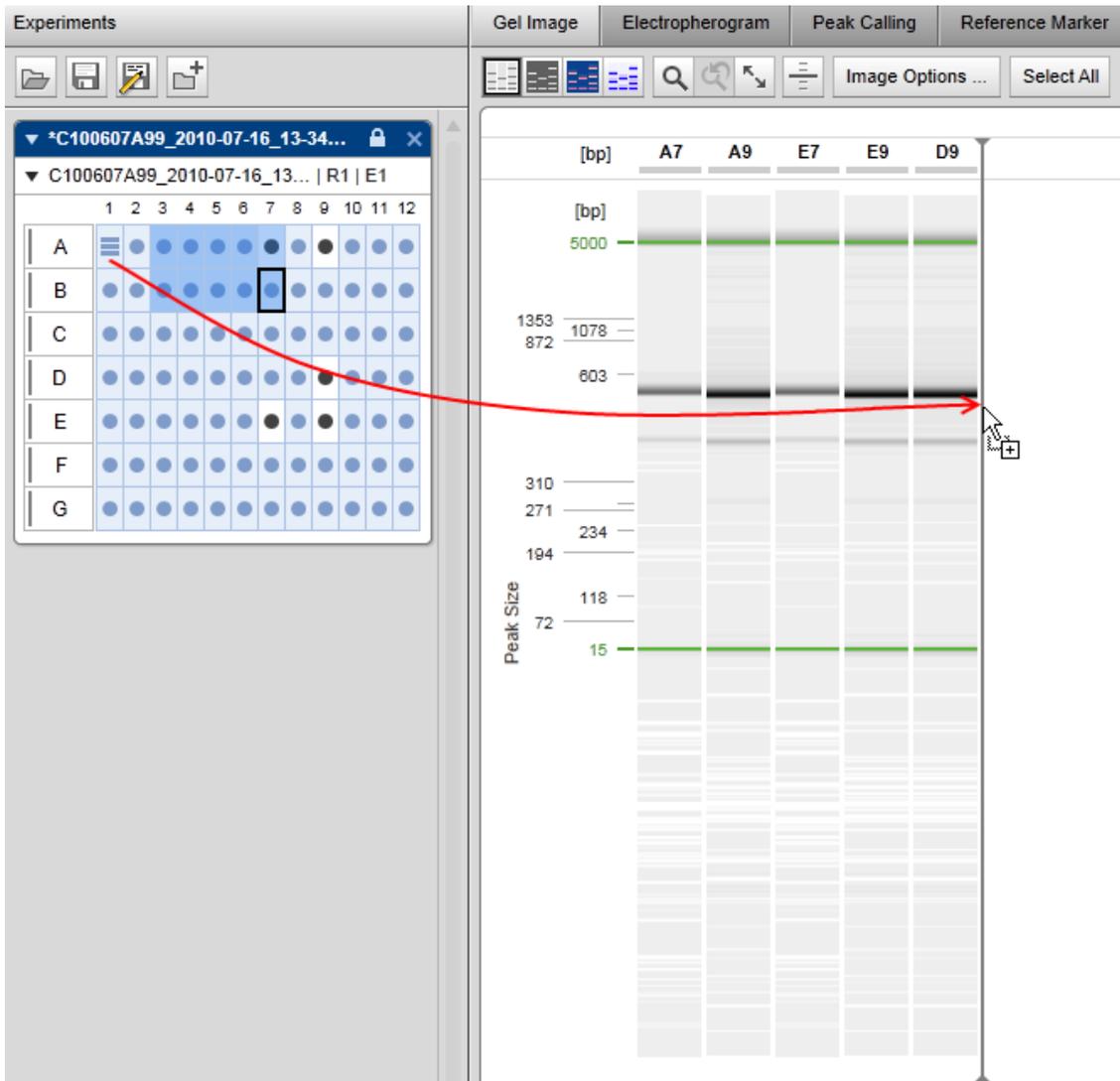
Samples can be added to a view by dragging samples from the **Experiment Explorer** to:

- The gel view
- The electropherogram overview
- The electropherogram superposition view (see description at the end of this section)

Proceed as follows:

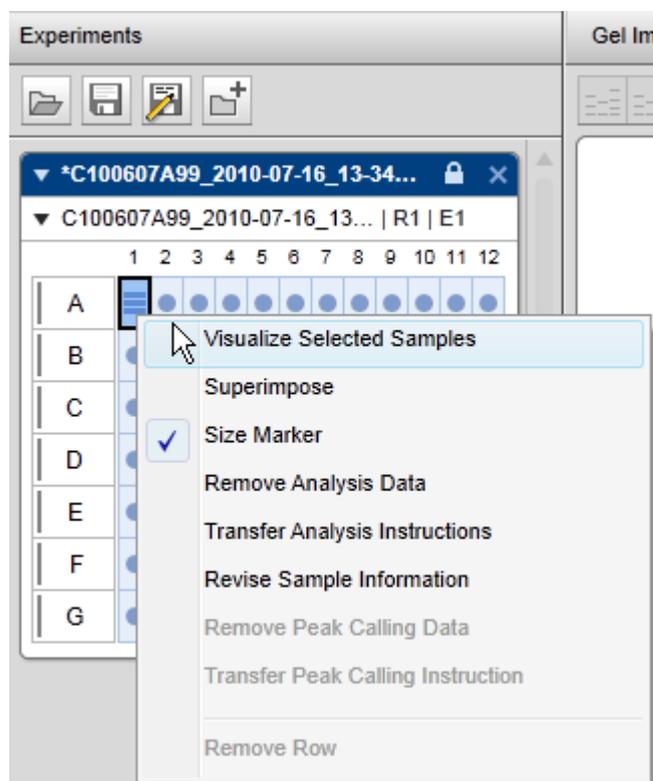
1. In the **Experiment Explorer** select the samples to be visualized.
2. Left-click the selected samples, drag to the view, and drop. All selected samples will be displayed in the view.

Note: In gel view and electropherogram overview a marker is shown that indicates the position when dropping. All samples will be displayed at the selected position. See also [Changing lane order](#).



Dragging sample A1 to the gel image, to the right of D9.

Alternatively, samples can be added to the views through the sample context menu of the experiment explorer. Use the **Visualize Selected Samples** option to add the selected samples to the views.



Visualize selected samples.

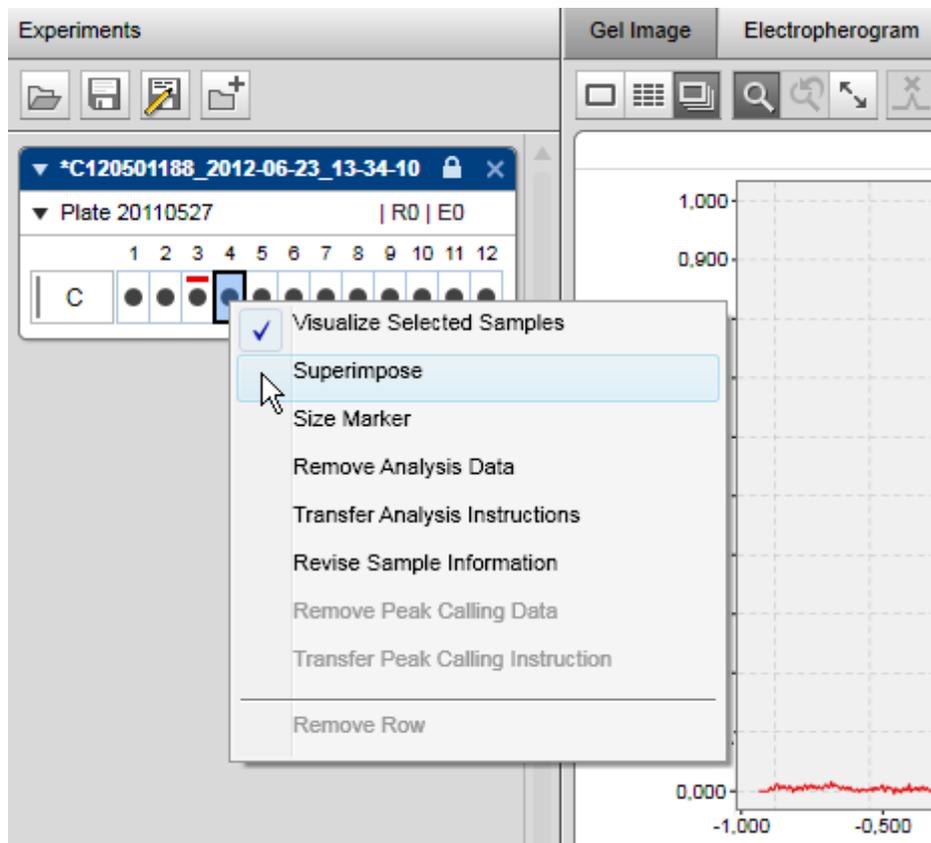
Finally, to visualize a plate, right-click the plate name and select the context menu option **Visualize Whole Plate**. To visualize the whole experiment, right-click the experiment name and select the context menu option **Visualize Whole Experiment**.

Unlike all other views, the **superposition view** does not automatically display all samples selected for visualization.

To add samples to the superposition view:

1. In the **Experiment Explorer** select the samples to be added.
2. Open the context menu of the selected samples in the **Experiment Explorer**.

3. Select the **Superimpose** option.



Adding sample C4 to superposition.

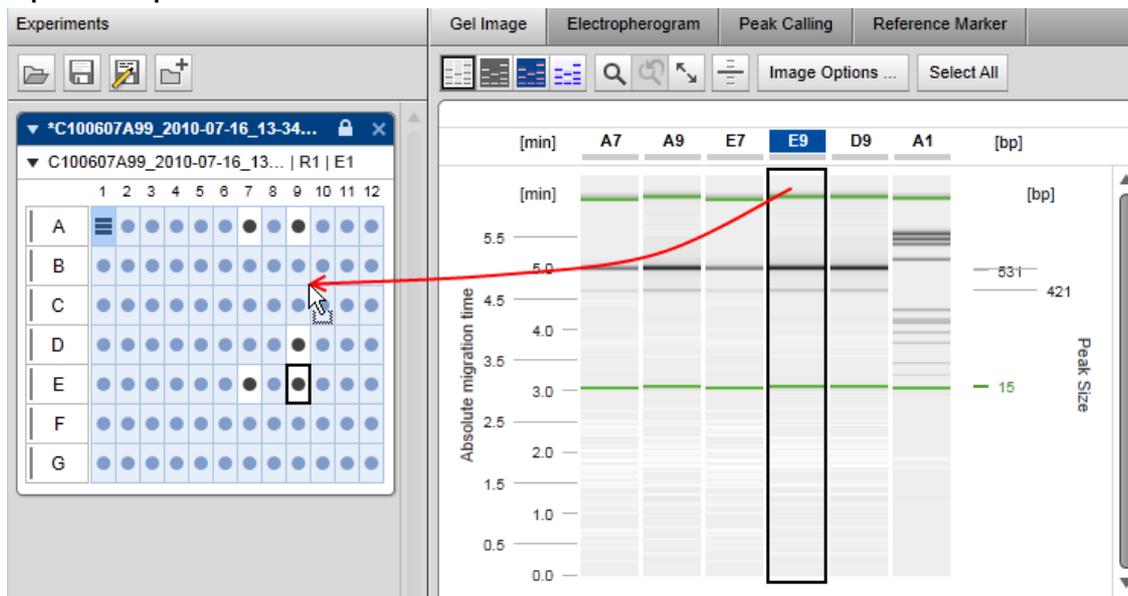
The selected samples will be added to the superposition view. In the **Experiment Explorer** all samples that are displayed in the superposition view are marked by a colored rectangular according to their color in the superposition.

Note: Up to 12 electropherograms can be superimposed. A warning will be displayed if the limit is exceeded.

Alternatively, drag and drop up to 12 selected samples from the **Experiment explorer** to the **superposition view**.

Removing samples from views

Samples can be removed from the views by dragging the selected samples from the view back to the **Experiment Explorer**.

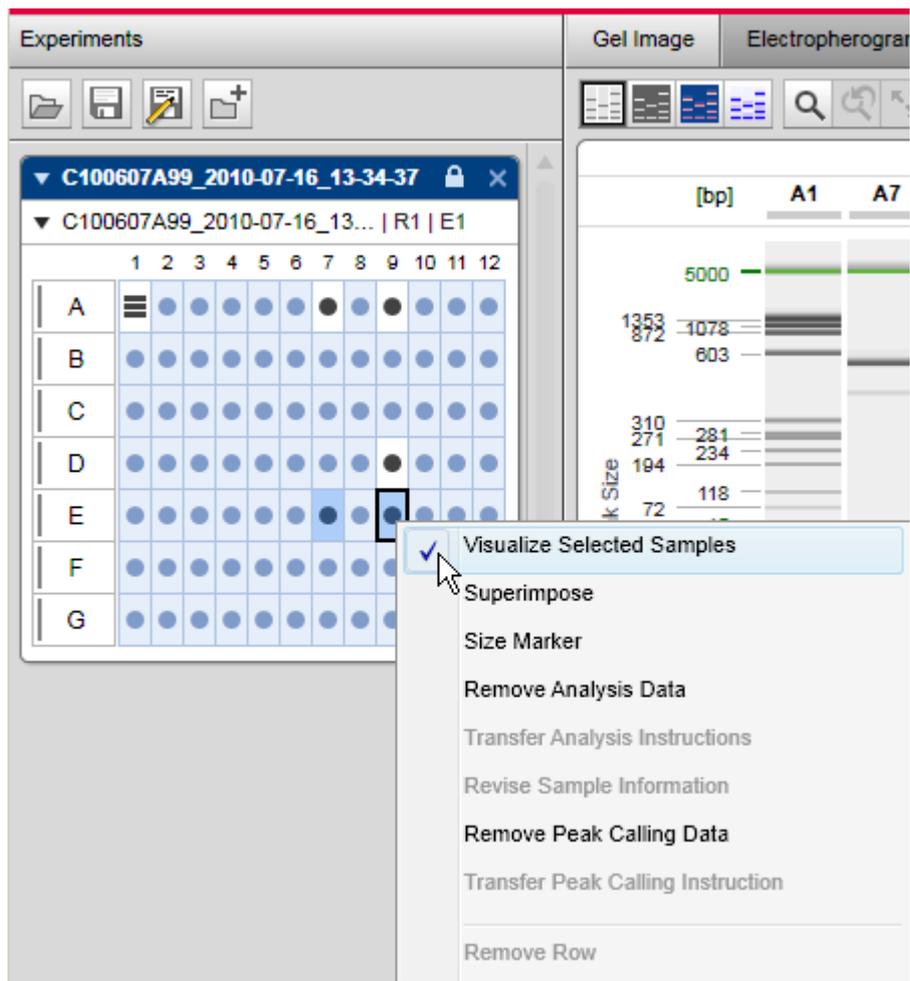


Removing samples E7 and E9 from the gel image.

Note: You can drop the samples elsewhere in the **Experiment Explorer**.

Alternatively, use the context menu of the samples in the **Experiment Explorer**:

1. Select the samples that should no longer be visualized.
2. Right-click a selected sample and uncheck the **Visualize Selected Samples** option to remove samples from the views.



Removing selected samples E7 and E9 via the context menu.

Finally, if a whole plate or a whole experiment is visualized, you can remove all the samples from the view. Right-click the plate name or the experiment name and uncheck the **Visualize Whole Plate** or **Visualize Whole Experiment** option from the appropriate context menu.

To remove samples from the superposition view, proceed as follows:

1. In the **Experiment Explorer** select the samples to be removed.
2. Open the context menu of the selected samples in the **Experiment Explorer**.
3. Unselect the **Superimpose** option.

Exporting view to clipboard

Sample views can be copied to the clipboard.

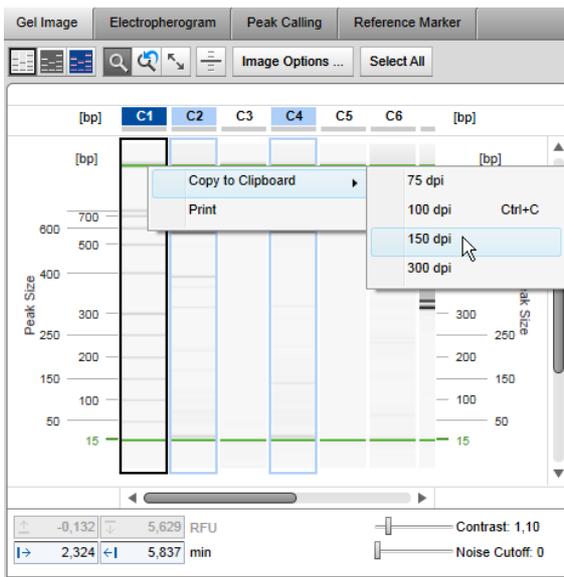
1. Select the lanes/electropherograms to be copied (in [gel view](#) or [electropherogram overview](#)).
2. Right-click the selected sample and select from the menu item **Copy to clipboard** the resolution you want have the image with.
3. Switch to the application you want the view to appear in and paste.

Note: You can use the keyboard shortcut **Ctrl+C** to copy selected images to clipboard. Keep in mind that using of key shortcut applies the default resolution value (96 dpi), not the last used one.

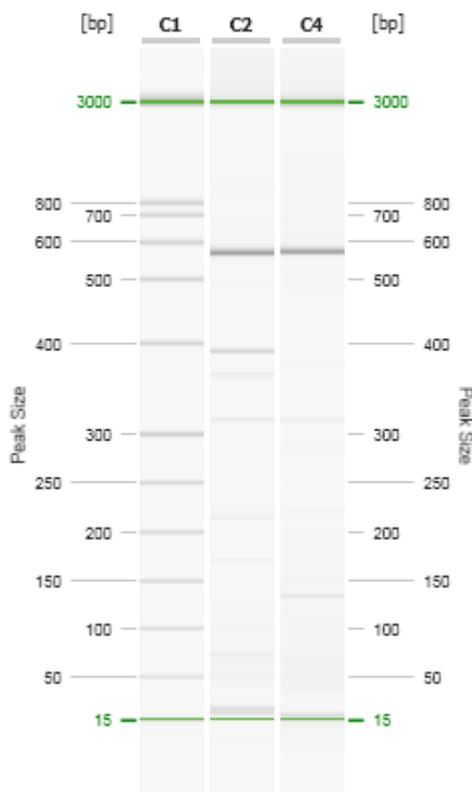
Note: When you paste the image in an application, make sure that it uses the right resolution. QIAxcel ScreenGel puts the pixel array on clipboard which adapted for desired resolution (this means that the image has the appropriate pixel size). The application you paste the image in, shall be able to interpret this information correctly.

Note: The samples that have been copied to clipboard, have the same image settings as in the visualization view (such as color palette, contrast, noise cutoff, and zoom factor).

Note: In the [single electropherogram view](#) and [electropherogram superposition view](#) the gel lane and C-channel diagram will be copied to clipboard too if they are displayed in visualization. If you hide both gel lane and C-channel diagram, only samples will be copied to clipboard. You can access the **Copy to clipboard** pop-up menu from gel lane and C-channel diagram as well.



Copying the gel image of the selected samples C1, C2, and C4 to the clipboard.



C1, C2, and C4 pasted.

Direct printing view

You can directly print images of selected samples:

1. Select the lanes/electropherograms to be printed.
2. Right-click the selected sample and select the context menu item **Print**.

This function works in a similar way to the 'copying to clipboard' function with default image resolution; the selected samples will be sent to the default printer. They have the same image settings as in the visualization view (such as contrast, noise cutoff, and zoom factor).

The image sent to the printer is identical to the image you would copy to the clipboard; if the gel lane and C-channel diagram are displayed in the [single electropherogram view](#) and [electropherogram superposition view](#), they will be printed as well.

Result table

The analysis result table of a sample is displayed in the **Analysis** environment below the electropherogram views or the gel view. Sample information, sample comment (if entered), position of the sample on the plate, and plate ID are displayed at the top of the result table. When an analyzed sample is selected, the results are shown in the result table. The displayed columns depend on the mode. Right-click the header line of the table, select **Show column**, and then select the property you are interested in.

Sample Info:				Position: A7	Plate ID:
#	Size [bp]	Conc. (ng/ul)	Saturated		
1	15				
2	426				
3	554				
4	5000				

Peak Result Peak Calling Result Smear/gDNA Result

DNA result table.

The **Peak Result** table lists the detected peaks of the sample. Use this result table for [Standard DNA analysis](#), for the [Fast Analysis of DNA samples](#) and for [RNA analysis](#). Refer to the [Peak result columns](#) section for detailed information on available peak properties.

The **Peak Calling Result** table lists the peak calling result of the sample. Use this result table also for [RNA quality control](#). Refer to the [Peak calling result columns](#) section for detailed information.

In **DNA** mode, the **Smear/gDNA Result** table lists the detected smear peaks of the sample and shows properties that are specific for smear peaks. Smear peaks are detected only when the analysis profile option **Smear** or **gDNA** had been selected in the **Analysis Properties** panel at the right of the **Analysis** environment ([Smear DNA analysis](#), [gDNA analysis](#)). Refer to the [Smear result columns](#) section for detailed information on smear peak properties.

If a distribution analysis was performed on **DNA** mode, the **Distribution** result table is visible instead of the **Peak Calling Result** table. Refer to the [Distribution result columns](#) for detailed information.

Note: Peak calling and distribution analysis generate an additional overview result table in the middle panel of the **Analysis** environment. For more information, refer to [Peak Calling](#) or [Distribution result](#), respectively.

Modifying the result table

The information displayed in the result table can be customized for the electropherogram single view and overview independently. The customization applies to all further viewing of the results.

Note: In the electropherogram superposition view, a small non-customizable result table is displayed.

Adding a column

To add a column:

1. Right-click the table header.

2. Select the column to be displayed from the **Show Column** selection.

Note: Select the **Show all Columns** option to display all columns. Select the **Restore Default Columns** option to display the default for the application.

Removing a column

To hide a column:

1. Right-click the column header.
2. Unselect the column from the **Show Column** selection.

Changing column order

The order of the displayed columns can be changed by dragging a column header to the desired position. While dragging, a marker is displayed that indicates the position of the column when dropping it.

Note: Columns of the peak calling and distribution result tables cannot be reordered.

Resizing column width

The column width can be changed by dragging a vertical cell border in the table header.

Note: Column widths of the peak calling and distribution result tables cannot be changed.

Interacting with the result table

Selecting and removing a peak

When selecting a peak in the result table, the peak is highlighted in the electropherogram (single electropherogram view and electropherogram overview). To select a peak in the result table, left-click the peak number in the # column. To unselect the peak, use the context menu option **Unselect Peak** or just click to another cell. To remove the selected peak from the result table, use the context menu option **Delete Selected Peak**. To remove multiple selected peaks from the result table, first select the peaks to delete by holding the **Ctrl** key and left-clicking the corresponding peak numbers in the # column. Alternatively, hold the **Shift** key and left-click the first and last peak numbers in the # column. All peaks in between will be selected. Right-click the selection and click **Delete Selected Peaks**.

Exporting analysis results

The contents of the result table can be exported to other applications using the Windows clipboard. There are several ways to select the table cells:

- Select the cells with the mouse while holding down the left mouse button.
- Click the first column of a row to select a row. You can also select multiple columns using the **Shift** and **Ctrl** key.
- Click the column header to select a column.

- Click the column header of the first column to select all cells.

To copy your selection:

1. Select cell(s).
2. Right-click a selected cell.
3. Click the **Copy selected cells to clipboard**.
4. Paste the data to other applications, for example, Microsoft Excel[®].

Note: The result data are exported using the local settings of the Windows system. Make sure that the target application also uses the local settings to interpret the numbers.

Peak result columns

The following columns are available:

#	Number of peaks in the sample.
Size [bp]	For DNA mode only. Fragment size in base pairs.
Size [nt]	For RNA mode only. Fragment size in nucleotides.
Conc. [ng/μl]	Concentration of the fragment in ng/μl. Note: This value is not calculated for alignment marker peaks.
Mol. [nmol/l]	Molar concentration (molarity) in nmol/l. The calculation is based on the fragment size and concentration. Note: This value is not calculated for alignment marker peaks.
Saturated	Indicator whether the peak intensity reaches the maximum possible intensity (see Saturated Signals section). The calculated height, area and concentration of saturated peaks are not correct.
S/N	Signal-to-noise ratio of the peak. The noise is approximated with three times the standard deviation of the noise data points from the baseline.
NA	Normalized area, also called corrected peak area. This is the peak area divided by the migration time of the peak apex.
Area	Peak area (integration of the area under the signal and above the baseline).
NA %	Normalized peak area relative to the sum of all normalized peak areas. Note: This value is not calculated for alignment marker peaks.
Ratio NA	The area ratio with respect to the previous peak. The alignment marker peaks and the first data peak in the table will have an empty field here.
Height	Height of the peak at its maximum.

Height %	Peak height relative to the sum of all peak heights. Note: This value is not calculated for alignment marker peaks.
Res.	The separation resolution relative to the next peak. Note: This value is not calculated for alignment marker peaks.
FWHM [sec]	The peak width at half the maximum intensity (full width at half maximum), which is a parameter for peak resolution and thus the precision of size calculation.
Start [min]	Start time/X-value of the peak in minutes.
Time [min]	Time/X-value for the peak maximum.
Stop [min]	Stop time/X-value of the peak in minutes.
Rel. Time	Relative time/X-value for the peak maximum. This value is mode-dependent: In DNA mode, in case of 2 alignment marker peaks, the relative position of the peak between lower alignment marker and upper alignment marker is mapped to the interval from zero to one, i.e. all peaks have a Rel. Time between zero and one. The alignment markers have a Rel. Time of zero and one, respectively. In case of one alignment marker peak, the relative migration time is calculated as in RNA mode. In RNA mode, the relative position of the peak in relation to the lower alignment marker is calculated, i.e. the alignment marker has a Rel. Time of 1 and all other peaks have Rel. Time higher than one.

Peak calling result columns

Each row in the table corresponds to a sample; the columns **Pos.** and **Sample Info** identify the sample. The **Pos** column is fixed. The following columns are defined by the peak calling instruction. Aggregated columns over all peaks of interest appear if they were selected in the **Calculated Columns** panel of the peak calling instruction. The following columns are grouped by the names of the peaks of interest and show several peak properties. To change the properties listed for each peak of interest, right-click the table header and select/unselect the property with the **Show Column** option. The change takes effect in the entire table.

Note: If a sample was not analyzed, it is not present in the peak calling result overview.

Parts of the peak calling result table can be copied to the clipboard. Select the cells to be copied and then press **Ctrl+C**. To copy the complete result of a peak calling instruction, right-click in the peak calling result table and select the **Copy Peak Calling Result of [...]** option.

Smear result columns

The following smear peak properties are available:

Number of peak in sample.

Note: As alignment marker peaks are no smear peaks, the peak number in this table usually starts with 2.

Median Size [bp]	Determines the fragment size that corresponds to the median of the area of interest. The median is the point in the peak curve, where geometrically the left part of the peak area has the same size as the right part. The value is given in base pairs.
Conc. Area of Interest [ng/μl]	Continuously calculated concentration of the fragments corresponding to the area of interest. Value is given in ng/μl.
Mol. Area of Interest [nmol/l]	Molar concentration (molarity) of the fragments corresponding to the area of interest. This calculation is based on the continuously calculated fragment size and concentration, not Median Size , and is given in nmol/l.
Start Area of Interest [bp]	Start of the area of interest given in base pairs.
End Area of Interest [bp]	End of the area of interest given in base pairs.
% Conc. Area of Interest	Percentage of concentration of fragments in the area of interest relative to the concentration of the smear peak (defined by the start and end of the peak).
NA Area of Interest	Normalized area based on the area of interest. Area of the smear peak normalized by the migration time.
% NA Area of Interest	Percentage of the normalized area relative to the normalized area of the smear peak (defined by the start and end of the peak).

Note: All values listed in the table above refer to the area of interest assigned to a smear peak. Moving the borders of the area of interest of a smear peak will trigger the recalculation of the corresponding properties.

In addition, two properties are calculated for the entire sample. The values are displayed just above the smear result table:

Total Concentration [ng/μl]	Total concentration of the fragments across the entire sample. The calculation is performed continuously for all data points with a signal above the baseline. The calculation starts after the end of the lower alignment marker peak and ends at the beginning of the upper alignment marker peak. The value is given in ng/μl.
Total Molarity [nmol/l]	Total molarity of the fragments across the entire sample. The calculation is based on continuously calculated fragment size and concentration for all data points with a signal above the baseline. The calculation starts after the end of the lower alignment marker peak and ends at the beginning of the upper alignment marker peak. The value is given in nmol/l. If the value is not visible, scroll the horizontal table scroll bar to the right to see the value.

Distribution result columns

Each row in the table corresponds to a sample, with the columns **Pos.** and **Sample Info** identifying the sample. Columns relevant to the entire sample appear first. Thereafter, columns are grouped according to the names of the defined areas of interest and display several smear peak properties. The remaining columns are then grouped by the name of defined ratios. Find a detailed description in the section [Distribution result columns](#).

To change the properties listed, right-click the table header and select or unselect the property with the **Show Column** option. The change takes effect in the entire table.

Note: If a sample was not analyzed with a smear or gDNA analysis profile, it will not appear in the distribution result overview. If a sample was not analyzed with a reference marker, the distribution values cannot be calculated. In this case, the sample **Quality** is listed as "Review." In both cases, follow the instructions in [Analysis of DNA samples](#) to check and correct the analysis steps that are required before **Distribution** analysis. Ensure using **Analysis** parameters as described in [Smear DNA analysis](#) and [gDNA analysis](#), respectively.

The distribution result table can be copied to the clipboard. To copy the complete result of a distribution profile, right-click in the distribution result table and select the **Copy Distribution Result of [...]** option.

Columns relevant to the entire sample:

Pos	Position on the plate.
Sample Info	Sample information
Total Conc. [ng/ μ l]	Total concentration of the fragments across the entire sample. Refer to Smear result columns for details. The column displays "n/a" for size marker samples.
Total Mol. [nmol/l]	Total molarity of the fragments across the entire sample. Refer to Smear result columns for details. The column displays "n/a" for size marker samples.
Quality	The overall quality assessment of the sample. The column reports "Passed" if all ratio assessments and height checks passed (if applicable). That is, if one sub-assessment failed, the overall quality reported is "Review" as well. The column displays "Not Analyzed" for size marker samples.

Note: If the sample was not analyzed with a reference marker table, i.e., if the [Size and concentration determination procedure](#) was unsuccessful, the **Quality** reported will be "Review," and **Total Conc.** and **Total Mol.** will display "n/a."

Columns relevant to an area of interest (grouped by name of the area of interest):

Mol. [nmol/l]	Molar concentration (molarity) of the fragments corresponding to the area of interest. Refer to Smear result columns for details. The column displays "n/a" for size marker samples.
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Conc. [ng/μl]	Concentration of the fragments corresponding to the area of interest. Refer to Smear result columns for details. The column displays "n/a" for size marker samples.
Height [S/N]	Maximum signal height of the area of interest, given as a Signal-to-noise ratio [S/N]. The noise is approximated by taking three times the standard deviation of the noise data points from the baseline. The column displays "n/a" for size marker samples.
Height Check	The quality assessment of an area of interest with regards to the Height [S/N]. The column reports "Not Analyzed" if the height of the area is not to be checked; "Passed" when the checked height of the area of interest is above the defined minimum height for that area; and "Review" when not. The column displays "Not Analyzed" for size marker samples.
Size Start [bp]	Start size of the area of interest given in base pairs. The column displays "n/a" for size marker samples. Note: The size may differ slightly from the start size defined in the distribution profile. The area of interest starts at the data point with a size nearest to the defined start size.
Size End [bp]	End size of the area of interest given in base pairs. The column displays "n/a" for size marker samples. Note: The size may differ slightly from the end size defined in the distribution profile. The area of interest ends at the data point with a size nearest to the defined end size.

Note: If the sample was not analyzed with a reference marker table, i.e., if the [Size and concentration determination procedure](#) was unsuccessful, the **Height Check** reported will be "Not Analyzed" and all other columns will display "n/a."

Note: If the signal in an area of interest does not exceed the baseline at any point (indicating that the area of interest is not present in the sample), the **Height Check** reports "Not Analyzed" when the height of the area is not to be checked, and "Review" when it is to be checked. All other columns display "n/a."

Columns relevant to a ratio (grouped by name of the ratio):

Ratio (Molarity)	This column is present only if the calculation basis Molarity has been selected for ratios. The value of the molarity ratio. That is, the molarity of the area of interest defined as the Numerator divided by Denominator, which may be either the molarity of another area of interest or the Total Molarity. The column displays "n/a" for size marker samples.
Ratio (Concentration)	This column is present only if the calculation basis Concentration has been selected for ratios.

	The value of the concentration ratio. That is, the concentration of the area of interest defined as the Numerator divided by Denominator, which may be either the concentration of another area of interest or the Total Concentration. The column displays "n/a" for size marker samples.
Ratio Quality	The quality assessment of the ratio. The column reports "Not Analyzed" if the quality of the ratio is not to be checked; "Passed" when the value of the ratio is within the defined range; and "Review" when not. The column displays "Review" for size marker samples.
Numerator	Defined in the distribution profile. This is the area of interest, of which the molarity or the concentration is used as numerator of the ratio, depending on the selected calculation method.
Denominator	Defined in the distribution profile. Either Total Sample or another area of interest, of which either the molarity or the concentration is used as denominator of the ratio, depending on the selected calculation method.

Note: If the sample was not analyzed with a reference marker table, i.e., if the [Size and concentration determination procedure](#) was unsuccessful, the **Ratio Quality** reported will be "Review" and the **Ratio** will display "n/a."

Note: If the signal of the area of interest used for the numerator does not exceed the baseline at any point (indicating that the area of interest is not present in the sample), the molarity/concentration value is assumed to be "0." If the signal of the area of interest used for the denominator does not exceed the baseline, the column **Ratio Quality** displays "Review." In both cases, the column **Ratio** displays "n/a."

For information about defining the distribution profile, refer to the [Modifying a distribution profile](#) section.

Gel view

The gel view displays the gel images of the samples.

The lanes in the gel view can be displayed in four view modes:



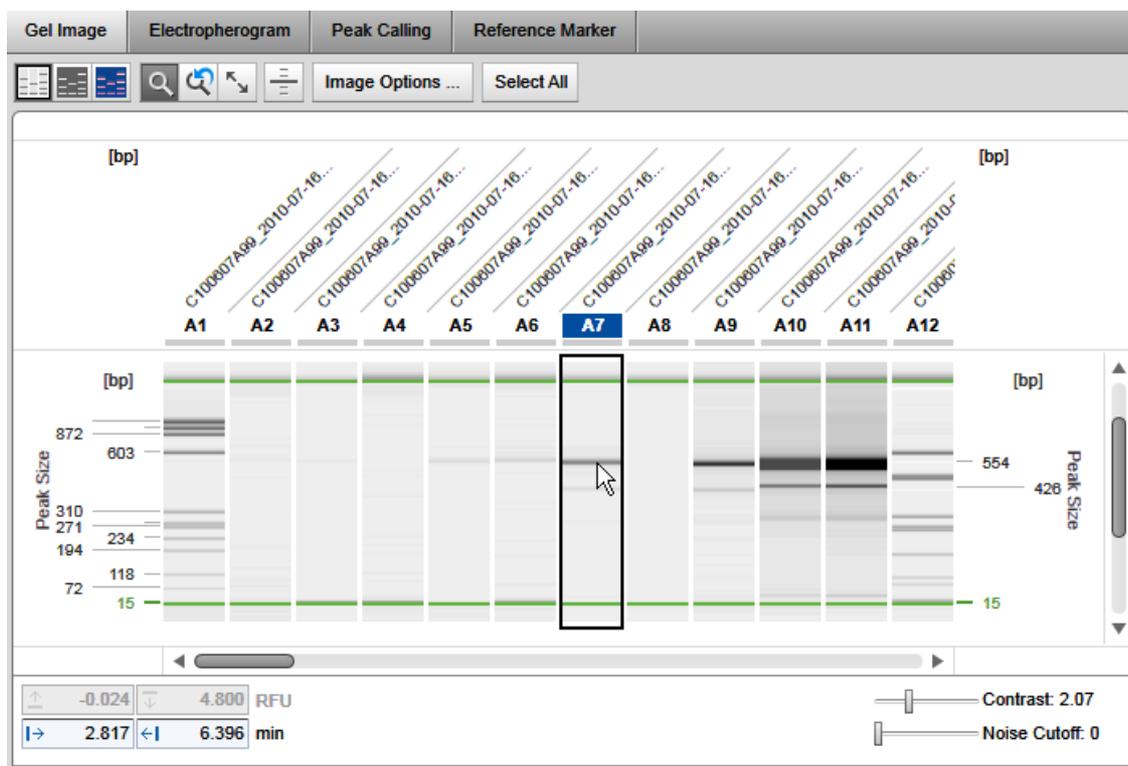
Normal mode



Inverted mode



False color rendering mode



Gel view with ruler, sample labels, and peak annotation.

The y-axis on the left-hand side is the main scale for the whole image. When the size scale is selected, it is based on the bands of the reference marker applied to all samples (see sample A1 in the image above).

The y-axis on the right-hand side describes the detected bands of the selected sample only (see above: highlighted with the black border, in the image above sample A7). It is available in the application only, not in report/export images (also not if the **Use Images as Displayed** option is selected).

Above each gel image the sample position is displayed (e.g., A1, A2, and so on). For a gel image a tool tip can be displayed by moving the mouse pointer to the sample number. This tool tip has information about the plate, the number of the run, and method that the sample was processed with.

If the mouse pointer hovers over the gel lanes, the values at the current cursor position are shown in the upper left corner of the view.

The [result table](#) of one sample is displayed below the gel view. This sample is marked in the **Experiment Explorer** and outlined with a black border in the gel view (see sample A7 in the image above). Select the sample to display in the result table by left-clicking it in the **Experiment Explorer** or in the gel view.

To view a sample in detail, double-click its gel lane. The view changes to single electropherogram view. To return to the gel view, select the **Gel Image** tab again.

You can interact with the gel view mainly through the buttons above the view:



Toggles zoom mode on/off.

In zoom mode (button pressed), the mouse is used to select a region for zooming into (Rubber band function — see [General software usage](#)). In addition, you can use the scroll wheel of the mouse to zoom in and out.

If this button is not pressed, the drag-and-drop function is activated to [change the lane order](#).

Note: The controls in the lower left corner of the gel view can be used to set the zoom region to absolute values, independently of the zoom mode.

Note: The drag-and-drop function is always possible if the mouse cursor is over the gel lane label, even in the zoom mode (button pressed).



Auto scale.

Resets the zoom region to the overall data range, undoing all zooming.



Undo zoom.

Returns to the previous zoom state.



Toggles a horizontal ruler at cursor position.

To configure the gel view, click the **Image** options button for the following options:

Unit of y-axis

Use this option to select the units of the y-axis scale on the left-hand side of the gel view.

If you select **Size**, the y-axis will show a size scale based on the reference marker. The lanes in the gel image will be aligned according to the alignment markers.

Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, a message will appear instead. In this case, reanalyze the samples with the same reference marker table and ensure that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.

If you select **Relative migration time**, the y-axis will show relative migration time. The lanes in the gel image will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the lanes cannot not be aligned and the y-axis will display a corresponding message. In this case, reanalyze the samples so that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.

If you select **Absolute migration time**, the lanes will not be aligned and the y-axis will show an absolute time scale.

Individual scaling	Select this option to auto-scale the contrast for each gel lane individually. Unselect this option for a comparison of samples.	
Show sample information	Select this option to display sample information at the top of each gel lane.	
Show plate ID	Select this option to display the plate ID at the top of the gel lane.	
Show method	Select this option to display the method applied at the top of each gel lane.	
Show analysis details	Highlight alignment markers	Select this option to highlight the alignment marker bands in green. Note: This highlighting is only possible for analyzed samples if the alignment markers have been correctly identified
	Show peak size	If this option is selected, the y-axis on the right-hand side will describe the sizes of the detected bands of the selected sample. Note: If the sample was not analyzed with a reference marker, the y-axis on the right hand will display "n/a." If the sample was not analyzed, a corresponding message will appear. Note: This option is always selected in the RNA mode.
	Show median of size	For DNA mode only. Select this option to show the median size of detected smear peaks for the selected sample. Note: If the sample was not analyzed with a DNA smear analysis profile or a reference marker , the y-axis on the right hand will display "n/a." If the sample was not analyzed, a corresponding message will appear.

Controls for contrast settings are located below the gel view to the right. The functions are described below:

Contrast	Use the slider to change the contrast according to your needs. The contrast value will be saved together with the experiment. Thus, you can customize the gel images independently of other experiments.
Noise cutoff	Use the slider to customize display of the noise in the signal. Move the slider to the extreme left position to see all signals. Move the slider to the right to suppress small signals, eliminating the noise. As for contrast, the noise cutoff value will be saved together with the experiment.

Changing lane order

The gel lanes can be reordered by drag-and-drop. The lane order takes effect for all views where the samples are visualized. The changed order will be saved when saving the experiment.

To change the lane order:

1. Select one or more lanes in the gel view.
2. Left-click the header of the selected lane or lanes and drag it to the new position. While dragging, a marker is shown indicating the new position of the lane(s) when dropping.
3. Drop the lane(s) when the marker indicates the correct new position. The lane(s) will be placed in that position. If more than one lane was selected, the lanes will be inserted in the same order as they were in before.

Note: If the zoom button  is toggled off, dragging can start also inside a gel lane.

Electropherogram view

The electropherogram view is activated by clicking on the **Electropherogram** tab in the analysis environment. Three electropherogram views can be selected using the following buttons in the tool bar:



Single electropherogram view.

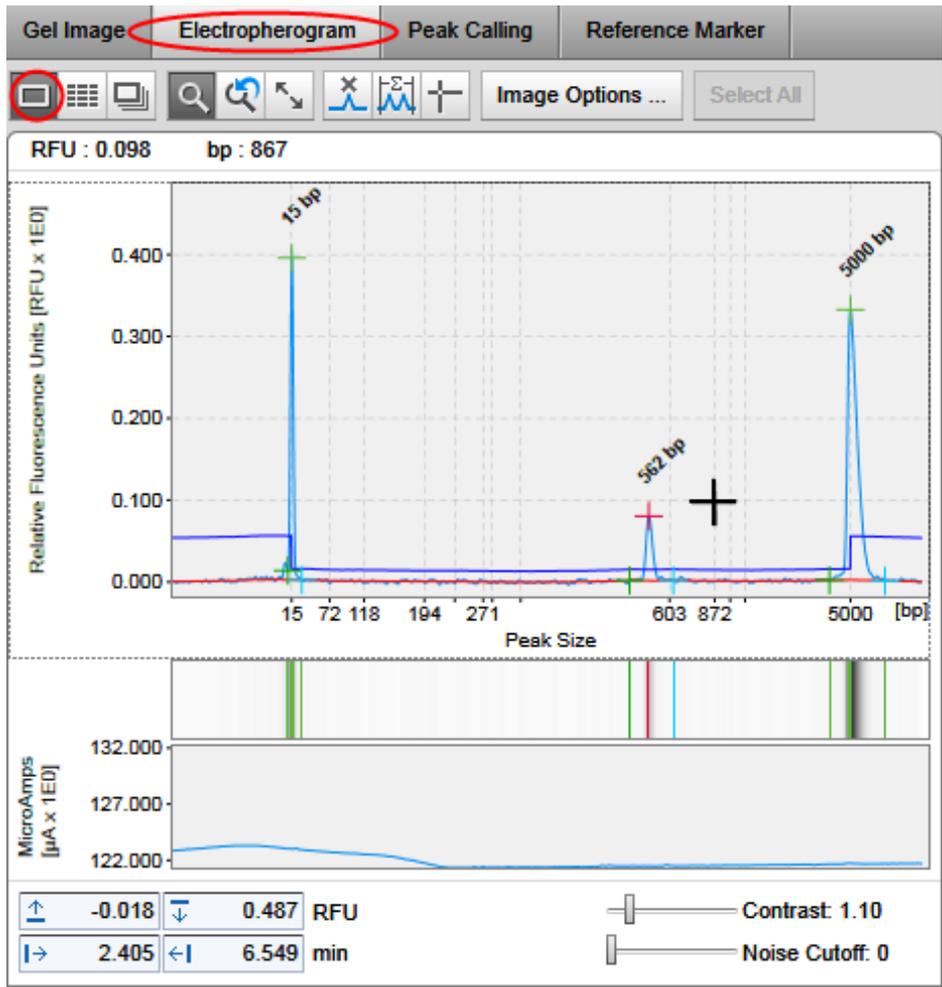


Overview mode with several single electropherograms.



Superposition view with several superimposed electropherograms.

The single electropherogram view is described in this section. The overview and superposition mode are described in the following sections.



Single electropherogram with peak annotation and displayed electrical current.

The single electropherogram view consists of a plot showing the recorded signal and the gel representation of the signal below the main plot.

Controls for the zoom region size and contrast settings of the gel view are located below the graphical representations of the signal. The current cursor position is shown in the upper left corner of the view.

The analysis result of the sample is displayed below the electropherogram view. Refer to section [Result table](#) for detailed information about the different types of result tables.

You can mainly interact with the electropherogram through the buttons in the tool bar (all buttons in this table are listed in "not pressed" state, left-click the button to press/release):

-  Toggles zoom mode on/off. For details, see [Zooming and scaling](#).
-  Auto scale. For details, see [Zooming and scaling](#).
-  Undo zoom. For details, see [Zooming and scaling](#).



Insert peak. For details, see [Adding a peak](#).



Manual integration of a time range. For details, see [Manual range integration](#).



Toggles ruler.

Activates vertical and horizontal rulers used to compare peak heights and positions.

To configure the electropherogram view, click the **Image** options button for the following options:

Unit of x-axis	<p>Use this option to select the units of the x-axis scale.</p> <p>If you select Size, the x-axis will show a size scale based on the reference marker, if the sample has been analyzed with a reference marker table and the alignment markers have been correctly identified. Otherwise, a message will be shown instead.</p> <p>If you select Rel. Time, the x-axis will show relative migration time, if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, a message will be shown instead.</p> <p>If you select Abs. Time [min], the x-axis will show an absolute time scale.</p> <p>Note: If the relative time scale is not created, reanalyze the sample so that the alignment markers are correctly identified. If the size scale is not created, reanalyze the sample with a reference marker table so that the alignment markers are correctly identified.</p>
Show gel lane	Select this option, to display the gel representation below the electropherogram in alignment with the x-axis.
Show electrical current curve	Select this option to display the diagram of the electrical current measured during data acquisition below the gel representation, if present, in alignment with the x-axis.
Show analysis details	Select this option to display analysis details for analyzed samples. Additional options can be selected.
Mark detected peaks	<p>Select this option to display the apex markers of detected peaks.</p> <p>If the option With label is selected, peak labels are displayed at the apex of each peak.</p> <p>Note: Only peak labels that do not overlap with an adjacent label are displayed. Hover the mouse cursor over the peak apex to get a tool tip with the peak label.</p> <p>Select the label units: Size, or absolute or relative migration time.</p>

Note: The label can be displayed as **Size** only if the sample was analyzed with a reference marker (for details refer to [Size and Concentration determination](#)). Otherwise, "n/a" is displayed.

Note: In **DNA** mode, a second option **Mark median of size** is available. If the sample was analyzed with a **DNA smear analysis profile**, select this option to display the marker with the median size of detected smear peaks. You can switch the corresponding label on and off.

Select the option **Mark peak start and end** to mark the start and end points of detected peaks.

Show areas of interest	For DNA mode only. If the sample was analyzed with a DNA smear analysis profile , select Show areas of interest to display the areas of interest of detected smear peaks.
Show suspend integration intervals	Select this option to display the suspend integration intervals.
Show threshold	Select this option to display the peak threshold (shown in blue). Note: The threshold parameter can be interactively changed by moving the threshold with the mouse. For details, see Modifying the threshold .
Show baseline	Select this option to display the baseline (shown in red).

Below the gel view at the right, controls for contrast settings are located. The controls are described below:

Contrast	Use the slider to change the contrast according to your needs. Contrast changes apply for further display of the gel lanes below electropherograms in single view for all experiments, but do not affect the contrast settings of the gel overview.
Noise cutoff	Use the slider to customize display of the noise in the signal. Move the slider to the extreme left position to see all signals. Move the slider to the right to suppress small signals, eliminating the noise. As for contrast, changes to the noise cutoff value do not affect the settings of the gel overview.

Zooming and scaling

The **Electropherogram** view allows exploration of the data via zooming and scaling.



Toggles zoom mode on/off.

When the button is clicked, the mouse is used to select a region for zooming into. For information on how to use the Rubber band function, see [General software usage](#). Additionally, you can use the scroll wheel of the mouse to zoom in and out.



Auto scale.

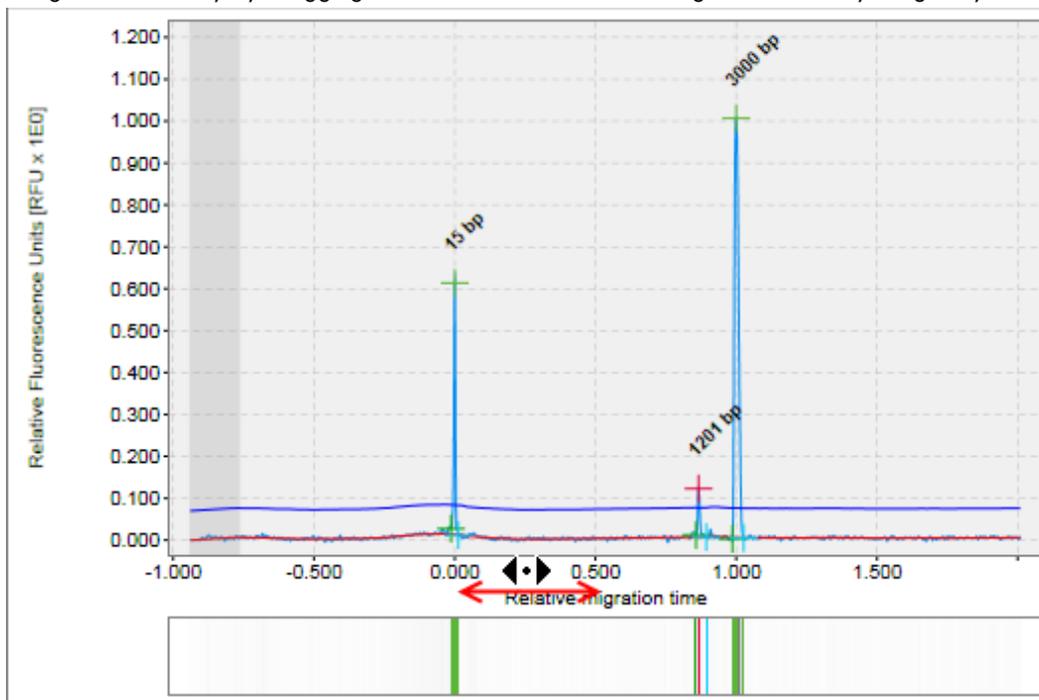
Resets the zoom region to the overall data range (both in time and RFU dimension), undoing all zooming.



Undo zoom.

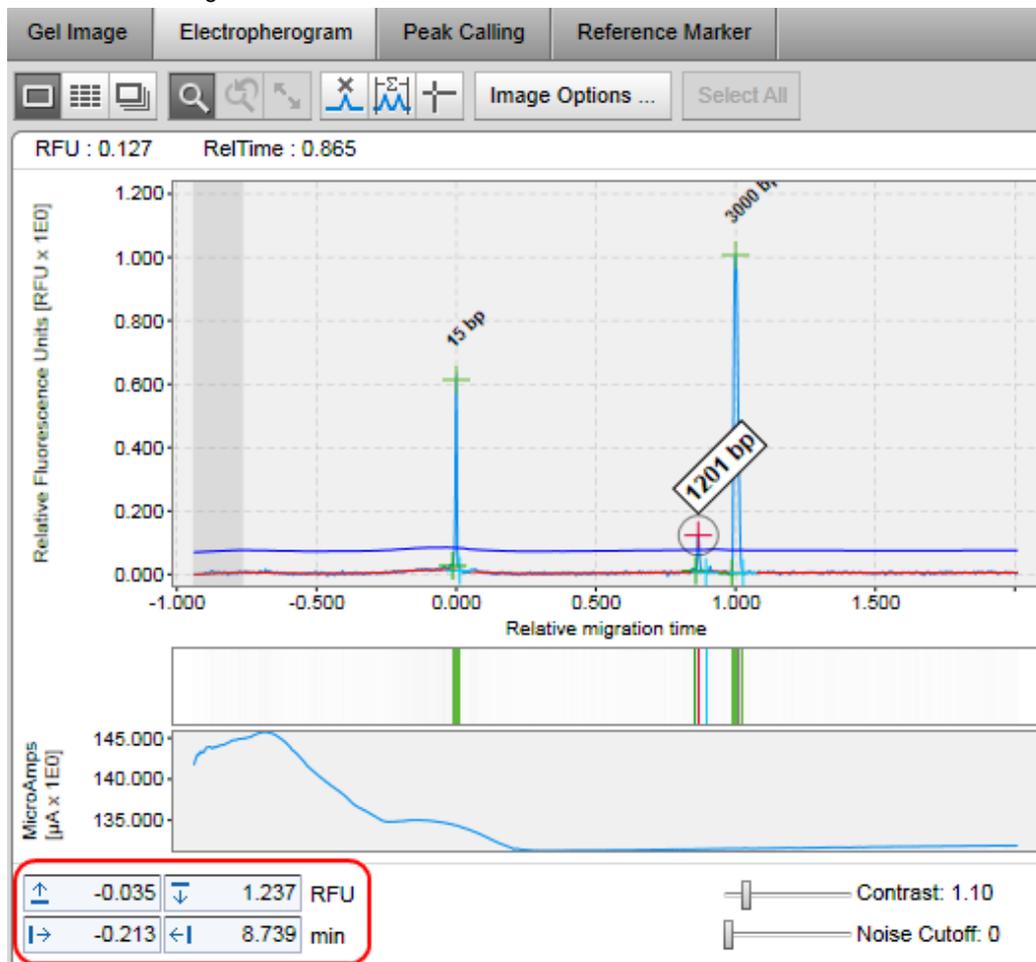
Returns to the previous zoom state.

Independent of the zoom mode, all electropherograms can be panned using the axes. You can shift the zoom region horizontally by dragging the x-axis. To shift the zoom region horizontally drag the y-axis.



Dragging the x-axis.

In addition to the tool buttons, the controls in the lower left corner of the **Electropherogram** view can be used to set the zoom region to absolute values.



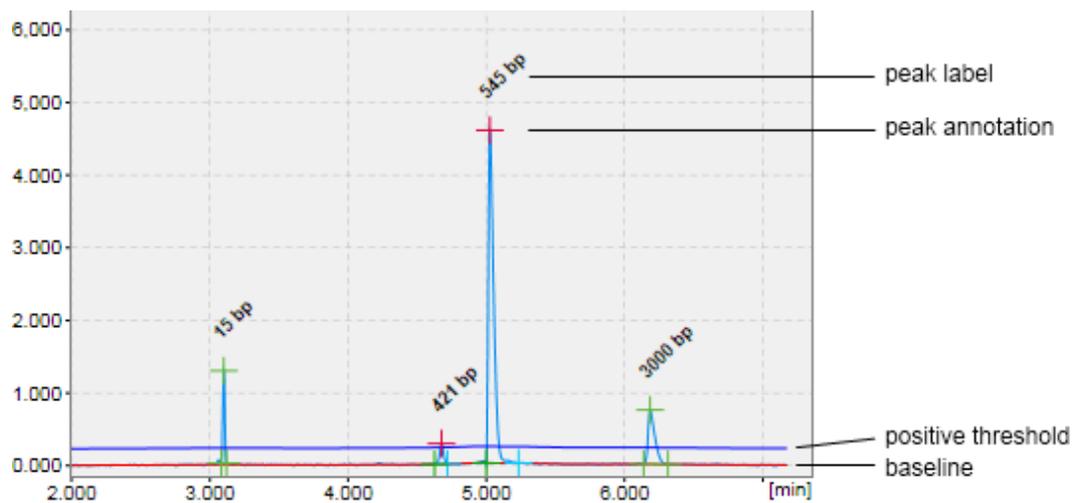
Input fields to set the zoom region to absolute values.

Note: For RFU values, only the values are permitted that are inside of the actual values. The values lying outside of the range of actual values range are not accepted and the background of the input field becomes yellow.

Note: For time values, the input of the upper range value up to an hour is allowed.

Peak annotations

In an analyzed sample the analysis result is displayed along with the raw signal. Each peak has peak markers for start (green), apex (red '+', green for alignment marker peaks), stop (turquoise), and a peak label. In **DNA** mode, if **smear** or **gDNA** analysis has been performed, i.e., if the sample has been analyzed with selected analysis profile option **Smear** or **gDNA**, the median of the peak can be marked (with a pink 'x') instead of the apex.



Peak annotations showing the apex.

In addition to the peaks, the detected baseline (in red) and the threshold for peak detection above the baseline (in blue) are displayed in the electropherogram.

The peak markers and units of the peak label can be configured by clicking the Image options button. Whether peak markers, the baseline or the threshold are displayed or hidden can be configured under **Image** options. For details, refer to [Electropherogram view](#).

Interacting with the result table

The functions are described below:

- | | |
|--------------------|---|
| Selecting a peak | In the electropherogram, left-click the apex marker of the peak.
Alternatively, in the result table, left-click the peak number in the # column.

The peak will be marked with a red circle in the electropherogram and highlighted in the result table. |
| Unselecting a peak | In the electropherogram or in the result table, open the context menu of the selected peak and select the Unselect Peak option.

The red circle in the electropherogram disappears as well as the highlighting in the result table. |
| Adding a peak | See Adding a peak for information on how to add a peak.

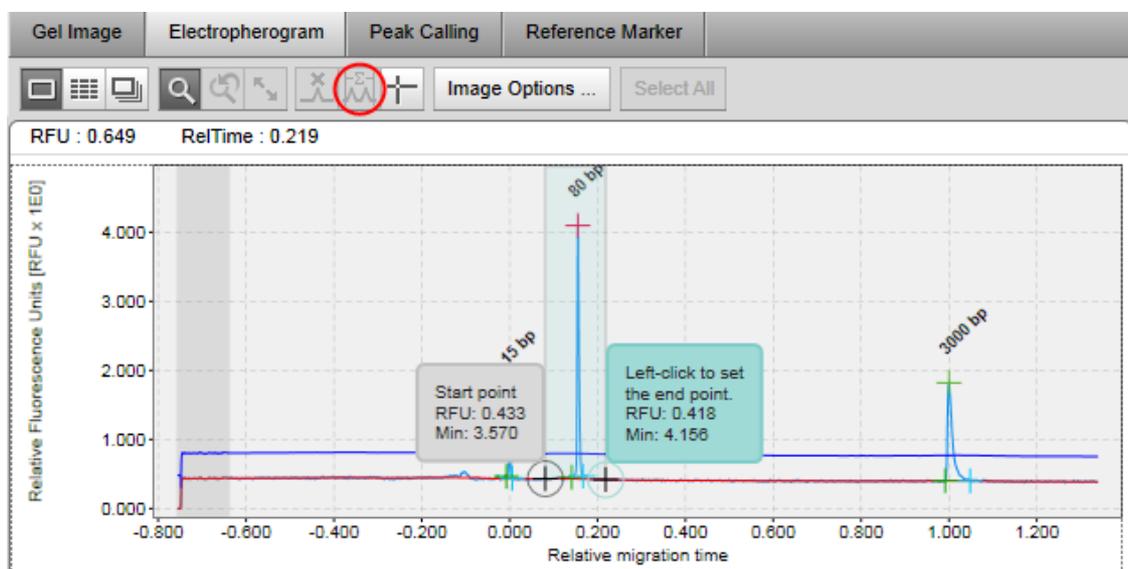
The peak will be added to the result table. |
| Deleting a peak | See Deleting a peak for information on how to delete a peak.

The peak will be removed from the result table, and the markers of the peak in the electropherogram disappear. |

Manual range integration

The manual integration of a time range is possible using the range integration tool ()

After clicking the **Range Integration** button, you need to specify a region. To do so, first click the left border of the region, then click the right border of the region.



Selection of a region for manual integration.

After selecting the region, a dialog is displayed which shows the selected time range borders, the normalized area sum of the region, and the percentage of normalized area in relation to the overall normalized area.

Note: The calculated values can be copied to the clipboard using the context menu of the dialog.

Note: The alignment marker peaks are not included in the normalized area calculation.

Electropherogram overview

The electropherogram overview displays several electropherograms in a gallery view. Twelve samples are always displayed on one page, arranged in a 3 x 4 matrix. It is intended for an overview inspection of the

acquired data. In the electropherogram overview the ruler tool () is especially useful. It provides a means to compare peak positions between several samples, both for alignment marker peaks and sample peaks. For analyzed samples, each peak has a peak marker for apex time (sample peaks are red, alignment marker peaks are green).



Overview after analysis using the ruler tool.

The zooming and scaling functionality is very similar to the single electropherogram view (see [Zooming and scaling](#)). The only difference is that zooming affects all electropherograms.

Use the **forward** and **backward** buttons at the bottom of the gallery view to navigate through the pages of the overview. Clicking on a sample in the experiment explorer will also navigate to the corresponding electropherogram in the gallery view. Use the scrollbars to navigate through the electropherograms on one page.

To enlarge the overview, collapse the parameters panel on the right side.

A result table displaying information on one sample appears below the electropherogram overview. Refer to the sections [Interacting with the result table](#) and [Result table](#) for more information.

To inspect an electropherogram in detail, double-click it. The view changes to single electropherogram

view. To return to the overview, click  again.

You can interact with the electropherogram mainly through the buttons in the tool bar:



Toggles zoom mode on/off. For details, see [Zooming and scaling](#).



Auto scale. For details, see [Zooming and scaling](#).



Undo zoom. For details, see [Zooming and scaling](#).



Toggles ruler.

Activates vertical and horizontal rulers used to compare peak heights and positions.

To configure the electropherogram overview, click the Image options button for the following options:

Unit of x-axis	<p>Use this option to select the units of the x-axis.</p> <p>If you select Size, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers.</p> <p>Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will show a corresponding message. In this case, reanalyze the samples with the same reference marker table and ensure that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.</p> <p>If you select Rel. Time, the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers.</p> <p>Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will display a corresponding message. In this case, reanalyze the samples so that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.</p> <p>If you select Abs. Time [min], the electropherograms will not be aligned and the x-axis will show an absolute time scale.</p>
Show sample position	Select this option to display the sample position in the upper left corner of each electropherogram.
Show sample information	Select this option to display the sample information at the top of each electropherogram.
Show plate ID	Select this option to display the plate ID at the top of each electropherogram.
Show method	Select this option to display the method applied at the top of each electropherogram.

Note: Only one of the options **Show sample information**, **Show plate ID** or **Show method** can be selected at a time.

Show analysis details

Select this option to show analysis details for analyzed samples. Additional options can be selected.

Mark detected peaks

Select this option to display the apex markers for detected peaks.

Note: In **DNA** mode, a second option **Mark median of size** is available. If the samples were analyzed with a **DNA smear analysis profile**, select this option to display the marker with the median size of detected smear peaks.

Show suspend integration intervals

Select this option to display the suspend integration intervals.

Changing order

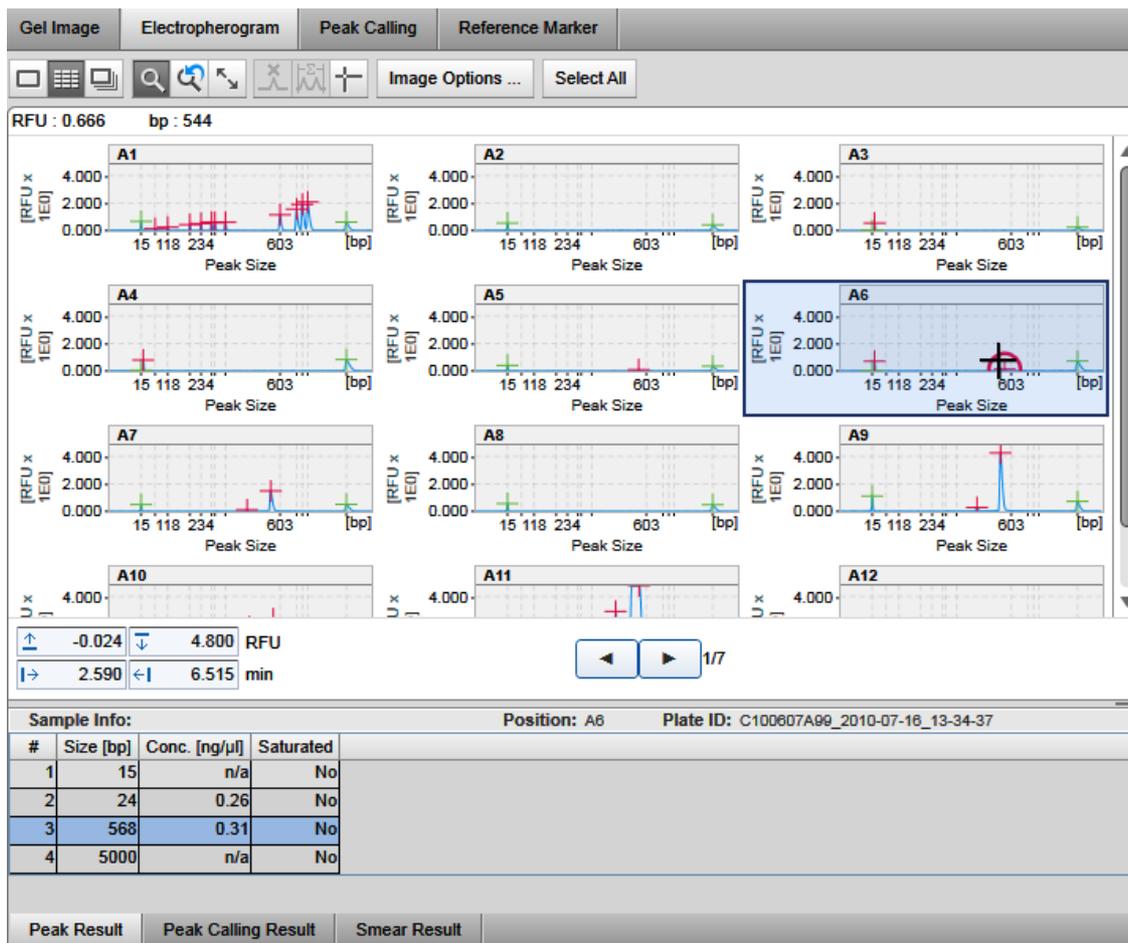
Remove samples from the electropherogram overview by dragging them from the overview into the experiment explorer.

Add samples to the electropherogram overview by dragging them from the experiment explorer into the overview. Added samples will be inserted at the end of the gallery.

To change the order of the electropherograms, switch to gel overview and reorder the samples there. See [Changing lane order](#) for details. Then switch back to the electropherogram overview.

Interacting with the result table

Below the electropherogram overview, the result table of one sample is displayed. This sample is marked in the **Experiment Explorer** and outlined with a black border in the gallery overview (see sample A6 in the image below). Select the sample in the **Experiment Explorer** or in the electropherogram overview by left-clicking it to view its result table.



Inspecting result table of sample A6.

The functions are described below:

- Selecting a peak In the electropherogram, left-click on the marker of the peak apex. Alternatively, in the result table, left-click the peak number in the # column.

The peak will be marked with a red circle in the electropherogram and highlighted in the result table.
- Unselecting a peak In the result table, open the context menu of the selected peak and select the **Unselect Peak** option.

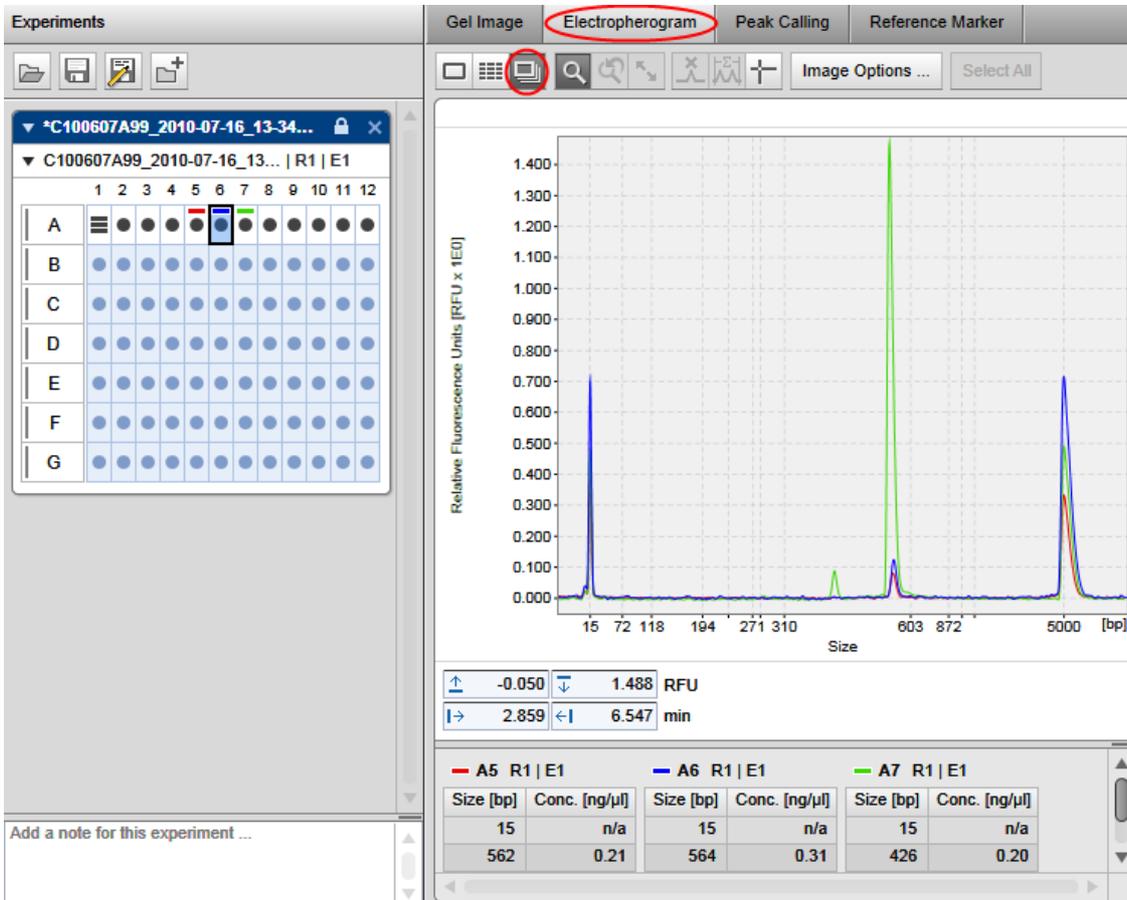
The red circle in the electropherogram disappears as well as the highlighting in the result table.
- Deleting a peak Select the peak to be deleted in the result table. Open the context menu of the result table and select the option **Delete selected peak**.

The peak will be removed from the result table, the marker of the peak in the electropherogram overview disappears.

Electropherogram superposition view

The electropherogram superposition view displays up to 12 electropherograms in one plot. It allows an easy comparison of several measurements.

In order to make the signals from different samples distinguishable, each sample has a distinct color.



Electropherogram superposition view.

In the lower part of the superposition view, small result tables of all samples are shown along with the corresponding colors. The order of the result tables is the same as the sample order in the gel view or electropherogram overview.

You can interact with the electropherogram through the buttons in the tool bar:



Toggles zoom mode on/off. For details see [Zooming and scaling](#).



Auto scale. For details see [Zooming and scaling](#).



Undo zoom. For details see [Zooming and scaling](#).



Toggles ruler.

Activates vertical and horizontal rulers used to compare peak heights and positions.

To configure the electropherogram superposition view, click the Image options button for the following options:

Unit of x-axis

Use this option to select the units of the x-axis.

If you select **Size**, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers.

Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will display a corresponding message. In this case, reanalyze the samples with the same reference marker table and ensure that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.

If you select **Rel. Time**, the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will display a corresponding message. In this case, reanalyze the samples so that the alignment markers have been correctly identified, or remove from the view the samples that have a different alignment marker or those samples for which alignment markers could not be correctly identified.

If you select **Abs. Time** [min], the electropherograms will not be aligned and the x-axis will show an absolute time scale.

Show electrical current curve

Select this option to display the diagram of the superimposed electrical current measured during data acquisition below the electropherogram superposition in alignment with the x-axis.

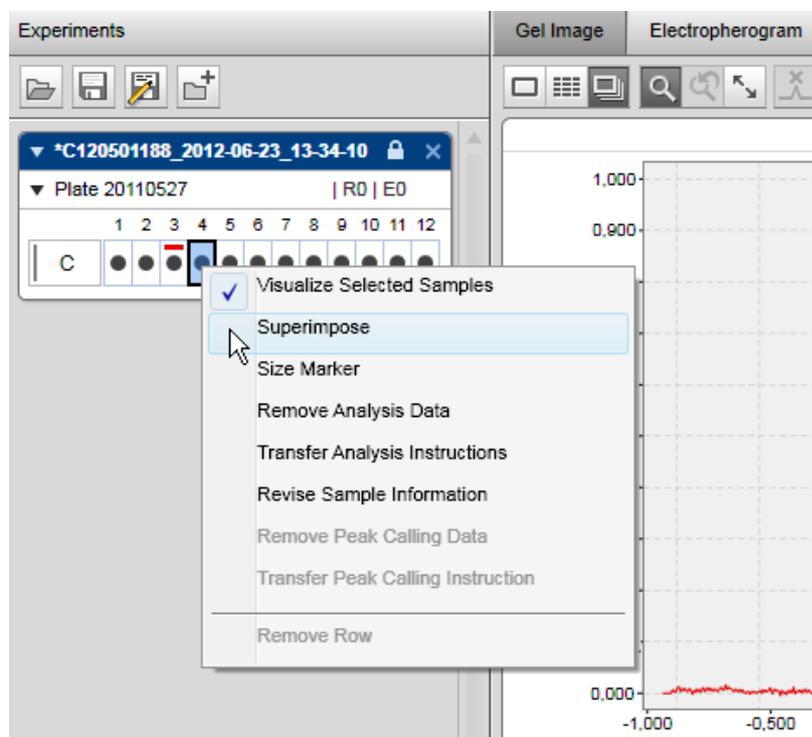
Show size marker peak labels If this option is selected, and if exactly one size marker is among the superimposed samples, the peak labels will be displayed for detected peaks of the marker sample. Select the units of the peak labels in the drop-down list.

Adding and removing samples

The superposition view does not automatically display all samples selected for visualization.

To add samples to the superposition view:

1. In the **Experiment Explorer** select the samples to be added.
2. Open the context menu of the selected samples in the **Experiment Explorer**.
3. Select the **Superimpose** option.



Adding sample C4 to superposition.

The selected samples will be added to the superposition view. In the **Experiment Explorer** all samples that are displayed in the superposition view are marked by a colored rectangular according to their color in the superposition.

Note: Up to 12 electropherograms can be superimposed. A warning will be displayed if the limit is exceeded.

Alternatively, drag and drop up to 12 selected samples from the **Experiment Explorer** to the superposition.

To remove samples from the superposition view, proceed as follows:

1. In the **Experiment Explorer** select the samples to be removed.
2. Open the context menu of the selected samples in the **Experiment Explorer**.
3. Unselect the **Superimpose** option.

Inspecting sample properties

To view sample properties:

1. Select the sample in the Experiment Explorer.
2. View the properties of the sample on the right-hand side of the analysis environment. If the toolbar on the right is not displayed, open it by clicking on the following icon:





In the properties view, there are six sections containing the following information:

- **Sample**
This section contains general information about the sample and the acquisition, for example, the date, experiment ID, and plate ID.
- **Analysis instructions**
The analysis instructions section shows the analysis parameters, alignment marker, and the reference marker used for the analysis.
- **Peak Calling Instruction or Distribution profile**
This section shows the peak calling instruction or distribution profile that was last applied to the sample.
- **Method**
This section shows the method name and actions used during the acquisition.
- **Cartridge**
The cartridge section shows information about the cartridge, such as the cartridge ID and the cartridge type.
- **Platform**
This section shows the software version and the instrument information (firmware version and serial number) for the run.

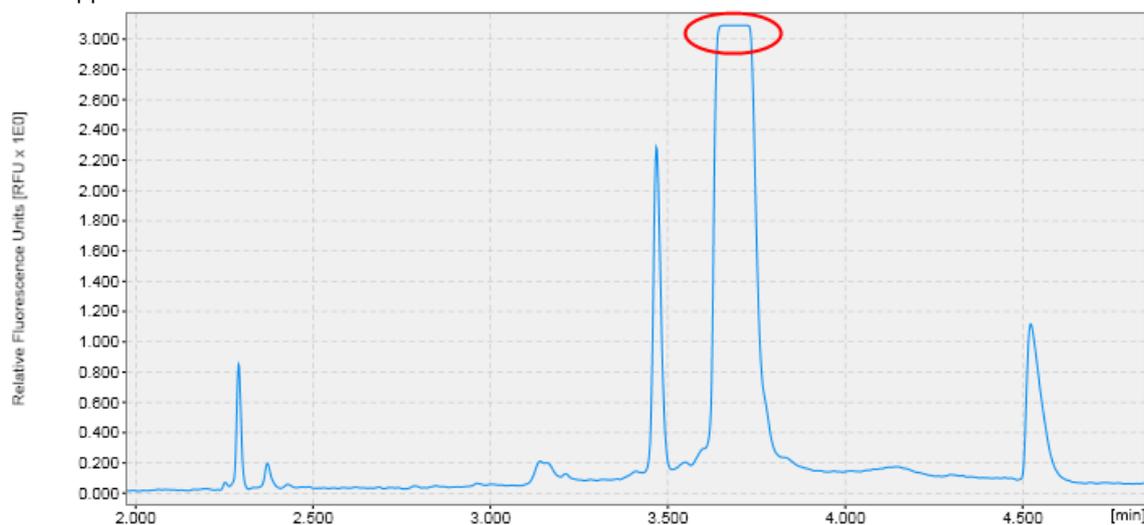
Note: It is not possible to perform peak calling and distribution analysis in the same experiment. Thus, either a peak calling instruction or a distribution profile is applied to a sample, but never both.

Saturated signals

Identifying a saturated signal

Overloading the signal by injecting highly concentrated DNA will cause the detector to saturate. Saturated signals are those in which the signal level exceeds the maximal detector limit.

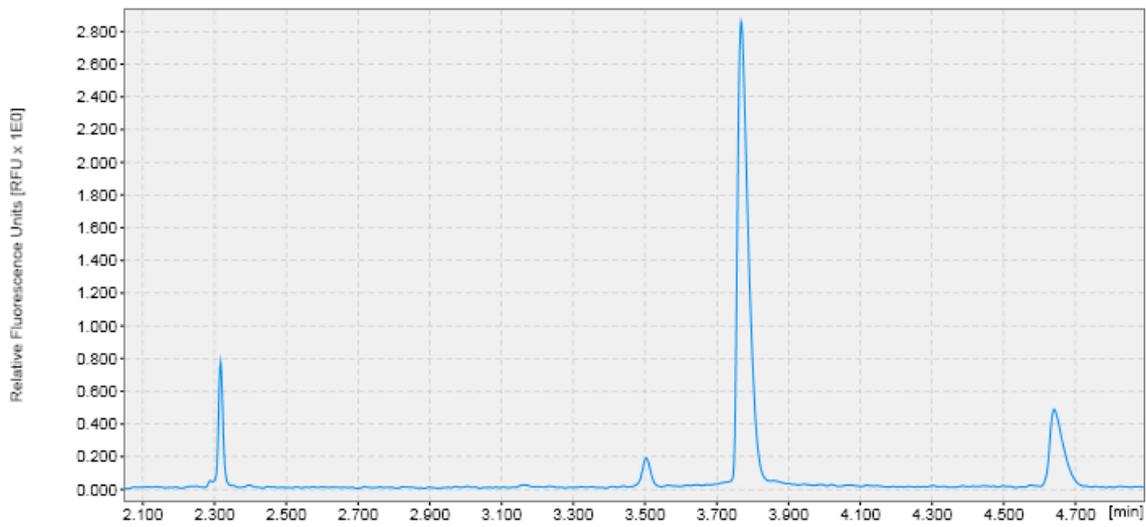
A saturated signal will usually display a flat top in its electropherogram. These signals are also referred to as “clipped.”



An example saturated signal.

Preventing a saturated signal

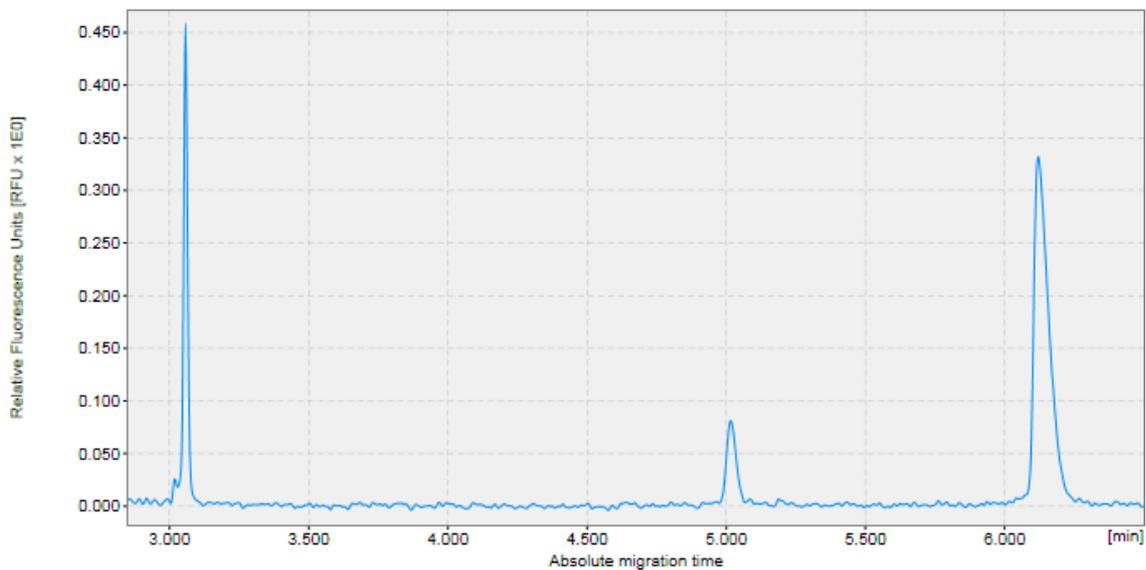
There are 2 ways to prevent overloading or saturation of the signal: dilute the samples in QX DNA Dilution Buffer or inject less sample. A smaller amount of sample can be injected by reducing the injection time (see section [Operating the QIAxcel](#)). A nonsaturated signal will display a sharp peak in the electropherogram.



An example normal (nonsaturated) signal.

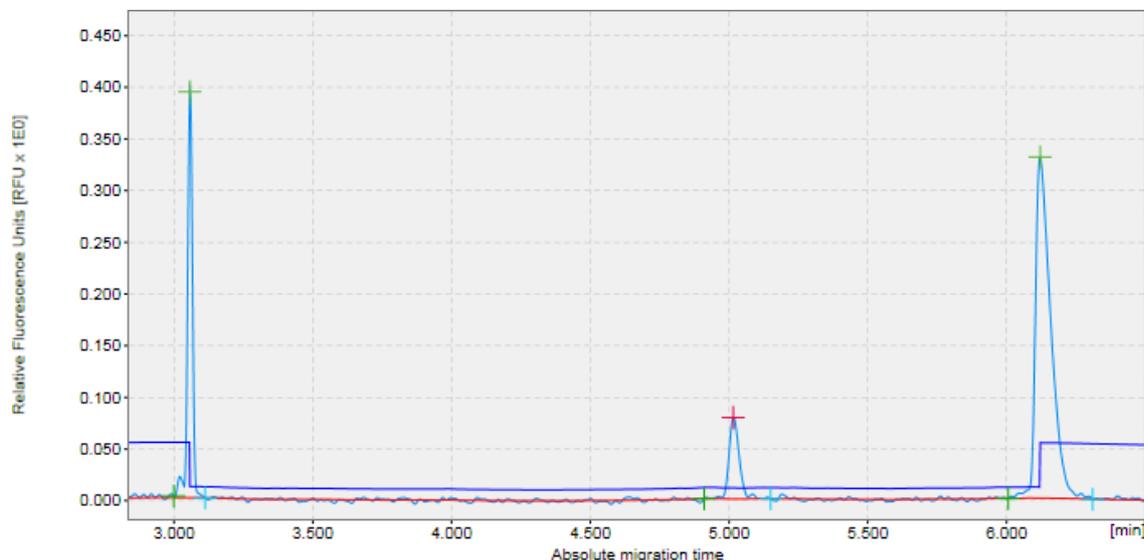
Peak detection

This section describes the peak detection procedure.



Unanalyzed raw data.

Analysis parameters for peak detection are provided in [Analysis Profiles](#).



Raw data after peak detection, without determination of size and concentration.

Alignment marker peaks are marked in [green](#). It is important that the correct peaks are marked as alignment marker peaks because this is the basis for all other analysis functions.

Note: In the image above, the **Analysis** parameter **Alignment Marker Threshold** (see dark blue line in the image above) was greater than the **Threshold** parameter. This leads to a peak in the threshold line at alignment marker positions.

Peak detection procedure

To perform peak detection, proceed as follows:

1. Load the samples you want to analyze using the **Experiment Explorer**. For details, refer to the [Loading sample data](#) section.
2. Visualize the samples you want to analyze. See the [Viewing sample data](#) section for details on data inspection.
3. Select the samples for analysis.
Note: Here, the selection inside the middle view is relevant — not the selection in the experiment explorer. See the [Selecting samples for analysis or report](#) section for details.
4. Open the **Analysis** parameters panel to be able to specify the analysis properties.

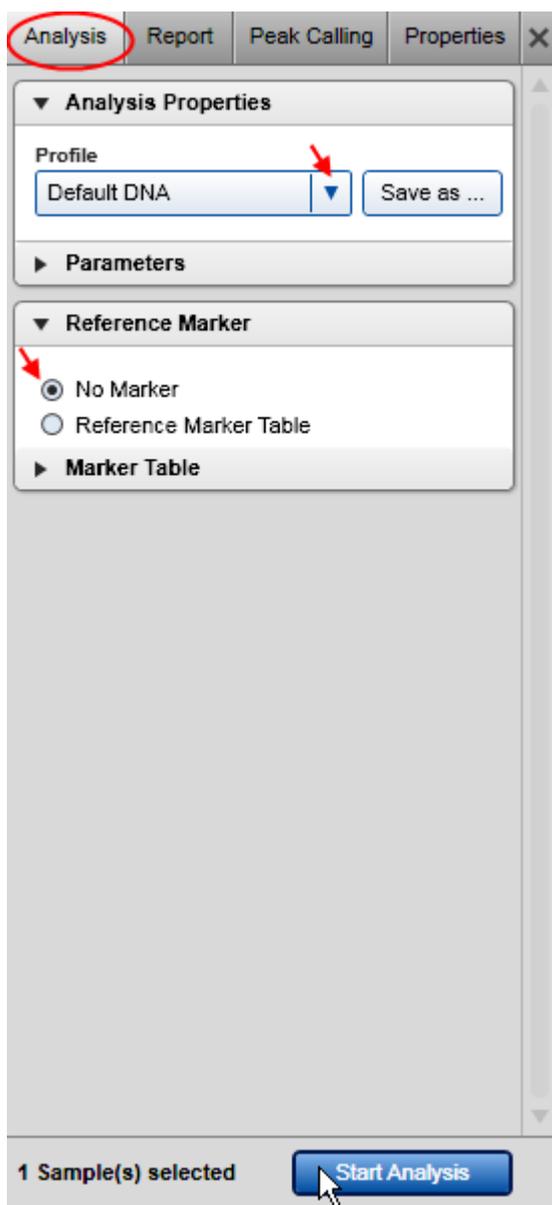
If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:



In the **Analysis** properties panel, define the parameters to use for analysis. This can be done by selecting a predefined analysis profile, which can be either a default (e.g., "Default DNA") or a user defined parameter set.

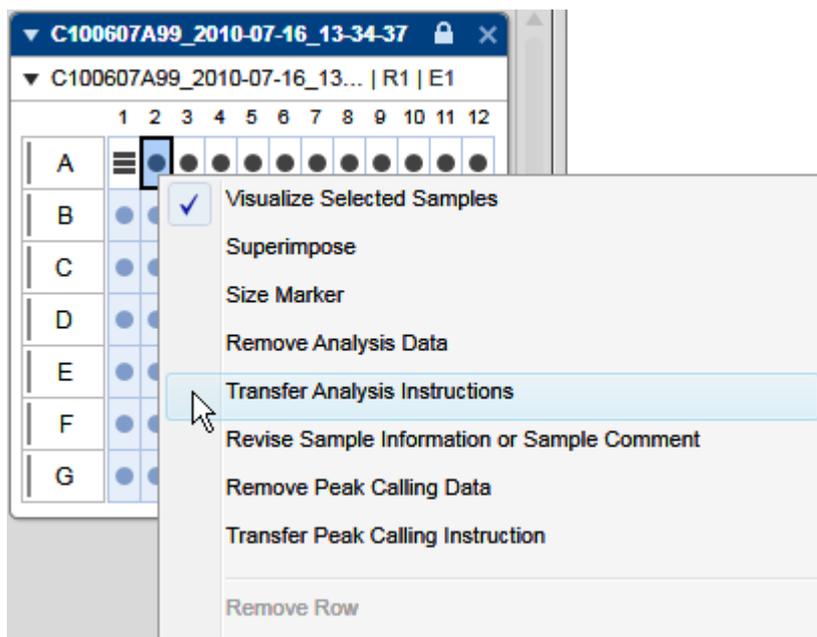
Refer to [Analysis of DNA samples](#) and [Analysis of RNA samples](#) for getting guidance as to which **Analysis** profile should be selected initially and how to use the analysis options for your specific samples.

Alternatively, a new analysis profile can be created. To modify or create an analysis profile, refer to sections [Modifying an analysis profile](#) and [Creating a new analysis profile](#), respectively. The analysis parameters of the selected profile are shown below the profile drop-down list. For general peak detection, no reference marker is required. Check **No Marker** in the **Reference Marker** section, as illustrated in the following figure.



No marker selected.

Note: If loaded samples have already been analyzed, the analysis parameters from the selected sample can be transferred to the **Analysis** parameters panel. To do this, right-click the sample in the **Experiment Explorer** and select the menu item **Transfer analysis parameters** from the context menu, as shown in the following figure.



Note: The alignment marker of a plate can be changed. To change the alignment marker, select the menu item **Overwrite alignment marker** from the context menu in the **Experiment Explorer** (the mouse cursor should be over the plate name). The **Overwrite Marker** dialog appears. Select the alignment marker from the drop-down list and confirm your choice by clicking **OK**.

5. Start the analysis by clicking the **Start Analysis** button.

6. View the analysis results. For each analyzed sample, the results are shown in tabular form at the bottom of the **Analysis** environment in the **Peak Result** tab (see [Result table](#) section) and in the plot of the single electropherogram view (see [Electropherogram view](#)).

Note: In the case of a smear or gDNA analysis, the **Smear Result** tab at the bottom of the **Analysis** environment shows the calculated properties that are specific to smear peaks. For more details, see the [Result table](#) section.

7. Make sure that the right peaks were detected. Firstly, it is important that the correct peaks are marked as alignment marker peaks (marked with a green '+') because this is the basis for all other analysis functions. If not, [adapt the analysis parameters](#) and repeat steps 5 to 7.

Refer to [Analysis of DNA samples](#) and [Analysis of RNA samples](#) for getting guidance as to which **Analysis** profile should be selected initially and how to use the analysis options for your specific samples.

As a last option, use the **Insert/Delete Peak** options described in the [Manually modifying analysis results](#) section.

8. [Save the analysis results](#) by clicking the **Save** button in the **Experiment Explorer**.

It is possible to automate the analysis (peak detection) during the data acquisition process. To do so, save any changes in the analysis parameters into a [customized analysis profile](#). Make sure that these analysis parameters work for all samples. Then [create a process profile](#). In the [Process Profile](#) step, select the option **Analysis** in the **Included steps** section. In the [Analysis](#) step, select the **customized analysis profile**. Save the process profile with these settings for reuse.

Modifying an analysis profile

To modify an analysis profile proceed as follows:

1. Open the **Analysis** tab at the right side of the **Analysis** environment.

If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:

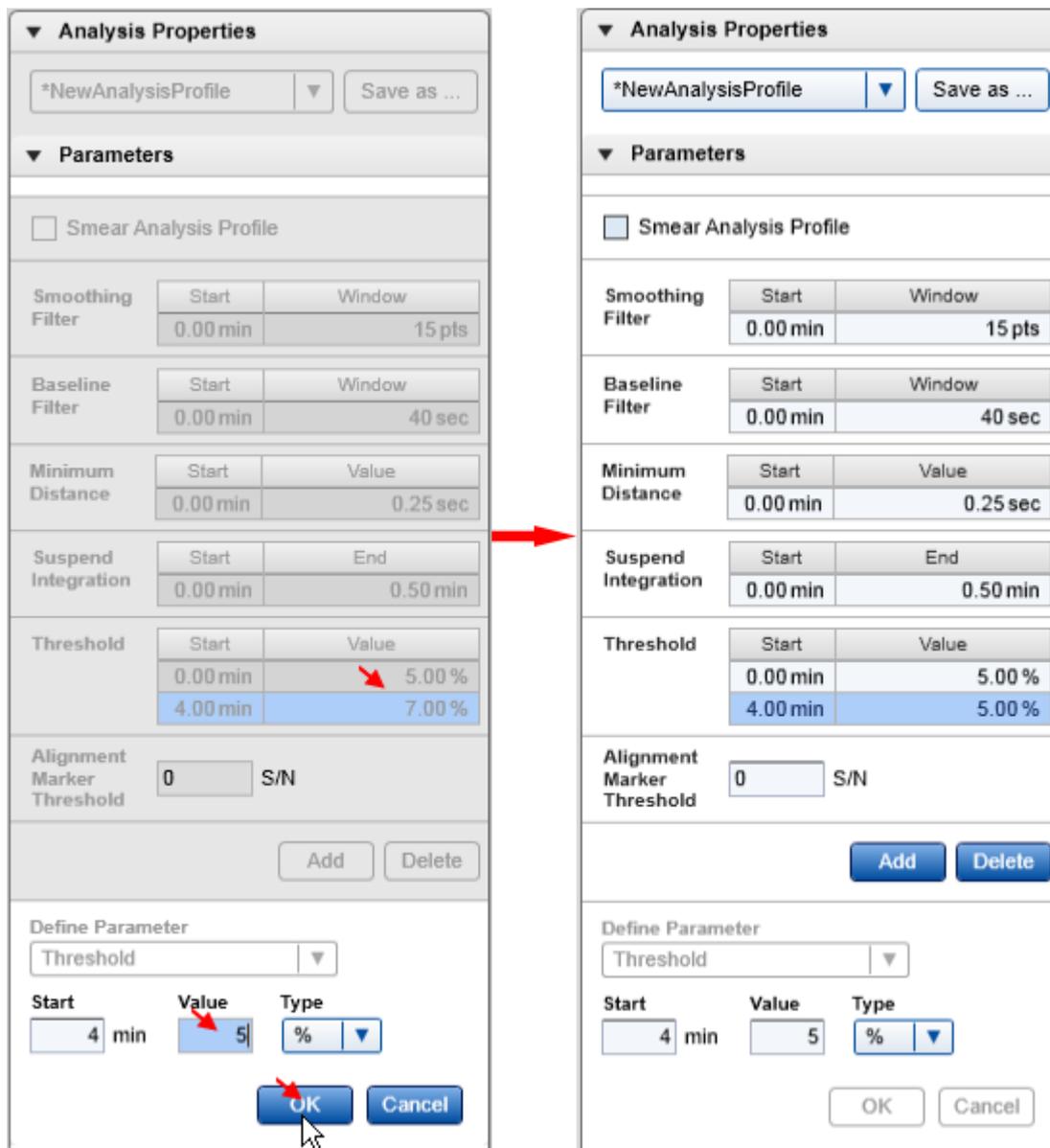


2. Select the analysis profile to be modified in the **Profile** drop-down list in the **Analysis Properties** panel .
3. Change the analysis parameters as described below.
4. To save the modified profile click the **Save as** button to the right of the **Profile** drop-down list.

Note: The parameters of an analysis profile can be modified by users with assigned user role **Advanced User** only.

Parameters can be changed by:

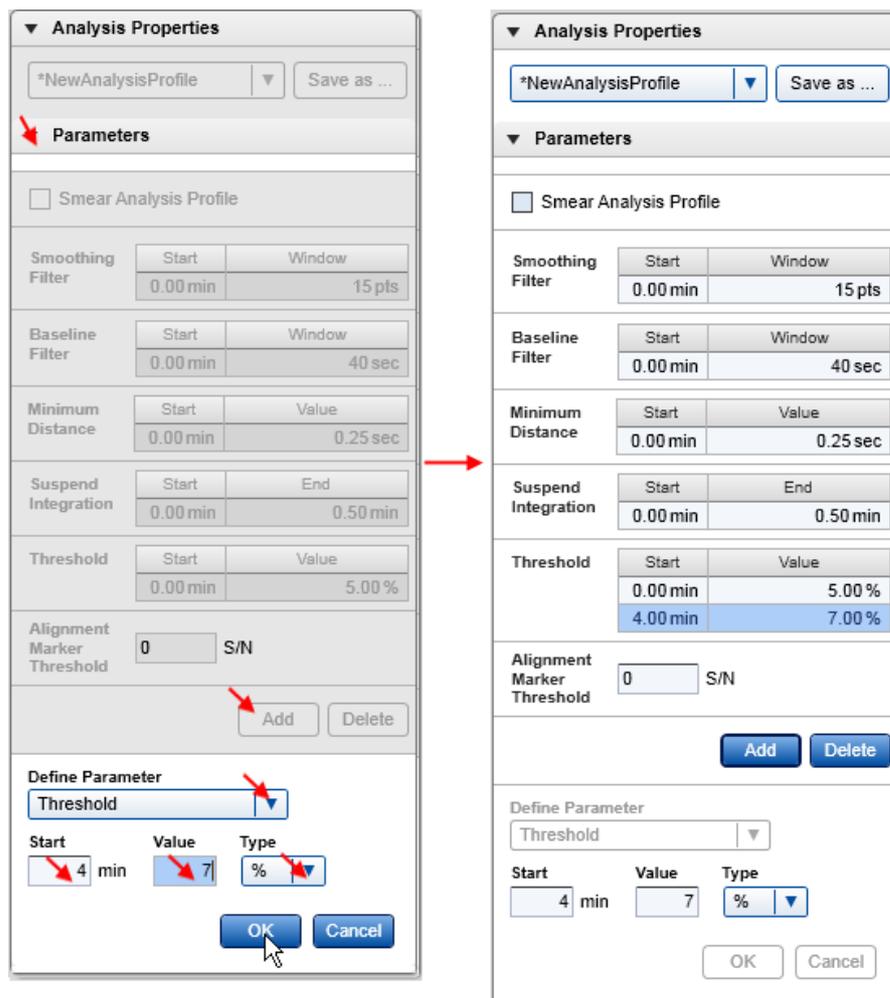
1. Clicking the parameter.
2. Changing the value (and unit if possible).
3. Clicking **OK**.



Changing the threshold parameter.

For example, to raise the threshold parameter to 7% starting from 4 minutes, perform the following:

1. Click the **Add** button below the parameters.
2. Select the parameter type **Threshold**.
3. Adjust the starting time (4 minutes), the threshold value (7), and its unit (%).
4. Accept the changes by clicking **OK**.



Each parameter displayed in the figure above has a corresponding time point. This is necessary because all parameters, except for **Alignment Marker Threshold**, can be changed with respect to time.

Note: The time of the initial parameter at 0.0 minutes cannot be changed. The suspend integration parameter is an exception. It is turned off by default and can be turned on to ignore a defined range of data during peak detection. This region does not necessarily start from 0.0 minutes.

The descriptions of the parameters and instructions on how to deduce suitable settings are in the table on the next page. Refer to sections [Standard DNA analysis](#), [Fast Analysis DNA analysis](#), [Smear DNA analysis](#), [gDNA analysis](#), and [Standard RNA analysis](#) for information on which parameters work best for your samples. More information about the analysis algorithms in QIAxcel ScreenGel and the respective parameters can be found in [Appendix D](#).

Parameter	Description	Adjusting the value
Peak	For DNA mode only. This parameter establishes the given profile as a DNA profile for sharp peaks.	Select this option if the profile has to be used for Standard DNA analysis or Fast Analysis DNA analysis .
Smear	For DNA mode only. This parameter establishes the given profile as a DNA smear profile .	Select this option if the profile has to be used for Smear DNA analysis of DNA libraries.
gDNA	For DNA mode only. This parameter establishes the given profile as a gDNA profile.	Select this option if the profile has to be used for gDNA analysis .
Baseline Filter	<p>This parameter governs the baseline detection (shown as a red line in electropherograms).</p> <p>Note: In case of a DNA smear and gDNA analysis, the software detects the baseline automatically and no parameterization by the user is needed. Thus, for smear and gDNA analysis profiles no baseline parameter is shown.</p>	<p>The default value for the Window parameter should be sufficient for most samples.</p> <p>If the baseline starts following the data, increase this value. Generally, the value should be set to twice the width of a single peak, but it must not be larger than half of the total migration time.</p> <p>If peak widths differ a lot over time, use distinct values for the Window parameter in different time intervals. For an example, see the "Default RNA" analysis parameter settings and Analyze RNA samples.</p>

Threshold	<p>The threshold parameter is used during peak detection. Signals that exceed the baseline by the threshold value are detected as peaks. The threshold can be given in RFU, as percentage of the highest signal in the sample, or as a multiple of the (estimated) noise level of the electropherogram.</p> <p>Note: The software uses the threshold for detection of alignment marker peaks whenever no higher alignment marker threshold is set.</p>	<p>The default setting is a good starting point for most samples. The threshold should be lowered if relevant peaks are below the threshold and not recognized as peaks.</p> <p>You can specify the threshold using different units. Use the RFU unit to set the threshold to a fixed RFU value. Use the % unit to specify the threshold as a percentage of the highest signal in the sample. Use the S/N unit to specify the threshold as a multiple of the noise level, which is estimated from the sample data.</p> <p>Note: For DNA smear and gDNA analysis, a higher S/N value is required as threshold.</p>
Minimum Distance	<p>The minimum distance parameter is used during the plausibility check of peaks. It defines the minimum distance two peak clusters must have to be detected as two distinct peaks.</p> <p>In noisy data with heavy tailing or fronting, noise spikes can cross the minimum peak threshold several times at the border of peaks. Detection of these noise peaks is prevented by this parameter.</p>	<p>The default setting is suitable for most samples.</p> <p>For very noisy data with fronting or tailing, in order to prevent the detection of noise peaks at cluster borders, increase the value.</p>
Suspend Integration	<p>The suspend integration parameter turns off peak detection for a defined period of time. The affected areas are marked with a grey bar in the single electropherogram view as well as in the electropherogram overview. Peaks that overlap with this bar are ignored by the analysis.</p>	<p>In the default setting, Suspend Integration is turned off, meaning that peak detection is performed on the entire duration of migration time. The time interval for Suspend Integration can be specified via absolute or relative migration time. In case the relative time unit is used, alignment marker peaks are not affected by Suspend Integration.</p>

Smoothing Filter	<p>The smoothing filter parameter defines the smoothing window width, i.e., the strength of the smoothing. The smoothing filter improves the signal-to-noise ratio (S/N) of the data but lowers the resolution.</p>	<p>Note: The suspend integration interval is shaded gray in the electropherogram single view and overview.</p> <p>Note: If relative time is chosen to describe the suspend integration interval, the following constraints apply: in case of 2 alignment marker peaks, all relative times must be between 0 and 1. In case of 1 alignment marker peak, all relative times must be above 1.</p> <p>The default window width is a good setting for most samples. If two close peaks cannot be resolved, the smoothing filter parameter can be lowered or disabled (i.e., set to 0 pts) to obtain the optimal resolution. One example for disabled smoothing is the Default Fast Analysis profile.</p> <p>Note: A different smoothing algorithm is applied in DNA smear analysis (Appendix D). The window length parameter of this algorithm is given in seconds.</p>
Alignment Marker Threshold	<p>This parameter allows to set a higher threshold for alignment marker peaks. It is useful to avoid that low intensity peaks are detected as alignment marker peaks, e.g., primer dimers before the lower alignment marker peak or noise peaks on the tail of the upper alignment marker.</p>	<p>A value between 5 and 10 should be suitable for most samples. If the alignment marker peaks have a lower S/N value, you can lower this threshold, or disable it by setting it to a value below the Threshold parameter.</p> <p>Note: For DNA smear and gDNA analysis, a higher S/N value is required as alignment marker threshold.</p>

Creating a new analysis profile

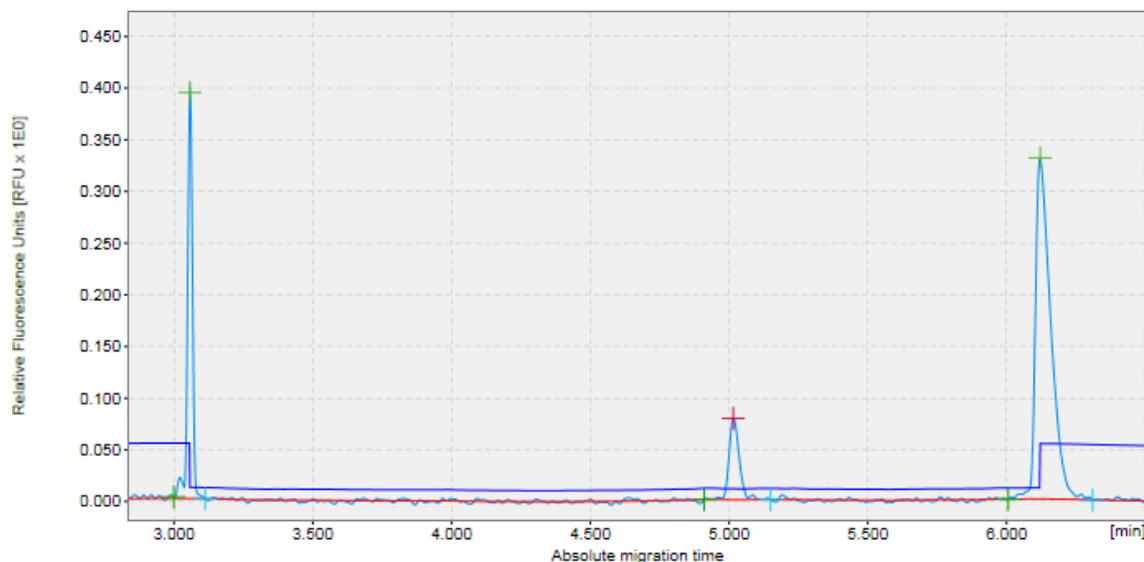
To create a new analysis profile:

1. Open the **Analysis** tab in the toolbar on the right-hand side of the **Analysis** environment.
2. Select an existing analysis profile from the **Profile** drop-down list. The selected profile serves as a template for the creation of the new profile. Select **NewAnalysisProfile** to start with default parameters.
3. Change the analysis parameters according to your needs as described in the [Modifying an analysis profile](#) section.
4. Store the new profile by clicking the **Save as** button to the right of the **Profile** drop-down list.
5. Assign a unique name to the profile and click **OK**.

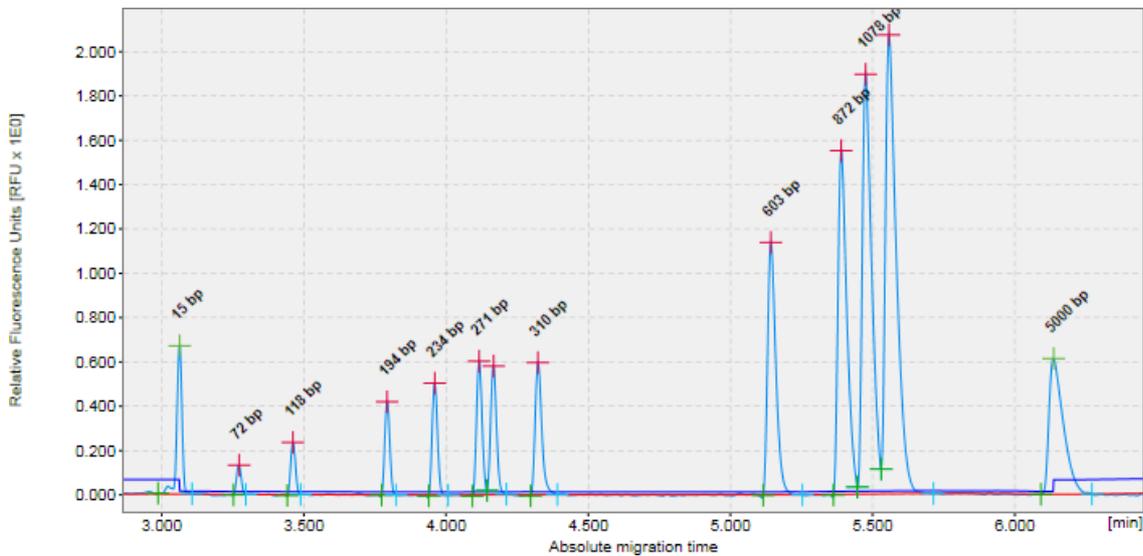
Note: Only users with assigned user role **Advanced User** can create new analysis profiles.

Size and concentration determination

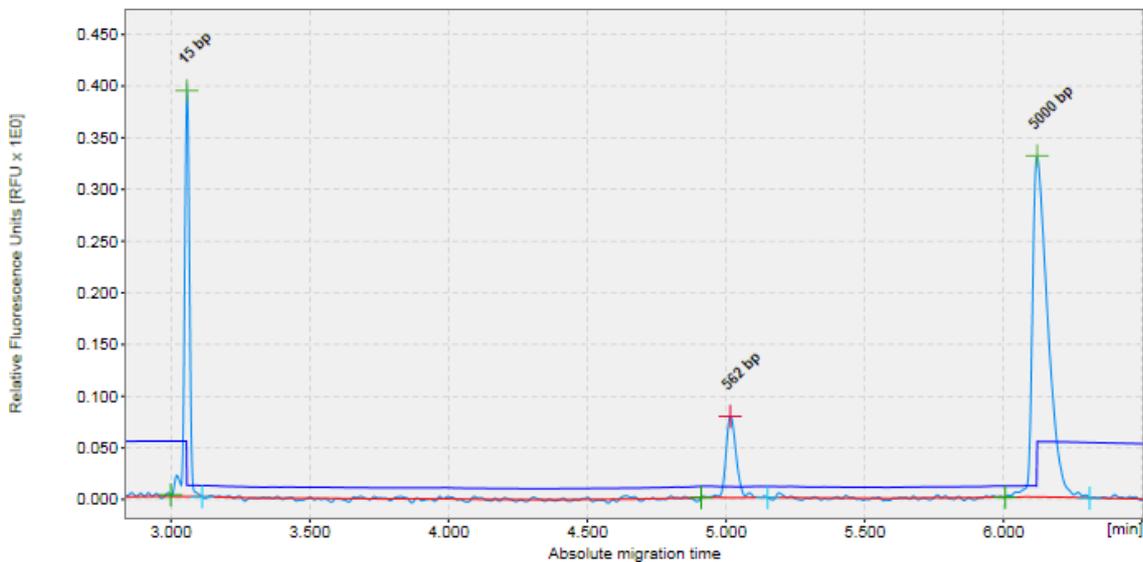
For a sample with detected peaks, the sizes and concentrations of the underlying analytes are calculated by referencing to a sample containing fragments of known size and concentration. The figures below show how a so-called reference marker (middle picture) is used to derive the sizes and concentrations for detected peaks (upper and lower picture). A reference marker can be created in two ways: either a size marker sample is run side by side with the samples that are being analyzed or a previously saved reference marker is selected in the **Reference Marker** section in the analysis tab. For details, see [Creating a reference marker](#).



Each detected peak is mapped to a corresponding reference marker peak. For peaks without unique corresponding reference marker peaks, the adjacent reference marker peaks are taken as reference (e.g., peaks with known size 310 bp and 603 bp, respectively).



Reference marker sample. Sizes and concentrations of contained molecules are known.



Sample with detected and annotated peaks.

The sizes for the newly detected peaks are either directly transferred from the matching reference marker peaks (15 bp peak) or interpolated using the two adjacent reference marker peaks (562 bp peak interpolated from 310 bp and 603 bp).

Similarly, the concentrations of detected analytes are referred from the known concentrations underlying the corresponding reference marker peaks.

This section describes how to proceed to determine size and concentration.

Note: Sample analysis can be performed by users with the assigned user roles **Basic User** and **Advanced User** only.

Size and concentration determination procedure

To determine size and concentration, proceed as follows:

1. Load the samples you want to analyze using the **Experiment Explorer**. For details, refer to the [Loading sample data](#) section.
2. In the **Analysis** parameters panel at the right side of the **Analysis** environment, define the parameters to use for analysis.

If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:



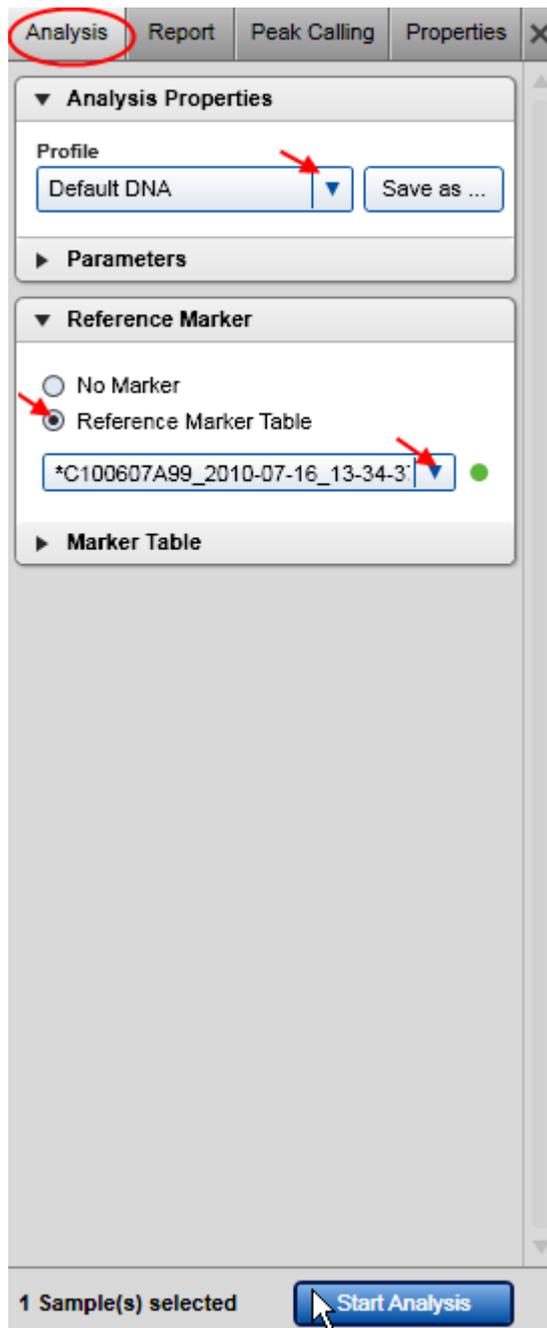
It is possible to [reuse](#) the analysis parameters and the reference marker table of an analyzed sample. This can be helpful if samples have already been analyzed during the data acquisition process, but analysis shall be reviewed or repeated. To do so, right-click one of the samples in the **Experiment Explorer** and select the context menu option **Transfer Analysis Instruction**. The analysis parameters and the reference marker table, if present, from the sample will be transferred to the analysis parameters tab. Otherwise, select a predefined analysis profile in the **Analysis** properties panel.

Refer to [Analysis of DNA samples](#) and [Analysis of RNA samples](#) for getting guidance as to which **Analysis** profile should be selected initially and how to use the analysis options for your specific samples.

To modify or create an analysis profile, refer to sections [Modifying an analysis profile](#) and [Creating a new analysis profile](#), respectively.

3. If the size marker was run side by side with samples, create a new reference marker as described in [Creating a reference marker](#). If samples should have been analyzed during data acquisition process, but either an error message has been shown or sample results are not as expected, use the procedure to check the correctness of the created reference marker step by step and recreate the reference marker, if needed. If the reference marker needs to be recreated, all other samples need to be reanalyzed too, as described in the next steps, using this new reference marker in step 6.
4. Visualize the samples you want to analyze. See the [Viewing sample data](#) section for details on data inspection.
5. Select the samples for analysis.
Note: Here, the selection inside the middle view is relevant – not the selection in the **Experiment Explorer**. See the [Selecting samples for analysis or report](#) section for details.
6. Define the reference marker to be used in the **Reference Marker** section of the **Analysis** panel. If you just created or recreated a reference marker in step 2, it is preselected for use. Proceed with step 7.

Otherwise, check **Reference Marker Table** and select a previously saved reference marker. Details of the reference marker are shown below the combo-box.



Reference marker checked.

Note: To ensure compatibility, the reference marker drop-down list contains only reference marker tables that match the alignment marker of the selected samples. The drop-down list is marked as invalid and empty if there is no matching reference marker table or no sample has been selected for analysis. In this case, select a sample. If the drop-down list is still marked as invalid, check the sample alignment marker and correct it if required (refer to [Checking alignment marker](#)), or create a new reference marker (refer to [Creating a reference marker](#)).

Note: If no sample is selected for analysis, the reference marker drop-down list is empty. Select the samples to analyze before selecting the reference marker. For details, see [Selecting samples for analysis or report](#).

Note: See the table below for explanation of the symbol at the right of the **Reference Marker Table** drop-down list:

●	<p>The selected reference marker table is fully compatible.</p> <p>That means that the size marker used for the reference marker table was processed no earlier or later than 90 days (DNA)/60 days (RNA) as the sample, and with the same cartridge and method as the sample. For analysis, it is not necessary to run the size marker first. The user can analyze older samples with a newer reference marker as well.</p>
●	<p>The size marker used for the reference marker table was processed more than 90 days (DNA)/60 days (RNA) earlier or later than the sample, with the same cartridge and method as the sample.</p>
●	<p>The reference marker table was processed with the same method as the sample, but with another cartridge of the same cartridge type.</p>
●	<p>The reference marker table is not compatible with the sample. This can happen if no reference marker matches the cartridge type, method and alignment marker of the sample.</p> <p>It is also shown when the software cannot check the compatibility because no sample has been selected for analysis.</p>

Important: Selecting the correct size marker will increase the accuracy of the size and concentration determination. Use the marker containing DNA fragments closest to the size of your targeted DNA fragments. The DNA fragments to be analyzed must fall within the smallest and largest fragment size of the size marker. In addition, the range of the alignment marker must cover the range of the size marker.

7. Start the analysis by clicking the **Start Analysis** button at the bottom of the **Analysis Parameters** panel.
8. View the analysis results. For each analyzed sample, the results are shown in tabular form at the bottom of the **Analysis** environment in the **Peak Result** tab. In the case of a smear or gDNA analysis in **DNA** mode, the **Smear/gDNA Result** tab shows the calculated properties that are specific to smear peaks. For more details, see the [Result table](#) section. The single electropherogram view is most suitable for checking peak detection. (see [Electropherogram view](#)).

Note: If the samples had been analyzed before with **Peak Calling** or **Distribution** analysis, these results will be automatically updated as well, based on the new calculations for peaks/smear peaks.

In case the sample was earlier analyzed with [distribution analysis](#) in DNA mode, the single electropherogram view shows smear peaks corresponding to the areas of interest as defined in the [distribution profile](#). In order to see a plot of the peak detection, the distribution analysis needs to be removed temporarily. To do so, right-click the sample in the **Experiment Explorer** to the right and select the option **Transfer Distribution Profile** to copy the parameters that had been used for distribution analysis into the **Distribution** panel to the right for later reuse. Then right-click the sample again and select the option **Remove Distribution Analysis Data** to remove the results of distribution analysis from the sample. The single electropherogram now shows the result of peak detection. It shows the alignment marker peaks (marked green at the apex) and the smear peaks according to the **Smear/gDNA Result** table.

9. Make sure that the right peaks were detected. First of all, it is important that the correct peaks are marked as alignment marker peaks (marked with a green '+') because this is the basis for all other analysis functions. If not, [adapt the analysis parameters](#) and repeat the steps 5 to 9.

Refer to [Analysis of DNA samples](#) and [Analysis of RNA samples](#) for getting guidance as to which **Analysis** profile should be selected initially and how to use the analysis options for your specific samples.

As a last option, use the **Insert/Delete Peak** options as described in the [Manually modifying analysis results](#) section.

10. In case the distribution analysis needs to be removed temporarily, it has to be repeated manually by using the distribution profile parameters that had been transferred before. Refer to [Distribution analysis](#) for instructions.

11. [Save the analysis results](#) by clicking the **Save** button in the **Experiment Explorer**.

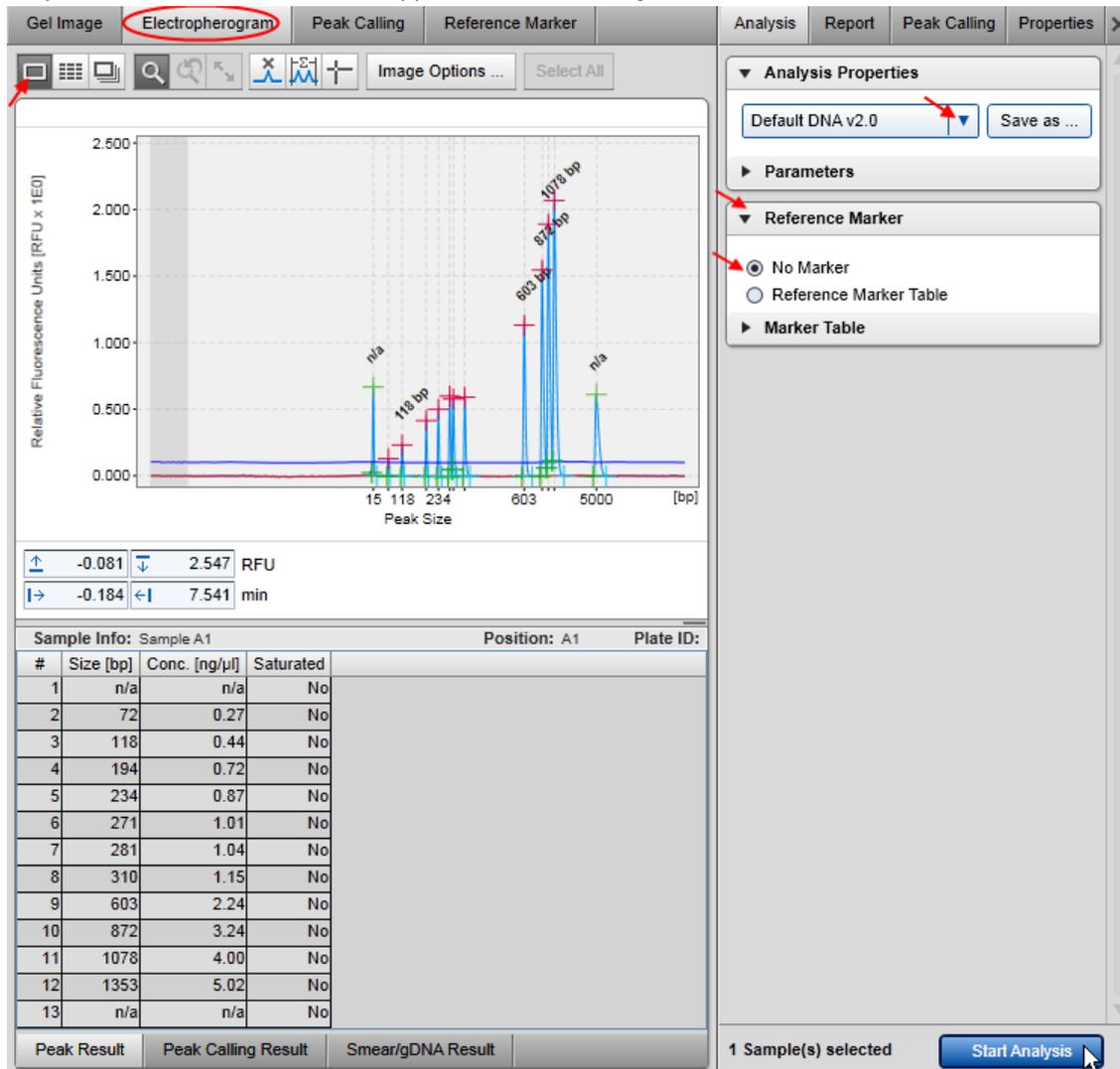
It is possible to automate the peak detection and size and concentration determination during the data acquisition process. To do so, save any changes in the analysis parameters into a customized analysis profile. Make sure that these analysis parameters work for all samples and also for the size marker sample. Then [create a process profile](#). In the [Process Profile](#) step, select the option **Analysis** in the **Included** steps section. In the [Analysis](#) step, select the customized analysis profile. If the size marker is to be run side by side with samples, define the size marker position for a run in the right part of the screen in the [Run Parameters](#) step, select the option **Run size marker** side by side with sample in the [Marker](#) step, and select the alignment marker and the size marker. If instead, a previously created reference marker shall be reused for several runs, select the option **Reference Marker Table** and select the previously created reference marker. For further details, refer to [Process profile options](#). Save the process profile with these settings for reuse. During each run setup, ensure to select the alignment marker in the **Sample Selection** step.

Creating a reference marker

To create a new reference marker, an analyzed size marker sample with annotated peak times and areas is required. A reference marker is formed by matching the peaks of the size marker sample to a size marker table (including alignment marker).

Proceed as follows:

1. In the [Experiment Explorer](#) select the sample that contains the size marker. If it is not flagged as a size marker (i.e., its symbol is  or ) , flag it with a right-mouse click and by selecting the **Size Marker** option from the context menu that appears. The icon changes to  or .



Analyzing the size marker sample.

2. Open the size marker sample in single electropherogram view by clicking the **Electropherogram** tab at the top of the middle view. If the size marker sample is already analyzed (i.e., its symbol is ) , proceed with step 6.

3. Select a profile in the **Analysis Properties** toolbar.

Refer to [Analysis of DNA samples](#) and [Analysis of RNA samples](#) for getting guidance as to which **Analysis** profile should be selected initially and how to use the analysis options for your specific samples.

Note: It is possible to [reuse](#) the analysis parameters of an analyzed size marker sample. This can be helpful if the sample has already been analyzed during the data acquisition process, but analysis shall be reviewed or repeated. Right-click the sample in the experiment explorer and select the context menu option **Transfer Analysis Instruction**. The analysis parameters and the reference marker table, if present, from the sample will be transferred to the analysis parameters tab.

4. Select **No Marker** as reference marker in the **Reference Marker** toolbar below.

5. Start the analysis by clicking the **Start Analysis** button.

The result of the analysis is a sample with annotated peak times and areas.

6. Make sure that the right peaks were detected. If not, [adapt the analysis parameters](#) and reanalyze the size marker sample.

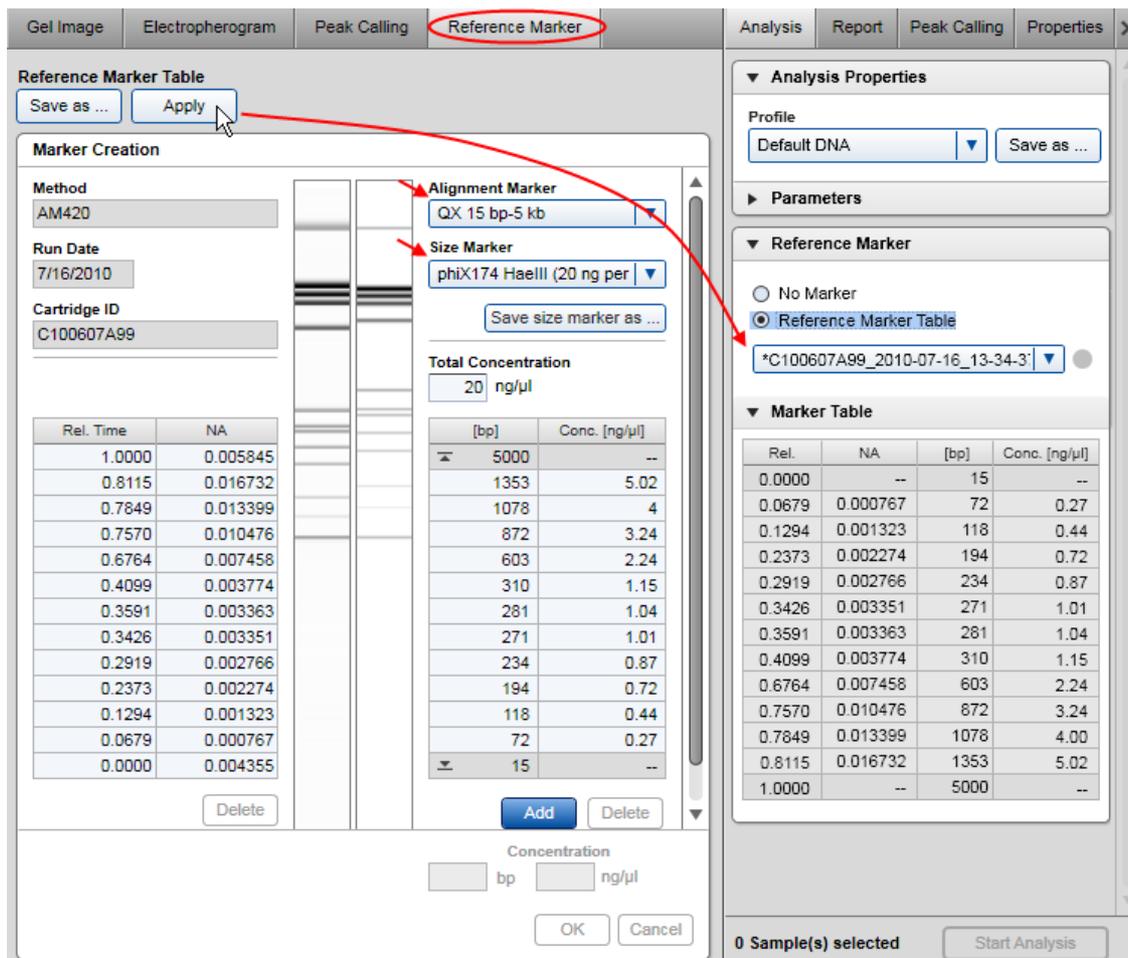
Refer to [Analysis of DNA samples](#) and [Analysis of RNA samples](#) for getting guidance as to which **Analysis** profile should be selected initially and how to use the analysis options for your specific samples.

As a last option, use the **Insert/Delete Peak** options described in the [Manually modifying analysis results](#) section.

7. Switch to the **Reference Marker** screen by clicking the **Reference Marker** tab on the top of the middle view.

The peak table (with the **Rel. Time and NA** columns) of the size marker sample is displayed at the left side of the screen.

Note: The panel is empty if no size marker sample is selected in the **Experiment Explorer** or if the selected size marker sample is not analyzed. In this case, repeat the steps above first.



Creating the reference marker.

Note: Depending on cartridge and method, a size marker creates different gel lanes. As the gel lane for the size marker (right-hand side) is a calculation based on the size marker table only, this image may differ from the gel lane from the actual run (left-hand side).

8. In the **Reference Marker** screen, check the alignment marker and select the size marker used in the size marker sample.

A comparison of the sample gel view (left) and the theoretical reference marker gel view (right) is displayed in the middle of the screen.

Note: If the alignment marker is not correct, change it as described in [Checking alignment marker](#).

Note: Creating new size markers is described in [Creating a new size marker table](#).

9. If the number of peaks in the size marker sample matches the number of peaks in the reference marker (two alignment marker peaks plus the size marker peaks), the reference marker can be used for sample analysis. Click the **Apply** button at the top of the **Reference Marker** screen to copy the created reference marker to the bottom of the **Reference Marker** panel of the **Analysis** parameters screen.

Optionally, save the reference marker using the **Save as** button at the top of the screen if you want to use the reference marker table for the analysis of further experiments.

Note: The **Apply** and **Save as** buttons are disabled and a warning is displayed at the top of the screen if the reference marker is invalid, e.g., if the number of peaks on the left and on the right does not match.

If more peaks than expected were detected in the size marker sample, you can delete them using the **Delete** button below the size marker samples peak table (with **Rel. Time** and **NA**).

Alternatively, switch to the single electropherogram view and check that the correct peaks were detected. Use the **Insert/Delete Peak** options described in the [Manually modifying analysis results](#) section or change the analysis parameters and reanalyze the size marker sample.

Note: A reference marker can be created by users with the assigned user role **Basic User** and **Advanced User** only.

It is possible to automate the creation of the reference marker during the data acquisition process if the size marker is to be run side by side with samples. To do so, save any changes in the analysis parameters into a customized analysis profile. Make sure that these analysis parameters also work for the samples. Then [create a process profile](#) defining the size marker position for a run in the [Run Parameters](#) step and selecting the customized analysis profile in the [Analysis](#) step. Save the process profile with these settings for reuse.

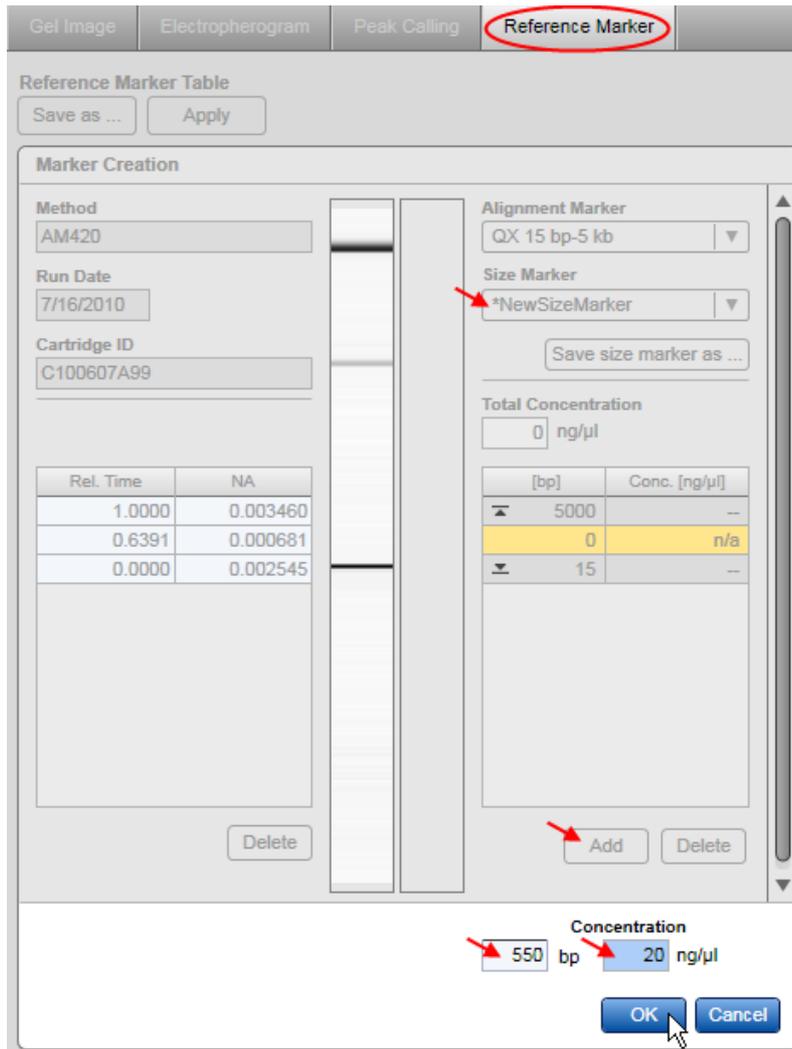
To continue sample analysis, refer to step 3 of the [Size and Concentration determination procedure](#).

Creating a new size marker table

To use a custom size marker, a new size marker table has to be created manually.

Proceed as follows:

1. In the **Experiment Explorer** select the sample that contains the size marker. If it is not flagged as a size marker (i.e., its symbol is  or ), flag it with a right-mouse click, selecting the **Size Marker** option from the context menu that appears. The icon changes to  or .
2. Open the **Reference Marker** screen of the **Analysis** environment.



Editing a new size marker.

3. Select **NewSizeMarker** from the size marker drop-down list to create an empty size marker table.
4. Click the **Add** button below the table to add a new row to the table.
5. Define the size and optionally the concentration.
6. Click **OK** to save the changes to the table. Repeat the steps from step 4 to define all rows.
7. Save the new size marker by clicking the **Save Size Marker** as button below the size marker drop-down list.

Note: A new size marker can be created by users with the assigned user role **Advanced User** only.

Note: If a sample is selected which is flagged as a size marker, a warning about mismatch of the number of rows of the size marker and peak table of the selected sample may be displayed. Ignore the warning and proceed with adding fragment sizes to the size marker table. If you entered all size marker fragments and the warning persists, switch to single electropherogram view and check that all peaks have been detected correctly.

Peak Calling

Based on the peak table, which is the result of the sample analysis, a peak calling step can be performed.

Peak calling shows whether corresponding peaks (e.g., because of the same size) are present in analyzed samples, and provides peak data for comparison.

To trigger peak calling, the definition of the peaks of interest must be provided by the user. Refer to the [Creating a new peak calling instruction](#) section for information on how to create it.

Note: Peak calling can be performed by users with the assigned user roles **Basic User** and **Advanced User** only.

To perform peak calling proceed as follows:

1. [Load](#) and [activate](#) the experiment for which sample peak calling should be carried out.
2. If not yet analyzed, analyze the samples of interest as described in [Standard DNA analysis](#).

Note: The samples must be analyzed before performing peak calling.

3. Select the visualized samples that the peak calling instruction shall be applied to.
4. Open the **Peak Calling** tab located on the right-hand side of the **Analysis** environment.

Note: In **DNA** mode, the **Peak Calling** tab is available only if peak calling features are active. Refer to [Activating peak calling features](#) for information on how to activate peak calling features.

5. Select the peak calling instruction from the **Peak Calling** Instruction drop-down box, which contains the set of peaks to search for.
6. Start peak calling by clicking the **Start Peak Calling** button at the bottom of the **Peak Calling** tab. The peak calling instruction is assigned to the selected samples and the **Peak Calling** screen in the middle of the **Analysis** environment is filled with the peak calling result.

Note: If you click **Start Peak Calling** the next time with the same unchanged peak calling instruction, the previous peak calling result for this instruction is completely replaced by the new one. If you would like to apply the same peak calling instruction to different data and don't want to overwrite the first set of results, save the instructions under different names, and apply them subsequently to the different sets of samples.

7. Switch to the **Peak Calling** screen in the middle of the **Analysis** environment to view the result. The structure of the result is described below.

The screenshot shows the Peak Calling software interface. The 'Peak Calling' tab is active. The interface is divided into several sections:

- Peak Calling Instruction:** my 1 RNA rat_mouse_human
- Peaks of Interest:** A table showing results for peaks 18 S and 28 S.

Name	Position	Tol. [%]
18 S	1869 nt	7.00
28 S	4700 nt	7.00
- Peak Calling Result of [my 1 RNA rat_mouse_human]:** A table showing results for samples A01 to A05.

Pos.	Sample Info	RIS	Ratio	Total RNA Conc. [ng/μl]	Found	Size [nt]	Found	Size [nt]
A01	Jurkat_RNeasy_486_1_1	10.0	1.92	571.71	Yes	1799	Yes	45
A02	Jurkat_RNeasy_486_1_2	10.0	1.93	593.40	Yes	1761	Yes	44
A03	Jurkat_RNeasy_400_1_3	10.0	1.83	649.36	Yes	1757	Yes	44
A04	Jurkat_RNeasy_400_1_4	10.0	1.85	580.75	Yes	1791	Yes	44
A05	Jurkat_RNeasy_300_1_5	10.0	1.89	504.75	Yes	1834	Yes	45
- Peak Calling Result of [my 2 RNA rat_mouse_human]:** A table showing results for samples B01 and B02.

Pos.	Sample Info	RIS	Ratio	Total RNA Conc. [ng/μl]	Found	Size [nt]	Found	Size [nt]
B01	Jurkat_RNeasy_486_1_1	9.7	1.68	715.29	Yes	1740	Yes	45
B02	Jurkat_RNeasy_486_1_2	9.9	1.80	779.96	Yes	1758	Yes	45

Separate RNA analysis for row A and B with RNA peak calling.

8. To save the result of peak calling, save the experiment by clicking the **Save** button  in the **Experiment Explorer**.

Peak calling result

Every sample can be analyzed individually (by means of peak calling). Therefore, the peak calling result overview is grouped by peak calling instructions, each of them named as the applied peak calling instruction (see image above). The result for each peak calling instruction can be collapsed individually. It has the following structure: the table peak calling instruction is placed at the top, followed by the list of the samples to which the peak calling instruction has been applied. The list of the samples is grouped by the plates to which the samples belong.

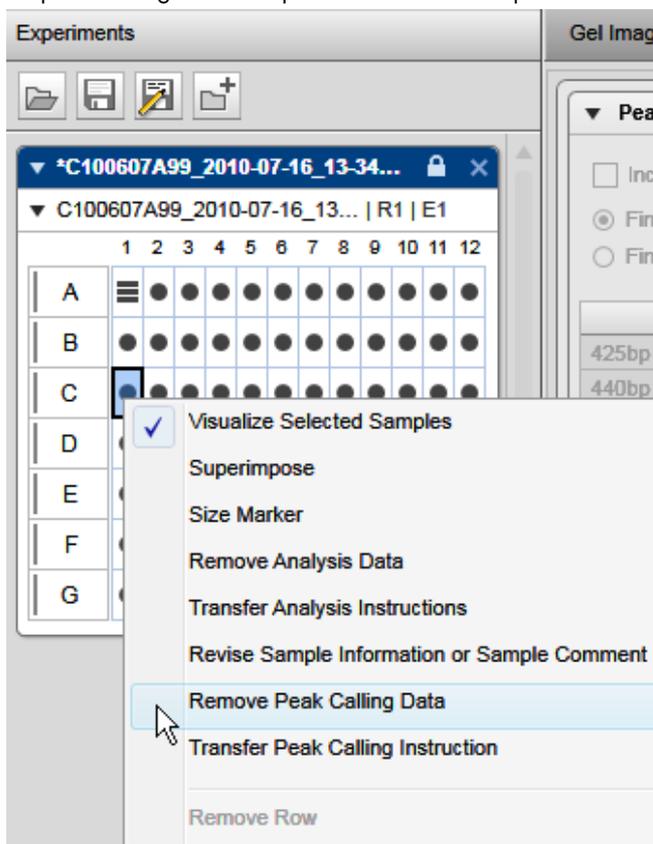
Each row in the table corresponds to a sample; the columns **Pos.** and **Sample Info** identify the sample. The **Pos** column is fixed. The following columns are defined by the peak calling instruction. Aggregated columns over all peaks of interest appear if they were selected in the **Calculated Columns** panel of the peak calling instruction. The following columns are grouped by the names of the peaks of interest and show several peak properties. To change the properties listed for each peak of interest, right-click the table header and select/unselect the property with the **Show Column** option. The change takes effect in the entire table.

Note: If a sample was not analyzed, it is not present in the peak calling result overview.

Parts of the peak calling result table can be copied to the clipboard. Select the cells to be copied and then press **Ctrl+C**. To copy the complete result of a peak calling instruction, right-click in the peak calling result table and select the **Copy Peak Calling Result of [...]** option.

Removing peak calling result

To remove the result of peak calling from a sample, right-click the sample in the experiment explorer and select **Remove Peak Calling Data** from the context menu that appears, as shown in the figure below. This menu item is only active if peak calling has been performed for the sample.



Remove the result of peak calling from a sample.

It is possible to automate peak calling during the data acquisition process. Ensure you have already automated the [Size and concentration determination procedure](#) for your samples using [Standard DNA analysis](#), [Fast Analysis DNA analysis](#) or [Standard RNA analysis](#). To automate peak calling, save any changes in the peak calling instructions into a customized peak calling instruction. Make sure that these parameters work for all samples. Then [modify the process profile](#) you have created to automate the size and concentration determination procedure for your samples. In the [Process Profile](#) step, select the option **Peak Calling** in the **Included** steps section additionally. If distribution analysis features are still active, activate peak calling features now. See the section [Activating distribution analysis features](#). In the [Peak Calling](#) step, select the customized peak calling instruction. For further details, refer to [Process profile options](#). Save the process profile with these settings for reuse. During each run setup, ensure selecting the alignment marker in the **Sample Selection** step.

Activating peak calling features

In **DNA** mode, either peak calling or distribution analysis features can be applied to samples of an active experiment.

To activate peak calling features for the current experiment, select **Activate Peak Calling Features** from the **View** menu. The peak calling result tables replace the distribution result tables and the peak calling parameter panel replaces the distribution parameter panel. The software keeps this setting until an experiment that used distribution analysis is activated or opened.

Note: It is not possible to activate peak calling features if a distribution analysis has already been performed in the current experiment. In this case, [remove the distribution analysis data](#) first.

Modifying a peak calling instruction

Peak calling instructions contain a set of parameters, defining the peaks to search for (peaks of interest).

Note: Peak calling instructions can be modified by users with the assigned user role **Advanced User** only.

To modify a peak calling instruction proceed as follows:

1. Open the **Peak Calling** tab at the right of the **Analysis** environment.
2. Select the peak calling instruction to be modified from the **Peak Calling Instruction** drop-down box.
3. Change the definitions for the peaks of interest according to your needs as described below.

Analysis Report **Peak Calling** Properties

Peak Calling Instruction
 b3_peaks Save as ...

▼ Peaks of Interest

Include size marker samples
 Find centered peak in interval
 Find highest peak in interval

Name	Position	Tol. [%]
15	15 bp	10,00
560	560 bp	10,00
603	603 bp	10,00
Peak 5000	5000 bp	10,00

Add Delete

Name
603

Position 603 Size Tolerance 10 %

OK Cancel

▼ Calculated Columns

Ratio Normalized Area ("Ratio")

Ratio

Relative Abundance

Modifying a row.

Note: The name in the **Peak Calling Instruction** drop-down box will appear with an asterisk to the left, indicating that the table has been changed.

4. Save the modified peak calling instruction by clicking the **Save as** button to the right of the **Peak Calling Instruction** drop-down box.

Peak calling configuration:

Include size marker samples

If this option is chosen, peak calling can be performed on the size marker sample  too. Otherwise, peak calling will be skipped for size marker samples.

Find centered / highest peak in interval

If more than one peak is found within the tolerance interval, this setting determines whether the centered peak (nearest to the sought position) or the highest peak is chosen.

To add a peak of interest:

1. Click the **Add** button. A new row with empty fields will appear at the bottom of the table.
2. Specify the peak of interest in the edit area below.

Name Specifies the name of the peak of interest. This will be the column header in the peak calling result table.

Note: The names of the peaks must be different.

Position Specifies the position of the peak to search for and the unit of the position (Size, Rel. Time, or Time).

Note: The positions of the peaks must be different.

Note: If **Rel. Time** is chosen to describe the position, the following constraints apply: In case of 2 alignment marker peaks, all relative times must be between 0 and 1. In case of 1 alignment marker peak, all relative times must be above 1.

Tolerance Tolerance for peak searching. In a sample the peak will be considered as detected if its position difference is less than the given tolerance from the defined position.

3. Click **OK** to add the new peak of interest to the table.

Note: The peaks of interest are sorted by position in the peak calling instruction table.

To delete a peak of interest:

1. Select the peaks row in the table.
2. Click the **Delete** button.

To modify a peak of interest:

1. Select the row of the peak of interest to be modified.
2. Edit the values of the peak of interest in the edit area below.
3. Click **OK**. The values in the selected row are changed.

Note: The peaks of interest are sorted by position in the peak calling instruction table.

Calculated columns:

In addition to finding the specified peaks, depending on the run mode, the following parameters can be calculated during peak calling:

Total Concentration	For RNA mode only. The total concentration of the RNA over the whole sample.
RNA Integrity Score	For RNA mode only. RNA integrity score (RIS) is a value from 0 to 10, where a value of 10 indicates completely intact RNA. This is especially useful for RNA QC . Note: The value is not calculated if the 18S peak was not found.
Ratio Normalized Area	Choose two peaks of interest. If both are found in the sample, the ratio of their normalized areas is calculated. This is especially useful for RNA QC using the 28S and 18S peaks.
Relative Abundance	For each peak of interest, the normalized area relative to the highest normalized area of corresponding peaks over all samples is calculated. (For the sample in which the normalized area of the peak is highest, the relative abundance is 100%. For all other samples, it is the percental fraction of its normalized area relative to the highest value.)

Creating a new peak calling instruction

To create a new peak calling instruction:

1. Open the **Peak Calling** tab at the right of the **Analysis** environment.
2. Select a peak calling instruction from the **Peak Calling Instruction** drop-down box. The selected peak calling instruction serves as a template for the creation of the new one. Select **NewPeakCallingInstruction** to start with an empty table.
3. Specify the peaks of interest according to your needs as described in the [Modifying a peak definition table](#) section.
4. Save the new peak calling instruction by clicking the **Save as** button to the right of the **Peak Calling Instruction** drop-down box. Enter a new unique peak calling instruction name and click **OK**.

Peak pattern matching

Based on a peak calling step, a peak pattern matching step can be performed.

Peak pattern matching shows whether certain patterns of peaks (determined in the peak calling step) are present in analyzed samples.

Note: Peak pattern matching can be performed by users with the assigned user roles **Basic User** and **Advanced User** only.

A peak pattern matching step is always based on a peak calling step. In order to perform peak pattern matching, proceed as follows:

1. Complete steps 1–5 described in the [Peak Calling](#) section.
2. In the **Peak Pattern Matching** panel, click the **Add** button to add a new pattern.
3. Entering a name for the new pattern and define the pattern. The definition of the pattern is done via the checkboxes presented for all peaks defined in the current peak calling instruction. Check the box for each peak to include in the pattern. Unchecked peaks will not be included in the pattern.
4. Click **OK** to confirm the pattern definition. By clicking **Cancel**, the definition step is canceled and no changes are made.

Note: You can define more than one pattern for a given peak pattern matching step. To add further patterns, repeat steps 2–4.

Note: To delete a pattern, click on it and press the **Delete** button.

5. Start peak calling and switch to the **Peak Calling** screen in the middle of the **Analysis** environment to view the results. For details see steps 6 and 7 of section [Peak Calling](#).

The peak calling result will indicate which pattern matches to each sample. Results are listed in the sample-specific column **Pattern** of the peak calling result table. If the peak calling result of a sample does not match any defined pattern, "n/a" will be displayed in the column and the result will be highlighted in light yellow.

For details about viewing the **Peak calling** result, refer to section [Peak Calling](#).

Note: Peak pattern matching is an extension to the peak calling instruction and is saved along with the peak calling instruction. It will also appear in any reports, exports, or print outs of the peak calling instruction.

Peak Calling Result of [my 1 RNA rat_mouse_human]

Include size marker samples
 Find centered peak in interval
 Find highest peak in interval

Total Concentration ("Total Conc.")
 RNA Integrity Score ("RIS")
 Ref. Peak: 18 S

Ratio Normalized Area ("Ratio")
 Ratio: 28 S / 18 S

Relative Abundance

Pos.	Sample Info	RIS	Ratio	Total RNA Conc. [ng/µl]	Pattern	Found	Size [nt]	Found	Size [nt]
A01	Jurkat_RNeasy_486_1_1	n/a	n/a	571.71	n/a	No	n/a	Yes	4516
A02	Jurkat_RNeasy_486_1_2	n/a	n/a	593.40	n/a	No	n/a	Yes	4422
A03	Jurkat_RNeasy_400_1_3	10.0	n/a	649.36	only 18 S	Yes	1757	No	n/a
A04	Jurkat_RNeasy_400_1_4	10.0	n/a	580.75	only 18 S	Yes	1791	No	n/a
A05	Jurkat_RNeasy_300_1_5	10.0	1.89	504.75	both	Yes	1834	Yes	4554
A06	Jurkat_RNeasy_300_1_6	10.0	1.97	519.17	both	Yes	1829	Yes	4538
A07	Jurkat_RNeasy_200_1_7	10.0	1.91	318.94	both	Yes	1869	Yes	4598
A08	Jurkat_RNeasy_200_1_8	10.0	2.04	316.96	both	Yes	1881	Yes	4633
A09	Jurkat_RNeasy_100_1_9	8.9	1.90	113.22	both	Yes	1931	Yes	4841
A10	Jurkat_RNeasy_100_1_10	9.5	2.03	131.73	both	Yes	1937	Yes	4856
A11	Jurkat_RNeasy_50_1_11	8.0	1.63	66.18	both	Yes	1945	Yes	4991

CF_Jurkat_RNeasy_Verd_051212 R1 | E1

Peak Calling Instruction: *my 1 RNA rat_mouse_huma | Save as ...

Name: 28 S
 Position: 4700
 Tolerance: 7%

Total Concentration ("Total Conc.")
 RNA Integrity Score ("RIS")
 Ref. Peak: 18 S

Ratio Normalized Area ("Ratio")
 Ratio: 28 S / 18 S

Relative Abundance

Peak Pattern Matching

only 18 S
 both

0 Sample(s) selected Start Peak Calling

Result of a peak pattern.

Analysis of DNA samples

This section describes how to analyze a DNA sample. Instructions are given for 4 types of analyses: (1) standard analysis of DNA samples, (2) analysis of samples using the high voltage method (fast analysis), (3) analysis of samples containing DNA libraries, and (4) analysis of samples containing genomic DNA. For all 4 samples types, perform steps 1–6 and follow the instructions corresponding to the relevant analysis type.

1. Select the **DNA** mode if this is not already selected. Check the current mode in the bottom right corner of the software screen. If another mode than DNA is selected, select **File/Logout** from the application menu bar to log out and then log in with selected DNA mode. For details, refer to section [User authentication](#).

Note: Only users with user role **Advanced User** can modify and save parameters of an analysis profile. Users with user role **Basic User** can select another analysis profile which is more suitable for the type of samples.

2. Switch to the **Analysis** environment by selecting the **Analysis** icon in the main toolbar.

3. If the samples you want to analyze are not yet listed in the **Experiment Explorer** at the left, select the **Load experiment** icon from the Experiment Explorer's toolbar. If the samples are listed, but not active (grayed out), right click it's experiment name and select **Activate**. For further details, refer to the [Loading sample data](#) or [Activating an experiment](#) section.
4. For the **Fast Analysis** of samples, or if the samples to analyze contain DNA libraries, or to perform quality control on gDNA purified with silica-based technologies, or for standard analysis of DNA samples for which size and concentration shall be determined, follow the instructions from the [Size and concentration determination procedure](#).
For information on which **Analysis** profile should be used as a starting point and which analysis parameters are required for your samples, refer to the respective sections: [Fast Analysis DNA analysis](#) for the **Fast Analysis** of samples, [Standard DNA analysis](#) for standard analysis of DNA samples, [Smear DNA analysis](#) for samples that contain DNA libraries, and [gDNA analysis](#) for samples containing gDNA purified with silica-based technologies.
Follow the [Size and concentration determination procedure](#) also if samples should have been analyzed during data acquisition process, but either an error message has been shown or sample results are not as expected. In this case, use the procedure to check the analysis step by step and correct if needed. Follow the instructions to reuse the analysis parameters that have been used for the samples.

If no size calculation shall be performed, follow the instructions of the [Peak detection procedure](#).
5. **Optional:** For the **Fast Analysis** of samples or standard analysis of DNA samples for which size and concentration have been determined, peak calling can be performed. Follow the instructions described in section [Peak Calling](#).
6. For DNA libraries with specific distribution expectations or to asses the quality of a library in routine use, or to assess the quality of gDNA, perform [Distribution analysis](#). Follow the instructions described in [Distribution analysis](#). For information on which **Distribution** profile should be used as a starting point for gDNA samples, refer to section [gDNA analysis](#).

The result table summarize all properties that the QIAxcel ScreenGel Software calculates for detected peaks. Right-click the header line of the table, select **Show column**, and then select the property you are interested in. Alternatively, right-click the header line of the table and select **Show all columns**. This option displays all the properties calculated by QIAxcel ScreenGel. For more information, refer to section [Result table](#) and sections [Standard DNA analysis](#), [Fast Analysis DNA analysis](#), [Smear DNA analysis](#), and [gDNA analysis](#), respectively.

Standard DNA analysis

During the [Size and concentration determination procedure](#) or the [Peak detection procedure](#) select the Default DNA v2.0 analysis profile as a starting point.

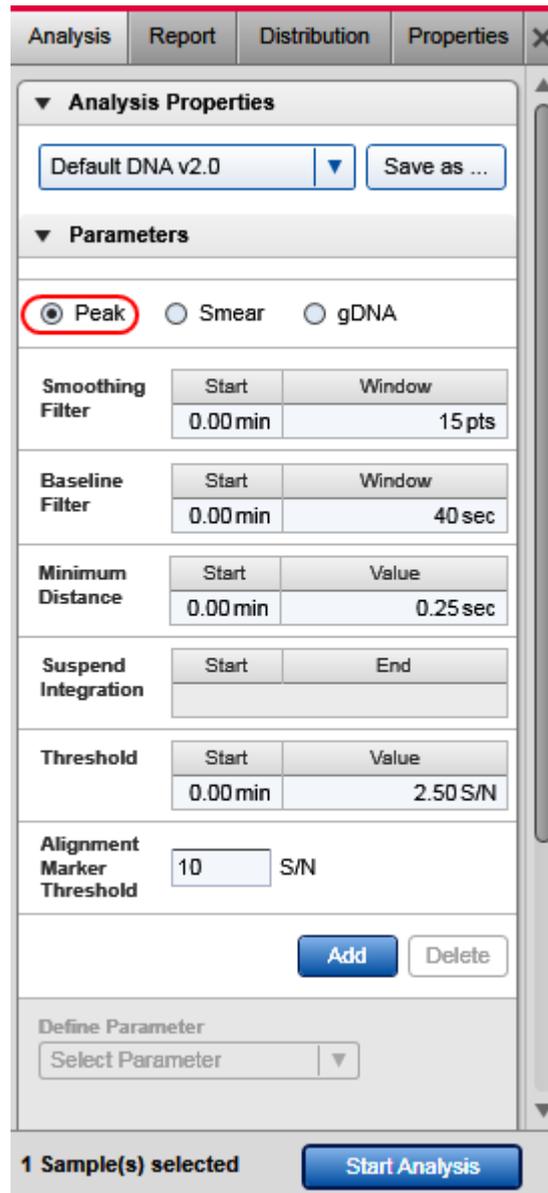
Note: The QIAxcel ScreenGel Software, version 1.2 and higher, comes with an improved default profile, named **Default DNA v2.0**. To be independent from the highest signal in the sample, in the new profile, the threshold parameter is defined as a multiple of the noise level which is estimated from the sample data.

The [single electropherogram view](#) is most suitable for checking peak detection. Ensure that the plot shows a red "+"-sign at the peak apex for all peaks between/after the alignment marker peak(s). If a pink "x"-sign is shown instead, click the **Image Options** button of the electropherogram toolbar and select the options **Mark peak apex** and **With Label**, with **Size [bp]** selected. Click **OK** to close the dialog. The electropherogram plot of the analyzed samples will show the size of the detected DNA molecules in base pairs above the apex of the corresponding peaks. Peak properties are shown in the **Peak Result** table below the electropherogram. For details, refer to the [Result table](#) section.

To switch the sample to be shown in the electropherogram, click on the next sample in the **Experiment Explorer** on the left.

Ensure that the peak detection has worked as expected. Firstly, it is important that the correct peaks are marked as alignment marker peaks (marked with a green '+') because this is the basis for all other analysis functions. If not, adapt the analysis parameters in the **Analysis** parameters panel on the right side of the **Analysis** environment. To do so, open the **Analysis Properties** section and then open the **Parameters** section. For details on how to change the parameters that are mentioned below, refer to section [Modifying an analysis profile](#).

Note: Collapse and expand parts of the analysis properties by clicking ▼ and ►, respectively.



Analysis profile for standard DNA analysis.

- Ensure that the **Peak** option is selected.
- If the raw data being analyzed are too noisy, increase the **Smoothing Filter window**. Click this parameter line and set the window size to 25 pts, for example, in the edit area below the parameters list and click **OK** to confirm. To apply time-dependent smoothing, add one or more smoothing filter parameter lines. To do so, click the **Add** button, select **Smoothing Filter**, and set the values for start time and window size. Click **OK** to confirm this setting. An example of time-dependent smoothing is represented by the **Default RNA analysis profile** in **RNA** mode.

- If peaks were detected before or after the alignment marker peak, increase the **Alignment marker threshold**. Click on the field and change the value.
- If peak detection is too sensitive, increase the **Threshold**. Click this parameter line and increase the value in the **Value** field in the edit area below the parameters list, and click **OK** to confirm.
- If in a certain range of migration time, peak detection is too sensitive, increase the **Threshold** in this region. To do so, click the **Add** button below the parameters list and select **Threshold** from the **Define parameter** drop-down list. As a starting point, set the time where the region for which to increase the threshold starts, and define a threshold of, for example 5 S/N. Click the **OK** button to confirm this setting. Then at the end of the affected region, reset the threshold to the default value (e.g., 2 S/N in Default DNA) by adding a third threshold definition. Set the start time of this threshold to the end of the affected region and set the threshold value to that of the first threshold parameter line. Click the **OK** button to confirm this setting.

Click the **Start Analysis** button again to start a new analysis according to this modified analysis profile.

In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the **Default DNA v2.0** analysis profile for future DNA analyses of similar samples.

Fast Analysis DNA analysis

For a run that contains the size marker, follow the [Size and concentration determination procedure](#). During the procedure, create and save a reference marker from the size marker sample. Use the **Default Fast Analysis** analysis profile as a starting point. If the run contains the size marker only, leave the procedure after the reference marker has been saved. If the run contains samples as well, continue the procedure to analyze the samples: in the **Reference Marker** section, check **Reference Marker Table** and select **use the just created and saved reference marker**.

For a run that contains samples only, follow the [Size and concentration determination procedure](#). During the procedure, use the **Default Fast Analysis** analysis profile as a starting point, and in the **Reference Marker** section, check **Reference Marker Table** and select the **previously created reference marker**.

The [single electropherogram view](#) is most suitable for checking peak detection. Ensure that the plot shows a red "+"-sign at the peak apex for all peaks between the alignment marker peaks. If a pink "x"-sign is shown instead, click the **Image Options** button of the electropherogram toolbar and select the options **Mark peak apex** and **With Label**, with **Size [bp]** selected. Click **OK** to close the dialog. The electropherogram plot of the analyzed samples will show the size of the detected DNA molecules in base pairs above the apex of the corresponding peaks. Peak properties are shown in the **Peak Result** table below the electropherogram. For details, refer to the [Result table](#) section.

To switch the sample to be shown in the electropherogram, click on the next sample in the **Experiment Explorer** on the left.

Ensure that the peak detection has worked as expected. Firstly, it is important that the correct peaks are marked as alignment marker peaks (marked with a green '+') because this is the basis for all other analysis functions. If not, adapt the analysis parameters in the **Analysis** parameters panel on the right side of the **Analysis** environment. To do so, open the **Analysis Properties** section and then open the **Parameters** section. For details on how to change the parameters that are mentioned below, refer to section [Modifying an analysis profile](#).

Note: Collapse and expand parts of the analysis properties by clicking ▼ and ►, respectively.

The screenshot shows the 'Analysis Properties' dialog box with the following settings:

- Analysis Properties:** Default Fast Analysis (dropdown), Save as ... (button)
- Parameters:**
 - Peak (circled in red), Smear, gDNA
 - Smoothing Filter:** Start: 0.00 min, Window: 0 pts (circled in red)
 - Baseline Filter:** Start: 0.00 min, Window: 40 sec
 - Minimum Distance:** Start: 0.00 min, Value: 0.25 sec
 - Suspend Integration:** Start: 0.00 min, End: 0.50 min
 - Threshold:** Start: 0.00 min, Value: 10.00 %
 - Alignment Marker Threshold:** 0 S/N
- Buttons:** Add, Delete
- Define Parameter:** Select Parameter (dropdown)
- Status:** 1 Sample(s) selected, Start Analysis (button)

Analysis profile for Fast Analysis.

- Ensure that the **Peak** option is selected.
- If you're analyzing samples, in the **Reference Marker** section, check **Reference Marker Table** and select a previously saved reference marker. If you're creating the reference marker, in the **Reference Marker** section, check **No Marker**.
- If peaks were detected before or after the alignment marker peak, increase the **Alignment marker threshold**. Click on the field and change the value.

- If peak detection is too sensitive, increase the **Threshold**. Click this parameter line and increase the value in the **Value** field in the edit area below the parameters list, and click **OK** to confirm.
- When analyzing **Fast Analysis** data, it may be that the default baseline filter window (40 seconds) is too large. In this case, a notification will arise suggesting to decrease the baseline filter window. To do so, click the **Baseline filter line** and set the **Window** size to 39 in the edit area below the parameters list, and click **OK** to confirm. In most cases, this will work.
- If in a region with many peaks close together, some peaks are not detected, decrease the minimum distance by clicking on the **Minimum Distance parameter line** and setting the distance **Value** from default 0.25 to 0.1 seconds, for example, in the edit area below the parameters list. Click **OK** to confirm this setting. If you do not need minimum distance between peaks, set the minimum distance value to 0 seconds.
- For **Fast Analysis** samples, smoothing should be deactivated as set in the **Default Fast Analysis** analysis profile. Here, in the **Smoothing Filter parameter line**, the **Window** value is set to 0 pts.

Click the **Start Analysis** button again to start a new analysis according to this modified analysis profile.

In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the **Default Fast Analysis** analysis profile for future **Fast Analysis** samples.

Smear DNA analysis

Use the analysis options described below to obtain basic information about DNA libraries in samples, such as minimum and maximum fragment sizes, molarity or concentration.

During the [Size and concentration determination procedure](#), select the **Default Smear DNA analysis** profile as a starting point.

The [single electropherogram view](#) is most suitable for checking peak detection. Ensure that the plot shows a pink "x"-sign for all smear peaks between the alignment marker peaks. If a red "+"-sign is shown instead, click the **Image Options** button of the electropherogram toolbar and select the options **Mark median of size** and **With Label**. Click **OK** to close the dialog. The electropherogram plot of the analyzed samples will mark the median of size in base pairs of the corresponding peaks.

Smear peak properties are shown in the **Smear/gDNA Result** table below the electropherogram. For details, refer to the [Result table](#) section.

To switch the sample to be shown in the electropherogram, click on the next sample in the **Experiment Explorer** on the left.

In case the sample was earlier analyzed with [distribution analysis](#) in DNA mode, the single electropherogram view shows smear peaks corresponding to the areas of interest as defined in the [distribution profile](#). In order to see a plot of the peak detection, the distribution analysis needs to be removed temporarily. To do so, right-click the sample in the **Experiment Explorer** to the right and select the option **Transfer Distribution Profile** to copy the parameters that had been used for distribution analysis into the **Distribution** panel to the right for later reuse. Then right-click the sample again and select the option **Remove Distribution Analysis Data** to remove the results of distribution analysis from the sample. The single electropherogram now shows the result of peak detection. It shows the alignment marker peaks (marked green at the apex) and the smear peaks according to the **Smear/gDNA Result** table.

Ensure that the peak detection has worked as expected. Firstly, it is important that the correct peaks are marked as alignment marker peaks (marked with a green '+') because this is the basis for all other analysis functions. If not, adapt the analysis parameters in the **Analysis** parameters panel on the right side of the **Analysis** environment. To do so, open the **Analysis Properties** section and then open the **Parameters** section. For details on how to change the parameters that are mentioned below, refer to section [Modifying an analysis profile](#).

Note: Collapse and expand parts of the analysis properties by clicking ▼ and ►, respectively.

The screenshot shows the 'Analysis Properties' dialog box with the following settings:

- Analysis Properties:** Default Smear DNA (dropdown), Save as ... (button)
- Parameters:**
 - Radio buttons: Peak, Smear, gDNA
 - Smoothing Filter:**

Start	Window
0.00 min	10 sec
 - Minimum Distance:**

Start	Value
0.00 min	0.25 sec
 - Suspend Integration:**

Start	End
 - Threshold:**

Start	Value
0.00 min	70.00 S/N
 - Alignment Marker Threshold:** 100 S/N
 - Buttons: Add, Delete
 - Define Parameter: Select Parameter (dropdown)
 - Buttons: OK, Cancel
- Footer:** 1 Sample(s) selected, Start Analysis (button)

Analysis profile for smear analysis.

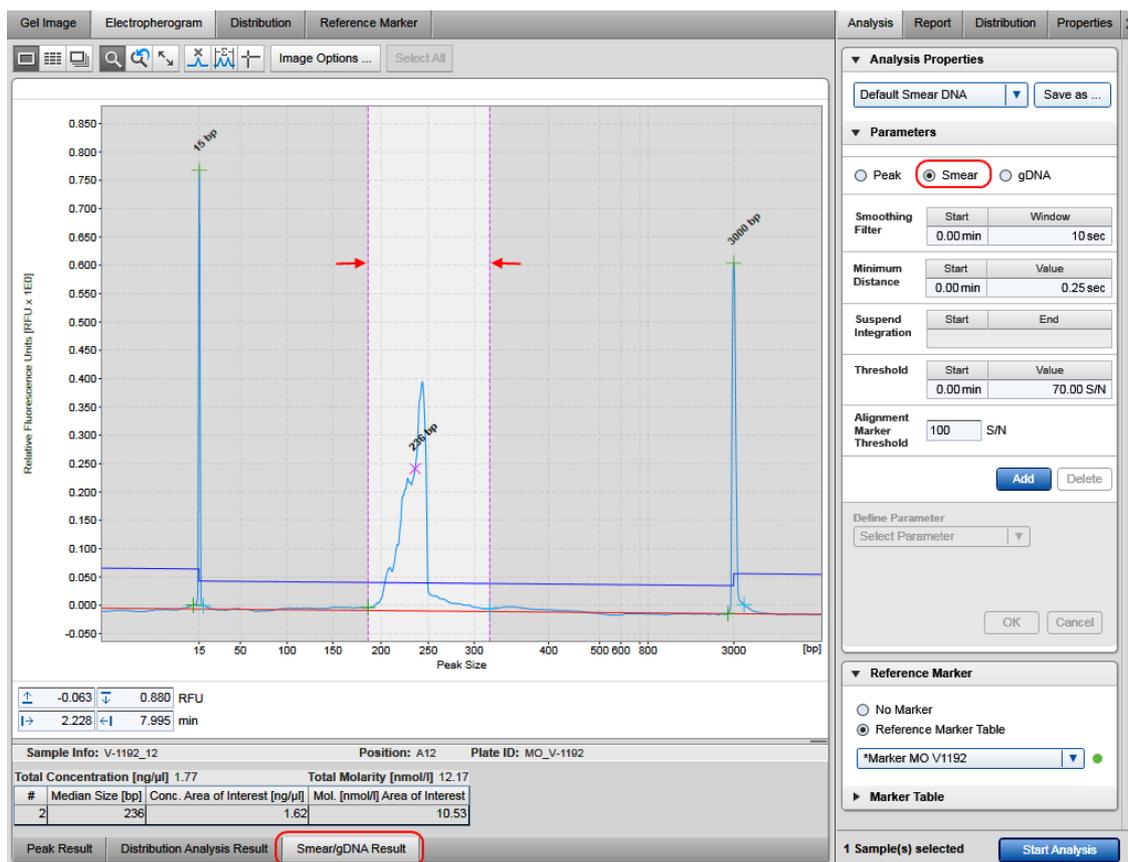
- Ensure that the **Smear** option is selected.
- If peaks were detected before the first or after the last alignment marker peak, increase the **Alignment marker threshold**. Click on the field and change the value.
- If signals were incorrectly detected as peaks, increase the threshold. Because the smoothing algorithm was optimized for the typical shape of smear data, a high S/N value is required as threshold.

Click the **Start Analysis** button again to start a new analysis using the modified analysis profile.

In some cases, it may be necessary to repeatedly adapt the analysis profile. If the peak detection worked as expected with a modified analysis profile, save and use the modified analysis profile for future DNA analyses of similar samples, instead of using the **Default Smear DNA analysis** profile.

Smear analysis distinguishes samples marked as size marker and does not define smear peaks for these samples. For all other samples, the analysis distinguishes between alignment marker peaks and smear peaks. The software assigns a so called area of interest to each detected smear peak. The borders of an area of interest are marked by two vertical pink lines and, by default, are the same as the borders of the corresponding peak. In case the detected peak borders do not describe the actual area of interest, move the borders to the correct positions. All properties displayed in the **Smear Result** table refer to the area of interest defined by the vertical pink lines.

Note: Upon clicking the **Start Analysis** button, the borders of the normalized areas will be reset to match the borders of the detected smear peak, even if they were previously corrected manually. Moving the threshold does not affect the borders of the area of interest.



Result of smear analysis.

However, for routine use, use **Distribution analysis** instead. There you can define the areas of the distribution you are interested in and use these settings for all samples in one step. For information on how to setup distribution analysis, refer to section [Distribution analysis](#). Distribution analysis can only be performed after the [Size and concentration determination procedure](#) has been completed successfully.

gDNA analysis

Use the analysis options described below for analysis of genomic DNA quality.

Note: Make sure to use the 15 bp alignment marker. For details, refer to [Checking alignment marker](#).

During the [Size and concentration determination procedure](#), select the **Default gDNA analysis** profile as a starting point.

The [single electropherogram view](#) is most suitable for checking peak detection. Ensure that the plot shows a pink "x"-sign for all smear peaks between the alignment marker peaks. If a red "+"-sign is shown instead, click the **Image Options** button of the electropherogram toolbar and select the options **Mark median of size** and **With Label**. Click **OK** to close the dialog. The electropherogram plot of the analyzed samples will mark the median of size in base pairs of the corresponding peaks.

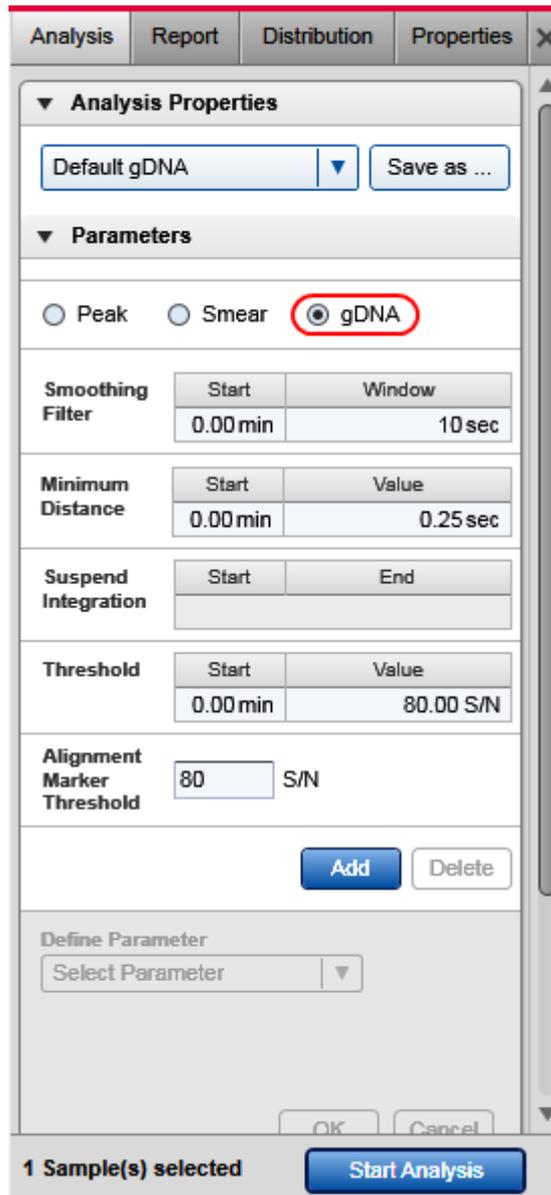
After the [Size and concentration determination procedure](#), the results are shown in the **Smear/gDNA Result** table below the electropherogram. Find the size estimation of the gDNA in base pairs in the column **Median Size** [bp]. The concentration estimation of the gDNA is displayed as **Total Concentration** just above the **Smear/gDNA Result** table. For further details, refer to the [Result table](#) section.

To switch the sample to be shown in the electropherogram, click on the next sample in the **Experiment Explorer** on the left.

In case the sample was earlier analyzed with [distribution analysis](#) in DNA mode, the single electropherogram view shows smear peaks corresponding to the areas of interest as defined in the [distribution profile](#). In order to see a plot of the peak detection, the distribution analysis needs to be removed temporarily. To do so, right-click the sample in the **Experiment Explorer** to the right and select the option **Transfer Distribution Profile** to copy the parameters that had been used for distribution analysis into the **Distribution** panel to the right for later reuse. Then right-click the sample again and select the option **Remove Distribution Analysis Data** to remove the results of distribution analysis from the sample. The single electropherogram now shows the result of peak detection. It shows the alignment marker peaks (marked green at the apex) and the smear peaks according to the **Smear/gDNA Result** table.

Ensure that the peak detection has worked as expected. Firstly, it is important that the correct peaks are marked as alignment marker peaks (marked with a green '+') because this is the basis for all other analysis functions. If not, adapt the analysis parameters in the **Analysis** parameters panel on the right side of the **Analysis** environment. To do so, open the **Analysis Properties** section and then open the **Parameters** section. For details on how to change the parameters that are mentioned below, refer to section [Modifying an analysis profile](#).

Note: Collapse and expand parts of the analysis properties by clicking ▼ and ►, respectively.



Analysis profile for gDNA analysis.

- Ensure that the **gDNA** option is selected.
- If the first detected peak is not the alignment marker peak, as a first step, increase the **Alignment marker threshold**. Click on the field and change the value. If this is not sufficient, click the **Add** button below the parameter list and select **Suspend Integration** from the **Define parameter** drop-down list. Use the **Absolute** time unit and define the starting point as 0 minutes. Set the ending point of this parameter to shortly before the start of the alignment marker peak (e.g., set end to 2 minutes if the first alignment marker peak appears at 2.5 minutes).

- If signals were incorrectly detected as peaks, increase the threshold. Click this parameter line and increase the value in the **Value** field in the edit area below the parameters list and click **OK** to confirm. Because the smoothing algorithm was optimized for the typical shape of smear data, a high S/N value is required as threshold.

Click the **Start Analysis** button again to start a new analysis using the modified analysis profile.

In some cases, it may be necessary to repeatedly adapt the analysis profile. If the peak detection worked as expected with a modified analysis profile, save and use the modified analysis profile for future DNA analyses of similar samples, instead of using the **Default gDNA analysis** profile.

To assess the quality of the gDNA, perform **Distribution analysis**. Select the **Default gDNA distribution** profile as a starting point. For information on how to perform distribution analysis, refer to section [Distribution analysis](#). Distribution analysis can only be performed after the [Size and concentration determination procedure](#) has been completed successfully.

Distribution analysis

Use this analysis type to assess the quality of DNA libraries or genomic DNA in routine use based on the size distribution.

Note: Distribution analysis is available in **DNA** mode only.

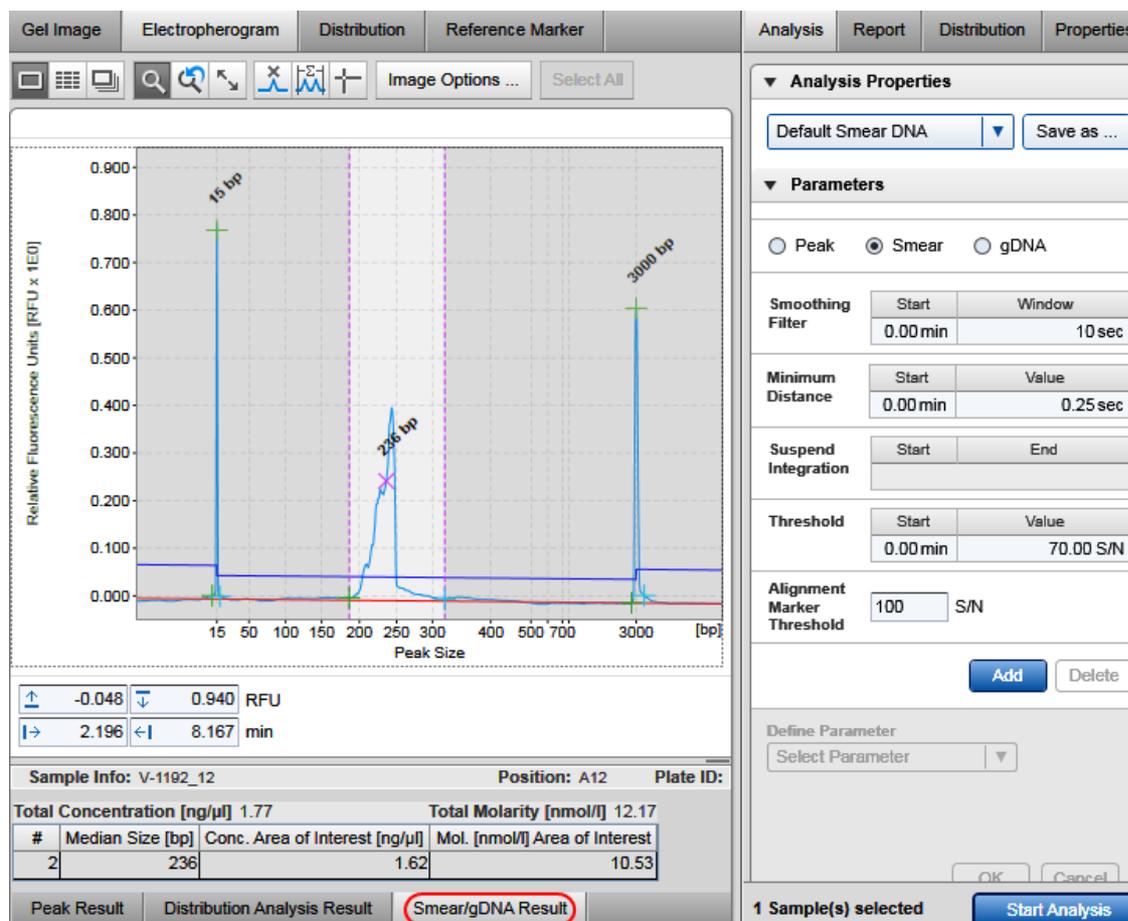
If the parameters panel is not yet open, open it by clicking the icon on the right-hand corner of the tab:



Note: If peak calling features are still active, activate distribution analysis features now. See the section [Activating distribution analysis features](#).

To perform the distribution analysis:

1. Before distribution analysis can start, ensure that the [Size and concentration determination procedure](#) has been performed using analysis profile parameters as described in the sections [Smear DNA analysis](#) or [gDNA analysis](#), respectively.

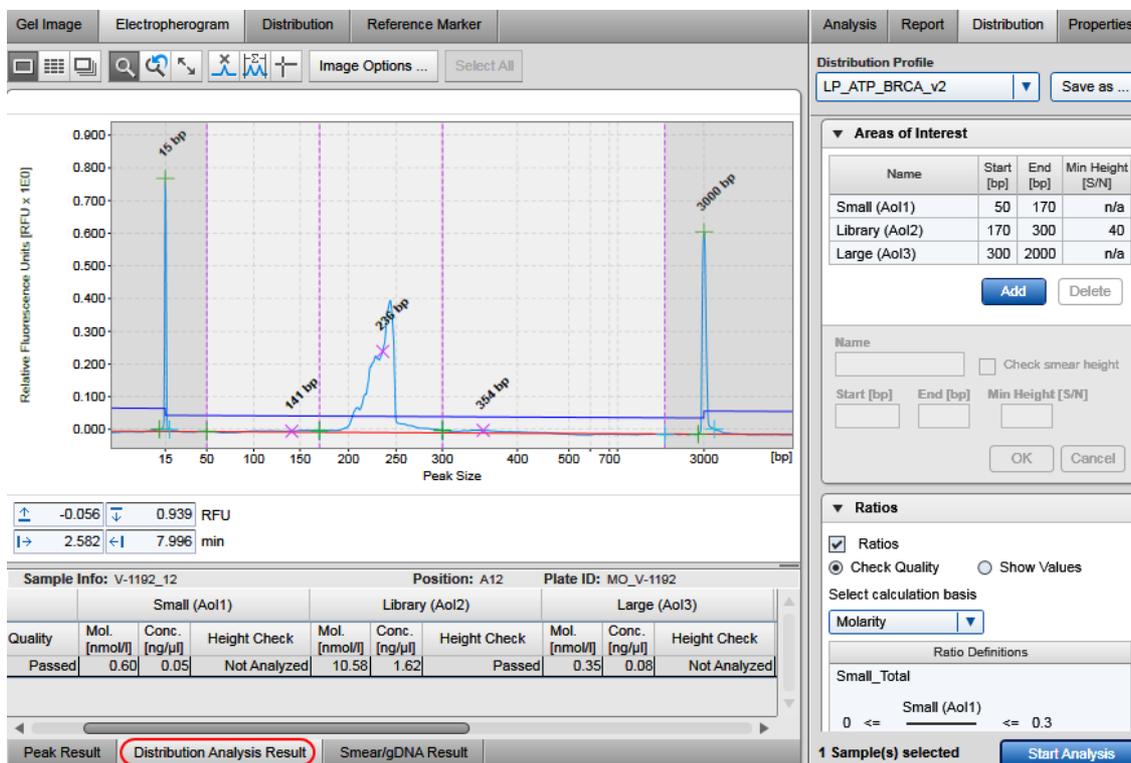


Intermediate result after the size and concentration determination procedure.

2. Open the **Distribution** tab located on the right side of the **Analysis** environment.
3. In case, the distribution analysis needs to be removed temporarily during the [Size and concentration determination procedure](#), use the distribution profile parameters that had been transferred before - they should be visible in the **Distribution** parameters tab at the right. Otherwise, select the distribution profile relevant for the samples from the **Distribution Profile** drop-down box. For gDNA quality analysis, select the **Default gDNA distribution profile**. A distribution profile defines the areas of interest that are, for example, expected for the library. For DNA libraries, refer to the section [Creating a distribution profile](#) for information on how to create the profile.

- Select the samples to be analyzed with this distribution profile.

Note: Here, the selection inside the middle view is relevant — not the selection in the **Experiment Explorer**. See the [Selecting samples for analysis or report](#) section for details.
- Click the **Start Analysis** button at the bottom of the **Distribution** tab at the right to start the distribution analysis.
- The result for one sample is displayed in the **Distribution Analysis Result** table below the electropherogram and an overview result table for all samples is available in the **Distribution** screen in the middle of the **Analysis** environment. Refer to the section [Distribution result](#) for a description of the result structure and to the section [Distribution result columns](#) for a description of the available columns.
- To save the result of the distribution analysis, save the experiment by clicking  in the **Experiment Explorer** at the left.



The screenshot displays the software interface for distribution analysis. The main window shows an electropherogram with relative fluorescence units (RFU x 1E0) on the y-axis and peak size in base pairs (bp) on the x-axis. Several peaks are labeled with their sizes: 15 bp, 141 bp, 239 bp, 354 bp, and 3000 bp. The interface is divided into several panels:

- Top Panel:** Contains tabs for 'Gel Image', 'Electropherogram', 'Distribution', and 'Reference Marker'. Below these are various tool icons and a 'Select All' button.
- Right Panel:** Contains the 'Distribution Profile' section with a dropdown menu set to 'LP_ATP_BRCA_v2' and a 'Save as ...' button. Below this is the 'Areas of Interest' section, which includes a table with columns for Name, Start [bp], End [bp], and Min Height [S/N]. The table lists three areas of interest: Small (AoI1), Library (AoI2), and Large (AoI3). Below the table are 'Add' and 'Delete' buttons. Further down is a form for adding a new area of interest with fields for Name, Start [bp], End [bp], and Min Height [S/N], along with a 'Check smear height' checkbox and 'OK'/'Cancel' buttons.
- Bottom Panel:** Contains the 'Ratios' section, which is checked. It includes options for 'Check Quality' (selected) and 'Show Values'. Below this is a 'Select calculation basis' dropdown menu set to 'Molarity'. At the bottom of this panel is a 'Ratio Definitions' section with a table for 'Small_Total' showing a range from 0 to 0.3 for 'Small (AoI1)'. At the very bottom of the interface, it shows '1 Sample(s) selected' and a 'Start Analysis' button.
- Sample Info Table:** Located below the electropherogram, it shows 'Sample Info: V-1192_12', 'Position: A12', and 'Plate ID: MO_V-1192'. It contains a table with columns for Quality, Mol. [nmol/l], Conc. [ng/ul], and Height Check for three areas of interest: Small (AoI1), Library (AoI2), and Large (AoI3).
- Distribution Analysis Result Table:** Located below the Sample Info table, it shows a table with columns for Quality, Mol. [nmol/l], Conc. [ng/ul], and Height Check for the three areas of interest.

Sample with completed distribution analysis.

Note: After distribution analysis, the single electropherogram shows the areas of interest as defined in the **Distribution** profile and the borders of areas of interest cannot be moved anymore.

Note: In some cases, the signal in an area of interest does not exceed the baseline at any point, indicating that the area of interest is not present in a sample.

It is possible to automate distribution analysis during the data acquisition process. Ensure that you have already automated the [Size and concentration determination procedure](#) for your samples using [Smear DNA analysis](#) or [gDNA analysis](#). To automate also the distribution analysis, save any changes in the distribution analysis parameters into a customized distribution profile. Make sure that these parameters work for all samples. Then [modify the process profile](#) you have created to automate the size and concentration determination procedure for your samples. In the [Process Profile](#) step, select the option **Distribution Analysis** in the **Included** steps section additionally. If peak calling features are still active, activate distribution analysis features now. See the section [Activating distribution analysis features](#). In the [Distribution Analysis](#) step, select the customized distribution profile. For further details, refer to [Process profile options](#). Save the process profile with these settings for reuse. During each run setup, ensure to select the alignment marker in the **Sample Selection** step.

Activating distribution analysis features

In **DNA** mode, either peak calling or distribution analysis features can be applied to samples of an active experiment.

To activate distribution analysis features for the current experiment, select **Activate Distribution Analysis Features** from the **View** menu. The distribution result tables replace the peak calling result tables and the distribution parameter panel replaces the peak calling parameter panel. The software keeps this setting until an experiment that used peak calling is activated or opened.

Note: It is not possible to activate distribution analysis features if peak calling has already been performed in the current experiment. In this case, [remove the peak calling data](#) first.

Distribution result

In the **Analysis** environment, each sample can be analyzed individually by means of distribution analysis. Therefore, the distribution result overview is grouped by distribution profiles and each group is labeled with the name of the applied distribution profile. The result for each distribution profile can be collapsed individually.

The result of each distribution profile lists the samples to which the profile was applied. This list is organized into groups of samples belonging to the same plate. Thus, in the screenshot below, a second group of samples from another plate might appear within the collapsible area of the distribution profile under a second heading MO_V-1192 R1 | E1.

Each row in the table corresponds to a sample, with the columns **Pos.** and **Sample Info** identifying the sample. Columns relevant to the entire sample appear first. Thereafter, columns are grouped according to the names of the defined areas of interest and display several smear peak properties. The remaining columns are then grouped by the name of defined ratios. Find a detailed description in the section [Distribution result columns](#).

To change the properties listed, right-click the table header and select or unselect the property with the **Show Column** option. The change takes effect in the entire table.

Note: If a sample was not analyzed with a smear or gDNA analysis profile, it will not appear in the distribution result overview. If a sample was not analyzed with a reference marker, the distribution values cannot be calculated. In this case, the sample **Quality** is listed as "Review." In both cases, follow the instructions in [Analysis of DNA samples](#) to check and correct the analysis steps that are required before **Distribution** analysis. Ensure using **Analysis** parameters as described in [Smear DNA analysis](#) and [gDNA analysis](#), respectively.

The distribution result table can be copied to the clipboard. To copy the complete result of a distribution profile, right-click in the distribution result table and select the **Copy Distribution Result of [...]** option.

▼ Distribution Analysis Result of [LP_ATP_BRCA_v2]																
MO_V-1192 R1 E1																
Pos.	Sample Info	Total Mol. [nmol/l]	Quality	Small (Ao11)			Library (Ao2)			Large (Ao3)			Small Total		Large Total	
				Mol. [nmol/l]	Conc. [ng/μl]	Height Check	Mol. [nmol/l]	Conc. [ng/μl]	Height Check	Mol. [nmol/l]	Conc. [ng/μl]	Height Check	Ratio (Molarity)	Ratio Quality	Ratio (Molarity)	Ratio Quality
A02	V-1192_2	4.14	Review	1.41	0.10	Not Analyzed	0.29	0.04	Review	0.11	0.03	Not Analyzed	0.34	Review	0.03	Passed
A03	V-1192_3	7.17	Passed	1.10	0.09	Not Analyzed	4.96	0.76	Passed	0.36	0.09	Not Analyzed	0.15	Passed	0.05	Passed
A04	V-1192_4	12.99	Passed	1.29	0.10	Not Analyzed	10.69	1.64	Passed	0.55	0.13	Not Analyzed	0.10	Passed	0.04	Passed
A05	V-1192_5	12.43	Passed	1.58	0.12	Not Analyzed	9.43	1.44	Passed	0.65	0.17	Not Analyzed	0.13	Passed	0.05	Passed
A06	V-1192_6	11.27	Passed	0.47	0.04	Not Analyzed	10.29	1.57	Passed	0.23	0.05	Not Analyzed	0.04	Passed	0.02	Passed
A07	V-1192_7	14.03	Passed	1.91	0.13	Not Analyzed	7.88	1.20	Passed	0.25	0.06	Not Analyzed	0.14	Passed	0.02	Passed
A08	V-1192_8	9.40	Passed	0.89	0.07	Not Analyzed	7.42	1.13	Passed	0.28	0.07	Not Analyzed	0.09	Passed	0.03	Passed
A10	V-1192_10	12.15	Passed	1.15	0.09	Not Analyzed	9.60	1.47	Passed	0.39	0.10	Not Analyzed	0.09	Passed	0.03	Passed
A12	V-1192_12	12.17	Passed	0.60	0.05	Not Analyzed	10.58	1.62	Passed	0.35	0.08	Not Analyzed	0.05	Passed	0.03	Passed
B02	SM	n/a	Not Analyzed	n/a	n/a	Not Analyzed	n/a	n/a	Not Analyzed	n/a	n/a	Not Analyzed	n/a	Not Analyzed	n/a	Not Analyzed

Distribution result overview with size marker at B2.

Note: If the distribution profile was modified but not saved, and then used for a subset of previously analysed samples, two distribution results will be listed with the same distribution profile name. To identify the differences between the used profiles, right-click one of the samples in the **Experiment Explorer** on the left and select the **Transfer Distribution Profile** item from the context menu. Inspect the parameters in the **Distribution** tab on the right. Do the same with a sample from the second distribution result.

Modifying a distribution profile

A distribution profile specifies the quality criteria for a DNA library or genomic DNA. The profile defines areas of interest by start and end size, as well as molarity or concentration ratios between defined areas of interest or against the total molarity or total concentration of the sample.

Note: Distribution profiles can only be modified by users with the assigned user role **Advanced User**.

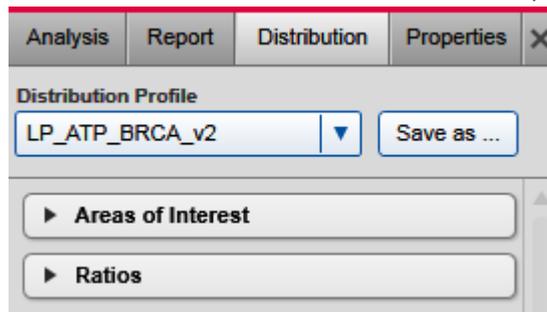
Note: Distribution analysis is available in **DNA** mode only.

To modify a distribution profile proceed as follows:

1. Open the **Distribution** tab on the right of the Analysis environment.

Note: The **Distribution** tab is available only if distribution features are active. Refer to [Activating distribution analysis features](#) for information on how to activate distribution analysis features.

2. Select the distribution profile to be modified from the **Distribution Profile** drop-down box.



Selected distribution profile.

3. Follow the instructions below to change definitions of areas of interest and/or of ratios as needed.

Note: The name of the profile in the **Distribution Profile** drop-down box will appear preceded by an "*", indicating that the profile has been modified.

4. Save the modified distribution profile by clicking the **Save as** button to the right of the **Distribution Profile** drop-down box.

Note: At least one area of interest must be defined.

Note: Collapse and expand parts of the distribution profile by clicking ▼ and ►, respectively.

To add an area of interest:

1. Click the **Add** button. A new empty row appears at the bottom of the table.
2. Define the area of interest in the editable fields:

Name	A unique name for the area of interest. This will be the column header in the distribution result table, grouping all columns relevant to this area. Note: Names of the areas must be unique and can have a maximum length of 20 characters. Total Molarity or Total Concentration cannot be used as a name for an area of interest.
Start [bp]	Define in base pairs the size where the area of interest starts.
End [bp]	Define in base pairs the size where the area of interest ends.
Check smear height	Select this option to check that the signal of the area of interest is above the threshold defined by Min Height (below).
Min Height [S/N]	Enabled if the option Check smear height has been selected.

Defines the threshold for the area of interest as a multiple of the noise level, which is estimated from the sample data.

Note: If **Check smear height** is not selected, "n/a" will appear in the table of areas of interest.

Note: Areas of interest may not overlap. The start or end field appears yellow in case of overlapping sizes. An area may, however, start at the size where another area ends.

Note: Make sure that size definitions of the areas of interest are in within the sizes of the alignment marker. Either use a suitable alignment marker or adapt the areas of interest. The distribution analysis will fail, otherwise, because all areas of interest are assumed to be within the range of the alignment marker. For gDNA analysis, refer to the **Default gDNA distribution** profile for the maximum size.

Example: Use areas of interest to distinguish between wanted (library) and unwanted (small or large artifacts) fragments during a library preparation reaction and use the option **Check smear height** for the library.

3. Click **OK** to add the new area of interest to the table.

Note: The areas of interest are sorted in the table by start size.

Note: At least one area of interest must be defined.

Name	Start [bp]	End [bp]	Min Height [S/N]
Small (Aol1)	50	170	n/a
Library (Aol2)	170	300	40
Large (Aol3)	300	2000	n/a

Name: Check smear height

Start [bp]: End [bp]: Min Height [S/N]:

Modifying an area of interest.

To delete an area of interest:

1. Select the corresponding row in the table.
2. Click the **Delete** button.

Note: If the deleted area of interest was used in the definition of a ratio, the ratio becomes invalid. Then delete the ratio as well.

To modify an area of interest:

1. Select the row of the area of interest to be modified.
2. Modify the values of the area of interest in the editable fields.
3. Click **OK**. The values in the selected row are changed.

Note: Areas of interest are sorted by position in the **Areas of Interest** table.

The QIAxcel ScreenGel allows to define ratios to assess the relationship between wanted and unwanted fragments in a distribution.

To add a ratio:

1. Expand the **Ratio** section.
2. Ensure that the **Ratios** option is selected.
3. If the QIAxcel ScreenGel shall include an assessment of the defined ratios into the overall sample quality, select the option **Check Quality**. In this case, you are forced to enter limits for the ratio value (see below). Select **Show Values**, otherwise, if you want to see the ratio calculations in the distribution result table without quality assessment based on the ratios.
4. Select the calculation basis for the ratios to be defined. It is possible to select **Concentration** or **Molarity**. This calculation basis will be used for all ratios.
5. Click the **Add** button. A new empty row will appear at the bottom of the **Ratio Definitions** list.
6. Define the ratio in the editable fields:

Ratio Name	A unique name for the ratio. This will be the column header in the distribution result table, grouping all columns related to this ratio. Note: Names of ratios must be unique and have a maximum length of 20 characters. The same name may not be used for ratios and for areas of interest.
Calculate ratio for	Define the nominator and denominator of the ratio by selecting the respective areas of interest from the drop-down boxes. In addition, the denominator drop-down box offers the option to select the Total Sample , which means the Total Molarity or Total Concentration , respectively, depending on the selected calculation method.
Acceptance range	These fields are available only if the option Check Quality has been selected.

Enter a minimum and maximum value in the Min. and Max. fields. The quality of the ratio will be considered as "Passed" for samples where the value of the ratio falls within this range, as "Review" otherwise.

Example: Select **Check Quality** and calculation basis **Concentration**, and define a ratio against the **Total Sample** for an area of unwanted fragments, and enter low values for the acceptance range.

Often, it is an iterative process to find out the acceptance range for a certain type of samples. If you find values that work for your samples, save the changes into this or a [new distribution profile](#) for reuse. If the ratio quality is frequently assessed as "Review" although the samples are good enough for downstream application, consider broadening the acceptance range or continuing without a quality check for ratios.

7. Click **OK** to add the new ratio to the list.

Note: Ratios appear in the list in the same order as in the distribution result table.

Note: Ratio names or range values that are too long may not be fully displayed in the list. A tool tip appears with the complete name by hovering the mouse over the truncated name or value.

▼ Ratios

Ratios

Check Quality Show Values

Select calculation basis

Molarity ▼

Ratio Definitions

Small_Total

$$0 \leq \frac{\text{Small (Aol1)}}{\text{Total Sample}} \leq 0.3$$

Large_Total

$$0 \leq \frac{\text{Large (Aol3)}}{\text{Total Sample}} \leq 0.2$$

Add Delete

Ratio Name

Large_Total

Calculate ratio for

Large (Aol3) ▼

Total Sample ▼

Acceptance range

Min. 0

Max. 0.2

OK Cancel

Modifying a ratio.

To delete a ratio:

1. Select the ratio row in the list.
2. Click the **Delete** button and approve the confirmation message.
3. If you deleted the last ratio, uncheck the **Ratios** option at the top of the **Ratios** section.

To modify a ratio:

1. Select the row of the ratio to be modified.
2. Modify the values of the ratio in the editable fields.
3. Click **OK**. The values in the selected row are changed.

Note: Ratios appear in the list in same order as in the distribution result table.

Creating a distribution profile

Note: Distribution analysis features must be active to create a distribution profile. Refer to [Activating distribution analysis features](#) for information on how to activate distribution analysis features.

To create a new distribution profile:

1. Open the **Distribution** tab on the right of the **Analysis** environment.
2. Select a distribution profile from the **Distribution Profile** drop-down box. The selected distribution profile serves as a template for the creation of the new one. Alternatively, select **NewDistributionProfile** to start with an empty profile.
3. Define the distribution profile as needed. Refer to the section [Modifying a distribution profile](#) for details.
4. Save the new distribution profile by clicking the **Save as** button to the right of the **Distribution Profile** drop-down box. Enter a unique distribution profile name and click **OK**.

Note: Only users with assigned user role **Advanced User** can create new distribution profiles.

Removing distribution results

To remove results of a distribution analysis from one or more samples:

1. Select the samples in the **Experiment Explorer**. Refer to the section [Selecting samples](#) for information on how to select multiple samples.
2. Right-click the selection and select **Remove Distribution Analysis Data** from the context menu.

The distribution analysis results for these samples are cleared from the distribution result tables. The electropherograms of the samples are updated because the areas of interest are no longer defined by a distribution profile.

In the experiment explorer, the samples will still appear as "analyzed."

Analysis of RNA samples

This section describes how to analyze an RNA sample. It distinguishes between two different kinds of analyses: size and concentration determination and RNA quality control. For both types of analyses, perform the steps below. Follow the instructions corresponding to the desired type of analysis.

1. Switch to **RNA** mode if this is not already selected. Check the current mode in the bottom right corner of the software screen. If another mode than RNA is selected, select **File/Logout** from the application menu bar to log out and then log in with selected **RNA** mode. For details, refer to section [User authentication](#).

Note: Only users with user role **Advanced User** can modify and save parameters of an analysis profile. Users with user role **Basic User** can select another analysis profile which is more suitable for their type of samples.

2. Switch to the **Analysis** environment by selecting the **Analysis** icon in the main toolbar.
3. If the samples you want to analyze are not yet listed in the **Experiment Explorer** at the left, select the **Load experiment** icon from the Experiment Explorer's toolbar. If the samples are listed but not active (grayed out), right click it's experiment name and select **Activate**. For further details, refer to the [Loading sample data](#) or [Activating an experiment](#) section.
4. To determine the size and concentration of RNA molecules, or to perform quality control for RNA samples with a size marker, follow the instructions of the [Size and concentration determination procedure](#). If quality control for RNA samples without a size marker shall be performed, follow the instructions of the [Peak detection procedure](#).
For both procedures refer to section [Standard RNA analysis](#) for information on which **Analysis** profile should be used as a starting point and which analysis parameters are required for your samples. Follow the [Size and concentration determination procedure](#) or [Peak detection procedure](#) also if samples should have been analyzed during data acquisition process, but either an error message has been shown or sample results are not as expected. In this case, use the procedure to check the analysis step by step and correct if needed. Follow the instructions to reuse the analysis parameters that have been used for the samples.
5. To perform quality control for RNA samples with or without a size marker, perform peak calling. Follow the instructions described in section [Peak Calling](#). For information on which peak calling instruction should be used as a starting point, refer to section [RNA quality control analysis](#).

The result tables summarize all the properties that the QIAxcel ScreenGel Software calculates for detected peaks. Right-click the header line of the table, select **Show column**, and then select the property you are interested in. Alternatively, right-click the header line of the table and select **Show all columns**. This option displays all the properties calculated by the QIAxcel ScreenGel. For more information, refer to section [Result table](#) and sections [Standard RNA analysis](#) and [RNA quality control analysis](#), respectively.

Standard RNA analysis

During the [Size and concentration determination procedure](#) or the [Peak detection procedure](#), select the **Default RNA** analysis profile as a starting point.

The [single electropherogram view](#) is most suitable for checking peak detection. Ensure that the plot shows a red "+" sign at the peak apex for all peaks after the alignment marker peak. If not, click the **Image Options** button of the electropherogram toolbar and select the options **Mark peak apex** and **With Label**, with **Size [nt]** selected. Click **OK** to close the dialog. To switch the sample to be shown in the electropherogram, click on the next sample in the **Experiment Explorer** at the left.

Peak properties are shown in the **Peak Result** table below the electropherogram. For details, refer to the [Result table](#) section. After the [Size and concentration determination procedure](#) has been completed, the single electropherogram views of the analyzed samples will show the size of the detected RNA molecules in nucleotides above the apex of the corresponding peaks.

The correct concentrations can be examined in the peak result table. If the concentrations are not shown by default, right-click the header line of the table, choose **Show column** and then select the **concentration column**, which displays the concentrations in ng/μl.

Ensure that the peak detection has worked as expected. Firstly, it is important that the correct peaks are marked as alignment marker peaks (marked with a green '+') because this is the basis for all other analysis functions. If not, adapt the analysis parameters in the **Analysis** parameters panel on the right side of the **Analysis** environment. To do so, open the **Analysis Properties** section and then open the **Parameters** section. For details on how to change the parameters that are mentioned below, refer to section [Modifying an analysis profile](#).

Note: Collapse and expand parts of the analysis properties by clicking ▼ and ►, respectively.

Analysis Report Peak Calling Properties X

▼ Analysis Properties

Default RNA Save as ...

▼ Parameters

Smoothing Filter	Start	Window
	0.00 min	5 pts
2.50 min	15 pts	
4.00 min	30 pts	
6.00 min	60 pts	

Baseline Filter	Start	Window
	0.00 min	40 sec
5.00 min	100 sec	

Minimum Distance	Start	Value
	0.00 min	5.00 sec

Suspend Integration	Start	End

Threshold	Start	Value
	0.00 min	5.00 S/N

Alignment Marker Threshold 10 S/N

Add Delete

Define Parameter Select Parameter

1 Sample(s) selected Start Analysis

Analysis profile for RNA analysis.

- If the first detected peak is not the alignment marker peak, as a first step, increase the **Alignment marker threshold**. Click on the field and change the value. If this is not sufficient, use the **Suspend Integration** parameter. To do so, click the **Add** button below the parameters list and select **Suspend Integration** from the **Define parameter** drop-down list. Select **Absolute** from the drop-down list next to **End to use the Absolute time unit**. Define the starting point as 0 minutes. Set the ending point of this parameter to shortly before the start of the alignment marker peak (e.g., set end to 2 minutes, if the first alignment marker peak appears at 2.5 minutes). Click the **OK** button to confirm this setting.

- If the analysis profile is too sensitive and detects peaks where there is only noise, increase the **Threshold** (e.g., from 2 S/N to 5 S/N). Click this parameter line and increase the value in the **Value** field in the edit area below the parameters list and click **OK** to confirm.
- If the baseline follows the 28S peak, increase the baseline filter window size for roughly the last third of the migration time. To add a second interval to the baseline filter parameter, click the **Add** button below the parameters list and select **Baseline Filter** from the **Define parameter** drop-down list. Then, e.g., set start to 6 minutes and the window size to 80 seconds. Click the **OK** button to confirm this setting.

Click the **Start Analysis** button again to start a new analysis according to this modified analysis profile.

In some cases, it may be necessary to repeat the adaptations to the analysis profile iteratively. If the peak detection worked as expected with the modified analysis profile, save this analysis profile and try to use this new profile instead of the **Default RNA analysis** profile for future RNA analyses.

RNA quality control analysis

This section provides instructions to investigate the integrity of RNA molecules. The RNA integrity check can be done with or without a size marker. Both approaches are described below.

If the parameters panel is not yet open, open it by clicking on the icon appearing on the right:



Performing quality control of RNA with a size marker

1. Ensure that the [Size and concentration determination procedure](#) has been performed using analysis profile parameters, as described in the section [Standard RNA analysis](#).
2. Switch to the **Peak Calling** tab of the parameters panel and select one of the provided peak calling instructions: Default RNA QC, Default RNA prokaryote, or Default RNA rat_mouse_human.
3. To determine the RNA integrity, select the **RNA Integrity Score** option and choose the 18S peak. To examine the 28S-to-18S-ratio in one sample, select the **Ratio Normalized Area** option and choose the 28S and the 18S peak. For prokaryotic RNA, choose the 23S and 16S peak, respectively. For detailed information on how to define peak calling instructions, refer to [Modifying peak calling instructions](#).

Analysis	Report	Peak Calling	Properties									
Peak Calling Instruction												
*Default RNA QC			Save as ...									
<p>▼ Peaks of Interest</p> <p><input type="checkbox"/> Include size marker samples</p> <p><input type="radio"/> Find centered peak in interval</p> <p><input checked="" type="radio"/> Find highest peak in interval</p> <table border="1"> <thead> <tr> <th>Name</th> <th>Position</th> <th>Tol. [%]</th> </tr> </thead> <tbody> <tr> <td>18 S</td> <td>1869 nt</td> <td>3.00 %</td> </tr> <tr> <td>28 S</td> <td>5025 nt</td> <td>4.00 %</td> </tr> </tbody> </table> <p>Add Delete</p> <p>Name</p> <p>Position <input type="text"/> Size <input type="text"/> Tol. [%] <input type="text"/> %</p> <p>OK Cancel</p>				Name	Position	Tol. [%]	18 S	1869 nt	3.00 %	28 S	5025 nt	4.00 %
Name	Position	Tol. [%]										
18 S	1869 nt	3.00 %										
28 S	5025 nt	4.00 %										
<p>▼ Calculated Columns</p> <p><input checked="" type="checkbox"/> Total Concentration ("Total Conc.")</p> <p><input checked="" type="checkbox"/> RNA Integrity Score ("RIS")</p> <p>Ref. Peak <input type="text" value="18 S"/></p> <p><input checked="" type="checkbox"/> Ratio Normalized Area ("Ratio")</p> <p>Ratio <input type="text" value="28 S"/> / <input type="text" value="18 S"/></p> <p><input type="checkbox"/> Relative Abundance</p>												

Peak calling instruction for RNA QC.

4. In the gel image overview, select all samples.
5. Click the **Start Peak Calling** button appearing at the bottom of the **Peak Calling** tab on the right.

6. Inspect the peak calling result in the peak calling result overview.



Each row in this table represents the peak calling result for one sample. The RNA integrity score is given in the column **RIS**. The 28S-to-18S-ratio, is given in the column **Ratio**. In addition, the total concentration of RNA is given in the column **Total RNA concentration**. Furthermore, for the 18S and 28S peak, it is listed whether or not this peak was found, based on the criterion given in the peak calling instruction. For detailed information on the peak calling result table, refer to [Peak Calling](#).

Performing quality control of RNA without the size marker

1. Ensure that the [Peak detection procedure](#) has been performed using analysis profile parameters as described in the section [Standard RNA analysis](#).
2. Switch to the **Peak Calling** tab of the parameters panel and select one of the provided peak calling instructions: Default RNA QC, Default RNA prokaryote, or Default RNA rat_mouse_human.
3. As the analysis was performed without the reference marker, adapt the peak calling instruction to search for peaks based on relative migration time instead of size. Click on the line of the 18S peak and update the position criterion in the parameter area below. Set the **Position** value to an average of the relative migration times that is shown in the result tables for the 18S peak of the selected RNA samples and change the unit from **Size** to **Rel. Time** in the drop-down list. Confirm this setting by clicking the **OK** button. Adjust the tolerance parameter, if the relative migration times differ from sample to sample. Do the same for the 28S peak. For prokaryotic RNA, change the 23S and 16S peak, respectively. For detailed information on how to define peak calling instructions, refer to section [Modifying peak calling instructions](#).
4. To determine the RNA integrity, select the **RNA Integrity Score** option and choose the 18S peak. To examine the 28S-to-18S-ratio in one sample, select the **Ratio Normalized Area** option and choose the 28S and the 18S peak.
5. In the gel image overview, select all samples.
7. Click the **Start Peak Calling** button appearing at the bottom of the Peak Calling tab on the right.
8. Inspect the peak calling result in the peak calling result overview.



Each row in this table represents the peak calling result for one sample. The RNA integrity score is given in the column **RIS**. The 28S-to-18S-ratio, is given in the column **Ratio**. In addition, the total concentration of RNA is given in the column **Total RNA concentration**. Furthermore, for the 18S and 28S peak, it is listed whether or not this peak was found, based on the criterion given in the peak calling instruction. For detailed information on the peak calling result table, refer to section [Peak Calling](#).

Manually modifying analysis results

The QIAxcel ScreenGel Software algorithms analyze the data fully automatically. The user can only influence the automated analysis through the analysis parameters.

After the analysis, the results can be modified manually by the user.

Modifying the threshold

In the single electropherogram view, the threshold parameter can be interactively changed by moving the threshold with the mouse. When doing so, the sample is reanalyzed using the analysis parameters of the sample properties and the new threshold value.

Deleting a peak

Deleting a peak is possible in the **Single Electropherogram View** only.

To delete a peak, proceed as follows:

1. Switch to the **Single Electropherogram View**.
2. Right-click the top of the peak in the electropherogram and select **Delete Peak** from the context menu that appears. The peak will be deleted.

To delete multiple peaks, proceed as follows:

1. Switch to the **Single Electropherogram View**.
2. Using the **Ctrl** key, left-click the top of the peaks to be deleted in the electropherogram.
3. Right-click in the electropherogram and select **Delete Selected Peaks** from the context menu that appears. The peaks will be deleted.

Note: After new analysis, deleted peaks may be detected again depending on the analysis parameters. Repeat the steps above to delete them again.

Note: A peak can be deleted by users with the assigned user roles **Basic User** and **Advanced User** only.

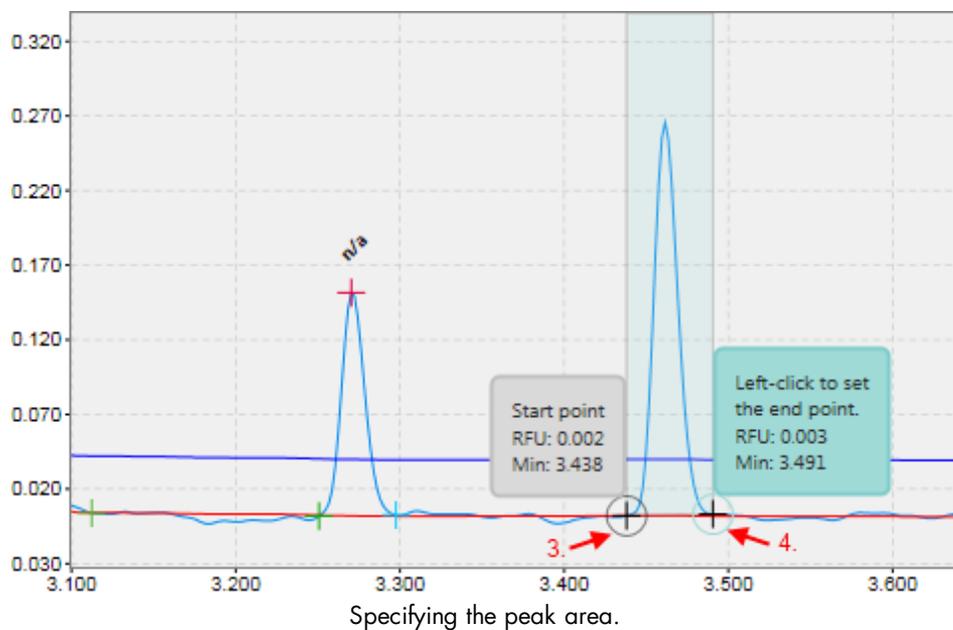
Adding a peak

Adding a peak is possible in the **Single Electropherogram View** only.

To add a peak, proceed as follows:

1. Switch to the **Single Electropherogram View**.
2. Right-click the electropherogram and select **Insert Peak** from the context menu that appears.
3. A marker is displayed that moves along the signal while the mouse is being moved. Move the marker to the left border of the peak that is to be added. Left-click to set the left border.

4. Accordingly, left-click to set the right border of the peak to be added. If a peak can be found in the marked area, the peak is added to the result table and the visualization is updated.



Note: Adding a peak before the first alignment marker peak or after the second alignment marker peak is only possible if the signal rises above the alignment marker threshold in the corresponding region.

Note: If the sample was analyzed with smear analysis, a new smear peak can be added as described above. The newly inserted peak may not overlap with the area of interest of another peak.

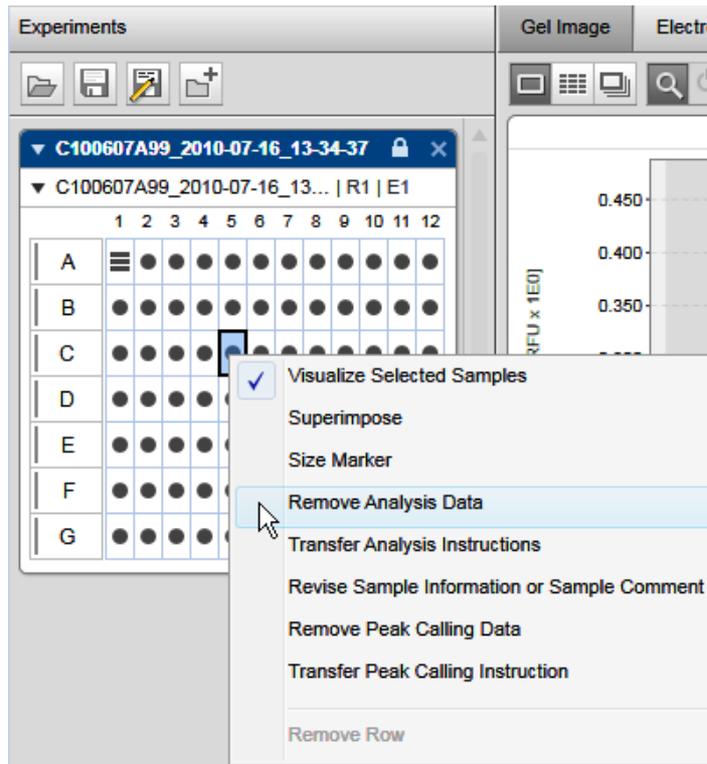
Note: A peak can be added by users with the assigned user roles **Basic User** and **Advanced User** only.

Removing analysis results

Removing the analysis result from samples is only possible using the **Experiment Explorer**.

To remove the analysis result from samples:

1. Select the samples in the **Experiment Explorer**. Refer to the [Selecting samples](#) section for information on how to select multiple samples.
2. Right-click the selection and select **Remove Analysis Data** from the context menu that appears.



Removing the analysis result of C5.

The result tables for these samples become empty. The representation of the sample in gel image and electropherogram view is updated: all peak annotations as well as baseline and threshold lines disappear.

If peak calling or distribution analysis was performed on the samples, the peak calling or distribution result tables for these samples also become empty and the samples are removed from the peak calling or distribution overview tables.

Note: To restore peak calling or distribution analysis results, reanalyze the samples with an analysis profile and reference marker, and repeat the peak calling or distribution analysis.

Refer to the sections [Peak Calling](#) and [Removing distribution results](#) for information on how to remove peak calling results or distribution analysis results independently.

Note: Only users with the assigned user roles **Basic User** and **Advanced User** can remove analysis results.

Checking alignment marker

To check the alignment marker of a sample:

1. Select the sample in the **Experiment Explorer**.
2. View the sample properties at the right side of the **Analysis** environment, in the **Analysis Instructions** panel. Refer to [Inspecting sample properties](#) for detailed information about how to view the properties.
3. Check if the alignment marker of the sample is correct. If not, the alignment marker of a plate can be changed. In the **Experiment Explorer**, right click the plate name. Select the context menu option **Overwrite alignment marker**. Select the correct alignment marker in the **Overwrite Marker** dialog that appears and confirm by clicking **OK**.

Note: Upon switching from one alignment mode to another (two alignment marker peaks vs. one alignment marker peak), the analysis data of the plate will be removed and the samples must be analyzed again.

Note: To ensure analysis compatibility, the reference marker drop-down list contains only reference marker tables that match the alignment marker of the samples.

Modifying areas of interest

In the single electropherogram view, if the sample was analyzed with a smear analysis profile and at least one smear peak was detected, the borders of the area of interest for each peak can be interactively changed. To do so, use the mouse to click and drag the pink vertical lines indicating the area borders to the desired position. The lines may be moved independently of any peak start or end point.

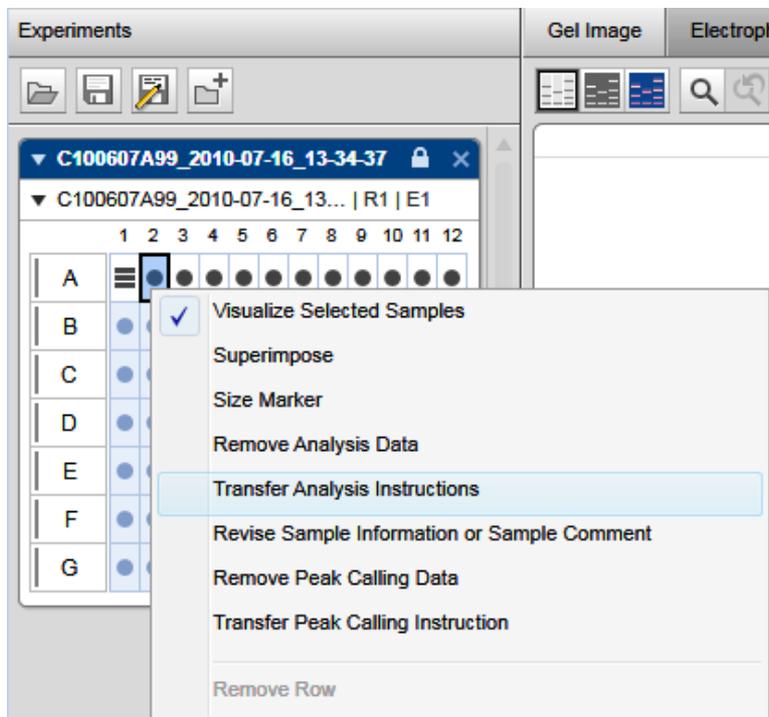
Note: Area of interest may not overlap. Thus, it is not possible to drag a vertical line into the area of interest of another peak.

After moving a border, the properties corresponding to the given area of interest are recalculated using the newly defined borders.

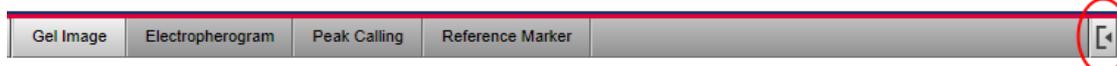
Reusing used analysis parameters

It is possible to reuse the analysis parameters of an analyzed sample.

1. Right-click the sample in the [Experiment Explorer](#).



2. Select one of the following options to transfer the parameters used for analysis of the sample into the toolbar on the right-hand side of the **Analysis** environment. If the toolbar on the right is not displayed, open it by clicking on the following icon:



Transfer Analysis Instructions

The option is available only if the sample has been analyzed.

The analysis profile and its parameters used for [peak detection](#) and the reference marker table used for [size and concentration determination](#), if present from the sample, will be transferred to the **Analysis** tab of the toolbar.

Transfer Peak Calling Instruction

The option is available only if peak calling has been performed on the sample.

The peak calling instruction that has been used with this sample for [peak calling](#) will be transferred to the **Peak Calling** tab of the toolbar

Transfer Distribution Profile

For **DNA** mode only. The option is available only if distribution analysis has been performed on the sample.

The distribution analysis profile that has been used with this sample for [distribution analysis](#) will be transferred to the **Distribution** tab of the toolbar.

Note: It is not possible to perform peak calling and distribution analysis in the same experiment. Thus, either a peak calling instruction or a distribution profile is applied to a sample, but never both.

Note: Only users with the assigned user role **Advanced User** can use these options. However, the parameters used with the sample can also be viewed in the [Properties](#) tab.

Reanalysis of multiple experiments

QIAxcel ScreenGel provides the possibility to analyze multiple experiments in the same way, without needing to open each experiment manually.

This section describes how to perform so called batch processing of experiments.

To perform batch processing of experiments proceed as follows:

1. In the **Analysis** environment, select **Batch** experiment processing in the **File** menu. The **Batch Processing** dialog will appear.
2. At the top of the dialog, select the directory containing the experiments to analyze. Click  and in the appearing dialog, navigate to and highlight the relevant directory. Click **OK**. The directory path should appear in the upper text field and the experiments contained in that folder should be listed in the lower text field.
3. Use the radio buttons below the directory path to indicate if all experiments in this folder and its subdirectories should be processed, or if only selected experiments should be processed. If the second option is chosen, select the experiments to process. Use the **Shift** or **Ctrl** key to select multiple experiments. **Ctrl+A** selects all entries.
4. Select the profiles to be applied to the selected experiments.

If a new analysis should be performed for the experiments, select the corresponding analysis profile from the drop-down list. For more details about the analysis of samples, see [Peak detection](#). Details about how to define a new analysis profile are available in [Modifying an analysis profile](#). If no analysis profile is selected, no new peak detection will be performed.

If a reference marker should be applied during analysis of the experiments, select the corresponding reference marker from the drop-down list. For details about the application of a reference marker, see [Size and concentration determination](#). Details about how to define a new reference marker are available in [Creating a reference marker](#). A reference marker can only be applied during analysis. Therefore, if a reference marker was chosen, batch processing can only be started if an analysis profile is also selected.

Note: Ensure that all selected experiments are run with the same alignment marker. Otherwise, the reference marker cannot be used for certain experiments.

If a new peak calling should be performed for the experiments, select the corresponding peak calling profile from the drop-down list. For details about peak calling, see [Peak Calling](#). Details about how to define a new peak calling profile are available in [Creating a new peak calling instruction](#). If no peak calling profile is selected, no peak calling will be performed.

If the results of the batch processing should be stored in a report, select the corresponding report profile from the drop-down list. The report/export will be written to the default report/export output path. For details about the report and export functionality, see [Report/Export](#). Details about how to define a new report profile are available in [Modifying a report/export profile](#). If no report profile is selected, no report will be created.

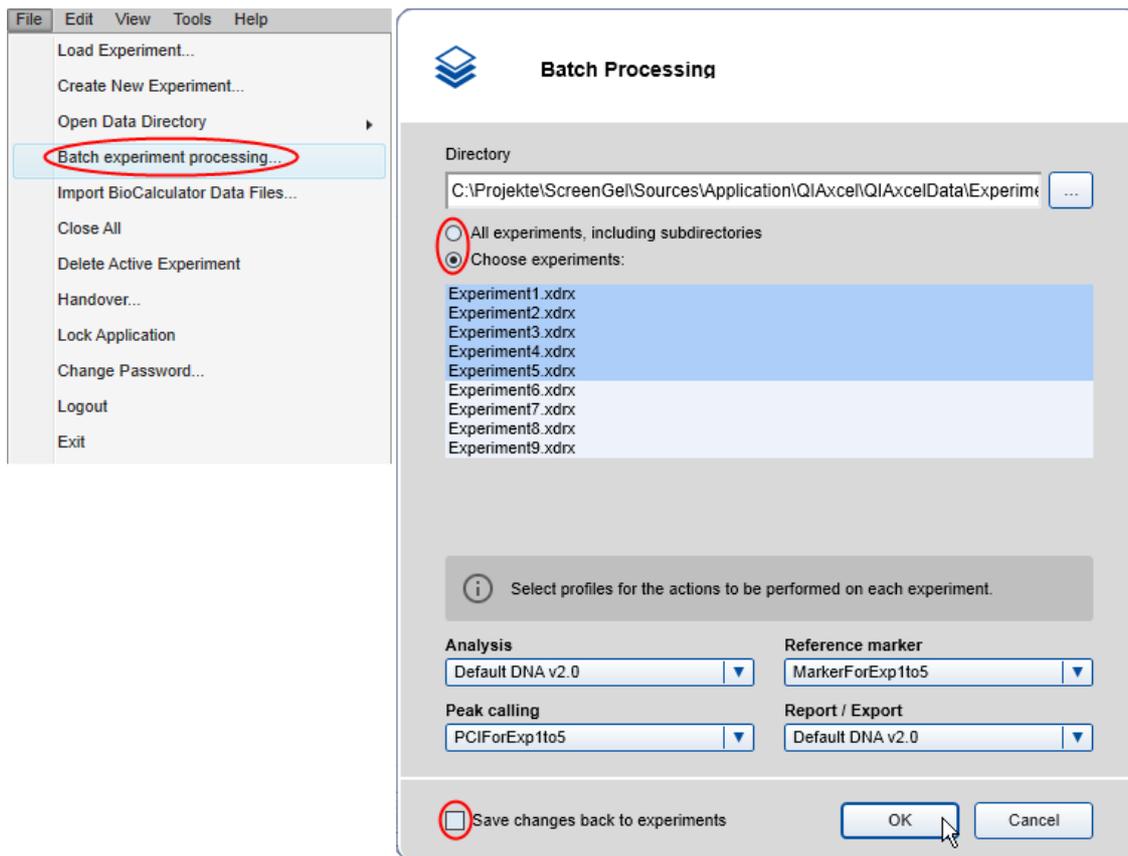
Note: If the **Use Images as Displayed** option is selected in a report/export profile, it will not be listed in the **Report/Export Profile** drop-down list. This option is not available for batch processing.

5. Check the box at the bottom of the dialog if the processed experiments should be overwritten with the results from the batch processing.

Note: Data in processed experiments may be lost if overwritten by results from the batch processing.

Note: If an experiment to be processed is open in the QIAxcel ScreenGel Software and the **Save changes back to experiments** option is checked, the results will not be written to the open experiment. When checking this option, ensure that all affected experiments are closed.

Note: If problems are encountered during processing, a warning message will appear at the end listing any issues that occurred (e.g., the analysis parameters do not fit the data).



Analyzing and reporting five experiments with size determination and peak calling.

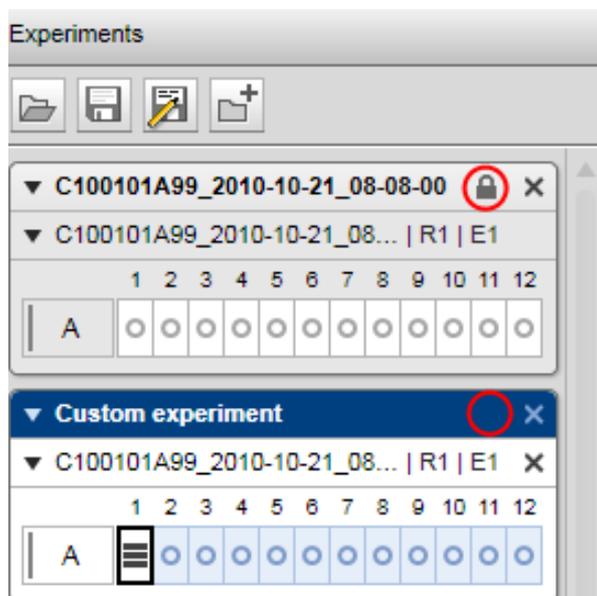
Customizing experiments

Experiments are created automatically from every process. Additionally, the user can create and modify experiments. This allows the user to compare samples from different experiments, and even different processes.

Note: Creating and modifying customized experiments requires the user role **Advanced User**.

A customized experiment may contain single rows or groups of rows as well as plates. However, within the experiment all rows will be still grouped in plate(s). Every time a row or plate is added to an experiment you get a copy of it. This means that the source experiment, from which the row/plate originates, will remain unaffected by all changes within the target experiment.

Note: You can modify the composition of customized experiments only. The composition of an experiment, which is the automatic result of a process, cannot be modified (see the image below).



Run results are marked with a padlock symbol. Custom experiments are not marked.

For general information about handling experiments and the **Experiment Explorer**, see the [Handling samples and experiments](#) section.

Creating a new experiment

To create a new customized experiment:

1. Click  at the top of the **Experiment Explorer**.
 2. Enter a unique name for the new experiment into the edit field of the dialog that appears and click **OK**.
- Important:** The experiment name cannot be changed later.
3. A new empty experiment will be created and displayed in the **Experiment Explorer** as the last experiment, at the bottom.

Use the scrollbar of the **Experiment Explorer** if the new experiment is outside the view. The new experiment will be activated automatically. If the previously active experiment was modified, the system asks you whether to save the changes or not. For more details about activating and deactivating, see the [Activating an experiment](#) section.

Refer to the [Modifying an experiment](#) section for information on how to collect samples for the new experiment.

Note: The composition of this experiment can be modified at any time, in comparison to experiments automatically generated by a process.

Note: New experiments can be created by users with the assigned user role **Advanced User** only.

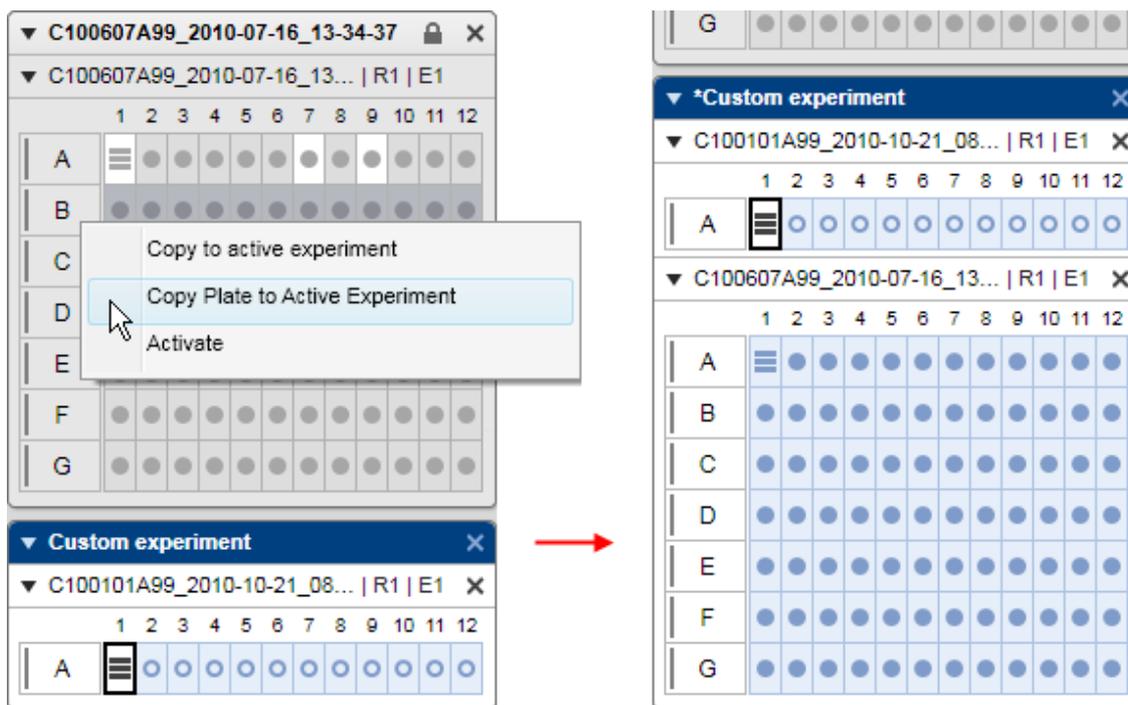
Modifying an experiment

If a customized experiment should be modified, make sure that it is activated. For more details about activating an experiment, see the [Activating an experiment](#) section.

Note: Only the composition of customized experiments can be modified. The composition of an experiment that is the automatic result of a process cannot be modified, and therefore the context menu options described below are disabled.

To modify an experiment:

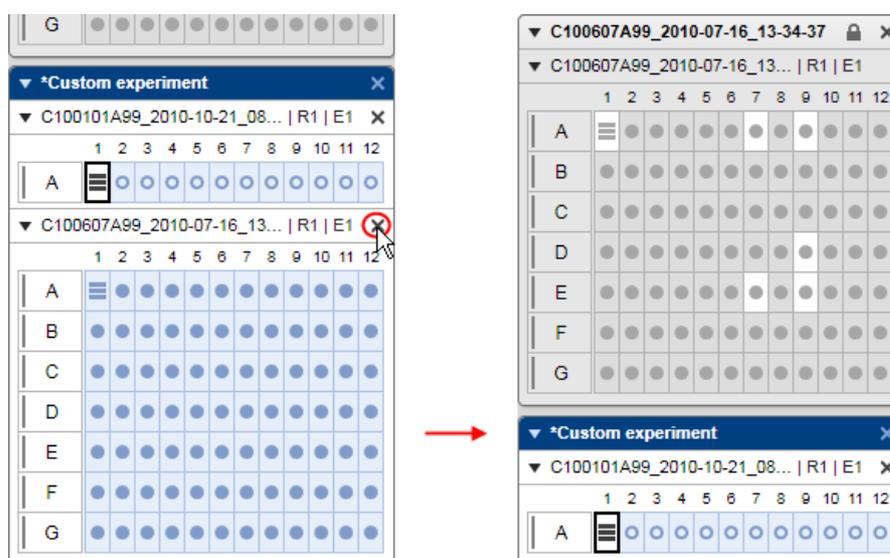
1. Load the source experiment that contains the samples. For further details on loading, see the [Loading samples](#) section.
2. Create or activate the experiment that is to be customized in the **Experiment Explorer**.
3. Expand the source experiment so that the required plates and rows are visible. The experiment can be expanded without activating. For more details about expanding, see the [Expanding and collapsing](#) section.
4. Modify the experiment as required:
 - To add a plate to the active experiment, right-click the plate to add and select the context menu option **Copy Plate to Active Experiment**. A copy of the plate will be created and added to the active experiment at the bottom.



Adding a plate to the active experiment.

Note: The complete plate will be copied to the experiment, but the original plate stays unchanged. Any further modification of this plate in the active experiment does not affect the original plate.

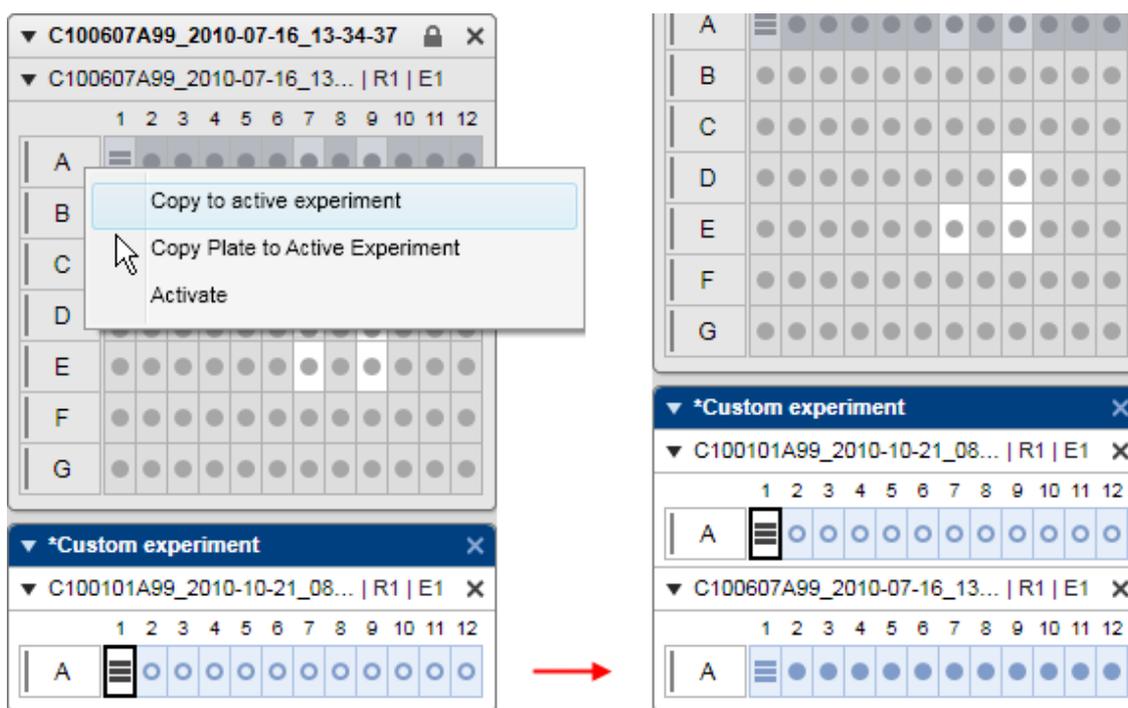
- To remove a plate from the active experiment, click the **Close** button of the plate. The plate will disappear from the experiment.



Removing a plate from the active experiment.

Note: This plate will be removed only from the active experiment, but the original plate remains unchanged.

- Adding a row is similar to adding a plate. Place the mouse cursor over the row to add to the active experiment and select the menu item **Copy to Active Experiment**. To preserve the context of the row, a copy of its plate will be created and added to the active experiment containing a copy of the selected row. If you add another row from the same plate to the active experiment, a copy of the row will be created and added to the copy of the plate inside the active experiment. Multiple rows of the same plate can be added in a similar way, but by simultaneously holding the **Shift** or **Ctrl** key during selection.

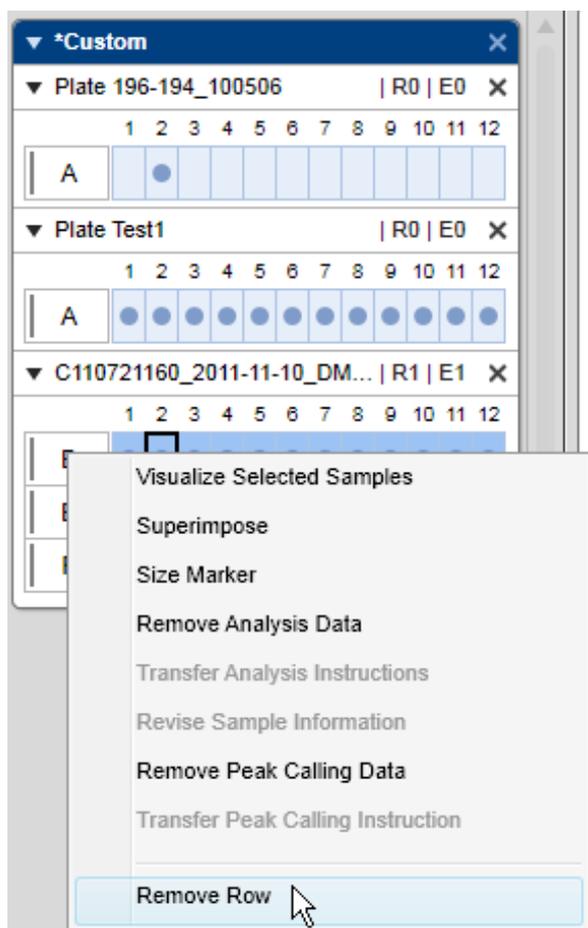


Adding a row to the active experiment.

Note: A row can be located in the experiment only once.

Note: Individual samples cannot be added to the active experiment. Add the complete row instead, but visualize the required samples only.

- To remove a row from the active experiment, right-click the row letter and select the option **Remove Row** from the context menu. The row will be removed from the active experiment. If the plate contains only one row, you cannot remove it; instead, please remove the plate.



Removing a row from the custom experiment.

Report/Export

The **Analysis** environment provides a flexible and powerful tool for reporting (**RTF** or **PDF** format) and data export (**XML** format).

For convenient reuse, corresponding report and export configurations can be stored together in report/export profiles. Thus, both reporting and data export may be integrated to form a fully automated process by including a report/export profile into a process profile.

You can specify which information has to be included in the report and export individually. The report and export files can be customized to suit your needs.

Each report contains of two main sections:

- The overview section for information about all samples, such as a gel overview
- The sample details section for detailed information about each sample

In the sample details section, the information related to each sample is reported for each sample grouped in the following subsections:

- Sample Header
- Sample Graphics
- Result Table
- Run Parameter
- Analysis
- Reference Marker

The order of the samples is the same as in the view.

For further details on customizing reports and export, see the [Modifying a report/export profile](#) section.

Generating a report

The basic procedure of manually generating a report in the **Analysis** environment is as follows:

1. Load the samples using the **Experiment Explorer**.
For further details on loading sample data, see section [Loading sample data](#).
2. Inspect the samples before reporting.
See the [Viewing sample data](#) section for more details on data inspection.
For this step, the **Gel view** or the **Electropherogram** overview are especially useful.
3. Select the samples you want to report.
For further details on selecting samples, see section [Selecting samples for analysis or report](#)
4. Select report settings and start reporting.

On the right-hand side of the **Analysis** environment, the report toolbar can be found.

If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:



Select the **Report** tab of the toolbar.

Select a predefined report/export profile. The report settings of the selected profile are shown below the drop-down list. For details, refer to the [Report options](#) section.

Make sure that at least one of the report formats **PDF** or **RTF** is selected. Additionally, ensure that at least one of the options (**Overview** or **Sample Details**) is selected. If not, select another predefined report/export profile. (Users assigned the user roles **Advanced User** or **Basic User** may modify the settings as they wish.)

Specify the directory where the report files will be saved (refer to section [Modifying a report/export profile](#) for information on how to specify the report directory).

Click the **Start Report/Export** at the bottom of the **Report** tab to start reporting.

Note: The button **Start Report/Export** is disabled if no samples are selected in the view (see Step 3).

The report files will be generated automatically and stored in the specified directory.

If you have selected the **Print report** option the report will be printed on the default printer.

Note: Ensure that you have defined a default printer on your system.

5. Inspect the report files.

If the options **Display Report** and **PDF** were selected, the generated report will be opened automatically in the default PDF reader.

Report options

The report/export settings are divided into two groups:

- **Report Options;** contains the report settings
- **Export Options;** contains the export settings

Note: You can collapse and expand each group by clicking ▼ and ► to the left of the group name.

Report Options

▼ Report Options

Directory

application\QIAxcel\QIAxcelData\Report ...

Save to origin experiment directory

Format

PDF RTF

Options

Display Report Print Report

Use Images as Displayed

Overview

Sample Details

Report options.

The options are described below:

Directory	Select the directory in which the generated report file should be stored by clicking  . In the dialog that appears, navigate to the correct directory and click OK .
Save to origin experiment directory	Check this option to save the report in the same directory as the experiment. If this option is checked, any selected path in Directory will be ignored.
PDF	A file in PDF format will be generated.
RTF	A file in RTF format will be generated. You can select both formats.
Display Report	If you select this option and the format option PDF is selected, the generated report will be displayed automatically using the default PDF reader.
Print Report	If you select this option the generated report file(s) will automatically be sent to the default printer. Note: Ensure that you have a default printer on your system.
Use Images as Displayed	Use this option to obtain images that look similar to the presentation in the QlAxcel ScreenGel Software regarding alignment, scales, labels, zoom, etc. Note: This option is available in the analysis environment only, it may not be used in a process profile.
Overview	The report contains of an overview section.
Sample Details	The report contains of a sample section.

Note: If one of the check boxes **PDF** or **RTF** is checked, the report/export profile is valid only if either the **Overview** or **Sample Details** check box is selected additionally.

Overview section

If the **Overview** option is selected, the following information is included automatically to the overview section of the report:

Report Date	Date and time of report generation.
Experiment Name	Name of the experiment the sample data belong to.
Cartridge ID	ID(s) of the cartridge(s) that the samples were processed with.
Cartridge Expiration Status	This information is automatically included if the cartridge has exceeded its expiration date.
Calibration Status	Calibration status of the cartridge(s) at process time.
Instrument ID	Serial number of the instrument(s) used to process the samples.
Data Acquisition Status	Only in case of an incomplete experiment . Gives information about planned and performed runs (e.g., 2 out of 8 runs performed successfully).

Corrupt Experiment Accepted by Only in case of an incomplete experiment, which was accepted by a user. Name of the user who has accepted the experiment.

Corrupt Experiment Accepted on: Only in case of an incomplete experiment, which was accepted by a user. Date and time when the experiment was accepted.

Select the following optional information that you want to include into the overview section:

Overview

- Experiment Plate Comment
- Reported by
- Experiment Path
- Lot Information
- Peak Calling Result Table
- Overall Result Table
- Overall Smear Result Table
- Gel Image Overview
- Electropherogram Overview
- Electropherogram Superposition View

Optional overview information.

Overview

- Experiment Plate Comment
- Reported by
- Experiment Path
- Lot Information
- Peak Calling Result Table

Result Table Columns	
<input checked="" type="checkbox"/>	Sample Information
<input checked="" type="checkbox"/>	Found
<input type="checkbox"/>	Size
<input type="checkbox"/>	Concentration
<input type="checkbox"/>	Molarity

Calculated Columns (if present)

Peak Calling Instruction Table

Special options for Peak Calling Result Table.

Overview

- Experiment Plate Comment
- Reported by
- Experiment Path
- Lot Information
- Peak Calling Result Table
- Overall Result Table
- Overall Smear Result Table
- Gel Image Overview

Image options ...

- Electropherogram Overview
- Electropherogram Superposition View

Special options for Gel Overview.

Overview

- Experiment Plate Comment
- Reported by
- Experiment Path
- Lot Information
- Peak Calling Result Table
- Overall Result Table
- Overall Smear Result Table
- Gel Image Overview
- Electropherogram Overview

Image options ...

- Electropherogram Superposition View

Special options for Electropherogram Overview.

The optional fields are described next.

Note: If a result table option but no result table column is selected, the check box is marked yellow, and the report/export profile is invalid.

Experiment Plate Comment	Experiment plate comment.
Reported by	The ID of the user who generated the report/export.
Experiment Path	The path where the experiment is stored.
Sample List	All samples of a plate are listed with position, sample information and comment. If the experiment contains samples from different plates, a sample list is included for each plate.
Lot Information	The entered lot numbers will be included.
Distribution Analysis Result Table	Use this option for a distribution analysis in DNA mode to include the distribution analysis result overview table. Each row in the table represents a sample. Note: This option is available only if distribution analysis features are active. Additional options to select are:
Show Profile Properties	Include the parameters of the distribution profile that was applied to the samples.
Sample Information	Include the Sample Information column.
Total Concentration	Include the column Total Concentration of the sample.
Total Molarity	Include the column Total Molarity of the sample.
Sample Quality	Include the Sample Quality column. This is the overall quality assessment of the sample, generated in the distribution analysis.
Aol Concentration	Include the Concentration column for each area of interest.
Aol Molarity	Include the Molarity column for each area of interest.
Aol Height	Include the Height column for each area of interest.
Aol Height Check	Include the Height Check column for each area of interest. This is the quality assessment of the height of the area of interest.
Ratio	Include the Ratio column for each defined ratio. Based on the selected calculation method, the column will show molarity or concentration ratio.
Ratio Quality	Include the Ratio Quality column for each defined ratio. This is the quality assessment of the ratio.

Note: If a report includes too many areas of interest or ratios, the table is split between two areas of interest or ratios. Sample information, total concentration, total molarity and sample quality columns appear only in the first table. The remaining tables are marked with "(continued)" in the header.

Note: If samples are selected to which different distribution profiles were applied, a new table is generated for each distribution profile. Furthermore, if samples from different plates are selected, a new table is generated for each plate.

Note: Cells with the value "Review" are highlighted in the report.

Peak Calling Result Table

The peak calling result overview table will be included. Each row in the table represents a sample. Additional options can be selected (see picture above).

Note: This option is available only if peak calling features are active.

Peak Calling Instruction Table Select this option to include the peak calling instruction table to the peak calling result overview table.

Sample Information Select this option to include the **Sample Information** column in the peak calling result overview table.

Found Select this option to include the **Found** column for each peak of interest to the peak calling result overview table.

Size Select this option to include the **Size** column for each peak of interest in the peak calling result overview table.

Concentration Select this option to include the **Concentration** column for each peak of interest in the peak calling result overview table.

Molarity Select this option to include the **Molarity** column for each peak of interest in the peak calling result overview table.

Note: Calculated columns (such as Ratio, RIS) are automatically included, if they are part of the applied peak calling instruction.

Note: If there are too many peaks of interest, the table is split between two peaks of interest, The sample info and the calculated columns appear only in the first table, the following tables are marked with "(continued)" in the header.

Note: If samples to which different peak calling instructions were applied are selected, a new table starts for each peak calling instruction. Additionally, if samples from different plates are selected, a new table starts for each plate.

Overall Result Table

Select this option to include a table that presents size and/or concentration and/or molarity results from all samples of a plate. A sub-table is included in the overall table for each selected sample. Sample position on the plate and, if available, sample information appear as the header of each sub-table. Each sub-table has as columns the result values that were selected for reporting. Each row then lists a detected peak and the corresponding results (size and/or concentration and/or molarity).

Note: If samples from different plates are selected, a new table starts for each plate.

Overall Smear Result Table For a smear or gDNA analysis in **DNA** mode, use this option to include an overview smear result table, including selected smear result properties.

If samples from different plates are selected, a new table starts for each plate. Each row in the table represents a sample.

Select each table column to specify the result values to display: Median Size, Conc. Area of Interest, Mol. Area of Interest, % NA Area of Interest, or % Conc. Area of Interest.

Note: The columns of the **Smear Result Table** can be selected and reordered as described for **Result Table** (below).

Select the options **Total Concentration** and **Total Molarity** to include the values for total concentration or total molarity of the sample.

Gel Image Overview Select this option to include the gel image of all selected samples.

Click the **Image** options button to specify the appearance of the gel image overview. Image options are described below.

Note: The **Image** options button is disabled if the **Use Images as Displayed** option is selected.

Note: The gel image in the report will have the left-hand y-axis on both sides, also if the **Use Images as Displayed** option is selected.

Unit of the y-axis

If you select **Size**, the y-axis will show a size scale based on the reference marker on both sides of the gel image, also if the **Use Images as Displayed** option is selected. The lanes in the gel image will be aligned according to the alignment markers.

Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, a corresponding message will appear.

If you select **Rel. Time**, the y-axis will show relative migration time. The lanes in the gel image will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the lanes cannot not be aligned and the y-axis will display a corresponding message.

If you select **Abs. Time** [min], the lanes will not be aligned and the y-axis will show an absolute time scale.

Zoom to Alignment Marker	<p>Select this option to scale the lanes so that the lanes start with the lower alignment marker band and end with the upper alignment marker band (crop data outside of the alignment markers).</p> <p>Note: This is possible only if all samples are analyzed.</p>
Individual Scaling	<p>Select this option to auto-scale the contrast for each gel lane individually.</p>
Show sample information	<p>Select this option to include the sample information in each lane.</p>
Show plate ID	<p>Select this option to display the plate ID, the repeat number, and the entry number of each lane.</p>
Show method	<p>Select this option to display the applied method above the sample lane.</p>
Gel Layout	<p>Use this option to determine the gel layout.</p> <p>Select Standard layout to order the lanes from left to right, as they are ordered in the view.</p> <p>Select Horizontal plate layout to order the lanes starting with A1 at the upper left and ending with H12 at the lower right.</p> <p>Select Vertical plate layout to order the lanes starting with H1 at the upper left and ending with A12 at the lower right.</p> <p>Select Reverse vertical plate layout for the vertical plate layout but starting with A1 at the upper left and ending with H12 at the lower right.</p> <p>Select Split plate layout to split the vertical plate layout. The left portion will start with H1 at the upper left and end with A6 at the lower right. The right portion will start with H7 at the upper left and end with A12 at the lower right.</p> <p>Note: Positions for samples not selected remain empty.</p>
Lanes per Row	<p>Use this option to specify the number of lanes per row: 4, 6, 8, 12, 16, 24, 32, 36, or 48.</p> <p>Note: This option is available only if Standard layout is selected in the Gel Layout option.</p>
Rows per Page	<p>Use this option to specify the number of rows to be included on one report page (a page split is introduced after the specified number of rows).</p> <p>Note: This option is not available if Standard layout is selected in the Gel Layout option.</p>

Analysis details	Select Highlight alignment markers to highlight in green the bands of the alignment marker peaks.
Electropherogram Overview	<p>Select this option to include an electropherogram overview of all selected samples. The order is the same as in the view. One gallery overview page with no more than 12 electropherograms will always be printed on one report page.</p> <p>Click on the Image options button to specify the appearance of the reported electropherogram overview. Image options are described below.</p> <p>Note: The Image options button is disabled if the Use Images as Displayed option is selected.</p>
Unit of x-axis	<p>If you select Size, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers.</p> <p>Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will display a corresponding message.</p> <p>If you select Rel. Time, the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers.</p> <p>Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will display a corresponding message.</p> <p>If you select Abs. Time [min], the electropherograms will not be aligned and the x-axis will show an absolute time scale.</p>
Zoom to Alignment Marker	<p>Select this option to scale the electropherograms so that the electropherograms start with the lower alignment maker peak and end with the upper alignment marker peak (crop data outside of the alignment markers).</p> <p>Note: This is possible only if all samples are analyzed.</p>
Individual Scaling	Select this option to auto-scale the y-axis for each electropherogram individually.
Show sample position	Select this option to display the sample position at the top of each electropherogram.

Show sample information	Select this option to display the sample information at the top of each electropherogram.
Show plate ID	Select this option to display the plate ID at the top of the electropherogram.
Show method	Select this option to display the applied method at the top of each electropherogram.
Show analysis details	Select this option to show analysis details for the analyzed samples. Select Mark detected peaks to display the apex markers of detected peaks. Note: In DNA mode, a second option Show median of size is available. If the sample was analyzed with a DNA smear analysis profile , select this option to display the markers with the median size of detected smear peaks. Select Show suspend integration intervals to display the suspend integration intervals.

Electropherogram Superposition View

Use this option to include the superposition electropherogram of all selected samples which have the superimposed flag set.

Note: The superposition view is restricted to 12 samples. In process environment and in batch processing, the superposition is created only if the experiment contains 12 samples or less.

Note: Use the **Use Images as Displayed** option to report the electropherogram superposition as displayed.

Click the **Image** options button to specify the appearance of the reported electropherogram superposition. Image options are described below.

Note: The **Image** options button is disabled if the **Use Images as Displayed** option is selected.

Unit of x-axis

If you select **Size**, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers.

Note: The size scale can be created only if all superimposed samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will show a message, instead.

If you select **Rel. Time**, the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all superimposed samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will show a message, instead.

If you select **Abs. Time** [min], the electropherograms will not be aligned and the x-axis will show an absolute time scale.

Zoom to Alignment Marker

Select this option to scale the electropherograms, so that the electropherograms start with the lower alignment maker peak, and end with the upper alignment marker peak, if available (crop data outside of the alignment markers).

Note: This is possible only if all samples are analyzed.

Show Electrical Current Curve

Select this option to include a diagram of the superimposed electrical current measured during data acquisition. The electrical current curve will appear below the electropherogram superposition, aligned with the x-axis.

Show size marker peak labels

If this option is selected, and if exactly one size marker is among the superimposed samples, the peak labels will be displayed for the detected peaks of the marker sample. Select the units for the peak labels in the drop-down list.

Note: In **RNA** mode, if you want the 28S/18S ratio or the RIS to be included in the report, select the overview option **Peak Calling Result Table** (refer to [Analyze RNA samples](#) for information on how to analyze RNA samples).

Sample details section

The following information is included automatically for each sample:

Information	Description	Report section
Experiment Name	Name of the experiment the sample data belong to.	Sample header
Plate ID	ID of the plate the sample belongs to.	Sample header
Position	Sample position on the plate.	Sample header

Run Number	If the same sample was processed multiple times, this number identifies the run that produced the sample data (for detailed information, refer to Run parameters and result structure).	Sample header
Run Entry Number	The run entry number of the plate (for detailed information, refer to Run parameters and result structure).	Sample header
Run Date	Date and time the process was started.	Run
Instrument ID	Serial number of the instrument the sample was processed with.	Run

Select the following optional information that you want to include in the sample section:

Sample Details

- Start Results on New Page
- Experiment Plate Comment
- Run Information
- Method Information
- Cartridge Information
- Sample Information
- Analysis Parameter
- Reference Marker Table
- Single Electropherograms
- Single Gel Images
- Lot Information
- Result Table
- Peak Calling Result Table
- Smear Result Table

Optional sample details.

Note: If a result table option but no result table column is selected, the check box is marked yellow, and the report/export profile is invalid.

The optional fields are described below:

Start Results on New Page	If you select this option, the results for each sample will start on a new page.
Experiment Plate Comment	If you select this option, the experiment plate comment is included in the Sample Header section.
Run Information	If you select this option, the following information is included in the Run section of the sample:
Rise time	The parameter for the applied Bessel filter (see also Settings).
Applied injection time	The applied sample injection time. Note: This time can differ from the methods sample injection time if there was another sample injection time specified in the process profiles run parameters. (see Selecting run parameters).
Applied separation time	The applied separation time during method run. Note: This time can differ from the methods separation time if the user adjusted the separation time during run.

	Processed by	The ID of the user who processed the sample.
Method Information	If you select this option, the following information is included in the Run section:	
	Applied method	Name of the method the sample was processed with.
	Method injection time	Sample injection time as it was defined in the method.
	Method injection voltage	Sample injection voltage as it was defined in the method.
	Method separation time	Separation time as it was defined in the method.
	Method separation voltage	Separation voltage as it was defined in the method.
Cartridge Information	If you select this option, the following information will be included in the Run section:	
	Cartridge ID	ID of the cartridge the sample was processed with.
	Cartridge Calibration Status	Calibration status of the cartridge at process time: " OK ", " Not calibrated ", or " Conditional OK ." For information on calibration status, refer to section Running the calibration wizard .
	Cartridge Expiry Date	The expiration date of the cartridge that was used for sample processing.
Sample Information	The sample information is included to the Sample Header section.	
Sample Comment	The sample comment is included to the Sample Header section.	
Analysis Parameter	The analysis parameters applied to the sample will be included in the report section Analysis .	
Reference Marker Table	The reference marker table used during analysis will be included.	
Electropherogram Single View	Use this option to include the electropherogram.	
	Select Use Images as Displayed to print the electropherogram as displayed.	
	Click the Image options button to specify the appearance of the reported single electropherograms. Image options are described below.	
	Note: If Use Images as Displayed is selected, the gel lane and the electrical current are combined with the electropherogram if they are visible in the view.	
	Note: The Image options button is disabled if the Use Images as Displayed option is selected.	

Unit of x-axis	<p>If you select Size, the x-axis will show a size scale based on the reference marker.</p> <p>Note: The size scale can be created only if the sample has been analyzed with a reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will display a corresponding message.</p> <p>If you select Rel. Time, the x-axis will show relative migration time.</p> <p>Note: The relative time scale can be created only if the sample has been analyzed, and the alignment markers have been correctly identified. Otherwise, the x-axis will display a corresponding message.</p> <p>If you select Abs. Time [min], the x-axis will show an absolute time scale.</p>
Zoom to Alignment Marker	<p>Select this option to scale the electropherograms so that the electropherograms start with the lower alignment marker peak and end with the upper alignment marker peak (crop data outside of the alignment markers).</p> <p>Note: This is possible only if all samples are analyzed.</p>
Individual Scaling	<p>Select this option to auto-scale the y-axis for each electropherogram individually.</p>
Show Gel Lane	<p>Select this option to display the gel representation below the electropherogram, aligned with the x-axis.</p>
Show Electrical Current	<p>Select this option to display a diagram of the electrical current measured during data acquisition below the electropherogram or below the gel lane.</p>
Select Show analysis details to enable the following configuration options:	
Mark detected peaks	<p>Select this option to display the apex markers for detected peaks.</p> <p>If the option With label is selected, peak labels are displayed at the apex of each peak.</p> <p>Note: Only peak labels that do not overlap with an adjacent label are displayed. Hover the mouse cursor over the peak apex to get a tool tip with the peak label.</p> <p>Select the label units: size, absolute or relative migration time.</p>

	<p>Note: The label can be displayed as Size only if the sample was analyzed with a reference marker (for details refer to Size and Concentration determination). Otherwise, "n/a" is displayed.</p> <p>Note: In DNA mode, a second option Mark median of size is available. If the sample was analyzed with a DNA smear analysis profile, select this option to display the marker with the median size of detected smear peaks. You can switch the corresponding label on and off.</p> <p>Select the option Mark peak start and end in order to mark the start and end points of detected peaks.</p>
	<p>For DNA mode only. If the sample was analyzed with a DNA smear analysis profile, select Show areas of interest to display the areas of interest of detected smear peaks.</p>
	<p>Select this option to display the suspend integration intervals.</p>
	<p>Select this option to display the peak threshold.</p>
	<p>Select this option to display the baseline.</p>
Gel Single View	<p>Use this option to report individual gel lanes for all selected samples.</p> <p>Click the Image options button to specify the appearance of the reported single gel images. Image options are described below.</p> <p>Note: The Image options button is disabled if the Use Images as Displayed option is selected.</p>
Unit of y-Axis	<p>If you select Size, the axis will show a size scale based on the sample peaks, if the sample has been analyzed with a reference marker table and the alignment markers have been correctly identified. Otherwise, the axis will display a corresponding message.</p> <p>If you select Rel. Time, the axis will show relative migration time, if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the axis will display a corresponding message.</p> <p>If you select Abs. Time [min], the axis will show an absolute time scale.</p>
Zoom to Alignment Marker	<p>Select this option to scale the lanes so that the lanes start with the lower alignment maker band and end with the upper alignment marker band (crop data outside of the alignment markers).</p> <p>Note: This is possible only if all samples are analyzed.</p>

	Individual Scaling	Select this option to auto-scale the contrast for each gel lane individually.
	Analysis details	Select Highlight alignment markers to highlight in green the bands of the alignment marker peaks.
Lot Information	Select this option to include the entered lot numbers.	
Result Table	If you select this option, the peak result table will be included in the report. Additional options appear to configure the result table (see below).	
Peak Calling Result Table	Select this option to include the peak calling result table in every sample section. Additional options can be selected.	
	Note: This option is available only if peak calling features are active.	
	Sample Information	Select this option to include the Sample Information column in the peak calling result overview table.
	Found	Select this option to include the Found column for each peak of interest to the peak calling result overview table.
	Size	For DNA and RNA mode only. Select this option to include the Size column for each peak of interest in the peak calling result overview table.
	Concentration	For DNA and RNA mode only. Select this option to include the Concentration column for each peak of interest in the peak calling result overview table.
	Molarity	For DNA and RNA mode only. Select this option to include the Molarity column for each peak of interest in the peak calling result overview table.
	Note: Calculated columns (such as Ratio, RIS) are automatically included if they are part of the applied peak calling instruction.	
	Note: If a report includes too many peaks of interest, the table is split between two peaks of interest. Sample information and the calculated columns appear only in the first table. The remaining tables are marked with "(continued)" in the header.	
Smear Result Table	For a smear or gDNA analysis in DNA mode, use this option to include a smear result table. The following columns can be selected: Median Size, Conc. Area of Interest, Mol. Area of Interest, Start Area of Interest, End Area of Interest, % Conc. Area of Interest, NA Area of Interest, and % NA Area of Interest. Refer to Smear result columns for further details.	
	Note: The columns of the Smear Result Table can be selected and reordered as described for the Result Table (see below).	
	Select the options Total Concentration and Total Molarity to include the values for total concentration or total molarity of the sample.	
Distribution Result Table	Use this option for a distribution analysis in DNA mode to include the distribution analysis result table for a sample.	

Note: This option is available only if distribution analysis features are active.

Additional options to select are:

Show Profile Properties	Include the parameters of the distribution profile that was applied to the sample.
Sample Information	Include the Sample Information column.
Total Concentration	Include the column Total Concentration of the sample.
Total Molarity	Include the column Total Molarity of the sample.
Sample Quality	Include the Sample Quality column. This is the overall quality assessment of the sample generated in the distribution analysis.
Aol Concentration	Include the Concentration column for each area of interest.
Aol Molarity	Include the Molarity column for each area of interest.
Aol Height	Include the Height column for each area of interest.
Aol Height Check	Include the Height Check column for each area of interest. This is the quality assessment of the height of the area of interest.
Ratio	Include the Ratio column for each defined ratio. Based on the selected calculation method, the column will show molarity or concentration ratio.
Ratio Quality	Include the Ratio Quality column for each defined ratio. This is the quality assessment of the ratio.

Note: If a report includes too many areas of interest or ratios, the table is split between two areas of interest or ratios. Sample information, total concentration, total molarity and sample quality columns appear only in the first table. The remaining tables are marked with "(continued)" in the header.

Note: In **RNA** mode, if you want the 28S/18S ratio or the RIS to be included in the report, select the overview option **Peak Calling Result Table** (refer to [Analysis of RNA samples](#) for further information).

Select the following optional information that you want to include in the peak result table:

<input checked="" type="checkbox"/> Result Table	
	Result Table Columns
<input type="checkbox"/>	Size
<input type="checkbox"/>	Concentration
<input type="checkbox"/>	Molarity
<input type="checkbox"/>	Saturated
<input type="checkbox"/>	Signal To Noise
<input type="checkbox"/>	Normalized Area
<input type="checkbox"/>	Area
<input type="checkbox"/>	Normalized Area Percentage
<input type="checkbox"/>	Ratio Normalized Area
<input type="checkbox"/>	Height
<input type="checkbox"/>	Height Percentage
<input type="checkbox"/>	Resolution
<input type="checkbox"/>	FWHM
<input type="checkbox"/>	Start
<input type="checkbox"/>	Time
<input type="checkbox"/>	Stop
<input type="checkbox"/>	Rel. Time

Result table options in DNA mode.

Note: If the **Result Table** option is selected, but no result table column is selected, the **Result Table** check box is marked yellow, and the report/export profile is invalid.

The peak result table options are described below:

Size	Adds the result table column Size [bp] or Size [nt] for DNA or RNA mode, respectively.
Concentration	Adds the result table column Conc. [ng/μl] . If you select this option, the total concentration is added automatically as last value of the column.
Molarity	Adds the result table column Mol. [nmol/l] .
Height Percentage	Adds the result table column Height % .
Normalized Area	Adds the result table column NA .
Normalized Area Percentage	Adds the result table column NA % .
Signal to Noise	Adds the result table column S/N (Signal-to-noise ratio).
FWHM	Adds the result table column FWHM [sec] (full width at half maximum).
Resolution	Adds the result table column Res .
Ratio Normalized Area	Adds the result table column Ratio NA .
Time	Adds the result table column Time .
Rel.Time	Adds the result table column Rel. Time .
Start	Adds the result table column Start .
Stop	Adds the result table column Stop .
Height	Adds the result table column Height .
Area	Adds the result table column Area .

Note: Refer to section [Peak result columns](#) for more information about the columns.

Note: You can specify the field order of the result table in the report by drag and drop. Left-click on a column name and drag it to the new position.

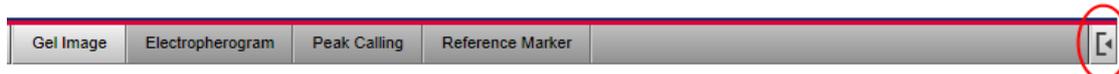
Exporting data

The basic procedure of exporting data in the **Analysis** environment is as follows:

1. Load the samples using the **Experiment Explorer**.
For more details about loading sample data, see section [Loading sample data](#).
2. Inspect the samples before exporting.
See the [Viewing sample data](#) section for more details on data inspection.
For this step, the **Gel view** or the **Electropherogram overview** are especially useful.
3. Select the samples you want to export.
For more details about selecting samples, see section [Selecting samples for analysis or report](#)
4. Select export settings and start exporting.

On the right side of the analysis environment, the report toolbar can be found.

If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:



Select the **Report** tab of the toolbar.

Select a predefined report/export profile. The export settings of the selected profile are shown below the report settings. For details, refer to the [Export options](#) section.

Make sure that at least one of the export options is selected. If not, select another predefined report/export profile. (Users assigned the user roles **Advanced User** or **Basic User** may modify the settings as they wish.)

Specify the directory in which the export files will be saved (refer to section [Export options](#) for information on how to specify the export directory).

Click the **Start Report/Export** at the bottom of the **Report** tab to start exporting.

Note: The button **Start Report/Export** is disabled if no samples are selected in the view (see Step 3).

The export files will be generated automatically and stored in the specified directory.

Export options

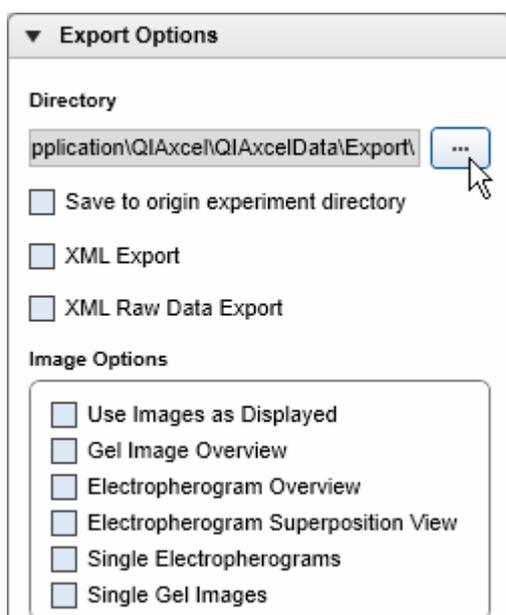
The report/export settings are divided into two groups:

- **Report Options** containing the report settings
- **Export Options** containing the export settings

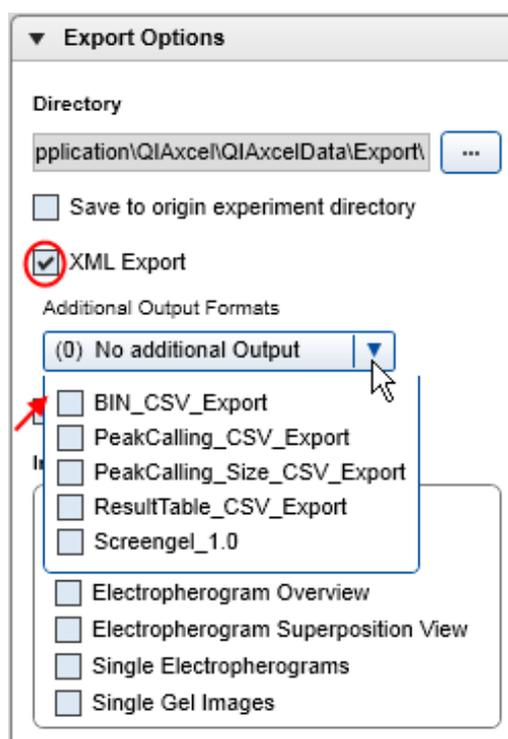
Note: You can collapse and expand each group by clicking ▼ and ► to the left of the group name.

Collapse the report options or scroll down to see the export options.

Export Options



Export Options.



Additional output formats.

The options are described below:

- Directory** Select the directory to which the export files will be saved by clicking . In the dialog that appears, navigate to the correct directory and click **OK**.
- Save to origin experiment directory** Check this box to save the report in the same directory as the experiment. If this option is selected, any selected path in **Directory** will be ignored.
- XML Export** If you select this option, an export file in XML format will be generated. This file contains all general experiment and sample details of the selected samples, except electropherogram raw data. If the samples are analyzed, it contains the analysis results.

An additional option to select additional output formats appears. The software provides two formats. You can select all of them.

BIN_CSV_Export Use this option to export the peak calling result table in .csv format (similar to the file format that was exported by the BioCalculator 3.2 Software).

DistributionAnalysis_CSV_Export Use this option to export the distribution analysis overview result table in .csv format.

PeakCalling_CSV_Export Use this option to export the peak calling result table with all selected peak properties in .csv format.

ResultTable_csv_table Use this option to export the analysis results in .csv format (similar to the file format that was exported by the BioCalculator 3.2 Software).

ScreenGel_1.0 Use this option to convert the export file to the .xml export format of the QIAxcel ScreenGel Software version 1.0.

SmearResultTable_CSV_Export Use this option to export the smear result overview table in .csv format.

Note: You can customize your own output formats. Define xslt scripts based on the .xml export file and store them in the %DATA_DIR%\ReportExportProfile\XSLT_Export directory. Script processing (e.g., VB- or Java-Script) within a XSLT style sheet is supported. In XSLT style sheets, the configured export directory is available as the parameter exportPath.

Note: To open generated .csv files in Excel, use the **New** from text option and select Unicode (UTF-8) as the file origin format. Fields are delimited by commas (,). Use **General** as the column data format. In the advanced options select period (.) as the decimal separator in numbers and make sure not to use a thousands separator. If the values are not listed in columns, highlight all cells, then use the **Text to Columns** function in Excel and select the correct delimiters. This option does not allow selecting the Unicode (UTF-8) format, which may result in unwanted characters in the column headers.

XML Raw Data Export If you select this option, electropherogram raw data of the selected files will be exported in XML format.

An additional option to select additional output formats appears. The software provides one format.

RawData_CSV_Export Use this option to export the electropherogram raw data in .csv format (similar to the file format which was exported by the BioCalculator 3.2 Software).

Note: You can customize your own output formats. Define xslt scripts based on the xml raw data export file and store them in the %DATA_DIR%\ReportExportProfile\XSLT_RawExport directory. Script processing (e.g., VB- or Java-Script) within a XSLT style sheet is supported. In XSLT style sheets, the configured export directory is available as the parameter exportPath.

The image options are described below:

Use Images as Displayed	<p>Use this option to obtain images that look similar to the presentation in the QIAxcel ScreenGel Software regarding alignment, scales, labels, zoom, etc.</p> <p>Note: This option is available in the analysis environment only, it may not be used in a process profile.</p>
Gel Image Overview	<p>Use this option to export the gel image of all selected samples.</p> <p>Click on the Image options button to specify the appearance of the exported gel image overview. Image options are described below.</p> <p>Note: The Image options button is disabled if the Use Images as Displayed option is selected.</p>
Unit of y-axis	<p>If you select Size, the y-axis will show a size scale based on the reference marker on both sides of the gel image, also if the Use Images as Displayed option is selected. The lanes in the gel image will be aligned according to the alignment markers.</p> <p>Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, a corresponding message will appear.</p> <p>If you select Rel. Time, the y-axis will show relative migration time. The lanes in the gel image will be aligned according to the alignment markers.</p> <p>Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the lanes cannot not be aligned and the y-axis will show a corresponding message.</p> <p>If you select Abs. Time [min], the lanes will not be aligned and the y-axis will show an absolute time scale.</p>
Zoom to Alignment Marker	<p>Select this option to scale the lanes, so that the lanes start with the lower alignment maker band, and end with the upper alignment marker band, if available (crop data outside of the alignment markers).</p> <p>Note: This is possible only if all samples are analyzed.</p>
Individual scaling	<p>Select this option to auto-scale the contrast for each gel lane individually.</p>

Show sample information	Select this option to include the sample information in each lane.
Show plate ID	Select this option to display the plate ID, the repeat number, and the entry number of each lane.
Show method	Select this option to display the applied method above the sample lane.
Gel Layout	<p>Select this option to determine the gel layout.</p> <p>Select Standard Layout to order the lanes from left to right, as they are ordered in the view.</p> <p>Select Horizontal plate layout to order the lanes starting with A1 at the upper left and ending with H12 at the lower right.</p> <p>Select Vertical plate layout to order the lanes starting with H1 at the upper left and ending with A12 at the lower right.</p> <p>Select Reverse vertical plate layout for the vertical plate layout but starting with A1 at the upper left and ending with H12 at the lower right.</p> <p>Select Split plate layout to split the vertical plate layout. The left portion will start with H1 at the upper left and end with A6 at the lower right. The right portion will start with H7 at the upper left and end with A12 at the lower right.</p> <p>Note: Positions for samples not selected remain empty.</p>
Lanes per Row	<p>Use this option to specify the number of lanes per row: 4, 6, 8, 12, 16, 24, 32, 36, or 48.</p> <p>Note: This option is available only if Standard layout is selected in the Gel Layout option.</p>
Rows per File	<p>Use this option to specify the number of rows to be included in one file (the image is split into several files according to the specified number of rows).</p> <p>Note: This option is not available if Standard layout is selected in the Gel Layout option.</p>
Highlight alignment markers	Select this option to highlight in green the bands of the alignment marker peaks.

Electropherogram Overview Select this option to export the electropherogram overview for all selected samples. The order is the same as in the view. One gallery overview page (at most 12 electropherograms) will always be exported to one file.

Click on the **Image** options button to specify the appearance of the exported electropherogram overview. Image options are described below.

Note: The **Image** options button is disabled if the **Use Images as Displayed** option is selected.

Unit of x-axis If you select **Size**, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers.

Note: The size scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will show a corresponding message.

If you select **Rel. Time**, the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all selected samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will show a corresponding message.

If you select **Abs. Time** [min], the electropherograms will not be aligned and the x-axis will show an absolute time scale.

Zoom to Alignment Marker Select this option to scale the electropherograms so that the electropherograms start with the lower alignment maker peak, and end with the upper alignment marker peak (crop data outside of the alignment markers).

Note: This is possible only if all samples are analyzed.

Individual Scaling Select this option to auto-scale the y-axis for each electropherogram individually.

Show sample position	Select this option to show the sample position at the top of each electropherogram.
Show sample information	Select this option to show the sample information at the top of each electropherogram.
Show plate ID	Select this option to show the plate ID at the top of the electropherogram.
Show method	Select this option to show the applied method at the top of each electropherogram.
Show analysis details	Select this option to show analysis details for the analyzed samples. Select Mark detected peaks to show the apex markers of detected peaks. Note: In DNA mode, a second option Show median of size is available. If the sample was analyzed with a DNA smear analysis profile , select this option to display the markers with the median size of detected smear peaks. Select Show suspend integration intervals to display the suspend integration intervals.

Electropherogram Superposition View

Use this option to export a superposition view of all selected samples which have the "superimposed" flag set.

Note: The superposition view is restricted to 12 samples. In process environment and in batch processing, the superposition is created only if the experiment contains 12 samples or less.

Note: Use the **Use Images as Displayed** option to export the electropherogram superposition as displayed.

Click the **Image** options button to specify the appearance of the reported electropherogram superposition. Image options are described below.

Note: The **Image** options button is disabled if the **Use Images as Displayed** option is selected.

Unit of x-axis If you select **Size**, the x-axis will show a size scale based on the reference marker. The electropherograms will be aligned according to the alignment markers.

Note: The size scale can be created only if all superimposed samples have been run with the same alignment marker, have been analyzed with the same reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will show a message, instead.

If you select **Rel. Time**, the x-axis will show relative migration time. The electropherograms will be aligned according to the alignment markers.

Note: The relative time scale can be created only if all superimposed samples have been run with the same alignment marker, have been analyzed, and the alignment markers have been correctly identified. Otherwise, the electropherograms will not be aligned and the x-axis will show a message, instead.

If you select **Abs. Time [min]**, the electropherograms will not be aligned and the x-axis will show an absolute time scale.

Zoom to Alignment Marker

Select this option to scale the electropherograms, so that the electropherograms start with the lower alignment marker peak, and end with the upper alignment marker peak, if available (crop data outside of the alignment markers).

Note: This is possible only if all samples are analyzed.

Show Electrical Current Curve

Select this option to include a diagram of the superimposed electrical current measured during data acquisition. The electrical current curve will appear below the electropherogram superposition, aligned with the x-axis.

Show size marker peak labels

If this option is selected, and if exactly one size marker is among the superimposed samples, the peak labels will be displayed for the detected peaks of the marker sample. Select the units for the peak labels in the drop-down list.

Single Electropherograms

Select this option to export the electropherograms for all selected samples in separate files.

Use the **Use Images as Displayed** option to export the electropherogram as displayed.

Click on the **Image** options button to specify the appearance of the exported single electropherograms. Image options are described below.

Note: If the **Use Images as Displayed** option is selected, the gel lane and the electrical current are combined with the electropherogram if these are visible in the view.

Note: The **Image** options button is disabled if the **Use Images as Displayed** option is selected.

Unit of x-axis	<p>If you select Size, the x-axis will show a size scale based on the reference marker.</p> <p>Note: The size scale can be created only if the sample has been analyzed with a reference marker table, and the alignment markers have been correctly identified. Otherwise, the x-axis will show a corresponding message.</p> <p>If you select Rel. Time, the x-axis will show relative migration time.</p> <p>Note: The relative time scale can be created only if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the x-axis will show a corresponding message.</p> <p>If you select Abs. Time [min], the x-axis will show an absolute time scale.</p>
Zoom to Alignment Marker	<p>Select this option to scale the electropherograms, so that the electropherograms start with the lower alignment maker peak, and end with the upper alignment marker peak, if available (crop data outside of the alignment markers).</p> <p>Note: This is possible only if all samples are analyzed.</p>
Individual Scaling	Select this option to auto-scale the y-axis for each electropherogram individually.
Show Gel Lane	Select this option to export the gel lane combined with the electropherogram (the gel lane is below the electropherogram).
Show Electrical Current	Select this option to export the electrical current curve below the electropherogram or below the gel lane.
Select Show analysis details to enable the following options for analyzed samples:	
Mark detected peaks	<p>Select this option to display the apex markers for detected peaks.</p> <p>If the option With label is selected, peak labels are displayed at the apex of each peak.</p> <p>Note: Only peak labels that do not overlap with an adjacent label are displayed. Hover the mouse cursor over the peak apex to get a tool tip with the peak label.</p>

Select the label units: size, absolute or relative migration time.

Note: The label can be displayed as **Size only**, if the sample was analyzed with a reference marker (for details refer to [Size and Concentration determination](#)). Otherwise, "n/a" is displayed.

Note: In **DNA** mode, a second option **Mark median of size** is available. If the sample was analyzed with a **DNA smear analysis profile**, select this option to display the marker with the median size of detected smear peaks. You can switch the corresponding label on and off.

Select the option **Mark peak start and end** to mark the starting and ending points of detected peaks.

Show areas of interest For **DNA** mode only. If the sample was analyzed with a **DNA smear analysis profile**, select **Show areas of interest** to display the areas of interest of detected smear peaks.

Show suspend integration interval Select this option to display the suspend integration intervals.

Show threshold Select this option to display the peak threshold.

Show baseline Select this option to display the baseline.

Single Gel Images Use this option to individually export the gel lanes for all selected samples.

Click on the **Image** options button to specify the appearance of the exported single gel images. Image options are described below.

Note: The **Image** options button is disabled if the **Use Images as Displayed** option is selected.

Unit of y-axis If you select **Size**, the axis shows a size scale based on the sample peaks, if the sample has been analyzed with a reference marker table and the alignment markers have been correctly identified. Otherwise, the axis will show relative migration time, if possible.

If you select **Rel. Time**, the axis will show relative migration time, if the sample has been analyzed and the alignment markers have been correctly identified. Otherwise, the axis will show an absolute time scale.

If you select **Abs. Time** [min], the axis will show an absolute time scale.

	Note: This option is not available if the Use Images as Displayed option is selected.
Zoom to Alignment Marker	Select this option to scale the lanes so that the lanes start with the lower alignment marker band, and end with the upper alignment marker band (crop data outside of the alignment markers).
	Note: This is possible only if all samples are analyzed.
Individual Scaling	Select this option to auto-scale the contrast for each gel lane individually.
Analysis details	If you select Show detected peaks and if the sample was analyzed, the y-axis will be labeled with the apex for detected peaks.
	Note: In DNA mode, a second option Show median of size is available. If the sample was analyzed with a DNA smear analysis profile , select this option to display the median size for detected smear peaks.
	Select Highlight alignment markers to highlight in green the bands of the alignment marker peaks.

The image export settings are described below. They appear if at least one image type is selected for export.

File Type	Select the file type for the image files.
Resolution	Select the resolution for the image files; the available resolutions are: 75 dpi (dots per inch), 150 dpi, 300 dpi, and 600 dpi. For small bands, use 150 dpi.

Modifying a report/export profile

Note: Only users with the **Advanced User** or **Basic User** role can modify report/export options.

To modify a report/export profile proceed as follows:

1. Open the **Report** tab.

If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:



Select the **Report** tab.

2. Select the report/export profile you want to modify.

Select the report/export profile in the **Report/Export Profile** drop-down list.

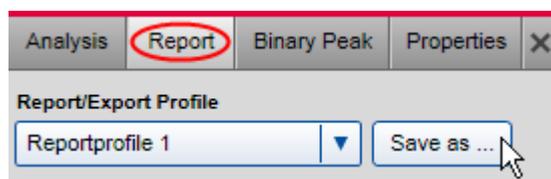
3. Change the profile options according to your needs.

See the [Report options](#) and [Export options](#) sections for detailed information.

Note: The system notifies modifications on the profile by displaying a "*" at the beginning of the profile name.

4. Save the modified report/export profile.

Click the **Save as** button. Click **OK** in the **Save Profile** dialog which appears.



Saving a report/export profile.

Note: If you want to use the modified report/export options only once, just click **Start Report/Export** without saving the modifications. However, your changes will be lost when you select another report/export profile.

Note: Report profiles provided by QIAGEN cannot be modified. However, to save your modifications enter a new unique profile name in the **Save Profile** dialog. A new profile will be created containing your modifications. This is possible for users with the **Advanced User** role only.

Creating a new report/export profile

Note: Only users with the **Advanced User** role can create a new report/export profile.

To create a new report/export profile proceed as follows:

1. Open the **Report** tab.

If it is not visible, you can display it using the **View** menu (selecting the menu item **View/Show Analysis Parameters**) or by clicking the icon at the extreme right of the view selection bar:



Select the **Report** tab.

2. Select a report/export profile.

Select the profile from the **Report/Export Profile** drop-down list. The selected profile serves as a template for the creation of the new profile.

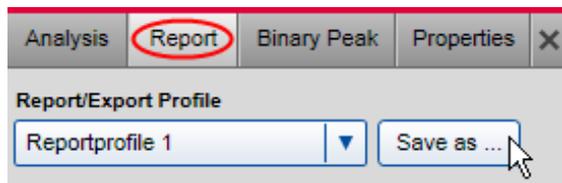
Note: Select **NewReport/ExportProfile** to create a report/export profile from scratch. The system will show ***NewReport/ExportProfile** after selection.

3. Set the profile options according to your needs. See the [Report options](#) and [Export options](#) sections for detailed information about report/export options.

Note: The system notifies modifications on the profile by displaying a "*" at the beginning of the profile name.

4. Save the modified report/export profile under a new name.

Click the **Save as** button and enter a new unique profile name in the **Save Profile** dialog that appears.

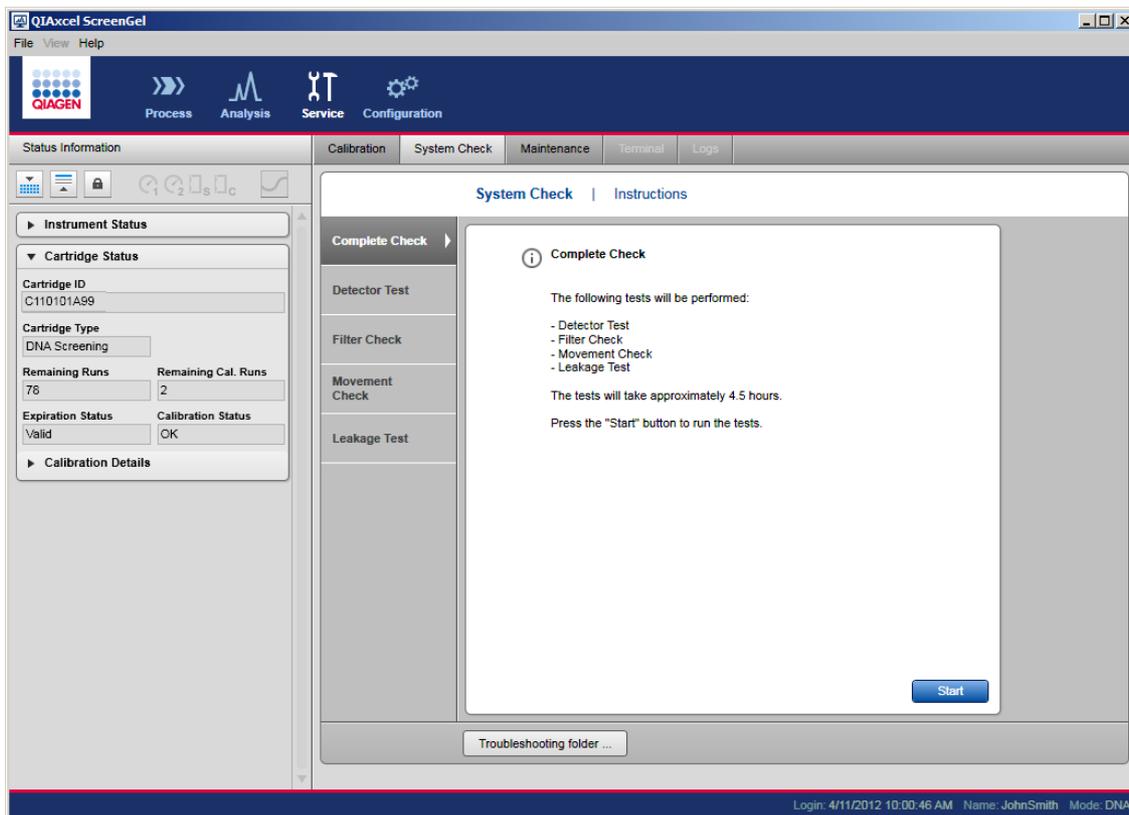


Saving a report/export profile.

Service

The **Service** environment provides functionality for cartridge calibration as well as troubleshooting and maintenance tools for the QIAxcel Advanced instrument.

On the left side of the **Service** environment, a **Status Information** panel is displayed (See [Status Information panel](#)).



Service environment with active System Check screen. The Status Information panel is shown to the left of the screen.

Note: The **Terminal** and **Logs** screens of the **Service** environment may be accessed by service personnel only and are not described in this manual.

Calibrating a cartridge

Every new cartridge requires intensity calibration prior to sample analysis. The intensities of each capillary are normalized and a factor is applied for every subsequent run. This corrects for natural intensity reading variations between each capillary in the cartridge. The data for each cartridge intensity calibration are stored in a single file named **<cartridge-id>_<instrument-id>.xcc**. This file is saved in the directory %DATA_DIR%\CartridgeCalibrationData\.

Note: To inspect calibration data, switch to the analysis environment and click the **Load experiment** button of the **Experiment Explorer**. In the file dialog that appears, select the path ending with "[**Calibration results**]."

Note: If for any reason a different computer is used to the one containing the calibration file, the file should be transferred to the new computer. Otherwise, recalibration of the cartridge is required.

Running the calibration wizard

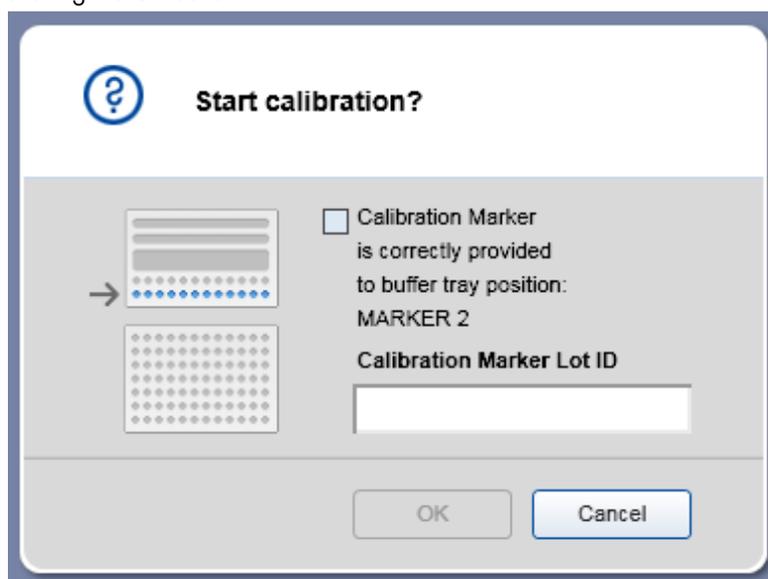
Intensity calibration of the cartridge is performed in the **Calibration** screen of the **Service** environment:

1. Load **QX Intensity Calibration Marker** onto the buffer tray position **MARKER2** as detailed in step 7 of [Preparing the buffer tray](#).

2. Launch the calibration run by clicking the **Start calibration** button.

Note: The total run time for the calibration routine is about 16 minutes.

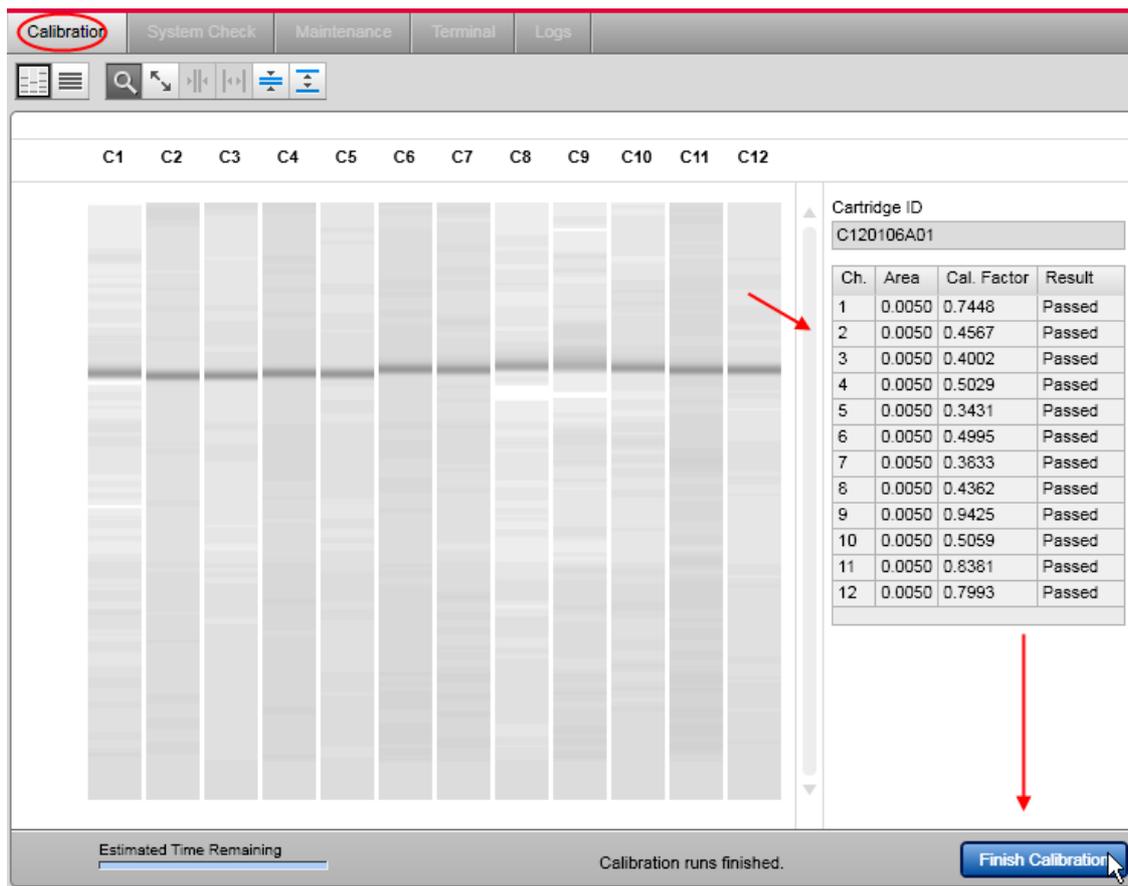
3. Confirm that the **QX Intensity Calibration Marker** is loaded. Optionally, enter the lot ID. Start the calibration by clicking the **OK** button.



Confirmation dialog.

If the **QX Intensity Calibration Marker** is not loaded correctly, cancel the dialog. Load it again and repeat step 1.

4. Once the calibration is complete, the calibration results are displayed next to the gel/electropherogram view. The result table shows the area, calibration factor, and the result ("Passed" or "Failed") for each channel.



Calibration results.

Note: A successfully calibrated cartridge should have a normalized area in a range as described in the respective kit handbooks.

Note: If one or more channels fail, the calibration process should be repeated. If the issue persists, please contact QIAGEN Technical Services or refer to the **Troubleshooting** section in the handbook supplied with the QIAxcel Kit you are using.

5. Accept the calibration result. The cartridge is now calibrated.

Note: Discard the calibration result if one or more channels fail.

Note: A user with user role **Advanced User** can accept calibration results even if one or more channels failed. In this case, the calibration status will be "**Conditional OK.**" Only users with the user role **Advanced User** can perform processes using cartridges with calibration status "**Conditional OK.**"

Recalibrating a cartridge

To recalibrate a cartridge, repeat the procedure detailed in [Running the calibration wizard](#). The calibration results of previous calibration procedures are discarded when recalibrating a cartridge.

Note: It is possible to calibrate a cartridge that has no calibration runs left. In this case, three regular runs are used instead of one calibration run.

System check

The **System Check** screen of the **Service** environment provides several procedures for detecting problems with the QIAxcel Advanced instrument:

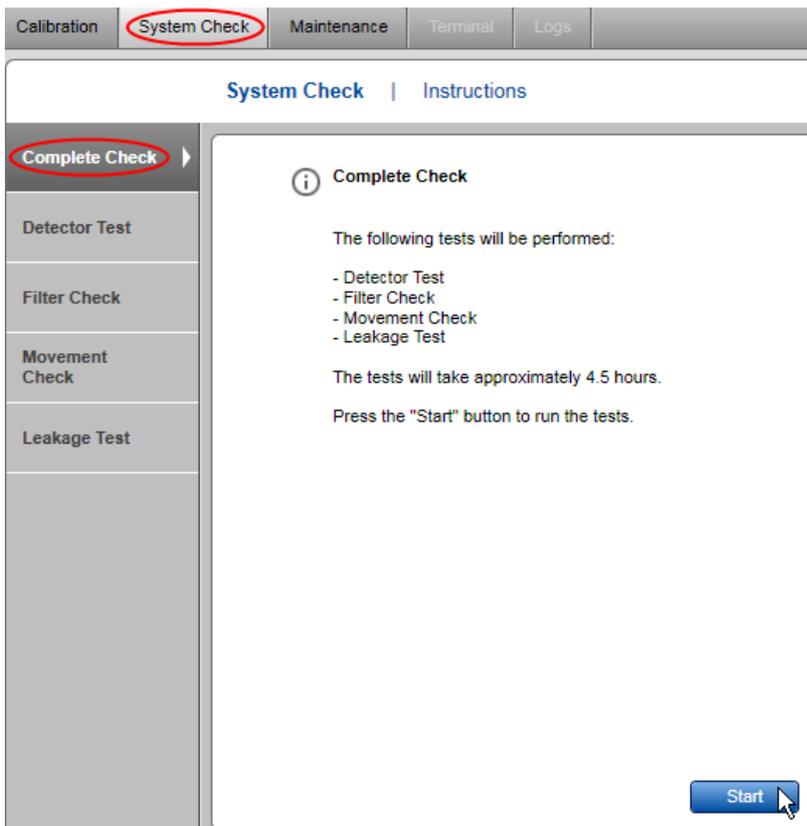
- **Complete Check**
The complete check performs all the system checks listed below.
- **Detector Test**
The detector test checks the raw count of all 12 channels.
- **Filter Check**
The filter check detects blockage of the purge filter.
- **Movement Check**
The movement test verifies that the sample tray can be moved properly and that the position sensors work as expected.
- **Leakage Test**
The leakage test checks for N₂ leakage.

Note: The test results are stored to the directory %DATA_DIR%\SystemTest\.

Note: The troubleshooting folder functionality is described in the [Troubleshooting folder](#) section.

Complete check

A **Complete Check** performs all available system checks: **Detector Test**, **Filter Check**, **Movement Check** and **Leakage Test**.



Complete check.

Note: The complete check takes approximately 4.5 hours.

Detector test

The **Detector Test** verifies that the detectors of all 12 channels of the QIAxcel Advanced instrument work as expected. It may be performed when one or more channels in a new cartridge do not provide data signals and the baseline is flat.

Perform the **Detector Test** by following the instructions shown on the screen. The test takes only several seconds. At the end of the test, the acquired data is shown, and the results are stored.

Note: If not instructed otherwise, perform this test with a cartridge inserted and latched.

Calibration **System Check** Maintenance Terminal Logs

System Check | Instructions

Complete Check

Detector Test

Filter Check

Movement Check

Leakage Test

Detector Test Results

The acquired values should be greater than or equal to 200. Otherwise contact QIAGEN Technical Services.

The following values were acquired during the detector test:

C01	C02	C03	C04	C05	C06	C07	C08	C09	C10	C11	C12
1847	3132	2205	2970	2149	2451	2872	1620	1559	3245	2221	1973
2467	2699	2019	2220	1024	1407	5683	2094	2311	1679	1260	1480
4568	2026	8034	2064	2656	1217	1815	1289	8971	8409	1561	2259
2110	2883	1594	8816	3218	1838	1542	2954	1084	2515	3496	5637
3243	2925	6007	2664	1382	1953	2796	1441	229	2441	2348	1770
5484	4075	2555	7249	2768	3781	1548	2020	2873	1636	1563	1131
5751	4815	1591	7272	2367	2273	1915	1764	2115	1208	1654	1190
1318	3262	3397	3969	1730	3202	3190	1271	4279	2818	1816	2083
8317	2322	3203	1677	2167	4263	3098	1356	1047	1005	3270	5390
6082	1703	1444	2567	1017	3118	6414	3127	2376	7032	430	9966
1669	1083	2930	1847	2136	2127	1278	1426	1945	2183	626	3651
4523	2091	3004	1914	1624	2694	2567	6808	2419	1220	1127	2136
5186	1183	3175	1079	2272	3263	7031	2460	1166	865	2203	3012
1364	1699	2218	1501	2940	2634	3216	1860	1679	1138	3275	1909
2923	3177	1368	9067	2793	2876	1352	2845	4517	1532	1389	4411
2031	2652	1640	2290	2075	2334	3007	6719	1430	1802	754	3118

OK

Finished!
The detector test has finished and the results are saved.

Restart

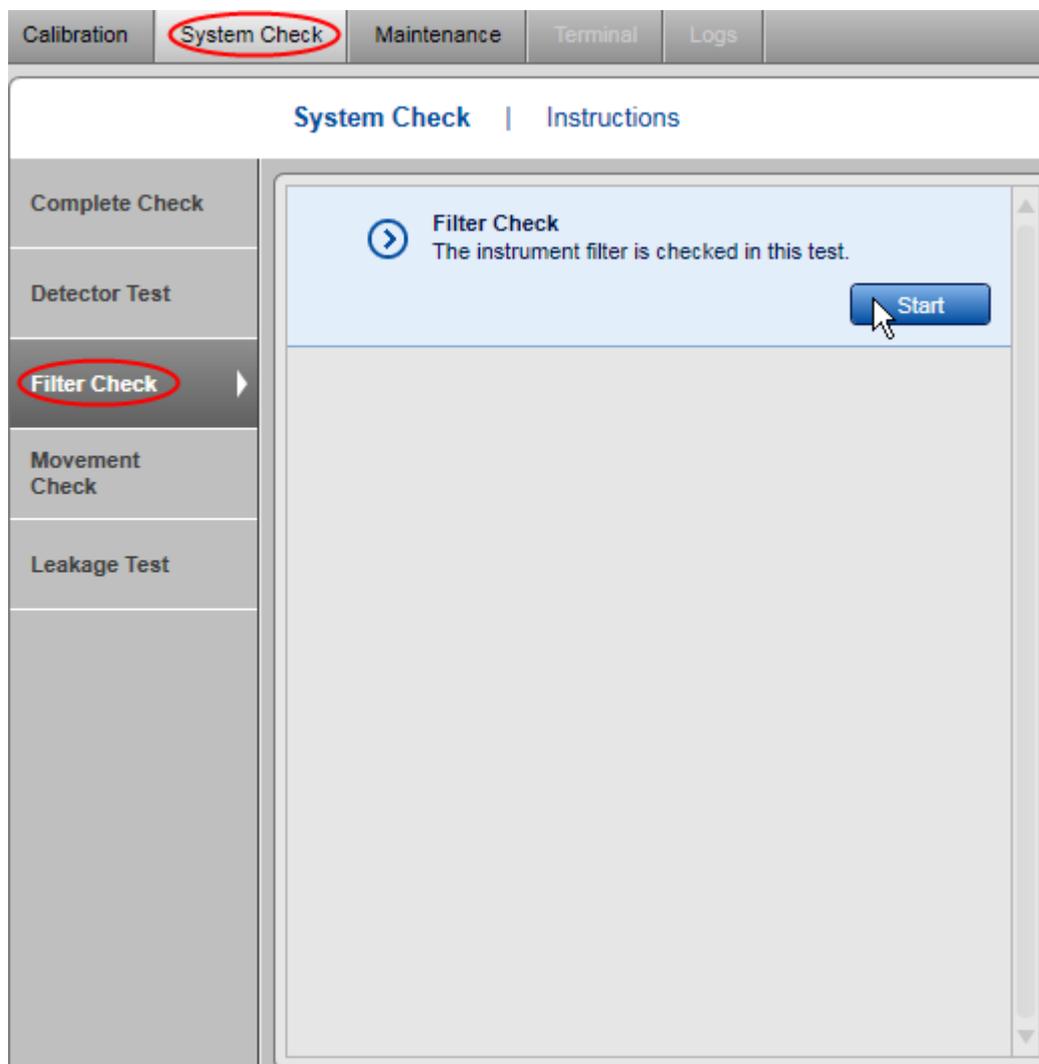
Detector test finished.

Filter check

In rare instances, the purge filter that sits inside the QIAxcel Advanced instrument may become blocked with gel carryover. This blockage can be diagnosed using the **Filter Check**. It takes about two minutes. At the end of the check, the filter status (passes or failed) is shown and the results are stored.

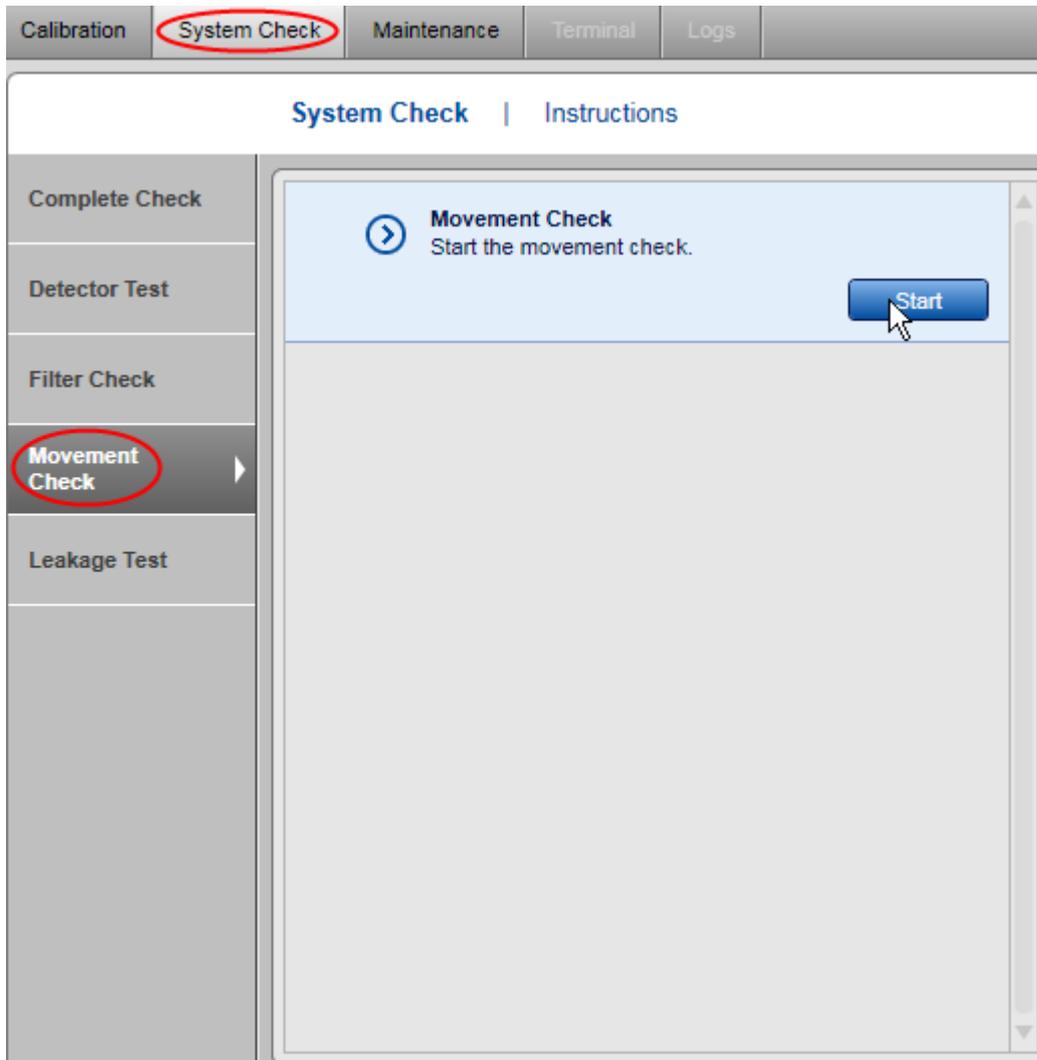
Note: A cleaning tissue, for example Kimwipe, is needed for this check.

The **Filter Check** is performed by following the instructions shown in the wizard:



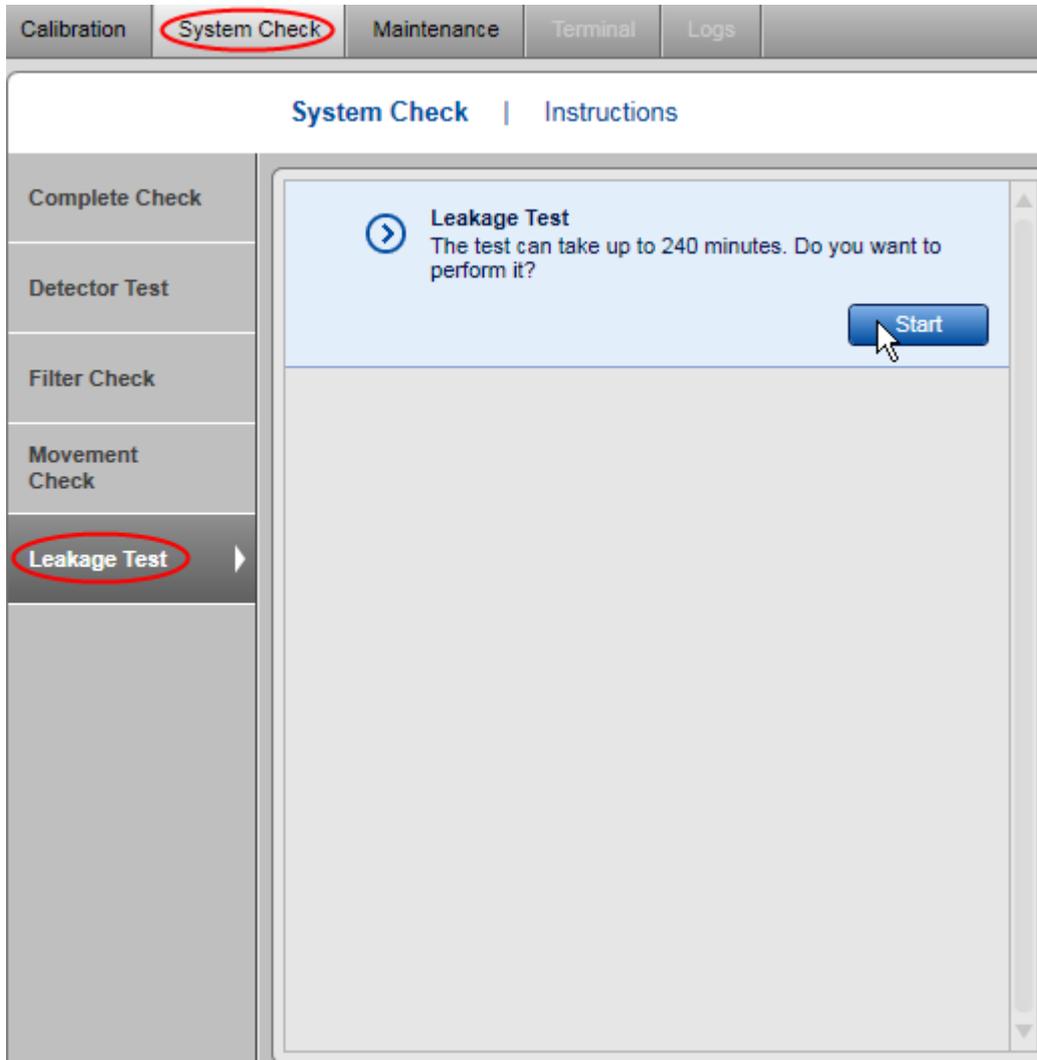
Movement check

The **Movement Check** verifies that the tray motors and tray sensors work as expected. This test is fully automated and requires no user interaction except cartridge removing. It takes several seconds. At the end of the test, a test summary (passed or failed) is shown and the results are stored.



Leakage test

The **Leakage Test** checks for leakages in the N₂ tubing of the QIAxcel Advanced instrument. This fully automated test takes approximately 240 minutes. After the test, the leakage rate is calculated if a leakage is detected and the results of the test are stored.



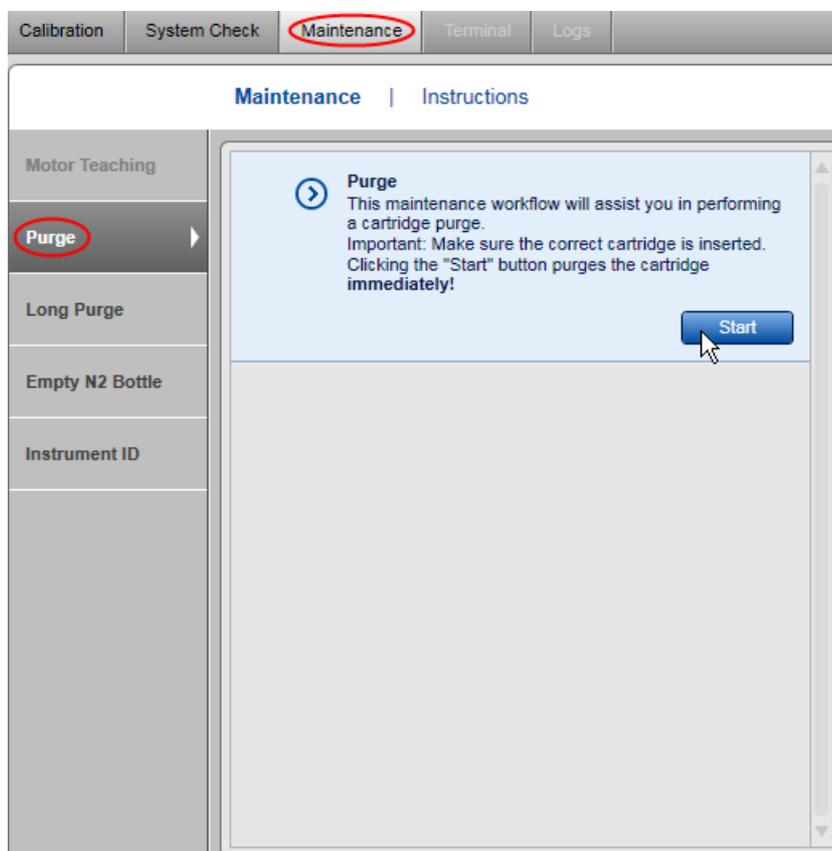
Maintenance

The **Maintenance** screen of the **Service** environment provides several maintenance and troubleshooting procedures for the QIAxcel Advanced instrument and cartridges:

- Motor teaching (for service personnel only; not described here)
- Purge
- Long purge
- Empty N₂ bottle
- Set instrument ID
- Troubleshooting folder

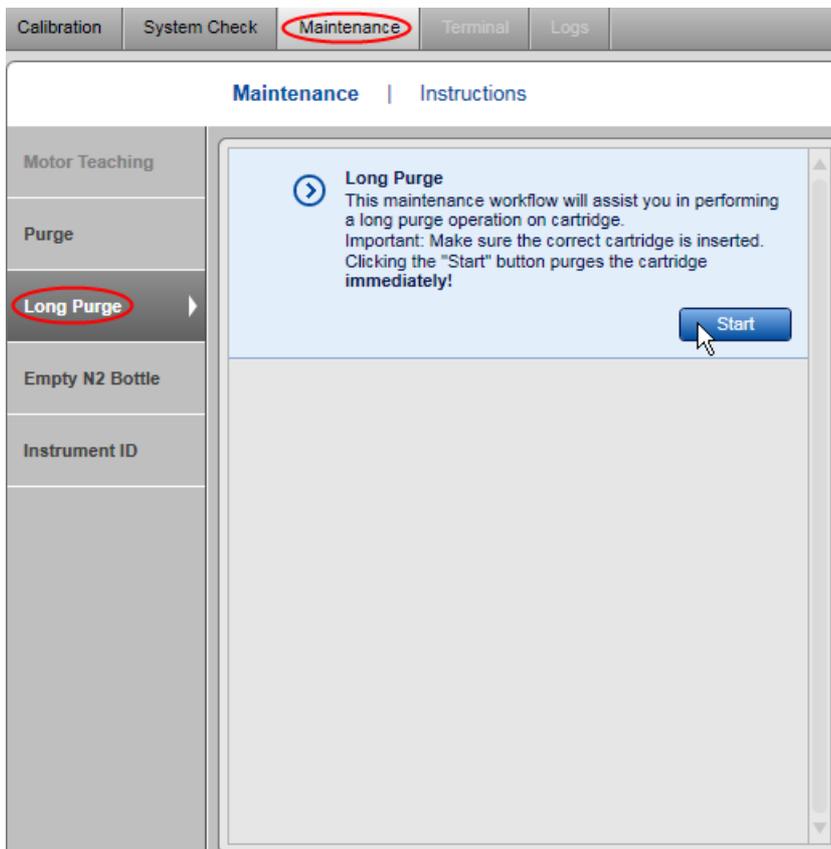
Purge

The **Purge** method allows the user to remove air bubbles from the gel cartridge and clean the capillaries. The process is fully automated and takes less than a minute.



Long purge

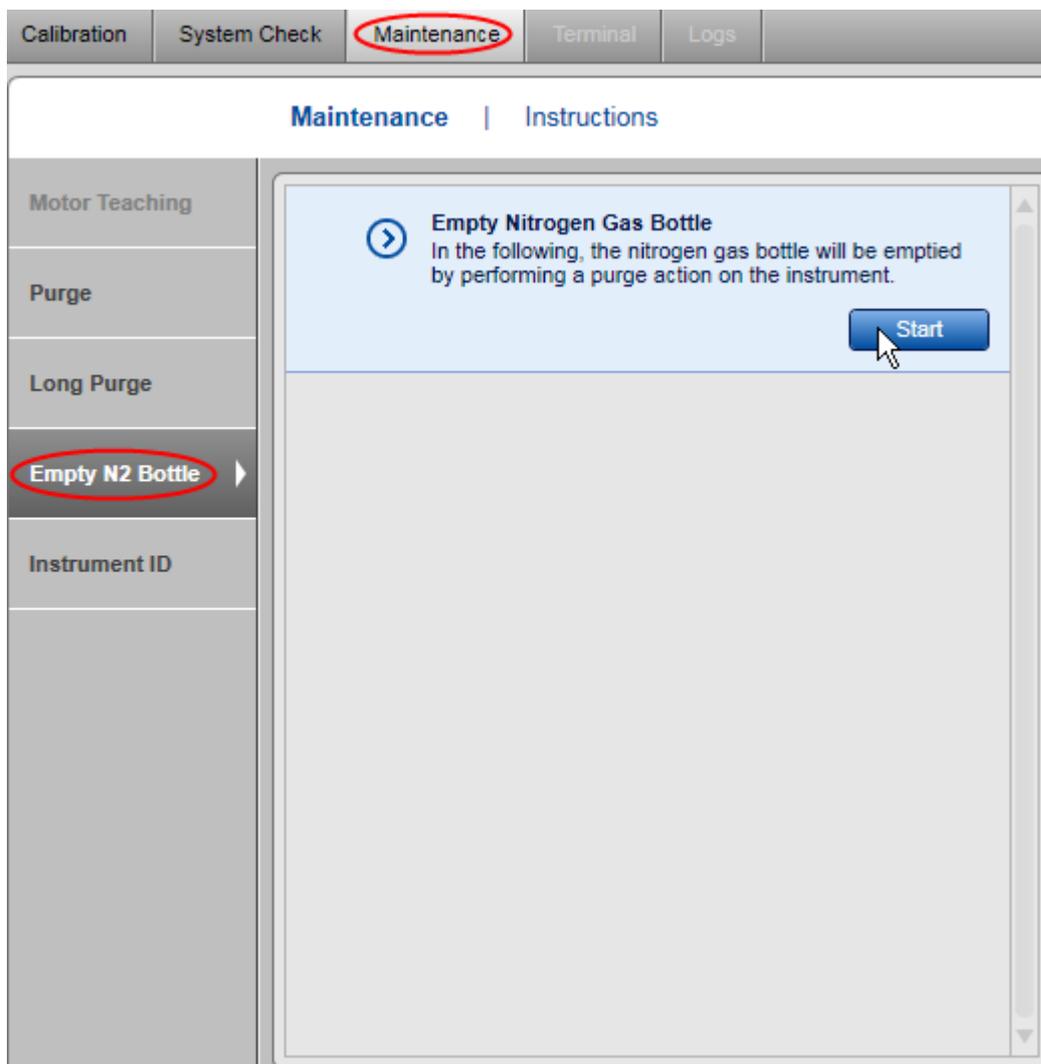
The **Long Purge** method allows the user to remove air bubbles from the gel cartridge and clean the capillaries extensively. The process is fully automated and takes about 3 minutes.



Empty N2 bottle

To remove a pressurized N₂ cylinder, you must release the remaining pressure first. The **Empty N₂ Bottle** function purges the nitrogen, which takes about a minute.

Note: You must first remove the QIAxcel gel cartridge before performing this action.



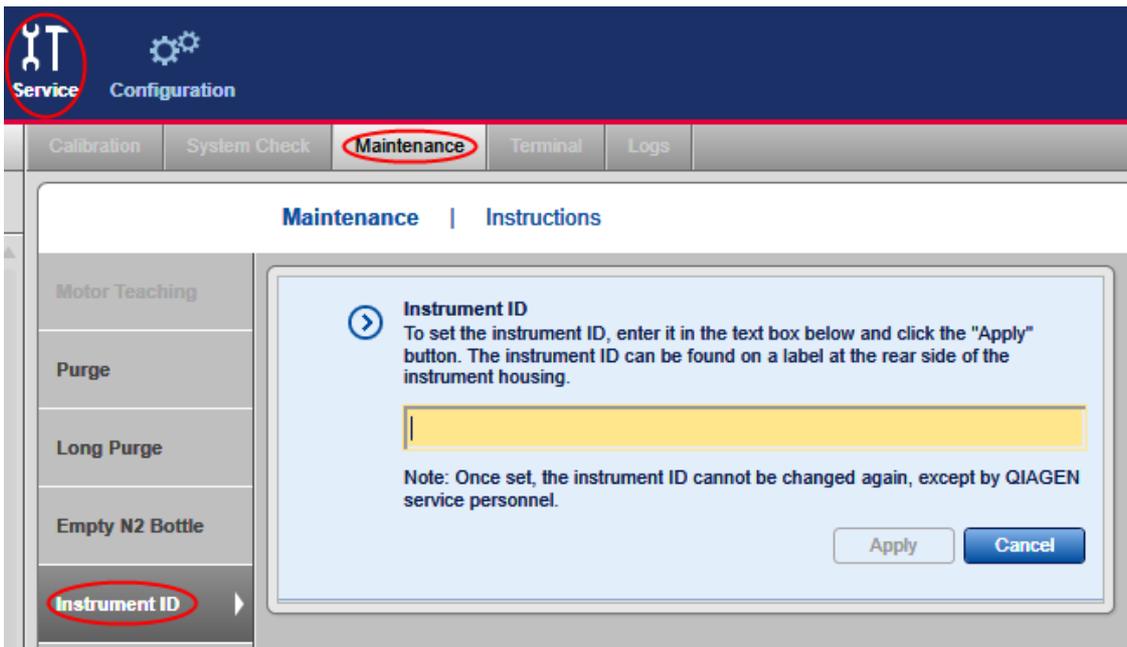
Important: Repeat this operation until no hissing sound can be heard at the end of the purge operation.

Setting the instrument ID

Setting the **QIAxcel instrument ID** (serial number) is possible only if the instrument is connected and the instrument ID has not been set. The instrument ID can be found on a label at the rear side of the instrument housing.

The instrument ID is required to identify each instrument and check that a cartridge is calibrated on a certain instrument (see [Calibrating a cartridge](#)).

Important: Make sure you have entered the correct instrument ID before clicking the **Apply** button. Once set, the instrument ID cannot be changed again, except by a QIAGEN service personnel.



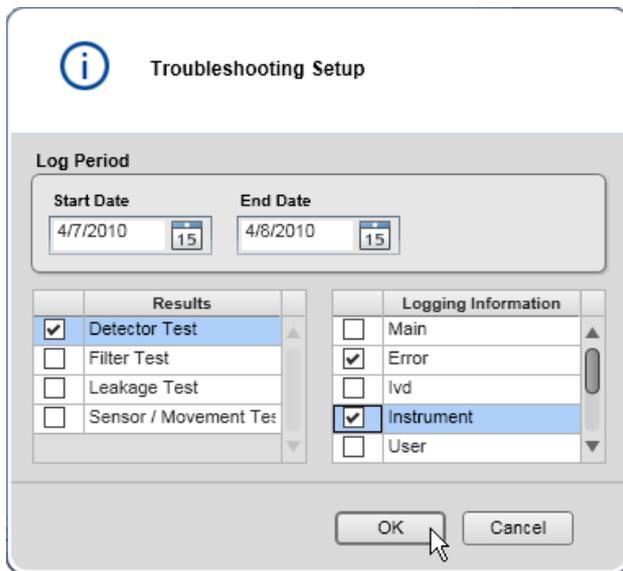
Troubleshooting folder and log files

The **Troubleshooting** folder function allows export of log files and test results produced within a specified time period.

To export log files or test results, proceed as follows:

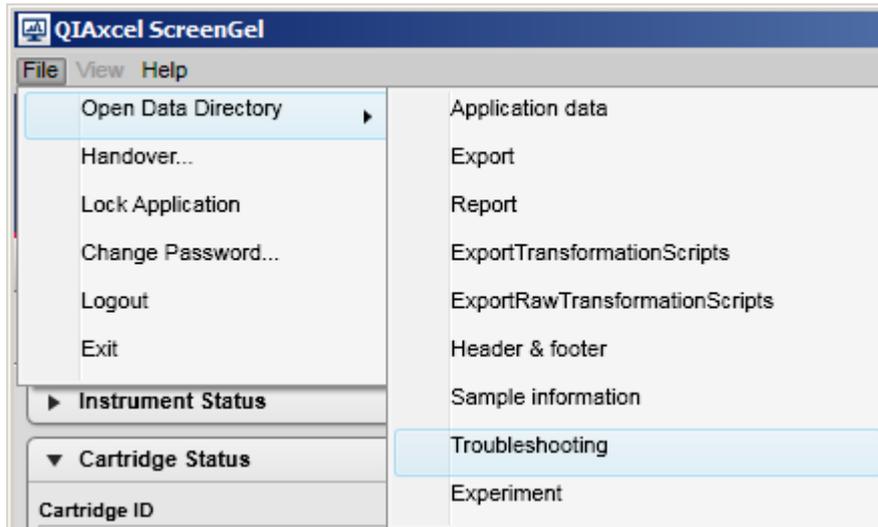
1. Switch to the **Service** environment.
2. Select the **Maintenance** or **System Check** screen.

3. Click the **Troubleshooting** folder, which is located at the bottom of the screen. It opens the following dialog:



Select information to be exported.

4. Select the time period in which the test results were produced or a problem occurred. In most cases, this is **Start Date**: yesterday, and **End Date**: today.
5. In the **Results** column, select the test results to be exported.
6. In the **Logging Information** column, select all log file types.
7. Click **OK**. The exported files are stored under the **Troubleshooting** directory defined in the [Settings](#).
8. To navigate to the **Troubleshooting** directory, select the **Open Data Directory->Troubleshooting** option from the **File** menu .



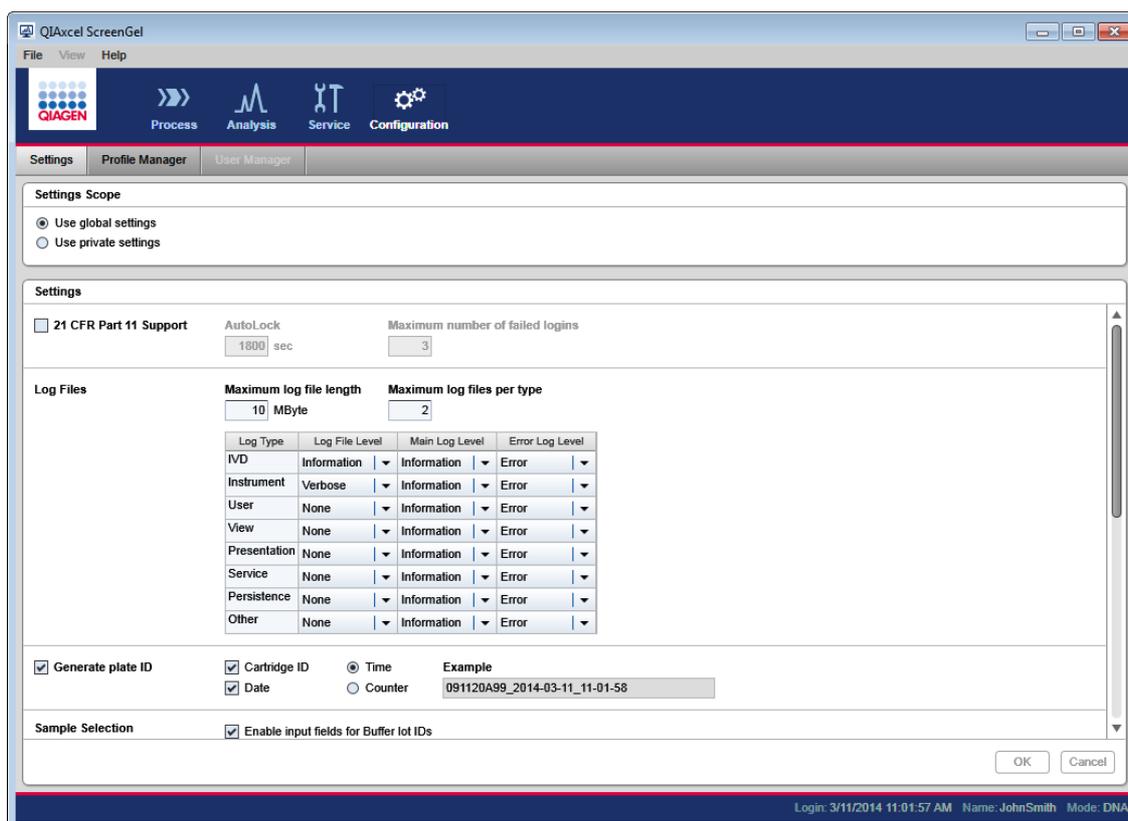
Open Data Directory function.

9. Select the just created file **Troubleshooting_..._...zip**.

Refer to the [Settings](#) section for information about log file levels.

Configuration

Application settings, users and profiles are managed in the **Configuration** environment:



Configuration environment with active Settings screen.

Settings

The **Configuration** environment of the QIAxcel ScreenGel Software provides several settings options as described below.

Note: Global settings options are read only for users with the assigned role **Routine User** or **Basic User**. Refer to the [User roles](#) section for more information.

Use global settings The global settings option is used to share both general settings and profiles among several users.

Use private settings When using private settings, both the general settings and the created profiles of the user are private.

Note: The private settings option can be activated only if the user has the right to maintain private settings (see [User management](#)).

The settings are grouped according to functionality. The following table gives an overview of the sections:

21 CFR Part 11 Support Controls functionality required by 21 CFR Part 11 (FDA guidelines on electronic records). Select this option to enable auto-lock and to limit the number of failed logins.

Option	Description
AutoLock	The system automatically locks the QIAxcel ScreenGel Software after the specified period of idle time, except when a process is running. To unlock, the user must login again. Refer to the User authentication section for more information about how to unlock. Note: Idle time means time without user action or instrument action.
Maximum number of failed logins	After the specified number of failed logins, the system automatically locks the user account. It can be unlocked by the administrator only.

Log files The QIAxcel ScreenGel Software writes all log messages to one main log file. In addition, separate log files can be created for individual log message types (IVD, Instrument, etc) and for errors. The language of all log files is English. An exception is the separate IVD log file (audit trail). If the software language is other than English, the file exists twice, one in English, and one in the selected language.

Start with the levels as shown in the following image.

Maximum log file length

 MByte

Maximum log files per type

Log Type	Log File Level	Main Log Level	Error Log Level
IVD	Information ▾	Information ▾	Error ▾
Instrument	Warning ▾	Error ▾	Error ▾
User	None ▾	Information ▾	Error ▾
View	None ▾	None ▾	None ▾
Presentation	None ▾	None ▾	None ▾
Service	None ▾	Information ▾	Error ▾
Persistence	None ▾	Information ▾	Error ▾
Other	None ▾	Error ▾	Error ▾

The size of a log file is limited; this size is configured by the **Maximum log file length**. To always have the latest log files available, a new file will be created when the maximum size has been reached. The number of log files to be kept is configured by the **Maximum log files per type**. When, for a particular log file type, the maximum number of files has been reached, the oldest file of that type will be deleted.

The verbosity increases from **Critical** to **Verbose**. When **Critical** is selected, only critical log messages are written to the log file. When **Verbose** is selected, all log messages are written to the log file.

Note: The **Verbose** level can decrease the performance of the QIAxcel ScreenGel Software. Keep the information as short as possible for each log and file type. Start with the levels as shown in the image above.

The main log file gives an overview of the last actions in the software. The verbosity of the main log file is set in the Main Log Level column of the above table. This describes how much information of a log type will be added to the main log file.

The verbosity of the individual log files is set in the **Log File Level** column. Increase the log level for special types of error tracking.

The error log file gives an overview of the last errors. The verbosity of the error log file is set in the **Error Log Level** column of the table shown above. This describes how much information of a log type will be added to the error log file. Typically, only the verbosity **Error** and **None** are used for the error log file.

Log Type	Description
IVD	Audit trail. If this is also included in the main log file, it helps to understand the last actions.
Instrument	In case of communication problems, it can be useful to increase the Log File Level to Verbose for a certain time span and to reproduce the situation. With these settings, the Instrument log file reaches the maximum log file length very soon (after one run). Therefore, disconnect from the instrument just after the situation occurred, export the log files, and return to verbosity Warning. Use verbosity Error in the columns Main Log Level and Error Log Level to keep the overview character of the main log file and the error log file.
User	Traces the user management actions.
View	Information from the graphical user interface of the software.
Presentation	Information from the graphical user interface of the software.
Service	Information from the software logic.
Persistence	Information about loading and saving. Increase verbosity of the Log File Level if there are problems with loading and saving experiments or profiles.
Other	All other information.

Refer to the [Troubleshooting folder and log files](#) section for information how to export log files.

Generate plate ID When enabled, defines how automatically generated plate IDs are constructed.

The following options define construction of the plate ID.

Generate plate ID
 Cartridge ID
 Time
 Example
 Date
 Counter
 091120A99_2010-11-10_13-49-29

Option	Description
Cartridge ID	If this option is selected, the generated plate ID will contain the Cartridge ID at the start.
Date	If this option is selected, the generated plate ID will contain the date of the data acquisition. If Cartridge ID is included, the date will be placed next to the Cartridge ID .
Time or Counter	Specifies how the uniqueness of the plate ID is achieved: with the time of the process start (including hours, minutes, and seconds) or with the counter incremented for the next plate ID generation. Note: If the plate ID is edited during process setup after automatic generation, the time will not reflect the exact process start time, but will reflect the time the plate ID was generated during process setup.

The **Example** field shows what the generated plate ID may look like.

Sample Selection Specifies which optional information can be entered at the Sample Selection screen of the process wizard.

Option	Description
Enable input fields for Buffer lot IDs	Select this option only, if you want to provide lot IDs for Buffers . If this option is not selected, you cannot provide lot IDs for Buffers during process setup.
Enable input fields for Marker lot IDs	Select this option only, if you want to provide lot IDs for Markers . If this option is not selected, you cannot provide lot IDs for Markers during process setup.
Provide Sample Information	Select this option, if you usually provide sample information. Even if this option is not selected, you can provide sample information, but have to select the Provide Sample Information option at the Sample Selection screen of the process wizard manually.
Prevent modification of imported sample information	Select this option if you want sample information from imported rack files to be "read only."

Instrument

Option	Description
Latch cartridge automatically	If this option is selected, the system latches the cartridge automatically after a cartridge is inserted and the cartridge door is closed.
Perform calibration automatically	If this option is selected, the system performs cartridge calibration automatically, if the inserted cartridge has not yet been calibrated.
COM Channel	Specifies the COM channel the QIAxcel Advanced instrument is connected to. After login, the system automatically tries to connect to the QIAxcel Advanced instrument using the specified COM port .

Rise Time

The rise time is a parameter of the **Bessel** filter applied to the raw data during acquisition. This parameter should not be changed unless you know the function of the **Bessel** filter and the effects of changes to the rise time parameter.

Directories

Specifies the directories for acquired raw data and all other application data.

The base directory for the directories listed below is initially (i.e., after the QIAxcel ScreenGel installation) the **Application Data** directory which is specified during the [Installation of the ScreenGel Software](#). All these directories are configurable.

The following directories can be specified:

Directory name	Description
Export	Default export directory. This is the default directory in which export files are generated, unless a different directory is chosen in the export profile.
Report	Default report directory. This is the default directory in which report files are generated, unless a different directory is chosen in the report profile.
Header & footer	Directory for report header and footer. During report generation the system looks here to find a header and footer to be included in the report.
Sample information	Default directory for importing or exporting sample information (see Running procedure or Running a process with advanced options , respectively). An example import rack file can be found in the default directory %DATA_DIR%\SampleInfo.
Troubleshooting	Directory where files created by the Troubleshooting folder are stored.

Experiment	Directory that contains 3 sub-directories: DNA and RNA . The experiment data files (both acquired as a process run result or combined in the Analysis environment) are saved by default in these sub-directories (according to the application mode), unless a different directory was chosen in the process profile.
Local Experiment	During a process, the experiment is saved in this directory. It is hard-coded to %DATA_DIR%\LocalExperiment. After the process has finished, the experiment is moved to the experiment path defined in the process profile. Only if this transfer fails (e.g., if it is a remote drive, and someone has tripped over the network cable), the experiment can still be found in the Local Experiment directory.
ExportTransformationScripts	This directory contains XSLT scripts for transforming export XML files. XSLT is a declarative language that enables transformation of the export XML file into a different format, for example, another XML, HTML, or plain text. Some example XSLT files can be found in the default directory %DATA_DIR%\ReportExportProfile\XSLT_Export, for creating files in .csv format from the export.
ExportRawTransformationScripts	This directory contains XSLT scripts for transforming raw data export XML files. An example XSLT file can be found in the default directory %DATA_DIR%\ReportExportProfile\XSLT_RawExport, for creating a file in .csv format from the raw data export.

Note: The directories above can be opened in the Windows Explorer directly from QIAxcel ScreenGel Software through the menu item **File/Open Data Directory**.

Most settings changes take immediate effect after clicking **OK**. The following table lists settings that require additional actions:

Generate plate ID section	Active after next login.
Instrument-COM channel	Active after reconnection with instrument. Note: After clicking OK , the system asks you to reconnect to the new COM channel.
Directories	Next login.

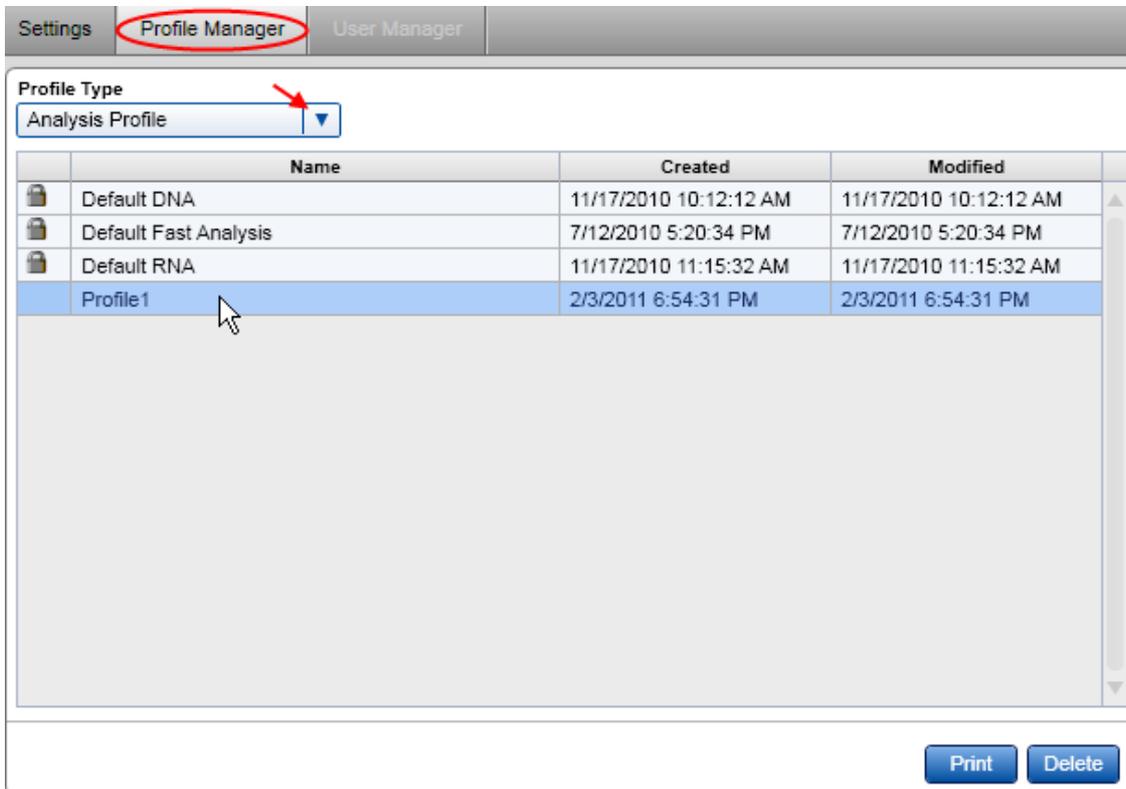
Changing the language

To view the languages supported by the software or to change the language:

1. In the **File** menu select the **Language** option.
2. Select the language in the drop-down box.
3. Close and restart the software.

Profile management

Several dialog boxes of the QIAxcel ScreenGel Software allow the creation of new profiles, for example analysis profiles, size marker tables, and reference marker tables. The **Profile Manager** lists all profiles grouped by type. Profile details can be printed and profiles can be deleted using the **Profile Manager**.



Note: Profiles that are marked with a padlock symbol are default profiles provided by QIAGEN. These profiles cannot be deleted.

User management

Administrators have access to the **User Manager** tab, in which user accounts can be modified:

User ID	Role	First Name	Last Name	DNA	RNA	Private Settings	Skip Run Checks	Revise Sample Information	Accept incomplete experiments	Last Password Change
Administrator	Administrator			✓	✓	✓				8/29/2014 2:27:32 PM
JohnBase	Basic User	John	Base	✓	✓					8/29/2014 2:37:04 PM
JohnSmith	Advanced User	John	Smith	✓	✓	✓	✓	✓	✓	8/29/2014 2:36:04 PM
JonnySmith	Routine User	Jonny	Smith	✓	✓					8/29/2014 2:36:31 PM

Show deactivated user accounts

Define user account Add

User ID: JonnySmith Initial password: First name: Jonny Mode: DNA Activated

Role: Routine User Confirm password: Last name: Smith RNA Allow private settings

May skip confirmation of run checks
 May revise sample information after run
 May accept incomplete experiments

Apply Cancel

The User Manager.

Editing user accounts

To edit an existing user account:

1. Select the user account to be modified.
2. The details are displayed in the section at the bottom of the dialog.
3. Modify the parameters as required.
4. Click the **Apply** button.

Note: In the **User Manager**, the user name, role, password, and authorizations of existing user accounts can be changed. The user ID (login name) is the unique identifier of a user and cannot be changed.

Adding users

To add a new user:

1. Click the **Add** button.
2. Specify a user ID not already in use, a user role, and a password. For details about user roles, refer to the [User roles](#) section.

Note: The password must contain one upper-case character, one lower-case character, and one digit. The minimum size of the password is eight characters.

3. Set the allowed run modes and user options.

4. Click the **Apply** button.

Note: You can create several user accounts for one person by giving the accounts different user IDs. This may be useful to distinguish different roles.

Deactivating user accounts

User accounts cannot be deleted, but they can be deactivated if users no longer work with QIAxcel ScreenGel Software data.

To deactivate a user account:

1. Select the user account to be deactivated from the list of users.
2. Uncheck the **Activated** option in the user settings. Deactivated users cannot log in anymore.
3. Click the **Apply** button.

Note: Only activated users are shown in the user table. To show deactivated users, check the **Show deactivated user accounts** checkbox below the user table.

User options

Allow private settings	Allows the user to maintain private settings.
May skip confirmation of run checks	On the Run Check page of the process wizard, the user may skip the confirmation of check messages.
May revise sample information after run	Enables the user to Revise sample information in the Experiment Explorer .
May accept incomplete experiments	If an experiment has run incompletely, the user can mark it as complete in the Experiment Explorer , overriding all warnings.

Maintenance procedures

The following maintenance procedures must be carried out to ensure reliable operation of the QIAxcel Advanced:

- Cleaning of the QIAxcel Advanced
- Minor corrective maintenance

Following these procedures ensures that the QIAxcel Advanced is free of dust and liquid spills.

Important: Disconnect the line power cord from the power outlet before servicing.

Servicing

The QIAxcel Advanced is supplied with a warranty that lasts for 1 year, starting from the date of shipment. The warranty includes all repairs due to mechanical breakdown. Application development, software upgrades, accessories, and disposable items are not included in the warranty.

QIAGEN offers comprehensive Service Support Agreements, including Warranty Extensions, Full Cover Support Agreements, and instrument/application training, including on-site installation. Service Support Agreements maximize productivity and ensure high performance from your instrument. In addition, service histories are fully documented and all parts are certified and guaranteed.

Contact your local QIAGEN Field Service Specialist or your local distributor for more information about flexible Service Support Agreements from QIAGEN.

Cleaning of the QIAxcel Advanced

Cleaning agents

CAUTION 	Damage to the instrument [C2] Do not use bleach, solvents, or reagents containing acids, alkalis, or abrasives to clean the QIAxcel Advanced.
---	---

WARNING 	Risk of electric shock [W11] Do not open any panels on the QIAxcel Advanced other than described in this user manual. Risk of personal injury and material damage Only perform maintenance that is specifically described in this user manual.
---	--

Wipe the instrument with a damp cloth only.

The sample plate holder inside the instrument should be cleaned occasionally using a moist, soft cloth.

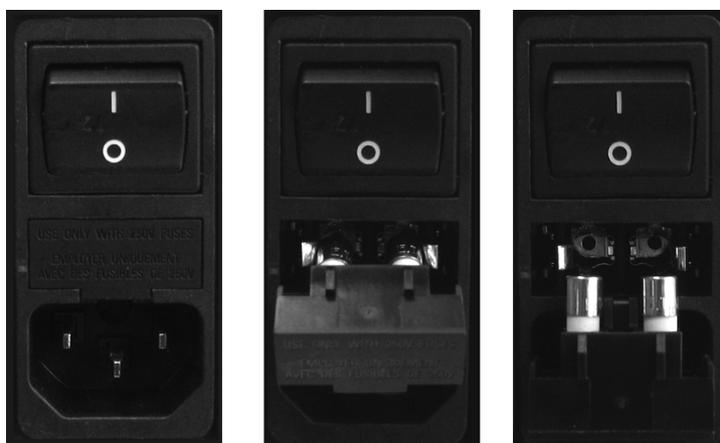
Wash the buffer tray in warm water using a mild detergent, rinse thoroughly with deionized water or reverse-osmosis water, and let it dry before filling with fresh buffer. The buffer tray should be cleaned before using a new QIAxcel gel cartridge.

Minor corrective maintenance

This section makes you familiar with the activities which may be required to maintain the QIAxcel Advanced or correct a failure.

Fuse replacement and cleaning

1. Switch off the QIAxcel Advanced using the main power switch.
2. Unplug the power cord from the power outlet and from the rear of the instrument.
3. Use a small flat-bladed screwdriver to remove the fuse-carrier assembly located above the area where the cord connector enters into the inlet.



Replacing the fuse.

4. Replace the fuse.
Replace only with time-delay 4 A (250 V) fuses, marked "T4A250V" cat. no. 9241 178. If replacement fuses are not available, contact QIAGEN Technical Services.
5. Re-insert the fuse-carrier assembly and plug in the power cord.
6. Turn on the power and check the instrument for normal operation, i.e., check that the status changes in the status panel (see section [Operating the QIAxcel Advanced](#)). If the instrument does not function normally, or continues to blow fuses, unplug the system and contact QIAGEN Technical Services.

N₂ cylinder replacement

N₂ cylinders should be changed when one or both low pressure warnings are shown in the [Status Information panel](#).

Remove the old N₂ cylinder:

Note: To remove a pressurized N₂ cylinder, empty the N₂ bottle first (see [Empty N₂ bottle](#)).

1. Open the sample door and remove the buffer tray.
2. Gently pull up on the N₂ cylinder port. Do not pull past the detent hole.
3. Turn the cylinder counter-clockwise to allow the remaining N₂ to gradually leak out.

Note: Dispose of empty N₂ cylinders as recyclable steel material according to your local regulations.

Insert a new N₂ cylinder:

4. Screw a new, unpunctured N₂ cylinder into the cylinder port in a clockwise direction.

Important: Only use N₂ cylinders provided by QIAGEN (cat. no. 929705).

5. Turn until the needle inside the port punctures the N₂ cylinder. Do not over-tighten: the cylinder should only be finger tight.
6. Gently push down on the N₂ cylinder until it is in the stowed (down) position.

Alternate N₂ supply

The QIAxcel Advanced external N₂ port (located at the rear of the instrument) can be supplied with clean, noncondensing compressed nitrogen. This external N₂ source can be used instead of the internal N₂ cylinder. The regulated N₂ minimum input pressure must be 50 psi (345 kPa) and the maximum input pressure should not exceed 75 psi (517 kPa).

To connect an external N₂ source, use the supplied urethane tubing (2 mm inner diameter x 3.18 outer diameter) rated for 150 psi. Additional tubing can be purchased separately (cat. no. 9018435).

Connect the urethane tubing from the output of the external N₂ source to the QIAxcel Advanced by firmly inserting the tubing into the fitting located on the rear panel of the instrument.

Turn on the external N₂ source pressure, and set the input pressure to 50–75 psi (345–517 kPa).

Blocked purge filter

Before a new sample run, fresh gel is purged from the gel reservoir of the cartridge into the capillaries by applying pressure through the purge line and purge port of the instrument. In rare cases when the QIAxcel gel cartridge was not stored in an upright position and equilibration conditions were not maintained, gel may run into the purge line of the instrument. A purge filter that is placed in the instrument prevents gel from running into the instrument's pressure valves. Gel in the filter or purge line will dry and thus block the filter or purge line.

To diagnose a blocked purge filter or purge line, the **Filter Check** with the QIAxcel ScreenGel Software can be performed. If the filter is blocked, a replacement of the purge filter is required. In very rare cases the purge line needs to be rinsed with water to resolve gel debris blocking the purge line tubing.

Note: Replacement of the purge filter and cleaning of the purge line is only required when the filter test failed and tubing is clogged.

Note: It is not required to replace the purge filter or cleaning the purge line as a preventive maintenance.

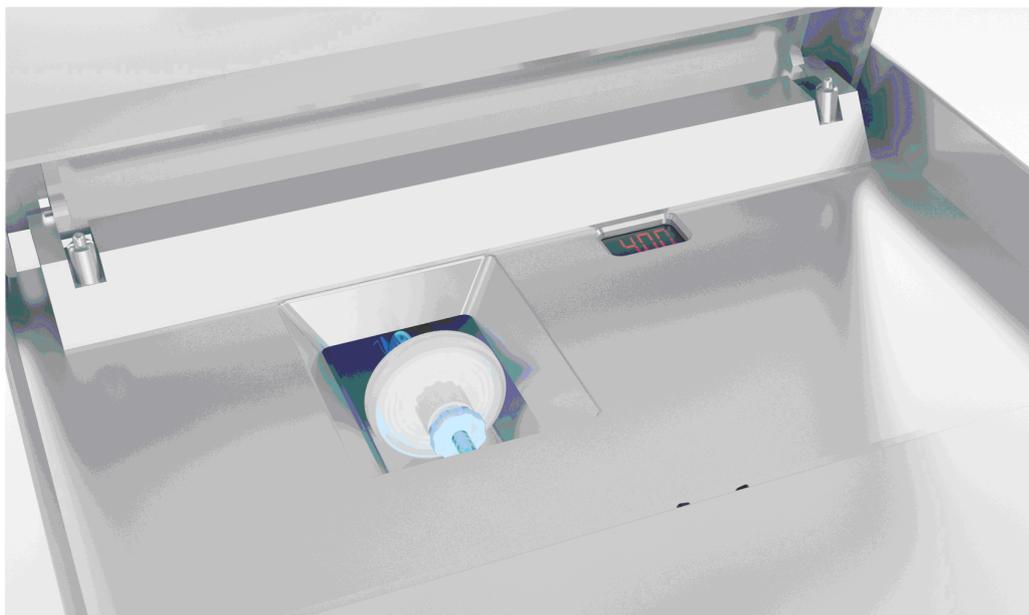
Performing a Filter Check

1. Switch on the QIAxcel Advanced.
2. Launch the QIAxcel ScreenGel Software .
3. Go to the **System Check** tab in the service environment and perform the guided **Filter Check** (see [Filter check](#)).
4. If **Filter Check** fails, replace the filter and test again.

Replacement of purge filter

1. Open the service door.
2. Remove the purge filter.

Note: Do not pull on the tubing.



3. Place a new purge filter and attach tightly to the connectors.
4. Perform the **Filter Check** again.

Note: If the **Filter Check** fails again, contact QIAGEN Technical Services.

Additional filters can be ordered from QIAGEN.

9021980 Set, Purge Filters (10), QX; please contact QIAGEN Technical Services.

Troubleshooting

This section provides information about what to do if an error occurs when using the QIAxcel Advanced and QIAxcel ScreenGel.

If you need to contact QIAGEN Technical Services about an error, note down the steps leading to the error and the information from any dialog that appear. This will help the QIAGEN Technical Service Specialist to resolve the error.

Refer to the [Troubleshooting folder and log files](#) section for detailed information on how to retrieve log files and system test results.

System setup

	Comments and suggestions
Instrument does not turn on	
a) Power cord not connected	Check the power connection.
b) Fuse blown	Replace the fuse.
Computer software cannot communicate with system	
a) RS232 cable is not connected between PC and system	Check the connection of the RS232 cable. To retry the connection to the instrument, click the  icon in the software in the Process environment.
b) Incorrect COM channel settings	Check the COM channel setting (see section Settings). At the bottom of the settings screen, click OK to confirm the changes. Click Yes in the message shown to connect again to the newly selected COM channel. If the  icon is visible, the instrument is ready to operate. If the problem persists, change the log level of the instrument log to verbose (see section Settings for information how to do this). Close the software, restart it, and login. Wait until the message appears as "the instrument is not available." Then collect the troubleshooting folder as described in the section Troubleshooting folder and log files . Ensure to check the boxes in the list at the right to include the logging information. Send the file created to QIAGEN Technical Services.
c) Instrument software version does not match the software version	If switching between the QIAxcel ScreenGel and the BioCalculator Software, close the software, turn the QIAxcel Advanced off at the power switch, wait 20 seconds and then turn it on again before launching the other software. Ensure you have opened only one of the software at a time.

Comments and suggestions

- d) Software cannot detect the COM port. Check the user permission for the registry entries that are concerned the COM ports. The pertained registry entry is typically named **HKEY_LOCAL_MACHINE\SYSTEM\ControlSet001\Enum\ACPI\PNP0501\XXXXXX\Device Parameters**. Make sure that user **Everyone** has at least read permission for this entry, otherwise the COM port scan procedure (which is invoked at start of the application) might fail if the QIAxcel ScreenGel is being operated by a user who does not have administrator permissions.
- e) Firmware update is not successful The QIAxcel ScreenGel Software comes with an up-to-date instrument software for instruments with serial number 30281 and higher. If the update process could not be completed, the QIAxcel Advanced instrument cannot connect to the QIAxcel ScreenGel Software any longer. In this case, the software provides an option to repeat the update process. Ensure that the cable between the instrument and the computer is connected correctly. Turn on the instrument. Restart the QIAxcel ScreenGel Software and login. Wait until the  icon changes to . In this case, the instrument is ready to operate again. Otherwise, a message appears that the instrument is not available. Click the **Troubleshoot** button. In the next message, click **Retry instrument update**. Wait for the **Updating Instrument** dialog. Wait a few minutes until the update is complete and the message closes. If the update is successful, the  icon is visible and the instrument is ready to operate. Otherwise, if the  icon is visible, change the log level of the instrument log to verbose (see section [Settings](#) for information how to do this) and repeat the steps to update the instrument again. Then collect the troubleshooting folder as described in the section [Troubleshooting folder and log files](#). Ensure to check the boxes in the list at the right to include the logging information. Send the file created to QIAGEN Technical Services.

No serial port in laptop computer

Some laptops do not have a serial port

Contact the PC manufacturer to request the correct serial port connector.

QIAxcel ScreenGel Software does not start

- a) QIAxcel ScreenGel Software not installed Install the QIAxcel ScreenGel Software.
- b) Old version of Microsoft Windows The QIAxcel ScreenGel Software operates with Windows 7 (32 and 64 bit) and Windows 10 (64 bit) (see section [Computer and software](#) for more details).

Operation

Comments and suggestions

N₂ cylinders do not last long

- a) Air leak Double check the N₂ cylinder to make sure it is tight.
- b) Internal leak if N₂ cylinder last only a couple of days Contact QIAGEN Technical Services.

Samples tray does not move

- a) Transport lock is in place Remove the transport lock.
- b) Sample door is not closed Close the sample door.

Cannot insert cartridge into system

Cartridge installed backwards Make sure the cartridge front cover faces the front of the system and check that the purge cap seal has been removed.

Cartridge cannot be latched

- a) N₂ pressure low Replace the N₂ cylinder.
- b) Cartridge door is open Close the cartridge door.
- c) Cartridge smart key not inserted Insert the smart key.

Cannot run system

- a) Sample door and/or cartridge door are open Close the sample door and/or cartridge door.
- b) Cartridge smart key not detected Insert the cartridge smart key
- c) Pressure low Replace the N₂ cylinder

QIAXcel ScreenGel Software is slow

- a) Too many experiments open in experiment explorer Close some of the opened experiments and then restart the QIAXcel ScreenGel Software. Try to keep the number of opened experiments low.
- b) Too many applications running concurrently. Close all unnecessary applications.

Problems when files are/shall be located on the network folder

- a) Network folder is not visible in the file dialog If the network folder is not visible in the software although it has been mapped, e.g., by an administrator, try the following to make the mapping visible for all Windows users. Delete the existing mapping. Then use the net use command together with a UNC name to map the network location. For example, in the command prompt, type the following command and press Enter:
net use \\< computername >\< sharename > /user:< username >
>

Comments and suggestions

- b) It takes too long to open a network folder
- Ask your local IT for assistance, if required.
- If you are using only one of the sub-folders of the network folder, map directly to the sub-folder instead of mapping the entire network folder. Use the net use command as described above.

DNA applications

Comments and suggestions

DNA peaks signal variation in channels

- New cartridge requires calibration
- Calibrate the cartridge (see section [Calibrating a cartridge](#)).

Slow peak migration time in channels

- a) Air bubbles in gel cartridge capillaries
- Perform a purge or 3-minute purge (see [Maintenance](#)) to remove air bubbles, or change the QX Separation Buffer.
- b) Current too low due to low temperature
- Increase the room temperature.
- c) Current too low due to partially dry capillary tips
- Perform a purge or 3-minute purge to clean the capillary tips (see [Maintenance](#)).

Weak signal of the QX Alignment Marker

- Degraded/old QX Alignment Marker
- Change the QX Alignment Marker.

No signal in channels

- a) No samples injected
- Check the volume of sample (10 µl minimum).
- b) Blocked capillary channel
- Purge the instrument to remove the blockage (see [Maintenance](#)). If this does not work, replace the cartridge.
- c) Broken capillary or optical fiber in cartridge
- Replace the cartridge.
- d) Light source problem (LEDs off)
- Check if all LEDs are illuminated. Contact QIAGEN Technical Services.
- e) No purging of the cartridge/purge filter blocked
- Perform a Filter Check.

Comments and suggestions

Loss of resolution in channels

- a) Old gel in some channels or clogged channels Perform a purge or 3-minute purge to fill the channels with new gel, or repeat the purge method several times to remove clogging (see [Maintenance](#)).
- b) Saturated signals Reduce the sample injection time or select a more suitable method.
- c) Expired cartridge Use a new cartridge.

Broad or saturated DNA peak/band

- a) DNA concentration too high Dilute the DNA solution in QX DNA Dilution Buffer.
Reduce the injection time.
Choose a method for high DNA concentration samples (e.g., 0H500 [see [Appendix B](#)]).
- b) Broken channel with high background Call QIAGEN Technical Services and replace cartridge.

DNA signal too low

- a) DNA concentration too low Increase the sample injection time.
Choose a method for low DNA concentration samples (e.g., 0L500 [see [Appendix B](#)]).
- b) Salt concentration too high in sample solution Desalt or dilute the DNA samples to reduce the salt concentration and enhance DNA injection.

Separation current (μA) too low

- a) QX Separation Buffer is contaminated Replace the QX Separation Buffer.
- b) Blocked capillary channel Replace the QIAxcel gel cartridge.

Separation current (μA) too high

- a) QX Separation Buffer contaminated Replace the QX Separation Buffer.
- b) Salt concentration too high in sample solution Desalt or dilute the DNA samples in QX DNA Dilution Buffer.

Data squeezed together on gel image folder

- a) Extra peaks before the first peak or after the last peak were detected Repeat the analysis as described in [Analysis of DNA samples](#). During the procedure, follow the instructions to increase the Alignment Marker Threshold.

Comments and suggestions

- b) Wrong peaks were identified as the first and last peaks for alignment
Repeat the analysis as described in [Analysis of DNA samples](#). During the procedure, follow the instructions to increase the Alignment Marker Threshold.
- c) Upper alignment markers were missing or below the threshold setting
Repeat the analysis as described in [Analysis of DNA samples](#). During the procedure, follow the instructions to decrease the Alignment Marker Threshold. Replace the new markers for the next run.
- d) Sample signals too strong and cause the alignment below the threshold setting
Dilute the samples or use the H Methods (see [Appendix B](#)) for sample analysis.

Data not aligned

- a) Upper marker missing
Change to a new alignment marker.
- b) Migration problem due to air bubbles
Purge and run the sample again.
- c) Migration problem due to low temperature
Increase the separation time.
- d) **Start Analysis** button in the "Analysis" environment not clicked
Click the **Start Analysis** button to perform analysis.
- e) Samples with different alignment markers visualized
Remove samples with a different alignment marker from the view.
- f) Alignment markers not identified correctly
Repeat the analysis as described in [Analysis of DNA samples](#). During the procedure, follow the instructions to adapt the analysis parameters.

No size calling in the result table

- a) The reference marker is turned off
Repeat the analysis as described in [Analysis of DNA samples](#). Select the right marker table.
- b) Peak detection failed
Repeat the analysis as described in [Analysis of DNA samples](#). During the procedure, ensure that peaks are detected correctly, especially the alignment marker peaks.

Wrong size calling

- a) Wrong reference marker table used
Repeat the analysis as described in [Analysis of DNA samples](#). Select the right marker table.

Comments and suggestions

- b) Reference marker table setting problems
- Repeat the analysis as described in [Analysis of DNA samples](#). Make sure that the correct alignment marker is set (refer to [Checking alignment marker](#)). Make sure the number of peaks in the Rel. Time and size (bp) columns are equal in the reference marker table.

No size scale in gel image

- a) Data not aligned
- Remove samples with a different alignment marker from the view. Repeat the analysis as described in [Analysis of DNA samples](#). Make sure all alignment marker peaks have been identified correctly.
- b) Samples analyzed with different reference marker tables
- Repeat the analysis as described in [Analysis of DNA samples](#) using the same reference marker table for all samples.

Required scale type not created

- a) Samples not analyzed
- Click the **Start Analysis** button to perform the analysis.
- b) Samples with different alignment markers visible
- Remove samples with a different alignment marker from the view.
- c) No size determination
- Repeat the analysis as described in [Analysis of DNA samples](#) using the same reference marker table for all samples.

Upper alignment markers resolved in double peaks

- High salt sample
- Dilute the sample or change the parameter setting.

RNA applications

Comments and suggestions

Alignment is off

- a) The first peak is below the threshold
- Repeat the analysis as described in [Analysis of RNA samples](#). During the procedure, follow the instructions to decrease the Alignment Marker Threshold.
- Contamination, for example, by salt may result in aberrant migration of individual lanes that may be too large for proper alignment. Use less sample or perform an additional cleanup of RNA samples that show delayed migration.
- b) Degraded/old calibration marker
- Replace the calibration marker.

Required scale type not created

- a) Samples not analyzed
- Click the **Start Analysis** button to perform the analysis.

Comments and suggestions

- | | |
|---|--|
| b) Samples with different alignment markers visible | Remove the samples with a different alignment marker from the view. |
| c) No size determination | Repeat the analysis as described in Analysis of RNA samples using the same valid reference marker table for all samples. |

The ratio of rRNA (28S/18S) is too low

Degraded RNA samples Change the RNA sample.

The signal of RNA sample is too low

- | | |
|---------------------------------|--|
| a) Low RNA sample concentration | Increase the sample volume up to 5 µl. Mix an equal volume of RNA loading buffer to sample. For example, if 2 µl of RNA sample was used, mix the RNA sample with 2 µl of RNA loading buffer. |
| b) Degraded RNA samples | Change the RNA samples. |

Broad RNA peaks

- | | |
|--|--|
| a) Degraded RNA samples | Change the RNA samples. |
| b) Incomplete RNA denaturation process | Repeat the RNA denaturation process. |
| c) Aged buffer | Replace the separation buffer every 25 runs. |

Only 18S RNA peak detected

- | | |
|-------------------------------------|--|
| Incomplete RNA denaturation process | Repeat the RNA denaturation process.

RNA degradation will also result in disappearance of the 28S peak first. |
|-------------------------------------|--|

Calibration marker signal variation in channels

- | | |
|---|---|
| a) New cartridge requires calibration | Calibrate the cartridge (see section Calibrating a cartridge). |
| b) Cartridge intensity calibration is incorrect | Calibrate the cartridge (see section Calibrating a cartridge). |
| c) Degraded/old QX Calibration Marker | Change the QX Calibration Marker. |

Delayed peak migration in some channels

- | | |
|--|--|
| a) Air bubbles in capillaries | Use the Long purge to remove air bubbles (see Maintenance). |
| b) Air bubbles in calibration marker or RNA sample vials | Remove the air bubbles from the vials. |

Glossary

Term	Description
Buffer tray	The buffer tray is a removable plastic tray that sits in the buffer tray holder of the QIAxcel Advanced and holds QX Separation and Wash Buffers and QX Intensity and Alignment Markers.
Buffer tray holder	The buffer tray holder is located inside the QIAxcel Advanced under the sample door. The buffer tray, which holds QX Separation and Wash Buffers and QX Intensity and Alignment Markers, is placed in the buffer tray holder prior to sample analysis.
Cartridge door	The door that allows the QIAxcel gel cartridge to be loaded into the QIAxcel Advanced. This door should remain closed during operation of the QIAxcel Advanced.
Channel(s)	Each QIAxcel gel cartridge has 12 channels (capillaries) through which the samples for analysis pass.
Method	A method is the collection of commands and parameters that are applied to an individual sample run. A number of default methods are preinstalled.
Mineral oil	For covering solutions and/or samples to prevent evaporation.
N ₂ door	The N ₂ door, located to the right of the sample door, allows insertion and removal of the N ₂ cylinder.
Position	An area of a rack/plate that can contain something. Examples of positions include the wells of a microplate or slots in the sample plate holder.
Power switch	A button located at the back of the QIAxcel Advanced in the bottom-left corner. It allows the user to switch the QIAxcel Advanced on and off.
Process Profile	This defines settings for data acquisition. Defines all parameters for the electrophoresis run.
Purge port	The purge port is located inside the QIAxcel Advanced instrument and aligns with the purge hole of the QIAxcel gel cartridge.
QX Alignment Marker	Allows sample migration time to be calibrated.
QX DNA or RNA Dilution Buffer	Allows dilution of concentrated samples.
QX DNA or RNA Separation Buffer	Enables separation of DNA or RNA molecules in the QIAxcel gel cartridge.
QX DNA or RNA Size Marker	Enables creation of a reference marker table allowing DNA/RNA size and/or concentration determination.

Term	Description
QX DNA or RNA Wash Buffer	For washing the capillary tips to prevent cross-contamination.
QX Intensity Calibration Marker	Allows calibration of the signal intensity for each new gel cartridge.
Sample door	The door that provides access to the sample plate holder and the buffer tray holder. This door should remain closed during operation of the QIAxcel Advanced.
Sample plate holder	The sample plate holder is located inside the QIAxcel Advanced under the sample door. 96-well plates or sample strips containing the samples for analysis are placed in the sample plate holder.
Service door	The service door allows access to the purge filter and a manometer.
Smart key	This key attached to the QIAxcel gel cartridge holds information about the cartridge (i.e., cartridge identifier, calibration status, number of runs). The smart key should be inserted into the smart key socket on the QIAxcel Advanced to enable sample analysis.
Smart key socket	The smart key socket allows the QIAxcel Advanced instrument to read and display the information on the smart key.

Appendices

The appendices contain technical data, QIAxcel methods and accessories, descriptions of the data analysis algorithms, and warranty terms.

Appendix A

Technical data

QIAGEN reserves the right to change specifications at any time.

Environmental conditions

Operating conditions

Power	100–240 V AC, 50–60 Hz, 360 VA
Fuse rating	4 A (250 V) time-delay fuse (for 100–240 V AC)
Overvoltage category	II
Air temperature	15–30°C (59–86°F)
Relative humidity	10–75% (noncondensing)
Altitude	Up to 2000 m (6500 ft.)
Place of operation	For indoor use only
Pollution level	2
Environmental class	3K2 (IEC 60721-3-3)

Transportation conditions

Air temperature	–25°C to 60°C (–13°F to 140°F) in manufacturer's package
Relative humidity	Max. 75% (noncondensing)

Storage conditions

Air temperature	15°C to 30°C (59°F to 86°F) in manufacturer's package
Relative humidity	Max. 75% (noncondensing)

Mechanical data and hardware features

Dimensions (door closed)	Width: 370 mm (14.57 in.) Height: 405 mm (15.94 in.) Depth: 555 mm (21.85 in.)
Dimensions (doors open)	Width: 370 mm (14.57 in.) Height: 706 mm (27.80 in.) Depth: 555 mm (21.85 in.)
Mass	27 kg (59.52 lb.)
Capacity	Up to 96 samples per run
Software	Default protocols are provided with the QIAxcel ScreenGel Software supplied with the QIAxcel Advanced. Updated protocols are available from www.qiagen.com/QIAxcelAdvanced .

Waste Electrical and Electronic Equipment (WEEE)

This section provides information about disposal of waste electrical and electronic equipment by users.

The crossed-out wheeled bin symbol (see below) indicates that this product must not be disposed of with other waste; it must be taken to an approved treatment facility or to a designated collection point for recycling, according to local laws and regulations.

The separate collection and recycling of waste electronic equipment at the time of disposal helps to conserve natural resources and ensures that the product is recycled in a manner that protects human health and the environment.



Recycling can be provided by QIAGEN upon request at additional cost. In the European Union, in accordance with the specific WEEE recycling requirements and where a replacement product is being supplied by QIAGEN, free recycling of its WEEE-marked electronic equipment is provided.

To recycle electronic equipment, contact your local QIAGEN sales office for the required return form. Once the form is submitted, you will be contacted by QIAGEN either to request follow-up information for scheduling collection of the electronic waste or to provide you with an individual quote.

FCC Declaration

The "United States Federal Communications Commission" (USFCC) (in 47 CFR 15. 105) declared that the users of this product must be informed of the following facts and circumstances.

This device complies with part 15 of the FCC. Operation is subject to the following two conditions: (1) This device may not cause harmful interference, and (2) this device must accept any interference received, including interference that may cause undesired operation.

This Class B digital apparatus complies with Canadian ICES-003.

The following statement applies to the products covered in this manual, unless otherwise specified herein. The statement for other products will appear in the accompanying documentation.

NOTE: This equipment has been tested and found to comply with the limits for a Class B digital device, pursuant to part 15 of the FCC Rules. These limits are designed to provide reasonable protection against harmful interference in a residential installation. This equipment generates, uses and can radiate radio frequency energy and, if not installed and used in accordance with the instructions, may cause harmful interference to radio communications. However, there is no guarantee that interference will not occur in a particular installation. If this equipment does cause harmful interference to radio or television reception, which can be determined by turning the equipment off and on, the user is encouraged to try to correct the interference by one or more of the following measures:

- Reorient or relocate the receiving antenna.
- Increase the separation between the equipment and receiver.
- Connect the equipment into an outlet on a circuit different from that to which the receiver is connected.
- Consult the dealer or an experienced radio/ TV technician for help.



QIAGEN GmbH, Germany is not responsible for any radio television interference caused by unauthorized modifications of this equipment or the substitution or attachment of connection cables and equipment other than those specified by QIAGEN GmbH, Germany. The correction of interference caused by such unauthorized modification, substitution or attachment will be the responsibility of the user.

Declaration of conformity

Name and address of the legal manufacturer

QIAGEN GmbH
QIAGEN Strasse 1
40724 Hilden
Germany

An up-to-date Declaration of Conformity can be requested from QIAGEN Technical Services.

Appendix B

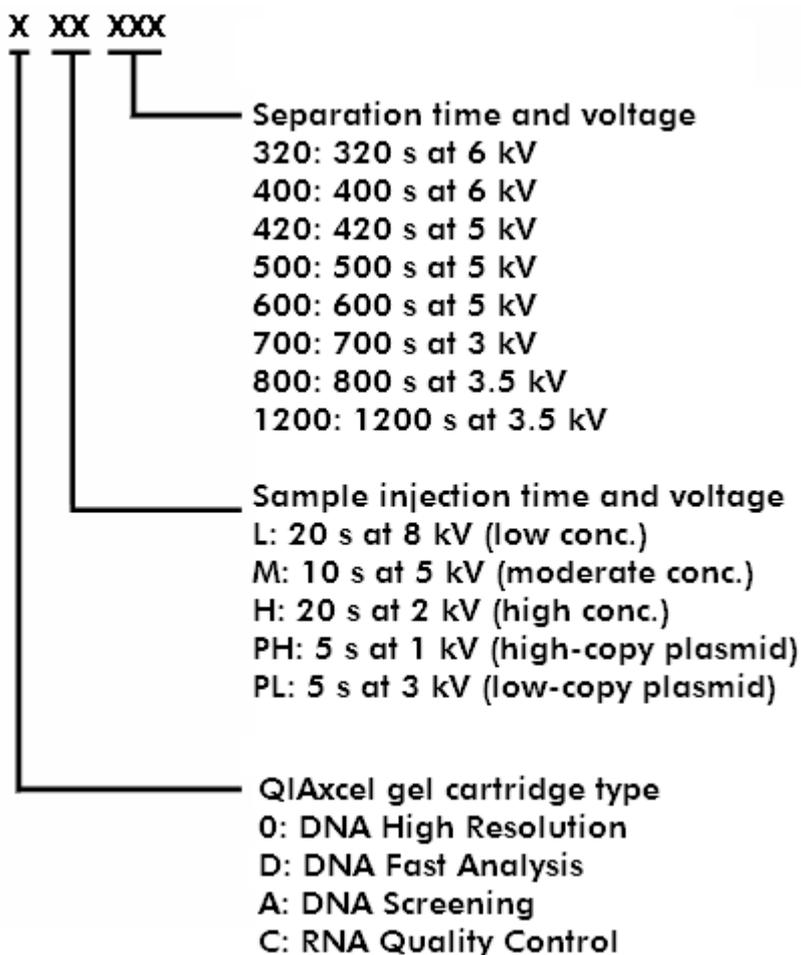
QIAxcel Advanced methods

A number of default methods are available for each QIAxcel Kit. Note that only the methods available for the particular cartridge type can be selected.

Note: If you require a custom method to be created, please contact QIAGEN Technical Services.

DNA/RNA methods

Each method name is an acronym, providing information on the specific QIAxcel Kit/QIAxcel gel cartridge being used, the sample injection time and voltage, and the separation time and voltage, as described below.



Description of method name acronyms.

Please find below a complete list of methods available for each QIAxcel gel cartridge type and information regarding their associated fragment sizes and best resolution.

QIAxcel DNA High Resolution methods

The QIAxcel DNA High Resolution Gel Cartridge is designed for high-resolution (3–5 bp) genotyping, high-resolution multiplex PCR, and AFLP/RFLP analysis of less than 20 fragments. The gel cartridge can separate fragment sizes ranging from 15 bp to 10 kb. The resolution depends on the fragment size and the method chosen to run the assay:

Guidelines for method selection using the QIAxcel DNA High Resolution Kit

Method	Fragment size			
	100–500 bp	500 bp – 1 kb	1–5 kb	5–10 kb
	Best resolution			
OM400*	20 bp	100 bp	500 bp	N/A
OL400†				
OH400‡				
OM500*	10 bp	50 bp	200 bp	N/A
OL500†				
OH500‡				
OM700*	3–5 bp	N/A	N/A	N/A
OL700†				
OH700‡				
OM800*	3–5 bp	N/A	N/A	N/A
OL800†				
OH800‡				
OM1200*	N/A	N/A	500 bp – 1 kb	1– 1.5 kb
OL1200†				
OH1200‡				

* We recommend the OM400, OM500, OM700, OM800, and OM1200 methods for DNA concentrations of 10–100 ng/μl (e.g., PCR products amplified from genomic DNA with 30–40 cycles).

† We recommend the OL400, OL500, OL700, OL800, and OL1200 methods for DNA concentrations of <10 ng/μl.

‡ We recommend the OH400, OH500, OH700, OH800, and OL1200 methods for DNA concentrations of >100 ng/μl (e.g., high-yield PCR products).

M Methods

We recommend the OM400, OM500, OM700, OM800, and OL1200 methods for DNA concentrations of 10–100 ng/μl.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
OM400	5	10	6	400
OM500	5	10	5	500
OM700†	5	10	3	700
OM800	5	10	3	800
OM1200	5	10	3.5	1200

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 5%.

† We recommend using method OM800 instead.

L Methods

We recommend the OL400, OL500, OL700, OL800, and OL1200 methods for DNA concentrations of <10 ng/μl.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
OL400	8	20	6	400
OL500	8	20	5	500
OL700†	8	20	3	700
OL800	8	20	3	800
OL1200	8	20	3.5	1200

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 5%.

† We recommend using method OL800 instead.

H Methods

We recommend the OH400, OH500, OH700, OH800, and OH1200 methods for DNA concentrations of >100 ng/ μ l.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
OH400	2	20	6	400
OH500	2	20	5	500
OH700†	2	20	3	700
OH800	2	20	3	800
OH1200	2	20	3.5	1200

* Sample injection time can be adjusted (minimum 1 s; maximum 60 s). Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 5%.

† We recommend using method OH800 instead.

Note: Unpurified PCR products contain dNTPs and primers, which can contribute to the optical density (OD) and cause over estimation of the DNA concentration.

QIAxcel DNA Screening methods

The QIAxcel DNA Screening Kit is designed for low-resolution (>20 bp) genotyping, low-resolution multiplex PCR, single PCR screening, plasmid DNA digestion checking, plasmid and oligo DNA quantity checking, and gDNA quality checking. The gel cartridge can separate the fragment size range from 15 bp to 5 kb. The resolution depends on the fragment size and the method chosen to run the assay:

Guidelines for method selection using the QIAxcel DNA Screening Kit

Method	Fragment size		
	<500 bp	500 bp – 1 kb	1–5 kb
AM320*	20 bp	100 bp	500 bp
AL320†			
AH320‡			
AM420*	20 bp	100 bp	500 bp
AL420†			
AH420‡			
APH600	Uncut plasmid DNA checking		
APL600			
AM900	gDNA quality checking		

* The AM320 and AM420 methods are recommended for DNA concentrations 10–100 ng/μl (e.g., PCR products [30–40 cycles] amplified from genomic DNA).

† The AL320 and AL420 methods are recommended for DNA concentrations <10 ng/μl.

‡ The AH320 and AH420 methods are recommended for DNA concentrations >100 ng/μl (e.g., high-yield PCR products).

M Methods

The AM320 and AM420 methods are recommended for DNA concentrations 10–100 ng/μl, while method APH600 is recommended for purified high-copy plasmid DNA (50–300 ng/μl) in elution buffer. Method AM900 is recommended for a visual quality check of gDNA purified using silica-based methods.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
AM320	5	10	6	320
AM420	5	10	5	420
APH600	1	5	6	600
AM900	2	40	3.5	900

L Methods

The AL320 and AL420 methods are recommended for DNA concentrations <10 ng/μl, while method APL600 is recommended for purified low-copy plasmid DNA (<50 ng/μl) in elution buffer.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
AL320	8	20	6	320
AL420	8	20	5	420
APL600	3	5	6	600

* Sample injection time can be adjusted from 5 to 40 seconds to obtain optimal signals. Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 7%.

H Methods

The AL320 and AL420 methods are recommended for DNA concentrations >100 ng/μl.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
AH320	2	20	6	320
AH420	2	20	5	420

* Sample injection time can be adjusted from 5 to 40 seconds to obtain optimal signals. Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 7%.

Note: Unpurified PCR products contain dNTPs and primers, which can contribute to the optical density (OD) and cause overestimation of the DNA concentration.

QIAxcel DNA Fast Analysis methods

The QIAxcel DNA Fast Analysis Gel Cartridge is designed for rapid analysis of PCR fragments. The gel cartridge can separate fragments ranging from 15 bp to 3 kb in size.

Note: The QIAxcel DNA Fast Analysis Cartridge, QX DNA Size Marker 50 bp – 1.5 kb, and the corresponding methods are not suited for concentration determination.

Methods for use with the QIAxcel DNA Fast Analysis Cartridge

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
DM80	15	8	15	80
DM80 v2.0†	15	8	15	80
DM150	10	10	10	150
DM190	10	15	10	190

* Sample injection time can be adjusted (minimum 1 s; maximum 40 s). To obtain optimal signals, we recommend using a minimum of 5 s and a maximum of 15 s.

† DM80 v2.0 includes a longer purge time between runs and thus improves the background level.

QIAxcel RNA Quality Control methods

The QIAxcel RNA Quality Control Gel Cartridge is designed for quality control of total RNA, cRNA, fragmented RNA, and single-stranded cDNA.

- Method CM-F-RNA is recommended for use with fragmented RNA and fragmented DNA at a concentration of 250–500 ng/μl.
- Method CM-RNA is recommended for use with total RNA at a concentration of 300–1000 ng/μl or cRNA at a concentration of 100–500 ng/μl.
- Method CL-RNA is recommended for use with total RNA at a concentration of 50–300 ng/μl or cRNA at a concentration of <100 ng/μl.

Note: Total RNA and cRNA concentrations >1 μg/μl should be diluted to 1 μg/μl in sterile DEPC water before denaturing.

Method	Sample injection voltage (kV)	Sample injection time (s)*	Separation voltage (kV)	Separation time (s)
CM-F-RNA	7	20	3	600
CM-RNA	5	20	6	600
CL-RNA	8	20	6	600

* Sample injection time can be adjusted from 5 to 40 seconds to obtain optimal signals. Reduce the injection time if the signal is saturated, as indicated by peaks with flat tops. Increase sample injection time if the signal is below the default setting of the threshold of 7%.

Appendix C

QIAxcel accessories

Product	Contents	Cat. no.
QIAxcel Advanced Instrument	Automated system for fast and fully automated DNA fragment analysis or qualitative and quantitative RNA analysis, QIAxcel ScreenGel software, 1-year warranty on parts and labor	9001941
QIAxcel Advanced Priority Package	Capillary electrophoresis device: includes Priority Package with computer, QIAxcel ScreenGel Software, installation, training, 2-year warranty on parts and labor, and 2 preventive maintenance visits	9002124
QIAxcel Advanced Priority Package Plus	Capillary electrophoresis device: includes Priority Package Plus with computer, QIAxcel ScreenGel Software, installation, training, 3-year warranty on parts and labor, and 3 preventive maintenance visits	9002125

QIAxcel Kits

QIAxcel DNA High Resolution Kit (1200)	QIAxcel DNA High Resolution Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, 12-Tube Strips	929002
QIAxcel DNA Screening Kit (2400)	QIAxcel DNA Screening Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, 12-Tube Strips	929004
QIAxcel DNA Fast Analysis Kit (3000)	QIAxcel DNA Fast Analysis Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, QX DNA Size Marker 50 bp – 1.5 kb, QX Alignment Marker 15 bp/3 kb, 12-Tube Strips	929008
QIAxcel RNA QC Kit v2.0 (1200)	For 100 runs of 12 samples: QIAxcel RNA Quality Control Cartridge, Buffers, Mineral Oil, QX Intensity Calibration Marker, QX RNA Alignment Marker, QX RNA Size Marker 200-6000 nt, QX RNA Denaturation Buffer, 12-Tube Strips	929104

DNA size markers

QX DNA Size Marker pUC18/HaeIII (50 µl)	DNA size marker with 9 fragments: 80–587 bp	929550
QX DNA Size Marker FX174/HaeIII (50 µl)	DNA size marker with 11 fragments: 72–1353 bp	929551

QX DNA Size Marker 100 bp – 2.5 kb (50 µl)	50 µl DNA size marker with 14 fragments: 100 bp – 2.5 kb	929559
QX DNA Size Marker 25–500 bp v2.0	50 µl DNA size marker with 17 fragments: 25–500 bp	929560
QX DNA Size Marker 50–800 bp v2.0	50 µl DNA size marker with 11 fragments: 50–800 bp	929561
QX DNA Size Marker 250 bp – 4 kb v2.0	50 µl DNA size marker with 11 fragments: 250 bp – 4 kb	929562
QX DNA Size Marker 250 bp – 8 kb v2.0	50 µl DNA size marker with 11 fragments: 250 bp – 8 kb	929563

Alignment markers

QX Alignment Marker 15 bp/600 bp (1.5 ml)	Alignment marker with 15 bp and 600 bp fragments	929530
QX Alignment Marker 15 bp/1 kb (1.5 ml)	Alignment marker with 15 bp and 1 kb fragments	929521
QX Alignment Marker 15 bp/3 kb (1.5 ml)	Alignment marker with 15 bp and 3 kb fragments	929522
QX Alignment Marker 15 bp/10 kb (1.5 ml)	Alignment marker with 15 bp and 10 kb fragments	929523
QX Alignment Marker 15 bp/5 kb (1.5 ml)	Alignment marker with 15 bp and 5 kb fragments	929524
QX Alignment Marker 50 bp/1 kb (1.5 ml)	Alignment marker with 50 bp and 1 kb fragments	929526
QX Alignment Marker 50 bp/5 kb (1.5 ml)	Alignment marker with 50 bp and 5 kb fragments	929529
QX RNA Alignment Marker (1.5 ml)	1.5 ml RNA alignment marker	929510

Calibration marker

QX Intensity Calibration Marker (600 µl)	600 µl QX Intensity Calibration Marker	929500
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Buffers

QX DNA Dilution Buffer (15 ml)	15 ml QX DNA Dilution Buffer	929601
QX RNA Dilution Buffer (15 ml)	15 ml QX RNA Dilution Buffer	929602
QX Separation Buffer (40 ml)	40 ml QX Separation Buffer	929603
QX FA Separation Buffer (40 ml)	40 ml QX Separation Buffer; for use with QIAxcel DNA Fast Analysis Cartridges	929606
QX Wash Buffer (40 ml)	40 ml QX Wash Buffer	929604
QX Mineral Oil (50 ml)	50 ml QX Mineral Oil	929605

Accessories

QX Cartridge Stand	QX Cartridge Stand	929701
QX Cartridge Stand Cover	QX Cartridge Stand Cover	929707
QX Buffer Tray	QX Buffer Tray	929702
QX 0.2 ml 12-Tube Strip (80)	80 x QX 0.2 ml 12-Tube Strips	929703
QX Multicolor 0.2 ml 12-Tube Strip (80)	80 x QX Multicolor 0.2 ml 12-Tube Strips	929704
QX Nitrogen Cylinder (6)	6 x QX Nitrogen Cylinder	929705
QX Cartridge Purge Tool	QX Cartridge Purge Tool	9241169

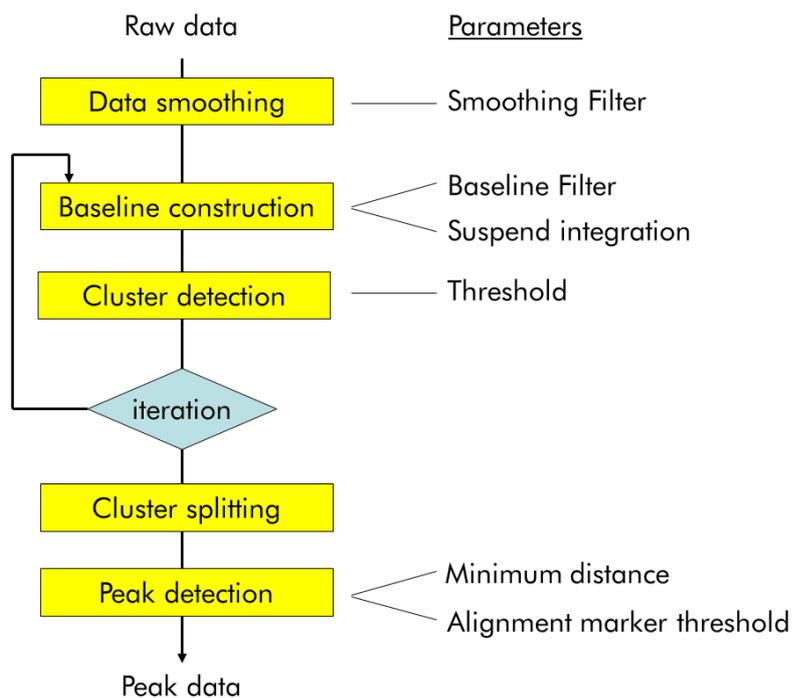
For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

Appendix D

DNA analysis algorithm description

Summary

The figure below shows a flow diagram of the algorithm. The first step of the data analysis is smoothing. Then, an iterative approach is used to construct the baseline. The objective of this baseline construction is to effectively remove the peaks but accurately follow any other disturbances, e.g. baseline drift and shifts, in the electropherogram. The next step is the cluster detection. Clusters are defined as data subsets in the electropherogram where there is a certain minimal difference in signal between the actual data and the constructed baseline. In this step, no distinction is made between a single peak or multiple not baseline separated peaks. The next step is to split clusters that contain more than one peak. Finally, the actual peak detection is performed, in which peak apex, start point, end point and area are determined.



Smoothing

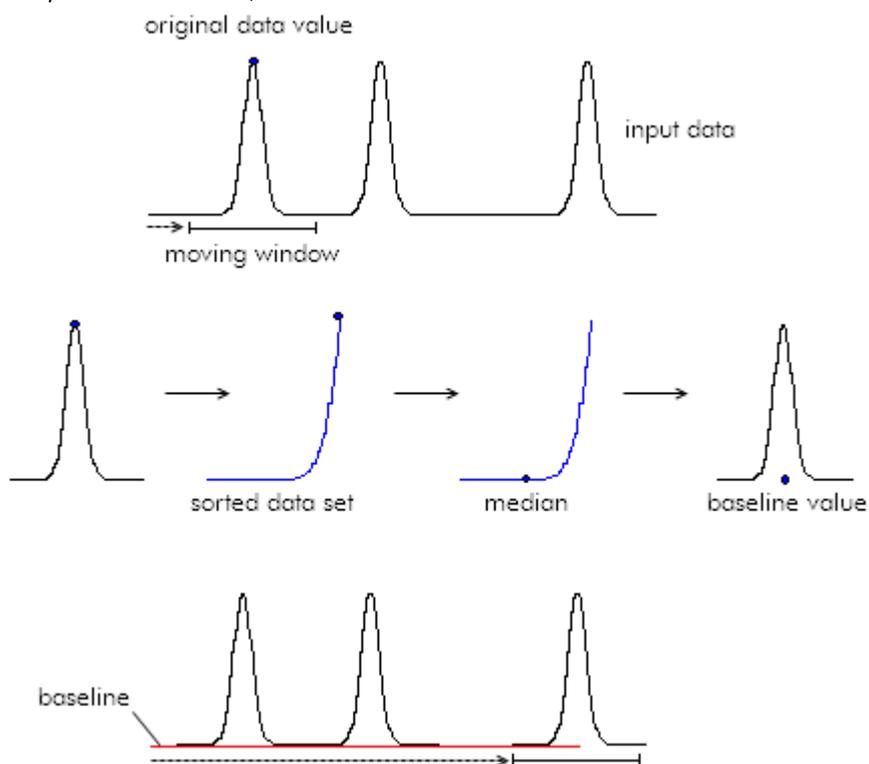
Smoothing is performed to increase the signal-to-noise ratio (S/N) of the data.

Smoothing is performed with a Savitzky-Golay filter using a second order polynomial. One exception is the analysis of smear DNA samples. A weighted average filter is applied to smooth this type of data.

Baseline construction

The baseline construction is based on a moving median filter. The median of a dataset is defined as the center point of a dataset sorted in ascending order. A moving median filter processes the input data by replacing each data point by the median of a data subset centered around that datapoints.

If the original dataset is an electropherogram, the electrophoretic peaks will be sorted towards the high end because they have a higher intensity than the noise peaks. This means that as long as the size of the moving median filter (Filter Size) is at least twice the baseline peak width, datapoints of that peak will never reach the center (median) of the data subset, and will therefore be removed.



Mathematically the construction of the baseline using a moving median filter can be described as follows:

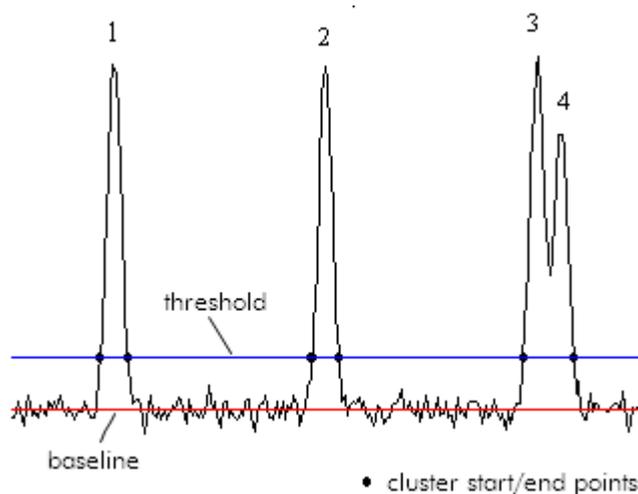
$$B(i) = \underset{x=i-r}{\overset{i+r}{\text{Median}}}(E(x))$$

in which B(i) represents the constructed baseline, E(i) the electropherogram, and r the filter rank.

An exception is the analysis of smear DNA and gDNA samples. The baseline for smear DNA analysis is constructed by taking the straight line that results from interpolating between the average signal values of ranges specified at the beginning and at the end of the electropherogram. The baseline for gDNA analysis is constructed by taking a horizontal straight line that starts from the average signal values at the beginning of the electropherogram.

Cluster detection

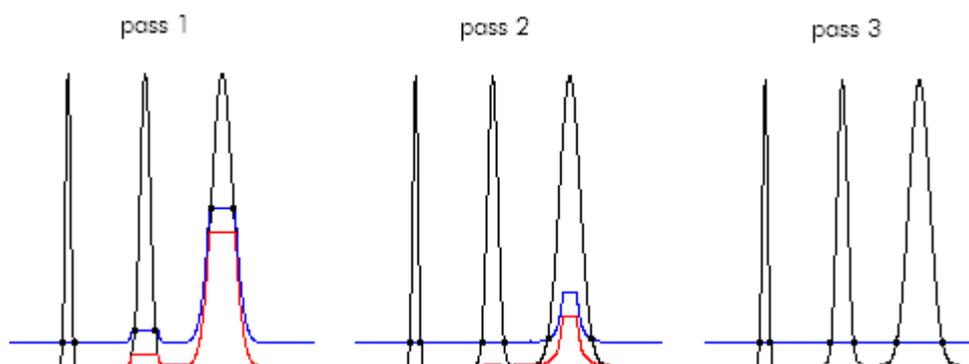
After the baseline construction, the actual peak detection is started. The first step of this process is called cluster detection. Clusters are defined as regions, i.e. data subsets, in the electropherogram where there is a significant difference between the raw data and the constructed baseline (see figure below). The parameter used to find these regions is the Threshold. The threshold is an imaginary line parallel to the constructed baseline, which marks the minimal height a peak must have (in reference to the constructed baseline) to be detected.



The identified regions can contain either one peak (peaks 1 and 2) or multiple, not baseline separated, peaks (peaks 3 and 4). In either case the region is called a cluster. Initially, the cluster start- and end points are marked as the points where the raw datapoints and the Minimum Peakheight threshold line cross.

The iteration process

As pointed out before, the successful removal of peaks during the baseline construction is dependent on the baseline filter size and peak width. In some cases it is not easy, or even impossible, to find a baseline filter size for optimal removal of all peaks in the electropherogram. This is especially the case in electropherograms with a wide variety of peak widths (requiring a large filter size on a very unstable baseline (requiring a small filter size to accurately preserve these relative high frequency baseline disturbances). The following Figure shows the effect of a too small filter size on the results of the baseline construction.



In the first pass, peak 1 is removed, but in peaks 2 and 3, the constructed baseline starts following the peak. Without any further modifications to the algorithm, this would result in inaccurate peak integration. To solve this problem the algorithm was made iterative. This means that multiple passes through the baseline construction and cluster detection are made, improving the baseline in each pass. The whole iteration process is based on the fact that even though the baseline construction during the first pass was not optimal, normally most of the clusters are still detected.

The principle of the iteration process is that the cluster information obtained in the previous pass is used to optimize the baseline construction in the current pass. In every additional pass, similar to the first pass, a moving median filter is used for the baseline construction. However, before determining the baseline, a check is made for overlaps between the clusters detected in the previous pass and the current filter position. If an overlap is detected, those points are deleted from the sorted data subset, leaving virtually only datapoints corresponding to baseline points in the original electropherogram. The value for the baseline is now determined by taking the median of this new shortened data subset.

The figure of pass 2 shows the new baseline calculated after two passes. The baseline under peak 2 is now correct but the baseline under peak 3 is still incorrect. Note, however, that the cluster start- and end points in peak 3 have shifted considerably closer to the correct position. A third pass therefore will remove a larger part of the peak from the sorted data subset leading to an improved baseline as shown after pass 3.

Cluster splitting

During the cluster detection, clusters with one or several peaks are determined. In cluster splitting step splits clusters with more than one peak into several clusters. This facilitates the peak detection in the next step. The algorithm used is very similar to the cluster detection algorithm. Cluster splitting is performed by iteratively increasing the threshold until clusters with more than one peak decompose to several clusters.

Note: During **Smear Analysis** the goal is to detect smear peaks. As these peaks are relatively broad, the cluster splitting step is omitted during smear peak detection.

Peak detection

After the cluster splitting, each cluster contains exactly one peak. The apex of the peak is determined by looking up the maximum data point in the cluster. Then, the exact start- and end points of the peak are determined. Two criteria are used for this purpose; the first criterion locates the start- and end points of a cluster at the first point (in both directions, starting from the center of the cluster) where the raw data and the constructed baseline cross each other. The second criterion is used to detect cluster borders in case of overlapping peaks (where the raw data and baseline do not cross). In this case the start- and end points of a peak are located at the points where the absolute value of the first derivative remains below a certain threshold for several datapoints. Starting at the center of the cluster, the actual start- and end points of a cluster are found at the first points where one of these two criteria is met.

Note: During the peak detection, peaks that are too close to each other are merged (based on the *Minimum distance* parameter). To ensure detection of overlapping peaks, make sure that the value of the *Minimum distance* is less than the distance between two peaks. Lower the *Minimum distance* if necessary, especially if your peaks are very sharp and closely resolved.

Note: During **Smear** and **gDNA Analysis** alignment marker peaks are detected as normal peaks and smear peaks are detected as smear peaks. Each smear peak has an assigned **Area of Interest**. The borders of the **Area of Interest** are initially set to the borders of the detected peak.

Appendix E

Liability clause

QIAGEN shall be released from all obligations under its warranty in the event repairs or modifications are made by persons other than its own personnel, except in cases where the Company has given its written consent to perform such repairs or modifications.

All materials replaced under this warranty will be warranted only for the duration of the original warranty period, and in no case beyond the original expiration date of original warranty unless authorized in writing by an officer of the Company. Read-out devices, interfacing devices and associated software will be warranted only for the period offered by the original manufacturer of these products. Representations and warranties made by any person, including representatives of QIAGEN, which are inconsistent or in conflict with the conditions in this warranty shall not be binding upon the Company unless produced in writing and approved by an officer of QIAGEN.

Appendix F

Informations de sécurité

Avant d'utiliser le QIAxcel Advanced, il est impératif de lire attentivement ce manuel et de porter une attention particulière aux informations de sécurité. Afin de garantir un fonctionnement de l'appareil en toute sécurité et de maintenir l'appareil en bon état de marche, il est impératif de suivre les instructions et les informations de sécurité fournies dans le présent manuel d'utilisation.

Les types d'informations de sécurité suivants sont fournis tout au long du manuel.

WARNING 	La formule « WARNING » (DANGER) est utilisée pour avertir des situations pouvant occasionner des dommages corporels à l'utilisateur ou à d'autres personnes. Les détails sur ces circonstances sont donnés dans un encadré semblable à celui-ci.
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CAUTION 	Le terme « CAUTION » (AVERTISSEMENT) est utilisé pour signaler les situations susceptibles de provoquer des détériorations de l'instrument ou d'autre matériel. Les détails sur ces circonstances figurent dans un encadré semblable à celui-ci.
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Les conseils donnés dans ce manuel ont pour but de venir compléter les exigences de sécurité habituelles en vigueur dans le pays de l'utilisateur et non de s'y substituer.

Utilisation appropriée

WARNING/ CAUTION 	Risque de dommages corporels et matériels [W1] L'utilisation non convenable du QIAxcel Advanced peut causer des blessures ou des détériorations de l'instrument. Le QIAxcel Advanced ne doit être utilisé que par du personnel qualifié qui a été formé de façon appropriée. Seul un ingénieur du service après-vente QIAGEN est autorisé à effectuer des travaux d'entretien sur le QIAxcel Advanced.
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Procéder à la maintenance comme décrit dans la section « [Maintenance Procedures](#) » (Procédures de Maintenance). QIAGEN facture les réparations rendues nécessaires suite à une maintenance inappropriée.

<p>WARNING/ CAUTION</p> 	<p>Risque de dommages corporels et matériels [W2]</p> <p>Le QIAxcel Advanced est trop lourd pour être soulevé par une personne. Pour éviter des dommages corporels ou matériels, ne pas soulever l'instrument tout seul.</p>
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<p>WARNING/ CAUTION</p> 	<p>Risque de dommages corporels et matériels [W3]</p> <p>Ne pas essayer de bouger le QIAxcel Advanced pendant son fonctionnement.</p>
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<p>CAUTION</p> 	<p>Détérioration de l'appareil [C1]</p> <p>Eviter de renverser de l'eau ou des substances chimiques sur le QIAxcel Advanced. Tout dommage causé par de l'eau ou des produits chimiques mettra fin à la garantie.</p>
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En cas d'urgence, éteignez le QIAxcel Advanced à l'aide de l'interrupteur d'alimentation situé à l'arrière de l'appareil et débranchez le câble d'alimentation de la prise de courant.

<p>CAUTION</p> 	<p>Détérioration de l'appareil [C2]</p> <p>Si « Pressure 1 » indique « Low » (bas) augmentez la pression du système avant d'utiliser la commande « unlatch » (décrochage). En enlevant la cartouche et la décrochant à pression réduite, l'appareil peut se détériorer.</p>
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<p>CAUTION</p> 	<p>Détérioration de l'instrument [C3]</p> <p>Ne pas utiliser d'eau de Javel, de solvants ou de réactifs contenant des acides, alcalins ou abrasifs pour nettoyer le QIAxcel Advanced</p>
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Sécurité électrique

Avant l'entretien, débranchez le cordon d'alimentation de la prise de courant.

<p>WARNING</p> 	<p>Risque d'électrocution [W4]</p> <p>Toute interruption du conducteur de protection à l'intérieur ou à l'extérieur de l'instrument, ou</p>
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	<p>déconnexion du raccord du conducteur de protection (terre) peut rendre l'instrument dangereux. Il est interdit d'interrompre volontairement ce conducteur.</p> <p>Présence de tensions mortelles dans l'instrument</p> <p>Lorsque l'instrument est relié au secteur, les raccords peuvent être sous tension, et des parties sous tension peuvent être découvertes en ouvrant des capots ou en retirant des pièces (à l'exception de celles auxquelles il est possible d'accéder manuellement).</p>
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Afin que le QIAxcel Advanced fonctionne de manière satisfaisante et en toute sécurité, conformez-vous aux conseils suivants :

- Le câble d'alimentation doit être relié à une prise d'alimentation disposant d'un conducteur de protection (terre/masse).
- Ne réglez ni ne remplacez aucune pièce interne à l'appareil.
- Ne faites pas fonctionner l'appareil si des capots ou des pièces ont été retirés.
- Si du liquide a été renversé à l'intérieur de l'appareil, éteignez-le et débranchez-le de la prise d'alimentation, puis contactez le support technique de QIAGEN.
- Si vous remplacez les fusibles, ne les remplacer qu'avec des fusibles du même type et équivalent en voltage, comme indiqué sur le fusible.

Si l'appareil devient dangereux sur le plan électrique, empêchez d'autres membres du personnel de l'utiliser et contactez le support technique de QIAGEN ; l'appareil peut être dangereux électriquement si :

- celui-ci ou le câble d'alimentation semble endommagé ;
- il a été stocké dans des conditions défavorables pendant une longue période ;
- il a subi des chocs sévères durant le transport.

Environnement

Conditions de fonctionnement

<p>WARNING</p> 	<p>Atmosphère explosive [W5]</p> <p>Le QIAxcel Advanced n'est pas conçu pour fonctionner dans une atmosphère explosive.</p>
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<p>WARNING</p> 	<p>Risque d'explosion [W6]</p> <p>Le QIAxcel Advanced a été conçu pour l'utilisation des réactifs et substances fournis par les kits QIAxcel. L'utilisation des réactifs et substances autres que celles indiquées peut entraîner un risque d'incendie ou d'explosion.</p>
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<p>CAUTION</p> 	<p>Détérioration de l'appareil [C4]</p> <p>La lumière directe du soleil peut décolorer des parties de l'instrument et endommager des parties en plastique. Placer le QIAxcel Advanced en dehors de la lumière directe du soleil.</p>
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<p>CAUTION</p> 	<p>Détérioration de la cartouche [C5]</p> <p>Lors de l'utilisation de la cartouche de Gel, ne pas la laisser plus de 15 minutes hors de la position d'arrêt (« Wash park ») du compartiment des liquides. Au-delà de cette période, les extrémités des capillaires risquent de se dessécher et d'influencer le bon fonctionnement de la cartouche. Des capillaires desséchés mettront fin à la garantie.</p> <p>Les extrémités des capillaires sont en verre et sont très fragiles.</p> <p>Faites attention à ne pas heurter une surface dure. Cela pourrait les casser et influencer le bon fonctionnement de la cartouche. Des extrémités de capillaires cassées mettront fin à la garantie.</p>
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<p>CAUTION</p> 	<p>Détérioration de la cartouche [C6]</p> <p>Si vous utilisez moins de 12 échantillons, les puits vides doivent être remplis de tampon de dilution QX ADN ou ARN. Si les puits restent vides, les capillaires non-utilisés peuvent s'abîmer.</p>
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Produits chimiques

<p>WARNING</p> 	<p>Substances chimiques dangereuses [W7]</p> <p>Certaines substances chimiques utilisées avec cet instrument peuvent être dangereuses ou peuvent le devenir après que le protocole ait été effectué.</p> <p>Toujours porter des lunettes de protection, deux paires de gants et une blouse de laboratoire.</p> <p>La personne responsable (par exemple le Chef du laboratoire) doit prendre les précautions nécessaires pour assurer la sécurité de l'environnement du poste de travail et pour être sûr que les opérateurs de l'instrument sont suffisamment formés et non exposés à des quantités dangereuses de substances toxiques (chimiques ou biologiques) comme défini dans « Material Safety Data Sheets (MSDS) » ou des documents « OSHA, ACGIH ou COSHH ».</p> <p>L'évacuation des vapeurs et déchets doit être conforme à tous règlements et dispositions légales - au plan national, départemental et local - concernant la santé et la sécurité.</p>
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* OSHA: Occupational Safety and Health Administration (United States of America).

† ACGIH: American Conference of Government Industrial Hygienists (United States of America).

‡ COSHH: Control of Substances Hazardous to Health (United Kingdom).

<p>WARNING</p> 	<p>Risque de feu [W8]</p> <p>Lors du nettoyage du QIAxcel Advanced avec un désinfectant à base d'alcool, laisser la porte du QIAxcel Advanced ouverte pour permettre aux vapeurs inflammables de s'évaporer.</p>
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Mise au rebut des déchets

Les consommables et flacons utilisés peuvent contenir des agents chimiques dangereux. Ces déchets doivent être convenablement collectés et mis au rebut conformément aux règles de sécurité locales.

Pour savoir comment mettre au rebut le QIAxcel Advanced, voir l'annexe A (« [Appendix A](#) »).

Dangers mécaniques

La porte à cartouche et la porte à échantillons du QIAxcel Advanced doivent être fermées à tout moment pendant l'usage de l'instrument.

<p>WARNING</p> 	<p>Éléments mobiles [W9]</p> <p>Afin d'éviter tout contact avec les éléments mobiles du QIAxcel Advanced lorsqu'il est en marche, toujours fermer les portes de l'instrument pour les échantillons et pour la cartouche.</p> <p>Si les détecteurs ne fonctionnent pas correctement, contacter le Support Technique QIAGEN.</p>
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Symboles sur le QIAxcel Advanced

Symbole	Emplacement	Description
	Plaquette à l'arrière de l'appareil	Marquage CE
	Plaquette à l'arrière de l'appareil	Marquage CSA pour le Canada et les États-Unis
	Plaquette à l'arrière de l'appareil	Fabricant légal
	Plaquette à l'arrière de l'appareil	Symbole DEEE
	Plaquette à l'arrière de l'appareil	Marquage FCC de la commission fédérale des communications des États Unis
	Plaquette à l'arrière de l'appareil	Marque RCM pour l'Australie et la Nouvelle-Zélande

Appendix G

Sicherheitshinweise

Vor der Inbetriebnahme des QIAxcel Advanced sollten Sie dieses Handbuch sorgfältig durchlesen – beachten Sie insbesondere die Sicherheitshinweise. Die Gebrauchsanweisungen und Sicherheitshinweise im Handbuch müssen befolgt werden, um einen sicheren Betrieb des Geräts zu gewährleisten und das Gerät in einem sicheren Zustand zu erhalten.

In diesem Handbuch werden die folgenden beiden Kategorien von Sicherheitshinweisen verwendet:

WARNING 	<p>„WARNING“ (WARNUNG) weist auf Situationen und Umstände hin, die zu einer Verletzung des Benutzers oder anderer Personen führen können.</p> <p>Nähere Angaben zu der Art der Gefährdung und der Vermeidung solcher Situationen werden in einem Textfeld wie diesem neben der Warnung gemacht.</p>
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CAUTION 	<p>Der Begriff „CAUTION“ (ACHTUNG) weist Sie auf Situationen hin, in denen das Gerät oder andere Geräte beschädigt werden könnten.</p> <p>Nähere Einzelheiten über diese Situationen werden in einem Textfeld wie diesem beschrieben.</p>
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Die in diesem Handbuch enthaltenen Hinweise stellen eine Ergänzung und keinen Ersatz der üblichen Sicherheitsanforderungen dar, die im jeweiligen Land gelten.

Sachgemäße Handhabung

WARNING/ CAUTION 	<p>Verletzungsgefahr und Beschädigung des Gerätes [W1]</p> <p>Die unsachgemäße Bedienung des QIAxcel Advanced kann zu einer Verletzung des Benutzers oder zur Beschädigung des Gerätes führen.</p> <p>Die Bedienung des QIAxcel Advanced darf nur durch qualifiziertes Personal, das entsprechend geschult wurde, erfolgen.</p> <p>Die Wartung des QIAxcel Advanced darf nur durch Mitarbeiter des QIAGEN Kundendienstes durchgeführt werden.</p>
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Führen Sie alle Wartungsarbeiten gemäß den Anweisungen in Abschnitt „[Maintenance Procedures](#)“ (Wartungsarbeiten) dieses Handbuchs durch. QIAGEN stellt alle Reparaturen in Rechnung, die nachweislich auf eine inkorrekte Wartung zurückzuführen sind.

<p>WARNING/ CAUTION</p> 	<p>Verletzungsgefahr und Beschädigung des Gerätes [W2]</p> <p>Der QIAxcel Advanced ist zu schwer um von einer Person gehoben zu werden. Um Verletzungen des Benutzers oder eine Beschädigung des Gerätes zu vermeiden ist davon abzusehen, das Gerät alleine zu heben.</p>
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<p>WARNING/ CAUTION</p> 	<p>Verletzungsgefahr und Beschädigung des Gerätes [W3]</p> <p>Den QIAxcel Advanced während eines Laufes nicht bewegen.</p>
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<p>CAUTION</p> 	<p>Beschädigung des Gerätes [C1]</p> <p>Vermeiden Sie es, Wasser oder Chemikalien auf dem QIAxcel Advanced zu verschütten. Durch verschüttetes Wasser oder verschüttete Chemikalien verursachte Geräteschäden sind nicht durch die Garantie abgedeckt.</p>
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Schalten Sie im Notfall den QIAxcel Advanced aus (der Netzschalter befindet sich auf der Geräterückseite), und ziehen Sie den Netzstecker aus der Steckdose.

<p>CAUTION</p> 	<p>Beschädigung des Gerätes [C2]</p> <p>Wenn die Statusanzeige Pressure 1, Low (niedrig) anzeigt, erhöhen Sie den Systemdruck bevor Sie unlatch (Enriegelung) auslösen. Das Herausnehmen der Kartusche und die Enriegelung bei niedrigem Druck kann das Gerät beschädigen.</p>
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<p>CAUTION</p> 	<p>Beschädigung des Gerätes [C3]</p> <p>Verwenden Sie keine Bleichmittel, Lösungsmittel oder säure-, laugen- oder scheuermittelhaltige Reagenzien zur Reinigung des QIAxcel Advanced.</p>
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Schutz vor Stromschlag

Ziehen Sie die Netzanschlusskabel aus den Steckdosen, bevor Sie Wartungsarbeiten am Gerät vornehmen.

<p>WARNING</p> 	<p>Gefährdung durch Elektrizität [W4]</p> <p>Jede Unterbrechung des Schutzleiters (Erdungs- bzw. Masseleiter) im Gerät oder außerhalb des Geräts und jede Abtrennung des Schutzleiters am Anschluss der Netzleitung erhöht die Gefahr eines Stromschlags.</p> <p>Eine absichtliche Unterbrechung der Schutzleiterverbindung ist verboten.</p> <p>Gefährliche Spannung im Gerät</p> <p>Auch in ausgeschaltetem Zustand kann an einigen Stellen im Gerät Netzspannung anliegen, wenn das Gerät am Stromnetz angeschlossen ist. Das Öffnen oder Entfernen von Gehäuseteilen kann diese stromführenden Teile freilegen.</p>
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Um einen zufriedenstellenden und sicheren Betrieb des QIAxcel Advanced zu gewährleisten, befolgen Sie bitte die nachstehenden Hinweise:

- Die Geräte-Netzkabel müssen an Wechselstrom-Steckdosen mit Schutzleiter (Erdungs-/Masseleiter) angeschlossen werden.
- Nehmen Sie im Geräteinneren keine Einstellungen an Teilen vor und wechseln Sie keine Teile aus.
- Nehmen Sie das Gerät nicht in Betrieb, wenn Abdeckungen oder Teile entfernt worden sind.
- Falls Flüssigkeit auf dem Gerät verschüttet wird und in das Gerät läuft, dann schalten Sie es sofort aus, trennen Sie es von der Netzspannung (Stecker ziehen!) und setzen Sie sich mit dem Technischen Service von QIAGEN in Verbindung.
- Beim Austausch der Netzsicherung ersetzen Sie diese nur durch eine desselben Typs und der Stromstärke, die auf dem Etikett/Typenschild angegeben ist.
- Falls die elektrische Sicherheit bei der Bedienung des Geräts nicht mehr gewährleistet werden kann, muss das Gerät gegen unbefugte oder unabsichtliche Benutzung gesichert werden. Kontaktieren Sie anschließend den Technischen Service von QIAGEN. Die elektrische Sicherheit des Geräts ist nicht mehr gegeben, wenn:
 - das Gerät oder das Netzkabel beschädigt erscheint;
 - das Gerät längere Zeit unter ungünstigen Bedingungen gelagert wurde;
 - das Gerät unsachgemäß transportiert worden ist.

Umgebungsbedingungen

Betriebsbedingungen

WARNING 	Explosionsfähige Atmosphären [W5] Der QIAxcel Advanced darf nicht in explosionsfähigen Atmosphären betrieben werden.
---	--

WARNING 	Explosionsgefahr [W6] Der QIAxcel Advanced ist ausschließlich mit Reagenzien und Substanzen aus den QIAxcel Kits zu benutzen. Die Benutzung von anderen Reagenzien oder Substanzen kann Feuer oder eine Explosion auslösen.
---	---

CAUTION 	Beschädigung des Gerätes [C4] Direktes Sonnenlicht kann Teile des Gerätes bleichen und Plastikteile schädigen. Der QIAxcel Advanced darf nicht ins direkte Sonnenlicht gestellt werden.
---	---

CAUTION 	Beschädigung der Kartusche [C5] Die Gel Cartridge sollte nicht länger als 15 Minuten außerhalb der Parkposition (Wash park) des Solution Trays aufbewahrt werden. Wird dieser Zeitrahmen überschritten, trocknen die Spitzen der Kapillaren aus. Ausgetrocknete Kapillarspitzen sind nicht durch die Garantie abgedeckt. Die Kapillarspitzen sind aus Glas und sehr zerbrechlich. Achten Sie darauf, die Spitzen nicht auf harte Oberflächen aufzusetzen. Dadurch können die Kapillaren brechen und damit die Funktion der Cartridge beeinträchtigen. Zerbrochene Kapillarspitzen sind nicht durch die Garantie abgedeckt.
---	---

<p>CAUTION</p> 	<p>Beschädigung der Kartusche [C6]</p> <p>Wenn weniger als 12 Proben verarbeitet werden, füllen Sie die leeren Probenbehältern mit QX DNA Verdünnungspuffer oder QX RNA Verdünnungspuffer. Andernfalls können Schäden an den kapillaren Kanälen entstehen.</p>
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Chemikalien

<p>WARNING</p> 	<p>Gefährliche Chemikalien [W7]</p> <p>Einige der in Verbindung mit diesem Gerät verwendeten Chemikalien sind gesundheitsgefährdend oder können nach Beendigung eines Protokoll-Laufs gesundheitsgefährdend werden. Es sollten immer Sicherheitsbrille, zwei Paar Handschuhe und ein Laborkittel getragen werden. Der Betreiber der Anlage ist für die Gewährleistung der Sicherheit am Arbeitsplatz verantwortlich. Er hat sicherzustellen, dass die Bediener des Gerätes ausreichend geschult sind und nicht gesundheitsgefährdenden Konzentrationen toxischer Substanzen (chemischer oder biologischer) ausgesetzt sind, so wie dies in den Sicherheitsdatenblättern oder in anderen zu beachtenden Dokumenten festgelegt ist.</p> <p>Bei der Behandlung von Abluft und bei der Abfallbeseitigung sind alle gesetzlichen Regelungen zur Gesundheit und Sicherheit auf nationaler, regionaler und lokaler Ebene zu berücksichtigen.</p>
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* OSHA: Occupational Safety and Health Administration (United States of America).

† ACGIH: American Conference of Government Industrial Hygienists (United States of America).

‡ COSHH: Control of Substances Hazardous to Health (United Kingdom).

<p>WARNING</p> 	<p>Feuergefahr [W8]</p> <p>Beim Reinigen des QIAxcel Advanced mit einem auf Alkohol basierendem Desinfektionsmittel muss die Tür des QIAxcel Advanced offen gelassen werden, damit die brennbaren Dämpfe entweichen können.</p>
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Entsorgen von Abfällen

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Weitere Informationen zur Entsorgung vom QIAxcel Advanced finden Sie im Anhang A („[Appendix A](#)“).

Gefahren durch mechanische Teile

Die Klappen für den Proben- und Cartridge-Einsatz des QIAxcel Advanced müssen während des Betriebs geschlossen sein.

<p>WARNING</p> 	<p>Bewegliche Geräteteile [W9]</p> <p>Um jeglichen Kontakt mit beweglichen Geräteteilen während des Laufes zu vermeiden, darf der QIAxcel Advanced nur benutzt werden, wenn die Klappen für den Proben- und Cartridge-Einsatz geschlossen sind. Sollten die Sensoren nicht ordnungsgemäß funktionieren, kontaktieren Sie bitte den Technischen Service von QIAGEN.</p>
---	---

Symbole auf dem QIAxcel Advanced

Symbol	Fundstelle	Beschreibung
	Plakette auf der Rückseite des Gerätes	CE-Zeichen
	Plakette auf der Rückseite des Gerätes	CSA-Zeichen für Kanada und die USA
	Plakette auf der Rückseite des Gerätes	Hersteller i.S.d. Gesetzes
	Plakette auf der Rückseite des Gerätes	WEEE-Zeichen
	Plakette auf der Rückseite des Gerätes	FCC Markierung der Federal Communications Kommission der USA
	Plakette auf der Rückseite des Gerätes	RCM-Zeichen für Australien und Neuseeland

Appendix H

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jzlib is based on zlib-1.1.3.

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Jean-loup Gailly jloup@gzip.org
Mark Adler madler@alumni.caltech.edu

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-----  
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