

3D HISTECH

QuantCenter 2.2 User Guide

August 6, 2018
Rev. 1

Contents

Disclaimer	3
Character Types and Symbols	5
1 Installation of QuantCenter 2.2 Bundled with CaseViewer 2.2	6
1.1 Prerequisites of the Installation.....	6
1.2 Licensing.....	6
1.3 Installation of Application Modules.....	7
2 Operation and workflow	12
2.1 Main application interface.....	12
2.2 Quantification workflow.....	13
2.2.1 Creating measurements.....	13
2.3 Defining a Measurement scenario.....	13
2.4 Gallery (FISHQuant and CISHQuant).....	15
2.5 Running measurements.....	17
2.6 Measurement results.....	19
2.7 QuantCenter menu.....	23
3 Available Quant applications	24
3.1 PatternQuant.....	24
3.2 NuclearQuant.....	27
3.3 MembraneQuant.....	30
3.4 CellQuant.....	33
3.5 HistoQuant.....	35
3.6 FISHQuant.....	39
3.7 CISHQuant.....	44
3.8 DensitoQuant.....	48
4 Data Visualization	50
4.1 Panels and functions.....	50
4.2 Scoring and creating a Secondary Probe.....	63
5 Running a Batch Process from CaseViewer	65
Alphabetical Index	67

Disclaimer

Copyright © 2001-2018 3DHISTECH Ltd.
All rights reserved.

Intellectual property related to the 3DHISTECH products are as follows:

- P1300124; PCT/HU2014/000020; EP 14745228.8.; US 14/771.380
- P0700404; PCT/HU2008/000065; EP 08762668.5.; US 12/663.537
- P1700279; PCT/HU2018/050030
- P1700483
- P1500394; PCT/HU2016/050039; EP 16840280.8.; US 15/756.370
- P0700409; US 2008/0306964
- P0800181; PCT/HU2009/000027; EP 09721248.4.
- P0600435; PCT/HU2007/000047; EP 2024772; US 12/301.781
- P0600177; PCT/HU2007/000018; EP 1.994.398; US 12/281.566
- P0900741; PCT/HU2010/000130; EP 10812989.1.
- P0900142; PCT/HU2010/000027; EP 10726183.6
- P101036; PCT/IB2005/050351; EP 1789831; US 7.663.078
- P0301911; PCT/HU04/00019; EP 1644767; US 7327515

The above mentioned granted patents, granted utility model, registered trademarks, pending international and national patent applications and the other corresponding IP are the sole properties of the 3DHISTECH Ltd.

3DHISTECH Ltd. is not liable for damage of whatever nature (including, but not limited to, general or specific damage, indirect damage, consequential damage or incidental damage, including the results of the analysis of the digitized slides, for example, change of health status related to erroneous diagnosis from the digitized slide(s)) that stems from or is associated with use of Product, digitized slides, quality of staining, quality of stained slides, quality of used method of staining. 3DHISTECH Ltd. assumes no responsibility for the functionality and fault-free condition of your “application programs” (Workflows, VBA macros, Commander scripts).

CAUTION

For research and education uses only, not for use in diagnostic procedures. This product has not been approved or cleared as a medical device by the U.S. Food and Drug Administration, nor any other regulatory authority. The data and images obtained or viewed using this product are not intended for clinical or diagnostic use.




For performance evaluation only, the performance characteristics of this product have not been established.

THE SOFTWARE IS PROVIDED "AS IS" AND WITHOUT WARRANTY OF ANY KIND, EXPRESSED, IMPLIED OR OTHERWISE, INCLUDING WITHOUT LIMITATION, ANY WARRANTY OF MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE.

Further Information

For the latest information on 3DHISTECH products and services, please visit our website at: <http://www.3dhitech.com>.

Character Types and Symbols

<i>Example</i>	Abbreviation or term that is explained in section Terms and Abbreviations .
Example	Words or characters that appear on the screen. These include field names, screen titles, pushbuttons and menu names, paths or options. Keys on the keyboard. For example, function keys (such as F11) or the Ctrl+O key combination.
<i>Example</i>	Cross-references to other documents or sections within this document.
 Warning!	Indicates that you need an additional module to use the feature or that there are prerequisites for the task.
 Important!	Contains an important piece of information or a recommendation. The application will work if you choose not to follow the recommendation but its performance might be less than optimal.
 Tip!	Contains a suggestion about using the application in some other way or to some interesting purpose.

1 Installation of QuantCenter 2.2 Bundled with CaseViewer 2.2

QuantCenter is not a stand-alone application. Because it runs under CaseViewer, you have to install CaseViewer before installing the application.

1.1 Prerequisites of the Installation

Prerequisites	Description
Hardware	Minimum: Intel 3,2 GHz i5 (Quad Core), 4GB RAM
Operating system	Microsoft Windows 7 Professional 64-bit, SP1
Display resolution	Recommended: 1280×720 or better
Disk space	CaseViewer 2.2 bundled with QuantCenter 2.2 Minimum: 400MB

1.2 Licensing

You receive a product-specific license when purchasing any of the 3DHISTECH applications.

Floating license can be used for running applications within a LAN (Local Area Network) segment. The dongle key must be plugged into a computer that can be accessed any time (switched on and continuously operating) and on which CaseViewer has been installed.



Important!

The license server using the dongle and the connecting clients have to be within the same LAN.

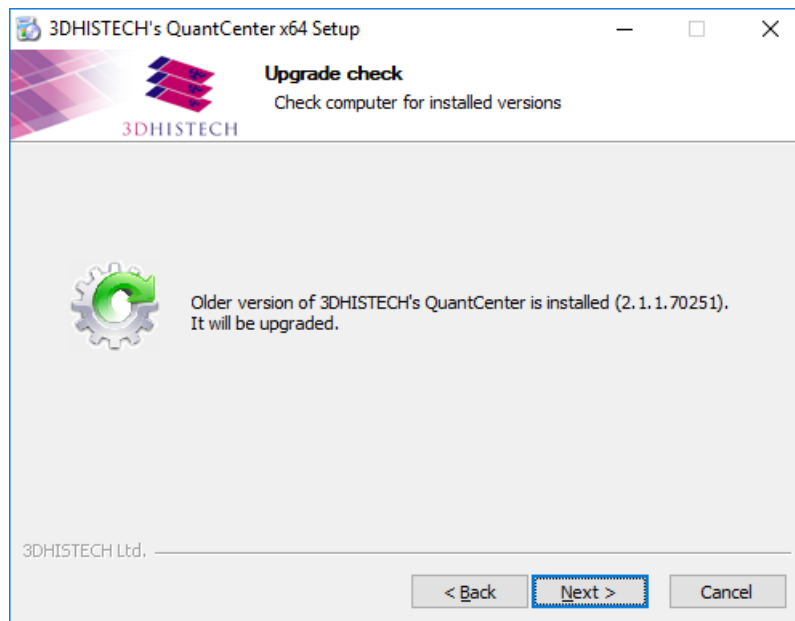
Contact 3DHISTECH support at support@3dhitech.com if you want to extend the license, as in this case some configuration of the license server and of the clients is required.

1.3 Installation of Application Modules

1. Install **CaseViewer 2.2** first. Please refer to section **1 Installation of CaseViewer** in **CaseViewer 2.2 User's Guide**.
2. Launch the **3DHISTECH_Apps_2.2_RTM.exe** file that you received on a 3DHISTECH installation disc or downloaded in a compressed file, then follow the instructions in the installation wizard.



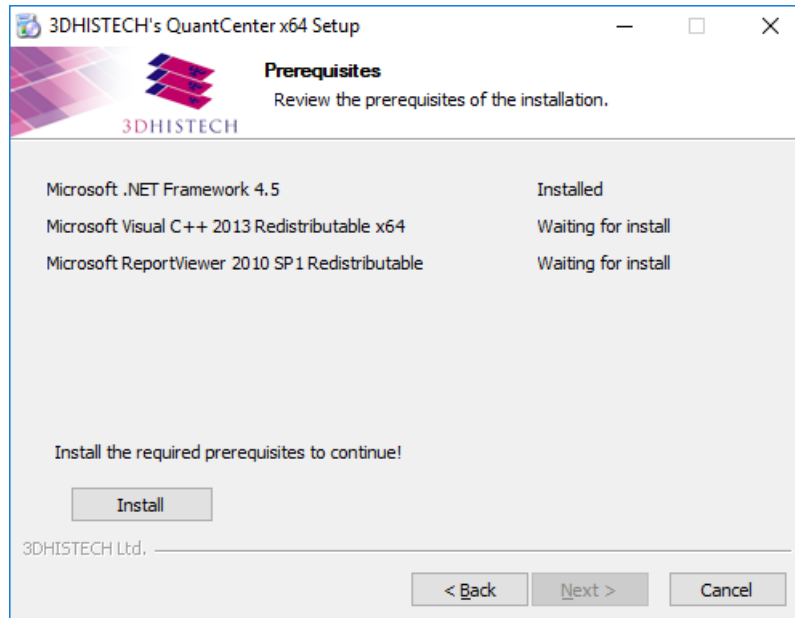
3. If there is an older version of the applications installed on your computer, it will be upgraded automatically after clicking **Next**.



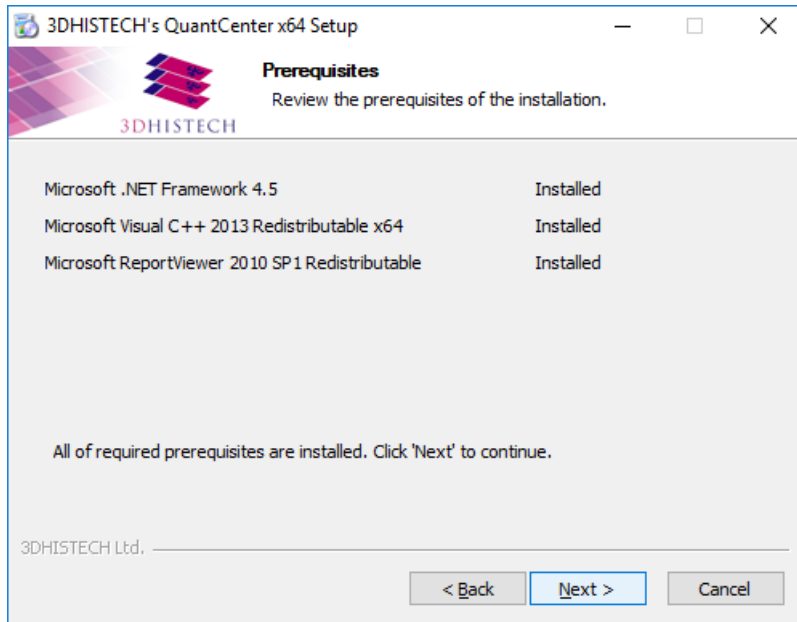
- 4. Accept the End-User License Agreement, and click **Next**.



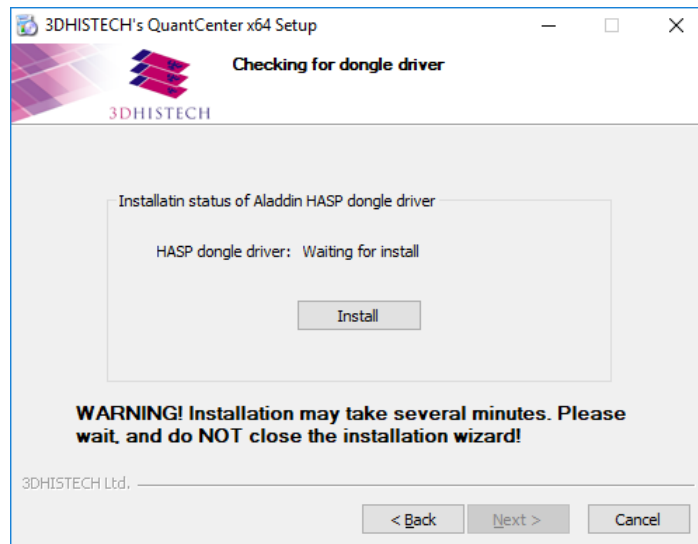
- 5. Click **Install** to install missing prerequisite software. Installations run in the background.



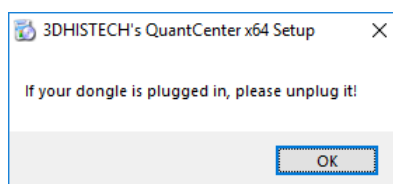
- 6. When all the prerequisites have been installed, click **Install** to continue with the installation of the selected components of the 3DHISTECH application package.



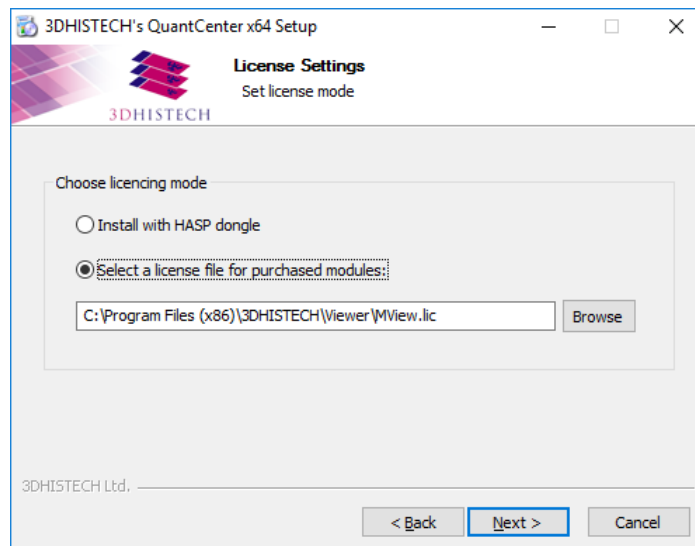
- 7. If the driver of the HASP dongle has not been installed yet, click **Install**.



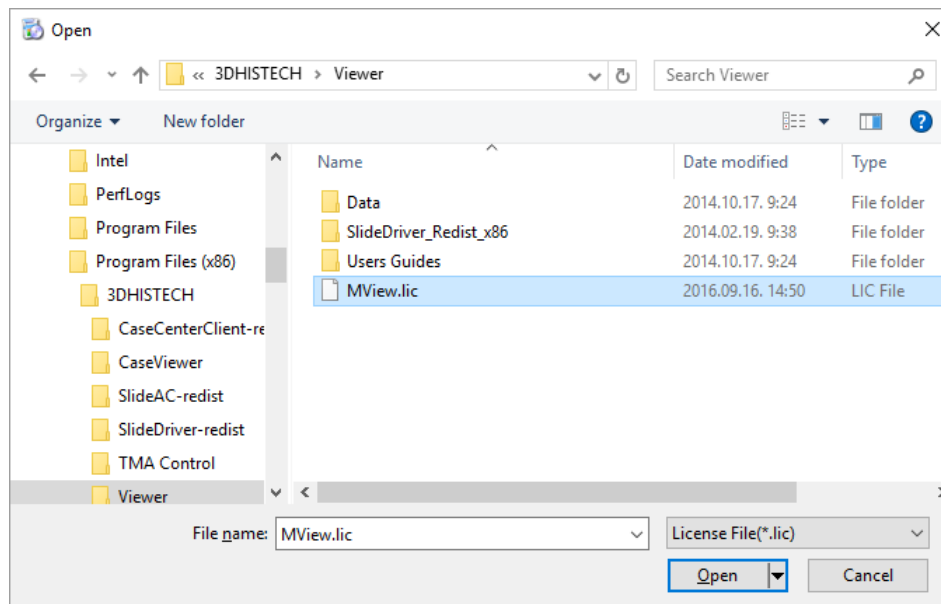
- 8. First, remove the HASP dongle from the USB port, then click **OK**.



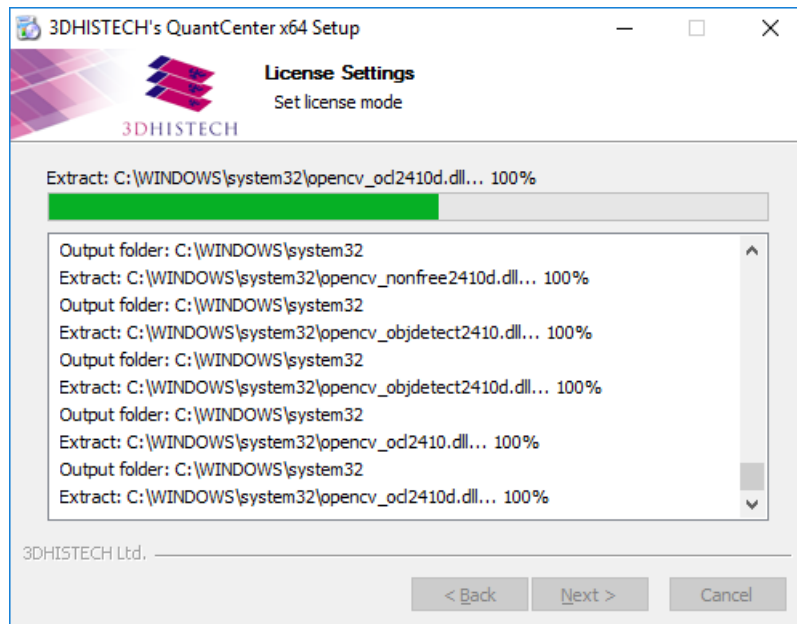
- Set the license mode. If you have a dongle key attached, select **Install with HASP dongle**, otherwise select a license file.



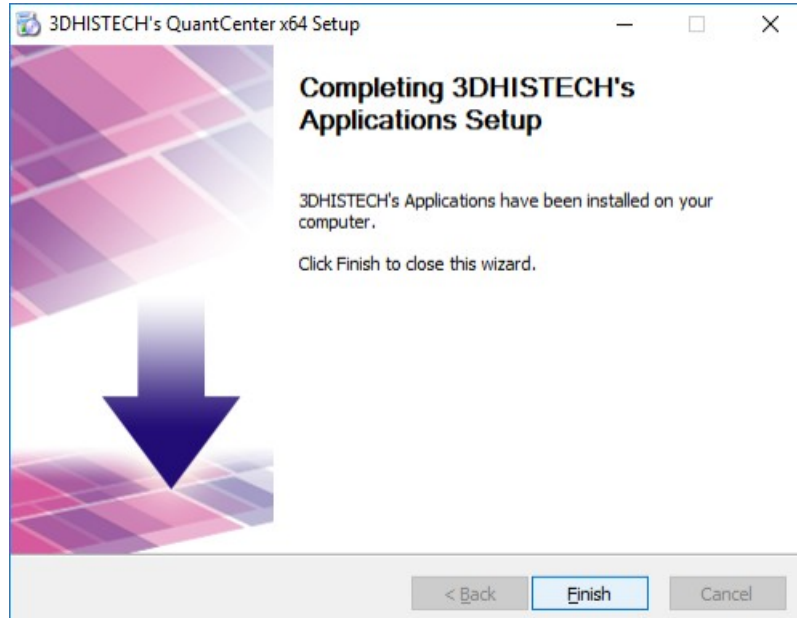
- If you want to use a license file, click **Browse** to locate and open **MView.lic** in the containing folder. Select the file, then click **Open** to continue.



- 11. A progress bar and an information box is displayed, showing the status of the installation procedure.



- 12. Click **Finish** to close installation wizard.

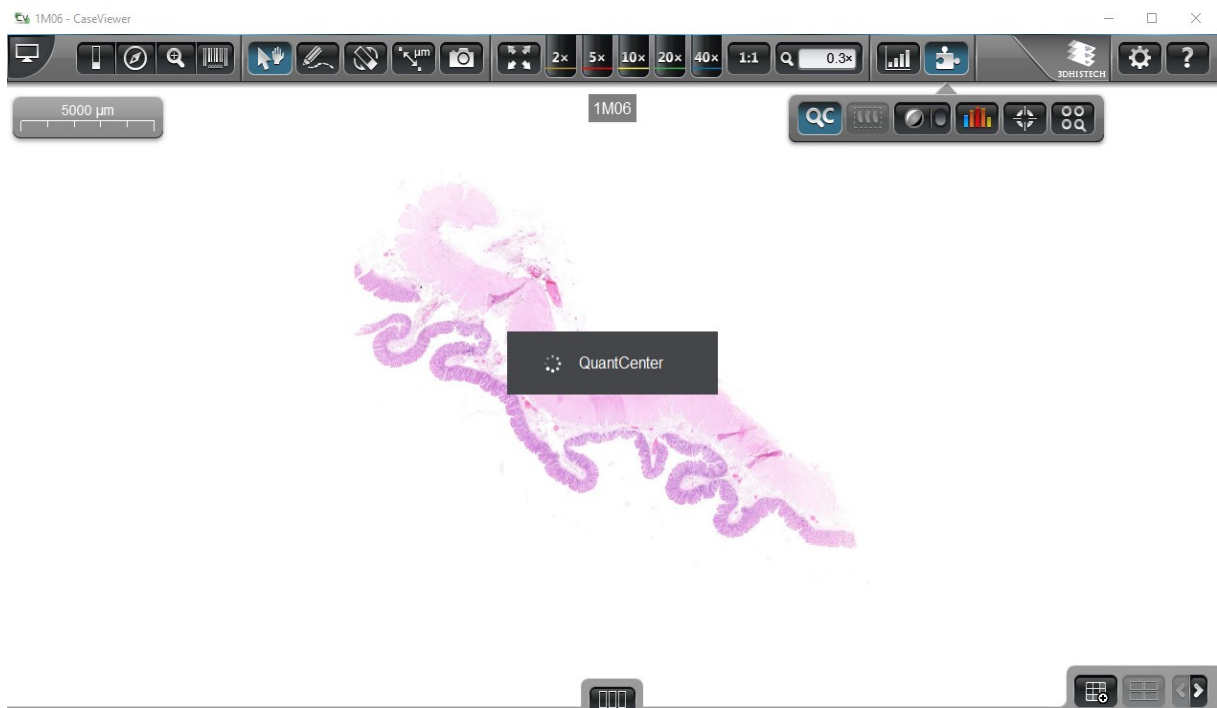


2 Operation and workflow

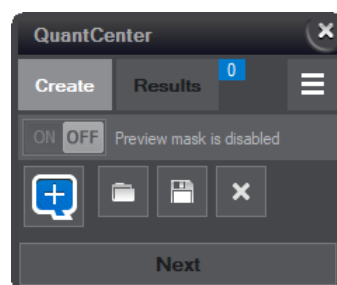
3DHISTECH QuantCenter is an embedded application for running quantification measurements on digital slides and is accessible from CaseViewer 2.2. For more information on how to open a slide in CaseViewer, and how to initiate measurement process through opening the slide in QuantCenter, see sections **2 Opening CaseViewer** and **3.2 Functions – 13. Plugins** in *CaseViewer 2.2 User's Guide*, and section **5 Running a Batch Process from CaseViewer** included in this guide.

2.1 Main application interface

Once QuantCenter is launched from CaseViewer, the splash screen is displayed.




QuantCenter 2.2 uses the CaseViewer slide canvas, and the visual result of each modification or adjustment (Quant measurements, preview, etc.) is applied to the opened slide in CaseViewer.

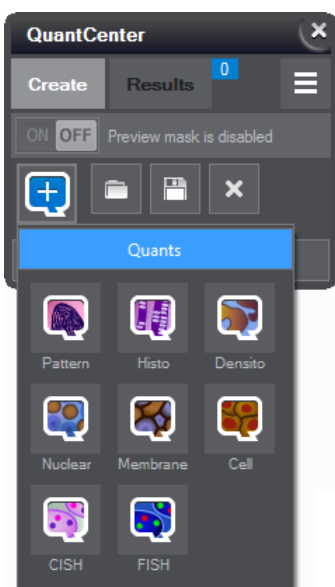



2.2 Quantification workflow


2.2.1 Creating measurements


The main advantage of QuantCenter is that the user is capable of defining a unique measurement scenario by creating a tree structure for the composition of Quant measurements.

Click  to open the Quant menu from which the required Quant module can be selected.




Click  to open a previously saved measurement scenario.

Click  to save the actual scenario that has been created.

Upon clicking  the whole scenario will be deleted, and only the root remains empty.

2.3 Defining a Measurement scenario

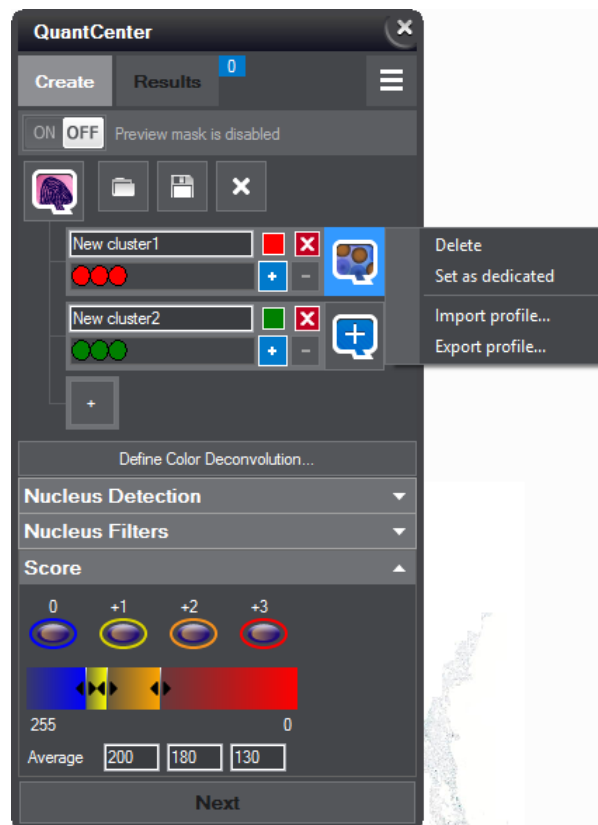
With the help of **Scenario Builder**, a unique measurement profile, a so-called „scenario” can be defined by linking Quant algorithms (PatternQuant, HistoQuant, DensitoQuant, NuclearQuant, MembraneQuant, CellQuant, CISHQuant, and FISHQuant).

1. Click the root element .
2. Select the icon of the desired Quant to start with as root.
3. The selected Quant is now added to the scenario.
4. If PatternQuant or HistoQuant is present in the measurement scenario, it must be trained first before running the measurement process (see **sections 3.1** and **3.5**).

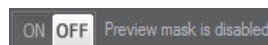
5. If a scenario is complete, specify the areas that will be included in the measurement (annotations / whole slide / current view). Before running the process make sure to set the desired selection on the panel.

When right-clicking the Quant button, you can delete that specific Quant item including selections, or you can select the **Set as dedicated** option by which the measurement of the dedicated Quant will be displayed on the **Measurement Card** form. If you do not set a Quant as dedicated manually, then the uppermost defined Quant will be set as dedicated by default.

It is also available for you to import a profile for the selected Quant by clicking **Import profile...**, and also to export the set parameters as profile for a later use by selecting the **Export profile...** option.



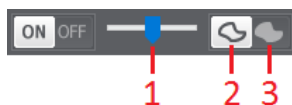
After the parameterization of a Quant is finished, **Mask** function can be activated on the preview image to show segmented objects related to the applied Quant application. To enable preview mask, click **ON** at the top of the selected form.



Once the preview mask is activated, additional options are available for you to select from. The rendering process of slide image with the applied mask is indicated by a processing indicator at the right side of the bar.



The transparency of the mask image can be set by dragging the slider (1) to a desired percentage value. **Outline** (2) or **Fill** (3) options can be selected as mask type (only **Fill** option is available for you if preview mask results are generated by PatternQuant or HistoQuant).



If you create or select a class (click the Quant button on the tree of the scenario), its Quant-related properties in which measurement parameters can be set are displayed at the bottom of the Scenario Builder form.


If a Quant is selected (except for PatternQuant or HistoQuant), and the **Mask** function is activated, a parameter table (Object Properties) is displayed upon right-clicking any of the segmented spots.

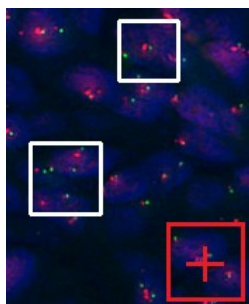
Name	Value
Area	27,019
Perimeter	23,356
Shape factor	0,622
Gray intensity	117,79
Brown intensity from C/D	102,933
Blue intensity from C/D	254,396
Score	3

2.4 Gallery (FISHQuant and CISHQuant)


NOTE: The Gallery function is available only if a FISHQuant or a CISHQuant process has been defined as the root element of a scenario.


Along with the Scenario Builder, desired areas of the slide can be imported into a Preview Gallery, or if a larger slide is loaded, the accuracy of segmentation/mask settings can be monitored by taking areas from farther locations of the slide.


After clicking the  button, move the red marking box above the desired area of the slide, then click with the left mouse button. The size of the marker can be adjusted by entering/increasing or decreasing the actual value in the box, or with the mouse wheel by rolling it back or forth (value ranges from 1 to 100um).

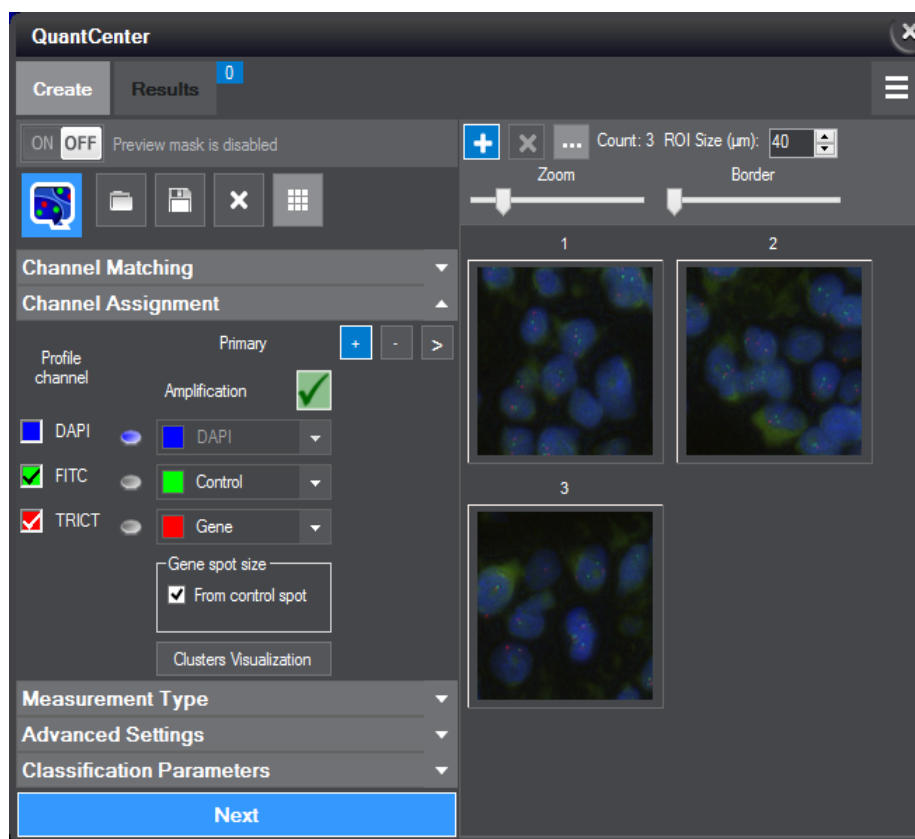


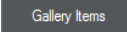
If you want to move the slide so to navigate to a different location when selecting desired areas of the slide to be added to the Gallery, the following options are available for you:

Click with the right mouse button, then drag the image. Click  again, then select slide area to be added as a Gallery item.

After clicking  it is available for you to increase/decrease item size by dragging the **Zoom** slider to the appropriate direction. The **Border** slider is responsible for enlarging the border of items.

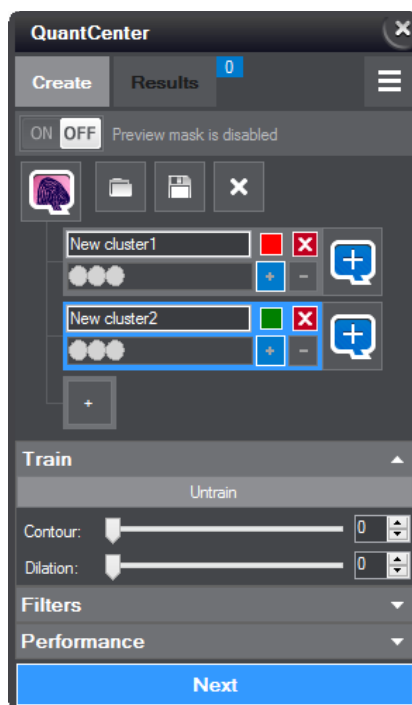
Click with the right mouse button if finished with adding items to the Gallery. In this window you can also delete selected gallery items by clicking . For multiple selection hold the **Ctrl** key pressed while selecting items with the left mouse button, or you can use the **Ctrl+A** hotkey for selecting all the items in the gallery.



To run measurement process on the gallery items (handled as annotations), click **Next** first at the bottom of the panel, then select . A separate job is added to the list in the Processing window, then measurement results are displayed both on the measurement card and the slide.

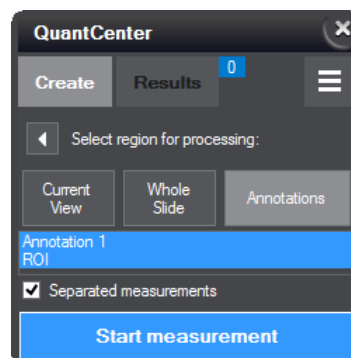
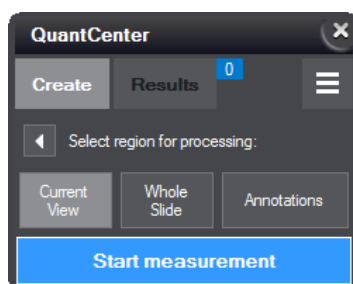
2.5 Running measurements


Once the scenario is built correctly and finished, the **Next** button at the bottom of the panel becomes active and the measurement process can be launched for the desired selection (**Current view**, **Whole slide**, and **Annotations**) by clicking this button.




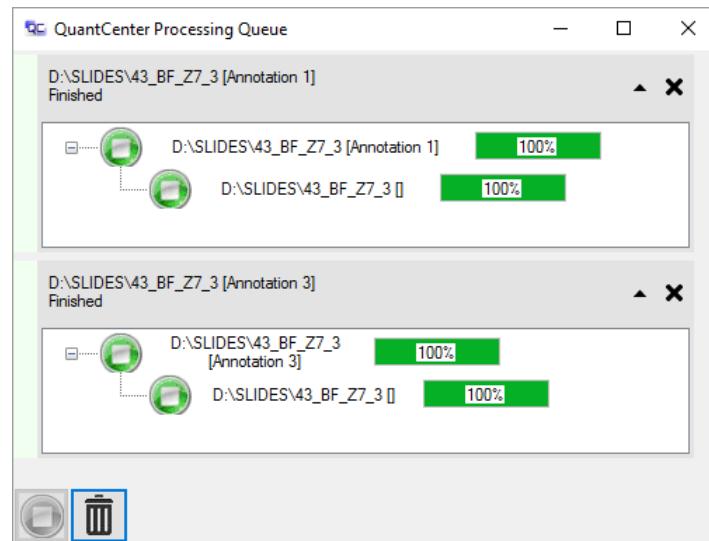
Current view and **Whole slide** options are available for you to select by default. If there are annotations on the slide, these annotations are listed on the **Annotations** panel. At least one annotation must be selected from the annotations list. The measurement will be run on the selected annotation(s). **Separated annotations** option allows you to run measurement processes in the queue separately.

The **Gallery items** option is available only if you run FISHQuant or CISHQuant measurements and you have marked areas on the **Scenario Builder and Gallery** form (see [section 2.4](#) for more information).




To get back to Scenario Builder, click  on the **Create** panel.

Upon running the measurement by clicking the **Start measurement** button, the **QuantCenter Processing Queue** window is displayed in which the running process or processes are displayed. For the detailed view of the progress click the  button.



The **QuantCenter Processing Queue** window can be minimized (runs in the background) and moved to the notification area at the right side of the system tray.

NOTE: Measurements are processed according to the scenario, so if a scenario has not already been created (or being untrained), they cannot be processed.

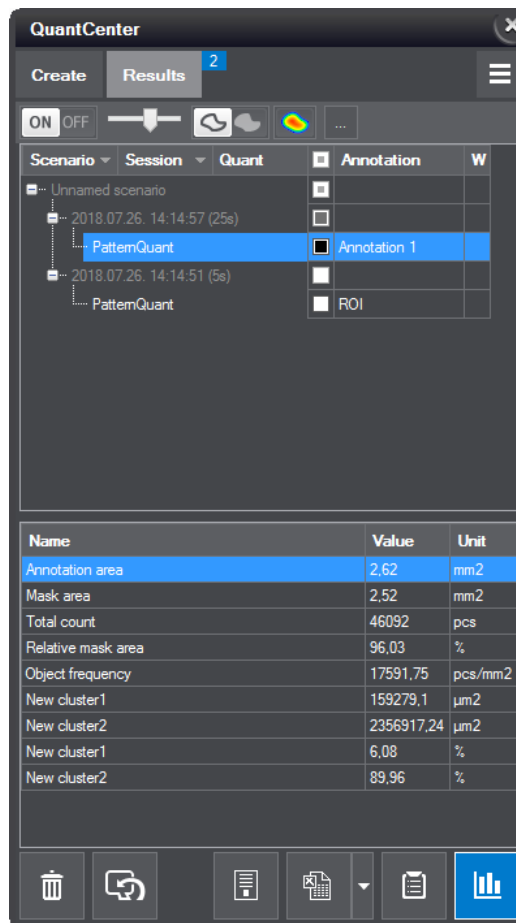
Measurement processes that are running in the background can be visualized by clicking  at the notification area of the system tray.

The measurement process is indicated by a  processing indicator at the right side of the bar.

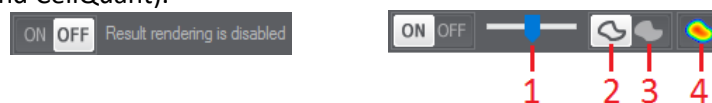
2.6 Measurement results


On the **Result** panel measurement data are shown. Segmented objects related to available measurement results can be displayed. To enable result rendering, click **ON** at the top of the selected form. If result rendering is active, additional options are available for you.


NOTE: The **Result** button is active only if there is a displayable measurement on the slide. Measurement results generated with version 2.2 are not compatible with older software versions than 2.1, and cannot be opened.

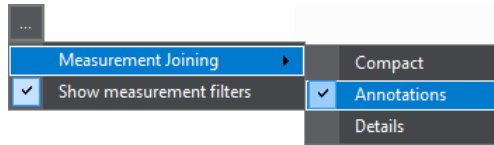


The transparency of the measurement result image can be set by dragging the slider (1) to a desired percentage value. **Outline** (2) or **Fill** (3) options can be selected as visualization type. The **Heatmap** (4) function offers you the visualization of stain positivity in the measured region by highlighting object density (for PatternQuant, HistoQuant, FISHQuant, and CISHQuant) and positivity (for NuclearQuant, MembraneQuant, and CellQuant).





The rendering process of slide image with the selected measurement(s) is indicated by a  processing indicator at the right side of the bar.

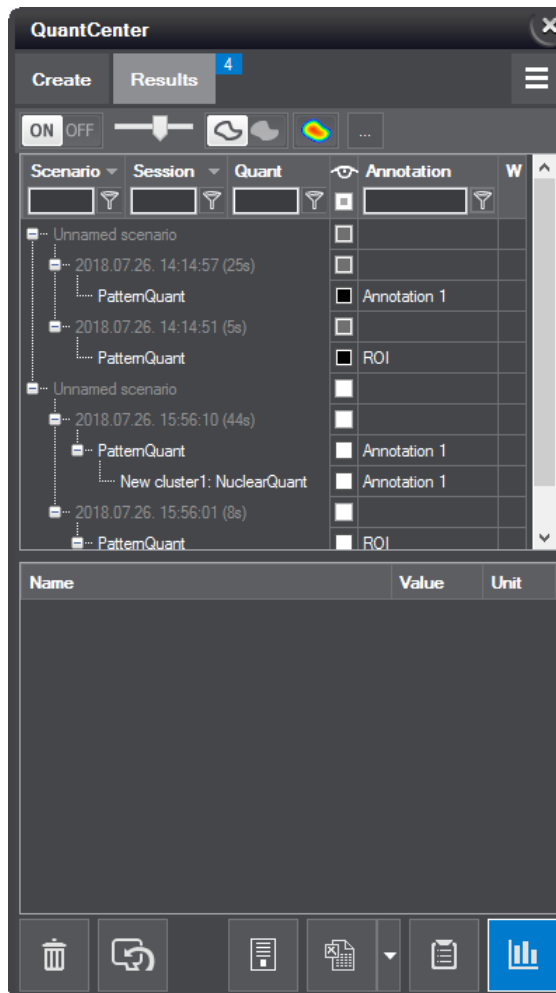
Click  to display further data visualization options.




Measurement data are classified according to three different aspects selectable from the **Measurement Joining** list.


- **Compact** – Default view, shows combined measurements in a simplified form.
- **Annotation** – Can be selected if a simple (one-element) scenario has been created, and measurements were run on different annotations.
- **Details** – If filters are applied, pre-segmented area-related (PatternQuant and HistoQuant) measurement data can be displayed.

Filtering options can be enabled by selecting **Show measurement filters** option. If enabled, **Scenario**, **Session**, **Quant**, and **Annotation** data can be filtered after typing a query and clicking the  button. Filtered results can be ordered within each group by clicking  at the right side of a column header.





If clicking a Quant-related measurement on the tree (under a scenario, by date), the related measurement data is displayed on the bottom pane of the form. Summarized data can be listed if selecting identical Quants in the tree (for multiple selection within a scenario, press **Ctrl / Shift** key during selection; alternatively, select items with your mouse by holding the left mouse button pressed).


Click the checkbox of a scenario/session in the  column to display detection results on the slide image, and by clicking the Quant name for which the measurement was created, data are displayed in the bottom pane of the form. The main checkbox activates the visualization of cumulative detection results on the slide image.

If you want to delete a measurement, first select the item on the tree, then click the  button or hit the **DEL** key. For multiple selection press **Ctrl/Shift** while selecting the items.


NOTE: PatternQuant and HistoQuant measurement values displayed as percentages (related to area) represent values regarding the original annotation (FA).


Click  to display the **Data Visualization** window. For more information on Data Visualization, see **section 4**.


Click  to reload the scenario based on which the measurement process has been initiated.


Click  to switch to Card View form.

Upon clicking left/right arrows in the card view of the form, data of the selected profile (scenario) will be displayed. If there are more than one scenario sessions (measurements) on the slide, up/down arrows are responsible for loading measurement data of the selected session.

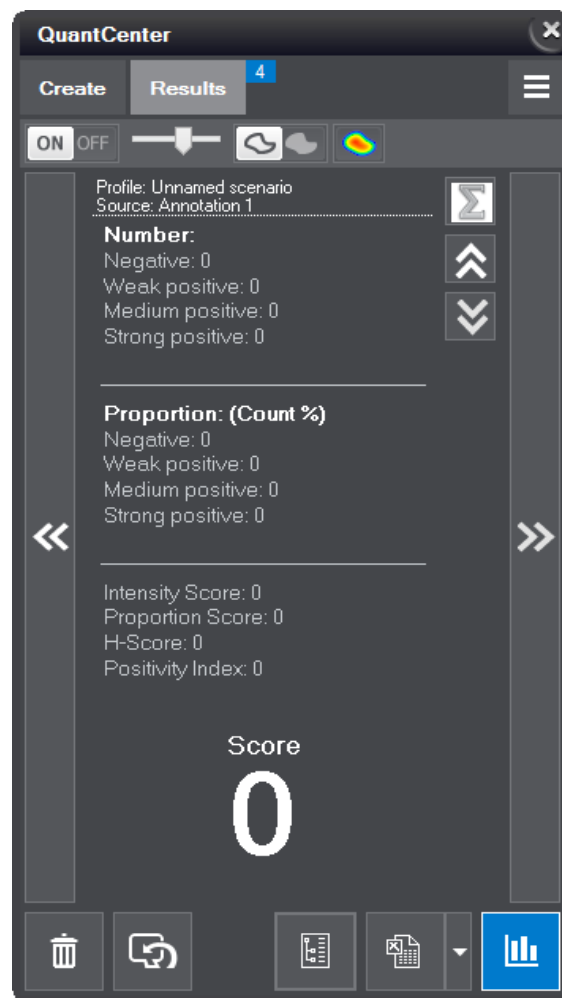
Click  to display merged measurement data related to a specific Quant module of all the sessions of a scenario.


To delete measurements, click  or hit the **DEL** key.

Click  to reload the scenario based on which the measurements have been created, then the software switches to Scenario Builder form.

 – Click this button to export measurement data as Excel worksheet. Click the down arrow at the right of this button and select **Transpose XLS table** to switch rows to columns or columns to rows when exporting measurement data.


NOTE: The selection of **Transpose XLS table** option is saved upon exiting, and will be used as default during export unless you deselect it.

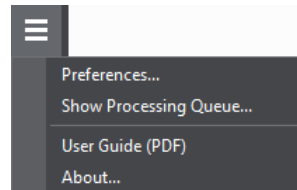


 – This button serves to open Data Visualization window in which spots are displayed. For more information on Data Visualization, see **section 4**.

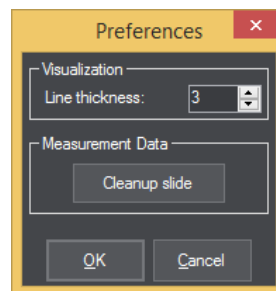
To go back to Tree View form, click .

2.7 QuantCenter menu

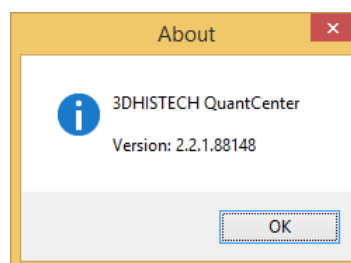
Click  at the top right corner of the QuantCenter window to open the menu from which the following options can be selected:



- Select **Preferences...** to display **Visualization** and **Measurement Data** settings. Set **Line thickness** to define the thickness of masking line. Click **Cleanup slide** to erase all measurement data saved for the slide.



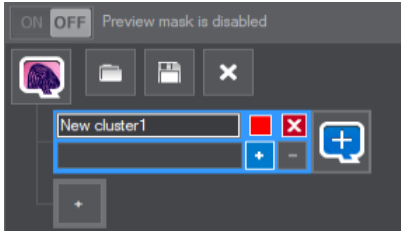
- The **Show Processing Queue...** option displays the QuantCenter Processing Queue window including all the processed measurements.
- Select **User Guide (PDF)** option to open the User Guide of the software.
- The **About...** option displays a window in which the name and the version number of the software is presented.




3 Available Quant applications


3.1 PatternQuant

This Quant module provides segmentation methods to decompose measurement area based on pattern and intensity.




One cluster is displayed by default, but a group of clusters is available for you to create, and extend to a maximum of 5 clusters by clicking .

For each cluster, a unique name and color can be defined. Name is presented in the tree on the measurement form, and the area defined by the cluster is marked with the color on the slide.

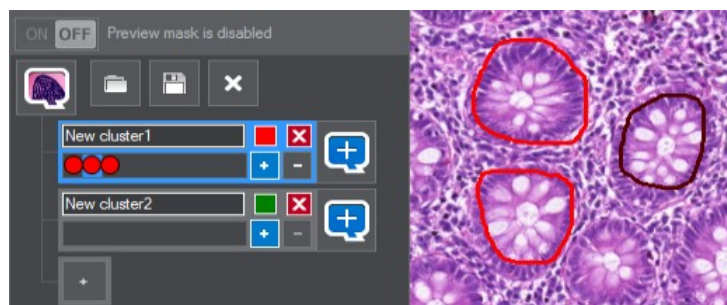




Important!


Before defining areas on the slide make sure to zoom on the slide in an adequate amount to support accurate drawing around specific target areas. Select the required zoom level in the CaseViewer window by clicking the appropriate button or enter a custom value in the text box at the main menu bar.

Click  first, then with the pen by using your mouse, define those areas on the slide that suits to the pattern of the specific cluster. Close selection border by releasing the left mouse button.

NOTE: It is advised to create more selections to get more accurate results. A maximum of 10 areas can be defined within a cluster.



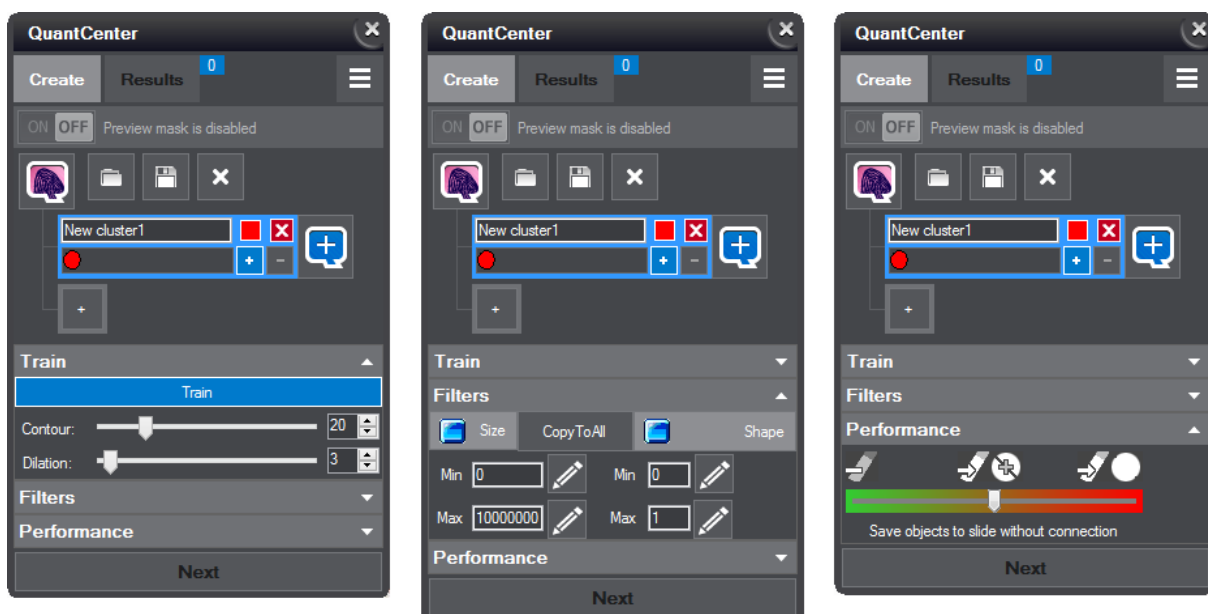
Click  to delete a selected area; first click selection item on the list (alternatively, hold **Ctrl** while clicking the item to select more one by one, or **Shift** to make group selection) then deletion can be performed. Click  to delete a cluster entirely.

Click  at the right side of the cluster panel to append an additional Quant to the cluster. The same window is displayed as in the root view of the tree. The selected Quant algorithm will run on determined areas specified by the cluster. The measurement process will run only on those areas of the annotation that match the properties defined by the cluster.

It is available for you not only to embed other Quants, but another PatternQuant in the tree as well. The additional Quant algorithms can be run on the resulting areas of the previous defined Quant application.

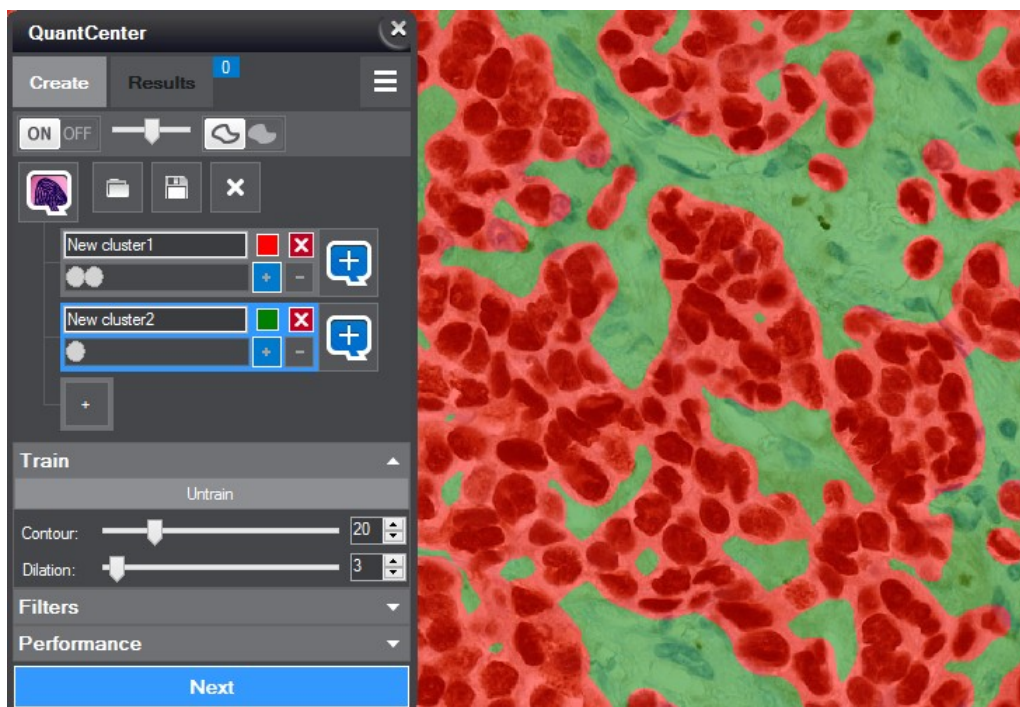
NOTE: The number of linked PatternQuant measurements is limited: the software is restricted to run only two PatternQuant measurements that are linked together (including the root).


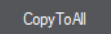
PatternQuant properties



- **Train** – click this button to launch the training process, at the end of which the software classifies slide areas based on all PatternQuant clusters and selected areas. After the training process is finished, the **Mask** function turns active, so the results are shown by coloring selected areas.

NOTE: Parameters and settings on the **Train** section of the panel are Quant-specific, while other sections are class-specific.



- **Contour** – the higher the set value is, the smoother the defined areas will be.
- **Dilation** – Mask boundaries can be set farther to surely include cells near the edge of the border.
- **Filter** – the result can be filtered based on **Size** and **Shape** either by typing values in the respective fields, or after clicking  you may specify these values by measuring length or by selecting area on the slide image with the drawing function of the mouse. If you click  each PatterQuant cluster will inherit the set values.

NOTE: PatternQuant filter settings affect the measurement only, parameter modifications are not visualized on the preview image.

NOTE: If filters are used, it is advised to set **Performance** to **Save objects to slide with connection**.

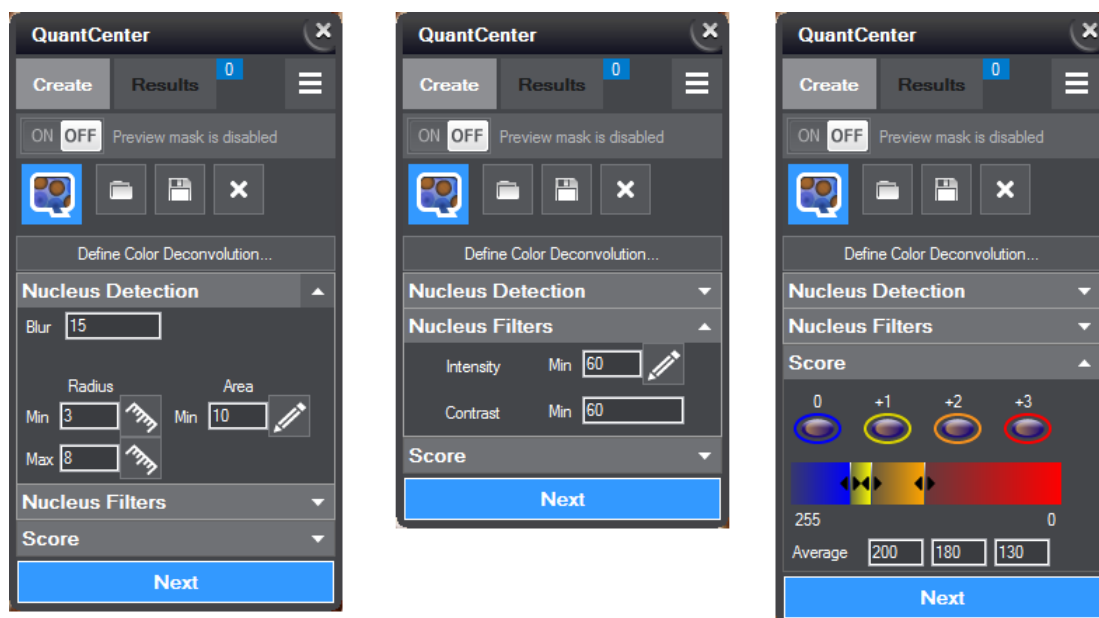
- **Performance** – 3 options are available to select from (measurement time will increase according to the following order):
 - **Save objects to slide disabled** (Green)
 - **Save objects to slide without connection** (Orange)
 - **Save objects to slide with connection** (Red)

3.2 NuclearQuant

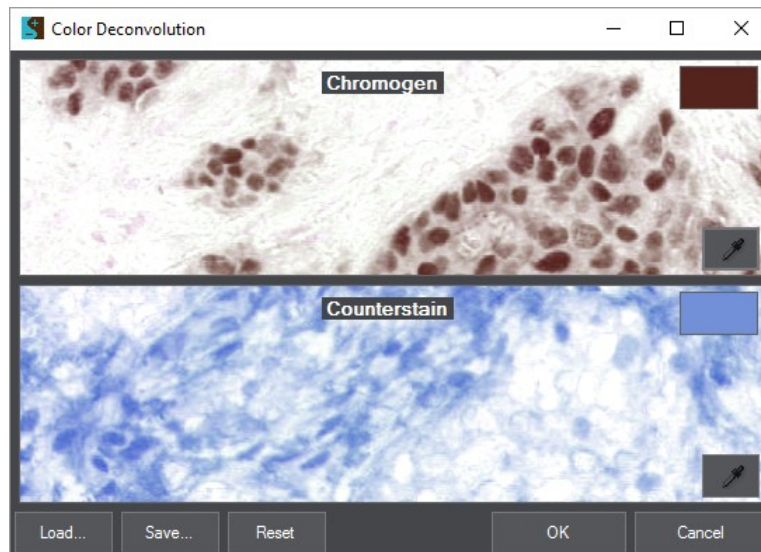
With the help of NuclearQuant image analyzing algorithm, cell nuclei can be detected and classified. It may be run as single (root) measurement, or embedded into PatternQuant or HistoQuant in which case NuclearQuant process will be run on areas segmented by the Quant into which it is embedded.

NuclearQuant properties


In this panel, the measurement parameters of NuclearQuant can be set.

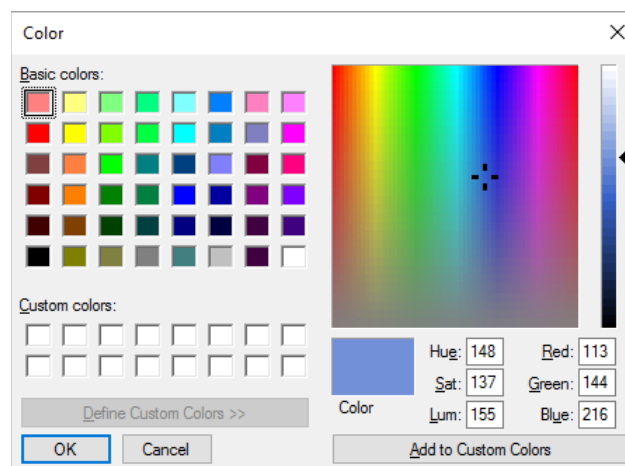


- **Define Color deconvolution:** the colors of positive and negative intensities can be defined in this window. The upper pane of the Color Deconvolution window represents objects of positive intensity (brown) and the lower pane represents objects of negative intensity (blue).



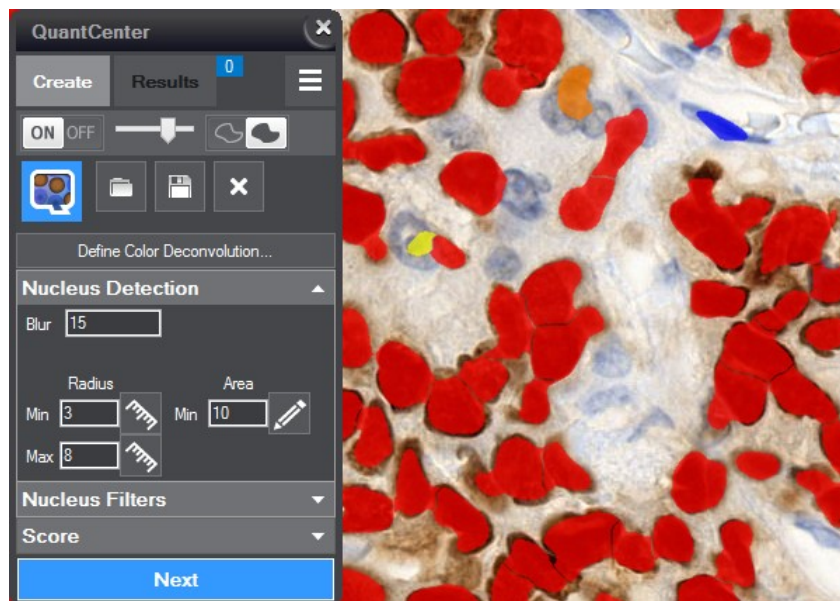
Representative colors can be set by either of the following two options:




- Click the pipette tool -  - to pick color sample from the relevant area of the slide image in the CaseViewer window.
- Click the color boxes of Chromogen and Counterstain panes, then set the desired color in the Color window. Click **OK** when finished.



A Color Deconvolution profile can be loaded by clicking **Load** or saved by clicking **Save**. A profile is stored in a CCC file at the specified folder.

Detection results according to the parameterization are displayed on the slide image that is automatically updated whenever you modify a parameter value.



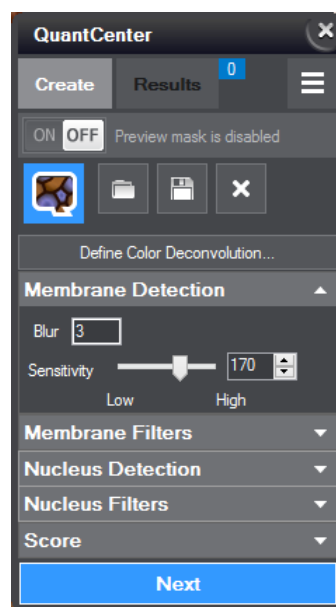
- **Nucleus Detection:** settings for nucleus detection
 - **Blur:** rough edges of the detected objects will be smoothed, therefore, besides decreasing noise-related flaws the resulting image appear more pleasing to the eye
 - Filtering based on **Radius** and **Area**. Set minimum and maximum values for Radius after clicking , and minimum area can be defined with the mouse by marking on the slide image after clicking .
- **Filters:** Set color **Intensity** (by entering value into the box, or by marking on the slide image after clicking ) and **Contrast** minimum values.
- **Score:** Scoring based on intensity. Ranges can be modified by dragging the dividers, or by defining **Average** values in the relevant boxes.

3.3 MembraneQuant

MembraneQuant is responsible for membrane detection and classification, furthermore it is capable of nuclei detection (since it cannot identify negative membranes, NuclearQuant is needed for this procedure).

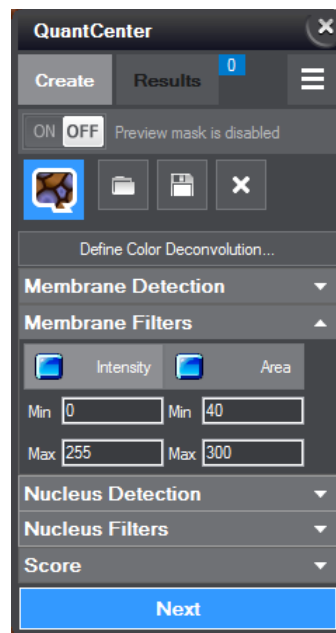
MembraneQuant properties

In this panel, the measurement parameters of MembraneQuant can be set.

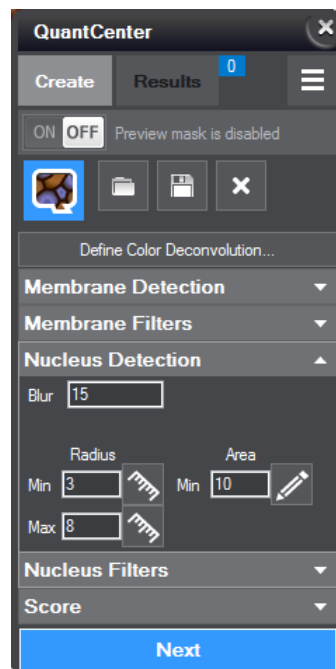


- **Define Color Deconvolution:** the type of Intensity can be set for MembraneQuant (positive) and nucleus detection (negative)
- **Membrane Detection:**
 - **Blur:** rough edges of the detected objects will be smoothed, therefore, besides decreasing noise-related image flaws the resulting image appear more pleasing to the eye
 - **Sensitivity:** sensitivity of the algorithm can be set either by dragging the slider bar, by entering a value to the box, or by clicking the arrows.




- **Membrane Filters:** Filtering based on the set value ranges of **Intensity** and **Area** by entering minimum and maximum values.

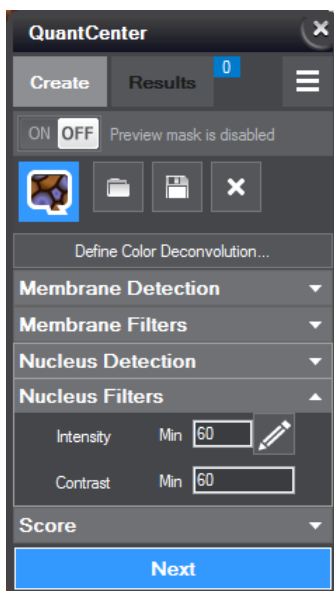


- **Nucleus Detection:** Settings for NuclearQuant algorithm used by MembraneQuant

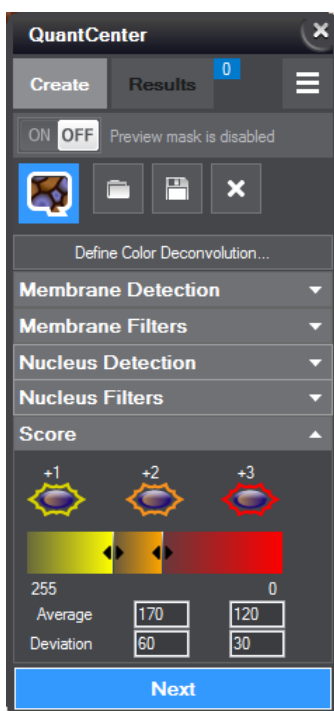


- **Blur:** rough edges of the detected objects will be smoothed, therefore, besides decreasing noise-related image flaws the resulting image appear more pleasing to the eye

- Filtering based on **Radius** and **Area**. Set minimum and maximum values for Radius after clicking , and minimum area can be defined with the mouse by marking on the slide image after clicking .
- Nucleus Filters: Intensity** and **Contrast** minimum values related to Nucleus settings. Set color **Intensity** (by entering value into the box, or by marking on the slide image after clicking ) , and **Contrast** minimum values.



- Score:** Scoring is based on intensity-related **Average** and **Deviation** values. Ranges can be modified by dragging the dividers, or by defining **Average** / **Deviation** values in their relevant boxes.



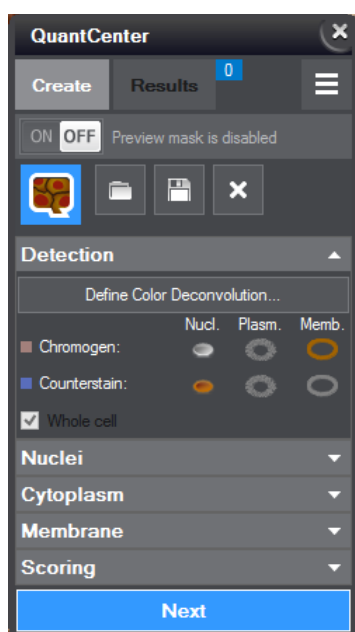
3.4 CellQuant

CellQuant is a tissue diagnosis module that can be adapted for nuclear-, cytoplasmic-, and membrane-localized IHC-stained biomarker identification based on intensity.

Quant Properties

In this panel, the measurement parameters of CellQuant can be set.

Detection



- **Define Color Deconvolution:** the colors of positive and negative intensities based on the staining protocol (brightfield slides) can be defined in this window.

Definition procedure is the same as detailed in **section 3.2** under NuclearQuant.

- **Channel matching:** Specify the intensities of objects (nucleus, plasm, membrane). Only one object can be selected for an intensity type (i. e. only one selection can be activated in a row).

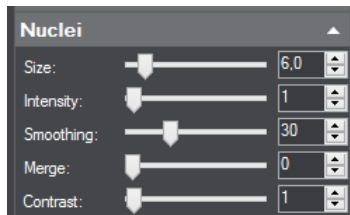


Important!

If you link an additional Quant to the actual scenario, and you specify channels and run measurements, after saving/exporting scenario or Quant, pairing will not be restored after reloading the scenario or Quant (when reloading, channels stored in the profile will be automatically matched with the channels of the slide). Channel matching is temporarily set and can be used to that specific measurement. If saving an additional Quant that is linked to a Fluorescent slide, the program saves which channels of the slide are selected, and those will be presented as profile channels pairable with slide channels after reloading.

- **Whole cell:** if selected, the algorithm (based on estimation) detects those objects that are not selected to be detected. If the selection box is not marked, only those objects will be displayed and measured that are being searched for.

Nuclei



- **Size:** average size of nuclei
- **Intensity:** minimum intensity of nuclei
- **Smoothing:** smoothing the contour of nuclei
- **Merge:** if the center area of nucleus is brighter (because of the type of the applied staining – e.g. Ki67), set the percentage value of filling these holes in the nucleus. 0 means no filling, 100 stands for filling in full. This option is useful for preventing objects from becoming over-segmented.
- **Contrast:** the minimum contrast (intensity difference) between the nucleus and the background.

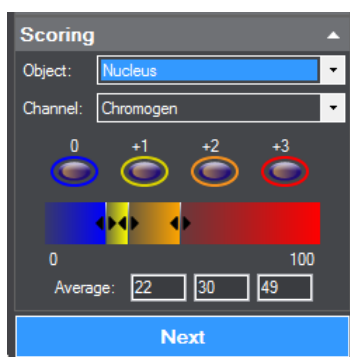
Cytoplasm

- **Width:** the maximum width of cytoplasm (distance between the edge of nucleus and membrane)

Membrane

- **Intensity:** minimum intensity of membrane

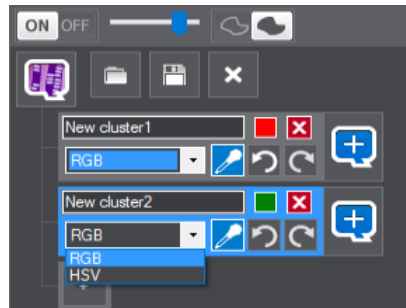
Scoring



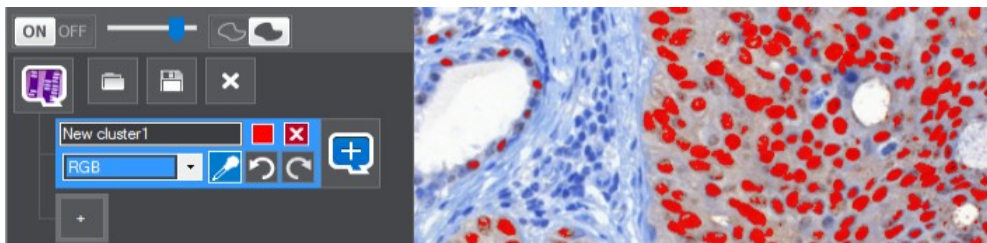
- **Object:** cell object selection for scoring
- **Channel:** select the channel for searching specified cell objects
- Set intensity-related **Average** and **Deviation** values


3.5 HistoQuant



HistoQuant is a quantification algorithm that can be used for performing segmentation and measurements on a Panoramic digital slide based on the colors of cell compartments.



If a Brightfield slide is opened, you can select from **RGB** and **HSV** color models, for Fluorescent slides **Channeled** or **HSV** can be selected in order to define the color channels or color reproduction area from which the samples are taken.



Color samples can be taken after clicking the pipette tool -  -, then move the mouse (this case, the pipette cursor) over the desired area of the slide, and click with the left mouse button.

To finish sampling, click with the right mouse button. Steps of sampling can be cancelled or repeated by clicking the  or  (undo/redo) buttons.



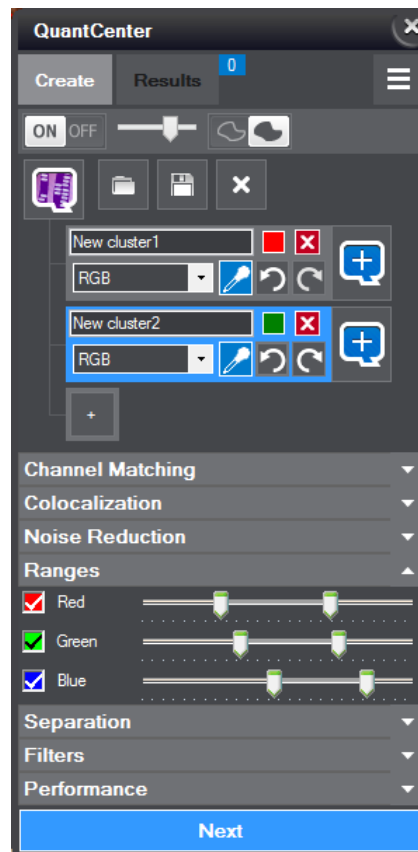
Important!

In Scenario Builder, the maximum number of definable HistoQuant classes is 8 (eight). Class name cannot be longer than 20 characters, and make sure that each class has unique name and representative colors.

If another Quant is linked to a PatternQuant or HistoQuant class, the settings of that specific Quant can be accessed only within the actual scenario, but can be saved by using the **Export** function.

HistoQuant Properties

In this panel, the measurement parameters of HistoQuant can be set.



Important!

If you link an additional Quant to the actual scenario, and you specify channels and run measurements, after saving/exporting scenario or Quant, pairing will not be restored after reloading the scenario or Quant (when reloading, channels stored in the profile will be automatically matched with the channels of the slide). Channel matching is temporarily set and can be used to that specific measurement.

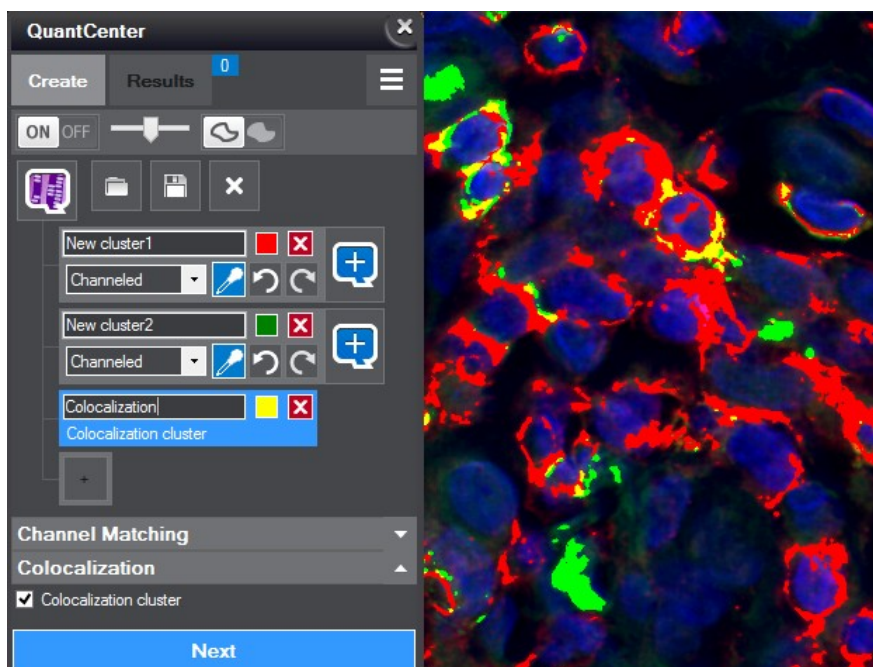
If saving an additional Quant that is linked to a Fluorescent slide, the program saves which channels of the slide are selected, and those will be presented as profile channels pairable with slide channels after reloading.

Channel Matching

This panel includes channel representation of the profile and the slide. When opening a slide for which channel matching is ambiguous, only this panel will be opened. Measurements can be run only if all the channels of the profile are conjugated with slide channels. Slide channel tabs include a dotted area showing that those channels are moveable. The pairing between a profile channel and the relevant slide channel is marked with a green line.

Colocalization

If a slide is opened, **Colocalization cluster** option can be activated to investigate stain colocalization, thus enabling a third, separate disjunct cluster to include colocalized objects.



Noise Reduction

To perform noise reduction on the slide image (to make it easier for HistoQuant algorithm to detect objects by colors that is crucial for detecting nuclei or cell compartments), Gauss or Median filters are available for you to select on this panel. Gauss reduces the noise and blurs the image. Median is a simple but fast filtering method, it uses the median of adjacent pixel values.

NOTE: If high noise reduction values are set, it is advised to activate the Gauss blur, as it is less sensitive for differences resulting from ROI shifts, zoom variations, etc.

Ranges

On this panel channel adjustments can be performed both for RGB (BF), Channeled (FL) and HSV (both) color models with the help of channel sliders. A tick mark is then visible in the checkbox of the relevant channel. If clicking the slider, a value box is displayed in which the desired value can be set or entered.

As for Fluorescent slides the number of channels is variable according to the defined channels set for digitization, so the relevant number of sliders for each channel are displayed in the Range panel if **Channeled** is selected for a cluster.

When **HSV** (Hue-Saturation Value) mode is selected from the drop-down menu, a color scale and a brightness slider is displayed in the panel, and during sampling a specific area can be defined on the scale that is marked with a white border. This area is both resizable and movable, therefore the selection is modifiable. Below the scale, four numeric fields are displayed, representing **Hue** and **Saturation** values. The combined slider at the right side of the color scale is responsible for adjusting brightness values within a range.

Separation

Two functions are available on this panel:

- **Fill holes** – Areas belonging together will be joined.
- **Separation** – If objects are too close to each other, they might be detected as one. If the value is 0 there will be no separation, and if value is set to 10, the area of the specific class is cut into several pieces.

Filters

Shape- and size-related filtering methods can be activated and set on this panel similar to PatternQuant.

Performance

3 options are available to select from (measurement time will increase according to the following order):

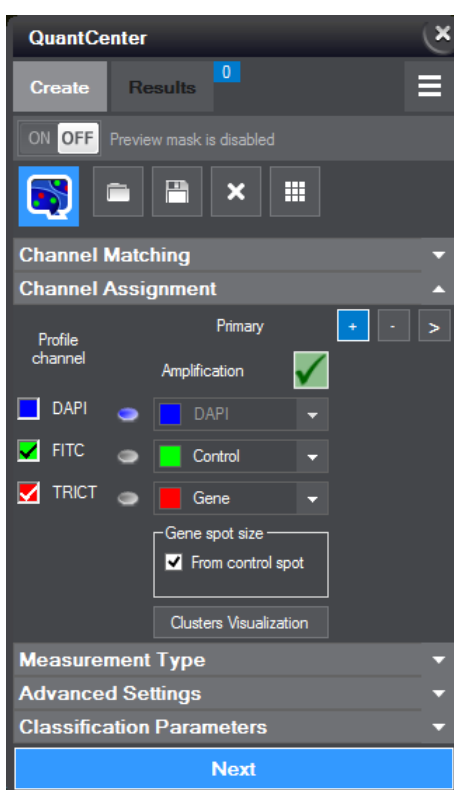
- **Save objects to slide disabled** (Green)
- **Save objects to slide without connection** (Orange)
- **Save objects to slide with connection** (Red)

3.6 FISHQuant

FISHQuant is an image analysis application, consisting of an automatic *segmentation* and a thresholding setup section. The information needed for the algorithm is not saved on the slide but in an XML file, which can be used later to evaluate other *annotations* on the same slide or on other slides.

NOTE: Since **FISHQuant** allows you to make measurements on the slides, and digital image processing can cause loss of quality, always make sure that the measurements are acceptable to you.

FISHQuant Properties



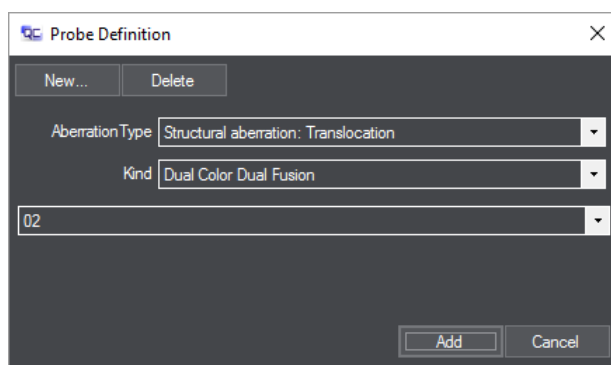
Channel Matching

This panel includes channel representation of the profile and the slide. When opening a slide for which channel matching is ambiguous, only this panel will be opened.

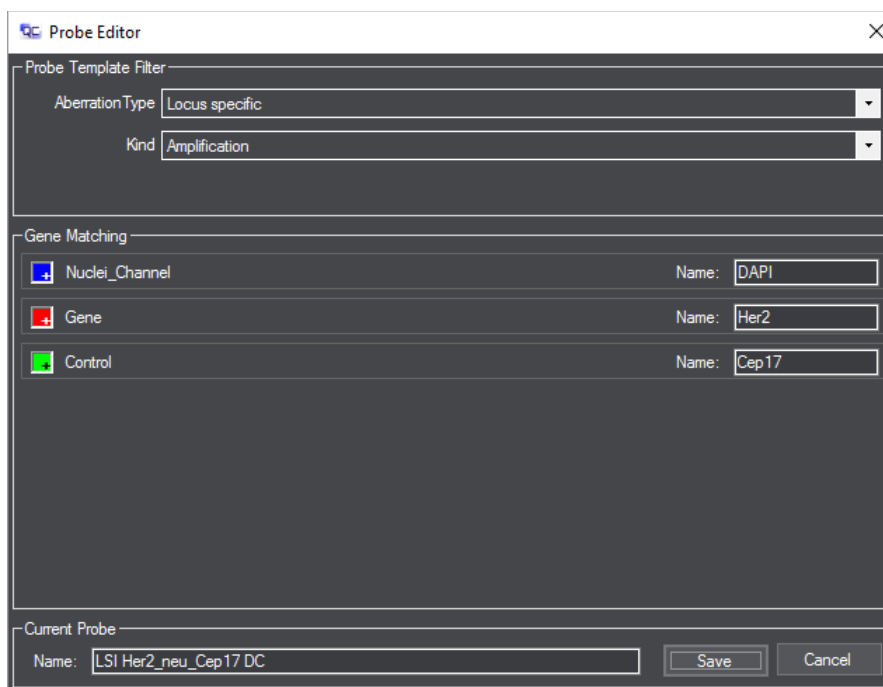
Measurements can be run only if all the channels of the profile are conjugated with slide channels. Slide channel tabs include a dotted area showing that those channels are movable. The pairing between a profile channel and the relevant slide channel is marked with a green line.

Channel Assignment

Under *Profile channel*, the color channels of the slide are listed. Click **+ Add Probe** to define a primary probe. In the appearing Probe Definition window, set **Aberration Type**, **Kind**, then select the probe from the bottom drop-down list. Click **New** to create a new probe, or click **Delete** to delete the selected aberration type.




If creating a new probe, the following window is displayed:

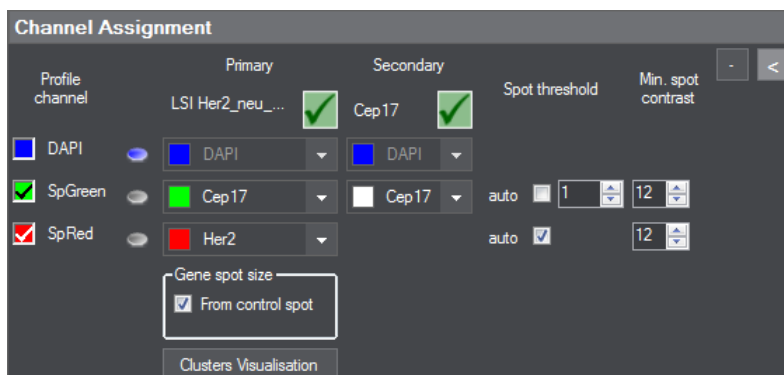


- Set **Aberration Type** and **Kind**, then fill in the fields of Gene Matching section.
- Add name to the probe, then click Save.
- In the Probe Definition window, click **Add** to set the created probe as *Primary*.
- To define a secondary probe, click **+** first, then define parameters from the drop-down lists.

NOTE: When defining a secondary probe, you can only select **Numerical deviation** as **Aberration type**.

Probes will be presented as *Primary* and *Secondary* above the probe name. If you want to delete a probe, first click the probe name, then the  button.

- By clicking the grey spot next a channel name, the desired channel can be selected as nuclei channel. If DAPI FISH slide is opened, the tick marks in the color boxes of the related channel, the detected signals on the displayed slide image can be switched on/off.



Click  to display further, spot-detection-related settings.

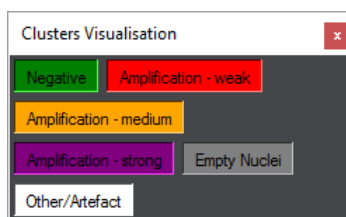
- The **Spot threshold** option is designed to set spot threshold value for the selected channel.
- Upon selecting the **auto** option to apply automated spot detection. The manual parameter setting for the detection of weaker spot signals is available in the **Min. spot contrast** value box.

Gene spot size

Upon selecting an amplification probe on the **Probe editor** panel, this option is displayed below the probe. Select one of the following options:

- From control spot** – breaks down the spot cloud of the highly amplified genes with the average size of the control spot
- Manual** – set a parameter value manually between 1.00 and 10.00 microns

Click **Clusters Visualization** to display the names and colors of the defined clusters of the primary probe. Clusters can be switched on/off in order to make them displayed/hidden on the mask image.



Measurement Type

Two types of segmentation algorithm are available for you to select from under this panel. By default, an automated nuclei segmentation algorithm parameters for the evaluation of tissue samples (optimally, the maximum thickness of a section is 3-4 micrometers) are listed under the Advance Settings panel. The parameters you can modify are the following:

- **Threshold**

Color intensity threshold for setting the least intensive pixels of the detected nuclei (value ranges from 0 to 255). Increment this value to find less intensive nuclei. Tick the check-box for automatic mode.

- **Blob contour smooth**

Circumference smoothing parameter (value ranges from 1 to 15, and only odd values are accepted) which defines the length that is taken to account when smoothing the circumferences of the detected nuclei. Increment this value to get smoother outlined nuclei.

- **Nuclei size**

The size of nuclei to be detected can be set here.

- **Min. nuclei contrast**

The minimum contrast value of spots can be set here.

- **Manual nuclei size setting**

If activated, minimum and maximum size values can be set as input data for segmentation algorithm.

If **Metaphase** option is selected, nuclei segmentation algorithm is activated (the related parameters are displayed in the **Advanced Settings** panel) for the evaluation of separate cells, cell cultures, and cytological specimens.

NOTE: If **Metaphase** option is activated, secondary probe cannot be defined.

Advanced Settings

- **Threshold**

Color intensity threshold for setting the least intensive pixels of the detected nuclei (value ranges from 0 to 255). Increment this value to find less intensive nuclei. Tick the check-box for automatic mode.

- **Blob contour smooth**

Circumference smoothing parameter (value ranges from 1 to 15, only odd values are accepted). Defines the length that is taken to account when Smoothing the circumferences of the detected nuclei. Increment this value to get smoother outlined nuclei.

- **Max blob area**
Nuclei size relative measure (value ranges from 0 to 50). Sets the size of the detected objects, that are not going to be split. Decrement this value to allow splitting of smaller objects.
- **Homogeneity**
Parameter of intensity difference (the difference between the most and the least intensive pixels). Decrementing this value allows nuclei to be formed on more homogeneous areas. Value range: [0,255]
- **Blobs area to shape**
Object convexity measure. Average area of nucleus circumference concavities. Decrement this value to detect more circular nuclei. Value range: [0,20]
- **Blobs num to shape**
Object convexity measure. Number of allowed nucleus circumference concavities. Decrement this value to detect more circular nuclei. Value range: [0,100]
- **Intensity scale**
Average intensity related measure. Uniformly dim objects will not be split. Increment this value to allow splitting of less intensive nuclei. Value range: [0,1]
- **Max trim pixel**
Iteration count of erosion operator. If multiple objects are connected with thin structures, they will be split. Increment this value to allow splitting through thicker connecting segments. Value range: [0,10]

Classification Parameters

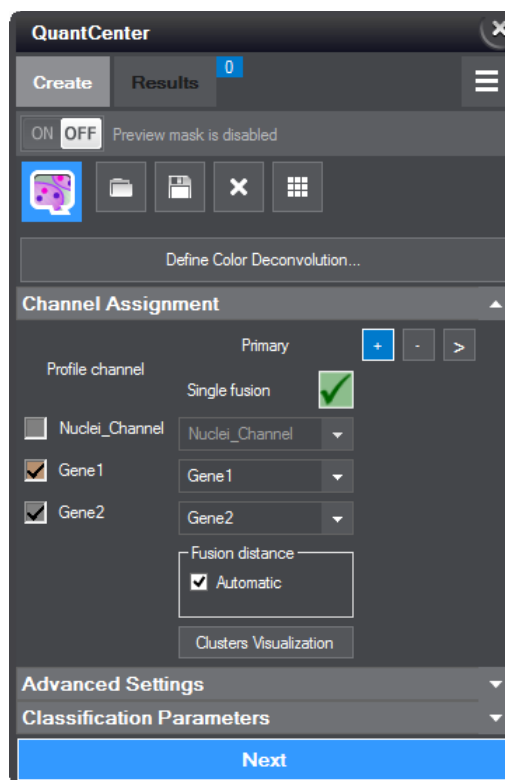
There are two functions that can be activated to assign limitation parameters for the classification.

- Activate **Show warning when Other/Artifact >** function to allow the software to display a warning message in the tree as a tooltip, if the percentage of objects found in the Other/Artifact clusters exceeds the set value.
- The **Stop when object count >** option is responsible for terminating classification if object count reaches the set maximum number of nuclei identified in negative and positive clusters.

3.7 CISHQuant

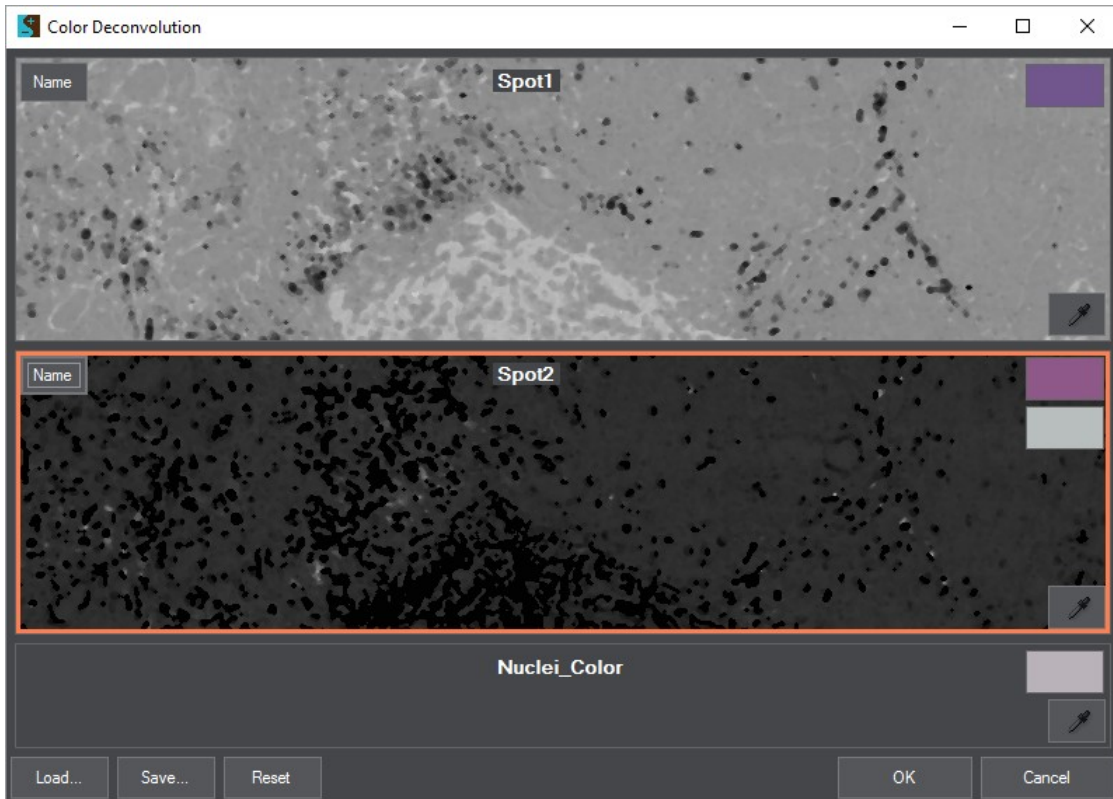
CISHQuant allows you to detect and separate CISH spots on the virtual slides digitized with Panoramic microscopes. This CISH-based application performs *segmentation* and *measurements* on Panoramic *digital slides* based on the colors of the gene spots and counter-stained nuclei. Based on the applied CISH probe, it can classify the detected objects.

CISHQuant Properties



Define Color Deconvolution

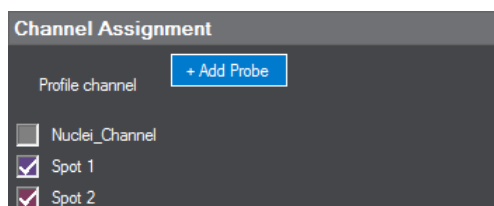
The representative colors of Nuclei, Spot channel 1, and Spot channel 2 can be defined in the Color Deconvolution window.



Use the pipette tool for setting the proper color for each channel (set a typical color of imperfections or impurities on the slide for the first channel, that will be removed before running the segmentation algorithm, then set colors of the two spot channel). Channel names can be edited by clicking the **Name** buttons. Click **Load** to import an existing Color Deconvolution profile and **Save** to export settings into a profile. Click **Reset** to undo all changes made to color selection since the window was opened, or **Cancel** to quit from the window, then **OK** to continue with probe definition.

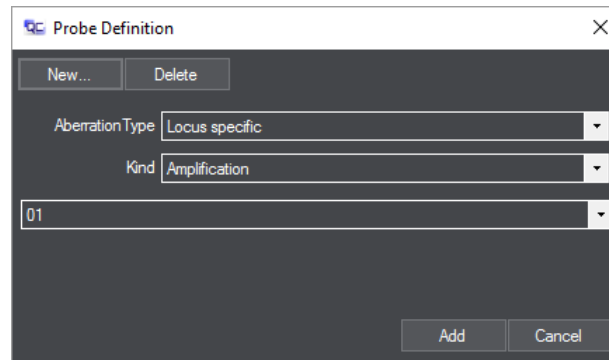
Channel Assignment

Click **Define Probe and slide colors** to define a probe. If you have loaded a Color Deconvolution profile, click [+ Add Probe](#).

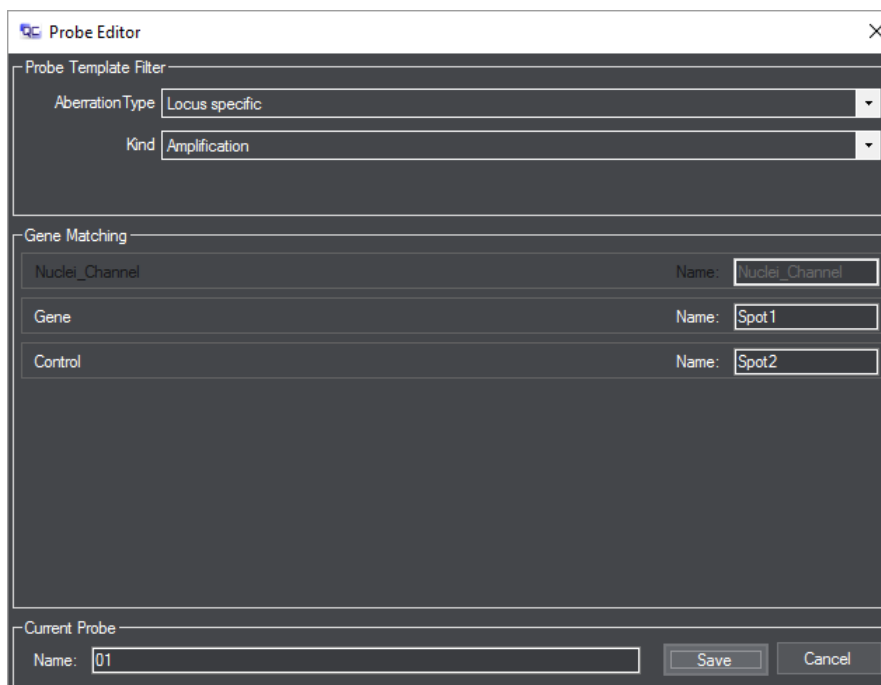


NOTE: After clicking **OK** in the Color Deconvolution window, the Probe Definition window is automatically displayed.

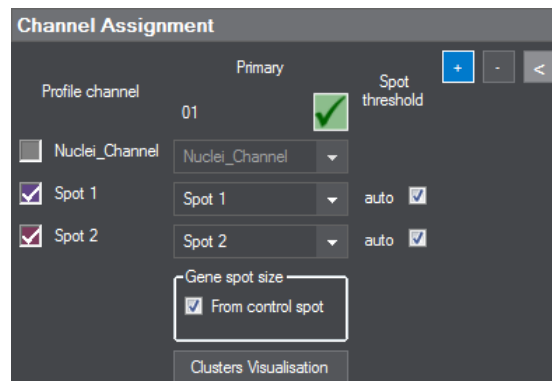
In the **Probe Definition** window, set **Aberration Type**, **Kind**, and probe from the relevant drop-down lists, delete probe by clicking **Delete**, or create new by clicking the **New** button.



If you want to create a new probe, click **New** first, then the Probe Editor window is displayed.



The primary probe created is shown in the **Channel Assignment** section of the panel. You can add a secondary probe by clicking **+** and remove a probe by selecting it first, then clicking **-**



Advanced Settings

This section of the panel includes parameters of the measurement that can be modified if necessary.

- **Threshold**

Color intensity threshold for setting the least intensive pixels of the detected nuclei (value ranges from 0 to 255). Increment this value to find less intensive nuclei. Tick the check-box for automatic mode.

- **Blob contour smooth**

Circumference smoothing parameter (value ranges from 1 to 15, only odd values are accepted) which defines the length that is taken to account when smoothing the circumferences of the detected nuclei. Increment this value to get smoother outlined nuclei.

- **Nuclei size**

The size of nuclei to be detected can be set here.

- **Min. nuclei contrast**

The minimum contrast value of spots can be set here.

- **Manual nuclei size setting**

If activated, minimum and maximum size values can be set as input data for segmentation algorithm.

Classification Parameters

There are two functions that can be activated to assign limitation parameters for the classification.

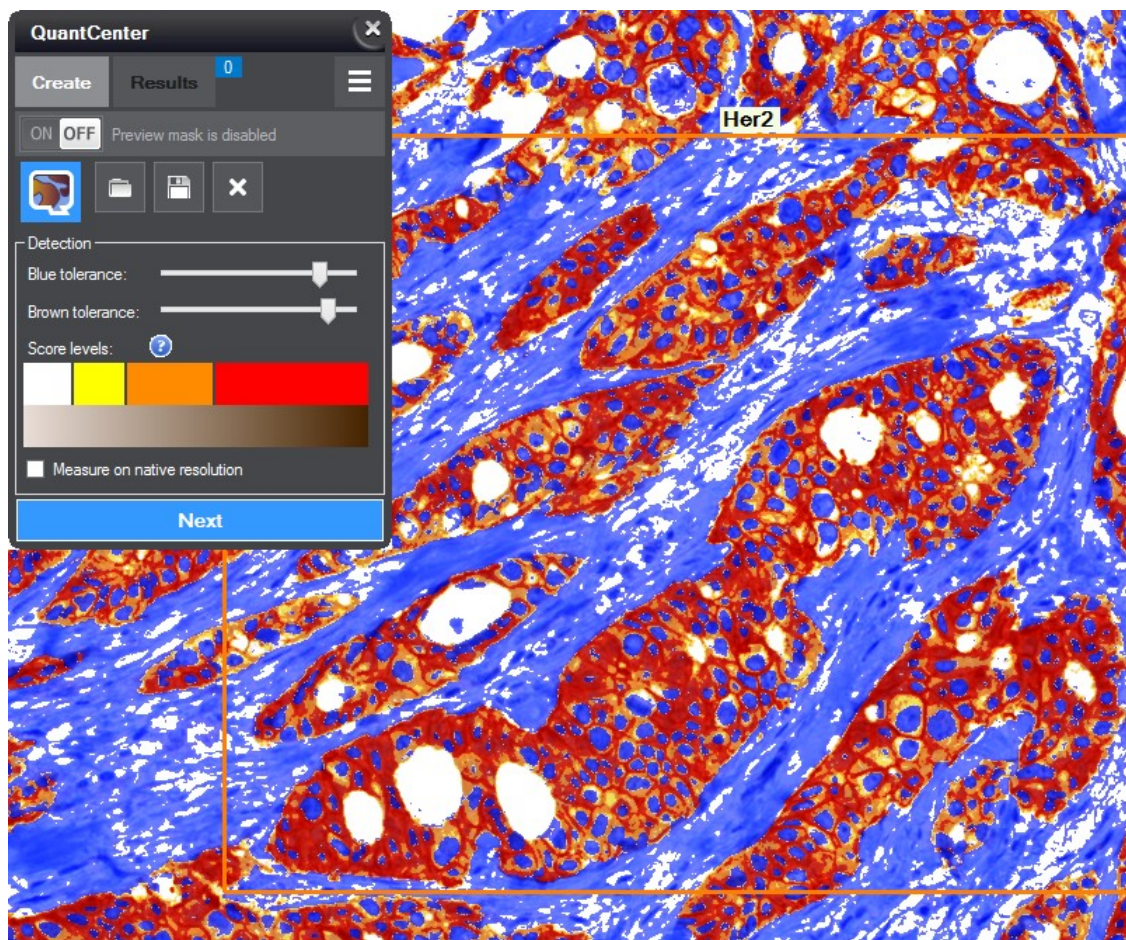
- Activate **Show warning when Other/Artifact >** function to allow the software to display a warning message in the tree as a tooltip, if the percentage of objects found in the Other/Artifact clusters exceeds the set value.
- The **Stop when object count >** option is responsible for terminating classification if object count reaches the set maximum number of nuclei identified in negative and positive clusters.

3.8 DensitoQuant

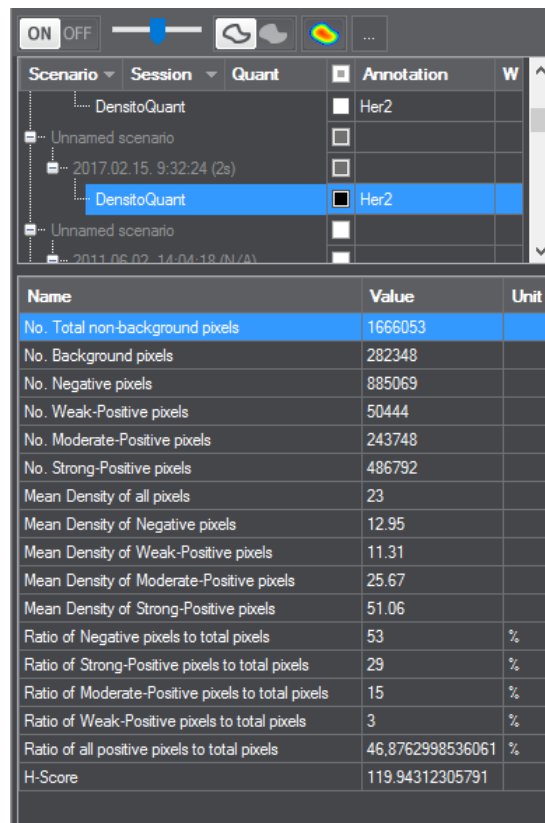
DensitoQuant offers a framework to configure, perform and visualize immunohistochemical measurements on slides, and measures the density of immunostain based on the colors of cell compartments from immunohistochemical stains.

1. Set **Detection** parameters **Blue tolerance** and **Brown tolerance**.
2. Activate **Measure on native resolution** if you want to run measurements at 1:1 magnification.
3. Select the annotations you want to run measurement on and run measurement process. The **Measurement Card** form is displayed after the process is finished.

On the **Scenario Builder** form turn **Mask** on to advert the shape of input annotation, and adjust parameters if necessary.




For detailed measurement results, activate **Measurement Tree** form first, then simply click the desired annotation name to show the related measurement data.



Name	Value	Unit
No. Total non-background pixels	1666053	
No. Background pixels	282348	
No. Negative pixels	885069	
No. Weak-Positive pixels	50444	
No. Moderate-Positive pixels	243748	
No. Strong-Positive pixels	486792	
Mean Density of all pixels	23	
Mean Density of Negative pixels	12.95	
Mean Density of Weak-Positive pixels	11.31	
Mean Density of Moderate-Positive pixels	25.67	
Mean Density of Strong-Positive pixels	51.06	
Ratio of Negative pixels to total pixels	53	%
Ratio of Strong-Positive pixels to total pixels	29	%
Ratio of Moderate-Positive pixels to total pixels	15	%
Ratio of Weak-Positive pixels to total pixels	3	%
Ratio of all positive pixels to total pixels	46.8762998536061	%
H-Score	119.94312305791	

NOTE: Data Visualization function is not available for DensitoQuant.


4 Data Visualization



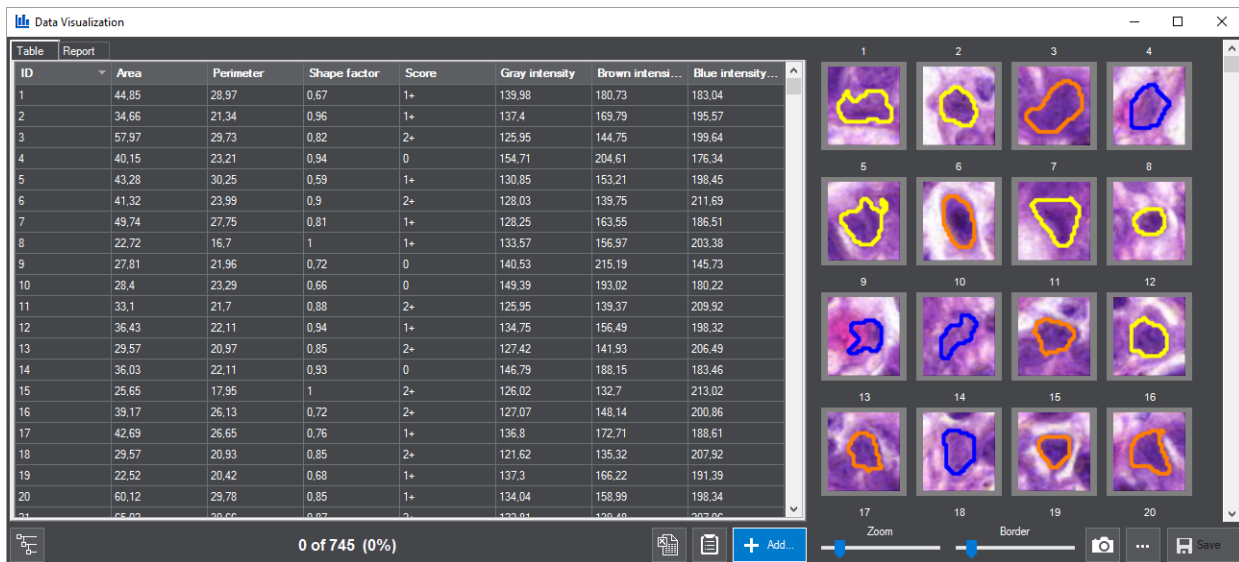
Important!

For the perfect visualization of the application make sure that the display is set to **Smaller – 100% (default)** under **Control Panel\Appearance and Personalization\Display** menu in Windows. Running the application using different display settings results in unexpected behavior of visual appearance.

4.1 Panels and functions

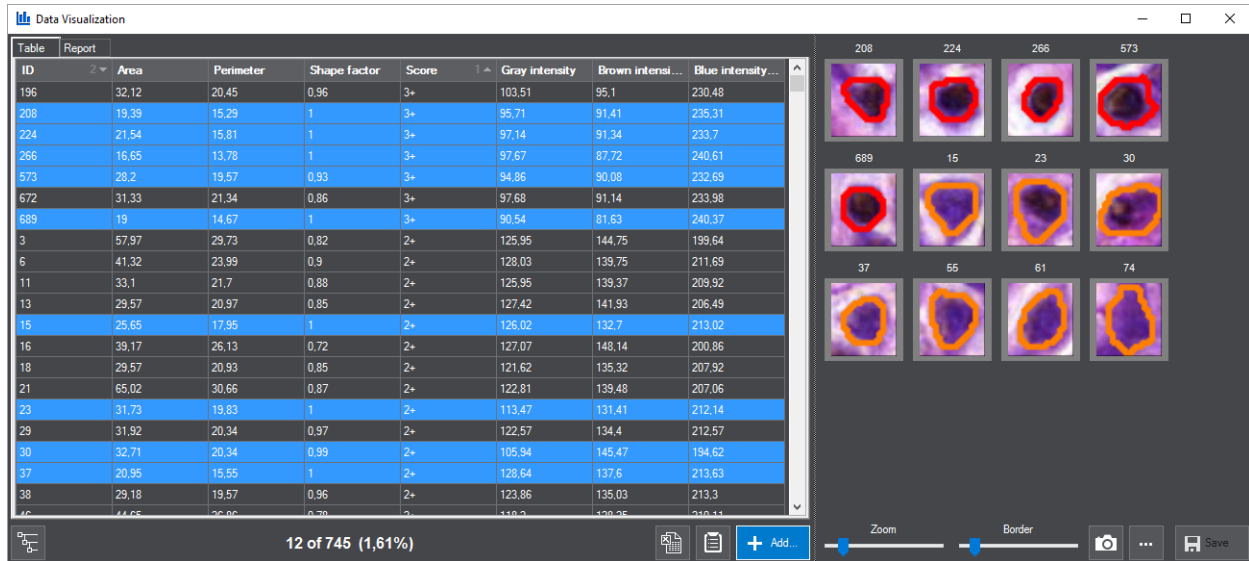
Upon clicking the  button both on Measurement Card and Measurement Tree forms, the Data Visualization window can be displayed.

Upon opening the Data Visualization window, the **Table** view is shown by default (except for FISHQuant and CISHQuant) in which detected objects and their detailed data related to the measurement are listed.



Each column can be ordered by clicking the header, so values will be listed in descending or increasing order. Upon clicking a list item, the image of the specific object is displayed on the right panel.

By keeping the **Ctrl** key pressed and clicking with the mouse, detected objects can be selected from the list and displayed in the right side of the window. Upon selecting any of the objects in the Gallery, its specific location on the slide is shown in the CaseViewer window. If more objects are selected, the area within these objects are located, is fitted in the slide view of CaseViewer.

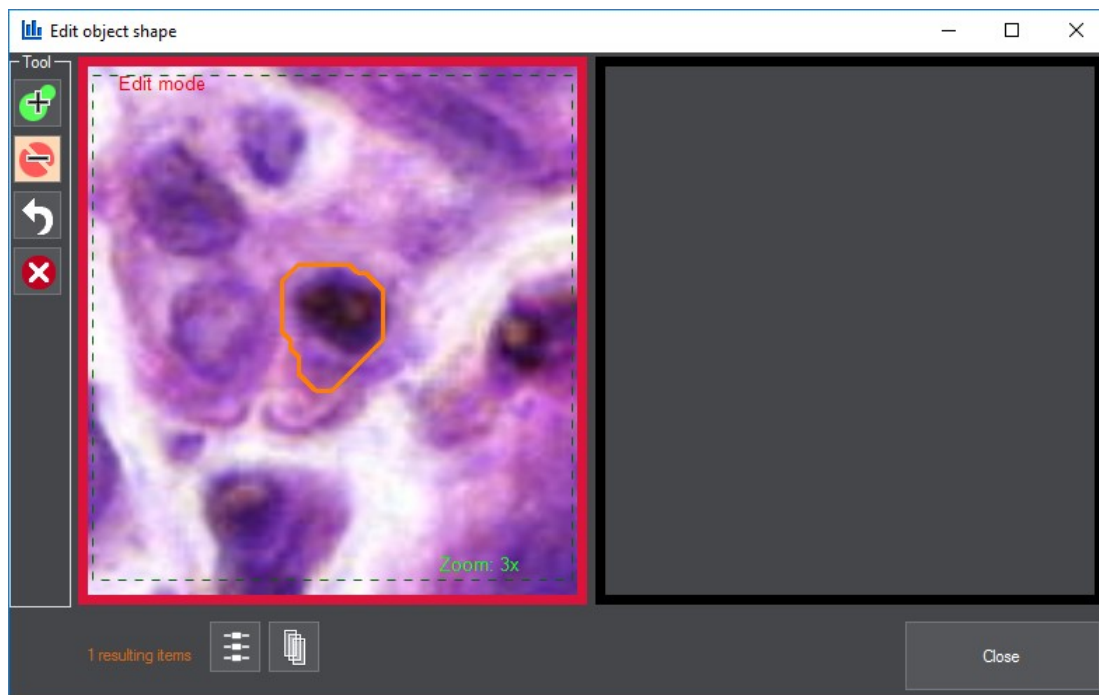


The visualization of gallery objects can be adjusted by dragging the Border and Zoom sliders. Item size can be increased/decreased by dragging the **Zoom** slider to the appropriate direction. The **Border** slider is responsible for enlarging the border of items.

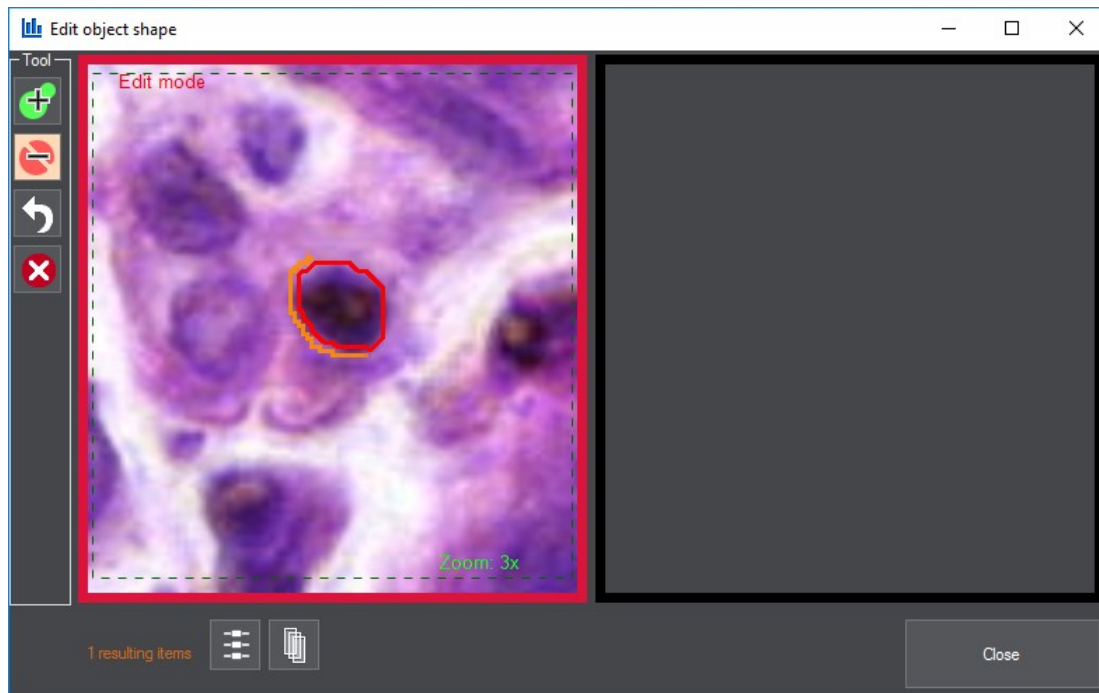
To turn on masking controls, select **Gallery controls** after clicking **...**


Upon right-clicking an object in the gallery, you can select from the following options:

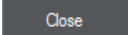
- **Edit shape** – Use this tool to alter masking boundary of detected objects or separate two or more objects that have been detected incorrectly as one.



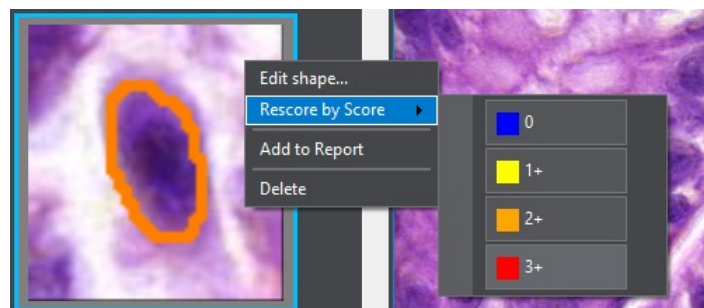
You can add area to nuclei by clicking the + button or cut nuclei (subtract area from nuclei) by clicking -, then moving the mouse with holding the left mouse button down.



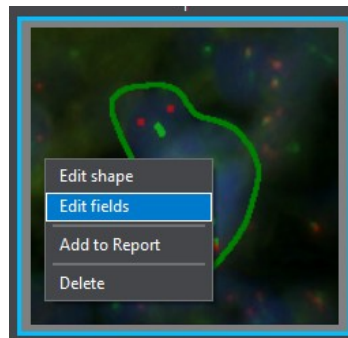
Click  to undo changes made after the window was opened.

Click  (or right-click on the slide area) to apply changes, then the images of the modified object and its neighboring objects are displayed on the right pane of the window. After double clicking on them, the shape of these objects can be further modified.

- **Rescore by Score** – Set a different score for an object



- **Edit fields** – Spot counts in channels for the selected objects can be modified in the **Edit Fields** window (available only for Fluorescent slides).

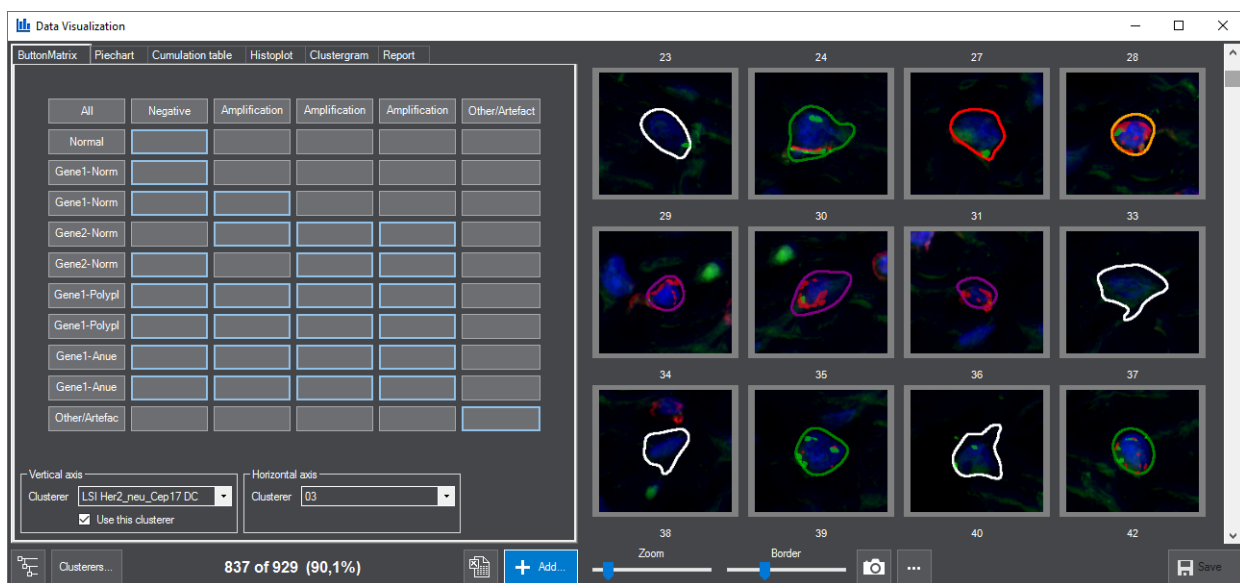


Editable fields	
Spot count in channel AF488	3
Spot count in channel AF594	0
Calculated fields	
Spot count in channel Gene in Probe LSI Her2_neu_Cep17 DC	0
Spot count in channel Control in Probe LSI Her2_neu_Cep17 DC	3
LSI Her2_neu_Cep17 DC cluster	Other/Artefact
03 cluster	Other/Artefact

1 cell(s) OK Cancel

- **Add to Report** – Add object to Report
- **Delete** – Remove object from the gallery

If you have opened the **Data Visualisation** window for FISHQuant or CISHQuant, the **ButtonMatrix** panel is displayed by default, in which the active clusters are displayed in the matrix.



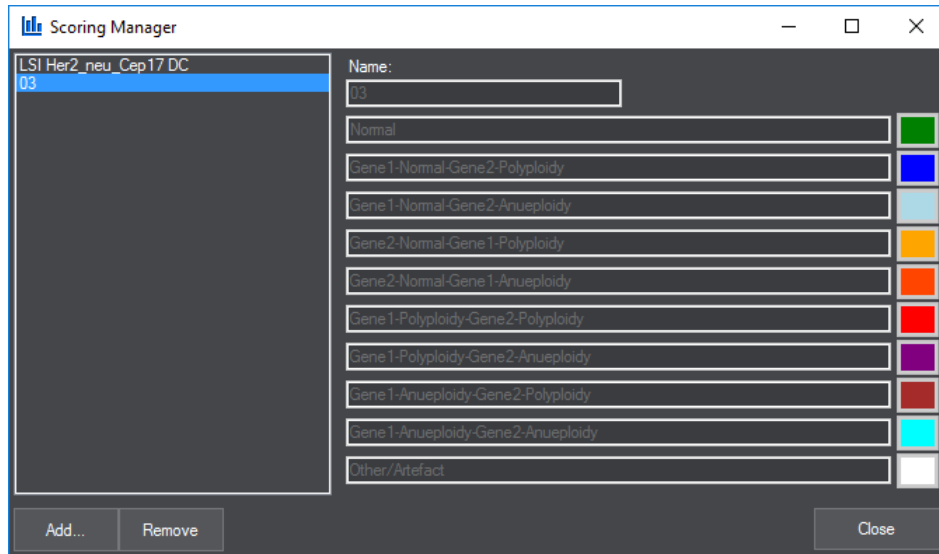
At the bottom of the window you can find buttons by which additional functions can be activated:



– Tree view of panels



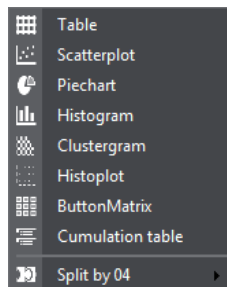
– Opens Scoring manager



– Export data to an Excel file



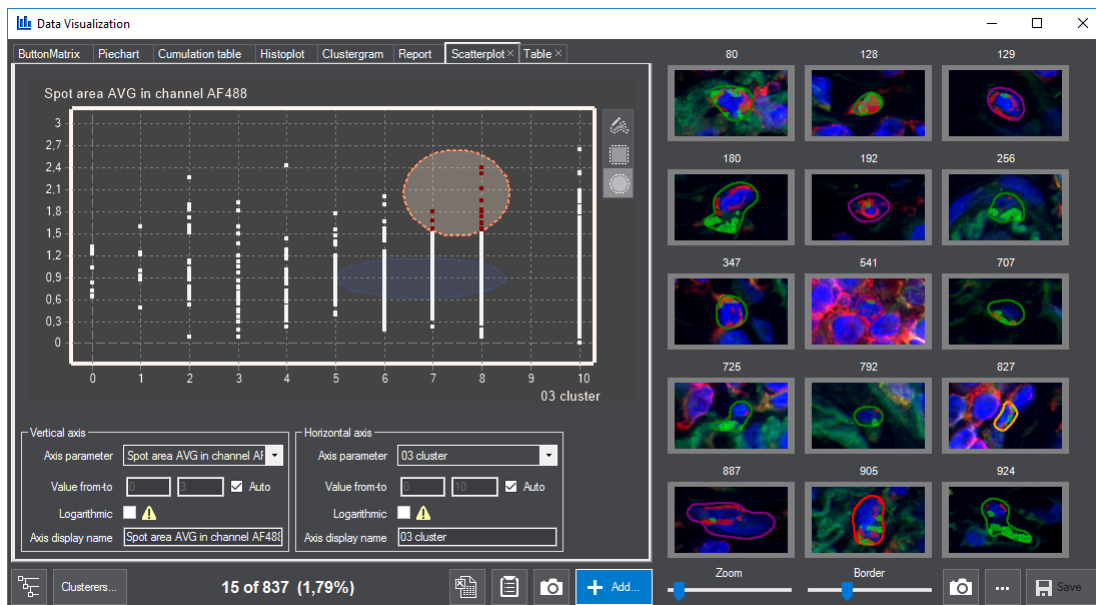
– Additional presentation forms can be activated after clicking this button:



• **Table**

ID	Gene/Control	Area	Perimeter	Shape fa...	LSI Her2_ne...	03 cluster	Cell state	Spot count in...	Spot area AV...
145	2.17	67.05	34.47	0.71	Amplification - we...	Gene1-Anueploid...	1	6	0.72
157	1.17	34.78	24.79	0.71	Negative	Gene1-Anueploid...	1	6	0.67
620	1.5	50.67	29.73	0.72	Negative	Gene1-Anueploid...	1	10	1.03
268	0.2	87.67	38.77	0.73	Negative	Gene1-Anueploid...	1	5	1.09
589	2	65.78	33.49	0.74	Amplification - we...	Gene1-Polyploidy...	1	15	0.9
56	2	54.71	30.5	0.74	Amplification - we...	Gene1-Polyploidy...	1	13	0.79
137	42	59.33	31.75	0.74	Amplification - str...	Gene1-Polyploidy...	1	1	0.69
744	0.5	59.89	31.83	0.74	Negative	Gene1-Anueploid...	1	6	1.13
142	0.38	81.2	37.04	0.74	Negative	Gene1-Anueploid...	1	8	1.12
783	3.91	80.38	36.84	0.74	Amplification - me...	Gene1-Anueploid...	1	11	0.82
681	0.82	92	39.35	0.75	Negative	Gene1-Polyploidy...	1	17	0.75
560	33	63.16	32.59	0.75	Amplification - str...	Gene1-Anueploid...	1	1	1.06
482	2.75	68.55	33.71	0.76	Amplification - me...	Gene1-Anueploid...	1	12	0.68
69	1.17	51.86	29.32	0.76	Negative	Gene1-Anueploid...	1	6	0.74
619	1.4	97.23	39.83	0.77	Negative	Gene1-Anueploid...	1	5	0.96
246	1.33	48.96	28.2	0.77	Negative	Gene1-Polyploidy...	1	3	0.92
828	1.25	52.31	29.14	0.77	Negative	Gene1-Anueploid...	1	4	1.09
478	1	41.59	25.98	0.77	Negative	Gene1-Anueploid...	1	7	0.7
654	5	44.1	26.7	0.78	Amplification - str...	Gene1-Anueploid...	1	1	0.95
807	1.6	22.42	19.03	0.78	Negative	Gene1-Polyploidy...	1	5	0.8
170	0.12	90.21	22.16	0.79	Negative	Gene1-Anueploid...	1	8	0.72

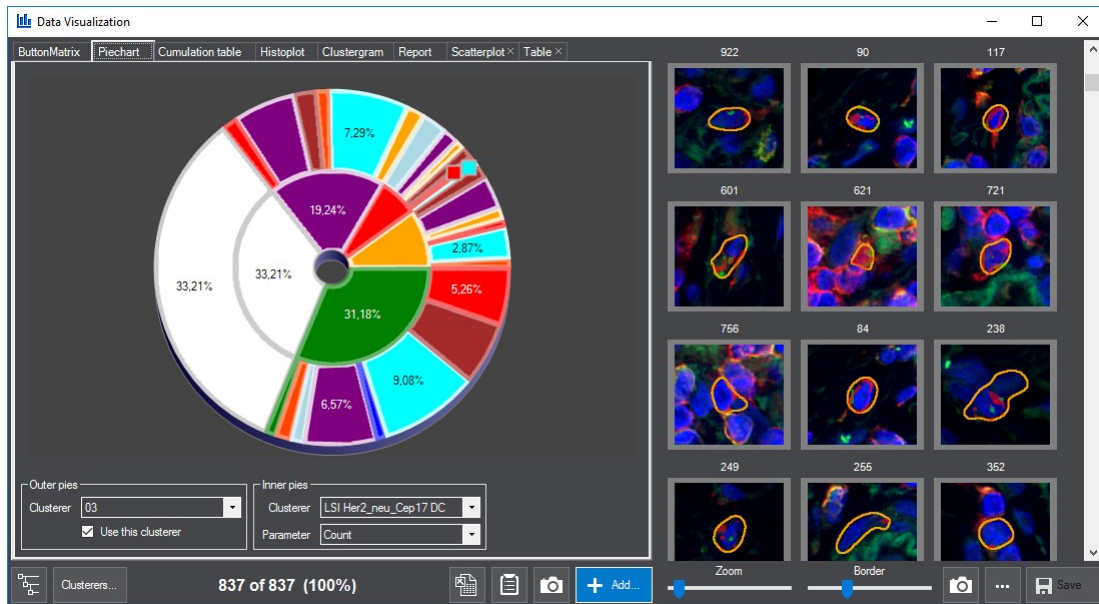
• **Scatterplot**



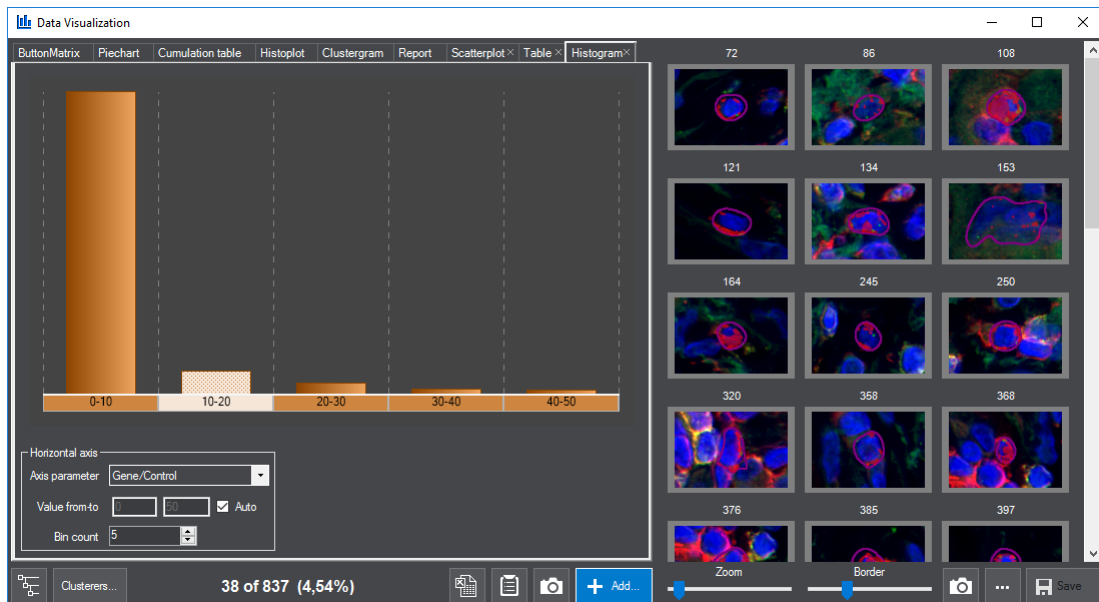
Cluster-related measurement data are displayed on an X-Y axis graph of the scatterplot (linear or logarithmic representations are both available). The axis parameter can be selected from the **Axis parameter** drop-down lists both for the **Vertical** and the **Horizontal** axis. If you deactivate the **Auto** function, value ranges of X and Y axis can be modified.

- **Piechart**

Another option for graphic representation of cluster-related measurements is the Piechart, by which percentage values of clusters are shown.



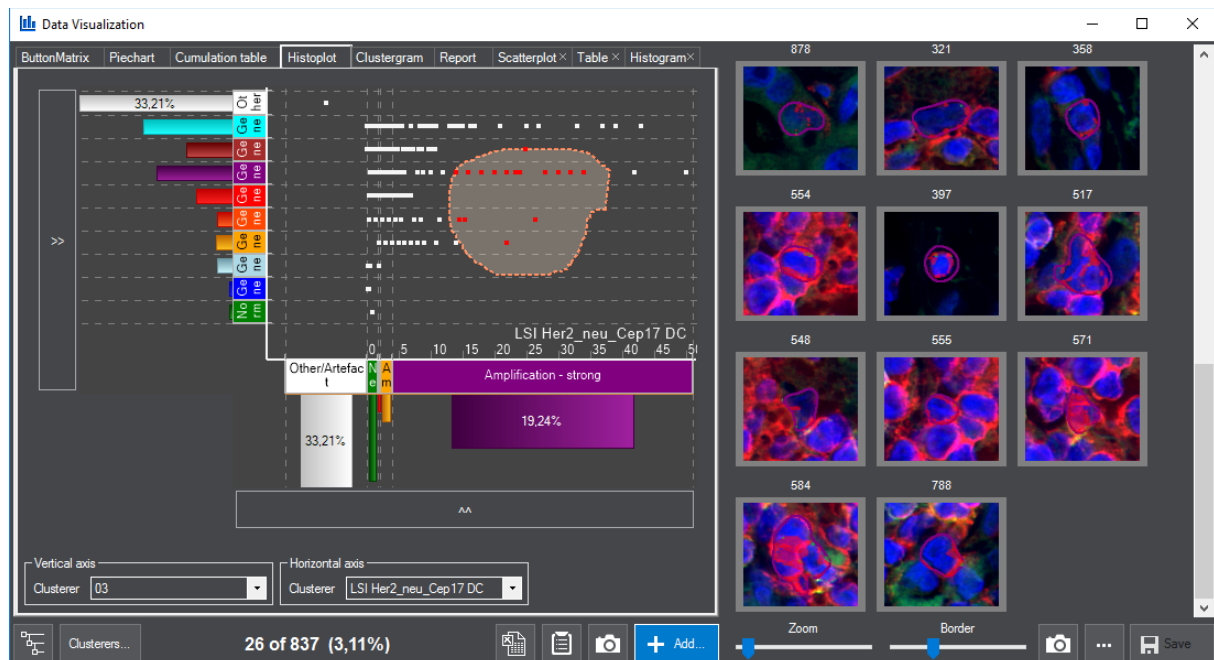
- **Histogram**



- **Histplot**

Activated clusters are displayed on this diagram. Items of selected columns are included in the gallery. Cluster editing/deletion is available only if the probe is amplified, therefore the axis is not editable if other types of probe have been defined.

Cluster column and row width can be modified by dragging the divider, or right-click to enter new value.



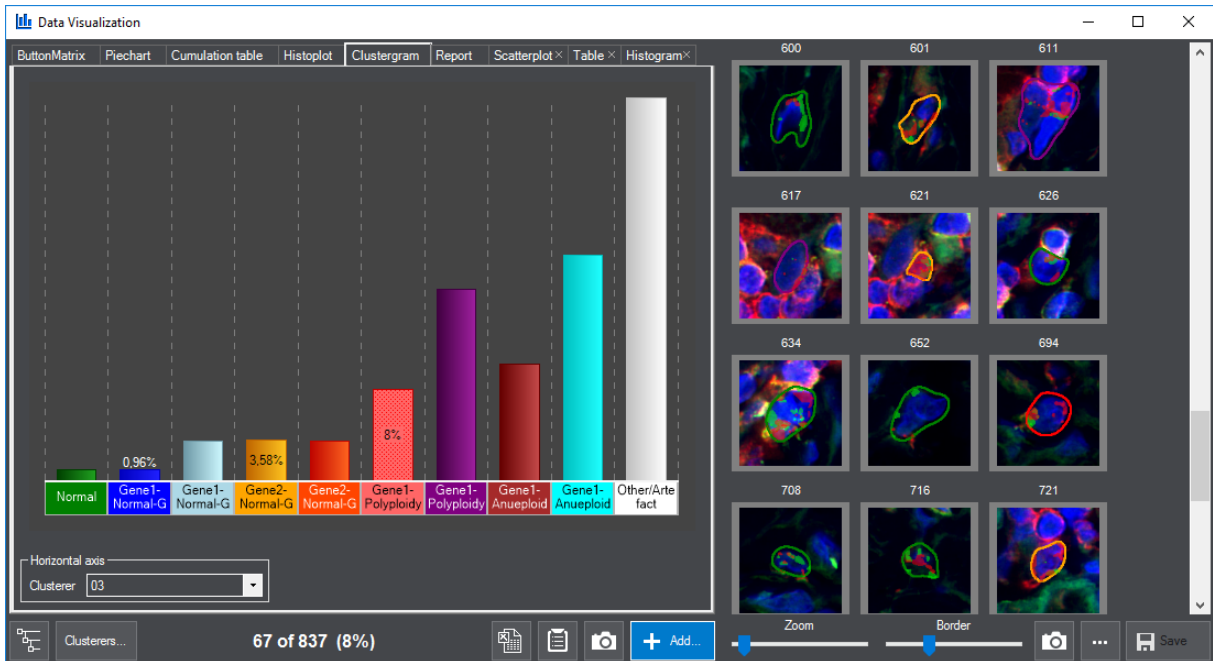
After right-clicking on the selected object displayed in the matrix can be deleted or moved to another cluster if needed. You can filter nuclei on the histplot by drawing a circle around the objects.

On the X axis of the Histplot, right-click the clusters to select from the following options:

- Change name
- Change color
- Create new cluster here
- Remove this cluster



NOTE: Any of the clusters can be removed, but at least one cluster must be present in the matrix. Cluster editing/deletion is available only if the probe is amplified, therefore the axis is not editable if other types of probe have been defined.

• **Clustergram**

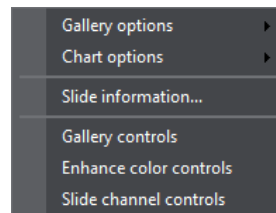


• **Cumulation table**

Name	Gene/Control	Percent	Count
Negative (LSI Her2_neu_Cep17 DC)	0.93	31.18%	261
Normal (03)	1	3.07%	8
Gene1-Normal-Gene2-Polyploidy (03)	0.35	3.07%	8
Gene1-Normal-Gene2-Anueploidy (03)	0.43	3.83%	10
Gene2-Normal-Gene1-Anueploidy (03)	0.67	4.6%	12
Gene1-Polyploidy-Gene2-Polyploidy (03)	1.02	16.86%	44
Gene1-Polyploidy-Gene2-Anueploidy (03)	1.19	21.07%	55
Gene1-Anueploidy-Gene2-Polyploidy (03)	0.78	18.39%	48
Gene1-Anueploidy-Gene2-Anueploidy (03)	0.95	29.12%	76
Amplification - weak (LSI Her2_neu_Cep17 DC)	2.01	6.57%	55
Gene1-Normal-Gene2-Anueploidy (03)	2	34.55%	19
Gene2-Normal-Gene1-Polyploidy (03)	2	12.73%	7
Gene1-Polyploidy-Gene2-Polyploidy (03)	1.98	9.09%	5
Gene1-Polyploidy-Gene2-Anueploidy (03)	2.01	21.82%	12
Gene1-Anueploidy-Gene2-Polyploidy (03)	2.04	16.36%	9
Gene1-Anueploidy-Gene2-Anueploidy (03)	2.1	5.45%	3
Amplification - medium (LSI Her2_neu_Cep17 DC)	3.2	9.8%	82
Gene2-Normal-Gene1-Polyploidy (03)	3.44	10.98%	9
Gene2-Normal-Gene1-Anueploidy (03)	2.93	8.54%	7
Gene1-Polyploidy-Gene2-Polyploidy (03)	3.24	7.22%	6

-  – The complete list is copied to clipboard
-  – Creates a snapshot of the selected item(s) that can be saved as a PNG/JPG/BMP/TIF file

⋮ – Further options are accessible by clicking this button:



- **Gallery options**

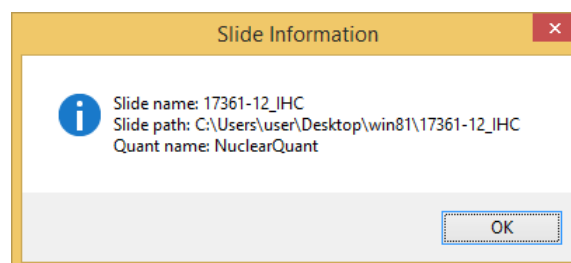
- Fit objects to same size – Fits objects into their frames in the gallery
- Single click selection mode – Multiple selection is available for you upon activating this function (alternatively, hold the **Ctrl** key while clicking on an item with the mouse)
- Show information tooltip on items – Object data are displayed in a tooltip when pointing the mouse cursor over an item if activated



- **Chart options**

- Show grid
- Show text

- **Slide information** – Slide name and the name of the applied Quant is displayed in a window.

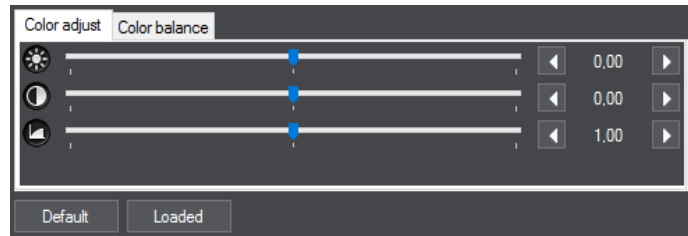


- **Gallery controls** – Object rendering, Outline and Fill masking modes

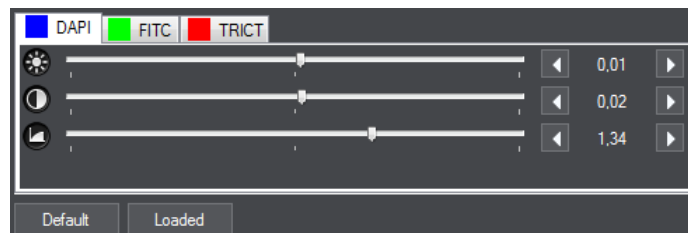
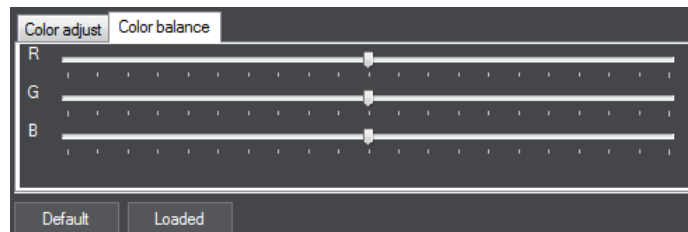



- **Enhance color controls** – A **Color adjust** and **Color Balance** window is displayed to modify values if necessary
- **Slide channel controls** – Fluorescent channel buttons are displayed
- **Z-stack controls**

 – **Brightness, Contrast, and Gamma** values can be adjusted on the **Color adjust** panel




Color channels can be adjusted separately. Channels of a color model are represented in accordance with the type of slide (RGB color model for Brightfield slides, FL channels for Fluorescent slides).



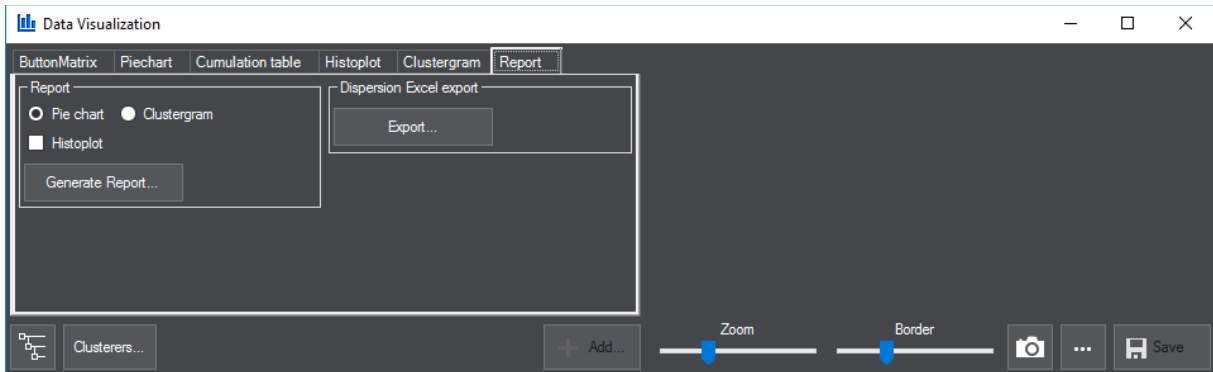
 – Click this button to activate Z-stack displaying function, then drag the slider bar left or right to switch between the focal planes of a Z-stack slide



 – FL channel buttons can be displayed, channels can be turned off/on separately (available for Fluorescent slides only)

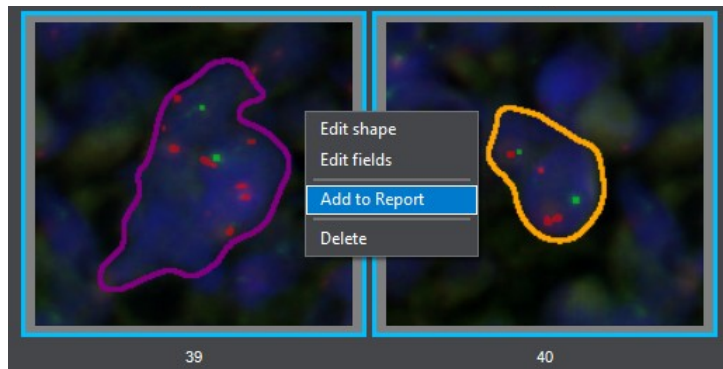
 – Saves data to slide

The **Report** panel offers you a reporting tool by which the selected gallery items and their data supplemented by additional diagrams (Piechart, Clustergram, and Histogram) can be presented on the Report form.

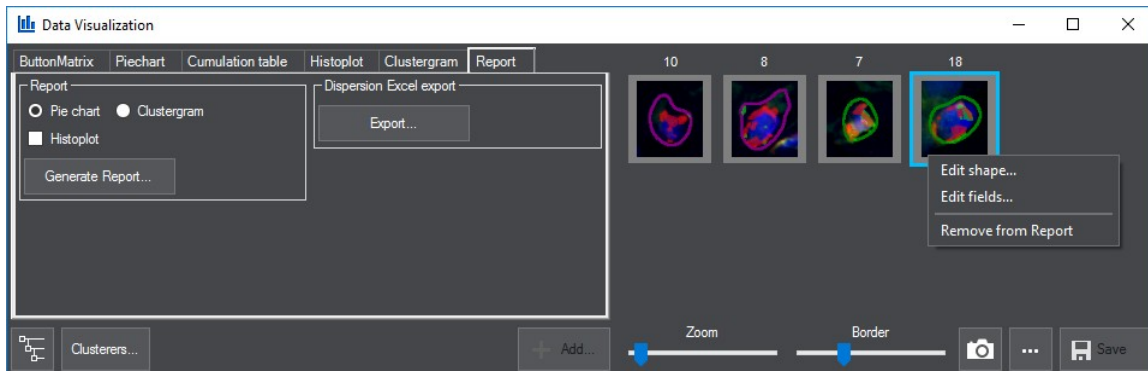


NOTE: Results of secondary measurements (numeric deviation) are visualized by a Histogram (function can be activated only if a secondary measurement is created).

Items can be added to the Report by right clicking one of the selected gallery items, then selecting the **Add to Report** option from the menu.

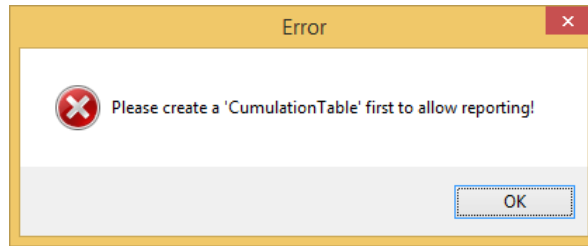


Selected items on the **Report** form can be deleted if right-clicking on the item(s) you want to exclude from the report, then selecting the **Remove from Report** option from the menu.



If you have finalized the settings of the Report, click **Generate Report** to create the report on the selected gallery items.

NOTE: The report can be generated only if you have added a Cumulation table to the DVT. Otherwise you receive a warning message informing you about this issue.

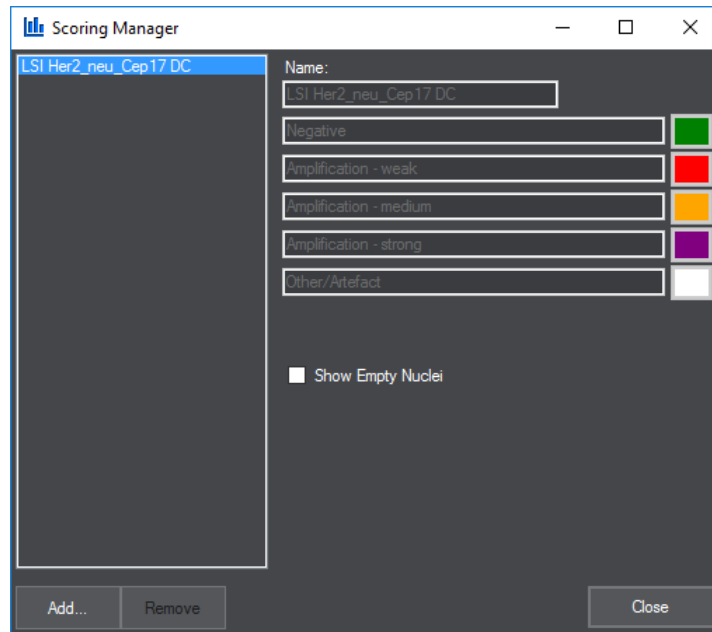


Upon clicking **Export** in the Dispersion Excel export field, spot number-related data of specific clusters can be exported to an Excel file.

Amplification - medium; Red-Polyploidy-Green-Polyploidy				
SpGreen				
Spot channel - spot number	SpGreen (spot number)	Nucleus count		
SpGreen - 04	4	3		
SpRed				
Spot channel - spot number	SpRed (spot number)	Nucleus count		
SpRed - 10	10	3		
Spots altogether				
Spot channel - spot number	SpGreen (spot number)	SpRed (spot number)	Nucleus count	
SpGreen - 04 ; SpRed - 10	4	10	3	

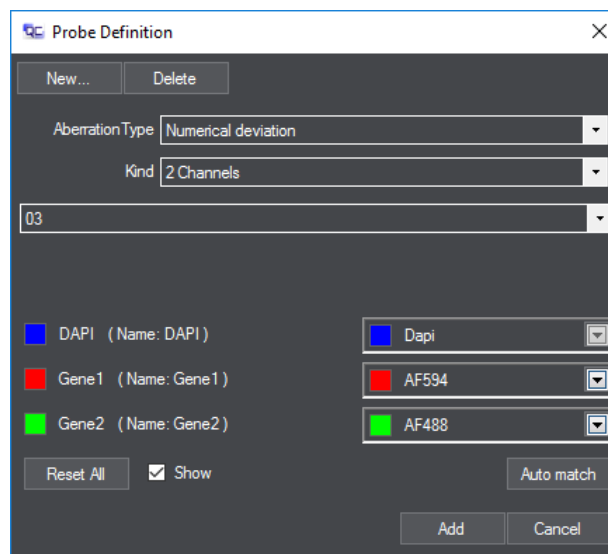
4.2 Scoring and creating a Secondary Probe

Click **Clusters...** to open the **Scoring Manager** window.



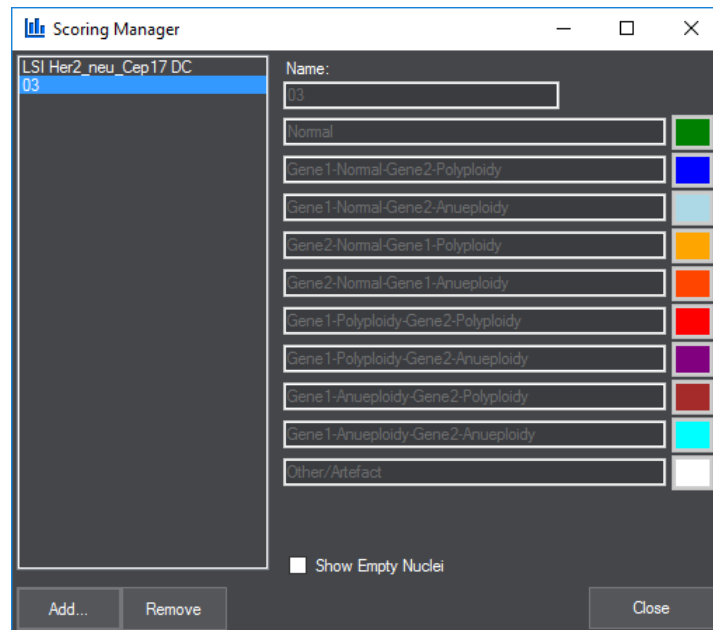
Upon clicking **Add...**, then selecting **Secondary probe**, the probe of secondary measurement can be created.

In the Probe Definition window, set parameters, channels, then click **Add**.



The clusters of the created secondary probe are presented with their colors in the Scoring Manager window. If you want to remove a secondary probe, select the probe name from the list first, then click




Remove.

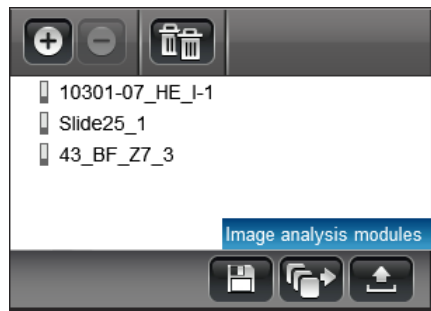



Click **Close** when finished.

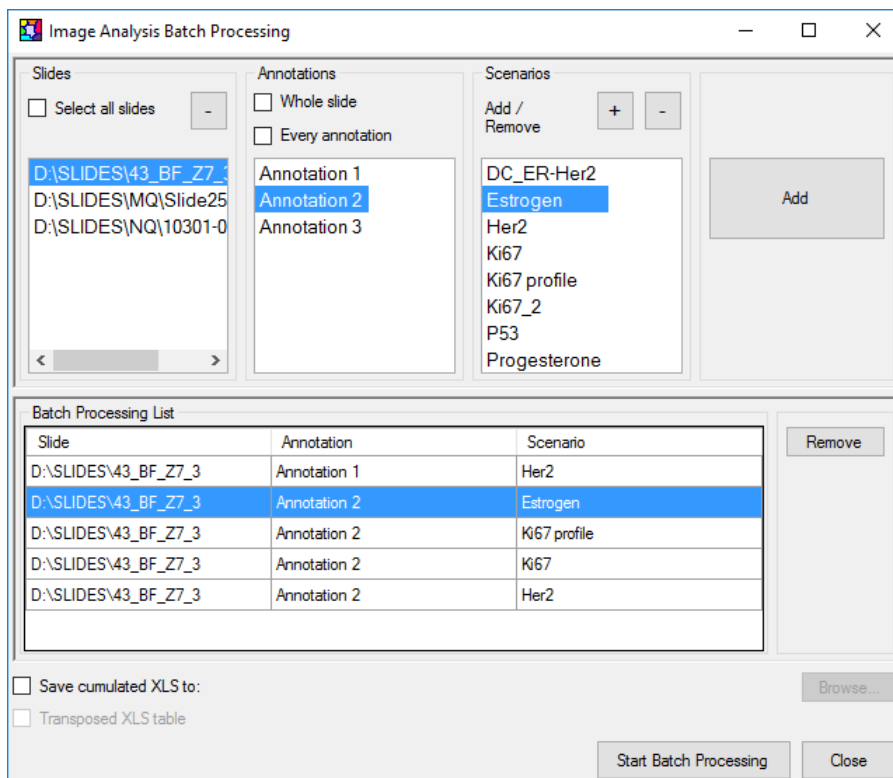
5 Running a Batch Process from CaseViewer

CaseViewer allows you to batch process a set of slides. You can find the batch processing panel at the bottom section of the tree-view panel on the left side of the CaseViewer main window. Please, refer to **CaseViewer 2.2 User's Guide** for more information.

1. In CaseViewer, select a slide or folder in the tree-view panel, then click the  button to add them to the list. Remove a slide from the list by clicking the  button, or remove all the slides by clicking .

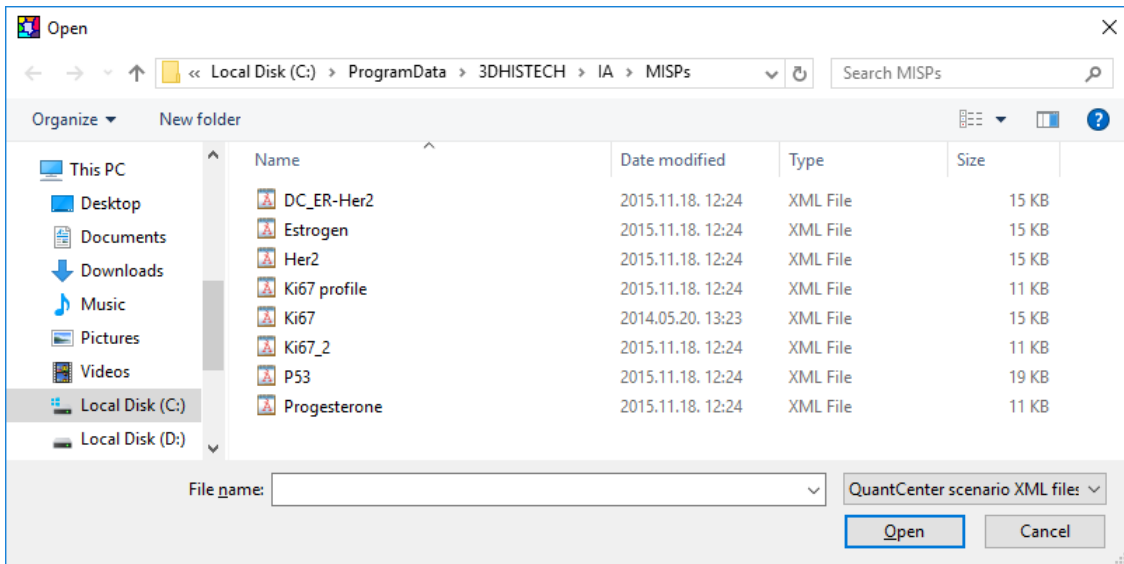


2. Click the  button when finished, then the Image Analysis Batch Processing window is displayed.

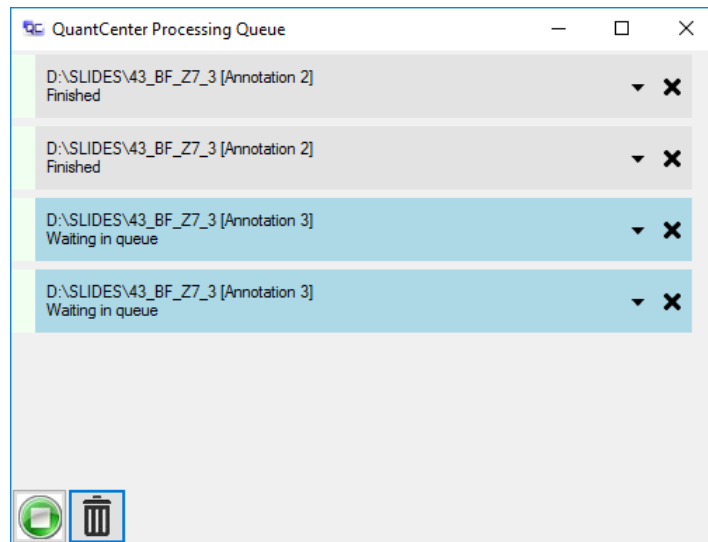


3. Select the slides you want to work with and specify Annotations and Scenarios for which they should be analyzed.

4. Click **+** to add more scenario XML files to the list of **Scenarios**. Select the file from the designated folder, then click **Open** to add them.



5. Click the **Add** button to add the slide to the **Batch Processing List**.
6. Tick **Save cumulated XLS to:** if you want to save a cumulated data sheet to a specified location. Click **Browse** to locate a folder. If you have already saved a cumulated XLS file, it is available for you to save a **Transposed XLS table** by ticking this option.
7. Click **Start Batch Processing** when finished. In QuantCenter, processes are displayed in the **QuantCenter Processing Queue** window.



NOTE: Scenarios that can be used during batch processing are listed from the following folder by default: *C:\ProgramData\3DHISTECH\IA\MISPs*.

Alphabetical Index

A

Amplification.....41
 Annotation.....14, 16, 17, 20, 21, 25, 39, 48, 49, 65

B

Batch Process.....12, 65

C

CellQuant.....2, 13, 19, 33
 CISHQuant.....2, 13, 15, 17, 19, 44, 50, 53

D

DensitoQuant.....48

F

Filter.....20, 26, 29, 31, 32, 37, 38, 57
 FISHQuant.....2, 13, 15, 17, 19, 39, 50, 53

H

HistoQuant.....2, 13, 15, 19, 20, 21, 27, 35, 36, 37

M

Mask.....14, 15, 23, 25, 26, 41, 48, 51, 59
 Measurement 2, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 24, 25, 26, 27, 30, 33, 35, 36, 37, 38, 39, 42, 44, 47, 48, 49, 50, 55, 56, 61, 63
 MembraneQuant.....2, 13, 19, 30, 31

N

NuclearQuant.....2, 13, 19, 27, 30, 31, 33

P

PatternQuant.....2, 13, 15, 19, 20, 21, 24, 25, 26, 27, 35, 38

S

Scenario.....2, 13, 14, 15, 17, 18, 20, 21, 33, 35, 36, 48, 65, 66
 Segmentation.....15, 24, 35, 39, 42, 44, 45, 47
 Slide....3, 12, 14, 15, 16, 17, 19, 21, 23, 24, 25, 26, 28, 29, 30, 32, 33, 35, 36, 37, 38, 39, 40, 41, 44, 45, 48, 51, 52, 53, 59, 60, 65, 66

T

Train.....13, 18, 25