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Supplementary Figures: 7

Supplementary Tables: -

Supplementary Videos:

Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read Reporting Life Sciences Research.

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

Statistics reporting, by figure

- Please specify the following information for each panel reporting quantitative data, and where each item is reported (section, e.g. Results, & paragraph number).
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the paragraph number instead of the figure number.

Note: Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

		TEST USED		n			DESCRIPTIVE STATS (AVERAGE, VARIANCE)		P VALUE		DEGREES OF FREEDOM & F/t/z/R/ETC VALUE	
	FIGURE NUMBER	WHICH TEST?	SECTION & PARAGRAPH #	EXACT VALUE	DEFINED?	SECTION & PARAGRAPH #	REPORTED?	SECTION & PARAGRAPH #	EXACT VALUE	SECTION & PARAGRAPH #	VALUE	SECTION & PARAGRAPH #
example	1a	one-way ANOVA	Fig. legend	9, 9, 10, 15	mice from at least 3 litters/group	Methods para 8	error bars are mean +/- SEM	Fig. legend	p = 0.044	Fig. legend	F(3, 36) = 2.97	Fig. legend
example	results, para 6	unpaired t-test	Results para 6	15	slices from 10 mice	Results para 6	error bars are mean +/- SEM	Results para 6	p = 0.0006	Results para 6	t(28) = 2.808	Results para 6

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		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 #
+ -	1d	two way ANOVA Frequency distribution of positive cells with Tukeys Post-test	Figure legends, Fig1d, Paragraph 1	WT n=4 KO n=5 KO +FMRP n=4	WT 4 brains from 3 litters 14 brain slices, total 4032 cells KO 5 brains from 2 litters 11 brain slices, total 2594 cells KO+FMRP 4 brains from 2 litters 14 brain slices, total of 2903 cells	Figure legends, Fig1d, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig1d, Paragraph 1	Bin 1: WT vs KO P= 0.1777 Bin 1: WT vs KO+Fmrp P=0.9786 Bin 1: KO vs KO+Fmrp P=0.2579 Bin 2: WT vs KO P= 0.0824 Bin 2: WT vs KO+Fmrp P=0.9217 Bin 2: KO vs KO+Fmrp P=0.1888 Bin 3: WT vs KO *P= 0.0326 Bin 3: WT vs KO+Fmrp P=0.7015 Bin 3: KO vs KO+Fmrp P=0.2090 Bin 4: WT vs KO **P= 0.0045 Bin 4: WT vs KO+Fmrp P=0.2649 Bin 4: KO vs KO+Fmrp P=0.2527 Bin 5: WT vs KO **P= 0.0065 Bin 5: WT vs KO+Fmrp P=0.9044 Bin 5: KO vs KO+Fmrp *P=0.0234	Figure legends, Fig1d, Paragraph 1	F (9, 100) = 21.37	Figure legends, Fig1d, Paragraph 1

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+ -	1d	two way ANOVA Frequency distribution of positive cells with Tukeys Post test	Figure legends, Fig1d, Paragraph 1	WT n=4 KO n=5 KO +FMRP n=4	WT 4 brains from 3 litters 14 brain slices, total 4032 cells KO 5 brains from 2 litters 11 brain slices, total 2594 cells KO+FMRP 4 brains from 2 litters 14 brain slices, total of 2903 cells	Figure legends, Fig1d, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig1d, Paragraph 1	Bin 6: WT vs KO P= 0.4251 Bin 6: WT vs KO+Fmrp P=0.5245 Bin 6: KO vs KO+Fmrp P=0.9937 Bin 7: WT vs KO P= 0.9960 Bin 7: WT vs KO+Fmrp P=0.0797 Bin 7: KO vs KO+Fmrp P=0.0741 Bin 8: WT vs KO P= 0.0753 Bin 8: WT vs KO+Fmrp P=0.8259 Bin 8: KO vs KO+Fmrp *P=0.0156 Bin 9: WT vs KO ***P< 0.0001 Bin 9: WT vs KO+Fmrp ***P=0.0001 Bin 9: KO vs KO+Fmrp **P=0.0012 Bin 10: WT vs KO ***P< 0.0001 Bin 10: WT vs KO+Fmrp *P=0.0127 Bin 10: KO vs KO+Fmrp P=0.1733	Figure legends, Fig1d, Paragraph 1	F (9, 100) = 21.37	Figure legends, Fig1d, Paragraph 1
+ -	2a	unpaired two-tailed T test	Figure legends, Fig2a, Paragraph 1	WT n=3 KO n=3	3 brains WT cells analyzed 2607 (8 slices) 3 brains KO cells analyzed 3017 (11 slices)	Figure legends, Fig2a, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig2a, Paragraph 1	NS: P=0.9393	Figure legends, Fig2a, Paragraph 1	t=0,08108 df=4	Figure legends, Fig2a, Paragraph 1

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+ -	2b	two way ANOVA Frequency distribution of positive cells with Tukeys Post test	Figure legends, Fig2b, Paragraph 1	WT n=4 KO n=4	4 brains from 2 litters for WT and KO total 656 cells(WT) and 609 (KO) cells analysed	Figure legends, Fig2b, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig2b, Paragraph 1	Bin 1: WT vs KO P= 0.9904 Bin 2: WT vs KO P= 0.7500 Bin 3: WT vs KO P= 0.9997 Bin 4: WT vs KO P= 0.9999 Bin 5: WT vs KO P= 0.5344 Bin 6: WT vs KO P > 0.9999 Bin 7: WT vs KO P > 0.9999 Bin 8: WT vs KO P > 0.9999 Bin 9: WT vs KO P > 0.9999 Bin 10: WT vs KO P > 0.9999	Figure legends, Fig2b, Paragraph 1	F (9, 60) = 206.7	Figure legends, Fig2b, Paragraph 1
+ -	2c	unpaired two-tailed T test	Figure legends, Fig2c, Paragraph 1	WT n=3 KO n=3	3 brains, 3 slices analysed per animal	Figure legends, Fig2c, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig2c, Paragraph 1	NS: p= 0.1503	Figure legends, Fig2c, Paragraph 1	t=1.776 df=4	Figure legends, Fig2c, Paragraph 1
+ -	2d	unpaired two-tailed T test	Figure legends, Fig2d, Paragraph 1	WT n=3 KO n=3	3 brains from 2 litters 3 brains from 2 litters	Figure legends, Fig2d, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig2d, Paragraph 1	NS: P=0.7439	Figure legends, Fig2d, Paragraph 1	t=0.3370 df=9	Figure legends, Fig2d, Paragraph 1
+ -	3b	unpaired two-tailed T test	Figure legends, Fig3b, Paragraph 1	WT n=4 KO n=4	4 brains from 1 litter (1 slice analyzed for each brain) 4 brains from 1 litter (1 slice analyzed for each brain)	Figure legends, Fig3b, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig3b, Paragraph 1	**P= 0.0078	Figure legends, Fig3b, Paragraph 1	t=3.915 df=6	Figure legends, Fig3b, Paragraph 1
+ -	3c	unpaired two-tailed T test	Figure legends, Fig3c, Paragraph 1	WT n=4 KO n=4	WT: 4 brains from 1 litter (1 slice for each brain) 65 cells analyzed 4 brains from 1 litter (1 slice analyzed for each brain) 43 cells analyzed	Figure legends, Fig3c, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig3c, Paragraph 1	* P=0.0421	Figure legends, Fig3c, Paragraph 1	t=2.575 df=6	Figure legends, Fig3c, Paragraph 1
+ -	3d	one way ANOVA	Figure legends, Fig3d, Paragraph 1	WT n=6 KO n=5 KO + Fmrp n=4	3-4 slices analysed per animal	Figure legends, Fig3d, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig3d, Paragraph 1	WT vs KO *** P < 0.0001 WT vs KO +Fmrp, p=0.8462 KO vs KO + Fmrp ***P < 0.0001	Figure legends, Fig3d, Paragraph 1	F (2, 12) = 35.94	Figure legends, Fig3d, Paragraph 1

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+ -	4a	unpaired two-tailed T test	Figure legends, Fig4a, Paragraph 1	WT n=7 KO n=7	7 brains from one litter for both WT and KO	Figure legends, Fig4a, Paragraph 1	error bars are mean +/- % SEM	Figure legends, Fig4a, Paragraph 1	*P=0.0228	Figure legends, Fig4a, Paragraph 1	t=2.611 df=12	Figure legends, Fig4a, Paragraph 1
+ -	4b	NA	Figure legends, Fig4b, Paragraph 1	n=4	4 independent IP experiments	Figure legends, Fig4b, Paragraph 1	relative expression	Figure legends, Fig4b, Paragraph 1	NA	Figure legends, Fig4b, Paragraph 1	NA	Figure legends, Fig4b, Paragraph 1
+ -	4c	unpaired one-tailed T test	Figure legends, Fig4c, Paragraph 1	WT n=4 KO n=4	WT 4 brains from 1 litter KO 4 brains from 1 litter	Figure legends, Fig4c, Paragraph 1	error bars are mean +/- % SEM	Figure legends, Fig4c, Paragraph 1	* P=0.0475	Figure legends, Fig4c, Paragraph 1	t=1.981 df=6	Figure legends, Fig4c, Paragraph 1
+ -	4d	unpaired two-tailed T test	Figure legends, Fig4d, Paragraph 1	WT n=4 KO n=4	4 independent cultures (embryos from different pregnant mothers) 4 independent cultures (embryos from different pregnant mothers)	Figure legends, Fig4d, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig4d, Paragraph 1	* P=0.0307	Figure legends, Fig4d, Paragraph 1	t=2.8101 df=6	Figure legends, Fig4d, Paragraph 1
+ -	5a	two way ANOVA Frequency distribution of positive cells with Tukeys Post test	Figure legends, Fig5a, Paragraph 1	KO + N-Cadherin n=6	KO+N-cadherin 6 brains analyzed from at least 3 litters 14 brain slices total of 2615 cells	Figure legends, Fig5a, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig5a, Paragraph 1	Bin 1: WT vs KO+ N-Cadherin P=0.9870 Bin 1: KO vs KO+ N-Cadherin P=0.1706 Bin 2: WT vs KO+ N-Cadherin P=0.9748 Bin 2: KO vs KO+ N-Cadherin P=0.0831 Bin 3: WT vs KO+ N-Cadherin P=0.4583 Bin 3: KO vs KO+ N-Cadherin P=0.2774005 Bin 4: WT vs KO+ N-Cadherin P=0.1489 Bin 4: KO vs KO+ N-Cadherin P=0.2611	Figure legends, Fig5a, Paragraph 1	F (9, 120) = 27.10	Figure legends, Fig5a, Paragraph 1

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+ -	5a	two way ANOVA Frequency distribution of positive cells with Tukeys Post test	Figure legends, Fig5a, Paragraph 1	KO + N-Cadherin n=6	KO+N-cadherin 6 brains analyzed from at least 3 litters 14 brain slices total of 2615 cells	Figure legends, Fig5a, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig5a, Paragraph 1	Bin 5: WT vs KO+ N-Cadherin **P=0.0005 Bin 5: KO vs KO+ N-Cadherin P=0.7599 Bin 6: WT vs KO+ N-Cadherin P=0.6276 Bin 6: KO vs KO+ N-Cadherin P=0.9164 Bin 7: WT vs KO+ N-Cadherin P=0.1821 Bin 7: KO vs KO+ N-Cadherin P=0.1744 Bin 8: WT vs KO+ N-Cadherin P=0.6559 Bin 8: KO vs KO+ N-Cadherin P=0.2972 Bin 9: WT vs KO+ N-Cadherin ***P<0.0001 Bin 9: KO vs KO+ N-Cadherin ***P=0.0005 Bin 10: WT vs KO+ N-Cadherin ***P=0.0001 Bin 10: KO vs KO+ N-Cadherin P=0.7092	Figure legends, Fig5a, Paragraph 1	F (9, 120) = 27.10	Figure legends, Fig5a, Paragraph 1
+ -	5b	NA	Figure legends, Fig5b, Paragraph 1	WT n=3 KO n=3	3-5 slices of 3 animals analysed	Figure legends, Fig5b, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig5b, Paragraph 1	NA	Figure legends, Fig5b, Paragraph 1	NA	Figure legends, Fig5b, Paragraph 1
+ -	5c	unpaired two-tailed T test	Figure legends, Fig5c, Paragraph 1	KO n=5 KO + N-Cad n=4	3-4 slices analysed per animal	Figure legends, Fig5c, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig5c, Paragraph 1	KO vs KO +Ncad p*=0.0347	Figure legends, Fig5c, Paragraph 1	t=2.615 df=7	Figure legends, Fig5c, Paragraph 1

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+ -	6d	ANOVA with posthoc t-test	Figure legends, Fig6d, Paragraph 1	WT (P0-1) 6 pups, (P2-3) 3 pups, (P4-5) 10pups , P(6-7) 2 pups KO (P0-1) 4 pups, (P2-3) 5 pups, (P4-5) 8 pups , P(6-7) 4 pups	slices from animals of differing postnatal ages WT n=52 slices (P0-1: 15 Slices, P2-3: 15 Slices, P4-5: 17 Slices, P6-7: 5 Slices) KO n=44 (P0-1:11 Slices, P2-3: 7 Slices, P4-5: 19 Slices, P6-7: 7Slices)	Figure legends, Fig6d, Paragraph 1	mean +/- SEM	Figure legends, Fig6d, Paragraph 1	ANOVA: p<0.001, Posthoc bonferroni t-test: P0-1 vs. 6-7 p=0.002, P2-3 vs. 4-5: p=0.021, P2-3 vs. P6-7, p<0.001	Figure legends, Fig6d, Paragraph 1	F(3,92)=7.892	Figure legends, Fig6d, Paragraph 1
+ -	6e	independent samples t-test; GLM with posthoc t-tests	Figure legends, Fig6e, Paragraph 1	WT (P0-1) 6 pups, (P2-3) 3 pups, (P4-5) 10pups , P(6-7) 2 pups KO (P0-1) 4 pups, (P2-3) 5 pups, (P4-5) 8 pups , P(6-7) 4 pups	slices from animals of differing postnatal ages WT n=52 Slices (P0-1: 15 Slices, P2-3: 15 Slices, P4-5: 17 Slices, P6-7: 5Slices) KO n=44 (P0-1:11 Slices, P2-3: 7 Slices, P4-5: 19 Slices, P6-7: 7Slices)	Figure legends, Fig6e, Paragraph 1	mean +/- SEM for both graphs	Figure legends, Fig6e, Paragraph 1	t-test: p=0.026; GLM age:p=0.003, gen=0.024 gen*age:p=0.70, t-test: P4-5 p<0.05, other groups NS	Figure legends, Fig6e, Paragraph 1	t=-2.25, df=94 GLM: genotype F(1,88)=5.238, p=0.024, age F(3,88)=5.034, p=0.003, genotype*age F(3,88)=0.471, p=0.703 P4-5: t=-3.34, p=0.002	Figure legends, Fig6e, Paragraph 1
+ -	6f	Welch's t test	Figure legends, Fig6f, Paragraph 1	P4-P5 WT + empty vector = 3 animals (7 slices,68 cells), P4-P5 Fmr1 KO + empty vector = 3 animals (9 slices, 118 cells), P4-P5 Fmr1 KO + N-cadherin = 6 animals (16 slices,295 cells), Fmr1 KO + Fmrp = 3 animals (7 slices, 203 cells).	P4-P5 WT + empty vector = 14 hemispheres, P4 Fmr1 KO + empty vector = 18 hemisphere, P4 Fmr1 KO + N-cadherin = 32 hemispheres), Fmr1 KO + Fmrp = 14 hemispheres.	Figure legends, Fig6f, Paragraph 1	mean +/-SEM	Figure legends, Fig6f, Paragraph 1	** P=0.003 * P=0.028	Figure legends, Fig6f, Paragraph 1	df=58 df=92 df=129, respectively	Figure legends, Fig6f, Paragraph 1
+ -	7 P4	unpaired two-tailed T test	Figure legends, Fig7, Paragraph 1	12 Slices	3 slices from 4 different animals	Figure legends, Fig7, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig7, Paragraph 1	p*=0.0139	Figure legends, Fig7, Paragraph 1	t=2.879 df=12	Figure legends, Fig7, Paragraph 1

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+ -	7 P18	unpaired two-tailed T test	Figure legends, Fig7, Paragraph 1	7 Slices	7 slices from 2 different animals	Figure legends, Fig7, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig7, Paragraph 1	p*= 0.0314	Figure legends, Fig7, Paragraph 1	t=2.090 df=25	Figure legends, Fig7, Paragraph 1
+ -	8	two-way ANOVA with Bonferroni correction	Figure legends, Fig8, Paragraph 1	WT n=3 KO n=5	3 WT brains/ 5 KO brains	Figure legends, Fig8, Paragraph 1	error bars are mean +/- SEM	Figure legends, Fig8, Paragraph 1	Bonferroni's Multiple Comparison FA: WT vs KO P> 0.9999 MD: WT vs KO P=0.008 AD: WT vs KO P=0.0008 RD: WT vs KO P=0.012	Figure legends, Fig8, Paragraph 1	F (3, 24) = 173.2	Figure legends, Fig8, Paragraph 1
+ -	Supp Fig 1b	two way ANOVA Frequency distribution of positive cells with Tukeys Post test	Supplementary Information Figure legends, Supp Fig1b, Paragraph 1	WT n=6 KO n=5	WT 6 brains from 2 litters 6 brain slices, total of 1066 cells KO 5 brains from 2 litters 11 brain slices, total 1874 cells	Supplementary Information Figure legends, Supp Fig1b, Paragraph 1	error bars are mean +/- SEM	Supplementary Information Figure legends, Supp Fig1b, Paragraph 1	Bin10: P> 0.9999 Bin 9: P> 0.9999 Bin 8: P=0.9973 Bin 7: P=0.9880 Bin 6: P> 0.9999 Bin 5: P> 0.9999	Supplementary Information Figure legends, Supp Fig1b, Paragraph 1	F (10, 165) = 51.97	Supplementary Information Figure legends, Supp Fig1b, Paragraph 1
+ -	Supp Fig2a	unpaired two-tailed T test	Supplementary Information Figure legends, Supp Fig2a, Paragraph 1	WT n=3 KO n=3	3 slices analysed per animal	Supplementary Information Figure legends, Supp Fig2a, Paragraph 1	error bars are mean +/- SEM	Supplementary Information Figure legends, Supp Fig2a, Paragraph 1	P =0.1503	Supplementary Information Figure legends, Supp Fig2a, Paragraph 1	t=1.776, df = 4	Supplementary Information Figure legends, Supp Fig2a, Paragraph 1
+ -	Supp Fig2b	unpaired two-tailed T test	Supplementary Information Figure legends, Supp Fig2b, Paragraph 1	WT n=3 KO n=3	3 brains total 1628 (WY) and 1859 (KO) cells analysed	Supplementary Information Figure legends, Supp Fig2b, Paragraph 1	error bars are mean +/- SEM	Supplementary Information Figure legends, Supp Fig2b, Paragraph 1	P =0.423	Supplementary Information Figure legends, Supp Fig2b, Paragraph 1	t=0.86, df = 6	Supplementary Information Figure legends, Supp Fig2b, Paragraph 1
+ -	Supp Fig4	unpaired two tailed t-test	Supplementary Information Figure legends, Supp Fig4, Paragraph 1	WT (71 cells monitored) KO (59 cells monitored)	WT from 6 different explants KO from 5 different explants	Supplementary Information Figure legends, Supp Fig4, Paragraph 1	mean values are represented	Supplementary Information Figure legends, Supp Fig4, Paragraph 1	Speed: p=0.8122 Directionality: p=0.9857	Supplementary Information Figure legends, Supp Fig4, Paragraph 1	Speed: t=0.2447, df=9, Directionality: t=0.01844, df=9	Supplementary Information Figure legends, Supp Fig4, Paragraph 1

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+ -	Supp Fig 5a	ANOVA	Supplementary Information Figure legends, Supp Fig5a, Paragraph 1	WT (P0-1) 6 pups, (P2-3) 3 pups, (P4-5) 10pups , P(6-7) 2 pups KO (P0-1) 4 pups, (P2-3) 5 pups, (P4-5) 8 pups , P(6-7) 4 pups	slices from animals of different postnatal ages. WT (P0-1: 15 Slices, P2-3: 15 Slices, P4-5: 17 Slices, P6-7: 5 Slices) KO (P0-1: 11 Slices, 2-3: 7 Slices, 4-5: 19 Slices, 6-7: 7Slices)	Supplementary Information Figure legends, Supp Fig5a, Paragraph 1	mean +/- SEM	Supplementary Information Figure legends, Supp Fig5a, Paragraph 1	age: P<0.001 genotype: p=0.64 genotype*age interaction: p=0.504	Supplementary Information Figure legends, Supp Fig5a, Paragraph 1	age: F(3,88)=8,618, p<0.001 genotype: F(1,88)=0.221, p=0.64, age*genotype: F(3,88)=0.787, p=0.504	Supplementary Information Figure legends, Supp Fig5a, Paragraph 1
+ -												

Representative figures

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

   If so, what figure(s)?

Yes

1b; 1c; 2a; 2b; 2c; 2d; 2e; 3a; 3b; 4a; 4b; 5a; 5b; 6a; 6f, 7, 8
Suppl. Figs.: 1a/b; 2a; 3a/b; Fig4; Fig 5e; Fig 6, Fig7.

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, see n above
1b; 1c (quantification in Figure legends Fig 1d, paragraph 1):
2a (quantification in Figure legends Fig 2a, paragraph 1);
2b (quantification in Figure legends Fig 2b, paragraph 1);
2c (quantification in Figure legends Fig 2c, paragraph 1);
2d (quantification in Figure legends Fig 2d, paragraph 1);
2e (quantification in Figure legends Fig 2d, paragraph 1);
3a/b (quantification in Figure legends Fig 3b/c, paragraph 1);
4a (quantification in Figure legends Fig 4a, paragraph 1);
4b (quantification in Figure legends Fig 4b, paragraph 1);
5a (quantification in Figure legends Fig 5a, FIg 5c, paragraph 1);
5b (quantification in Figure legends Fig 5b, paragraph 1);
6a (quantification in Figure legends Fig 6d-e, paragraph 1)
6f (quantification in Figure legends Fig 6f, paragraph 1)
7 (quantification in Figure legends Fig7, paragraph 1)
8 (quantification in Figure legends Fig8, paragraph 1)

Supp Fig1b (quantification/distribution in Supplementary Information Figure legends Fig1b, paragraph 1);
Supp Fig2a (quantification in supplementary Information Figure legends Fig2a, paragraph 1);
Supp Fig. 3a/b (n=3 slices from 2 animals)
Supp Fig. 4 (quantification in supplementary Information Figure legends Fig4, paragraph 1);
Supp Fig. 5e
Supp Fig. 6 (quantification in supplementary Information Figure legends Fig6, paragraph 1));
Supp Fig. 7a (quantification in Figure legends Fig 4a, paragraph 1)
Supp Fig. 7b (quantification in Figure legends Fig 4b, paragraph 1)

All the informations are in this file as well as in the figure legends.

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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 experiments we performed produced statistically significant results with the sample size we used. All the informations are in this file as well as in the figure legends for each Figure specifically.
2. Are statistical tests justified as appropriate for every figure? Where (section, paragraph #)?	The statistical analysis used in this manuscript is standard and according to similar studies found in the literature.
a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?	Statistics used is described in the figure legends.
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 #)?	We used parametric tests.
c. Is there any estimate of variance within each group of data? Is the variance similar between groups that are being statistically compared? Where is this described (section, paragraph #)?	Yes yes Online Methods, Statistics
d. Are tests specified as one- or two-sided?	Yes, in this file.
e. Are there adjustments for multiple comparisons?	Yes
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	Data points were not excluded (experimentally). In Fig 6, Spikes were detected using an in house-made algorithm that evaluates peak height and slope, and the spike frequency for active cells was calculated. After removing outliers (automatically
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 method for randomization was used.
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 #)?	No Online Methods, Statistics

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6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes Online Methods - section: a) Transgenic mice, paragraph 1 b) In utero electroporation, paragraph 5
7. Is the species of the animals used reported? Where (section, paragraph #)?	Yes In the text and in the Methods section (paragraph 1).
8. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes In the Methods section. a) Transgenic mice (paragraph 1)
9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	For our experiments we used embryos and for Figures 7 and 8 we used P18 males.
10. Is the age of the animals/subjects reported? Where (section, paragraph #)?	Yes In the text and in the figure legends.
11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	Yes, in the Online Methods - section. We state under Transgenic mice: "Animal care was conducted conforming the institutional guidelines followed by the KULeuven (Belgium) and VU University Amsterdam (Netherlands). A 14-h light/10 h dark cycle was used"
12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?	No, but in the Online Methods - section under the Transgenic mice we state:""Animal care was conducted conforming the institutional guidelines followed by the KULeuven (Belgium) and VU University Amsterdam (Netherlands).
13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?	N/A (not applicable)
14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? Where (section, paragraph #)?	N/A (not applicable)
a. If multiple behavioral tests were conducted in the same group of animals, is this reported? Where (section, paragraph #)?	N/A (not applicable)
15. If any animals/subjects were excluded from analysis, is this reported? Where (section, paragraph #)?	N/A (not applicable)
a. How were the criteria for exclusion defined? Where is this described (section, paragraph #)?	N/A (not applicable)

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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 (not applicable)

Reagents

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

The antibodies used in this study have been purchased and validated by the suppliers.
FMRP antibodies was characterized in Ferrari et al 2007. Additionally, it was largely validated by us and other laboratories, here a few examples (Napoli et al., 2008, Harlow et al., 2010, Till et al., 2012, Luca et al 2013).

a. Is antibody catalog number given?

Where does this appear (section, paragraph #)?

Name of the companies selling the antibodies we used, the catalog number and the concentration are described in the Online Methods section.

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

Where does this appear (section, paragraph #)?

See above

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

Where (section, paragraph #)?

N/A

a. Were they recently authenticated?

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

N/A

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

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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.

Figure 6
Customized scripts in Matlab and C++ algorithm were used to analyze Ca imaging data.

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.

NO
Upon request.

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

Nature Neuroscience: doi:10.1038/nn.3870

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 #)?	
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?	
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?	
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?	N/A

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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?	
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?	
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?	
20. Are the results based on an ROI (region of interest) analysis?	N/A
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?	N/A
22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?	N/A

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Additional comments

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