

quanTLC manual

May 31, 2018

QuanTLC can be accessed online: 134.176.7.66/quanTLC.
The github repository with the code source is [here](#)
The peer review article is available [here](#).



Select a chromatogram image or a Rdata file

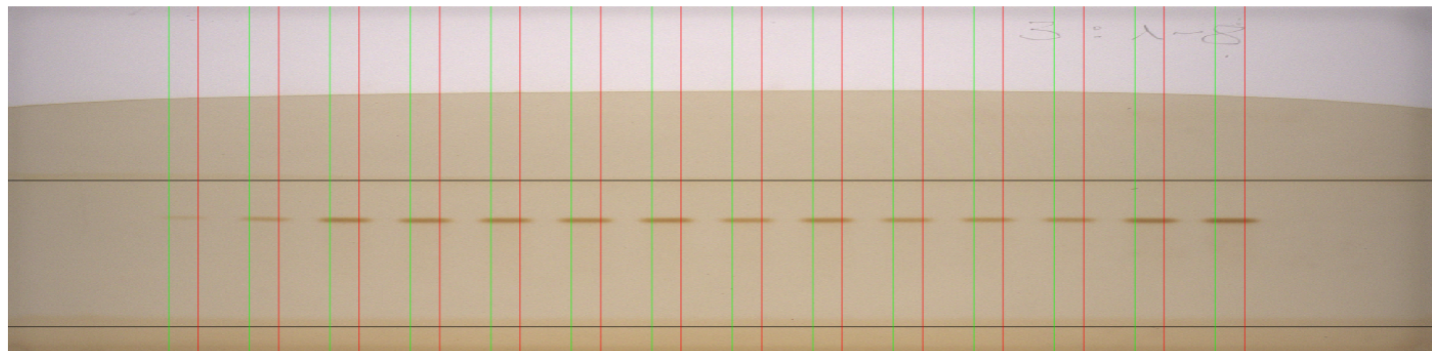
Select a demonstration file

	Value
Plate length [mm]	200.00
Plate width [mm]	100.00
Cropping [mm]	2.00
Migration front [mm]	50.00
Distance to lower edge [mm]	8.00
First application position [mm]	26.00
Band length [mm]	6.00
Distance between tracks [mm]	11.00
Edge cut [mm]	1.00
Number of bands	14.00

☒ Change to distance calculated from the middle of the band
☐ Development from both sides

☒ Preprocessing options

Select the preprocessing algorithms (order is important)



Selection of the track

1

Extract the video densitograms.

Preprocess the video densitograms.

Data Input

1. Upload an image file (jpeg, png, tiff and bmp are supported). A saved *.Rdata file can also be be uploaded here for reprocessing (cf. Data output section)
2. Optionally, select a demonstration data file. The experiment shown here is available as demonstration file “sucralose”.

Input and preprocessing Integration and statistics Report Help

Select a chromatogram image or a Rdata file

Browse... sucralose.tif

Upload complete

Select a demonstration file

None

	Value
Plate length [mm]	200.00
Plate width [mm]	100.00
Cropping [mm]	2.00
Migration front [mm]	50.00
Distance to lower edge [mm]	8.00
First application position [mm]	26.00
Band length [mm]	6.00
Distance between tracks [mm]	11.00
Edge cut [mm]	1.00
Number of bands	14.00

1

☒ Change to distance calculated from the middle of the band

☐ Development from both sides

Extract the video densitograms

Preprocessing options

Select the preprocessing algorithms (order is important)

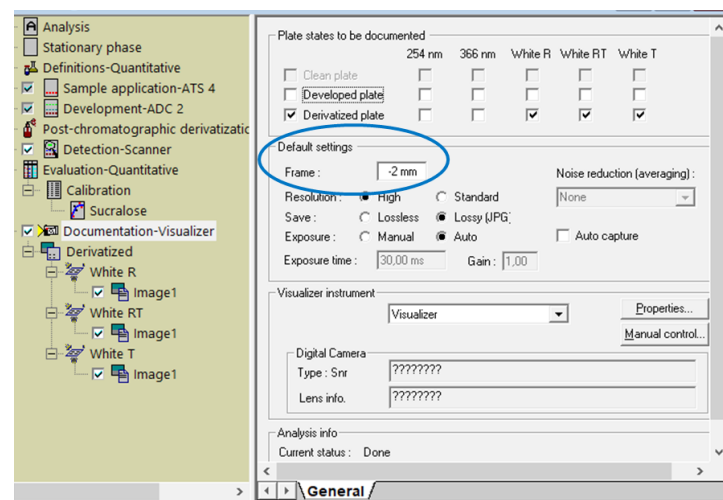
Negative peak inversion Smoothing Baseline correction

Apply the preprocesses

Videodensitogram extraction

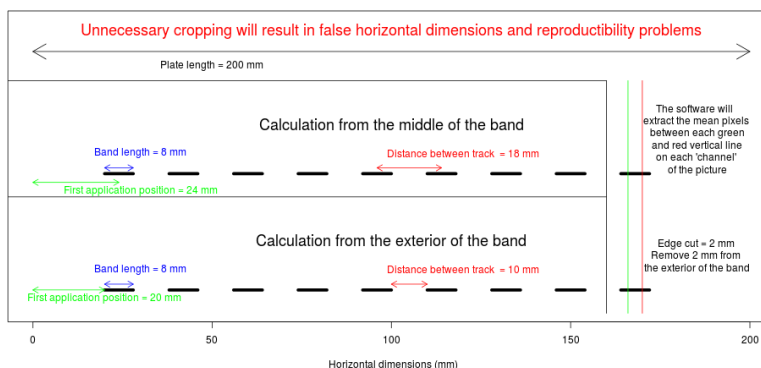
1. Input the plate size, track pattern information and migration distance used during the experiment.

Cropping [mm]: refers to “Frame” in the General settings for the Visualizer in WinCATS (cutting the image).



Use “Edge cut [mm]” to only use the center of the zones for evaluation, as 4 mm for a Band length of 6 mm.

Illustration of the chromatogram extraction



2

Input and preprocessing | Integration and statistics | Report | Help

Select a chromatogram image or a Rdata file

Browse... sucralose.tif

Upload complete

Select a demonstration file

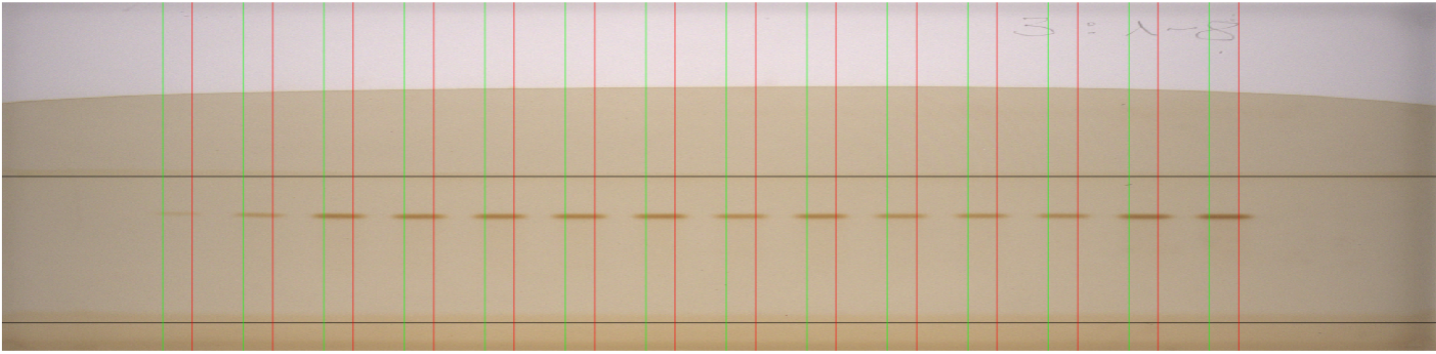
None

	Value
Plate length [mm]	200.00
Plate width [mm]	100.00
Cropping [mm]	2.00
Migration front [mm]	50.00
Distance to lower edge [mm]	8.00
First application position [mm]	26.00
Band length [mm]	6.00
Distance between tracks [mm]	11.00
Edge cut [mm]	1.00
Number of bands	14.00

☒ Change to distance calculated from the middle of the band

☐ Development from both sides

Extract the video densitograms



Preprocessing options

Select the preprocessing algorithms (order is important)

Negative peak inversion | Smoothing | Baseline correction

Apply the preprocesses

Selection of the track

1

Extract the video densitograms.

Preprocess the video densitograms.

2. The chromatogram image update directly the band position, bands will be extracted between the green and red vertical lines.

3. Check for a calculation from the middle of the band, as is standard for winCATS.

4. Check here in case of double side development.

5. Finally, click on this button to extract the videodensitograms.

Note that it is possible to extract automatically the track information by clicking on the image (2). Hover the image for instructions.

Select a chromatogram image or a Rdata file

Browse... sucralose.tif

Upload complete

Select a demonstration file

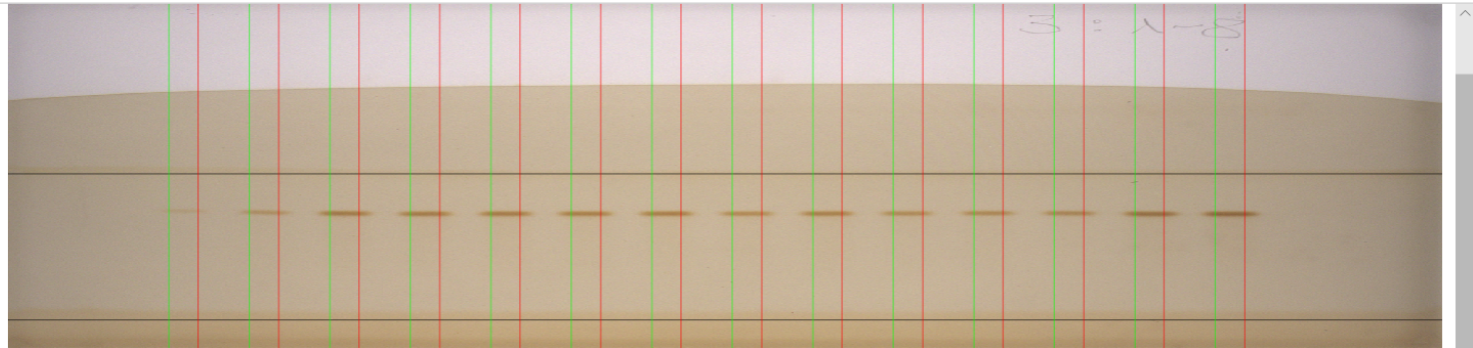
None

	Value
Plate length [mm]	200.00
Plate width [mm]	100.00
Cropping [mm]	2.00
Migration front [mm]	50.00
Distance to lower edge [mm]	8.00
First application position [mm]	26.00
Band length [mm]	6.00
Distance between tracks [mm]	11.00
Edge cut [mm]	1.00
Number of bands	14.00

☒ Change to distance calculated from the middle of the band

☐ Development from both sides

Extract the video densitograms



☒ Preprocessing options

Select the preprocessing algorithms (order is important)

Negative peak inversion Smoothing Baseline correction

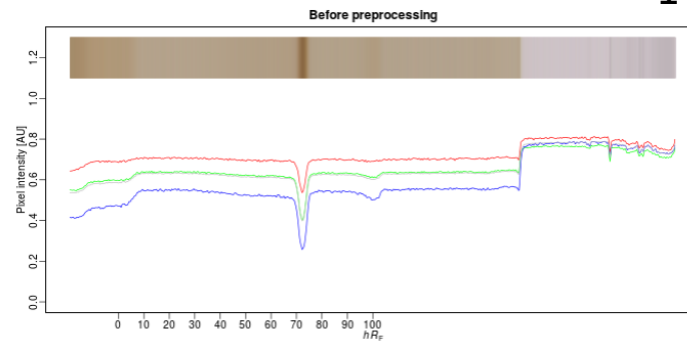
Apply the preprocesses

Selection of the track

14

2

1



Data Preprocessing

1. The raw extracted videodensitograms are plotted.
2. Each track can be selected for preview.

Select a chromatogram image or a Rdata file

Browse... sucralose.tif

Upload complete

Select a demonstration file

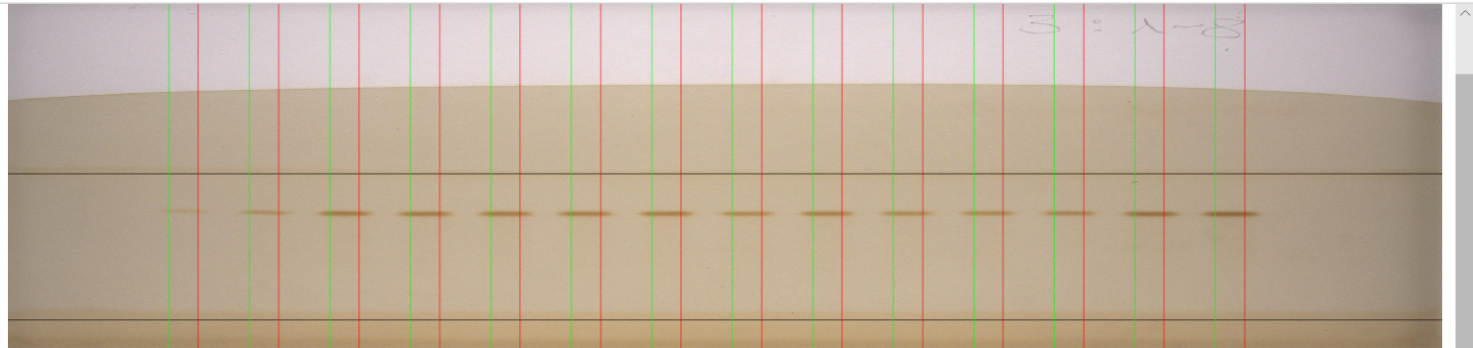
None

	Value
Plate length [mm]	200.00
Plate width [mm]	100.00
Cropping [mm]	2.00
Migration front [mm]	50.00
Distance to lower edge [mm]	8.00
First application position [mm]	26.00
Band length [mm]	6.00
Distance between tracks [mm]	11.00
Edge cut [mm]	1.00
Number of bands	14.00

☒ Change to distance calculated from the middle of the band

☐ Development from both sides

Extract the video densitograms



☒ Preprocessing options

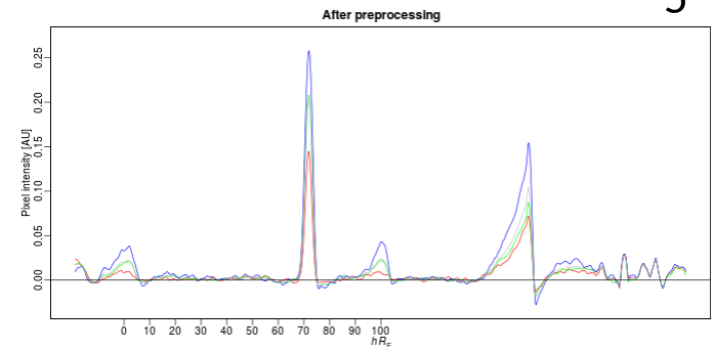
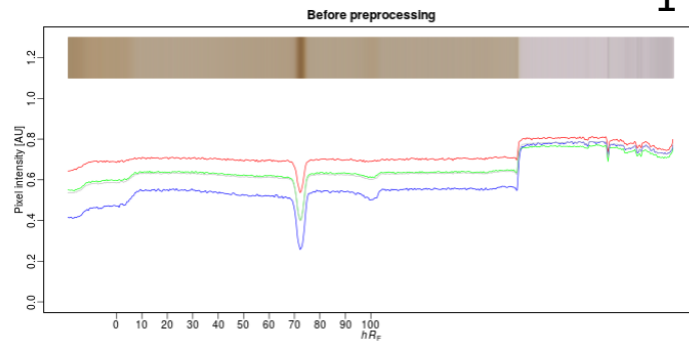
Select the preprocessing algorithms (order is important)

Negative peak inversion Smoothing Baseline correction

Apply the preprocesses

Selection of the track

14



Data Preprocessing

3. Select a set of preprocessing parameters by clicking the input line and the on the parameters (normally, smoothing then baseline correction works correctly, preceded by peak inversion if needed).
4. Click on this button to perform the preprocessing.
5. The preprocessed videodensitograms are plotted.
6. Optionally, more choices are possible for the preprocessing (open the Options windows and try), but the default should work though.

1

Input and preprocessing Integration and statistics Report Help

Minimum number of increasing steps before a peak is reached

10

Minimum number of decreasing steps after the peak

10

The minimum (absolute) height a peak has to have to be recognized as such

0.01

☐ Perform automatic integration☒ Show peak list

hRF range

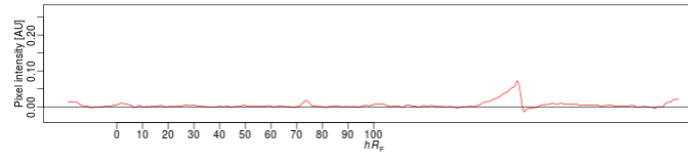
5

☐ Use peak height

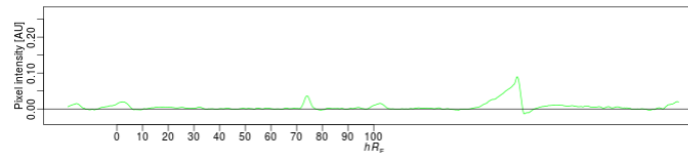
Selection of the track

1

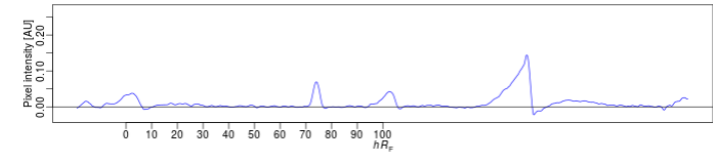
Red channel



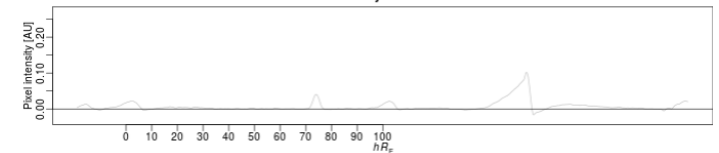
Green channel



Blue channel



Grayscale



Select at least one peak.

Select at least one peak.

Track	Standard	Quantity [AU]
Track 1	<input checked="" type="checkbox"/>	1.00
Track 2	<input checked="" type="checkbox"/>	2.00
Track 3	<input checked="" type="checkbox"/>	3.00
Track 4	<input checked="" type="checkbox"/>	4.00
Track 5	<input checked="" type="checkbox"/>	5.00
Track 6	<input checked="" type="checkbox"/>	6.00
Track 7	<input checked="" type="checkbox"/>	7.00
Track 8	<input checked="" type="checkbox"/>	8.00
Track 9	<input checked="" type="checkbox"/>	9.00
Track 10	<input checked="" type="checkbox"/>	10.00
Track 11	<input checked="" type="checkbox"/>	11.00
Track 12	<input checked="" type="checkbox"/>	12.00
Track 13	<input checked="" type="checkbox"/>	13.00
Track 14	<input checked="" type="checkbox"/>	14.00

Peak detection

1. Select the tab "Integration and statistics"
2. The options used for peak detection and the button for peak detection. Note that this algorithm is not the best and you may need to fine tune the preprocessing if not all peak are detected.
3. Click on "Perform automatic integration".

1

Input and preprocessing Integration and statistics Report Help

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Minimum number of decreasing steps after the peak

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The minimum (absolute) height a peak has to have to be recognized as such

0.01

Perform automatic integration

Show peak list

hRF range

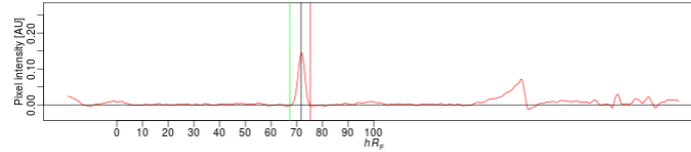
5

☐ Use peak height

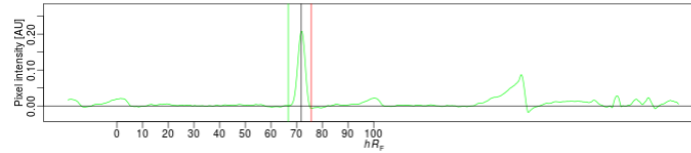
Selection of the track

14

Red channel

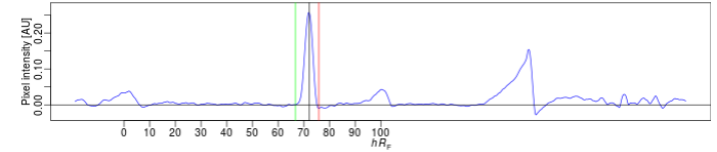


Green channel

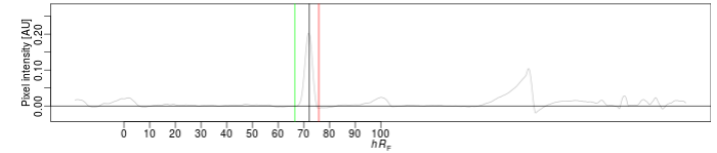


4

Blue channel



Grayscale



Select at least one peak.

Select at least one peak.

Track	Standard	Quantity [AU]
Track 1	<input checked="" type="checkbox"/>	1.00
Track 2	<input checked="" type="checkbox"/>	2.00
Track 3	<input checked="" type="checkbox"/>	3.00
Track 4	<input checked="" type="checkbox"/>	4.00
Track 5	<input checked="" type="checkbox"/>	5.00
Track 6	<input checked="" type="checkbox"/>	6.00
Track 7	<input checked="" type="checkbox"/>	7.00
Track 8	<input checked="" type="checkbox"/>	8.00
Track 9	<input checked="" type="checkbox"/>	9.00
Track 10	<input checked="" type="checkbox"/>	10.00
Track 11	<input checked="" type="checkbox"/>	11.00
Track 12	<input checked="" type="checkbox"/>	12.00
Track 13	<input checked="" type="checkbox"/>	13.00
Track 14	<input checked="" type="checkbox"/>	14.00

4. The detected peaks are plotted for each channel.

5. Each track can be selected for preview.

6. It is possible to look in detail by showing the peak list opening in a new window.

Input and preprocessing

Integration and statistics

Report

Help

Minimum number of increasing steps before a peak is reached

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Minimum number of decreasing steps after the peak

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The minimum (absolute) height a peak has to have to be recognized as such

0.01

Perform automatic integration

Show peak list

hRF range

5

Use peak height

Selection of the track

14

Red channel

Blue channel

Green channel

Grayscale

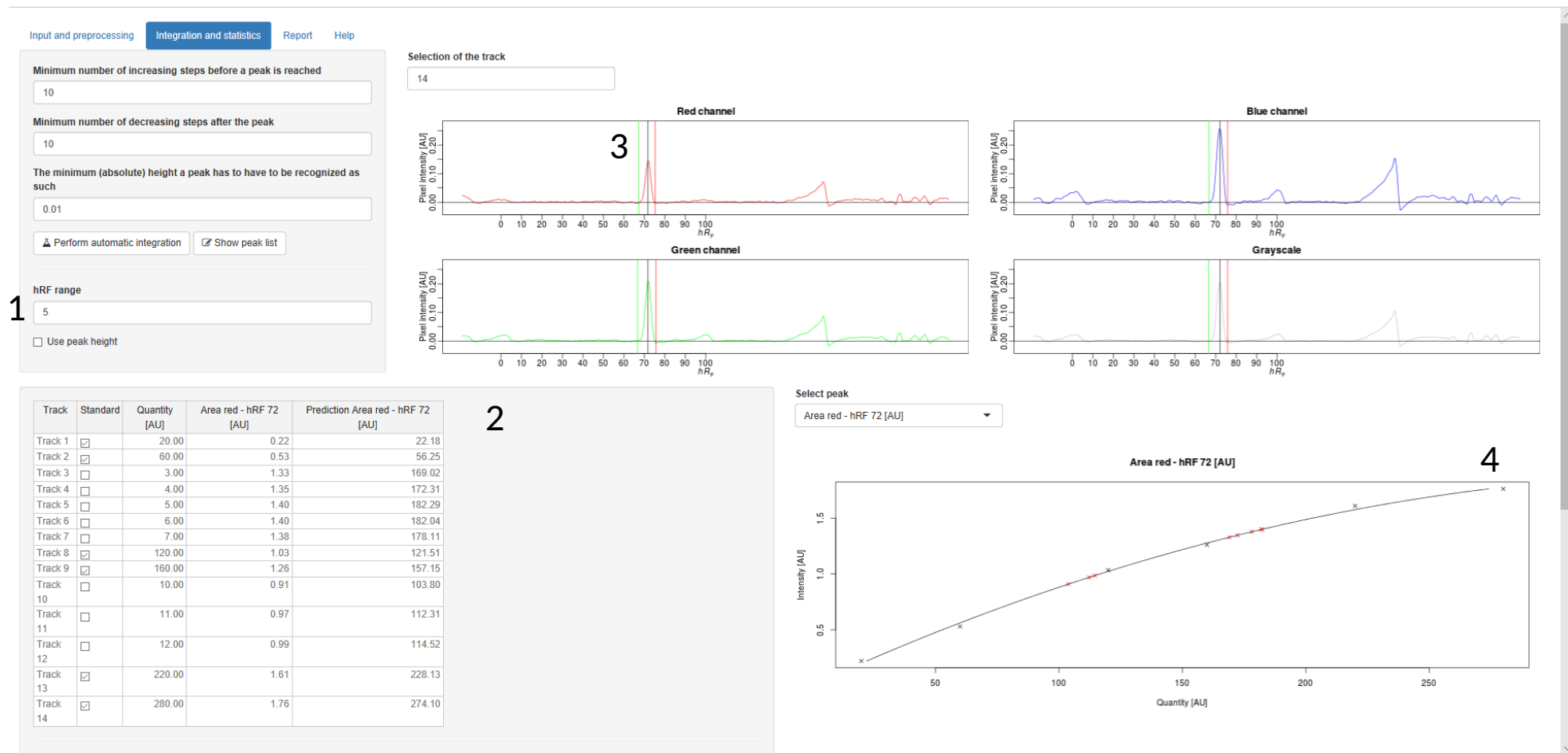
Track	Standard	Quantity [AU]
Track 1	<input checked="" type="checkbox"/>	20.00
Track 2	<input checked="" type="checkbox"/>	60.00
Track 3	<input type="checkbox"/>	3.00
Track 4	<input type="checkbox"/>	4.00
Track 5	<input type="checkbox"/>	5.00
Track 6	<input type="checkbox"/>	6.00
Track 7	<input type="checkbox"/>	7.00
Track 8	<input checked="" type="checkbox"/>	120.00
Track 9	<input checked="" type="checkbox"/>	160.00
Track 10	<input type="checkbox"/>	10.00
Track 11	<input type="checkbox"/>	11.00
Track 12	<input type="checkbox"/>	12.00
Track 13	<input checked="" type="checkbox"/>	220.00
Track 14	<input checked="" type="checkbox"/>	280.00

Select at least one peak.

Select at least one peak.

Calibration

1. Select the pixel window (tolerance for peak selection) and if you want to use peak height instead of area.
2. Input which tracks provide standards and what is the targeted value for each in units you want to use (AU), like ng/zone.



3. Click on a peak on the plot.

4. The calibration curve is plotted, multiple clicks in the other channels will lead to multiple calibration. Note that once a peak is selected, the table become read-only to avoid inconsistency.

The predicted values for each sample and standard are updated in the table (2) to be used for calculating the sample concentrations.

1

Input and preprocessing

Integration and statistics

Report

Help

Include in report

- ☒ Chromatogram
- ☒ Dimension table
- ☒ Preprocessing options
- ☒ Integration options
- ☒ Video-densitograms
- ☒ Peak list
- ☒ Peak list for each sample
- ☒ Regression results

2

Document format

- ☒ PDF ☐ HTML ☐ MS Word

3

Report

4

Save data

Upload this Rdata file instead of the chromatogram

Export as CSV format

Data output

1. Select the “Report tab”
2. Check the information to be included in the report.
3. Select the format of report.
4. Click here to download the report

1

Input and preprocessing

Integration and statistics

Report

Help

Include in report

- ☒ Chromatogram
- ☒ Dimension table
- ☒ Preprocessing options
- ☒ Integration options
- ☒ Video-densitograms
- ☒ Peak list
- ☒ Peak list for each sample
- ☒ Regression results

Document format

- ☒ PDF ☐ HTML ☐ MS Word

Report

Save data

Upload this Rdata file instead of the chromatogram

Export as CSV format

5. Save the data as *.Rdata file to be uploaded again. This is very useful for multiple HPTLC analyses using the same method, plate size and track pattern. After uploading the Rdata file (master) simply upload the plate image of the new analysis and everything is fine, immediately. Continue with densitogram extraction and calibration.
6. Export the results as *.csv file to evaluate them in another software or to make your own plot for publication in your software of choice.