Hypomyelination leads to alterations in inhibitory function and parvalbumin-positive neuron density in auditory cortex

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ABSTRACT

Myelination increases axonal conduction velocity and contributes to neural circuit function. Consequently, myelin disruption causes behavioral and cognitive defects. Myelin was thought to be restricted to excitatory neurons, and studies on dysmyelination focused primarily on these cells. However, axons of inhibitory neurons are also myelinated (Micheva et al., 2016), but the effects of myelin on inhibitory circuits are unknown. We thus studied mice that have mild hypomyelination due to loss of oligodendrocyte ErbB receptor signaling, focusing on primary auditory cortex (A1). We found that mutant mice have reduced A1 myelin and inhibitory connections to L2/3 neurons without affecting excitatory inputs, thus altering excitatory/inhibitory balance. These effects are not associated with altered expression of GABAergic and glutamatergic synaptic components, but with reduced parvalbumin-positive (PV^+) neuron density and PV mRNA levels. These results demonstrate that mild hypomyelination can impact cortical neuronal networks, reducing inhibitory activity, and shifting networks towards excitation.

Impact Statement

Mild hypomyelination alters excitatory/inhibitory balance in the primary auditory cortex by reducing the number of parvalbumin-positive interneurons and reducing inhibition.

INTRODUCTION

It has long been known that myelination of central neurons increases conduction velocity of action potentials and provides metabolic support to axons (Foster et al., 2019, Monje, 2018). Therefore, myelination is critical for the normal patterns of neural circuits' activation and synchronization, as well as for normal physiological, cognitive and behavioral performance. Given the abundant presence of myelin, myelin disruption can cause severe information processing defects, and has been associated with neurodegenerative and psychiatric disorders (Meuth et al., 2010, Du and Ongur, 2013, Gibson et al., 2018).

Whereas myelin was thought to be restricted primarily to excitatory neurons, it has recently been appreciated that myelin is also present on inhibitory neurons (Micheva et al., 2016). Recent EM-based studies indicate that axon collaterals of inhibitory neurons, especially those of a large proportion of parvalbumin-positive (PV^+) cells, are myelinated (Peters and Proskauer, 1980, Tamas et al., 1997, Micheva et al., 2016). PV^+ cell axons constitute about half of all myelinated axons in cortical layer 2/3 (L2/3), and a quarter of myelinated axons in L4, and myelination of GABAergic axons is enriched in MBP expression (Micheva et al., 2016). However, the impact of myelin defects on inhibitory circuits and neurons remains unknown.

Most insights into the impact of myelin on the function of neural circuits have been obtained by analyzing the consequences of severe demyelination, which can affect regions throughout the brain, including the cerebral cortex. For example, cuprizone-induced demyelination promotes hyper- and depolarizing shifts of the resting membrane potential of auditory thalamocortical pathway neurons and reduction in action potential firing of primary auditory cortex (A1) neurons (Ghaffarian et al., 2016). Furthermore, focal demyelination in A1 permanently disrupts its tonotopic organization (Cerina et al., 2017) and auditory frequency-specific responses in MGB (Narayanan et al., 2018).

However, in recent years there has been an increased appreciation that myelination is not an all-or-none process, but rather a continuum based on subtle differences in myelin thickness of the density of myelin segments (Monje, 2018). Furthermore, we now know that central nervous system (CNS) myelin thickness and density is influenced by experience, i.e. myelin is negatively influenced by deprivation (Makinodan et al., 2012, Liu et al., 2012) and increased by neuronal activity and novelty (Gibson et al., 2014, McKenzie et al., 2014). However, much less is known about how subtle changes in myelin alters excitatory/inhibitory balance.

To gain insights into the impact of hypomyelination on inhibitory and excitatory neuronal network function in A1, we took advantage of mice in which ErbB receptor signaling in oligodendrocytes has been eliminated by expression of a dominant-negative ErbB4 in cells of the oligodendrocyte lineage under the control of the CNPase promoter (CNP-DN-ErbB4, (Roy et al., 2007)). DN-ErbB4 expression completely blocks the signaling of NRG1 receptors ErbB2, 3 and 4 (Chen et al., 2006, Rio et al., 1997, Prevot et al., 2003), without affecting signaling by ErbB1, the receptor for EGF (Prevot et al., 2003). We previously showed that these mice have a mild but significant hypomyelination in all tested CNS axons, as well as slower conduction in the optic nerve (Roy et al., 2007, Makinodan et al., 2012). To evaluate whether hypomyelination alters intracortical neural circuits in primary auditory cortex, we used laser-scanning photostimulation (LSPS) to optically probe functional circuits to L2/3 neurons. We found that hypomyelination leads to reduced A1 inhibitory function and a consequent alteration in excitatory/inhibitory balance in this cortical area. The functional alterations are not associated with changes in gene expression for GABAergic and glutamatergic markers, but rather to a reduced density of parvalbumin (PV) expressing neurons in A1. These results strengthen the role of NRG1-ErbB signaling in the regulation of CNS myelin maturation and suggest that subtle defects in myelin thickness can lead to large-scale changes in network activity in auditory cortex.

RESULTS

Disruption of oligodendrocyte ErbB signaling results in reduced myelin basic protein and mRNA levels in the auditory cortex

We previously showed that CNP-DN-ErbB4 mice have reduced myelin thickness in optic nerve and corpus callosum axons (Roy et al., 2007) as well as reduced levels of MBP protein and mRNA levels in peripheral nerves (Chen et al., 2006). To determine if A1 myelin is also affected in the mutant mice, we measured myelin basic protein (MBP) expression (Bonnefil et al., 2019). Immunofluorescence and Western blot analysis showed that A1 MBP protein expression is markedly reduced in the adult mutant mice compared with their wild type (WT) littermates (Fig. 1a-d). Quantitative RT-PCR analysis showed a similar reduction in MBP gene expression in A1 (Fig. 1e). These results indicate that, like in other brain regions, loss of oligodendrocyte ErbB receptor signaling leads to A1 hypomyelination.

Hypomyelination does not alter sensitivity of cortical neurons to photostimulation.

We next examined the impact of hypomyelination on A1 intracortical neural circuits using laser-scanning photostimulation (LSPS) with caged glutamate (Meng et al., 2015, Meng et al., 2020, Meng et al., 2017) in brain slices of adult mice. We first tested if oligodendrocyte DN-ErbB4 expression affects the ability of A1 neurons to fire action potentials to photoreleased glutamate by performing cell-attached patch recordings from cells in L2/3 and L4 (N=27 L4 and N=38 L2/3 neurons in WT, N=20 L4 and N=36 L2/3 neurons in CNP-DN-ErbB4) (Fig. 2a). Short UV laser pulses (1ms) to focally release glutamate were targeted to multiple stimulus spots covering the extent of A1 (Fig. 2b). Stimulation close to the cell body led to action potentials (Fig. 2b). There were no differences between the genotypes in the area around targeted neurons where action potentials could be generated (Fig. 2b, c, $p>0.05$) or in the number of evoked action potentials (Fig. 2c). Thus, we concluded that the spatial resolution of LSPS is not affected by hypomyelination.

Hypomyelination does not alter excitatory connections to L2/3 neurons.

To map and quantify functional excitatory inputs to L2/3 neurons we performed whole-cell recording combined with LSPS while cells were held at a holding potential of -70mV. All recorded cells were from similar laminar positions (Fig. 2a, $p>0.05$). We targeted the laser pulse to multiple stimulus locations and recorded the resulting membrane currents (Fig. 3a). Targeting the cell body and the proximal dendrites of the cell under study caused large amplitude and short-latency (<8ms) currents (Fig. 3b), reflecting direct activation of glutamate receptors on the neuron. These ‘direct’ currents were excluded from the analysis. Targeting other sites could result in longer-latency (> 8ms) currents, which under our recording conditions, reflect monosynaptically evoked post-synaptic currents (PSCs) (Meng et al., 2015, Meng et al., 2020, Meng et al., 2017) (Fig. 3b). We activated 600-900 stimulus locations spanning all cortical layers around the recorded neuron.

We mapped 68 L2/3 cells (36 cells in WT, 32 cells in CNP-DN-ErbB4) and aligned and averaged all individual spatial connection maps to the soma position of the individual cells (Fig. 3c). By averaging the individual connection maps, we obtained the spatial connection probability map for excitatory inputs where each value (represented as color in the maps) denotes the fraction of neurons in the population that received input from a particular location (Fig. 3d). Qualitatively, a comparison of the excitatory connection probability maps from WT and in CNP-DN-ErbB4 animals showed no differences (Fig. 3d).

Since spatial averaging can obscure differences in functional connections, we quantified the laminar changes of the connection properties for each cell as in prior studies (Meng et al., 2015, Meng et al., 2020, Meng et al., 2017). For each neuron, we quantified the total area in each

layer where stimulation resulted in a response. The total area within each layer where stimulation can evoke EPSCs in L2/3 neurons was similar in all layers between genotypes (Fig. 3e). The thalamocortical slices are cut such that the macroscale rostro-caudally oriented tonotopic map is preserved in the slice plane. Thus, the spatial extent of functional integration along the slice is a proxy for the integration along the tonotopic axis. To assess this laminar connection width, we calculated the distance in each layer that covers 80% of input sites. We found that the laminar connection width is similar between genotypes indicating that the functional integration across the tonotopic axis was unchanged in CNP-DN-ErbB4 mice (Fig. 3e). Circuit changes can result from both connection probability and input strength. Thus, we measured the average charge of the evoked EPSC and the relative EPSC charge contribution from each layer to L2/3 cells (Fig. 3f). Evoked EPSCs and relative contribution from all layers were not different between genotypes (Fig. 3f, $p>0.05$). Together, these results indicate that hypomyelination does not affect the spatial pattern of functional excitatory connectivity.

Hypomyelination leads to reduced inhibitory connectivity to L2/3 neurons.

To map and quantify functional inhibitory input to L2/3 neurons we held cells at 0 mV and repeated the LSPS. Qualitatively comparison of the resulting connection probability maps from WT and CNP-DN-ErbB4 animals showed an apparent reduction in inputs from L4 and from within L2/3 (Fig. 4a). We confirmed this observation by quantifying the total area within each layer where stimulation evoked IPSCs in the recorded L2/3 neurons. We found that total input from L2/3, L4 and L5/6 was reduced in CNP-DN-ErbB4 animals (Fig. 4b). Moreover, the laminar connection width was lower in all layers of CNP-DN-ErbB4 mice than in cells from WT (Fig. 4b). The average charge of the evoked IPSC within L2/3 in CNP-DN-ErbB4 animals was reduced but the relative contribution from L2/3 is increased (Fig. 4c). These results suggest hypomyelination causes a spatial hypoconnectivity of inhibitory connections. As expected from the decreased inhibitory connectivity, calculating the balance between excitation and inhibition showed that this balance is shifted towards excitation (Fig. 4d).

Individual cells can vary in their inputs and functional circuit diversity can emerge through development (Meng et al., 2020). We thus investigated the spatial diversity of the circuits impinging on L2/3 cells by calculating the similarity (spatial correlation) between connection maps within each population (Meng et al., 2020). We found that the circuit similarity is increased for both excitatory and inhibitory circuits in cells from CNP-DN-ErbB4 mice (Fig. 5). Thus, loss of oligodendrocyte ErbB signaling causes a reduction of inhibitory circuits and a reorganization of excitatory circuits.

Hypomyelination does not alter expression of inhibitory or excitatory synaptic components, but reduces PV^+ cell numbers and PV mRNA levels in the auditory cortex.

Since ErbB receptor signaling has been reported to regulate neurotransmitter receptor expression in diverse cells, we tested if the levels of mRNA for several genes central to inhibitory and excitatory neurotransmission are altered in A1 in CNP-DN-ErbB4 mice. Quantitative RT-PCR analysis revealed normal levels of mRNA for molecules associated with GABAergic signaling (GAD65, GAD67, VGAT and GABARα1) (Fig. 6a), and glutamatergic signaling (VGLUT1, VGLUT2, GRIA1, GRIA2, GRIA3 and GRIA4) (Fig. 6b). Thus, the observed circuit differences do not appear to result from alteration in expression of components of GABAergic or glutamatergic synapses.

We wondered if the observed reduction in functional connections could be due to loss of synaptic connections, a reduction in presynaptic neurons or a combination of both factors. To test these scenarios, we quantified the number of neurons expressing PV in A1 of CNP-DN-ErbB4 and WT mice. Remarkably, the number of PV^+ neurons was significantly reduced in

mutant mice (Fig. 7a,b). Furthermore, A1 PV mRNA levels were also significantly reduced (Fig. 7c).

Cell-specific ErbB3 KO confirms that the reduced auditory cortex PV mRNA level is due to loss of oligodendrocyte ErbB signaling.

NRG1-ErbB signaling is critical for several aspects of PV^+ neuron development (Li et al., 2011, Neddens and Buonanno, 2010, Ting et al., 2011, Yin et al., 2013). Since DN-ErbB4 expression should increase the number of NRG1 binding sites in the brain, we needed to account for the possibility that the loss of PV expression reflects a loss of NRG1 signaling on inhibitory neurons rather than changes in oligodendrocyte function. Therefore, we analyzed mice with inducible oligodendrocyte specific knockout of ErbB3 using mice carrying an ErbB3 floxed allele (ErbB3 fl/fl, (Qu et al., 2006)) and mice expressing the tamoxifen-inducible Cre recombinase (CreERT) under the control of the PLP promoter (PLP/CreERT) (Doerflinger et al., 2003). We previously showed that these mice have CNS hypomyelination comparable to that seen in the CNP-DN-ErbB4 mice (Makinodan et al., 2012). As expected, tamoxifen injections from P6 to P56 lead to a reduction in A1 ErbB3 mRNA levels (Fig. 7e). Importantly, A1 PV mRNA levels was also reduced by oligodendrocyte ErbB3 KO (Fig. 7f). Interestingly, the correlation between the levels of PV and MBP mRNA expression in CNP-DN-ErbB4 mice ($R^2 = 0.3627$, $p = 0.0064$; Fig. 7d) and in PLP/creERT – ErbB3fl/fl mice ($R^2 = 0.32$, $p = 0.035$; Fig. 7g) were similar in spite of the mice being in different backgrounds (FVB/N for CNP-DN-erbB4, C57/Bl6 for ErbB3 KO), further supporting the notion that the reduction in PV expression is due to hypomyelination caused by loss of oligodendrocyte ErbB signaling.

DISCUSSION

Our results indicate that hypomyelination leads to altered excitatory/inhibitory balance in A1 cortical circuits due to diminished inhibitory connections to L2/3 neurons. These functional changes appear to result, at least in part, from a reduced density of PV expressing neurons in A1. While hypomyelination does not affect excitatory connectivity in A1, we found a significant spatial hypoconnectivity of inhibitory connections to L2/3 neurons in CNP-DN-ErbB4 mice, i.e. individual L2/3 neurons in mutant mice receive inhibitory inputs from fewer locations, especially from L2/3 and L4. Interestingly, individual inhibitory connections are of comparable strength. Thus, our data uncover a novel role of myelin in neural circuit function, regulation of PV^+ neurons density.

Our analysis of the balance between excitation and inhibition showed that hypomyelination induces a shift towards excitation. This imbalance is likely due to reduced PV^+ neurons and not due to changes in the expression of multiple enzymes, transporters and receptors from GABAergic and glutamatergic systems. The specific effects of myelin on inhibitory circuits suggest that myelin might play multiple roles beyond controlling timing of axonal conduction. Our results suggest that hypomyelination affects axons of PV^+ cells, which are fast-spiking neurons with high metabolic demands (Hu et al., 2014). It has been proposed that myelin plays a role in metabolic support of PV^+ cells, as well as to improve the energy efficiency of signal propagation (Rinholm et al., 2011, Micheva et al., 2016, Lee et al., 2012). Thus, a loss of myelin could cause impaired PV^+ cell function and the reduction of PV^+ cells in CNP-DN-ErbB4 mice is consistent with this idea. Since PV levels are known to be regulated by activity (Dehorter et al., 2015, Lagler et al., 2016, Favuzzi et al., 2017, Stedehouder et al., 2018), the reduction in PV levels could also reflect an altered maturation of PV^+ cells, altered migration, premature death of PV^+ cells, or a combination of these factors. Whatever the underlying mechanism, our data point to a powerful regulation of PV^+ cells by myelination.

Our findings of altered circuits, suggests that hypomyelination might lead to degraded fidelity of sound representation. This is consistent with the observation that focal demyelination of A1 L4

alters auditory frequency-specific responses (Narayanan et al., 2018) and abolishes tonotopic organization (Cerina et al., 2017). Since A1 neurons that encode the fast fluctuation of acoustic stimuli tend to receive balanced and concurrent excitation and inhibition (Bendor, 2015, Wang et al., 2008), our observation of altered inhibitory circuits in CNP-DN-ErbB4 mice are consistent with the functional deficits after hypomyelination.

Thus, hypomyelination could play a role in the development of cognitive deficits. Indeed, we previously showed that CNP-DN-ErbB4 mice have behavioral phenotypes consistent with psychiatric disorders (Roy et al., 2007) and interneuron hypomyelination was reported in rat models of schizophrenia (Maas et al., 2020). Hence, our results showing reduced density of PV^+ cells and altered network connection to excitation neurons suggest that the absence of myelin might lead to circuit changes that manifest as impaired cognitive functions.

MATERIALS AND METHODS

Animals. All animal procedures were carried out with prior approval from the University of Michigan and the University of Maryland Committees on Use and Care of Animals in accordance with the National Research Council Guide for the Care and Use of Laboratory Animals. Mice were housed in an Association for Assessment and Accreditation of Laboratory Animal Care–accredited facility in the University of Michigan. Mice were kept in a light- (12 h on/off) and temperature- (21-23°C) controlled environment and were fed with a standard chow diet (5LOD, LabDiet, USA).

Transgenic mice expressing a dominant-negative ErbB4 receptor under control of the CNPase promoter (CNP-DN-ErbB4) (Chen et al., 2006) were crossed to wild type FVB/N J mice (JAX® mice, stock # 001800). The experimental mice were those hemizygous for CNP-DN-ErbB4 or wild type littermates. To evaluate the role of NRG-1/ErbB3 signaling in the hypomyelination and expression of PV in the A1, mice expressing inducible cre recombinase under the control of the proteolipid protein promoter (PLP/creERT) were crossed to ErbB3flox/flox mice (Makinodan et al., 2012). Floxed allele recombination was induced by ip injection of tamoxifen (Sigma, St. Louis, MO, USA) dissolved in corn oil (10 mg/ml), by the time the peripheral myelination is known to be stablished (from P6). For recombination between P6 and P30, mice were treated with a dose of 33 mg/kg/day. From P30 to P56, tamoxifen dose was 100 mg/kg body weight, every other day. This regimen was used because PLP expressing oligodendrocytes differentiate and mature over time until adulthood. The experimental mice were those homozygous for ErbB3 flox expressing creERT, and homozygous ErbB3 flox littermates without cre recombinase expression. All mice were treated with tamoxifen, regardless genotype. Experiments were performed in 2-month age mice.

The genotypes of mice were confirmed by PCR detection of the transgenes in tail-derived DNA from the CNP-DN-ErbB4, wild type, PLP/creERT and ErbB3fl/fl mice at weaning and at the end of experiments. The following pairs of primers were used: CNP-DN-ErbB4: F: 5' TGCTGAAGGAATGGTGTGC 3'; R: 5' CTTGTCGTCATCGTCTTTG 3'; PLP/CreERT: F: 5' GATGTAGCCAGCAGCATGTC 3; R: 5' ACTATATCCGTAACCTGGAT 3' and ErbB3-flox: F: 5' CCAACCCTTCTCCTCAGATAGG 3'; R: 5' TGTTTGTGAAATGTGGACTTTACC 3' and R: 5' GGCAGGCATGTTGACTTCACTTGT 3'. Expression of the DN-ErbB4 FLAG transgene was also validated by RT-qPCR in the primary auditory cortex, using the following pair of primers: F: 5' GAGCCTTGAGAAGATTCTTG 3'; R: 5' TGTCGTCATCGTCTTTGTAG 3'.

Dissection of the primary auditory cortex. Male mice were anesthetized with isoflurane (Fluoriso, Vet One) and euthanized by decapitation. Brain was collected and the primary auditory cortex (A1) fragments were micro dissected (thickness: 1.0 mm) from an area located laterally to the border of the hippocampus, according to the coordinates from Paxinos and Franklin Mouse Brain Atlas (2.06 mm posterior to bregma, 3.5 mm lateral to the midline and 2.0

mm dorsoventrally). Tissues were immediately frozen in dry ice for posterior processing for RT-qPCR (n = 7-12/group) or Western blotting (n = 6/group) analyses. Tissue harvesting was performed between 8-10am.

Real-time quantitative RT-PCR. Total RNA was isolated from the A1 samples using RNA extraction kit, Qiazol Reagent (RNeasy mini kit; Qiagen, Germany), and DNase treatment was performed (RNase-free; Qiagen). The complementary DNA was synthesized using iScript cDNA synthesis kit (Bio-Rad, #1708891, USA), according to the manufacturers' protocol. Quantitative RT-PCR was performed on a CFX-96 Bio-Rad reverse transcription polymerase chain reaction detection system (Hercules, CA, USA) using iTaq Universal SYBR® Green supermix (Bio-Rad, # 172-5121, USA) and primer pairs were synthesized by IDT (Coralville, IA, USA). All samples and standard curves were run in triplicate. Water instead of complementary DNA was used as a negative control. The mRNA expression in transgenic versus control mice was determined by a comparative cycle threshold (Ct) method and relative gene copy number was calculated as normalized gene expression, defined as described previously (Stankovic and Corfas, 2003). Ribosomal protein L19 (RPL19) and GAPDH were used as housekeeping genes. The following specific oligo primers were used for the target genes: RPL19, F: 5'ACCTGGATGAGAAGGATGAG 3'; R: 5'ACCTTCAGGTACAGGCTGTG 3'; GAPDH, F: 5' TCACTGCCACCCAGAAGA 3'; R: 5' GACGGACACATTGGGGGTAG 3'; MBP, F: 5'ATCCAAGTACCTGGCCACAG 3'; R: 5'CCTGTCACCGCTAAAGAAGC 3'; GAD65, F: 5' CATTGATAAGTGTTTGGAGCTAGCA 3'; R: 5' GTGCGCAAACTAGGAGGTACAA 3'; GAD67, F: 5' TCGATTTTTCAACCAGCTCTCTACT 3'; R: 5' GTGCAATTTCATATGTGAACATATT 3'; VGAT, F: 5' TCCTGGTCATCGCTTACTGTCTC 3'; R: 5' CGTCGATGTAGAACTTCACCTTCTC 3'; GABARα1, F: 5' CCCCGGCTTGGCAACTA 3'; R: 5' TGGTTTTGTCTCAGGCTTGAC 3'; VGLUT1, F: 5' TCGCTACATCATCGCCATC 3'; R: 5' GTTGTGCTGTTGTTGACCAT 3'; VGLUT2, F: 5' CTGCGATACTGCTCACCTCTA 3'; R: 5' GCCAACCTACTCCTCTCCAA 3'; GRIA1, F: 5' GCTATTCCTACCGACTTGA 3'; R: 5' CCACATCTGCTCTTCCATA 3'; GRIA2, F: 5' CCTCATCATCATCTCCTCCTAC 3'; R: 5' GAGCCAGAGTCTAATGTTCCA 3'; GRIA3, F: 5' TCTAAGCCTGAGCAATGTG 3'; R: 5' CCTTCTCTGTATGTAGCGTAAT 3' and GRIA4, F: 5' GCATACCTTGACCTCCTTCTG 3'; R: 5' GCACGAACTGGCTCTCTC 3', PARVALBUMIN: F: 5' GCAAGATTGGGGTTGAAGAA 3'; R: 5' GTGTCCGATTGGTACAGCCT 3', and ErbB3: F: 5' TTGCCTACAGGAACGCTTACCCG 3'; R: 5' ACCCCCCAAAACCGCAGAATC 3". Changes in mRNA expression were calculated as relative expression (arbitrary units) respective to the wild type group.

Western blot analysis. Total protein from A1 was extracted using RIPA buffer (#R0278, Sigma Aldrich, USA) and protease inhibitor cocktail kit (#78410, ThermoFisher Scientific, USA). Homogenates were centrifuged at 4°C and 14,000 g for 15 minutes. Aliquots of the lysates containing 10 mg of protein were denatured in Laemmli buffer and β-mercaptoethanol (Bio-Rad, USA) at 95°C for 5 min. After electrophoresis (Mini-protean TGX gel, #456-1086, Bio-Rad, USA), samples were blotted onto nitrocellulose membranes (Immobilon-PSQ, #ISEQ00010, Merk Millipore, USA). Nonspecific binding was prevented by immersing the membranes in blocking buffer (5% BSA in Tris-buffered saline -Tween 20, TBS-T) for 60 minutes at room temperature. The membranes were then exposed overnight to the primary antibodies: mouse anti-GAPDH (1:3000, MA5-15738, ThermoFisher Scientific, USA) and rat anti-MBP (1: 1,000, MAB386, Millipore, Germany). The blots were rinsed in TBS-T and then incubated with horseradish peroxidase-conjugated anti-mouse antibody (1:4,000, SC-516102, Santa Cruz, USA) or anti-rat antibody (1: 4,000, #7077, Cell Signaling, USA) for one hour at room temperature. Antibody-antigen complexes were visualized by detecting enhanced chemiluminescence using a Pierce ECL detection system (#32209, ThermoFisher Scientific, USA) and digital images with Chemi Doc Touch Image System (Bio-Rad, USA). Expression of

MBP was normalized to the expression of GAPDH. Data were analyzed as relative expression (arbitrary units) respective to wild type group.

Immunostaining and image processing. To assess the pattern of expression of the MBP or PV in the A1, CNP-DN-ErbB4 or wild type mice (7 – 10/group) were anesthetized using isoflurane (Fluriso, Vet One) and transcardially perfused with saline, followed by 4% formaldehyde in 0.1 M phosphate buffer (PBS). Brains were dissected, post-fixed in the same fixative for 1 hour, placed in PBS containing 30% sucrose and sectioned on a cryostat (30-mm sections, 4 series) in the frontal plane. For MBP staining, brain coronal sections were rinsed with PBS and nonspecific binding was prevented by immersing the sections in blocking buffer (PBS, 5% normal horse serum and 0.3% Triton X-100) for one hour at room temperature. The sections were incubated overnight at 37°C with primary antibody rat anti-MBP (1:1,000, MAB386, Millipore, Germany) in PBS, 1% normal horse and 0.3% Triton X-100 solution. After rinses, sections were incubated for one hour with the chicken anti-rat AlexaFluor 647 secondary antibody (1:400, #A-21472, Life Technologies, USA). For PV staining, brain coronal sections were rinsed with TBS and nonspecific binding was prevented by immersing the sections in blocking buffer (TBS, 5% normal goat serum and 0.2% Triton X-100) for one hour at room temperature. The sections were incubated overnight at 4°C with primary antibody rabbit anti-PV (1:1,000, PV25, Swant). After rinses, sections were incubated for one hour with the goat anti-rabbit AlexaFluor 488 secondary antibody (1:400, Life Technologies, USA). Finally, the sections were mounted on superfrost microscope slides (Fisher Scientific, USA) and coversliped with Fluoro-Gel II with DAPI mounting medium (#17985-50, Electron Microscopy Sciences, USA).

Series of systematically selected brain sections representing the A1 (30-mm thick, every 120-mm, starting on 2.06 mm posterior to bregma and ending on bregma – 3.5) were acquired using a Leica SP8 confocal laser scanning microscope and 10X or 63X oil-immersion lens. The immunoreactive structures were excited using lasers with the excitation and barrier filters set for the fluorochromes used (magenta for MBP, green for PV, and blue for DAPI). Quantification of MBP immunofluorescence signal or the number of PV positive cells were performed in 10 different fields of the A1 per mice using the Image J software (FIJI version, NIH, USA). MBP signal intensity was calculated by converting each magenta frame into grayscale with homogeneously adjusted threshold. Histograms indicating the number of pixels of MBP staining within the same area of each image were recorded and expressed as Integrated Density. Averaged Integrated Density of the 10 fields analyzed per mice was used to compare the levels of MBP expression between groups. All immunofluorescence images shown are representative of at least three individual mice from each group.

In vitro Laser-Scanning Photostimulation (LSPS). LSPS experiments were performed as previously described (Meng et al., 2020, Meng et al., 2017, Meng et al., 2015).

Slice preparation. Mice were deeply anesthetized with isofluorane (Halocarbon). A block of brain containing A1 and the medial geniculate nucleus (MGN) was removed and thalamocortical slices (500 µm thick) were cut on a vibrating microtome (Leica) in ice-cold ACSF containing (in mM): 130 NaCl, 3 KCl, 1.25 KH_2PO_4, 20 $NaHCO_3$, 10 glucose, 1.3 $MgSO_4$, 2.5 $CaCl_2$ (pH 7.35 – 7.4, in 95%O_2-5%CO_2). The cutting angle was ~15 degrees from the horizontal plane (lateral raised) and A1 was identified as described previously (Meng et al., 2020, Meng et al., 2017, Meng et al., 2015). Slices were incubated for 1 hr in ACSF at 30°C and then kept at room temperature. Slices were held in a chamber on a fixed-stage microscope (Olympus BX51) for recording and superfused (2-4 ml/min) with high-Mg^{2+} ACSF recording solution at room temperature to reduce spontaneous activity in the slice. The recording solution contained (in mM): 124 NaCl, 5 KCl, 1.23 NaH_2PO_4, 26 $NaHCO_3$, 10 glucose, 4 $MgCl_2$, 4 $CaCl_2$. The location of the recording site in A1 was identified by landmarks (Meng et al., 2020, Meng et al., 2017, Meng et al., 2015).

Electrophysiology. Whole-cell recordings from L2/3 cells were performed with a patch clamp amplifier (Multiclamp 700B, Axon Instruments) using pipettes with input resistance of 4 – 9 MΩ. Data acquisition was performed with National Instruments AD boards and custom software (Ephus) (Suter et al., 2010), which was written in MATLAB (Mathworks) and adapted to our setup. Voltages were corrected for an estimated junction potential of 10 mV. Electrodes were filled with (in mM): 115 cesium methanesulfonate ($CsCH_3SO_3$), 5 NaF, 10 EGTA, 10 HEPES, 15 CsCl, 3.5 MgATP, 3 QX-314 (pH 7.25, 300 mOsm). Cesium and QX314 block most intrinsic active conductances and thus make the cells electrotonically compact. Series resistances were typically 20-25 MΩ. Photostimulation: 0.5 – 1 mM caged glutamate (*N*-(6-nitro-7-coumarinylmethyl)-L-glutamate; Ncm-Glu) (Muralidharan et al., 2016) is added to the ACSF. This compound has no effect on neuronal activity without UV light (Muralidharan et al., 2016). UV laser light (500 mW, 355 nm, 1 ms pulses, 100 kHz repetition rate, DPSS) was split by a 33% beam splitter (CVI Melles Griot), attenuated by a Pockels cell (Conoptics), gated with a laser shutter (NM Laser), and coupled into a microscope via scan mirrors (Cambridge Technology) and a dichroic mirror. The laser beam in LSPS enters the slice axially through the objective (Olympus 10×, 0.3NA/water) and has a diameter of < 20 μm. Laser power at the sample is < 25 mW. Laser power was constant between slices and recording days. We typically stimulated up to 30 × 25 sites spaced 40 μm apart, enabling us to probe areas of 1 mm^2; such dense sampling reduces the influence of potential spontaneous events. Repeated stimulation yielded essentially identical maps. Stimuli were applied at 1 Hz. Analysis was performed essentially as described previously with custom software written in MATLAB (Meng et al., 2020, Meng et al., 2017, Meng et al., 2015). To detect monosynaptically evoked postsynaptic currents (PSCs), we detected PSCs with onsets in an approximately 50-ms window after the stimulation. This window was chosen based on the observed spiking latency under our recording conditions (Meng et al., 2020, Meng et al., 2017, Meng et al., 2015). Our recordings were performed at room temperature and in high-Mg^{2+} solution to reduce the probability of polysynaptic inputs. We measured both peak amplitude and transferred charge; transferred charge was measured by integrating the PSC. While the transferred charge might include contributions from multiple events, our prior studies showed a strong correlation between these measures (Meng et al., 2020, Meng et al., 2017, Meng et al., 2015). Traces containing a short-latency (< 8 ms) 'direct' response were discarded from the analysis (black patches in color-coded maps) as were traces that contained longer latency inward currents of long duration (> 50 ms) (Fig. 3b). The short-latency currents could sometimes be seen in locations surrounding (< 100 μm) areas that gave a 'direct' response. Occasionally some of the 'direct' responses contained evoked synaptic responses that we did not separate out, which leads to an underestimation of local short-range connections. Cells that did not show any large (>100 pA) direct responses were excluded from the analysis as these could be astrocytes. It is likely that the observed PSCs at each stimulus location represent the activity of multiple presynaptic cells.

Stimulus locations that showed PSC were deemed connected and we derived binary connection maps. We aligned connection maps for L2/3 cells in the population and averaged connection maps to derive a spatial connection probability map (Fig. 3c). In these maps the value at each stimulus location indicates the fraction of L2/3 cells that received input from these stimulus locations. Layer boundaries were determined from the infrared pictures. We derived laminar measures. Input area is calculated as the area within each layer that gave rise to PSCs. Mean charge is the average charge of PSCs from each stimulus location in each layer. Intralaminar integration distance is the extent in the rostro-caudal direction that encompasses connected stimulus locations in each layer. We calculated E/I balance in each layer for measures of input area and strength as (E-I)/(E+I), thus $(Area_E-Area_I)/(Area_E+Area_I)$, resulting in a number that varied between -1 and 1 with 1 indicating dominant excitation and -1 indicating dominant inhibition.

Spatial connection probability maps show the average connection pattern in each group. To compare the large-scale connectivity between cells in each group we calculated the spatial correlation of the binary connection maps in each group by calculating the pairwise cross-correlations (Meng et al., 2020).

Statistical analysis. Results are expressed as means ± SEM and were analyzed using MATLAB or GraphPad Prism 8 software. Comparisons of mRNA and protein expression, MBP Integrated Density, number of PV expressing cells and LSPS results were carried out using the unpaired two-tailed Student's t-test or Mann-Whitney non-parametric test depending if the variables passed a test for normal distribution or not. To evaluate the correlation between PV and MBP mRNA expression a Person's correlation test was performed. Differences were accepted as significant at $P < 0.05$.

FIGURE LEGENDS

Figure 1: MBP protein and mRNA expression are reduced in A1 of CNP-DN-ErbB4 mice.
a, Representative photomicrographs of primary auditory cortex of WT and CNP-DN-ErbB4 male mice showing the expression of myelin basic protein (MBP) (magenta) and nuclear DAPI staining (blue). Scale bar: 20μm.
b, Quantification of MBP staining intensity (WT: black; CNP-DN-ErbB4: red) (n = 4 – 8 mice per genotype).
c, Representative Western blots analysis of A1 samples for MBP and GAPDH.
d, Quantification of MBP protein expression normalized by GAPDH in A1 of WT and CNP-DN-ErbB4 mice (n = 6).
e, Relative mRNA expression of MBP in A1 of WT and CNP-DN-ErbB4 mice (n = 7 – 12). Unpaired two-tailed Student's t was performed. Data are expressed as mean ± SEM. * $p < 0.05$; **** $p < 0.0001$.

Figure 2: Sensitivity to photoreleased glutamate is unchanged in A1 of CNP-DN-ErbB4 mice.
a, Left, Infrared image of cortical field with patch pipette on a Layer 2/3 cell. Scale bar is 200 μm. Cortical layers are identified based on the DIC image. Right, Position of recorded cells within Layer 2/3. Plotted are the relative positions within Layer 2/3 for WT (black) and CNP-DN-ErbB4 (red) mice. 0 refers to the border with Layer 4 and 100 refers to the border with Layer 1.
b, Left Graphic illustration on how cell attach LSPS experiments were performed. The cortical field were divided into approximate 30 by 25 grids. UV laser scans all the grids with a pseudorandom pattern to make sure that two nearby locations won't be scanned sequentially to avoid adaptation. Cells under laser activation site could be activated and generate action potentials (APs). Right, Cell attach recordings on Layer 2/3 and 4 cells show areas that evoke action potentials. Maps show first spike latencies encoded by color and overlaid on infrared images.
c, Cumulative distributions of number of spikes (Left) and distances from locations that resulted in APs to the soma of L2/3 (solid) and L4 (dashed) cells for both WT (black) and CNP-DN-ErbB4 (red) mice.

Figure 3: Excitatory circuits to L2/3 neurons are normal in A1 of CNP-DN-ErbB4 mice.
a, Schematic diagram shows how whole-cell voltage-clamp combined with LSPS experiments are performed.
b, Whole-cell voltage-clamp recordings at holding potential of -70mV (top) and 0mV (bottom). Left, shows the traces obtained with photostimulation at different locations. Solid lines indicate time of photostimulation. Green shaded area is the analysis window. It started at 8 ms and ended at 50ms after laser onset. Right, example of excitatory and inhibitory maps for a L2/3 cell. Pseudocolor indicates the PSC charge at each stimulation location. Black area indicates where direct responses are. White circle marks the soma location. Horizontal bars indicate layer borders and are 100 μm long.
c, Cartoon illustrating how the connection probability (P(connection)) map is calculated. All the input maps contain 0 (gray, the area has no connection to the recorded cell) and 1 (black square, the area has monosynaptic connection to the recorded cell) and are aligned to soma (white circles). The P (connection) map is calculated by averaging all the input maps along z-axis.
d, Spatial connection probability of excitatory connections for WT (left) and CNP-DN-ErbB4 (right) mice, n=36 cells for WT and n = 32 cells for CNP-DN-ErbB4. The border bars are the averaged borders across all the cells in each group. Scale bar is 200μm long.

e, Bar graph of total area (left) and laminar connection width (right) of excitatory inputs from L2/3, L4 and L5/6 to L2/3 neurons of WT (black) and CNP-DN-ErbB4 (red) mice. Data are expressed as mean ± SEM, p>0.05. F, Bar graph of mean charge (left) and relative laminar charge contribution (right) from L2/3, L4 and L5/6 to L2/3 neurons of WT (black) and CNP-DN-ErbB4 (red) mice. Data are expressed as mean ± SEM, p>0.05.

Figure 4: Reduced connectivity of inhibitory circuits to L2/3 neurons in A1 of CNP-DN-ErbB4 mice.
a, Spatial connection probability of inhibitory connections for WT (left) and CNP-DN-ErbB4 (right) mice. The border bars are the averaged borders across all the cells in each group. Scale bar is 200μm long.
b, Bar graph of total area (left) and laminar connection width (right) of inhibitory inputs from L2/3, L4 and L5/6 to L2/3 neurons of WT (black) and CNP-DN-ErbB4 (red) mice. Data are expressed as mean ± SEM. * p<0.05, **p<0.01, ***p<0.001. Loss of myelin reduce the inhibitory inputs from all layers.
c, Bar graph of inhibitory mean charge (left) and relative laminar charge contribution (right) from L2/3, L4 and L5/6 to L2/3 neurons of WT (black) and CNP-DN-ErbB4 (red) mice. Data are expressed as mean ± SEM, *p<0.05.
d, Excitatory/inhibitory ((E-I)/(E+I)) balance for inputs from L2/3, L4, and L5/6 based on charge (left), peak (middle) and area (right). L2/3 neurons in CNP-DN-ErbB4 mice receive more excitation than inhibition, * p<0.05, **p<0.01, ***p<0.001.

Figure 5: Reduction in inhibitory circuits and reorganization of excitatory circuits in A1 of CNP-DN-ErbB4 mice.
a, Graphical representation of calculation of pairwise correlation between functional connection maps. Each black square represents the area that has monosynaptic connection to the recorded cell. Each connection map will be first vectorized and pairwise correlation between all the vectors will be calculated.
b, The mean and SEM of pairwise correlations of both excitatory (left) and inhibitory (right) maps for WT (black) and CNP-DN-ErbB4 (red) mice. Hypomyelination reduced the pairwise correlation of both excitatory and inhibitory maps, **p<0.01, ****p<0.0001

Figure 6: mRNA levels for excitatory and inhibitory synaptic proteins is normal in A1 of CNP-DN-ErbB4 mice.
mRNA expression for synaptic proteins in A1 of WT (black) and CNP-DN-ErbB4 (red) male mice were measured by real-time RT-PCR.
a, GABAergic markers: GAD65, GAD67, VGAT and GABARα1.
b, Glutamatergic markers: VGLUT1, VGLUT2, GRIA1, GRIA2, GRIA3 and GRIA4.
Unpaired two-tailed Student's t test or Mann-Whitney non parametric test were performed. Data are expressed as mean ± SEM. No difference was found between groups (n = 7 – 12).

Figure 7: Loss of oligodendrocyte ErbB signaling leads to reduced A1 PV cell density and PV mRNA levels.
a, Representative photomicrographs of A1 sections from WT and CNP-DN-ErbB4 mice showing PV^+ cells (green). Scale bar: 100μm.
b, A1 PV^+ cell density is reduced in A1 of CNP-DN-ErbB4 mice (n = 7 – 10).
c, A1 PV mRNA levels are reduced in A1 of CNP-DN-ErbB4 mice (n = 7 – 11).
d, PV mRNA levels correlate with MBP mRNA levels in A1 (WT, black dots; CNP-DN-ErbB4, red dots) mice.
e, Reduced ErbB3 mRNA levels in A1 after oligodendrocyte-specific ErbB3 KO (PLP/creERT:$ErbB3^{fl/fl}$) (n = 7).

f, A1 PV mRNA levels are reduced in PLP/creERT:ErbB3$^{fl/fl}$ (n = 7 – 11).
g, PV mRNA levels correlate with MBP mRNA levels in A1 (ErbB3$^{fl/fl}$, black dots; PLP/creERT:ErbB3$^{fl/fl}$, blue dots) mice.
Unpaired two-tailed Student's t test and Pearson's correlation test were performed. Data are expressed as mean ± SEM. * $p < 0.05$; ** $p < 0.01$.

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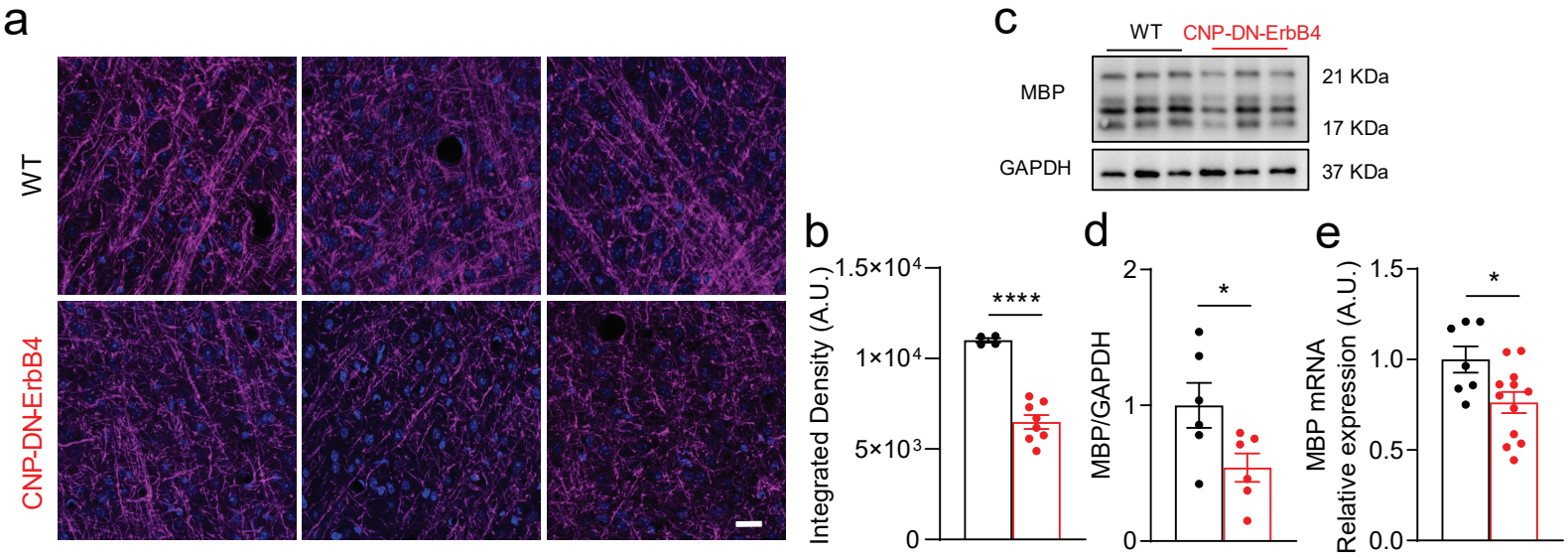
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Figure 1

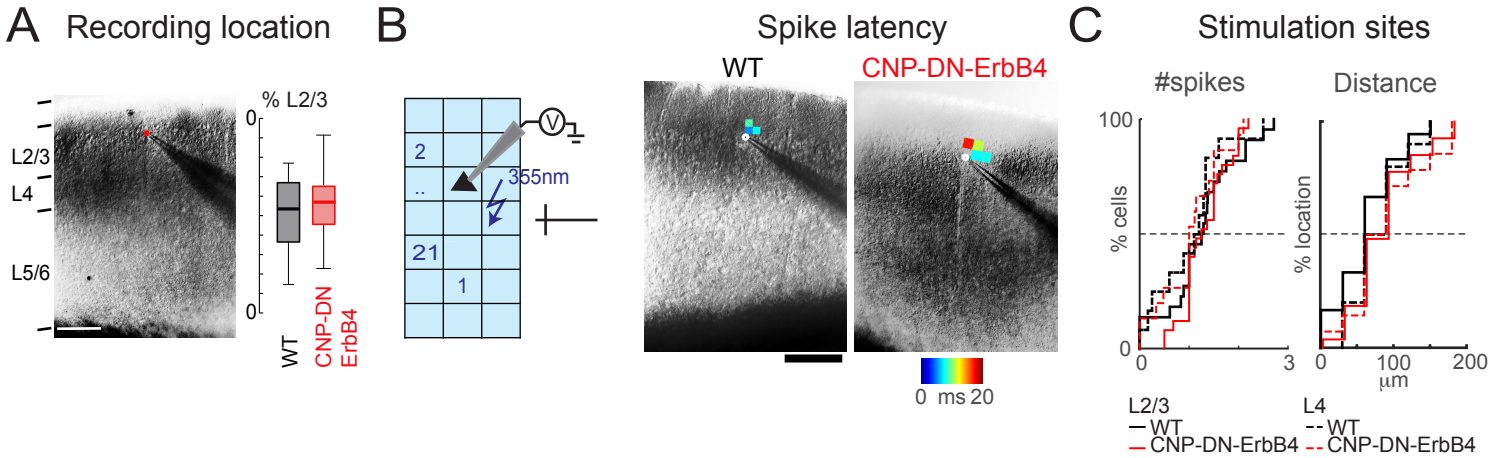
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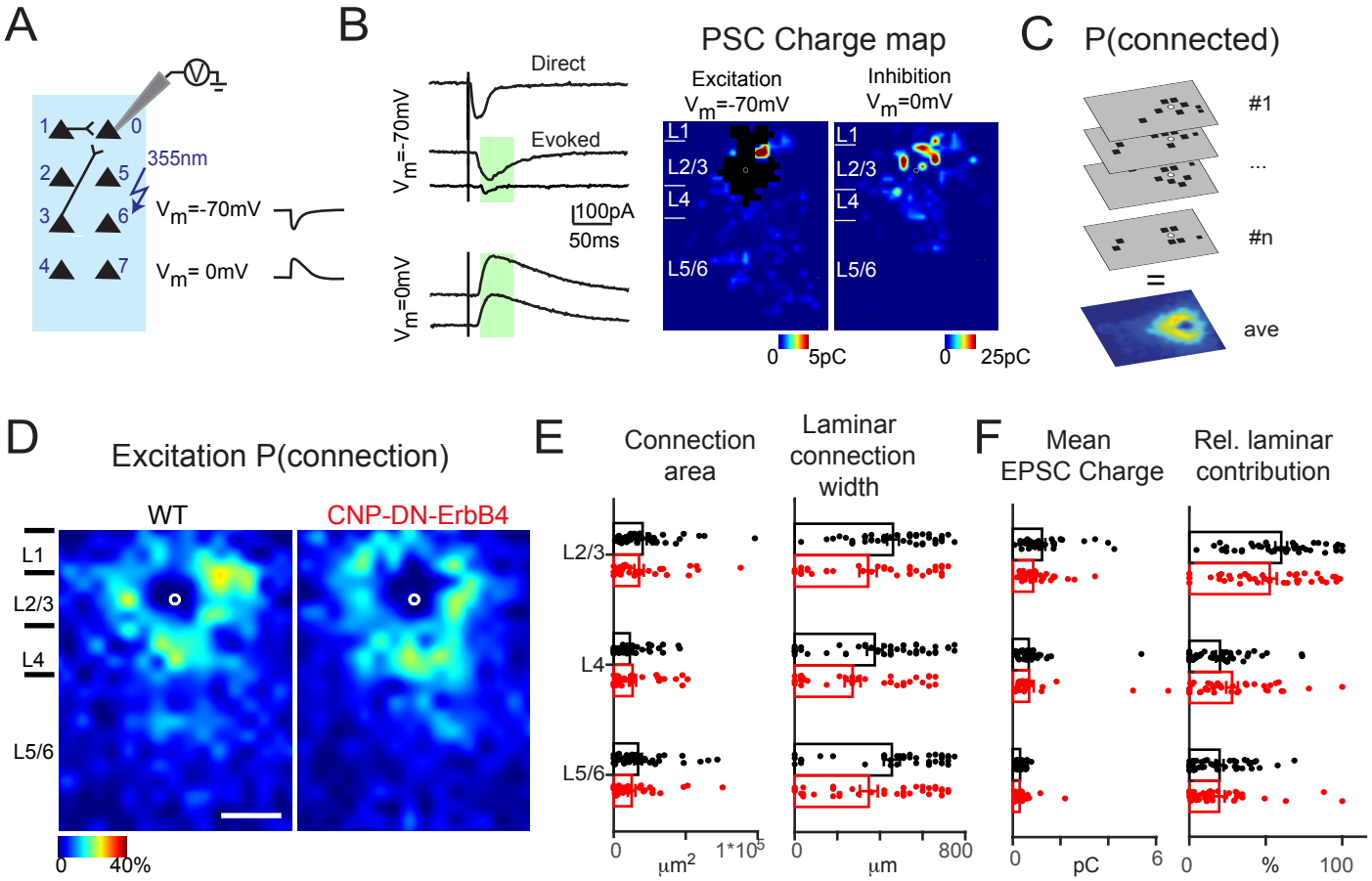
Figure 2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Excitation P(connection)
WT
CNP-DN-ErbB4
L1
L2/3
L4
L5/6
0
40%
E
Connection area
Laminar connection width
L2/3
L4
L5/6
0
μm2
1*10^5
0
μm
800
F
Mean EPSC Charge
Rel. laminar contribution
0
pC
6
0
%
100

Figure 3

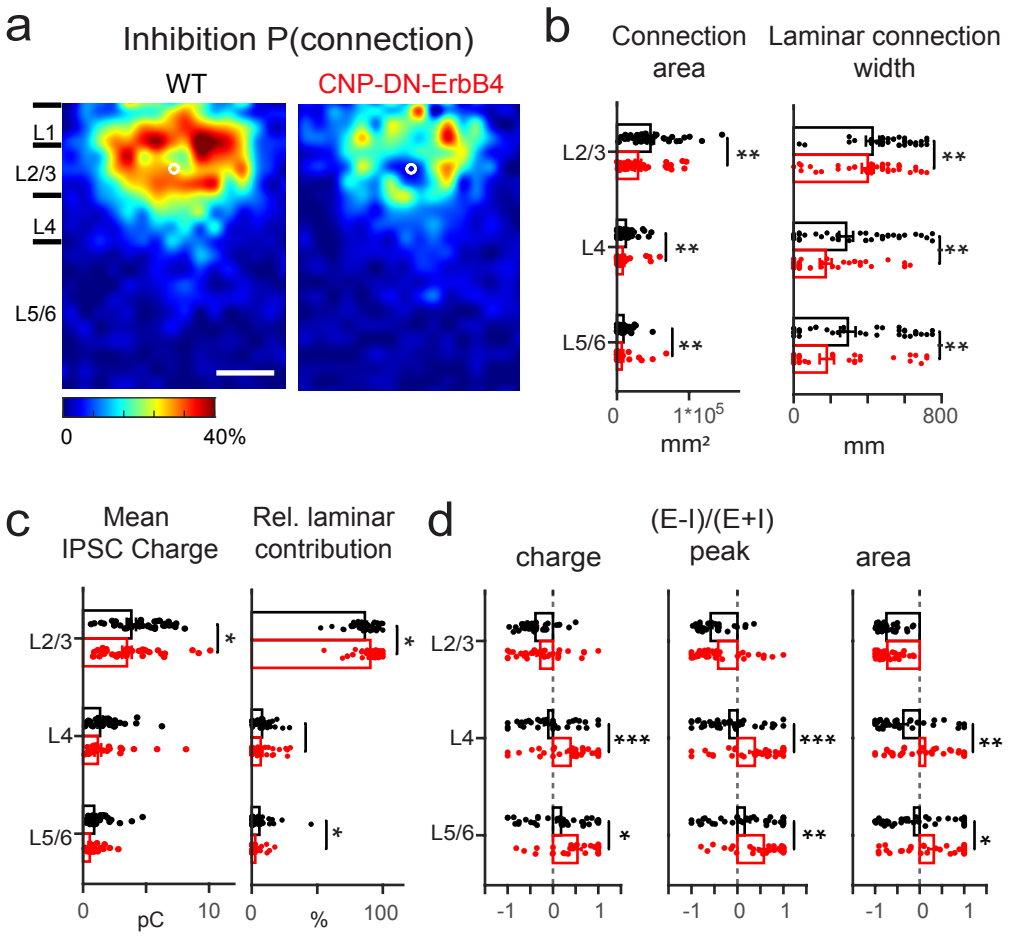
a
Inhibition P(connection)
WT
CNP-DN-ErbB4
L1
L2/3
L4
L5/6
0
40%
b
Connection area
Laminar connection width
L2/3
L4
L5/6
**
0
1*10^5
mm²
800
mm
c
Mean IPSC Charge
Rel. laminar contribution
*
0
pC
10
%
100
d
charge
(E-I)/(E+I)
peak
area
***
-1
0
1

Figure 4

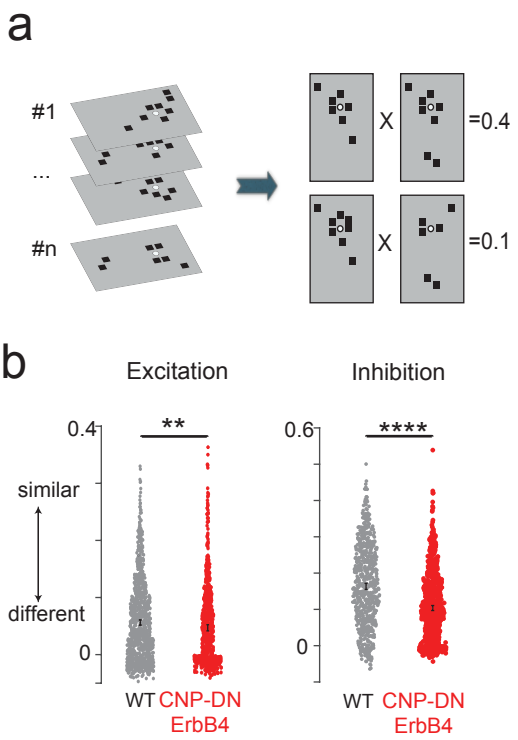
a
#1
...
#n
X
=0.4
X
=0.1
b
Excitation
Inhibition
0.4
similar
different
0
**
WT
CNP-DN
ErbB4
0.6
0
****
WT
CNP-DN
ErbB4

Figure 5

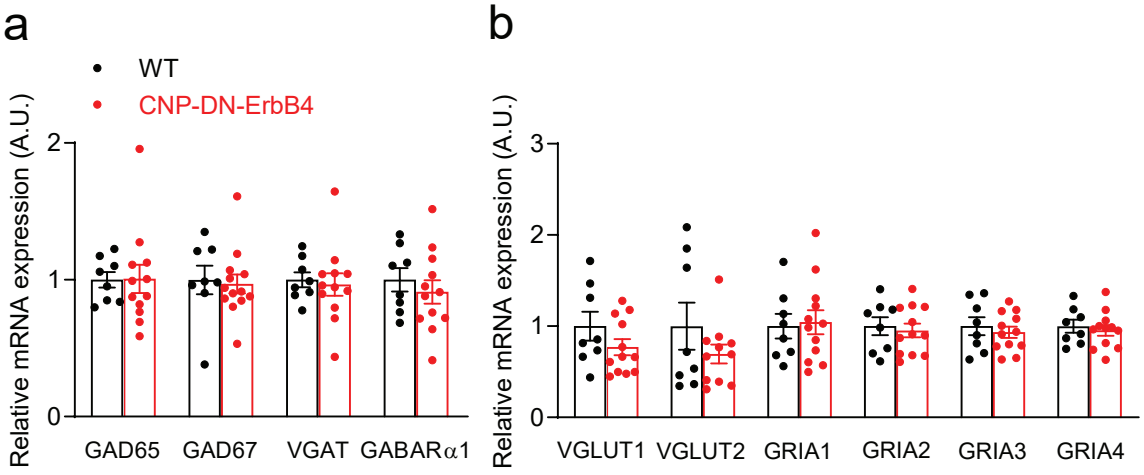
a
WT
CNP-DN-ErbB4
Relative mRNA expression (A.U.)
2
1
0
GAD65
GAD67
VGAT
GABARα1
b
Relative mRNA expression (A.U.)
3
2
1
0
VGLUT1
VGLUT2
GRIA1
GRIA2
GRIA3
GRIA4

Figure 6

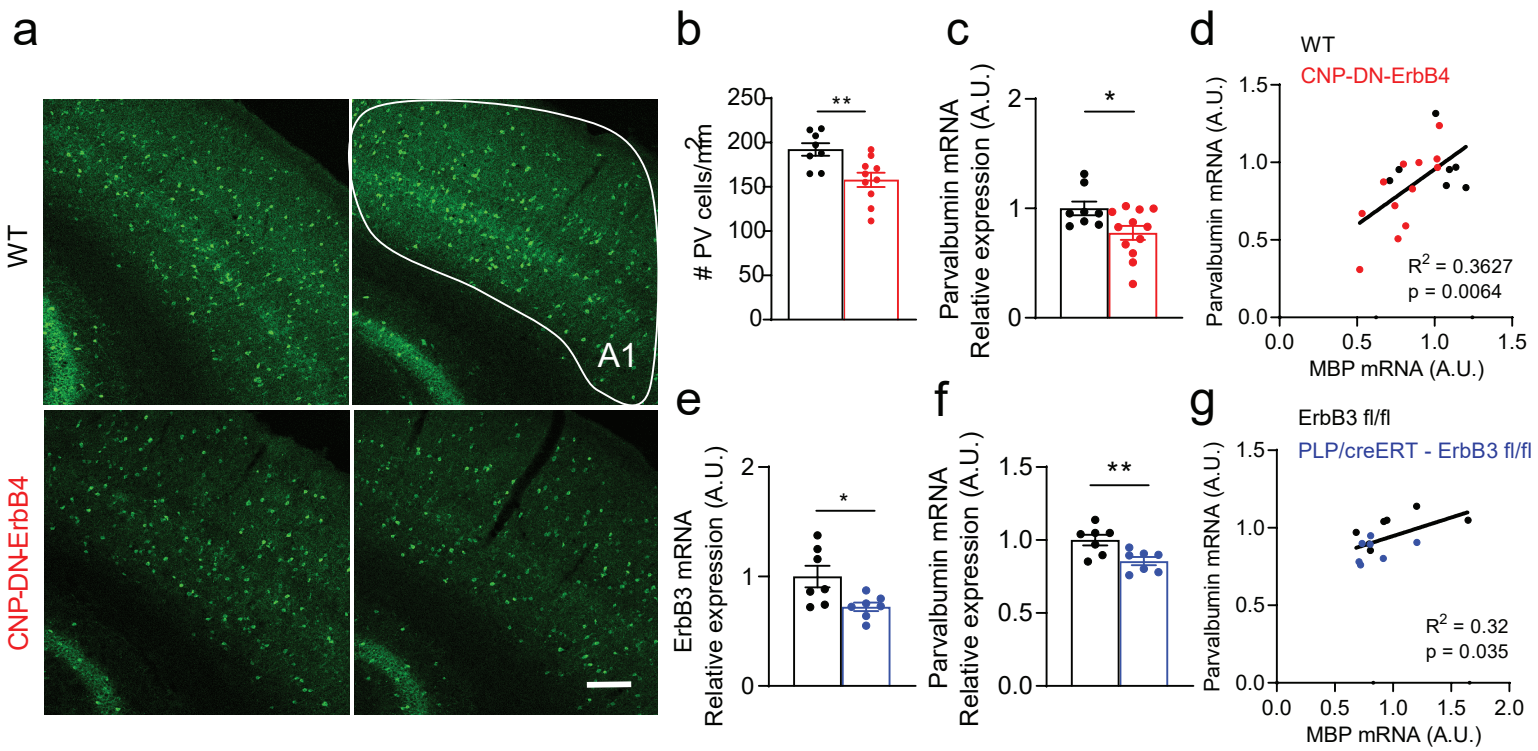
a
WT
CNP-DN-ErbB4
A1
b
PV cells/mm2
250
200
150
100
50
0
**
c
Parvalbumin mRNA
Relative expression (A.U.)
2
1
0
*
d
WT
CNP-DN-ErbB4
Parvalbumin mRNA (A.U.)
MBP mRNA (A.U.)
1.5
1.0
0.5
0.0
0.0
0.5
1.0
1.5
R2 = 0.3627
p = 0.0064
e
ErbB3 mRNA
Relative expression (A.U.)
2
1
0
*
f
Parvalbumin mRNA
Relative expression (A.U.)
1.5
1.0
0.5
0.0
**
g
ErbB3 fl/fl
PLP/creERT - ErbB3 fl/fl
Parvalbumin mRNA (A.U.)
MBP mRNA (A.U.)
1.5
1.0
0.5
0.0
0.0
0.5
1.0
1.5
2.0
R2 = 0.32
p = 0.035

Figure 7