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Supplementary Materials for

Fluid assessment in dialysis patients by point-of-care magnetic relaxometry

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The PDF file includes:

Table S11. Summary of $\mathrm{RA}_{\mathrm{long}}$ values from MRI small voxel: Lateral 1 with subcutaneous and muscle.
Table S12. Summary of $\mathrm{RA}_{\mathrm{long}}$ values from MRI small voxel: Lateral 2 with muscle only.
Table S13. Summary of whole-body R_{e} BI values.
Table S14. Summary of whole-body R_{inf} BI results.
Table S15. Summary of leg segmental R_{e} BI results.
Table S16. Summary of leg segmental R_{inf} BI results.
Table S17. Change in T_2 relaxation time of phantom measured with each human NMR sensor measurement.

Other Supplementary Material for this manuscript includes the following:

(available at stm.sciencemag.org/cgi/content/full/11/502/eaau1749/DC1)

Table S1 (Microsoft Excel format). Individual-level demographics of the study population.

Computer code for statistical tests

1. **Comparison of HC and HD groups (two-sample)**
   - **Welch Test**: Matlab command: ttest2(HC, HD, ‘VarType’, ‘unequal’)
   - **Permutation Test (two-sample)**: R command (from *perm* package): permTS(HC, HD, method='exact.mc', control=permControl(nmc=10^5-1))
2. **Comparison of a single group at two time points (paired)**
   - **Permutation Test (one-sample):** R command (from *EnvStats* package): oneSamplePermutationTest(diff_HD, n.permutations=1e5)
   - **Paired t-Test**: paired, two-sided Student t-test
3. **Quantile regression of pixel-wise MRI data**

   Used to calculate results in table S4.

   - **Quantile Regression with Clustering**: R command (from *quantreg* package):

     data is table with columns: SubjectNum | HD | HC | AM | PM | T_2_Values

     ```
     quantileList <- c(0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9)
     nReps <- 1000
     q <- quantileList[i]
     model <- rq(T2_Values ~ PM * HD, tau = q, method = "fn", data)
     result <- summary(model, se = "boot", tau = q, R = nReps, bsmethod = "wild", cluster
     = SubjectNum)
     ```

4. **Determination of optimal model for T_2 data fitting**

   An F distribution look-up table requires knowing the degrees of freedom of the numerator (DF1-DF2) and denominator (DF2) of the F ratio.

   Matlab command for *P* value calculation: 1 – fcdf(fratio, df1 – df2, df2)

5. Cumulative distribution function (cdf) plots for pixel-wise MRI data

Used to generate figs. 2D-F and fig. S7.

The Matlab code to calculate the MRI pixel-wise cdfs:

Values = vector of pixel values
Bins = vector for how to bin the pixel values
cdf = ecdf2(Values, Bins) *(Fig 2D-E and fig. S7A-B)*

The final value of the integral curve describes the total difference between the pre- and post-cdfs.

cdf_difference = cdf_pre – cdf_post *(Fig. S7C)*
cdf_integral_difference = cumtrapz(Bins(2:end), cdf_difference) *(Fig 2F and fig. S7D)*

The 95% CI is calculated by dividing the standard deviation of the cdf of all subjects by the square root of the number of subjects and multiplying by 1.96. Matlab code:

CI vector = 1.96 * std(cdfs of all subjects) / sqrt(n subjects)

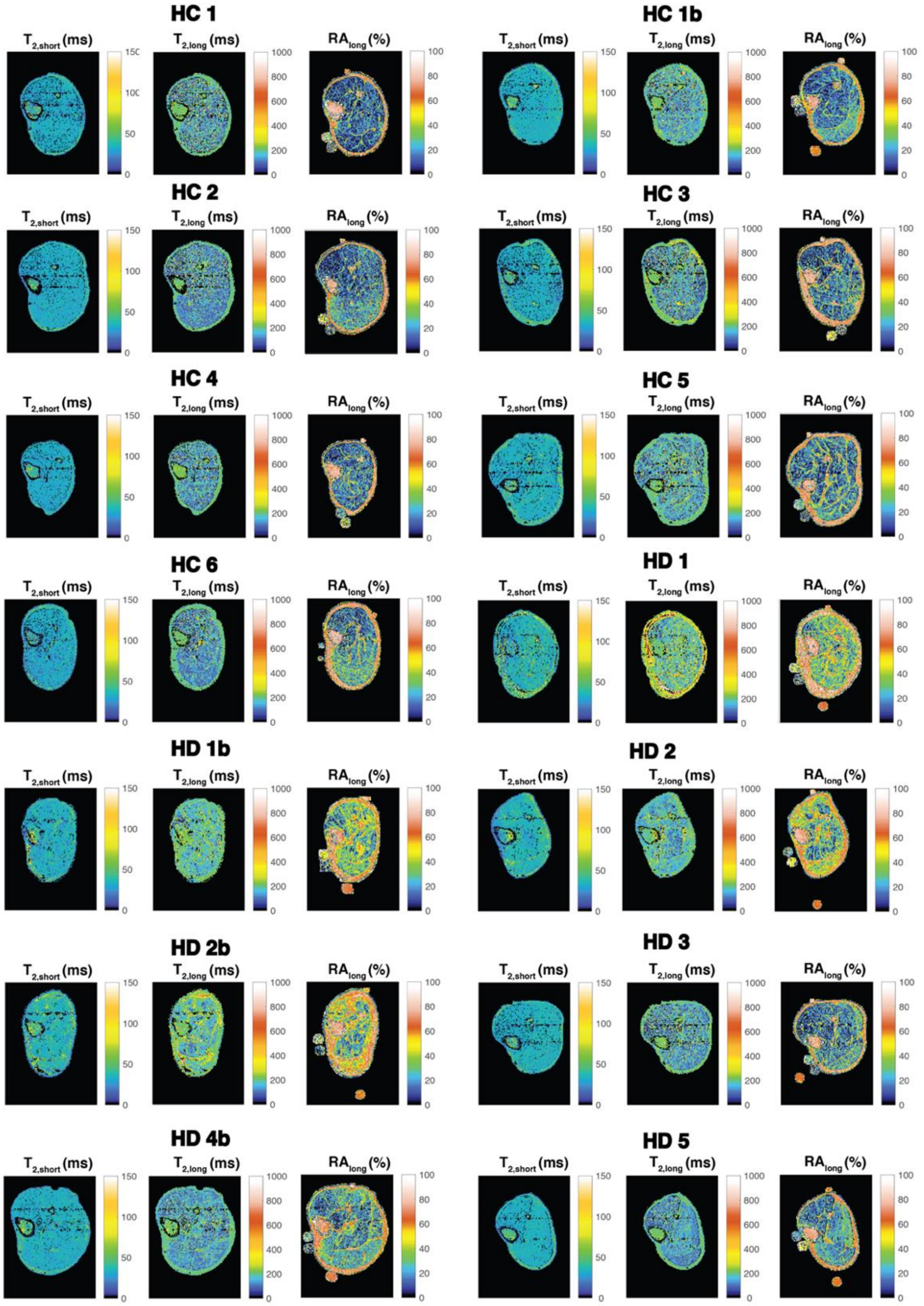

Fig. S1. Pixel-wise heatmap of MRI biexponential T_2 fit results. The pixel-wise biexponential fit results for each subject (n = 14). $T_{2,short}$, $T_{2,long}$, and RA_{long} values for slice 1 of the baseline (pre) MRI scan are shown. RA_{short} is equal to 100% - RA_{long}. The color scaling is different between the three types of heatmaps – $T_{2,short}$, $T_{2,long}$, and RA_{long} – but equal across subjects. All pixel values are shown (fitting criteria not applied). HC: healthy control; HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. Values in heatmaps plotted as histograms in figs. S2-S6.

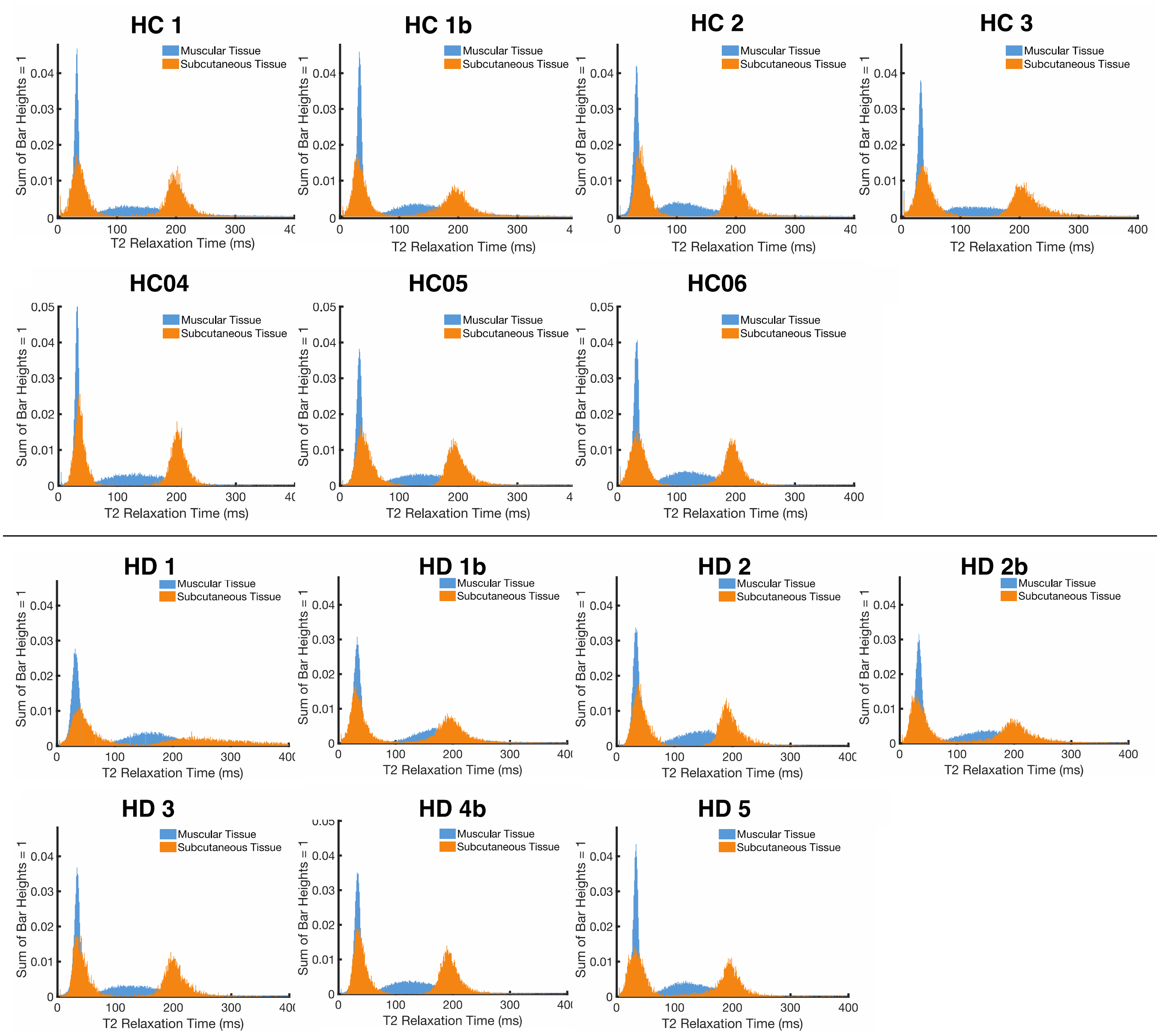

Fig. S2. Histogram of MRI pixel-wise T_2 relaxation time values in muscular and subcutaneous tissue at baseline. The muscular (blue) and subcutaneous (orange) histograms of pixel-wise T_2 relaxation time values for each subject (n = 14) are overlaid. $T_{2,short}$ values form first peak and $T_{2,long}$ values form second peak. Data is shown for baseline (pre) MRI scans. The sum of each histogram's bar heights equals 1. HC: healthy control; HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. Histogram from HD 4b is shown in fig. 1C.

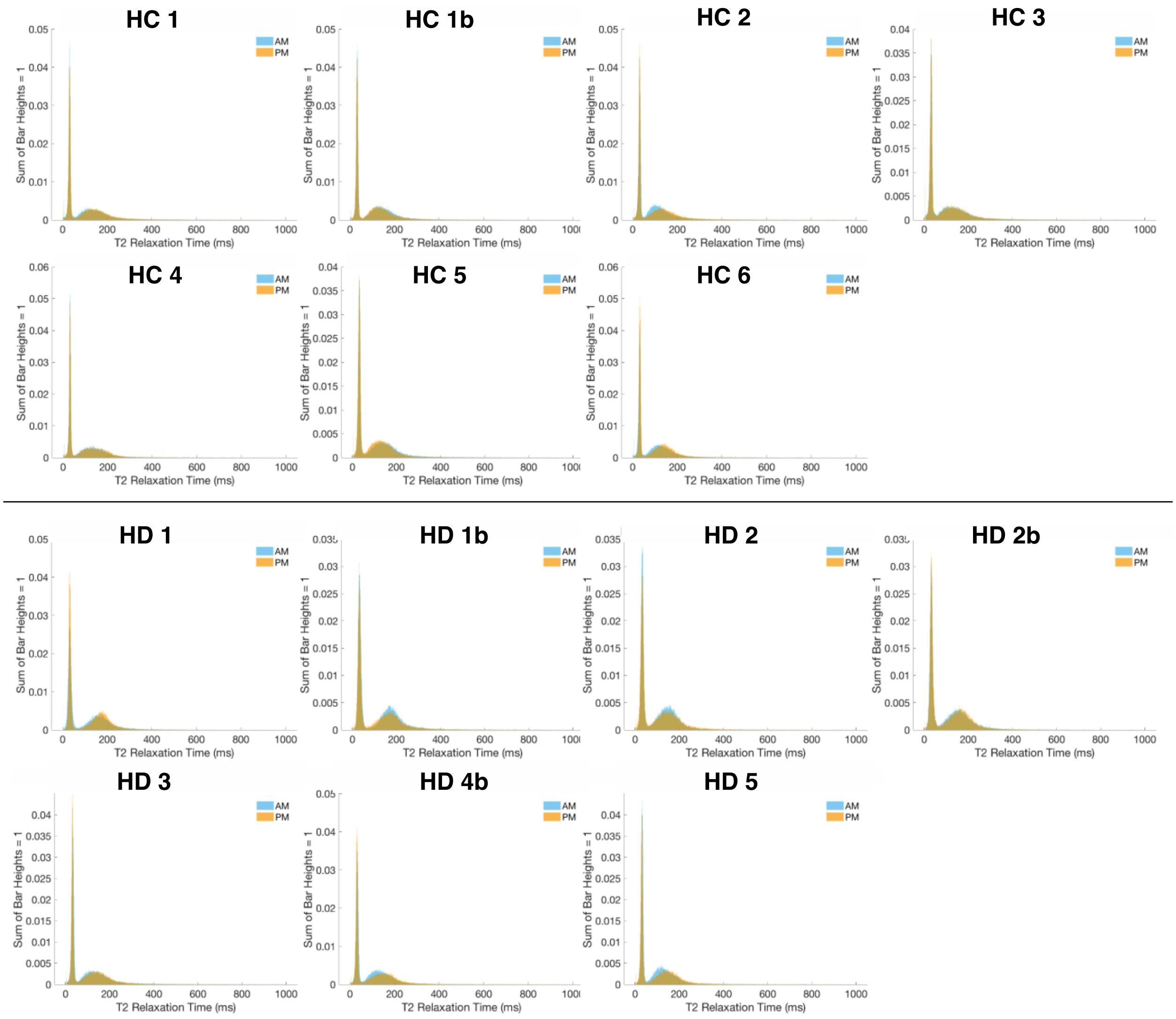

Fig. S3. Histogram of MRI pixel-wise T_2 relaxation time values in muscular tissue. Pre (blue) and post (orange) histograms of MRI pixel-wise T_2 relaxation time values for each subject (n = 14). $T_{2,short}$ values form first peak and $T_{2,long}$ values form second peak. Sum of histogram bar heights equals 1. HC: healthy control; HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. AM = pre, PM = post. For statistics comparing HC vs HD ΔT_2 values, see table S3. The pre-to-post ΔT_2 values from these histograms were aggregated to produce the "All muscle" data in fig. 1D-E.

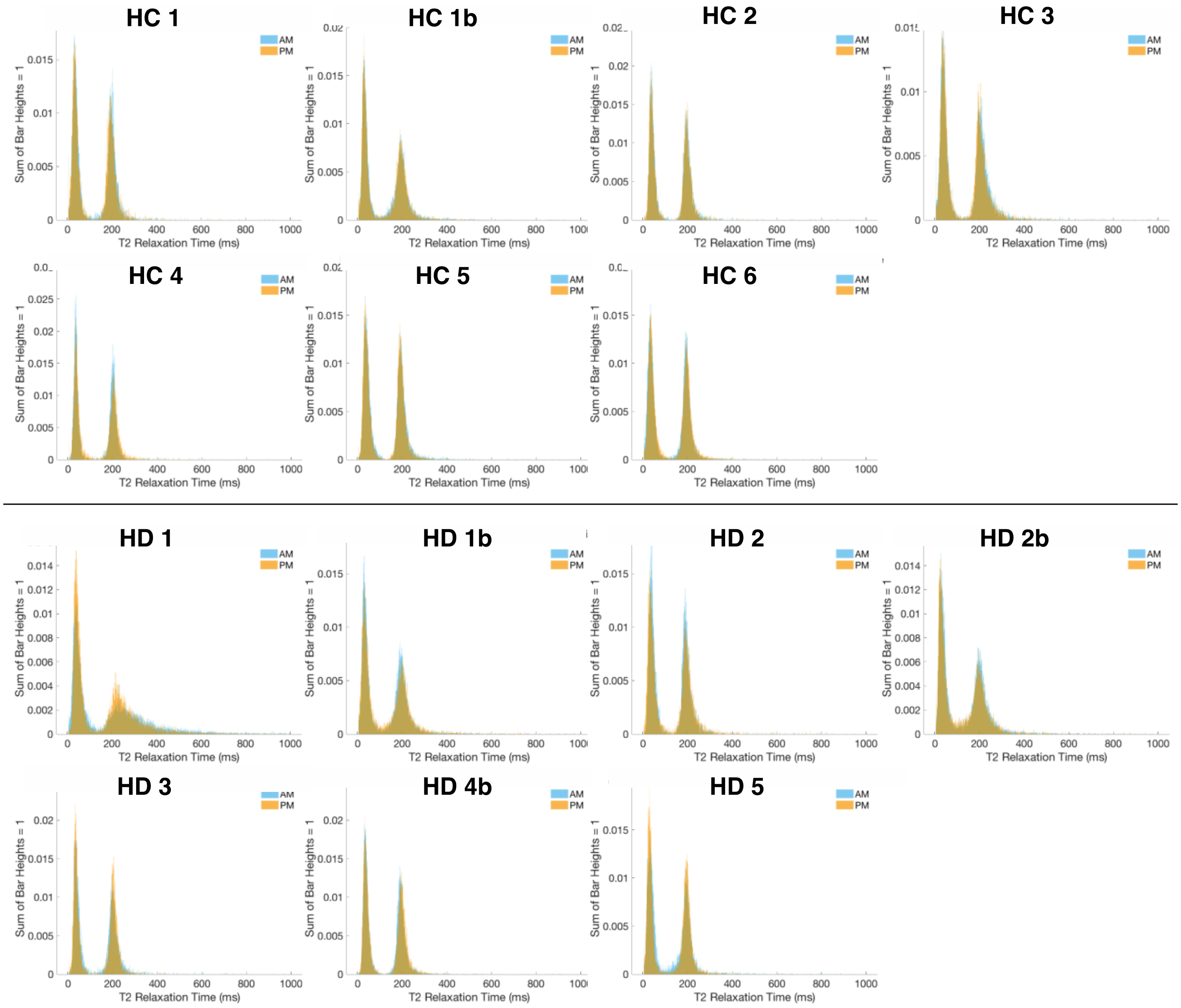

Fig. S4. Histogram of MRI pixel-wise T_2 relaxation time values in subcutaneous tissue. Pre (blue) and post (orange) histograms of MRI pixel-wise T_2 relaxation time values for each subject (*n* = 14). $T_{2,\mathrm{short}}$ values form first peak and $T_{2,\mathrm{long}}$ values form second peak. Sum of histogram bar heights equals 1. HC: healthy control; HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. AM = pre, PM = post. For statistics comparing pre-to-post ΔT_2 values, see table S3. The pre-to-post ΔT_2 values from these histograms were aggregated to produce the “All subcu” data in fig. 1D-E.

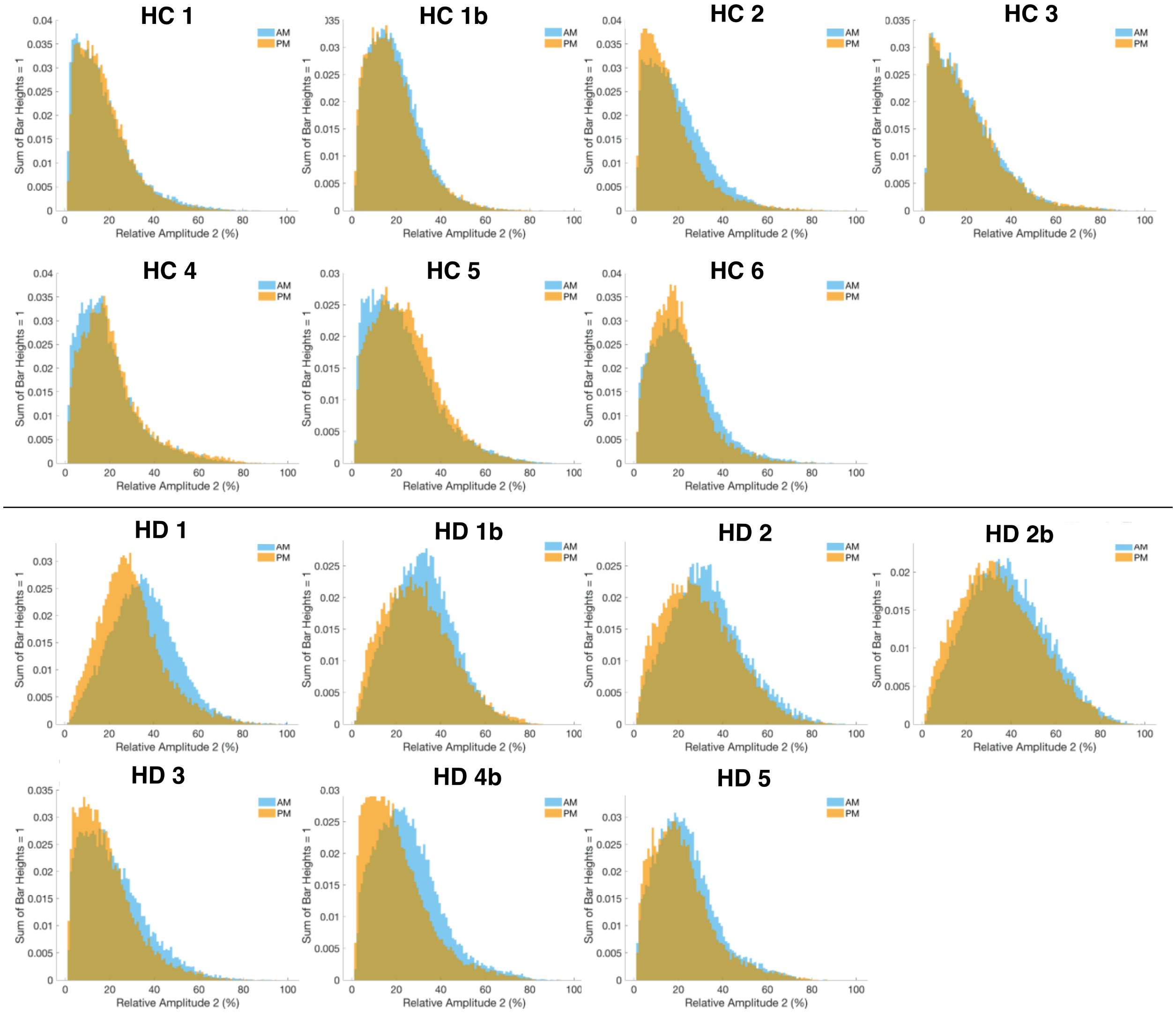

Fig. S5. Histogram of MRI pixel-wise RA_{long} values in muscular tissue. Pre (blue) and post (orange) histograms of MRI pixel-wise RA_{long} values for each subject ($n = 14$). Sum of histogram bar heights equals 1. HC: healthy control; HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. Relative amplitude 2 = RA_{long}, AM = pre, PM = post. For statistics comparing pre-to-post ΔRA_{long} values, see table S3. The values from these histograms were aggregated to produce figs 2D-F and the "All muscle" data in fig. 1F.

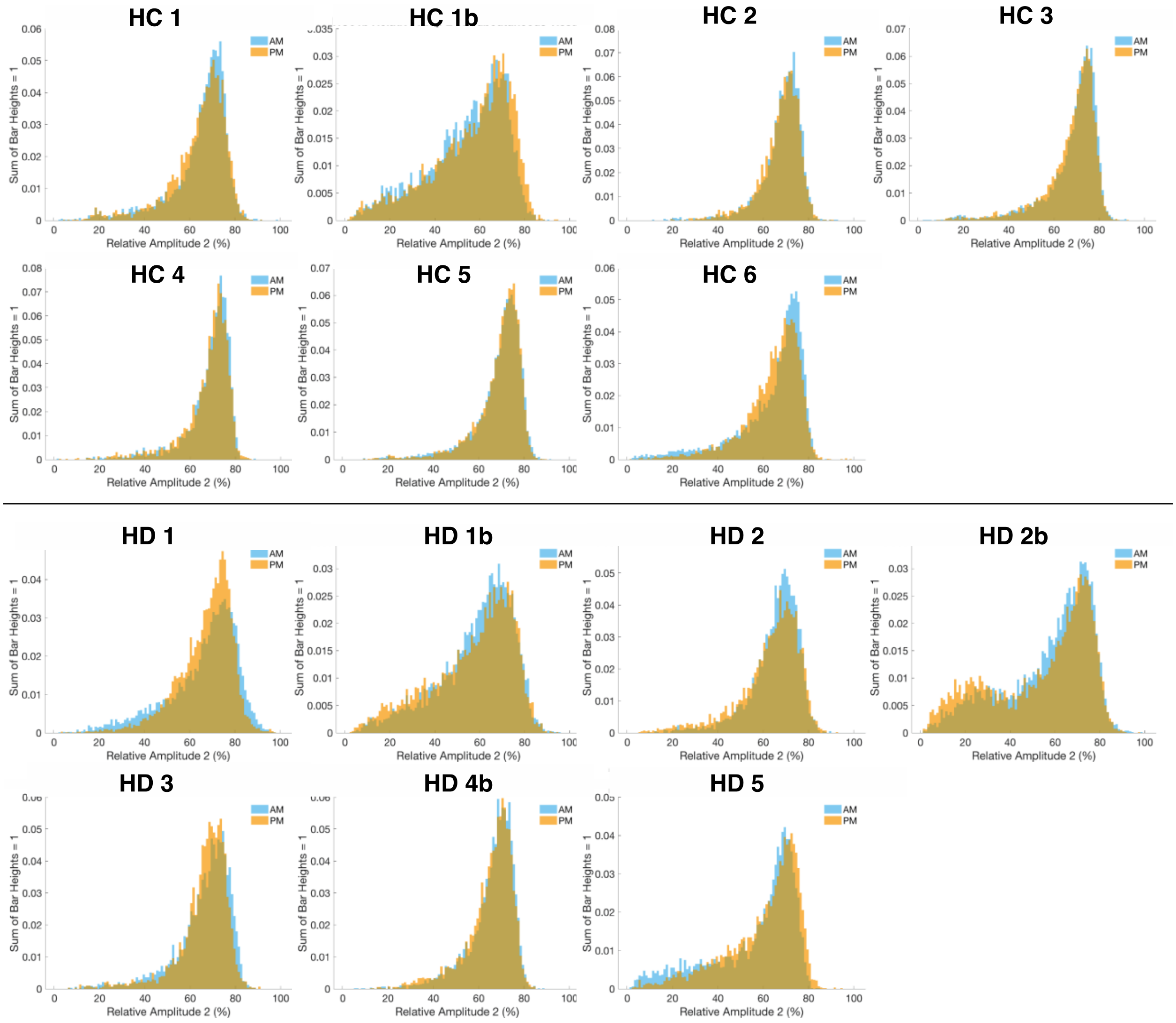

Fig. S6. Histogram of MRI pixel-wise RA_{long} values in subcutaneous tissue. Pre (blue) and post (orange) histograms of pixel-wise RA_{long} values for each subject (*n* = 14). Sum of histogram bar heights equals 1. HC: healthy control; HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. Relative amplitude 2 = RA_{long}, AM = pre, PM = post. For statistics comparing pre-to-post ΔRA_{long} values, see table S3. The values from these histograms were aggregated to produce “All subcu” data in fig. 1F.

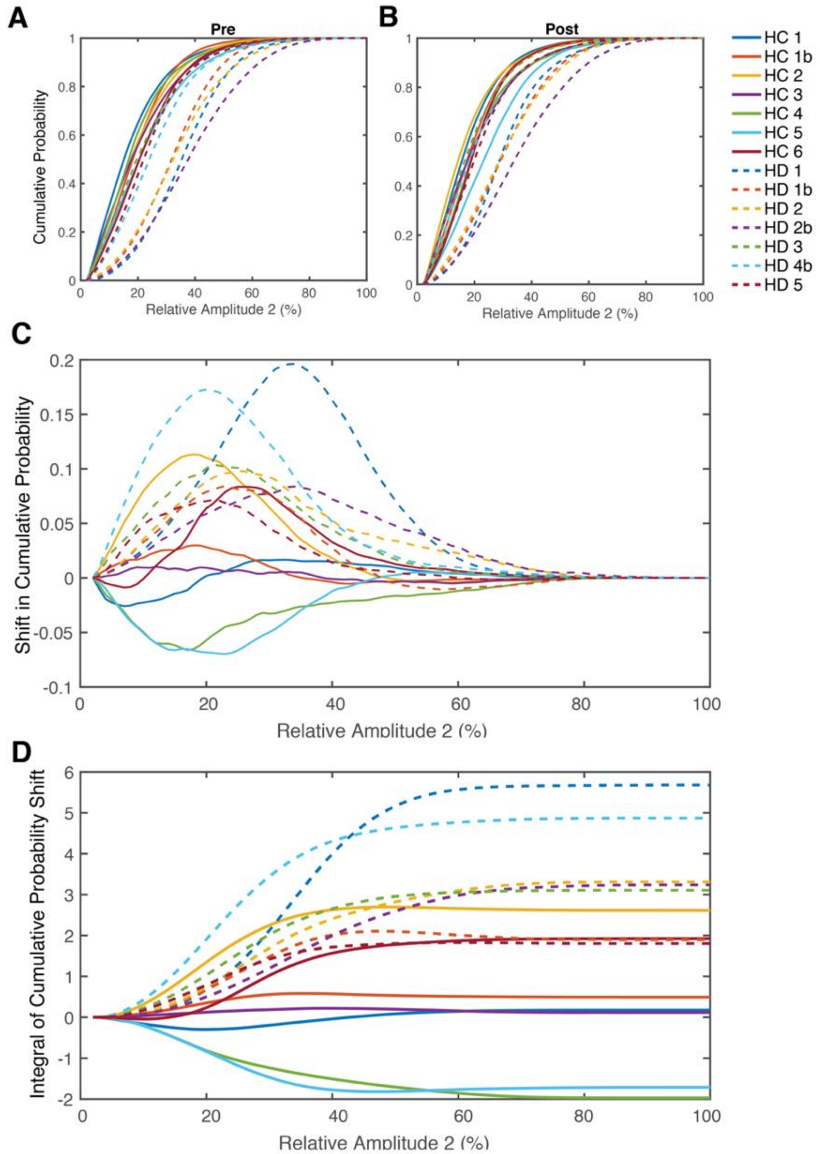

Fig. S7. CDFs of MRI pixel-wise RA_{long} values in muscular tissue. (**A**) CDFs of pixel-wise RA_{long} MRI values in muscular tissue at baseline (pre) for each subject (*n* = 14). This figure more clearly shows that only HD3 overlaps completely with HCs at baseline compared to fig. 2D. (**B**) CDF of pixel-wise RA_{long} MRI values in muscular tissue at post-time point for each subject (*n* = 14). This figure more clearly shows that HD5, HD4b, and HD3 overlap with HC subjects compared to fig. 2E. (**C**) Difference between pre- and post-CDFs shown in subplots A and B for each subject (*n* = 14). (**D**) Integral of pre- and post-CDF difference curve shown in subplot C for each subject. HD 1, who was one of the most fluid overloaded subjects in the study, had one of the largest shifts in pre-to-post CDF. The results from individual subjects in this figure are averaged together to create fig. 2D-F. Corresponding statistics are tabulated in table S4. Note: subtraction is in a different order than in fig. 2F so signs are reversed between fig. 2F and fig. S7D. Code to generate each subplot is summarized in "Suppl. Mat.: Computer code used for statistical tests - #5 Cumulative distribution function (cdf) plots for pixel-wise MRI data." HC: healthy control; HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. Relative amplitude 2 = RA_{long}.

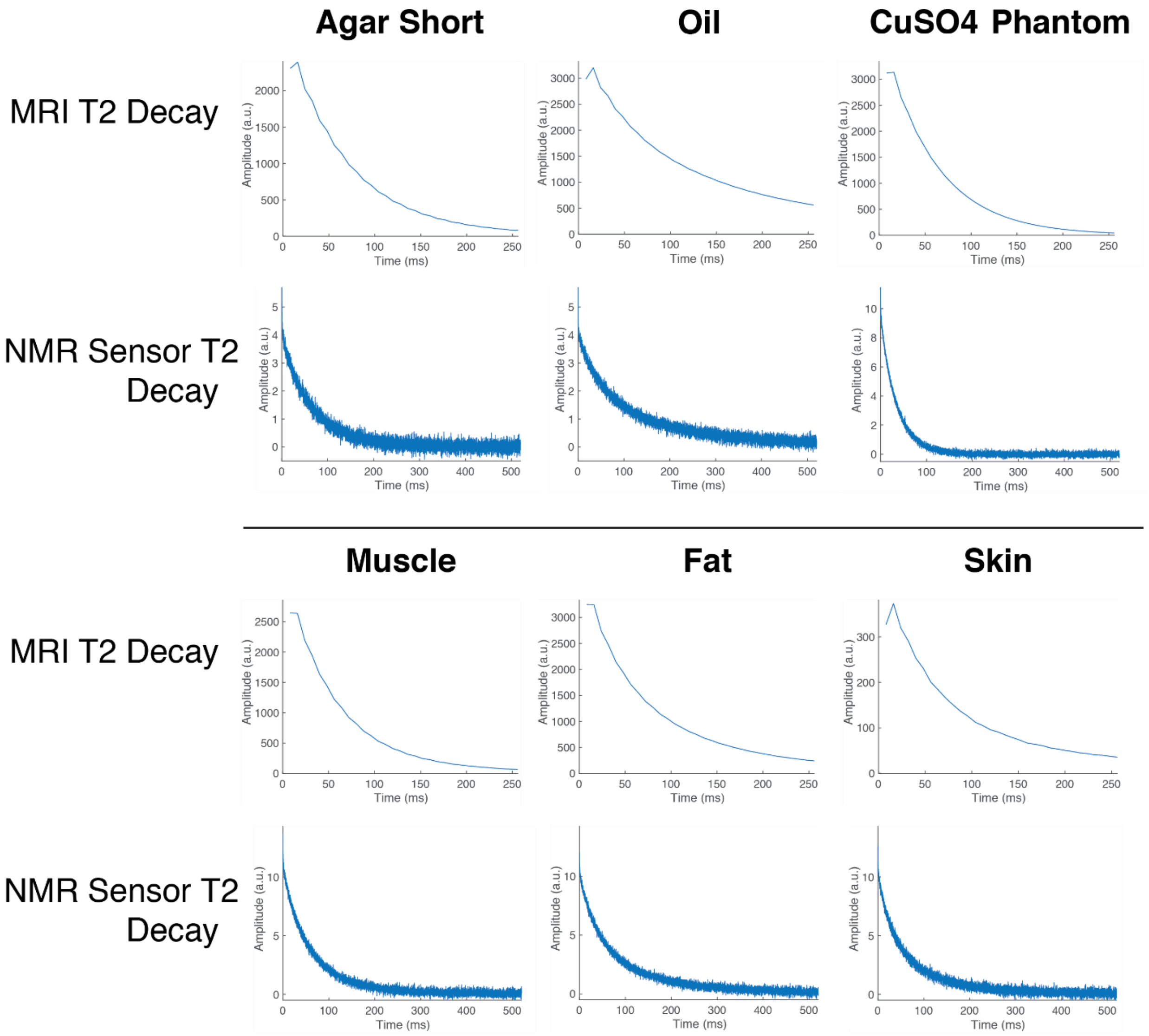

Fig. S8. *T*$_2$ decays of phantoms measured on MRI and NMR sensor. Side-by-side comparison of the raw T_2 decays from the MRI (whole ROI) and NMR sensor for each of the six phantoms and ex vivo tissues. The NMR Sensor collects 8,000 points on the T_2 decay from 0.065 ms to 520 ms by 65 μs intervals (echo time). The MRI collects 32 points from 8 ms to 256 ms with 8 ms spacing.

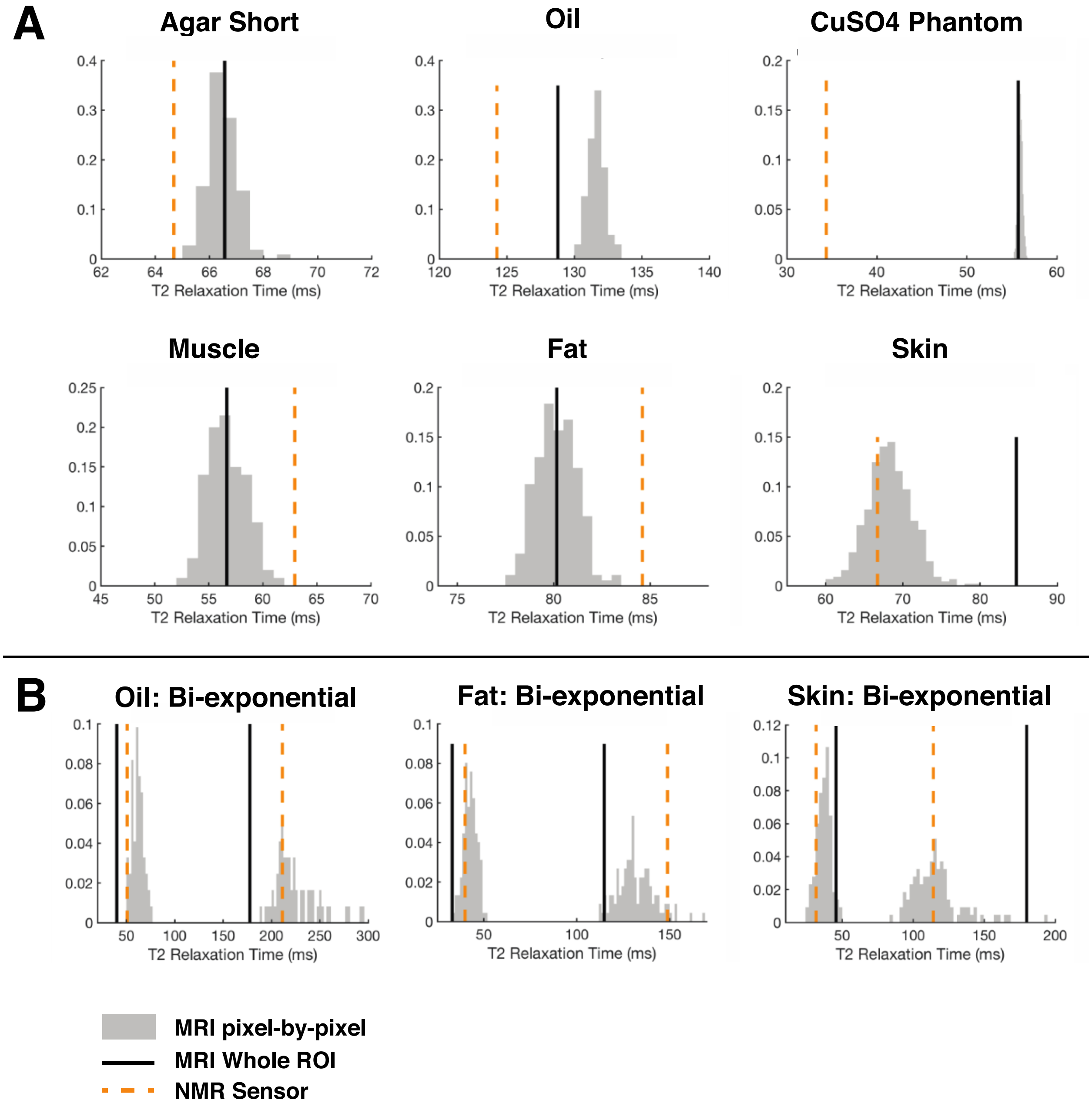

Fig. S9. T_2 results of phantoms measured on MRI and NMR sensor. (**A**) Mono-exponential fit results for phantoms and ex-vivo tissues. (**B**) Bi-exponential fit results for phantoms and ex-vivo tissues that were best fit by a bi-exponential fit. Grey histogram shows MRI pixel-wise fit results where sum of each histogram's bar heights equals 1. Solid black line shows T_2 relaxation time from MRI whole ROI fit. Orange dotted line shows T_2 relaxation time from NMR sensor fit. All NMR sensor (orange dotted) and MRI pixel-wise (grey histogram) fit results are summarized in fig. 5 and mono-exponential results in table S7.

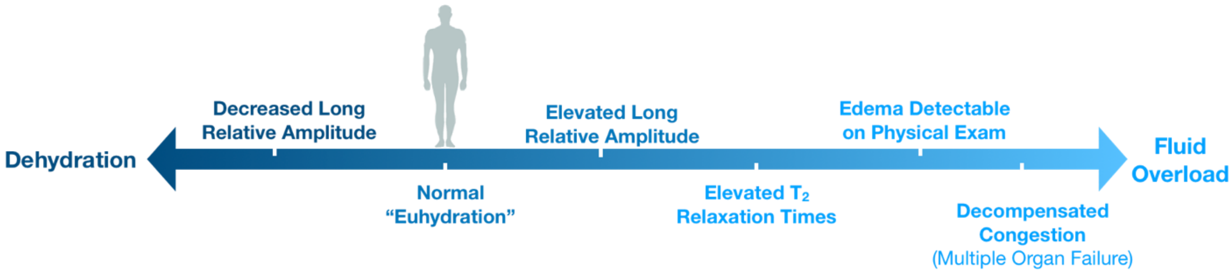

Fig. S10. Quantitative NMR relaxometry findings at different fluid states. Graphical summary of the relaxometry findings – through both bedside NMR sensor and/or traditional MRI measurements – at different clinical fluid states. All findings were observed in the muscular tissue.

Fig. S11. Pixels deleted by the MRI pixel-wise fitting criteria. Pixels (highlighted in blue) on each slice of each scan (*n* = 14 subjects) that were deleted by the four fitting criteria (described in “Materials and Methods: MRI analysis: Pixel-wise”). All pixel-wise MRI data presented in this study (except when otherwise noted) does not have data from these pixels included. HC: healthy control; HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice.

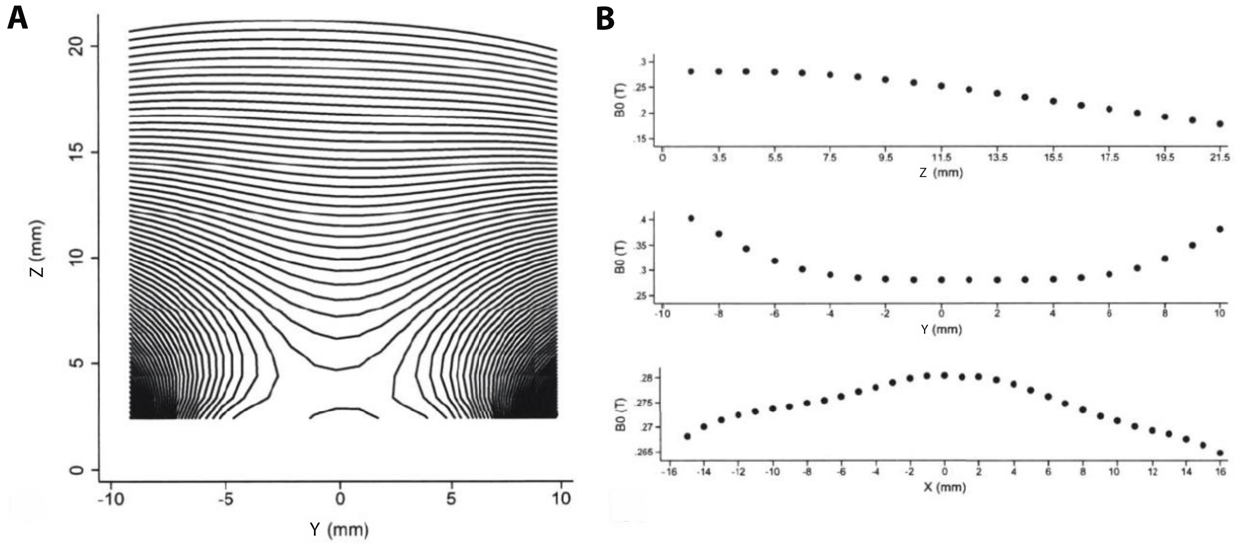

Fig. S12. B_o magnetic field map of the NMR sensor. The B_o magnetic field of the NMR sensor is produced by a unilateral linear Halbach magnet array. (**A**) Map of Y-Z plane shows saddle region. Contour line gradations represent 3.2mT. (**B**) 1D plots of each axis shows flat zones indicating uniform regions of the magnetic field. The field strength of the flat regions is approximately 0.28 T and about 80 mm^3 in volume (4 x 5 x 4 mm). Z represents the direction perpendicular from the flat face of the coil. The X-Y plane represent the plane delineated by the flat face of the sensor.

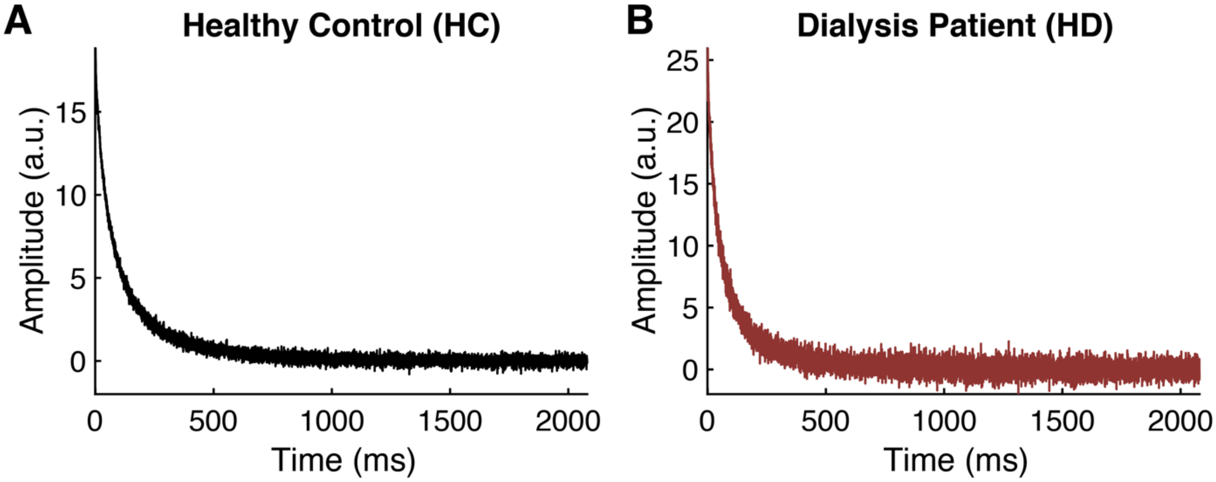

Fig. S13. NMR sensor T_2 decay signal from a representative HC and HD participant. (**A**) Raw T_2 relaxation time decay signal from healthy control 6 (HC 6) at baseline (SNR 98.2). (**B**) Raw signal from dialysis patient 4 (HC 4) at baseline (SNR 49.4). The average SNR across all subjects and time points is 80.4 ± 24.5 (mean ± std). The HC and HD signals shown in this figure are above and below the mean SNR, respectively. The SNR is calculated as the maximum T_2 signal value divided by the standard deviation of the noise floor.

Table S1. Individual-level demographics of the study population. Demographic information of each study subject (*n* = 14) as well as the means and standard deviations for HC and HD groups. 1 HC subject and 2 HD subjects completed the study twice (denoted by ‘b’ in the subject ID). Blood values are reported at baseline. Fluid loss (in kg) is based on the difference in pre- and post-weight. Percentage fluid loss is calculated by 100% * Fluid Loss / (0.6 * Baseline weight) because approximately 60% of the body is water. HC: healthy control; HD: hemodialysis patient.

(see Excel data file)

Table S2. *F* test comparison of multiexponential fits for pixel-wise MRI data. Results of an extra sum-of-squares F-test comparison of (1) mono- versus bi-exponential and (2) bi- versus 3-exponential fits for MRI pixels across multiple tissue types. **P* < 0.05 indicates that the more complex of the two models being compared is correct. The data shown are from randomly chosen pixels in slice 1 of an HC subject's baseline scan.

		Mono- vs bi-exponential		**Bi- vs. 3-exponential**	
	SNR	**F ratio**	***P* value**	**F ratio**	***P* value**
Muscular tissue	70.74	45.16	2.44E-09*	1.46	0.25
Subcutaneous tissue	140.1	86.76	1.76E-12*	1.77	0.19
Bone	5.41	0.092	0.91	-7.45E-5	1
Marrow	130.11	60.88	9.87E-11*	7.5E-8	0.99

Table S3. Summary of change in pixel-wise MRI values within ROIs. Change in pixel-wise MRI values between pre- and post-MRI scans summarized as the mean and standard deviation for HC and HD groups. Values for each of the 3 indicators – $T_{2,\text{short}}$, $T_{2,\text{long}}$, and RA_{long} – for each ROI are tabulated. . HC: healthy control. HD: hemodialysis patient. *P* values calculated with both a two-sample permutation test and two-sample Welch test are shown. * signifies $P < 0.05$, ** signifies $P < 0.01$, *** signifies $P < 0.001$. Data is visualized in bar-plot form in figs. 1D-F.

ROI		**HC**		**HD**		**HC vs HD, *P* value**	
		Mean	Std	Mean	Std	Welch test	Permutation test
Bone (1-exp fit)	$T_{2,\text{short}}$	6.03	10.52	-2.74	10.03	0.1365	0.1398
Whole leg	RA_{long}	-0.65	1.20	1.77	2.10	0.0253*	0.0248*
	$T_{2,\text{short}}$	0.02	1.13	0.95	0.68	0.0925	0.0758
	$T_{2,\text{long}}$	-4.47	12.66	-9.57	11.43	0.4445	0.4541
Marrow	RA_{long}	-0.06	1.98	-0.67	1.34	0.5212	0.5102
	$T_{2,\text{short}}$	-0.99	5.40	1.03	4.11	0.4475	0.4464
	$T_{2,\text{long}}$	-0.71	8.66	-1.09	9.43	0.9386	0.9374
Muscular tissue (all)	RA_{long}	0.23	1.70	3.42	1.43	0.0026**	0.0032**
	$T_{2,\text{short}}$	0.13	0.72	1.03	0.81	0.0487*	0.0445*
	$T_{2,\text{long}}$	-3.65	14.97	-11.50	11.31	0.2914	0.2973
Muscle: Anterior	RA_{long}	-0.96	2.06	4.13	2.12	0.0006***	0.0017**
	$T_{2,\text{short}}$	0.66	1.47	0.99	1.36	0.6741	0.6690
	$T_{2,\text{long}}$	7.26	11.98	-13.25	25.09	0.0841	0.0849
Muscle: Deep Posterior	RA_{long}	-1.52	3.23	3.06	1.79	0.0089**	0.0057**
	$T_{2,\text{short}}$	-0.14	1.80	1.62	0.94	0.0481*	0.0407*
	$T_{2,\text{long}}$	-3.62	17.86	-3.84	27.37	0.9862	0.9886
Muscle: Gastrocnemius	RA_{long}	2.14	2.98	5.67	2.61	0.0364*	0.0376*
	$T_{2,\text{short}}$	0.00	1.34	2.21	2.10	0.0404*	0.0305*
	$T_{2,\text{long}}$	-13.94	17.61	-6.38	31.29	0.5902	0.5818
Muscle: Lateral	RA_{long}	-0.24	1.65	3.32	2.71	0.0142*	0.0078**
	$T_{2,\text{short}}$	0.06	0.61	1.27	1.12	0.0332*	0.0283*
	$T_{2,\text{long}}$	4.48	15.14	-7.00	30.76	0.3992	0.4027
Muscle: Soleus	RA_{long}	0.25	2.96	1.79	2.12	0.2887	0.2829
	$T_{2,\text{short}}$	-0.13	1.34	1.66	1.61	0.0432*	0.0437*
	$T_{2,\text{long}}$	-4.63	17.18	0.31	16.77	0.5960	0.5926
Subcu. tissue (all)	RA_{long}	0.02	1.03	0.53	2.37	0.6161	0.6276
	$T_{2,\text{short}}$	-0.32	2.44	1.58	2.03	0.1400	0.1404
	$T_{2,\text{long}}$	-0.08	4.75	2.48	13.04	0.6395	0.7876

Table S4. Summary of quantile regression results for MRI pixel-wise RA$_{\text{long}}$ values from the muscle ROI. Results of quantile regression with clustering for MRI pixel-wise RA$_{\text{long}}$ values of muscle ROI. (**Left**) Difference between HC and HD values at each quantile with corresponding *P* values. (**Right**) Difference between pre- and post-values at each quantile with corresponding *P* values. * signifies $P < 0.05$, ** signifies $P < 0.01$, *** signifies $P < 0.001$, **** signifies $P < 0.0001$. HC: healthy control. HD: hemodialysis patient. Table results correspond to fig. 2D-F. For code to run quantile regression with clustering, see "SM: Computer code used for statistical tests - #3 Quantile regression of pixel-wise MRI data."

	Difference between HD vs HC				**Difference between Pre vs Post**			
Quantile (%)	Pre	*P* value	Post	*P* value	HC	*P* value	HD	*P* value
10	4.27	0.00271**	1.97	0.09462	0.13	0.64171	2.18	4.57E-06****
20	6.48	0.00101**	3.23	0.08903	0.08	0.85664	3.17	1.01E-09****
30	7.89	0.00053***	4.15	0.06936	0.03	0.96468	3.72	2.35E-12****
40	9.01	0.00027***	5.00	0.05520	-0.07	0.91417	4.08	2.73E-14****
50	9.92	0.00034***	5.98	0.03279*	-0.24	0.74761	4.18	2.66E-14****
60	10.73	0.00008****	6.83	0.02165*	-0.38	0.65668	4.28	1.18E-10****
70	11.41	0.00009****	7.75	0.02025*	-0.49	0.60580	4.14	2.93E-07****
80	12.12	0.00004****	8.83	0.01099*	-0.54	0.62938	3.83	0.00016***
90	12.82	0.00006****	10.03	0.00520**	-0.31	0.75714	3.11	0.00123**

Table S5. Summary of MRI $\mathrm{RA}_{\mathrm{long}}$ values for muscle (whole ROI average). Summary of the $\mathrm{RA}_{\mathrm{long}}$ values of the muscle ROI (whole ROI average) for each HC (*n* = 7) and HD (*n* = 7) subject as well as the change between pre- and post-measurements. Values are obtained by fitting the average T_2 decay of the whole muscle ROI with a bi-exponential fit. HC: healthy control. HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparisons calculated with a one-sample permutation test and paired Student t-test. * signifies $P < 0.05$, ** signifies $P < 0.01$, *** signifies $P < 0.001$. Data corresponds to fig. 3.

Subject	Pre	Post	Change	Pre vs Post, *P* value
HC 1	13.84	13.95	0.11	Permutation test **0.7499** Paired t-test **0.7293**
HC 1b	16.54	14.97	-1.57	
HC 2	15.14	12.88	-2.27	
HC 3	15.70	15.57	-0.14	
HC 4	15.86	18.12	2.27	
HC 5	19.79	21.43	1.64	
HC 6	18.85	17.15	-1.71	
HD 1	34.75	29.25	-5.50	Permutation test **0.01572*** Paired t-test **0.00023*****
HD 1b	31.34	27.58	-3.77	
HD 2	32.25	28.28	-3.97	
HD 2b	37.35	34.22	-3.13	
HD 3	17.80	14.83	-2.97	
HD 4b	23.24	17.39	-5.85	
HD 5	20.34	18.10	-2.25	
HC vs HD, *P* value				
Permutation test	**0.0025****	**0.02706***	**0.00122****	
Welch test	**0.00610****	**0.02965***	**0.00091*****	

Table S6. Comparison of specifications of the NMR sensor with those of a traditional MRI scanner. The ability of the NMR sensor to take more points in the T_2 measurement and have those points be spaced closer together allows the data to be fit by a higher number of exponentials. Although the NMR sensor does not have spatial resolution, its ability to decompose its signal into many components allows much of the same quantitative information to be obtained about the sample. $^{\otimes}$ 32 echoes is a limitation of Siemens MRI scanners. Other scanner types were not evaluated. CPMG: Carr-Purcell-Meiboom-Gill pulse sequence.

	MRI	**NMR sensor**
Cost of sensor	$1.5 Million	~$1,000
Cost of scan	$2000	<<$120 (cost of bedside x-ray)
Field strength	1.5T	0.28T
Time for T_2 measurement	10 minutes	45 seconds
# Echoes in CPMG	$32^{\otimes}$	8,000
Echo time (TE)	8 ms	65 µs
# of exponentials	2	3+

Table S7. Summary of phantom T_2 relaxation time results for MRI and NMR sensor. T_2 relaxation times measured by the MRI (pixel-wise) and NMR sensor for each phantom and ex-vivo tissue ($n = 6$) with a mono-exponential fit. Results correspond to fig. S9.

Sample	**MRI pixelwise** (ms)	**NMR sensor** (ms)	**Difference** (ms)	(%)
Agar short	66.2	64.7	1.5	2.3
Oil	132	124.3	7.7	6.2
$CuSO_4$ phantom	56	34.4	21.6	62.8
Muscle	56.7	63	6.3	10
Fat	79.5	84.6	5.1	6
Skin	69	66.7	2.3	3.4

Table S8. Summary of RA_b values from NMR sensor. Summary of the RA_b values (relative amplitude of the ECF of the muscular tissue) for each HC (*n* = 7) and HD (*n* = 7) subject as well as the change between pre- and post-measurements. Values are obtained by fitting NMR sensor measurements with a forced 3-exponential fit. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. * denotes $P < 0.05$. Data corresponds to fig. 6A,C.

Subject	Pre	Post	Change	Pre vs Post, *P* value
HC 1	35.99	33.90	-2.09	Permutation test **0.6995** Paired t-test **0.7245**
HC 1b	34.66	35.67	1.01	
HC 2	32.18	32.19	0.01	
HC 3	36.29	37.59	1.31	
HC 4	29.54	30.24	0.70	
HC 5	35.57	33.90	-1.67	
HC 6	31.98	34.27	2.29	
HD 1	41.33	43.13	1.80	Permutation test **0.0477*** Paired t-test **0.0317***
HD 1b	45.10	40.29	-4.80	
HD 2	33.06	27.93	-5.12	
HD 2b	30.94	30.69	-0.25	
HD 3	35.92	28.97	-6.95	
HD 4b	21.04	12.96	-8.09	
HD 5	25.11	22.31	-2.81	
HC vs HD, *P* value				
Permutation test	**0.5292**	**0.2945**	**0.0223***	
Welch test	**0.8790**	**0.2975**	**0.0264***	

Table S9. Summary of $\mathrm{RA}_{\mathrm{long}}$ values from MRI small voxel: Anterior 1 with subcutaneous and muscle. The anterior 1 voxel is 0.5 cm^3 in volume located in the anterior muscle group of the lower leg including both subcutaneous tissue and muscle. Tabulated summary of the $\mathrm{RA}_{\mathrm{long}}$ values (relative size of ECF space) for each HC ($n = 7$) and HD ($n = 7$) subject in this voxel as well as the change between pre- and post-measurements. Values are obtained by fitting the average T_2 decay of the small voxel ROI with a bi-exponential fit. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. *$P < 0.05$. Data corresponds to fig. 6F.

Subject	Pre	Post	Change	Pre vs Post, *P* value
HC 1	15.85	19.92	4.08	Permutation test **0.4386** Paired t-test **0.4607**
HC 1b	27.45	20.89	-6.56	
HC 2	13.73	20.63	6.90	
HC 3	20.45	18.69	-1.75	
HC 4	14.15	18.99	4.84	
HC 5	35.74	34.50	-1.24	
HC 6	39.22	42.82	3.60	
HD 1	52.57	31.53	-21.03	Permutation test **0.0631** Paired t-test **0.0547***
HD 1b	33.84	27.91	-5.94	
HD 2	54.74	49.04	-5.70	
HD 2b	49.18	51.07	1.89	
HD 3	30.36	19.03	-11.33	
HD 4b	18.22	9.56	-8.67	
HD 5	20.42	21.75	1.34	
HC vs HD, *P* value				
Permutation test	**0.085**	**0.4920**	**0.0284***	
Welch test	**0.0853**	**0.5008**	**0.0349***	

Table S10. Summary of $\mathrm{RA}_{\mathrm{long}}$ values from MRI small voxel: Anterior 2 with muscle only. The anterior 2 voxel is $0.5\mathrm{cm}^3$ in volume located in the anterior muscle group close to, but not including, the subcutaneous tissue. Tabulated summary of the $\mathrm{RA}_{\mathrm{long}}$ values (relative size of ECF space) for each HC ($n = 7$) and HD ($n = 7$) subject in this voxel as well as the change between pre- and post-measurements. Values are obtained by fitting the average T_2 decay of the small voxel ROI with a bi-exponential fit. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. *$P < 0.05$. Data corresponds to fig. 6F.

Subject	Pre	Post	Change	Pre vs Post, *P* value
HC 1	8.92	10.55	1.63	Permutation test **0.1407** Paired t-test **0.1396**
HC 1b	8.97	10.59	1.62	
HC 2	6.34	10.15	3.81	
HC 3	9.40	10.28	0.88	
HC 4	9.91	11.60	1.69	
HC 5	18.31	17.96	-0.34	
HC 6	11.67	10.09	-1.58	
HD 1	25.82	9.67	-16.15	Permutation test **0.0622** Paired t-test **0.0692**
HD 1b	24.30	26.05	1.75	
HD 2	46.27	41.94	-4.32	
HD 2b	46.15	43.20	-2.95	
HD 3	8.80	9.90	1.10	
HD 4b	12.75	5.85	-6.90	
HD 5	14.79	6.28	-8.51	
HC vs HD, *P* value				
Permutation test	**0.0198***	**0.2315**	**0.0179***	
Welch test	**0.0413***	**0.2129**	**0.0366***	

Table S11. Summary of $\mathrm{RA}_{\mathrm{long}}$ values from MRI small voxel: Lateral 1 with subcutaneous and muscle. The lateral 1 voxel is $0.5\mathrm{cm}^3$ in volume located in the lateral muscle group including both subcutaneous tissue and muscle. Tabulated summary of the $\mathrm{RA}_{\mathrm{long}}$ values (relative size of ECF space) for each HC (*n* = 7) and HD (*n* = 7) subject in this voxel as well as the change between pre- and post-measurements. Values are obtained by fitting the average T2 decay of the small voxel ROI with a bi-exponential fit. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. $^*P < 0.05$. Data corresponds to fig. 6F.

Subject	Pre	Post	Change	Pre vs Post, *P* value
HC 1	39.83	27.65	-12.18	Permutation test **0.5301** Paired t-test **0.5167**
HC 1b	32.49	34.21	1.73	
HC 2	25.07	18.78	-6.29	
HC 3	46.26	41.80	-4.46	
HC 4	23.96	24.85	0.88	
HC 5	30.18	36.29	6.11	
HC 6	46.23	48.98	2.75	
HD 1	53.60	61.34	7.74	Permutation test **0.3761** Paired t-test **0.3348**
HD 1b	45.17	51.32	6.15	
HD 2	49.09	47.35	-1.74	
HD 2b	66.05	63.10	-2.95	
HD 3	31.05	32.54	1.49	
HD 4b	36.05	34.40	-1.65	
HD 5	21.81	24.18	2.36	
HC vs HD, *P* value				
Permutation test	**0.2296**	**0.1162**	**0.2772**	
Welch test	**0.2341**	**0.1185**	**0.2761**	

Table S12. Summary of RA_{long} values from MRI small voxel: Lateral 2 with muscle only. The lateral 2 voxel is 0.5cm^3 in volume located in the lateral muscle group close to, but not including, the subcutaneous tissue. Tabulated summary of the RA_{long} values (relative size of ECF space) for each HC ($n = 7$) and HD ($n = 7$) subject in this voxel as well as the change between pre- and post-measurements. Values are obtained by fitting the average T2 decay of the small voxel ROI with a bi-exponential fit. HC: healthy control. HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. P values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. * signifies $P < 0.05$. ** signifies $P < 0.01$. Data corresponds to fig. 6F.

Subject	Pre	Post	Change	Pre vs Post, *P* value
HC 1	12.15	13.47	1.32	Permutation Test **0.5589** Paired t-test **0.5443**
HC 1b	18.70	15.95	-2.75	
HC 2	11.85	7.01	-4.83	
HC 3	11.05	19.40	8.35	
HC 4	14.05	13.79	-0.27	
HC 5	18.79	19.84	1.05	
HC 6	7.84	12.48	4.64	
HD 1	30.50	32.08	1.58	Permutation Test **0.0316*** Paired t-test **0.0209***
HD 1b	29.08	27.41	-1.67	
HD 2	34.59	27.06	-7.53	
HD 2b	60.19	49.74	-10.45	
HD 3	15.20	10.78	-4.42	
HD 4b	23.61	13.52	-10.09	
HD 5	14.37	10.53	-3.83	
HC vs HD, *P* value				
Permutation Test	0.0091**	0.0912	0.0237*	
Welch Test	0.0327*	0.1215	0.0210*	

Table S13. Summary of whole-body R_e BI values. Tabulated summary of the whole-body R_e values (ECF-associated resistivity) for each HC ($n = 7$) and HD ($n = 7$) subject as well as the change between pre- and post-measurements. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. * denotes $P < 0.05$. ** denotes $P < 0.01$. Data correspond to fig. 7A-B.

Whole body bioimpedance R_e				
Subject	**Pre**	**Post**	**Change**	**Pre vs Post, *P* value**
HC 1	651.03	693.26	42.23	Permutation test: **0.03059*** Paired t-Test: **0.0037***
HC 1b	588.64	646.38	57.74	
HC 2				
HC 3	531.55	548.82	17.27	
HC 4	727.65	759.08	31.43	
HC 5	445.20	462.07	16.87	
HC 6	747.07	799.23	52.16	
HD 1	438.79	535.94	97.15	Permutation test: **0.03098*** Paired t-Test: **0.0070****
HD 1b	-	-	-	
HD 2	439.05	445.22	6.17	
HD 2b	354.59	398.65	44.06	
HD 3	434.80	520.92	86.12	
HD 4b	518.24	609.45	91.21	
HD 5	568.34	622.37	54.04	
HC vs HD, Permutation test *P* value	**0.02008***	**0.06864**	**0.12494**	
HC vs HD, Welch test, *P* value	**0.0230***	**0.0720**	**0.1354**	

Table S14. Summary of whole-body R_{inf} BI results. Tabulated summary of the whole-body R_{inf} values (TBW-associated resistivity) for each HC (*n* = 7) and HD (*n* = 7) subject as well as the change between pre- and post-measurements. HC: healthy control. HD: hemodialysis patient. A 'b' in the subject ID indicates a subject's second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. * denotes $P < 0.05$. ** denotes $P < 0.01$. Data correspond to fig. 7C-D.

Whole body bioimpedance R_{inf}				
Subject	**Pre**	**Post**	**Change**	**Pre vs Post, *P* value**
HC 1	446.38	470.08	23.70	Permutation test: **0.0321*** Paired t-test: **0.0286***
HC 1b	404.33	444.45	40.13	
HC 2				
HC 3	359.84	367.96	8.12	
HC 4	506.85	512.11	5.26	
HC 5	306.11	311.55	5.44	
HC 6	500.71	520.16	19.45	
HD 1	314.59	371.29	56.69	Permutation test: **0.0624** Paired t-test: **0.0212***
HD 1b	-	-	-	
HD 2	345.63	340.28	-5.35	
HD 2b	276.68	315.38	38.70	
HD 3	281.20	338.36	57.16	
HD 4b	342.81	377.49	34.67	
HD 5	417.54	433.05	15.50	
HC vs HD, Permutation test *P* value	**0.0449***	**0.0771**	**0.1924**	
HC vs HD, Welch test, *P* value	**0.0448***	**0.0851**	**0.2014**	

Table S15. Summary of leg segmental R_e BI results. Tabulated summary of the leg segmental R_e values (ECF-associated resistivity) for each HC ($n = 7$) and HD ($n = 7$) subject as well as the change between pre- and post-measurements. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. P values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. * denotes $P < 0.05$. ** denotes $P < 0.01$. *** denotes $P < 0.001$. Data corresponds to fig. 7E-F.

Leg Bioimpedance R_e				
Subject	**Pre**	**Post**	**Change**	**Pre vs Post, *P* value**
HC 1	104.63	113.00	8.37	Permutation Test: **0.0313*** Paired t-Test: **0.0021****
HC 1b	106.43	123.54	17.11	
HC 2	82.81	88.62	5.80	
HC 3	80.01	86.79	6.78	
HC 4	135.61	149.81	14.21	
HC 5	73.22	83.79	10.56	
HC 6	-	-	-	
HD 1	41.55	57.44	15.88	Permutation Test: **0.0163*** Paired t-Test: **0.0006*****
HD 1b	110.16	137.54	27.38	
HD 2	85.56	98.03	12.48	
HD 2b	58.85	66.01	7.16	
HD 3	84.81	110.53	25.73	
HD 4b	102.99	130.52	27.53	
HD 5	118.82	138.41	19.59	
HC vs HD, Permutation test *P* value	**0.4572**	**0.9009**	**0.0383***	
HC vs HD, Welch test, *P* value	**0.45346**	**0.90151**	**0.03011***	

Table S16. Summary of leg segmental R_{inf} BI results. Tabulated summary of the leg segmental R_{inf} values (TBW-associated resistivity) for each HC (*n* = 7) and HD (*n* = 7) subject as well as the change between pre- and post-measurements. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice. *P* values for (1) HC vs HD comparisons calculated with a two-sample permutation test and two-sample Welch test, and (2) pre vs post comparison calculated with a one-sample permutation test and paired Student t-test. * denotes $P < 0.05$. ** denotes $P < 0.01$. *** denotes $P < 0.001$. Data corresponds to fig. 7G-H.

Leg segmental bioimpedance R_{inf}				
Subject	**Pre**	**Post**	**Change**	**Pre vs Post, *P* value**
HC 1	56.43	58.29	1.87	Permutation test: **0.0308*** Paired t-test: **0.0161***
HC 1b	64.37	70.61	6.24	
HC 2	40.00	41.21	1.22	
HC 3	41.10	42.12	1.02	
HC 4	73.76	78.78	5.02	
HC 5	37.30	41.14	3.84	
HC 6	-	-	-	
HD 1	29.40	37.47	8.08	Permutation test: **0.0152*** Paired t-test **0.0005*****
HD 1b	74.07	81.44	7.36	
HD 2	72.00	78.34	6.34	
HD 2b	49.69	56.47	6.78	
HD 3	50.71	60.56	9.85	
HD 4b	51.90	57.50	5.60	
HD 5	80.26	95.33	15.07	
HC vs HD, Permutation test *P* value	**0.5122**	**0.2690**	**0.0023****	
HC vs HD, Welch test, *P* value	**0.5158**	**0.2780**	**0.0055****	

Table S17. Change in T_2 relaxation time of phantom measured with each human NMR sensor measurement. A phantom filled with an aqueous solution of copper sulfate of known T_2 relaxation time was taken with each human measurement so that any sensor malfunctions could be immediately identified. The phantom was measured with the same pulse sequence as used in human measurements except with 0 dummy echoes instead of 3, due to historical reasons of how the phantom had been characterized in past experiments. The T_2 relaxation time was calculated by fitting the CPMG data with a mono-exponential decay curve. The difference between the measured T_2 relaxation time at the pre- and post-time points is quantified in this table. The average pre-to-post change in measured phantom T_2 value was 0.84 ± 0.78 ms. The maximum T_2 difference was 2.8 ms, which occurred one time. HC: healthy control. HD: hemodialysis patient. A ‘b’ in the subject ID indicates a subject’s second study visit for those that completed the study twice.

Subject	Difference in T_2 relaxation time (ms)
HC 1	0.87
HC 1b	0.20
HC 2	0.27
HC 3	0.20
HC 4	0.10
HC 5	1.37
HC 6	0.67
HD 1	2.80
HD 2	1.63
HD 3	0.07
HD 4b	1.34
HD 5	1.32
HD 2b	0.62
HD 1b	0.33
Mean	**0.84**
Std. dev.	**0.78**