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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	TrakEM2 part of Fiji version date 2014-06-02
Data analysis	Cytoscape 3.7.1, Python v3.6.7, igraph (v0.7.1) implementation of Louvain clustering algorithm, custom code at https://github.com/cabrittin/parsetrakem2 and https:/github.com/cabrittin/elegansbrainmap

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 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 volumetric datasets generated during the current study, associated connectivity databases and associated analysis are available at https://doi.org/10.5281/zenodo.4383277 and http://wormwiring.org/. The raw data for volumetric reconstructions for Figs. 1 and 3, Extended Data Fig. 8 and all Supplementary Videos is available at https://doi.org/10.5281/zenodo.4383277. Extracted adjacency data is available in Supplementary Information 1. The reference datasets are available in Supplementary Information 3. The Cytoscape files use to generate the brain map (Fig. 4 and Extended Data Fig. 10) and network motifs (Extended Data Fig. 10) are available at https://doi.org/10.5281/zenodo.4383277 . See associated Source Data for the data used to generate plots. The collection of C. elegans nervous system electron micrographs are also available at https://www.wormatlas.org/ and https://wormimage.org.

Field-specific reporting

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

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

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

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

Sample size	We used two legacy serial section EM series, which provided 4 bilateral datasets. No sample-size calculation was performed. Our core-variable model analysis (Fig. 2) indicates that 4 datasets is sufficient to decipher that there is a core component and that the core component can be estimated.
Data exclusions	Our segmentation was restricted to the nerve ring. Cell bodies were excluded from our segmentation because their large sizes skew membrane contact distributions. Dendrites were excluded from our analysis because the contain few synapses. we removed from our analysis a number of neurons that exhibit appreciable differences in synaptic connectivity or process morphology laterally (PLN, PVN, HSN), between the L4 and adult (HSN, PVR, SABD), or those that make minimal membrane contact in the nerve ring (in VB, VC and VD classes), leaving 173 cells in 93 cell classes (the "restricted dataset", Supplementary Information 1). For most of our analyses, we excluded the smallest 35% of membrane contacts because these smaller membrane contacts appear to be highly variable (Extended Data Fig. 2a).
Replication	We exploited the bilateral symmetry of the datasets as a means of replication. We also applied our models to datasets from White et al. (1986) and Witvliet et al. (2020). All attempts at replication were successful.
Randomization	Allocation into experimental groups was not random. In our assessment of the variability of synaptic contacts, we restricted our analysis to synaptic contacts on core (M4) contacts in order to control for differences in process placement. To determine that our core-variable results were not an artifact of synaptic scoring used in this study (Cook et al. 2019), we repeated our analysis using different synaptic scoring (White et al. 1986). and on different datasets (Witvliet et al., 2020). To assess that our clustering is not sensitive to natural variability in membrane contact areas, we derived our clusters from population spatial models (Fig 1c), which yielded consistent results across different datasets (Extended Data Fig. 5i), biological noise levels (Extended Data Fig. 5j) and spatial domains (Extended Data Fig. 5k,l).
Blinding	Blinding is not relevant to the study because test groups were not randomly assigned. Moreover, our analyses depend on knowing and comparing specific neurons between datasets.

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