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Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☒	☐	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☒	☐	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☒	☐	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☒	☐	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	The commercially available EM simulation software (CST microwave studio Darmstadt, Germany) was used, but this is not central to the paper.
Data analysis	MatLab 2016b (Mathworks, MA, USA) was used to analyze the data. The custom Matlab code used to perform the SNR analysis implements methods and procedures well known in our community and described in detail in the referenced publication (this code is available upon request). The custom Matlab code used to evaluate the high-impedance detector design space is available at https://bitbucket.org/macloos/hic/wiki/Home The open source latex package Tikz (http:// www.texample.net/tikz) was used to generate the main figures. Mathematica 10 (Champagne, IL, USA), was used to create supplemental figure 2 (showing the data obtained using CST based EM simulation).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The data that support the findings of this study are available within the paper and its Supplementary Information. All datasets generated for this study are available from the corresponding author upon reasonable request.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences

Study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	In-vitro (phantom) experiments were performed to evaluate the performance of different MR detector configurations. Two phantoms were used, both with a conductivity that approximates human tissue. SNR measurements were performed in one spot 1/2 the detector radius underneath the center detector. This is the approximate location where a given detector works optimally. The SNR was averaged over a small ~30 voxel ROI to minimize the influence of noise like contributions form the transmit normalization procedure. Three human volunteers were scanned to highlight the various possible applications of the HIC detector. Considering the diverse examples we wanted to show, three subjects were scanned in subsequent sessions. The total time inside the magnet for each subject was less than 1 hour.
Data exclusions	No data were excluded.
Replication	All attempts to replicate the results were successful. The results from the rectangular phantom experiments were reproduced several times (with consistent results). Initial experiments were performed with a courser sampling (10% steps in overlap not shown in the paper). Subsequent experiment used a refined step size of 5% and also included B1 mapping measurements to account for transmit sensitivity variations. Finally, we also considered possible variations in the RF receive chain of the system and repeated the measurement after performing a receive chain calibration procedure. Each of these experiments were performed on separate days, sometimes weeks apart. All of the measurements show the same behavior as shown in the paper. Only the final (most refined and precise) measurements are shown in the paper. Measurements performed on the cylindrical phantom were repeated twice (both using a 5% step size, B1 mapping, and receiver gain calibration). Both measurements show the same trend, with small variations most likely due to variability in coil placement on the curved surface. The graphs in the supplemental figure showing these results corresponds to the mean of the two measurements. The quantitative in-vivo SNR comparison was performed once and all three in-vivo scanning sessions consistently produced the same high-quality, high-SNR images.
Randomization	Randomization was not applicable.
Blinding	The subject data was anonymized to protect possible leaking of HIPPA information. No blinding was used, all comparative analysis contained in the manuscript is based on objective quantitative measures.

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☐	☒ Unique materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Research animals
☐	☒ Human research participants

Unique materials

Obtaining unique materials	The preamplifiers used in this work were provided by Siemens. Although Siemens may not be able to provide these specific

Obtaining unique materials	amplifiers to all sites, there are many alternatives with similar performance characteristics (both from MR vendors and general electronic stores). All the essential parts needed to build the coil can be bought directly from various sources such as digikey (and other suppliers).

Human research participants

Policy information about studies involving human research participants

Population characteristics	The left hand of three healthy volunteers was imaged at 3 Tesla. Volunteers were between 27-40 years old. The study was approved by our institutional review board (IRB), and written informed consent was obtained prior to the examination.

Method-specific reporting

n/a	Involved in the study	
☒	☐	ChIP-seq
☒	☐	Flow cytometry
☐	☒	Magnetic resonance imaging

Magnetic resonance imaging

Experimental design

Design type	Evaluation of signal-to-noise ratio (SNR), and structural imaging.
Design specifications	Phantom and invivo SNR measurements. In addition, high-resolution structural and dynamic images of the left hand were acquired. No performance/task-based/resting-state fMRI or clinical trials were performed.
Behavioral performance measures	N/A

Acquisition

Imaging type(s)	Structural and SNR
Field strength	3T
Sequence & imaging parameters	For the SNR evaluation: Gradient recalled echo (GRE) images, axially through the center coil, were acquired, one signal image (flip angle = 25 degrees) and one noise image (flip angle = 0 degrees). Sequence parameters were as follows: 3 ms echo time, 200 ms repetition time, 256 x 256 matrix, 384 x 384 mm field of view, 5 mm slice thickness, and 300 Hz/pixel readout bandwidth. In addition, a B1+ map was acquired using the pre-saturation turbo-flash method (same resolution) [Chung S. et al., Magn. Reson. Med. 64, 439-446 (2010)]. Structural images: T1-weighted turbo spin echo (TSE) images of the left hand were acquired in coronal and sagittal planes (TSE, 1024 x 786 matrix, 256 x 192 field of view, 2 mm slice thickness, Turbo factor 2, excitation / refocusing angle of 90 / 180 degrees, TR = 400 ms, TE = 15 ms, total scan time 2 min and 37 s). In addition, 150- mm resolution images were acquired in sagittal only (TSE, 2048 x 512 matrix, 303 x 76 mm field of view). A proton-density-weighted 3D GRE dataset was acquired covering only a single finger (0.5 mm isotropic, 512 x 64 x 104 matrix, 256 x 32 x 52 mm field of view, TR = 12 ms, TE = 5 ms, 10-degree flip angle, total scan time, 1 min and 20 s). A Golden angle radial GRE (0.8 mm x 0.8 mm, 192 x 192 matrix, 160 x 160 mm field of view, 2.5 slice thickness, TR = 6.5 ms, TE = 3.5 ms, total acquisition time 25 s) was used to make the MR videos.
Area of acquisition	Phantom and left hand of healthy adult volunteers.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	N/A
Normalization	SNR maps are B1+ normalized.
Normalization template	N/A
Noise and artifact removal	N/A
Volume censoring	N/A

Statistical modeling & inference

Model type and settings	N/A
Effect(s) tested	N/A

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference (See Eklund et al. 2016)	N/A
Correction	N/A

Models & analysis

n/a	Involved in the study
☒	☐ Functional and/or effective connectivity
☒	☐ Graph analysis
☒	☐ Multivariate modeling or predictive analysis