Healthy Brain and Child Development Study (HBCD)

MRI-Tech SOP for Siemens XA30

(General Distribution Version derived from v1.7 for XA30)

Table of contents:

Section 1: Important Notes

A NOTE ON SETTING UP THE SEQUENCES

We recommend that the sequences be loaded to your machine as a group. This will keep the appropriate linkages between scans so that positioning is correct. This can be seen via the 'ribbon' icon next to each of the sequences. Thus, we do not recommend copying the individual scans over one-by-one by ones will break the links. If the links are broken between scans, please see the sections below on "what to do if the baby comes out of the scanner", as this section explains how to manually re-establish the links.

WHAT TO DO IF YOU HAVE ANY CONCERNS OR PROBLEMS WITH THE SCAN PROTOCOL

The protocol below was tested and worked on multiple scanners. **Please do not make any adjustments to the sequences unless the machine will not run unless changes are made**.

A NOTE ON PA/AP ACQUISTIONS

Sequences that are collected AP vs PA (e.g.., BOLD, field maps, DWI) have been tested and correctly acquired in the specified direction. Parameters have been properly set and you should NOT adjust these (or any other) parameters.

HEAD COIL

The 32-channel head coil is preferred. If your site has access to both the 32channel and 64-channel coils, please use the 32-channel.

STIMULATION ERRORS

The protocol below was tested and did not elicit any stim or SAR errors during piloting

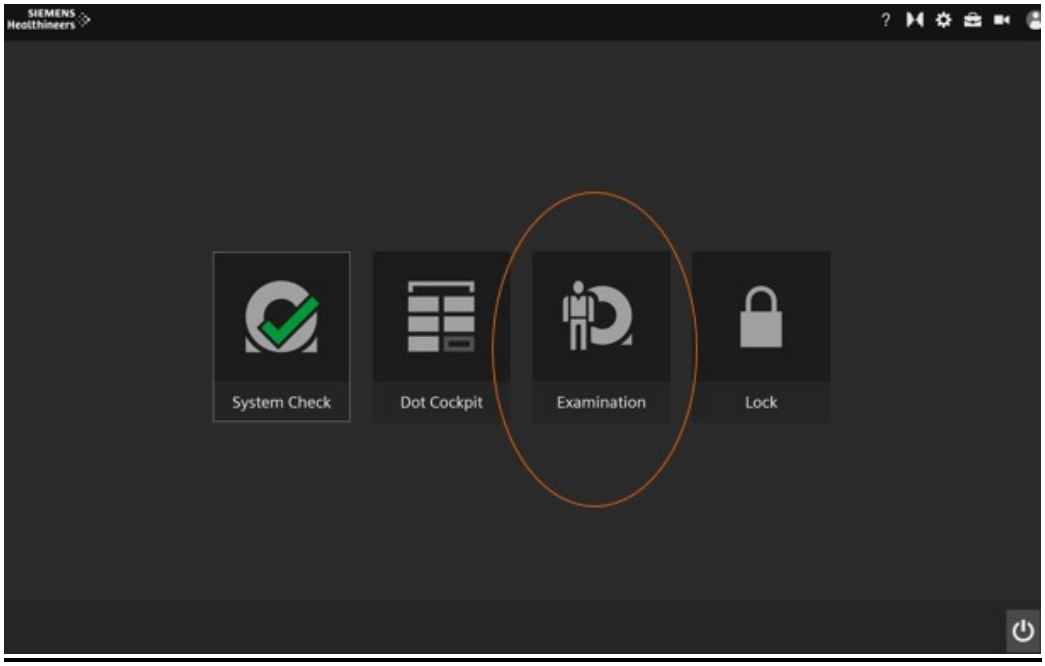
IF BABY COMES OUT OF THE SCANNER DURING THE PROTOCOL:

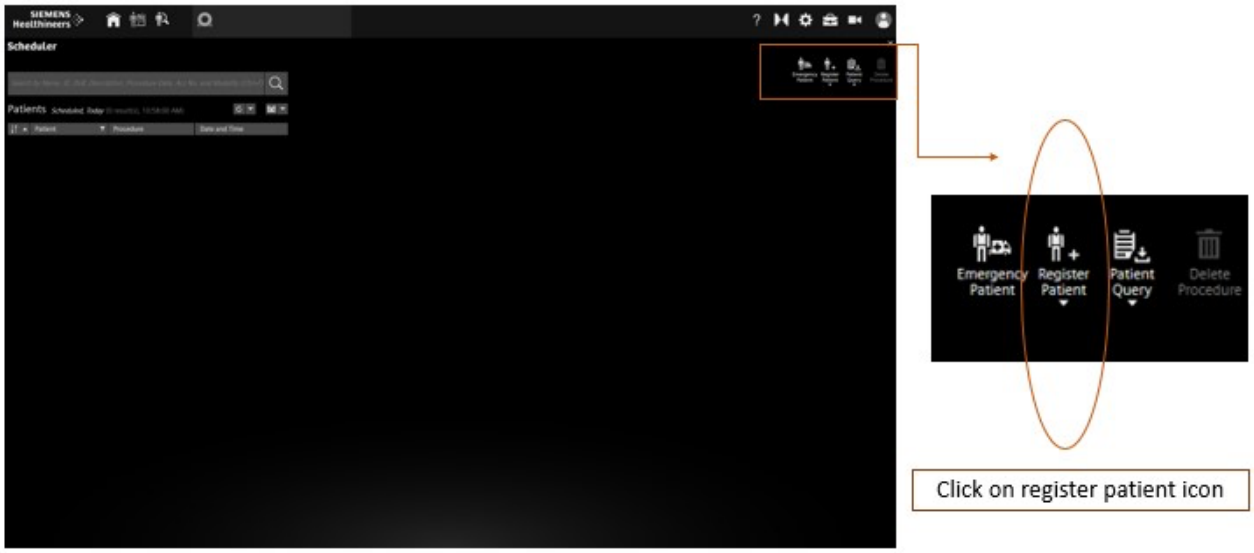
Please follow instructions located towards the end of this document.

Section 2: MRI Scanning

2.1 PARTICIPANT REGISTRATION

From the home screen (as seen on the picture), click on Examination icon and click on register patient icon shown in the picture.

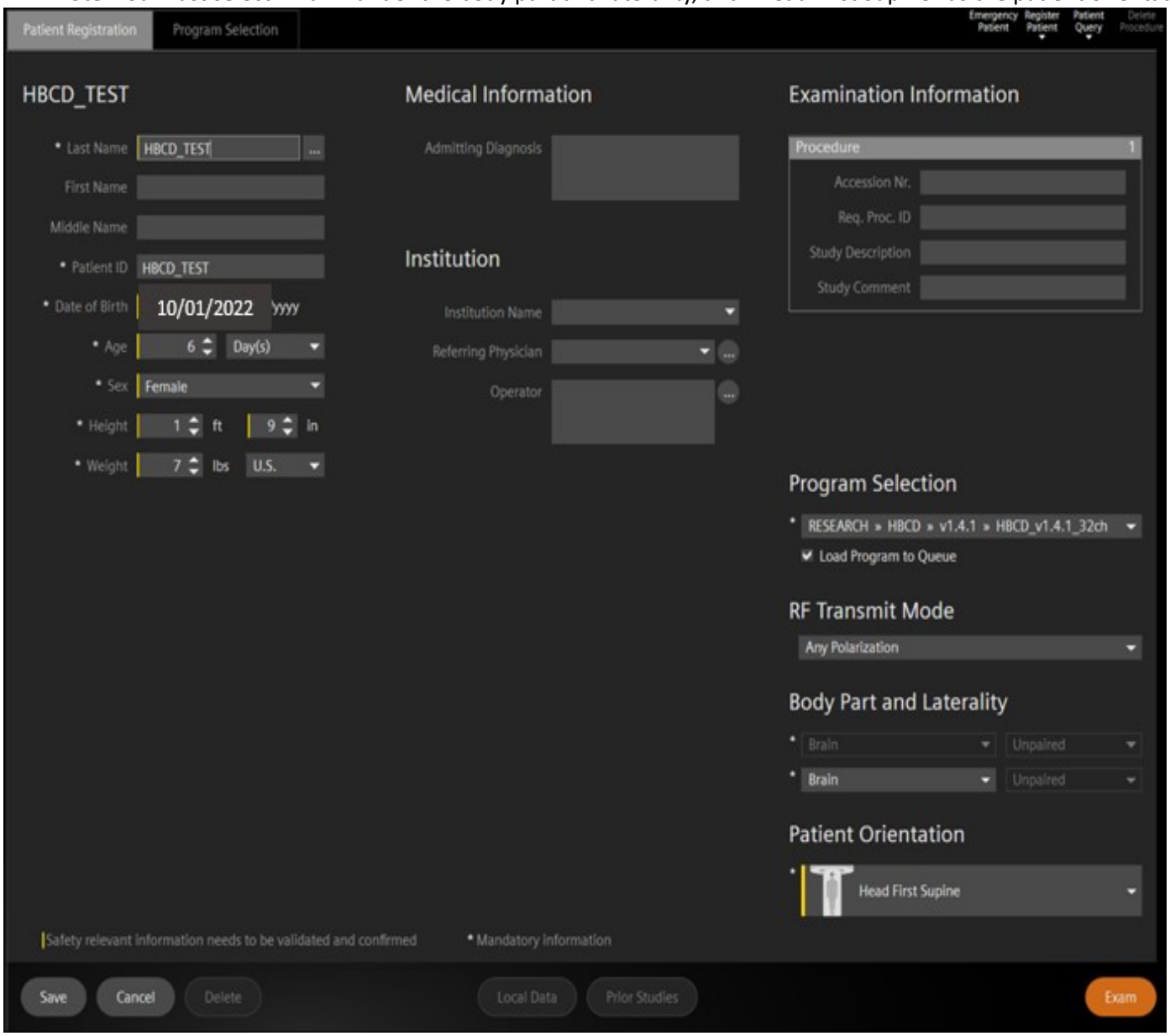




2.2 REGISTRATION INFO

Enter participant information as seen in the image of a typical registration page for an MRI scan (see below). All sections marked with * in subject registration page must have data input to start the exam. Click on the orange **Exam** icon when you complete all the required fields in the registration form, and you are ready to begin the scan.

Note: You must select "Brain" under the body part and laterality, and "Head First Supine" as the patient orientation.



Your exam card should look like as shown in the picture (for XA30 seq version 2.1)

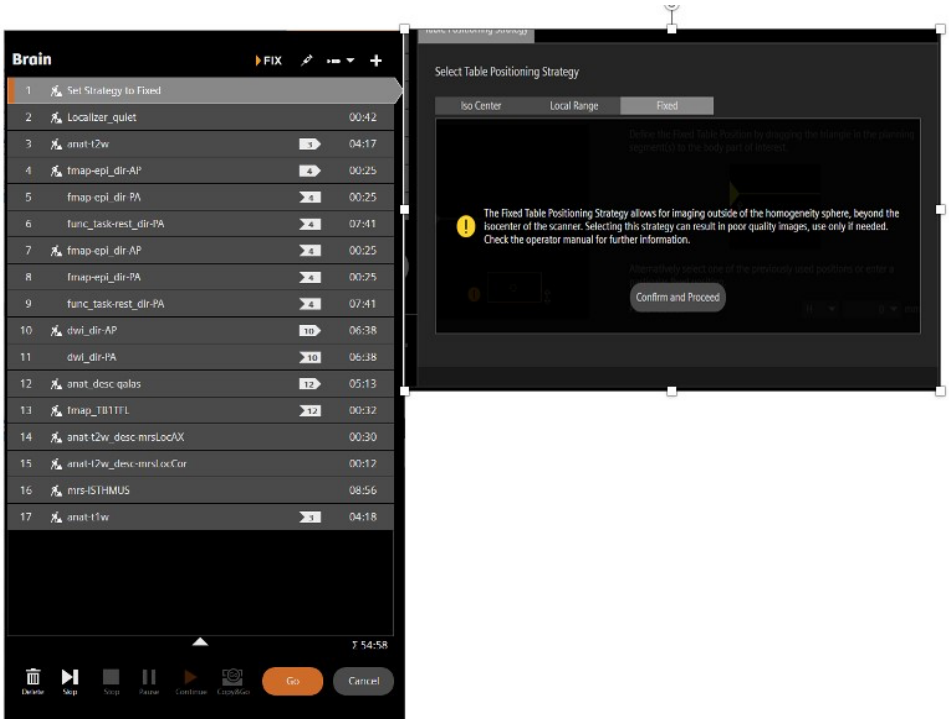
2.3 MRI ACQUISITION

First, to avoid unwanted table movement during scanning, we provide a table positioning strategy called "**Set Strategy to Fixed".**

Please note, your protocol may already be in FIX mode when you load the protocol (depending on how you get the protocol to load, selecting on registration vs dragging it over).

If you see the orange arrow next to “FIX” then the procol is in the correct mode. You can open “Set Strategy to Fixed” by double clicking it, click the orange “Go” Button, and proceed to **Localizer_quiet**.

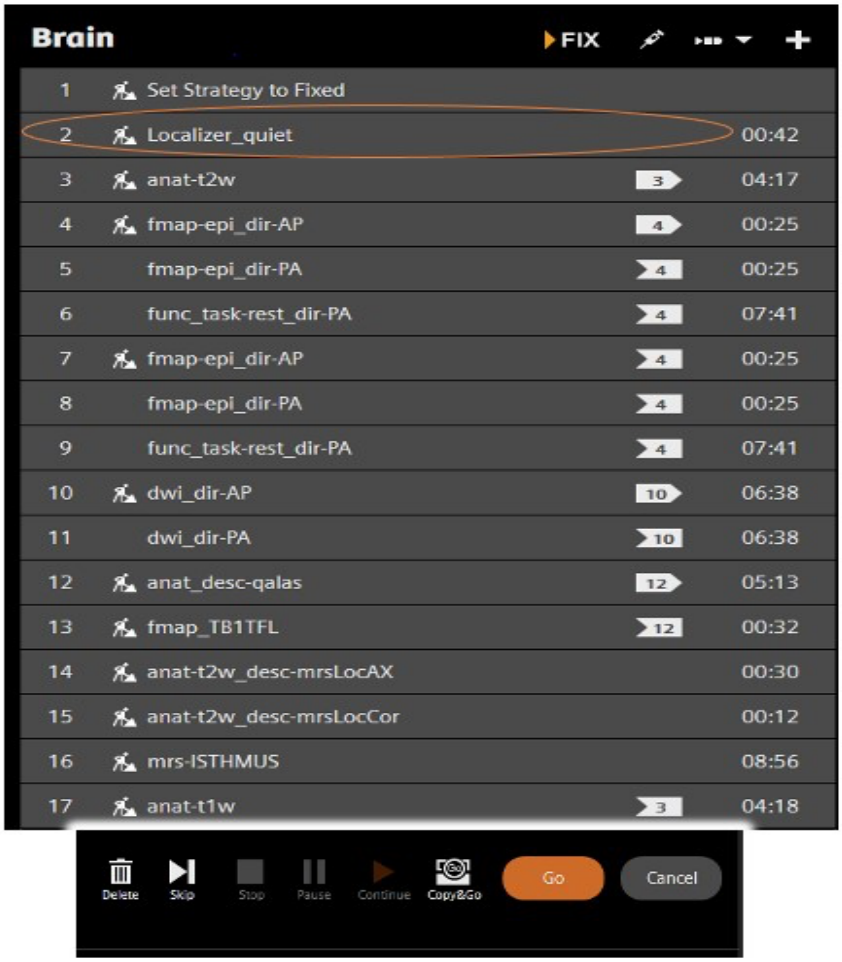
If the protocol is not in FIX mode (e.g., if you see the letters LOC instead of FIX): Double-click "Set Strategy to Fixed" to open it. Then, select "Fixed" and click "Confirm and Proceed" as shown in the figure below, and then click the orange "Go" icon [to save].



● Press **continue** (a red triangular button located at the lower middle area of the sequence card as seen in the picture) and proceed to "**Localizer_quiet**."

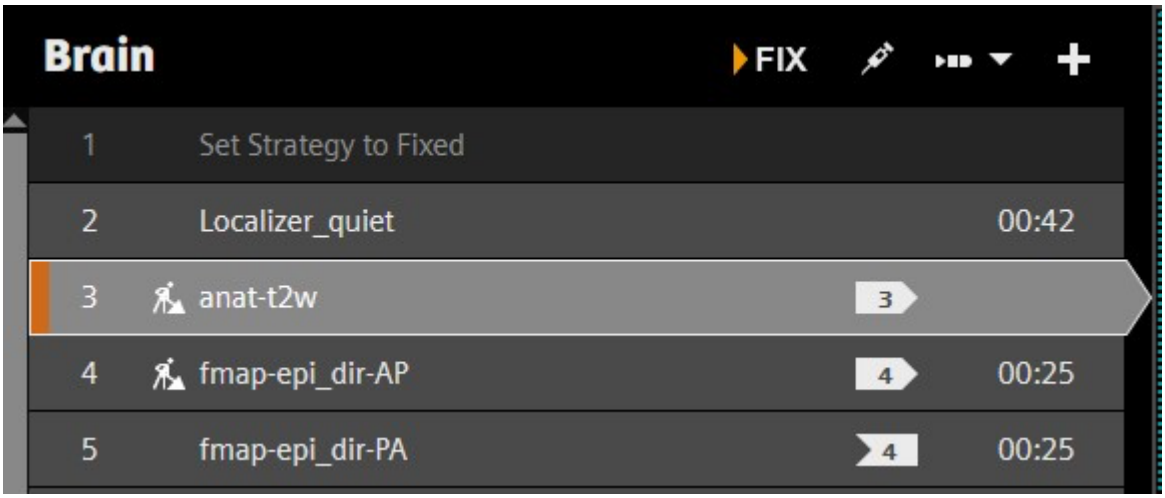
2.3.1 LOCALIZER_QUIET

● Double-click the **Localizer_quiet**
● Click the orange "Go" icon when ready to start collecting localizer scan.



2.3.2 ANAT-T2W

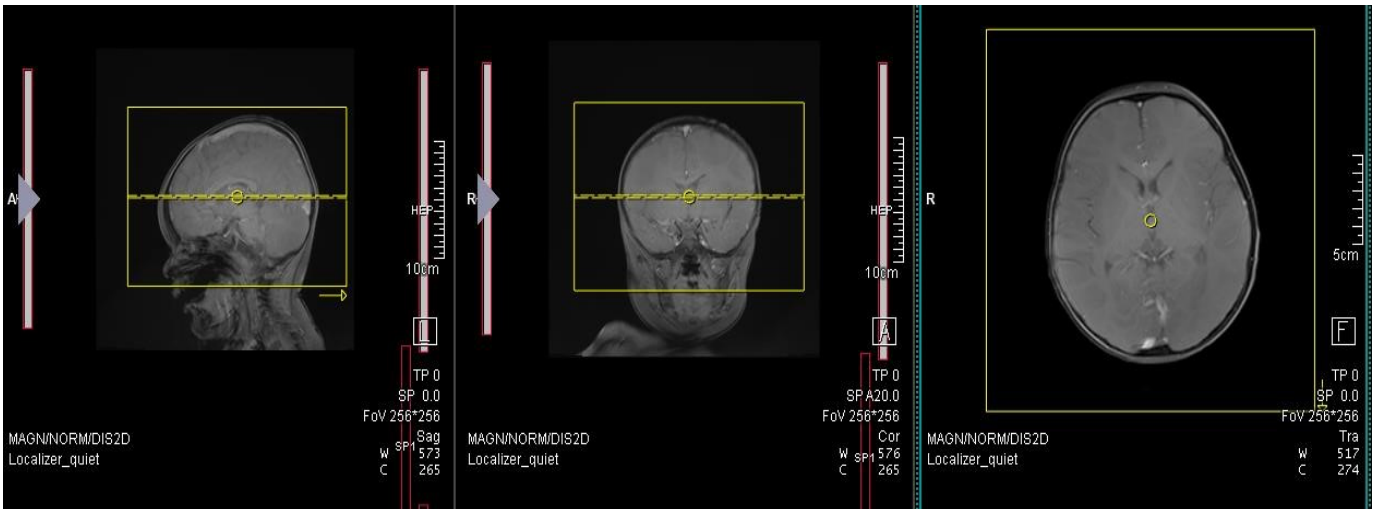
- Important: In v2.1 of the HBCD protocol, the anat-t2 is not configured to send motion data to FIRMM. This is intentional.
- After you run **Localizer_quiet**, the **anat-t2w** will be ready to be set up. Before making any change/setting up the **anat-t2w** sequence, please read below the "**IMPORTANT NOTE ON ALIGNMENT BOX".**

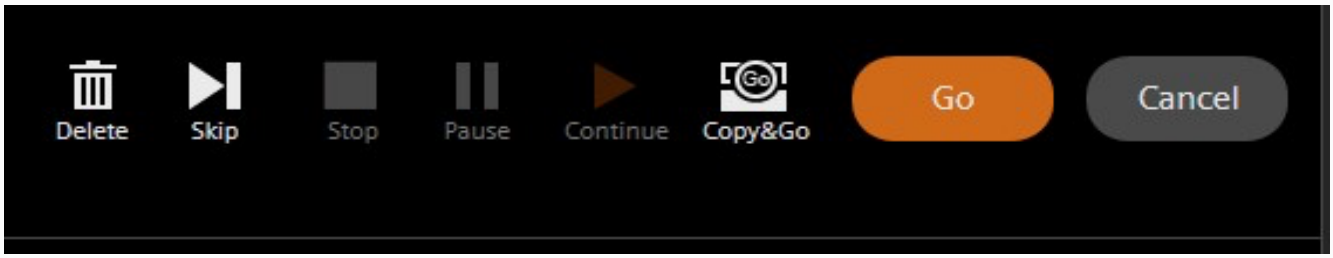


- Once **anat-t2w** is open, **DO NOT ROTATE OR ANGLE THE YELLOW BOX**. Only move the yellow box to center the brain and make sure you have full coverage (first image shown below). Then, you can click the orange 'go' button (second image shown below) to save changes. You may also see a blue navigator FOV box. Do not move the navigator box.

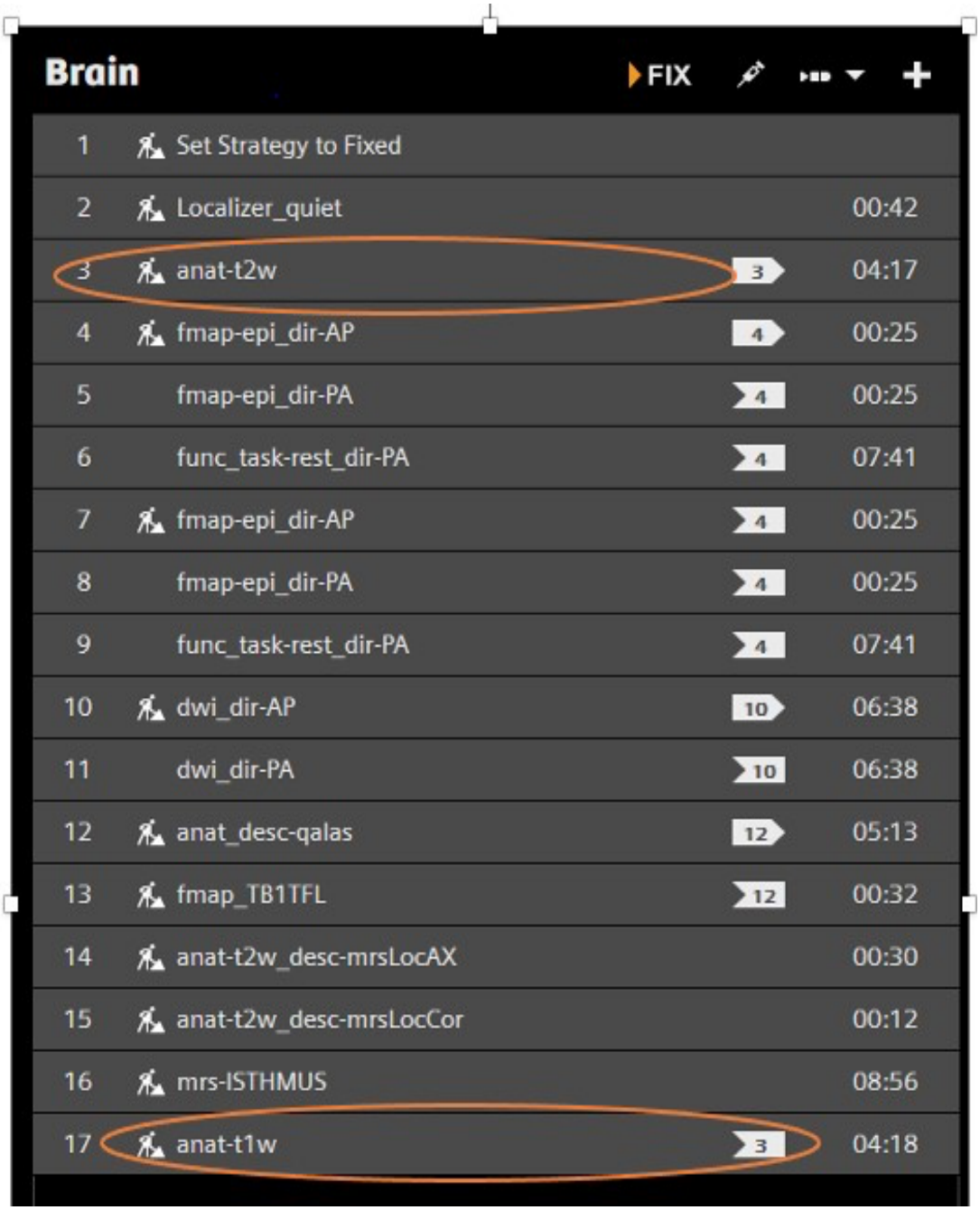
AN IMPORTANT NOTE ON ALIGNMENT:

- Please note that the general strategy is to center image acquisitions but NOT to rotate the field of views. i.e., we are **NOT** doing ACPC alignment, **NOR** do we rotate the FOV even if the localizer indicates that the brain is rotated a bit.
- The exception to this rule is the acquisition of the two MRS localizers used to position the MRS scan that immediately follows (mrs-ISTHMUS). See acquisition-specific instructions below for details.



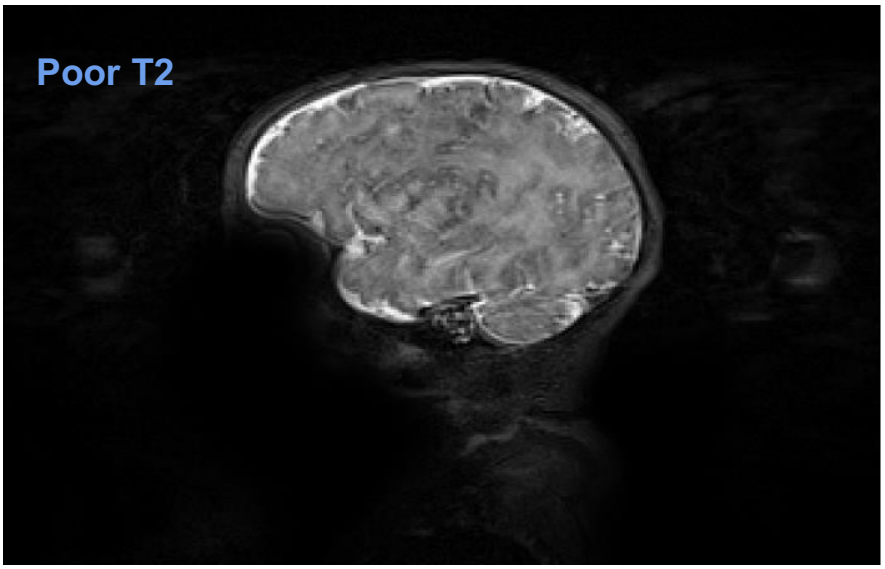


- Once **anat-t2w** parameters are applied (i.e., saved in the previous step), they will automatically copy over to **anat-t1w** sequence. See the image below: yellow circled sequence (currently labeled with "3" ribbon, note- ribbon number may slightly vary from version to version, in case there are future changes, currently we are using **version 2.1 of HBCD-sequence for this demonstration**)

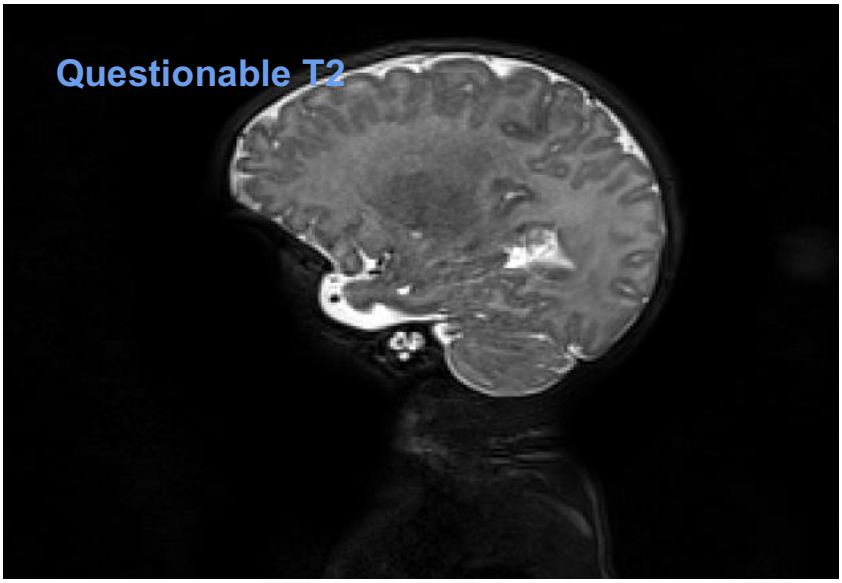

Brain
FIX
1 Set Strategy to Fixed
2 Localizer_quiet 00:42
3 anat-t2w 3 04:17
4 fmap-epi_dir-AP 4 00:25
5 fmap-epi_dir-PA 4 00:25
6 func_task-rest_dir-PA 4 07:41
7 fmap-epi_dir-AP 4 00:25
8 fmap-epi_dir-PA 4 00:25
9 func_task-rest_dir-PA 4 07:41
10 dwi_dir-AP 10 06:38
11 dwi_dir-PA 10 06:38
12 anat_desc-qalas 12 05:13
13 fmap_TB1TFL 12 00:32
14 anat-t2w_desc-mrsLocAX 00:30
15 anat-t2w_desc-mrsLocCor 00:12
16 mrs-ISTHMUS 08:56
17 anat-t1w 3 04:18

anat-t2w-IMAGE QUALITY

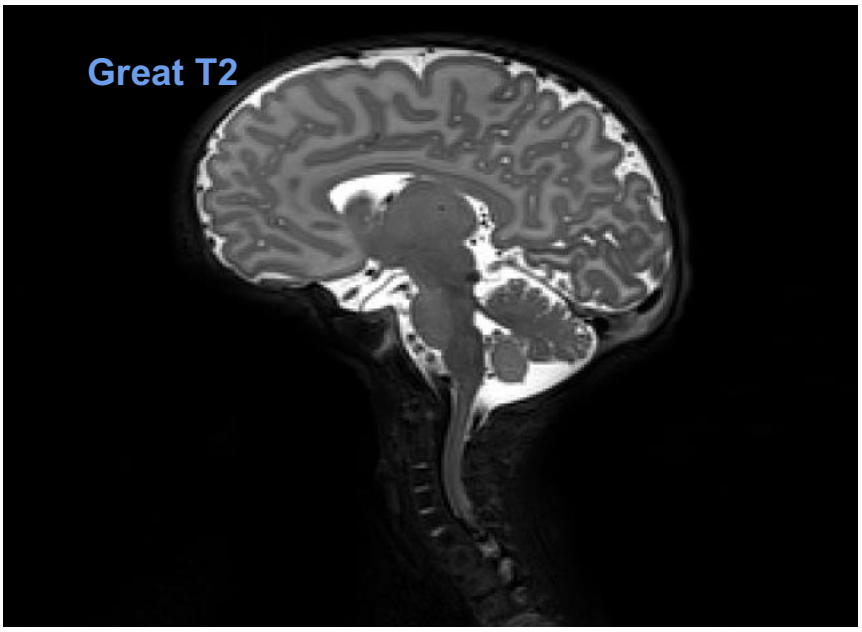
Poor T2: Below is an example of a **poor T2**; note the ghosting around the brain and the lack of distinction between white and grey matter.



Questionable T2: Below is an example of a **questionable T2**; you would ideally like to have a better image than below, but this can still be run for analysis. Note the banding at the top part of the brain; while there is some clarity it would be helpful to train and obtain an image with more clarity and distinction.



Great T2- note the very clear distinction of white and grey matter, lack of banding, and ghosting.



Also, look at the last image is from the **same T2 above**; note that it's typical to get something looking like this in the area between hemispheres, and it's OK! There is still clarity of white and grey matter with no ghosting or banding.

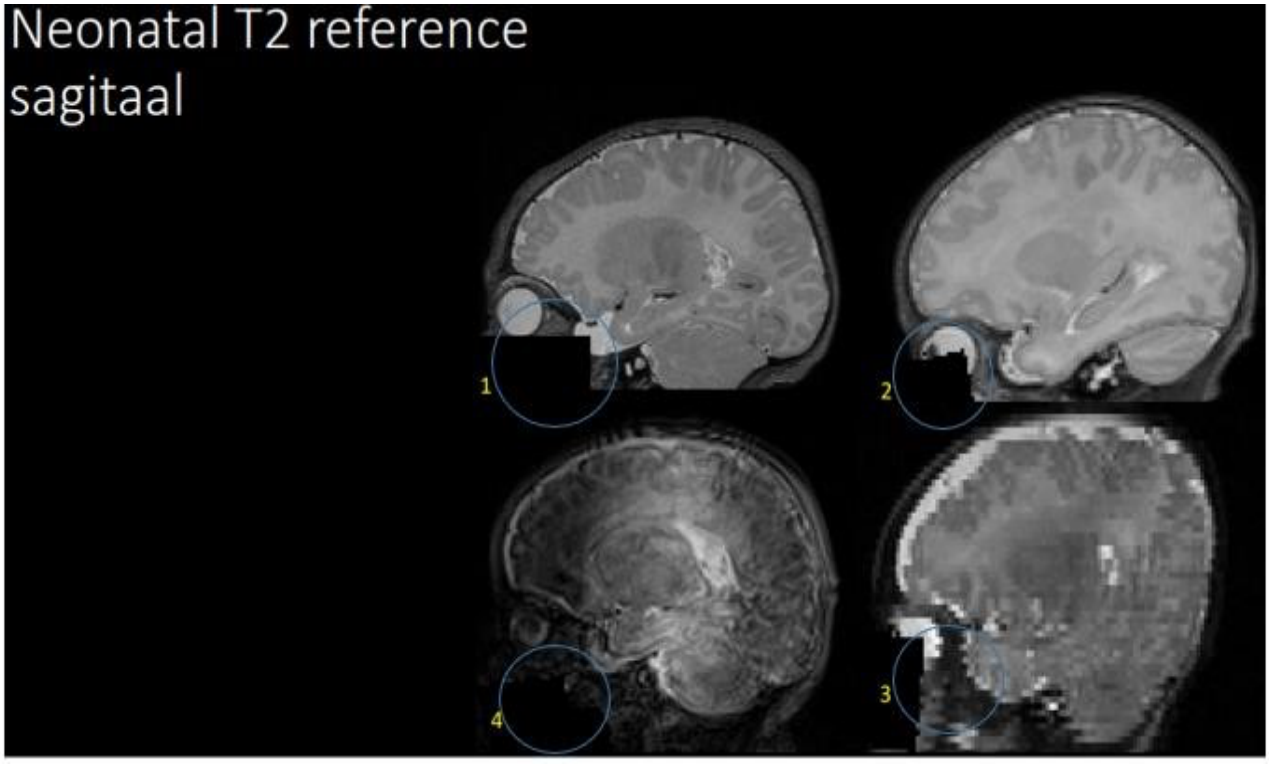
<u>** USABLE T2W-Image ***</u>**

<u>T2 Marker of Success:</u>

******Image quality has to be at least a "2" based on the images below in order to be usable. Ideally, the #2 is closer to the 'good' image *****.

The images below show a T2 sagittal reference picture. The pictures are rated on a scale of 1-4 (1 and 2 being passing brain images).

- The **number 1** on the first brain image below shows **a "good" T2.** This is indicated by no visible motion or minor artifacts throughout the image and minor banding.
- The **number 2** on the second brain image below shows a **"mild" T2**. This is indicated by moderate artifacting such as hemodynamic and eye motion artifact (noted most often in the ventral part of the brain) or mild artifacts on many slices throughout the image. In the example image below, we have rated it "mild" due to "ringing" artifacts at the top of the brain.
- The **number 3** on the third brain image below shows a **"moderate" T2**. This one is considered questionable. This is indicated by heavy artifact on more than two slices when scrolling through the images but not throughout all acquired images in the T2 or moderate artifact throughout the image.
- The **number 4** on the fourth brain image below shows a **"severe,"** and this would be a failing T2. This is indicated by heavy artifact throughout the image.



2.3.3 FIELD MAP PAIR (fmap-epi_dir-AP, fmap-epi_dir-PA)

The current version of the HBCD protocol has two field map pairs.

After **anat-t2w** is finished running (or even while it is still running), double click on the 1st field map scan (**fmap-epi_dir-AP**, red circle below). Then, adjust the yellow boxes (Field of View) in 'positioning window'. See the image on next page.

- Move yellow boxes so it covers the to the entire brain.
- Yellow dot should be in the middle of the brain.
- ONLY MOVE THE FIELD OF VIEW UP AND DOWN AND SIDE TO SIDE TO CENTER. DO **NOT** ROTATE THE FIELD OF VIEW, WE ARE NOT ACPC ALIGNING THE ACQUISITIONS.
- Apply changes by clicking the orange 'go' button (also to run field map scans)
- These parameters will copy over to all sequences with the same ribbon number (see light blue circle in image).

Note: If the 'working man' icon goes away after applying these changes and if you would like them back, please click on the location of the working man icon to bring them back.

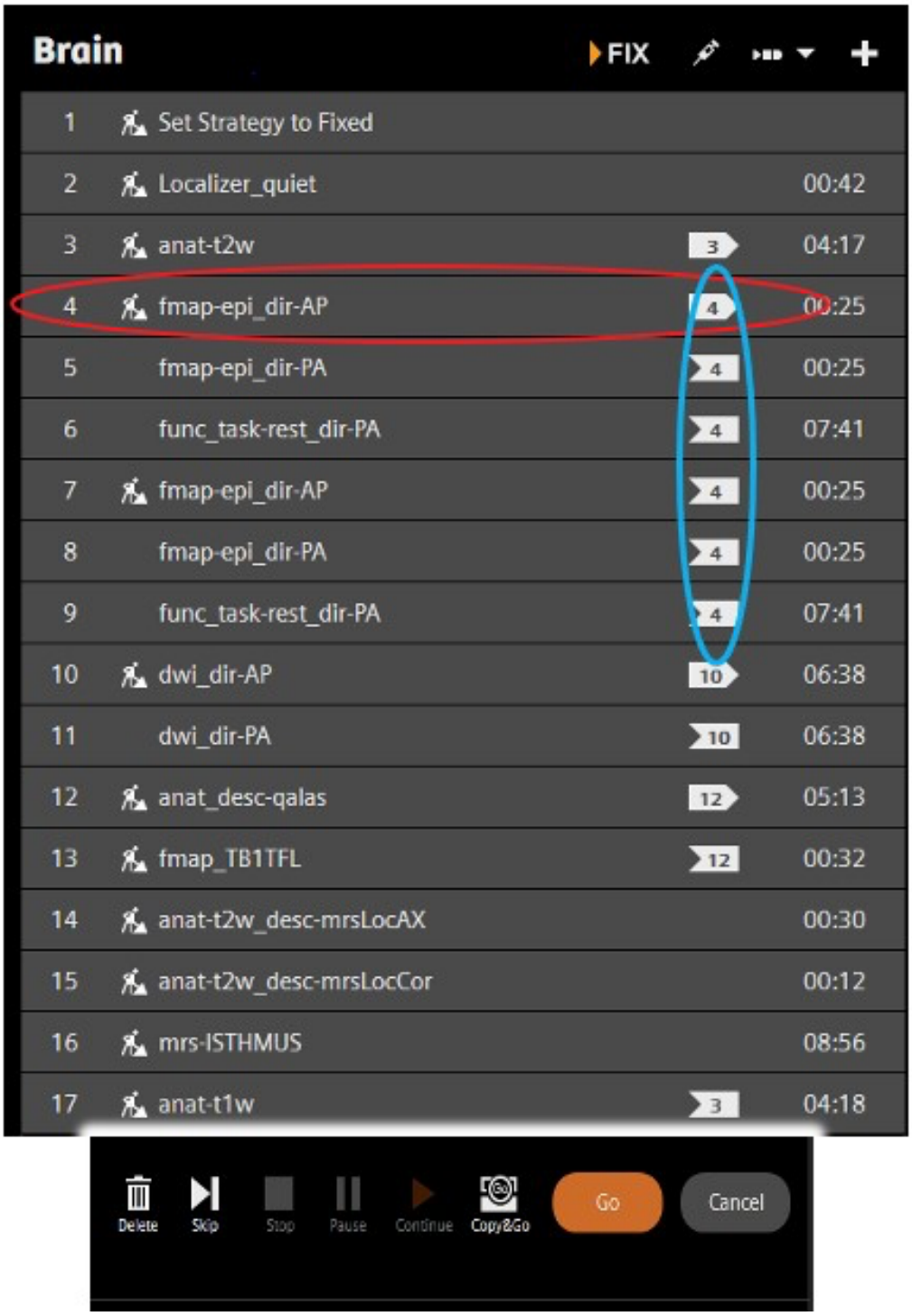
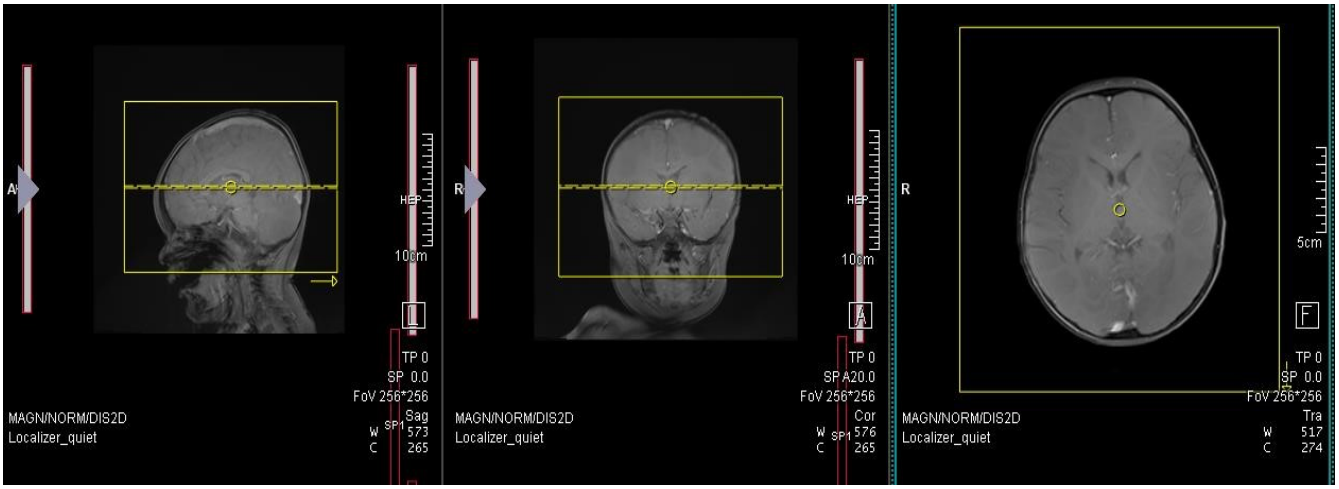


Image of aligning acquisition of field map:



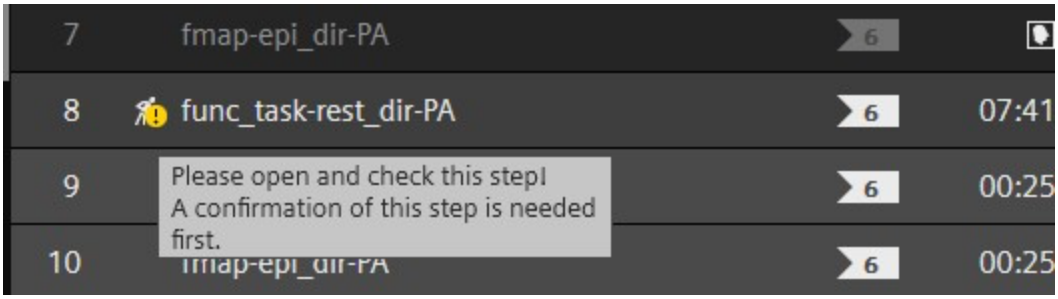
Note: Any following field maps will automatically run after aligning the first set.

****** USABLE FIELDMAP *****

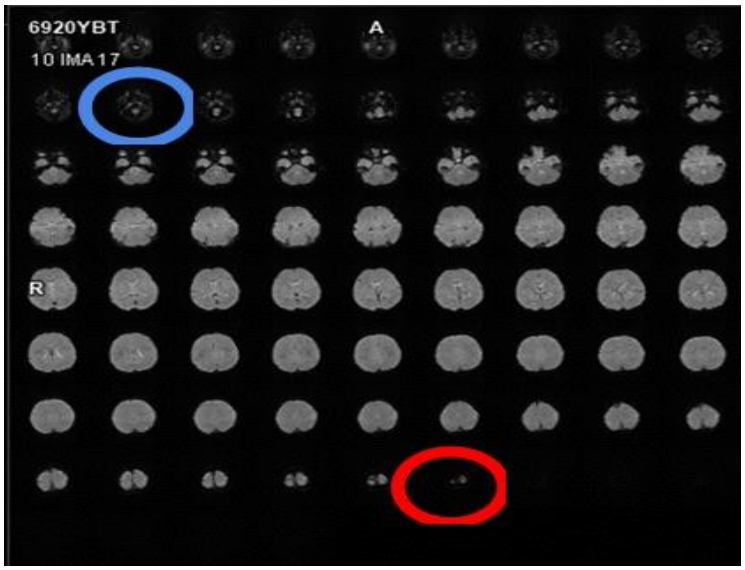
Field Map Marker of Success: In order to have usable data, we need acquired volumes (least one of the field maps) to have little or no movement artifact. For this, check if there is blurring/ field of view cut off or any evidence of a significant movement.

2.3.4 BOLD (func_task-rest_dir-PA)

- The BOLD sequences should run automatically following the field maps and not require any additional user input. However, your scanner may pause showing a yellow exclamation mark (see below) asking you to open the sequence to confirm before proceeding. Double-click the sequence to open it and click the orange GO button without making changes. If there are concerns about alignment (e.g., not automatically copying the parameters from the field maps) see the section on what to do if the baby comes out of the scanner at the beginning of this document.



- During BOLD acquisition, please monitor (1) the inline display images as they are being collected, (2) FIRMM, and (3) the baby video monitor (if available).
- As you watch the BOLD data as they are being collected (in the inline display), verify that you have adequate coverage of the whole brain (see images below).



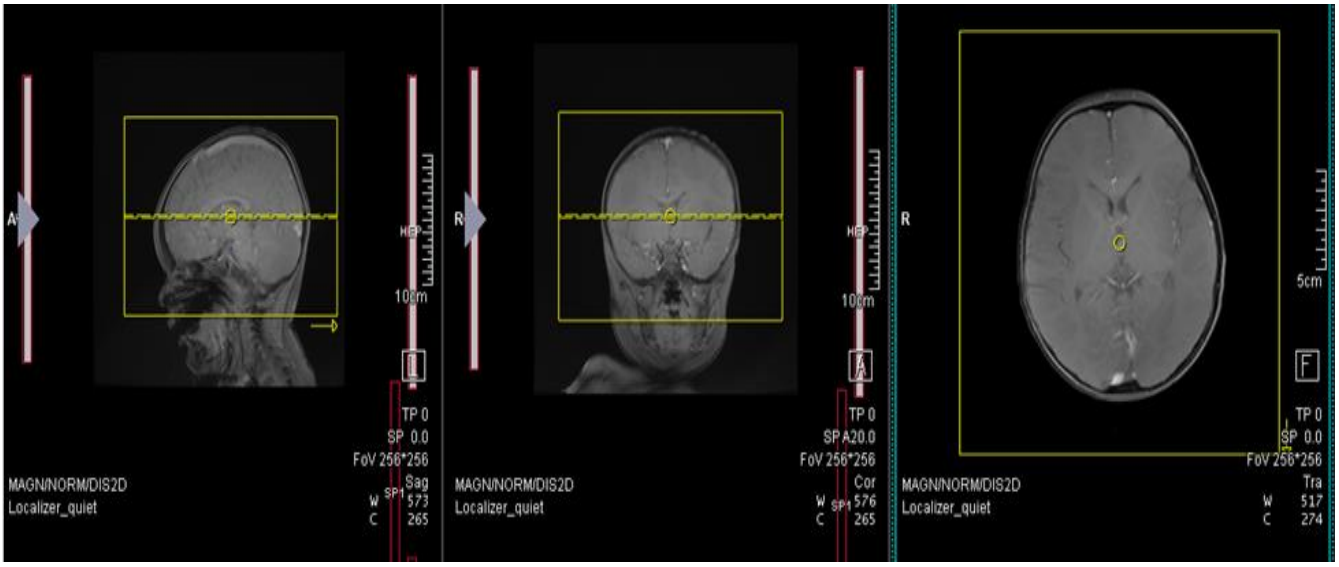
← In this picture, the blue circle shows where the bottom of the baby's brain ends and the red circle shows where the top of the baby's brain ends. Both top and bottom need to be seen to ensure that no part of the brain is being cut off in image collection.

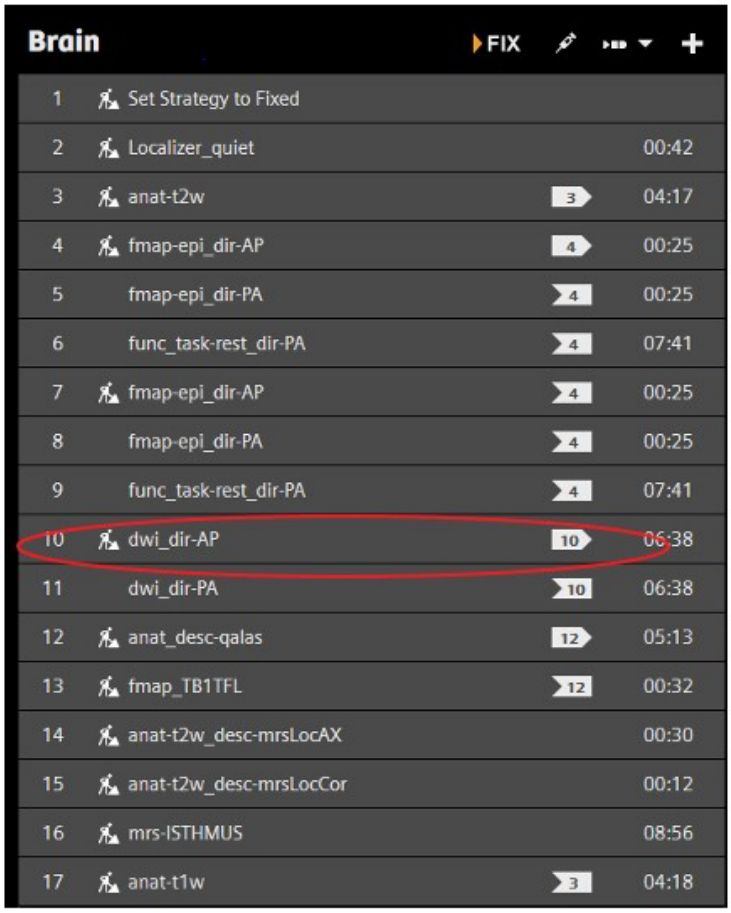
****** USABLE BOLD (REST) SCANS *****

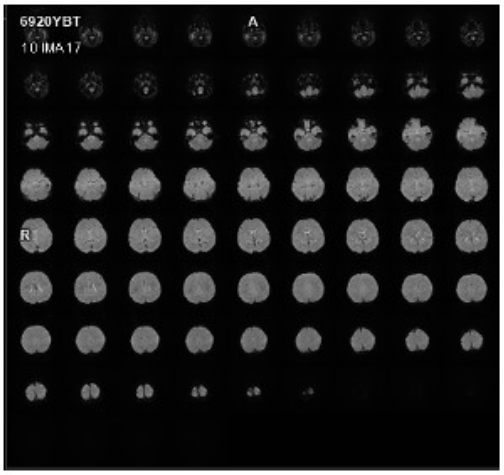
BOLD Data Marker of Success: In order to have usable BOLD data, we need to have (1) full brain coverage as indicated in the example images above and (2) at least 7.5 minutes of usable BOLD data as indicated by FIRMM (see FIRMM instruction for detail). Note that we also need at least one of the field map volumes to not have much movement artifact (see "Field Map Marker of Success").

2.3.5 Diffusion Weighted Images (DWI; dwi_dir-AP, dwi_dir-PA)

- Now open the first DWI sequence (you can do this while other sequences are running or wait until you are ready to run the DWI).
- Line this up just like you would the BOLD field map (move the yellow box to center the brain and make sure you have full brain coverage like first image below). Do not rotate the field of view. Once lined up, click 'go' to start DWI sequences (At the same time, the parameters will copy to the remaining DWI sequence (which are currently labeled with "10" ribbon, shown in the second image below with a red circle).





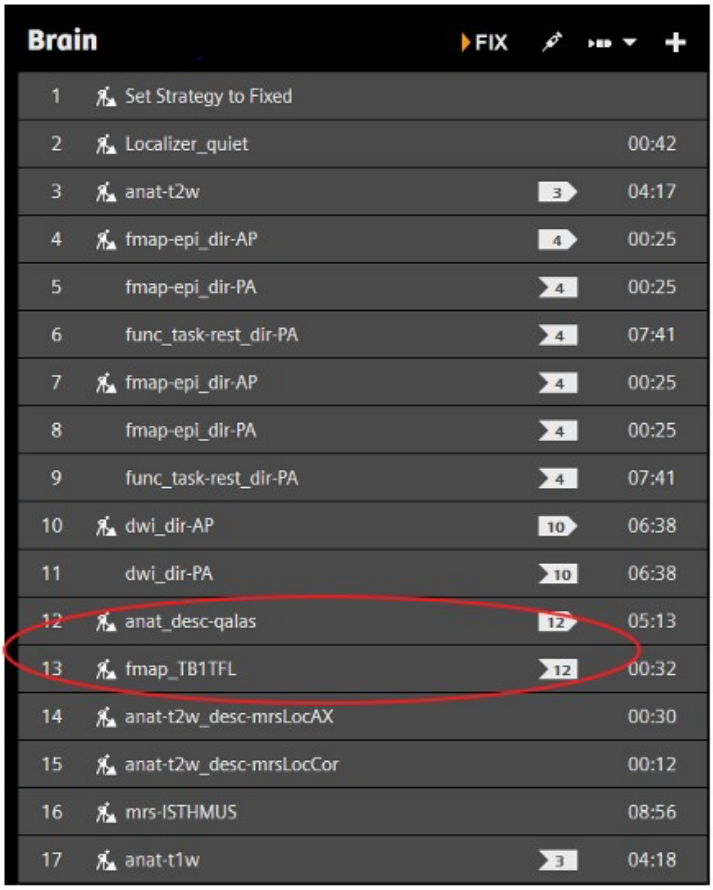


- The image above shows DWI sequence acquisition from the inline display (see BOLD protocol above for how to open this window). Note the full brain coverage, with the same markers for adequate coverage as the BOLD protocol above.

****** USABLE DWI SCANS *****

DWI Marker of Success: The marker of success is to obtain both A/P and P/A phase encoding series, with whole-brain coverage and no obvious artifacts. From the FIRMM objective markers, the success criteria will include a **minimum of 3 b=0 images** in each DWI series and a minimum of 60% diffusion encoding volumes from all DWI series.

2.3.6 QALAS (anat_desc-qalas) & FMAP_TB1TFL



- Open the **anat_desc-qalas** sequence to set it up, which should be prescribed in the same way as the **anat-t2w** scan. Do **NOT** rotate/angle/oblique the FOV box and only translate it in any direction so that it is centered around the brain, and you have full brain coverage (same procedure as described in the previous sections for other scan types). Once properly lined up, click on the orange "Go" button, and the FOV prescription parameters will copy over to the **'fmap_TB1TFL'** (which is currently labeled with the "12" ribbon)

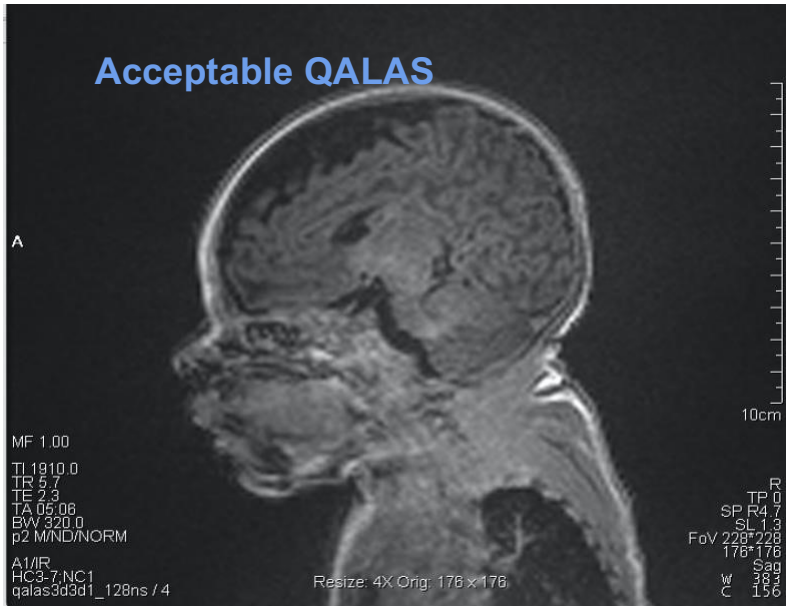
  anat_desc-qalas outputs several (5 sets) volumes each with different T1/T2 weightings. The third one is the most similar in contrast to a standard T1w, so we will use this one for quality review (see below), using the same rating methods and scales as **anat-t1w**. Rare problems, such as brain cutoff, will be noted.

**** USABLE QALAS SCANS ****

QALAS Marker of Success:

- We will be using a similar measure of success for the QALAS scans as we do for the **anat-t2w** images, as described above. Assess the image quality by examining the distinction of gray and white matter and whether motion artifacts are present.
- When deciding whether to repeat a QALAS scan or not, it is instructive to inspect the 3rd (out of 5) contrast of the QALAS images. On the XA30A platform, simply load the 3rd DICOM series in the "3D View" tool on the scanner's console. To do this, go to the MR "View&Go" Tab. Select the Series tab to view all images. Click on the QALAS images you just ran and click on dropdown arrow icon. Drag and drop the third image ("Volume_03") to view.

- Below is an example from a neonate. This image is also acceptable in quality.



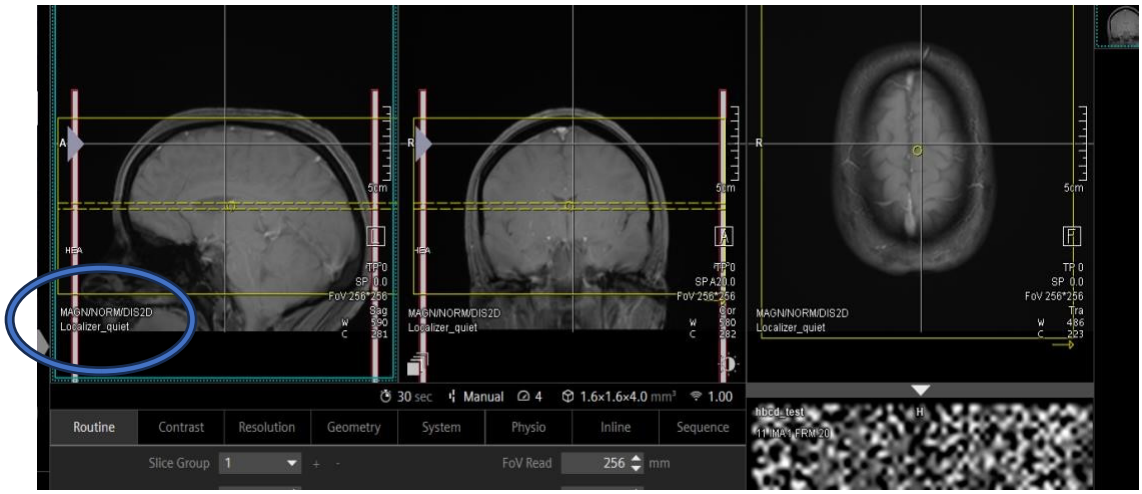
- Run **fmap_TB1TFL** sequence. Do not move the yellow box or change any parameters.

2.3.7 MRS LOCALIZERS (anat-t2w_desc-mrsLocAX, anat-t2w_descmrsLocCor)

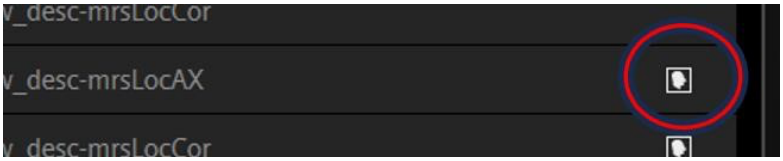
- The two MRS localizers are acquired to correctly position the subsequent Magnetic Resonance Spectroscopy (MRS) sequence (ISTHMUS) and are used in data processing.

2.3.7.1 anat-t2w_desc-mrsLocAX (also called the axial localizer)

- **Open anat-t2w_desc-mrsLocAX** by double clicking it. It should look like the picture below once opened. You should center the yellow box so that the whole brain is covered. You may angle the yellow box so that it is angled relative to the head position but the critical step is to make sure the ENTIRE brain is in the yellow box. **The yellow FOV box can be rotated ONLY for MRS localizers**.



- For accuracy in placement, **anat-t2w_desc-mrsLocAX** should **be planned/positioned** on the most recent imaging scan. If you believe that subject has not moved significantly after you ran the **localizer_quiet** then you can continue to position the box, otherwise **anat-t2w_desc-mrsLocAX** should **be planned/positioned** on the most recent imaging scan, which would be **fmap_TB1TF1** as lined up before this in the sequence chain. To load other images in the viewing windows, click and drag the image from the white box (see below) next to the desired sequence to the viewing window.



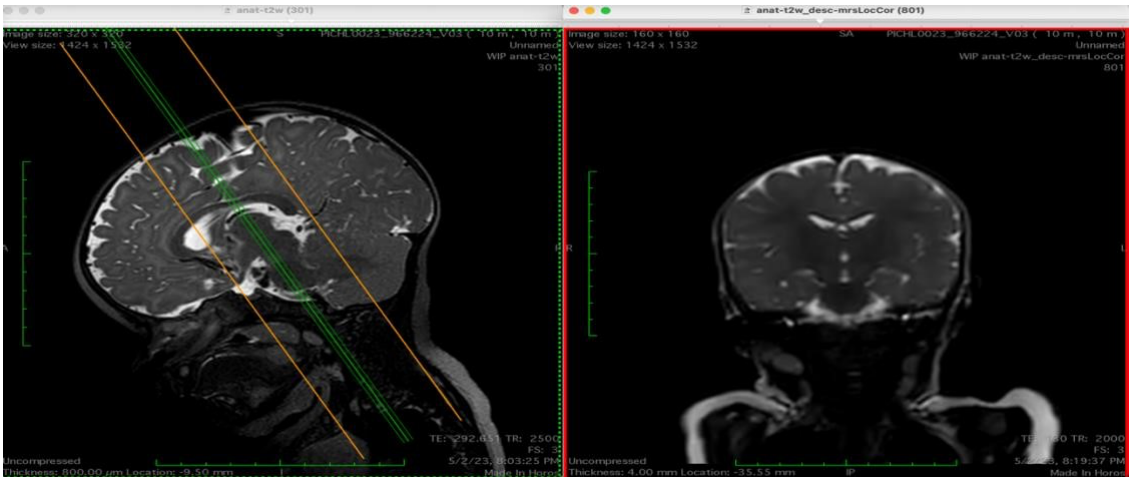
  - The yellow dot should be in the middle of the brain and the entire brain should fall in the yellow FOV box.
  - Once you are finished making changes, click orange 'go' button to apply.

2.3.7.2 anat-t2w_desc-mrsLocCor (also called coronal localizer)

- **If it did not open automatically, open anat-t2w_desc-mrsLocCor** by doubleclicking. It should look like the picture below once opened. This box does not cover the whole brain. This yellow box **MUST** be rotated and centered. Rotate the yellow box so that the angle of the volume is roughly aligned with the angle of the brainstem and the center of the box covers the mid-part of the brain. See

below examples. NOTE THAT THE FOV CAN BE ROTATED ONLY FOR MRS LOCALIZERS.

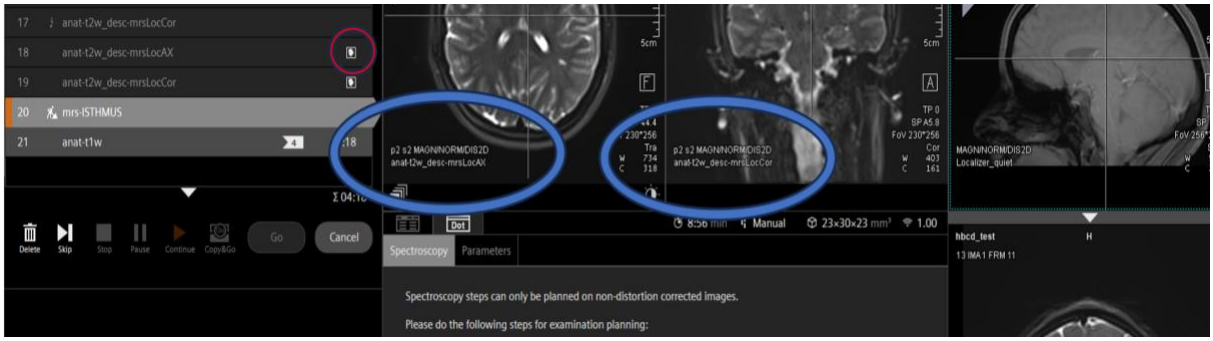
- 



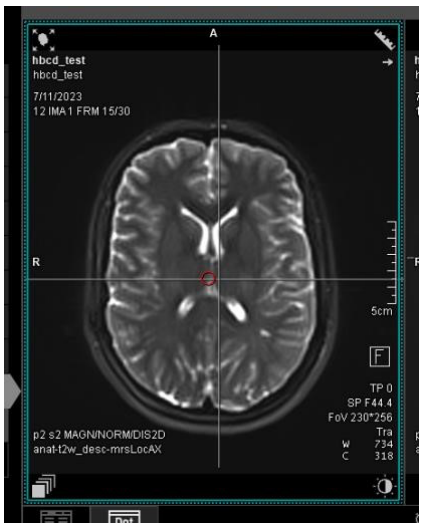
- The yellow dot should be in the middle of the brain to align this localizer.
- Once you are finished making changes, click the orange 'go' button to apply.

2.3.8 MRS-ISTHMUS

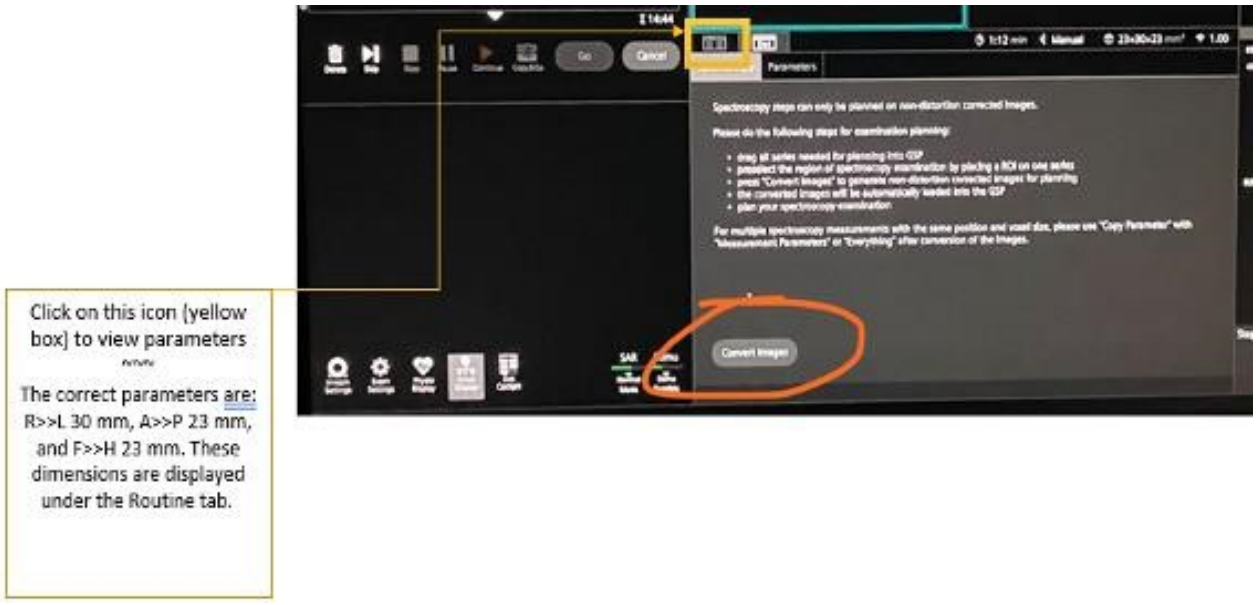
- If mrs-ISTHMUS is not already open, open **mrs-ISTHMUS** sequence by double clicking it. MRS-ISTHMUS is the main MRS sequence.
- Once you have run the two localizers, the images in the viewing panels may have shifted around. Check the lower left-hand side of the viewing panels to check which sequences are displayed (blue ovals in the below image).



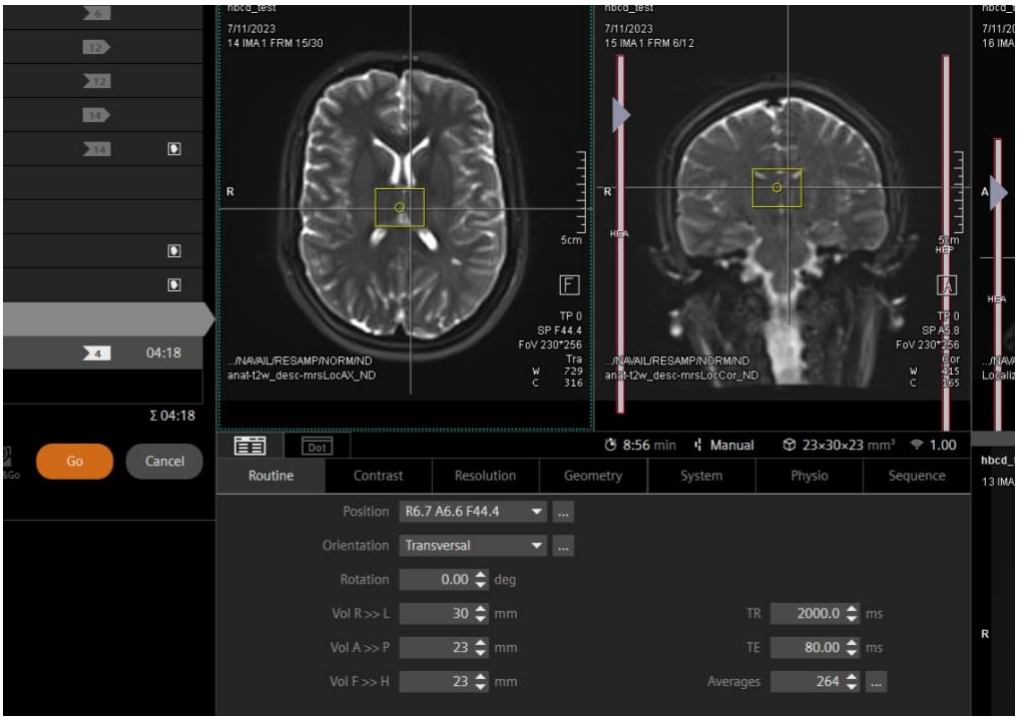
- You can load **anat-t2w_desc-mrsLocAX** into leftmost panel by clicking and dragging from the small white box next to the sequence name (indicated by the red circle in the image above).
- In the same way, load **anat-t2w_desc-mrsLocCor** into middle panel.
- Focus on the two MRS localizers. Ignore any other image (e.g. localizer_quiet.)
- Click once in the middle of the **anat-t2w_desc-mrsLocAX** image. You will see a red circle appear (if done correctly).



- Click "Convert images" (orange circle) and double check your parameters as seen in the below image. **The correct parameters are: R>>L 30 mm, A>>P 23 mm, and F>>H 23 mm.**



After you click "Convert Images", yellow boxes will appear in every panel (see below). This yellow box is your voxel. The arrangement of which localizer appears in which panel may have shifted. Position your voxel using the two MRS localizers and ignore any other image (e.g. localizer_quiet.)



Note: The image above is of an adult brain. Please refer to Section 3 for guidance on positioning the voxel in an infant.

Position MRS sequences (aligning with the thalamus)

The yellow box should be positioned as described in the section: **aligning with the thalamus** (see guidance on where to place the voxel in Section 3). Use both axial and coronal view images from the localizers to plan the voxel.

If the voxel boundaries are displayed in dotted lines, then the acquisitions are not happening on this slice. **Browse through the slices to find the voxel boundaries in**

solid line. Ensure that the planned location has voxel boundaries shown in solid line.

Once your voxel is in a desired location, please ensure that the voxel measurements are correct (it is possible that the voxel dimension might have changed accidentally because of dragging the edge of the voxel around while moving it, or the exam card settings might not have carried over correctly). The correct parameters are: R>>L 30 mm, A>>P 23 mm, and F>>H 23 mm. These dimensions are displayed under the Routine tab (as shown in a picture above).

- Once you are finished with the changes **on mrs-ISTHMUS**, click the orange 'go' button to apply. Run without further intervention.

2.3.8.1 MOTION DURING MRS

- PLEASE NOTE ALL MOTION IN THE SCAN LOG. Please include which sequence (e.g., **anat-t2w_desc-mrsLocAX** and **anat-t2w_desc-mrsLocCor, mrs-ISTHMUS**) and approximately when (e.g., minute 2), if possible.
- Mild motion (e.g., slight head movements during sleep or a few transient movements) will be managed during post-processing. No need to re-scan.
- Major motion (e.g., baby wakes up crying during the scan) such that you need to stop the scan, soothe the infant and re-start. If motion occurs in the middle of the ISTHMUS: please re-acquire **both MRS localizers followed by mrsISTHMUS.**

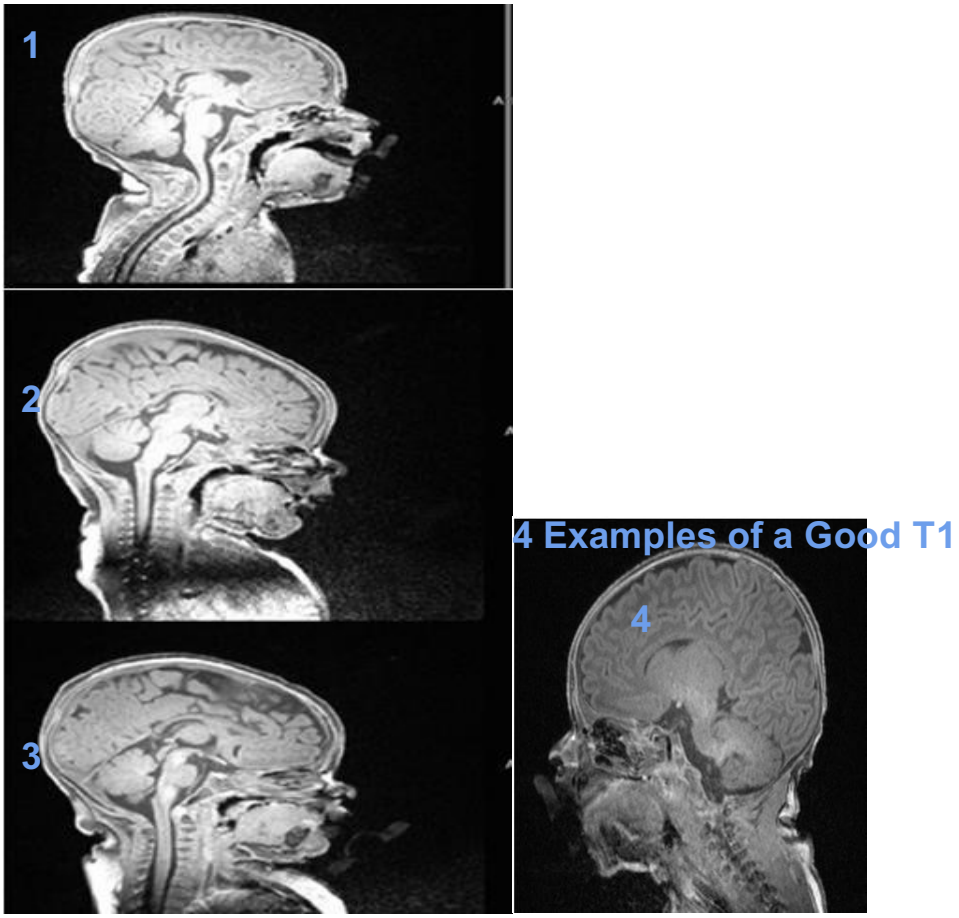
- Less than 2 minutes from the end, keep going through the end. (We can discard bad acquisitions in the post-processing.)

2.3.9. ANAT-T1W

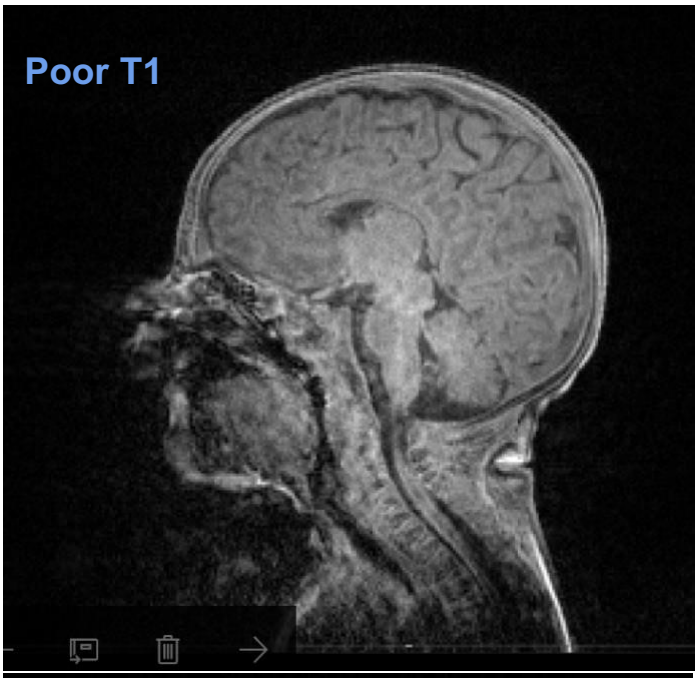
- Important: In v2.1 of the HBCD protocol, the anat-t2 is not configured to send motion data to FIRMM. This is intentional.
- Run **anat-t1w**. These parameters have already been applied previously with the **anat-t2w**. No aligning is needed. You may also see a blue navigator FOV box. Do not move the navigator box. In case, parameter is not copied, follow instruction on section: IF BABY COMES OUT OF THE SCANNER DURING THE PROTOCOL. The T1 sequences will start automatically. If it does not, double click the T1 and apply with the "go (or continue) button to begin T1 scan.

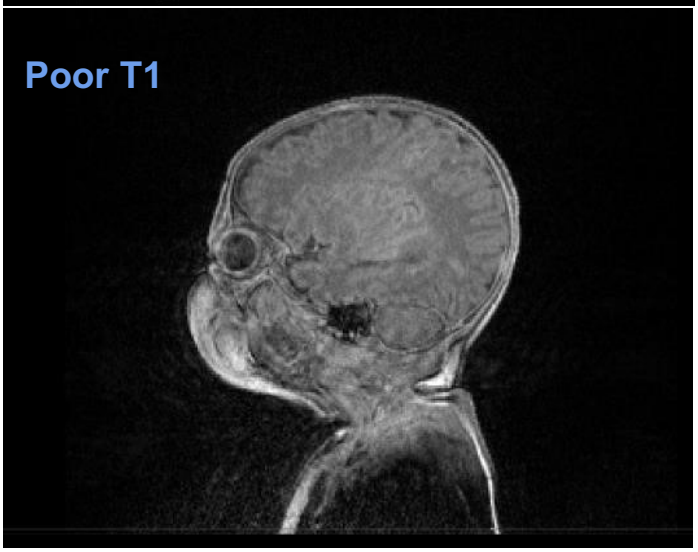
**** T1W-IMAGE QUALITY ***

Below are a few examples of a **good T1** in an infant:



Below are examples of a **poor T1** in an infant:


Poor T1

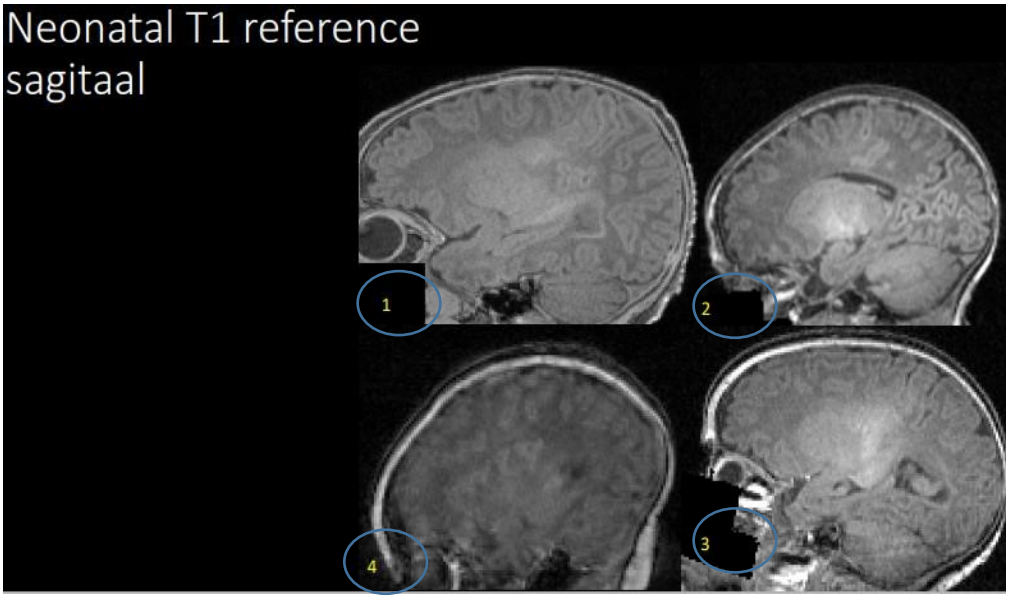

Poor T1

**** USABLE T1W-Image ***

T1 Marker of Success: Image quality has to be at least a "2" based on the images above in order to be usable.

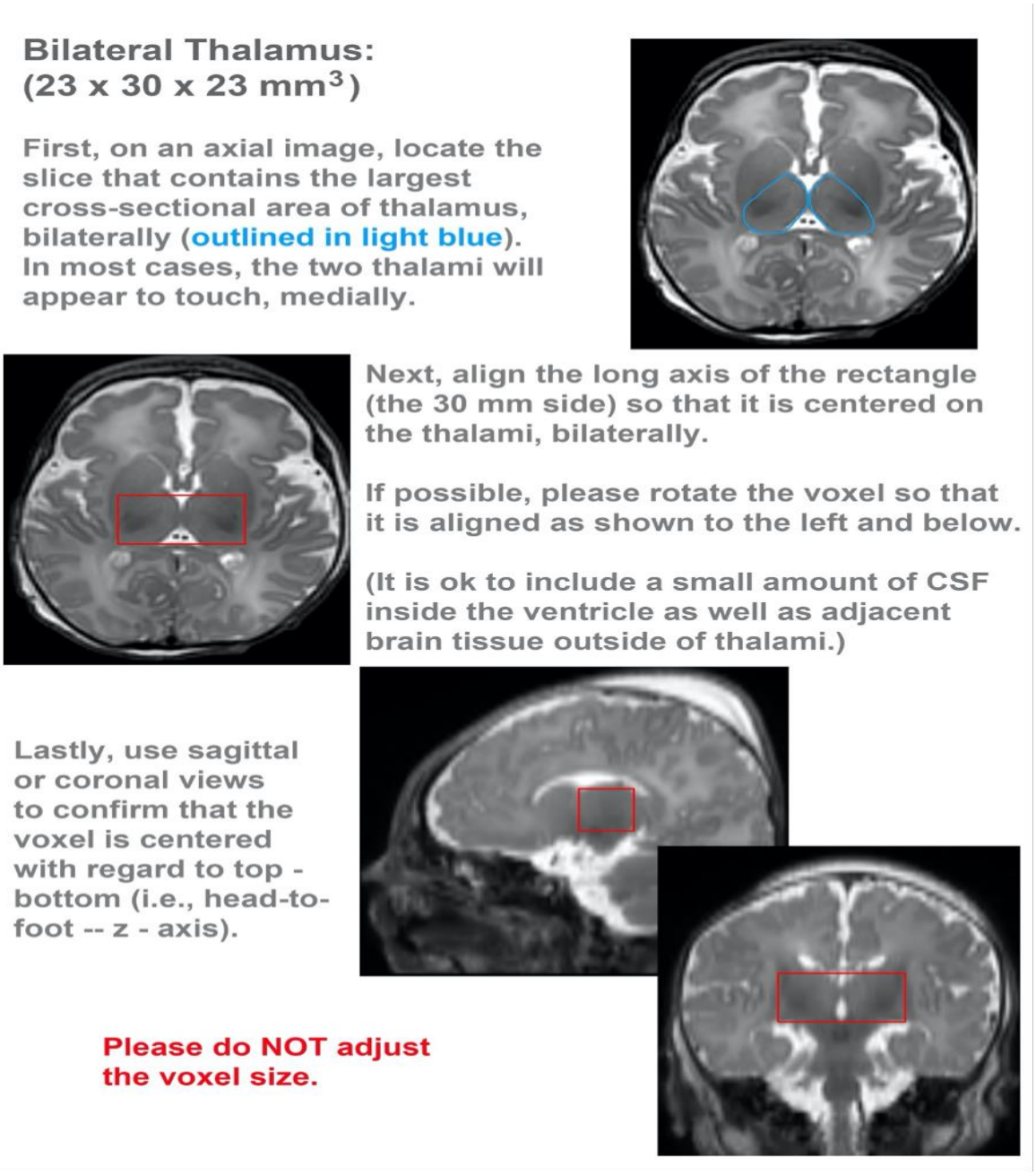
The images below show a T1 sagittal reference picture. The pictures are rated on a scale of 1-4 (**1 and 2 being passing** brain images).

- The number 1 on the first brain image below shows a "**good" T1**. This is indicated by no visible motion or minor artifacting throughout the image and minor banding.
- The number 2 on the second brain image below shows a **"mild" T1**. This is indicated by moderate artifacting such as hemodynamic and eye motion artifact (often noted in the ventral part of the brain) or mild artifacting on many slices throughout the image.
- The number 3 on the third brain image below shows a "moderate" T1. This one is considered questionable. This is indicated by heavy artifacting on more than two slices but not throughout or moderate artifacting throughout the image.
- The number 4 on the fourth brain image below shows a "severe" and this would be a failing T1. This is indicated by heavy artifacting throughout the image.



Section 3: Aligning MRS

3.1.1. Region of interest (ROI): All HBCD MRS sequences will be localized to the same region of interest: the bilateral thalamus. The graphic below describes general principles of aligning the MRS voxel.



Section 4: IF BABY COMES OUT OF THE SCANNER DURING THE PROTOCOL

4.1. Re-positioning the remaining sequences

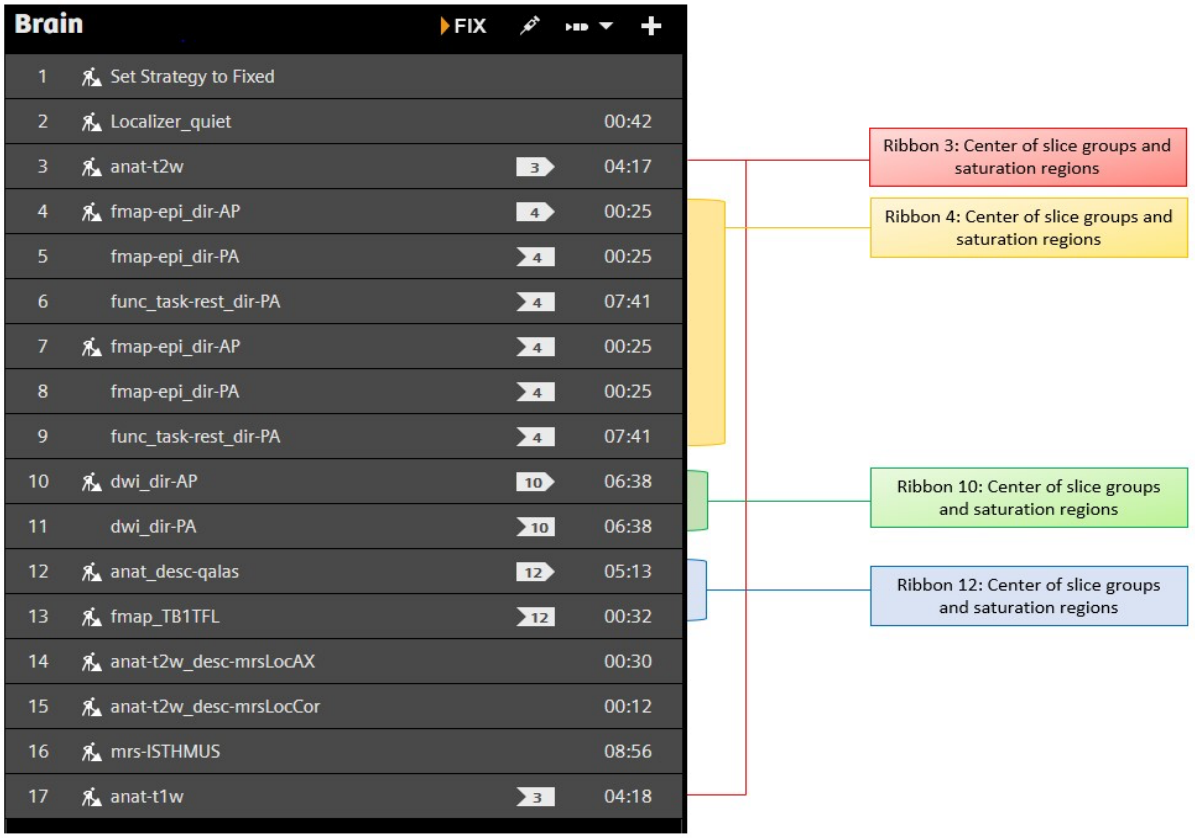
**** always rerun localizer and apply new parameters to all scans any time you put the subject back in the scanner****

1.) Pull down "localizer_quiet" and any sequences that were not completed prior to bringing baby out.
2.) Run the localizer that you copied.
3.) Position the first remaining sagittal sequence (T1, T2, and QALAS are sagittal sequences) and the first remaining transverse sequence. (BOLD, DWI, and field maps are transverse sequences). The details for how to position each scan type are listed above in the sequence-specific instructions. Remember to center the sequences but do not rotate the field of view (the exceptions in which the FOV is rotated are the MRS localizers).
4.) Copy the parameters of the remaining sagittal from the first sagittal and the remaining transverse from the first transverse by doing as follows:
    i.) Open the sequence you'd like to copy the parameters to (you can do this by double-clicking on the sequence).
    ii.) Right click on the sequence you'd like to copy the parameters from
    iii.) Click "copy parameters" and use diagram below to know specific parameter to copy from. From example, if copying petameters from T2w to T1w, then you copy "center of slice groups and saturation regions" (as shown on the figure)
    iv.) Click "OK" and parameters should load to that sequence.
    v.) Click orange 'go' button to apply these changes. Make sure your 'working man' icon is still on each sequence.
    vi.) This will have to be done for every sequence that applies.
    vii.) To check that the parameters are applied, double click on sequence to open it and yellow boxes should be aligned with yellow dot in the middle.
5.) T1, T2, QALAS are collected sagittal.
6.) BOLD, DWI, and field maps are all collected transverse
7.) **If the baby is taken out during MRS**, repeat all MRS steps (starting from **MRS LOCALIZERS,** Section 2.3.7)

4.2 REORDERING SEQUENCES:

If you decide to run the sequences in an order different from the default, please ensure that all scans are properly aligned based on HBCD protocol. If you're unsure how to do this, see the instructions at the end of this document on what to do "if the baby comes out of the scanner during the protocol".

Figure below, shows what parameter to copy based on the sequence type

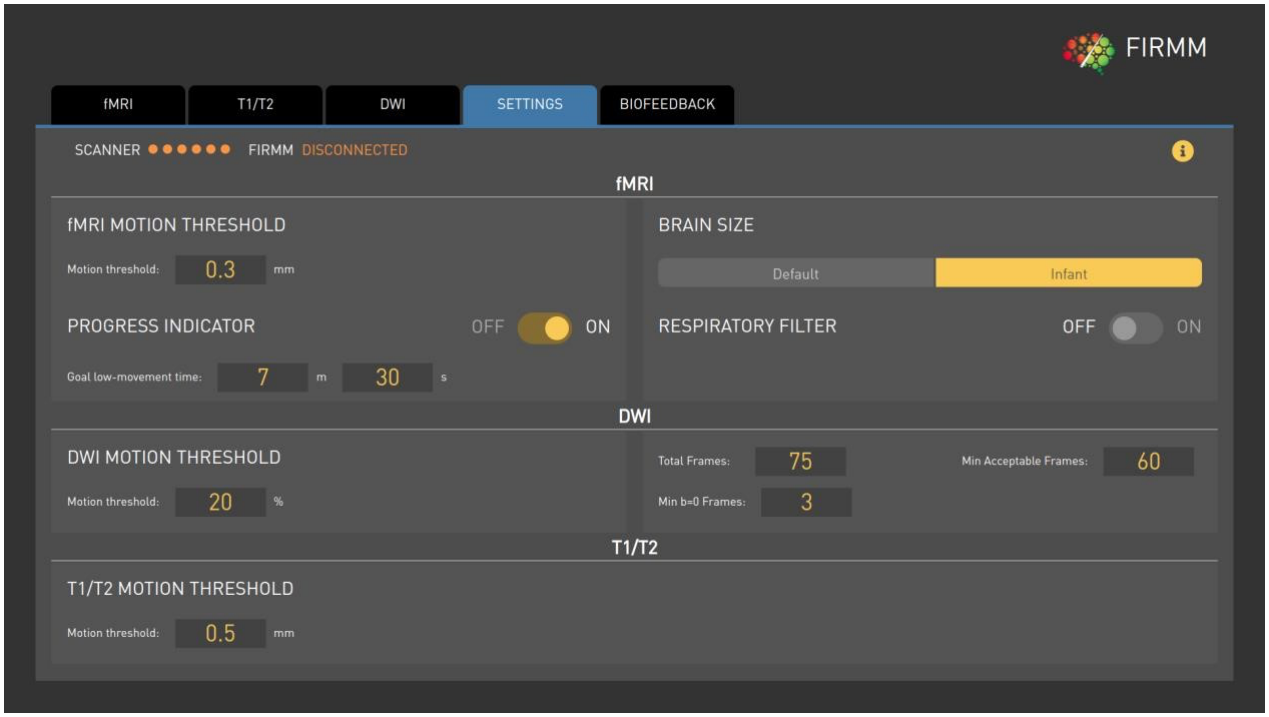


Section 6: FIRMM

FIRMM has provided "FIRMM Quick Reference Guide for HBCD" please follow this document for detail, if needed. For summary of the FIRMM set up, see below:

6.1. FIRMM settings for HBCD Study

- **Need to change this figure__"** Progress Indicator (default is off)**: please turned this on.**



- The image above shows how to apply different settings to an infant MRI scan on FIRMM. The fMRI Motion Threshold (red circle) shows the FD cutoff for usable frames. **This number should be set to 0.3 mm**.
- The Brain Size setting should be set on **"infant"** for infant scanning.
- The Respiratory Filter has an "on/off" button. This filter should be switched to **"OFF".**
- **Under DWI**; motion thereshold= 20 %, Min. Acceptable Frames =60%, Min b=0 frame=3, Total Frames=75 (per AP/PA direction)

• Under T1/T2**; Motion threshold= 0.5** • Progress Indicator **: please turned this on (if not)**

6.2. GUI display:

FIRMM should start running automatically once images start to be collected.

6.2.1 fMRI

Quality Score and Quality Time

The image above shows FIRMM tracking movement on a BOLD run. The 53% shows the percentage of usable data that is being collected (low motion data). The 10m 27s shows how much time of usable data has been collected. **Our goal for piloting is for at least 7m 30s of usable data.** (Can be "concatenated" across runs; FIRMM can keep track across runs.)

Motion Trace

A scrollable trace of the acquired motion data. Each data bar is the calculated motion result from the scan frame. The bar color denotes if the motion is low (white) or exceeds the user selected threshold (yellow). Pointers indicate the minimum and maximum motion thresholds value (the 0.2 markers in the figure) that has been selected in the fMRI Settings on the Settings Tab.

To select an individual series/run, tap the yellow "I" (circled in red) and select the appropriate series. The quality score and quality time will change based on the series that are selected.

NOTE: Upon acquisition of fMRI data, remember to document the Quality Score and Quality Time measures for each separate run into the HBCD LORIS Scan Log.

6.2.2 T1/T2

NOTE: Upon acquisition of the T1w or T2w data, remember to document the Quality Score, measure into the HBCD LORIS Scan Log.

6.2.3 DWI

To select an individual series/run, tap the yellow “I” (circled in red) and select the appropriate series. The quality score and quality time will change based on the series that are selected.

NOTE: Upon acquisition of DWI data, remember to document the Quality Score, Good Frames, and Good b=0 measures for each individual series into the HBCD LORIS Scan Log.