nature neuroscience

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Manuscript Number: NN-A49958A

Manuscript Type: Article

Main Figures: 6

Supplementary Figures: 9

Supplementary Tables: 1

Supplementary Videos: -

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 #
+ -	1c	Wilcoxon-rank sum and signed rank tests	Fig. legend	Fibroblasts: 11 (major), 6 (minor), iN: 20 (major), 10 (minor)	3 independent reprogramming in at least duplicate	Figure and Figure legend	error bars are mean +/- SEM	Methods	WFibroblasts= nsp > 0.1802; WiN = *p < 0.0157	Fig. legend	WFibroblasts= 19, r = -0.33; WiN= 65, *p = 0.0157, r = -0.40	Fig. legend
+ -	1e	Welch two sample t-test and ANOVA, with shown post-hoc Analysis after BH	Fig. legend	Psi (10/10), Ezh2 (7/8), Cplx1 (9/9), Cplx1 delta (4/4), Nsf (7/7), Nsf delta (3/3), Syn3 s1 (10/10), Syn3 s1 delta (4/3), Syn3 s2 (12/12), Syn3 s2 delta (7/7), Syt1 (15/15), Syt1 delta (16/16), Hcrt (8/8), Hcrt delta (7/7), Syt7 (8/8), Syt7 delta (8/8), Stx17 (9/9), Stx17 delta (5/5)	number of experiments, each in triplicate	Figure and Figure legend	error bars are mean +/- SEM	Methods	Anova psiCheck2: p-value = 0.8969 Ezh2: p-value = 3.749e-11, Cplx1: p-value: 0.0004483, Nsf: p-value: < 2.2e-16, Syn3 s1: p-value: 2.156e-08, Syn3 s2: p-value: 4.21e-05, Syt1: p-value: < 2.2e-16, Hcrt: p-value: 1.512e-07, Syt7: p-value: 8.172e-15, Stx17: p-value: 0.02072	Fig. legend	tpsiCheck2(52.511) = 0.40, nsp = 0.6932, r = 0.06; tEzh2(40.7) = -8.94, ***p < 0.001, r = 0.81; FCplx1(3, 74) = 6.73, ***p < 0.001; FNsf(3, 54) = 97.32, ***p < 0.001; FSyn3-1(3, 75) = 16.67, ***p < 0.001; FSyn3-2(3, 108) = 8.47, ***p < 0.001; FSyt1(3, 181) = 67.12, ***p < 0.001, FHcrt(3, 85) = 14.12, ***p < 0.001, FSyt7(3, 74) = 37.38, ***p < 0.001, FStx17(3, 80) = 3.44, *p = 0.0207	Fig. legend

+ -	1f	Welch two sample t-test and Wilcoxon-rank sum and signed rank tests	Fig. legend	Cplx1 (5/4), Nsf (6/6), Syn3 (5/7), Syt1 (3/3), Hcrt (6/7), Syt7 (5/7), Stx17 (3/4)	number of experiments	Figure and Figure legend	error bars are mean +/- SEM	Methods	Cplx1: p-value = 0.008993, Nsf: p-value = 0.002165, Syn3: p-value = 0.007023, Syt1: p-value = 0.05347, Hcrt: p-value = 0.4452, Syt7: p-value = 0.3481, Stx17: p-value = 0.6337,	Fig. legend	tCplx1(6.98) = -3.58, **p = 0.0090, r = 0.81; WNsf= 0, **p = 0.0022, r = -0.89; tSyn3(9.71) = -3.40, **p = 0.007, r = 0.74; tSyt1(3.21) = -2.99, nsp = 0.0535, r = 0.86; WHcrt= 15, nsp = 0.4452, r = -0.21; tSyt7(6.06) = -1.02, nsp = 0.3481, r = 0.38; tStx17(4.31) = 0.51, nsp = 0.6337, r = 0.24	Fig. legend
+ -	1g	Welch two sample t-test and Wilcoxon-rank sum and signed rank tests	Fig. legend	Cplx1 (6/6), Nsf (6/4), Syn3 (5/6), Syt1 (4/4), Hcrt (6/6), Syt7 (5/6), Stx17 (6/6),	number of experiments	Figure and Figure legend	error bars are mean +/- SEM	Methods	Cplx1: p-value = 0.0001546, Nsf: p-value = 0.03453, Syn3 = p-value = 0.0001549, Syt1 = p-value = 0.02857, Hcrt: p-value = 0.01031, Syt7: p-value = 0.3962, Stx17: p-value = 0.03316	Fig. legend	tCplx1(9.10) = -6.18, ***p < 0.001, r = 0.90; tNsf(4.43) = -3.01, *p = 0.3453, r = 0.82; tSyn3(8.99) = -6.23, ***p < 0.001, r = 0.90; WSyt1 = 0, *p = 0.0286, r = -0.77, tHcrt(10) = -3.15, *p = 0.0103, r = -0.71; tSyt7(6.27) = 0.91, nsp = 0.3962, r = 0.34 tStx17(9.96) = -2.47, *p = 0.033, r = 0.62	Fig. legend
+ -	1h	Welch two sample t-test	Fig. legend	Cplx1 (5/3), Nsf (12/8), Syn3 (10/7), Syt1 (10/8), Pclc (16/12), Stx8 (16/12), Synj1 (16/12)	number of samples from at least three reprogramming	Figure and Figure legend	error bars are mean +/- SEM	Methods	Cplx1: p-value = 0.043, Nsf: p-value = 0.01069, Syn3: p-value = 0.01181, Syt1: p-value = 0.004158, Pclo: p-value = 0.3034, Stx8: p-value = 0.7013, Synj1: p-value =0.2398	Fig. legend	tCPLX1 (5.97) = 2.56, *p = 0.043, r = 0.72; tNSF (17.89) = 2.85, *p = 0.0107, r = 0.56; tSYN3 (11.29) = 3.00, *p = 0.0118, r = 0.67; tSYT1 (13.40) = 3.45, **p = 0.004, r = 0.69; tPCLO (22.95) = 1.05, nsp = 0.3034, r = 0.22, tSTX8 (20.36) = -0.49, nsp = 0.7013, r = 0.22, tSYNJ1 (18.94) = -1.21, nsp = 0.2398, r = 0.27.	Fig. legend
+ -	1i	Kruskal-Wallis rank sum test	Fig. legend	Major allele (37), minor allele (28)	number of analyzed cells, usually one cell per coverslip from two reprogramming from each fibroblast line	Figure and Figure legend	error bars are mean +/- SEM	Methods	p-value = 6.56e-10	Fig. legend	H(1) = 38.15, ***p <0.001	Fig. legend

+ -	2d	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (5), miR-137 (12), naive (9)	number of dissected dorsal DG regions from at least three animals	Figure and Figure legend	error bars are mean +/- SEM	Methods	tΔmiR-137OE-miR-137OE (2.53), *p = 0.028, tmiR-137OE-naive (-2.72), *p = 0.028, tΔmiR-137OE-naive (0.26), nsp = 0.796	Fig. legend	H(2) = 7.68, *p = 0.0215	Fig. legend
+ -	2e	Welch two sample t-test	Fig. legend	Cplx1 (4/5), Nsf (6/5), Syn3 (9/5), Syt1 (6/6)	number of dissected dorsal DG/CA3 regions from at least three animals	Figure and Figure legend	error bars are mean +/- SEM	Methods	Cplx1: p-value = 0.0009697, Nsf: p-value = 0.01234, Syn3:p-value = 0.01351, Syt1: p-value = 0.04182	Fig. legend	tCplx1(5.43) = -6.46, ***p < 0.01, r = 0.94; tNsf(6.47) = -3.43, *p = 0.0123, r = 0.80; tSyn3(9.89) = -3.00, *p = 0.0135, r = 0.69; tSyt1(7.21) = -2.47, *p = 0.0418, r = 0.68	Fig. legend
+ -	3b	Pillai's trace in the multivariate test statistic	Fig. legend	miR-137 delta (84), miR-137 (112)	number of analyzed synapses of at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value: 4.821e-08	Fig. legend	V=0.26, F(11, 184) = 5.81, ***p < 0.001, FDocked(1, 194)=2.91, nsp = 0.0892; F50nm(1, 194)=6.83, *p 0.0097; F100nm(1, 194)=37.7, ***p < 0.001; F150nm(1, 194)=32.5, ***p < 0.001; F200nm(1, 194)=12.4, ***p < 0.001; F250nm(1, 194)=0.87, nsp = 0.3517; F300nm(1, 194)=1.57, nsp 0.211; F350nm(1, 194)=4.00, *p 0.0471; F400nm(1, 194)=27.3, ***p < 0.001; F450nm(1, 194)=7.46, **p = 0.0069	Fig. legend
+ -	3d	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (6), miR-137 (5)	number of analyzed hippocampal slices from at least 3 animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 2.279e-16	Fig. legend	H(1) = 67.34, ***p < 0.001	Fig. legend
+ -	4a	ANOVA Wilcox ranksum test	Fig. legend	miR-137 delta (9), miR-137 (9)	number of analyzed hippocampal slices from at least 3 animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value Anova: <2e-16, p-value (50-60min) = 3.453e-09	Fig. legend	F(1, 1060) = 144.6, ***p < 0.001, W = 7283, ***p < 0.001, r = -0.42	Fig. legend
+ -	4b	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (12), miR-137 (14)	number of analyzed hippocampal slices from at least 3 animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.8774	Fig. legend	nsp = 0.8774	Fig. legend

+ -	4c	Welch two sample t-test	Fig. legend	miR-137 delta (13), miR-137 (13)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	Context: p-value = 0.001135.	Fig. legend	t(17.76) = 3.87, **p = 0.0011, r = 0.68	Fig. legend
+ -	4d	Welch two sample t-test	Fig. legend	miR-137 delta (13), miR-137 (13)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	Cue: p-value = 0.07091	Fig. legend	t (22) = 1.90, nsp = 0.0709	Fig. legend
+ -	4e	ANOVA, post-hoc: Wilcoxon-rank sum and signed rank tests	Fig. legend	miR-137 delta (8), miR-137 (9)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	0.000245	Fig. legend	F(1, 117) = 14.32, ***p < 0.001, posthoc: WDay1= 30, nsp = 0.5535, r = -0.14; WDay2= 28.5, nsp = 0.495, r = -0.16; WDay3= 29, nsp = 0.5309, r = -0.15; WDay4= 17.5, nsp = 0.0831, r = -0.41; WDay5= 14, *p = 0.0380, r = -0.50; WDay6= 16.5, nsp = 0.0673, r = -0.43; WDay7= 7, **p = 0.061, r = -0.65	Fig. legend
+ -	4f	Welch two sample t-test	Fig. legend	miR-137 delta (8), miR-137 (9)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	0.5224	Fig. legend	t(13.51) = -0.66, nsp = 0.5224, r = 0.18	Fig. legend
+ -	4g	ANOVA	Fig. legend	miR-137 delta (8), miR-137 (9)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	0.000107, 0.0438	Fig. legend	F(3, 28) = 10.16, ***p < 0.001; F(7, 60) = 7.24, *p = 0.0438	Fig. legend
+ -	5a	Welch two sample t-test	Fig. legend	Cplx1 (6/5), Nsf (6/5), Syn3 (6/6), Syt1 (6/4)	number of experiments	Figure and Fig. legend	error bars are mean +/- SEM	Methods	tCplx1(8.80) = 3.02, *p = 0.0149, r = 0.71; tNsf(2.46) = 9.00, *p = 0.036, r = 0.64; tSyn3(7.70) = -3.24, *p = 0.0125, r = 0.76; tSyt1(7.96) = 3.00 *p = 0.0173	Fig. legend	tCplx1(8.80) = 3.02, *p = 0.0149, r = 0.71; tNsf(2.46) = 9.00, *p = 0.036, r = 0.64; tSyn3(7.70) = -3.24, *p = 0.0125, r = 0.76; tSyt1(7.96) = 3.00 *p = 0.0173	Fig. legend

+ -	5b	Welch two sample t-test and Wilcoxon-rank sum and signed rank tests	Fig. legend	Cplx1 (17/9), Nsf (21/8), Syn3 (18/7), Syt1 (24/11), Pclo (16/5), Stx8 (17/4), Synj1 (16/5)	number of transduced minor allele SNP fibroblast lines with either construct from three reprogramming	Figure and Fig. legend	error bars are mean +/- SEM	Methods	WCPLX1 = 27, **p = 0.0064, r = -0.53; WNSF = 13, ***p < 0.001, r = -0.70; WSYN3 = 117, ***p < 0.001, r = -0.71; WSYT1 = 66.5 *p = 0.0209, r = -0.39; tPCLO(4.82) = 0.52 nsp = 0.6282, r = 0.23; tSTX8(5.63) = 1.54 nsp = 0.1782, r = 0.54; tSYNJ1(5.56) = 1.06 nsp = 0.3338, r = 0.41	Fig. legend	WCPLX1 = 27, **p = 0.0064, r = -0.53; WNSF = 13, ***p < 0.001, r = -0.70; WSYN3 = 117, ***p < 0.001, r = -0.71; WSYT1 = 66.5 *p = 0.0209, r = -0.39; tPCLO(4.82) = 0.52 nsp = 0.6282, r = 0.23; tSTX8(5.63) = 1.54 nsp = 0.1782, r = 0.54; tSYNJ1(5.56) = 1.06 nsp = 0.3338, r = 0.41	Fig. legend
+ -	5c	Kruskal-Wallis rank sum test	Fig. legend	Sponge control (11), Sponge (18)	number of analyzed transduced induced neurons of the two minor allele fibroblast lines from three reprogramming	Fig. legend	error bars are mean +/- SEM	Methods	p-value < 2.2e-16	Fig. legend	H(1) = 152.06, ***p <0.001	Fig. legend
+ -	5d	Welch two sample t-test	Fig. legend	Cplx1 (13/11), Nsf (17/18), Syn3 (13/14), Syt1 (16/19)	number of dissected dorsal DG/CA3 regions from at least three animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	tCplx1(21.97) = -2.69, *p = 0.0140, r = 0.5; tNsf(29.0) = -2.36, *p = 0.0251, r = 0.40; tSyn3(16.11) = 3.43, **p 0.0034, r = 0.65; tSyt1(21.41) = -2.17, *p 0.0415, r = 0.42	Fig. legend	tCplx1(21.97) = -2.69, *p = 0.0140, r = 0.5; tNsf(29.0) = -2.36, *p = 0.0251, r = 0.40; tSyn3(16.11) = 3.43, **p 0.0034, r = 0.65; tSyt1(21.41) = -2.17, *p 0.0415, r = 0.42	Fig. legend

+ -	5f	Pillai's trace in the multivariate test statistic	Fig. legend	Sponge control (50), Sponge (43)	number of analyzed synapses of at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	V=0.25, F(11, 91) = 2.40, *p = 0.0125, posthoc analysis: FDocked(1, 91)=4.01, *p = 0.0483; F50nm(1, 91)=4.13, *p = 0.045; F100nm(1, 91)=1.68, nsp = 0.1977; F150nm(1, 91)=3.04, nsp = 0.0845; F200nm(1, 91)=2.18, nsp = 0.1429; F250nm(1, 91)=0.09, nsp = 0.7687; F300nm(1, 91)=0.29, nsp = 0.5886; F350nm(1, 91)=3.22, nsp = 0.0759; F400nm(1, 91)=0.55, nsp = 0.4619; F450nm(1, 91)=1.53, nsp = 0.2188	Fig. legend	V=0.25, F(11, 91) = 2.40, *p = 0.0125, posthoc analysis: FDocked(1, 91)=4.01, *p = 0.0483; F50nm(1, 91)=4.13, *p = 0.045; F100nm(1, 91)=1.68, nsp = 0.1977; F150nm(1, 91)=3.04, nsp = 0.0845; F200nm(1, 91)=2.18, nsp = 0.1429; F250nm(1, 91)=0.09, nsp = 0.7687; F300nm(1, 91)=0.29, nsp = 0.5886; F350nm(1, 91)=3.22, nsp = 0.0759; F400nm(1, 91)=0.55, nsp = 0.4619; F450nm(1, 91)=1.53, nsp = 0.2188	Fig. legend
+ -	5g	Anova	Fig. legend	Sponge control (5), Sponge (6)	number of analyzed hippocampal slices from at least three animals	Fig. and Fig. legend	error bars are mean +/- SEM	Methods	<2e-16 ***	Fig. legend	F(1, 305) = 77.73, ***p < 0.001	Fig. legend
+ -	5h	Kruskal-Wallis rank sum test, Wilcoxon-rank sum and signed rank tests	Fig. legend	Sponge control (5), Sponge (5)	number of analyzed hippocampal slices from at least three animals	Fig. and Fig. legend	error bars are mean +/- SEM	Methods	p-value < 2.2e-16, p-value = 2.552e-12	Fig. legend	H(1) = 125.92, ***p < 0.001; W = 341, ***p < 0.001	Fig. legend
+ -	5i	Welch two sample t-test	Fig. legend	Sponge control (10), Sponge (9)	number of animals	Fig. and Fig. legend	error bars are mean +/- SEM	Methods	p = 0.1707	Fig. legend	t(17.0) = -1.43, nsp = 0.1707	Fig. legend
+ -	5j	Welch two sample t-test	Fig. legend	Sponge control (10), Sponge (9)	number of animals	Fig. and Fig. legend	error bars are mean +/- SEM	Methods	p = 0.873	Fig. legend	t(16.21) = 0.16, nsp = 0.873	Fig. legend
+ -	6c	Pillai's trace in the multivariate test statistic	Fig. legend	miR-137 delta (46), miR-137 (47), miR-137-Syt1 (70), miR-137-delta-Syt1 (58)	number of analyzed synapses of at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	< 2.2e-16, < 2.2e-16, < 2.2e-16	Fig. legend	Vgrey-red=0.72, F(11, 97) = 22.9, ***p < 0.001, Vgrey-green=0.66, F(11, 100) = 17.7, ***p < 0.001, Vgrey-purple=0.57, F(11, 102) = 12.3, ***p < 0.001.	Fig. legend

+ -	6d	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (5), miR-137 (7), miR-137-Syt1 (4), miR-137-delta-Syt1 (4)	number of hippocampal slice preparation from at least 3 animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value < 2.2e-16	Fig. legend	H(3) = 217.81 ***p < 0.001	Fig. legend
+ -	6e	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (5), miR-137 (8), miR-137-Syt1 (8), miR-137-delta-Syt1 (6)	n: number of analyzed hippocampal slices of at least 3 animals	Fig. and Fig. legend	error bars are mean +/- SEM	Methods	p-value < 2.2e-16	Fig. legend	H(3) = 106.41, ***p < 0.001	Fig. legend
+ -	6f	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (15), miR-137 (15), miR-137-Syt1 (15), miR-137-delta-Syt1 (15)	number of analyzed hippocampal slices from at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.2776	Fig. legend	H(3) = 3.85, nsp = 0.2776	Fig. legend
+ -	6g	Anova	Fig. legend	miR-137 delta (8), miR-137 (10), miR-137-Syt1 (11), miR-137-delta-Syt1 (9)	number of animals	Fig. and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.00887, posthoc analysis: tmiR-137-miR137-Syt1(3.57), **p = 0.0060; tΔmiR-137-miR137 (-2.28), nsp = 0.1236, tΔmiR-137-miR137-Syt1(1.03), nsp = 0.7317, tΔmiR-137-ΔmiR137-Syt1(-0.93), nsp = 0.789, tmiR-137-ΔmiR137-Syt1 (1.37), nsp = 0.5278, tmiR-137-Syt1-ΔmiR137-Syt1 (-2.07), nsp = 0.1825	Fig. legend	F(3, 34) = 4.53, **p = 0.0089, posthoc analysis: tmiR-137-miR137-Syt1(3.57), **p = 0.0060; tΔmiR-137-miR137 (-2.28), nsp = 0.1236, tΔmiR-137-miR137-Syt1(1.03), nsp = 0.7317, tΔmiR-137-ΔmiR137-Syt1(-0.93), nsp = 0.789, tmiR-137-ΔmiR137-Syt1 (1.37), nsp = 0.5278, tmiR-137-Syt1-ΔmiR137-Syt1 (-2.07), nsp = 0.1825	Fig. legend

+ -	S1a	Anova	Fig. legend	3	number of experiments	Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.000124; tpGL3-rs2660304 = 0.000692; trs2660304-rs2802535 = 0.000511; trs2660304-rs1625579 = 0.000540; tpGL3-rs2660304 = 0.478149	Fig. legend	F(4) = 7.87, ***p < 0.001, posthoc analysis: tpGL3-rs2660304 (4.482), ***p < 0.001, r = 0.91; trs2660304-rs2802535 (-4.57), ***p < 0.001, r = 0.92; trs2660304-rs1625579 (-4.57), ***p < 0.001, r = 0.92; tpGL3-rs2660304 (1.65), nsp = 0.4781, r = 0.64	Fig. legend
+ -	S1d	Welch two sample t-test	Fig. legend	mir-9 (9/6), mir-19b (9/7), mir-124 (12/10)	number of samples from at least three reprogramming	Figure and Fig. legend	error bars are mean +/- SEM	Methods	tmiR-9(7.87) = -0.2, nsp = 0.8475, r = 0.07, tmiR-19b(8.28)=0.12, nsp = 0.9047, r = 0.04, tmiR-124(13.89) = -0.16, nsp > 0.8773, r = 0.04	Fig. legend	tmiR-9(7.87) = -0.2, nsp = 0.8475, r = 0.07, tmiR-19b(8.28)= 0.12, nsp = 0.9047, r = 0.04, tmiR-124(13.89) = -0.16, nsp > 0.8773, r = 0.04	Fig. legend

+ -	S2b	Welch two sample t-test and Wilcoxon-rank sum and signed rank tests	Fig. legend	Calb1 (5/5), CamK2 (5/5), Nrxn1 (7/7), Nrxn1 delta (7/7), Stx8 (7/7), Stx8 delta (3/3), Stxbp5 (6/6), Sv2a(3/3), Sv2a (2/2), Syn2a (7/7), Syn2b (6/6), Syn2b delta (7/7), Synj1 (7/7), Synj1 delta (3/3), Synpr (7/7), Syt9 (6/6), Vamp1 (6/6), Vamp2 (12/12), Vamp2 delta (3/3), Vamp7 (6/6)	number of experiments, each in triplicates	Figure and Fig. legend	error bars are mean +/- SEM	Methods	WCalb1= 170, *p = 0.0180, r = -0.43; tCamK2(14.58) = -0.14, nsp = 0.8888, r = 0.04; FNrxn1(3, 80) = 13.89, ***p < 0.001; FStx8(3, 56) = 0.60, nsp = 0.6159; WStxbp5= 187, nsp = 0.4381, r = -0.13; FSv2a(3, 20) = 0.05, nsp = 0.9831; WSyn2a= 201, nsp = 0.6326, r = -0.07; FSyn2b(3, 74) = 0.72, nsp = 0.545; FSynj1(3, 56) = 1.30, nsp = 0.2845; WSynpr= 278, nsp = 0.1515, r = -0.22; WSyt9= 121, nsp = 0.2983, r = -0.18; WVamp1= 119, nsp = 0.1786 r = -0.22; FVamp2(3, 81) = 3.92, *p = 0.0115; WVamp7= 172, nsp = 0.7637, r = -0.05	Fig. legend	WCalb1= 170, *p = 0.0180, r = -0.43; tCamK2(14.58) = -0.14, nsp = 0.8888, r = 0.04; FNrxn1(3, 80) = 13.89, ***p < 0.001; FStx8(3, 56) = 0.60, nsp = 0.6159; WStxbp5= 187, nsp = 0.4381, r = -0.13; FSv2a(3, 20) = 0.05, nsp = 0.9831; WSyn2a= 201, nsp = 0.6326, r = -0.07; FSyn2b(3, 74) = 0.72, nsp = 0.545; FSynj1(3, 56) = 1.30, nsp = 0.2845; WSynpr= 278, nsp = 0.1515, r = -0.22; WSyt9= 121, nsp = 0.2983, r = -0.18; WVamp1= 119, nsp = 0.1786 r = -0.22; FVamp2(3, 81) = 3.92, *p = 0.0115; WVamp7= 172, nsp = 0.7637, r = -0.05	Fig. legend
+ -	S3a	independent t-test	Fig. legend	miR-137 delta (3), miR-137 (3)	number of experiments	Figure and Fig. legend	error bars are mean +/- SEM	Methods	0.0004961368	Fig. legend	Ty(2) = 44.89, ***p < 0.001, r = 1	Fig. legend
+ -	S3b	independent t-test	Fig. legend	miR-137 delta (3), miR-137 (3)	number of experiments	Figure and Fig. legend	error bars are mean +/- SEM	Methods	0.01119	Fig. legend	Ty(3.97) = 4.48, *p = 0.0112, r = 0.91	Fig. legend
+ -	S4b	Wilcoxon-rank sum and signed rank tests	Fig. legend	miR-137 delta (84), miR-137 (112)	number of analyzed synapses of at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.2973	Fig. legend	W = 4294, nsp = 0.2973, r = -0.07	Fig. legend

+ -	S5a	Welch two sample t-test	Fig. legend	miR-137 delta (8), miR-137 (8)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	Margin distance: p-value = 0.5547; Margin time: p-value = 0.083; Center distance: p-value = 0.02307; Center time: p-value = 0.083; Total distance: p-value = 0.2117; Horizontal activity: p-value = 0.06852; Vertical activity: p-value = 0.1962; Stereotype: p-value = 0.05167	Fig. legend	Margin distance: t(12.94) = -0.61, nsp = 0.5547, r = 0.17; Margin time: t(12.20) = -1.89, nsp = 0.083, r = 0.48; Center distance: t(13.83) = 2.55,*p = 0.023, r = 0.57; Center time: t(12.20) = 1.89, nsp = 0.083, r = 0.48; Total distance: t(12.89) = 1.31, nsp = 0.2117, r = 0.34; Horizontal activity: t(13.52) = 1.98, nsp = 0.0685, r = 0.47; Vertical activity: t(13.15) = 1.36, nsp = 0.1952, r = 0.35; Stereotype: t(13.87) = 2.13, nsp = 0.05167, r = 0.50	Fig. legend
+ -	S5b	Welch two sample t-test	Fig. legend	miR-137 delta (8), miR-137 (8)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.3709, p-value = 0.5585	Fig. legend	Frequency of exploration: t(9.90) = 0.94, nsp = 0.3709, r = 0.29; time spend in light: t(11.88) = 0.60, nsp = 0.5585	Fig. legend
+ -	S5c	Anova, Welch two sample t-test	Fig. legend	miR-137 delta (7), miR-137 (8)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	F(1, 26) = 2.09, nsp = 0.161, F(1, 26) = 0.40, nsp = 0.535. Distance and velocity did not differ for the conditions, tdistance(12.98) = 0.36, nsp = 0.7259, r = 0.10, tvelocity(12.97) = 0.35, nsp = 0.7298	Fig. legend	F(1, 26) = 2.09, nsp = 0.161, F(1, 26) = 0.40, nsp = 0.535. Distance and velocity did not differ for the conditions, tdistance(12.98) = 0.36, nsp = 0.7259, r = 0.10, tvelocity(12.97) = 0.35, nsp = 0.7298	Fig. legend
+ -	S5d	Wilcoxon-rank sum and signed rank tests	Fig. legend	miR-137 delta (6), miR-137 (6)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	W= 20.5, nsp = 0.7471, r= -0.09	Fig. legend	W= 20.5, nsp = 0.7471, r= -0.09	Fig. legend
+ -	S5e	Welch two sample t-test	Fig. legend	miR-137 delta (13), miR-137 (12)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.2381	Fig. legend	t(41.97) = -1.20, nsp = 0.2381, r = 0.18	Fig. legend
+ -	S5f	Welch two sample t-test	Fig. legend	miR-137 delta (8), miR-137 (9)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value Time = 0.4165, p-value Path = 0.8838	Fig. legend	tTime(24.07) = -0.83, nsp = 0.4165, r= 0.17; tPath(25.57) = -0.15, nsp = 0.8838, r= 0.03	Fig. legend

+ -	S5g	Anova	Fig. legend	miR-137 delta (10), miR-137 (10)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	3.23e-06, 6.83e-09, 0.10, 0.0673	Fig. legend	new versus a familiar mouse (left panel, F(2, 24) = 22.41, ***p < 0.001), and a mouse versus an object (right panel, F(2, 24) = 45.5, ***p < 0.001); Ffamiliar mouse (2, 48) = 2.41, nsp = 0.10 and Fempty cage (2, 48) = 2.86, nsp = 0.0673	Fig. legend
+ -	S6b	Welch two sample t-test	Fig. legend	Sponge control (50), Sponge (43)	number of analyzed hippocampal slices from at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	0.07513	Fig. legend	t(88.82) = -1.80, nsp = 0.0751, r = -0.19	Fig. legend
+ -	S6c	Anova	Fig. legend	Sponge control (4), Sponge (4)	number of analyzed hippocampal slices from at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value =0.229	Fig. legend	F(1, 129) = 1.46, nsp = 0.229	Fig. legend
+ -	S6d	Welch two sample t-test	Fig. legend	Sponge control (10), Sponge (9)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	Total distance: p-value = 0.4809; Time moving: p-value = 0.3285; Moves/ Counts: p-value = 0.389; Distance periphery: p-value = 0.8617; Time periphery: p-value = 0.01826; Distance center: p-value = 0.01512; Time center: p-value = 0.01822	Fig. legend	Total distance: t(16.5) = -0.72, nsp = 0.4809, r = 0.18; Time moving: t(16.33) = -1.01, nsp = 0.3285, r = 0.24; Moves/Counts: t(17.51) = -0.88, nsp = 0.389, r = 0.21; Distance periphery: t(16.37) = -0.18, nsp = 0.8617, r = 0.04; Time periphery: t(16.19) = 2.62, *p = 0.0182, r = 0.55; Distance center: t(12.89) = -2.80, *p = 0.0151, r = 0.62; Time center: t(16.21) = -2.63, *p = 0.0182, r = 0.55	Fig. legend
+ -	S6e	Welch two sample t-test	Fig. legend	Sponge control (10), Sponge (10)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.7664	Fig. legend	t(13.47)= 0.30, nsp = 0.7664, r= 0.08	Fig. legend
+ -	S6f	Welch two sample t-test	Fig. legend	Sponge control (10), Sponge (9)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 1	Fig. legend	t(17.12)= 0, nsp = 1, r= 0	Fig. legend
+ -	S7e	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (56), miR-137 (53), miR-137-Syt1 (56), miR-137-delta-Syt1 (58)	number of analyzed synapses of at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value < 2.2e-16	Fig. legend	H(3) = 77.75, ***p < 0.001	Fig. legend

+ -	S7f	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (8), miR-137 (10), miR-137-Syt1 (11), miR-137-delta-Syt1 (9)	number of animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.1068	Fig. legend	H(3) = 6.10, nsp = 0.1068	Fig. legend
+ -	S8a	Kruskal-Wallis rank sum test, Wilcoxon-rank sum and signed rank tests	Fig. legend	Syt1 KD control (5), Syt KD (5)	number of analyzed hippocampal slices from at least three animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = <2.2e-16 p-value = 2.9e-12	Fig. legend	H(1) = 129,44 ***p < 0.001, W = 2681, ***p < 0.001, r = -0.39	Fig. legend
+ -	S8b	Kruskal-Wallis rank sum test	Fig. legend	Syt1 KD control (5), Syt KD (5)	number of analyzed hippocampal slices from at least three animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.01004	Fig. legend	H(1) = 6.63, *p = 0.0100	Fig. legend
+ -	S8c	Kruskal-Wallis rank sum test	Fig. legend	Syt1 KD control (5), Syt KD (5)	number of analyzed hippocampal slices from at least three animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	p-value = 6.041e-12	Fig. legend	H(1) = 47.32, ***p < 0.001	Fig. legend
+ -	S8d	Welch two sample t-test	Fig. legend	miR-137 delta (4), miR-137 (4)	number of animals	Fig. legend	error bars are mean +/- SEM	Methods	p-value = 0.02636	Fig. legend	t(4.77)=-3.18, *p = 0.0264	Fig. legend
+ -	S8e	Kruskal-Wallis rank sum test, Wilcoxon-rank sum and signed rank tests	Fig. legend	miR-137 delta (5), miR-137 (5)	number of analyzed hippocampal slices from at least three animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	H(1) = 3.19, nsp = 0.0741, W = 1528, nsp = 0.9285, r = -0.01	Fig. legend	H(1) = 3.19, nsp = 0.0741, W = 1528, nsp = 0.9285, r = -0.01	Fig. legend
+ -	S8f	Kruskal-Wallis rank sum test	Fig. legend	miR-137 delta (12), miR-137 (14)	number of analyzed hippocampal slices from at least three animals	Figure and Fig. legend	error bars are mean +/- SEM	Methods	F(1,66) = 0.91, nsp = 0.4543	Fig. legend	F(1,66) = 0.91, nsp = 0.4543	Fig. legend

Representative figures

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

   If so, what figure(s)?

   Figure 2c, 2e, 3a, 5d, 5e, 6b
   Supplementary Figure 1c, 2c, 3c-d, 4a, 6a, 7b-d, 8d

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 #)?

   See 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.	Method section, Statistical methods: Sample size. For biochemical (immunohistochemistry, western blotting) and molecular (quantitative PCR, luciferase) the minimum number of biological replicates needed for non-parametric statistical analysis is three animals per condition, per experiment. To improve our statistical power and ensure that our hypotheses are rigorously tested, we try to include 4 to 5 biological replicates in each experiment, and to replicate each experiment at least once, when possible. Behavior and in vivo experiments have a higher variability inherent to behavioral experiments. It is customary to include in > 8 animals to achieve appropriate statistical power. For behavior, these experiments are typically repeated at least once with a separate cohort of animals. The number of animals used for survival surgery is dictated by the subsequent experiments that those animals will be engaged in (behavior, tissue harvesting, both).
2. Are statistical tests justified as appropriate for every figure? Where (section, paragraph #)?	See section "Statistical methods" in the "Method" part of the manuscript. Each statistical test is included in the Figure legend. Details of post-hoc analysis result can be found in the Method part "Statistical methods"
a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?	Yes. Welch two sample t-test (t), independent t-test (Ty, yuen), analysis of variance for one or more fitted model objects (F), multivariate analysis of variance (V), Wilcoxon-rank sum and signed rank tests (W) Kruskal-Wallis rank sum test (H)
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. See section "Statistical methods" in the "Method" part of the manuscript. "Each data set was analyzed for its ability to meet the statistical assumptions for equality of the variance, for normal distribution, and for sphericity"... "The assumption of the parametric test was calculated using the Levene test"
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 #)?	see above. "If the assumption was met, the following tests were used: Welch two sample t-test, independent t-test, analysis of variance for one or more fitted model objects (F), multivariate analysis of variance (V). If the assumption was validated, the following tests were performed: Wilcoxon-rank sum and signed rank tests (W) and Kruskal-Wallis rank sum test (H)."
d. Are tests specified as one- or two-sided?	see above
e. Are there adjustments for multiple comparisons?	see above
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	Before data collection the following criteria were established: Experiments, in which the control failed, were excluded from the study. Animals, in which the virus expression could not be observed, were excluded.

4. Define the method of randomization used to assign subjects (or samples) to the experimental groups and to collect and process data. If no randomization was used, state so. Where does this appear (section, paragraph #)?	Behavior, electrophysiological measurements, image taking as well as analysis have been performed blindly, as indicated in the Method part, sections: "Behavior experiments", "Electrophysiology", "Electron microscopy".
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 #)?	See above. Behavior, electrophysiological measurements, image taking as well as analysis have been performed blindly, as indicated in the Method part, sections: "Behavior experiments", "Electrophysiology", "Electron microscopy".
6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes. Method part, section" Animals": "All animal experiments were performed with approval from the MIT Committee on Animal Care (CAC)."
7. Is the species of the animals used reported? Where (section, paragraph #)?	Yes. Method part, section" Animals": "If not otherwise indicated, at least 2 month old, male C57BL/6 mice from Jackson Laboratory were used for all experiments. "
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes. Method part, section" Animals": "If not otherwise indicated, at least 2 month old, male C57BL/6 mice from Jackson Laboratory were used for all experiments. "
9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Yes. Method part, section" Animals": "If not otherwise indicated, at least 2 month old, male C57BL/6 mice from Jackson Laboratory were used for all experiments. "
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes. Method part, section" Animals": "If not otherwise indicated, at least 2 month old, male C57BL/6 mice from Jackson Laboratory were used for all experiments. "
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	Yes. Method part, section" Animals": "Mice were housed groups of 3-5 animals in a 12 h light/ 12 h dark cycle, with standard mouse chow and water ad libitum."
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	Yes. Method part, section" Animals": "Mice were housed groups of 3-5 animals in a 12 h light/ 12 h dark cycle, with standard mouse chow and water ad libitum."
13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?	Yes. Method part, section"Behavior experiments": "All the experiments were done during the light phase, in the second half of the day,..."
14. 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 #)?

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

N/A

Where (section, paragraph #)?

a. How were the criteria for exclusion defined?

Where is this described (section, paragraph #)?

b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study.

Where is this described (section, paragraph #)?

Reagents

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

Yes, we have used commercially available antibodies.

a. Is antibody catalog number given?

Where does this appear (section, paragraph #)?

Yes,
1.) Immunohistochemistry: Primary antibody: rat BrdU (AbD Serotec, MCA2060GA, 1:500), rabbit GFP (Invitrogen, A11122, 1:300), rabbit Complexin-1 (Proteintech, 10246-2-AP, 1:300), mouse GFAP (G6171, 1:500), mouse Nsf-1 (MA1-12435, 1:300) and rabbit Syn3 (OSS00018W, 1:300) from Thermo Scientific, guinea pig Iba1 (234 004, 1:500), mouse Syt1 (105 011, 1:300), guinea pig ZnT3 (197 004, 1:1000) from Synaptic Systems.
Secondary antibodies were diluted 1:400 (all obtained from Jackson Laboratory).

2.) Western blot, Transfer: mouse β-actin (Sigma Aldrich, A5316)

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

Where does this appear (section, paragraph #)?

References are listed on the webpage of the antibody distributor.

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

Where (section, paragraph #)?

Yes. Method part, section" Human fibroblasts": "Human fibroblasts were obtained from the Coriell Institute, McLean Hospital, the Massachusetts General Hospital, and the American Type Culture Collection (ATCC)."

a. Were they recently authenticated?

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

Data deposition

Data deposition in a public repository is mandatory for:

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

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

1. Are accession codes for deposit dates provided?

   Where (section, paragraph #)?

N/A

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. Is computer source code/software provided with the paper or deposited in a public repository? Indicate in what form this is provided or how it can be obtained.

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	N/A