Supporting Information

Tissue specimens

Table S1: **Tissue specimens**. Five whole brains from chimpanzees were studied. Sex, age at death, *postmortem* time, cause of death, brain averaged (median ± IQR) R1 and R2* values are reported.

Specimen	Sex	Age	*Postmortem* time	Cause of death	R1 / s^{-1}	R2* / s^{-1}
1	F	13 years	15 hours	poaching	2.56 ± 0.93	22.22 ± 17.69
2	F	43 years	1 hour	during surgery	1.08 ± 0.37	37.34 ± 24.83
3	M	16 years	$<$ 16 hours	bacterial septicemia	1.90 ± 0.94	35.28 ± 17.71
4	M	15 years	$<$ 12 hours	bacterial septicemia	2.11 ± 0.70	33.26 ± 18.21
5	M	12 years	6 hours	conspecific aggression	1.78 ± 0.49	24.85 ± 15.59

Supplementary methods

Postmortem acquisition setup

For MRI data acquisition, the brains were placed in a spherical acrylic container filled with perfluoropolyether (Fomblin) and stabilised in place with sponges. Brains were stored at room temperature for at least two hours before scanning. A warm air stream was directed at the specimen during scanning to achieve constant temperatures closer to normal body temperature. The sample temperature was monitored by a sensor (LUXTRON Corporation, CA, USA) attached to the container surface and ranged from 27.5°C to 33.5°C across the specimens.

Order of MT pulse flip angles

The pseudo-random order of MT pulse flip angles during the calibration was: 620°, 300°, 240°, 500°, 400°, 320°, 740°, 520°, 460°, 340°, 280°, 760°, 600°, 680°, 720°, 700°, 560°, 480°, 200°, 640°, 220°, 260°, 540°, 660°, 440°, 360°, 580°, 380°, 420°.

Supplementary statistics

Table S2: **Evaluation of the bias correction in the low resolution calibration data. A**: Quantification of the bias in the maps. For each brain, the correlation coefficient between B_1^+ and MTsat across all voxels in the brain was quantified using a partial Spearman correlation coefficient (regressing out R2*), using the uncorrected maps "uncorr", the maps using the voxel-wise estimated calibration coefficients "vox", the maps corrected with the individual-based calibration coefficients "ind", and the maps corrected with the group-based calibration coefficients "group". **B**: Quantification of the absolute effect of the bias correction. Median ± interquartile range of the percent change in MTsat due to the correction were calculated across all voxels in the brain and reported in absolute values. We also report maximum absolute difference for the maps. Changes are reported between uncorrected maps and correction with voxel-wise parameters, uncorrected maps and correction with individual-based parameters, between correction with voxel-wise parameters and correction with individual-based parameters, and between the the two global correction approaches.

	A: MTsat vs B_1^+ correlation (ρ)				**B: Average absolute % difference**			
Brain	**uncorr**	**vox**	**ind**	**group**	**uncorr vs vox**	**uncorr vs ind**	**vox vs ind**	**ind vs group**
brain 1	0.422	−0.116	−0.115	−0.097	11.14 ± 12.37 (max = 121.14)	11.32 ± 12.46 (max = 63.36)	0.32 ± 0.71 (max = 43441)	0.37 ± 0.40 (max = 2.00)
brain 2	0.586	0.087	0.091	0.078	14.78 ± 20.83 (max = 104.83)	14.75 ± 20.34 (max = 95.22)	0.20 ± 0.39 (max = 13413)	0.25 ± 0.35 (max = 1.64)
brain 3	0.632	0.299	0.303	0.307	15.91 ± 20.52 (max = 307.20)	15.95 ± 19.96 (max = 88.03)	0.37 ± 0.81 (max = 25470)	0.13 ± 0.16 (max = 0.72)
brain 4	0.611	0.178	0.181	0.175	15.89 ± 19.21 (max = 1759)	16.21 ± 18.51 (max = 107.32)	0.39 ± 0.84 (max = 61624)	0.14 ± 0.16 (max = 0.91)
brain 5	0.633	0.046	0.053	0.074	14.20 ± 21.01 (max = 496.17)	14.42 ± 20.73 (max = 83.60)	0.39 ± 0.88 (max = 62469)	0.35 ± 0.50 (max = 2.00)

Table S3: **Evaluation of the high-resolution bias correction. A: Quantification of the bias in the maps.** For each brain, the correlation coefficient between B_1^+ and MTsat across all voxels in the brain was quantified using a partial Spearman correlation coefficient (regressing out R2*), using the uncorrected maps "uncorr" (left column), the maps corrected with the individual-based calibration coefficients "ind" (middle column) and the maps corrected with the group-based calibration coefficients "group" (right column). **B: Quantification of the absolute effect of the bias correction**: Median ± interquartile range % in MTsat due to the correction were calculated across all voxels in the brain. Absolute changes are reported between uncorrected maps and correction with individual-based parameters (left column), between uncorrected and correction with group-based parameters (middle column), and between the the two correction approaches (right column).

	A: MTsat vs B_1^+ correlation (ρ)			**B: Average absolute % difference**		
Brain	**uncorr**	**ind**	**group**	**uncorr vs ind**	**uncorr vs group**	**ind vs group**
brain 1	0.440	−0.087	−0.069	12.17 ± 9.33	11.75 ± 8.95	0.39 ± 0.38
brain 2	0.523	0.018	0.004	18.33 ± 15.95	18.74 ± 16.39	0.31 ± 0.34
brain 3	0.556	0.196	0.201	17.28 ± 13.67	17.10 ± 13.50	0.14 ± 0.15
brain 4	0.589	0.099	0.092	18.70 ± 16.52	18.90 ± 16.75	0.16 ± 0.14
brain 5	0.469	−0.094	−0.077	17.19 ± 14.28	16.67 ± 13.76	0.42 ± 0.43

Accounting for different reference flip angles without recalibration

Once we have estimated the calibration constant C for a given β_{ref}, MTsat may be scaled to any target flip angle β'_{ref} that lies within the range of validity of the model using

$$\mathrm{MTsat}(\beta'_{\mathrm{ref}}) = \left(1 + \left[\frac{\beta'_{\mathrm{ref}}}{\beta_{\mathrm{ref}}} - 1\right] C\right) \frac{\mathrm{MTsat}(\beta_{\mathrm{loc}})}{1 + (r f_{\mathrm{T}} - 1)C}, \qquad [S.1]$$

i.e. changing the target flip angle from β_{ref} to β'_{ref} amounts to multiplication of the correction in Eq. [10] by a scaling factor $(1 + [(\beta'_{\mathrm{ref}}/\beta_{\mathrm{ref}}) - 1]C)$. This relation was derived by setting $\beta_{\mathrm{loc}} = \beta'_{\mathrm{ref}}$ in Eq. [9], solving for $\mathrm{MTsat}(\beta'_{\mathrm{ref}})$, and then inserting $\mathrm{MTsat}(\beta_{\mathrm{ref}})$ from Eq. [10] into the resulting equation.

In the special case where $\beta'_{\mathrm{ref}} = \beta_{\mathrm{nom}}$, then $\beta'_{\mathrm{ref}}/\beta_{\mathrm{ref}} = r$ which allows Eq. [S.1] to be written in the same form as Eq. [12]:

$$\mathrm{MTsat}(\beta'_{\mathrm{ref}} = \beta_{\mathrm{nom}}) = \frac{\mathrm{MTsat}(\beta_{\mathrm{loc}} = f_{\mathrm{T}}\beta_{\mathrm{nom}})}{1 + (f_{\mathrm{T}} - 1)C'}, \qquad [S.2]$$

where

$$C' = \frac{rC}{1 + (r - 1)C}, \qquad [S.3]$$

i.e. in this case we can just update the calibration constant to compute the correction to β'_{ref} rather than multiplying by a prefactor. The validity of Eqs. [S.2] and [S.3] can be proven by equating Eqs. [S.1] and [S.2] under the assumption that $\beta'_{\mathrm{ref}}/\beta_{\mathrm{ref}} = r$ and then solving for C'.

Supplementary residual C dependence on tissue type and B_1^+

To quantitatively illustrate this effect of small residual dependence of calibration coefficient C on tissue type and B_1^+ in all brains, partial Spearman correlation coefficients between the bias corrected MTsat (as an indicator of tissue type) and C (accounting for B_1^+) were calculated. Spearman correlations were used so as to also be sensitive to nonlinear monotonic relationships. The coefficients ranged from $\rho = -0.532$ to $\rho = -0.749$ across the brains (Table 1). This suggests that the tissue type explains up to a half of the residual 3–9% variance in the estimated calibration parameter and that the assumption is to some extent violated. We found low to medium degrees of partial Spearman correlation between B_1^+ and the calibration parameters (correcting for MTsat).

Comparison with the previous calibration model

In Refs. (21) and (24) an alternative method for B_1^+ correction of MTsat (intended for weaker MT pulses as commonly used *in vivo*) was presented which is different to that which we used. The heuristic model used as the basis of the correction method was constructed so that $\mathrm{MTsat}(\beta_{\mathrm{loc}} = 0) = 0$ and the behaviour at small β_{loc} is purely quadratic. It is intended to interpolate between the quadratic and linear regions in Fig. 2A. Here we compare the alternative model with the model we used in the main article.

The model used in Refs. (21) and (24) (Helms' model) can be written as

$$\mathrm{MTsat}(\beta_{\mathrm{loc}}) = A_0{\beta_{\mathrm{loc}}}^2(1 - A_1\beta_{\mathrm{loc}}), \qquad [S.4]$$

and interpolates between the quadratic and transition regions in Fig 2A. A_0 and A_1 are parameters to be fit from multi-flip angle calibration data of the same sort as we used, but for weaker MT pulses. The generality of this correction method relies on the assumption that A_1 is independent of the underlying tissue (21). This model has the same number of fitting parameters as the model we used (Lipp's model) (Eq. [7]).

Fig. S1 shows both models fitted to our experimental calibration data for two example voxels (one in splenium and one in caudate, corresponding to the same data as presented in Fig. 2B). The fits in Fig. S1 show that Helms' model (Eq. [S.4]) is not a good representation of our data, undershooting at both the lower and upper range of β_{loc}. In contrast, Lipp's model (Eq. [7]) is a better representation of the data over the whole measured range of β_{loc}. The relatively poorer fit of Helms' model in these data would give rise to a larger variance of the A_1 parameter distribution over voxels and brains compared to the variance of the A parameter from Lipp's model.

Adding additional parameters to Helms' model (e.g. a ${\beta_{\mathrm{loc}}}^2$ term within the parentheses of Eq. [S.4]) would help to reduce the undershoot at higher β_{loc}, but at the expense of greater model complexity and sensitivity to noise. We thus decided to follow the path of using Lipp's model rather than Helms' model in the main article.

Figure S1: Comparison of model fits using the MTsat correction model using Eq. [S.4] (Helms' model) and that using Eq. [7] (Lipp's model). Raw data (black ×'s) are from the same single voxels as shown in Fig. 2B. The models were fit separately in each case. The gray shaded area shows the range of β_{loc} values over the sample when $\beta_{\mathrm{nom}} = \beta_{\mathrm{ref}}$, the reference MT flip angle (here 700°), which is shown by the dashed line.