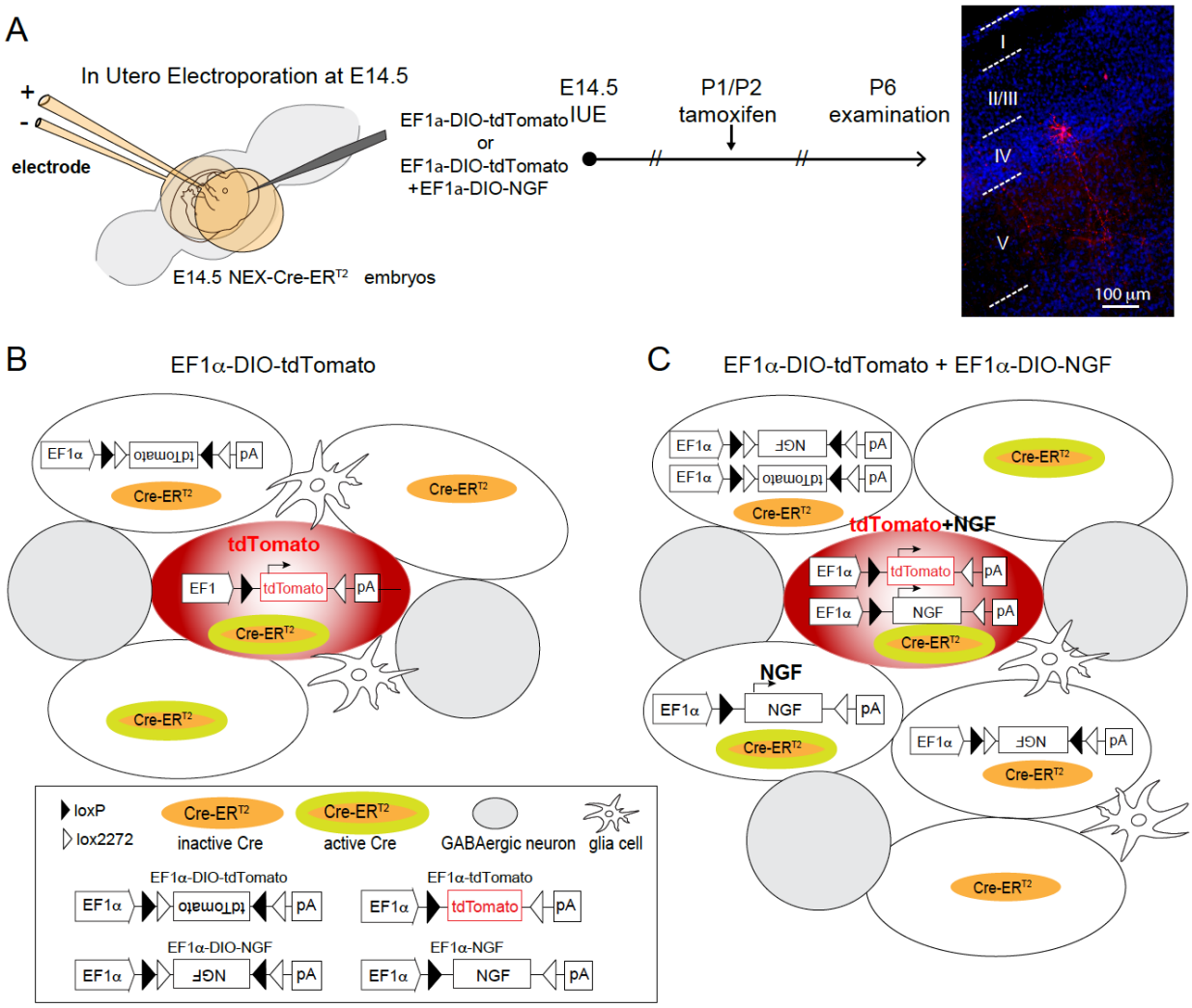
Supplementary Data

Supplementary Table 1. Summary of normalized mRNA levels of selected candidates in P4 S1 cortex determined by qPCR experiments. N/A: not available; ND: not detectable; &, for TrkA, TrkB, TrkC, p75 NTR expression levels. The statistical analysis (*) refers to wild-type compared with mGluR5 KO, Glu-mGluR5 cKO, or GABA-mGluR5 cKO S1 cortex. *$p < 0.05$, **$p < 0.01$, ***$p <$ 0.0001 by Mann-Whitney test. Bold highlights the *p values* that are statistically significant.

Gene		**mGluR5 KO**			**Glu-mGluR5 cKO**			**GABA-mGluR5 cKO**		
		WT (n=7)	Homo (n=7)	*p value*	Ctrl (n=7)	KO (n=7)	*p value*	Ctrl (n=5)	KO (n=7)	*p value*
mGluR5		1.00±0.07	ND	----	1.00±0.03	0.27±0.02	**0.0012 ****	1.00±0.04	0.85±0.03	**0.048 ***
EphrinA5		1.00±0.09	1.21±0.12	0.2593	1.00±0.07	1.12±0.07	0.2086	1.00±0.22	0.85±0.07	0.1255
Fmrp		1.00±0.09	1.35±0.19	0.1282	1.00±0.06	1.03±0.06	p>0.9999	1.00±0.02	0.95±0.05	0.149
Nr2b		1.00±0.12	1.18±0.09	0.3176	1.00±0.06	1.09±0.06	0.62	1.00±0.10	1.04±0.08	p>0.9999
Bdnf		1.00±0.12	1.28±0.21	0.2949	1.00±0.09	1.12±0.11	0.4557	1.00±0.13	1.02±0.12	0.8763
Ngf		1.00±0.09	1.51±0.15	**0.0064 ****	1.00±0.10	1.30±0.05	**0.0379 ***	1.00±0.13	1.05±0.15	0.8763
TrkA		N/A	N/A	N/A	1.00±0.06[&]	1.52±0.12	**0.0051 ****	N/A	N/A	N/A
TrkB		N/A	N/A	N/A	1.00±0.02[&]	1.06±0.10	0.5038	N/A	N/A	N/A
TrkC		N/A	N/A	N/A	1.00±0.09[&]	1.47±0.27	0.1136	N/A	N/A	N/A
P75 NTR		N/A	N/A	N/A	1.00±0.01[&]	1.16±0.07	0.2677	N/A	N/A	N/A
FGF4 subfamily	*Fgf4*	ND								
	Fgf6	ND								
FGF7 subfamily	***Fgf7***	1.00±0.08	1.40±0.12	**0.02 ***	1.00±0.07	1.38±0.11	**0.0262 ***	1.00±0.04	0.96±0.08	0.8763
	Fgf10	1.00±0.07	1.43±0.11	**0.0111 ***	1.00±0.10	1.31±0.09	**0.0239 ***	1.00±0.06	0.97±0.06	0.8763
	Fgf22	1.00±0.03	1.34±0.15	**0.0361 ***	1.00±0.04	1.32±0.10	**0.0111 ****	1.00±0.07	1.03±0.07	p>0.9999
FGF8 subfamily	*Fgf8*	ND								
	Fgf17	1.00±0.19	0.88±0.19	0.6282	1.00±0.05	1.60±0.22	**0.0223 ***	1.00±0.13	0.88±0.07	0.4318
FGF9 subfamily	***Fgf9***	1.00±0.11	1.36±0.07	**0.0262 ***	1.00±0.03	1.27±0.07	**0.007 ****	1.00±0.10	1.01±0.17	0.7551
FGF11 subfamily	*Fgf14*	1.00±0.11	1.79±0.19	**0.0023 ****	1.00±0.04	1.11±0.10	0.4557	N/A	N/A	N/A
Fgfr1-IIIb		N/A	N/A	N/A	1.01±0.08	1.62±0.15	**0.0041 ****	N/A	N/A	N/A
Fgfr1-IIIc		N/A	N/A	N/A	1.08±0.18	0.97±0.22	0.7104	N/A	N/A	N/A
Fgfr2-IIIb		N/A	N/A	N/A	1.05±0.13	0.65±0.05	**0.0262 ***	N/A	N/A	N/A
Fgfr2-IIIc		N/A	N/A	N/A	1.00±0.05	0.93±0.08	0.62	N/A	N/A	N/A
Fgfr3-IIIb		N/A	N/A	N/A	1.03±0.10	1.60±0.07	**0.0006 *****	N/A	N/A	N/A
Fgfr3-IIIc		N/A	N/A	N/A	1.01±0.05	0.84±0.10	0.2086	N/A	N/A	N/A

Supplementary Table 2 mRNA expression of *Fgf7*, *10*, *22*, and *Ngf* in P4 S1 cortex (n=6) and/or DIV7 primary cortical neurons (n=6). Values are copies/ng RNA.

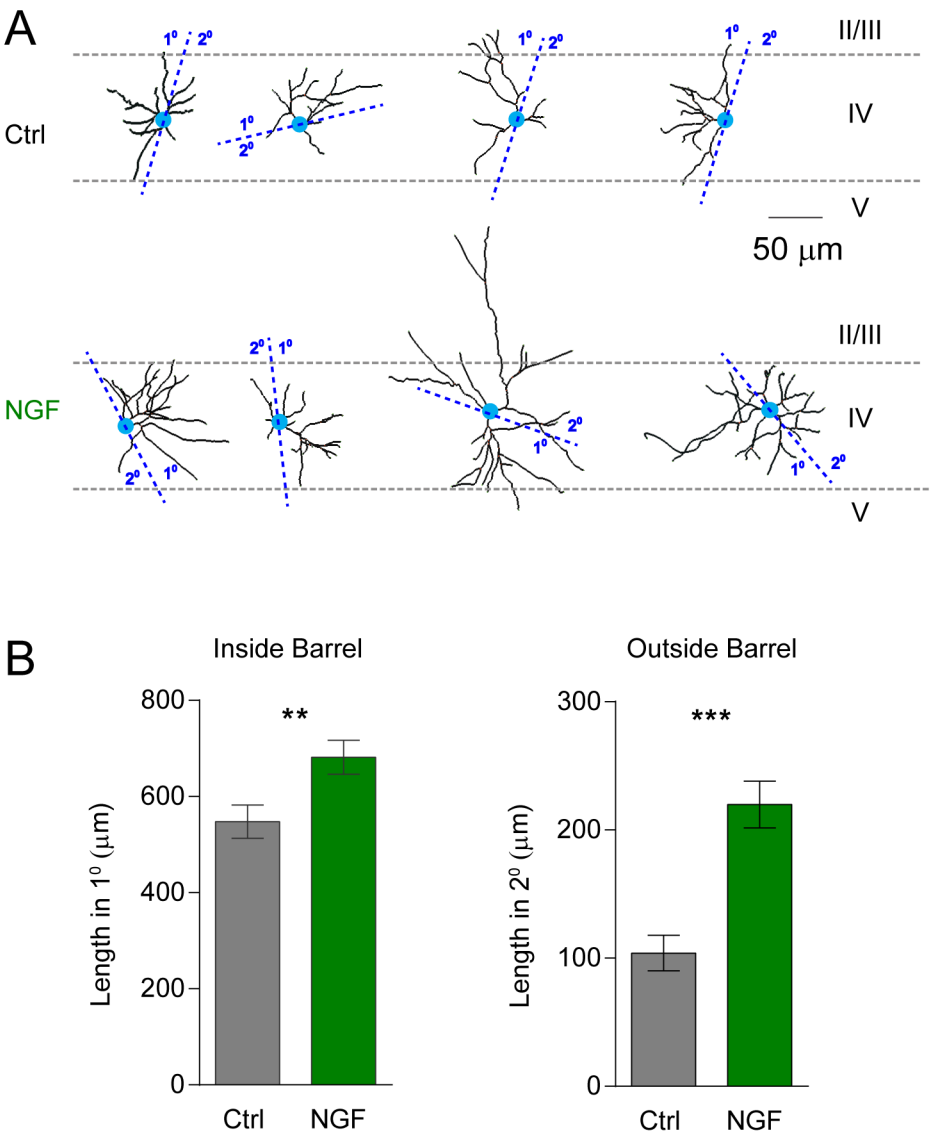
	Values (copies/ng RNA)	
Gene	P4 S1 cortex	DIV7 cortical neurons
Ngf	63.16±3.232	47.51±5.77
Fgf7	15.27±1.85	27.34±2.48
Fgf10	123.80±9.21	118.6±15.5
Fgf22	49.49±3.44	114.1±15.47



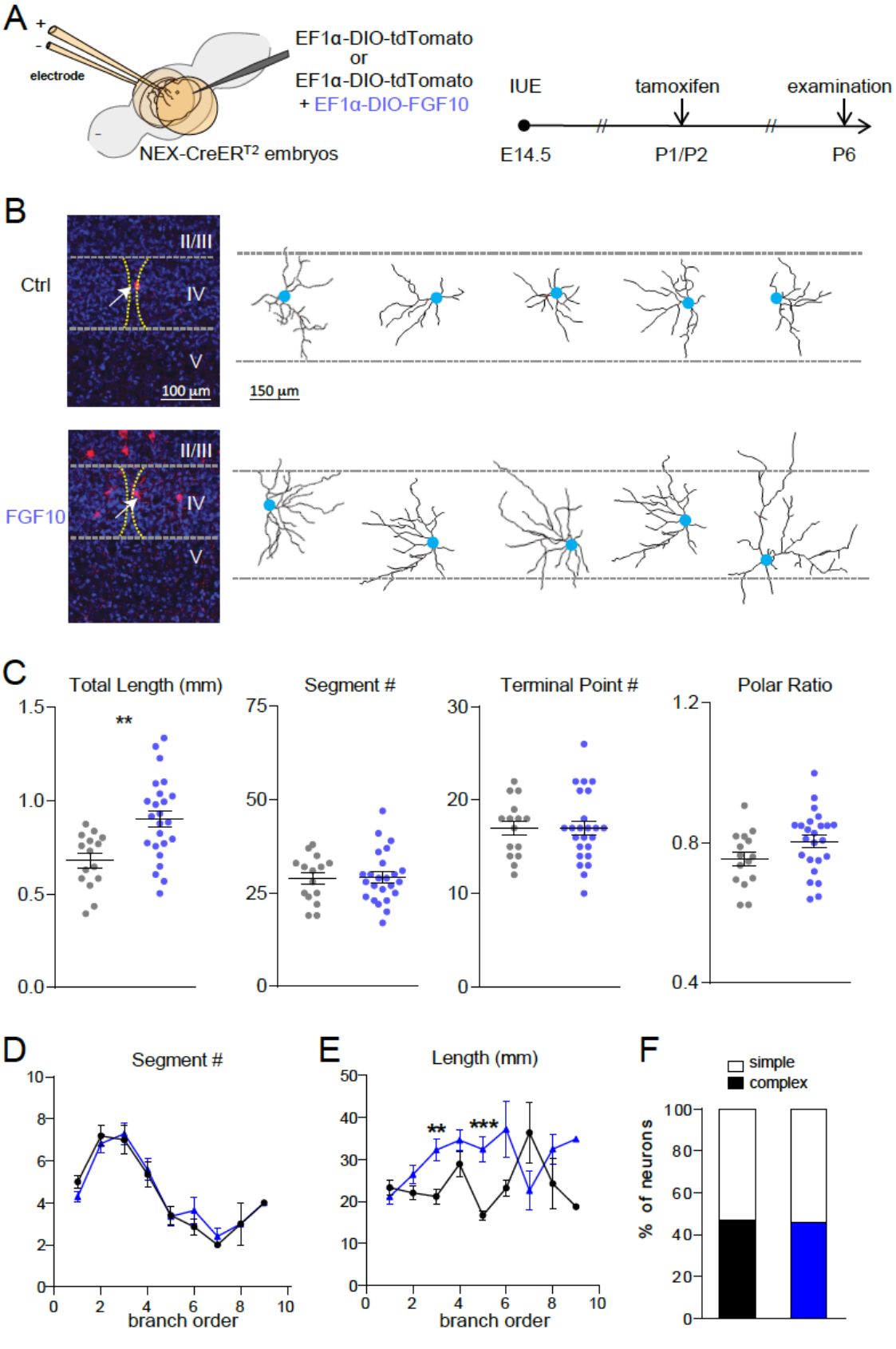
Supplementary Figure 1. Diagrams illustrate the methodology used to express tdTomato with or without NGF overexpression only in a few cortical layer IV neurons. (A) Mosaic brains were generated by electroporating a mixture of EF1α-DIO-tdTomato alone (0.1 μg/μl) or together with EF1α-DIO-NGF (mixed in a molar ratio of 1:20, with a final concentration of reach 1 μg/μl) into the cortical plate of E14.5 NEX-Cre-ER^{T2} embryos. Conducting IUE at E14.5 with low concentration of EF1α-DIO-tdTomato allows one to electroporate a small percentage of cortical layer IV neurons without targeting GABAergic neurons or glial cells (because they are not present in cortical plate or away from the ventricle at E14.5). At P1 or P2, Cre-ER^{T2} in cortical glutamatergic neurons was activated by a single tamoxifen injection (i.p. 100 mg/10 ml/kg). At P6, brains from these pups were collected for immunostaining and confocal imaging. (B, C) A single tamoxifen injection activates Cre in a subset of cortical layer IV glutamatergic

neurons. Using the IUE procedure at E14.5, only a small percentage of cortical layer IV neurons express the EF-1α-DIO-tdTomato construct alone, EF-1α-DIO-NGF construct alone, or a mixture of EF-1α-DIO-tdTomato and EF-1α-DIO-NGF constructs. Within the neurons expressing these DIO constructs if Cre-ER^{T2} becomes activated, the expression of either tdTomato, NGF, or both will occur following Cre-mediated recombination. For control experiment, embryos were only electroporated with EF-1α-DIO-tdTomato (B). To both express NGF and label those neurons with tdTomato, a mixture of EF-1α-DIO-tdTomato and EF-1α-DIO-NGF at the molar ratios of 1 to 20 was used for electroporation (C).

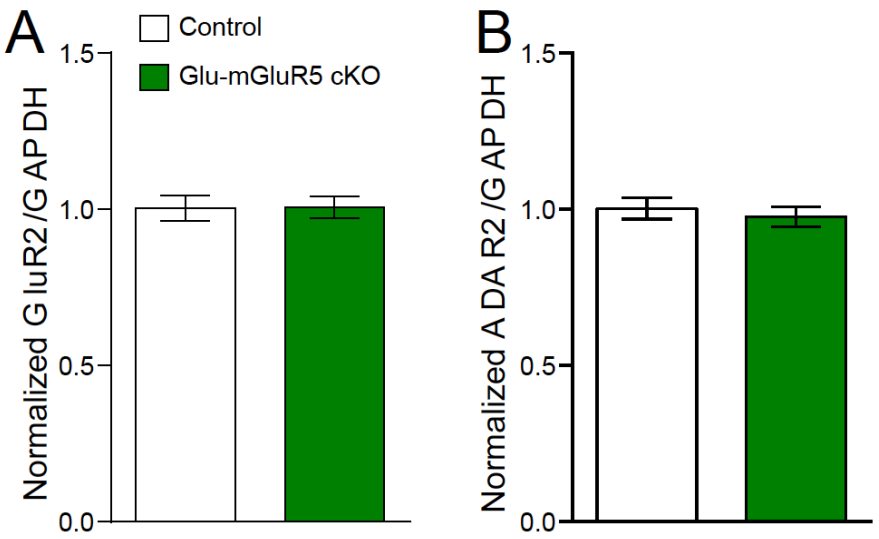
Supplementary figure 2



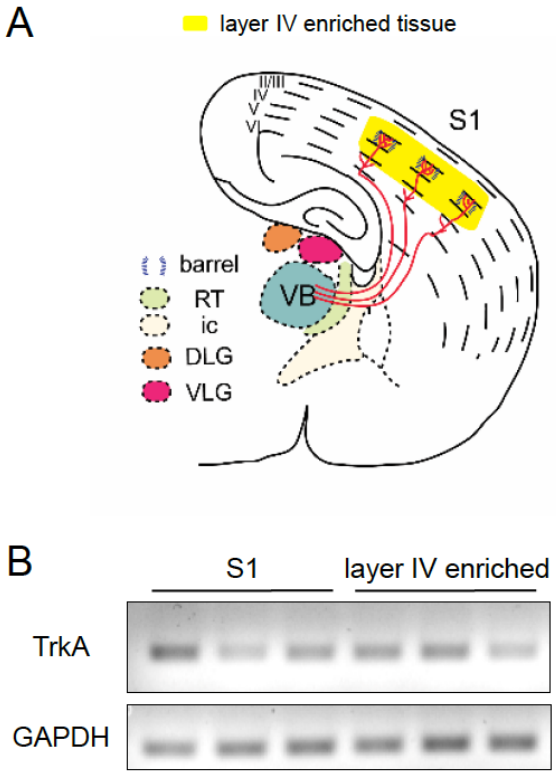
Supplementary Figure 2. Postnatal NGF expression increases dendritic growth both inside and outside the principal barrel. (A) Representative traced images of neurons are shown. (B) Quantitative analysis of dendritic length inside (1°) and outside (2°) the principal barrel that was used to calculate dendritic polarity in figure 4. Statistical analysis: Mann-Whitney test. The statistical analysis (*) compared NGF group to control (Ctrl) group. $^{**}p < 0.01$; $^{***}p < 0.001$.


A
+
-
electrode
-
EF1α-DIO-tdTomato
or
EF1α-DIO-tdTomato
+ EF1α-DIO-FGF10
NEX-CreER^{T2} embryos
IUE
tamoxifen
examination
E14.5
P1/P2
P6
B
Ctrl
II/III
IV
V
100 μm
150 μm
FGF10
II/III
IV
V
C
Total Length (mm)
**
Segment #
Terminal Point #
Polar Ratio
D
Segment #
branch order
E
Length (mm)
**
***
branch order
F
simple
complex
% of neurons

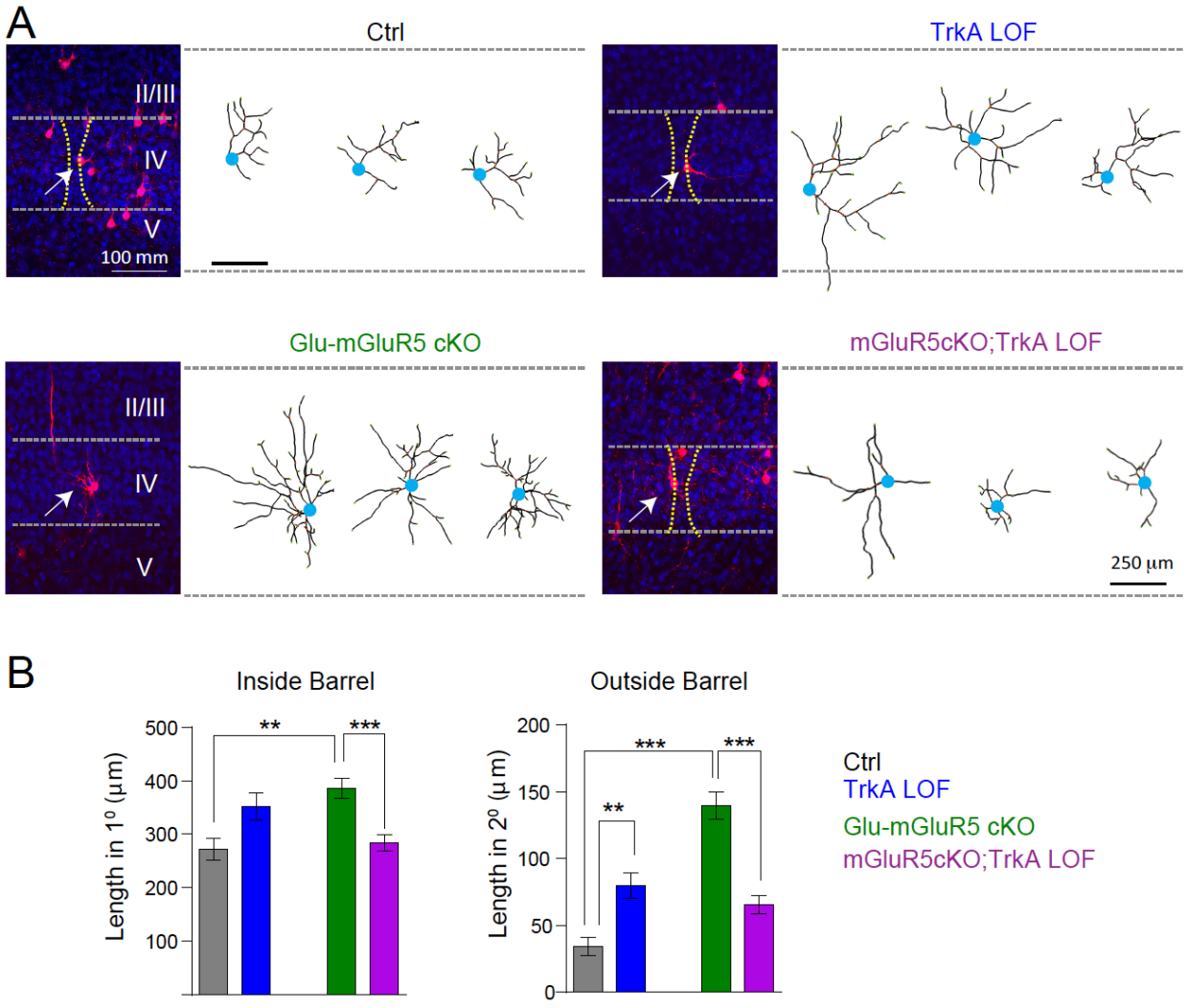
Supplementary Figure 3. Postnatal FGF10 expression in layer IV glutamatergic cortical neurons promotes dendritic elongation. (A) Schematic representation of the electroporation and tamoxifen treatment protocols that were used to express FGF10. (B) Examples of original images and computer-aided reconstructions. The region between the dashed lines indicates layer IV. The reconstructed neuron is identified by a yellow arrowhead. (C) The total dendritic length is significantly increased in FGF10-overexpressing neurons. However segment number, terminal points, and polar ratios were not. (D, E) Summaries of segment length (D) and number (E) per branch order. (F) Summary of neuron complexity determined by grouping branch order < 5 (simple neurons) or branch order ≥ 5 (complex neurons). Statistical analysis: Mann-Whitney test. The statistical analysis (*) compared FGF10 to Ctrl group. *$p < 0.05$; **$p < 0.01$.



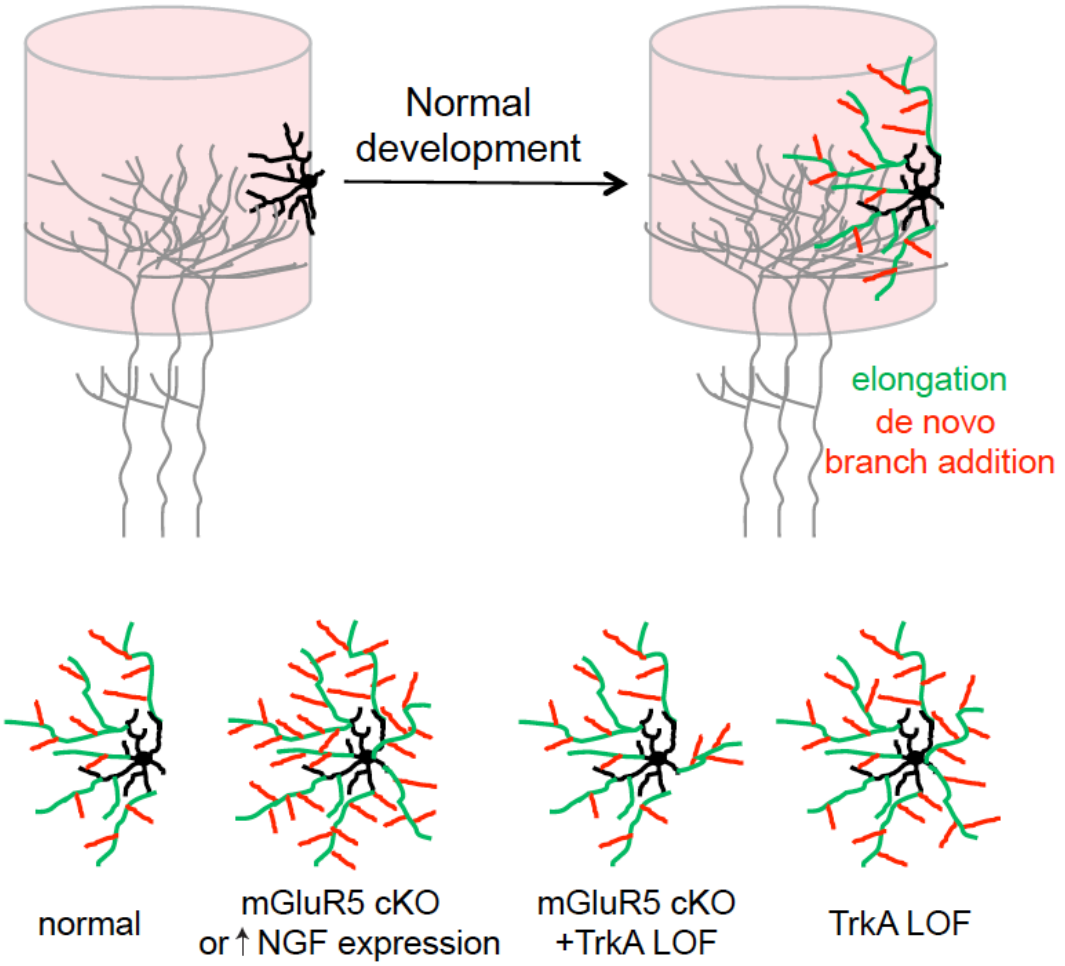
Supplementary Figure 4. Absence of mGluR5 does not change *GluR2* and *Adar2* mRNA expression level in at P4 levels in S1 cortex. The mRNA levels of *GluR2* (A) and *Adar2* (B) were measured using real-time qPCR ($n \geq 5$).



Supplementary Figure 5. RT-PCR data shows that TrkA is expressed in the cortical layer IV of S1 cortex. (A) The Layer IV enriched tissue (indicated by yellow shading) was excised from acute brain slices prepared from P6 mouse brains using a vibratome. (B) The S1 cortex or cortical layer IV enriched tissue was subjected to RNA extraction and RT-PCR to detect TrkA mRNA expression.



Supplementary Figure 6. Inhibiting TrkA kinase activity rescued mGluR5 deletion-induced aberrant dendritogenesis. (A) The cortical locations of traced neurons shown in Figure 6B. (B) Quantitative analysis of dendritic length inside (1°) and outside the principal barrel (2°) that was used to calculate dendritic polarity in figure 6C. One-Way ANOVA with post hoc Tukey's multiple comparisons test was conducted for (B). The statistical analysis (*) compared the indicated groups. $^{**}p < 0.01$; $^{***}p < 0.001$.



Supplementary Figure 7. Schematic illustrating the orientation of spiny stellate neuron dendrites towards thalamocortical axonal terminals within barrels at P6. Layer IV spiny stellate neurons extensively extend their dendrites by elongating pre-existing dendrites (green) or adding de-novo branches (red) towards thalamocortical axons terminating within the barrel hollow, culminating in a polarized dendritic pattern. In mGluR5 KO or NGF overexpressing neurons, dendrites outside the barrels elongate and more de-novo dendritic branches are added both inside barrel and outside the barrel, causing neurons to lose their polarized morphology. Inhibiting NGF-TrkA signaling in mGluR5 KO neurons attenuated de-novo branching inside the barrel and partially reduced excess dendritic growth outside the barrel. Interestingly, blocking TrkA kinase activity in WT neurons also disrupted the polarized dendritic pattern and de novo branch points were added outside of the barrel.