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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 #
+ -	1b	Welch two-sample unpaired t test	Fig. legend	4 Nx and 4 Hx Nx= normoxia Hx = hypoxia	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	IGL thickness Nx versus Hx P = 0.21	Fig. legend	t(5.97) = 1.42	Fig. legend
+ -	1b	Welch two-sample unpaired t test	Fig. legend	6 Nx and 5 Hx	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	ML thickness Nx versus Hx P = 8.42e-5	Fig. legend	t(7.46) = 7.69	Fig. legend
+ -	1b	Welch two-sample unpaired t test	Fig. legend	6 Nx and 5 Hx	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	EGL thickness Nx versus Hx 0.00037	Fig. legend	t(6.0) = –7.17	Fig. legend
+ -	1d	Two-way ANOVA Welch heteroscedastic F test followed by unpaired Welch two-sample t tests t	Fig. legend	7, 6, 4 and 4 Nx and 7, 4, 4 and 6 Hx (at P7,11,15 and 30)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Purkinje cell No. treatmnt. 0.045 age 0.71 interact. 0.83 Nx vs Hx P7 0.077 P11 0.28 P15 0.72 P30 0.45	Fig. legend	F(1,34)=4.32 F(3,34)=0.46 F(3,34)=0.30 t(7.9) = 2.03 t(7.89) = 1.16 t(3.80) = 0.540 t(7.83) = 0.79	Fig. legend
+ -	1e	Two-way ANOVA Welch heteroscedastic F test followed by unpaired Welch two-sample t tests	Fig. legend	7, 5, 5 and 4 Nx and 5, 5, 5 and 5 Hx (at P7,11,15 and 30)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Purkinje cell length treat. 2.76e-13 age 8.69e-23 interact. 0.018 Nx vs Hx P7 0.00039 P11 3.76e-6 P15 0.0087 P30 0.41	Fig. legend	F(1,33)=136.89 F(3,33)=251.15 F(3,33)=3.86 t(9.80) = 5.26 t(7.62) = 11.74 t(4.86) = 4.24 t(5.58) = 0.90	Fig. legend
+ -	1g	Two-way ANOVA Welch heteroscedastic F test followed by unpaired Welch two-sample t tests (Holm's sequential Bonferroni correction)	Fig. legend	6, 6, 6 and 10 Nx and 5, 6, 6 and 12 Hx (at P7,11,15 and 30)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	NF200 int. treat. 4.11e-6 age 0.96 interact. 0.98 Nx vs Hx P7 0.015 P11 0.042 P15 0.019 P30 0.0099	Fig. legend	F(1,49)=26.87 F(3,49)=0.10 F(3,49)=0.053 t(8.97) = 3.01 t(7.38) = 2.45 t(7.98) = 2.93 t(18.61) = 2.87	Fig. legend

+ -	1h	Two-way ANOVA Welch heterosceda stic F test followed by unpaired Welch two-sample t tests (Holm's sequential Bonferroni correction)	Fig. legend	5, 6, 9 and 10 Nx and 4, 6, 9 and 9 Hx (at P7,11,15 and 30)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	MBP int. treat. 6.18e-10 age 0.059 interact. 0.40 Nx vs Hx P7 0.014 P11 0.0028 P15 0.0039 P30 0.00058	Fig. legend	F(1,46)=60.58 F(3,46)=2.66 F(3,46)=1.01 t(4.66) = 3.83 t(6.05) = 4.85 t(11.24) = 3.62 t(10.49) = 4.86	Fig. legend
+ -	1j	Welch two-sample unpaired t test	Fig. legend	3 Nx and 3 Hx (P11)	mice	Fig. legend	g ratio mean ± sem Nx 0.81 ± 0.02 Hx 0.91 ± 0.004	Fig. legend	g ratio Nx versus Hx 0.024	Fig. legend	t(5.61) = 2.23	Fig. legend
+ -	2c	Welch two-sample unpaired t test	Fig. legend	5 and 7 (Olig2) 10 and 7 (Ki67) 7 and 6 (CC1) at P7	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Cell counts Nx vs. Hx 0.00074 (OliG2) 9.73e-5 (Ki67) 0.0089 (CC1)	Fig. legend	t(10.0)=4.79 t(13.25)=5.48 t(2.90)=19.75	Fig. legend
+ -	2c	Welch two-sample unpaired t test	Fig. legend	9 and 9 (Olig2) 6 and 8 (Ki67) 8 and 8 (CC1) at P11	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Cell counts Nx vs. Hx 9.27e-5 (OliG2) 4.13e-5 (Ki67) 0.0015 (CC1)	Fig. legend	t(9.42)=6.48 t(10.38)=6.76 t(7.48)=4.85	Fig. legend
+ -	2c	Welch two-sample unpaired t test	Fig. legend	6 and 7 (Olig2) 7 and 8 (Ki67) 10 and 11 (CC1) at P15	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Cell counts Nx vs. Hx 0.012 (OliG2) 2.37e-6 (Ki67) 9.47e-5 (CC1)	Fig. legend	t(6.33)=3.50 t(11.80)=8.46 t(13.77)=5.42	Fig. legend
+ -	2c	Welch two-sample unpaired t test	Fig. legend	14 and 7 (Olig2) 6 and 4 (Ki67) 8 and 5 (CC1) at P30	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Cell counts Nx vs. Hx 3.99e-5 (OliG2) 0.039 (Ki67) 0.00090 (CC1)	Fig. legend	t(9.33)=7.25 t(3.55)=3.17 t(10.35)=4.62	Fig. legend
+ -	2c	Welch two-sample unpaired t test	Fig. legend	3 and 3 (Olig2) 3 and 3 (Ki67) 3 and 3 (CC1) at P60	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Cell counts Nx vs. Hx 0.93 (OliG2) – (Ki67) 0.34 (CC1)	Fig. legend	t(0.10)=2.13 – t(1.11)=3.45	Fig. legend
+ -	3b	Welch two-sample unpaired t test	Fig. legend	5 Nx 4 Hx at P11	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	GAD65-GFP cell counts Nx vs. Hx 0.0056	Fig. legend	t(6.40) = 4.10	Fig. legend
+ -	3b	Welch two-sample unpaired t test	Fig. legend	5 Nx 5 Hx at P15	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	White matter cell counts Nx vs. Hx 0.0021	Fig. legend	t(7.36) = 4.65	Fig. legend
+ -	3d	Welch two-sample unpaired t test	Fig. legend	5 Nx 5 Hx at P11	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Molecular layer cell counts Nx vs. Hx 0.025	Fig. legend	t(4.28) = 3.40	Fig. legend

+ -	3d	Welch two-sample unpaired t test	Fig. legend	6 Nx 5 Hx at P15	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Molecular layer cell counts Nx vs. Hx 0.039	Fig. legend	t(6.11) = 2.62	Fig. legend
+ -	3f	Welch two-sample unpaired t test	Fig. legend	11 Nx 12 Hx at P15	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	White matter Pax2 GFP cell count Nx vs. Hx 0.00020	Fig. legend	t(5.30) = 11.73	Fig. legend
+ -	4b	Fisher's exact test	Fig. legend	13 Nx 9 Hx (P7-8)	mice	Fig. legend	IPSC prevalence (NG2 cells) 20/31 cells Nx 2/29 cells Hx	Fig. legend	2.86e-6	Fig. legend	–	–
+ -	4b	Welch two-sample unpaired t test	Fig. legend	13 Nx 9 Hx (P7-8)	mice	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	IPSC freq. Nx vs. Hx 0.0036	Fig. legend	t(30.01) = 3.16	Fig. legend
+ -	4b	Welch two-sample unpaired t test	Fig. legend	13 Nx 9 Hx (P7-8)	mice	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	IPSC charge Nx vs. Hx 0.00021	Fig. legend	t(34.53) = 4.14	Fig. legend
+ -	4d	Fisher's exact test	Fig. legend	10 Nx 7 Hx (P7-9)	mice	Fig. legend	IPSC prevalence (neurons) 27/31 cells Nx 8/18 cells Hx	Fig. legend	0.0027	Fig. legend	–	–
+ -	4d	Welch two-sample unpaired t test	Fig. legend	10 Nx 7 Hx (P7-9)	mice	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	IPSC freq. Nx vs. Hx 0.0022	Fig. legend	t(44.94) = 3.25	Fig. legend
+ -	4d	Welch two-sample unpaired t test	Fig. legend	10 Nx 7 Hx (P7-9)	mice	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	IPSC charge Nx vs. Hx 0.0042	Fig. legend	t(40.74) = 3.04	Fig. legend
+ -	5a	Welch two-sample paired t test	Fig. legend	11 Nx (P7-8)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	IPSC Freq. Cntrl vs. Carbachol 0.0013	Fig. legend	t(14) = 4.02	Fig. legend
+ -	5a	Welch two-sample paired t test	Fig. legend	6 Hx (P7-8)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	IPSC Freq. Cntrl vs. Carbachol 0.47	Fig. legend	t(13) = 0.75	Fig. legend
+ -	5b	Welch two-sample paired t test	Fig. legend	4 cells from 3 Nx mice (P7-9)	cells	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	Interneuron AP Freq. Cntrl vs. Carbachol 0.0076	Fig. legend	t(3) = –6.44	Fig. legend
+ -	5c	Welch two-sample paired t test	Fig. legend	7 cells from 3 Nx mice (P7-9)	cells	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	Purkinje cell AP Freq. Cntrl vs. Carbachol 0.39	Fig. legend	t(6) = 0.92	Fig. legend
+ -	5d	Welch two-sample paired t test	Fig. legend	6 cells from 3 Nx mice (P7-9)	cells	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	Purkinje cell AP Freq. Cntrl vs. Apamin 0.025	Fig. legend	t(5) = –3.15	Fig. legend

+ -	5e	One-way Repeated measures ANOVA followed by unpaired Welch two-sample t tests (Holm's sequential Bonferroni correction)	Fig. legend	9 cells from 9 Nx mice (P7-8)	cells	Fig. legend	Symbols are mean Error bars are SEM	Fig. legend	Interneuron AP freq. 0.0027 Cntrl vs. Apamin 0.72 vs. Carbachol 0.048	Fig. legend	F(2,24) = 7.67 t(15.2) = 0.37 t(8.0) = 2.8	Fig. legend
+ -	6a	Welch two-sample unpaired t test	Fig. legend	5 and 7 (Bic.) 6 and 6 (Vigab.) 6 and 5 (Tiag.) at P11	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	NG2+/Olig2+ cell counts Drug vs. cntrl. 0.0077 (bic.) 0.014 (vigab.) 0.0032 (tiag.)	Not in text.	t(6.06) = 3.91 t(10.00) = 2.95 t(8.99) = 3.97	Not in text.
+ -	6a	Welch two-sample unpaired t test	Fig. legend	6 and 8 (Bic.) 8 and 4 (Vigab.) 9 and 10 (Tiag.) at P11	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	NG2+/Ki67+ cell counts Drug vs. cntrl. 0.0044 (bic.) 0.0042 (vigab.) 0.0023 (tiag.)	Not in text.	t(5.49) = 4.65 t(7.17) = 4.13 t(9.05) = 4.19	Not in text.
+ -	6a	Welch two-sample unpaired t test	Fig. legend	6 and 6 (Bic.) 5 and 5 (Vigab.) 7 and 8 (Tiag.) at P11	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	CC1+ cell counts Drug vs. cntrl. 0.027 (bic.) 0.0099 (vigab.) 0.0015 (tiag.)	Not in text.	t(7.57) = 2.71 t(6.39) = 3.62 t(12.99) = 4.00	Not in text.
+ -	6b	Welch two-sample unpaired t test	Fig. legend	6 and 6 (P7) 4 and 4 (P11) 4 and 4 (P15)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	NG2+/Olig2+ cell counts wt vs. NKCC1-/- 0.041 (P7) 0.00050 (P11) 0.013 (P15)	Not in text.	t(2.35) = 4.11 t(4.31) = 9.58 t(5.95) = 3.47	Not in text.
+ -	6b	Welch two-sample unpaired t test	Fig. legend	6 and 5 (P7) 3 and 5 (P11) 5 and 5 (P15)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	NG2+/Ki67+ cell counts wt vs. NKCC1-/- 0.047 (P7) 0.049 (P11) 0.034 (P15)	Not in text.	t(7.19) = 2.38 t(5.15) = 2.55 t(4.75) = 2.93	Not in text.
+ -	6b	Welch two-sample unpaired t test	Fig. legend	6 and 4 (P7) 4 and 4 (P11) 5 and 4 (P15)	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	CC1+ cell counts wt vs. NKCC1-/- 0.00016 (P7) 0.0061 (P11) 0.021 (P15)	Not in text.	t(7.06) = 7.19 t(4.00) = 5.29 t(6.70) = 2.98	Not in text.
+ -	6d	Welch two-sample unpaired t test	Fig. legend	4 Nkcc1fx 4Nkcc1fx /fx	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	NG2+/GFP+ cell counts Nkcc1fx vs. Nkcc1fx/fx 0.00021	Not in text.	t(7.96) = 6.00	Not in text.
+ -	6d	Welch two-sample unpaired t test	Fig. legend	4 Nkcc1fx 4Nkcc1fx /fx	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Ki67+/GFP+ cell counts Nkcc1fx vs. Nkcc1fx/fx 0.015	Not in text.	t(3.49) = 5.61	Not in text.

+ -	6d	Welch two-sample unpaired t test	Fig. legend	4 Nkcc1fx 4Nkcc1fx /fx	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	CC1+/GFP+ cell counts Nkcc1fx vs. Nkcc1fx/fx 0.00022	Not in text.	t(8.65) = 5.46	Not in text.
+ -	6d	Welch two-sample unpaired t test	Fig. legend	4 Nkcc1fx 4Nkcc1fx /fx	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	MBP intens. Nkcc1fx vs. Nkcc1fx/fx 0.042	Not in text.	t(2.58) = 5.95	Not in text.
+ -	7a	Two-way ANOVA Welch heterosceda stic F test	Fig. legend	6 Nx ctrl. 6 Nx vig. 6 Hx ctrl. 7 Hx vig.	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Olig2+ cell count cond. 0.00094 drug 6.21e-9 interact. 0.017	Not in text.	F(1,21) = 14.78 F(1,21) = 87.42 F(1,21) = 6.97	Not in text.
+ -	7a	Two-way ANOVA Welch heterosceda stic F test	Fig. legend	10 Nx ctrl. 4 Nx vig. 8 Hx ctrl. 5 Hx vig.	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Ki67+ cell count cond. 8.57e-11 drug 0.78 interact. 2.08e-4	Not in text.	F(1,23) = 125.55 F(1,23) = 0.077 F(1,23) = 19.35	Not in text.
+ -	7a	Two-way ANOVA Welch heterosceda stic F test	Fig. legend	6 Nx ctrl. 6 Nx vig. 6 Hx ctrl. 8 Hx vig.	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	CC1+ cell count cond. 0.0014 drug 0.020 interact. 0.23	Not in text.	F(1,22) = 13.43 F(1,22) = 6.34 F(1,22) = 1.49	Not in text.
+ -	7b	Two-way ANOVA Welch heterosceda stic F test	Fig. legend	4 Nx ctrl. 4 Nx tiag. 7 Hx ctrl. 6 Hx tiag.	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Olig2+ cell count cond. 2.16e-7 drug 0.0035 interact. 0.0021	Not in text.	F(1,17) = 69.07 F(1,17) = 11.44 F(1,17) = 13.18	Not in text.
+ -	7b	Two-way ANOVA Welch heterosceda stic F test	Fig. legend	6 Nx ctrl. 6 Nx tiag. 6 Hx ctrl. 7 Hx tiag.	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Ki67+ cell count cond. 6.00e-4 drug 0.67 interact. 3.80e-5	Not in text.	F(1,21) = 16.26 F(1,21) = 0.18 F(1,21) = 26.97	Not in text.
+ -	7b	Two-way ANOVA Welch heterosceda stic F test	Fig. legend	7 Nx ctrl. 6 Nx tiag. 7 Hx ctrl. 5 Hx tiag.	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	CC1+ cell count cond. 8.83e-7 drug 7.88e-9 interact. 0.75	Not in text.	F(1,21) = 47.08 F(1,21) = 85.00 F(1,21) = 0.11	Not in text.
+ -	7d	Two-way ANOVA Welch heterosceda stic F test	Fig. legend	5 Nx ctrl. 6 Nx tiag. 6 Hx ctrl. 5 Hx tiag.	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	MBP intens. cond. 3.20e-7 drug 3.65e-6 interact. 0.81	Not in text.	F(1,18) = 61.63 F(1,18) = 43.04 F(1,18) = 0.063	Not in text.
+ -	S1	Welch two-sample unpaired t test	Fig. legend	3 P7 3 P11 3 P15 3 P30	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	Cerebellar area Nx vs. Hx 0.21 (P7) 0.0072 (P11) 0.82 (P15) 0.52 (P30)	Not in text.	t(3.27) = 1.56 t(2.73) = 7.32 t(2.67) = 0.26 t(2.16) = 0.68	Not in text.

+ -	S3b	Welch two-sample unpaired t test	Fig. legend	Western 3 Nx 3 Hx at P11	mice	Fig. legend	MBP/NF200 ratio P11 mean ± sem Nx 0.80 ± 0.086 Hx 0.39 ± 0.094	Fig. legend	MBP/NF200 ratio Nx versus Hx 0.032	Fig. legend	t(4.0) = 3.25	Fig. legend
				Western 3 Nx 3 Hx at P11			MMBP/NF200 ratio P30 mean ± sem Nx 1.07 ± 0.22 Hx 0.72 ± 0.16		MBP/NF200 ratio Nx versus Hx 0.29		t(3.7) = 1.23	
	S3d			E.M. 3 Nx 3 Hx at P30			g ratio P30 mean ± sem Nx 0.80 ± 0.007 Hx 0.85 ± 0.005		g ratio Nx versus Hx 0.0084		t(5.1) = 3.77	
+ -	S4b	Welch two-sample unpaired t test	Fig. legend	3 P7 3 P11 3 P15 3 P30	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	CNPase/Actin Nx vs. Hx 0.016 (P7) 0.0097 (P11) 0.0084 (P15) 0.016 (P30)	Fig. legend	t(2.38) = 6.29 t(2.14) = 9.03 t(3.07) = 6.06 t(3.18) = 4.66	Fig. legend
+ -	S4c	Welch two-sample unpaired t test	Fig. legend	3 P7 3 P11 3 P15 3 P30	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	MBP/Actin Nx vs. Hx 0.028 (P7) 0.0004 (P11) 0.0003 (P15) 0.0011 (P30)	Fig. legend	t(2.10) = 5.57 t(2.68) = 22.31 t(3.48) = 14.46 t(3.80) = 8.81	Fig. legend
+ -	S5b	Wilcoxon Mann-Whitney Rank Sum test	Fig. legend	40 cells from 3 Nx mice and 35 cells from 3 Hx mice (P10-11)	cells	Fig, legend	Box-and-whisker plots showing median values, mean values, 25-7th percentiles and 10-90th percentiles	Fig. legend	Nx vs. Hx 3.67e-9 (rate) 1.03e-6 (CV) 0.00021 (CV2)	Fig. legend	Z = 5.50 Z = -4.67 Z = -3.70	Fig. legend
+ -	S6c	Welch two-sample unpaired t test	Fig. legend	6 Nx 6 Hx at P11	mice	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	BrdU+ GAD65 cell count 0.0019 (ML) 0.00030 (IGL) 0.045 (WM)	Fig. legend	t(5.96) = 5.01 t(6.14) = 7.77 t(2.61) = 5.30	Fig. legend
+ -	S7a	Welch two-sample paired t test	Fig. legend	4 cells from 3 Nx mice	cells	Fig. legend	NG2 cell IPSC freq. (Hz) mean ± sem 0.059 ± 0.025 (cntrl.) 0.56 ± 0.012 (sucr.)	Fig. legend	Freq cntrl. vs. sucr. 0.028	Fig. legend	t(3) = 3.97	Fig. legend
+ -	S8b	One-way ANOVA Welch heterosceda stic F test	Fig. legend	5 cntrl. 5 musc. 5 bic.	cultures	Fig. legend	Columns are mean Error bars are SEM	Fig. legend	BrdU+ NG2 cell count F test 0.014 cntrl. vs musc. 0.014 cntrl. vs bic. 0.47	Fig. legend	F(2,5.37) = 10.34 t(7.54) = 3.68 t(4.74) = -0.78	Fig. legend
+ -	Result s para 3	Welch two-sample unpaired t test	Results para 3	3 Nx and 3 Hx (P11)	mice	Results para 3	MBP/NF200 ratio Nx 0.80 ± 0.09 Hx 0.39 ± 0.09	Result s para 3	MBP/NF200 ratio Nx vs. Hx 0.032	Results para 3	t(3.97) = 3.25	Results para 3
+ -	Result s para 3	Welch two-sample unpaired t test	Results para 3	3 Nx and 3 Hx (P30)	mice	Results para 3	MBP/NF200 ratio Nx 1.06 ± 0.22 Hx 0.73 ± 0.16	Result s para 3	MBP/NF200 ratio Nx vs. Hx 0.29	Results para 3	t(1.23) = 3.65	Results para 3
+ -	Result s para 5	Welch two-sample unpaired t test	Results para 5	5 Nx 4 Hx (P11)	mice	Results para 5	PDGFaR+/BrdU+ cell count Nx 13.2 ± 2.1 Hx 37.4 ± 3.6	Result s para 5	Nx vs. Hx. 0.0019	Results para 5	t(5.95) = 4.96	Results para 5

+ -	Results para 10	one sample t test	Results para 10	4 Nx cells	cells	Results para 10	norm. IPSC freq. 0.50 ± 0.12	Results para 10	cntrl. vs. TTX 0.026	Results para 10	t(3) = -4.11	Results para 10
+ -	Results para 11	Welch two-sample unpaired t test	Results para 11	31 cells in 10 Nx mice 18 cells in 7 Hx mice	cells	Results para 11	sIPSC amp. (pA) in neurons 22.9 ± 2.5 (Nx) 18.8 ± 4.2 (Hx)	Results para 11	Nx vs. Hx 0.51	Results para 11	t(5.44) = 0.70	Results para 11
+ -	Results para 11	Welch two-sample unpaired t test	Results para 11	25 cells in 10 Nx mice 4 cells in 3 Hx mice	cells	Results para 11	sIPSC decay (ms) in neurons 52.0 ± 5.5 (Nx) 51.0 ± 13.7 (Hx)	Results para 11	Nx vs. Hx 0.95	Results para 11	t(4.03) = 0.06	Results para 11
+ -	Results para 13	Welch two-sample paired t test	Results para 13	6 cells from 3 Nx mice (P7-9)	cells	Results para 13	IPSC freq. in NG2 cells 0.034 ± 0.045 Hz (cont) 0.053 ± 0.020 Hz (apamin)	Results para 13	IPSC freq. in NG2 cells Cntrl vs. Apamin 0.30	Results para 13	t(5) = −1.16	Results para 13

Representative figures

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

   If so, what figure(s)?

Fig 1 (immuno and EM)
Fig2 (immuno)
Fig 3 (immuno)
Fig 6 (immuno)
Fig 7 (immuno)

Fig S1 (brain sections)
Fig S2 (immuno)
Fig S3 (EM)
Fig S4 (western)
Fig S6 (immuno)
Fig S8 (immuno)
Fig S9 (immuno)
Fig S10 (immuno)

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.
All images are representative of data that was replicated and quantified - this is reported in the respective Figure legends.

Statistics and general methods

1. Is there a justification of the sample size?

   If so, how was it justified?

   Where (section, paragraph #)?

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

No.

Sample sizes are based on the standard used in the field and on previous experience analyzing similar datasets. This is stated in the Methods (paragraph 18 'Data presentation and statistical analysis').

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

   Where (section, paragraph #)?

This is described once, in the Methods (paragraph 18 'Data presentation and statistical analysis').

a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?	Yes Yes
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 - by visual assessment of Q-Q plots and/or density histograms. Testing for normality is not always appropriate. One set of data (Purkinje cell firing; Supplementary Fig. 5b) was tested using non-parametric tests. This is described in Methods (paragraph 18 'Data presentation and statistical analysis').
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 #)?	No. Welch F and t tests were used that do not assume equal variance (stated in Methods paragraph 18 'Data presentation and statistical analysis').
d. Are tests specified as one- or two-sided?	All tests are two-sided. Specified in Methods paragraph 18 ('Data presentation and statistical analysis').
e. Are there adjustments for multiple comparisons?	Yes - Holm's sequential Bonferroni correction (stated in Methods paragraph 18 'Data presentation and statistical analysis').
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	NA
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 #)?	No randomization was used, except in the quantification of purified NG2-cells in cultures (MBF Bioscience StereoInvestigator system). This is stated in Methods paragraph 18 ('Data presentation and statistical analysis').
5. Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included? If no blinding was done, state so. Where (section, paragraph #)?	Yes (stated in Methods paragraph 18 'Data presentation and statistical analysis').
6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes Methods, para 1, 'Mice'.
7. Is the species of the animals used reported? Where (section, paragraph #)?	Yes Introduction, para 3 and Methods, para 1.
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes Methods, para 1.

9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Yes - both male and female mice were used. Methods, para 1.
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes Throughout text and in all Figure legends.
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	No
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	NA
13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?	NA
14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? Where (section, paragraph #)?	NA
a. If multiple behavioral tests were conducted in the same group of animals, is this reported? Where (section, paragraph #)?	NA
15. If any animals/subjects were excluded from analysis, is this reported? Where (section, paragraph #)?	Yes This is stated in Methods paragraph 17 ('Drug injections')
a. How were the criteria for exclusion defined? Where is this described (section, paragraph #)?	Two mice were excluded following bicuculline-induced seizures - stated in Methods paragraph 17 ('Drug injections').
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 #)?	NA

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 #)?	Catalog numbers are given of commercial sources. Sources of non-commercial antibodies are clearly stated (Methods paragraphs 4 and 8).

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

Where does this appear (section, paragraph #)?

Validation data reported in publications, Antibodypedia, CiteAb or by commercial suppliers; this is stated in Methods paragraphs 8.

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

Where (section, paragraph #)?

NA

a. Were they recently authenticated?

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

NA

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 #)?

NA

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.

NA

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.

NA

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