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Supplementary Videos: None

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

		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 #
+ -	1b	unpaired t-test	Fig. legend	3,3	Yes(n=3 control and 3 mutant tissues)	20	error bars are mean +/- SEM	Fig. legend	P=0.024(Brg1) P=0.0018(Mbp) P=2.12715E-06(Plp1) P=0.448(Hes5) P=0.007(Chd7)	Fig. legend	df=4 t= 7.40454 (Mbp) t=40.9407(Plp1) t=1.71615(Hes5) t=3.52193(Brg1) t=5.02164(Chd7)	20
+ -	2f	unpaired t-test	Fig. legend	P9 (3,2) P15(4,4)	Yes(n=3-4 control and 2-4 mutant tissues)	21	error bars are mean +/- SEM	Fig. legend	P=0.026(P9) P=0.009(P15)	Fig. legend	t(3)=4.11611 t(6)=3.79473	21
+ -	2h	unpaired t-test	Fig. legend	P9 (3,3) P15(4,4)	Yes(n=3-4 control and 3-4 mutant tissues)	21	error bars are mean +/- SEM	Fig. legend	P=0.002 (P9) P=0.009(P15)	Fig. legend	t(4)=7.22 t(6)=3.74	21
+ -	2k	unpaired t-test	Fig. legend	for P14: 3,3 for P28: 3,3	Yes(n=3 control and 3 mutant animals for each stage)	21	error bars are mean +/- SEM	Fig. legend	P=0.0017(P14) P=0.0217(P28)	Fig. legend	t(4)=10.73 (P14) t(4)=3.656(P28)	21
+ -	2l	unpaired t-test	Fig. legend	202, 196	Yes(n=196 axons from three Chd7cKO mice, and n=202 axons from three control mice)	21	mean +/- SEM of Ctrl:0.7227 +/- 0.007414 mean +/- SEM of Chd7cKO: 0.8325 +/-0.003235 N=196	Fig. legend	P<0.0001	Fig. legend	t=13.44	21
+ -	3d	unpaired t-test	Fig. legend	3,3	yes (n=3 control and 3 mutant animals)	22	error bars are mean +/- SEM	Fig. legend	P=0.7091	Fig. legend	t=0.4104 df=3	22
+ -	3f	unpaired t-test	Fig. legend	4,4	yes (n=4 independent cultures)	22	error bars are mean +/- SEM	Fig. legend	P<0.001	Fig. legend	t(6)=5.937	22
+ -	3j	unpaired t-test	Fig. legend	3,3	yes (n=3 control and 3 mutant animals)	22	error bars are mean +/- SEM	Fig. legend	P<0.0001(CC1) P=0.0123(Mog)	Fig. legend	df=4 t=32.609(CC1) t=4.331(Mog)	22
+ -	4e	unpaired t-test	Fig. legend	4,4	yes (n=4 control and 4 mutant animals)	22	error bars are mean +/- SEM	Fig. legend	P=0.022(dpl7) P=0.0098(dpl14)	Fig. legend	df=6 t=3.07893(dpl7) t=3.72552(dpl14)	22
+ -	4h	unpaired t-test	Fig. legend	4,4	yes (n=4 control and 4 mutant animals)	23	error bars are mean +/- SEM	Fig. legend	P=0.0015	Fig. legend	t=5.523 df=6	23
+ -	4j	unpaired t-test	Fig. legend	4,4	yes (n=4 control and 4 mutant animals)	23	error bars are mean +/- SEM	Fig. legend	P=0.0188	Fig. legend	t=3.191 df=6	23
+ -	4k	unpaired t-test	Fig. legend	126,128	Yes(n=126 axons from four Chd7cKO mice, and n=128 axons from four control mice)	23	mean +/- SEM of Ctrl:0.8943 +/- 0.005128 mean +/- SEM of Chd7cKO: 0.9330 +/-0.003088	Fig. legend	P<0.0001	Fig. legend	t=6.440	23

+ -	5c	unpaired t-test	Fig. legend	3,3	Yes (n=3control and 3 mutant tissues)	23	error bars are mean +/- SEM	Fig. legend	P=0.0008(Mbp) P=0.028(Plp1) P=0.0001(Cnp) P=0.0005(Sox10) P=0.0049(Tcf7l2) P=0.03(Myrf) P=0.168(Pdgfra) P=0.027(Hes1) P=0.98(Hes5) P=0.049(Id2) P=0.03(Id4)	Fig. legend	df=4 t=9.11(Mbp) t=3.37(Plp1) t=14.63(Cnp) t=10.05(Sox10) t=5.62(Tcf7l2) t=3.29(Mrf) t=1.68(Pdgfra) t=3.38(Hes1) t=0.02(Hes5) t=2.81(Id2) t=3.29(Id4	23
+ -	5f	unpaired t-test	Fig. legend	3,3	Yes (n=3control and 3 mutant tissues)	23	error bars are mean +/- SEM	Fig. legend	P=0.002(Enpp2) P=0.0018(Nfya) P=0.046(Pik3r3) P=0.0012(Elovl7)	Fig. legend	df=4 t=6.67(Enpp2) t=7.41(Nfya) t=2.86(Pik3r3) t=8.22(Elovl7)	23
+ -	5g	unpaired t-test	Fig. legend	3,3	Yes (n=3control and 3 mutant tissues)	23	error bars are mean +/- SEM	Fig. legend	P<0.001	Fig. legend	t=14.809 (Gsn) t=8.65895(Ermn) t=10.1806(Mtap7) t=9.90701(Tppp)	23
+ -	6f	paired t-test	Fig. legend	144	Yes(n=144 differentially expressed genes directly targeted by Chd7)	24	mean (+), median, quartiles (boxes), range (whiskers)	Fig. legend	P=3.1X10-20	Fig. legend	t(143)=10.79	24
+ -	6o	paired t-test	Fig. legend	For Cnp: 3,3 For Plp1: 4,4	Yes(n=3-4 independent experiments)	24	error bars are mean +/- SEM	Fig. legend	P=0.0138 (Cnp) P=0.0385 (plp1)	Fig. legend	df=2,t=8.437 (Cnp) df=3 t=3.534 (Plp1)	24
+ -	6p	One-Way ANOVA test	Fig. legend	3,3	Yes(n=3 independent experiments)	24	error bars are mean +/- SEM	Fig. legend	Chd7 to pCIG P=0.008(Mbp) P=0.017(Plp1) P=0.013(Cnp) P=0.028(Myrf) Sox10+Chd7 to Sox10 P=0.0002(Mbp) P=0.01(Plp1) P=0.01(Cnp) P=0.02(Myrf)	Fig. legend	Chd7 to pCIG t=6.397 t=4.792 t=5.344 t=4.042 Sox10+pCIG to Sox10 only t=9.876 t=5.836 t=5.794 t=4.53	24

+ -	6q	unpaired t-test (left) One-way ANOVA test (right)	Fig. legend	5,5(left) 4,4(right)	Yes(n=4-5 independent experiments)	24	error bars are mean +/- SEM	Fig. legend	P=0.016(Chd7) P=0.0003(Sox10) for Chd7 siRNAs compared to scrambled siRNAs: P=0.03(Mbp) P=0,015(Plp1) P=0.033(Cnp) for Sox10 siRNAs compared to scrambled siRNAs: P=0.0004(Mbp) P=0.0005(Plp1) P=0.0002(Cnp) P=0.002(Myrf) for Sox10+Chd7 siRNAs compared to Sox10 siRNAs: P=0.006(Mbp) P=0.004(Plp1) P=0.01(Cnp) P=0.03(Myrf)	Fig. legend	t(8)=3.04(Chd7) t(8)=6.02(Sox10) for Chd7 siRNAs compared to scrambled siRNAs: df=6 t=2.82(Mbp) t=3.34(Plp1) t=2.74(Cnp) for Sox10 siRNAs compared to scrambled siRNAs: df=6 t=6.84(Mbp) t=6.68(Plp1) t=7.55(Cnp) t=5.74(Myrf) for Sox10+Chd7 siRNAs compared to Sox10 siRNAs: df=8 t=3.7(Mbp) t=3.86(Plp1) t=3.15(Cnp) t=2.69(Myrf)	24
+ -	6r	One-Way ANOVA	Fig. legend	4,4,4,4	Yes(n=4 independent experiments)	25	error bars are mean +/- SEM	Fig. legend	P= 0.022 (Mbp, Sox10 to pCIG) P=0.035 (Cnp, Sox10 to pCIG) P=0.014(Myrf, Sox10 to pCIG) P=0.031(Myrf, K998R to pCIG) P=0.025(Mbp, K998R+Sox10 to Sox10) P=0.035(Cnp, K998R+Sox10 to Sox10) P=0.014(Myrf, K998R+Sox10 to Sox10)	Fig. legend	df=6 t=3.06(Mbp,Sox10 to pCIG) t=2.71 (Cnp,Sox10 to pCIG) t=3.447(Myrf,Sox10 to pCIG) t=2.79(Myrf,K998R to pCIG) t=2.97(Mbp, K998R+Sox10 to Sox10) t=2.71Cnp, K998R+Sox10 to Sox10) t=3.41(Myrf, K998R+Sox10 to Sox10)	25
+ -	7b	unpaired t-test	Fig. legend	3,3	Yes(n=3control and 3 mutant tissues)	25	error bars are mean +/- SEM	Fig. legend	P=0.005(Sp7) 0.0019(Creb3l2)	Fig. legend	df=4 t=5.64(Sp7) t=7.26(Creb3l2)	25
+ -	7c	unpaired t-test	Fig. legend	3,3,3,3	Yes(n=3 independent experiments)	25	error bars are mean +/- SEM	Fig. legend	P=0.005(Creb3l2_pro) P=0,024(Sp7_pro) P<0.0001(Creb3l2_diff) P=0.031(Sp7_diff)	Fig. legend	df=4 t=5.565(Creb3l2_pro) t=3.551(Sp7_pro) t=17.1576(Creb3l2_diff) t=3.268(Sp7_diff)	25
+ -	7g	unpaired t-test	Fig. legend	3,3,3,3	Yes(n=3 independent experiments)	25	error bars are mean +/- SEM	Fig. legend	P=0.0067(Sp7) P=0.0022(Creb3l2)	Fig. legend	df=4 t=5.17(Sp7) t=6.97(Creb3l2)	25

+ -	7h	unpaired t-test	Fig. legend	3,3,3	Yes(n=3 independent experiments)	25	error bars are mean +/- SEM	Fig. legend	Creb3l2KD: P=0.01(Cnp) P=0.001(mbp) P=0.0002(Plp1) P=0.005(Mag) P=0.014(Myrf) Sp7 KD P=0.0008(Cnp) P<0.0001(Mbp) P=0.0011(Plp1) P=0.002(Mag) P=0.0014(Myrf)	Fig. legend	df=4 Creb3l2 KD t=4.60(Cnp) t=8.73(Mbp) t=12.97(Plp1) t=5.65(Mag) t=4.11(Myrf) Sp7 KD t=9.013(Cnp) t=16.48(Mbp) t=8.49(Plp1) t=7.43(Mag) t=7.91(Myrf)	25
+ -	7i	unpaired t-test	Fig. legend	4,4 5,5	Yes(n=4-5 independent experiments)	25	error bars are mean +/- SEM	Fig. legend	P=0.013(Osterix) P=0.001(Creb3l2)	Fig. legend	df=6 t=3.468(Osterix) df=8 t=5.07(Creb3l2)	25
+ -	7j	One-way ANOVA test	Fig. legend	3,3,4,4	Yes(n=3-4 independent experiments)	26	error bars are mean +/- SEM	Fig. legend	Chd7 siRNA +pCIG compared to scrambled siRNA+pCIG: P=0.012(Mbp) P=0.022(Plp1) P=0.047(Myrf) Chd7 siRNA +Sp7 compared with Chd7 siRNA+pCIG: P=0.036(Mbp) P=0.045(Plp1) P=0.049(Myrf)	Fig. legend	Chd7 siRNA +pCIG compared to scrambled siRNA+pCIG:df=4 t=4.30(Mbp) P=3.63(Plp1) P=2.84(Myrf) Chd7 siRNA+Sp7 compared with Chd7 siRNA +pCIG: df=5 t=2.83(Mbp) t=2.65(plp1) t=2.62(Myrf)	26
+ -	s1c	unpaired t-test	Fig. legend	3,3,3,3	Yes (n=3control and 3 mutant tissues)	Supplementary Form_Page 1	error bars are mean +/- SEM	Fig. legend	P=0.03(P4) P=0.008(e17.5)	Fig. legend	t=3.23(P4) t=4.89(e17.5)	Supplementary Form_Page 1
+ -	s2b	unpaired t-test	Fig. legend	2,2,3,3	Yes (n=2-3control and 2-3 mutant tissues)	Supplementary Form_Page 2	error bars are mean +/- SEM	Fig. legend	P=0.007(P4) P=0.0027(P15)	Fig. legend	t(2)=11.359(P4) t(4)=6.575(P15)	Supplementary Form_Page 2
+ -	s2d	unpaired t-test	Fig. legend	For Sox10: 3,3,4,4 For Olig2: 3,3,4,4	Yes (n=3-4control and 3-4 mutant tissues)	Supplementary Form_Page 2	error bars are mean +/- SEM	Fig. legend	For Sox10: P=0.017(P9) P=0.0027(P15) For Olig2: P=0.02(P9) P=0.014(P15)	Fig. legend	For Sox10: t(4)=3.93(P9) t(6)=4.877(P15) for Olig2: t(4)=3.74(P9) t(6)=3.38(P15)	Supplementary Form_Page 2
+ -	s3b	unpaired t-test; two-way anova test	Fig. legend	3,3	Yes (n=3 control and 3 mutant tissues)	Supplementary Form_Page 3	error bars are mean +/- SEM	Fig. legend	For CC1 density: P=0.03(P1) P=0.0029(P4) P=0.012(P7) P=0.045(P14) P=0.71(P60) For CC1 of Sox10%: P < 0.0001	Fig. legend	t(3)=3.89(P1) t(4)=6.49(P4) t(4)=4.36(P7) t(4)=2.87(P14) t(4)=0.39(P60) For CC1 of Sox10%: F (1, 19) = 56.75	Supplementary Form_Page 3
+ -	s5b	unpaired t-test	Fig. legend	4,4,4,3	Yes (n=4control and 3-4 mutant tissues)	Supplementary Form_Page 5	error bars are mean +/- SEM	Fig. legend	For Sox10: P=0.048 (dpl7) P=0.037(dpl14) For Olig2: P=0.03dpl7) P=0.02(dpl14)	Fig. legend	For Sox10: t(6)=2.47 (dpl7) t(5)=2.82(dpl14) For Olig2: t(6)=2.81 (dpl7) t(5)=3.33(dpl14)	Supplementary Form_Page 5

+ -	s6c	unpaired t-test	Fig. legend	3,3	Yes(n=3control and 3 mutant mice)	Supplementary Form_Page 6	error bars are mean +/- SEM	Fig. legend	0.0001	Fig. legend	t(4)=15.05	Supplementary Form_Page 6
+ -	s8d	Mann–Whitney–Wilcoxon rank test	Fig. legend	704	Yes(n=704 genes with Chd7 occupancy within 5Kb from TSS)	Supplementary Form_Page 8	mean (+), median, quartiles (boxes), range (whiskers)	Fig. legend	P<10-10	Fig. legend	t(703)=7.955 (astrocyte) t(703)=6.790 (Neuron) t(703)=12.62 (Microglia) t(703)=8.312 (Endothelial)	Supplementary Form_Page 8

Representative figures

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

   If so, what figure(s)?

Yes
Western blots: Fig 6j,6k,
In Situ Hybridization: Fig 2c,2d;4d
Electron Microscopy: Fig. 2i, 2j; 3a;4i;7i
Immunohistochemistry: Fig. 1c,1d,1e,1f,1g,1i,1j,1k;1l,1m,2b,2e,2g; 3c,3e,3g,3h,3i;4a,4b,4c,4d,4g;7e,7f,7l,7m

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 #)?

Yes.
For representative images that used for statistical analysis, the number of independent experiments or animals is the n described in individual figure legends.
There are no limitations of reproducibility for any experiments.

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.

Sample sizes were indicated in the legend of each Figure and Supplementary Figure.

For cell-based and gene expression assays (Figs 3f,6o-r,7g-j), the sample size ($n \geq 3$) allows us to achieve at least 80% power (standard power) to detect the difference with 95% confidence.

For animal phenotype analysis (Fig. 1b, 2f,2h,2k,2l,3j,4e-f,4h,4j-k, 5c,5f,5g,) the animals with the same genotypes at the same age exhibit very similar phenotypes. The sample size ($n \geq 3$) should allow us to achieve at least 80% power (standard power) to detect the difference with 95% confidence.

2. Are statistical tests justified as appropriate for every figure?

   Where (section, paragraph #)?

Yes. Reported on Methods (Statistical Analysis, page 28: para 4). In each figure, the statistical test was stated in the corresponding legend and justified to detect the difference with 95% confidence.

   a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?

Yes, we summarized in the statistical methods in page 28: para 4. each statistical test is defined in the corresponding figure legend.

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 #)?

For statistical tests reported in legends of each Figure, the data meet the assumption of normal distribution and are appropriate for ANOVA or t-tests.

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. For statistical tests reported in Figs. 1-7, there is an estimate of variation within each group of data (Error bars show SEM). Data are presented as mean ± SEM or as a Box-and-whisker plot (reported in Methods; page 28, para 4). The variance is similar between the groups that are being statistically compared.

d. Are tests specified as one- or two-sided?

Yes, two-sided tests were used and specified in the last paragraph of Methods.

e. Are there adjustments for multiple comparisons?

N/A

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 or samples were excluded from the analysis.

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 #)?

N/A

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 #)?

For cell-based experiments, EM, histochemistry, the genotypes of cells/animals were known before the conduction of experiments. LPC- induced injuries in Fig. 4 (page 7, para 2) were conducted in a genotype-blinded manner. For image quantification analysis in Fig. 2(f,h,k,i),Fig. 3(b,d,f,h),and Fig. 4(e,f,h,j,k), data were quantified blindly.

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included?

Where (section, paragraph #)?

Yes, in Methods section "Animals" (page 26, para 1)

7. Is the species of the animals used reported?

Where (section, paragraph #)?

Yes, in Methods section "Animals" (page 26, para 1)

8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported?

Where (section, paragraph #)?

Yes, in Methods section"Animals" (page 26, para 1). The mouse strains used in this study were generated and maintained on a mixed C57Bl/6;129Sv background.

9. Is the sex of the animals/subjects used reported?

Where (section, paragraph #)?

Yes, reported in Methods for the information of animals (page 26, para 1). Both male and female mice were used for the present study.

10. Is the age of the animals/subjects reported?

    Where (section, paragraph #)?

Yes, they are indicated in individual figure legends.

11. For animals housed in a vivarium, is the light/dark cycle reported?

    Where (section, paragraph #)?

Animals were housed in a vivarium with a 12-hour light/dark cycle (page 26, para 1)

12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?

    Where (section, paragraph #)?

The number of animals per cage is three or less in the animal facilities (page 26, para 1)

13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?

    Where (section, paragraph #)?

N/A

14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?

    Where (section, paragraph #)?

No

    a. If multiple behavioral tests were conducted in the same group of animals, is this reported?

       Where (section, paragraph #)?

N/A

15. If any animals/subjects were excluded from analysis, is this reported?

    Where (section, paragraph #)?

No animals were excluded from the analysis.

    a. How were the criteria for exclusion defined?

       Where is this described (section, paragraph #)?

N/A

    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 #)?

N/A

Reagents

1. Have antibodies been validated for use in the system under study (assay and species)?

Yes

    a. Is antibody catalog number given?

       Where does this appear (section, paragraph #)?

Yes, in the Methods section "Immunohistochemistry " and "Chromatin-immunoprecipitation and sequencing (ChIP-Seq)" (page 26 para 4 and page 28 para 2)

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

Where does this appear (section, paragraph #)?

Antibody validation was reported from the companies that provide the antibodies or from cited literatures (page 26 para 4 and page 28 para 2).

2. Cell line identity

a. Are any cell lines used in this paper listed in the database of commonly misidentified cell lines maintained by ICLAC and NCBI Biosample?

Where (section, paragraph #)?

No

b. If yes, include in the Methods section a scientific justification of their use--indicate here in which section and paragraph the justification can be found.

N/A

c. For each cell line, include in the Methods section a statement that specifies:

- the source of the cell lines
- have the cell lines been authenticated? If so, by which method?
- have the cell lines been tested for mycoplasma contamination?

Where (section, paragraph #)?

Oli-neu used in this study was a commonly used oligodendroglial cell line and obtained from Dr. Patricia Wight. Cells were cultured under the same condition as reported in the literature (See reference 30).

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 #)?

Yes, all gene expression profiling data have been submitted to NCBI repository site GEO with accession number GSE72727 provided on page 16 (para 1).

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.

N/A

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.

N/A

Human subjects

1. Which IRB approved the protocol?

   Where is this stated (section, paragraph #)?

The study was approved by institutional review board at the Cincinnati Children's Hospital Medical Center (See Methods page 26, para 1)

2. Is demographic information on all subjects provided?

   Where (section, paragraph #)?

N/A

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

   Where (section, paragraph #)?

Yes. The information was provided in the Methods section (page 26 para1), and in the text page 5 (para 2) and page 20 (Fig.1n,o). Male and female subjects from age 2 to age 15 were included in the study approved by the CCHMC institutional review board.

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

   Where (section, paragraph #)?

N/A

5. How well were the groups matched?

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

N/A

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

   Where (section, paragraph #)?

The informed consent was obtained from all subjects as outlined by the CCHMC institutional review board (page 26, para 1)

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

   Where (section, paragraph #)?

N/A

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?

N/A

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

      Where (section, paragraph #)?

N/A

2. Is the number of blocks, trials or experimental units per session and/or subjects specified? Where (section, paragraph #)?	N/A
3. Is the length of each trial and interval between trials specified?	N/A
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.	N/A
5. Is the task design clearly described? Where (section, paragraph #)?	N/A
6. How was behavioral performance measured?	N/A
7. Is an ANOVA or factorial design being used?	N/A
8. For data acquisition, is a whole brain scan used? If not, state area of acquisition.	N/A
a. How was this region determined?	N/A
9. Is the field strength (in Tesla) of the MRI system stated?	N/A
a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?	N/A
b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?	N/A
10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?	N/A
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 #)?	N/A
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 #)?	N/A
13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?	N/A

14. Were any additional regressors (behavioral covariates, motion etc) used?	N/A
15. Is the contrast construction clearly defined?	N/A
16. Is a mixed/random effects or fixed inference used?	N/A
a. If fixed effects inference used, is this justified?	N/A
17. Were repeated measures used (multiple measurements per subject)?	N/A
a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?	N/A
18. If the threshold used for inference and visualization in figures varies, is this clearly stated?	N/A
19. Are statistical inferences corrected for multiple comparisons?	N/A
a. If not, is this labeled as uncorrected?	N/A
20. Are the results based on an ROI (region of interest) analysis?	N/A
a. If so, is the rationale clearly described?	N/A
b. How were the ROI's defined (functional vs anatomical localization)?	N/A
21. Is there correction for multiple comparisons within each voxel?	N/A
22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?	N/A

Additional comments

Additional Comments	