May 2024

Important Note

QIAxcel® ScreenGel® Software V2.1

Dear valued QIAxcel Connect customer,

We would like to inform you about the improvements and bug fixes in QIAxcel ScreenGel Software V2.1.

This document contains information about the following:

- Changes from QIAxcel ScreenGel Software version 2.0 to 2.1
  - Improvements
  - Fixed bugs
- Known bugs and behavior observations in V2.1.
- Compatibility
- System requirements
- Firmware update
- Experiment data downward compatibility
- Profile data downward compatibility
- Important Information
- Updating the QIAxcel ScreenGel Software
- Appendix: Updated and deleted profiles

Improvements in ScreenGel V2.1

Only most relevant improvements listed.

- **Languages**

  Support for 4 additional languages for graphical user interface (French, German, Japanese, and Spanish) in the QIAxcel ScreenGel application (installer, application and IVD logs, out of scope: user manual, other log files, and profiles)

- **Process Profiles & Sub profiles**

  Several process profiles, marker profiles, run methods, as well as analysis and report/export profiles were updated to reflect the need of specific analytical experiments. A detailed overview of the updates can be found in the Appendix. Note, previously created or stored profiles are still available when upgrading the SW and are not overwritten (see **www.qiagen.com/HB-3573**).

  Furthermore, there is a new size marker profile for the size range 1–8 kb using Thermo Scientific® GeneRuler 1 kb DNA-Ladder, see **www.qiagen.com/HB-3574**

- **RNA Integrity Score (RIS) for QX RNA High Sensitivity Cartridges**

  RIS algorithm for the RNA High-Sensitivity Cartridge (cat. no. 929112) has been updated and trained with additional data points to further improve the stability of RIS determination.

  Note: When analyzing RIS with the QIAxcel RNA High Sensitivity Kit, samples must be in the concentration range of 1–50 ng/µL.

- **RNA analysis smoothing filter**

  Improvement of the Smoothing filter algorithm for RNA analysis for higher Signal/Noise (S/N) values and improved LOD. This can lead to slight difference in assignment of start and end point of peaks, thus, slightly different concentration and size determination than QIAxcel ScreenGel Software version 2.0.

- **QIAsphere®**

  Implementation of new QIAsphere features (QIAsphere notifications, file download, and software update)

- **Double-click feature**

  Experiments can be opened by double-clicking the experiment file in the file explorer or on the desktop. After double-clicking the experiments, ScreenGel 2.1 will start automatically. If the application is already open, it is only possible to open experiments via double-clicking that match the mode (RNA/DNA) which is currently selected in the application.

Fixed Bugs in ScreenGel V2.1

Only most relevant fixes are listed.

- **Inaccurate size detection (Peak analysis)**

  When using the QX High-Resolution Kit in combination with the QX DNA Size Marker Large-Fragment Kit (cat. no. 929710) that uses only a lower (single fragment) alignment marker for alignment, ScreenGel 2.0 provided an inaccurate peak sizes prediction for fragments larger than the last fragment of the Size Marker peak. The mathematical model for size extrapolation after the 20 kb peak of the Large Fragment Marker was improved.

- **Run was not saved/could not be loaded**

  In the event that the Experiment Directory is not available, completed experiments confirmed by the user could not be saved in the Experiment Directory. It was not obvious to the user that the file had not been saved. If the application was then closed, the experiment file could not be saved afterwards.

  When saving experiment fails (e.g., when the Experiment Directory is not available when closing the application), application displays an error message and stay open so that the user can try to save it once again to same destination.

- **Negative values for Mol. Area of Interest in report**

  In ScreenGel V2.0 in some cases reports contained negative values for the Molarity of the Area of Interest in (Smear Analysis) instead of “n/a”. Values in the application were not affected.

Behavior observations and user-relevant known bugs in ScreenGel V2.1

Behavior

- **Instrument connection is not established at the first attempt**

  The QIAxcel Connect needs around 15 seconds to boot. During this period, ScreenGel cannot connect to the instrument and recognize the state of booting. The timeout for the connection functionality in ScreenGel is shorter, and an error message regarding the instrument connection will occur. This message only provides the options “Instrument not needed” & “Troubleshoot”. The latter option leads to the Troubleshoot dialog and may falsely suggest that a firmware update is needed. We recommend waiting around 15 seconds to try to connect again.

- **Manual smear analysis**

  Results for manually inserted Smear Peaks were removed when sample is analyzed with distribution analysis after. This means manual insertion of peaks might need to be repeated for Distribution analysis. We therefore recommend checking exactly the Peak assignment in the electropherogram of the Distribution Analysis results if you have manually inserted peaks in the preceding smear analysis.

- **Acoustic feedback does not work, app is not in mixer sound after run**

  To use the Acoustic feedback function, the Windows Media Player must be installed manually because it is not included in the Operating System version that is provided on the QIAxcel Connect notebook.

- **Distribution profile edit – missing authorization for Admin**

  If the user is logged in as Administrator, the distribution profile in process environment cannot be selected/exchanged. If the user is logged in as Developer user, it is possible.

User-relevant known bugs in ScreenGel V2.1

- **Concentration display with High Sensitivity Cartridges**

  The concentration display in the "Distribution Analysis Result" table is cut when working with high concentration of nucleic acid in combination with DNA High Sensitivity Cartridge or RNA High Sensitivity Cartridge and Distribution Analysis. Thus, the value for concentration is not fully displayed in the analysis result table.

  See **www.qiagen.com/HB-3572**

- **"No connection" pop-up while moving the Application window results in inoperability**

  If the ScreenGel application window is moved, while the "no connection error" pops-up, the application is no longer operable. The only way is to close the application via task manager.

- **Non-applicable profiles shown in drop-down**

  The Analysis Profile from the experiment that was previously analyzed is preselected in the **Analysis Profile** drop-down menu (**Analysis Properties**), even if it does not fit to the current cartridge type. After changing the profile, the non-applicable profile disappears.

- **Invalid marker table validation in analysis parameter "drawer"**

  After experiment load and applying the correct reference marker table (**Apply** button on experiment **Marker** tab) the marker table validation in parameter drawer is active {yellow background}) and the tooltip says "Reference Marker does not match; please select another one." The warning is gone only after whatever cell selection in Experiment Explorer.

- **Mouse capture during window resizing connection process**

  When user resizes the window of application during the set-up of the connection to the instrument then troubleshooting pop-up with no instrument detection appears and it is no possibility to close pop-up (only via [ESC] but app is still disabled). Cursor is still resized shape.

Compatibility

The QIAxcel ScreenGel 2.1 is compatible with QIAxcel Connect (third generation) instruments. The QIAxcel ScreenGel 2.1 software is not compatible with the discontinued QIAxcel and QIAxcel Advanced (first and second generation) instruments.

System requirements

The QIAxcel ScreenGel 2.1 software should only be installed on a computer that meets the following minimal specifications:

- 2.3 GHz CPU
- 80 GB free hard drive capacity, NTFS formatted
- 4 GB RAM
- 1920 x 1080 screen resolution
- USB port
- Pointer device (mouse or similar)
- Windows 10 with minimum required version 1607
- Ethernet or Wi-Fi network adapter in the case of QIAsphere usage

Firmware update

The ScreenGel Software V2.1 comes in combination with instrument firmware 5.0.3, for QIAxcel Connect instruments. If the software connects to the instrument, it checks if the instrument firmware on the instrument is up to date. If not up to date, it automatically updates the instrument firmware. This process takes a few minutes. A message is shown during that time. Do not turn off the instrument or disconnect the cable between the computer and the instrument, and do not close the software until the update is complete. After a successful update, the software automatically connects to the instrument.

The software contains a feature to repeat this step if the firmware update fails and the instrument cannot be connected anymore. In this case, follow the instructions outlined in the user manual, "System Setup" of the "Troubleshooting" section.

Experiment data downward compatibility

It is possible to load experiments created by a former version of the ScreenGel software in the QIAxcel ScreenGel V2.1 software. The QIAxcel ScreenGel V2.1 software migrates the experiment data during loading but does not save back the migrated experiment automatically. It is not possible to save experiment data in the format of a former ScreenGel version in the QIAxcel ScreenGel V2.1 software.

Profile data downward compatibility

The QIAxcel ScreenGel V2.1 software provides the user with the ability to use profiles (analysis, process, report/export profiles, methods, size marker, alignment marker, and calibration data) that were created by a former ScreenGel software version. The QIAxcel ScreenGel V2.1 software migrates the data during loading, saves it back automatically, and overwrites the file. Please also refer to **www.qiagen.com/HB-3573**

Important Information

- To view reports in PDF format, a PDF reader must be installed on the computer.
- Enable acoustic feedback from ScreenGel by enabling sound in Windows Sound Control Panel.
- To play **.mp3** or **.wav** files, Windows Media Player must be installed on the computer.
- For Windows 10 only – If UEFI Boot is used, the **Secure Boot** option must be disabled to ensure successful software installation.
- For proper time estimation presented in QIAsphere, the time zone on the notebook where ScreenGel is installed must be aligned with the time zone where QIAsphere is hosted.

Updating the QIAxcel ScreenGel Software

Visit **qiagen.com/qiaxcel-connect-system** and go the **Resource** section of the QIAxcel Connect product page to download the latest software and user guides. For software installation instructions, please refer to the *QIAxcel Connect Quick Start Guide* and *QIAxcel Connect User Manual*.

Best regards,

QIAGEN

Appendix: Update of Pre-Installed Profiles

Please note, when upgrading from ScreenGel 2.0 to ScreenGel 2.1, the new profile version will be added to the directory automatically while the old versions will stay in the same folder. If you do not want to keep the old versions within the same folder, and consequently showing up in the drop-down selection within the software, please refer to **www.qiagen.com/HB-3573** for handling of profiles.

Process Profiles

Process profiles include sub profiles such as run method and parameters, as well and profiles for marker, analysis, and report/export.

Profile Name	Status	Predecessor Profile in SG 2.0	Description
ccfDNA Analysis_V3.xpp	Updated	ccfDNA Analysis.xpp ccfDNA Analysis_V2.xpp (via web download)	• new Analysis profile "ccfDNA Analysis" • new AM "QX 15 bp HS" • new Distribution Profile "ccfDNA Analysis" • new ReportExportProfile "DNA Distribution Analysis HS" • Uses updated Method "DNA High-Sensitivity_V2", see important note regarding change of solvent to improve resolution and corresponding introduction of longer run-time with V2 of method.
Default DNA Fast Analysis_V2.xpp	Updated	Default DNA Fast Analysis.xpp	• Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section
Default DNA High Resolution_V2.xpp	Updated	Default DNA High Resolution.xpp	• Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section

Profile Name	Status	Predecessor Profile in SG 2.0	Description
Default DNA High-Sensitivity_V3.xpp	Updated	Default DNA High-Sensitivit.xpp/ Default DNA High-Sensitivity_V2.xpp	• Updated Report/Export "DNA Fragment Analysis HS_V2" • Updated Notes section • Uses updated Method "DNA High-Sensitivity_V2", see important note regarding change of solvent to improve resolution and corresponding introduction of longer run-time with V2 of method.
Default DNA Screening_V2.xpp	Updated	Default DNA Screening.xpp	• Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section
Default RNA High-Sensitivity_V2.xpp	Updated	Default RNA High-Sensitivity.xpp	• Updated Analysis Profile "RNA High-Sensitivity Analysis_V2" • Updated Report/Export "RNA Report HS_V2" • Updated Notes section
DNA High Resolution Plus_V2.xpp	Updated	DNA High Resolution Plus.xpp	• Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section
gDNA Analysis (0M1200).xpp	Updated	gDNA Quality Control (Template-HR).xpp	• replacement for gDNA Quality Control (Template-HR).xpp • Updated Analysis Profile "gDNA Analysis_V2" • Updated Notes section • Addition of Report/Export " DNA Smear Analysis"
gDNA Analysis_V2.xpp	Updated	gDNA Analysis.xpp	• Updated Analysis Profile "gDNA Analysis_V2" • Removal of Distribution Profile "Default gDNA Integrity Ratio" • Updated Notes section • Update of Report/Export " DNA Smear Analysis"

Profile Name	Status	Predecessor Profile in SG 2.0	Description
Large Fragment Analysis_V2.xpp	Updated	Large Fragment Analysis.xpp	• Updated Analysis Profile "DNA Large Fragment Analysis_V2" • Updated Notes section • Updated Report/Export "DNA Fragment Analysis_V2"
Multiplex PCR Analysis_V2.xpp	Updated	Multiplex PCR Analysis.xpp	• Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section
NGS Library Control_V2.xpp	Updated	NGS Library Control.xpp	• SM changed from "QX 15 bp-10 kb" to "QX 15 bp-5 kb" • Updated Report/Export "DNA Smear Analysis" • Updated Notes section
PCR Amplicon Analysis.xpp	Updated	DNA Amplicon Analysis.xpp	• replacement for DNA Amplicon Analysis.xpp • Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section
Restriction Digest Analysis HR_V2.xpp	Updated	Restriction Digest Analysis HR.xpp	• Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section
Restriction Digest Analysis SC_V2.xpp	Updated	Restriction Digest Analysis SC.xpp	• Updated Report/Export "DNA Fragment Analysis_V2" • Updated Notes section
RNA mammalian QC_V2.xpp	Updated	RNA mammalian QC.xpp	• Updated Analysis Profile "Default RNA QC_V2" • Updated Peak Calling instruction "Default RNA rat_mouse_human v3" • Updated Report/Export "RNA Report_V2" • Updated Notes section

Profile Name	Status	Predecessor Profile in SG 2.0	Description
RNA Prokaryote QC_V2.xpp	Updated	RNA Prokaryote QC.xpp	• Updated Analysis Profile "Default RNA QC_V2" • Updated Peak Calling instruction "Default RNA prokaryote v3" • Updated Report/Export "RNA Report_V2" • Updated Notes section
n/a	Removed	gDNA Quality Control (Template-SC).xpp	
n/a	Removed	NGS Library QC - High Conc.xpp	New Process profile will be released independently
n/a	Removed	NGS Library QC - Medium Conc.xpp	New profile will be released independently

Alignment Marker Profiles

Profile Name	Status	Description
QX 15 bp HS.xam	New	Additional profile for DNA High-Sensitivity Kit, single Alignment Marker peak of 15 bp. Requires use of diuted QX RNA Alignment Marker (1.5 mL) cat. no. 929510 see notes in process profile ccfDNA Analysis_V3

Size Marker Profiles

Profile Name	Status	Description
GeneRuler 1 kb DNA-Ladder - Thermo Scientific (TM).xsm	New	New marker profile for use of Thermo Scientific GeneRuler 1kb DNA-Ladder, see **www.qiagen.com/HB-3574** for dilution recommendations
100 bp - 2.5 kb (10 ng per ul).xsm	Removed	
100 bp - 2.5 kb (100 ng per ul).xsm	Removed	
phiX174 HaeIII (20 ng per ul).xsm	Removed	Marker discontinued
pUC18 HaeIII (20 ng per ul).xsm	Removed	Marker discontinued

Analysis Profiles

Profile Name	Status	Predecessor Profile in SG 2.0	Description
ccfDNA Analysis.xap	new	n/a	additional profile for DNA High-Sensitivity kit including Smear Analysis
Default RNA QC_V2.xap	updated	Default RNA QC	Threshold and AM threshold increased due to improved smoothing filter for RNA QC V2 kit
DNA High-Sensitivity Analysis_V2.xap	updated	DNA High-Sensitivity Analysis.xap	Change of Alignment Marker threshold from 10 S/N to 20 S/N
DNA Large Fragment Analysis_V2.xap	updated	DNA Large Fragment Analysis.xap	Change of Alignment Marker threshold from 20 S/N to 10 S/N
gDNA Analysis_V2.xap	updated	gDNA Analysis.xap	Change of threshold from 50 to 80; Additional minimum distance parameter: Start: 7 min, Value: 7 sec
NGS Library Analysis HS.xap	new	n/a	additional profile for DNA High-Sensitivity Kit
RNA High-Sensitivity Analysis_V2.xap	updated	RNA High-Sensitivity Analysis	Threshold & AM threshold increased due to new smoothing filter for RNA High-Sensitivity kit)

Distribution Analysis Profiles

Profile Name	Status	Description
ccfDNA Analysis.xda	new	Additional profile for DNA High-Sensitivity Kit

Method

Profile Name	Status	Predecessor Profile in SG 2.0	Description
DNA High-Sensitivity_V2.xmt	updated	DNA High-Sensitivity.xmt	Separation time increased to address running time of adjusted DNA High-Sensitivity Kit
RNA High-Sensitivity medium.xmt	(removed)	RNA High-Sensitivity medium.xmt	no longer Default Method, only in InitialData folder

Peak Calling Instruction

Profile Name	Status	Description
Default RNA prokaryote v3.xbp	updated	Ratio Normalized Area included
Default RNA rat_mouse_human v3.xbp	updated	Ratio Normalized Area included

Report Export Profiles

Profile Name	Status	Predecessor Profile in SG 2.0	Description
RNA Report_V2.xre	updated	RNA Report.xre	Additional parameters: Overview *Experiment Plate comment* *Reported by* *Gel Image Overview* Sample Details *Start Results on New Page* *Sample Information* *Sample Comment* *Single Electropherogram*

Profile Name	Status	Predecessor Profile in SG 2.0	Description
RNA Report HS_V2.xre	updated	RNA Report HS.xre	Additional parameters: Overview *Experiment Plate comment* *Reported by* *Gel Image Overview* Sample Details *Start Results on New Page* *Sample Information* *Sample Comment* *Single Electropherogram*
DNA Smear Analysis.xre	new	n/a	new profile for smear analysis with regular DNA Kit
DNA Smear Analysis HS.xre	new	n/a	new profile for smear analysis with DNA High-Sensitivity Kit
DNA Peak Calling.xre	new	n/a	new profile for Peak Calling analysis with regular DNA Kit
DNA Peak Calling HS.xre	new	n/a	new profile for Peak Calling analysis with DNA High-Sensitivity Kit
DNA Fragment Analysis_V2.xre	updated	DNA Fragment Analysis.xre	Additional parameters: Overview *Experiment Plate comment* *Reported by* *Overall Result Table* *Gel Image Overview* Sample Details *Start Results on New Page* *Sample Information* *Sample Comment* *Single Electropherogram*
DNA Fragment Analysis HS_V2.xre	updated	DNA Fragment Analysis HS.xre	Additional parameters: Overview *Experiment Plate comment* *Reported by* *Overall Result Table* *Gel Image Overview* Sample Details *Start Results on New Page* *Sample Information* *Sample Comment* *Single Electropherogram*

Profile Name	Status	Predecessor Profile in SG 2.0	Description
DNA Distribution Analysis.xre	new	n/a	new profile for Distribution analysis with regular DNA kits
DNA Distribution Analysis HS.xre	new	n/a	new profile for Distribution analysis with DNA High-Sensitivity Kit
NGS Libraries.xre (removed)	removed		
NGS Libraries HS.xre	removed		
gDNA Analysis.xre	removed		
gDNA Analysis HS.xre	removed		

Calibration Process Profile

Profile Name	Status	Description
Calibration_Default_Rna.xcp	updated	Parameter added for improved smoothing filter
Calibration_HighSens_Rna.xcp	updated	Parameter added for improved smoothing filter