

Investigating localization
within a sample section

Examples

1. Which compounds have which distributions within the sample section?
2. What components colocalize with known localization?
3. Divide up pixels into specified cluster numbers.

Examples

1. Which compounds have which distributions within the sample section?

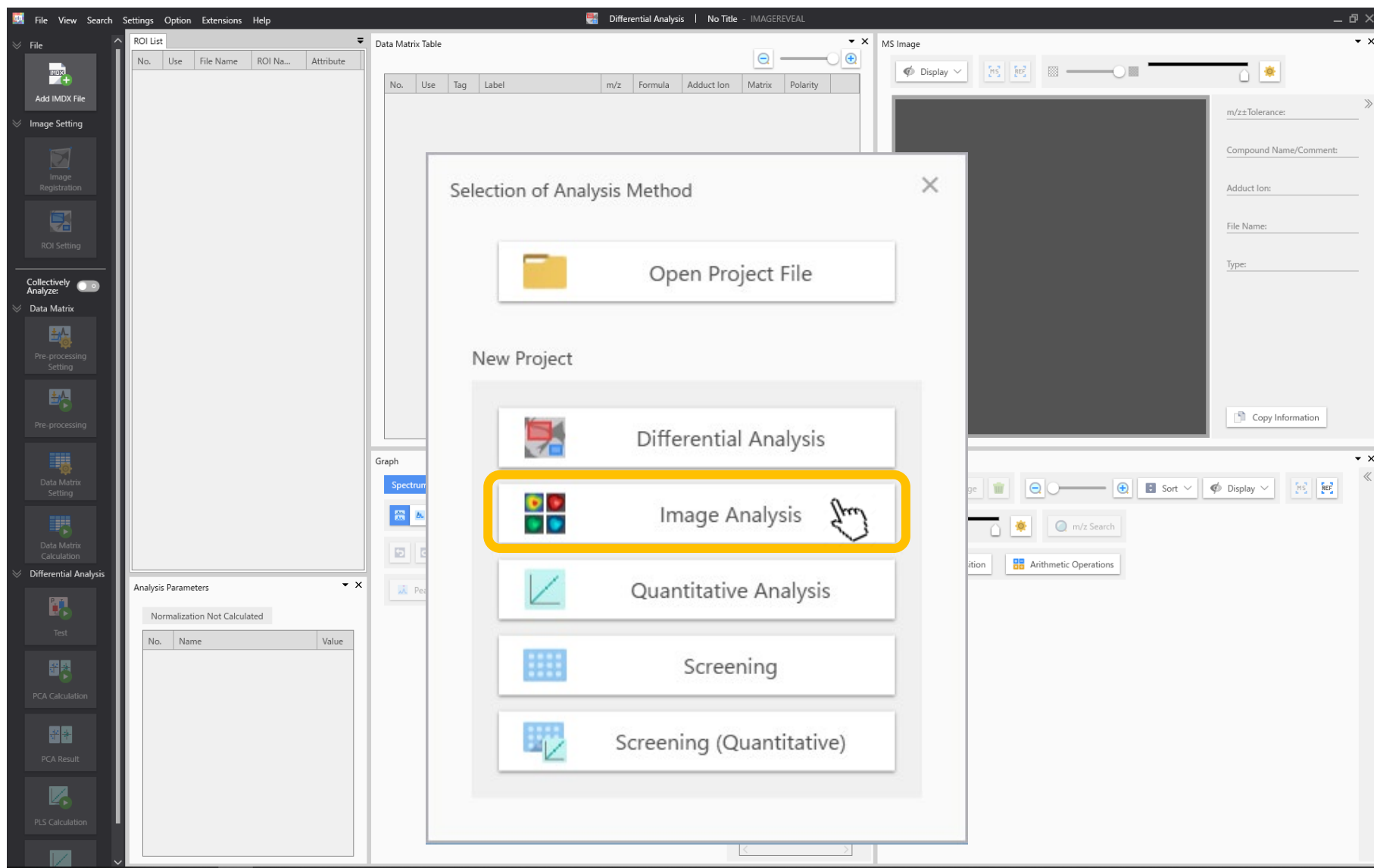
2. What components colocalize with known localization?

3. Divide up pixels into specified cluster numbers.

Steps

1. Select “Image Analysis” mode
2. Read in data
3. Read in reference images (from previous localization analysis)
4. Alignment (image registration)
5. ROI settings if necessary
6. Data matrix table calculations
7. Similar image extraction calculation

1. Select “Image Analysis”



2. Read in data (.imdx)

The screenshot displays the IMAGEREVEAL software interface. The left sidebar contains a vertical list of icons for various functions. The 'Add IMDX File' icon, located at the top of this list, is highlighted with a yellow rectangular box. A white mouse cursor icon is positioned over this button. The main window is divided into several panels:

- ROI List:** A table with columns: No., Use, File Name, ROI Na..., and Data Points.
- Data Matrix Table:** A table with columns: No., Use, Tag, Label, m/z, Formula, Adduct Ion, Matrix, and Polarity.
- MS Image:** A large dark rectangular area for displaying mass spectra images. To its right are input fields for 'm/z Tolerance:', 'Compound Name/Comment:', 'Adduct Ion:', 'File Name:', and 'Type:'. A 'Copy Information' button is at the bottom right.
- Graph:** A panel with a 'Display' dropdown, a 'Peak Picking' button, and an 'Add MS Image' button.
- MS Image List:** A panel with an 'Add MS Image' button, a 'Sort' dropdown, a 'Display' dropdown, and buttons for 'Superimposition' and 'Arithmetic Operations'.
- Analysis Parameters:** A section at the bottom left with a 'Normalization Not Calculated' status and a table with columns: No., Name, and Value.

3. Read in reference images

Load the image file to be used as a reference image.
Select from the menu bar, “File” → Reference Image Management .

The screenshot shows the software interface with the 'File' menu open. The 'Reference Image Management...' option is highlighted with a yellow box and a mouse cursor. The main window displays a mass spectrum graph titled 'Testicle_9AA_PL_SL_5x_1_AREA01.imdx Whole_Ave.' with peaks labeled at m/z 721.48186, 767.49182, 795.52084, 796.52363, 797.52374, 798.52545, 837.53900, and 885.53782. The y-axis is labeled 'Intensity' and ranges from 0E+00 to 2E+06. The x-axis is labeled 'm/z' and ranges from 700 to 900. The MS Image List panel on the right shows a list of images with 'Testicle_9AA_PL...' selected. The 'Analysis Parameters' panel at the bottom left shows 'Normalization Not Calculated'.

File View Search Settings Option Extensions Help

- New Project
- Open Project File...
- Save Project File
- Save Project File As...
- Project File Conversion
- Convert to IMDX File...
- ROI Average Spectrum CSV Export...
- Add IMDX File...
- Reference Image Management...**
- Normalize between files...
- MS/MS Spectrum Normalization...
- Exit

Pre-processing Setting

Pre-processing

Data Matrix Setting

Data Matrix Calculation

Image Analysis

Image Classification Calculation

Image Classification Result

Similar Image Extraction Calculation

Similar Image Extraction Result

Analysis Parameters

Normalization Not Calculated

| No. | Name | Value |
|-----|------|-------|
|-----|------|-------|

Graph

Display

Add MS Image

m/z Search

Peak Picking

The normalization calculation

| D... | File Name | Sp |
|-------------------------------------|-----------------|----|
| <input checked="" type="checkbox"/> | Testicle_9AA... | Wh |

MS Image List

Add MS Image

Sort

Display

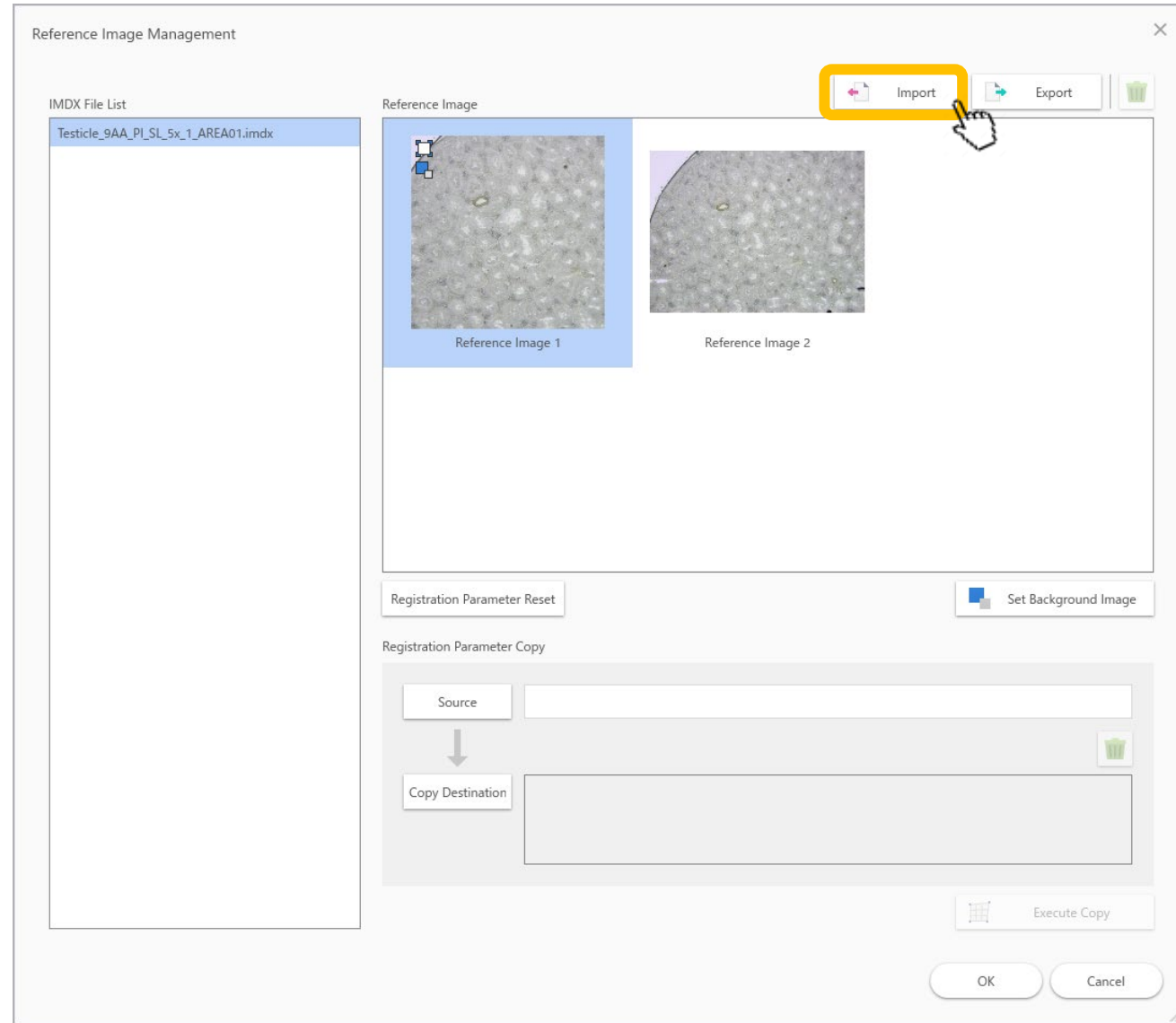
Superimposition

Arithmetic Operations

Testicle_9AA_PL...

TIC

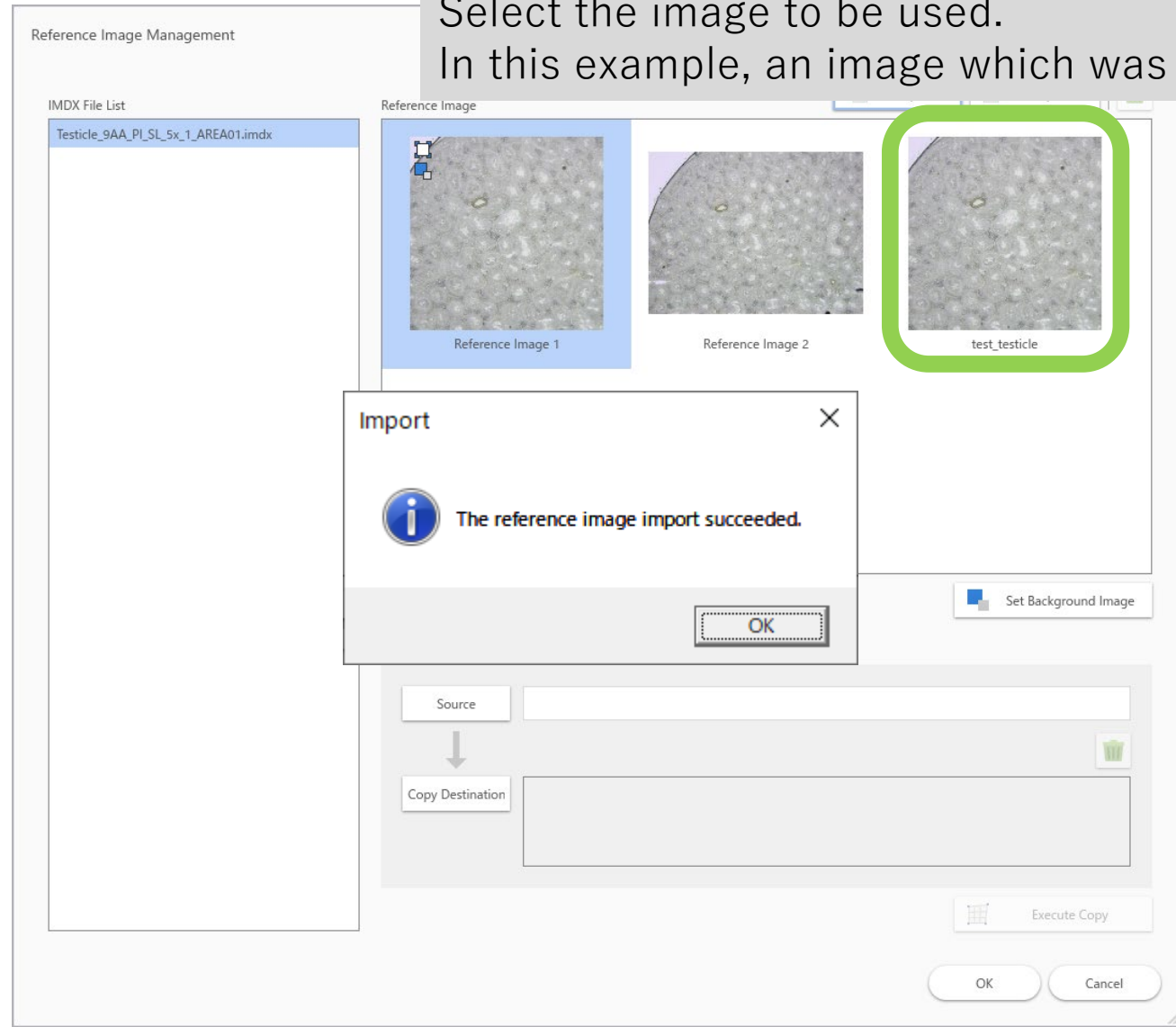
3.1 The “Reference Image Management” screen opens



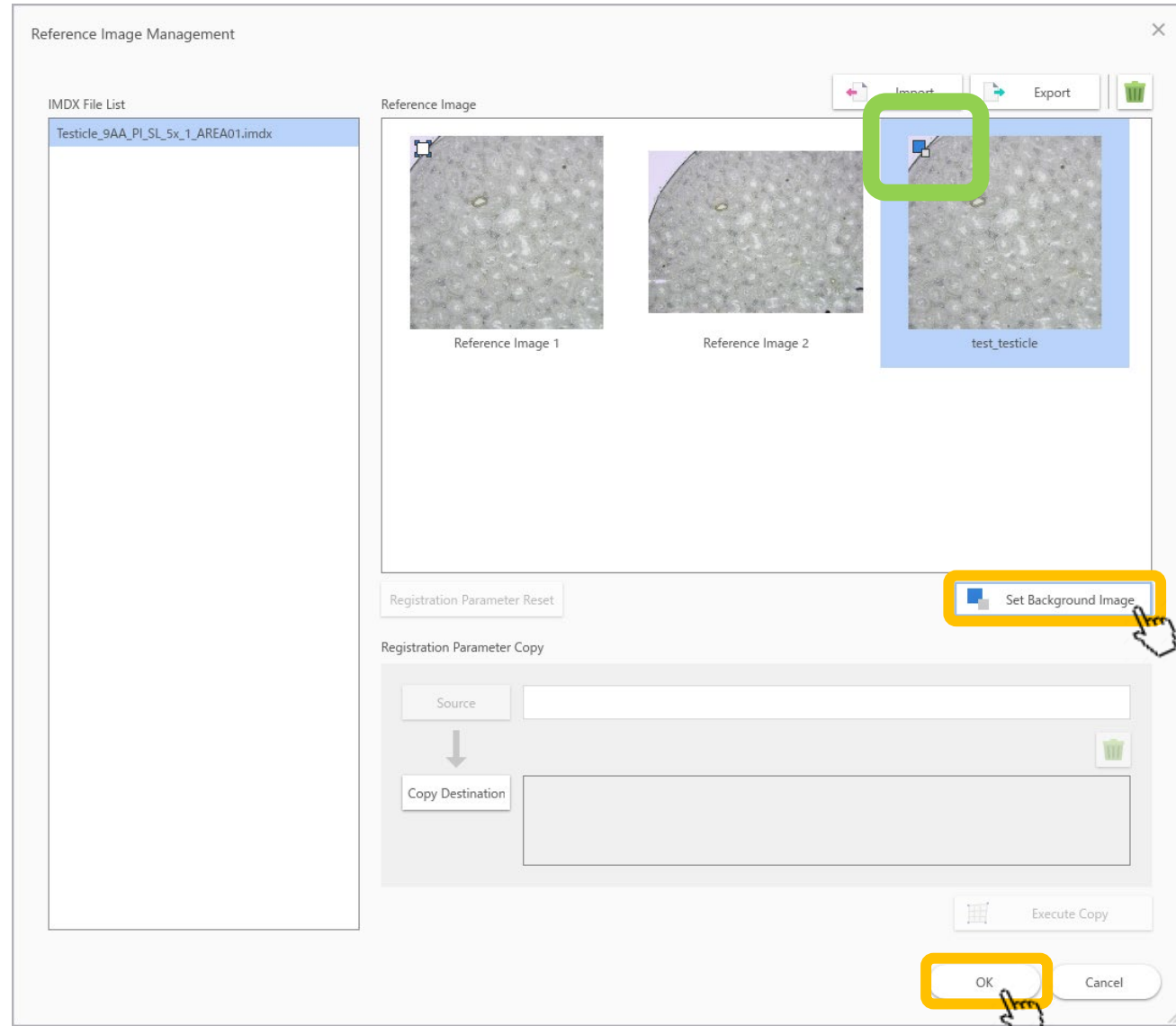
3.2 Import an image to use

Select the image to be used.

In this example, an image which was already read in is imported.



3.3 Set the imported image as a background image



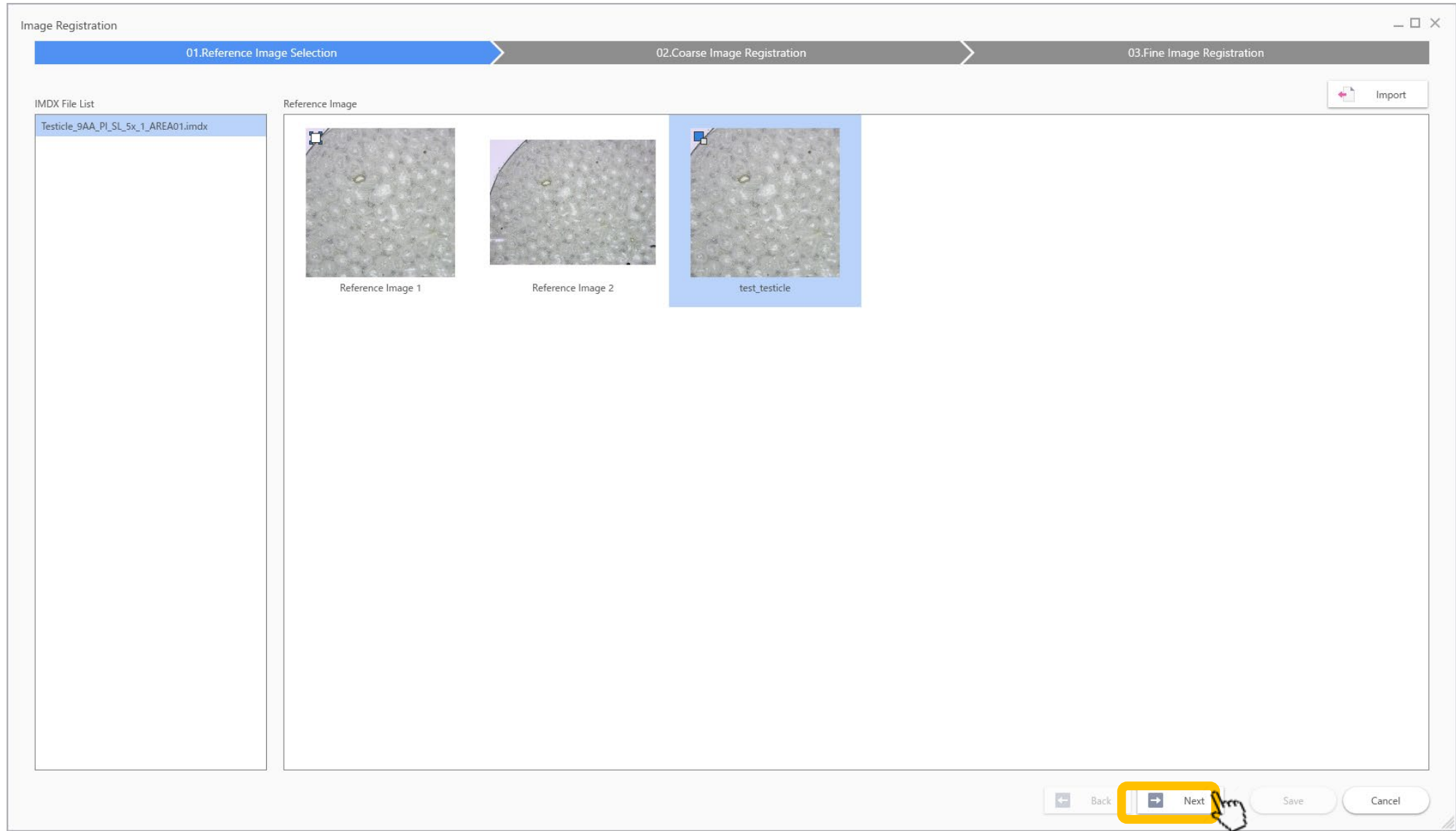
4. Image registration

Select "Image registration"

The software interface displays the following components:

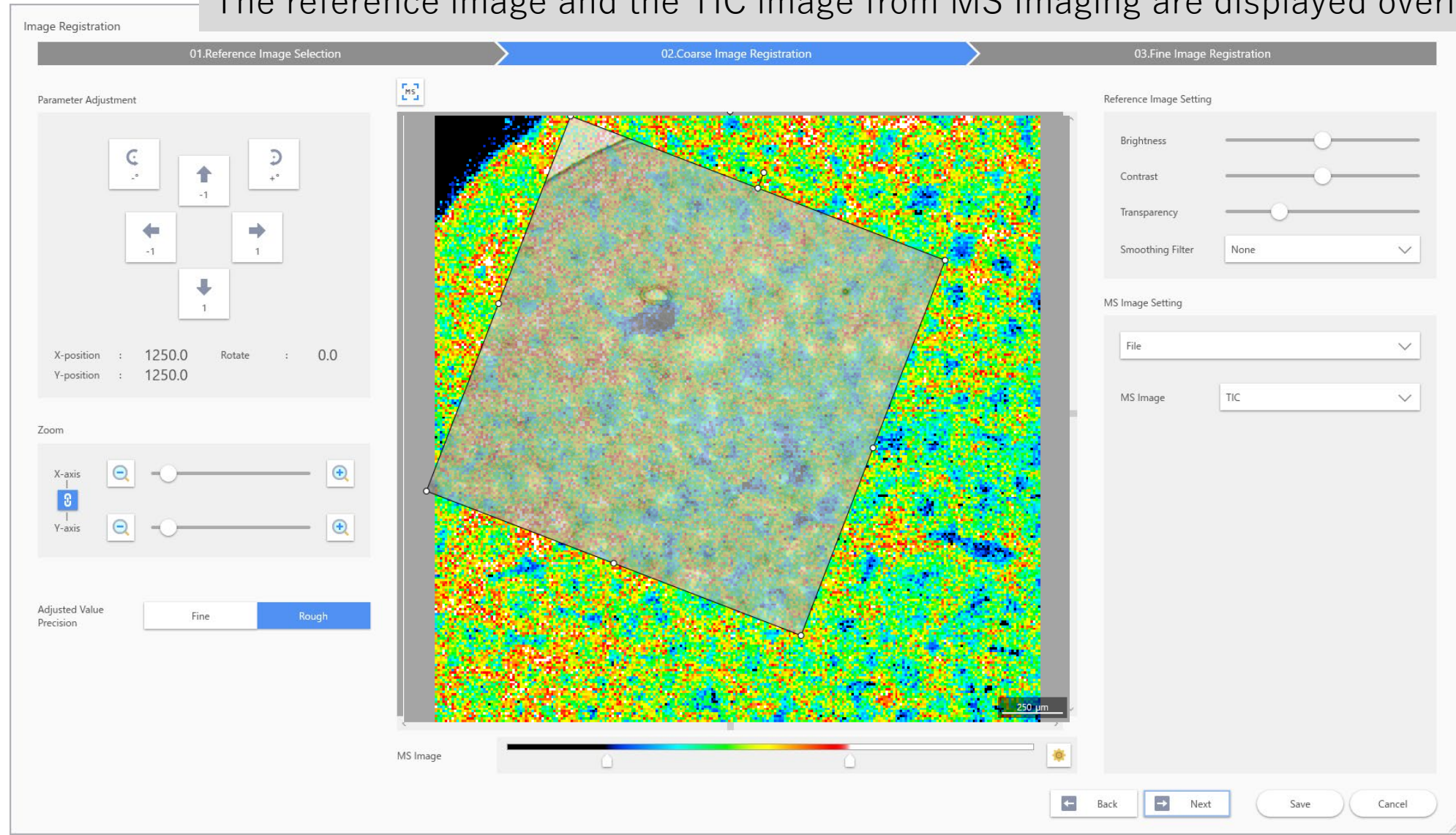
- Left Sidebar:** Contains various tool icons. The 'Image Registration' icon is highlighted with a yellow box and a mouse cursor.
- Top Panel:** Includes a menu bar (File, View, Search, Settings, Option, Extensions, Help) and a 'Data Matrix Table'.
- ROI List:** A table with columns: No., Use, File Name, ROI Name, Data Points.
- Data Matrix Table:** A table with columns: No., Use, Tag, Label, m/z, Formula, Adduct Ion, Matrix, Polarity.
- Main Image:** A large color-coded mass spectrum image (TIC) with a 250 µm scale bar. The image shows a complex pattern of peaks and valleys.
- Bottom Panel:** Contains a 'Graph' showing a mass spectrum plot with peaks labeled at m/z 721.48186, 767.49182, 795.52545, 796.52363, 797.52374, 837.53900, and 885.53782. The y-axis is labeled 'Intensity' and the x-axis is labeled 'm/z'.
- MS Image List:** A panel showing the selected image 'Testicle_9AA_Pi...' and a smaller thumbnail of the image.
- Analysis Parameters:** A section titled 'Normalization Not Calculated' with a table for parameters.

4.1 The background image is selected



4.2 The image registration window opens

The reference image and the TIC image from MS Imaging are displayed overlaid.



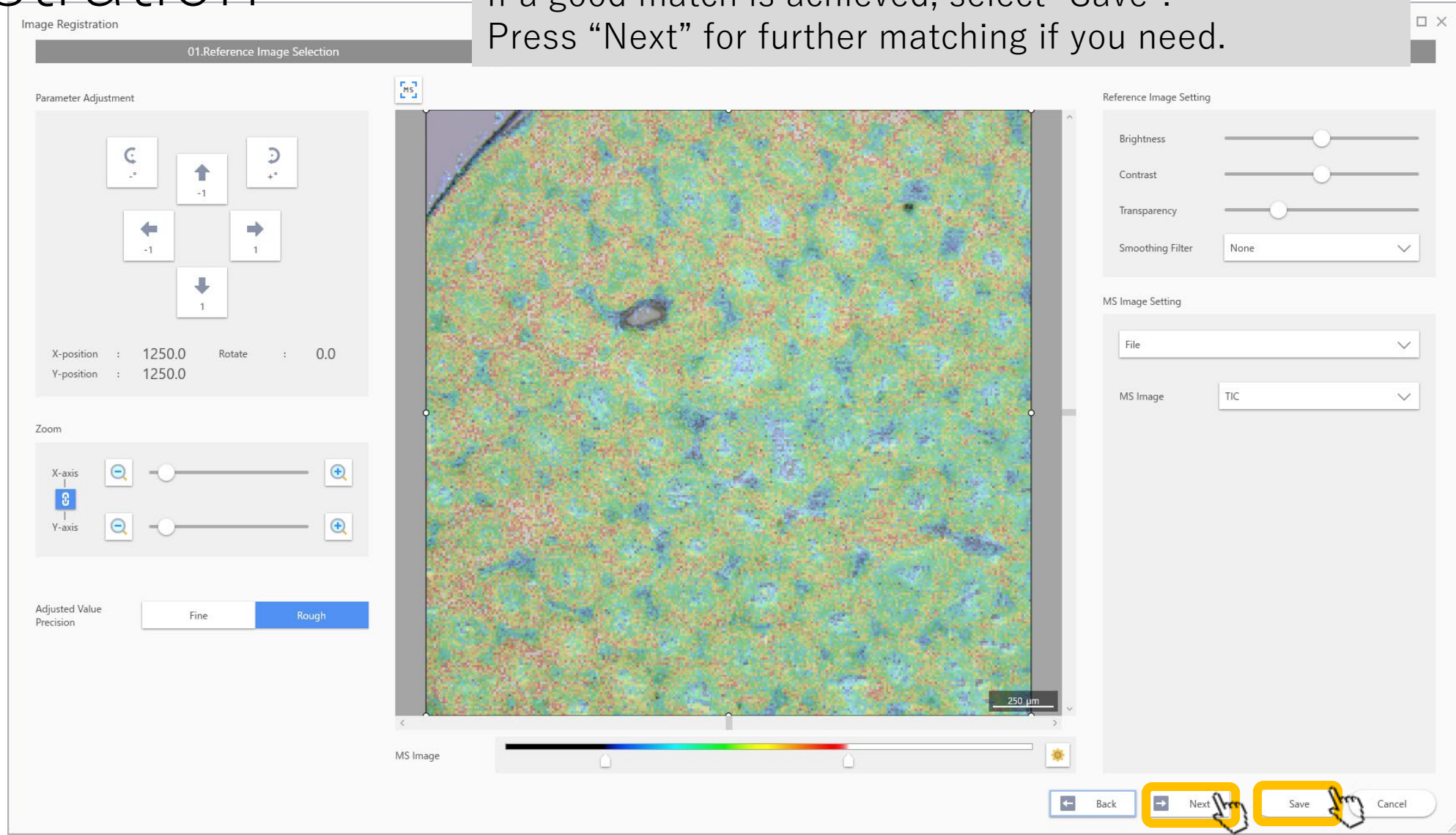
4.3 Coarse image registration

Use the parameter adjustment buttons and the zoom tool on the left-hand side of the window to get a good match between the reference image and the TIC image.

The screenshot displays the coarse image registration software interface. On the left, the 'Parameter Adjustment' panel includes directional buttons (up, down, left, right, and rotation) and numerical input fields for X-position (1250.0), Y-position (1250.0), and Rotate (0.0). Below this is the 'Zoom' panel with sliders for X-axis and Y-axis, and a 'Fine'/'Rough' precision toggle. The central area shows a reference image (a grayscale micrograph of a cell) overlaid on a TIC image (a colorful, noisy map). Yellow arrows indicate the registration adjustments being made. The bottom of the central area features a color scale bar and a '250 μm' scale indicator. On the right, the 'Reference Image Setting' panel contains sliders for Brightness, Contrast, and Transparency, and a 'Smoothing Filter' dropdown set to 'None'. Below that, the 'MS Image Setting' panel has a 'File' dropdown and an 'MS Image' dropdown set to 'TIC'. At the bottom right, there are 'Back', 'Next', 'Save', and 'Cancel' buttons.

4.4 If you need, go to next “Fine image registration”

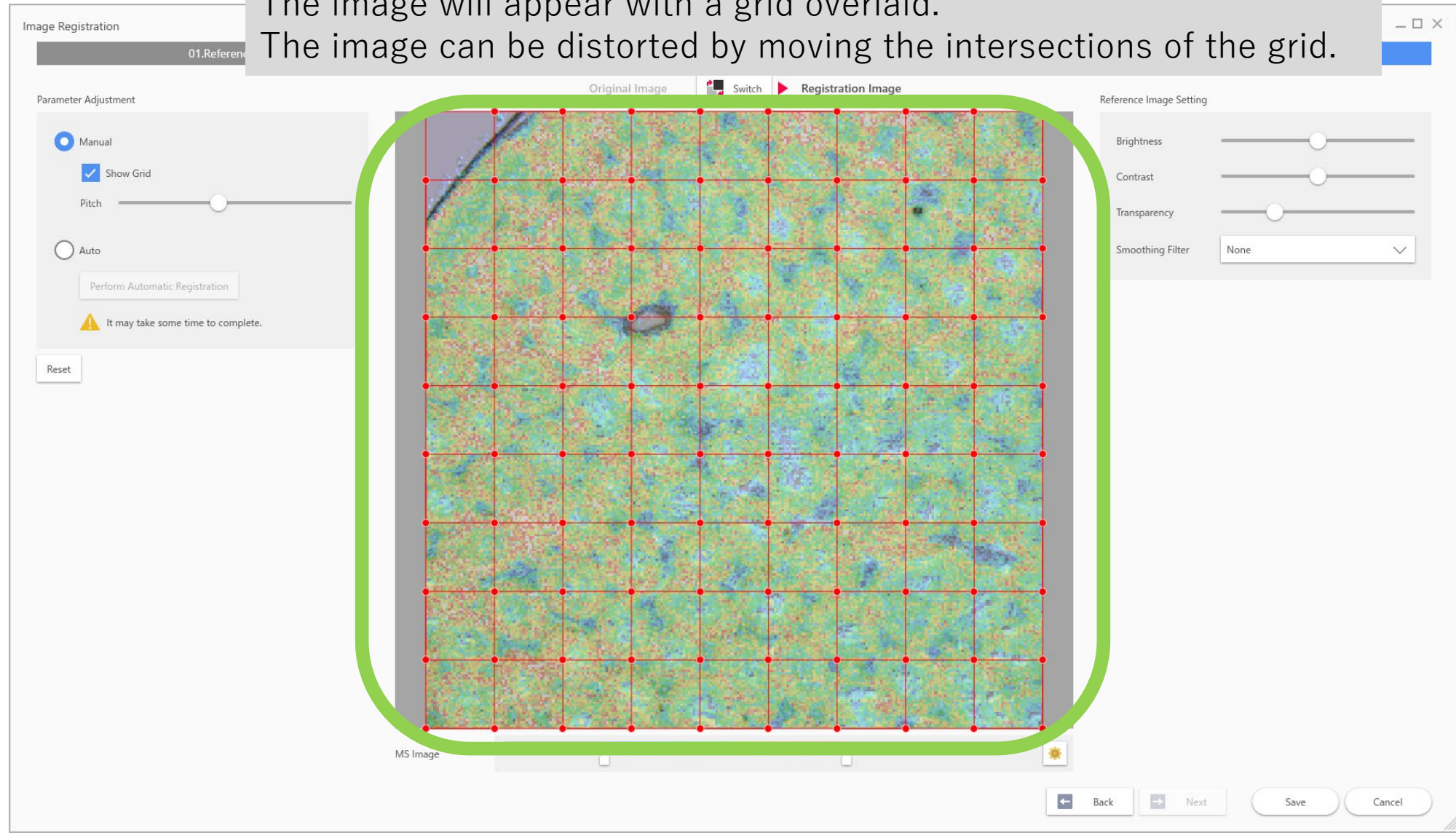
If a good match is achieved, select "Save".
Press “Next” for further matching if you need.



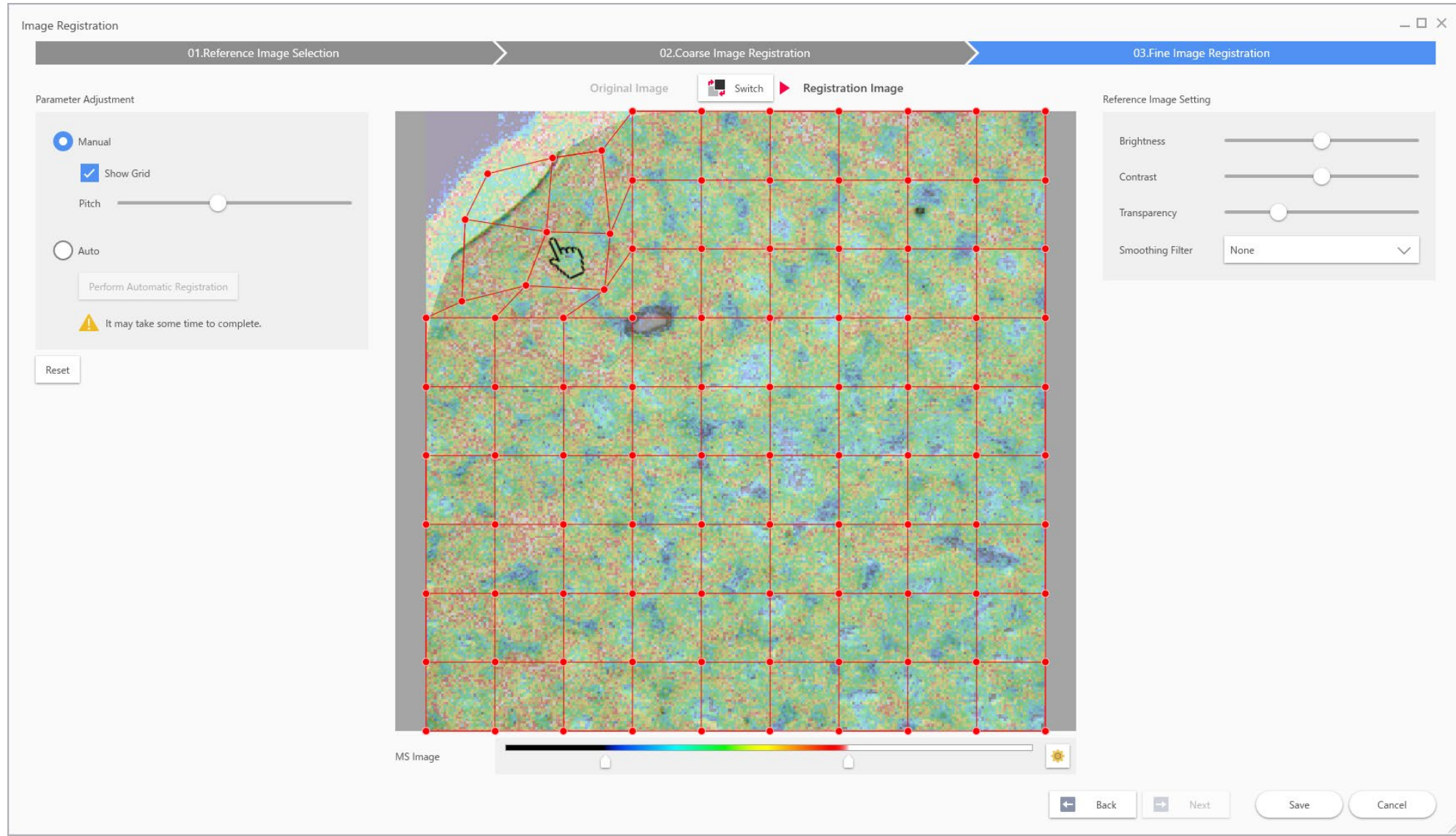
4.5 Fine image registration

The image will appear with a grid overlaid.

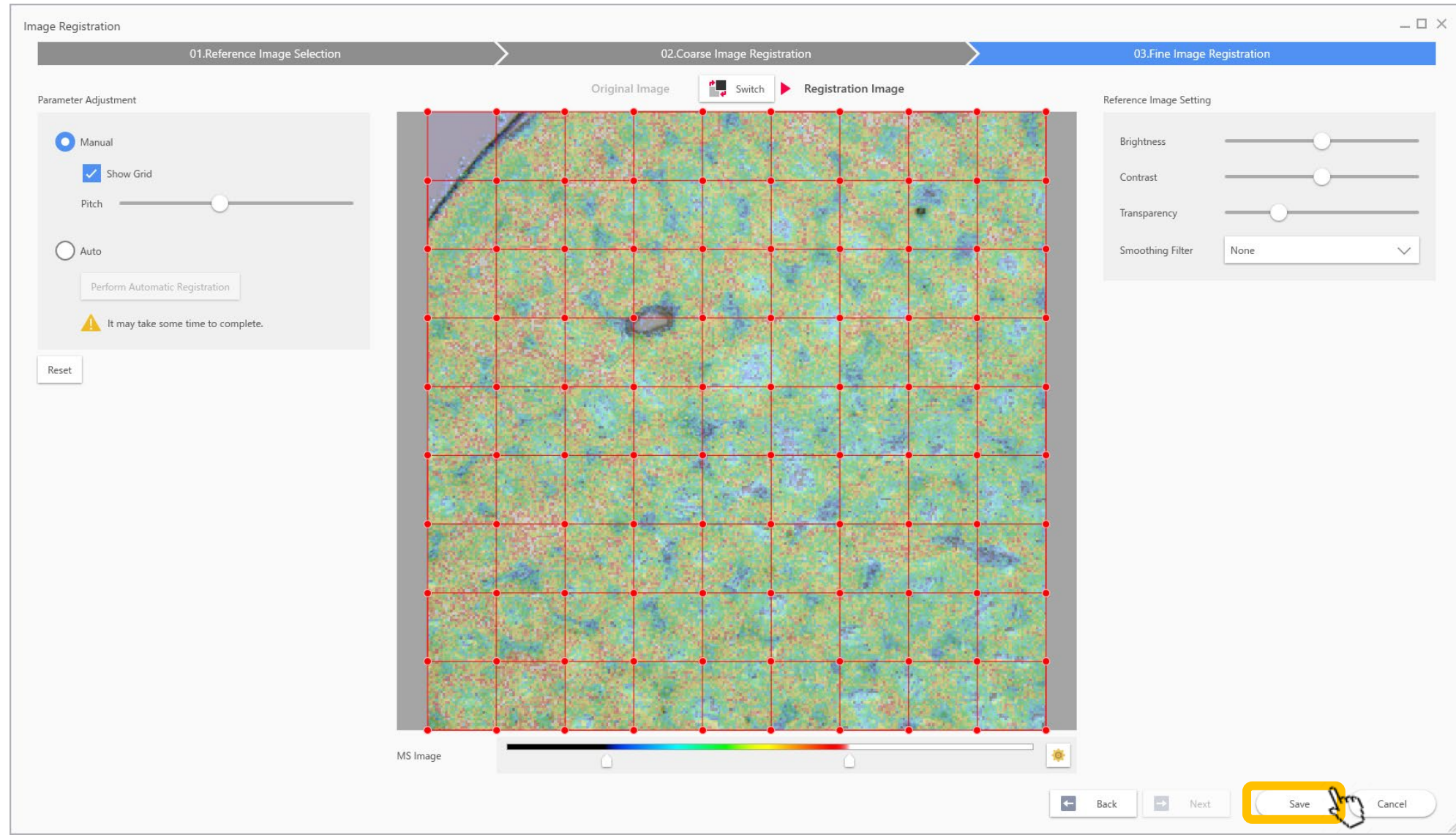
The image can be distorted by moving the intersections of the grid.



4.6 Example of a manipulated image



4.7 Alignment is complete, click “save”



5 Set ROI if necessary

The screenshot displays the IMAGEREVEAL software interface, which is used for mass spectrometry image analysis. The interface is divided into several panels:

- Left Panel (Navigation):** Contains a vertical list of icons for various functions. The 'ROI Setting' icon is highlighted with a yellow box, and a mouse cursor is pointing at it.
- ROI List Panel:** A table with columns: No., Use, File Name, ROI Name, and Data Points. It contains one entry: No. 1, Use checked, File Name 'Testicle_9AA...', ROI Name 'All', and Data Points '62500'.
- Data Matrix Table Panel:** A table with columns: No., Use, Tag, Label, m/z, Formula, Adduct Ion, Matrix, and Polarity. It is currently empty.
- MS Image Panel:** Displays a large, colorful mass spectrometry image. A scale bar in the bottom right corner indicates '250 μm'. To the right of the image, there is a metadata section with fields for Compound Name/Comment (TIC), File Name (Testicle_9AA_PL_SL_5x_1_AREA01.i.mdx), and Type (TIC). A 'Copy Information' button is located below the image.
- Graph Panel:** Shows a mass spectrum plot titled 'Testicle_9AA_PL_SL_5x_1_AREA01.mdx Whole_Ave.'. The x-axis is labeled 'm/z' and ranges from 700 to 900. The y-axis is labeled 'Intensity' and ranges from 0E+00 to 2E+06. Several peaks are labeled with their m/z values: 721.48186, 767.49182, 795.52084, 796.2363, 797.2374, 798.52545, 837.53900, and 885.53782.
- MS Image List Panel:** A panel at the bottom right showing a list of MS images. It includes buttons for 'Add MS Image', 'Sort', 'Display', 'Superimposition', and 'Arithmetic Operations'. A small thumbnail of the current MS image is shown below the list.

The 'Analysis Parameters' panel at the bottom left shows 'Normalization Not Calculated'.

5.1 Select the region to be processed

ROI can be depicted as squares, circles or polygons.

The screenshot displays the 'ROI Setting' software interface. The main window shows a mass spectrum image with a color scale bar at the bottom. A yellow box highlights the selection tools (square, circle, and polygon) in the top-left corner. The 'Reference Image Setting' panel on the right includes sliders for Brightness, Contrast, and Transparency, and a dropdown for Smoothing Filter. The 'MS Image Setting' panel includes a File dropdown and an MS Image dropdown set to 'TIC'. The 'ROI List' panel on the right shows a table with one entry.

ROI Setting

IMDX File: Testicle_9AA_Pi_SL_5x_1_AREA01.imdx Reference Image: Reference Image 1

MS REF

Import Export

Brightness Contrast Transparency Smoothing Filter: None

MS Image Setting

File MS Image: TIC

MS Image

ROI Display Setting Transparency Label ☒ Display

ROI List

| No. | Use | File Name | ROI Name | Attribute | Date |
|-----|--------------------------|----------------------------|----------|-----------|------|
| 1 | <input type="checkbox"/> | Testicle_9AA_Pi_SL_5x_1... | All | Center | |

OK Cancel

5.2 The ROI is listed in the ROI list.

After drawing the ROI, set the attributes.

The screenshot displays the 'ROI Setting' dialog box. The 'IMDX File' is 'Testicle_9AA_Pi_SL_5x_1_AREA01.imdx' and the 'Reference Image' is 'test_testicle'. The main image shows a red and purple histological section with a red ROI boundary. The 'Reference Image Setting' section includes sliders for Brightness, Contrast, and Transparency, and a 'Smoothing Filter' dropdown set to 'None'. The 'MS Image Setting' section has a 'File' dropdown and an 'MS Image' dropdown set to 'TIC'. The 'ROI List' table on the right shows two entries, with the second entry highlighted in green. The 'MS Image' section at the bottom has a color scale and a 'Label' checkbox checked. The 'ROI Display Setting' section has a 'Transparency' slider and a 'Label' checkbox checked.

| No. | Use | File Name | ROI Name | Attribute | Date |
|-----|-------------------------------------|----------------------------|----------|-----------|------|
| 1 | <input type="checkbox"/> | Testicle_9AA_Pi_SL_5x_1... | All | Group A | |
| 2 | <input checked="" type="checkbox"/> | Testicle_9AA_Pi_SL_5x_1... | ROI001 | Group A | |

6. pre-processing settings

The screenshot displays the IMAGEREVEAL software interface with the following components:

- Left Panel:** A vertical toolbar with icons for File, Image Setting, ROI Setting, Pre-processing Setting (highlighted with a yellow box and a hand cursor), Data Matrix Setting, Data Matrix Calculation, and Image Analysis.
- ROI List:** A table with columns: No., Use, File Name, ROI Na..., and Data Points. It contains one entry: No. 1, Use checked, File Name Testicle_9AA..., ROI Na... All, Data Points 62500.
- Data Matrix Table:** A table with columns: No., Use, Tag, Label, m/z, Formula, Adduct Ion, Matrix, and Polarity. It is currently empty.
- MS Image:** A large color-coded mass spectrum image. To its right, a panel shows: Compound Name/Comment: TIC, File Name: Testicle_9AA_PL_SL_5x_1_AREA01.i.mdx, Type: TIC, and a Copy Information button.
- Graph:** A mass spectrum plot titled "Testicle_9AA_PL_SL_5x_1_AREA01.mdx Whole_Ave." showing Intensity vs. m/z. The x-axis ranges from 700 to 900, and the y-axis ranges from 0E+00 to 2E+06. Labeled peaks include m/z values: 721.48186, 767.49182, 795.52084, 796.52363, 797.52374, 798.52385, 837.53900, and 885.53782.
- Analysis Parameters:** A section titled "Normalization Not Calculated" with a table with columns: No., Name, and Value. It is currently empty.
- MS Image List:** A panel at the bottom right showing a list of MS images. It includes buttons for Add MS Image, Sort, Display, Superimposition, and Arithmetic Operations. A small thumbnail of the MS image is shown below the list.

6.1 Pre-processing (normalization) settings

Pre-processing Setting

Normalize None TIC XIC

Import Export + -

| No. | Use | m/z | Tolerance |
|-----|-----|-----|-----------|
|-----|-----|-----|-----------|

☐ Reference Value Setting

Minimum Threshold Value (%)

Specified Method ☐ Range ☒ Center \pm Tolerance

OK Cancel

Sets the "normalisation" criterion.
"TIC" are common.

6.2 Data matrix settings

The screenshot displays the IMAGEREVEAL software interface with the 'Data Matrix Setting' panel highlighted in the left sidebar. The main window is divided into several sections:

- ROI List:** A table with columns: No., Use, File Name, ROI Na..., Data Points. It contains one entry: No. 1, Use checked, File Name 'Testicle_9AA...', ROI Na... 'All', Data Points '62500'.
- Data Matrix Table:** A table with columns: No., Use, Tag, Label, m/z, Formula, Adduct Ion, Matrix, Polarity. It is currently empty.
- MS Image:** A large color-coded mass spectrum image. To its right, a panel shows 'Compound Name/Comment: TIC', 'File Name: Testicle_9AA_PL_SL_5x_1_AREA01.i.mdx', and 'Type: TIC'. A 'Copy Information' button is at the bottom.
- Graph:** A mass spectrum plot titled 'Testicle_9AA_PL_SL_5x_1_AREA01.i.mdx Whole_Ave.' showing Intensity vs. m/z. The x-axis ranges from 700 to 900. The y-axis ranges from 0E+00 to 2E+06. Several peaks are labeled with their m/z values: 721.48186, 767.49182, 795.32084, 796.32363, 797.2374, 798.52545, 837.53900, and 885.53782.
- Analysis Parameters:** A section titled 'Normalization Not Calculated' with a table with columns: No., Name, Value. It is currently empty.
- MS Image List:** A panel at the bottom right showing a list of MS images. The first entry is 'Testicle_9AA_PL...' with a small thumbnail and the label 'TIC'.

A hand cursor is pointing at the 'Data Matrix Setting' icon in the left sidebar.

6.3 Data matrix settings

Data Matrix Setting

Analysis Method: ☐ Target ☒ Non-target ☐ Threshold Value: 0.000 %

m/z Range: ☒ Auto ☐ Manual 10.00000 - 1000.00000 Da

Bin Size: 1.0000 Da

☐ Labeling: Matrix Clusters

☐ Specified Peak Exclusion: Exclude Specified m/z

OK Cancel

Non-targets cut the signal intensity from the spectrum at a fixed width. Targets specify a specific m/z value and bin size.

6.4 Data matrix calculations

The screenshot displays the IMAGEREVEAL software interface with several panels and a dialog box.

Left Panel (Navigation):

- File
- Image Setting
 - Image Registration
 - ROI Setting
- Collectively Analyze: ☐
- Data Matrix
 - Pre-processing Setting
 - Pre-processing
 - Data Matrix Calculation** (highlighted with a yellow box)
- Image Analysis
 - Image Classification Calculation
 - Image Classification Result
 - Similar Image Extraction Calculation
 - Similar Image Extraction Result

ROI List:

| No. | Use | File Name | ROI Na... | Data Points |
|-----|-------------------------------------|-----------------|-----------|-------------|
| 1 | <input checked="" type="checkbox"/> | Testicle_9AA... | All | 62500 |

Data Matrix Table:

| No. | Use | Tag | Label | m/z | Formula | Adduct Ion | Matrix | Polarity |
|-----|-----|-----|-------|-----|---------|------------|--------|----------|
|-----|-----|-----|-------|-----|---------|------------|--------|----------|

MS Image:

Compound Name/Comment: TIC
File Name: Testicle_9AA_PL_SL_5x_1_AREA01.i.mdx
Type: TIC

MS Image List:

- Testicle_9AA_PL... (TIC)

Graph:

Testicle_9AA_PL_SL_5x_1_AREA01.mdx Whole_Ave.

Intensity vs m/z plot showing peaks at:

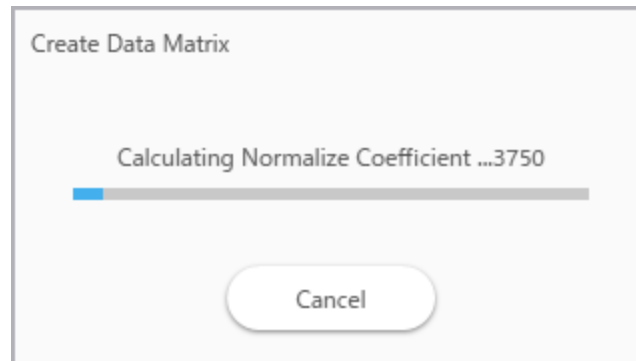
- 721.48186
- 767.49182
- 795.52084
- 796.52363
- 797.52374
- 798.52545
- 837.53900
- 885.53782

Execute Processing Dialog:

Execute the following calculation.
Normalize
Data Matrix Creation

Buttons: OK, キャンセル

6.5 Calculations window



6.6 Data matrix calculations are complete

The screenshot displays the IMAGEREVEAL software interface with the following components:

- ROI List:** A table with 2 rows. Row 1: No. 1, Use (unchecked), File Name: Testicle_9A..., ROI Na...: All, Data Points: 62500. Row 2: No. 2, Use (checked), File Name: Testicle_9A..., ROI Na...: ROI001, Data Points: 61700.
- Data Matrix Table:** A table with 21 rows of data points. The columns are No., Use, Tag, Label, m/z, and ROI001. The m/z values range from 699.9849 to 720.4849, and the ROI001 values range from 11504.753 to 8185.359.
- MS Image:** A large, colorful mass spectrum image showing a complex pattern of peaks. A scale bar indicates 250 μm.
- Compound Name/Comment:** TIC. File Name: Testicle_9AA_PL_SL_5x_1-AREA02.i.mdx. Type: TIC.
- Graph:** A section for displaying and manipulating data. It includes a 'Display' button, a 'Peak Picking' button, and a 'm/z Search' input field.
- MS Image List:** A list of images, including 'Testicle_9AA_PL_...' and 'TIC'.
- Analysis Parameters:** A table showing parameters for the TIC analysis. The parameters are: No., Name, and Value. The values are: 1. Normalize (TIC), 2. Normalize Reference Value Setting (Off), 3. Normalize Minimum Threshold(%) (0), 4. Data Matrix Analysis Method (Non-tar), 5. m/z Range (699.9849), 6. Tolerance/Bin Size (Da) (1.0000), 7. Labeling (Off), 8. Exclusion List (Off), 9. Threshold Setting (Off).

7. Select “Similar image extraction calculation”

The screenshot displays the IMAGEREVEAL software interface with the following components:

- Left Sidebar:** A vertical menu of analysis tools. The 'Similar Image Extraction Calculation' option is highlighted with a yellow box and a mouse cursor.
- ROI List:** A table listing regions of interest (ROIs) for analysis.
- Data Matrix Table:** A table showing mass spectrometry data points for each ROI.
- MS Image:** A large, colorful mass image representing the data for a selected ROI.
- MS Image List:** A list of processed mass images.
- Analysis Parameters:** A panel for configuring analysis settings.

ROI List

| No. | Use | File Name | ROI Na... | Data Points |
|-----|-------------------------------------|----------------|-----------|-------------|
| 1 | | Testicle_9A... | All | 62500 |
| 2 | <input checked="" type="checkbox"/> | Testicle_9A... | ROI001 | 61700 |

Data Matrix Table

| No. | Use | Tag | Label | m/z | ROI001 |
|-----|-------------------------------------|-----|-------------------|----------|-----------|
| 1 | <input checked="" type="checkbox"/> | | 699.9849-700.9849 | 700.4849 | 11904.753 |
| 2 | <input checked="" type="checkbox"/> | | 700.9849-701.9849 | 701.4849 | 10861.376 |
| 3 | <input checked="" type="checkbox"/> | | 701.9849-702.9849 | 702.4849 | 7137.776 |
| 4 | <input checked="" type="checkbox"/> | | 702.9849-703.9849 | 703.4849 | 9499.758 |
| 5 | <input checked="" type="checkbox"/> | | 703.9849-704.9849 | 704.4849 | 6598.998 |
| 6 | <input checked="" type="checkbox"/> | | 704.9849-705.9849 | 705.4849 | 10954.193 |
| 7 | <input checked="" type="checkbox"/> | | 705.9849-706.9849 | 706.4849 | 7085.682 |
| 8 | <input checked="" type="checkbox"/> | | 706.9849-707.9849 | 707.4849 | 10111.607 |
| 9 | <input checked="" type="checkbox"/> | | 707.9849-708.9849 | 708.4849 | 7323.618 |
| 10 | <input checked="" type="checkbox"/> | | 708.9849-709.9849 | 709.4849 | 14103.264 |
| 11 | <input checked="" type="checkbox"/> | | 709.9849-710.9849 | 710.4849 | 9111.132 |
| 12 | <input checked="" type="checkbox"/> | | 710.9849-711.9849 | 711.4849 | 9957.518 |
| 13 | <input checked="" type="checkbox"/> | | 711.9849-712.9849 | 712.4849 | 6569.451 |
| 14 | <input checked="" type="checkbox"/> | | 712.9849-713.9849 | 713.4849 | 10506.920 |
| 15 | <input checked="" type="checkbox"/> | | 713.9849-714.9849 | 714.4849 | 7621.135 |
| 16 | <input checked="" type="checkbox"/> | | 714.9849-715.9849 | 715.4849 | 8599.440 |
| 17 | <input checked="" type="checkbox"/> | | 715.9849-716.9849 | 716.4849 | 7888.463 |
| 18 | <input checked="" type="checkbox"/> | | 716.9849-717.9849 | 717.4849 | 8757.440 |
| 19 | <input checked="" type="checkbox"/> | | 717.9849-718.9849 | 718.4849 | 6989.884 |
| 20 | <input checked="" type="checkbox"/> | | 718.9849-719.9849 | 719.4849 | 12290.908 |
| 21 | <input checked="" type="checkbox"/> | | 719.9849-720.9849 | 720.4849 | 8185.359 |

Analysis Parameters

| No. | Name | Value |
|-----|-----------------------------------|----------|
| 1 | Normalize | TIC |
| 2 | Normalize Reference Value Setting | Off |
| 3 | Normalize Minimum Threshold(%) | 0 |
| 4 | Data Matrix Analysis Method | Non-tar |
| 5 | m/z Range | 699.9849 |
| 6 | Tolerance/Bin Size (Da) | 1.0000 |
| 7 | Labeling | Off |
| 8 | Exclusion List | Off |
| 9 | Threshold Setting | Off |

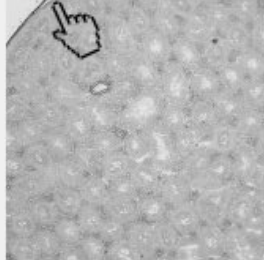
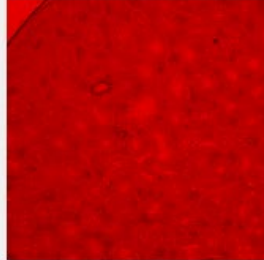
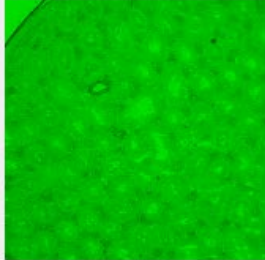
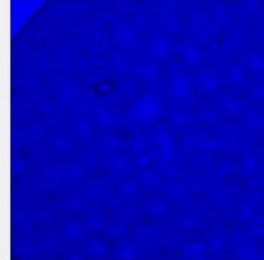
7.1 Select colours to be used (Grayscale in this case)

Similar Image Extraction Setting

IMDX File : Testicle_9AA_PL_SL_5x_1_AREA02.imdx

Reference Image

☒ Grayscale Image ☐


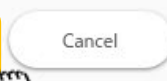
Number of Latent Variables : ☐ Auto ☒ Manual 15

m/z Range : 700.48492 - 899.48492 Da Auto Setting

Number of Extracted Images : 5

Data Point Thinning : None

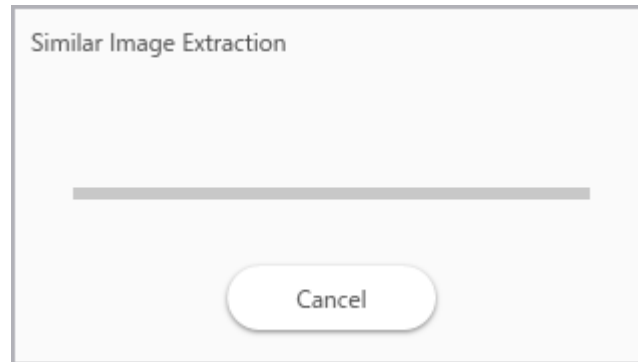
m/z Width for Image Extraction : 1.00000 Da

 Execute  Cancel

Only single colour in the image can be handled.
Specify the colour to be used in the reference image.
For black and white photo, select greyscale.

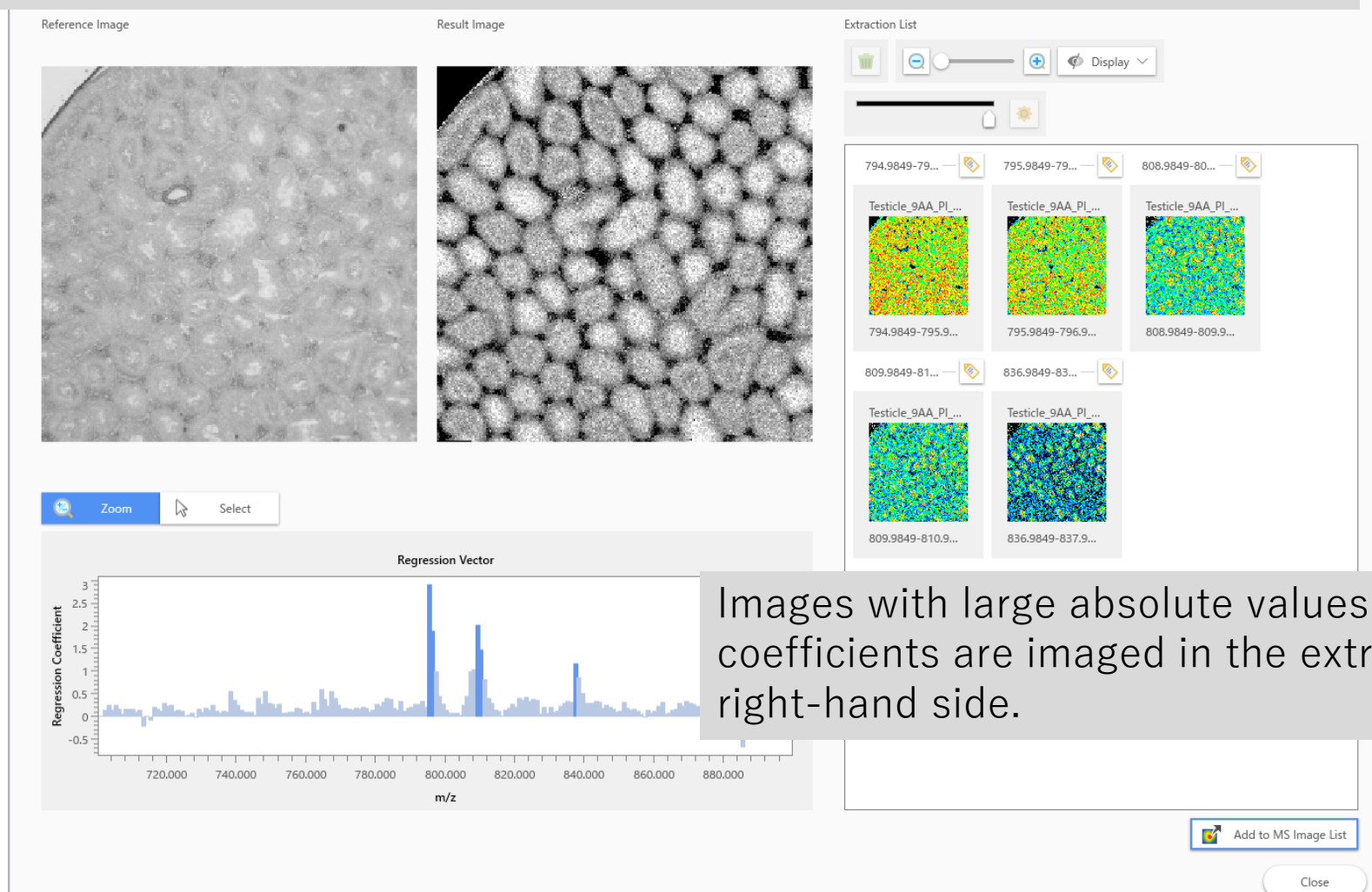
“Number of Latent Variable” is “automatic”, which is more accurate but takes longer.
“Number of Extracted Image” is the number of m/z's that are automatically imaged.
If “Data Point Thinning” is effective, the resulting image is also thinned out.
“m/z Width for Image Extraction” is a range intended to prevent the emergence of similar isotope peaks, and only the m/z value with the highest regression coefficient within that range will be extracted.

7.2 Calculations dialogue



7.3 Similar image extraction calculation result

On the left-hand side is the “Reference Image”,
and in the centre is the “Regression Image” calculated from the MS imaging data.



Images with large absolute values of the regression coefficients are imaged in the extraction list on the right-hand side.

7.4 Adding images to the main screen

Similar Image Extraction Result

Reference Image

Result Image

Extraction List

794.9849-79... 795.9849-79... 808.9849-80...

Testicle_9AA_Pi... Testicle_9AA_Pi... Testicle_9AA_Pi...

794.9849-795.9... 795.9849-796.9... 808.9849-809.9...

809.9849-81... 836.9849-83...

Testicle_9AA_Pi... Testicle_9AA_Pi...

809.9849-810.9... 836.9849-837.9...

Regression Vector

Regression Coefficient

m/z

Zoom Select

Add to MS Image List

Close

Selecting images from the “Extraction List” and clicking the “Add to MS image list” button, the highlighted images will be added to the main screen.

7.5 The images are added to the MS image list

The screenshot displays the IMAGEREVEAL software interface, which is used for mass spectrometry image analysis. The interface is divided into several panels:

- Left Panel:** A vertical toolbar containing icons for various functions such as Image Registration, ROI Setting, Data Matrix, Pre-processing, and Image Classification.
- ROI List:** A table listing regions of interest (ROIs) with columns for No., Use, File Name, ROI Name, and Data Points.
- Data Matrix Table:** A large table showing mass spectrometry data with columns for No., Use, Tag, Label, m/z, PLS Coefficient, and ROI Name. It contains 21 rows of data.
- MS Image:** A panel displaying a mass spectrometry image (TIC) with a color scale and a 'Copy Information' button.
- MS Image List:** A panel showing a list of mass spectrometry images. Two images are highlighted with a yellow box: 'Testicle_9AA_PLI_SL_Sx_1_AREA02.indx' and 'Testicle_9AA_PLI_SL_Sx_1_AREA02.indx'.
- Graph:** A panel for displaying and analyzing data, including a 'Peak Picking' button.
- Analysis Parameters:** A panel showing parameters for the analysis, such as 'TIC', 'Normalize', 'Normalize Reference Value Setting', 'Normalize Minimum Threshold(%)', 'Data Matrix Analysis Method', 'm/z Range', 'Tolerance/Bin Size (Da)', 'Labeling', 'Exclusion List', and 'Threshold Setting'.