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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 #
+ -	2d	Two-way ANOVA	Fig. legend	4, 3, 3	mice from at least 3 litters/group	Fig. 2d	error bars are mean +/- SEM	Fig. legend	P = 0.033 for interaction, P = 0.000006 for compartment, P = 0.033 for age	Fig. legend	F(2, 16) = 4.400 for interaction, F(1, 16) = 49.072 for compartment, F(2, 16) = 4.400 for age	Fig. legend
+ -	2e	Two-way ANOVA	Fig. legend	4, 3, 3	mice from at least 3 litters/groupmice from at least 3 litters/group	Fig. 2e	error bars are mean +/- SEM	Fig. legend	P = 0.060 for interaction, P = 0.000000 for compartment, P = 0.060 for age	Fig. legend	F(2,16) = 3.456 for interaction, F(1,16) = 110.852 for compartment, F(2,16) = 3.001 for age	Fig. legend
+ -	2f	One-way ANOVA	Fig. legend	6, 6, 6	mice from at least 3 litters/group	Fig. 2f	error bars are mean +/- SEM	Fig. legend	P = 0.000001	Fig. legend	F(2, 15) = 41.852	Fig. legend
+ -	2g	Two-way ANOVA	Fig. legend	for Foxp2, 60 in DLS and 89 in DMS; for Mef2C, 63 in DLS and 82 in DMS	cells from 3 mice that were from 3 litters/group	Fig. 2g	error bars are mean +/- SEM	Fig. legend	for Foxp2, P = 0.962 for interaction, P = 0.000000 for region, P = 0.962 for age; for Mef2C, P = 0.004 for interaction, P = 0.000001 for region. P = 0.004 for age	Fig. legend	for Foxp2, F(2, 139) = 0.039 for interaction, F(1, 139) = 40.321 for region, F(2, 139) = 0.039 for age; for Mef2C, F(2, 141) = 5.838 for interaction, F(1, 141) = 25.477 for region, F(2, 141) = 5.838 for age	Fig. legend
+ -	2h	One-way ANOVA	Fig. legend	3, 3, 3	mice from 3 litters/ group	Fig. 2h	error bars are mean +/- SEM	Fig. legend	for Foxp2, P = 0.000128 in DLS, P = 0.000078 in DMS; for Mef2C, P = 0.000177 in DLS, P = 0.000056 in DMS	Fig. legend	for Foxp2, F(2, 6) = 56.571, in DLS, F(2, 6) = 67.197, in DMS; for Mef2C, F(2, 6) = 50.443, in DLS, F(2, 6) = 75.536	Fig. legend
+ -	3a	One-way ANOVA	Fig. legend	3, 3, 3	striatal lysate of animals from 3 littermates/group	Fig. 3a	error bars are mean +/- SEM	Fig. legend	for VGluT1, P = 0.005, for PSD-95, P = 0.002	Fig. legend	for VGluT1, F(2, 6) = 14.649; for PSD-95, F(2, 6) = 19.954	Fig. legend
+ -	3b	Student's t test	Fig. legend	5, 5	striatal lysate of animals from 5 littermates/group	Fig. 3b	error bars are mean +/- SEM	Fig. legend	for VGluT1, P = 0.014; for PSD-95, P = 0.036	Fig. legend	for VGluT1, t(8) = -3.155; for PSD-95, t(8) = 2.518	Fig. legend
+ -	3c	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 5 littermates/group	Fig. 3c	error bars are mean +/- SEM	Fig. legend	for PSD-95, P = 0.003; for VGluT1, P = 0.049	Fig. legend	for PSD-95, t(4) = -6.442; for VGluT1, t(4) = -2.795	Fig. legend

+ -	3d	One-way ANOVA	Fig. legend	30, 30, 30	cells from 3 animals that were from 3 littermates/ group	Fig. 3d & supp table 1	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.055; for thin/Filopodia, P = 0.000463; for mushroom P = 0.000013; for branched, P = 0.019; for atypical, P = 0.747; for sum, P = 0.000000	Fig. legend	for stubby, F(2, 87) = 2.992; for thin/Filopodia, F(2, 87) = 8.396; for mushroom, F(2, 87) = 12.889; for branched, F(2, 87) = 4.169; for atypical, F(2, 87) = 0.293; for sum, F(2, 87) = 28.470	Fig. legend
+ -	3e	Student's t test	Fig. legend	30, 30	cells from 3 animals from 3 littermates/group	Fig. 3e & supp table 2	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.538; for thin/Filopodia, P = 0.032; for mushroom P = 0.050; for branched, P = 0.029; for multiple branched, P = 0.001 for atypical, P = 0.448; for sum, P = 0.000383	Fig. legend	for stubby, t(29) = 0.623; for thin/ Filopodia, t(29) = -2.249; for mushroom, t(29) = -2.041; for branched, t(29) = -2.300; for multiple branched, t(29) = -3.525 for atypical, t(29) = 0.769; for sum, t(29) = -4.216	Fig. legend
+ -	3f	One-way ANOVA	Fig. legend	38, 38, 33	cells from 3 animals from 3 littermates/group	Fig. 3f & supp table 3	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.000000; for thin/filopodia, P = 0.139; for mushroom, P = 0.007; for branched, P = 0.000153; for multiple branched, P = 0.004 for atypical, P = 0.000021; for sum, P = 0.000000	Fig. legend	for stubby, F(2,106) = 34.658; for thin/ filopodia, F(2,106) = 2.012; for mushroom, F(2,106) = 5.182; for branched, F(2,106) = 9.555; for multiple branched, F(2,106) = 5.965 for atypical, F(2,106) = 11.944; for sum, F(2,106) = 38.448	Fig. legend
+ -	3g	Student's t test	Fig. legend	23, 10	cells from 3 animals from 3 littermates	Fig. 3g	error bars are mean +/- SEM	Fig. legend	P = 0.000000	Fig. legend	t(31) = 9.429	Fig. legend
+ -	3h	Student's t test	Fig. legend	12, 13	cells from 4 and 3 animals in each group	Fig. 3h	error bars are mean +/- SEM	Fig. legend	P = 0.000001	Fig. legend	t(23) = -7.612	Fig. legend
+ -	3i	Student's t test	Fig. legend	14, 14	cells from 3 and 5 animals/group	Fig. 3i	error bars are mean +/- SEM	Fig. legend	P = 0.002	Fig. legend	t(26) = -3.509	Fig. legend
+ -	3j	Student's t test	Fig. legend	23, 17	cells from 4 animals from 2 littermates	Fig. 3j	error bars are mean +/- SEM	Fig. legend	P = 0.269	Fig. legend	t(38) = -1.122	Fig. legend
+ -	3k	Student's t test	Fig. legend	17, 13	cells from 3 animals/group	Fig. 3k	error bars are mean +/- SEM	Fig. legend	P = 0.000000	Fig. legend	t(28) = 9.453	Fig. legend
+ -	3l	Student's t test	Fig. legend	8, 7	cells from 4, 3 mice/group	Online methods	error bars are mean +/- SEM	Fig. legend	for frequency, P = 0.013; for amplitude, P = 0.043	Fig. legend	for frequency, t(13) = 2.890; for amplitude, t(13) = -2.2505	Fig. legend
+ -	3m	Mann-Whitney U test	Fig. legend	23, 27	cells from 6, 4 animals/group	Online methods	error bars are mean +/- SEM	Fig. legend	for frequency, P = 0.009; for amplitude, P = 0.471	Fig. legend	for frequency, U = 167.5; for amplitude, U = 273	Fig. legend
+ -	3n	Student's t test	Fig. legend	7, 6	cells from 3, 3 animal/group	Online methods	error bars are mean +/- SEM	Fig. legend	for frequency, P = 0.001, for amplitude, P = 0.237	Fig. legend	for frequency, t(14) = -4.022 ;for amplitude, t(14) = -1.131	Fig. legend

+ -	4c, left	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	Fig. 4c	error bars are mean +/- SEM	Fig. legend	P = 0.012	Fig. legend	t(4) = -4.317	Fig. legend
+ -	4c, right	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	Fig. 4c	error bars are mean +/- SEM	Fig. legend	P = 0.002	Fig. legend	t(4) = -7.692	Fig. legend
+ -	4d	Student's t test	Fig. legend	3, 3, 3	striatal lysate of animals from 3 littermates/group	Fig. 4d	error bars are mean +/- SEM	Fig. legend	for WT vs. Hetero, P = 0.022; for Hetero vs. KO, P = 0.018; for WT vs. KO, P = 0.016	Fig. legend	for WT vs. Hetero, t(4) = -3.645; for Hetero vs. KO, t(4) = -3.875; for WT vs. KO, t(4) = -7.913	Fig. legend
+ -	4e	Student's t test	Fig. legend	5, 5	striatal lysate of animals from 5 littermates/group	Fig 4e	error bars are mean +/- SEM	Fig. legend	P = 0.038	Fig. legend	t(8) = 2.480	Fig. legend
+ -	4f	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	Fig 4f	error bars are mean +/- SEM	Fig. legend	P = 0.000203	Fig. legend	t(4) = -12.987	Fig. legend
+ -	4g	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	Fig. 4g	error bars are mean +/- SEM	Fig.Fig. legend	P = 0.010	Fig. legend	t(4) = 4.540	Fig. legend
+ -	4h	Student's t test	Fig. legend	3, 3	independent experiments	Fig. 4h	error bars are mean +/- SEM		P = 0.046	Fig. legend	t(4) = 2.853	Fig. legend
+ -	5c	Student's t test	Fig. legend	3, 3	independent experiments	Fig. 5c	error bars are mean +/- SEM	Fig. legend	WT: control vs. mFoxp2, P = 0.039; control vs. hFoxp2, P = 0.032	Fig. legend	WT: control vs. mFoxp2, t(4) = 3.017; control vs. hFoxp2, t(4) = 3.237	Fig. legend
+ -	6a	Kruskal-Wallis one-way ANOVA followed by Dunn's pairwise multiple comparisons test	Fig. legend	10, 12, 17	animals from 30 litters/group	Fig. 6a	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P < 0.001	Fig. legend	test statistic = 21.474	Fig. legend
+ -	6b	One-way ANOVA	Fig. legend	10, 12, 17	animals from 30 litters/group	Fig. 6b	error bars are mean +/- SEM	Fig. legend	P = 0.000238	Fig. legend	F(2, 36) = 10.768	Fig. legend
+ -	6c	Kruskal-Wallis one-way ANOVA followed by Dunn's pairwise multiple comparisons test	Fig. legend	10, 12, 17	animals from 30 litters/group	Fig. 6c	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P < 0.001	Fig. legend	test statistic = 15.832	Fig. legend
+ -	6d	One-way ANOVA	Fig. legend	10, 12, 17	animals from 30 litters/group	Fig 6d	error bars are mean +/- SEM	Fig. legend	P = 0.002	Fig. legend	F(2, 36) = 7.296	Fig. legend
+ -	6e	One-way ANOVA	Fig. legend	3, 3, 3	striatal lysate of animals from 3 littermates/group	Fig. 6e	error bars are mean +/- SEM	Fig. legend	for PSD-95, P = 0.007; for VGluT1, P = 0.002	Fig. legend	for PSD-95, F(2, 6) = 12.645,for VGluT1, F(2, 6) = 21.487	Fig. legend

+ -	6f	One-way ANOVA	Fig. legend	30, 36, 35	cells from 3 animals from 3 littermates/group	Fig. 6f	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.013; for thin/filopodia, P = 0.000005; for mushroom, P = 0.025; for branched, P = 0.000031; for multiple branched, P = 0.138, for atypical, P = 0.011; for sum, P = 0.000000	Fig. legend	for stubby, F(2, 98) = 4.521; for thin/filopodia, F(2, 98) = 13.875; for mushroom, F(2, 98) = 3.816; for branched, F(2, 98) = 11.563; for multiple branched, F(2, 98) = 2.023; for atypical, F(2, 98) = 4.709; for sum, F(2, 98) = 30.941	Fig. legend
+ -	6g-i	One-way ANOVA	Fig. legend	3, 3, 3	animals from 3 littermates/group	Fig. 6g-i	error bars are mean +/- SEM	Fig. legend	for striosome, P = 0.000145; for matrix, P = 0.005; for total striatum, P = 0.000015	Fig. legend	for striosome, F(2, 6) = 54.063; for matrix, F(2, 6) = 15.055; for total striatum, F(2, 6) = 117.718	Fig. legend
+ -	6j	Student's t test	Fig. legend	16, 23	cells from 4, 3 animals/group	Fig. 6j	error bars are mean +/- SEM	Fig. legend	P = 0.000000	Fig. legend	t(26) = -7.410	Fig. legend
+ -	6k	Student's t test	Fig. legend	8, 8	animals from 10 litters/group	Fig. 6k	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.014	Fig. legend	t(14) = -2.789	Fig. legend
+ -	6l	Student's t test	Fig. legend	8, 8	animals from 10 litters/group	Fig. 6l	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.016	Fig. legend	t(14) = -2.727	Fig. legend
+ -	7a	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.000196	Fig. legend	F(2, 66) = 11.001	Fig. legend
+ -	7b	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.000475	Fig. legend	F(2, 66) = 8.613	Fig. legend

+ -	7c	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.003	Fig. legend	F(2, 66) = 6.444	Fig. legend
+ -	7d	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.005	Fig. legend	F(2, 66) = 5.723	Fig. legend
+ -	7e	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.090	Fig. legend	F(2, 66) = 2.497	Fig. legend
+ -	7f	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.016	Fig. legend	F(2, 66) = 4.404	Fig. legend
+ -	7g	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.933	Fig. legend	F(2, 66) = 0.069	Fig. legend
+ -	7h	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.273	Fig. legend	F(2, 66) = 1.325	Fig. legend
+ -	7i	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.303	Fig. legend	F(2, 66) = 1.218	Fig. legend

+ -	7j	One-way ANOVA	Fig. legend	23, 22, 15	animals from 25 litters/group	Fig. 7	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	P = 0.000371	Fig. legend	F(2, 66) = 10.022	Fig. legend
+ -	supp 1c	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp1c	error bars are mean +/- SEM	Fig. legend	P = 0.000001	Fig. legend	t(4) = 56.963	Fig. legend
+ -	supp 1f	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp1f	error bars are mean +/- SEM	Fig. legend	P = 0.000016	Fig. legend	t(4) = 24.504	Fig. legend
+ -	supp 2c	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp2c	error bars are mean +/- SEM	Fig. legend	for Striosome, P = 0.013; for matrix, P = 0.024; for total striatum, P = 0.013	Fig. legend	for Striosome, t(4) = 4.228; for matrix, t(4) = 3.535; for total striatum, t(4) = 4.298	Fig. legend
+ -	supp 2f	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp2f	error bars are mean +/- SEM	Fig. legend	for Striosome, P = 0.002; for matrix, P = 0.012; for total striatum, P = 0.004	Fig. legend	for Striosome, t(4) = -7.426; for matrix, t(4) = -4.343; for total striatum, t(4) = -6.013	Fig. legend
+ -	supp 2i	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp2i	error bars are mean +/- SEM	Fig. legend	for Striosome, P = 0.115; for matrix, P = 0.014; for total striatum, P = 0.032	Fig. legend	for Striosome, t(4) = -2.007; for matrix, t(4) = -4.201; for total striatum, t(4) = -3.240	Fig. legend
+ -	supp 3a	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp3a	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.810; for middle, P = 0.755, for caudal, P = 0.549	Fig. legend	for rostral, t(4) = 0.257; for middle, t(4) = -0.334; for caudal, t(4) = -0.654	Fig. legend
+ -	supp 3b	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3b	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.640; for middle, P = 0.758, for caudal, P = 0.236	Fig. legend	for rostral, t(4) = -0.505; for middle, t(4) = 0.330; for caudal, t(4) = 1.392	Fig. legend
+ -	supp 3c	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3c	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.974; for middle, P = 0.460, for caudal, P = 0.972	Fig. legend	for rostral, t(4) = -0.035; for middle, t(4) = -0.816; for caudal, t(4) = -0.037	Fig. legend
+ -	supp 3d	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3d	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.744; for middle, P = 0.972, for caudal, P = 0.825	Fig. legend	for rostral, t(4) = 0.350; for middle, t(4) = -0.037; for caudal, t(4) = -0.236	Fig. legend
+ -	supp 3e	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3e	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.283; for middle, P = 0.341, for caudal, P = 0.850	Fig. legend	for rostral, t(4) = -0.035; for middle, t(4) = -0.816; for caudal, t(4) = -0.037	Fig. legendFig. legend

+ -	supp 3f	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3f	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.844; for middle, P = 0.362, for caudal, P = 0.173	Fig. legend	for rostral, t(4) = 0.210; for middle, t(4) = 1.029; for caudal, t(4) = 1.655	Fig. legend
+ -	supp 3g	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3g	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.208; for middle, P = 0.432, for caudal, P = 0.476	Fig. legend	for rostral, t(4) = -1.501; for middle, t(4) = 0.873; for caudal, t(4) = -0.786	Fig. legend
+ -	supp 3h	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3h	error bars are mean +/- SEM	Fig. legend	for rostral, P = 0.883; for middle, P = 0.728, for caudal, P = 0.171	Fig. legend	for rostral, t(4) = 0.157; for middle, t(4) = 0.374; for caudal, t(4) = -1.669	Fig. legend
+ -	supp 3k	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3k	error bars are mean +/- SEM	Fig. legend	P = 0.716	Fig. legend	t(4) = 0.390	Fig. legend
+ -	supp 3n	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3n	error bars are mean +/- SEM	Fig. legend	P = 0.400	Fig. legend	t(4) = -0.940	Fig. legend
+ -	supp 3q	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3q	error bars are mean +/- SEM	Fig. legend	P = 0.519	Fig. legend	t(4) = -0.707	Fig. legend
+ -	supp 3t	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3t	error bars are mean +/- SEM	Fig. legend	P = 0.146	Fig. legend	t(4) = -1.800	Fig. legend
+ -	supp 3u	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 3u	error bars are mean +/- SEM	Fig. legend	P = 0.627	Fig. legend	t(4) = 0.569	Fig. legend
+ -	supp 4a	One-way ANOVA	Fig. legend	30, 30, 30	cells from 3 animals from 3 littermates/group	supp 4a & supp table 1	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.275; for thin/Filopodia, P = 0.000002; for mushroom P = 0.000094; for branched, P = 0.002; for atypical, P = 0.158; for sum, P = 0.000000	Fig. legend	for stubby, F(2, 87) = 1.309; for thin/Filopodia, F(2, 87) = 15.251; for mushroom, F(2, 87) = 10.333; for branched, F(2, 87) = 6.699; for atypical, F(2, 87) = 1.882; for sum, F(2, 87) = 28.470	Fig. legend
+ -	supp 4b	Student's t test	Fig. legend	30, 30, 30	cells from 3 animals from 3 littermates/group	supp 4b & supp table 2	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.677; for thin/Filopodia, P = 0.041; for mushroom P = 0.106; for branched, P = 0.393; for multiple branched, P = 0.083; for atypical, P = 0.823; for sum, P = 0.000383	Fig. legend	for stubby, t(29) = -0.421; for thin/Filopodia, t(29) = -2.134; for mushroom, t(29) = -1.670; for branched, t(29) = -0.867; for multiple branched, t(29) = -1.795; for atypical, t(29) = 0.226; for sum, t(29) = -4.016	Fig. legend

+ -	supp 4c	One-way ANOVA	Fig. legend	47, 30, 36	cells from 3 animals from 3 littermates/group	supp 4c & supp table 3	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.000000; for thin/filopodia, P = 0.000009; for mushroom, P = 0.000001; for branched, P = 0.000003; for multiple branched, P = 0.000106; for atypical, P = 0.000105; for sum, P = 0.000000	Fig. legend	for stubby, F(2, 110) = 61.760; for thin/ filopodia, F(2, 110) = 12.941; for mushroom, F(2, 110) = 16.513; for branched, F(2, 110) = 14.529; for multiple branched, F(2, 110) = 9.961; for atypical, F(2, 110) = 9.982; for sum, F(2, 110) = 86.254	Fig. legend
+ -	supp 4d	One-way ANOVA	Fig. legend	30, 30, 30	cells from 3 animals from 3 littermates/group	supp 4d & supp table 4	error bars are mean +/- SEM	Fig. legend	for stubby, P = 0.038; for thin/filopoida, P = 0.000000; for mushroom, P = 0.000366; for branched, P = 0.000128; for multiple branched, P = 0.094; for atypical, P = 0.027; for sum, P = 0.000000	Fig. legend	for stubby, F(2, 89) = 3.391; for thin/filopoida, F(2, 89) = 22.339; for mushroom, F(2, 89) = 8.687; for branched, F(2, 89) = 10.016; for multiple branched, F(2, 89) = 2.433,; for atypical, F(2, 89) = 3.759; for sum, F(2, 89) = 57.917	Fig. legend
+ -	supp 6c	Student's t test	Fig. legend	3, 3	animals from 3 littermates/group	supp 6c	error bars are mean +/- SEM	Fig. legend	for M1, P = 0.103; for S1, P = 0.108	Fig. legend	for M1, t(4) = -2.102; for S1, t(4) =-2.063	Fig. legend
+ -	supp 6d	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp 6d	error bars are mean +/- SEM	Fig. legend	P = 0.340	Fig. legend	t(4) = 1.243	Fig. legend
+ -	supp 6e	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp 6e	error bars are mean +/- SEM	Fig. legend	for GluR1, P = 0.204; for PSD-95, P = 0.166; for VGluT1, P = 0.105; for Mef2C, P = 0.883	Fig. legend	for GluR1, t(4) = 1.859; for PSD-95, t(4) = -2.138; for VGluT1, t(4) = -2.086; for Mef2C, t(4) = 0.167	Fig. legend
+ -	supp 6f	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp 6e	error bars are mean +/- SEM	Fig. legend	for GluR1, P = 0.034; for PSD-95, P = 0.038; for VGluT1, P = 0.015; for Mef2C, P = 0.043	Fig. legend	for GluR1, t(4) = 3.169; for PSD-95, t(4) = 3.055; for VGluT1, t(4) = 4.114; for Mef2C, t(4) = -2.919	Fig. legend
+ -	supp 6g	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp 6e	error bars are mean +/- SEM	Fig. legend	for GluR1, P = 0.000287; for PSD-95, P = 0.048; for VGluT1, P = 0.032; for Mef2C, P = 0.049	Fig. legend	for GluR1, t(4) = 11.890; for PSD-95, t(4) = 2.823; for VGluT1, t(4) = 3.226; for Mef2C, t(4) = -2.789	Fig. legend
+ -	supp 6h	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp 6h	error bars are mean +/- SEM	Fig. legend	for GluR1, P = 0.042; for PSD-95, P = 0.113; for VGluT1, P = 0.011; for Mef2C, P = 0.004	Fig. legend	for GluR1, t(4) = -2.952; for PSD-95, t(4) = 2.020; for VGluT1, t(4) = -4.518; for Mef2C, t(4) = 5.838	Fig. legend

+ -	supp 6i	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp 6h	error bars are mean +/- SEM	Fig. legend	for GluR1, P = 0.003; for PSD-95, P = 0.048; for VGluT1, P = 0.004; for Mef2C, P = 0.027	Fig. legend	for GluR1, t(4) = -6.268; for PSD-95, t(4) = -2.826; for VGluT1, t(4) = -5.797; for Mef2C, t(4) = 3.392	Fig. legend
+ -	supp 6j	Student's t test	Fig. legend	3, 3	striatal lysate of animals from 3 littermates/group	supp 6h	error bars are mean +/- SEM	Fig. legend	for GluR1, P = 0.002; for PSD-95, P = 0.002; for VGluT1, P = 0.042; for Mef2C, P = 0.000406	Fig. legend	for GluR1, t(4) = -7.169; for PSD-95, t(4) = -7.396; for VGluT1, t(4) = -2.958; for Mef2C, t(4) = 10.873	Fig. legend
+ -	supp 7b	Student's t test	Fig. legend	4, 4	independent experiments	supp 7b	error bars are mean +/- SEM	Fig. legend	Mock vs. hFoxp2, P = 0.003; hFoxp2 vs. mtFoxp2, P = 0.006	Fig. legend	Mock vs. hFoxp2, t(6) = 8.032; hFoxp2 vs. mtFoxp2, t(6) = -6.723	Fig. legend
+ -	supp 8a	Student's t test	Fig. legend	10, 12	animals from 30 litters/group	supp 8a	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	for Events, P = 0.004; for Duration, P = 0.001; for Elements, P = 0.000100 ; for frequency jump, P = 0.001; for Peak freq (start), P = 0.756; for Peak ampl (start), P = 0.188; for Peak freq (end), P = 0.012; for Peak ampl (end), P = 0.002; for Peak freq (max), P = 0.443; for Peak ampl (max), P = 0.001.	Fig. legend	for Events, t(20) = 3.902; for Duration, t(20) = 3.870; for Elements, t(20) = 4.965; for frequency jump, t(20) = 4.494; for Peak freq (start), t(20) = 0.316; for Peak ampl (start), t(20) = 1.364; for Peak freq (end), t(20) = 2.765; for Peak ampl (end), t(20) = 3.615; for Peak freq (max), t(20) = 0.790; for Peak ampl (max), t(20) = 3.782.	Fig. legend
+ -	supp 8b	One-way ANOVA	Fig. legend	10, 11	animals from 30 litters/group	supp 8b	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	for duration, P = 0.002; for Peak freq (start), P = 0.218; for Peak ampl (start), P = 0.431; for Peak ampl (end), P = 0.007; for Peak freq (max), P = 0.080; for Peak ampl (max), P = 0.003.	Fig. legend	for duration, F(2, 36) = 7.317; for Peak freq (start), F(2, 36) = 1.590; for Peak ampl (start), F(2, 36) = 0.861; for Peak ampl (end), F(2, 36) = 5.729; for Peak freq (max), F(2, 36) = 2.705; for Peak ampl (max), F(2, 36) = 6.949	Fig. legend

+ -	supp 8c	Student's t test	Fig. legend	10, 11	animals from 30 litters/group	supp 8c	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	for Events, P = 0.515; for Duration, P = 0.587; for Elements, P = 0.286 ; for frequency jump, P = 0.480; for Peak freq (start), P = 0.976; for Peak ampl (start), P = 0.369; for Peak freq (end), P = 0.345; for Peak ampl (end), P = 0.222; for Peak freq (max), P = 0.464; for Peak ampl (max), P = 0.976.	Fig. legend	for Events, t(19) = -0.664; for Duration, t(19) = -0.552; for Elements, t(19) = -1.099; for frequency jump, t(19) = -0.720; for Peak freq (start), t(19) = -0.031; for Peak ampl (start), t(19) = -0.921; for Peak freq (end), t(19) = -0.968; for Peak ampl (end), t(19) = -1.263; for Peak freq (max), t(19) = -0.747; for Peak ampl (max), t(19) = -0.031.	Fig. legend
+ -	supp 8d	Student's t test	Fig. legend	8, 8	animals from 10 litters/group	supp 8d	median (horizontal line in the box), range between the 25th and 75th percentiles (box), and 1.5 times this interquartile range (T-bars). Outlying values are marked as circles	Fig. legend	for Duration, P = 0.964; for Elements, P = 0.160; for Peak freq (start), P = 0.054; for Peak ampl (start), P = 0.350; for Peak freq (end), P = 0.959; for Peak ampl (end), P = 0.362; for Peak freq (max), P = 0.518; for Peak ampl (max), P = 0.526.	Fig. legend	for Duration, t(14) = 0.046; for Elements, t(14) = 1.483; for Peak freq (start), t(14) = -2.104; for Peak ampl (start), t(14) = 0.096; for Peak freq (end), t(14) = 0.053; for Peak ampl (end), t(14) = -0.943; for Peak freq (max), t(14) = -0.663; for Peak ampl (max), t(14) = -0.650.	Fig. legend

Representative figures

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

   If so, what figure(s)?

Fig. 1
Fig. 2
Fig. 3
Fig. 4
Fig. 5
Fig. 6
Supplementary Fig. 1
Supplementary Fig. 2
Supplementary Fig. 3
Supplementary Fig. 4
Supplementary Fig. 5
Supplementary Fig. 6

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 #)?	For each representative figure, it is one of the figures that are used for statistical analysis. The repeating number is the n that is described in individual figure legends or in figures.

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.	The sample size was chosen based on literatures in the field.
2. Are statistical tests justified as appropriate for every figure? Where (section, paragraph #)?	Based on the properties of the data, appropriate statistics were used , and they were described in individual figure legends.
a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?	Yes, the statistical methods were summarized in the "Online method" part, and each statistical test is described in each 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 #)?	Yes. If the data points represent normal distribution, ANOVA or Student's t-test were used. If the data points did not fit with normal distribution, Mann-Whitney U or Kruskal-Wallis one-way ANOVA were used. The statistical details were summarized in the "Online method" part.
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. Either bar with standard error of mean or box plot was used to analyze our data. Details were described in individual figure legends.
d. Are tests specified as one- or two-sided?	We use two-tailed analysis in the entire paper.
e. Are there adjustments for multiple comparisons?	Yes. Some post-hoc tests were used, and they were described in individual figure legends and online methods.
3. To promote transparency, *Nature Neuroscience* has stopped allowing bar graphs to report statistics in the papers it publishes. If you have bar graphs in your paper, please make sure to switch them to dot-plots (with central and dispersion statistics displayed) or to box-and-whisker plots to show data distributions.	Yes. We have combined all bar graphs with dot-plots to show data distributions.
4. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	N/A

5. 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
6. 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 USV recordings and mEPSC recording were performed with mouse genotypes blinding to the experimenter.
7. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes, it is described in Online Methods, 1st paragraph "Animals".
8. Is the species of the animals used reported? Where (section, paragraph #)?	Yes, described in Online Methods "Animals".
9. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes, they are described in Online Methods "Animals".
10. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	No. We include both male and female mice, and described in Online Methods "Animals".
11. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes, they are described in each figure legend.
12. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	Yes, they are described in Online Methods "Animals".
13. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	Yes, 2-3 adult mice/cage and 6-8 pups/cage, described in Online Methods "Animals".
14. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?	Yes, described in Online Methods "Ultrasonic vocalization analysis".
15. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? Where (section, paragraph #)?	N/A

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

Where (section, paragraph #)?

N/A

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

Where (section, paragraph #)?

N/A

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, described in Online methods "Immunohistochemistry" & "Western blotting".

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

Where does this appear (section, paragraph #)?

The validation data are described in the first paragraph of Results and Supplementary Fig. 1. Other data were from the companies that provided the antibodies.

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 #)?

N/A

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 #)?

N2A and SH-SY5Y cell lines were derived from ATCC. None tested for authentication and mycoplasma contamination.

Data availability

Provide a Data availability statement in the Methods section under "Data availability", which should include, where applicable:

- Accession codes for deposited data
- Other unique identifiers (such as DOIs and hyperlinks for any other datasets)
- At a minimum, a statement confirming that all relevant data are available from the authors
- Formal citations of datasets that are assigned DOIs
- A statement regarding data available in the manuscript as source data
- A statement regarding data available with restrictions

See our data availability and data citations policy page for more information.

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.

Where is the Data Availability statement provided (section, paragraph #)?

We have stated that "The data that support the findings of this study are available from the corresponding authors upon request." in the subsection of Data availability in Online Methods.

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 #)?

   N/A

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 #)?

   N/A

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 #)?

   N/A

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	