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| **MRSinMRS checklist** | |
| 1. Hardware |  |
| a. Field strength [T] | 7 |
| b. Manufacturer | Siemens |
| c. Model (software version if available) | Magnetom 7T |
| d. RF coils: nuclei (transmit/ receive), number of channels, type, body part | 1H, 32 ch, head, Nova Medical |
| e. Additional hardware | N/A |
| 2. Acquisition |  |
| a. Pulse sequence | FID-MRSI |
| b. Volume of Interest (VOI) locations | Parallel to the anterior commissure-posterior commissure line, superior to the lateral ventricles, and covering the centrum semiovale region |
| c. Nominal VOI size [cm3, mm3 ] | 220×220×20 mm3 |
| d. Repetition Time (TR), Echo Time (TE) [ms, s] | TR=200 ms / 1.3 ms acquisition delay |
| e. Total number of Excitations or acquisitions per spectrum | 1 average |
| In time series for kinetic studies | N/A |
| i. Number of Averaged spectra (NA) per time-point | N/A |
| ii. Averaging method (e.g. block-wise or moving average) | N/A |
| iii. Total number of spectra (acquired / in time-series) | N/A |
| f. Additional sequence parameters (spectral width in Hz, number of spectral points, frequency offsets); If STEAM: Mixing Time TM; If MRSI: 2D or 3D, FOV in all directions, matrix size, acceleration factors | BW 6000 Hz, 1024 spectral points, MRSI: 2D, FOV 220×220 mm2 , 8mm slice thickness, matrix size 100×100, Acc. factor: 4 |
| g. Water Suppression Method | WET |
| h. Shimming Method, reference peak, and thresholds for “acceptance of shim” chosen | Standard shim + manual adjustment, water peak < 40 Hz |
| i. Triggering or motion correction method (respiratory, peripheral, cardiac triggering, incl. device used and delays) | N/A |
| 3. Data analysis methods and outputs |  |
| a. Analysis software | LCModel 6.3-1 |
| b. Processing steps deviating from quoted reference or product | N/A |
| c. Output measure (e.g. absolute concentration, institutional units, ratio) | institutional units, ratio |
| d. Quantification references and assumptions, fitting model assumptions | Simulated in NMRScope-B, macromolecular background |
| 4. Data Quality |  |
| a. Reported variables (SNR, Linewidth (with reference peaks)) | SNR was calculated using the pseudoreplica method, and linewidth as FWHM of the NAA fit (see Supplementary Table 2) |
| b. Data exclusion criteria | Volume below 20mm³ for all lesions, volume between 100-400mm³ for lesion periphery analysis |
| c. Quality measures of postprocessing Model fitting (e.g. CRLB, goodness of fit, SD of residual) | CRLB (see Supplementary Table 2) |
| d. Sample Spectrum | See Supplementary Figure 1 |

**Supplementary Table 1:** Minimum Reporting Standards for ***in vivo*** MR Spectroscopy