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An Intrinsic Transcriptional Program Underlying Synaptic Scaling during Activity Suppression

Graphical Abstract

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In Brief

Schaukowitch et al. demonstrate that an intrinsic transcriptional program in neurons underlies the homeostatic plasticity induced in response to chronic activity suppression. Calcium-dependent signaling through the T-type calcium channel is critical for transcriptional activation and synaptic upscaling in cultured neurons.

Highlights

- A transcription program is activated by TTX-mediated activity suppression
- Upregulated gene products functionally contribute to synaptic upscaling
- T-type calcium channel activity is required for transcriptional activation
- Transcriptional induction also occurs in an in vivo context

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An Intrinsic Transcriptional Program Underlying Synaptic Scaling during Activity Suppression

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SUMMARY

Homeostatic scaling allows neurons to maintain stable activity patterns by globally altering their synaptic strength in response to changing activity levels. Suppression of activity by the blocking of action potentials increases synaptic strength through an upregulation of surface α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA) receptors. Although this synaptic upscaling was shown to require transcription, the molecular nature of the intrinsic transcription program underlying this process and its functional significance have been unclear. Using RNA-seq, we identified 73 genes that were specifically upregulated in response to activity suppression. In particular, *Neuronal pentraxin-1* (*Nptx1*) increased within 6 hr of activity blockade, and knockdown of this gene blocked the increase in synaptic strength. *Nptx1* induction is mediated by calcium influx through the T-type voltage-gated calcium channel, as well as two transcription factors, SRF and ELK1. Altogether, these results uncover a transcriptional program that specifically operates when neuronal activity is suppressed to globally coordinate the increase in synaptic strength.

INTRODUCTION

Traditional forms of Hebbian synaptic plasticity have the potential to modify synaptic strength too far in either direction, potentially leading to runaway activity in a circuit. Homeostatic plasticity provides a way to globally scale up or down synapses to maintain the relative strengths of individual synapses without maxing out the system. Neurons are able to homeostatically regulate synaptic strength by controlling α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA) receptor (AMPAR) surface expression. This can be seen by measuring changes in the amplitudes of AMPAR-mediated miniature excitatory postsynaptic currents (mEPSCs), as well as staining of surface AMPARs (Thiagarajan et al., 2005; Turrigiano et al., 1998). These changes are inducible in culture using pharmacological reagents that increase or decrease activity levels. Tetrodotoxin (TTX), a sodium channel blocker, blocks the action potentials in the culture, decreasing neuronal activity. Conversely, bicuculline (Bic), a γ-aminobutyric acid type A ($GABA_A$) receptor antagonist, blocks the major inhibitory input in the cultures, leading to a burst of synaptic activity. Deficits in the homeostatic regulation of synaptic strength (synaptic scaling) have been identified in many models of psychiatric disorders, such as autism spectrum disorders and schizophrenia (Wondolowski and Dickman, 2013), suggesting that the tight control of network activity is crucial for proper neuronal function.

Several gene products have been shown to function in scaling (Turrigiano, 2011). For example, BDNF, tumor necrosis factor alpha (TNF-α), integrin beta-3 (β3), PICK1, and PSD95 have all been implicated in upregulating the synaptic strength in response to chronic activity deprivation, mainly by increasing AMPAR accumulation at synapses. Polo-like kinase 2 (Plk2), CDK5, ARC, Homer1a and EphA4 mediate the opposite effect (scaling down) in response to a chronic increase in neural activity. Therefore, although synaptic scaling occurs bidirectionally depending on the level of intracellular calcium, different sets of effector molecules mediate each direction of the scaling process.

Although increases in AMPAR levels can be seen as early as 4–6 hr after activity silencing, this increase in synaptic strength can continue for up to 24 or 48 hr (Ibata et al., 2008). This time window of synaptic upscaling suggests that nuclear signaling and transcription might be involved. Consistently, addition of the transcription inhibitor actinomycin D in cortical neuronal cultures blocked the TTX-induced increase in mEPSC amplitude (Ibata et al., 2008), suggesting the importance of gene transcription in synaptic upscaling in response to activity suppression. However, the mechanism and function of activity-regulated transcription in neurons have mostly been studied in conditions during which activity is increased, as with Bic, rather than when activity is absent. Upon an increase in neural activity, calcium influx through the NMDA receptor (NMDAR) and/or L-type voltage-gated calcium channel (L-VGCC) triggers activation of distinct calcium-dependent signaling pathways, which then modulate the activity of various transcription factors (e.g., CREB, MEF2, and SRF) to induce expression of a specific

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gene set (Flavell and Greenberg, 2008). Gene products from the transcription induced by increased neural activity then mediate the cell-wide adaptive responses important for proper neuronal development and plasticity. However, little is known about whether there is a neuronal transcription program that is inherently designed to mediate the adaptive response to the opposite condition, when neuronal activity is suppressed.

To determine the transcription program responsible for gene induction during the quiescent state that invokes synaptic upscaling, we performed RNA sequencing (RNA-seq), as well as global nuclear run-on sequencing (GRO-seq) in mouse cortical neurons before and after TTX treatment and identified 73 genes whose expression is reproducibly upregulated by TTX-mediated activity blockade. One gene in particular, *Neuronal pentraxin-1* (*Nptx1*) was found to be necessary for the TTX-induced scaling effect, fitting with its known role in promoting the clustering of AMPARs (Sia et al., 2007; Xu et al., 2003). Further characterization of the *Nptx1* induction mechanism revealed that calcium-regulated transcription factors appear to mediate this pathway, and we discovered that the T-type voltage-gated calcium channels (T-VGCCs) initiate this pathway, providing insight into a role for this channel in neuronal activity-dependent gene regulation.

RESULTS

Genome-wide Identification of Genes that Are Upregulated in Response to TTX

To examine the transcription program that specifically mediates TTX-induced homeostatic scaling, we performed RNA-seq analysis from neuron cultures treated with TTX for 2 or 6 hr at 12 days in vitro (DIV). We reasoned that because actinomycin D blocked TTX-induced homeostatic upscaling (Ibata et al., 2008), genes whose expression is increased upon activity suppression might be functionally implicated in the process. As a control, we also treated neurons with Bic for the same periods to ensure the neurons are transcriptionally responsive to bidirectional activity manipulations (Figure 1A). We took the data from two biological replicates and identified differentially regulated genes at a false discovery rate (FDR) < 0.05 and a fold change cutoff of 1.25 (see Experimental Procedures). A total of 73 genes were reproducibly induced by TTX, whereas the Bic-mediated synaptic activity burst induced 888 genes at either time point. These two gene sets showed little overlap, suggesting that gene induction in response to TTX and Bic are mediated by distinct pathways (Figure 1B). However, a large fraction of each gene set showed bidirectional changes such that genes induced by TTX tend to be downregulated by Bic, and vice versa (Figure 1C). Under our filtering criteria, 28 of 73 TTX-induced genes are significantly downregulated by Bic (Figure S1C). If TTX-induced genes were to actively mediate synaptic upscaling by promoting AMPAR expression and/or trafficking to the surface, their expression should be decreased when neuronal activity is chronically increased; otherwise, their gene products would functionally interfere with the synaptic downscaling process. In principle, gene expression changes in any direction could be functionally relevant to homeostatic plasticity. Our data identify members of the cadherin family, such as *Chd10* and *Pcdh20*, to be bidirectionally regulated, with their expression decreasing in response to TTX and increasing in response to Bic (Table S1), and cell adhesion molecules, including N-cadherin (*Chd2*), have been previously implicated in scaling (Fernandes and Carvalho, 2016). Stargazin (*Cacng2*), a gene that is downregulated in response to Bic, has previously been identified as having a role in scaling in the visual cortex (Louros et al., 2014).

Gene Ontology analysis of TTX-induced genes did not show strong enrichment of any particular functional category but instead distributed throughout diverse functional categories such as mitogen-activated protein kinase (MAPK) signaling, RNA metabolism, and transcription (Figure 1D). When compared to a well-curated list of autism susceptibility genes, 7 of the 73 TTX-induced genes have been implicated in autism spectrum disorders (ASDs) (*Auts2*, *Cacna1h*, *Bbs4*, *Fan1*, *Ogt*, *Smg6*, and *Upf2*); previously published studies identified associations of another 5 genes, including *Nptx1*, with disorders like schizophrenia and bipolar disorder (Table S2) (Fernandez-Enright et al., 2014; Girirajan et al., 2013; Howerton et al., 2013; Ionita-Laza et al., 2014; Kalscheuer et al., 2007; Nguyen et al., 2013; Rajkumar et al., 2015; Sanders et al., 2013; Shinkai et al., 2002; Splawski et al., 2006; Sultana et al., 2002). The observed association of TTX-induced genes with psychiatric disorders suggests that activity suppression-induced gene expression might be important for proper cognitive function.

Among the 73 TTX-induced genes, we have chosen 8 candidate genes (*Auts2*, *Cacna1h*, *Rps6ka5*, *Nos1*, *Elk1*, *Mical3*, *Txnip,* and *Nptx1*) for further analysis, in parallel with traditional immediate-early genes like *Arc* and *c-fos* that show strong induction in response to Bic (Figures 1E–1G). Manual qRT-PCR was able to confirm the changes seen in the genome-wide data (Figure S1). A more extensive time course experiment revealed that there are roughly two groups of genes based on their induction kinetics, with one group peaking around 6 hr of TTX treatment and another increasing until 24 hr (Figure S2). Although the significance of the different kinetics of the two groups is unknown, this is reminiscent of the transcription induction profiles in response to an increase in neuronal activity (e.g., a Bic- or KCl-treated condition), in which rapid induction of immediate-early genes is followed by a second wave of transcription of slowly induced genes (Flavell and Greenberg, 2008). The slower overall expression kinetics of TTX-induced genes also fit nicely with the previously shown time window for TTX-induced scaling of 4–48 hr.

To examine the transcriptional response to activity suppression more directly, we used GRO-seq to globally measure actively transcribed genes in response to TTX treatment. For the 73 genes that we identified as TTX-inducible based on mRNA sequencing (mRNA-seq), we find that most of them show a similar increase in transcription levels determined by GRO-seq (Figures 2A and 2B). Because GRO-seq only detects nascent transcription activity of RNA polymerase II (RNA Pol II) during the nuclear run-on (NRO) procedure, it generally shows faster expression kinetics than mRNA-seq. Several genes identified in our list are extremely long genes with multiple isoforms. One such gene, *Auts2*, showed only a slight increase by GRO-seq when looking at the longest isoform, but two of the shorter isoforms (uc008zut.1 and uc008zuu.1) showed much higher induction (Figure 2C), suggesting isoform-specific changes in

GO Term	Count	p Value
metal ion binding	21	0.00274
MAPK signaling pathway	4	0.002968
Immediate early response	2	0.008757
Basic-leucine zipper (bZIP) transcription factor	3	0.010914
regulation of transcription, DNA-dependent	10	0.012232
regulation of RNA metabolic process	10	0.013474

Figure 1. RNA-Seq Identifies a Subset of Genes Upregulated in Response to TTX

(A) Heatmap demonstrating the expression of genes that are regulated by either TTX or Bic at 2 or 6 hr of indicated treatments in cortical neurons. The 2 and 6 hr columns each contain two lanes showing replicates of the indicated treatments.

(B) Venn diagram showing the overlap between TTX- and Bic-upregulated (left) and TTX- and Bic-downregulated (right) genes.

(legend continued on next page)

expression in response to activity suppression. In addition, by using primers targeting intronic regions to detect nascent transcripts, we measured the levels of *Nptx1*, *Auts2,* and *Txnip* pre-mRNAs and saw induction upon treatment with TTX (Figure 2D). In parallel, we examined whether changes in mRNA stability would contribute to the TTX-induced increase in mRNA levels (Figure 2E). We blocked RNA Pol II transcription in TTX-pretreated or untreated control neurons by adding actinomycin D and monitored the decay rate of several candidate RNAs. Among tested genes, *Elk1* and *Mical3* showed a noticeable increase in mRNA stability when neurons were treated with TTX, but the rest of the tested genes showed little change in their mRNA stability. Altogether, our combined analysis of RNA-seq and GRO-seq strongly suggests that neurons have an intrinsic transcription network that can be induced in the absence of action potentials.

Nptx1 Is Necessary for Homeostatic Upregulation of Synaptic Strength

To evaluate the functional significance of the transcriptional response in neurons under activity blockade, we tested one of our candidate genes, *Nptx1* for its role in synaptic upscaling. NPTX1 protein (also known as NP1) plays a role in clustering AMPARs at the cell surface, which may imply its function in synaptic scaling. In addition to an increase in RNA levels, the total protein level of NP1 increased over time but peaked around 24 hr of TTX treatment (Figure 3A), supporting the idea that this protein could be playing a role in increasing synaptic strength. We further observed an increase in surface expression of NP1 protein in neurons treated with TTX for 24 hr (Figure 3B). To directly test the functional role of NP1 in homeostatic scaling, we measured AMPAR mEPSC amplitudes and frequencies in dissociated hippocampal cultures after knocking down *Nptx1*. Although TTX treatment of neurons with the scrambled (Scr) control for 24 hr significantly increased AMPA-mediated mEPSC amplitude without a significant change in mEPSC frequency (Scr, vehicle [veh]: 6.04 ± 1.41; Scr, TTX: 8.83 ± 2.60; not significant [NS] via Tukey's multiple comparisons test), knockdown of *Nptx1* blocked this increase in mEPSC amplitude (Figures 3C and 3D). However, there was no difference in the cumulative distributions of mEPSC amplitude between neurons infected with the scrambled control and *Nptx1* knockdown in the vehicle condition, illustrating that the knockdown does not change baseline AMPAR surface expression ($p = 0.17$ via Kolmogorov-Smirnov [K-S] test; $D = 0.4$) (Figures 3E and 3F). Conversely, sustained overexpression of NP1 protein alone caused a significant increase in AMPAR amplitude, occluding the effect of TTX treatment (Figures S3A and S3B). There were no significant changes in mEPSC frequency when NP1 was knocked down or overexpressed (Scr, veh: 6.04 ± 1.41; knockdown, veh: 7.72 ± 2.37; overexpression, veh: 9.88 ± 1.36; NS via Tukey's multiple comparisons test). These results suggest that the TTX-induced increase in NP1 is functionally important for the homeostatic synaptic upscaling process and that the precise level of NP1 within the cell is critical for maintaining proper AMPAR levels at the surface.

SRF and ELK1 Mediate TTX-Dependent *Nptx1* Induction

We next conducted a screen of several activity-regulated transcription factors (SRF, CREB, MEF2A, or MEF2D) in cortical neurons to see if any were necessary for *Nptx1* induction. While knocking down CREB and MEF2A individually showed a slight decrease in the TTX-dependent induction of *Nptx1*, MEF2D knockdown had no effect (Figures S4A and S4B). Knockdown of SRF significantly impaired the induction of several candidate genes: *Nptx1*, *Rps6ka5*, and *Auts2* (Figures 4A and S5A). These activity-regulated transcription factors have been extensively characterized for their roles in transcription when neural activity is increased (Flavell and Greenberg, 2008). Their activities are tightly regulated by various calcium-dependent signaling pathways triggered by influx of extracellular calcium through the NMDAR and/or L-VGCC. However, our finding suggests that at least some of these transcription factors might also promote transcription under the opposite condition, when neural activity is chronically suppressed.

SRF has been known to work with other cofactors to convert specific signal inputs into differential gene activation (Knöll and Nordheim, 2009). The two best characterized cofactor families are the ternary complex factors (TCFs) and members of the myocardin family (MRTF). Both MAPK and Ca^{2+} signaling have been shown to regulate the activity of TCFs through extensive phosphorylation. Actin signaling dynamically controls MRTF trafficking in which monomeric G-actins sequester them in the cytoplasm, whereas filamentous F-actins trigger translocation of MRTFs into the nucleus to drive transcription with SRF. MRTFs are mainly composed of MRTF-A and MRTF-B, and ternary complex factors (TCFs) are made up of ELK family members. Based on our RNA-seq data, MRTF-A (*Mkl-1*), MRTF-B (*Mkl-2*), ELK1 (*Elk1*), and ELK4 (*Elk4*) are highly expressed in cortical neurons, while ELK3 (*Elk3*) is expressed at an extremely low level (Figure S5B). To determine which cofactor or cofactors are required for SRF-mediated transcription of the *Nptx1* gene, knockdown of both MRTF-A and MRTF-B, with a short hairpin RNA (shRNA) targeting a common region between the two genes, and knockdown of ELK1 or ELK4 were performed in cortical cultures. Despite similar knockdown efficiency of each of the factors (Figures 4B and S5C), only knockdown of ELK1 impaired the TTX-mediated induction of *Nptx1*, suggesting that the activating signal to increase *Nptx1* expression works through the SRF cofactor ELK1 (Figure 4B). *Elk1* is the only cofactor gene that

(C) Boxplots of the log2 values for TTX-upregulated genes (left) or Bic-upregulated genes (right) in each condition normalized to the untreated (UN) condition. A gray dotted line is present at 0 to represent no change.
(D) Select GO terms identified for the TTX-upregulated genes.
(E) Genome browser views of example genes that are upregulated by TTX: *Nptx1*, *Rps6ka5*, *Auts2*, and *Cacna1h*.
(F) Genome browser views of an example gene that is upregulated in response to Bic: *Arc*.
(G) Graphs displaying the reads per kilobase of transcript per million mapped reads (RPKM) values of the example genes for the indicated conditions.
See also Figures S1 and S2.

Figure 2. GRO-Seq Confirms an Active Transcription Program in Response to Activity Suppression

(A) Heatmap of the 73 TTX-upregulated genes identified by mRNA-seq, showing their expression normalized to unstimulated. Each time point shows the data of two biological replicates.

(B) Genome browser views showing the global nuclear run-on sequencing (GRO-seq) tracks aligned with four of the candidate genes in response to 30 min, 2 hr, or 4 hr TTX treatment. Below the tracks are graphs displaying the RPKM values for each condition.

(C) Genome browser view of the shorter isoforms of *Auts2* (top), along with isoform-specific RPKM values for the indicated time points (bottom).

(D) qRT-PCR results from cells that were treated with TTX for the indicated time points. Pre-mRNA levels were measured for the indicated genes.

(E) RNA levels of the indicated genes after treatment with actinomycin D (Act D) for the indicated time points, with or without a 15 min pretreatment with TTX. n = 3 biological replicates. *$p < 0.05$. The p values were determined by a two-way ANOVA. Error bars represent SEM.

Figure 3. *Nptx1* Is Functionally Important for Homeostatic Scaling

(A) Western blot of NP1 and β-actin expression in cortical neurons that were treated with TTX for the indicated time points (top) and the quantification of the induction (bottom). n = 3 biological replicates.

(B) Staining of surface NP1 levels on neuronal dendrites in untreated (UN) or TTX-treated (24 hr) conditions, with the quantification below. n = 13 and 15 dendrites for UN and TTX conditions, respectively.

(C and D) Example traces, cumulative probability histograms, and rank order plots of AMPA-mediated mEPSC amplitudes from cells treated with either vehicle or TTX after infection with the scrambled control (C) or NP1 knockdown (D). Scramble vehicle (n = 9) versus scramble TTX (n = 8): $p = 1.5 \times 10^{-74}$, D = 0.31. Knockdown vehicle (n = 7) versus knockdown TTX (n = 8): $p = 7.3 \times 10^{-5}$, D = 0.08.

(E) Cumulative probability histograms from vehicle-treated conditions of either scrambled or knockdown cells from (C) and (D) overlaid. p = 0.03, D = 0.17. See also Figure S3.

(F) Representative western blot of the efficiency of NP1 knockdown in the scaling experiments.

*p < 0.05; **p < 0.01. The p values were determined by an unpaired Student's t test. Statistical significance between cumulative probability graphs was determined by the Kolmogorov-Smirnov test. Error bars represent SEM.

shows increased expression in response to TTX, which might be due to an increase in mRNA stability (Figures 1E, 2E, and 4B). ELK1 knockdown also blocked induction of *Auts2* and *Cacna1h* (Figure S5D). Therefore, ELK1 also participates in the TTX-dependent transcriptional induction, possibly in conjunction with SRF.

To determine whether the *Nptx1* gene is a direct target of SRF, we examined the promoter and enhancer regions of the *Nptx1* gene for SRF binding. We used the histone H3 lysine 27 acetylation (H3K27Ac) profiles determined for neuron cultures treated with 55 mM KCl or TTX to identify potential enhancer regions near the *Nptx1* gene, because H3K27Ac is a marker for active enhancers (Malik et al., 2014). Based on these profiles, we identified one potential enhancer downstream of *Nptx1* (E1) (Figure 4C). The H3K27Ac level was high at this enhancer under TTX-mediated activity suppression (overnight treatment of TTX) but then decreased when neurons were depolarized by KCl, implying that the enhancer became activated by activity blockade. Further supporting this idea, qRT-PCR primers directed against this region detected enhancer RNAs (eRNAs) that were induced in response to TTX (Figure 4D). Because eRNAs have been shown to be a reliable marker of active enhancers within a given cell type (Kim and Shiekhattar, 2015), this also suggests that this region is an enhancer that is activated in response to activity suppression. To address whether this was a feature common to enhancers of TTX-induced genes, we compared the peaks that decreased in response to KCl genome-wide with our list of TTX-induced genes. Of the ~2,000 H3K27Ac peaks that decreased in response to KCl, 600 genes were found within 10 kb of a peak, including 12 of our TTX-upregulated genes (Figure 4E, left). Expanding the distance to within 50 kb of an H3K27Ac peak, there were 2,130 genes identified, 22 of which overlapped with our 73 TTX-upregulated genes (Figure 4E, right), including *Txnip*, *Nos1,* and *Syt13* (Figure S6A). The overlaps at both distances are significant

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(p = 0.0001689 and p = 0.0031693, respectively). This analysis suggests that there might be a genome-wide epigenetic mechanism to regulate the activity of a large number of enhancers, which in turn promotes transcriptional induction of specific gene sets in response to low activity levels.

We also looked for serum response elements (SREs) containing the motif of $CC(A/T)_6GG$ in the genomic regions surrounding the *Nptx1* locus, using the Regulatory Sequence Analysis Tool (RSAT) (Miano, 2003; Thomas-Chollier et al., 2011). There are two canonical SRE sites: the first is ~20 kb downstream of *Nptx1* (SRE1), and the second is ~10 kb upstream of *Nptx1* within an H3K27Ac peak present in the forebrain early in development (SRE2) (Figures 4C and S6B) (Nord et al., 2013). When allowing for one mismatch in the motif, there is another potential SRE found within an intron (Intron) (Figure 4C) of *Nptx1* that is highly conserved evolutionarily. Our chromatin immunoprecipitation (ChIP) analysis revealed that the SRF binding level increases ~2-fold in response to TTX at the site within the intron of *Nptx1* (Figure 4F). These results suggest that SRF is directly regulating the transcriptional induction of *Nptx1* in response to activity suppression. We also observed TTX-induced ELK1 binding at the potential downstream enhancer (E1), suggesting that this cofactor is also directly affecting *Nptx1* transcription (Figure 4G).

Calcium-Mediated Signaling through T-type VGCC Is Critical for TTX-Induced Transcription

Previous studies suggested that TTX-induced synaptic upscaling can be mimicked by a reduction in calcium (Ca^{2+}) influx through the L-type channel or by reduced activity of Ca^{2+}/calmodulin-dependent protein kinase (CaMK) K and CaMKIV (Ibata et al., 2008; Turrigiano et al., 1998). However, we found that influx of extracellular calcium is necessary to activate the TTX-specific nuclear signaling. Pretreatment of neurons with the calcium chelator, EGTA, or a cell-permeable form of the compound, EGTA-AM, that only becomes active once inside the cell was able to block the induction of *Nptx1* in response to TTX (Figure 5A).

To determine the source of calcium entry, we then tested inhibitors of calcium channels important for nuclear gene expression upon an increase in neural activity: 2,3-dihydroxy-6-nitro-7-sulfamoyl-benzo[f]quinoxaline-2,3-dione (NBQX), a selective inhibitor of AMPARs; AP-5, an inhibitor of NMDARs; and nimodipine, a blocker of the L-type VGCC. None of these compounds were able to block TTX-mediated *Nptx1* induction, even though they were all, to varying degrees, able to block *Arc* induction by Bic (Figure 5B). Next, we pretreated neurons with cadmium (Cd^{2+}), a general VGCC blocker, before addition of TTX and observed a dose-dependent decrease in *Nptx1* induction (Figure 5C). To elucidate which VGCC is regulating the induction of genes during TTX treatment, we tested inhibitors of all known VGCCs (L-, N-, P/Q-, R-, and T-type VGCCs) and found that only T-type VGCC blockers NNC 55-0396 dihydrochloride, mibefradil, and TTA-A2 significantly inhibited the *Nptx1* induction in response to TTX (Figures 5D and 5E). All three subtypes of T-VGCC are expressed in our cortical neuronal culture: CaV3.1 (*Cacna1g*), CaV3.2 (*Cacna1h*), and CaV3.3 (*Cacna1i*). One in particular, *Cacna1h*, is also induced in response to TTX and has been implicated in ASD (Figures 1, 2, and S7A; Table S2). Knockdown of *Cacna1h* or treatment with the T-type blocker TTA-A2 was able to block induction of several TTX-induced genes in addition to *Nptx1* (Figures 5F, S7B, and S7C).

Furthermore, TTA-A2 blocked the TTX-induced increase in AMPA-mediated current, suggesting that the T-VGCC is also functionally required for homeostatic synaptic upscaling (Figure 6A). Unlike other VGCCs (L-, R-, N-, and P/Q-type VGCCs), the T-VGCC is a low-voltage activated (LVA) channel that can operate even when Na^+ channels are blocked by TTX (Iftinca and Zamponi, 2009). The T-VGCC only opens within a small voltage window near resting membrane potential (Iftinca and Zamponi, 2009; Tsien, 1998). If the T-VGCC activity is required for mediating gene induction in the TTX-treated condition, mild depolarization of neurons to potentials past the channel's window current should block the induction seen with TTX. To test this idea, the external K^+ concentration was raised from 5 to 11 mM KCl during the TTX exposure, and we found that this was able to block the induction of *Nptx1* and *Auts2,* while there was no effect with an increase of NaCl (Figure 6B). This result is consistent with the premise that T-VGCC channels are responsible for this induction. We next performed a time course experiment with the T-VGCC blocker NNC 55-0396, which revealed that the inhibitory effects of T-VGCC block decrease with greater delay in drug treatment (Figure 6C). This suggests that prolonged channel activity throughout the duration of activity suppression

Figure 4. SRF and Its Cofactor ELK1 Regulate the Expression of *Nptx1*

(A) qRT-PCR results from cells that were infected with the scrambled control or shSRF knockdown. Cells were left untreated (UN) or treated with TTX or Bic. n = 3 biological replicates. See also Figure S4.

(B) qRT-PCR results from cells that were infected with an shRNA targeting the indicated cofactor family member (shMRTFA/B, shElk1, or shElk4) compared to a scrambled control. Cells were either left untreated or treated with TTX or Bic. n = 3 biological replicates. The p values determined by a two-way ANOVA with Tukey's multiple comparisons test.

(C) University of California, Santa Cruz (UCSC) genome browser view of the *Nptx1* locus aligned with H3K27Ac ChIP-seq from Malik et al. (2014) and the RNA-seq data from TTX-treated cells. The qPCR primer sets used in the ChIP experiments below are labeled with black bars. SRE1 and SRE4 are potential serum response elements (SREs) based on SRF's consensus sequence. E1 aligns with the H3K27Ac peak, with the blue bar highlighting the decreasing peak. Intron amplifies an intronic conserved region. Neg1 is a negative control region upstream of *Nptx1*, while Neg2 is a negative control on another chromosome. See also Figure S6.

(D) qRT-PCR results of an eRNA expressed from the potential enhancer region of *Nptx1* in response to 6 hr TTX treatment. n = 3 biological replicates.

(E) Venn diagrams demonstrating the overlap of genes throughout the genome that were within 10 kb (left) or 50 kb (right) of a H3K27Ac peak that decreased in response to KCl and the 73 genes found to be significantly upregulated in response to TTX. The p values determined by the hypergeometric test.

(F and G) ChIP results of SRF binding (F) or ELK1 binding (G) at the indicated loci around the *Nptx1* gene. n = 4 biological replicates for the SRF ChIP, n = 3 biological replicates for the ELK ChIP. The p values determined by a two-way ANOVA with Tukey's multiple comparisons test, comparing the primer set of interest with the negative region (Neg2).

*p < 0.05; **p < 0.01; ***p < 0.001. Error bars represent SEM.

Figure 5. T-type VGCC Mediates *Nptx1* Induction in Response to TTX Treatment

(A) Cortical neurons at 14 DIV were pretreated with EGTA or EGTA-AM before being treated with TTX for 4 hr. Levels of *Nptx1* were measured by qRT-PCR. The vehicle control for EGTA-AM is DMSO.

(B) Expression levels of *Nptx1* and *Arc* were measured with qRT-PCR from cortical neurons that were pretreated with NBQX, (*2R*)-amino-5-phosphonovaleric acid (AP-V), or nimodipine (Nimo) before treatment with TTX or Bic.

(C) Cortical neurons were pretreated with 100 or 200 μM cadmium (Cd^{2+}) before treatment with TTX or treated with 200 μM Cd^{2+} alone. n = 3 biological replicates.

(D) Cortical neurons were pretreated with nimodipine (Nimo), ω-agatoxin IVA (ω-Aga), ω-conotoxin GVIA (ω-Cono), or SNX-482 before treatment with TTX or Bic. Vehicle is DMSO. n = 3 biological replicates.

(E) Blockers of the T-VGCC, NNC 55-0396 (NNC), mibefradil, or TTA-A2 were used to pretreat cortical neurons for 15 min before treatment with TTX. n = 5 biological replicates. In all preceding bar graphs, black bars represent untreated cells. Dark gray bars represent cells treated with TTX and pretreated with the indicated compounds. Light gray bars represent cells treated with Bic and pretreated with the indicated compounds. See also Figure S7.

(F) Cells were infected with a lentivirus containing either an shRNA targeting the CaV3.2 gene (*shCacna1h*) or a scrambled control. The levels of the indicated genes were measured by qRT-PCR. n = 3 biological replicates.

*$p < 0.05$; **$p < 0.01$; ***$p < 0.001$. The p values determined by a one-way ANOVA using Dunnett's multiple comparisons test, except for (F), for which multiple t tests were performed and statistical significance was determined using the Holm-Sidak multiple comparison test.

mediates the upregulation of TTX-induced genes. This is in contrast to the gene induction in response to an increase in activity, in which an immediate-early phase of calcium signaling through L-VGCC and/or NMDAR following the activity increase seems critical for ensuring late long-term potentiation (LTP) (Deisseroth et al., 1996; Saha et al., 2011; West et al., 2002).

To further characterize the calcium signaling pathway, we tested the necessity of components of the MAPK signaling pathways, because MAPK signaling is known to regulate ELK1/SRF transcription (Hill et al., 1993), and components of this pathway were identified in our Gene Ontology (GO) analysis (Figure 1D). However, different inhibitors of this pathway did not show significant effects on *Nptx1* induction (Figure S8A). A previous study showed that inhibition of CaMKIV, by blocking its upstream kinase CaMKK with STO-609, or a drop in somatic calcium influx through the L-VGCC was sufficient to induce synaptic upscaling in a manner similar to TTX (Ibata et al., 2008). However, addition of STO-609 alone or together with TTX had no significant effect on the expression of *Nptx1* and other TTX-induced genes (Figure S8B). In contrast, the CaMKII inhibitor KN-62 alone was sufficient to cause *Nptx1* induction to a level similar to TTX and occluded the effect of TTX (Figure S8C). Three additional TTX-induced genes showed a similar increase in their mRNA levels by KN-62 alone, suggesting KN-62 alone is sufficient to mimic these TTX-induced transcriptional changes. Blocking the L-VGCC and NMDAR individually induces *Nptx1* and *Auts2* expression as well, similar to when activity is suppressed by TTX (Figure 6D). The gene expression driven by these treatments is also commonly inhibited by blocking the T-VGCC, which suggests a common mechanism (Figure 6E). Therefore, the TTX-induced transcription program we have defined is related to the signaling pathway previously characterized for synaptic upscaling (Ibata et al., 2008; Turrigiano et al., 1998), and T-VGCC activity is required for this TTX-induced transcription program.

Gene Induction Occurs during Activity Suppression In Vivo

Homeostatic scaling has been shown to occur in layer 2/3 (L2/3) pyramidal neurons of the visual cortex upon visual deprivation (Goel and Lee, 2007; Lambo and Turrigiano, 2013; Maffei and Turrigiano, 2008). To see whether the synaptic upscaling observed in the visual cortex is accompanied by a transcriptional

Figure 6. T-VGCC Is Necessary for Scaling

(A) Example traces, cumulative probability histograms, and rank order plots of cells that were pretreated with either TTA-A2 or vehicle and then treated with TTX for 24 hr. n = 9 cells for the untreated condition, n = 10 cells for both TTX-treated conditions. TTA-A2/TTX versus vehicle/TTX (n = 10 cells each): $p = 2.11 \times 10^{-27}$, D = 0.185. Vehicle/TTX versus untreated (n = 9 cells): $p = 4.79 \times 10^{-6}$, D = 0.08. Statistical significance between cumulative probability graphs was determined by the Kolmogorov-Smirnov test.

(B) Cells were pretreated with 6 mM KCl or 6 mM NaCl before the addition of TTX for 6 hr.

(C) T-VGCC blocker was added either 15 min before the addition of TTX or 30 min, 2 hr, or 4 hr after the addition of TTX. The total time of TTX treatment was 6 hr. *Nptx1* and *Auts2* RNA levels were measured with qRT-PCR.

(D) Neurons were treated with the indicated blockers for 6 hr, and the RNA levels of the indicated genes were measured with qRT-PCR.

(E) Cells were pretreated with the VGCC blocker TTA-A2, before the addition of the NMDAR or L-VGCC blocker. RNA levels of the indicated genes were measured with qRT-PCR.

For bar graphs, *$p < 0.05$; **$p < 0.01$. The p values determined by a one-way ANOVA using Dunnett's multiple comparisons test. Error bars represent SEM.

response during dark rearing (DR), we housed mice in the dark for 24 hr and then measured RNA levels in the visual cortex compared to those of mice that were housed in a normal 12 hr light/dark cycle (Figure 7A). While the DR condition led to a significant decrease in the expression of activity-induced genes such as *c-fos* and *Arc*, a subset of TTX-induced genes, including *Nptx1*, was upregulated (Figure 7B). In addition to an increase in RNA levels, we observed an increase in NP1 protein levels by both western blot and immunohistochemistry in the visual cortex following 3 days of DR (Figures 7C and 7D). Though dark rearing represents a physiological method to induce synaptic scaling, it does not suppress all spontaneous action potentials in the retina (Hengen et al., 2016). To better reproduce the in vitro findings, we performed intraocular injections of TTX, which silence all activity coming from the retina and have previously been shown to trigger scaling up of AMPAR activity in the visual cortex (Desai et al., 2002; Frenkel and Bear, 2004) This alternative visual deprivation protocol was also able to show an increase in most of the tested TTX-induced genes in a more reliable manner than the dark rearing paradigm (Figure 7E). Altogether, these results indicate the existence of an intrinsic transcription program that can induce expression of specific genes in response to activity suppression in vivo.

DISCUSSION

In this study, we have identified a transcriptional program that is activated in response to neuronal activity suppression and drives a homeostatic increase in synaptic strength. This program requires T-VGCC-dependent Ca^{2+} signaling and the function of activity-regulated transcription factors like SRF and ELK1. Transcriptional induction during neuronal inactivity appears to be an important process for homeostatic plasticity, because one of the genes induced by activity blockade, *Nptx1*, is necessary and sufficient to increase AMPAR amplitude.

Homeostatic scaling is crucial for proper neuronal function and maintaining balance between excitation and inhibition. This is highlighted by several models of psychiatric disorders showing deficits in scaling (Wondolowski and Dickman, 2013). Multiple genes in our list of TTX-induced genes have also been linked to neurological disorders such as ASD and schizophrenia (Table S2), which further implies a functional relevance of this program. *Auts2* has gained attention as an autism susceptibility gene (Gao et al., 2014), as has *Cacna1h,* which encodes a subtype of T-VGCC that we have shown to be the critical VGCC mediating this response. Other genes in our list have been implicated previously in homeostatic scaling. *Rps6ka5* encodes a kinase (MSK1) that is necessary for TTX-induced scaling, and *Nos1*, a gene linked to schizophrenia, was identified in a study looking at transcriptional changes after long-term (48 hr) treatment of TTX, although no functional

(legend on next page)

studies for this gene were performed (Corrêa et al., 2012; Lee and Chung, 2014).

Studies suggest that activity-dependent changes in DNA methylation levels mediated by enzymes such as DNA methyltransferase (DNMT) or the Ten-eleven translocation (Tet) family protein Tet3 are a critical mechanism of synaptic scaling (Meadows et al., 2015; Nelson et al., 2008; Yu et al., 2015). However, how these enzymes selectively alter the expression of genes related to synaptic scaling has not been demonstrated. When neural activity is suppressed, many activity-induced genes show slightly dampened expression compared to the basal culture condition, which could also be related to the neuron's compensatory response to maintain a stable firing rate. For example, chronic activity blockade of hippocampal neurons resulted in an overall reduction of potassium current with a concomitant decrease in expression levels of voltage-gated K_V1 and K_V7 potassium channels, which was explained as a mechanism for the homeostatic increase in intrinsic excitability (Lee et al., 2015).

The transcription program characterized in our study appears to be related to the previously defined signaling pathway, because we observed that pharmacological inhibition of the L-VGCC or NMDAR alone could mimic the gene induction mediated by TTX (Figure 6D). A time course experiment of the T-VGCC inhibitor NNC 55-0396 elucidates that the continuous activity of T-VGCC for a prolonged period might underlie gene induction (Figure 6C). These results could further imply that the tonic activity or signaling of the T-VGCC at rest might be suppressed or overridden by other calcium channel activities such as by the L-VGCC and NMDAR. The T-VGCC signaling to the nucleus might then become effective when the other calcium channel activities are directly inhibited by specific blockers or when neuronal firing is silenced by TTX.

Knockdown of *Nptx1* was able to block the TTX-induced upscaling of synaptic strength, which suggests a functional relevance of gene induction. A previous study proposed that *Nptx1* might be a proapoptotic gene based on the findings that it is overexpressed in cerebellar granule cells (CGNs) cultured with a low potassium concentration that causes cell death and that reducing *Nptx1* mRNA significantly attenuated cell death (DeGregorio-Rocasolano et al., 2001). A subsequent study in rat cortical neurons described that knockdown of *Nptx1* increases the number of excitatory synapses and neuronal excitability, suggesting a function in the negative regulation of excitatory synaptic plasticity (Figueiro-Silva et al., 2015). These functions of *Nptx1* are ostensibly incompatible with the previously defined role of *Nptx1* in AMPAR clustering and potentiating postsynaptic response, as well as our finding in homeostatic synapse upscaling. We speculate that the previous studies and ours examine different stages of physiological consequences that might result from alterations in *Nptx1* levels. Our study investigates the early stage (12–24 hr) of homeostatic synapse plasticity initiated by activity blockade, at which point we only observed increased AMPAR amplitude and ~2- to 2.5-fold increases in *Nptx1* mRNA and protein levels, peaking at 6 and 24 hr, respectively. During this period, *Nptx1* knockdown blocked the TTX-induced upscaling of synaptic strength. However, a prolonged period of activity suppression (e.g., TTX treatment for 2 days or longer) or *Nptx1* knockdown might force neurons to trigger additional, more drastic homeostatic responses, such as changes in intrinsic excitability, presynaptic release probability, or even synapse numbers (Bacci et al., 2001; Burrone et al., 2002; Murthy et al., 2001), in which *Nptx1* might also be functionally involved. Chronic activity blockade by TTX has been widely used and does not cause significant cell death for at least a few days. The previously shown proapoptotic function of *Nptx1* was studied in CGNs under low potassium concentration, which caused 40% cell death within 24 hr and induced a more dramatic increase of *Nptx1* mRNA and protein. We think that a mild increase in *Nptx1* levels during the early period of activity blockade is a physiologically important process for a neuron's homeostatic synaptic plasticity.

Nptx1 induction was mediated through the activity of the transcription factors SRF and ELK1, which have a well-known role in transcription in the opposite scenario, when activity is increased. However, to a lesser degree, other activity-regulated transcription factors, such as CREB and MEF2A, appear to participate in the transcription program in response to activity blockade as well (Figure S4). These findings provide important insight into the understanding of the activity-regulated transcription program in neurons, showing that at least some transcription factors can engage in transcriptional induction in two opposing conditions: when neural activity is high or low. Despite the bidirectional function of transcription factors, our RNA-seq data show that each activity condition induces a distinct set of genes, suggesting that those bidirectional transcription factors might coordinate with condition-specific factors to confer the target gene specificity. Therefore, it would be interesting to determine a more comprehensive list of transcription factors for their unique or specialized role in the transcription program at rest.

Our findings suggest a key function of the T-VGCC in homeostatic synaptic plasticity through the regulation of nuclear transcription. T-VGCCs are abundant in hippocampal neuronal dendrites, along with other key VGCCs (Kavalali et al., 1997;

Figure 7. *Nptx1* Is Induced In Vivo

(A) Schematic timeline of the dark rearing behavior experiment. Mice were either housed in a normal 12 hr light/dark cycle or placed in a completely dark chamber for 24 hr.

(B) qRT-PCR results of the indicated genes that are induced in the visual cortex in response to dark housing for 24 hr. n = 3 biological replicates.

(C) Staining of the visual cortex with an antibody against NP1, costained with the nuclear marker DAPI. Images taken at 10× magnification.

(D) Western blot results from the visual cortices of mice that were dark reared for 3 days compared to those reared in a normal light/dark cycle. Quantification of the western blot results of NP1 normalized to β-actin. n = 5 biological replicates.

(E) qRT-PCR results of the visual cortices of mice that were injected intraocularly with either PBS or TTX. n = 4 biological replicates.

*$p < 0.05$; **$p < 0.01$; ***$p < 0.001$. The p values were determined with an unpaired Student's t test for dark rearing experiments. The p values for the intraocular injections were determined using a paired t test. Error bars represent SEM.

Magee and Johnston, 1995). However, they are also unique among the VGCCs, because these channels are low-voltage activated (LVA) channels, while the other types (L-, R-, N-, and P/Q-type VGCCs) are high-voltage activated (HVA) (Randall and Tsien, 1997). The T-VGCC can operate even when Na^+ channels are blocked by TTX (Iftinca and Zamponi, 2009). Compared to HVA channels, T-VGCCs open in response to smaller depolarizations, have smaller conductances, and inactivate slowly near resting potential. After opening, increased voltage produces greater inactivation such that these channels operate over a small voltage window near resting membrane potential. Recovery from inactivation is facilitated by a brief hyperpolarization, at which point they may trigger bursts of action potentials. These properties make T-type calcium channels ideal candidates to produce calcium signals near resting potential (Iftinca and Zamponi, 2009; Tsien, 1998). Our findings further suggest that these properties would make the T-VGCC ideal for transmitting the signal to the nucleus when neural activity is suppressed. The identification of this channel as a regulator of gene expression opens up a new avenue of research in understanding the role of the T-VGCC in neuronal function.

EXPERIMENTAL PROCEDURES

Cell Culture

All experiments carried out with the use of animals were reviewed and approved by the Institutional Animal Care and Use Committee (IACUC) committee at University of Texas Southwestern Medical Center. Primary cortical cultures were made from embryonic day 16–18 (E16– E18) mice, and they were grown in Neurobasal media supplemented with B-27 and Glutamax. AraC was added at 6 DIV to prevent glial proliferation. Cells were used in experiments 12–15 days in vitro (DIV), as indicated. Hippocampal cultures were made from postnatal day 1–3 (P1–P3) rat pups and cultured as described previously (Kavalali et al., 1999).

Whole-Cell Voltage Clamp Recordings

At 14–18 DIV, dissociated hippocampal cultures were voltage-clamped at −70 mV, as previously described (Reese and Kavalali, 2015), using an Axon Instruments Axopatch 200B amplifier. For detailed procedures, see the Supplemental Experimental Procedures.

RNA-Seq

Total RNA was extracted using Trizol reagent (Life Technologies), and the library was prepared using the TruSeq RNA Library Preparation Kit (Illumina) according to the manufacturer's instructions. The analysis procedure is described in the Supplemental Experimental Procedures.

GRO-Seq

GRO-seq was carried out as previously described (Core et al., 2008; Hah et al., 2011) with modifications (Danko et al., 2013; Lam et al., 2013), using 10 million nuclei per sample. Detailed procedures are described in the Supplemental Experimental Procedures.

qRT-PCR

Total RNA was extracted from neurons using Trizol reagent (Life Technologies) according to the manufacturer's protocol. cDNA was made with a high-capacity reverse transcription kit (Life Technologies), and amplification was performed with SybrGreen (Life Technologies) using the primers indicated in the Supplemental Experimental Procedures.

Visual Cortex Experiments

For all visual cortex experiments, male C57BL/6 mice were used at P21–P25. For detailed procedures, see the Supplemental Experimental Procedures.

ACCESSION NUMBERS

The accession number for the datasets reported in this paper is GEO: GSE90988.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, eight figures, and two tables and can be found with this article online at http://dx.doi.org/10.1016/j.celrep.2017.01.033.

AUTHOR CONTRIBUTIONS

T.-K.K., K.S., and E.T.K. designed the project. K.S. performed RNA-seq, transcription factor knockdown, ChIP, and RNA analysis of pharmacological experiments and T-type channel knockdown. A.L.R. performed the whole-cell patch clamping. S.-K.K. performed GRO-seq and nascent RNA analysis. G.K. performed the analysis for the sequencing data. J.-Y.J. provided the transcription factor knockdown constructs and helped with the visual cortex experiments. K.S. and T.-K.K. wrote the manuscript with input from E.T.K. and A.L.R. All authors discussed the results and commented on the manuscript.

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Supplemental Information

An Intrinsic Transcriptional Program Underlying Synaptic Scaling during Activity Suppression

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Figure S1. Confirmation of genome-wide data with RT-qPCR, Related to Figure 1. qRT-PCR results of TTX induced genes **(A)** and Bic induced genes **(B)** from cells that were treated with TTX or Bic for the indicated time points. n = 2 biological replicates. (C) Venn diagrams of bidirectional genes, comparing genes upregulated by bicuculline and downregulated by TTX (left) or genes downregulated by bicuculline and upregulated by TTX. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. p values determined by a one-way ANOVA using Dunnett's multiple comparisons test.

Figure S2. There are two waves of TTX-dependent gene induction, Related to Figure 1. qRT-PCR results from cells that were treated with TTX for the indicated time points. RNA levels were measured for the indicated genes. The columns represent distinct classes of genes based on their induction patterns. The left column contains genes that peak around 6 h of TTX treatment, while the middle column contains genes that continue to rise until 24 h. The right column contains immediate early genes that are induced in response to Bic, and decrease with TTX treatment. n = 3 biological replicates. Error bars represent SEM.

Figure S3. Overexpression of *Nptx1* occludes TTX-induced scaling, Related to Figure 3. (A) Example traces of AMPA-mediated mEPSCs from either vehicle or TTX treated cells. **(B)** Cumulative probability histograms of AMPA-mediated mEPSC amplitudes from cells overexpressing NP1 in either vehicle or TTX treated conditions indicate that TTX-induced scaling is occluded by high NP1 levels. NP1/TTX (n = 11) vs NP1/veh (n = 10), p = 0.005, D = 0.055.

Figure S4. Effects of activity-regulated transcription factors in TTX-dependent induction, Related to Figure 4. Cortical neurons were infected with lentiviruses containing a scrambled shRNA control or an shRNA targeting CREB, MEF2A, or MEF2D. **(A)** RNA levels of the indicated TTX or Bic induced gnes were measured with qRT-PCR. **(B)** RNA levels of the indicated transcription factor genes were measured with qRT-PCR to test knockdown efficiency. n = 3 biological replicates. *, $p < 0.05$; **, $p < 0.01$; ***, $p<0.001$. p values determined by a two-way ANOVA with Tukey's multiple comparisons test using GraphPad Prism. Error bars represent SEM.

A
Auts2
Cacna1h
Rps6ka5
Nos1
Mical3
Txnip
Elk1
Arc
Scr
shSRF
Fold Induction
(Normalized to Gapdh)
UN
TTX
Bic

B
Scale
50 kb
100 kb
5 kb
20 kb
10 kb
mm10
chr15:
81,100,000
chr16:
13,400,000
chrX:
20,940,000
20,950,000
chr10:
93,300,000
chr1:
132,030,000
UN
TTX 2h
TTX 6h
Bic 2h
Bic 6h
Mkl1
Mkl2
Elk1
Elk3
Elk4

C
Mkl1
Mkl2
Elk4
Scr
shMRTFA/B
shELK1
shELK4
Fold Induction
(Normalized to Tbp)
UN
TTX
Bic

D
Auts2
Cacna1h
Rps6ka5
Scr
shMRTFA/B
shELK1
shELK4
Fold Induction
(Normalized to Tbp)
UN
TTX
Bic

Figure S5. SRF and its cofactor ELK1 regulate the expression of TTX-induced genes, related to Figure 4. **(A)** qRT-PCR results of TTX-induced genes from cells that were infected with the scrambled control or shSRF knockdown. Cells were left untreated (UN) or treated with TTX or Bic. n = 3 biological replicates. The Bic induced gene *Arc* was tested as a control of knockdown efficiency. **(B)** UCSC genome browser views of the SRF cofactor family members: *Mkl1*, *Mkl2*, *Elk1*, *Elk3*, and *Elk4* (*left to right*). **(C)** qRT-PCR results of the other cofactor family members after knockdown of the indicated family member (shMRTFA/B or shElk4) compared to a scrambled control. Cells were either left untreated or treated with TTX or Bic. **(D)** qRT-PCR results of TTX-induced genes after the indicated cofactor knockdown. n = 3 biological replicates. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. p values determined by a two-way ANOVA with Tukey's multiple comparisons test. Error bars represent SEM.

Figure S6. H3K27Ac peaks surround TTX up regulated genes, Related to Figure 4. (A) UCSC genome browser views of genes with a decreasing H3K27Ac peak nearby: *Txnip*, *Nos1*, and *Syt13*. The H3K27Ac data from Malik et al., 2014 is aligned with the RNA-seq data for the idicated conditions. Blue bars represent the decreasing H3K27Ac peaks. **(B)** A UCSC genome browser view of the *Nptx1* gene aligned with RNA-seq data from the indicated conditions and H3K27Ac ChIP data from Nord et al., 2013. The H3K27Ac ChIP was performed with forebrain tissue at the indicated time points throughout development. A potential SRE (SRE2) is located within a peak that decreases throughout development, while the peak around the promoter expands into the intronic region (Intron) as develpment progresses. Red bars highlight the regions amplified in ChIP experiments.

A
Scale
20 kb
mm10
chr11:
94,450,000
UN
TTX 2h
TTX 6h
Cacna1g
Scale
20 kb
mm10
chr17:
25,400,000
Cacna1h
Scale
50 kb
mm10
chr15:
80,400,000
Cacna1i
B
Auts2
Nos1
Rps6ka5
Mical3
Elk1
Txnip
Scr
shCacna1h
Fold Induction
(Normalized to Tbp)
UN
TTX
C
Cacna1h
Nptx1
Auts2
Nos1
Rps6ka5
Mical3
Elk1
Txnip
UN
TTX+DMSO
TTX+TTA-A2
TTA-A2 only

Figure S7. Cortical neurons express all three isoforms of the T-VGCC, related to Figure 5. (A) UCSC genome browser views of the RNA-seq data from cells treated with TTX for 2 or 6 h, aligned with the genomic loci of the three T-VGCC genes: *Cacna1g*, *Cacna1h*, and *Cacna1i*. These genes encode the CaV3.1, CaV3.2, and CaV3.3 subtypes, respectively. **(B)** RNA expression levels of the indicated genes after knockdown of *Cacna1h* (CaV3.2) or infection with a scrambled control, in either untreated or TTX-treated conditions. n = 3 biological replicates. **(C)** RNA expression levels of the indicated genes in response to TTA-A2 treatment. Cells were either untreated (UN), treated with TTX for 6 h pretreated with DMSO or TTA-A2, or treated with TTA-A2 alone. n = 7 biological replicates. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. p values for **(B)** were determined by multiple t tests, as performed, where statistical significance was determined using the Holm-Sidak method. p values for **(C)** were determined using a one-way ANOVA using Dunnet's multiple comparisons test. Error bars represent SEM.

Figure S8. Calcium signaling pathways mediating induction, Related to Figure 7. (A) qRT-PCR results of cells treated with TTX for 6 h and pretreated with the indicated blockers of comoponents of the MAPK signaling pathway. n = 5 biological replicates. **(B)** qRT-PCR results of cells treated with TTX and/or STO-609. n = 4 biological replicates. **(C)** qRT-PCR results of cells treated with TTX and/or KN-62. DMSO was used as a vehicle when indicated. n = 5 biological replicates. In the above bar graphs, black bars represent untreated cells. Grey bars represent cells treated with TTX and pretreated with the indicated compounds. White bars represent cells treated only with the indicated compound. *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. p values determined by a one-way ANOVA using Dunnett's multiple comparisons test. Error bars represent SEM.

Supplemental Table 1, related to Figure 1: Genes that are differentially regulated by TTX and BIcuculline, attached as an excel file.

Supplemental Table 2, related to Figure 1: TTX-induced genes that have been associated with neurodevelopmental disorders (Gene information from SFARI and other published sources)

Gene ID	Gene Name	Associated Disorder	Reference
Auts2	*Autism susceptibility candidate 2*	ASD, ADHD, epilepsy	Sultana et al., 2002; Kalscheuer et al., 2007
Cacna1h	*Calcium channel, voltage-dependent, alpha 1H subunit*	ASD	Splawski et al., 2006
Bbs4	*Bardet-Biedl syndrome 4*	Bardet-Biedl syndrome, ASD	Girirajan et al., 2013
Fan1	*FANCD2/FANCI-associated nuclease 1*	ASD and schizophrenia	Ionita-Laza et al., 2013
Ogt	*O-linked N-acetylglucosamine (GlcNAc) transferase*	Maternal stress marker	Howerton et al., 2013
Smg6	*Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)*	ASD, neurodevelopmental disorders	Nguyen et al., 2013
Upf2	*UPF2 regulator of nonsense transcripts homolog (yeast)*	ASD, neurodevelopmental disorders	Nguyen et al., 2013
Nos1	*Nitric Oxide Synthase I*	Schizophrenia	Shinkai et al., 2002
Elk1	*Elk1, member of ETS oncogene category*	Schizophrenia	Sanders et al., 2013
Nptx1	*Neuronal pentraxin 1*	Bipolar Disorder	Rajkumar et al., 2015
Myt1	*Myelin transcription factor 1*	Schizophrenia	Fernandez-Enright et al., 2013
Dbp	*D site of albumin promoter binding protein 1*	Schizophrenia	Sanders et al., 2013

Supplemental Experimental Methods

Lentiviral infections

Lentiviral constructs containing the indicated shRNAs in the pLLX vector were transfected into HEK293T cells with the helper plasmids Δ8.9 and VsVg using Fugene HD (Promega) before incubating for 48-72 h. Viral supernatant was then added directly to the cultures to infect the neurons. shRNA sequences were designed using GE Dharmacon siDesign Center or as previously described (Abad et al., 2006; Joo et al., 2015; Lee et al., 2010; Rodriguez-Gomez et al., 2012). The shRNA sequences used are: *Scrambled,* 5'-GCCCTGCCACCGTAATTTA-3'; *shNP1*, 5'-GTACAGCCGCCTCAATTCT-3'; *shSRF*, 5'-AAGATGGAGTTCATCGACAAC-3'; *shCREB*, 5'-GGAGTCTGTGGATAGTGTA-3'; *shMEF2A*, 5'-GTTATCTCAGGGTTCAAAT-3'; *shMEF2D*, 5'-GTAGCTCTCTGGTCACTCC-3'; *shMRTFA/B*, 5'-CATGGAGCTGGTGGAGAAGAA-3'; *shELK1*, 5'-GGGATGGTGGTGAGTTCAAGT-3'; *shELK4*, 5'-GCAACGAGCCCTAGTCTTTCT-3'; *shCacna1h*, 5'-GGGCTTCCTTTAGTAGCAA-3'.

Pharmacological Inhibitors

To induce scaling, 1 μM TTX (Tocris) or 50 μM bicuculline (Sigma) was used. Cells were also pretreated with the following inhibitors at the indicated concentrations: 5 μM NBQX (Tocris), 100 μM AP-5 (Tocris), 10 μM Nimodipine (Tocris), 5 mM EGTA (Bio-world), 10 μM EGTA-AM (Life Technologies), 2 μM ω-Conotoxin GVIA (Alomone labs), 2 μM ω-Agatoxin IVA (Alomone labs), 2 μM SNX-482 (Alomone labs), 10 μM NNC 55-0396 dihydrochloride (Alomone labs), 1 μM Mibefradil (Alomone labs), 50 μM TTA-A2 (Alomone labs), 10 μM KN-62 (Tocris), 3 μM STO-609 (Tocris), and 10 μM each of the MAPK inhibitors: U0126, SB 203580, PD 98059, SB 202190, SP 600125 (Tocris). 5 μg/mL Actinomycin D was added to block transcription. EGTA-AM, Nimodipine, TTA-A2, STO-609, KN-62, Actinomycin D, and the MAPK inhibitors were dissolved in DMSO to make stock solutions. Cells were pretreated with EGTA-AM for 30 min before exchanging the media and being stimulated with TTX. Cells were pretreated with EGTA for 5 min before stimulation, and for all other inhibitors, cells were pretreated for 15 min before stimulation by either TTX or bicuculline.

Whole cell voltage clamp recordings

At DIV14-18, dissociated hippocampal cultures were voltage-clamped at -70 mV, as previously described (Reese and Kavalali, 2015), using an Axon Instruments Axopatch 200B amplifier. Access resistance was less than 25MΩ for each recording. The internal pipette solution contained (in mM): 120 K-Gluconate, 20 KCl, 10 NaCl, 10 HEPES, 0.6 EGTA, 4 Mg-ATP and 0.3 Na-GTP at pH 7.3. In order to isolate AMPA-mEPSCs, the extracellular solution contained 1 μM TTX, 50 μM picrotoxin (to block mIPSCs), 50 μM (2R)-amino-5-phosphonovaleric acid (AP5), 2 mM Ca^{2+} and 1.25 mM Mg^{2+}. All recordings were performed under continuous perfusion, and cells were perfused for 3 min before recording to achieve stable baselines. The AMPA-mEPSCs were quantified with Synaptosoft MiniAnalysis software. 4 minutes were analyzed per recording. To ensure that high frequency cells did not skew the amplitude comparisons by being overrepresented, 200 mEPSC amplitudes were randomly selected from each recording to generate the cumulative probability histograms and rank order plots. Significance was determined using the Kolmogorov-Smirnov test, which was performed using PAST 3.1 (http://folk.uio.no/ohammer/past/).

Chromatin Immunoprecipitation (ChIP)

ChIP was performed as previously described (Joo et al., 2015; Kim et al., 2010; Schaukowitch et al., 2014). Briefly, neurons were crosslinked with 1% formaldehyde for 10 min before quenching with 2M glycine (125 mM final concentration). Cells were washed with cold PBS and harvested in PBS with proteinase inhibitors (Roche). Cells were lysed with Buffer I (50 mM Hepes KOH, pH 7.5, 140 mM NaCl, 1 mM EDTA, pH 8.0, 10 % Glycerol, 0.5% NP-40, protease inhibitors) and nuclei were resuspended in Buffer II (300 mM NaCl, 1 % Triton-X 100, 0.1% Sodium deoxycholate, 1 mM EDTA, pH 8.0, 0.5 mM EGTA, pH 8.0, 10 mM Tris, pH 8.0, protease inhibitors) before being sonicated to shear the DNA on a Misonix sonicator. Lysates were incubated with 4 μg of the following antibodies overnight at 4°C: anti-SRF (H-300, Santa Cruz Biotechnology Cat# sc-13029, RRID:AB_2302440), anti-ELK1 (I-20 X, Santa Cruz Biotechnology, Cat# sc-355, RRID:AB_631429). The next day, Protein A/G beads (Santa Cruz) were added for 2 h at 4°C, and then the beads were washed with Low, High, and LiCl buffers. DNA was eluted with Elution buffer (10 mM Tris, pH 8.0, 1 mM EDTA, pH 8.0, 1 % SDS) at 65°C for 10 min, and then reverse crosslinked at 65°C for 5-8 h. DNA was incubated with RNAse A (Qiagen), followed by Proteinase K (NEB), and purified by Phenol:Chloroform extraction, followed by a commercial DNA purification kit (Qiagen). Regions were amplified using qPCR with the primers listed below.

Immunostaining
Hippocampal neurons from P3 rats were cultured until DIV14-17. Cells were treated with 1 μM TTX overnight. Cells were washed once with PBS before fixation with 4% paraformaldehyde in PBS for 20 min at room temperature. Cells were washed three times with PBS. To stain for surface NP1, neurons were left unpermeabilized, and blocked with 10% Normal Donkey Serum (NDS; Jackson ImmunoResearch Laboratories) in PBS for 1 h at room temperature. Primary antibody incubation was performed for 2 h at room temperature in 2% NDS in PBS at the following dilution: anti-NP1 (BD Biosciences Cat# 610369, RRID:AB_397754, 1:300). Cells were washed three times with PBS before secondary incubation for 1 h at room temperature. The secondary antibody Alexa-Fluor anti-Mouse 555 was diluted 1:1000 in 2% NDS in PBS. Cells were washed three times in PBS, and mounted using hard-set mounting solution (VectaShield). Images were taken on a Zeiss LSM 150 using a 63x objective, and were quantified using ImageJ. For immunohistochemistry, mice were perfused with 4% formaldehyde and brains were incubated in 4% paraformaldehyde overnight. After three washes with PBS, the brains were incubated with 30% sucrose and then mounted in Tissue-tek (Sakura). The brains were sliced at 40 μm, and the slices were incubated with blocking solution (10% NDS in PBS) for 1 h at room temperature. Primary antibody incubation was performed overnight at 4°C in 0.1% TX-100 in PBS at a dilution of 1:50. Cells were washed four times with 0.1% TX-100 in PBS, and incubated with secondary antibody Alexa-Fluor anti-Mouse 555 at a dilution of 1:200 in 0.1% TX-100 in PBS for 1 h at room temperature. Slices were again washed four times with 0.1% TX-100 and coverslips were applied with hard-set mounting solution (VectaShield).

RNA-seq analysis
The sequencing reads were mapped to the mm10 UCSC annotation using TOPHAT (Trapnell et al., 2009) with the parameters (-a 8 -m 0 -I 500000 -p 8 -g 20 --library-type fr-firststrand --no-novel-indels --segment-mismatches 2). RPKM calculations were done using the HOMER package by normalizing to 10 million reads. Tracks for visualization on UCSC browser are generated using HOMER. Heatmaps were generated in JavaTreeView from log transformed fold change values, normalized to the unstimulated condition, using hierarchical clustering in Cluster. Venn diagrams were created using BioVenn (Hulsen et al., 2008).

ChIP-seq analysis
H3K27Ac ChIP-seq (GSE60192) data was downloaded from GEO. Bowtie2 (Langmead et al., 2009) aligner was used to align the fastq reads to mm10 UCSC annotation. Duplicates were removed using Picard MarkDuplicates (http://broadinstitute.github.io/picard/) and visualization tracks were generated using HOMER. Using MACS, the KCl-K27ac peaks were identified by using the Unstimulated-K27ac samples as control at a p-value of 1E-5. Closest genes were identified near the negative peaks generated for KCl-K27ac through MACS by using in-house downstream scripts.

GRO-seq analysis
10 million nuclei per sample were extracted and used for global run-on, and base hydrolysis was performed as previously described (Core et al., 2008). Nascent RNAs were immunoprecipitated with anti-BrdU antibody-conjugated beads (Santa Cruz Biotech) twice. Between two immunoprecipitations, purified run-on RNAs were subjected to polyA tailing by using Poly(A)-polymerase (NEB). Subsequently, RNAs are subjected to first-strand cDNA synthesis using Superscript III Reverse Transcriptase (Invitrogen) with the oNTI223 primer. Extra oNTI223 primers were removed by Exonuclease I (NEB) and cDNAs were size-selected in an 8 % polyacrylamide TBE-urea gel. Purified cDNAs were subsequently circularized using CircLigase (Epicentre) and relinearized with ApeI (NEB). The relinearized DNA template were subjected to PCR amplification by using Phusion High-Fidelity DNA Polymerase (NEB) and Illumina TrueSeq small-RNA sample barcoded primers. Subsequently, PCR products were isolated by 6 % polyacrylamide TBE gel and purified. The final libraries were sequenced using an Illumina HiSeq per the manufacturer's instructions. The raw fastq reads were trimmed using CUTADAPT with parameters -a AAAAAAAAAAAAAAAAAAAA -z -e 0.10 -f fastq -m 32 (Chae et al., 2015). Then the surviving reads were submitted to BWA aligner for mapping to the mm10 UCSC annotation. Samtools and the HOMER package were used to make visualization tracks and RPKM calculations. RPKM was calculated by normalizing to 10 million reads.

Western blotting
Protein was extracted from neurons using sample buffer (60 mM Tris-HCl, pH 6.8, 2% SDS, 10% glycerol). Before loading, samples were mixed with loading buffer (5% 2-mercaptoethanol, 0.1% bromophenol blue) and denatured at 95°C. Proteins were run on a 12% SDS-PAGE gel, and analyzed by western blotting with the following antibodies:

anti-NP1 (BD Biosciences Cat# 610369, RRID:AB_397754, 1:1000) or anti-β-actin (Sigma-Aldrich Cat#A5441, RRID:AB_476744, 1:5000).

Visual Cortex experiments

For dark rearing experiments, male C57Bl6/J mice were placed into completely dark chambers at P21-25 at the end of their light cycle. The visual cortices were removed, and RNA was extracted in Trizol after 24 h in the dark. For measuring protein levels, mice were taken out of the dark after 3 d. Intraocular injections of TTX were performed as in (Frenkel and Bear, 2004). Briefly, 1 μL of 1 mM TTX or PBS was injected into each eye of the mouse using a glass pipette at a rate of 1 μL/1 min (Joo et al., 2015). RNA was then extracted from visual cortex of the opposite hemisphere with Trizol.

Primer Sequences

Primers for RT-qPCR

Nptx1-forward	GAAGAAGAGCCTGCCAGAGAT
Nptx1-reverse	CAGGCACAGCATAAGAGAAGG
Rps6ka5-forward	CTTGACGCACAATGGCTACG
Rps6ka5-reverse	CCTGCCCTGACAGCATTGTA
Auts2-forward	TGAGGGATCCTTACCGTGAC
Auts2-reverse	ATCGGTCGGCTTCATACAAC
Cacna1h-forward	GCCAGAAATGCTACCTGGGT
Cacna1h-reverse	CAGAGAGGCTCACGTTGTGT
Nos1-forward	GGTTTAAGGACCTGGGGCTC
Nos1-reverse	CCAGCCACTAAAGGGACAGG
Txnip-forward	TGCAGGAAATGAAGCATCTG
Txnip-reverse	GTTCCCCGCTGTAGAGACTG
Elk1-forward	CTCTGCATCCACCAACTTGA
Elk1-reverse	CTGCTGCAGCTTCTGAGAGA
Mical3-forward	TTCTCACCTTGCGCAAAAGC
Mical3-reverse	CGATGCCGCCATATCAGAGT
Arc-forward	GTGAAGACAAGCCAGCATGA
Arc-reverse	CCAAGAGGACCAAGGGTACA
c-fos-forward	ATCCTTGGAGCCAGTCAAGA
c-fos-reverse	ATGATGCCGGAAACAAGAAG
Nptx1-pre-mRNA-forward	AACACGCCTTAAGATGGCAC
Nptx1-pre-mRNA-reverse	CCCTGCTCGGACTGCAAAAT
Auts2-pre-mRNA-forward	CCATTTTCCCAGGGCTTTGC
Auts2-pre-mRNA-reverse	GCCTCTTGGGTGTGTTCTCA
Txnip-pre-mRNA-forward	TGCTATTCTCACAGGGTCAACA
Txnip-pre-mRNA-reverse	GGGGAATAGAGAGGAAATTTTCAG
Arc-pre-mRNA-forward	GTGCCAGTGCCCACTACAAT
Arc-pre-mRNA-reverse	CCAAGTCCACTTTCCAGGAG
Auts2-short-forward	CGGCTAGGTCCACAAGTCTG
Auts2-short-reverse	CTGCCGTTTAGGATCCGGTT
Srf-forward	GGTGCCAGGTAGTTGGTGAT
Srf-reverse	TGAAGCCAGCATTCACAGTC
Mkl1-forward	CTGTCTAAGCCCTGGTGCTC
Mkl1-reverse	GCTCCTCAATCTGCTTGTCC
Mkl2-forward	TCATGCAACTTTTCGCTCAC
Mkl2-reverse	GCATAGCACGTGGTCAAAGA
Elk4-forward	TGCAACGAGCCCTAGTCTTT
Elk4-reverse	TTCCAGGGAAGGTAGTGTGG
Creb-forward	AAACATACCAGATCCGCACA
Creb-reverse	CTCTCTCTTCCGTGCTGCTT

Mef2a-forward	AGGGCTGCTTGTCCTAGATG
Mef2a-reverse	ACCAGCGCTGACCTGTCT
Mef2d-forward	CTGGCACTAGGCAATGTCAC
Mef2d-reverse	AGTGGGGCTGTTGCTGAG
Tbp-forward	TGACTCCTGGAATTCCCATC
Tbp-reverse	TTGCTGCTGCTGTCTTTGTT
Gapdh-forward	AGGTCGGTGTGAACGGATTTG
Gapdh-reverse	TGTAGACCATGTAGTTGAGGTCA
eNptx1-forward (eRNA-F)	ACATGCTCACGGTTGTGGAT
eNptx1-reverse (eRNA-R)	TTCTCTAGCCAGCAGTTGCC

Primers for ChIP qPCR

Nptx1-SRE1-forward	CAGGCTGTGTGAGGTAGTGG
Nptx1-SRE1-reverse	CACCAGGGTTTCCACGATCA
Nptx1-E1-forward	AGCAAAACCAGGAGCCAAGA
Nptx1-E1-reverse	CCACGCTGTGAACTCGGTAG
Nptx1-Intron-forward	AACACGCCTTAAGATGGCAC
Nptx1-Intron-reverse	CCCTGCTCGGACTGCAAAAT
Nptx1-Promoter-forward	TGAGACCGGGATCGGGC
Nptx1-Promoter-reverse	GAAGACTGTGCGGCGTAGAA
Nptx1-Neg1-forward	CACAGCGGTGAGCTCTAACT
Nptx1-Neg1-reverse	AAGAGGAATGTGGGCTGGTG
Nptx1-SRE2-forward	AGGGACAGCTTTTCGGATGG
Nptx1-SRE2-reverse	CTTGCCAATGAGATGGGGGT
Neg2-forward	GCAGAGCGGACCATAAACAT
Neg2-reverse	CCGTGAAATGAGTTGCCTTT
c-fos-Promoter-forward	CCTCCCTCCTTTACACAGGA
c-fos-Promoter-reverse	ACCTTCCGCGTGTAGGATTT

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