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Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the 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
☐	☒ A statement on 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 statistical parameters 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

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	No custom software was used.
Data analysis	Data analysis was carried out in MATLAB version 2019a. The Java Information Dynamics Toolbox v1.5 is freely available online: (https://github.com/jlizier/jidt), and an updated version with MATLAB/Octave code and instructions to compute synergy and redundancy from Integrated Information Decomposition has been made available as Supplementary Information. The CONN toolbox version 17f is freely available online (http://www.nitrc.org/projects/conn). DSI Studio is freely available online (https://dsi-studio.labsolver.org). The version available in April 2020 was used. The Brain Connectivity Toolbox code used for graph-theoretical analyses is freely available online (https://sites.google.com/site/bctnet/). The code used for NeuroSynth meta-analysis is freely available online: (https://www.github.com/gpreti/GSP_StructuralDecouplingIndex), and NeuroSynth is also freely available online: https://neurosynth.org/. The HRF deconvolution toolbox v2.2 is freely available online: (https://www.nitrc.org/projects/rshrf). The Pypreclin pipeline code v1.0.1 is freely available at GitHub (https://github.com/neurospin/pypreclin). The code for PLS analysis of gene expression profiles is freely available online: https://github.com/SarahMorgan/Morphometric_Similarity_SZ. The GOrilla platform is available online at http://cbl-gorilla.cs.technion.ac.il The REVIGO platform is available online at http://revigo.irb.hr The R package plsgenomics v1.5 is freely available online: https://CRAN.R-project.org/package=plsgenomics. The code for the dynamic mean-field model is freely available at http://www.gitlab.com/concog/fastdmf. FreeSurefer v5.3.0 is available at https://surfer.nmr.mgh.harvard.edu/ SPM12 is available at www.fil.ion.ucl.ac.uk/spm/software/spm12/ The code for spin-based permutation testing of cortical correlations is freely available online at https://github.com/frantisekvasa/rotate_parcellation.

The code for gene enrichment relative to an ensemble of null phenotypes is freely available online at https://github.com/benfulcher/GeneCategoryEnrichmentAnalysis/wiki/Ensemble-enrichment.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The HCP DWI data in SRC format are available online (http://brain.labsolver.org/diffusion-mri-data/hcp-dmri-data).
The HCP fMRI data are available online (https://www.humanconnectome.org/study/hcp-young-adult/data-releases).
Macaque MRI data are available from the PRIMatE Data Exchange (PRIME-DE) through the Neuroimaging Informatics Tools and Resources Clearinghouse (NITRC; http://fcon_1000.projects.nitrc.org/indi/indiPRIME.html).
The PET data that support the findings of this study are available from author James Rowe (James.Rowe@mrc-cbu.cam.ac.uk) upon reasonable request for academic (non-commercial) purposes, subject to restrictions required to preserve participant confidentiality.
The macaque connectome is available online on Zenodo: DOI: 10.5281/zenodo.1471588, and it is based on the CoCoMac database, available at http://cocomac.g-node.org/main/index.php?
The Genotype-Tissue Expression (GTEx) database (data source: GTEx Analysis Release V6p) is available at https://www.gtexportal.org/.
The BrainSpan Study [BSS] database is available at http://brainspan.org
Cortical gene expression patterns were taken from the transcriptomic data of the Allen Human Brain Atlas (AHBA, http://human.brain-map.org/static/download).
Region-wise maps of chimpanzee-to-human cortical expansion and HAR gene expression are available as Supplementary Materials from Wei et al. (2019). DOI: https://doi.org/10.1038/s41467-019-12764-8.
The NMT anatomical volume and associated probabilistic tissue segmentation maps (GM, WM and CSF) are freely available online: https://afni.nimh.nih.gov/pub/dist/atlases/macaque/nmt and http://github.com/jms290/NMT.
The maps of average regional Glycolytic Index (GI) are available as Supplementary Materials from Vaishnavi et al. (2010). DOI: https://doi.org/10.1073/pnas.1010459107.
The genes whose expression is associated with the regional distribution of GI in the human brain are available as Supplementary Materials from Goyal et al. (2014); DOI; doi: 10.1016/j.cmet.2013.11.020.
Anonymized receptor autoradiography data from Goulas et al. (2021) are available online: https://github.com/AlGoulas/receptor_principles.
The measure of cortical wiring distance is available as Supplementary Information from Paquola et al. (2020). DOI: https://doi.org/10.1371/journal.pbio.3000979.

Field-specific reporting

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☐ Life sciences ☒ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

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Behavioural & social sciences study design

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

Study description	This was a quantitative study, re-analyzing previously collected data from multimodal neuroimaging datasets.
Research sample	HCP dataset: The dataset of human MRI data used in this work came from the Human Connectome Project (HCP, http://www.humanconnectome.org/), Release Q3. These data contained fMRI and diffusion weighted imaging (DWI) acquisitions from the widely-used 100 unrelated subjects (54 females and 46 males, mean age = 29.1 ± 3.7 years) of the HCP 900 data release [51]. Full details can be found in a specific publication dedicated to the description of this widely-used, openly available dataset: Van Essen et al (2013) NeuroImage. PET dataset: 15 healthy volunteers (8 females; age: 68 ± 7 years) underwent simultaneous 3T MRI and [11C]UCB-J PET at the Wolfson Brain Imaging Centre, University fo Cambridge [97]. The volunteers were chosen as age-/sex-/education-matched healthy controls for a cohort of patients, and recruited from the UK National Institute for Health Research Join Dementia Research register. Both healthy controls and patient volunteers were pre-screened by telephone; participants were excluded based on any of the following: history of cancer within the last 5years; concurrent use of the medication levetiracetam; any severe physical illness or co-morbidity that limited ability to fully participate in the study; any contraindications to performing MRI. Participants were also excluded based on history of ischaemic or haemorrhagic stroke evident on MRI available from the clinic. The PET data used in the present study are available from author James Rowe (James.Rowe@mrc-cbu.cam.ac.uk) upon reasonable request for academic (non-commercial) purposes, subject to restrictions required to preserve participant confidentiality. Macaque dataset: We used fMRI data from rhesus macaques (Macaca mulatta) scanned at Newcastle University. This samples includes 14 exemplars (12 male, 2 female); Age distribution: 3.9-13.14 years; Weight distribution: 7.2-18 kg (full sample description available online: http://fcon_1000.projects.nitrc.org/indi/PRIME/files/newcastle.csv and http://fcon_1000.projects.nitrc.org/indi/PRIME/newcastle.html). To ensure comparability with the human data, we did not include data from anaesthetized animals. Out of the 14 total animals present in the Newcastle sample, 10 had awake resting-state fMRI data.

	Data from the Allen Brain Atlas was collected from 6 post-mortem brains from adult human donors with no history of psychiatric or neuropathological disorders (age: 24-57 years). Receptor autoradiography data were obtained from four postmortem cerebral hemispheres obtained from three human donors with no known history of neurological or psychiatric diseases (one female; age 75 ± 3 years) with their previous written consent.
Sampling strategy	HCP dataset: the 100 unrelated subjects used for our study were identified and made available by members of the HCP consortium. Recruiting efforts were used by the HCP consortium to ensure that participants broadly reflect the ethnic and racial composition of the U.S. population as represented in the 2000 decennial census. We did not use statistical methods to pre-determine sample size, but this 100-subject dataset has been extensively studied, so that our sample size is similar to those reported in previous publications [25,56]; no data-points were excluded, and there was no assignment into sub-groups. The dataset is extensively described in a dedicated publication: Van Essen et al (2013) NeuroImage. Macaque dataset: we used all available data from the awake scanning of the Newcastle sample of the PRIME-DE database, chosen due to relatively large sample size and availability of awake rather than anaesthetised acquisition. Data acquired during anaesthesia were not used. PET dataset: The volunteers were chosen as age-/sex-/education-matched healthy controls for a cohort of patients, and recruited from the UK National Institute for Health Research Join Dementia Research register. Here we only used the healthy control data. See above and Holland et al., 2020 (Movement Disorders) for details. All participants were reimbursed for their travel costs.
Data collection	As our study did not collect any dedicated new data, the researchers who collected the original datasets were not aware of the hypotheses of the present study. HCP dataset: structural, functional, and diffusion MRI data were collected with a 3-Tesla Skyra scanner at Washington University. Extensive details are provided in a dedicated publication: Van Essen et al (2013) NeuroImage. PET dataset: participants underwent simultaneous 3T MRI and [11C]UCB-J PET on a GE SIGNA PET/MR (GE Healthcare, Waukesha, USA). The radioligand [11C]UCB-J was synthesized at the Radiopharmacy Unit, Wolfson Brain Imaging Centre, Cambridge University. No other individuals were present in the PET scanning room apart from the participant, during the scan. Participants were under continuous visual observation from the adjacent control room, and there was an open microphone channel in case a participant needed to be in contact with the radiographers. The radiographer was present throughout with medical cover on site in case of need (such a need did not arise). Please see Holland et al., 2020 (Movement Disorders) for details. Macaque dataset: Animals were scanned in a vertical Bruker 4.7T primate dedicated scanner. Please see Milham et al., 2019 (Neuron) and http://fcon_1000.projects.nitrc.org/indi/PRIME/newcastle.html for details.
Timing	HCP dataset: Data were acquired between August 2012 and April 2013; please see Van Essen et al., 2013 (NeuroImage) for details. PET dataset: data were acquired between June 2019 and June 2020. Please see Holland et al., 2020 (Movement Disorders) for details. Macaque dataset: please see Milham et al., 2019 (Neuron) and http://fcon_1000.projects.nitrc.org/indi/PRIME/newcastle.html.
Data exclusions	To ensure comparability with human fMRI data, which were acquired from awake participants, we excluded a priori any macaque fMRI data obtained under anaesthesia. Of 14 macaques, 12 had resting-state functional MRI data available. Of these 12, 2 had fMRI data acquired during anaesthesia, and were excluded for this reason. Of the remaining 10 exemplars, one only had available fMRI data fro one session, whereas the remaining 9 exemplars each had two sessions. No data were excluded from the HCP or PET datasets.
Non-participation	HCP dataset: the dedicated publication by Van Essen et al., 2013 (NeuroImage) that describes data collection of the HCP dataset reports that on average, approximately 6–7 families had to be screened in order to identify one family who met all the inclusion criteria and were willing to participate. PET dataset: No participants dropped out or declined participation.
Randomization	HCP dataset: we did not allocate the subjects from the HCP dataset into different experimental groups. PET dataset: volunteers were chosen as healthy controls for a patient study, selected to match age, sex and education of patients. Here we only used data from the healthy controls. please see Holland et al., 2020 (Movement Disorders) for details.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☐	☒ MRI-based neuroimaging

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Functional MRI data were obtained from 10 exemplars of Macaca Mulatta, out of 14 (12 male, 2 female); Age distribution: 3.9-13.14 years; Weight distribution: 7.2-18 kg (full sample description available online: http://fcon_1000.projects.nitrc.org/indi/PRIME/files/newcastle.csv and http://fcon_1000.projects.nitrc.org/indi/PRIME/newcastle.html).
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All of the animal procedures performed were approved by the UK Home Office and comply with the Animal Scientific Procedures Act (1986) on the care and use of animals in research and with the European Directive on the protection of animals used in research (2010/63/EU). We support the Animal Research Reporting of In Vivo Experiments (ARRIVE) principles on reporting animal research. All persons involved in this project were Home Office certified and the work was strictly regulated by the U.K. Home Office. Local Animal Welfare Review Body (AWERB) approval was obtained. The 3Rs principles compliance and assessment was conducted by National Centre for 3Rs (NC3Rs). Animal in Sciences Committee (UK) approval was obtained as part of the Home Office Project License approval.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Human research participants

Policy information about studies involving human research participants

Population characteristics	HCP dataset: 100 unrelated subjects (54 females and 46 males, mean age = 29.1 ± 3.7 years). PET dataset: N=15 healthy controls (8 females; age: 68 ± 7 years).
Recruitment	HCP dataset: please see Barch et al., 2013 (NeuroImage) for details. PET dataset: The volunteers were chosen as age-/sex-/education-matched healthy controls for a cohort of patients, and recruited from the UK National Institute for Health Research Join Dementia Research register. Please see Holland et al., 2020 (Movement Disorders) for details.
Ethics oversight	HCP dataset: All HCP scanning protocols were approved by the local Institutional Review Board at Washington University in St. Louis. PET dataset: The research protocol was approved by an NHS Research Ethics Committee (REC: 18/EE/0059) and the Administration of Radioactive Substances Advisory Committee (ARSAC), and all participants provided written informed consent in accordance with the Declaration of Helsinki.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Magnetic resonance imaging

Experimental design

Design type	Resting-state (for PET dataset: simultaneous MR/PET).
Design specifications	HCP dataset: Two sessions of 15 min resting-state fMRI were acquired (here, we only used data acquired in the LR encoding direction) PET dataset: Dynamic PET data acquisition was performed for 90 minutes starting immediately after [11C]UCB-J injection. Macaque dataset: Resting-state scanning was performed for 21.6 minutes, with awake animals.
Behavioral performance measures	No behavioural measures were collected during scanning.

Acquisition

Imaging type(s)	HCP dataset: fMRI and diffusion MRI. Macaque dataset: fMRI PET dataset: Positron Emission Tomography with [11C]UCB-J radioligand, and simultaneous T1-weighted MRI.
Field strength	HCP and PET datasets: 3T. Macaque dataset: 4.7T.
Sequence & imaging parameters	HCP dataset: resting-state fMRI: gradient-echo EPI, TR= 720 ms, TE= 33.1 ms, flip angle = 52°, FOV= 208 × 180, voxel size = 2 mm isotropic. Macaque dataset: TR of 2600ms, 17ms TE, voxels size 1.22 x 1.22 x 1.24. Effective Echo Spacing of 0.63ms. Phase Encoding Direction: Encoded in columns.
Area of acquisition	Whole-brain scanning.

Diffusion MRI ☒ Used ☐ Not used

Parameters: The spatial resolution was 1.25 mm isotropic. TR=5500ms, TE=89.50ms. The b-values were 1000, 2000, and 3000 s/mm2. The total number of diffusion sampling directions was 90, 90, and 90 for each of the shells in addition to 6 b0 images.

Preprocessing

Preprocessing software

HCP dataset fMRI: the minimally preprocessed HCP functional data were used, with further denoising using the CONN toolbox V17f (please see Glasser et al., 2013 (NeuroImage) for details on HCP minimal preprocessing pipelines).
HCP dataset diffusion MRI: DSI Studio was used on the minimally preprocessed HCP diffusion data.
PET dataset: SPM12 software was used.
Macaque fMRI: Pypreclin pipelines for preprocessing (lease see Grigis et al., 2020 (NeuroImage) for details). Briefly, it includes the following steps: (i) Slice-timing correction. (ii) Correction for the motion-induced, time-dependent B0 inhomogeneities. (iii) Reorientation from acquisition position to template; here, we used the recently developed National Institute of Mental Health Macaque Template (NMT). (iv) Realignment to the middle volume using FSL MCFLIRT function. Subsequent denoising was performed using the CONN toolbox V17f.

Normalization

HCP dataset FMRI: please see Glasser et al., 2013 (NeuroImage) for details on HCP minimal preprocessing pipelines.
HCP dataset diffusion MRI: DWI data were then reconstructed using q-space diffeomorphic reconstruction (QSDR), as implemented in DSI Studio (www.dsi-studio.labsolver.org). QSDR first reconstructs diffusion-weighted images in native space and computes the quantitative anisotropy (QA) in each voxel. These QA values are used to warp the brain to a template QA volume in Montreal Neurological Institute (MNI) space using the statistical parametric mapping (SPM) nonlinear registration algorithm. A diffusion sampling length ratio of 2.5 was used, and the output resolution was 1 mm.

Macaque dataset: as part of the Pypreclin pipeline, the following steps were performed: (v) Normalisation and masking using Joe's Image Program (JIP) -align routine (http://www.nmr.mgh .harvard.edu/~jbm/jip/, Joe Mandeville, Massachusetts General Hospital, Harvard University, MA, USA), which is specifically designed for preclinical studies: the normalization step aligns (affine) and warps (non-linear alignment using distortion field) the anatomical data into a generic template space. (vi) B1 field correction for low-frequency intensity non-uniformities present in the data. (vii) Coregistration of functional and anatomical images, using JIP -align to register the mean functional image (moving image) to the anatomical image (fixed image) by applying a rigid transformation. The anatomical brain mask was obtained by warping the template brain mask using the deformation field previously computed during the normalization step. Then, the functional images were aligned with the template space by composing the normalization and coregistration spatial transformations.

Normalization template

HCP dataset: MNI152 template. Please see original study for details.
Macaque data: we used the National Institute of Mental Health Macaque Template (NMT): a high-resolution template of the average macaque brain generated from in vivo MRI of 31 rhesus macaques (Macaca mulatta).

Noise and artifact removal

The anatomica CompCor (aCompCor) method was used for denoising of both human and macaque fMRI data.
The aCompCor method involves regressing out of the functional data the following confounding effects: the first five principal components attributable to each individual's white matter signal, and the first five components attributable to individual cerebrospinal fluid (CSF) signal; six subject-specific realignment parameters (three translations and three rotations) as well as their first- order temporal derivatives . Linear detrending was also applied, and the subject-specific denoised BOLD signal timeseries were band-pass filtered to eliminate both low-frequency drift effects and high-frequency noise, thus retaining frequencies between 0.008 and 0.09 Hz.

For macaques, white matter and CSF masks were obtained from the corresponding probabilistic tissue maps of the high-resolution NMT template (eroded by 1 voxel); their first five principal components were regressed out of the functional data, as well as linear trends and 6 motion parameters (3 translations and 3 rotations) and their first derivatives. Following previous work on macaque functional MRI (see e.g. Barttfeld et al., 2015 (PNAS)), data were bandpass-filtered in the range of 0.0025-0.05 Hz. When comparing directly between human and macaque data, results were also replicated using the same bandpass filter of 0.008-0.09Hz used for human data.

Volume censoring

No volume censoring was used in this study.

Statistical modeling & inference

Model type and settings

One-sample non-parametric t-tests with 10,000 permutations were used to determine whether the synergy-redundancy scores were significantly different from zero for each of the Yeo resting-state subnetworks and for each cytoarchitectonic class of Von Economo; FDR correction for multiple comparisons was adopted according to the Benjamini-Hochberg procedure.
The statistical significance of within-group differences in network properties was determined with non-parametric permutation t-tests (repeated-measures), with 10,000 permutations. Between-subjects non-parametric t-tests (also with 10,000 permutations) were instead used to test the statistical significance of human-macaque comparisons. All tests were two-sided, with an alpha value of 0.05. The effect sizes were estimated using Hedges's g.
Meta-analytic results were obtained from NeuroSynth; please refer to Preti et al., 2019 (Nature Communications) for details.
Following Partial Least Squares analysis of gene expression data (see below for details), goodness of fit of low-dimensional PLS components was tested non-parametrically by repeating the analysis 1000 times after shuffling the regional labels. The error on the PLS weights associated with each gene were tested by resampling with replacement of the 308 ROIs (bootstrapping); the ratio of the weight of each gene to its bootstrap standard error was used to Z-score the genes and rank their contributions to each PLS component. We also demonstrated the robustness of this analysis using ridge-regularised PLS regression with a binarised target vector. The ridge (L2) penalty norm was determined by 10-fold cross-validation. For the hypothesis-driven enrichment analysis testing for enrichment of HAR-Brain genes and Aerobic Glycolysis genes, we also used non-parametric permutation testing. We randomly drew 1000 samples of the same number of genes and estimated

their PLS weighting, and compared the PLS weights of the HAR-Brain/AG genes to this permutation distribution. This provided an estimate of the probability of HAR-Brain/AG gene enrichment of each PLS component under the null hypothesis.
A further alternative approach was designed to account for the potential confound of spatial autocorrelation. To this end, we obtained a z-score for each AHBA gene, by dividing its empirical Spearman correlation with the redundancy-to-synergy cortical map, with the standard deviation of the distribution of correlations obtained from 5000 randomly rotated cortical maps having preserved spatial autocorrelation 95,96. Enrichment for HAR-Brain genes and genes related to aerobic glycolysis was then computed using permutation testing as described above, by comparing the weights of the genes of interest with the weights of 1000 random selections of the same number of genes.
To ensure robustness to possible outliers, all correlations were quantified using Spearman's rank-based correlation coefficient. To further ensure the robustness of our results to the potential confounding effect of spatial autocorrelation and contralateral symmetry 32,108, we also estimated p-values from a spatial permutation test which generates a null distribution of 10,000 randomly rotated brain maps with preserved spatial covariance ("spin test") 95,96. This analysis is only applicable for parcellations with full cortical coverage; when data were only available for the left cortical hemisphere, they were mirrored to the corresponding regions of the right hemisphere in order to perform the spatial rotations, since this test explicitly controls for contralateral symmetry 95,96 and then we only considered this hemisphere for computing the empirical and permuted correlations.

Effect(s) tested

For each of the Yeo resting-state subnetworks and for each cytoarchitectonic class of Von Economo, we tested whether they had significant prevalence of synergy or redundancy.
We also tested whether synergy and redundancy significantly differened in terms of their network structural-functional similarity, global efficiency, and modularity.
We tested whether synergy and redundancy vary between edges that do or do not have an underlying direct structural connection, or that connect region in the same or different subnetworks.
We also tested whether diversity of cortico-cortical wiring between regions correlates with synergy and redundancy.
We tested whether humans and macaques differed in global proportion of synergy or redundancy, and whether the resulting effect size is greater than the effect size obtained from traditional FC or from its global efficiency or modularity.
We tested whether the redundancy-to-synergy cortical gradient was significantly associated with meta-analytic cognitive domains, and with the distributions of HAR-Brain gene expression, cortical expansion, synaptic density, Glycolytic Index, and receptor diversity. We compared these results against surrogate data.
We also tested for significant enrichment of HAR-BRAIN genes and genes related to aerobic glycolysis among the PLS components.

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

Anatomical location(s)

200 cortical ROIs from Schaefer (2018) cortical atlas, supplemented with 32 subcortical ROIs from Tian (2020) subcortical atlas.
Alternative analyses were performed with the Desikan-Killiany atlas (68 cortical ROIs) and its 114-ROI and 308-ROI subparcellations, as well as the Lausanne 129 ROI cortical-subcortical parcellation, the Brodmann parcellation (for Glycolytic Index), a 40-region cytoarchitectonic parcellation (for the receptor diversity) and the HCP 360-ROI multimodal cortical parcellation.

Statistic type for inference
(See Eklund et al. 2016)

t-tests: permutation-based with 10,000 permutations. Correlation: Spearman's rank-based correlation coefficient. Gene enrichment: Z-score after random resampling. Comparison of effect sizes: Z-test as per Borenstein et al (2009).

Correction

The False Discovery Rate was controlled by means of the Benjamini-Hochberg procedure, across resting-state networks and across cytoarchitectonic classes, and for the Ensemble Phenotype null model. For GOrilla analysis, we used the "P-value threshold 10-4" setting in order to best approximate FDR correction with $\alpha = 0.05$.

Models & analysis

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

Functional and/or effective connectivity

See Methods for details of the computation of time-delayed mutual information, synergy and redundancy.
Traditional functional connectivity was obtained from Pearson correlation of timeseries.

Graph analysis

For each subject, weighted, fully dense whole-brain networks of synergistic and redundant interactions between each pair of ROIs were obtained (note that these measures are guaranteed non-negative). The modularity quality function (Newman's spectral algorithm) and global efficiency were computed. Null models were obtained as follows. For each individual we obtained a random network whereby the weight of the edge between each pair of regions i and j is randomly sampled from the range between 0 and the time-delayed mutual information (TDMI) between i and j – thereby being in the same theoretical range as both synergy and redundancy. We then computed the global efficiency and modularity of this synthetic network, and repeated the procedure 100 times, comparing the global efficiency and modularity averaged across 100 simulations, with the corresponding measures obtained from the empirical networks of synergy and redundancy, for each individual. When comparing the global efficiency and modularity of humans versus macaques for functional connectivity, negative values were removed by taking the absolute value.

Multivariate modeling and predictive analysis

To explore analogous associations between the redundancy-to-synergy regional gradient and all 20,647 genes measured in the AIBS microarrays, at each of 308 regions, we used the dimension-reducing multivariate technique of partial least squares (PLS). PLS finds components from the predictor variables (308

× 20,647 matrix of regional gene expression scores) that have maximum covariance with the response variables (308 × 1 matrix of regional redundancy-to-synergy gradient).

Goodness of fit of low-dimensional PLS components was tested non-parametrically by repeating the analysis 1000 times after shuffling the regional labels. The error on the PLS weights associated with each gene were tested by resampling with replacement of the 308 ROIs (bootstrapping); the ratio of the weight of each gene to its bootstrap standard error was used to Z-score the genes and rank their contributions to each PLS component.