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Supplementary Videos: 0

Reporting Checklist for Nature Neuroscience

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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 #
+ -	1g	paired t-test	Fig. legend	3	biological replicates of cultured neurons	Fig. legend	error bars are mean +/- SEM	Fig legend	p=0.0057	Fig. legend	t=4.195	Fig. legend
+ -	2b	paired t-test	Fig. legend	14	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p= 0.0014	Fig. legend	t = 3.133	Fig. legend
+ -	2c	paired t-test	Fig. legend	14	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=1.86E-5	Fig. legend	t=4.064	Fig. legend
+ -	2d	paired t-test	Fig. legend	14	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.0178	Fig. legend	t=2.53	Fig. legend
+ -	2e	paired t-test	Fig. legend	7	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.0186	Fig. legend	t=2.475	Fig. legend
+ -	2f	paired t-test	Fig. legend	8	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.0264	Fig. legend	t=2.1998	Fig. legend
+ -	2g	paired t-test	Fig. legend	4	yes	Figure legend	error bars are mean +/- SEM		p=0.0406	Fig. legend	t=2.456	Fig. legend
+ -	2h	Unpaired t-test	Fig. legend	N = 6 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p = 0.035	Fig. legend	t = 2.502	Fig. legend
+ -	2i	Unpaired t-test	Fig. legend	N = 6 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p = 0.045	Fig. legend	t = 2.327	Fig. legend
+ -	2j	Unpaired t-test	Fig. legend	N = 6 biological replicates	yes	Fig. legend	box plot whisker bars	Fig. legend	p = 0.0311	Fig. legend	t = 2.551	Fig. legend
+ -	2l	unpaired t-test	Fig. legend	N = 232 neurons for control, 185 neurons for BDNF, 245 for Jq1, and 200 for Jq1 +BDNF from 5 biological replicates per group.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=8.52E-26, jq1 v. jq1 +bdnf p=0.00084 bdnf v. jq1 +bdnf p=0.00012	Fig. legend	control v. bdnf t = 11.447, jq1 v. jq1+bdnf t = 3.363, bdnf v. jq1 +bdnf t = 3.867	Fig. legend

+ -	2m	unpaired t-test	Fig. legend	N = 105 neurons for control, 80 for BDNF, 85 for Brd2 siRNA, 71 for Brd2 +BDNF, 88 for Brd3, 63 for Brd3 +BDNF, 80 for Brd4, and 71 for Brd4 +BDNF from 11 biological replicates.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.0012 for control v. control+bdnf, p=8.57x10^-5 for brd2 v. brd2+bdnf, p=0.017 for brd3 v. brd3 +bdnf, p=0.66 for brd4 v. brd4+bdnf, p = 0.0157 for bdnf vs brd4 +bdnf	Fig. legend	for control vs BDNF t = 3.296, for Brd4 siRNA vs Brd4 siRNA + BDNF t = 0.438, for Brd2 siRNA vs Brd2 siRNA + BDNF t = 4.035, for Brd3 siRNA vs Brd3 siRNA + BDNF t = 2.42, Brd4 siRNA + BDNF t = 2.445.	Fig. legend
+ -	3b	paired t-test	Fig. legend	N=3 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=2.98E-5	Fig. legend	t = 3.357	Fig. legend
+ -	4a	paired t-test	Fig. legend	N=10 for dmso samples, n= 6 for tbb samples, n=3 for jq1 samples	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=0.0095, tbb v. tbb+bdnf p=0.064,	Fig. legend	t=1.693	Fig. legend
+ -	4b	paired t-test	Fig. legend	N=8 for dmso samples, n= 6 for tbb samples, n=3 for jq1 samples	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=0.0303, tbb v. tbb +bdnf p=0.2	Fig. legend	t=2.791	Fig. legend
+ -	4c	paired t-test	Fig. legend	N=8 for dmso samples, n= 5 for tbb samples, n=3 for jq1 samples	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=0.0411, tbb v. tbb +bdnf p=0.11	Fig. legend	t=1.987	Fig. legend
+ -	4d	paired t-test	Fig. legend	14	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=0.0215, 0.116 for tbb	Fig. legend	t=2.505	Fig. legend
+ -	4e	paired t-test	Fig. legend	14	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=0.0175, 0.047 for tbb	Fig. legend	t=2.496	Fig. legend
+ -	4f	paired t-test	Fig. legend	13	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=0.0122, 0.69 for tbb	Fig. legend	t=2.926	Fig. legend
+ -	4g	paired t-test	Fig. legend	8	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. tbb p=0.0451, 0.518 for tbb +bdnf	Fig. legend	t=2.485	Fig. legend

+ -	4h	paired t-test	Fig. legend	8	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. tbb p=0.0179, 0.0.88 for tbb +bdnf	Fig. legend	t=2.726	Fig. legend
+ -	4i	paired t-test	Fig. legend	6	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. tbb p=0.0437	Fig. legend	t=2.938	Fig. legend
+ -	4k	unpaired t-test	Fig. legend	N = 108 neurons for control, 131 for BDNF, 117 for TBB, 118 for TBB +BDNF from 13 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf p=7.4E-14, tbb v tbb +bdnf p=0.001, bdnf vs tbb+bdnf p=7.598E-10	Fig. legend	control vs bdnf t = 7.962, for TBB vs TBB+BDNF t = 3.331, for BDNF vs TBB+BDNF t = 6.408	Fig. legend
+ -	4n	unpaired t-test	Fig. legend	for control n = 120 neurons, for BDNF n = 113, for TBB n = 39, for TBB +BDNF n = 50 from 6 biological replicates,	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control v. bdnf P = 9.98E-7	Fig. legend	t = 5.02	Fig. legend
+ -	5d	Unpaired T-test with bonforroni correction	Fig. legend	N = 68 for GFP, 61 for Brd4, 46 for CK2 deletion, 44 for deletion 492-494, 54 for S492A, 51 for SSS492ESE from 5 biological replicates.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=1.22x10^-8 for gfp v. Brd4, 0.067 for CK2del, 0.19 for 492-494del, 0.034 for S492a For Brd4 vs CK2 deletion P = 0.0011, for Brd4 vs deletion 492-494 P = 0.00037, for Brd4 vs S492A P = 0.0075, for Brd4 vs Brd4-pm P = 0.0204	Fig. legend	For GFP vs Brd4 t = 6.09, for GFP vs Brd4-pm t = 2.353, for Brd4 vs CK2 deletion t = 3.36, for Brd4 vs deletion 492-494 t = 3.689, for Brd4 vs S492A t = 2.724, for Brd4 vs Brd4-pm t = 2.353	Fig. legend
+ -	5e	Unpaired t-test	Fig. legend	N = 57 neurons for Brd4, N = 52 for S492A and N = 38 for Brd4-pm from 3 biological replicates.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for Brd4 vs S492A P = 0.0001, for Brd4 vs Brd4-pm P = 0.0085	Fig. legend	for Brd4 vs S492A t = 4.042, for Brd4 vs Brd4-pm t = 2.488	Fig. legend

+ -	5f	Unpaired t-test	Fig. legend	N = 35 neurons for Brd4, 21 for Brd4 with BDNF, 29 for S492A, and 18 for Brd4-pm from 3 biological replicates.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.0164 for Brd4 v. Brd4 +BDNF, p=0.00167 for Brd4 v. S492A, p= 0.035038 for Brd4 v. Brd4-pm	Fig. legend	for Brd4 vs Brd4 + BDNF t = 2.477, for Brd4 vs S492A t = 3.286, for Brd4 vs SSS492A t = 2.166	Fig. legend
+ -	6a	Univariate analysis	Fig. legend	N = 12 biological replicates for gria1 and 6 biological replicates for gria2.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=6.4x10^-8 for gria1, 0.77 for gria2	Fig. legend	t = 7.959	Fig. legend
+ -	6d	Unpaired t-test	Fig. legend	N = 33 neurons for control and 26 neurons for Jq1 from 4 biological replicates.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 4.242E-8	Fig. legend	t = 6.322	Fig. legend
+ -	6f	Unpaired t-test with bonforroni correction	Fig. legend	N = 33 neurons for control siRNA, 31 for Brd2 siRNA, 28 for Brd3 siRNA, and 28 for Brd4 siRNA from 5 biological replicates.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.0096 for Brd4 sirna, 0.74 for Brd2 sirna, 0.78 for Brd3 sirna	Fig. legend	t = 2.667	Fig. legend
+ -	6i	Unpaired t-test	Fig. legend	N = 33 neurons for GFP and N = 24 neurons for GFP-Brd4 from 4 biological replicates.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.00167	Fig. legend	t = 3.264	Fig. legend

+ -	7a	2-way ANOVA	Fig. legend	N = 10 mice for DMSO, 9 mice for 1 week Jq1 and 10 mice for 3 weeks Jq1.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	two-way ANOVA (zone) P = 2E16, two-way ANOVA (treatment) P = 0.986,	Fig. legend	two-way ANOVA (zone) F = 598.57, two-way ANOVA (treatment) F = 0.015, df = 54	Fig. legend
+ -	7c	Univariate analysis and unpaired two sided t-test	Fig. legend	N = 10 mice for DMSO, 9 mice for 1 week Jq1 and 10 mice for 3 weeks Jq1.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	dmso univariate analysis = 0.00127. For control vs 1 week jq1 p=0.00107, for control vs 3 weeks jq1 0.00941	Fig. legend	for DMSO vs 1 week Jq1 t = 2.88, for DMSO vs 3 weeks Jq, t = 2.927	Fig. legend
+ -	7d	Univariate analysis and unpaired t-test	Fig. legend	N = 10 mice per group.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	univariate analysis for dmso p=0.00262. t-test for DMSO vs post-learning Jq1 P = 0.0376	Fig. legend	univariate analysis for dmso t = 4.11. t-test for DMSO vs post-learning t = 2.25	Fig. legend
+ -	7f	2-way anova with posthoc ttest	Fig. legend	N = 10 mice for DMSO, 9 mice for 1 week Jq1 and 10 mice for 3 weeks Jq1.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	Anova P =0.0135, Ttest P=0.008	Fig. legend	Anova: F = 4.67, df = 54, P =0.0135 Ttest: t=2.23	Fig. legend
+ -	8b	Unpaired t-test	Fig. legend	N = 7 mice for DMSO and 6 mice for Jq1.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.002	Fig. legend	t=3.155	Fig. legend
+ -	8c	Unpaired t-test	Fig. legend	N = 7 mice for DMSO and 6 mice for Jq1.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p=0.036	Fig. legend	t=2.388	Fig. legend
+ -	83	one sample ttest univariate analysis	Fig. legend	one safor DMSO n = 4 mice, for Jq1 n = 4 mice and for non-kindled n = 6 micempl e ttest univariat e analysis	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0473	Fig. legend	t = 2.415	Fig. legend

+ -	8f	n.a.	Fig. legend	N = 8 mice for DMSO and Jq1 and N = 6 mice for non-kindled group.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	n.a.	Fig. legend	n.a.	Fig. legend
+ -	8g	Unpaired t-test	Fig. legend	N = 8 mice for DMSO and Jq1 and N = 6 mice for non-kindled group.	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	unpaired one-tailed t testday 13 P = 0.00555, day 15 P = 0.0486, unpaired two-tailed t test for day 30 t = 2.715	Fig. legendFig. legend	unpaired one-tailed t testday 13 t = 2.494, day 15 t = 0.928, unpaired two-tailed t test for day 30 t = 2.715	Fig. legend
+ -	S1d	One-sample t-test	Fig. legend	for 0.5 hours n = 14, for 2 hours n = 13, for 4 hours n = 14, for 8 hours n = 12, for 24 hours n = 13,	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	p= 0.0338	Fig. legend	t = 2.01	Fig. legend
+ -	S2d	One-sample t-test	Fig. legend	7	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 6.18E-6	Fig. legend	t = 13.07	Fig. legend
+ -	S2g	unpaired t-test	Fig. legend	n = 45 neurons for control siRNA and 37 neurons for Brd4 siRNA from 5 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 6.38E-16	Fig. legend	t = 10.093	Fig. legend
+ -	S2h	One-sample t-test	Fig. legend	3	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0157	Fig. legend	t = 5.51	Fig. legend
+ -	S2i	One-sample t-test	Fig. legend	3	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.019	Fig. legend	t = 4.92	Fig. legend
+ -	S2j	unpaired t-test	Fig. legend	for control n = 47 for Brd4 siRNA1 n = 43 and for Brd4 siRNA2 n = 37 neurons from 2 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for siRNA1 P = 2.24E-38, for siRNA2 P = 2.82E-25	Fig. legend	for siRNA1 t = 22.91, for siRNA2 t = 15.18	Fig. legend

+ -	S2l	upaired two-tailed t test	Fig. legend	for control n = 25 , for control + BDNF n = 23 , for Brd4 siRNA1 n = 22 , for Brd4 siRNA1 + BDNF n = 22 , for Brd4 siRNA2 n = 14 , and for Brd4 siRNA2 + BDNF n = 26 from 2 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 9.53E-4	Fig. legend	t = 3.432	Fig. legend
+ -	S2m	upaired two-tailed t test for control	Fig. legend	test for control n = 42 neurons, for long Brd4 n = 26 neurons and for short Brd4 n = 30 neurons	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for control vs long Brd4 P = 0.015, for long vs short Brd4 P = 0.0016	Fig. legend	for control vs long Brd4 t = 2.48, for long vs short Brd4 P = 0.0016	Fig. legend
+ -	S2n	one sample t test	Fig. legend	for Arc n = 13 biological replicates, for Fos n = 13 biological replicates, for Nr4a1 n = 11	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for Arc P = 3.098E-5, for Fos biological replicates P = 0.013, and for Nr4a1 P = 0.00104	Fig. legend	for Arc biological replicates t = 6.58, for Fos t = 2.65, and for Nr4a1 t = 4.75	Fig. legend
+ -	S3n	unpaired two-tailed t test	Fig. legend	for control siRNA n = 24 neurons and for CK2 siRNA n = 26 neurons from 3 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 8.05E-5	Fig. legend	t = 3.29	Fig. legend

+ -	S3o	unpaired two-tailed t test	Fig. legend	for control siRNA n = 50 neurons, n = 39 for BDNF, for CK2 siRNA n = 39, and for CK2 siRNA + BDNF n = 37 from 5 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	control vs BDNF, P = 1.21E-5, for BDNF vs CK2 siRNA + BDNF P = 7.09E-7	Fig. legend	control vs BDNF, t = 5.244, for BDNF vs CK2 siRNA + BDNF t = 5.42	Fig. legend
+ -	S3q	unpaired two-tailed t test	Fig. legend	for control n = 15 for BDNF 18 neurons	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 5.389E-5	Fig. legend	t = 4.73	Fig. legend
+ -	S5c	unpaired two-sided t test	Fig. legend	for GFP n = 68, for Brd4 n = 61, for CK2 deletion n = 46, for deletion 492-494 n = 44, for S492A n = 54, for SSS492ESE n = 51 from 5 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for GFP vs Brd4 P = 4.596E-17, for CK2 deletion P = 1.26E-27, for deletion 492-494, P = 1.48E-22,for S492A, P = 4.14E-34, for SSS492ESE P = 7.82E-24	Fig. legend	for GFP vs Brd4 t = 9.73, for CK2 deletion t = 14.57, for deletion 492-494, t = 12.37, for S492A t = 17.17, for SSS492ESE t = 12.73	Fig. legend
+ -	S6b	unpaired two-sided t test	Fig. legend	for control n = 13 neurons and for Jq1 n = 12 neurons from 2 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 0.0015	Fig. legend	t = 3.56	Fig. legend
+ -	S6d	unpaired two-sided t test	Fig. legend	for control siRNA n = 14 neurons, for Brd4 siRNA1 n = 13 neurons, and for Brd4 siRNA2 n = 14 neurons from 2 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for control vs siRNA1 P = 0.0114, for control vs siRNA2 P = 0.0078	Fig. legend	for control vs siRNA1 t = 2.61, for control vs siRNA2 t = 2.76	Fig. legend

+ -	S6e	unpaired two-sided t test	Fig. legend	n = 68 neurons for control for Jq1 and n = 66 from 2 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	nonsignificant	Fig. legend	nonsignificant	Fig. legend
+ -	S6f	unpaired two-sided t test	Fig. legend	n = 15 neurons, for long Brd4 n = 17, and for short Brd4 n = 18 from 2 biological replicates	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for control vs long Brd4 P = 0.0161, for long vs short Brd4 P = 0.0308	Fig. legend	for control vs long Brd4 t = 2.55, for long vs short Brd4 t = 2.26	Fig. legend
+ -	S7j	one sample t test	Fig. legend	n = 10 mice for DMSO and 9 mice for 1 week Jq1	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for DMSO P = 0.00325, for Jq1 P = 0.00103	Fig. legend	for DMSO t = 4.14, for Jq1 t = 5.017	Fig. legend
+ -	S7k	2-way ANOVA with posthoc t test	Fig. legend	N = 10 mice for control and 3 week Jq1 and 9 mice for 1 week Jq1	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 2E-16	Fig. legend	F = 165.7, df = 130	Fig. legend
+ -	S7l	2-way ANOVA with posthoc t test	Fig. legend	N = 10 mice for control and 3 week Jq1 and 9 mice for 1 week Jq1	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	P = 2E-16	Fig. legend	F = 80.72, df = 110	Fig. legend
+ -	S8a	unpaired two-sided t test	Fig. legend	test for dmso n = 9 brains and for Jq1 n = 8	yes	Fig. legend	error bars are mean +/- SEM	Fig. legend	for gria1 P = 0.00517, for Nr4a1 P = 0.018	Fig. legend	for gria1 t value = 3.27, for Nr4a1 t value = 2.64	Fig. legend

Representative figures

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

   If so, what figure(s)?

   Figures 1, 2, 4, 5, and 6, supplementary figures 1, 2, 3, 4, 5, 6, 8.

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 state exact replicates.

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.	No statistical methods were used to predetermine sample sizes but our sample sizes are similar to those reported in previous publications (20,30,37).
2. Are statistical tests justified as appropriate for every figure? Where (section, paragraph #)?	All statistics are described in the methods section and each statistical test is listed in the figure legend.
a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?	In the methods section, a statistics summary describes when different tests are used.
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 #)?	Data distribution was assumed to be normal but this was not formally tested, described in the methods section
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 #)?	Variance was assumed to be normal but this was not formally tested, described in the methods section
d. Are tests specified as one- or two-sided?	Whether t-tests are one or two-sided are described in each figure elegend.
e. Are there adjustments for multiple comparisons?	Yes, a Bonforroni correction is applied for multiple comparisons as described in the methods section
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	Data was not generally not excluded except for one mouse during behavioral testing because the lights went off in the facility and the video recording was not visible. The behavioral section of the methods section describes the reasons for exclusion.
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 #)?	Mice were first randomly assigned to groups. Then, due to variable weights of the mice used for testing, we opted to ensure that groups were balance by weight. This ensured that the average weight per mouse of each group was equivalent and prevented differences in behavioral results due to differences in size of the mice. This is described in the methods within the behavioral testing section.
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 #)?	The investigator carryinag out the behavioral testing and analysis was fully blind to the treatment groups. Another investigator coded all cages during the behavioral testing and analysis. The extent of blinding is described in the methods section.

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Described in the methods within the behavioral testing section.
7. Is the species of the animals used reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? Where (section, paragraph #)?	Mice had no previous history.
a. If multiple behavioral tests were conducted in the same group of animals, is this reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
15. If any animals/subjects were excluded from analysis, is this reported? Where (section, paragraph #)?	Described in the methods in the behavioral testing section.
a. How were the criteria for exclusion defined? Where is this described (section, paragraph #)?	No animals were excluded from the analysis except for one mouse for the novel object testing because the lights went off in the facility during the test so the data could not be collected. This is described in the methods in the behavioral testing section.

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 #)?

During seizure testing some mice died after seizure induction resulting in fewer mice at the end of testing.

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 #)?

All information is provided in the methods section.

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

Where does this appear (section, paragraph #)?

All antibodies used are commonly used commercial antibodies except for the newly developed phospho-Brd4 antibody which is validated in Supplementary Figure 5.

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

Where (section, paragraph #)?

N2a cells were used and were tested for mycoplasma contamination before use, described in the methods section.

a. Were they recently authenticated?

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

N2a cell methods are described in the cell culture section.

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 deposits have been made available through a GEO link. This is provided in the RNA-sequencing description in the methods section.

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 #)?

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