Multichannel multislice B1+ mapping

In this study, multichannel multislice B1+ maps were obtained by using a hybrid method, which combines a single large tip angle AFI together with a series of small tip angle gradient echo images. Relevant imaging parameters for the AFI were: FOV=320(RO)×216(PE)×176.4(SS) mm3 (where RO, PE and SS designate readout, phase encode and slice selective dimensions, respectively), in-plane resolution= 4 mm, slice thickness=6.3 mm, TR1/TR2/TE=20/100/2.13 ms, nominal flip angle=60°, in-plane acceleration factor=2 (i.e., iPAT=2 in Siemens terminology), partial Fourier=6/8 (PE and SS), bandwidth=320 Hz/pixel and total acquisition time=3 minutes 11 seconds. The series of small tip angle gradient echo images were acquired with the relevant imaging parameters being FOV=320(RO)×216(PE) mm2, in-plane resolution=4 mm, 24 sagittal slices, slice thickness=6.3 mm, TR/TE=250/2.76 ms, nominal flip angle=10°, iPAT=2, partial Fourier=7/8 (PE), bandwidth=380 Hz/pixel and total acquisition time=1 minute 30 seconds.

T1 weighted 3D-MPRAGE acquisition

The T1-weighted image obtained for masking the brain was acquired using the MPRAGE sequence (1) with the following imaging parameters: FOV=224(RO)×224(PE) ×179.2(SS) mm^3, 0.7-mm isotropic resolutions, TR/TE/TI=2400/2.68/1300 ms, nominal flip angle=6°, iPAT=2, partial Fourier=7/8 (PE), phase oversampling=10%, bandwidth=210 Hz/pixel and total acquisition time=6 minutes 36 seconds. To reduce the impact of B_1^+ inhomogeneity on inversion, adiabatic pulses (2) using the phases obtained from the CP-like mode RF phase shimming were utilized.

Pilot high resolution dMRI with 2-fold slice acceleration

Using each of the three transmit configurations under consideration, we acquired the 1.05-mm, single-shell, whole brain dMRI data with: FOV=210(RO)×210(PE) ×151.2(SS) mm^3, anterior-posterior phase encoding, MB2, inter-slice shift=FOV/2, iPAT=3, partial Fourier=6/8, 144 sagittal slices, TR/TE=7400/71 ms, bandwidth=1388 Hz/pixel, and echo spacing=0.82 ms.

As in the 7T HCP dMRI protocol, excitation and refocusing MB pulses were formed using vendor optimized apodized sinc pulses with TBWP=3.2 for excitation, and TBWP=5.2 for refocusing. The pulse duration was set to 5120 μs for excitation and 10240 μs for refocusing. Furthermore, a time shift of 1920 μs was introduced between the two SB pulse components of the final MB2 pulses (3), as in the 7T HCP dMRI data (4), leading to total pulse duration of 7040 μs for excitation and 12160 μs for refocusing.

The pTx dMRI dataset was acquired with the pTx-enabled sequence, whereas the two 1Tx dMRI datasets were obtained with the sequence that had been used in the WashU-Minn-Oxford consortium of the HCP (4). For the pTx acquisition, the RF voltages were adjusted to achieve the nominal flip angles (i.e., 90° for excitation and 180° for refocusing) at the maximum B_1^+ field across the brain. For 1Tx acquisitions, because of the more inhomogeneous RF field across the brain, relatively higher reference RF voltages (set to achieve 10-15% greater than nominal flip angles) were utilized to increase the signals from the low B_1^+ regions in the periphery of the brain.

For the pTx dMRI acquisition, the same 24 RF shim sets were utilized for both excitation and refocusing. These RF shim sets were utilized to form 12 pairs of band-specific or slab-specific pTx excitation and refocusing MB2 pulses (a total of 48 pTx MB2 pulses). During data acquisition, each pair was applied six times with adjusted central frequencies to excite and refocus the 12, 1.05-mm thick image slices residing within the two corresponding 6.3-mm thick B_1^+ mapping slabs (each with 6 image slices), leading to the acquisition of a total of 144 image slices per image volume.

Original HCP 7T diffusion protocol

The HCP 7T diffusion protocol acquires whole brain dMRI data with 1.05 mm isotropic resolutions, FOV=210(RO) × 210(PE) × 138.6(SS) mm^3, MB2, iPAT=3 (3-fold in-plane acceleration), partial Fourier=6/8, inter-slice shift=FOV/2, 132 oblique axial slices, TR/TE=7000/71 ms, bandwidth=1388 Hz/pixel, echo spacing=0.82 ms, and two-shell q-space sampling (b-value=1000 and 2000 s/mm^2); it acquires a total of 286 image volumes, corresponding to 64 unique diffusion directions per shell plus 15 interspersed b=0 images, acquired twice using anterior-posterior (AP) and PA phase encode directions. The total acquisition time was ~40 minutes, which was divided into 4 segments of ~10 minutes each (the reader is referred to Vu et al. (4) for more details on the HCP 7T dMRI protocol).

Supporting Figures

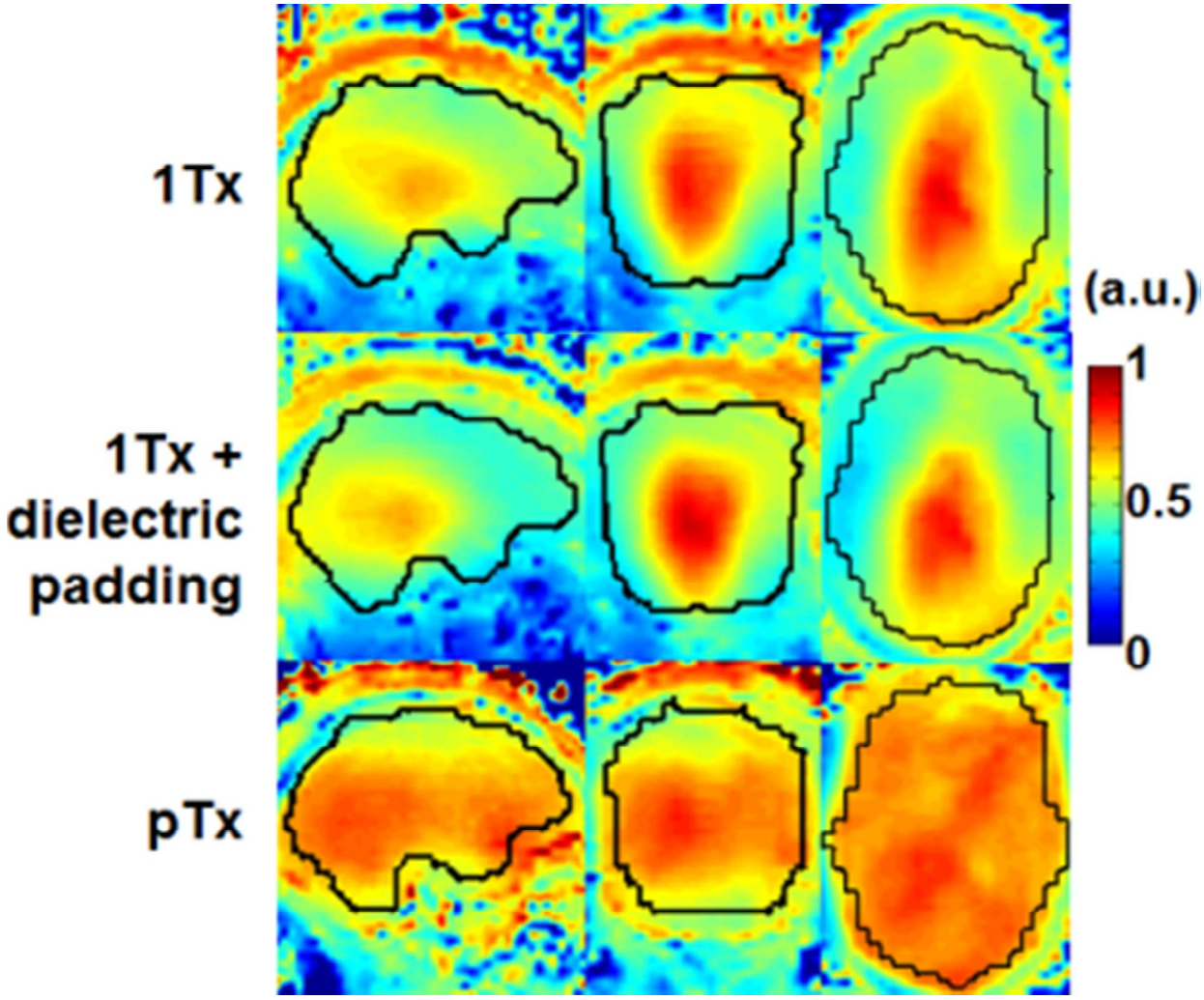

Fig. S1. Magnitude transmit B1 (B1+) maps for Nova single transmit (1Tx) coil alone (top row) and with dielectric padding (middle row), Nova 8 transmit (8Tx) coil with pTx multiband (MB) pulse design (bottom row). B1+ maps are shown in three orthogonal views with brain regions indicated by black curves. Following the slab-wise design framework, band-specific RF shimming was conducted on 24 contiguous, 6.3-mm thick sagittal B1+ mapping slabs covering the whole brain. The brain mask utilized was derived by extracting the brain from a 3D T1w image acquired with 0.7 mm isotropic resolutions. Note that pTx yielded best B1+ homogeneity across the whole brain.

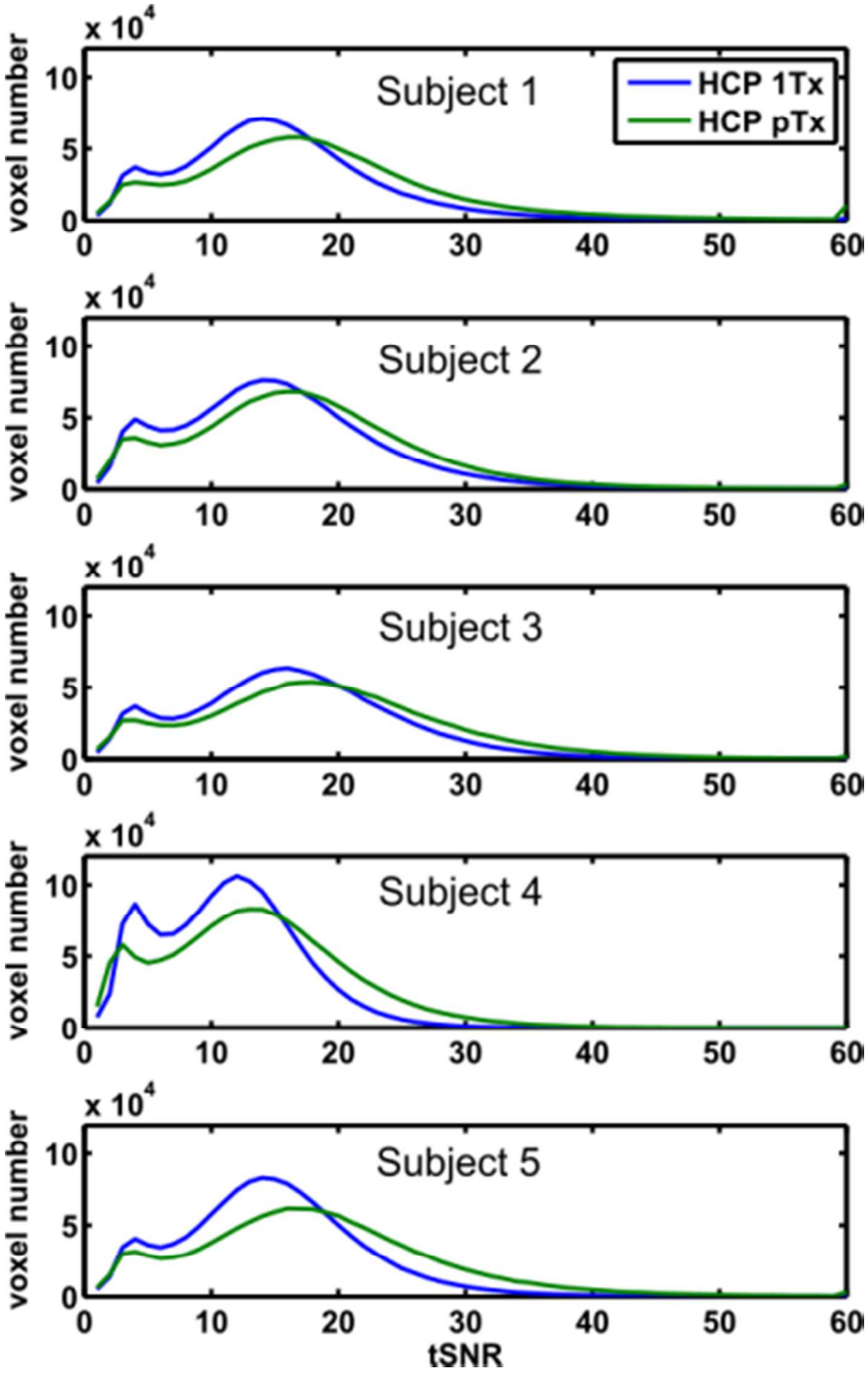

Fig. S2. Comparing HCP 7T dMRI protocol (HCP 1Tx) with HCP pTx protocol in terms of histograms of temporal SNR (tSNR). Each row shows tSNR histograms for one subject. For each subject, the tSNR histogram for HCP 1Tx (blue) or HCP pTx (green) dataset was created by counting the voxels in the brain mask and based on the tSNR map that were calculated on a voxel-wise basis from the corresponding 15, minimally preprocessed, b0 images obtained at different time points during the dMRI acquisition. Further quantitative analysis revealed that the use of pTx on average increased tSNR in ~63% of the brain volume.

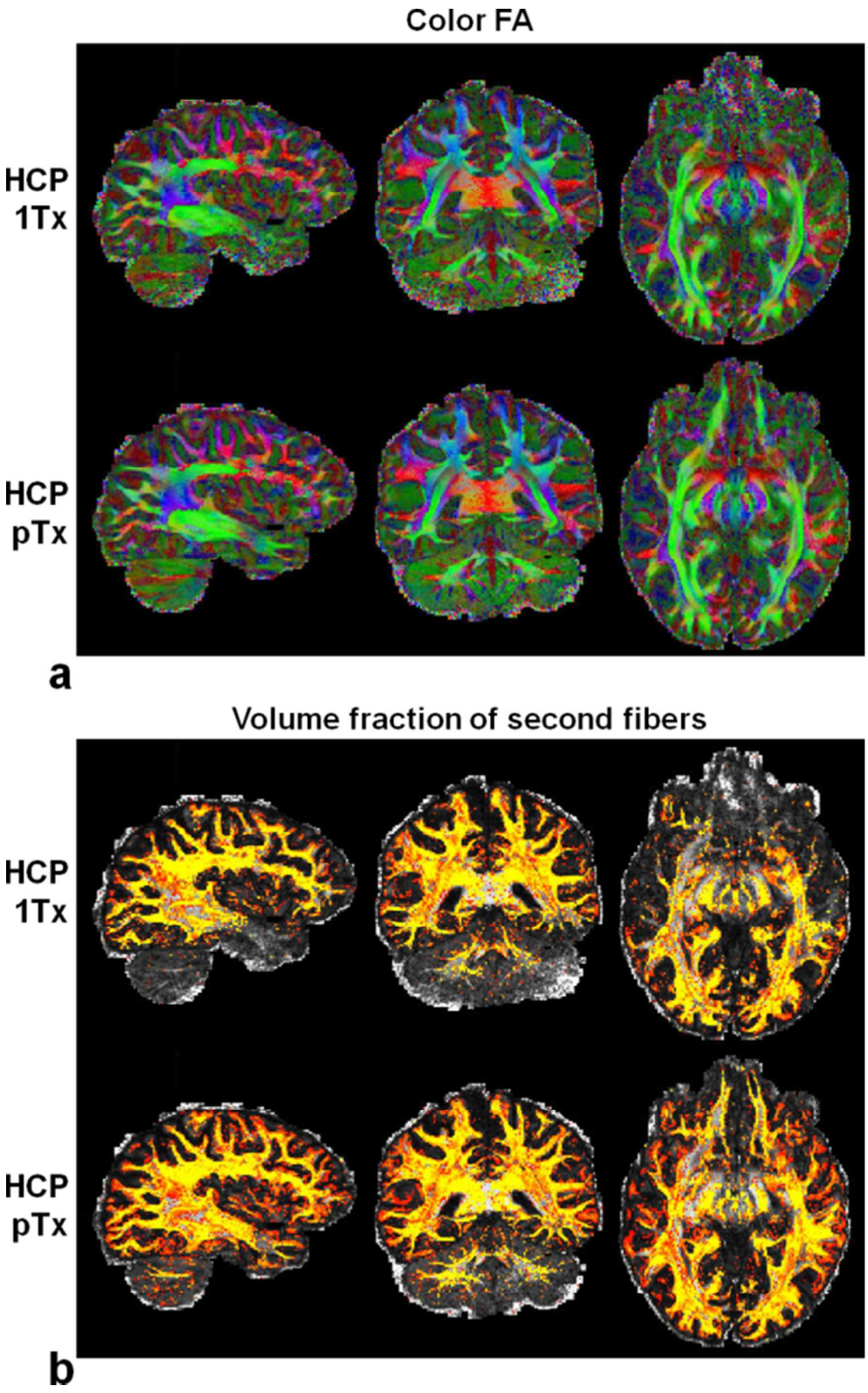

Fig. S3. Comparing HCP 7T dMRI protocol (HCP 1Tx) with HCP pTx protocol. Data are shown for another subject. (a) Color fractional anisotropy (FA) maps. (b) Volume fraction maps for second fiber orientations. The color FA is FA (in the range of [0 1]) with the color representing

the orientation of the principal fiber (red: left-right; green: anterior-posterior; blue: inferior-superior). The volume fraction map is shown in a colorscale of [0.05 0.2] (with yellow being high and red being low in volume fraction), overlaid on the respective FA map (in a grayscale of [0 1]). Both dMRI datasets were acquired with 1.05 mm isotropic resolutions, MB2, in-plane acceleration factor=3, and TE=71 ms. The TR for pTx acquisition was slightly longer (7400 vs 7000 ms). Both acquisitions utilized the same q-space sampling scheme (double shells, b-value=1000/2000 s/mm2), corresponding to 143 unique image volumes, each acquired twice with anterior-posterior (AP) and PA phase encode directions. Total scan time was kept constant for both datasets (i.e., 40 minutes divided into 4 segments of 10 minutes each). Note that the use of pTx improved fiber orientation estimation performances in such brain regions as the lower temporal lobe, the cerebellum and the inferior frontal lobe.

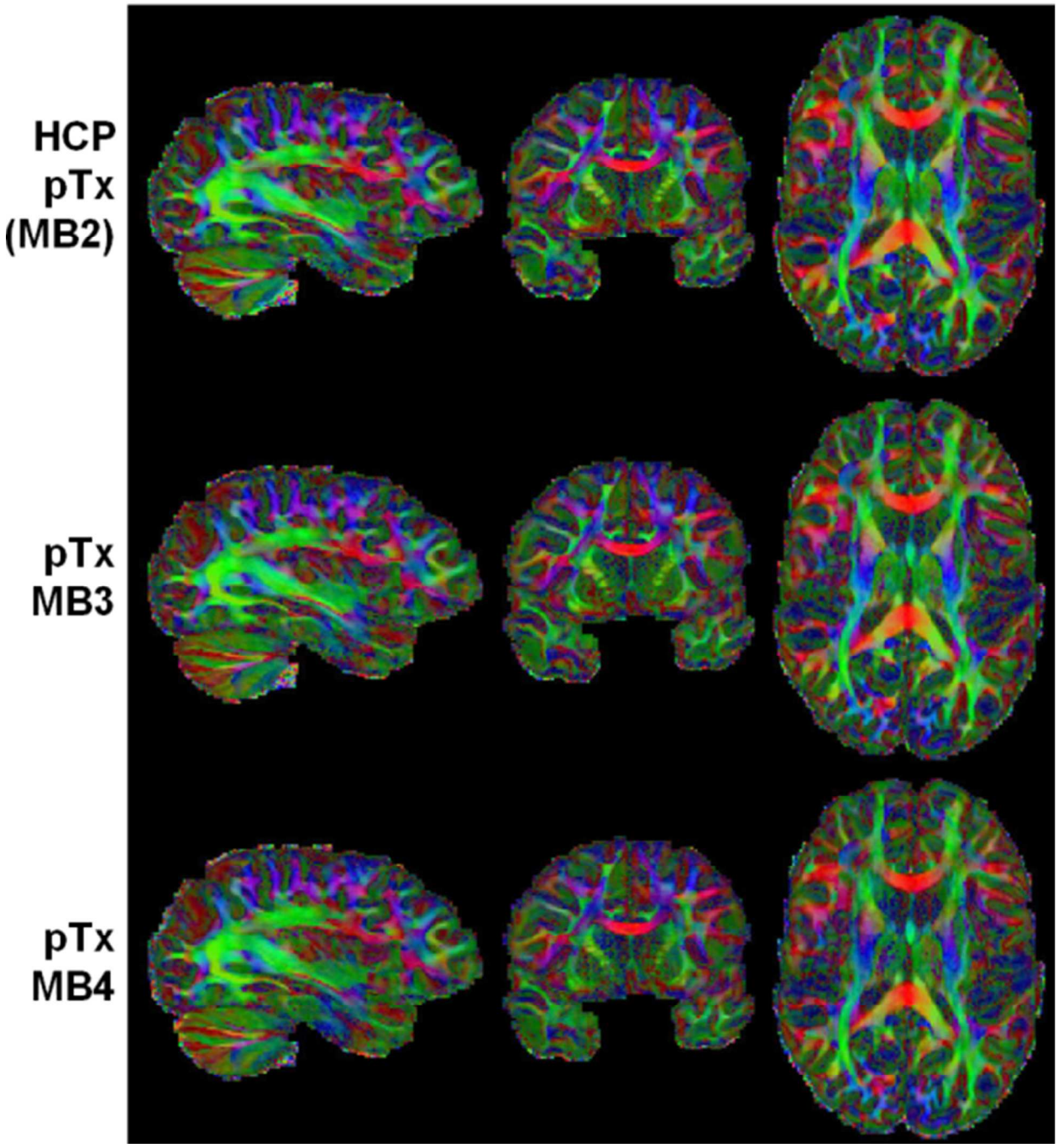

Fig. S4. Color fractional anisotropy (FA) maps of the HCP pTx MB2 protocol (top row) vs the pTx MB3 protocol (middle row) vs the pTx MB4 protocol (bottom row) in another subject. The color FA is FA (in the range of [0 1]) with the color representing the orientation of the principal fiber (red: left-right; green: anterior-posterior; blue: inferior-superior). All three dMRI datasets were acquired with 1.05 mm isotropic resolutions, in-plane acceleration factor=3, TE=71 ms, and double-shell q-space sampling (b-value=1000/2000 s/mm2). Total scan time was kept constant for all acquisitions (i.e., ~40 minutes divided into 4 segments of 10 minutes each).

Because of use of a shorter TR (3701 ms for MB4 and 4934 ms for MB3 vs 7400 ms for MB2), both MB3 and MB4 acquisitions obtained more data than the MB2 acquisition.

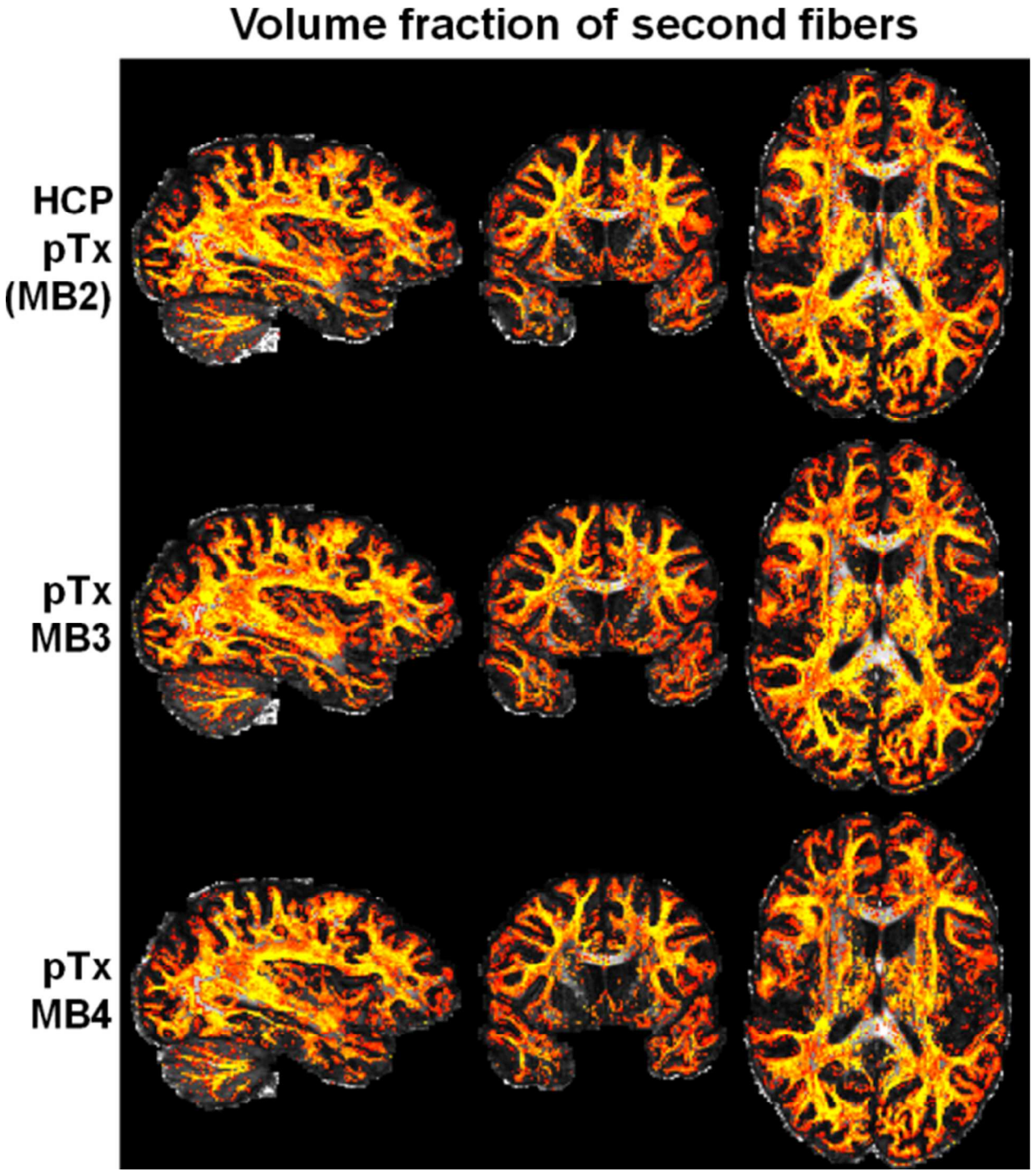

Fig. S5. Volume fraction maps of second fiber estimation for the HCP pTx MB2 protocol (top row) vs the pTx MB3 protocol (middle row) vs the pTx MB4 protocol (bottom row) in another

subject. These volume fraction maps derived using the same data as in Fig. S4, are overlaid on the respective fractional anisotropy map (defined in the grayscale of [0 1]) and shown in a colorscale of [0.05 0.2] (with yellow being high and red being low in volume fraction).

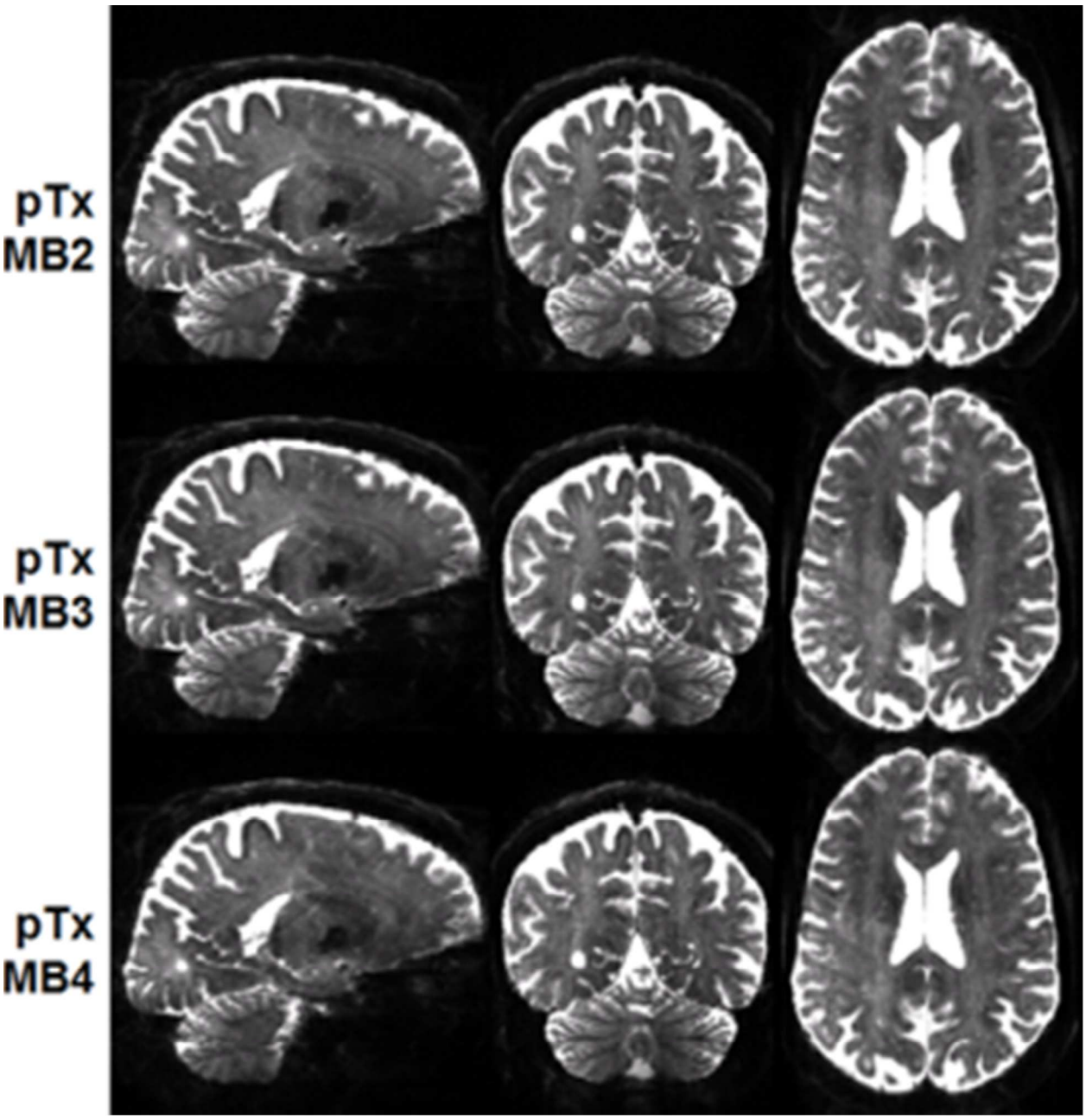

Fig. S6. Comparison of image quality for pTx acquisition with MB2 vs MB3 vs MB4, all with an in-plane acceleration of 3 (iPAT3). Shown are distortion corrected b=0 images acquired with 1.05 mm isotropic resolutions. Although enabling shorter TR values, both MB3 and MB4 data acquisitions used the same TR of 7400 ms as MB2 acquisition to avoid the TR dependent signal saturation effect for comparison purposes. All images were reconstructed using the split slice-

GRAPPA algorithm (Cauley et al. MRM 2014) to minimize the inter-band signal leakage. Note that both MB3 and MB4 acquisitions led to comparable image quality to the MB2 acquisition.

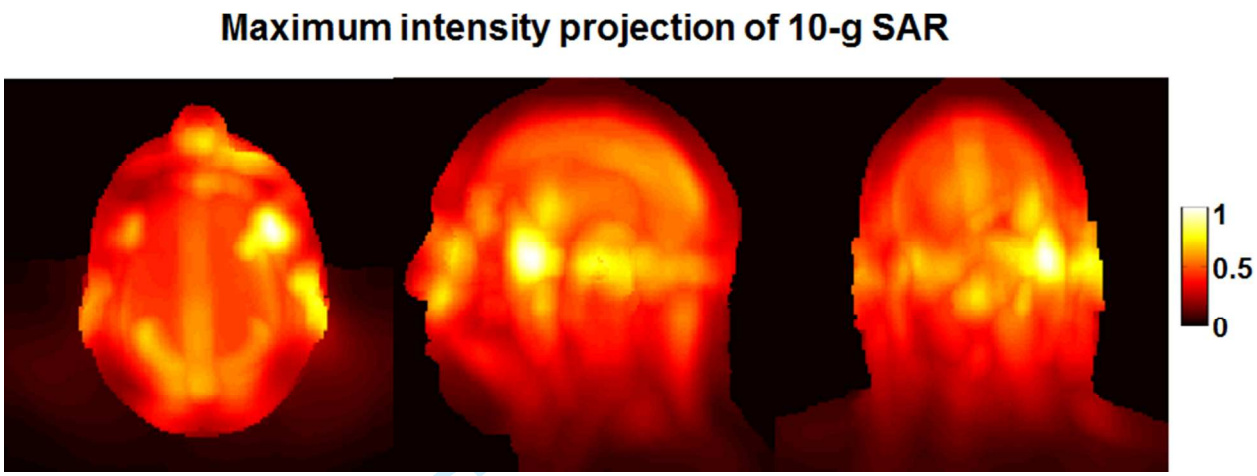

Fig. S7. Maximum intensity projection of the local SAR distribution in axial (left), sagittal (middle) and coronal (right) view for the pTx multiband pulses utilized in the current study. The local SAR map shown here is normalized to the maximum, mainly to appreciate the location of the hotspots. Note the SAR hotspots observed in various regions of the head. This same normalized local SAR distribution applies to all of the pTx dMRI acquisitions in the current study, but the absolute value for the maximum local SAR varies, depending on what MB factor is used for the acquisition. The maximum local SAR value was calculated to be 0.95, 1.42 and 1.70 W/kg for MB2, MB3 and MB4, respectively.

References

1. Mugler JP, 3rd, Brookeman JR. Three-dimensional magnetization-prepared rapid gradient-echo imaging (3D MP RAGE). Magn Reson Med 1990;15(1):152-157.

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4. Vu AT, Auerbach E, Lenglet C, Moeller S, Sotiropoulos SN, Jbabdi S, Andersson J, Yacoub E, Ugurbil K. High resolution whole brain diffusion imaging at 7T for the Human Connectome Project. NeuroImage 2015;122:318-331.