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Supplementary Figures: 15

Supplementary Tables: 11

Supplementary Videos: 1

Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read Reporting Life Sciences Research.

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

Statistics reporting, by figure

- Please specify the following information for each panel reporting quantitative data, and where each item is reported (section, e.g. Results, & paragraph number).
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the paragraph number instead of the figure number.

Note: Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

		TEST USED		n			DESCRIPTIVE STATS (AVERAGE, VARIANCE)		P VALUE		DEGREES OF FREEDOM & F/t/z/R/ETC VALUE	
	FIGURE NUMBER	WHICH TEST?	SECTION & PARAGRAPH #	EXACT VALUE	DEFINED?	SECTION & PARAGRAPH #	REPORTED?	SECTION & PARAGRAPH #	EXACT VALUE	SECTION & PARAGRAPH #	VALUE	SECTION & PARAGRAPH #
example	1a	one-way ANOVA	Fig. legend	9, 9, 10, 15	mice from at least 3 litters/group	Methods para 8	error bars are mean +/- SEM	Fig. legend	p = 0.044	Fig. legend	F(3, 36) = 2.97	Fig. legend
example	results, para 6	unpaired t-test	Results para 6	15	slices from 10 mice	Results para 6	error bars are mean +/- SEM	Results para 6	p = 0.0006	Results para 6	t(28) = 2.808	Results para 6
+ -	1a-h	no stats		5	mice	legend	no stats					

		TEST USED		n			DESCRIPTIVE STATS (AVERAGE, VARIANCE)		P VALUE		DEGREES OF FREEDOM & F/t/z/R/ETC VALUE	
	FIGURE NUMBER	WHICH TEST?	SECTION & PARAGRAPH #	EXACT VALUE	DEFINED?	SECTION & PARAGRAPH #	REPORTED?	SECTION & PARAGRAPH #	EXACT VALUE	SECTION & PARAGRAPH #	VALUE	SECTION & PARAGRAPH #
+ -	1i-m	no stats		3 stroke; 2 control	primate brains	legend	no stats					
+ -	1q-x	no stas		4 stroke; 7 control	human brains	legend	no stats					
+ -	2a-c	repeated-measures ANOVA followed by Tukey-Kramer's post hoc test	last paragraph Methods	All conditions were tested in quadruplicate, in two separate experiments	cultures	legend	mean+/- SEM	legend	* =P<0.05, ** =P<0.01, *** = P<0.005 compared to Medium only; ^ = P<0.05 compared to Medium +GDF10; # = P<0.05, ## = P<0.01 compared to Scrambled +GDF10; @ = P<0.05, @@ = P<0.01 compared to Protein control Cyto C.	legend	In (a) F (6, 105) = 7.220; (b) F (6, 105) = 8.384; (c) F (6, 105)	legend
+ -	2e	one tail , unpaired TT test	last paragraph Methods	Two independent cultures per condition and in each culture 4 wells repeating the condition .	culture condition	legend	mean+/-SEM	legend	* =P<0.05, ** =P<0.01, *** = P<0.005 compared to Medium only	legend	medium vs GDF10: t=2.852 df=13; fosk/mann vs fosk/man GDF10: t=2.371 df=14	legend
+ -	3a-d,g	repeated-measures ANOVA followed by Tukey-Kramer's post hoc test	last paragraph Methods	All conditions were tested in quadruplicate, in two separate experiments.	cultures	legend	mean+/-SEM	legend	* =P<0.05, ** =P<0.01, *** = P<0.005 compared to Medium only; ^ = P<0.05 compared to Medium +GDF10; # = P<0.05, ## = P<0.01 compared to Scrambled +GDF10; @ = P<0.05, @@ = P<0.01 compared to Protein control Cyto C	legend	(a) F (5, 186) = 10.28; (b) F (2, 93) = 6.138; (c) F (4, 155) = 10.23; (d) F (4, 155) = 11.49; (g) F (2, 93) = 4.435	legend
+ -	3h	two tailed T test	legend		cultures	legend					t test, two-tailed t=3.073	legend

+ -	4a,d	Hotellings T2 test	legend, "Statistical Analysis" section Methods	n=8 all conditions	mice	legend	population correlation method, defined in Statistical Analysis section, Methods	Methods section, legend	4a p=0.04; 4d p=0.033	legend	no value in this category, these are population correlation statistics: multivariate mean equality	legend, Statistical Analysis section of Methods
+ -	4b,e	Watson's nonparametric two-sample U2 test	legend, "Statistical Analysis" section Methods	n=8 all conditions	mice	legend	Filled polygons represent the 70th percentile of the distances of all BDA labeled connections from the injection site in each segment of the graph. Weighted polar vectors represent the median vector multiplied by the median of the normal distribution of the number of points in a given segment of the graph	Methods section, legend	4b p<0.05; 4e p<0.01	legend	(b) $U^2$647.176, df 90939, df2 180911; (e) U^2 78.616, df 38554, df2 5906	legend
+ -	4c,f	one-way ANOVA followed by Tukey-Kramer's post hoc test	legend, "Statistical Analysis" section Methods	n=8 all conditions	mice	legend	mean+/-SEM	Methods section, legend	* = P<0.05, **=P<0.01	legend	In (c) F (1, 10) = 12.03; (f) F (1, 10) = 20.24.	legend
+ -	5a	Please see spreadsheet, Suppl Table 11 for manuscript										
+ -	5c	Please see spreadsheet, Suppl Table 11 for manuscript										
+ -	5e	Please see spreadsheet, Suppl Table 11 for manuscript										

+ -	6a	multiple comparisons ANOVA followed by Tukey-Kramer's post hoc test	"Statistical Analysis" section Methods	n=7 all conditions	n=7 all conditions	legend	mean+/-SEM	legend	GDF10 treatment produces a significant recovery compared to stroke+vehicle (# = P<0.05) and stroke +cyto C (^ = P<0.05). Right graph: Stroke +GDF10 siRNA impairs the normal recovery seen in stroke +vehicle (# = p<0.01) and in stroke +scrambled siRNA ($ = P<0.05).	legend	F (1.958, 11.75)	legend
+ -	6b	multiple comparisons ANOVA followed by Tukey-Kramer's post hoc test	"Statistical Analysis" section Methods	n=7 all conditions	mice	legend	mean+/-SEM	legend	Stroke+GDF10 produces a significant recovery in forelimb function compared to stroke+cyto C (^ = P<0.05). Right graph: Stroke+GDF10 siRNA reduces the normal process of motor recovery after stroke (** = P<0.01, compared with stroke +vehicle) and impairs the forelimb function compared with stroke +scrambled siRNA ($ = P<0.05).	legend	F (1.869, 11.21) = 10.70	legend

+ -	6c	multiple comparisons ANOVA followed by Tukey-Kramer's post hoc test	"Statistical Analysis" section Methods	n=7 all conditions	mice	legend	mean+/-SEM	legend	Delivery of GDF10 results in a significant recovery in forepaw use compared to delivery of protein control cyto C (^ = P<0.05). Injection of GDF10 siRNA complex significantly reduces right forepaw function compared to injection of the scrambled siRNA ($ = p<0.05).	legend	F (2.101, 12.61) = 9.382	legend
+ -	7b	False Discovery Rate	RNAseq section of Methods, legend	Three samples from stroke, stroke +GDF10, P4 and 2 samples from control	pooled samples of 2 brains	RNAseq section of Methods	FDR<0.1	legend	FDR<0.1	legend	does not apply	
+ -	7c	unsupervised hierarchical clustering analysis	RNAseq section of Methods, legend	Three samples from stroke, stroke +GDF10, P4 and 2 samples from control	pooled samples of 2 brains	RNAseq section of Methods	unsupervised hierarchical clustering of genes with FDR<0.1	legend	FDR<0.1	legend	does not apply	
+ -	8a	Fisher's exact p value , Benjamini Hochberg correction for multiple comparisons	RNAseq section of Methods, legend	Three samples from stroke, stroke +GDF10, P4 and 2 samples from control	pooled samples of 2 brains	RNAseq section of Methods	is inverse log of p value corrected for multiple comparisons in Benjamini-Hochberg (B-H) test	legend	-Log(B-H p value)	legend	does not apply	

+ -	8b	1) obtain data for individual data sets in published expression analyses 2) find gene symbol for each probe 3) find duplicated symbols, get average expression data 4) combine with data from this manuscript (Fig. 7) 5) quantile normalization or variance stabilization transformation normalization 6) remove batch effect by comBat 7) MDS plot for individual study	legend, Suppl Fig 9, Methods section "RNAseq" section	principle component spatial analysis presented in Fig. 8b	transcriptome data taken from published studies listed in GEO or supplied to authors and listed in Suppl Table 9	Suppl Fig 9, legend to Fig. 8; Methods section "RNAseq" section	Principle component analysis of 180 microarray or RNAseq data sets	Results section, final part	Principle component analysis in a custom statistical test of published transcriptomes	legend, Suppl Fig 9, Methods section "RNAseq" section	does not apply	

Representative figures

1. Are any representative images shown (including Western blots and immunohistochemistry/staining) in the paper?

   If so, what figure(s)?

   Figure 1, Suppl Figs 1,2,4

2. For each representative image, is there a clear statement of how many times this experiment was successfully repeated and a discussion of any limitations in repeatability?

   If so, where is this reported (section, paragraph #)?

   Figure legends

Statistics and general methods

1. Is there a justification of the sample size?

   If so, how was it justified?

   Where (section, paragraph #)?

   Even if no sample size calculation was performed, authors should report why the sample size is adequate to measure their effect size.

   Yes, power analysis and, where power analysis not applicable, reference to previously published studies with same methodology. Methods, last section

2. Are statistical tests justified as appropriate for every figure? Where (section, paragraph #)?	Yes, last section of Methods
a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?	Yes, last section Methods
b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)? Where is this described (section, paragraph #)?	Yes, last section Methods
c. Is there any estimate of variance within each group of data? Is the variance similar between groups that are being statistically compared? Where is this described (section, paragraph #)?	Yes, data displayed for variance in Figs 2-6, variance described in statistical testing and reported in Figure legends and Results
d. Are tests specified as one- or two-sided?	Yes
e. Are there adjustments for multiple comparisons?	Yes
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	No data points excluded
4. Define the method of randomization used to assign subjects (or samples) to the experimental groups and to collect and process data. If no randomization was used, state so. Where does this appear (section, paragraph #)?	Animals were not grouped by experimental condition but were not randomized by a specific method
5. Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included? If no blinding was done, state so. Where (section, paragraph #)?	Yes, investigators were blinded to experimental condition. Specified in last section of Methods
6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes, first section of Methods
7. Is the species of the animals used reported? Where (section, paragraph #)?	Yes, first section of Methods
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes, first section of Methods

9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Yes, first section of Methods
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes first section of Methods
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	Yes, first section of Methods
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	Yes, first section of Methods
13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?	Yes, in Behavioral Assessment section of Methods
14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? Where (section, paragraph #)?	Yes, in Methods first section and Methods section "Non-human primate model of stroke"
a. If multiple behavioral tests were conducted in the same group of animals, is this reported? Where (section, paragraph #)?	Yes, in "Behavioral Assessment" section in Methods
15. If any animals/subjects were excluded from analysis, is this reported? Where (section, paragraph #)?	No animals were excluded
a. How were the criteria for exclusion defined? Where is this described (section, paragraph #)?	
b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study. Where is this described (section, paragraph #)?	

Reagents

1. Have antibodies been validated for use in the system under study (assay and species)?	Yes, compared to no-primary and no-secondary controls and in manufacturer literature, listed in Methods section and in Suppl Table 10
a. Is antibody catalog number given? Where does this appear (section, paragraph #)?	Suppl Table 10

b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?

Where does this appear (section, paragraph #)?

description of no-primary and no-secondary controls (for immunofluorescent staining) in Methods section, "Immunohistochemistry".

2. If cell lines were used to reflect the properties of a particular tissue or disease state, is their source identified?

Where (section, paragraph #)?

No cell lines

a. Were they recently authenticated?

Where is this information reported (section, paragraph #)?

Data deposition

Data deposition in a public repository is mandatory for:

a. Protein, DNA and RNA sequences
b. Macromolecular structures
c. Crystallographic data for small molecules
d. Microarray data

Deposition is strongly recommended for many other datasets for which structured public repositories exist; more details on our data policy are available here. We encourage the provision of other source data in supplementary information or in unstructured repositories such as Figshare and Dryad.

We encourage publication of Data Descriptors (see Scientific Data) to maximize data reuse.

1. Are accession codes for deposit dates provided?

Where (section, paragraph #)?

Data will be deposited in GEO.

Computer code/software

Any custom algorithm/software that is central to the methods must be supplied by the authors in a usable and readable form for readers at the time of publication. However, referees may ask for this information at any time during the review process.

1. Identify all custom software or scripts that were required to conduct the study and where in the procedures each was used.

2. If computer code was used to generate results that are central to the paper's conclusions, include a statement in the Methods section under "**Code availability**" to indicate whether and how the code can be accessed. Include version information as necessary and any restrictions on availability.

Human subjects

1. Which IRB approved the protocol?

Where is this stated (section, paragraph #)?

Not relevant

2. Is demographic information on all subjects provided?

   Where (section, paragraph #)?

3. Is the number of human subjects, their age and sex clearly defined?

   Where (section, paragraph #)?

4. Are the inclusion and exclusion criteria (if any) clearly specified?

   Where (section, paragraph #)?

5. How well were the groups matched?

   Where is this information described (section, paragraph #)?

6. Is a statement included confirming that informed consent was obtained from all subjects?

   Where (section, paragraph #)?

7. For publication of patient photos, is a statement included confirming that consent to publish was obtained?

   Where (section, paragraph #)?

fMRI studies

For papers reporting functional imaging (fMRI) results please ensure that these minimal reporting guidelines are met and that all this information is clearly provided in the methods:

1. Were any subjects scanned but then rejected for the analysis after the data was collected?

   a. If yes, is the number rejected and reasons for rejection described?

      Where (section, paragraph #)?

2. Is the number of blocks, trials or experimental units per session and/or subjects specified?

   Where (section, paragraph #)?

3. Is the length of each trial and interval between trials specified?

4. Is a blocked, event-related, or mixed design being used? If applicable, please specify the block length or how the event-related or mixed design was optimized.

5. Is the task design clearly described?

   Where (section, paragraph #)?

6. How was behavioral performance measured?

7. Is an ANOVA or factorial design being used?

8. For data acquisition, is a whole brain scan used?

   If not, state area of acquisition.

   a. How was this region determined?

9. Is the field strength (in Tesla) of the MRI system stated?

   a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?

   b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?

10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?

11. Is the coordinate space for the anatomical/functional imaging data clearly defined as subject/native space or standardized stereotaxic space, e.g., original Talairach, MNI305, ICBM152, etc? Where (section, paragraph #)?

12. If there was data normalization/standardization to a specific space template, are the type of transformation (linear vs. nonlinear) used and image types being transformed clearly described? Where (section, paragraph #)?

13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?

14. Were any additional regressors (behavioral covariates, motion etc) used?

15. Is the contrast construction clearly defined?

16. Is a mixed/random effects or fixed inference used?

   a. If fixed effects inference used, is this justified?

17. Were repeated measures used (multiple measurements per subject)?

   a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?

18. If the threshold used for inference and visualization in figures varies, is this clearly stated?

19. Are statistical inferences corrected for multiple comparisons?

    a. If not, is this labeled as uncorrected?

20. Are the results based on an ROI (region of interest) analysis?

    a. If so, is the rationale clearly described?

    b. How were the ROI's defined (functional vs anatomical localization)?

21. Is there correction for multiple comparisons within each voxel?

22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?

Additional comments

Additional Comments	Raw data for all bar or column graphs is uploaded as Excel files.