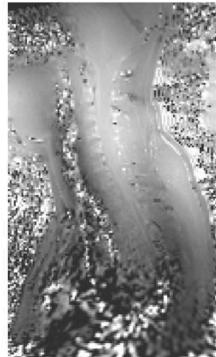


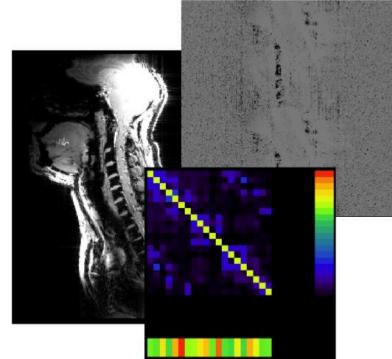
7 T C-Spine Coil QC Protocol: *In-Vivo* Acquisition Guidelines



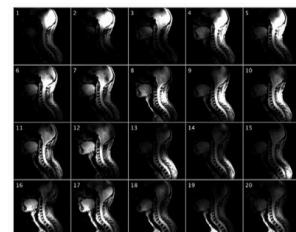
DREAM (2D)
B1+ mapping



turboFLASH (2D)
B1+ mapping



coilQA
SNR, g-factor, noise statistics



GRE (2D)
Coil Sensitivity

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>

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Subject Setup/Positioning

- When positioning the subject in the coil, make use of any available cushions and padding in order to ensure that the spine is as straight as possible (ie: minimize lordosis).
- Remind the subject that they should try to move as little as possible during scans and wait until between scans to swallow.
- **Position the isocenter** such that it is in the middle of the anatomical area covered by your coil. This may not correspond to your coil's isocenter mark.

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.

In Table 1, every site is coloured according to which boxes they have to follow.

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

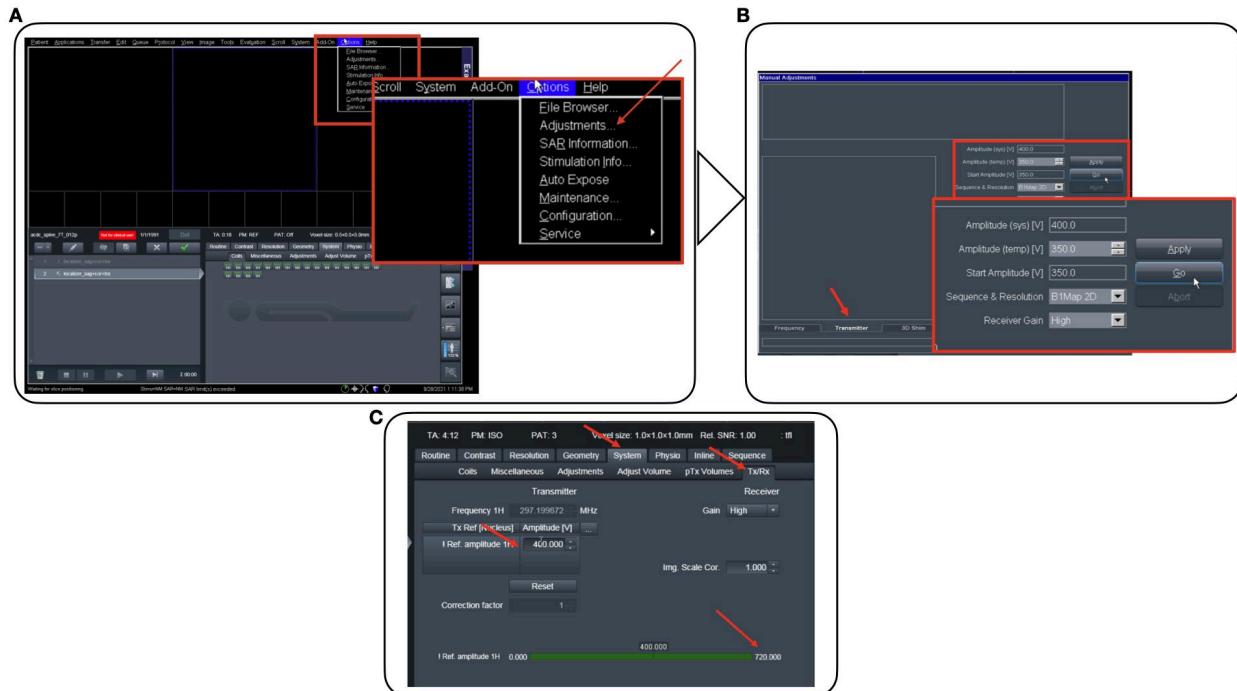


Figure 2. Manually setting the reference voltage and finding the hardware limit.

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 where you put 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.

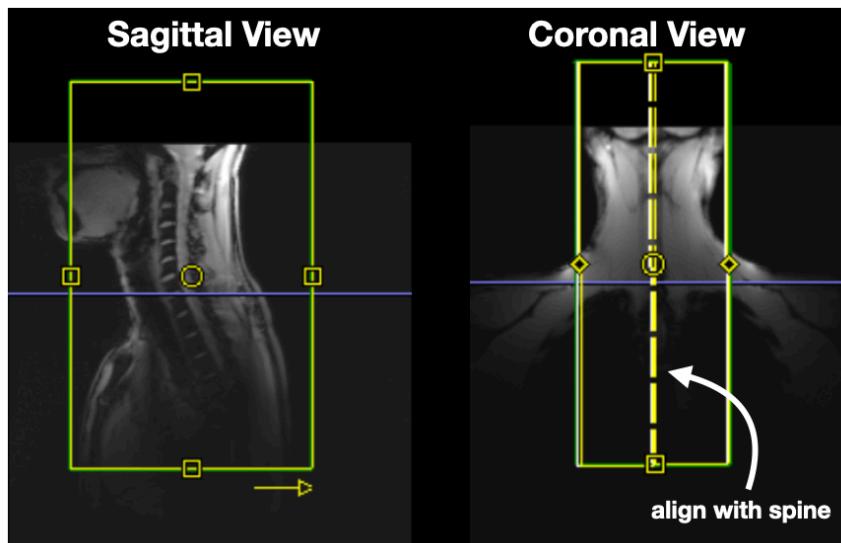


Figure 3. Positioning of FOV for turboFLASH scans.

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).

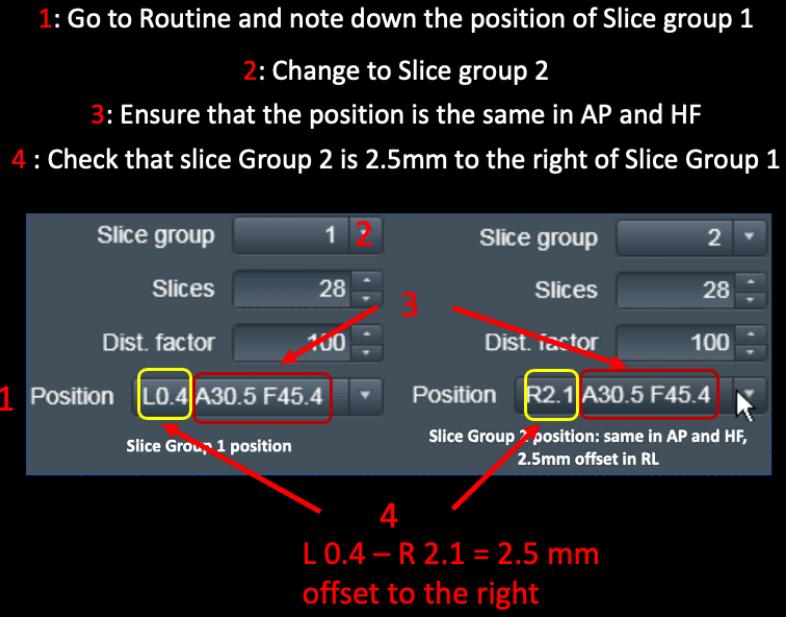


Figure 4. Positioning of the two slice groups for turboFLASH scans.

- **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.
- **Ensure that this Reference Voltage does not cause clipping in the SINC preparation pulse:**
 - Select the Prep_SINC1 1H Amplitude in the box at the lower-left of the System > Tx/Rx card, and check that the amplitude of this pulse is not at the upper allowable bound (the green bar at the bottom). If the amplitude is at the upper allowable bound (all the way to the right of the green bar), then the pulse will be clipped. If the pulse will be clipped then manually reduce the Ref. amplitude 1H by increments of 5 V, checking the Prep_SINC1 1H Amplitude each time, until the amplitude is no longer at the upper allowable bound. Note down the actual Ref. amplitude 1H used in this acquisition. It's wise to change the sequence name so that it contains the actual Ref. amplitude 1H (i.e., append _RefV320 to the sequence name, with the correct number)
- **Note down the table position** (referred to as **TablePos** throughout); found under *System > Miscellaneous > Position*. Note down both the letter (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 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 for the anatomical location your coil is optimized for, 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. It should NOT look like an anatomical scan, and the Image Comment in the bottom left will say “FLIP ANGLE MAP”) in the *Viewing card*
- Select the ROI tool and place a circular ROI about 200 pixels centered on the area your coil is optimized for disk. See **Figure 5** for ROI placement and size.
- Compute the Reference Voltage for the optimal level as:
- $RefVolOpt = RefVolSeq * \frac{900}{Mean\ in\ ROI} = \underline{\hspace{2cm}}$

Where $RefVol_{seq}$ is the reference voltage with which the sequence was run (i.e., the Reference Voltage determined in Adjustment Step 2), and “Mean in ROI” is the mean values in the ROI on **Figure 5**

- **Sanity check:** if the mean in the ROI is above 900, then the new RefVolOpt should be lower than RefVolSeq, if it is below 900, then the new RefVolOpt should be higher than RefVolSeq
- **Ensure that this Reference Voltage does not cause clipping in the SINC preparation pulse.** As before, step down in RefVol in increments of 5V until the Pre_SINC pulse does not clip anymore. **Note down this voltage, and for the TurboFLASH B1+ scan only, consider this new voltage to be RefVolOpt.**

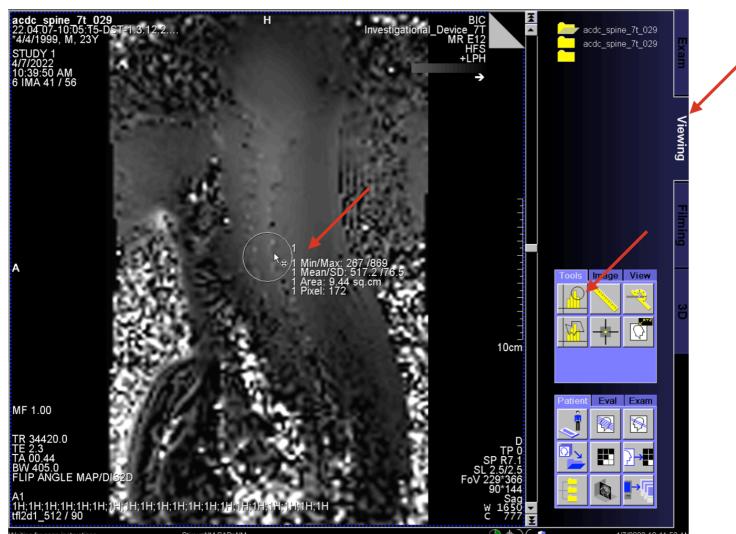


Figure 5. Mean turboFLASH flip angle measurement. In this case, the coil has been optimized for the C2/C3 level

Acquiring a B1+ map with the optimal Reference Voltage for the Optimal level:

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 $\text{RefVol}_{\text{Local_limit}}$
 - 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 $\text{RefVol}_{\text{CFOV}}$
 - 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 where you put 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.

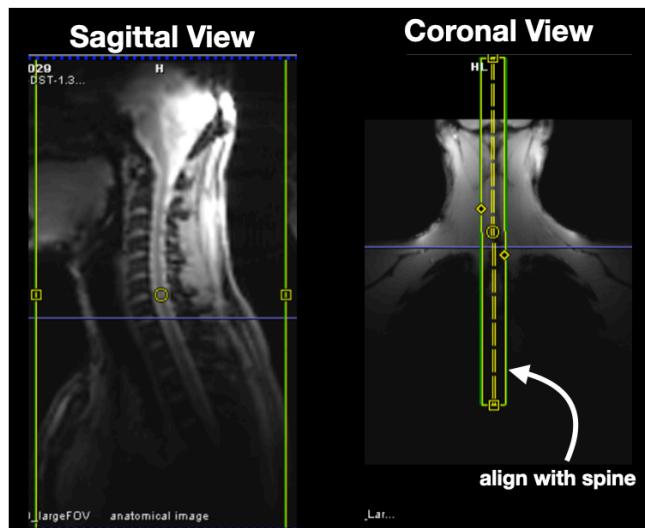


Figure 6. Positioning of Large FOV for DREAM scans.

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 $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - If $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{opt}}$
 - If you have a hardware limit:
 - If $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{HW_limit}}$ (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 $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{opt}}$

- Check that this Reference Voltage does not cause clipping in the SINC preparation pulse. If it does, change the *PrepRF duration* value under Sequence > Special until there is no more clipping. Make a note of this value (*PrepRFdur_DREAM*).
- Ensure the table position is correct by going to System > Miscellaneous > Table Position and making sure it is set to *TablePos*.
- Check that shim mode is set to “Brain” by going to System > Adjustments
- 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.
- Re-adjust the central frequency, as described in Adjustment Step 1.

MRI console:

- Run the DREAM scan

Medium FOV acquisition

MRI Console:

- Copy Table Position, Centre of Slice groups and Sat Regions from the Large FOV DREAM
- Copy Adjustment Volume from Large FOV DREAM and adjust in H-F until it covers the FOV
- Position the Field of View (FOV) according to Figure 7. The center of the FOV should roughly correspond to where you put 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.

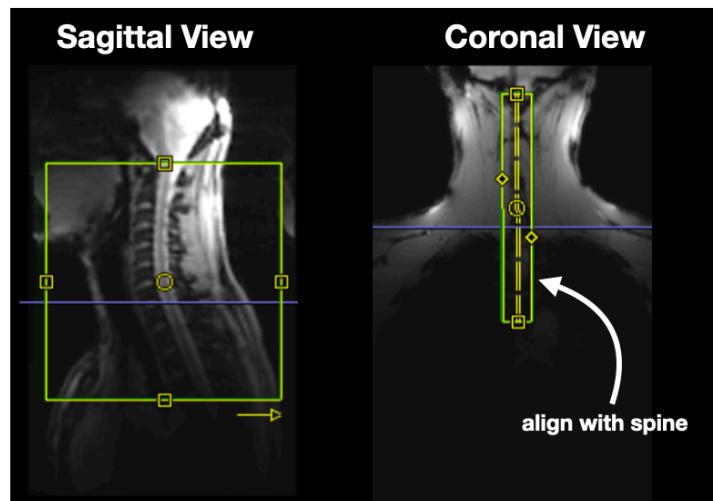


Figure 7. Positioning of Medium FOV for DREAM scans.

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 $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{local_limit}}$* (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - *If $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{local_limit}}$* (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{opt}}$
 - **If you have a hardware limit:**
 - *If $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{HW_limit}}$* (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 $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{HW_limit}}$* (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{opt}}$
- **Check that this Reference Voltage does not cause clipping in the SINC preparation pulse.** If it does, change the *PrepRF duration* value under *Sequence > Special* to *PrepRFdur_DREAM*
- **Ensure the table position is correct** by going to *System > Miscellaneous > Table Position* and making sure it is set to *TablePos*.
- **Check that shim mode is set to “Brain”** by going to *System > Adjustments*
- **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*.
- **Re-adjust the central frequency**, as described in Adjustment Step 1.

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

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

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolOpt_0p66”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{Opt}} * \frac{2}{3}$
- 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 “_RefVolOpt_1p5”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{Opt}} * 1.5$
- Under System > Miscellaneous, check that the Position is the same as the previous scan
- **Check that this Reference Voltage does not cause clipping in the SINC preparation pulse.** If it does, change the PrepRF duration value under Sequence > Special to avoid clipping. Note down this value

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 and If $\text{RefVol}_{\text{Opt}}$ is also within your limit (ie, you acquired the previous DREAM scan with $\text{RefVol}_{\text{Opt}}$)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolOpt_0p66”

Sequence card:

- Under System > Tx/Rx > Ref. amplitude 1H, enter $\text{RefVol}_{\text{Opt}} * \frac{2}{3}$

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

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

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolOpt_0p66”

Sequence card:

- Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{opt}} * \frac{2}{3}$
- 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 “_RefVolOpt_1p5”

Sequence card:

- Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{Opt}} * 1.5$
- Under *System > Miscellaneous*, check that the *Position* is the same as the previous scan
- **Check that this Reference Voltage does not cause clipping in the SINC preparation pulse.** If it does, change the *PrepRF duration* value under *Sequence > Special* to avoid clipping. Note down this value

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 and $\text{RefVol}_{\text{Opt}}$ is also within your limits (i.e. you acquired the DREAM Medium FOV acquisition with $\text{RefVol}_{\text{Opt}}$)

MRI Console:

- Drag the sequence down in the queue to create a copy
- Append its name with “_RefVolOpt_0p66”

Sequence card:

- Under *System > Tx/Rx > Ref. amplitude 1H*, enter $\text{RefVol}_{\text{Opt}} * \frac{2}{3}$
- 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 “_RefVolHWLimit_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

Large FOV sagittal acquisition

MRI Console:

- Copy Table Position, Centre of Slice groups and Sat Regions from the Large FOV DREAM
- Be sure to set Orientation to Sagittal and Phase Enc Dir to H-F
- Position the B0 shim adjust volume according to Figure 8

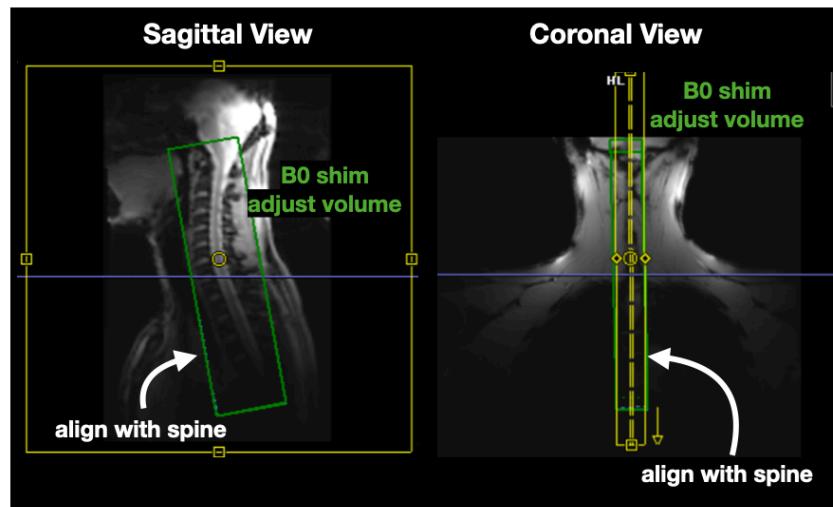


Figure 8. Positioning of FOV and B0 shim box for Large FOV sagittal coilQA scans.

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 $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - If $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{opt}}$
 - If you have a hardware limit:
 - If $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{HW_limit}}$ (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 $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{opt}}$
- 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*
- Re-adjust the central frequency, as described in Adjustment Step 1.

MRI console:

- Run the coilQA scan

Medium FOV sagittal acquisition

MRI Console:

- Copy Table Position, Centre of Slice groups and Sat Regions and adjustment volume from the Large FOV coil QA (the previous scan)
- Be sure to set Orientation to Sagittal and Phase Enc Dir to H-F

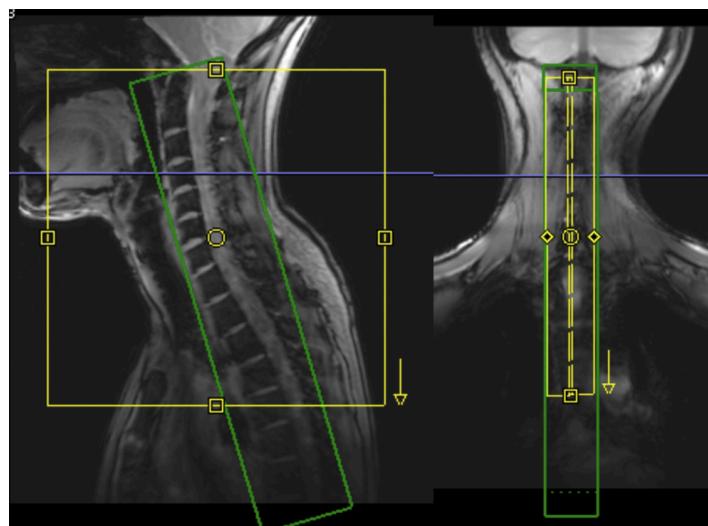


Figure 9. Positioning of FOV and B0 shim box for Medium FOV sagittal coilQA scans.

- 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"

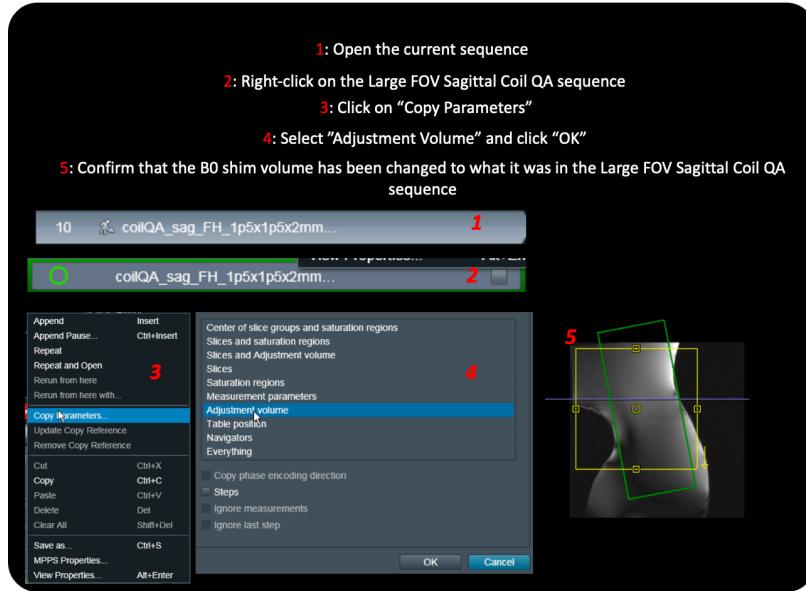


Figure 10. Guide on copying “Adjustment Volume”, eg the B0 shim box, from one scan to the next

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 $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - **If $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{opt}}$
 - **If you have a hardware limit:**
 - **If $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{HW_limit}}$** (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 $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{HW_limit}}$** (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{opt}}$
- **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*
- **Re-adjust the central frequency**, as described in Adjustment Step 1.

MRI console:

- Run the coilQA scan

Medium FOV axial acquisition

MRI Console:

- Copy Table Position, Centre of Slice groups and Sat Regions and adjustment volume from the Large FOV coil QA (the previous scan)
- Be sure to set Orientation to Transversal and Phase Enc Dir to R-L

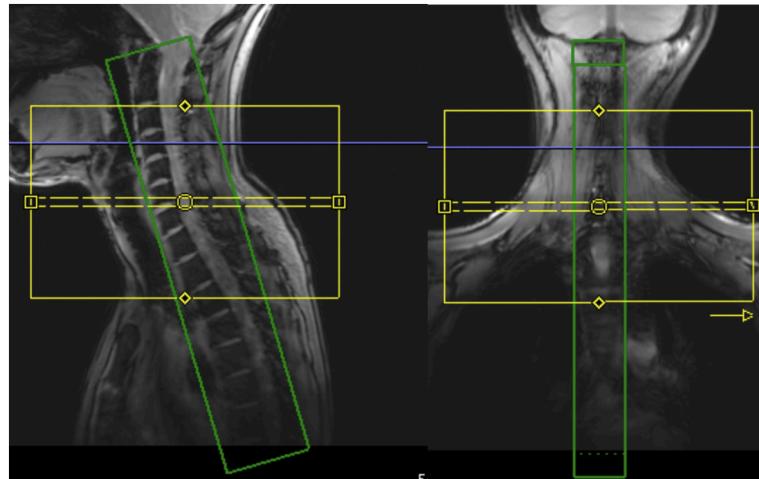


Figure 11. Positioning of FOV and B0 shim box for axial coilQA scans.

- 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 $\text{RefVol}_{\text{Opt}} > \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - If $\text{RefVol}_{\text{Opt}} < \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{Opt}}$
 - If you have a hardware limit:
 - If $\text{RefVol}_{\text{Opt}} > \text{RefVol}_{\text{HW_limit}}$ (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 $\text{RefVol}_{\text{Opt}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{Opt}}$

- **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*
- **Re-adjust the central frequency**, as described in Adjustment Step 1.

MRI console:

- **Run the coilQA scan.**

GRE

- Copy Table Position, Centre of Slice groups and Sat Regions from the Large FOV coil QA (the previous scan)
- Be sure to set Orientation to Sagittal and Phase Enc Dir to A-P
- The adjustment volume is the same as the FOV
- 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.

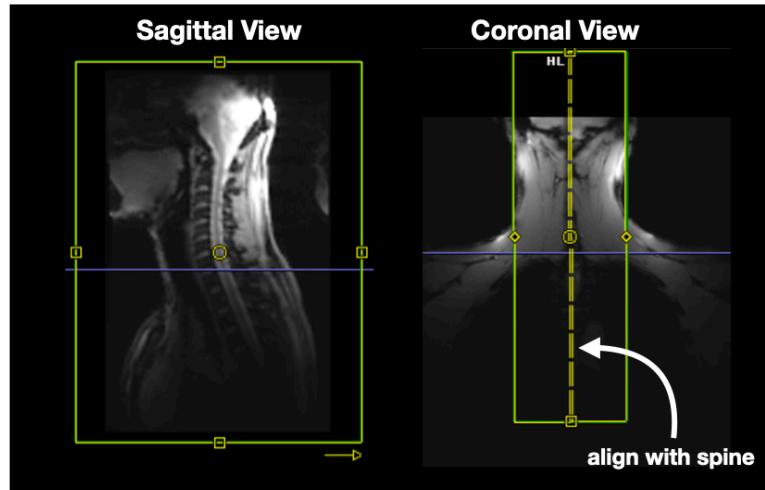


Figure 12. Positioning of FOV GRE scan.

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 $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - If $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{local_limit}}$ (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{opt}}$
 - If you have a hardware limit:
 - If $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{HW_limit}}$ (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 $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{HW_limit}}$ (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{opt}}$
- 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 on the scanner
- Navigate to C:/MedCom/MriProduct/PhysConfig
- Select the “SarDataUser.mat” file
- Check that it’s “Date Modified” value corresponds to the current scan sessions time

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 where you put 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 13 (the GRE scan).** The B0 shim volume should cover the whole FOV. If it does not, go to System > Adjust Volume, and click Reset.

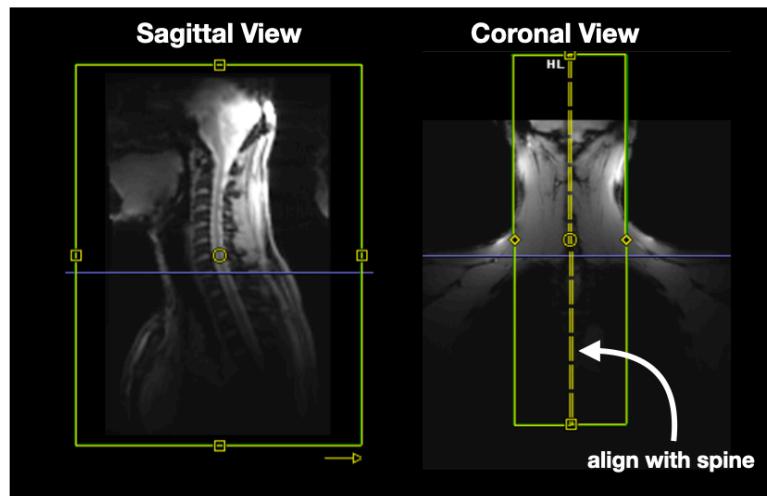


Figure 13. Positioning of FOV for TFL_rfmap scans

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 set correctly** by going to System > Tx/Rx > Ref. amplitude 1H
 - **If you have a local limit:**
 - **If $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is above your local limit): set it to $\text{RefVol}_{\text{local_limit}}$
 - **If $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{local_limit}}$** (i.e., the determined Reference Voltage is below your local limit): set it to $\text{RefVol}_{\text{opt}}$
 - **If you have a hardware limit:**
 - **If $\text{RefVol}_{\text{opt}} > \text{RefVol}_{\text{HW_limit}}$** (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 $\text{RefVol}_{\text{opt}} < \text{RefVol}_{\text{HW_limit}}$** (i.e., the determined Reference Voltage is below your hardware limit): set it to $\text{RefVol}_{\text{opt}}$

- 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*, and ticking *Unfiltered Images ON*.
- Re-adjust the central frequency, as described in Adjustment Step 1.

MRI console:

- Run the **RF_map 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 (<https://shimming-toolbox.org/en/latest>), Spinal Cord Toolbox (<https://spinalcordtoolbox.com/>), and FSLEYES (<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSLEYES>) 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 between C2/C3 and T2/T3. Enter first the bottom slice (T2/T3), then the top slice (C2/C3). 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.

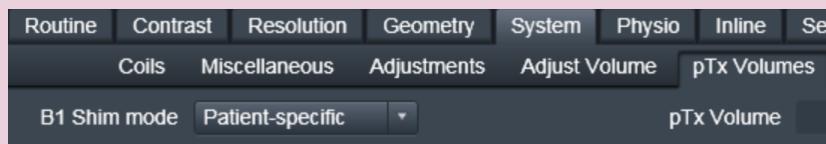


Figure 14. Location of the “B1 shim mode” switch

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



Figure 15. Workflow for applying B1+ shim weights

DREAM B1+ mapping

MRI Console:

- Drag the previously acquired **LARGE FOV DREAM 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”