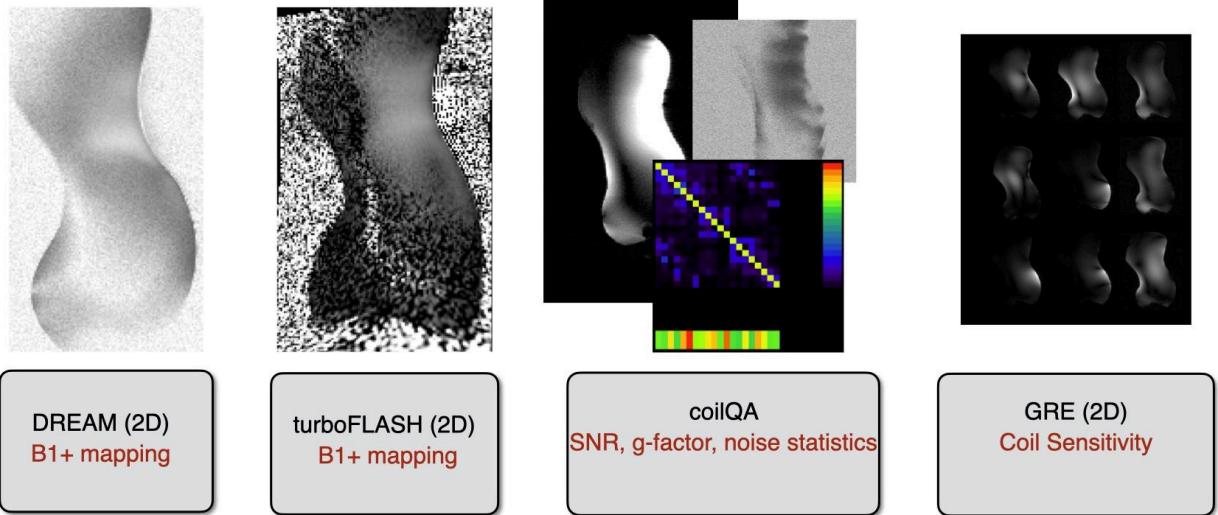


7 T C-Spine Coil QA Protocol: Spinoza V6 Phantom Acquisition Guidelines



This Standard Operating Procedure (SOP) accompanies the 7 T c-spine coil QC protocol available at: <https://github.com/spinal-cord-7t/coil-qc-protocol>

| | |
|---|-----------|
| Phantom positioning and subject registration | 3 |
| A note on Reference Voltages | 4 |
| Localizer | 5 |
| TurboFLASH B1+ mapping | 8 |
| Re-acquire the TurboFLASH B1+ map with optimal Reference Voltage for the center of the FOV, as described below. | 9 |
| DREAM | 14 |
| Large FOV acquisition | 14 |
| Medium FOV acquisition | 16 |
| Re-acquire the Medium FOV DREAM B1+ map with additional Reference Voltages | 17 |
| coilQA | 21 |
| Large FOV sagittal acquisition | 21 |
| Medium FOV sagittal acquisition | 22 |
| Medium FOV axial acquisition | 24 |
| GRE | 26 |
| Ensuring the correct VOPs are loaded | 28 |
| RF_map B1+ mapping | 29 |
| TurboFLASH B1+ mapping | 33 |
| coilQA | 34 |
| Large FOV sagittal acquisition | 34 |
| GRE | 35 |

Phantom positioning and subject registration

Position the phantom within your coil. As much as possible, try to align the center of the coil with the center of the neck of the phantom.

Mark the isotenter location, via the laser, approximately at the center of your coil.



Phantom Version: Spinoza V6

Phantom fill material:

15.4 liter solution containing demineralized water (641 ml/L), sugar (513 g/L), salt (16.5 g/L), mouthwash (40 ml/L), agar (7.5 g/L).

MRI console:

- Register the Subject
- Select “C-Spine” for “Body Part and Laterality”

A note on Reference Voltages

Through this document, the Reference Voltage is adjusted for several scans. Due to differences in local hardware and potentially, local limitations, this procedure is described in color-coded boxes throughout the document.

Sites with local Reference Voltage Limits should follow the Salmon-Coloured Boxes. A local limit refers to a limitation on Reference Voltage imposed by your scan site. If for reasons of safety, equipment, etc, you can not exceed this voltage, this applies to you.

If you are a Terra site without local Reference Voltage Limits, you need to follow the Light Orange Coloured Boxes.

If you are a **Magnetom site that can not automatically adjust the Reference Voltage**, you need to follow the Light Green Coloured Boxes.

For **TurboFlash B1+ mapping** and **DREAM** sequences, scans have to be re-acquired using a new Reference Voltage, typically one higher than previously used. Such voltages might come up against hardware limitations, which are accounted for in the SOP.

Localizer

MRI console:

- Make the sequence editable by double-clicking on it.
- Do not run the scan until *Adjustment Step 1* and *Adjustment Step 2* are completed.

Sequence card:

- Ensure that all coil elements are selected by going to the *System > Coils* and selecting all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements.
- Adjust the central frequency as described in the blue box below.

Adjustments step 1: Manually measuring the central frequency

Start the central frequency adjustment by opening the manual adjustments page: Under the *Options > Adjustments > Frequency* tab, click *Go*. See Figure 1.

If the central frequency converges adequately, click *Apply*. Otherwise, manually set the cursor to the center of the frequency distribution, then click *Apply*.

If the frequency distribution does not show a clear peak, change the measurement sequence (under the *Sequence & Resolution* drop box) from STEAM 10Hz (default) to FID 10 Hz or FID 400 Hz, then click *Go*. Once the central frequency converges, click *Apply*.



Figure 1. Manual central frequency measurement.

- Adjust the Reference Voltage as described in the color-coded boxes and Figure 2 below

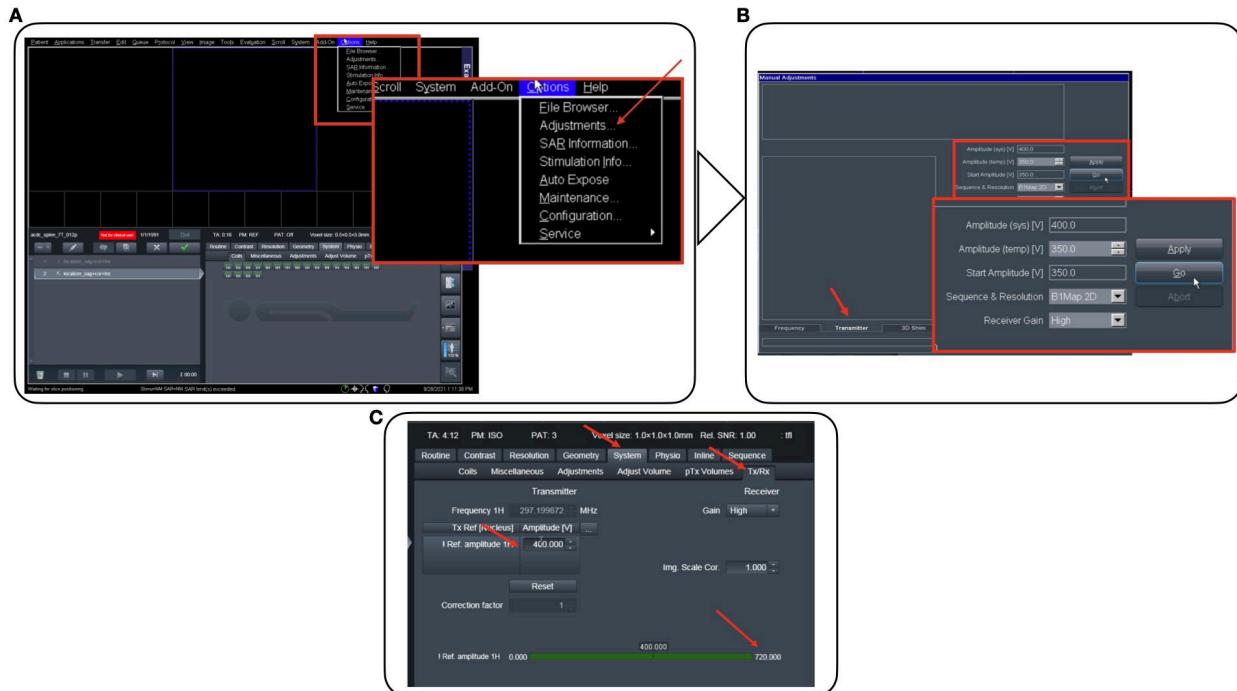


Figure 2. Manually setting the reference voltage and finding the hardware limit.

Adjustments step 2: Setting the Reference Voltage

For sites with limitations on the Reference Voltage:

- **MRI console:**
 - Go to *Options > Adjustments > Transmitter* and hit “go”. See Figure 2 (a).
 - Note down this Reference Voltage ($\text{RefVol}_{\text{Localizer}}$) and compare it to your local limitation ($\text{RefVol}_{\text{local_limit}}$).
 - Close the adjustments menu.

If $\text{RefVol}_{\text{local_limit}} > \text{RefVol}_{\text{Localizer}}$ then you are not affected by your local limit

- **Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, check that the amplitude has been updated to $\text{RefVol}_{\text{Localizer}}$, and update it if it has not. See Figure 2 (b).
 - Under *System > Tx/Rx > Ref. amplitude 1H*, check the maximum voltage that can be played out, note it down as $\text{RefVol}_{\text{HW_limit}}$, and fill in Table 1. See Figure 2 (c).

If $\text{RefVol}_{\text{local_limit}} < \text{RefVol}_{\text{Localizer}}$ then you are affected by your local limit, and all subsequent scans will be acquired in an underflipped regime.

- **Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{local_limit}}$. This step

- must be repeated for every subsequent scan. See Figure 2 (b).
- Under *System > Tx/Rx > Ref. amplitude 1H*, check the maximum voltage that can be played out, note it down as $\text{RefVol}_{\text{HW_limit}}$, and fill in Table 1. See Figure 2 (c).

For sites that can automatically adjust the Reference Voltage (Terra sites):

- MRI console:**
 - Go to *Options > Adjustments > Transmitter* and hit “Go”. See Figure 2 (a).
 - Note down this Reference Voltage ($\text{RefVol}_{\text{Localizer}}$), which is displayed in *Amplitude (temp)*.
 - Hit “Apply”, and check that the value in the *Amplitude (sys)* has been updated to $\text{RefVol}_{\text{Localizer}}$
 - Close the Adjustments menu.
- Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, check that the amplitude has been updated to $\text{RefVol}_{\text{Localizer}}$, and update it if it has not. See Figure 2 (b).
 - Under *System > Tx/Rx > Ref. amplitude 1H*, check the maximum voltage that can be played out, note it down as $\text{RefVol}_{\text{HW_limit}}$, and fill in Table 1. See Figure 2 (c).

For sites that can not automatically adjust the Reference Voltage (Some Magnetom sites):

- MRI console:**
 - Go to *Options > Adjustments > Transmitter* and set the *Amplitude (temp)* value to a voltage that has been shown to work with your coil ($\text{RefVol}_{\text{Convention}}$).
 - Hit *Apply*
 - Verify that *Amplitude (sys)* has been updated to $\text{RefVol}_{\text{Convention}}$.
 - Close the Adjustments menu.
- Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, check that the amplitude has been updated to $\text{RefVol}_{\text{Convention}}$, and update it if it has not. See Figure 2 (b).
 - Under *System > Tx/Rx > Ref. amplitude 1H*, check the maximum voltage that can be played out, note it down as $\text{RefVol}_{\text{HW_limit}}$, and fill in Table 1. See Figure 2 (c).

MRI console:

- Run the Localizer scan**
- Note: The scanner may complain about the Reference Voltage and the Adjustment Volume having been adjusted. Ignore these warnings**

TurboFLASH B1+ mapping

tfl_B1map sequence for Terra, WIP543 for Magnetom

MRI Console:

- **Position the Field of View (FOV) according to Figure 3.** The center of the FOV should roughly **correspond to the isocentre**. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.

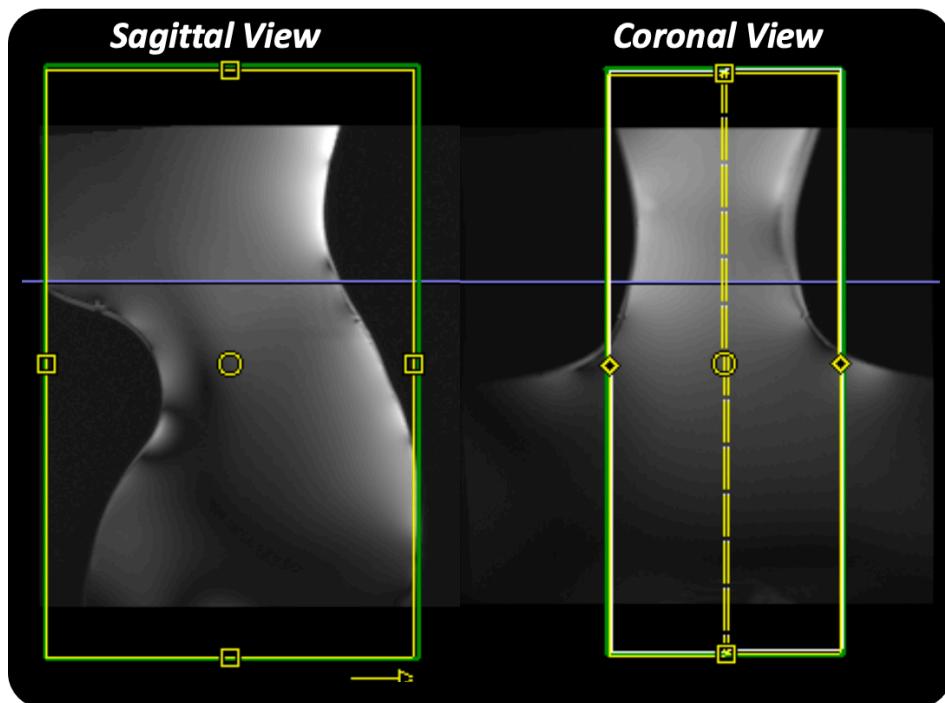


Figure 3. Positioning of FOV for turboFLASH scans.

Sequence card:

- **Make sure that you position BOTH slice groups.** The two slice groups should have the same Position information in the anterior-posterior and head-foot directions, with slice group 2 being offset by the slice thickness, 2.5mm (see example in Figure 4).

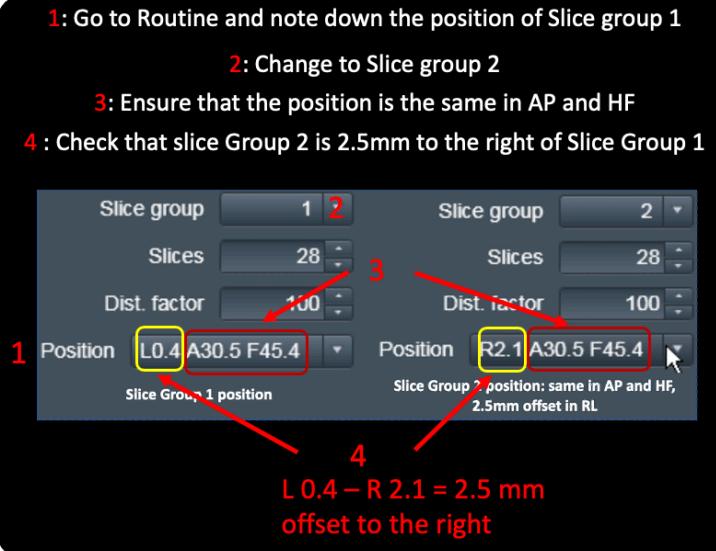


Figure 4. Positioning of the two slice groups for turboFLASH scans.

- **Ensure that all coil elements are selected** by going to the *System > Coils* and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements.
- **Ensure that the Reference Voltage is correctly set** by going to *System > Tx/Rx > Ref. amplitude 1H* and checking that the voltage determined for the Localizer in Adjustment Step 2 is being used here, and setting it if necessary.
- **Note down the table position** (referred to as *TablePos* throughout); found under *System > Miscellaneous > Position*. Note down both the latter (F or H) and the number
- **Ensure that Distortion correction is turned ON** by going to *Resolution > Filter Image* and tick *Distortion Corr ON* and set the *Mode* to 3D, and ticking *Unfiltered Images ON*.
- **IF you are a Magnetom Site Ensure that Distortion correction is turned OFF instead**
- **Re-adjust the central frequency**, as described in Adjustment Step 1.

MRI console:

- Run the scan.
- Wait for the scan to reconstruct.

Re-acquire the TurboFLASH B1+ map with optimal Reference Voltage for the center of the FOV, as described below.

On the Viewing card:

- Open the Flip Angle Map created by the scan (third image series of the scan for Terra, first image series for Magnetom) in the *Viewing card*
- Select the ROI tool and place a circular ROI about 200 pixels in area over the **center of the FOV** at the midline. The placing of the ROI should correspond to the area your coil's transmit profile has been optimized for. See **Figure 5** for ROI placement and size.

- The mean of the ROI is the measured flip angle (FA_{meas}) in units of [flip angle*10], so to get the FA_{meas} , divide the mean in the ROI by 10
 - Compute the Reference Voltage for the center of the FOV as:
 $RefVol_{CFOV} = 90 * (RefVol_{seq}/FA_{meas})$, where $RefVol_{seq}$ is the reference voltage with which the sequence was run (i.e., the Reference Voltage determined in Adjustment Step 2)

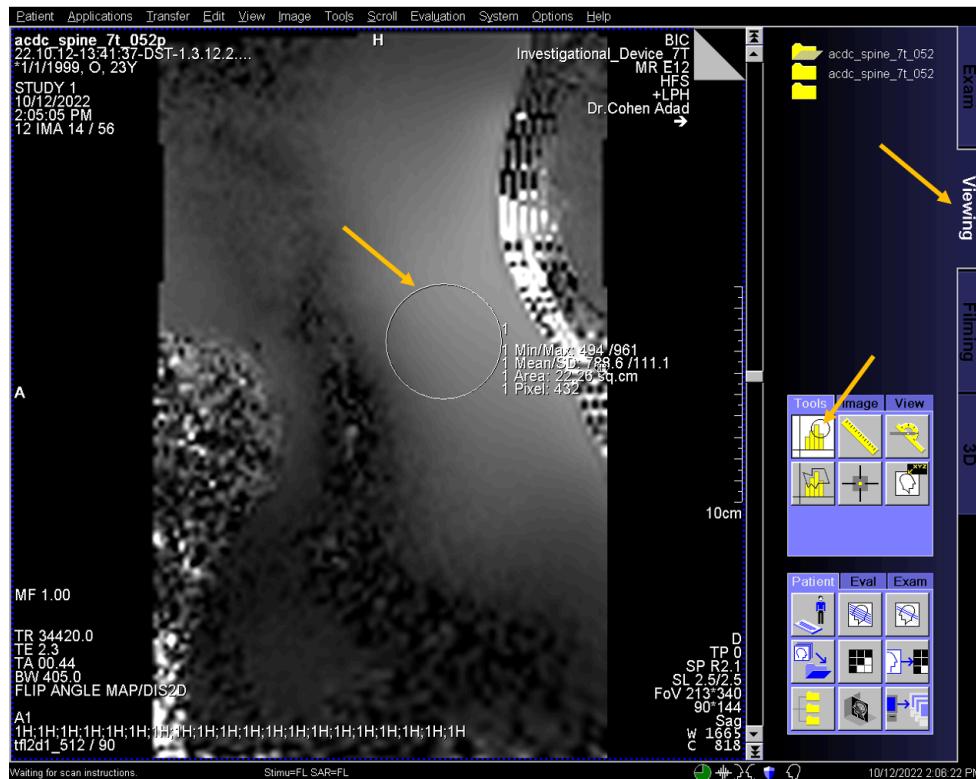


Figure 5. Mean turboFLASH flip angle measurement

Acquiring a B1+ map with the optimal Reference Voltage for the center of the FOV:

For sites with limitations on the Reference Voltage:

If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is above your local limit):

- **MRI Console:**
 - Drag the sequence down in the queue to create a copy
 - Append its name with “_RefVolLocal_limit”
 - **Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, enter *RefVol_{Local_limit}*

- Under *System > Miscellaneous > Table Position*, check that the *Position* is the same as the previous scan (*TablePos*)
- MRI Console:**
 - Run the turbo FLASH scan**
 - Note: the table should not move. If it did, please abort the scan, check the *System > Miscellaneous > Table Position* tab, and set it to the same as the previous scan (*TablePos*)
 - Sanity check for the measured flip angle:** Repeat the procedure described in Figure 5, and validate that the measured flip angle is 90 degrees

If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is below your local limit):

- MRI Console:**
 - Drag the sequence down in the queue to create a copy
 - Append its name with “_RefVolCFOV”
- Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{CFOV}}$
 - Under *System > Miscellaneous > Table Position*, check that the *Position* is the same as the previous scan (*TablePos*)
- MRI Console:**
 - Run the turbo FLASH scan**
 - Note: the table should not move. If it did, please abort the scan, check the *System > Miscellaneous > Table Position* tab, and set it to the same as the previous scan (*TablePos*)
 - Sanity check for the measured flip angle:** Repeat the procedure described in Figure 5, and validate that the measured flip angle is 90 degrees

For sites that can automatically adjust the Reference Voltage (Terra sites):

If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is above your hardware limit):

- MRI Console:**
 - Drag the sequence down in the queue to create a copy
 - Append its name with “_RefVolHW_Limit”
- Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{HW_limit}}$

- Under *System > Miscellaneous > Table Position*, check that the *Position* is the same as the previous scan (*TablePos*)
- MRI Console:**
 - Run the turbo FLASH scan**
 - Note: the table should not move. If it did, please abort the scan, check the *System > Miscellaneous > Table Position* tab, and set it to the same as the previous scan (*TablePos*)
 - Sanity check for the measured flip angle:** Repeat the procedure described in Figure 5, and validate that the measured flip angle is closer to 90 degrees than in the previous scan

If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit):

- MRI Console:**
 - Drag the sequence down in the queue to create a copy
 - Append its name with “_RefVolCFOV”
- Sequence card:**
 - Under *System > Tx/Rx > Ref. amplitude 1H*, enter **RefVol_{CFOV}**
 - Under *System > Miscellaneous*, check that the *Position* is the same as the previous scan (*TablePos*)

MRI Console:

- Run the turbo FLASH scan**
- Note: the table should not move. If it did, please abort the scan, check the *System > Miscellaneous > Table Position* tab, and set it to the same as the previous scan (*TablePos*).
- Sanity check for the measured flip angle:** Repeat the procedure described in Figure 5, and validate that the measured flip angle is 90 degrees

For sites that can not automatically adjust the Reference Voltage (Some Magnetom sites):

If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is above your hardware limit):

- MRI Console:**
 - Drag the sequence down in the queue to create a copy
 - Append its name with “_RefVolHW_Limit”
- Sequence card:**

- Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{HW_limit}}$
- Under *System > Miscellaneous > Table Position*, check that the *Position* is the same as the previous scan (*TablePos*)
- **MRI Console:**
 - Run the turbo FLASH scan
 - Note: the table should not move. If it did, please abort the scan, check the *System > Miscellaneous > Table Position* tab, and set it to the same as the previous scan (*TablePos*)
 - **Sanity check for the measured flip angle:** Repeat the procedure described in Figure 5, and validate that the measured flip angle is closer to 90 degrees than in the previous scan

If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit):

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolCFOV”

Sequence card:

- Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{CFOV}}$
- Under *System > Miscellaneous > Table Position*, check that the *Position* is the same as the previous scan

MRI Console:

- Run the turbo FLASH scan
- Note: the table should not move. If it did, please abort the scan, check the *System > Miscellaneous > Table Position* tab, and set it to the same as the previous scan (*TablePos*)
- **Sanity check for the measured flip angle:** Repeat the procedure described in Figure 5, and validate that the measured flip angle is 90 degrees

DREAM

ThreeDream_2d sequence on Terra, 3dream_2D on Magnetom

Large FOV acquisition

MRI Console:

- **Position the Field of View (FOV) according to Figure 6.** The center of the FOV should roughly **correspond to the Isocentre**. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.

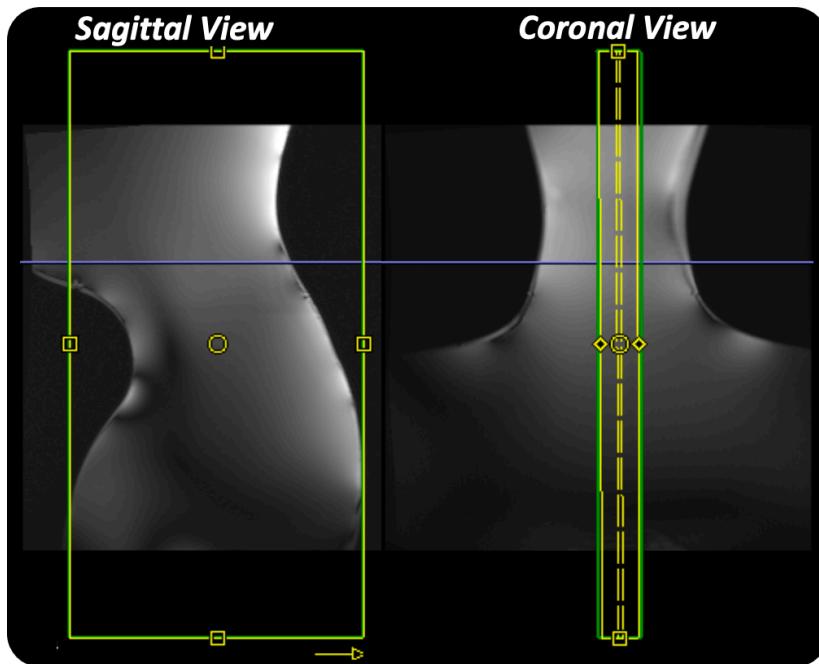


Figure 6. Positioning for Large FOV DREAM scans.

Sequence card:

- **Ensure that all coil elements are selected** by going to the *System > Coils* and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements.
- **Ensure that the Reference Voltage is set correctly** by going to *System > Tx/Rx > Ref. amplitude 1H*
 - **If you have a local limit:**
 - **If $\text{RefVol}_{\text{cFOV}} > \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - **If $\text{RefVol}_{\text{cFOV}} < \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{cFOV}}$
 - **If you have a hardware limit:**
 - **If $\text{RefVol}_{\text{cFOV}} > \text{RefVol}_{\text{HW_limit}}$** (i.e., the determined Reference Voltage is above your hardware limit): set it to the Reference Voltage used for the Localizer, $\text{RefVol}_{\text{HW_limit}}$

- If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{CFOV}}$
- Ensure the **table position is correct** by going to *System > Miscellaneous > Table Position* and making sure it is set to *TablePos*.
- Ensure that **Distortion correction is turned ON** by going to *Resolution > Filter Image* and tick *Distortion Corr ON*, setting *Mode* to 3D, and ticking *Unfiltered Images ON*.

MRI console:

- Run the DREAM scan

Medium FOV acquisition

MRI Console:

- **Position the Field of View (FOV) according to Figure 7.** The center of the FOV should roughly **correspond to the Isocentre**. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.

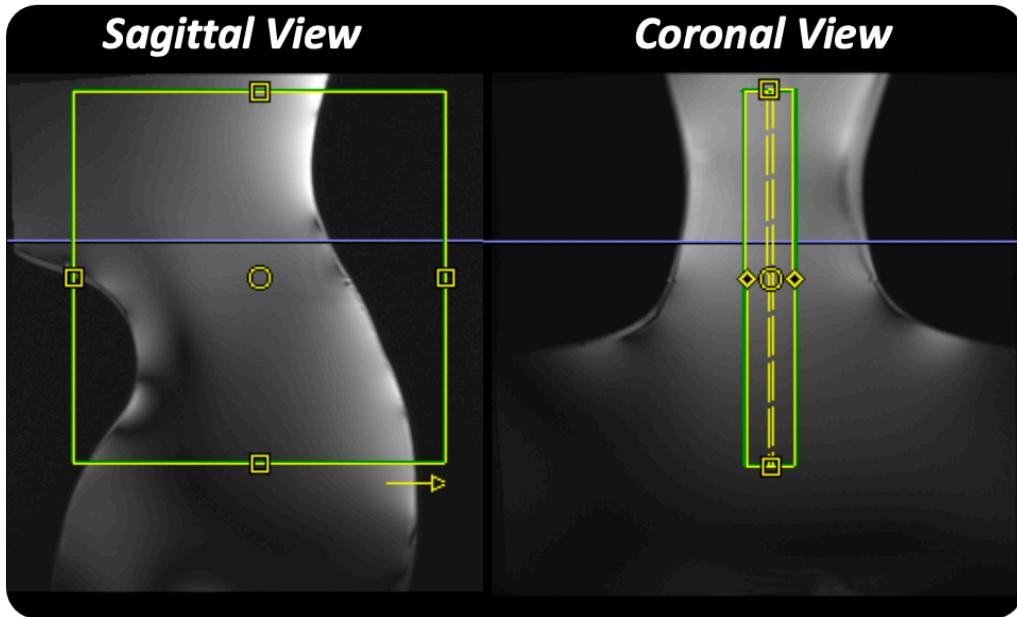


Figure 7. Positioning for Large FOV DREAM scans.

Sequence card:

- **Ensure that all coil elements are selected** by going to the *System > Coils* and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements.
- **Ensure that the Reference Voltage is set correctly** by going to *System > Tx/Rx > Ref. amplitude 1H*
 - **If you have a local limit:**
 - *If $\text{RefVol}_{\text{cFOV}} > \text{RefVol}_{\text{local_limit}}$* (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - *If $\text{RefVol}_{\text{cFOV}} < \text{RefVol}_{\text{local_limit}}$* (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{cFOV}}$
 - **If you have a hardware limit:**
 - *If $\text{RefVol}_{\text{cFOV}} > \text{RefVol}_{\text{HW_limit}}$* (i.e., the determined Reference Voltage is above your hardware limit): set it to the Reference Voltage used for the Localizer, $\text{RefVol}_{\text{HW_limit}}$
 - *If $\text{RefVol}_{\text{cFOV}} < \text{RefVol}_{\text{HW_limit}}$* (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{cFOV}}$
- **Ensure the table position is correct** by going to *System > Miscellaneous > Table Position* and making sure it is set to *TablePos*.

- Ensure that Distortion correction is turned ON by going to *Resolution > Filter Image* and tick *Distortion Corr* ON, setting *Mode* to 3D, and ticking *Unfiltered Images* ON.

MRI console:

- Run the DREAM scan

Re-acquire the Medium FOV DREAM B1+ map with additional Reference Voltages

After the scan has finished, **re-acquire the Medium FOV DREAM B1+ map with additional Reference Voltages**, as described in the box below.

Acquiring the Medium FOV DREAM B1+ map with additional Reference Voltages:

For sites with limitations on the Reference Voltage:

Calculate if $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$ and $\text{RefVol}_{\text{CFOV}} * 1.5$ are within your limits (i.e., if they are lower than $\text{RefVol}_{\text{local_limit}}$)

If both $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$ and $\text{RefVol}_{\text{CFOV}} * 1.5$ are within your limits:

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolCFOV_0p66”

Sequence card:

- Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$
- Under *System > Miscellaneous*, check that the *Position* is the same as the previous scan

MRI Console:

- Run the DREAM scan
- Note: the table should not move. If it did, please abort the scan, check the *System > Miscellaneous > Table Position* tab, and set it to the same as the previous scan (*TablePos*)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Change the end of its name to “_RefVolCFOV_1p5”

Sequence card:

- Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{CFOV}} * 1.5$

- Under System > Miscellaneous, check that the Position is the same as the previous scan

MRI Console:

- Run the DREAM scan**
- Note: the table should not move. If it did, please abort the scan, check the System > Miscellaneous > Table Position tab, and set it to the same as the previous scan (*TablePos*)

If $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$ is within your limits and If $\text{RefVol}_{\text{CFOV}}$ is also within your limit (ie, you acquired the previous DREAM scan with $\text{RefVol}_{\text{CFOV}}$)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolCFOV_0p66”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$
- Under System > Miscellaneous, check that the Table Position is the same as the previous scan

MRI Console:

- Run the DREAM scan**
- Note: the table should not move. If it did, please abort the scan, check the System > Miscellaneous > Table Position tab, and set it to the same as the previous scan (*TablePos*)

If $\text{RefVol}_{\text{CFOV}}$ is not within your limits (ie, you acquired the previous DREAM scan with $\text{RefVol}_{\text{local_limit}}$)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVollocal_limit_0p66”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{HW_limit}} * \frac{2}{3}$
- Under System > Miscellaneous, check that the Table Position is the same as the previous scan

MRI Console:

- Run the DREAM scan**
- Note: the table should not move. If it did, please abort the scan, check the System > Miscellaneous > Table Position tab, and set it to the same as the previous scan (*TablePos*)

For sites that can automatically adjust the Reference Voltage (Terra sites):

Calculate if $\text{RefVol}_{\text{CFOV}}$, $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$ and $\text{RefVol}_{\text{CFOV}} * 1.5$ are within your hardware limits (i.e., if they are lower than $\text{RefVol}_{\text{HW_limit}}$).

If both $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$ and $\text{RefVol}_{\text{CFOV}} * 1.5$ are within your limits:

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolCFOV_0p66”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$
- Under System > Miscellaneous, check that the Position is the same as the previous scan

MRI Console:

- Run the DREAM scan
- Note: the table should not move. If it did, please abort the scan, check the System > Miscellaneous > Table Position tab, and set it to the same as the previous scan (TablePos)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Change the end of its name to “_RefVolCFOV_1p5”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{CFOV}} * 1.5$
- Under System > Miscellaneous, check that the Position is the same as the previous scan

MRI Console:

- Run the DREAM scan
- Note: the table should not move. If it did, please abort the scan, check the System > Miscellaneous > Table Position tab, and set it to the same as the previous scan (TablePos)

If only $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$ is within your limits and $\text{RefVol}_{\text{CFOV}}$ is also within your limits, but $\text{RefVol}_{\text{CFOV}} * 1.5$ is not (i.e. you acquired the DREAM Medium FOV acquisition with $\text{RefVol}_{\text{CFOV}}$)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolCFOV_0p66”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{CFOV}} * \frac{2}{3}$
- Under System > Miscellaneous, check that the Table Position is the same as the previous scan

MRI Console:

- **Run the DREAM scan**
- Note: the table should not move. If it did, please abort the scan, check the System > Miscellaneous > Table Position tab, and set it to the same as the previous scan (TablePos)

If $\text{RefVol}_{\text{opt}} * \frac{2}{3}$ is within your limits but $\text{RefVol}_{\text{opt}}$ is not within your limits (i.e. you acquired the DREAM Medium FOV acquisition with $\text{RefVol}_{\text{HW_limit}}$)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolHW_limit_0p66”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{HW_limit}} * \frac{2}{3}$ (i.e., $\frac{2}{3}$ of the voltage of the DREAM Medium FOV acquisition)
- Under System > Miscellaneous, check that the Table Position is the same as the previous scan

MRI Console:

- **Run the DREAM scan**
- Note: the table should not move. If it did, please abort the scan, check the System > Miscellaneous > Table Position tab, and set it to the same as the previous scan (TablePos)

For sites that can not automatically adjust the Reference Voltage (Some Magnetom sites):

Instructions are identical to the previous box, “For sites that can automatically adjust the Reference Voltage (Terra sites)”

coilQA

Coil_utils sequence on Terra

Large FOV sagittal acquisition

MRI Console:

- **Position the Field of View (FOV) according to Figure 8.** The center of the FOV should roughly correspond to the Isocentre. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.
- **Position the B0 shim adjust volume according to Figure 8**

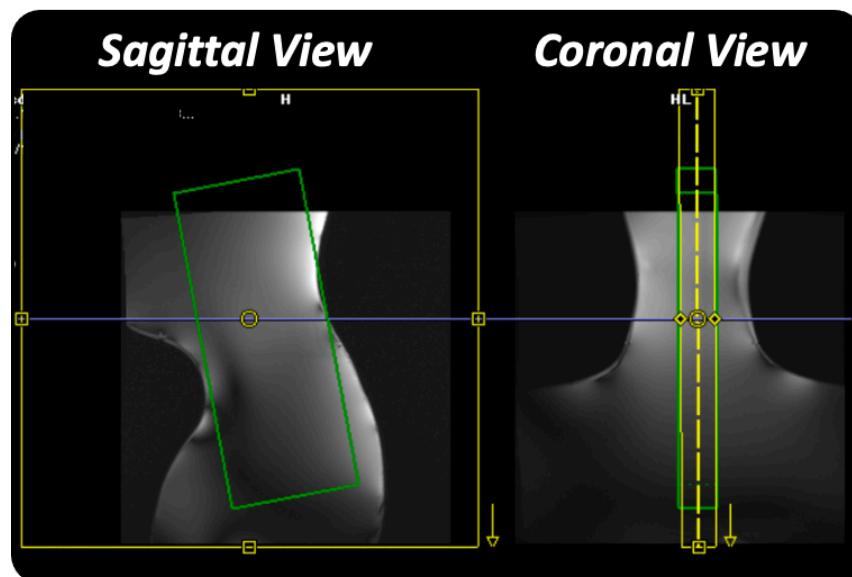


Figure 8. Positioning of FOV and B0 shim box for sagittal coilQA scans.

Sequence card:

- **Ensure that all coil elements are selected** by going to the System > Coils and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements
- **Ensure that the Reference Voltage is set correctly** by going to System > Tx/Rx > Ref. amplitude 1H
 - **If you have a local limit:**
 - **If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - **If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{CFOV}}$
 - **If you have a hardware limit:**
 - **If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{HW_limit}}$** (i.e., the determined Reference Voltage is above your hardware limit): set it to the Reference Voltage used for the Localizer, $\text{RefVol}_{\text{HW_limit}}$

- **If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{HW_limit}}$** (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{CFOV}}$
- **Ensure the table position is correct** by going to *System > Miscellaneous > Table Position* and making sure it is set to *TablePos*
- **Ensure that Distortion correction is turned OFF** by going to *Resolution > Filter Image* and tick *Distortion Corr OFF*.

MRI console:

- Run the coilQA scan

Medium FOV sagittal acquisition

MRI Console:

- **Position the Field of View (FOV) according to Figure 9.** The center of the FOV should roughly **correspond to the Isocentre**. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.

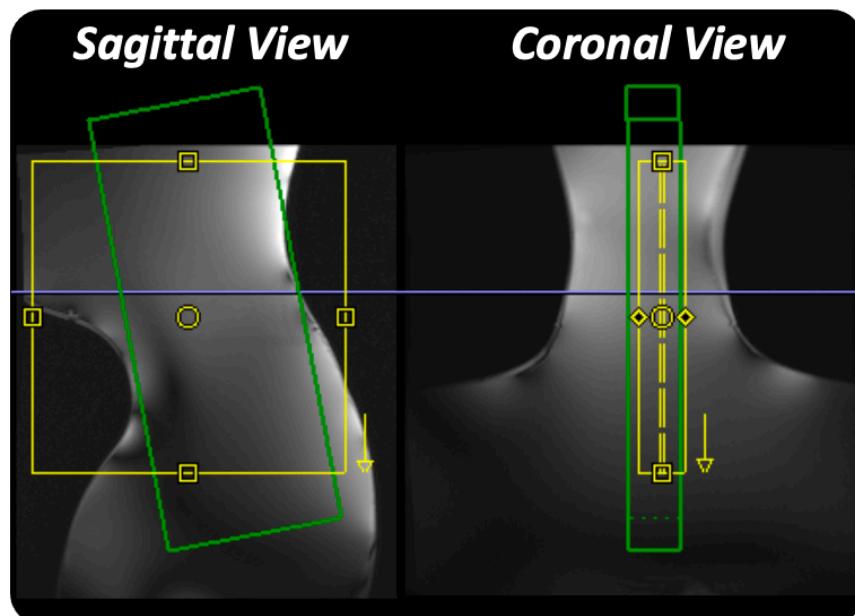


Figure 9. Positioning of FOV and B0 shim box for sagittal coilQA scans.

- **Copy the Adjustment Volume from the Large FOV Sagittal Coil QA scan, as shown in Figure 10,** by right clicking on the Large FOV Sagittal Coil QA scan, and selecting “Copy Parameters→ Adjustment Volume”

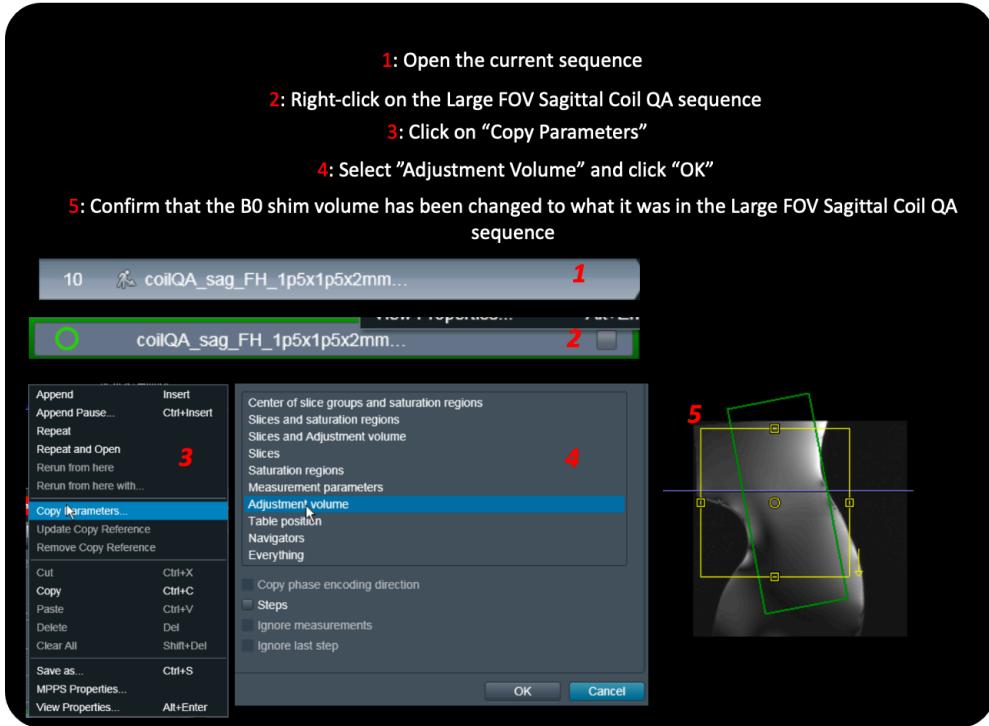


Figure 10. Guide on copying “Adjustment Volume”, eg the B0 shim box, from one scan to the next

Sequence card:

- Ensure that all coil elements are selected by going to the System > Coils and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements
- Ensure that the Reference Voltage is set correctly by going to System > Tx/Rx > Ref. amplitude 1H
 - If you have a local limit:
 - If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{CFOV}}$
 - If you have a hardware limit:
 - If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is above your hardware limit): set it to the Reference Voltage used for the Localizer, $\text{RefVol}_{\text{HW_limit}}$
 - If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{CFOV}}$
- Ensure the table position is correct by going to System > Miscellaneous > Table Position and making sure it is set to TablePos.
- Ensure that Distortion correction is turned OFF by going to Resolution > Filter Image and tick Distortion Corr OFF.

MRI console:

- Run the coilQA scan

Medium FOV axial acquisition

MRI Console:

- **Position the Field of View (FOV) according to Figure 11.** The center of the slice group should roughly **correspond to the Isocentre**. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.

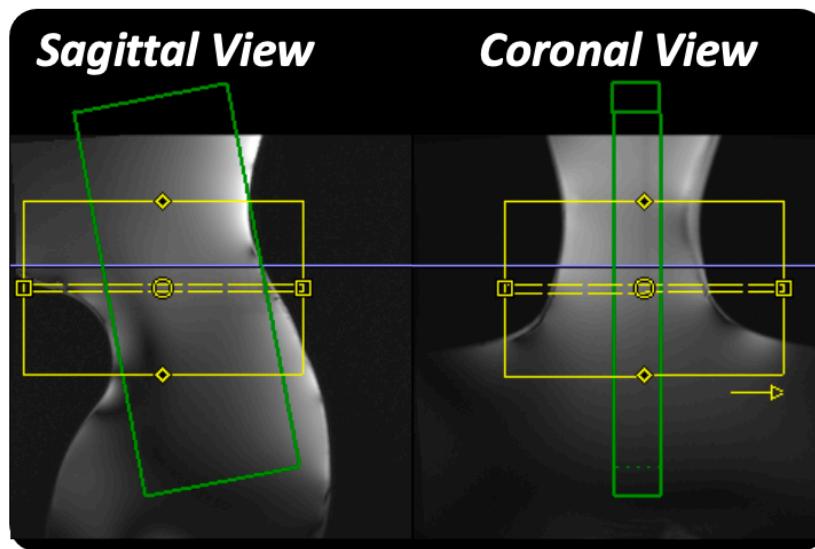


Figure 11. Positioning of FOV and B0 shim box for axial coilQA scans.

- **Copy the Adjustment Volume from the Large FOV Sagittal Coil QA scan, as shown in Figure 10,** by right clicking on the Large FOV Sagittal Coil QA scan, and selecting “Copy Parameters→ Adjustment Volume”

Sequence card:

- **Ensure that all coil elements are selected** by going to the *System > Coils* and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements.
- **Ensure that the Reference Voltage is set correctly** by going to *System > Tx/Rx > Ref. amplitude 1H*
 - **If you have a local limit:**
 - *If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{local_limit}}$* (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - *If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{local_limit}}$* (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{CFOV}}$
 - **If you have a hardware limit:**
 - *If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{HW_limit}}$* (i.e., the determined Reference Voltage is above your hardware limit): set it to the Reference Voltage used for the Localizer, $\text{RefVol}_{\text{HW_limit}}$

- If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{CFOV}}$
- Ensure the **table position is correct** by going to *System > Miscellaneous > Table Position* and making sure it is set to *TablePos*
- Ensure that **Distortion correction is turned OFF** by going to *Resolution > Filter Image* and tick *Distortion Corr OFF*.

MRI console:

- Run the coilQA scan.

GRE

Gre sequence on Terra and Magnetom

MRI Console:

- **Position the Field of View (FOV) according to Figure 12.** The center of the FOV should roughly correspond to the Isocentre. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.
- **Position the B0 adjust volume according to Figure 12.** The B0 shim volume should cover the whole FOV. If it does not, go to System > Adjust Volume, and click Reset.

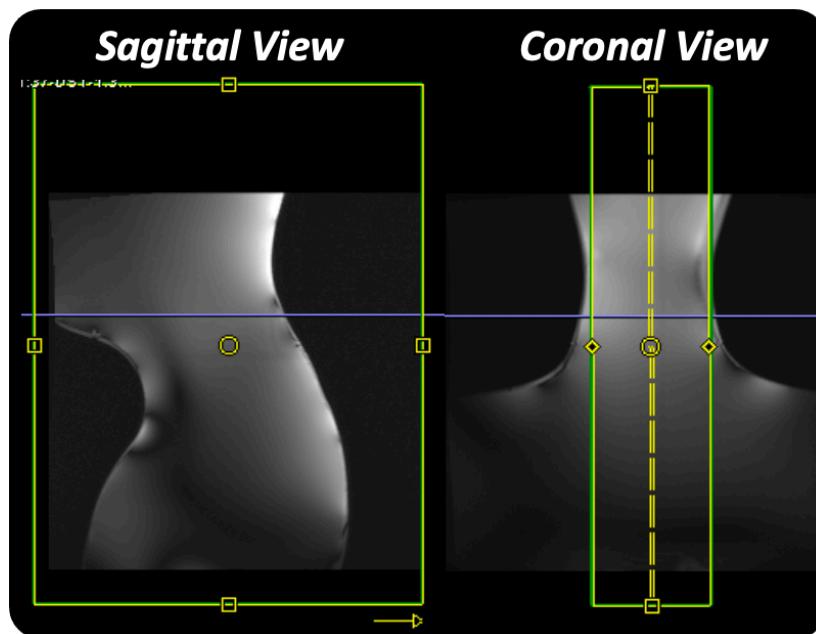


Figure 12. Positioning of FOV GRE scan.

Sequence card:

- **Ensure that all coil elements are selected** by going to the System > Coils and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements.
- **Ensure that the Reference Voltage is set correctly** by going to System > Tx/Rx > Ref. amplitude 1H
 - **If you have a local limit:**
 - **If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - **If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{CFOV}}$
 - **If you have a hardware limit:**
 - **If $\text{RefVol}_{\text{CFOV}} > \text{RefVol}_{\text{HW_limit}}$** (i.e., the determined Reference Voltage is above your hardware limit): set it to the Reference Voltage used for the

- Localizer, RefVol_{HW_limit}
- If $\text{RefVol}_{\text{CFOV}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to RefVol_{CFOV}
- Ensure the **table position is correct** by going to *System > Miscellaneous > Table Position* and making sure it is set to *TablePos*.
- Ensure that **Distortion correction is turned ON** by going to *Resolution > Filter Image* and tick *Distortion Corr* ON, setting *Mode* to 3D, and ticking *Unfiltered Images* ON. .

MRI console:

- Run the GRE scan
- If the scanner gives a warning about SAR, run in “First Level” mode

B1+ shimming using the Shimming Toolbox: Only for Terra pTx sites

Ensuring the correct VOPs are loaded

MRI Console:

- Drag the GRE sequence down in the queue to create a copy
- Set the B1 shim mode by going to System > pTx Volumes and set the *B1 Shim mode* to *Patient-specific*.
- Go to **Options > Adjustments > B1 shim** and click *Measure*
- Once the measurement is complete, click *Calculate*
- Exit the Options menu, and delete the copied scan from the queue
- Open a file explorer
- Navigate to C:/MedCom/MriProduct/PhysConfig
- Select the “SarDataUser.mat” file
- Check that it’s “Date Modified” value corresponds to the current scan session

RF_map B1+ mapping

Tfl_rfmap sequence on Terra

MRI Console:

- **Position the Field of View (FOV) according to Figure 13.** The center of the FOV should roughly correspond to the Isocentre. If the FOV in the FH direction for the imported protocol is too large for your coil, use the largest FOV possible in the FH direction for your coil.
- **Copy the Adjustment Volume from the TFL_B1map scan, as shown in Figure 10,** by right clicking on the TFL_B1map scan, and selecting “Copy Parameters→ Adjustment Volume”.

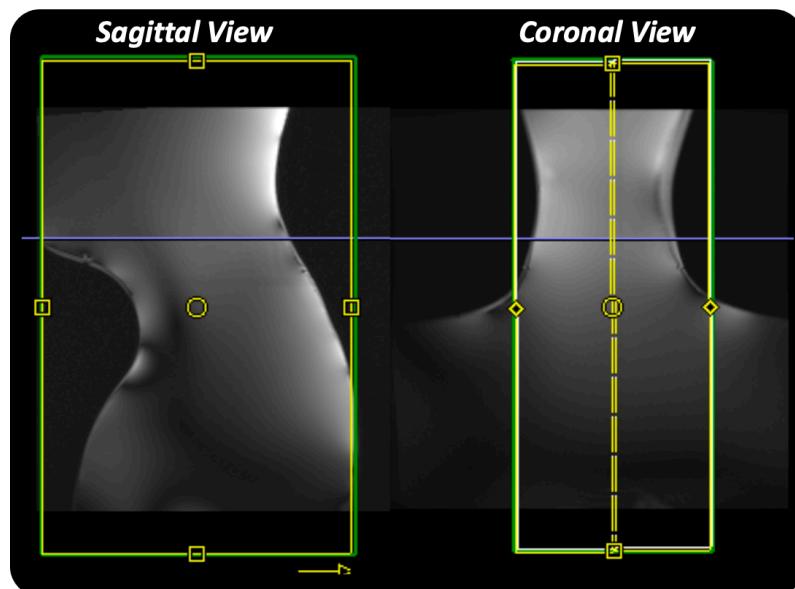


Figure 13. Positioning of FOV for TFL_rfmap scans

Sequence card:

- **Ensure that all coil elements are selected** by going to the *System > Coils* and select all coils. Because some coils used in this study are custom made, they may not AutoSelect all their coil elements.
- **Ensure that the Reference Voltage is correctly set** by going to *System > Tx/Rx > Ref. amplitude 1H* and checking that the voltage determined for the Localizer is being used here.
- **Ensure that Distortion correction is turned ON** by going to *Resolution > Filter Image* and tick *Distortion Corr* ON, and ticking *Unfiltered Images* ON.
- **Ensure the table position is correct** by going to *System > Miscellaneous > Table Position* and making sure it is set to *TablePos*

MRI console:

- **Run the scan**

After the scan has completed, **calculate the RF shim weights** as described in the box. This procedure takes about 15 minutes. This offline processing procedure requires Shimming Toolbox and Spinal Cord Toolbox to be installed.

B1+ shim weight calculation:

MRI Console:

- Go to *Patient > Browser* and select the *tfl_rfmap* scan and the *channel-combined magnitude of the GRE scan* (it should be the second series of the scan, with 44 images, with the suffix *_ND*)
- Go to *Transfer > Export to Off-Line*
- Wait for the transfer to finish
- Copy those files onto a new directory (named *DATADIR* in this example) on a pendrive
- Copy the “*SarDataUser.mat*” file from *C:/MedCom/MriProduct/PhysConfig* into *DATADIR*

Local laptop:

- Transfer *DATADIR* onto your local laptop
- Create a new Output Directory outside of *DATADIR* (here named *outputDIR*)
- Copy the *dcm2bids_QA.json* file into *DATADIR*
- Run the “*rfshim_QA.sh*” script, pointing it to *DATADIR*:
 - `./rfshim_QA.sh ~path/to/DATADIR ~path/to/outputDIR`
- The script will pop up FSLeyes windows and ask you to enter the slice number (in the Head-Foot direction, corresponding to the y direction of the GRE scan) to restrict the mask. Enter first the bottom slice, then the top slice. A new FSLeyes window will pop up confirming the restricted mask. Once this is done, the rest of the script will run. The whole process will take less than 2 minutes
- Open the “*b1_shim_weights.txt*” file in *OutputDIR/CVred*
- Copy the “*b1_shim_weights.txt*” file onto the scanner (see salmon-coloured box below)

MRI Console:

- **Drag the sequence down in the queue to create a copy**
- Append the end of its name to “*_RFshim_CVred*”
- **Acquire the scan with the B1+ shim weights applied**, as described in the mauve-coloured box below

Acquiring B1+ shimmed scans:

Sequence card:

- Set the **B1 shim mode** by going to *System > pTx Volumes* and set the *B1 Shim mode* to *Patient-specific*. See Figure 14.

MRI console:

- Open a terminal and a windows explorer
- Open the “**b1_shim_weights.txt**” in the Windows Explorer
- Open a terminal and type:
`adjvalidate -txscale -set Tx1_mag Tx1_phase T2x_mag Tx2_phase;`
Where TX1_mag TX1_phase, etc are the values in the **b1_shim_weights.txt** file

Sequence card:

- Set the **B1 shim mode** by going to *System > pTx Volumes* and set the *B1 Shim mode* to *Patient-specific*. See Figure 14.

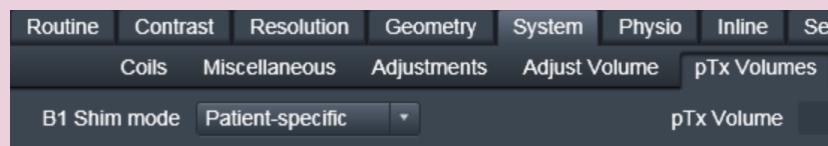


Figure 14. Location of the “B1 shim mode” switch

MRI Console:

- Double-check that the correct B1+ shim weights are set: Go to *Options > Adjustments > B1 shim*
- Enter the values in the “Temporary” column
- Hit “Apply”
- Double-check that the new values are transferred to the “System” column
- Exit the Adjustments menu
- Run the scan

- 1: Open the Adjustments Menu
- 2A: Check that the values in the "System" Column correspond to the values in the "b1_shim_weights.txt" file. If they **do**, proceed to point 5
- 2B: If they **don't**, enter them in the "Temporary" column
- 3: Click "Apply"
- 4: Check that the values in the "System" column correspond to the values in the "b1_shim_weights.txt" file

5: Exit the Adjustment menu

The screenshot shows a software interface for adjusting shim weights. On the left, a vertical menu is open with the following options:

- File Browser...
- Adjustments...** (highlighted with a blue box)
- SAR Information...
- Stimulation Info...
- Auto Expose
- Maintenance... **1**
- Configuration...
- Service

The main window displays a table titled "B1 Map" with two columns: "Temporary" and "System". The "Temporary" column contains values from Tx Sc. 0 to Tx Sc. 10, while the "System" column contains values from Tx Sc. 1 to Tx Sc. 10. The "System" column values are highlighted with red boxes and labeled with numbers 2A through 4.

| | Temporary | System |
|-----------|-----------|--------|
| B1 Map | ? | 2A |
| Tx Sc. 0 | 0 | 0.35 |
| Tx Sc. 1 | 0.21 | -80.0 |
| Tx Sc. 2 | 0.18 | 105.0 |
| Tx Sc. 3 | 0.37 | 89.0 |
| Tx Sc. 4 | 0.76 | 9.00 |
| Tx Sc. 5 | 0.38 | 150.0 |
| Tx Sc. 6 | 0.12 | 167.0 |
| Tx Sc. 7 | 0.46 | -47.0 |
| Tx Sc. 8 | | |
| Tx Sc. 9 | | |
| Tx Sc. 10 | | |
| Tx Sc. 11 | | |

The "Temporary" column has "mag" and "pha" headers, and the "System" column has "mag" and "pha" headers.

To the right, a "Measure" panel shows a table titled "System 4" with the following values:

| | System 4 |
|----------|-------------|
| ? | 0.21 0.00 |
| Tx Sc. 1 | 0.21 -80.00 |
| Tx Sc. 2 | 0.18 105.00 |
| Tx Sc. 3 | 0.37 89.00 |
| Tx Sc. 4 | 0.76 9.00 |
| Tx Sc. 5 | 0.38 150.00 |
| Tx Sc. 6 | 0.12 167.00 |
| Tx Sc. 7 | 0.46 -47.00 |

The "Measure" panel includes buttons for "Abort", "Calculate", "Load Circular", "Load Elliptical", and "Load System". The "Apply" button is highlighted with a red box and the number "3".

Figure 15. Workflow for applying B1+ shim weights

TurboFLASH B1+ mapping

tfl_B1map sequence for Terra, WIP543 for Magnetom

MRI Console:

- Drag the previously acquired sequence down in the queue to create a copy
- Append the end of its name to “_RFshim_CVred”
- Acquire the scan with the B1+ shim weights applied, as described in the salmon-coloured box under “RF_map B1+ mapping”

coilQA

Coil_utils sequence on Terra

Large FOV sagittal acquisition

MRI Console:

- Drag the previously acquired sequence Large FOV sagittal coil QA sequence down in the queue to create a copy
- Append the end of its name to “_RFshim_CVred”
- **Acquire the scan with the B1+ shim weights applied**, as described in the salmon-coloured box under “RF_map B1+ mapping”

GRE

MRI Console:

- **Drag the previously acquired GRE sequence down in the queue to create a copy**
- Append the end of its name to “_RFshim_CVred”
- **Acquire the scan with the B1+ shim weights applied**, as described in the salmon-coloured box under “RF_map B1+ mapping”