



Olink[®] NPX Signature for Olink[®] Target 96

User Manual

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Part 1: Introduction

1. About this manual

The Olink® NPX Signature User Manual provides you with the instructions needed for processing the raw data and performing quality control on the data from Olink® Target 96 panels with the Olink® NPX Signature software.

This manual contains step-by-step instructions for analysis in Olink NPX Signature and software troubleshooting.

1.1 Intended use

Olink® NPX Signature is a data analysis software that is designed for the OlinkTarget analysis platform, including Olink® Target 48, Olink Target 96, Olink® Focus as well as for Olink® Flex panels. It allows for importing run data, validating data quality, and normalizing Olink data for subsequent statistical analysis.

Olink NPX Signature is intended for research use only. Not for use in diagnostic procedures. All trademarks and copyrights contained in this material are the property of Olink Proteomics AB unless otherwise stated. For questions, guidance, and support, including questions regarding Olink Target 48, Olink Focus, and Olink Flex panels, contact Olink Support at support@olink.com.

1.2 Intended target group

Olink NPX Signature is intended to be used by trained users of the Olink Target 96 analysis platform. Quality control should be performed by trained users that determine whether data from a run can be approved for further analysis.

2. List of Abbreviations


%CV	Coefficient of Variation
IFC	Integrated Fluidic Circuit (also called "chip" in this document)
LLOQ	Lower Limit of Quantification
LOD	Limit of Detection
LOQ	Limit of Quantification
LQL	Lowest Quantifiable Level
NPX	Normalized Protein eXpression
PCR	Polymerase Chain Reaction
QC	Quality Control
ULOQ	Upper Limit of Quantification


3. Safety

This chapter contains important safety information.

3.1 Definition of alert levels

The following alert levels are used in the Olink Explore manuals:

 **IMPORTANT:** Indicates an important action that may impair the results if not performed correctly.

 **NOTE:** Contains information that can make it easier to understand or perform a certain task.

4. Associated documentation

Olink documentation

- Olink® Signature Q100 User manual, doc no 1172
- Olink® Target 96 User Manual, doc no 0935

All relevant Olink documentation is available from the Olink website:

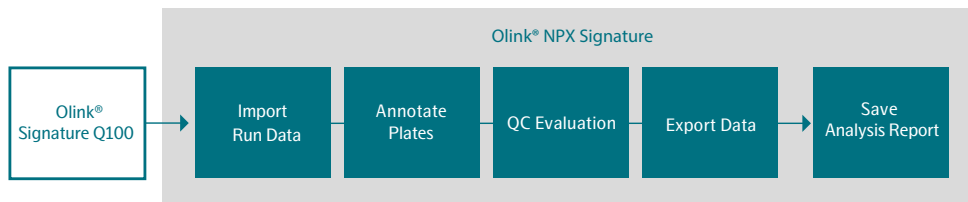
<https://www.olink.com/downloads>

5. Technical support

For questions, guidance and support, contact Olink Proteomics at support@olink.com.

6. Process

Olink NPX Signature is a standalone Windows software application that lets you import data from Olink® Signature Q100, validate its quality and normalize it. The data is not required to be annotated or processed before importing it into Olink NPX Signature. The software can also process Fluidigm® Biomark™ data.




7. Software and file requirements

Components	Minimum	Recommended
Operating System	Windows® 10 or higher	
Processor	Intel® Core™ i5	Intel® Core™ i7 or higher
Memory	8 GB RAM	16 GB RAM or more
Disk Space	500 MB	500 MB

7.1 Files and information

7.1.1 Olink® NPX Signature Study File (.npx)

 **IMPORTANT:** To enable Olink NPX Signature's remote data functions to Olink Signature Q100, ensure that the instrument is connected to the network and TCP port 8085 (enabled by default) is not blocked. For instructions on how to securely connect the Olink Signature Q100 to a network, refer to the Olink Signature Q100 User manual.

Olink NPX Signature stores all study data in a file with the extension .npx. This file is the single repository for all study-related data required by Olink NPX Signature to display, review, and export data for a study.

Place this NPX file on your local computer or in a folder on the network. NPX files are typical ~5–10 MB in size but can be larger if you save the run data in the .npx file.

7.1.2 Files and Information Needed for Analysis

Q100 Run Data

This is the Olink Signature Q100 run data that can be imported into Olink NPX Signature without the need for annotation or processing in advance. The file types and information accessible for analysis are:

- Olink Signature Q100 export file (.q100 or .zip);
- Olink Signature Q100 instrument with enabled remote connectivity;
- Olink NPX Manager project file (.oaf); or
- Fluidigm Real-time PCR exported heatmap or table file (.csv).


See the tutorials and the help sections in Olink NPX Signature for more information.

Plate Manifest File

Microsoft Excel file (.xlsx) that can be used to define the sample plate layout.

Panel Data File

Data file version provided on the insert that is delivered with the Reagent kit.

 **NOTE:** The size of the .zip file that is transferred via USB from Olink Signature Q100 might be larger than 20 MB. An NPX Signature study that includes run data in the .npx archive might be too large to email to Olink Support. If possible, email only the Olink NPX Signature project file with the .npx extension.

8. Installing


8.1 License agreement

You are required to accept the end-user license agreement when installing Olink NPX Signature or before using an updated version for the first time.

8.2 Install software

The installer performs a first-time installation or an update to the current installation if it is already installed on your local computer. Any updates to the software retain all existing user settings and custom data.

1. Download the latest version of the Olink NPX Signature software to your computer from olink.com/software.
2. Open the zip folder.
3. Double-click the installer (.msi) file.
4. Follow the on-screen instructions.
5. Olink NPX Signature will be displayed in the Windows Start menu for future use. To open the application, double-click on the icon.

 **IMPORTANT:** *Before using Olink NPX Signature for the first time or upon installation of an updated version, you are required to accept the end-user license agreement.*

8.3 Uninstall software

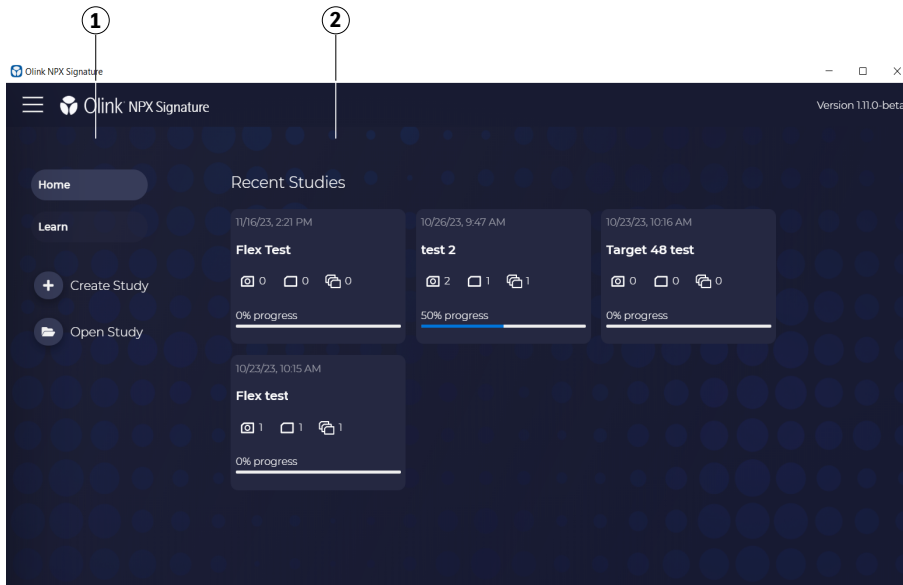
If you need to uninstall Olink NPX Signature, it can be uninstalled using the Windows Add found in Windows Settings, or Remove Programs in the Control panel. Select Olink NPX Signature from the program list and click **Uninstall**.

All user data is retained where it was saved before the application was uninstalled, and your custom Olink NPX Signature settings are retained on the system.

Part 2: User Interface

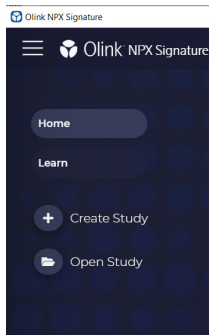
9.General

9.1 Start view



No	Function	Description
1	Main menu	Access main functions. Click on the three lines in the top left corner to expand the main menu.
2	Recent studies	Show recent opened studies. Click on a project to get to the Study Overview.

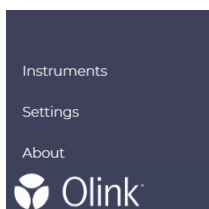
9.2 Main menu



Function	Description
Home	Access the main level of the application, where you see your most recently opened studies.
Learn	Access all the integrated tutorials. Refer to 11. Tutorials and in-line help for more information.
Create Study	Create a new study.
Open Study	Open an existing study.

The expanded menu lists three functions in the lower part of the menu.

9.2.1 Lower part of main menu



Function	Description
Instruments	Show a list of Olink Signature Q100 instruments available to the Olink NPX Signature software over the network.
Settings	Access the application settings. Refer to 10. Settings for more information.
About	For instructions on how to securely connect the Olink Signature Q100 to a network, refer to the Olink® Signature Q100 User Manual.

10.Settings

Click **Settings** on the main menu to customize the view.

General

- Change the color theme of the application and charts.
- Enable or disable the advanced user features.
- Customize the Analysis Report by adding a company name and logo.

Layout Templates

Review or create new sample plate layouts to define the sample types for each well.

Panels

- Review all Panel Data Files in the application.
- Import or remove Olink Flex Panel Data Files.

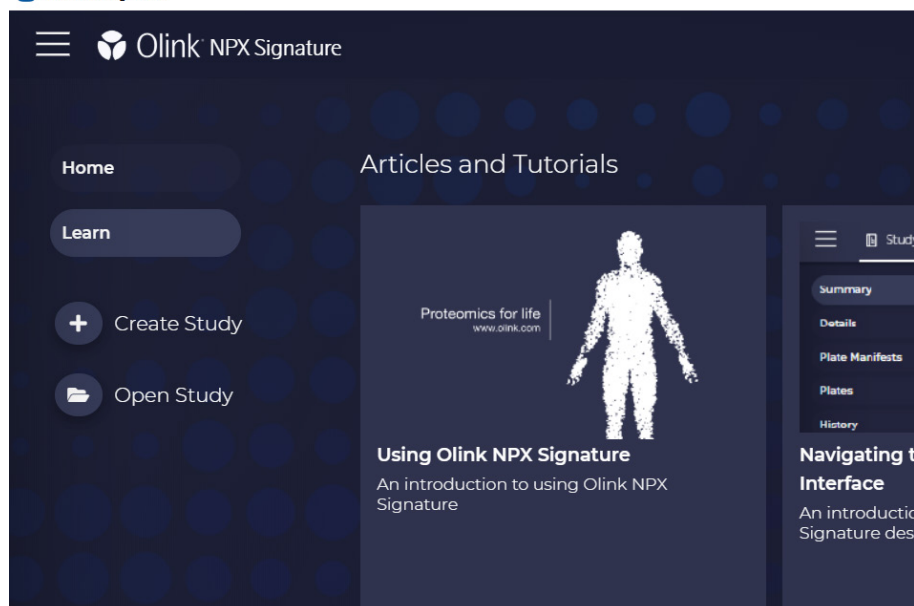
11.Tutorials and in-line help

Olink NPX Signature contains integrated tutorials and in-line help.

11.1 Tutorials


Click **Learn** on the main menu to access integrated tutorials meant to assist you in learning the various features of Olink NPX Signature. Click a tutorial and navigate through the pages using **Next** or **Previous**.

Olink NPX Signature



You can also launch a tutorial by clicking **TUTORIAL** in the end of the in-line help content.

11.2 In-Line help

Click the  icon in the upper-right corner of a view to access the in-line help, which contains information about the usage of the current view. If the contextual help is longer than the allowed space, a scroll bar appears that lets you read the full text.

Part 3: Operation

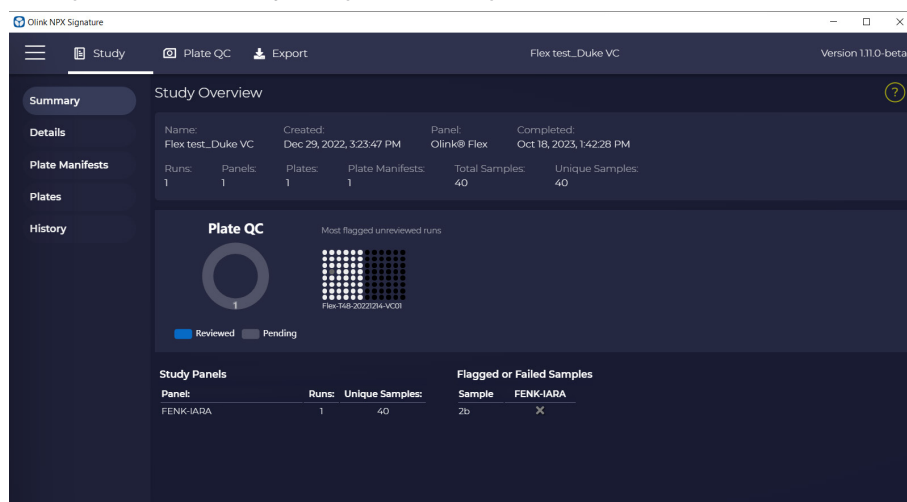
12. Introduction

Input data for Olink NPX Signature are run files from Olink Signature Q100, Ct values exported from the Fluidigm Real-Time PCR Analysis software, NPX Manager .oaf project files and NPX Signature .npx study files. After quality control and normalization against the Extension Control, the IPC, and a bridging factor, the output data are obtained in NPX values.

This section describes how you analyze data step-by-step in Olink NPX Signature.

The following steps are included in the standard operating procedure:

1. Create an Olink Target 96 Study.
2. Import run data.
3. Verify panel and plate layout information.
4. Under Details, enter optional study information.
5. Select normalization method.
6. Perform quality controls including additional quality assessment.
7. Export Data and Analysis Report under Export tab.



13. Start or open a project

13.1 Create a study

To create a study, perform the following steps:

1. Click Create Study.
2. Select Product.
3. Enter Study Name (required information), Sample Type and Notes.
4. Click Create.

13.2 Import run data

13.2.1 Add run data to a new study

When prompted, select your Run Data Source:

- To import run data directly from an Olink Signature Q100 instrument to Olink NPX Signature, select Olink Q100 Connect. Select the desired run(s) and press Next.



NOTE: Run data cannot be saved in the npx folder. Please make sure that the data is securely saved on disk, server or computer.

- Select Next again and verify panel, data file version and plate layout information. Click Add. The Study Overview will appear.
- To import run data files from your computer or a local server, select Run Data Files.
 - Select the desired run data file(s). Valid options are Olink Signature Q100 export files, .q100 or .zip, exported heatmap or table results files in .csv format from Fluidigm Real-time PCR analysis software.
- Add plate name for Plates 1 and 2.
- Select Sample Plate Dispensing: Left & Right or Even & Odd.



NOTE: A study cannot include different panel types at the same time. It can consist of only runs from one of the following panels: Olink Target 48, Olink Target 96, Olink Focus, or from Olink Flex.

If duplicate sample names are found, Olink NPX Signature prompts an alert message box. During data import, unique sample and assay names are necessary for proper handling of the data. Change sample names if needed. Sample names can be changed directly in Olink NPX Signature by importing a manifest in the Plate Manifests view. Refer to the built-in help for more information.

When the selected runs have been validated, click Next. Select the correct Panel and Panel Data File for each of the imported runs, and select if the plate should have the default plate layout or if the layout should be mapped based on a plate manifest. Click Add.

For instructions on how to securely connect the Olink Signature Q100 to a network, please refer to the Olink® Signature Q100 User Manual.

13.2.2 Add run data to existing study

Open your already saved study. Expand the main menu by clicking the three horizontal lines in the top left corner. Select Import Run Data, and follow the above instructions to add data directly from a Olink Signature Q100 instrument or from run data files on your computer.

13.3 Enter study information

Study information can be entered in the Study -> Details. Adding study details is optional but can be used to e.g., add information to the Analysis Report.

Enter information in some or all the following fields to be displayed in the Analysis Report:

- Sample Type
- Customer Info
- Business Development Manager
- Lab Info
- Report Notes
- QC Notes for Analysis Report

13.4 Verify plate layout and sample annotation

1. Select Plate QC-> Plate Layout to display the plate layout for each Olink panel and plate.
2. Under Plate Details, verify that the correct panel data file version is selected in the drop-down menu. The same data file version will be used for all runs of the same Olink panel in the study.
3. Verify that the plate layout is correct. To change the plate layout, select one or several wells and click preferred Sample Type in the list above the plate layout.

Available types are:

- Sample (S)
- Sample Control (SC)
- Negative Control (NEG)
- Inter-plate Control (IPC)
- N/A

Calibrator, Negative Control, and Sample Control must be annotated for calibration normalization and QC to be performed.


4. Repeat step 2 and 3 for all imported plates before continuing.

14. Perform quality controls

1. Perform the QC for each plate separately using the Sample QC tab.
2. Perform quality assessment for all plates using the other views and then make an overall assessment.


The acceptance criteria for passing QC are described below.

Criteria	Recommended value
Run QC	
Std. Dev. of Incubation Control 1	< 0.2 NPX
Std. Dev. of Incubation Control 2	< 0.2 NPX
Std. Dev. of Detection Control	< 0.2 NPX
Number of flagged samples	≤ 1/6 of total number of samples on plate (15 samples on a full plate)
Sample QC	
Incubation Control 2 deviation	< ±0.3 NPX from plate median
Detection Control deviation	< ±0.3 NPX from plate median

 **TIP:** If Std. Dev. is higher than the recommended values, evaluate the Control signal deviation from median/sample QC graph to identify any extreme outlier samples. Exclude these samples from the QC analysis (click on the sample in the graph and select **QC analysis: Excluded**) and re-evaluate the run QC again.

14.1 Perform a quality assessment

Parameters that need to be evaluated for each run are listed in the table below. The corresponding information in NPX Signature can be found in the lower left corner under Plate Metrics. If all plates pass quality control and assessment, the quality control is finished, and the data is ready for export and reporting.

Information	Recommended value	Comment
Assay LOD	$ \text{LOD} < 2.5 \text{ NPX}$	If $ \text{LOD} > 2.5$ please contact Olink Support for guidance. Plate ANOVA
	≤ 10 (number of assays)	No warning.
	> 10 (number of assays)	May be caused by insufficient randomization or other issues.
		 NOTE: These guidelines are based on a two-plate study. The larger a study is, the smaller the detectable differences become.
Row/Column	ANOVA < 30 (number of assays)	No warning.
	30 – 60 (number of assays)	Possible randomization issue. Refer to section 21.
	60 – 90 (number of assays)	Re-run plate or otherwise ensure that this is not the result of a poorly executed run.
		For high values, investigate the Assay QC view.
%CV Intra	$< 15\%$	Refer to sections 21 and 19.
%CV Inter	$< 25\%$	Refer to sections 21 and 19.
Detectability	$> 75\%$ of the samples	Refer to document on olink.com/software .

If all plates pass quality control and assessment, the data analysis is finished, and the data is ready for export and reporting.

14.2 Additional quality assessment



NOTE: Switch between Ct and NPX in each view e.g. to evaluate the effect of normalization or to search for position effects in internal controls and assays.

To perform additional quality assessment, follow these steps:

- On the Assay QC tab, view the values of internal controls and assays (change assay in the drop-down menu above the plate layout) for each sample. For example, search for specific patterns that may indicate technical errors.
- On the Table tab, evaluate patterns of data below LOD between sample plates in a study and/or remove specific assays or single datapoints from a study/sample plate.
- On the Heatmap tab, search for outlier samples and/or visualize homogeneity of Negative Controls and IPCs (change sample type in the drop-down menu).

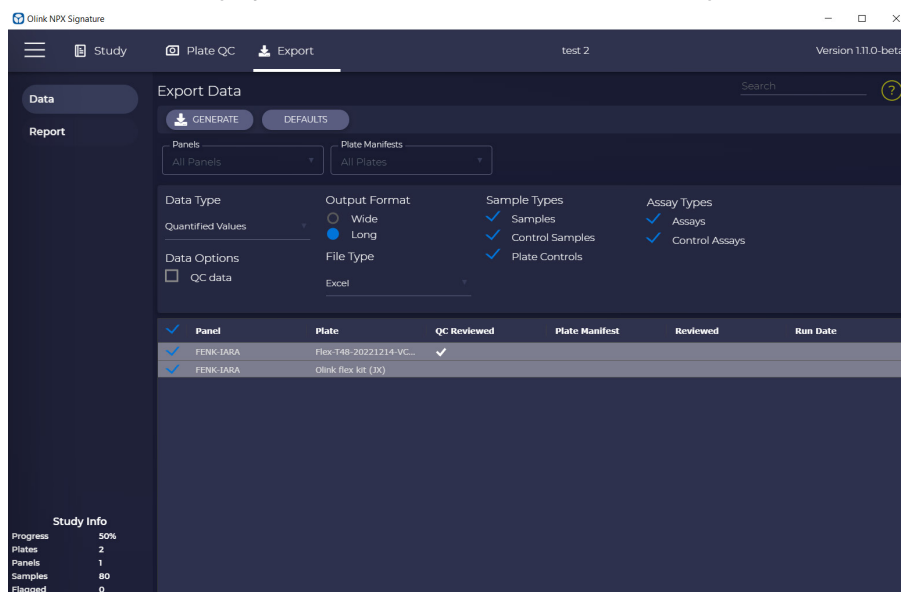
On the Detectability tab, evaluate the detection limit for each assay and sample plate (optimal range for $\text{LOD} \pm 2.5 \text{ NPX}$). Assess if deviating LOD for one sample plate affects detectability on other sample plates.

On the Z-scores tab, display differences between sample plates or distributions within a plate.


15. Export data

In the Export -> Data tab, Data can be exported to a XLSX file or CSV file for use in other applications.

1. Select **NPX Value** on the status bar in the upper left corner of the main window.
2. Under Study Options on the **Study** tab, select the output option for NPX values below LOD. The default is "Actual Value", which displays the actual measured value for each data point.



3. The settings in the **Export Data** view may be adjusted to change the format, layout, or to add additional data to the export. Refer to [14.1 Perform a quality assessment](#) for more information.
4. In the **Data** tab, mark the desired runs to be included in the report and click **Generate**.
5. Enter a filename and location in the **Save** dialog, select an export format (XLSX or CSV files) and click the **Save** button.

Setting	Description
Export format	XLSX or CSV For CSV format, column separator and decimal separator can be configured.
Layout	Wide format or Long format. Wide is the default matrix format and Long format will output one line per datapoint.  NOTE: In Excel, there is a number of rows limit of 1 048 576. If this number is exceeded, Excel export will not work, and CSV format should be selected instead.
Export Samples	Export data for customer samples
Export Control Samples	Export Control samples.
Export Plate Controls	Export IPC, Plate Control, Negative Control or Calibrators.
Export Assay Results	Export results for assays.
Export Control Assay Results	Export results for control assays.
Export QC data	Export deviation from median for Incubation Control 2 and Detection Control.
Export Plate LOD	Will export plate LOD for each plate as well as max LOD.

15.1 Considerations

- Samples that are flagged by the analysis are reported in red text. NPX-values that are below maximum plate LOD have a red background.
- Samples, assays, or data points that have been marked as failed in the software are reported as No Data.

The NPX results Excel file can be optionally exported and the data will be presented as follows:

- As NPX values.
- Values below maximum plate LOD have a red cell background.
- Data for samples with a QC warning are indicated in red text. Data from samples that do not pass QC should be treated with caution.
- The maximum plate LOD value for each assay is presented on a separate row below the data for the samples and is indicated as LOD.
- Missing data frequency is presented for each assay and indicates the percentage of samples with values below Maximum plate LOD.

The layout is described below. Parameters in brackets represent quantified data.

Study Name	Olink NPX Signature version																								
NPX data or Quantified data																									
Panel	Panel 1					...				Panel x					Panel 1		...	Panel x		Panel 1		...	Panel x		
Assay	1	2	3	...	96						1	2	3	...	96	Plate ID			Plate ID		QC Warning			QC Warning	
Uniprot ID	1	2	3	...	96						1	2	3	...	96										
Olink ID	1	2	3	...	96						1	2	3	...	96										
Sample #1	1	2	3	...	96						1	2	3	...	96	plate_1.csv			plate_x.csv		Pass / Warning			Pass / Warning	
Sample #2	1	2	3	...	96						1	2	3	...	96	plate_1.csv			plate_x.csv		Pass / Warning			Pass / Warning	
Sample #x	1	2	3	...	96						1	2	3	...	96	plate_1.csv		...	plate_x.csv		Pass / Warning			Pass / Warning	
...																									
[Assay warning]	1	2	3	...	96						1	2	3	...	96	plate_1.csv			plate_1.csv						
[Lowest quantifiablelevel]	1	2	3	...	96						1	2	3	...	96	plate_1.csv			plate_1.csv						
Max LOD [Plate LOD]	1	2	3	...	96						1	2	3	...	96	[plate_1.csv]			[plate_1.csv]						
[ULOQ]	1	2	3	...	96						1	2	3	...	96										
[LLOQ]	1	2	3	...	96						1	2	3	...	96										
Missing Data freq. (%)	1	2	3	...	96						1	2	3	...	96										
Normalization type	1	2	3	...	96						1	2	3	...	96										

Column	Description	Type
SampleID	The annotated sample ID	String
Index	Well index in 96 plate	Integer
OlinkID	OlinkID for assay	String
UniProt	UniProt ID for assay	String
Assay	Gene name for assay	String
MissingFreq.	Frequency of missing data (below LOD or NaN)	Float
Panel	Panel name assay belongs to	String
Panel_Lot_Nr	Lot number for the panel	Integer
PlateID	Name of the plate the sample was run on	String
QC_Warning	Indicates whether the sample passed QC or not	String PASS, WARN or FAIL
LOD	LOD value for assay	Float
NPX	NPX value	Float
Normalization	Type of normalization used in study	String Plate control or Intensity
Assay_Warning	Indicates whether the assay passed QC or not	String PASS or WARN

15.2 Create an Analysis Report

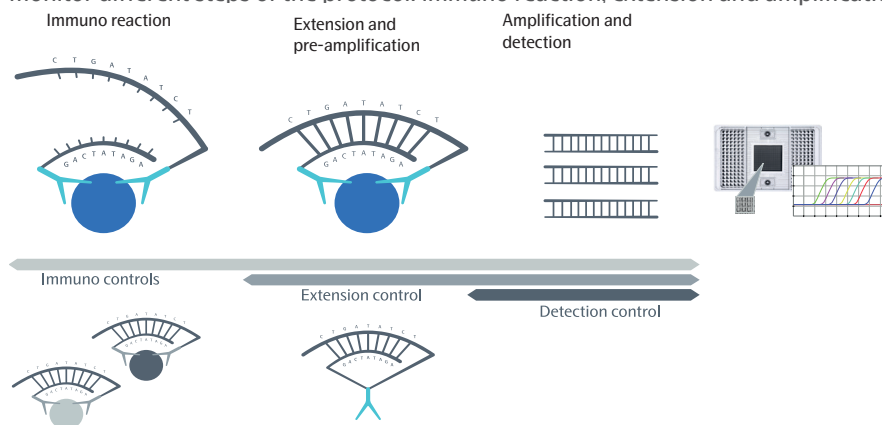
Once all data has been thoroughly checked, Olink NPX Signature can generate an Analysis Report for the study. The Analysis Report includes information and QC parameters for the study.

Go to Export -> Report and select all panels to be included in the Analysis Report. Click Create to save the Analysis Report as a PDF document. A preview of the document will appear.

Part 4: Quality control

16. Overview

Olink has built-in quality controls in all multiplex panels. Each 92-plex panel contains 96 assays. Four of these are internal controls that allow for an in-process quality control designed to monitor different steps of the protocol: immuno reaction, extension and amplification/detection.



- The two Incubation Controls consist of two different non-human antigens measured with PEA assays: Incubation Control 1 and 2. These controls monitor potential variation in all three steps of the reaction.
- The Extension Control is an antibody coupled to both DNA-tags (hence always in proximity). This control monitors the extension/pre-amplification and amplification/detection step and is used for normalization of the data.
- The Detection Control is a complete double stranded DNA amplicon which does not require any proximity binding or extension step. This control monitors the amplification/detection step.

The internal controls are used for both sample and run QC as described below. The quality control of data is performed separately for each sample plate.

16.1 Sample QC

Each of the internal controls is spiked into all samples at a set concentration. The signals for these are therefore expected to be the same over the entire plate. Sample QC is performed using the Detection Control and Incubation Control 2. Within each run, the levels of these controls are monitored for each sample and compared against the plate median of all samples. If either of the controls deviate more than the acceptance criteria allow (see below), the sample gets a QC Warning and the sample is flagged in Olink NPX Signature. The Extension Control is used in the normalization step and in generation of NPX, and hence is not included in the quality control of data.

Acceptance criteria for passing a sample:

- Incubation Control 2 and Detection Control deviates $< \pm 0.3$ NPX from the plate median.

Deviating values for the internal controls can be caused by, for example, errors in pipetting or pre-analytical factors in the samples that affect the performance of the controls. For more information on troubleshooting samples that do not pass QC. Refer to [19. Deviating controls](#) for more information.

16.2 Run QC

The internal controls are also used in the run QC. This QC assesses the variation over the plate for each of the Incubation Controls 1 and 2 and the Detection Control. If the variation for one of the controls is too large (see below) the entire run is considered unreliable.

For acceptance criteria for passing a run, refer to [14. Perform quality controls](#).

If a too large variation is observed for either of the controls, go to the Plate QC -> Assay QC tab to evaluate the data. For example, if individual samples show extreme values or if a certain sample column is affected, these samples can be marked as failed, and the QC redone and re-evaluated. For more information on troubleshooting of this step, refer to [19. Deviating controls](#).

In addition to passing or failing individual plates, ensure that no systematic bias is present in the data. The Plate metrics view in the bottom left corner alerts you to such issues.

%CV is calculated using control samples if present in duplicates on each sample plate. The reported %CV is the mean %CV over all assays, and this is only calculated using data over LOD. A high %CV does not fail a run automatically but should be a cause for further investigation.

- Reference value for Inter %CV: < 25%
- Reference value for Intra %CV: < 15%

17. Normalization methods

Olink NPX Signature supports three methods for between-plate normalization. Between-plate normalization adjusts median NPX levels based either on customer samples or IPC controls. An important concept when deciding on the normalization procedure is randomization, which in this context applies to the sample placement across the plates. For randomized studies with more than one plate, sample intensity normalization is the default normalization. For other studies, IPC normalization is the default. (See [Randomization FAQ](#) on the Olink website.)

Olink uses an arbitrary, relative quantification unit called Normalized Protein eXpression (NPX). In qPCR, the x-axis value of the point where the reaction curve intersects the threshold line is called the Cycle threshold (Ct). This indicates the number of cycles needed for the signal to surpass the fluorescent signal threshold line. NPX is derived from the Ct values obtained from the qPCR using the following equations:

Extension Control:

$$Ct_{\text{Analyte}} - Ct_{\text{Extension Control}} = dCt_{\text{Analyte}}$$

Inter-plate Control:

$$dCt_{\text{Analyte}} - dCt_{\text{Inter-plate Control}} = ddCt_{\text{Analyte}}$$

Adjustment against a correction factor:

$$\text{Correction factor} - ddCt_{\text{Analyte}} = NPX_{\text{Analyte}}$$

The correction factor is calculated by Olink during the validation of the panels.

17.1 IPC normalization

Three inter-plate controls (IPC) are included on each plate and run as normal samples. The inter-plate control is a pool of 92 antibodies, each with one of the pairs of unique DNA tags on it positioned in fixed proximity (i.e. 92 Extension Controls). The median of the three IPCs is subtracted for each assay, and this reduces variation between plates. This method is completely independent of the samples included on the plate and is therefore recommended for studies where complete randomization of samples cannot be guaranteed.

17.2 Intensity normalization v.2

The Intensity normalization v.2 adjusts the data so that the median NPX for a protein on each plate is equal to the overall median. Each plate is adjusted so that the median of all assays is the same on all plates. This method relies on the assumption that the true median of each plate is the same. One way of ensuring this is to randomize the samples beforehand. If there is total randomization, this method outperforms other normalization methods. If there are specific types of samples that are only available on certain plates, this normalization method should not be used.



NOTE: Only samples are included in this normalization. Negative Controls, IPCs and control samples are excluded. Compare with [17.3 Intensity normalization](#).

17.3 Intensity normalization

Intensity normalization has been replaced by Intensity normalization v.2 as standard. The function remains as a tool for troubleshooting older datasets using this normalization method. This method uses the median of all samples on the plate, including Sample Controls, Negative Controls and IPCs.

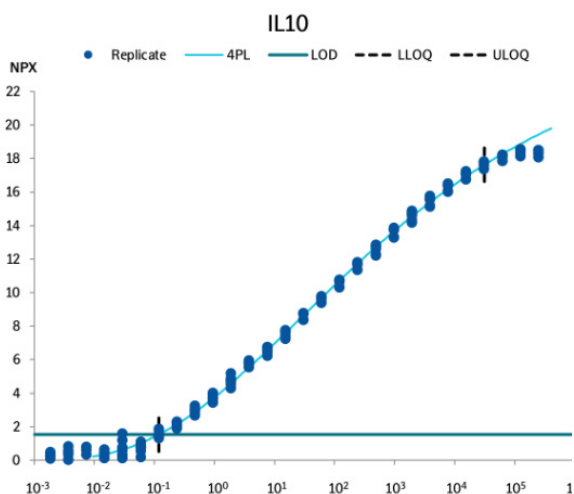
17.4 Calibrator normalization

17.4.1 Results in standard unit (pg/mL)

Standard curve

During development, a thorough fine-tuned 32-point standard curve is developed for each protein biomarker simultaneously, including all 45 proteins. Multichannel pipetting and numerous replicates of the curves are used to minimize errors and establish an accurate immunoassay curve fitting. Due to the wide dynamic range of the PEA assays in the panel, a large spread of measurement points is required to cover the entire range. Eight measurement points, which are commonly used in many technologies, would not suffice for Olink's multiplex measurement of 45 assays. The predefined standard curves avoid operator-dependent reconstitution and pipetting of standard curves at each lab and for each run. The figure below shows an example of a standard curve defined for one assay during development.

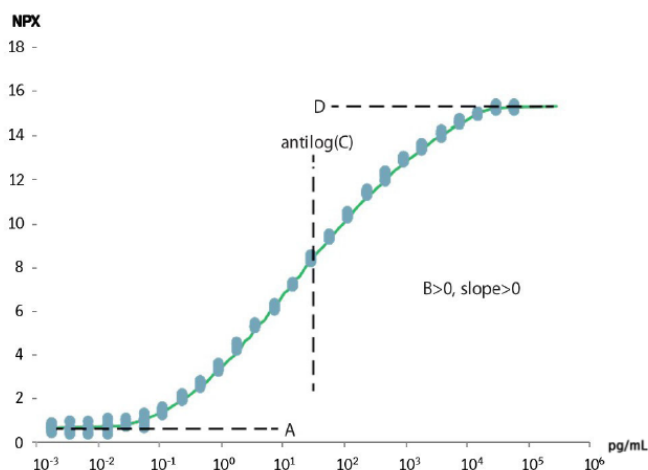
Standard curves for each assay can be found via the panel product page (olink.com/target/).



A standard curve defined for each assay during development.

4PL model

A 4PL model curve fit is used to describe the immunoassay standard curve, indicated by the turquoise line in the figure above. When running a study, the measured sample value (represented by the dotted blue arrows in the figure above) is related back to the adjusted standard curve model which translates the measured value to the protein concentration in pg/mL using the equation below. Where A = asymptote (a constant value) at low doses, B = slope factor, C = EC50 (mid-range concentration) and D = asymptote at high doses. These parameters are indicated in the figure below. An example of a point standard curve defined for each assay during development.



An example of a point standard curve defined for each assay during development.

$$\text{Concentration (pg/mL)}_{\text{Sample I, Assay J}} = \frac{10^{\left(10^{\left(\frac{\log_{10}\left(\frac{(A-D)}{(\text{NPXvalue}_{\text{Sample I, Assay J}} - D)} - 1\right)} + \log_{10}(C)\right)}\right)}}{B}$$

1000

Repeated testing and validation show that the 4PL curve fitting describes the standard curve well and can be used to correctly estimate the protein concentration in analyzed samples within the limits of quantification. The approximate lower and upper limits of quantification (ULOQ and LLOQ) are defined during the development of the panel, and specifications for LLOQ and ULOQ are established for each lot. This information is available in the individual Panel Validation Reports provided by Olink.

Results reported in pg/mL

The list below together with the figures provide an overview of how data in pg/mL is reported in the results file.

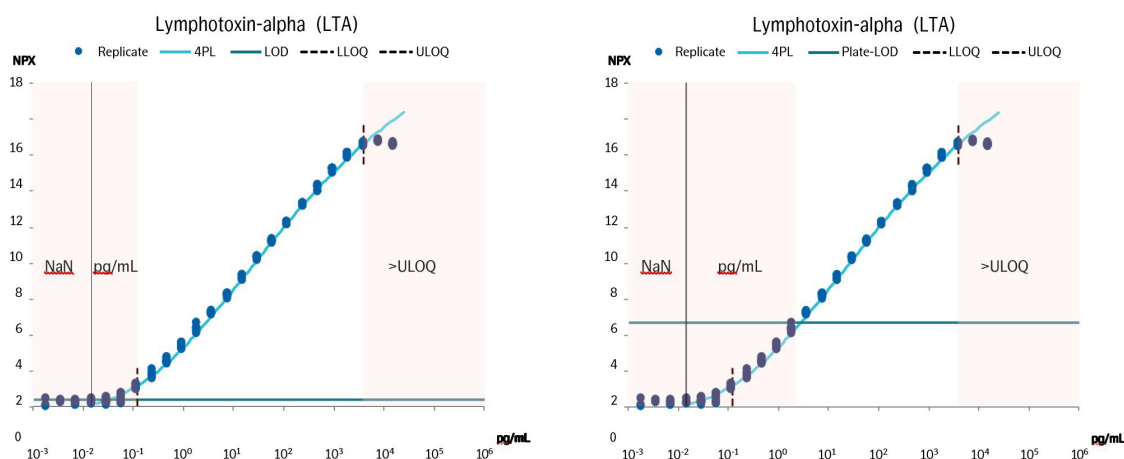
- Data between LQL and ULOQ is reported as a pg/mL value and shown in the white areas of the graphs.



NOTE: Lowest Quantifiable Level (LQL) is defined as the value used as the lower limit, LLOQ (default) or plate LOD (when plate LOD > LLOQ).

- Data below the lowest fitting parameter in the 4PL curve fit model cannot be calculated and is indicated as NaN in the red areas of the graphs.
- Data >ULOQ is indicated as >ULOQ in the red areas of the graphs. Values above ULOQ are not reported in pg/mL due to high risk of misinterpretation of hooking data.
- Data below LQL is presented in pg/mL value in the red areas of the graphs. Values below LQL should be treated with caution due to decreased precision and accuracy in the lower range and should not be used for individual comparison to reference values.

For a more detailed list describing the results file, refer to [15. Export data](#).



Overview of how data in pg/mL is reported in the results file.

Part 5: Troubleshooting

18. Introduction

This chapter describes issues that may arise during use of Olink NPX Signature, or data issues during analysis, and how to solve these issues.



NOTE: *The figures in troubleshooting are schematic only and might not reflect the current interface of Olink NPX Signature for Olink Target 96.*

18.1 Warning messages

The following warnings can be displayed:

1. Opening Study
 - a. Could not identify the panel
 - The panel datafile associated to plates in the study cannot be located and thus not identified. Navigate to Settings -> Panels and import the required panel data file.
2. Importing Run Data
 - a. Quality Threshold does not meet specified criteria 0.5.
 - The Quality Threshold defined for analysis was not set to 0.5. Open *Run data* in Fluidigm Real-Time PCR and export the data after analyzing with a quality threshold of 0.5.
 - b. Baseline Correction method is not set to Linear.
 - The Baseline Correction method defined for analysis was not set to Linear. Open run data in Fluidigm Real-Time PCR and export the data after analyzing with a baseline correction method of Linear.
 - c. Unsupported plate format
 - The run data was not acquired for a supported IFC.
 - d. Unsupported probe-type count, expected 1.
 - The run data was not acquired with a supported protocol
 - e. Panel types must match in study
 - The study already contains a plate for one-panel type (Olink Target 96, Olink Target 48, etc.). All plates in the study must be run for the same panel type.
 - f. Run barcode already exists in a study for the panel
 - The run data for this IFC has already been imported to the study.
 - g. Data integrity file not found in the archive
 - The run data checksum file was not found in the Olink Q100 Signature export. The run data must be analyzed and exported from Real-Time PCR before importing.
 - h. Could not locate data file in file
 - The run data analysis export was not located in the Olink Q100 Signature export file. This may be due to a corner finding error during analysis, due to:
 - o Insufficient amount of ROX dye in corner wells
 - o Contrast not optimal
 - o Edge sample or assay is not loaded (e.g. air bubbles or particle clogging of the IFC)

Unzip the run data archive and open the ChipRun.bml in Fluidigm Real-Time PCR to analyze and export data. Manually set the corners using Fluidigm Real-Time PCR Analysis Software, export in CSV format and import in Olink NPX Signature.

Make sure to zoom in to clearly see where the wells should be (if empty). All wells will not fit optimally, the important ones are the four corner wells.

- i. Datafile checksum not verified
 - The run data contained in the Olink Signature Q100 export file failed to validate using the checksum values generated when the analysis was performed. This may indicate that the run data has been modified after it was initially analyzed when the run was going to be completed. Unzip the run data archive and import the results_all.csv, results_all.csvx, or results_heatmap.csv file directly.
3. Importing Panel Datafiles
 - a. Data file already exists
 - A panel definition with the same name and version is already imported in the application.
4. Importing Sample Manifest Files
 - a. Unrecognized file extension for sample plate manifest
 - The file format could not be processed. Supported formats are Fluidigm Real-time PCR comma value separated plate definitions and NPX Signature XLSX format.
 - b. No Sample-ID defined in input data
 - The sample manifest import file does not define the Sample-ID column
 - c. No Plate-ID defined in input data
 - The sample manifest import file does not define the Plate-ID column

19. Deviating controls

If the normalized value for internal controls or a specific sample deviates from the rest of the sample set, the sample is flagged. A flagged sample should not be excluded from the data export but may be excluded from the QC analysis. Refer to [14. Perform quality controls](#) for evaluation of the data.

Issue	Explanation	Reason	Action
A sample is flagged.	A sample is flagged when one or several internal controls deviate from the plate median for that specific sample.	All flagged samples in a study are shown under Study -> Summary in the table Flagged or failed samples.	The behavior of the internal controls makes it possible to understand why the sample is flagged. See the rest of this section for more information. For more detailed information about flagged samples, click the Plate QC -> Sample QC tab (Figure 7) and the Assay QC tab (Figure 10).

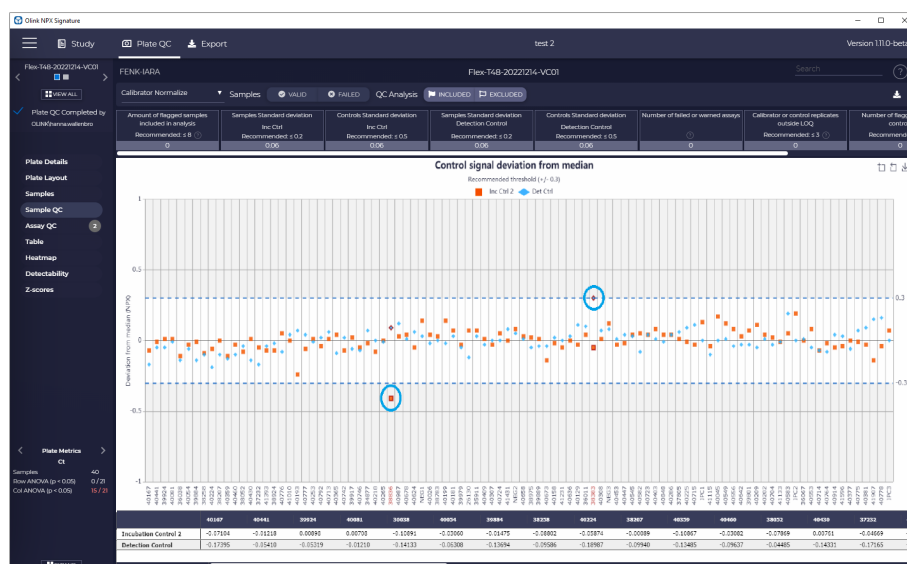


Figure 1. The Sample QC tab, where the left circled sample is flagged by Incubation Control 2, and the right circled sample is flagged by the Detection Control. Both of these datapoints are outside the recommended threshold.

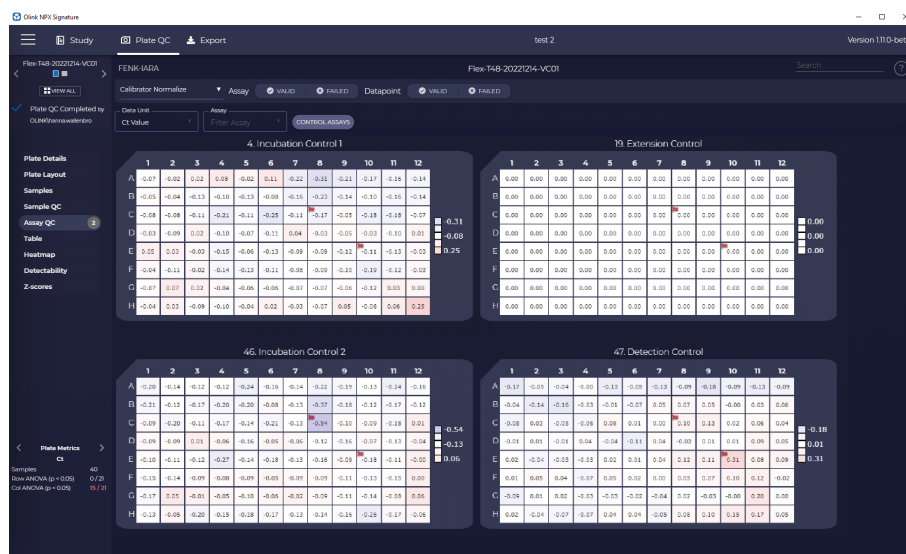


Figure 2. Assay QC tab for samples shown in Figure 1. The circled sample to the left has a lower NPX for Incubation Control 2 (well B3). The circled sample to the right has a higher NPX for the Detection Control (well F4) and lower NPX for the Extension Control.

19.1 Sample flagged by Incubation Controls

Issue	Explanation	Reason	Action
A sample is flagged by the Incubation Control.	The Incubation Controls deviate.	If the two Incubation Controls deviate, but not the Extension and Detection Controls, this is an indication that something (most likely in the sample) is affecting only the Incubation Controls.	See examples in 19.1.1 .

19.1.1 Common reasons for deviating Incubation Controls.

Possible cause	Explanation	Solution
Sample matrix	If the sample matrix for the flagged sample is different from the others on the same plate, the incubation environment can be different. This can make the reaction slightly more or less efficient.	Perform the QC evaluation for one sample type at a time.
Sample volume or concentration	The sample volume is too high or too low.	Set the sample as failed in the Plate Layout tab. If applicable, run the sample again and make sure the correct volume is used. See examples in Figure 1 .
Sample quality	If the sample is stored in a freezer for long periods of time, it can evaporate. A more concentrated sample can increase possible matrix effects, and thus make the internal controls more or less efficient.	
Sample type	Olink assays are validated for serum and plasma. Other sample matrices can contain factors that interfere with the immuno reaction step.	Standardize samples as much as possible (E.g.: for lysed cells and tissue, use similar concentration of protein in each sample).

20. Sample flagged by detection control

Issue	Explanation	Reason	Action
A sample is flagged by Detection Control.	The NPX value of the Detection Control for this specific sample deviates more than 0.3 NPX from the plate median.	One example can be seen in Figure 1 and Figure 2 . Data is normalized using the Extension Control. Since both Incubation Controls and the Extension Control display decreased Ct-values, the normalization step will adjust the data. The Detection Control that did not show decreased Ct-values will be overcompensated by normalization against the Extension Control and thereby deviate from the rest of the sample set after normalization.	This type of flag is generally caused by the same reasons as flagged Incubation Controls. It is not uncommon that both the Incubation Control 2 and Detection Control flag simultaneously, but with opposite "direction" in the Sample QC. This is seen when the flagged sample affects both the extension and immunoassay step, but to different extent. See examples in 19.1.1 .

20.1 Deviating external controls

Issue	Explanation	Reason	Action
High Intra- CV value	Intra-CV value is larger than 15%.	The Sample Controls differ within the sample plate.	Check sample annotation of the Sample Controls and that they pass QC. Check the row pattern for rows A and B to make sure that none of the rows is an outlier (e.g. issue with a channel on one of the multichannel pipettes). Fail one or both of the control samples if remaining data on the plate pass all QC analysis and assessment.

Issue	Explanation	Reason	Action
High Inter-CV value	Inter-CV value is larger than 25%.	The control samples differ between sample plates.	Check sample annotation of the control samples and that they pass QC. If intensity normalization has been used, ensure that randomization assumption is valid by comparing with IPC normalization.

Issue	Explanation	Reason	Action
High LOD (> 2.5 NPX)	Background levels, values in Negative Controls, are increased above expected levels.	<ul style="list-style-type: none"> Sample and/or primer columns double pipetted during loading of IFC. 	<ul style="list-style-type: none"> Rerun from Detection step.
		<ul style="list-style-type: none"> Technical issue (increased background may occur sporadically due to random interaction of probes or airborne contamination). Seen for all three Negative Control wells for specific assays. 	<ul style="list-style-type: none"> If high LOD does not affect the detectability for the assay, continue data analysis. If detectability is affected in a multi plate study, the affected assay can be excluded from the affected plate and data analysis continues for remaining plates or rerun from immuno reaction step . Please contact support@olink.com for further guidance.
		<ul style="list-style-type: none"> Sample/IPC contamination of Negative Control. 	<ul style="list-style-type: none"> If one well affected: Exclude contaminated Negative Control. If two or more Negative Controls are affected: Rerun samples.
		<ul style="list-style-type: none"> Sample and/or primer columns switched during loading of IFC. 	<ul style="list-style-type: none"> If noted during lab work, contact support@olink.com.
Large number of high and/or low LODs (outside ± 2.5 NPX)	Calculated LODs are out of expected range.	<ul style="list-style-type: none"> Wrong datafile Wrong panel. Contamination of Negative Controls. Wrong annotation of negative controls or IPCs. 	<ul style="list-style-type: none"> Confirm datafile; reanalyze data. Please contact support@olink.com for further guidance.
Large deviation in LOD between plates in study.	LOD values differ more than 1 NPX between sample plates in the same study.	<ul style="list-style-type: none"> Contamination of one or several wells Pipetting error Technical issue (increased background may occur sporadically due to random interaction of probes). Seen for all three Negative Control wells for specific assays. 	<ul style="list-style-type: none"> Evaluate which plate and/or well is contributing to the large deviation. Exclude affected well if that can be defined. Exclude assay on affected plate or rerun from immuno reaction step Please contact support@olink.com for further guidance.

Issue	Explanation	Reason	Action
Large deviation between triplicates of IPC and/or Negative Controls on the same plate.	NPX values for triplicate samples deviate > 0.5 NPX.	<ul style="list-style-type: none"> Contamination of one or several wells. Pipetting error 	<ul style="list-style-type: none"> If one well affected: Exclude that well. If several wells affected: Rerun

20.2 Missing sample data

Issue	Explanation	Reason	Action
Missing sample data in exported results file.	Data for some samples are not exported.	This can be caused by not using unique sample names.	Ensure that sample names are unique by checking Plate QC -> Samples tab or change sample type to Control for non- unique samples to force export of data for these samples.

21. Inconsistent results

21.1 Variation between plates - common reasons

Issue	Explanation	Reason	Action
The "Plate ANOVA" value in the Panel metrics box (Figure 3) shows a high value. The variation is also shown on the Plate QC -> Z-scores tab (Figure 4. Plate variation that should be solved by intensity normalization.).	The total NPX varies between plates.	May be caused by insufficient randomization, meaning that the distribution of samples from different groups is not the same for all plates in the study.	If the samples are completely randomized, make sure that intensity normalization has been used. The results will then look like the example in Figure 5, the same results as in Figure 4 after intensity normalization.
High Inter-CV value	Inter-CV value is larger than 25%.	The control samples differ between sample plates.	Check sample annotation of the control samples and that they pass QC. If intensity normalization has been used, ensure that randomization assumption is valid by comparing with IPC normalization.

Panel Metrics	
IPC Normalized	
Plates	25
Samples	2150
Plate ANOVA (p < 0.05)	92 / 92
Row ANOVA (p < 0.05)	55 / 92
Col ANOVA (p < 0.05)	45 / 92
Flagged	8
Proteins > 75%	85 / 92
%CV (Inter)	13
%CV (Intra)	5

Figure 3. The Panel metrics field, with a Plate ANOVA value that indicates variation between plates.



Figure 4. Plate variation that should be solved by intensity normalization.

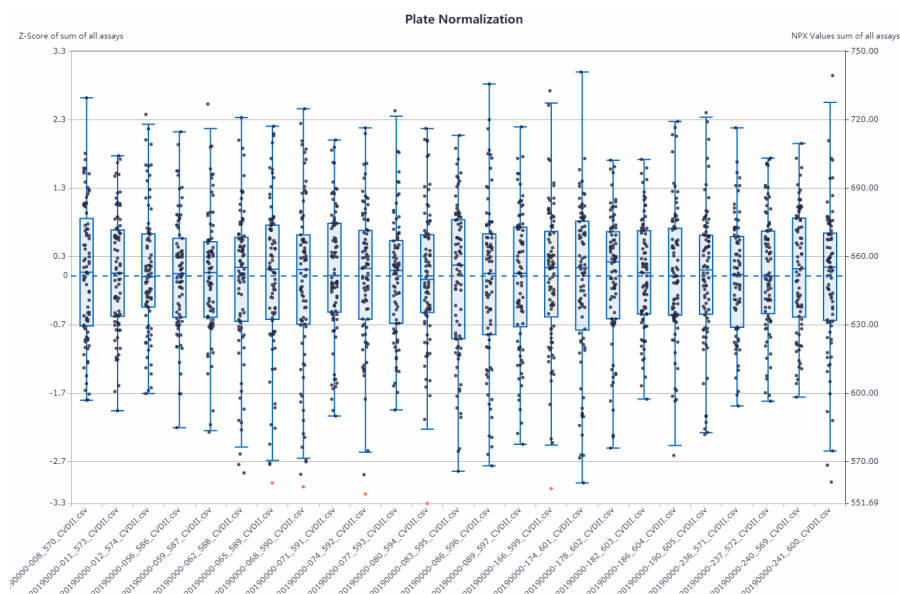



Figure 5. The same results as in Figure 4, after intensity normalization.


21.2 Variation within a plate - common reasons

Issue	Explanation	Reason	Action
The columns or row ANOVA in the Plate Metrics or Panel Metrics box show high values. The effects are visualized in the Assay QC tab.	Areas of a plate (rows and/or columns) have systematically higher or lower values (Ct and/or NPX) than the rest of the plate.	The variation is caused by the sample position on the plate. Within-plate effects are often caused by laboratory mistakes.	See examples in 21.2.1 .  NOTE: Make sure that the deviation cannot be explained with biological variation, i.e. that a unique sample group is placed on one column/row.
Position effects/patterns: visible only for Internal controls			
All internal controls are affected on Ct-level in a similar manner (all increased or decreased.)	One sample column or row consistently show deviating values.	Pipetting error, e.g. pipette not pre- conditioned.	Exclude data from analysis and/or rerun.
		Mistake during pipetting of the incubation solution, extension solution, detection solution or samples.	Refer to Figure 6 .
		Evaporation due to incomplete sealing of plate during incubation or PCR steps.	Exclude data from analysis and/or rerun.
		Different sample matrices.	QC matrices separately.
Incubation Controls and Extension Control differ from Detection Control on Ct-level.	Incubation and Extension Controls show the same pattern, Detection Control shows another pattern.	PCR instrument not good at keeping 50°C, Detection Control not affected by extension step.	Rerun from immuno reaction step.
		May be pre-analytical (interfering factors may affect all controls but the Detection Control).	Contact support@olink.com for further guidance.
Incubation Control(s) differ from Extension and Detection Controls.	One or both Incubation Controls show deviating pattern.	Pre-analytical factors in samples that interfere with the immuno reaction.	Few deviating samples: Exclude samples from subsequent statistical data analysis. > 1/6th of samples deviating: Contact support@olink.com for further guidance.
Position effects/patterns: visible for samples and Internal controls			
Columns/rows/parts of sample plate.	Patterning that follows sample naming/sample matrices.	Different sample matrices.	QC matrices separately.
Gradient over the sample plate.	Upper or lower part or left and right part of the plate affected with clearly deviating values.	IFC issue. Poor vortexing in extension step. Poor mixing of detection mix. Uneven temperature in PCR block.	Rerun. Contact support@olink.com for further guidance.

21.2.1 Common problems and reasons for within-plate effects.

Problem	Possible cause	Figure reference
First column different than the rest of the plate (observed for internal controls).	The pipette was not preconditioned.	
A specific column or columns is/are different than for the rest of the plate (observed for internal controls).	A mistake when the incubation solution, extension solution, detection solution or samples were pipetted.	Figure 7.
One row consistently different from the rest of the plate (observed for internal controls and/or samples).	The pipette tip in that specific position was not tight enough.	
A gradient from row A to row H.	Pipetting was done at an angle. The plates were not sufficiently vortexed.	Figure 10.
Deviating Z-score distribution for single assays on one plate.	Primer contamination.	Figure 9.

21.3 Extreme outliers - common reasons

Issue	Explanation	Reason	Action
<p>Extreme blue or red lines in heatmap (when only selecting “samples” in the drop-down menu) or outlier dots in z-score view.</p> <p> NOTE: Extreme outliers can be discovered in different views (Plate QC -> Z-scores, Assay QC, Heatmap). In Figure 6, two types of outliers are illustrated.</p>	Sample with extremely low or high protein quantification.	Incorrect dilution of sample No sample added.	Fail sample.

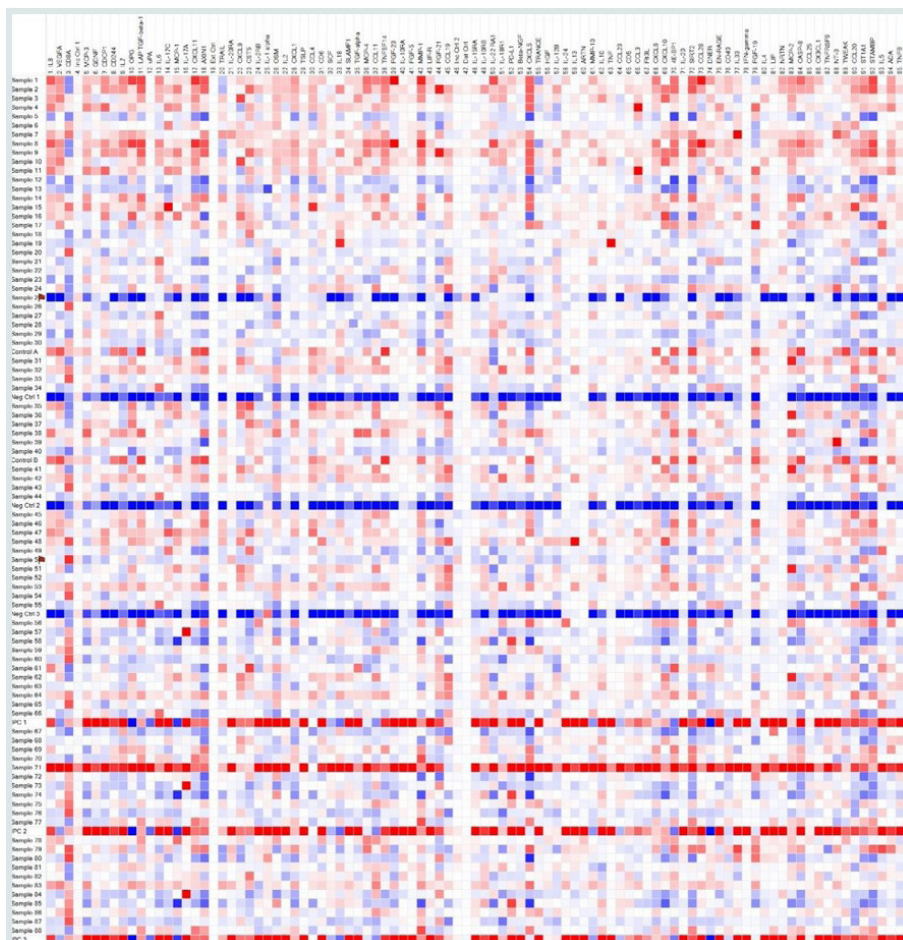


Figure 6. Heatmap with display type Delta with NPX values from a single plate run which contains two outliers. Sample 25 has the lowest NPX values for all assays and Sample 71 has the highest NPX values for all assays.

For Sample 25, most NPX values are below LOD and one conclusion for this outlier is that there is no biological sample present in that well.

For Sample 71, the NPX values are higher than for the rest of the samples. This can arise from poor dilution of a sample when running one of the high-abundant panels.



Figure 7. Ct-values that show results of laboratory mistakes. Refer to table below for a description of errors performed on this run.



Figure 8. NPX values that show results of laboratory mistakes. Refer to table below for a description of errors performed on this run.

Explanation of columns in Figure 7 and Figure 8. Red numbers indicate laboratory mistakes.

	Column 4 (correct)	Column 7	Column 8	Column 9	Column 10	Column 11	Column 12
Incubation mix (μL)	3	3	3	3	3	6	3
Sample volume (μL)	1	1	1	0	2	1	1
Extension mix (μL)	96	96	192	96	96	96	96
Detection mix (μL)	7.2	14.4	7.2	7.2	7.2	7.2	7.2
PCR product (μL)	2.8	2.8	2.8	2.8	2.8	2.8	5.6



Figure 9. Ct values that show primer contamination of Incubation Control 2.

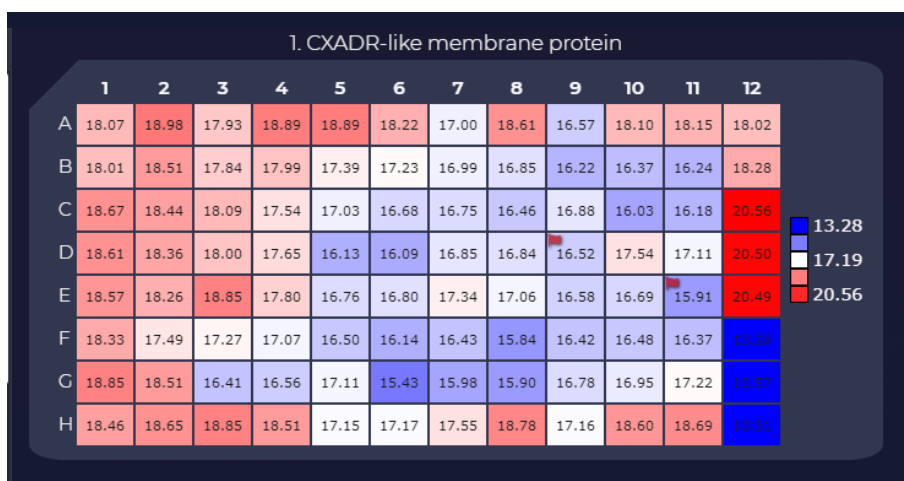


Figure 10. Within plate effects due to incorrect or insufficient vortexing of the sample plate during sample dilution.

21.3.1 High NPX signals - common reasons

Issue	Explanation	Reason	Action
Unexpectedly high NPX signals in diluted panel for the majority of samples.	Low variation between samples Saturated assays (may be visualized in Z-scores tab).	Samples were not diluted.	Rerun from sample dilution step.

22.Revision history

Version	Date	Description
1.11	2023-11-21	6 , flowchart updated. 13.3 , Note added. Updated version number to match software version (version 1.1–1.10 does not exist). Screenshots updated. Editorial changes.
1.0	2023-02-15	New

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1324, v1.11, 2023-11-21