Upgrading *syngo*.via VB30 to VB40 – What's New in MRI?

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In May 2020, the Economic Interest Group IRM74, upgraded its two *syngo*.via servers from software version VB30 to VB40.

Below, you can find details about the new features added to enhance daily use for radiographers and radiologists, together with a description of the advanced software.

General MR

Sorting has been redesigned in the **Series Navigator**, in particular by adding a number in front of each series for easier identification. The diffusion b-value is displayed between brackets (Fig. 1A), in a similar manner to the TE value for multiple scan series or when the series are sorted in Dixon, which makes viewing much clearer for the user.

Note also that the presence of an icon makes it easier to identify a series generated by the user in the list of series (Fig. 1B).

New **display types**, such as Cinematic VRT (Fig. 2A) and MIP/MinIP fusion (Fig. 2B), are available in the bottom left corner menu of the screen.
The display mode and slice thickness can now be changed more quickly with the aid of the blue shortcuts at the side (Fig. 3).

The system can now also memorize radiologists' habits when dragging and dropping their series so that they are displayed according to their preferences the next time. This tool can be used on new layouts created from a private account and when using them to improve memorization of the required series (**Smart Layout** tool: Segment learning button – Fig. 4).

The system then takes into account approximately 30 DICOM attributes from the dragged sequence in order to search for the series that best matches the required series.

If you wish to display several well-defined series, it is possible to zoom-in on specific segments. This is done by selecting the segments by holding down the Ctrl key and right-clicking on **Enlarge segments** (Fig. 5). Simply double-click to return to the original display.

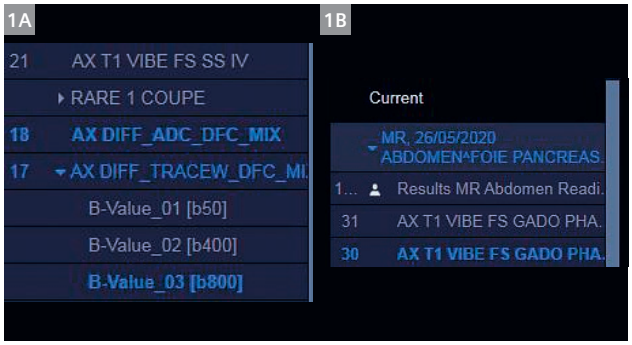
Easy Reading layout now displays series with the same orientation in segments of the same size.

When studying dynamic series (particularly if there are multiple phases as is the case with TWIST and GRASP-VIBE), the **4D cinematic imaging** tool facilitates the temporal location of the displayed phase (Fig. 6). This is now available in all MR workflows.

When **studying 3D volumes**, the reference line is now hidden automatically when scrolling through the series so that it does not interfere with viewing.

An **export in non-DICOM image format** (practical for saving images to an external storage device for presentation purposes, for example) is now available from any workflow (previously only available in MM Reading) (Fig. 7).

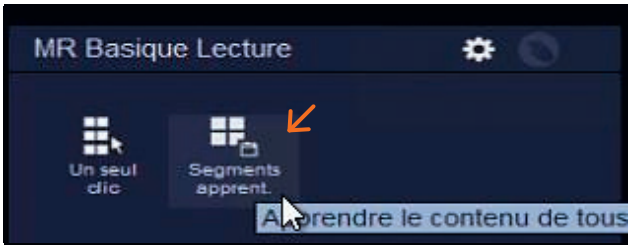
When the user closes an examination by 'ignoring the findings', the dialog box that asked for confirmation in the previous version has now disappeared.



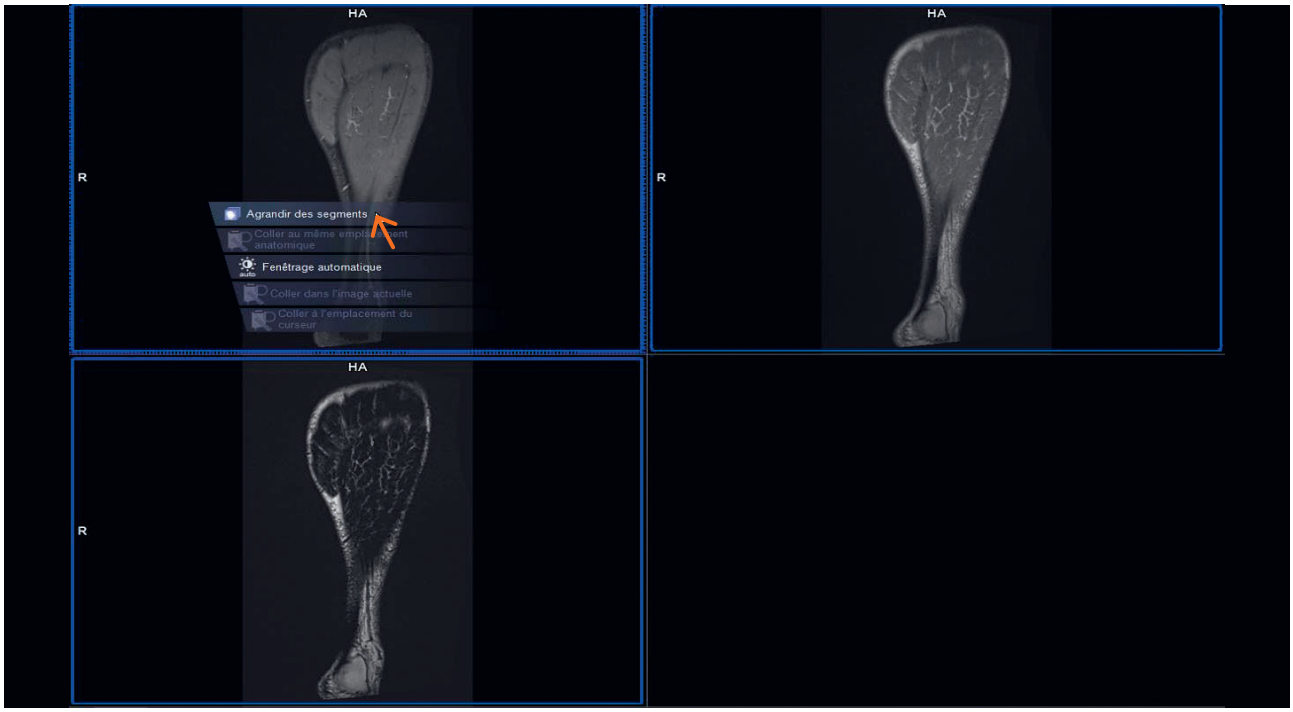
1 New display of series in *syngo*.via VB40.

2 New series display types.

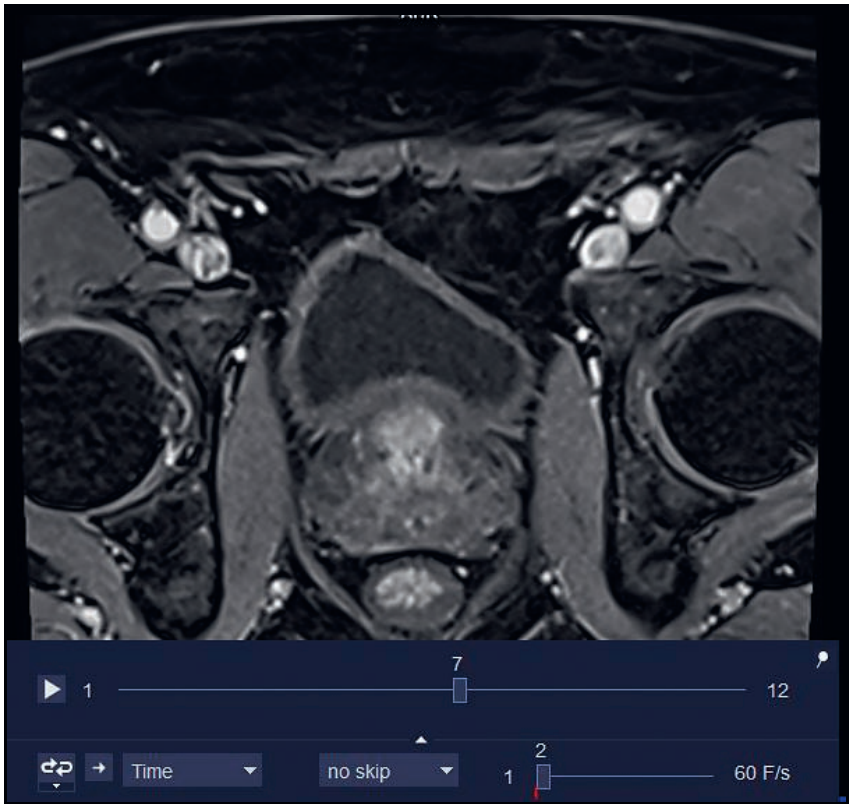
3 Rapid changing of display mode and slice thickness.



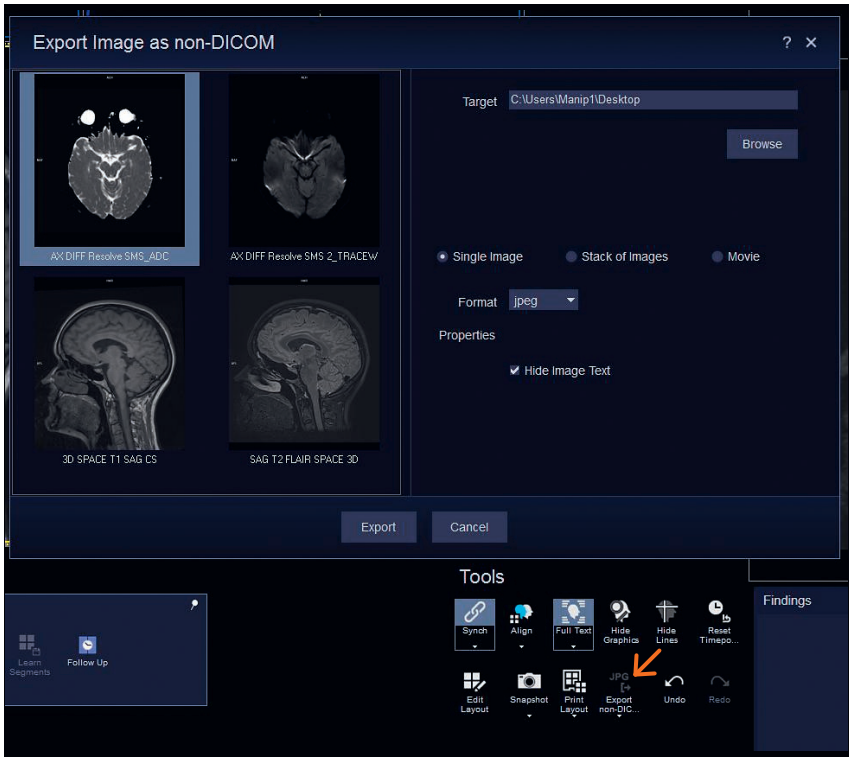
4 Segment learning button of the Smart Layout tool.



5 Enlarging segments.



6 4D cinematic imaging tool.



7 Exporting an image non DICOM format.

MR Prostate

A new feature for **automatic segmentation of the prostate gland** is now available from the Biopsy Support (Fig. 8A). An automatic prostate volume calculation is carried out if the system has been configured to do so (Fig. 8B). It can also be generated again afterwards at any time. Radiologists can then modify the contours according to their expectation, by using the manual correction tools (Fig. 8C).

A quick and easy configuration needs to be carried out once by clicking on the settings icon and indicating which series to use (depending on the sequence names used on the user's site): Prostate segmentation works for T2-weighted TSE or SPACE cross-sectional series (Fig. 9 orange arrow).

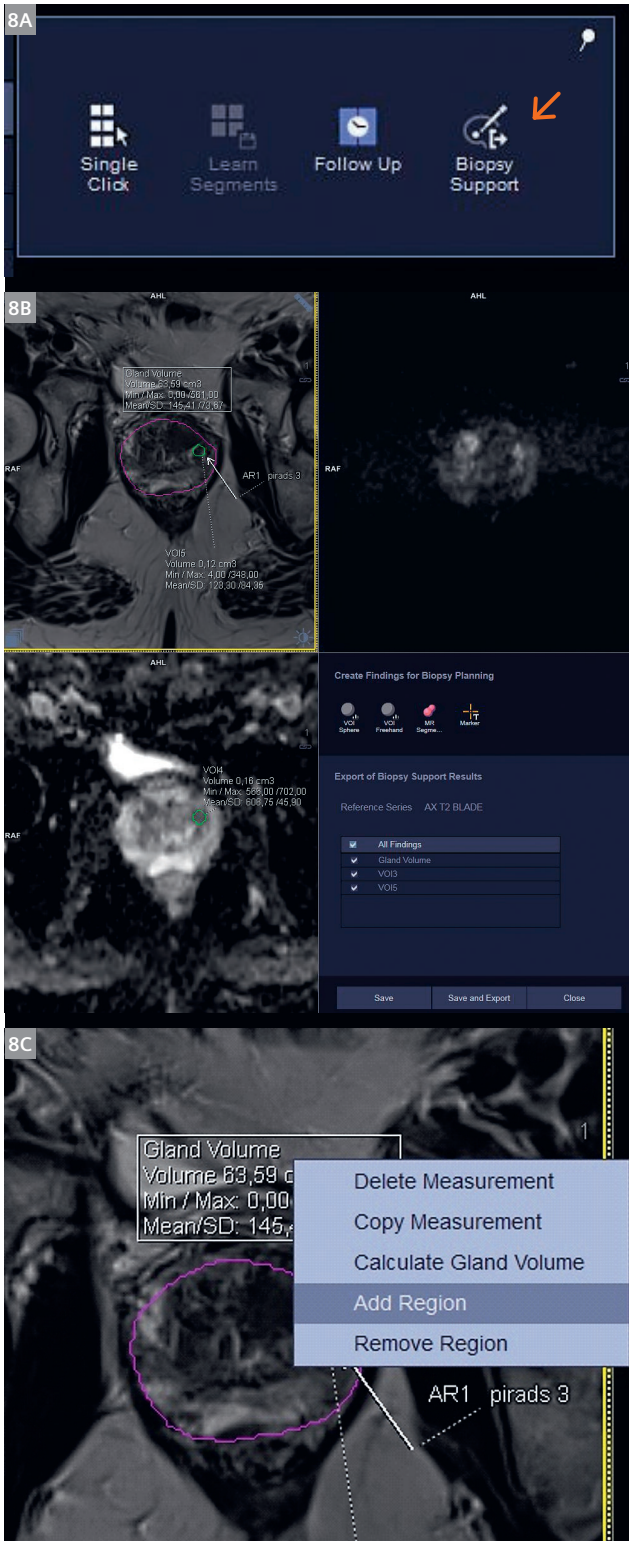
Note that it is still possible to analyze the gland volume using the three measurements technique. For that, you need to hold down the SHIFT button while drawing the three measures (one in each standard anatomic plan) and right-clicking on 'Calculate Gland Volume'.

The user can also create VOIs to define a target for an US-guided biopsy (Fig. 8B). The data can be exported to the PACS or to any fusion biopsy support system with the RTSS (Radiotherapy Structure Set) standard format. The fusion can then be used as a reference during the biopsy.

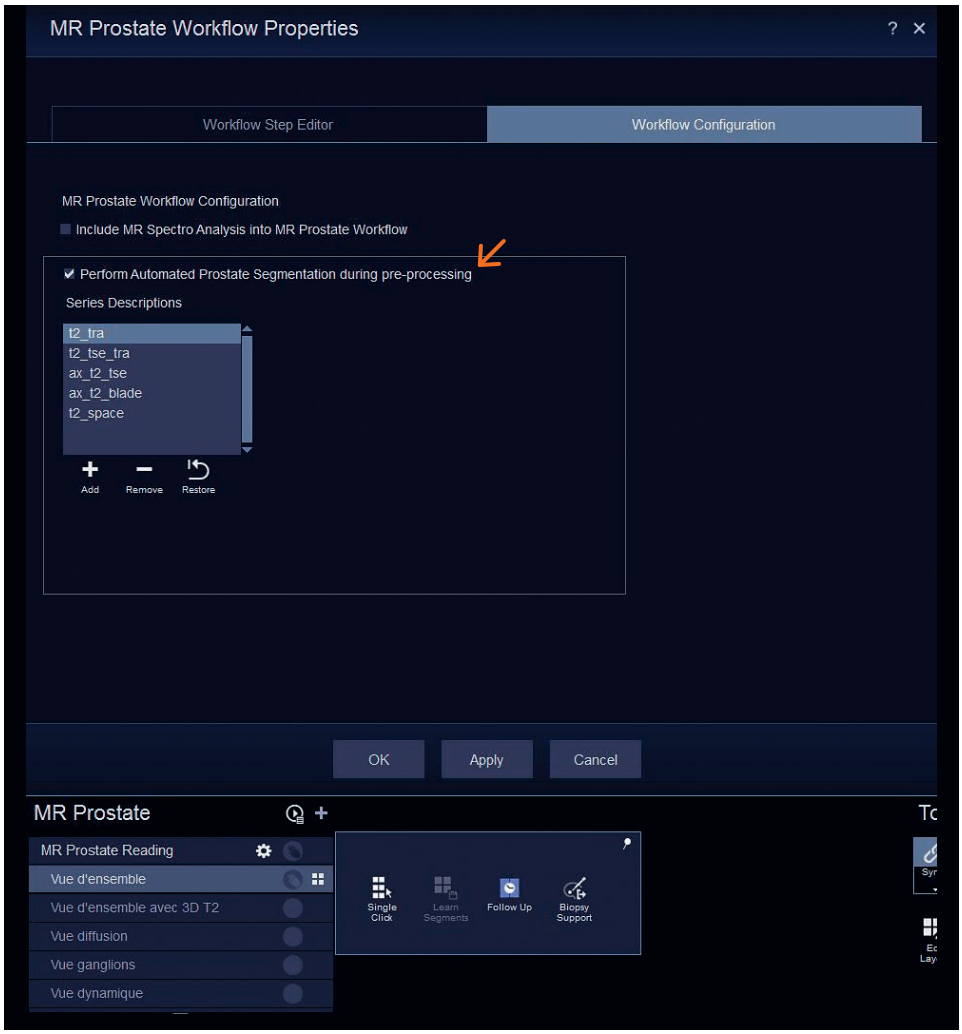
Displaying the MR Spectro Analysis step can also be disabled in the configuration settings to avoid overloading the list of viewing stages (Fig. 9).

The report has been completely revised. The display is now clear and much more complete, including the color scheme and PI-RADS 2 .1 report (see the 'Findings Wizard' section for the other workflows).

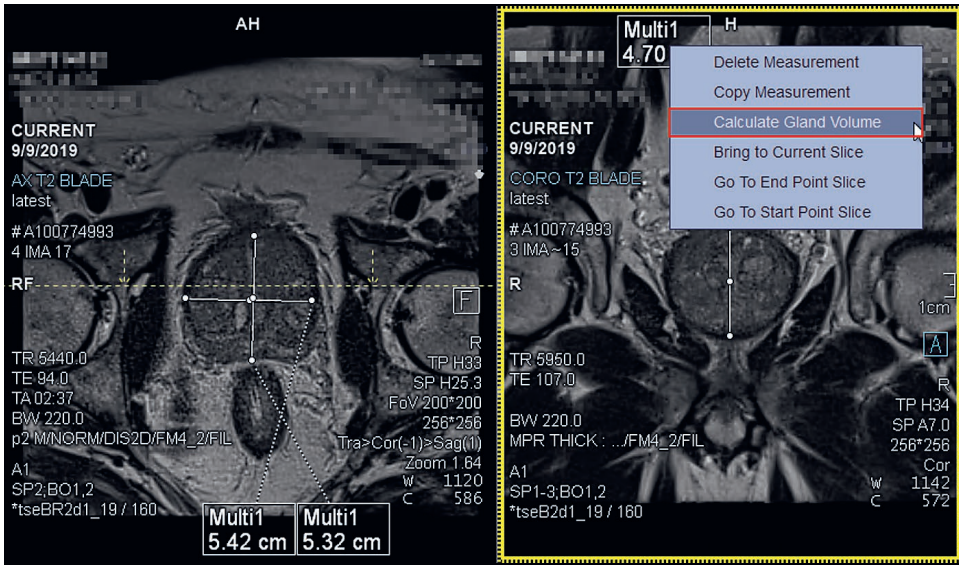
The report can be exported in various formats: CSV or standard PDF format (Fig. 12).



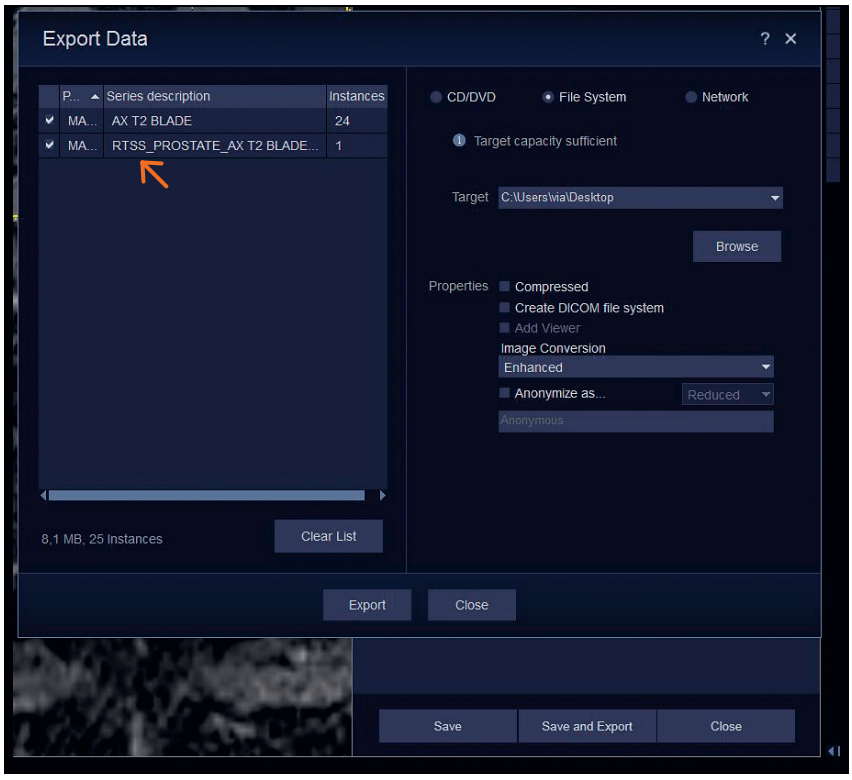
8 Prostate segmentation tool.



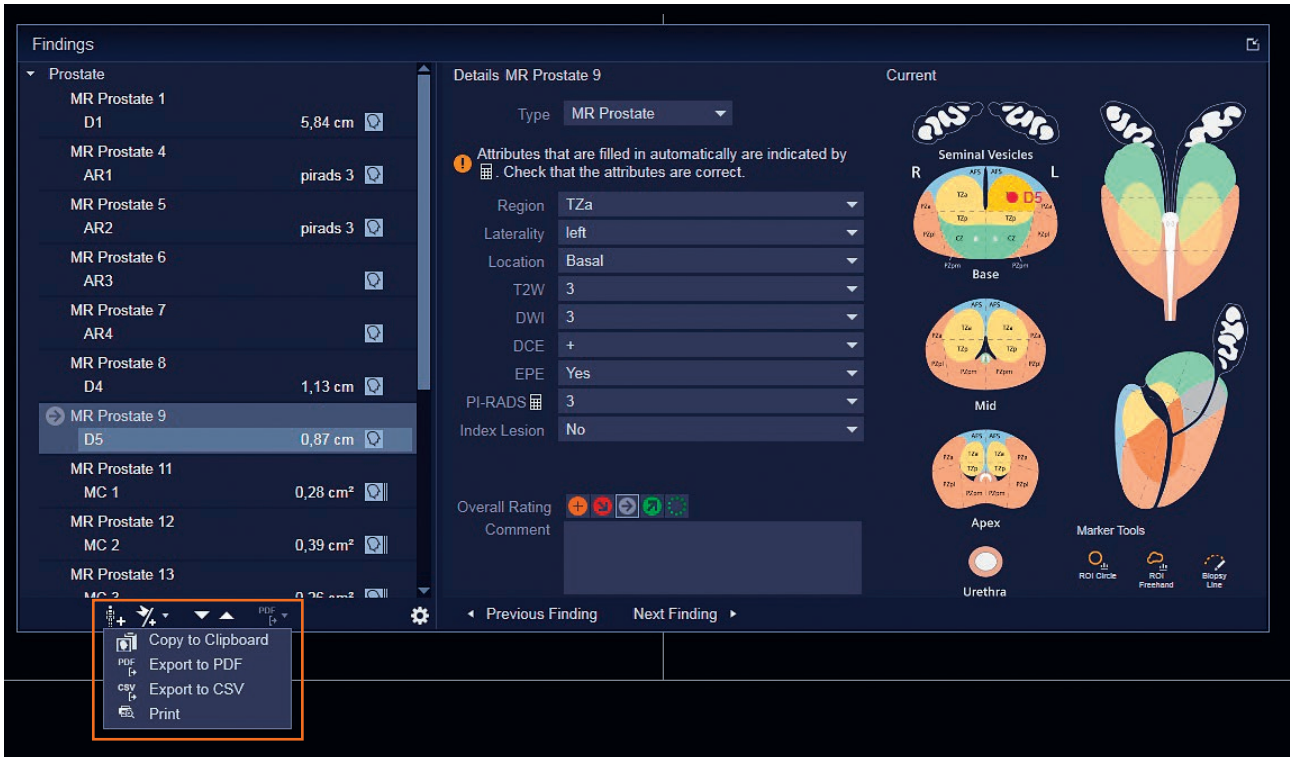
9 MR Prostate workflow configuration.



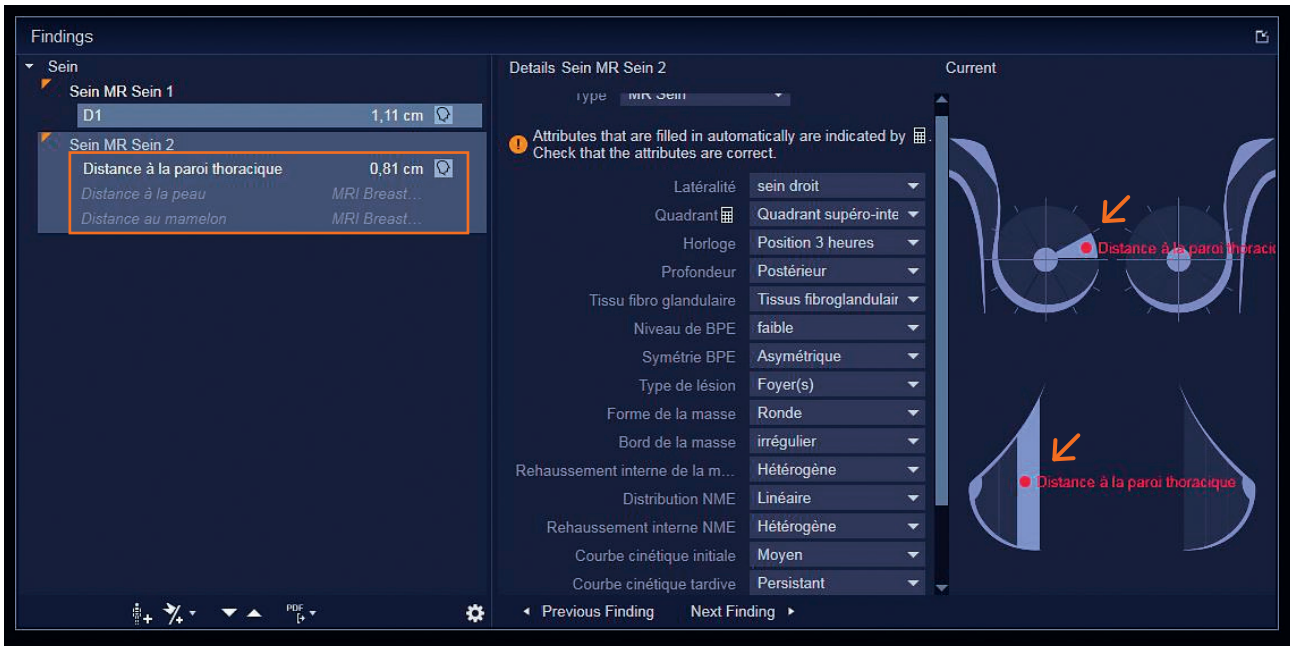
10 Analyzing the gland volume in MR Prostate.



11 Exporting biopsies in RTSS format.



12 Report and Findings Navigator.



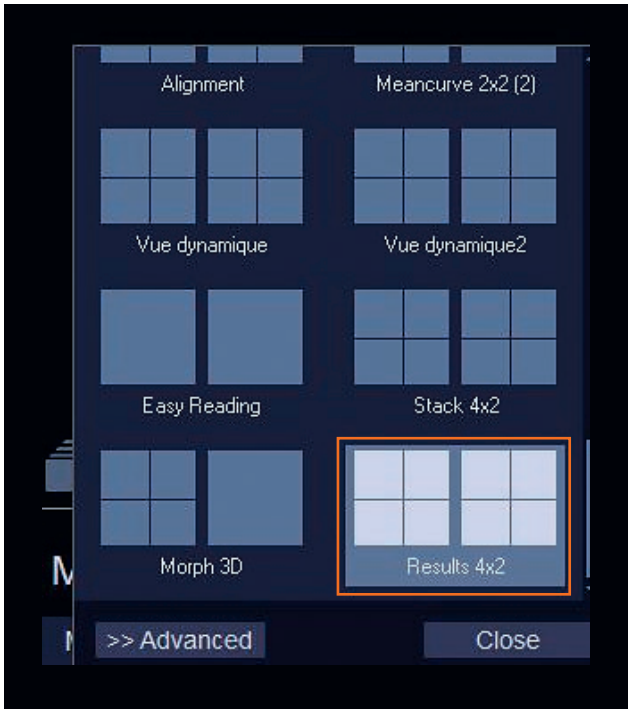
13 Findings Assistant in MR Breast.

MR Breast and Findings Assistant in the MRI workflow

The **Findings Assistant** has been developed, so that it is now easier to manage the measurements and snapshots made by the interpreting physician. It is now possible to group the findings together, to comment on them, and to classify them according to their level of severity.

For MR Breast, the distances to the chest wall, skin, and nipple are displayed in the report. The measurement determined can then simply be defined using the corresponding formulation (Fig. 13). The final report is clearer and easier to read.

Note that a **new layout view** available in the Siemens layout gallery makes it possible to display all the measurements and findings made by the radiologist for the examination (Fig. 14).



14 New Findings layout.

MM Reading

Mainly used for studying previous cases, the 'Previous study' and 'Next study' icons have been added, making it possible to move directly from one examination to another (Fig. 15).

New layouts specific to MRI studies are now available depending on the body region being investigated (Fig. 16).

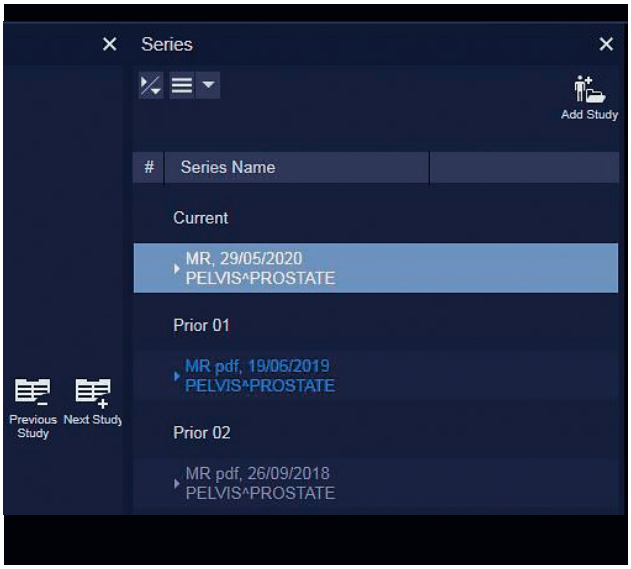
MRI-specific tools have also been added to the MM Reading workflow.

Calculation tools allowing, in particular, the subtraction or calculation of diffusion b-values or ADC values are now available as well as the MR Composing tool which is used to group different series together in order to generate one overall series (for example, to obtain a cervico-thoraco-lumbar spine series).

Images with the same orientation are placed side by side in Easy Reading mode for easier analysis.

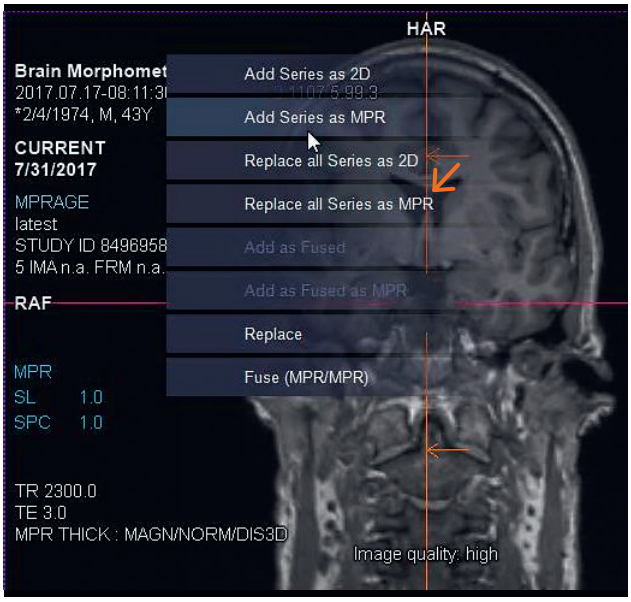
The display of several volumes in MM Reading has been enhanced with the 'Add Series as MPR' option, enabling direct 3D comparison of several series (Fig. 17).

Windowing can now also be reset with a simple click of the mouse.



15 Studying previous cases in MM Reading in *syngo*.via VB40.

16 New MRI layouts in MM Reading.

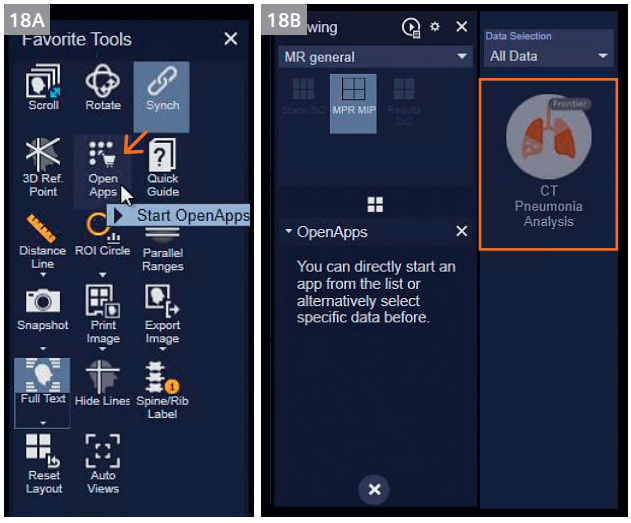


17 New rapid display options in MM Reading.

syngo.via OpenApps

It is now possible to open and use software available on Siemens Healthineers' Digital Marketplace in MM Reading (for a fee).

An icon is displayed, making it possible to switch views between *syngo*.via and the partner software integrated into *syngo*.via.



18 OpenApps icon in MM Reading.

Flight Recorder

A new **Flight Recorder** icon has been added to the desktop and can also be accessed from the top bar. This function makes it possible to take screen shots, make videos, and/or add comments when an incident occurs on *syngo*.via (Fig. 19).

The data is saved locally and directly on the *syngo*.via server. Siemens remote support can then access the saved items at any time in order to identify any problems more quickly and precisely.

19 Flight Recorder.

MR Oncology

New functions have been added/previous functions have been enhanced in MR Oncology such as with the new **Findings Assistant** tool.

The way in which the findings are organized has changed in VB40, making it possible to better define all the information relating to the finding that has been created.

Let's take the example of a lesion that has been identified and measured using distance lines in MR Oncology.

In the Findings section, a **classification** is carried out depending on the type of lesion for each workflow. Arrows on the right of each section/sub-section and finding make it possible to define the entire lesion in detail. In the lesion type, it is now possible to define details about the body region (Fig. 20).

Furthermore, the arrow to the right of 'MR Oncology 1' indicating the lesion and the associated finding provide access to details about the lesion observed and allow to link this lesion to another previous finding (Fig. 21).

It is now possible to carry out various actions directly from the Findings Assistant in *syngo*.via VB40:

- Create multiple findings
- Estimate the volume of the lesion
- Track the findings over time via previous examinations
- Ascertain details about the location of the lesion
- Follow-up in accordance with RECIST criteria

The volume of a lesion can be estimated by drawing distance lines along at least two different planes of orientation (Fig. 22):

1. Place the reference point on different planes (use the keyboard shortcut 'R').
2. Hold down the 'Shift' key on the keyboard while drawing the distance lines along the different planes (keyboard shortcut for distance lines: 'D').
3. The distance lines will be added to the automatically-generated finding.

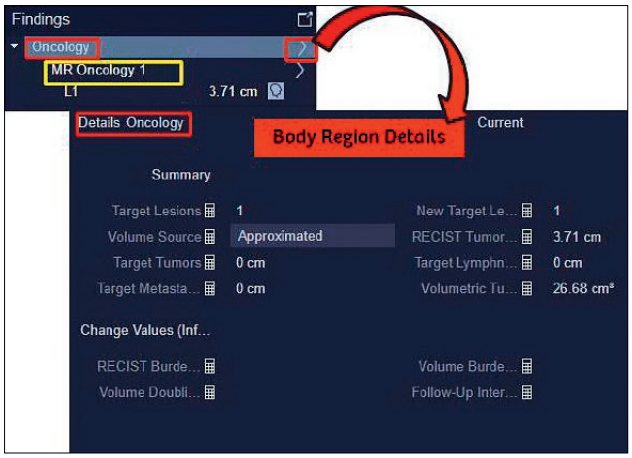
Tip: Use a layout in 3D MPR mode, e.g., the '3D MPR' layout, to directly display several planes in the same 3D series.

The finding can be added to an icon in the 'Details' section, and the body region in question can be filled in (Fig. 23).

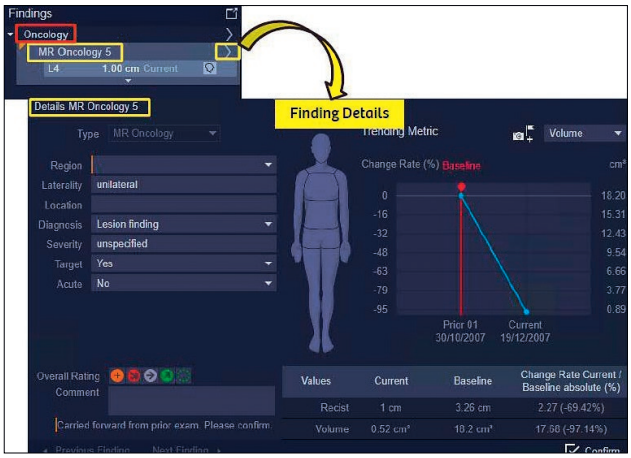
Several findings can be tracked at once using several time points.

To do this, select the different findings corresponding to the same lesion (CTRL + left-click), then right-click on 'Track selected Onco Finding' (Fig. 24).

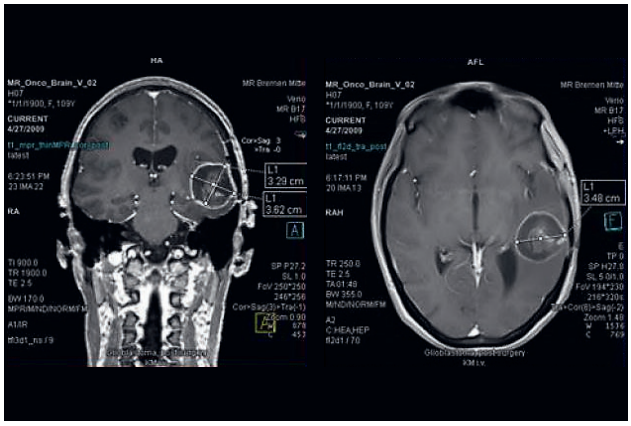
The findings will then be grouped into one finding for the lesion in question, together with all the details about the lesion and its development: Trending curve / RECIST / Volume (Fig. 25).



20 MR Oncology Findings Assistant.



21 Details of findings in MR Oncology.



22 Volume estimation.

23 Estimating the volume in the Findings Assistant with body region.

24 Tracking findings on several time points.

25 Trending curve in MR Oncology.

MR Oncology – OncoTrend

General information

MR Oncology's **OncoTrend** tool enables **ADC-based whole-body diffusion evaluation** for oncology follow-up. This makes it possible to produce efficient and reproducible measurements with associated quantitative findings.

The intuitive back-mapping of active disease and reactive areas on DWI images of the whole body helps oncologists to understand and interpret the complex information from the whole-body MRI (Fig. 26).

Among other things, this tool helps to support the standardization of whole-body MRI in order to determine the response to a treatment and to monitor bone diseases, in particular, based on diffusion-weighted imaging (DWI).

The icon for the **OncoTrend** tool can be found on the logon page of the MR Oncology workflow (Fig. 27).

The layout enables high ADC and b-values to be loaded by default. The required b-value series can also be calculated manually with the aid of the 'Calculate ADC and b-value' calculation tool.

When you click on the OncoTrend tool icon, the OncoTrend workflow commands are available in the OncoTrend layout segments.

To start the evaluation the user performs a threshold-based segmentation based in MPR or MIP view (Fig. 28).

By default, the segmentation mask is created over the images of the calculated b-value. The threshold can then be modified using the slider in the menu at the bottom of the screen.

Areas such as the brain and kidneys with a naturally high signal intensity without metastases must not be included in the calculation.

The mask can then be fine-tuned with the aid of the 'Punch tool' which can only be applied in the MIP and MPR views. It behaves differently depending on the display type (Fig. 29):

- In MPR view, the ROI is only applied on the visible slice.
- In MIP view, the ROI is applied for the whole volume.

To display the histogram, select 'Display histogram' and select the segment in which you wish to display the histogram. The mask is copied onto the ADC image and the corresponding VOI histogram is calculated. After confirming by clicking OK, the histogram is created, and the back-mapping is automatically applied to the image with the highest b-value.

Focusing the view on the response areas in relation to the active disease areas

On the b-value images, the back-mapping display can be toggled between the high and low values (Fig. 30).

High: MIP – The therapeutic response areas (higher ADC value) are displayed with higher priority.

Low: MinIP – The areas containing the remaining tumor load (low ADC value) are displayed with higher priority.

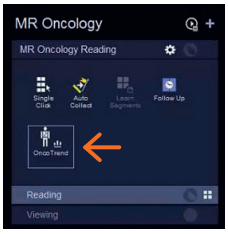
Quantifying the histogram

Users can compare the histograms with the aid of the 'Show Statistics' icon (Fig. 31A).

If the two histograms are selected, the difference between the values is calculated and displayed.

A snapshot of the statistics table can be recorded for the PACS and the table can also be exported to a spreadsheet in CSV format (Fig 31B).

26 Display of OncoTrend in MR Oncology.

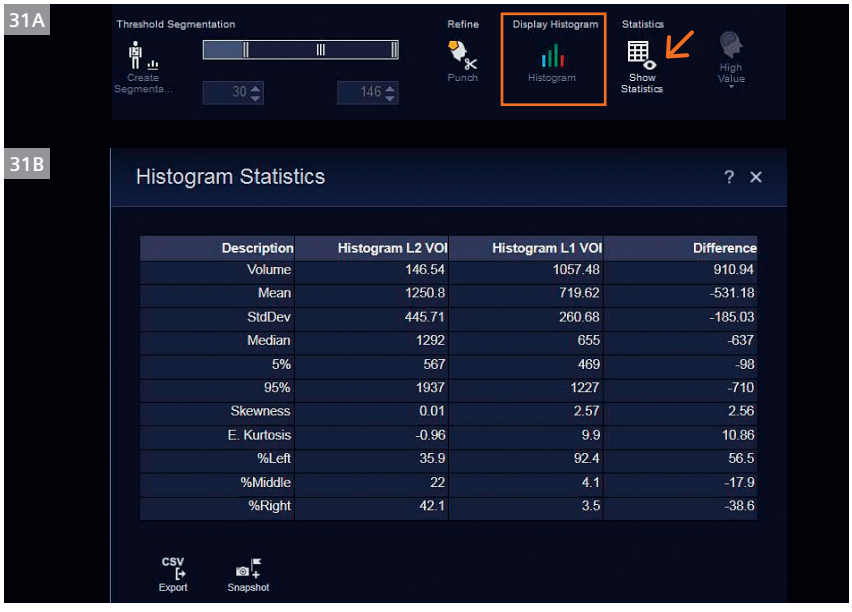


27 OncoTrend tool in MR Oncology.

28 Threshold segmentation.

29 Threshold segmentation.

30 Threshold segmentation.



31 OncoTrend histogram.

MR Neurology

The new functions in MR Neurology enable tracking of brain morphometry and the use of 'Perfusion PACS Ready'.

For **brain morphometry** (Fig. 32), a warning dialog box is displayed if image blending is used with distortion correction on data without distortion correction.

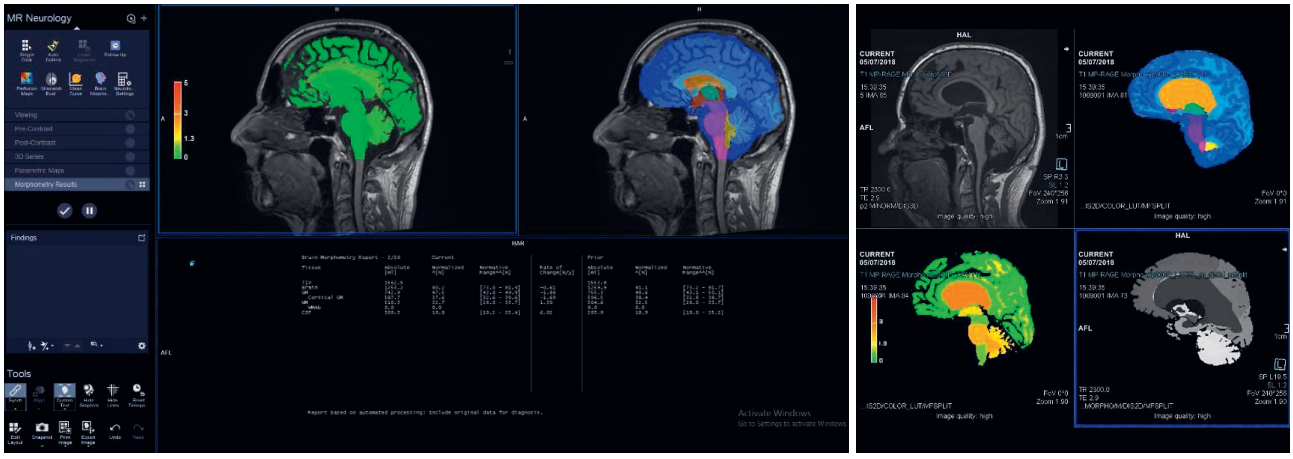
In addition, for patient tracking, the rate of change is now calculated between two time points (Fig. 33).

The trend graphics are then added in relation to the volume.

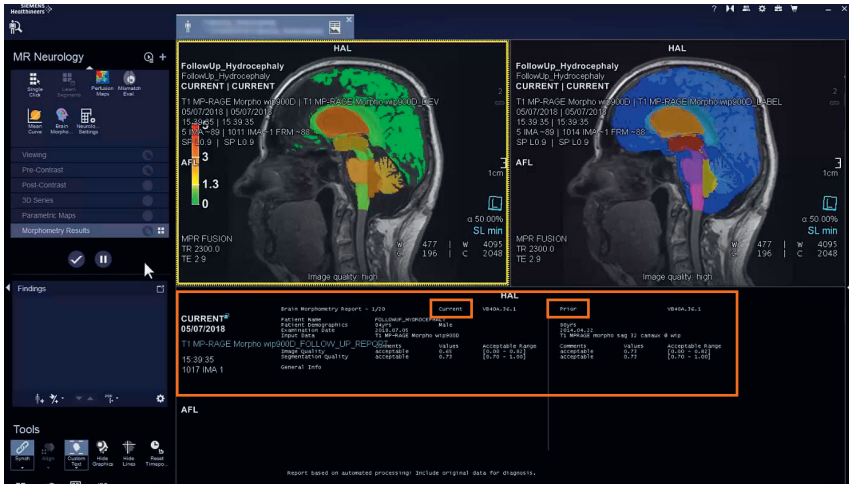
It is then possible to generate findings from a maximum of five DICOM series: volume report, label map, fused label map, deviation map, and fused deviation map.

Processing can be triggered interactively but it can also be fully automated and is then performed in MR Neurology's preprocessing area ('**PACS Ready**'). The PACS Ready feature is available for brain morphometry results as well as for parametric maps in neuro perfusion.

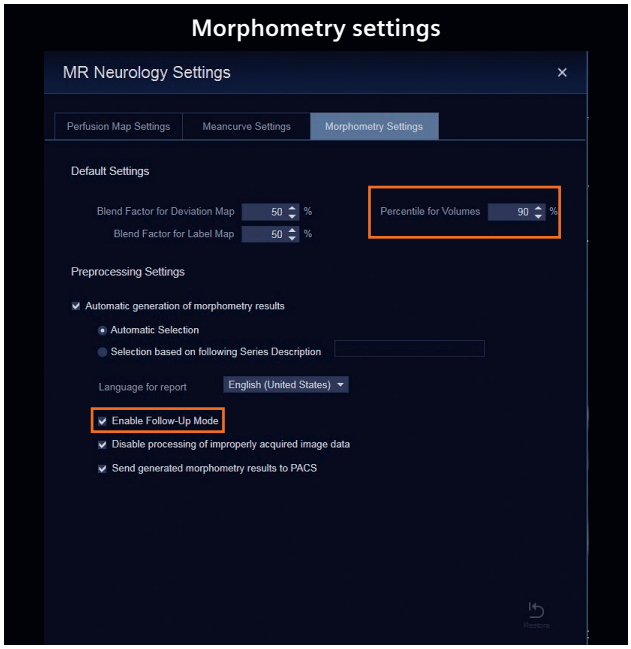
The findings can be analyzed in a dedicated findings step and are automatically sent to PACS (Fig. 34).



32 Morphometry.



33 Creation of morphometry findings with comparative analysis.

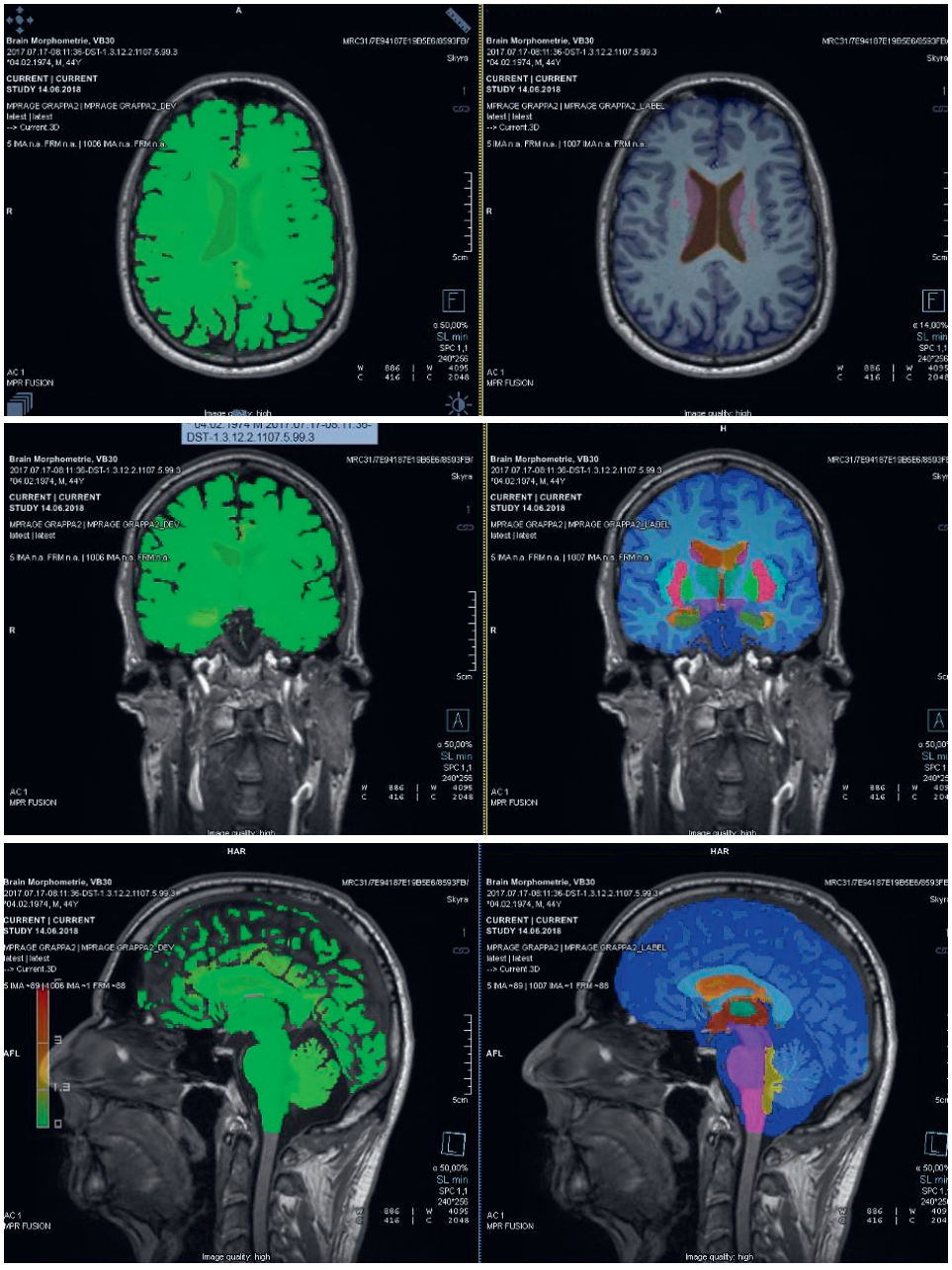


34 Morphometry settings for tracking.

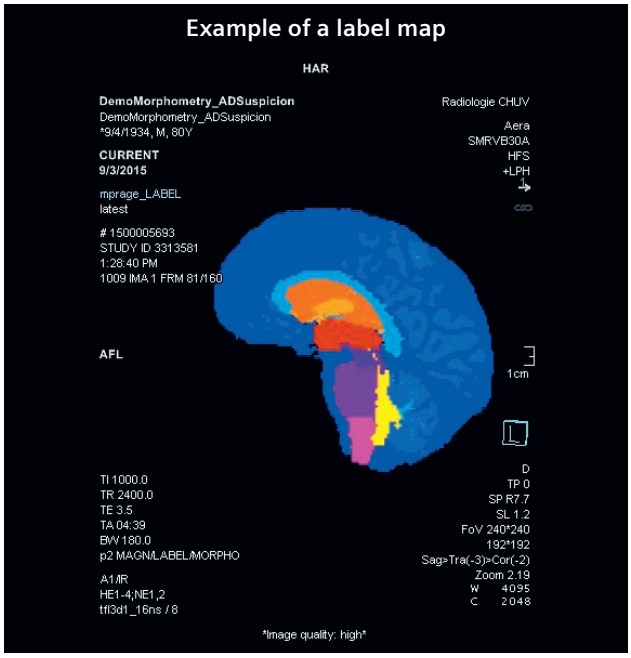
Scan/DICOM parameters	Value for 1.5T	Value for 3T
Manufacturer	= Siemens Manufacturer DICOM tag contains “Siemens”	
Image Type	Contains NORM One of the image type attributes is “NORM”	
Magnetic Field Strength	1.5T	3T
Repetition Time	TR ≥ 2400 ms	TR ≥ 2300 ms
Echo Time	≤ 10 ms	
Inversion Time	TI = 1000 ms	TI = 900 ms
Pixel Spacing (X & Y)	≤ 2 mm	
Flip Angle	FA = 8 deg	FA = 9 deg
Slice Thickness	≤ 1.2 mm	
MrAcquisitionType	3D	
3D Matrix size (Rows x Columns x SlicesPerSlab)	≤ 11534336 Recommended parameters: rows = 256, col = 256, slicesPerSlab = 176 = 256 * 256 * 176 = 11534336	
Contrast bolus agent	Not used No contrast agent used	
Orientation	Sagittal	
In-plane phase encoding direction	not “COL”	
Auto-align matrix	Scan was done with auto-alignment	
Slice Oversampling	sliceOS ≤ 0.3	sliceOS ≤ 0.2
FoV read (VoxelReadoutFoV)	fov ≥ 240	fov ≥ 256
FoV phase (VoxelPhaseFov / VoxelReadoutFov (ratio))	Ratio = 1	Ratio ≥ 0.9
Magn. Preparation	= 2	
Reconstruction (mode)	= 1	
Base Resolution	BR = 192	BR = 256
PhaseResolution	= 1	
PhasePartialFourier	= 16	
PAT Mode	> 2	
PAT Acceleration Factor	≤ 3	
No. of slab groups	= 1	
No. of slabs	= 1	
No. of excitations	≤ 192 If Swap re-ordering == (1 OR 2) NoE = slicesPerSlab * (1+ sliceOverSampling) else NoE = phaseEncodingLines * (1 + phaseOverSampling)	
SliceThickness * slicesPerSlab * (1 + sliceOverSampling)	≥ 211.2 Recommended parameters: thickness = 1.21 slicesPerSlab = slicesOverSampling = 0 1.2 * 176 * (1 + 0) = 221.2	
CoilCombineMode	= 2	
PE Swap Re-ordering	1 or 2	
AsymmetricEcho	= 1	
PixelBandwidth	170 ≤ BW ≤ 190	230 ≤ BW ≤ 250
Interpolation	Tag should not be present	
ImageFilter		
Normalize		
BiFicFilter		
RawFilter		
EllipticalFilter		
EllipticalScanning		

Calculation criteria in the user guide

The calculation of the morphometry results is contingent upon compliance of the input MPRAGE sequence protocol with a widely accepted standard. This table lists all criteria for the input MPRAGE protocol.



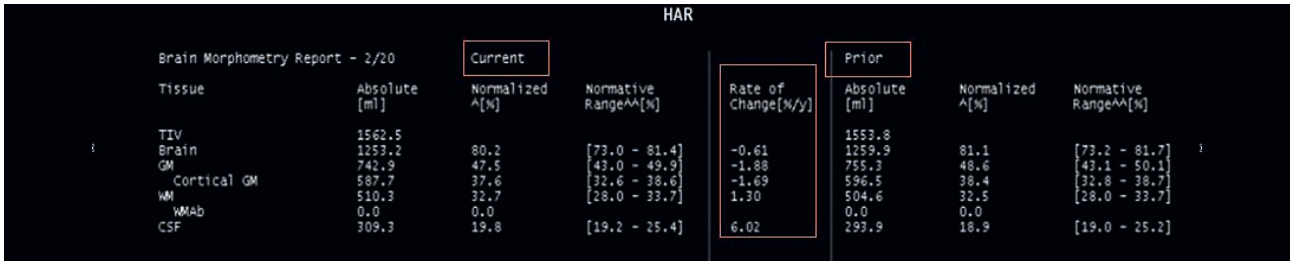
35 Anatomical image fusion and morphometric map.



36 Morphometric label map and its legend.

Color codes for different Brain areas			
	Lobar WM (white matter): • Frontal lobe • Parietal lobe • Occipital lobe • Temporal lobe • Corpus callosum • Deep WM • Cerebellum WM		Lobar GM (grey matter): • Frontal lobe • Parietal lobe • Occipital lobe • Temporal lobe • Clingulate gyrus • Cerebellum GM
	CSF		White Abnormal (WMAb)
	Thalamus (left/right)		Lateral ventricle left
	Caudate (left/right)		Lateral ventricle right
	Putamen (left/right)		3rd ventricle

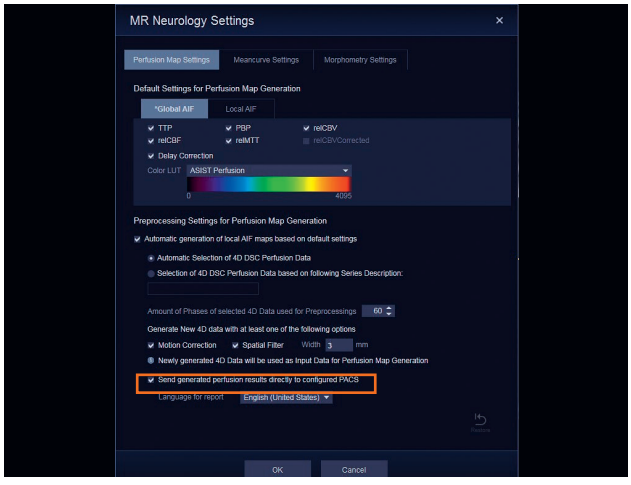
Color codes of the label map
In the label maps each brain region is visualized in a different color. Refer to the color assignments above.



37 Morphometric label map.
Volume estimations are calculated for the different brain regions, in both absolute and relative (percentage of total intracranial volume) values. For each region of the brain, a normative range is displayed corresponding to the 10th and 90th percentiles of a healthy population. Two time point reports with findings for each time point. A rate of change is displayed for each region of the brain.

The standard MPR *syngo*.via fusion (Fig. 35) can be used to check the findings of the segmentation. See figures 36 and 37 for a reminder of the colors assigned to each body region and the parametric volume report in tracking mode.

For **cerebral perfusion** (Fig. 38), it is possible to choose whether or not to send the AIF maps automatically to the PACS after preprocessing.



38 Configuration to send AIF maps automatically to the PACS.

MR Cardiac Analysis

For multi-phase cases, a user-defined layout can be created (Fig. 39A).

It is now possible to create private layouts with spatial and/or temporal synchronization. It is now also possible to set series in the most relevant segment position by dragging and dropping series (for example, SA and LA) and different time points (for example, sorted into columns) in the layout (Fig. 39B).

The synchronization tool can also be used to set up a movie synchronization group (Fig. 39C).

It is now possible to adapt the Endo/EPI contour more easily by moving the visible control points with the aid of the '**Control Point Edit**' tool (Fig. 40).

- Switch between Endo/Epi with the respective buttons (or the Alt + A shortcut).
- Add more control points simply by clicking on the contour or delete existing control points by right-clicking on them.
- The changes are propagated in the same way as with the Nudge tool.

Furthermore, all the relevant values (SV, EF, TD/TS volume, Mass) are now always visible for both ventricles in the TVG segment (Fig. 41). This facilitates comparison of the left and right ventricles.

It is now also possible to **modify the preferred normal ranges according to other criteria**, for example, on different publications or for pediatric patients (Fig. 42). You can view these normal ranges according to criteria in the Findings Details of the Findings Navigator, and edit the normal values if needed.

Don't forget to select the 'Edit' button again to save the changes.

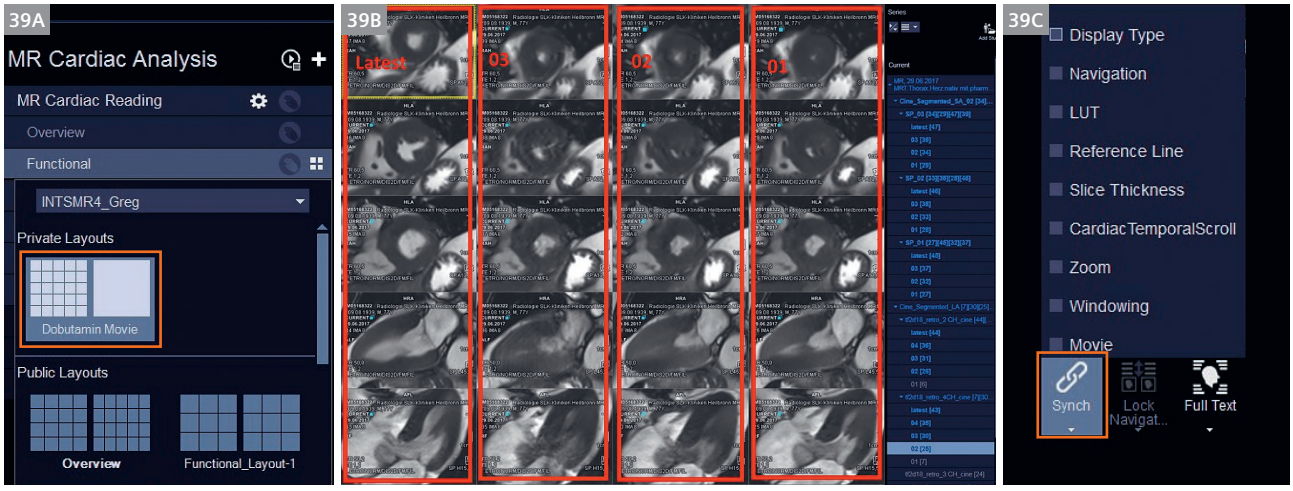
You can always 'Reset' the normal ranges to the factory settings after confirming the safety pop-up window (Fig. 43).

The normal values can be modified for all the available options (VG, VG NORM, VD, VD NORM).

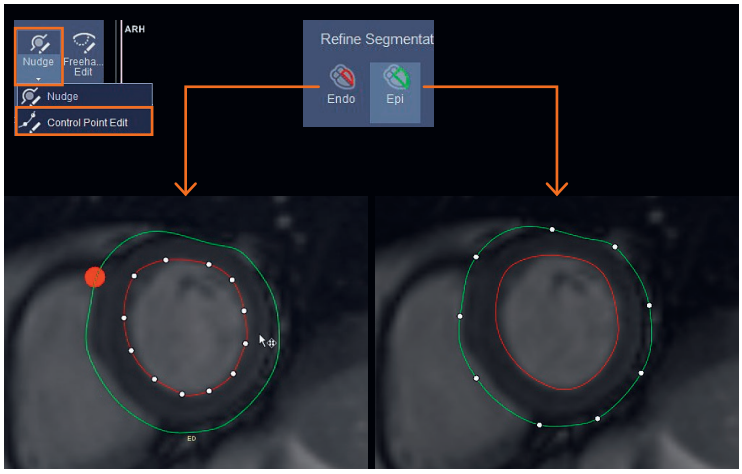
The modified normal values are saved by the user; consequently, a pediatric radiologist can use different values.

TD/TS mode can now be enabled by default when opening the MR Cardiac Analysis application. Open 'MR Cardiac Function Properties' and enable the contour drawing 'only within ED/ES' in your chosen mode (Fig. 44). Wall thickness is automatically included in the findings.

It is also possible to create a VG/VD finding directly from the 'Finding Details' dialog box (Fig. 45).

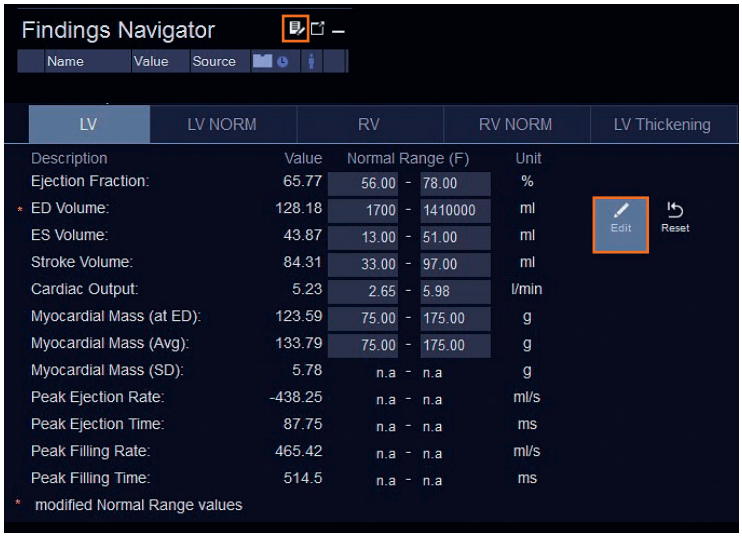


39 New configuration functionalities in MR Cardiac Analysis with the creation of a private layout **(39A)** and the possibility of spatial and/or temporal synchronization **(39B)** and **(39C)**.

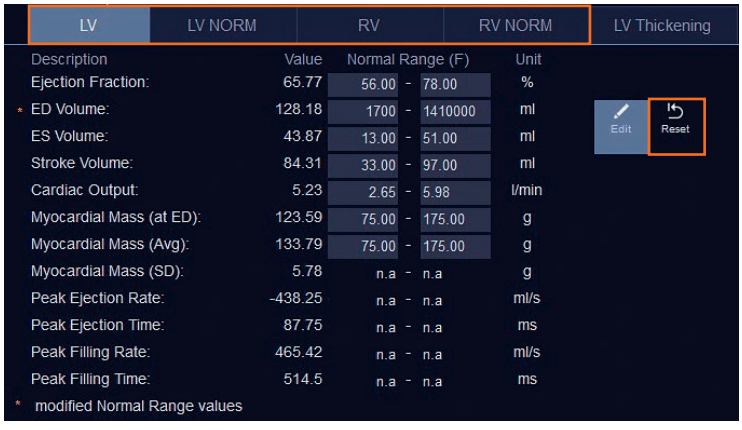


40 Control Point Edit tool.

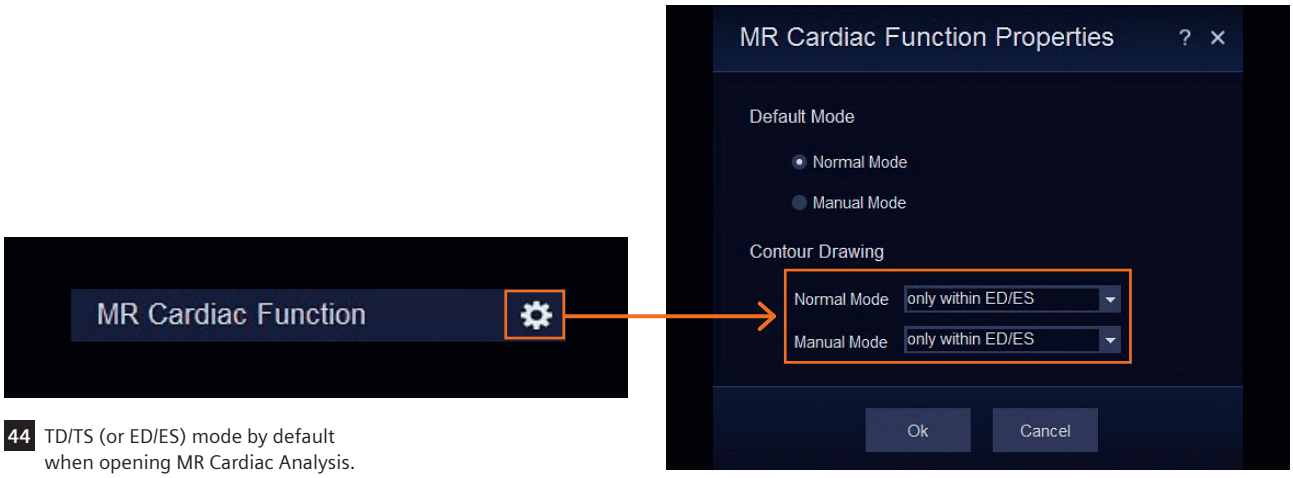
41 Displaying relevant values in the TVG segment.



42 Modifying the normal value ranges according to criteria.



43 Resetting the normal values.



44 TD/TS (or ED/ES) mode by default when opening MR Cardiac Analysis.

45 Creating the finding in the “Finding Details” dialog box.

MR Spectroscopy

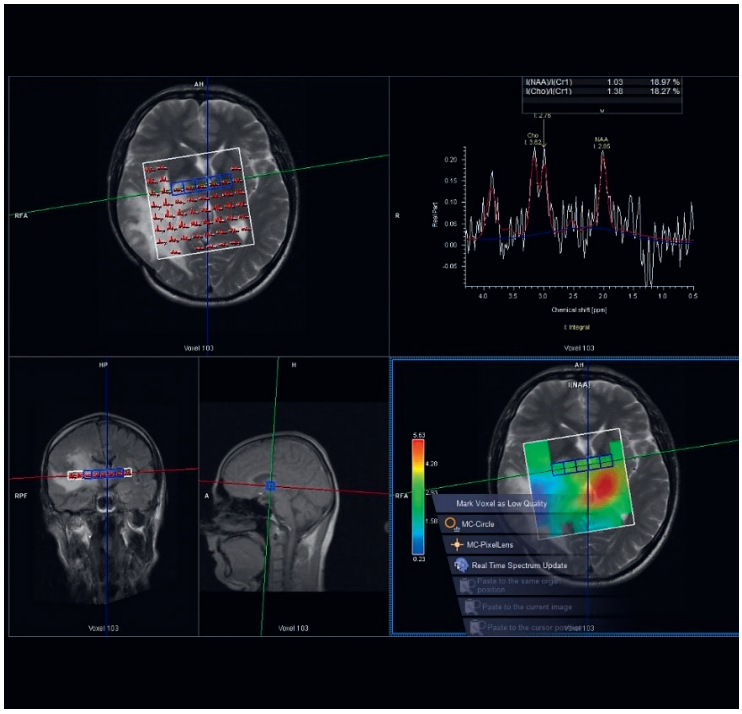
Several improvements have been made to the MR Spectroscopy workflow.

It is now possible to view the **selection of multiple voxels** in all orientations (Fig. 46). This makes it possible to adjust all the voxels selected in high/low quality at the same time.

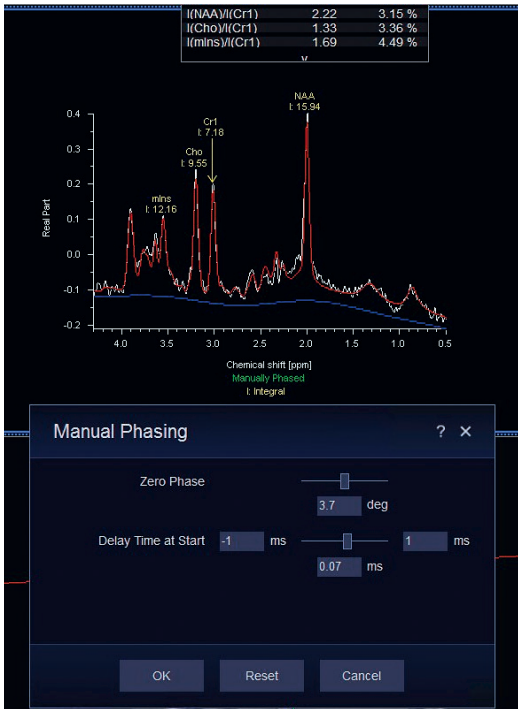
To do so, all the selected voxels must be of the same category (high quality or low quality). Voxels are selected simply by holding down the CTRL key and left clicking with the mouse.

In addition, **the display's performance in manual phasing** has been improved (Fig. 47).

Manual phasing is a tool from the Corner menu which is available for advanced users (requires the spectro_research license).



46 Selecting multiple voxels in the different planes.



47 Manual phasing of the spectrum.

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