NMDA Receptor Dysregulation by Defective Depalmitoylation in the Infantile 1 **Neuronal Ceroid Lipofuscinosis Mouse Model** 2

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16 Abstract

- 17 Protein palmitoylation and depalmitoylation alter protein function. This post-translational modification is critical
- 18 for synaptic transmission and plasticity. Mutation of the depalmitoylating enzyme palmitoyl-protein thioesterase
- 19 1 (PPT1) causes infantile neuronal ceroid lipofuscinosis (CLN1), a pediatric neurodegenerative disease. However,
- 20 the role of protein depalmitoylation in synaptic maturation is unknown. Therefore, we studied synapse
- 21 development in $Ppt1^{-/-}$ mouse visual cortex. We demonstrate the stagnation of the developmental N-methyl-D-22 aspartate receptor (NMDAR) subunit switch from GluN2B to GluN2A in $Ppt1^{-/-}$ mice. Correspondingly,
- 22 aspartate receptor (NMDAR) subunit switch from GluN2B to GluN2A in $Ppt1^{-/-}$ mice. Correspondingly, 23 GluN2A-mediated synaptic currents are diminished and $Ppt1^{-/-}$ dendritic spines maintain immature morphology
- 24 in vivo. Further, GluN2B is hyperpalmitoylated in *Ppt1*^{-/-} neurons and associated with extrasynaptic, diffuse
- calcium influxes and enhanced vulnerability to NMDA-induced excitotoxicity. Remarkably, $Ppt1^{-/-}$ neurons
- treated with palmitovlation inhibitors demonstrate normalized levels of palmitovlated GluN2B and Fyn kinase.
- 27 reversing susceptibility to excitotoxic insult. Thus, depalmitoylation of GluN2B by PPT1 plays a critical role in
- 28 postsynapse maturation and pathophysiology of neurodegenerative disease.

29 Introduction

The neuronal ceroid lipofuscinoses (NCLs) are a class of individually rare, primarily autosomal recessive, 30 neurodegenerative diseases occurring in an estimated 2 to 4 of 100,000 live births (Nita et al., 2016). Collectively, 31 NCLs represent the most prevalent class of hereditary pediatric neurodegenerative disease (Haltia, 2006). The 32 NCLs are characterized by progressive neurodegeneration, blindness, cognitive and motor deterioration, seizures, 33 and premature death. The cardinal feature of all NCLs is the intracellular accumulation of proteolipid material. 34 termed lipofuscin (Jalanko and Braulke, 2009: Nita et al., 2016). While lipofuscin accumulates in all cells of 35 affected individuals, it deposits most robustly in neurons. This accumulation is concurrent with rapid and 36 progressive neurodegeneration, particularly of thalamic and primary sensory cortical areas (Bible et al., 2004; 37 38 Kielar et al., 2007). The NCLs are categorized into CLN1-14 based on the age of onset and the causative gene 39 mutated. The products of CLN genes are lysosomal and endosomal proteins, therefore NCLs are also classified 40 as lysosomal storage disorders (LSDs) (Bennett and Hofmann, 1999; Jalanko and Braulke, 2009). The infantile form of disease. CLN1, presents as early as 6 months of age with progressive psychomotor deterioration, seizure, 41 42 and death at approximately five years of age (Haltia, 2006; Jalanko and Braulke, 2009; Nita et al., 2016). CLN1 disease is caused by mutations in the gene CLN1, which encodes the enzyme palmitoyl-protein thioesterase 1 43 44 (PPT1) (Camp and Hofmann, 1993; Camp et al., 1994; Vesa et al., 1995; Jalanko and Braulke, 2009). PPT1 is a depalmitovlating enzyme responsible for the removal of palmitic acid from modified proteins (Camp and 45 46 Hofmann, 1993; Lu and Hofmann, 2006).

47 Protein palmitovlation, the addition of a 16-carbon fatty acid (palmitic acid) to cysteine residues, is a crucial 48 regulator of protein trafficking and function, particularly in neurons (Havashi et al., 2005; Kang et al., 2008; 49 Noritake et al., 2009; Fukata and Fukata, 2010; Fukata et al., 2013; Han et al., 2015). This post-translational 50 modification is mediated by palmitovl acyltransferases (PATs) of the zDHHC enzyme family (Fukata et al., 2006; 51 Fukata and Fukata, 2010; Korycka et al., 2012). In contrast to other types of protein acylation, palmitoylation 52 occurs via a reversible thioester bond (s-palmitoylation), permitting dynamic control over target protein interactions and function. Further, palmitovlated proteins require depalmitovlation prior to lysosomal degradation 53 54 (Lu et al., 1996; Lu and Hofmann, 2006). Consequently, protein palmitovlation and depalmitovlation contribute significantly to mechanisms underlying synaptic plasticity and endosomal-lysosomal trafficking of proteins 55 (Hayashi et al., 2005, 2009; Lin et al., 2009; Noritake et al., 2009; Fukata and Fukata, 2010; Thomas et al., 2013; 56 Keith et al., 2012; Thomas et al., 2012; Fukata et al., 2013; Woolfrey et al., 2015; Han et al., 2015; Kaur et al., 57 58 2016). Indeed, PPT1 is a lysosome-targeted depalmitoylating enzyme that localizes to the axonal and synaptic compartments (Verkruyse and Hofmann, 1996; Ahtiainen et al., 2003; Kim et al., 2008). The synaptic association 59 of PPT1 and prominence of palmitovlated synaptic proteins suggests that PPT1 influences synaptic functions 60 through, at least, protein turnover. Many synaptic proteins undergo palmitoylation, including, but not limited to: 61 postsynaptic density protein 95 (PSD-95), all GluA subunits of AMPARs, and the GluN2A/2B subunits of 62 NMDARs (Kang et al., 2008). However, the role of depalmitovlation in regulating synaptic protein function 63 remains less clear. 64

N-methyl-D-aspartate receptors (NMDARs) are voltage-dependent, glutamate-gated ion channels consisting
of two obligatory GluN1 subunits and two GluN2 subunits that undergo a developmental change (Cull-Candy et
al., 2001; van Zundert et al., 2004; Lau and Zukin, 2007; Paoletti et al., 2013). NMDARs play a crucial role in
synaptic transmission, postsynaptic signal integration, synaptic plasticity (Cull-Candy et al., 2001; Van Dongen,
2009; Paoletti et al., 2013), and have been implicated in various neurodevelopmental and psychiatric disorders
(Lau and Zukin, 2007; Lakhan et al., 2013; Yamamoto et al., 2015; Hu et al., 2016). NMDAR subunit composition,
receptor localization, and downstream signaling mechanism undergo developmental regulation (Watanabe et al.,

1992; Monyer et al., 1994; Sheng et al., 1994; Li et al., 1998; Stocca and Vicini, 1998; Tovar and Westbrook, 72 73 1999; Losi et al., 2003; van Zundert et al., 2004; Paoletti et al., 2013; Wyllie et al., 2013). In particular, GluN2B-74 containing NMDARs, which are abundant neonatally and allow copious calcium entry, are supplanted by 75 GluN2A-containing NMDARs in response to experience-dependent neuronal activity (Quinlan et al., 1999a, 76 1999b; Philpot et al., 2001; Liu et al., 2004; Paoletti et al., 2013). This developmental switch of GluN2B- to 77 GluN2A-containing NMDARs during brain maturation is mediated by the postsynaptic scaffolding receptors. 78 SAP102 and PSD-95, respectively; SAP102-GluN2B-NMDAR complexes are replaced by PSD-95-GluN2A-79 NMDAR complexes in response to developmental, experience-dependent neuronal activity (Sans et al., 2000; 80 van Zundert et al., 2004; Elias et al., 2008). While PSD-95, GluN2B, and GluN2A all undergo palmitovlation, how depalmitovlation regulates the turnover of these proteins, let alone during the GluN2B to GluN2A subunit 81 switch, is unclear. 82

83 In the current study, we investigated the cellular and synaptic effects of PPT1-deficiency using the *Ppt1*^{-/-} 84 mouse model of CLN1 disease. We focused on the visual system in *Ppt1*^{-/-} animals for two reasons. First, cortical blindness is a characteristic feature of CLN1 disease. Second, the rodent visual system is a well-studied model of 85 86 cortical development and synaptic plasticity/maturation and it therefore serves as an optimal experimental model 87 to examine the role of PPT1-mediated depalmitovlation during development. We found that lipofuscin accumulated very early in the *Ppt1^{-/-}* visual cortex, shortly after eve-opening at postnatal day (P) 14, a timing 88 89 earlier than previously documented (Gupta et al., 2001). Using biochemistry and electrophysiology, we found impeded developmental NMDAR subunit switch from GluN2B to GluN2A in *Ppt1^{-/-}* mice compared to wild-type 90 (WT). This NMDAR disruption is associated with disrupted dendritic spine morphology in vivo. To gain further 91 92 mechanistic insight into neurodegeneration in CLN1, we used cultured cortical neurons and found that Ppt1^{-/-} neurons recapitulate the disrupted GluN2B to GluN2A switch, leading to excessive extrasynaptic calcium 93 94 transients and enhanced vulnerability to NMDA-mediated excitotoxicity. We directly examined protein 95 palmitovlation state and found hyperpalmitovlation of GluN2B as well as Fyn kinase, which facilitates GluN2B surface retention, in *Ppt1*^{-/-} neurons. Finally, we demonstrate that chronic treatment of *Ppt1*^{-/-} neurons with 96 97 palmitoylation inhibitors normalized GluN2B and Fyn kinase hyperpalmitoylation and rescued the enhanced 98 susceptibility to excitotoxicity. Our results indicate that PPT1 plays a critical role in the developmental GluN2B 99 to GluN2A subunit switch and synaptic maturation. Further, our results indicate that these dysregulated 100 mechanisms contribute to CLN1 pathophysiology and may be shared features of common adult-onset neurodegenerative diseases. 101

102 Results

To understand synaptic dysregulation in CLN1 disease, we utilized the visual cortex of *Ppt1*^{-/-} animals as 103 a model system. The rodent visual cortex undergoes timed, experience-dependent plasticity, which has been well-104 characterized at the systemic, cellular, and molecular levels (Bear et al., 1990; Gordon and Stryker, 1996; Hensch 105 et al., 1998; Quinlan et al., 1999a, 1999b; Fagiolini and Hensch, 2000; Mataga et al., 2001, 2004; Philpot et al., 106 2001: Desai et al., 2002: Yoshii et al., 2003: Hensch, 2005: Cooke and Bear, 2010). We examined WT and Ppt1⁻ 107 ⁻ littermates at the following ages: P11, P14, P28, P33, P42, P60, P78, P120, which correspond to particular 108 developmental events in visual cortex. In mice, P11 and P14 are prior to and just after eye opening (EO) 109 respectively. Further, the critical period in the visual cortex peaks at P28 and closes from P33 to P42. Postnatal 110 111 day 60, P78, and P120 were selected as adult time points. We determined whether experience-dependent synaptic 112 maturation is altered during the progression of CLN1 pathology.

113 Lipofuscin deposits immediately following eye opening in visual cortex of *Ppt1^{-/-}* mice

Although it remains controversial whether lipofuscin is toxic to neurons or an adaptive, neuroprotective 114 mechanism, its accumulation correlates with disease progression. Therefore, we examined lipofuscin deposition 115 in the visual cortex as a marker of pathology onset and progression. Lipofuscin aggregates are readily visible as 116 autofluorescent lipopigments (ALs) without staining under a confocal microscope. To examine the temporal and 117 spatial accumulation of ALs in *Ppt1^{-/-}* mice, we performed quantitative histology on the visual cortex (area V1) 118 119 of WT and *Ppt1^{-/-}* mice during early development. Visual cortical sections were imaged at the above-mentioned 120 developmental time points and ALs were quantified in a laminar-specific manner. We found that ALs are detectable first at P14 in *Ppt1*^{-/-} visual cortex, much earlier than previously reported (Figure 1A, B, C). 121

Further, AL accumulation accelerated rapidly through the critical period (Berardi et al., 2000; Hensch, 2005; Maffei and Turrigiano, 2008) and plateaued by adulthood (P60). This result indicates that neuronal AL load is saturable, and that this saturation occurs early on in disease, as $Ppt1^{-/-}$ animals do not perish until around 10 months old (Gupta et al., 2001). Interestingly, we noticed a trend that AL accumulation became more robust in the deep cortical layers beginning at P28, particularly layer IV, the termination site of thalamocortical neurons projecting from the dorsal lateral geniculate nucleus (dLGN) that relay retinal inputs (**Figure 1C**). WT mice accumulate a miniscule amount of ALs, even at the oldest time point examined (**Figure 1A-C**).

Whether lipofuscin accumulation is directly neurotoxic or not, profiling the temporospatial and subregional pattern of AL deposition will be valuable for assessing therapeutic interventions in future studies. Further, the pattern of deposition revealed herein suggests a correlation between systemic neuronal activation and lipofuscin accumulation. In particular, our result that AL deposition starts immediately following EO, the onset of patterned visual activity, and is detectable prominently in layer IV (**Figure 1A, C, Supplementary Table 1**) suggests that neuronal activity or experience-dependent plasticity are linked to lipofuscin deposition.

135 NMDAR subunit composition is biased toward immaturity in *Ppt1-/-* visual cortex

To examine the role of PPT1 in excitatory synapse function, we focused on the NMDAR subunits, GluN2B and GluN2A, which are both palmitoylated (Hayashi et al., 2009). Developmental GluN2B to GluN2A subunit change (Paoletti et al., 2013) is critical for NMDAR function and maturation, which facilitates refinement of neural circuits and a higher tolerance to glutamate-mediated excitotoxicity (Hardingham and Bading, 2002, 2010; Hardingham et al., 2002). Furthermore, previous work shows evidence for NMDA-induced excitotoxicity in the pathogenesis of CLN1 (Finn et al., 2012). We biochemically analyzed WT and *Ppt1*-^{/-} visual cortices from

P11 to P60, and measured levels of GluN2B and GluN2A subunits in whole lysates and synaptosomes of WT and *Ppt1^{-/-}* visual cortices. Whereas GluN2B levels were comparable between WT and *Ppt1^{-/-}* at all ages, GluN2A levels in synaptosomes were significantly lower in *Ppt1^{-/-}* than WT (Figure 2A). This decrease was present at time points during, and just following, the critical period in visual cortical development (P33, P42, and P60).
When analyzed as a ratio of GluN2A/GluN2B, a robust and persistent decrease is observed in *Ppt1^{-/-}* visual cortex (Figure 2B). GluN1 levels were unchanged between WT and *Ppt1^{-/-}* in synaptosomes (Figure 2C), indicating the selective obstruction of GluN2A incorporation into NMDARs.

149 The developmental shift from GluN2B-containing NMDARs to synaptic GluN2A-containing NMDARs is mediated by the postsynaptic scaffolding proteins, SAP102 and PSD-95 (Townsend et al., 2003; Yoshii et al., 150 2003: Elias et al., 2008). SAP102 preferentially interacts with GluN2B-containing NMDARs, which are enriched 151 152 neonatally (Chen et al., 2000, 2011; Sans et al., 2000; Liu et al., 2004; van Zundert et al., 2004; Zheng et al., 153 2010). In contrast, PSD-95 has greater affinity to GluN2A-containing NMDARs, particularly in the mature brain 154 (Sans et al., 2000; van Zundert et al., 2004; Van Dongen, 2009; Yan et al., 2014). Thus, we examined the expression of these scaffolding proteins in WT and Ppt1^{-/-} visual cortex. Similar to the results obtained for 155 GluN2B and GluN2A, while SAP102 levels remained unchanged, we observed a decrease in PSD-95 levels at 156 157 P33-P60, the same developmental time points where GluN2A expression was reduced (Figure 2D). Together, these results suggest reduced incorporation and scaffolding of GluN2A-containing NMDARs in *Ppt1-/-* synapses, 158 indicating immature or dysfunctional synaptic composition. 159

To examine whether the reduction in GluN2A is due to selective exclusion from the postsynaptic site or 160 alterations in the total protein amount, we also measured NMDAR subunit levels in whole lysates. These findings 161 closely match our findings in synaptosomes. Namely, GluN2A levels showed reductions in Ppt1^{-/-} lysates 162 beginning at the same time point (P33), while GluN2B levels were stable (Supplementary Figure 1A). The 163 GluN2A/2B ratios in *Ppt1*^{-/-} whole lysates were also lower than those in WT lysates and the reduction was 164 comparable to that observed in synaptosomes. (Supplementary Figure 1B). GluN1 levels, however, were 165 unaltered between genotypes (Supplementary Figure 1C). Collectively, these results indicate a selective 166 decrease in the total amount of mature synaptic components in *Ppt1*^{-/-} brains and suggest that synaptosomal 167 reductions in GluN2A and PSD-95 may result from altered transcription or translation. 168

169 NMDAR-mediated EPSCs are altered in *Ppt1^{-/-}* visual cortex

Next, we sought to correlate our biochemical findings electrophysiological changes in NMDAR 170 functionality (Figure 2). While human CLN1 patients present with retinal degeneration and the *Ppt1*^{-/-} mouse 171 model of CLN1 phenocopies the human disease, the electroretinogram (ERG) is effectively unaltered at 4 moths 172 173 in the mouse model (Lei et al., 2006), allowing for detailed study of the electrophysiological changes in the visual 174 cortex associated with early disease states. We recorded evoked, NMDAR-mediated excitatory postsynaptic currents (EPSCs) in layer II/III cortical neurons in visual cortical slices of WT and Ppt1^{-/-} mice at P42. The 175 NMDA-EPSCs were pharmacologically isolated (see Methods section) and were recorded in whole cell patch 176 177 mode clamped at +50mV (Figure 3A). As GluN2A- and GluN2B-containing NMDARs exhibit differential receptor kinetics, with GluN2A displaying fast (~50ms) and GluN2B displaying slow decay kinetics (~300ms), 178 their relative contribution is reliably interpolated by fitting the EPSC decay phase with a double exponential 179 function (Stocca and Vicini, 1998; Vicini et al., 1998). From the fitting, we measured the following parameters: 180 the amplitude (A) of the fast (A_f) and slow (A_s) components; the ratio $A_{f}/A_{f}+A_{s}$; the decay time constants (τ) of 181 the fast (τ f) and the slow components (τ s), and the weighted decay (τ w). *Ppt1*^{-/-} mice showed significant decreases 182 in the A_f and ratio of $A_f/A_f + A_s$ as compared to WT, while A_s showed no significant change (Figure 3B). Further, 183

the τf significantly decreased in $Ppt1^{-/-}$ mice vs. WT, while τw and τs were comparable (**Figure 3C**). As the fast components of both the amplitude and decay constant are reduced in $Ppt1^{-/-}$ neurons, these data indicate a functional decrease in the contribution of GluN2A in NMDAR-mediated EPSCs in layer II/III visual cortical neurons and corroborate our biochemical findings.

188 Dendritic spine morphology is immature in *Ppt1-/-* visual cortex

The morphology of dendritic spines is dynamic, and synaptic activities directly alter spine morphology 189 during synaptic plasticity (Engert and Bonhoeffer, 1999; Parnass et al., 2000; Matsuzaki et al., 2001; Yuste and 190 Bonhoeffer, 2001). During visual cortical development and concomitant with the GluN2B to GluN2A switch, 191 excitatory synaptic architecture and dendritic spine morphology undergo robust structural plasticity. In particular, 192 dendritic spines contribute to experience-dependent synaptic plasticity via the generation, maturation, and long-193 term stabilization of spines, ultimately giving rise to the established synaptic circuit. Typically, by P33, dendritic 194 spines demonstrate reduced turnover, reduced motility, and mushroom-type spine morphology, indicating 195 synaptic maturity. Importantly, dendritic spines are morphologically disrupted in many neurodevelopmental 196 disorders, typically skewing towards an immature phenotype (Purpura, 1979; Irwin et al., 2001; Penzes et al., 197 198 2011).

We hypothesized that dendritic spine morphology is immature or disrupted in $Ppt1^{-/-}$ neurons, particularly given that GluN2A subunit incorporation is disrupted *in vivo*. Thus, we used *in utero* electroporation to sparsely label layer II/III cortical neurons in visual cortex using a GFP construct (Matsuda and Cepko, 2004). GFPexpressing cells from WT and $Ppt1^{-/-}$ animals were imaged for detailed analysis of dendritic spine morphology (spine length, spine volume, and spine head volume) at P33, a time point when dendritic spine morphology is typically considered mature and GluN2A is reduced at $Ppt1^{-/-}$ synapses.

Electroporated, GFP-expressing cells (procedure schematized in Figure 4A) from WT and *Ppt1*^{-/-} visual 205 cortex (Figure 4B) were analyzed in Imaris (Bitplane) for dendritic spine characteristics. While WT neurons 206 exhibited mushroom-type spine morphology with high-volume spine heads (Figure 4C, arrows). Pnt1^{-/-} neurons 207 showed longer, filipodial protrusions or stubby spines (Figure 4C, arrowheads). Quantification of spine length 208 and spine volume demonstrated that Ppt1^{-/-} spines were longer and less voluminous compared to WT (Figure 4D-209 E). Further, the volume of dendritic spine heads was reduced in $Ppt1^{-/-}$ neurons (Figure 4E, inset). These data 210 indicate that dendritic spine morphology is disrupted in the developing CLN1 visual cortex, correspond with the 211 finding that NMDAR composition is immature at P33, and suggest a reduced ability to compartmentalize calcium 212 and other localized biochemical signals in CLN1. 213

NMDAR subunit composition and dendritic spine morphology are also immature in *Ppt1-/-* primary cortical neurons

The GluN2B to GluN2A switch and maturation of dendritic spine characteristics in WT primary neurons has been previously demonstrated (Williams et al., 1993; Zhong et al., 1994; Papa et al., 1995). We established that the developmental switch from GluN2B- to GluN2A-containing NMDARs and dendritic spine morphology are impaired in the $Ppt1^{-/-}$ mouse brain. To understand these mechanisms more comprehensively and examine protein palmitoylation more directly, we used dissociated neuronal cultures. First, we analyzed these developmental events in WT and $Ppt1^{-/-}$ primary cortical neurons to determine whether the biochemical and structural features of disease are recapitulated *in vitro*.

Cortical neurons cultured for 7, 10, or 18 days *in vitro* (DIV 7, 10, or 18) were harvested and lysates subjected to immunoblot analysis for markers of immature (GluN2B) or mature (GluN2A, PSD-95) excitatory

synapses. Expression of GluN2B clearly preceded that of mature synaptic markers, peaking in both WT and *Ppt1*^{-/-} neurons at DIV10 and decreasing thereafter (**Figure 5A**). In contrast, levels of both GluN2A and PSD-95 remained low until DIV18, at which point expression was robust (**Figure 5B, C**). Importantly, GluN2A, PSD-95, and GluN2A/GluN2B ratio levels were reduced in *Ppt1*^{-/-} neurons compared to WT at DIV18, indicating that the biochemical phenotype is recapitulated to an extent *in vitro* (**Figure 5B-D**).

To analyze dendritic spine morphology, primary cortical neurons from fetal WT and Ppt1^{-/-} mice were 230 transfected with a GFP construct (Matsuda and Cepko, 2004) and were cultured until DIV 15 or 20 when live cell 231 imaging was performed (Figure 6A). We measured dendritic spine length and volume in transfected cells using 232 the Imaris software (Bitplane). At both DIV 15 and 20, we observed a significant shift in the dendritic spine length 233 and volume (Figure 6B and C). Ppt1-/- neurons demonstrated a significantly higher percentage of long, thin 234 235 protrusions (filipodia-type; Figure 6B), and a significant reduction in the percentage of mature, mushroom-type dendritic spines with volumes greater than 0.2 µm³ (Figure 6C). When averaged, the data demonstrate a robust 236 increase in mean spine length and a decrease in spine volume in Ppt1^{-/-} neurons compared to WT controls at both 237 time points (Figure 6B and C, right). Together, these data demonstrate that *Ppt1*^{-/-} neurons in culture give rise 238 to morphologically immature dendritic spines and corroborate our in vivo findings. 239

240 Calcium imaging reveals extrasynaptic calcium dynamics in *Ppt1-/-* neurons

Intracellular calcium dynamics, compartmentalization, and signaling play a critical role in synaptic 241 transmission and plasticity. These properties are altered by glutamate receptor composition and location (Lau and 242 Zukin, 2007; Hardingham and Bading, 2010; Paoletti et al., 2013). GluN2B-containing NMDARs maintain a 243 prolonged open conformation compared to GluN2A-containing receptors, allowing increased calcium entry per 244 synaptic event (Sobczyk et al., 2005). Moreover, previous studies indicate that GluN2A-containing NMDARs are 245 generally inserted in the PSD whereas GluN2B-containing NMDARs are localized extrasynaptically and 246 associated with SAP102 (Tovar and Westbrook, 1999; Hardingham et al., 2002; Townsend et al., 2003; 247 Washbourne et al., 2004; Hardingham and Bading, 2010). To determine more directly the effects of our 248 biochemical and electrophysiological findings on calcium dynamics, we analyzed calcium signals in WT and 249 Ppt1^{-/-} neurons transfected with the genetically encoded calcium sensor, GCaMP3 (Tian et al., 2009). 250

While WT neurons exhibited primarily compartmentalized, dendritic spine-specific calcium signals 251 (Figure 7A-C, left, see Video 1), Ppt1^{-/-} neurons demonstrated diffuse calcium influxes that spread through the 252 253 dendritic shaft (Figure 7A-C, right, see Video 2). These extrasynaptic transients appear rarely in WT cells (Figure 7, see Videos). To analyze the calcium dynamics in more detail, measurements of $\Delta F/F_0$ were made for 254 each dendritic segment, from each cell over the course of the captured videos (see Methods). Multiple transients 255 from the same synaptic site are shown as a heat map of $\Delta F/F_0$ measurements and they are largely consistent across 256 time in both WT and $Ppt1^{-/-}$ neurons (Figure 7B). Further, plotting of the averaged $\Delta F/F_0$ transients at an 257 individual synaptic site demonstrates that local fluorescence increases in WT cells are confined to a short distance 258 from the peak $\Delta F/F_0$ at synaptic sites (Figure 7B and C, left), while those of $Ppt1^{-/-}$ neurons diffuse longer 259 distances within the dendrite (Figure 7B and C, right). To quantitatively compare these properties, we performed 260 measurements of area under the curve (AUC) and calcium diffusion distance (see shaded region in Figure 7C) 261 for each synaptic site from WT and Ppt1^{-/-} neurons. These analyses revealed a robust increase in both the AUC 262 (Figure 7D) and the calcium diffusion distance (Figure 7E) in $Ppt1^{-/-}$ neurons compared to WT. Furthermore, 263 performing correlation analysis of calcium events across time (see Methods) within a given neuron demonstrates 264 that calcium influxes are more synchronous (increased correlation coefficient) in Ppt1^{-/-} neurons compared to WT 265 (Figure 7F). This result may involve the mechanisms underlying synaptic cluster plasticity, including synaptic 266

integration via translational activation (SITA) influenced by excessive Ca^{2+} entry in *Ppt1^{-/-}* neurons (Govindarajan et al., 2006). Together, these data indicate that calcium entry and dispersion are enhanced at *Ppt1^{-/-}* synapses *in vitro*.

These data are in line with our biochemical and electrophysiological findings and suggest that GluN2B-270271 containing NMDARs mediate the observed calcium signals. To further test this possibility, we next treated WT and Ppt1^{-/-} neurons with Ro 25-6981 (1µM, added in imaging medium following 2.5min imaging at baseline), a 272 GluN2B-containing NMDAR specific antagonist, and performed calcium imaging. Ro 25-6981 had virtually no 273 effect on calcium signals recorded from WT cells (Figure 7G-I, see Video 3). In contrast, Ppt1-/- neurons treated 274 275 with Ro 25-6981 showed a reduction in dendritic calcium influxes within shafts, while few residual, compartmentalized transients persisted (Figure 7G-I, see Video 4). Quantitatively, both AUC (Figure 7H) and 276 277 calcium diffusion (Figure 7I) distance were rescued to WT levels following Ro 25-6981 treatment of Ppt1-/neurons. Together, these data suggest that Ppt1-/- neurons have extrasynaptic calcium signaling compared to WT 278 that is sensitive to GluN2B-NMDAR blockade. 279

280 *Ppt1-/-* cultured neurons show enhanced vulnerability to NMDA-mediated excitotoxicity

GluN2B-predominant NMDARs are implicated in enhanced neuronal susceptibility to NMDA-mediated 281 neuronal death (Hardingham and Bading, 2002, 2010; Hardingham et al., 2002; Martel et al., 2012). Our results 282 from biochemical, electrophysiological, and live-imaging analyses indicate decreased GluN2A/2B ratio 283 suggesting an intriguing possibility that *Ppt1*^{-/-} neurons are more vulnerable to excitotoxicity (Finn et al., 2012). 284 Therefore, we treated WT and *Ppt1^{-/-}* cultured neurons with NMDA (varying doses, 10-300µm) and glycine (1-285 30µm, always in 1:10 ratio with NMDA) for 2 hours and assayed cell viability 24 hours later using the 286 PrestoBlue® reagent (ThermoFisher Scientific) (Figure 8A). As expected, both WT and Ppt1^{-/-} neurons 287 288 demonstrated dose-dependent reductions in cell viability in response to increasing concentrations of NMDA/glycine (Figure 8B). Importantly, Ppt1^{-/-} neurons were more vulnerable to NMDA insult, as exposure to 289 10µM NMDA was sufficient to reduce cell viability significantly in $Ppt1^{-/-}$ neurons but not WT cells (WT = 93 ± 290 4.1%; $Ppt1^{-/-} = 76 \pm 3.5\%$; *p=0.046; Figure 8B). Further, at 100µM NMDA, WT neuron viability decreased by 291 35%, while $Ppt1^{-/-}$ neuron viability was reduced significantly further, by 58% (WT = 65 ± 1.8%; $Ppt1^{-/-}$ = 42 ± 292 4.5%; **p=0.0043; Figure 8B). At 300µM NMDA treatment this effect plateaued, as cell viability between WT 293 and *Ppt1^{-/-}* neurons was comparable (Figure 8B). 294

Palmitoylation inhibitors rescue enhanced vulnerability to NMDA-mediated excitotoxicity in *Ppt1-/*cultured neurons

We next asked whether this enhanced vulnerability to excitotoxicity is due to hyperpalmitoylation of 297 neuronal substrates, and if it can be corrected by balancing the level of synaptic protein 298 palmitoylation/depalmitoylation. First, we found that 77% of cultured Ppt1-/- neurons accumulate ALs 299 spontaneously at DIV18-20 (Figure 9A and B). Immunostaining for a marker of lysosomal compartments, 300 lysosomal-associated membrane protein-2 (LAMP-2), corroborated these findings, revealing that the observed 301 accumulates within lysosomes of *Ppt1^{-/-}* but not WT neurons (vehicle treatment in Figure 9B). Further, 302 AL lysosomes appeared swollen in vehicle-treated Ppt1^{-/-} neurons (see arrows in Figure 9B). Treatment with the 303 palmitoylation inhibitors, 2-bromopalmitate (2-BP, 1µM, 7-day treatment) and cerulenin (1µM, 7-day treatment) 304 reduced the percentage of AL-positive neurons (Figure 9C) and the area occupied with ALs per neuron (Figure 305 9D). Further, the mean lysosomal size also normalized in Ppt1^{-/-} neurons when these cells were treated with 2-BP 306 307 or cerulenin (Figure 9E).

To examine the efficacy of these compounds in preventing NMDA-mediated toxicity, we pretreated a subset of neurons with the same palmitoylation inhibitors, 2-BP (1 μ M, DIV12-18) and cerulenin (1 μ M, DIV12-18) prior to treatment with NMDA and glycine. Notably, pretreatment with both 2-BP and cerulenin improved cell viability of *Ppt1^{-/-}* neurons to that of WT following excitotoxicity induction (**Figure 8F**). These results indicate *Ppt1^{-/-}* neurons are more vulnerable to excitotoxicity and are consistent with our calcium imaging data that demonstrated the predominance of extrasynaptic, GluN2B-mediated NMDAR activity.

Palmitoylation inhibitors rescue GluN2B and Fyn kinase hyperpalmitoylation in *Ppt1-/-* neurons

Finally we directly examined the palmitovlation state of neuronal proteins to determine the mechanisms by 315 which hyperpalmitovlation of neuronal substrates may lead to NMDA-mediated excitotoxicity and asked whether 316 palmitovlation inhibitors correct these abnormalities. In particular, we focused on GluN2B palmitovlation, given 317 our evidence implicating GluN2B in the synaptic dysfunction present in *Ppt1*^{-/-} neurons. We employed a modified 318 319 acvl-biotin exchange procedure (Drisdel and Green, 2004), termed the APEGS assay (acvl-PEGyl exchange gelshift) (Yokoi et al., 2016). The APEGS assay effectively tags the palmitoylation sites of neuronal substrates with 320 a 5kDa polvethylene glycol (PEG) polymer, causing a molecular weight-dependent gel shift in immunoblot 321 analyses. Thus, we quantitatively analyzed the palmitovlated fraction of synaptic proteins and palmitovlated 322 signaling molecules that may influence NMDAR function. 323

We subjected DIV18 WT and Ppt1-/- primary cortical neuron lysates to the APEGS assay to determine the 324 palmitovlation state of GluN2B. Indeed, GluN2B palmitovlation was increased in Ppt1^{-/-} neurons compared to 325 WT at DIV18 (Figure 10A). This suggests enhanced surface retention of GluN2B-containing NMDARs in *Ppt1*⁻ 326 neurons (Mattison et al., 2012). Next, we asked whether palmitoylation inhibitors mitigated excitotoxic 327 vulnerability in Ppt1-/- neurons by correcting GluN2B hyperpalmitoylation. Both 2-BP and cerulenin treatment 328 (1um, DIV12-18) as in Figure 9 normalized levels of GluN2B palmitovlation to those of WT (Figure 10B). 329 implying enhanced turnover or reduced surface retention of GluN2B. We also examined another palmitovlated 330 protein. Fyn kinase, as a candidate for facilitating the enhanced surface retention of GluN2B-containing NMDARs. 331 Fyn is a prominent member of the Src kinase family known to directly interact with and affect the synaptic 332 333 stabilization of GluN2B (Prybylowski et al., 2005; Trepanier et al., 2012). Fyn palmitovlation was increased in Ppt1^{-/-} neurons compared to WT (Figure 10C). Importantly, the palmitovlation of Fvn significantly decreased in 334 both WT and Ppt1^{-/-} neurons following treatment with 2-BP and cerulenin (Figure 10D). Together, these data 335 point to two potentially overlapping mechanisms by which palmitoylation inhibitors reduce the stabilization or 336 retention of GluN2B at the synaptic compartment, thereby reducing cellular calcium load in *Ppt1*^{-/-} neurons and 337 338 mitigating the enhanced susceptibility to excitotoxicity. Further, these data implicate the palmitoylation of Fyn kinase, a molecule that is being targeted for the treatment of Alzheimer's disease (Nygaard et al., 2014, 2015; 339 340 Kaufman et al., 2015), in the progression of CLN1.

341 Discussion

The first mouse model of CLN1 was developed in 2001 by Gupta and colleagues (Gupta et al., 2001). 342 Since the development of this, and alternative models of CLN1, much progress has been made in understanding 343 the temporal, regional, and cell-type specific effects of lipofuscin accumulation and neuronal degeneration, 344 particularly in late stage disease (Gupta et al., 2001; Bible et al., 2004; Kielar et al., 2007; Bouchelion et al., 2014). 345 In addition, comprehensive data characterizing the behavioral dysfunction of the *Ppt1*^{-/-} mouse has recapitulated 346 clinical symptoms of the disease (Dearborn et al., 2015). Recent data demonstrate that PPT1 localizes to synaptic 347 compartments and influences presynaptic localization and mobility of prominent presynaptic proteins, including 348 349 SNAP25 (Kim et al., 2008). These findings correlate with histological and electrophysiological findings in cultured *Ppt1^{-/-}* neurons, demonstrating a depletion of presynaptic vesicle pool size (Virmani et al., 2005). 350 Moreover, presynaptic protein localization and function are altered in CLN1 models and in human tissue (Kanaani 351 et al., 2004; Virmani et al., 2005; Kim et al., 2008; Aby et al., 2013). 352

In the current study, we examined the role of PPT1 in cortical development and postsynaptic maturation 353 in the Ppt1^{-/-} mouse model of CLN1. Our principal finding demonstrates a role for PPT1 and, more broadly, 354 protein depalmitovlation in the regulation of NMDAR composition and function during visual cortical 355 356 development. Specifically, we show reductions of GluN2A-containing NMDARs and their preferential synaptic scaffold, PSD-95, in the Ppt1-/- mouse visual cortex at distinct developmental time points (P33-P60). These 357 biochemical alterations are recapitulated *in vitro* and correlate with immature dendritic spine morphology *in vivo* 358 and in vitro, extrasynaptic calcium transients, and enhanced susceptibility to NMDA-induced excitotoxicity. 359 360 These data are in agreement with previous studies demonstrating markedly enhanced NMDA-, but not AMPA-, mediated toxicity in *Ppt1^{-/-}* neurons and improved behavioral phenotype of *Ppt1^{-/-}* mice treated with the NMDAR 361 antagonist, memantine (Finn et al., 2012, 2013). Furthermore, *Ppt1^{-/-}* neurons exhibit hyperpalmitovlation of both 362 363 GluN2B and Fyn kinase, which facilitates retention of GluN2B-containing receptors on the cell surface. This dysregulation likely deviates the GluN2A/2B composition and spine morphology toward immaturity, causing 364 enhanced vulnerability to excitotoxic insult. Importantly, chronic palmitovlation inhibitor treatment alleviates 365 Ppt1^{-/-}-induced dysfunction. Together, these data implicate dysregulated GluN2 subunit switch as a major 366 pathogenic mechanism in CLN1. 367

368 GluN2B to GluN2A subunit switch

Numerous studies have demonstrated the biochemical and functional switching of GluN2B- to GluN2A-369 containing NMDARs in various brain regions, including the cortex, hippocampus, cerebellum, and brainstem 370 371 (Paoletti et al., 2013). This developmental event is experience-dependent. Specifically, acute ex vivo hippocampal 372 preparations from young (P2-P9) rats reveal rapid, evoked activity-dependent synaptic GluN2A incorporation in response to LTP-induction (Bellone and Nicoll, 2007). Further, Dark rearing rats, effectively removing visual 373 stimuli and consequent afferent activity, delays the GluN2 subunit switch and extends critical period plasticity 374 375 (Carmignoto and Vicini, 1992; Quinlan et al., 1999b; Philpot et al., 2001). Conversely, environmental enrichment causes an acceleration of visual cortical maturation (Cancedda et al., 2004; Sale et al., 2004; Guzzetta et al., 2009). 376 Here, we have identified the novel mechanism whereby impaired GluN2B to GluN2A subunit switch contributes 377 to the core pathophysiology of a pediatric neurodegenerative disease. 378

We have demonstrated a novel role for PPT1 in the regulation of palmitoylated postsynaptic proteins. In particular, lack of PPT1 disrupts the NMDA receptor GluN2B to GluN2A subunit switch characteristic of excitatory synaptic maturation. Initially, we predicted synaptic markers, particularly PSD-95, would be

overrepresented at postsynaptic sites, since their synaptic distribution depends on the balance between 382 palmitovlation and depalmitovlation (Craven et al., 1999; El-Husseini et al., 2000; Jevifous et al., 2016). As PSD-383 95 facilitates the GluN2 subunit switch and preferentially interacts with GluN2A, we also hypothesized an 384 increase in the GluN2A subunit. However, our biochemical data indicate reductions in the total amount as well 385 as the synaptic incorporation of GluN2A and PSD-95 in the PPT1-deficient brain (Figure 2, Supplementary 386 Figure 1). Interestingly, a recent study suggests that PSD-95 is depalmitovlated by ABHD17 family enzymes. 387 388 not PPT1 (Yokoi et al., 2016). Further, the palmitoylation state of PSD-95 is reduced with increased synaptic 389 activity (El-Husseini et al., 2002). Consequently, we now postulate that the lack of functional PPT1 results in surface retention of GluN2B-containing NMDAR complexes, either directly or indirectly via the mechanisms 390 discussed below, thereby impeding the developmental switch to GluN2A-containing receptors. 391

It remains unclear whether impaired GluN2B to GluN2A subunit switch in *Ppt1*^{-/-} neurons is entirely 392 attributable to GluN2B hyperpalmitovlation or if Fyn hyperpalmitovlation is also involved. Fyn kinase is 393 394 developmentally regulated (Umemori et al., 1992; Inomata et al., 1994) and a major palmitoylated downstream kinase of reelin signaling that affects GluN2B surface stabilization (Alland et al., 1994; Koegl et al., 1994; 395 Prybylowski et al., 2005; Kang et al., 2008). Moreover, Fyn kinase is currently being investigated in phase 3 396 clinical trials as a pharmacological target in AD (Nygaard et al., 2014, 2015; Kaufman et al., 2015). Thus, Fyn 397 dysfunction (in varying contexts) may be a common feature of these neurodegenerative phenotypes. While protein 398 palmitovlation is associated with many of the signaling pathways underlying synaptic development, further study 399 is needed to elucidate precisely (i.e. the direct substrates) how PPT1 influences the GluN2B to GluN2A switch 400 and if Fyn is indeed a key mediator. Studying developmental mechanisms that are 1) associated with GluN2 401 switching in vivo and 2) regulated by protein palmitoylation/depalmitoylation will likely reveal targets for 402 pharmacological intervention in CLN1. 403

Several other mechanisms underlying this GluN2 subunit switch have been proposed, including reelin, 404 Wnt-5a, and mGluR5 signaling (Groc et al., 2007; Cerpa et al., 2011; Matta et al., 2011). The accumulation of 405 reelin at excitatory synapses during development, for example, mobilizes GluN2B-containing NMDARs and 406 enhances the synaptic contribution of GluN2A-containing NMDARs (Groc et al., 2007; Iafrati et al., 2013). 407 Similarly, evoked activation of mGluR5 at hippocampal synapses is necessary for incorporation of GluN2A-408 containing NMDARs, and mGluR5-null mice demonstrate deficient GluN2B to GluN2A switching (Matta et al., 409 2011). Importantly, Wnt-5a and mGluR5 function are directly regulated by palmitoylation (Kurayoshi et al., 2007; 410 Yokoi et al., 2016), suggesting that disruptions in protein depalmitovlation may lead to impaired synaptic 411 412 maturation through several pathways.

The current work supports a role for PPT1 in regulating postsynaptic proteins. However, whether the pre-413 or postsynaptic site is affected foremost in *Ppt1^{-/-}* mouse visual cortex during development is still unknown. 414 Indeed, we detect a significant reduction in GluN2A and PSD-95 beginning at P33, but not before, while 415 lipofuscin deposition begins as early as P14. However, our electrophysiological, biochemical, and in vitro calcium 416 imaging data suggest that this reduction is manifested postsynaptically. Furthermore, we show direct evidence for 417 hyperpalmitoylation of two postsynaptic proteins, the GluN2B subunit and Fyn. One direction of our future work 418 is to examine in more detail the timing, subcellular specificity, and trafficking of both pre- and post-synaptic 419 proteins in *Ppt1*^{-/-} mouse. 420

421 Excitotoxicity and NMDAR regulation

Patients afflicted with later-onset NCLs typically exhibit an enlarged VEP prior to degeneration, concurrent with seizure (Pampiglione and Harden, 1977; Pagon et al., 1993; Haltia, 2006). While this

phenomenon has not been directly observed in CLN1, it is plausible that disrupted GluN2 subunit switch 424 contributes to hyperexcitability and accelerates cell death leading to the rapid degeneration of neuronal circuits 425 before the diagnosis can be made. In line with this notion, NMDAR subunit dysregulation is implicated in various 426 neuropsychiatric and neurodegenerative disorders (Paoletti et al., 2013; Zhou and Sheng, 2013). Furthermore, 427 recent evidence describing the effects of GluN2 subunit incorporation on NMDAR function suggests a 428 mechanism linking subunit specificity to excitotoxicity and neuronal degeneration (Martel et al., 2009, 2012; 429 Hardingham and Bading, 2010). GluN2 subunit composition and NMDAR localization activate opposing 430 downstream transcriptional programs. Specifically, GluN2A-containing NMDARs in the postsynaptic density 431 activate cyclic-AMP response element binding protein (CREB) and other transcription factors associated with 432 cell-survival and learning. In contrast, activation of GluN2B-containing, extrasynaptic NMDARs preferentially 433 434 triggers pro-apoptotic signaling pathways and causes inhibition of CREB (Hardingham and Bading, 2002; Hardingham et al., 2002). Though this system is likely more intricate than described here (Thomas et al., 2006), 435 these previous studies are consistent with our observations that *Ppt1*^{-/-} neurons are biased toward extrasynaptic 436 calcium transients (Figure 7 and Video 2) and that they are more susceptible to excitotoxicity (Figure 8). 437 Furthermore, the most significant outcome of this study is that palmitoylation inhibitors mitigated the pro-438 apoptotic predisposition of $Ppt1^{-/-}$ neurons in vitro (Figure 9). 439

The incorporation of GluN2A into NMDARs is experience-dependent (Stocca and Vicini, 1998; Quinlan 440 et al., 1999a, 1999b). An intriguing possibility is that *Ppt1^{-/-}* neurons in sensory cortices are unable to tolerate 441 normal sensory experiences, in part because this experience-dependent GluN2 subunit switch is disrupted. Indeed, 442 443 PPT1-defeciency results in selective degeneration of thalamic nuclei and primary sensory cortices (Bible et al., 2004; Kielar et al., 2007). Further, PPT1 expression is developmentally-regulated in WT rodents, such that 444 functional PPT1 increases with cortical maturation and peaks in early adulthood, when it may regulate this 445 switching phenomenon (Suopanki et al., 1999a, 1999b). Together, we argue that intact PPT1 plays a critical role 446 in regulating NMDAR functional properties in response to external stimuli, thereby facilitating synaptic 447 maturation and preventing excitotoxicity. Whether manipulating neuronal activity or experience-dependent 448 synaptic plasticity ameliorates disease progression remains unknown and is a focus of ongoing experiments. 449

450 **Implications for other neurodegenerative diseases**

While substantial progress has been made in our understanding of adult-onset neurodegenerative diseases 451 including Alzheimer's disease and Parkinson's disease, effective, disease-modifying therapeutics are yet to be 452 developed for most of these disorders. In part, this is likely due to the genetic complexity and heterogeneity of 453 454 these diseases as well as lifestyle and environmental factors limiting the translational success of seemingly promising therapeutic strategies. Recently, studies in monogenic diseases have attracted attention because they 455 share common pathological hallmarks with adult-onset neurodegenerative diseases. This approach has turned out 456 457 to be valuable to decipher underlying disease mechanisms (Peltonen et al., 2006). For instance, heterozygous mutations in the glucocerebrosidase (GBA) gene, which cause Gaucher disease if homozygous, confer risk to 458 Parkinson's disease (Neudorfer et al., 1996; Tavebi et al., 2001; Sidransky, 2012; Sidransky and Lopez, 2012). 459 The link between the two diseases exemplifies the critical role of lysosomal degradation in inclusion body 460 formation and corroborates mounting evidence for autophagy as a key mechanism to clear neuronal waste and 461 maintain cellular health (Nixon, 2005, 2013). 462

Lipofuscin is not only the cardinal hallmark of the NCLs, but also accumulates in many neurodegenerative disorders, including Alzheimer's and Huntington's diseases. However, it remains inconclusive whether lipofuscin aggregation is an adaptive, neuroprotective mechanism, or a direct cause of neuronal degeneration. Clinical

therapies in CLN1 patients aimed at targeting storage material are largely unsuccessful (Gavin et al., 2013; Levin 466 et al., 2014). For instance, clinical trials using small compounds that effectively depleted lipofuscin in CLN1 467 patients demonstrated minor subjective improvements. Nevertheless, patients progressed to a vegetative state by 468 52 months (Levin et al., 2014). Therefore, it is likely that CLN1 pathology involves not only lipofuscin deposition. 469 but also an excess of palmitovlated proteins, which alters synaptic functions. Indeed, emerging evidence indicates 470 that both endosomal sorting and lysosomal proteolysis dynamically contribute to mechanisms underlying synaptic 471 plasticity (Shehata et al., 2012; Gokhale et al., 2015; Goo et al., 2017). Despite detectable NMDAR disruption 472 473 not beginning before P33, it remains plausible that synaptic dysregulation of some type starts either before or 474 concurrent with the deposition of storage material in CLN1 disease. Understanding synaptic mechanisms that are regulated by PPT1 and other NCL-associated gene products will shape the foundation for treating these 475 476 devastating diseases. Our data point to NMDARs as a potential therapeutic target and corroborate the efficacy of memantine in *Ppt1^{-/-}* mice (Finn et al., 2013). However, other receptor subunits and ion channels also undergo 477 palmitovlation, including AMPARs (Havashi et al., 2005) and GABARs (Fang et al., 2006). Further studies are 478 needed to reveal the role of PPT1 in regulating these palmitoylated synaptic proteins. 479

Lastly, several proteins associated with adult-onset neurodegenerative disorders, such as amyloid precursor protein (APP) and huntingtin, are palmitoylated and regulate synaptic functions (Huang et al., 2004; Smith et al., 2005; Zheng and Koo, 2006; Bhattacharyya et al., 2013). Therefore, understanding how the balance between protein palmitoylation and depalmitoylation affects neuronal functions has broad implications and will have a novel impact on the therapeutic strategies against these and other brain disorders.

In conclusion, we have demonstrated that an imbalance between protein palmitoylation and depalmitoylation accelerates lipofuscin accumulation. Further, we have shown that lack of PPT1 function results in the stagnation of developmental GluN2 subunit switch, leading to enhanced vulnerability to glutamatemediated excitotoxicity. Our results indicate a vital role for PPT1 in the regulation of postsynaptic maturation and set the stage for further investigating protein depalmitoylation in NCLs as well as adult-onset neurodegenerative diseases associated with lipofuscin.

491 Materials and methods

492 Animals

All animal procedures were performed in accordance with the guidelines of the University of Illinois of Chicago Institutional Animal Care and Use Committee. $Ppt1^{+/-}$ (heterozygous) mice were obtained from Jackson Laboratory and maintained on 12h light/dark cycle with food and water *ad libitum*. Breeding of $Ppt1^{+/-}$ animals results in litters containing $Ppt1^{-/-}$, $Ppt1^{+/-}$, and $Ppt1^{+/+}$ (WT) animals. $Ppt1^{-/-}$ and WT littermate controls at specified developmental time points: P11, P14, P28, P33, P42, P60, P78, and P120 were genotyped in-house (Gupta et al., 2001) and used for experiments.

499 Brain fractionation and Western blot

For collection of brain for biochemistry (immunoblot), Ppt1-/- and WT animals were decapitated following 500 isoflurane anesthesia, then the brain was removed, and washed in ice cold PBS. The occipital cortex (visual 501 cortex), hippocampus, and remaining cortex were separately collected on ice. Isolated visual cortices from Ppt1-502 ^{-/-} and WT animals were homogenized in ice-cold synaptosome buffer (320mM sucrose, 1mM EDTA, 4mM 503 504 HEPES, pH7.4 containing 1x protease inhibitor cocktail (Roche), 1x phosphatase inhibitor cocktail (Roche) and 1mM PMSF) using 30 strokes in a Dounce homogenizer. Aliquots for whole lysate (WL) were stored and the 505 remaining sample was used for synaptosome preparation, performed as previously with slight modification. In 506 brief. WLs were centrifuged at 1,000 x g to remove cellular debris, supernatant was then centrifuged at 12,000 x 507 g for 15min to generate pellet P2. P2 was resuspended in synaptosome buffer and spun at 18,000 x g for 15min 508 to produce synaptosomal membrane fraction, LP1, which was used for downstream biochemical analyses 509 510 (synaptosomes). For immunoblot, protein concentration of each sample was determined using BCA protein assay (Pierce). Samples were then measured to 20µg total protein in 2x Laemmli buffer containing 10% β-511 mercaptoethanol (Bio-rad), boiled at 70°C for 10min and loaded into 10% tris-glycine hand cast gels (Bio-rad). 512 513 or 4-20% precast gels (Bio-rad) for electrophoresis (110V, 1.5-2h). Proteins were wet-transferred to PVDF membranes (Immobilon-P, Millipore), blocked in TBS, pH7.4 containing 5% non-fat milk and 0.1% Tween-20 514 (TBS-T+5% milk). Membranes were incubated in primary antibody solutions containing 2% BSA in TBS-T for 515 516 2h at RT or overnight at 4°C. Primary antibodies were used as follows: GluN2A (Cat: NB300-105, 1:1,000, Novus 517 Biologicals), GluN2B (Cat: 75/097, 1:1,000, Neuromab), GluN1 (Cat: 75/272, 1:1000, Neuromab), PSD-95 (Cat: 518 K28/74, 1:2,000, Neuromab), SAP102 (Cat: N19/2, 1:2,000, Neuromab), Fyn kinase (Cat: 4023, 1:1,000, Cell signaling) and B-actin-HRP (Cat: MA5-15739-HRP, 1:2,000, ThermoFisher). Membranes were then incubated 519 with appropriate secondary, HRP-conjugated antibodies (Jackson ImmunoResearch) at either 1:5,000, 1:10,000, 520 or 1:30,000 (PSD-95 only) for 1h at RT. Visualization and quantification was performed using Pierce SuperSignal 521 ECL substrate and Odyssey-FC chemiluminescent imaging station (LI-COR). Signal density for each synaptic 522 523 protein was measured using the LI-COR software, Image Studio Lite (version 5.2) and was normalized to the 524 signal density for β-actin loading control for each lane. A total of four independent experiments was performed for both WL and LP1 analyses, with a minimum of two technical replicates for each experiment averaged together. 525

526 Histology and autofluorescent lipopigment quantification

Ppt1^{-/-} and WT mice were anesthetized using isoflurane and transcardially perfused with ice cold PBS (pH 7.4, \sim 30ml/mouse) followed by 4% paraformaldehyde (PFA) in PBS (\sim 15ml/mouse). Brains were removed and post-fixed for 48h at 4°C in 4% PFA and transferred to PBS, pH7.4 containing 0.01% sodium azide for storage if

necessary. Brains from *Ppt1^{-/-}* and WT animals were incubated in 30% sucrose solution for 48h prior to sectioning

using Vibratome 1000 in cold PBS. For imaging and quantification of AL, sagittal sections were cut at 100µm. 531 Every third section was mounted on Superfrost Plus microscope slides (VWR) using Vectamount mounting media 532 containing DAPI (Vector Laboratories, cat: H-5000). Interlaced/overlapping images of visual cortex area V1 from 533 the cortical surface to subcortical white matter (or subiculum), which was localized using Paxino's mouse atlas 534 (sagittal), were collected for 2-4 sections from each animal using a Zeiss LSM710 confocal laser scanning 535 microscope at 40x magnification (excitation at 405nm to visualize DAPI and 561nm to visualize AL). All sections 536 were imaged using identical capture conditions. Quantification of AL was performed by thresholding images in 537 538 FIJI (NIH), generating a binary mask of AL-positive pixels (satisfied threshold) vs. background. The identical threshold was applied to each image (from cortical surface to subcortical white matter and across animals). 539 Percent area occupied by AL puncta that satisfied the threshold was then calculated using the "analyze particles" 540 541 tool in FIJI. This analysis was performed for 2-4 sections (total of ~10-20 images, as imaging an entire cortical column is typically 5 interlaced images) from each animal and averaged together to give a single value, 542 representative of the total area occupied by AL in the cortical column imaged. Three to six animals per group 543 544 were analyzed this way and averaged to give the mean area occupied by AL at each time point, for both genotypes 545 (n=4-6 animals/group).

546 Electrophysiology

WT and *Ppt1*^{-/-} animals at P42 were deeply anesthetized using isoflurane drop method and decapitated. 547 Brains were resected in semi-frozen oxygenated (95% O₂ and 5% CO₂) artificial cerebrospinal fluid (aCSF, in 548 mM: NaCl 85, sucrose 75, KCl 2.5, CaCl₂ 0.5, MgCl₂ 4, NaHCO₃ 24, NaH₂PO₄ 1.25, D-glucose 25, pH 7.3), and 549 350um sections containing visual cortex area V1 were sectioned using a Leica VT1200 S vibratome in semi-550 frozen aCSF. After recovery (1h) in aCSF at 30°C, sections were transferred to the recording chamber, perfused 551 at 2ml/min with aCSF at 30°C. Following localization of visual cortex area V1 using Paxinos mouse brain atlas. 552 a stimulating electrode was placed in layer IV, and pyramidal neurons from layer II/III were blindly patched 553 554 (patch solution in mM: CsOH monohydrate 130, D-Gluconic acid 130, EGTA 0.2, MgCl₂ 1, CsCl 6, Hepes 10, 555 Na₂-ATP 2.5, Na-GTP 0.5, Phoshocreatine 5, OX-314 3; pH 7.3, osmolarity 305 mOsm) and recorded in voltage clamp mode at +50mV (V_H) to remove Mg²⁺ block from NMDARs. NMDA-EPSCs were pharmacologically 556 isolated via addition of CNOX (10µM), (+)-Bicuculline (60 µM) and SCH 50911 to block AMPA, GABAA and 557 558 GABA_B receptors, respectively. Stimulation intensity was titrated to give a saturating postsynaptic response, and 559 EPSCs were then recorded, averaging 5-10 sweeps. The decay phase of the averaged NMDAR-EPSCs were then fitted to a double exponential (Carmignoto and Vicini, 1992). We calculated for each cell: the amplitude of the 560 561 fast (Af) component (GluN2A-mediated), the amplitude of the slow (As) component (GluN2B-mediated), the contribution of the fast component Af/ Af+As to the overall decay phase, the τ fast (τ f), the τ slow (τ s) and the 562 τ weighted (τ w) in WT and *Pnt1^{-/-}* mice following this formula: τ w= τ fx(Af/Af+As) + τ sx(As/Af+As) (n=10/4 563 (cells/animals), WT; n=12/5 PPT-KO). 564

565 In utero electroporation

In utero electroporation was performed as previous(Yoshii et al., 2011, 2013). Timed-pregnant dams at E16.5 were deeply anesthetized via isoflurane (3% induction, 1-1.5% for maintenance of anesthesia during surgery) and laparotomized. The uterus was then externalized and up to $\sim 1\mu$ l of solution containing GFP construct ($2\mu g/\mu$ l) and fast green dye was delivered into the left lateral ventricle through the uterine wall using a micropipette. Using an ECM 830 Square Wave electroporator (Harvard Apparatus, Holliston MA), brains were electroporated with 5 pulses of 28V for 50msec at intervals of 950msec at such an angle to transfect neurons in visual cortex. After recovery, pregnancies were monitored and pups were delivered and nursed normally. Electroporated pups were

genotyped, raised to P33, and sacrificed via transcardial perfusion as described above. Electroporated brains from WT and $Ppt1^{-/-}$ mice (procedure schematized in **Figure 4A**) were sectioned and sequentially mounted. Transfected neurons in visual cortex (**Figure 4B**) were imaged to capture all apical neurites and 3D reconstructed images were analyzed in Imaris (Bitplane) for dendritic spine characteristics known to be associated with synaptic maturity (spine length, spine volume, and spine head volume). At least two z-stack images (typically >100 z-planes/image) were stitched together to capture the prominent apical neurites and extensions into the cortical surface for each cell. Each stitched image, equivalent to one cell, was considered one n.

580 **Primary cortical neuron culture**

For primary cortical neuron cultures, embryos from timed-pregnant, Ppt1-/+ dams were removed, 581 decapitated, and cortices resected at embryonic day (E) 15.5. All dissection steps were performed in ice cold 582 HBSS, pH7.4. Following cortical resection, tissue from each individually-genotyped embryo were digested in 583 HBSS containing 20U/ml papain and DNAse (20min total, tubes flicked at 10min) before sequential trituration 584 with 1ml (~15 strokes) and 200µl (~10 strokes) pipettes, generating a single-cell suspension. For live-cell imaging 585 experiments, cells were counted then plated at 150,000-180,000 cells/well in 24-well plates containing poly-D-586 lysine/laminin-coated coverslips. For biochemical experiments, i.e. immunoblot, APEGS assay in vitro, cells 587 were plated on poly-D-lysine/laminin-coated 6-well plates at 1,000,000 cells/well. Cells were plated and stored 588 in plating medium (Neurobasal medium containing B27 supplement, L-glutamine and glutamate) for 3-5 DIV, 589 before replacing half medium every 3 days with feeding medium (plating medium without glutamate). Cultures 590 used in chronic palmitovlation inhibitor treatment were exposed to either DMSO (vehicle), 2-BP (1µm, Sigma, 591 cat: 238422) or cerulenin (1um, Cayman Chemicals, cat: 10005647) every 48 hours between DIV 11 and 18. 592

593 **Primary cortical neuron harvest and immunoblotting**

Primary cortical neurons from E15.5 WT and *Ppt1-/-* embryos were cultured for 7, 10, or 18 DIV prior to harvest for immunoblot or APEGS assay (only DIV18 used for APEGS). To harvest protein extracts, cells were washed 2x with ice-cold PBS before addition of lysis buffer containing 1% SDS and protease inhibitor cocktail, 500µl/well. Cells were incubated and swirled with lysis buffer for 5 minutes, scraped from the plate, triturated briefly, and collected in 1.5ml tubes. Lysates were centrifuged at 20,000g for 15min to remove debris, and the supernatant was collected for biochemical analysis. Immunoblotting analyses were performed as in section 2.2. APEGS assay was carried out as described in section 2.7.

601 **APEGS assay on primary cortical neuron lysates**

The APEGS assay was performed as utilized in Yokoi, 2016 and recommended by Dr. M. Fukata (personal 602 communication, 06/2018). Briefly, cortical neuron lysates were brought to 150µg total protein in a final volume 603 of 0.5ml buffer A (PBS containing 4% SDS, 5mM EDTA, protease inhibitors, remaining sample used in aliquots 604 "input"). Proteins were reduced by addition of 25mM Bond-Breaker™ TCEP (0.5M stock solution, 605 for ThermoFisher) and incubation at 55°C for 1h. Next, to block free thiols, freshly prepared N-ethylmaleimide 606 (NEM) was added to lysates (to 50mM) and the mixture was rotated end-over-end for 3h at RT. Following 2x 607 chloroform-methanol precipitation (at which point, protein precipitates were often stored overnight at -20°C). 608 lysates were divided into +hydroxylamine (HA) and -HA groups for each sample, which were exposed to 3 609 volumes of HA-containing buffer (1M HA, to expose palmitolylated cysteine residues) or Tris-buffer control (-610 HA, see Figure 10), respectively, for 1h at 37°C. Following chloroform-methanol precipitation, lysates were 611 solubilized and exposed to 10mM TCEP and 20mM mPEG-5k (Laysan Bio Inc., cat# MPEG-MAL-5000-1g) for 612 613 1h at RT with shaking (thereby replacing palmitic acid with mPEG-5K on exposed cysteine residues). Following

the final chloroform-methanol precipitation, samples were solubilized in a small volume (60µl) of PBS containing

1% SDS and protein concentration was measured by BCA assay (Pierce). Samples were then brought to 10μg

616 protein in laemmli buffer with 2% β-mercaptoethanol for immunoblot analyses as in section 2.2. Quantification

of palmitoylated vs. non-palmitoylated protein was carried out as in section 2.2, with the added consideration that

618 palmitoylated protein was taken as the sum of all (typically two-three distinct bands, see Figure 9) bands 619 demonstrating the APEGS-dependent molecular weight shift compared to the –HA control lane. Non-

palmitoylated protein was quantified from the band size-matched to the –HA control sample. The ratio was taken

as the palmitoylated protein divided by non-palmitoylated protein, all divided by β -actin control from the same

622 lane.

623 Transfection, dendritic spine and calcium imaging analyses

For analysis of dendritic spine morphology, WT and Ppt1^{-/-} neurons were transfected between DIV6-8 624 with GFP using Lipofectamine® 2000 (ThermoFisher) according to manufacturer protocol. Briefly, GFP DNA 625 construct (~2µg/µl, added at ~1µg/well) was mixed with Lipofectamine-containing Neurobasal medium, 626 incubated for 30min to complex DNA-Lipofectamine, equilibrated to 37°C, and added to the cells 250µl/well for 627 1-1.5h. Following incubation, complete medium was returned to the cells. Neurons were then imaged at DIV15 628 and DIV20 for dendritic spine morphology using a Zeiss LSM 710 confocal microscope equipped with a heated 629 stage at 63x magnification. GFP-positive neurons were imaged at 0.2µm Z-plane interval (typically 25 Z-630 planes/image). Three to seven overlapping Z-stacks were stitched to visualize an entire neuron. Z-stack images 631 were collapsed into a single plane and dendritic spines were analyzed using semi-automated image processing 632 software. Imaris (Bitplane). The same dendrite and dendritic spine processing parameters were used for each 633 image. For DIV15: n=4-5 neurons/group, 3-independent experiments, WT=21,514 spines; *Ppt1*^{-/-}=18,013 spines. 634 For DIV20: n=3 neurons/group, 2-independent experiments, WT=11,335 spines; *Ppt1*^{-/-}=9,958 spines. 635

To directly image calcium signals in WT and *Ppt1*^{-/-} neurons, cells were transfected as above using the 636 construct encoding GCaMP3 (see Acknowledgments) at DIV6-8. Cells were grown to DIV18 then imaged at 637 room temperature in Tyrode's solution (imaging medium, 139mM NaCl, 3mM KCl, 17mM NaHCO₃, 12mM 638 glucose, and 3mM CaCl₂) for a maximum of 15min using a Mako G-507B camera mounted onto a Leica inverted 639 microscope. Videos were acquired at ~7 frames per second using StreamPix software (NorPix). A maximum of 640 5min per neuron was recorded (thus, minimum 3 neurons per coverslip were acquired). N=3-6 neurons/group, 641 three independent experiments. For treatment with Ro 25-6981, neurons were imaged at baseline for 2-2.5min 642 before adding Ro 25-6981 (1µM) directly to the imaging medium. Neurons were then imaged for an additional 643 2.5min. 644

To analyze the area under the curve (AUC) and width (diffusion distance) of calcium transients, 500-600 frames from the middle of each video (average frame count for whole videos= \sim 2000 frames) for WT and *Ppt1*^{-/-} neurons were analyzed using FIJI (NIH). Dendritic segments, excluding primary dendrites, were traced using a segmented line ROI with pixel width of 50, which reliably encompassed the dendritic segment and accompanying dendritic spines. Next, the following macro derived from the ImageJ forum (http://forum.imagej.net/t/how-toobtain-xy-values-from-repeated-profile-plot/1398) was run on each individual ROI:

```
651 macro "Stack profile Plot" {
652 collectedValues="";
653 ymin = 0;
654 ymax = 255;
655 saveSettings();
```

```
656
          if (nSlices==1)
657
             exit("Stack required");
658
          run("Profile Plot Options...",
             "width=400 height=200 minimum="+ymin+" maximum="+ymax+" fixed");
659
660
          setBatchMode(true);
          stack1 = getImageID;
661
          stack2 = 0;
662
663
          n = nSlices;
664
          for (i=1; i<=n; i++) {</pre>
665
               showProgress(i, n);
666
               selectImage(stack1);
667
               setSlice(i);
668
               run("Clear Results");
669
                 profile = getProfile();
670
               for (j=0; j<profile.length; j++) {</pre>
671
                  collectedValues=collectedValues+profile[j] + "\t";
672
               }
673
               collectedValues=collectedValues+"\n";
674
675
               run("Plot Profile");
676
               run("Copy");
677
               w = getWidth; h = getHeight;
678
               close();
679
               if (stack2==0) {
                   newImage("Plots", "8-bit", w, h, 1);
680
681
                   stack2 = getImageID;
682
               } else {
                   selectImage(stack2);
683
684
                   run("Add Slice");
685
               }
               run("Paste");
686
687
          }
688
          f = File.open("C:/"cell#, ROI #".xls");
689
690
          print(f, collectedValues);
691
          setSlice(1);
692
          setBatchMode(false);
693
          restoreSettings();
694
             }
695
```

696 This gives the fluorescence intensity at each pixel along the ROI across the time/frame dimension. The background fluorescence for each ROI was then subtracted by averaging the fluorescence across the ROI in an 697 inactive state (no calcium transients), giving the measure $\Delta F/F_0$ when examined across time/frame. For each ROI 698 (up to 1265 pixels in length), each calcium transient at individual synaptic sites (dendritic spines and adjacent 699 shafts) was averaged. Those averages were then compiled to give the average transient signal, which was then 700 used to analyze the AUC and calcium diffusion distance (WT=55 ROIs, 170 synaptic sites, 1630 transients; Ppt1-701 ⁻=38 ROIs, 131 synaptic sites, 1281 transients; n=3-6 neurons/group/experiment, 3 repetitions). For Ro 25-6981-702 treated neurons, the same protocol was followed with the exception that calcium transients at an individual 703 synaptic site were split into "before application" and "after application" groups. 704

To analyze synaptic synchrony, $\Delta F/F_0$ measurements for 20 randomly-chosen sites of synaptic activity per neuron were correlated across the time dimension (500 frames of each video). A correlation matrix was

707 generated to determine the average correlation of each synaptic site with all other chosen sites. The average values 708 for each synaptic site, for 5 neurons/group are plotted in **Figure 7**.

709 NMDA toxicity assays

To measure cell viability following exposure of WT and *Ppt1^{-/-}* neurons to NMDA and glycine, neurons 710 were plated as above and grown to DIV18. For experiments presented in Figure 6, feeding medium was removed 711 from neurons, stored at 37°C, and replaced with B27-free Neurobasal medium with or without NMDA/glycine at 712 the following concentrations: 10/1µM, 100/10µM, or 300/30µM (ratio maintained at 10:1). Cells were incubated 713 for 2h at 37°C in treatment medium Following incubation treatment medium was removed and replaced with 714 the original feeding medium. Cells were then incubated an additional 22h before addition of PrestoBlue® cell 715 viability reagent (ThermoFisher). At 24h, fluorescence intensity of each well was measured using a Beckman 716 Coulter DTX 800 Multimode Detector. Cell viability for each treatment condition was calculated and expressed 717 as percentage of vehicle-treated control wells (no pretreatment, no NMDA application). Experiments in Figure 7 718 were performed similarly except that cultures were pretreated with either DMSO (vehicle), 2-BP (1µM, Sigma, 719 cat: 238422) or cerulenin (1µM, Cayman Chemicals, cat: 10005647) every 48 hours between DIV 11 and 18. 720

AL accumulation *in vitro*, palmitoylation inhibitor treatment, imaging and analysis

WT and Ppt1^{-/-} neurons were cultured as above. To examine AL deposition, neurons were grown to 722 DIV18-20, fixed in 4% PFA for 10min at RT, and stored in PBS for up to 72 hours prior to immunocytochemistry. 723 To examine AL accumulation alone, cells were immunostained for the microtubule associated protein, MAP2 724 (Millipore Sigma, cat: AB5622) and mounted in DAPI-containing mounting medium. To assess AL localization, 725 DIV18-DIV20 neurons were immunostained for MAP2 and LAMP-2 (Abcam, cat: ab13524). Neurons were then 726 imaged at random using a Zeiss LSM 710 confocal microscope at 63x magnification. Z-stacks (0.4µm Z-plane 727 interval, 12-22 Z-planes/image) were taken at 512 x 512 pixel density. 7-10 neurons/group for three independent 728 experiments. 729

To semi-automatically analyze the percentage of AL-containing cells, the cytosolic area covered by AL 730 deposits, and the cytosolic area covered by lysosomes, images immunostained for MAP2 and LAMP-2 were 731 processed in FIJI. Each channel of the image: LAMP-2 (488nm), MAP2 (633nm), DAPI (405nm), AL (561nm) 732 was thresholded separately as to display only the lysosomes, cell soma, the nucleus, and AL deposits, respectively. 733 Thresholds were kept identical between images. Next, the areas of these compartments/deposits were measured 734 using the "analyze particles" tool restricted to an ROI tracing the cell soma. Lysosomes needed to have a 735 circularity of >0.5 to avoid counting small clusters of lysosomes as a single unit (Bandyopadhyay et al., 2014; 736 Grossi et al., 2016). To measure AL deposits, the same approach was used with the additional constraint: AL 737 738 deposits were required to have a circularity >0.4 and comprise more than 8 adjacent pixels. Cytosolic area was 739 calculated by measuring MAP2 signal area and subtracting the area occupied by DAPI stain.

740 Immunocytochemistry

Coverslips were stained in runs so that all experimental and control groups were immunostained simultaneously. Coverslips were washed 3x with TBS, permeabilized for 20min at RT with TBS containing 0.5% Triton X-100, and blocked for 1h at RT in TBS containing 0.1% Triton X-100 and 5% BSA. Then, primary antibody (MAP2 or LAMP-2) at 1:400 dilution was added to coverslips in TBS containing 0.1% Triton X-100 and 1% BSA and incubated for 2h at RT or overnight at 4°C. Following 4X washes with TBS containing 0.1%

Triton X-100, cells were incubated with 1:400 secondary, fluorophore-linked antibody (either Alexa Fluor 488, cats: A-11034, A-11006; or Alexa Fluor 633, ThermoFisher, cat: A-21070) in TBS containing 0.1% Triton x-100 and 1% BSA. These steps are repeated for double immunostained cells. For LAMP-2/MAP2 double immunostaining, saponin was used in place of Triton X-100 at the same concentrations. Coverslips are then mounted on SuperFrost Plus slides in DAPI Vectamount medium.

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756 Author contributions statement

A.Y. conceptualized and oversaw experiments, provided resources, prepared and revised the manuscript. K.P.K designed and performed experiments, performed data analysis, prepared and revised the manuscript as well as the figures. W.F. and F.B. performed electrophysiological recordings (Figure 3) and aided in the revision of the manuscript. S.A. and R.S. analyzed calcium dynamics data (Figure 7) and aided in manuscript revision.

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762 **Conflict of interest statement**

The authors declare no conflicts of interest.

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249 Figure legends

Figure 1. ALs deposit immediately following eye opening in visual cortex of *Ppt1-/-* mice. (A) Representative 250 composite confocal images through area V1 of visual cortex in WT (top) and Ppt1^{-/-} mice (bottom) during 251 development and into adulthood. DAPI nuclear stain (blue, 405nm excitation) and AL signals (red, 561nm 252 excitation) are visualized. Cortical layers are marked (left). Scale=50um. (B) Ouantification of the mean percent 253 area occupied by ALs through all cortical layers (see methods). Ppt1-/- and WT were compared (n=4-6 254 animals/group) at each age using t-test and the significance was indicated as follows: *p<0.05, **p<0.01, and 255 ***p<0.001. Significant AL increase in *Ppt1^{-/-}* mouse brain between two consecutive ages (e.g. P28 vs. P33) are 256 shown as # p < 0.05 and # p < 0.01. Error bars represent s.e.m. (C) Cortical layer-specific quantification of area 257 occupied by ALs separated by each cortical layer (x-axis) and age (z-axis). Averaged values, s.e.m., and n for 258 each condition are represented in Supplementary table 1. 259

Figure 2. NMDAR subunit composition is biased toward immaturity in Pot1--- visual cortex. (A) 260 Representative immunoblots of GluN2 subunits, GluN2A and GluN2B across age and genotype as indicated (top) 261 and quantification of band density (bottom) normalized to β-actin loading control within lane. (B) Representative 262 immunoblots of GluN2A and GluN2B (top) and quantification of the ratio of GluN2A/GluN2B band density 263 264 within animal (bottom). (C) Representative immunoblots of GluN1 from synaptosomes across age and genotype as indicated (top) and quantification of band density (bottom) normalized to β-actin loading control within lane. 265 (D) Representative immunoblots of scaffolding molecules PSD-95 and SAP102 across age and genotype as 266 indicated (top) and quantification of band density (bottom) normalized to β-actin loading control within lane. For 267 all experiments in Figure 2, Ppt1^{-/-} and WT were compared (n=4 independent experiments/animals with 2 268 repetitions/group) at each age using t-test and the significance was indicated as follows: *p<0.05, and **p<0.01. 269 270 Error bars represent s.e.m.

Figure 3. NMDAR-mediated EPSCs are altered in *Ppt1-/-* visual cortex. (A) Representative traces of NMDA-271 EPSCs recorded from pyramidal neurons in layer II/III of the visual cortex (V1) of WT and Ppt1^{-/-} mice. Red 272 arrows indicate onset of evoked stimulus. Neurons were voltage clamped at +50mV and NMDA-EPSCs evoked 273 in layer IV. (B) Quantification of amplitude of the fast component, Af, slow component, As, and Af/Af+As derived 274 from fitting the decay phase of the evoked NMDA-EPSCs with the double exponential function: $Y(t) = A_{f^*}e^{-t/t}$ fast 275 + $A_{s*}e^{-t/t}$ slow. (C) Quantification of the decay constant of the fast component, τf , slow component, τs , and weighted 276 decay, tw. derived from fitting the decay phase of the evoked NMDA-EPSCs with the double exponential 277 function: $Y(t) = A_{f*}e^{-t/t}_{fast} + A_{s*}e^{-t/t}_{slow}$. For experiments in Figure 3, $Ppt1^{-/-}$ and WT were compared (n=10 cells, 278 4 mice (WT); n=12 cells, 5 mice ($Ppt1^{-/-}$)) using t-test and the significance was indicated as follows: *p<0.05, and 279 **p<0.01. Error bars represent s.e.m.A 280

Figure 4. Dendritic spine morphology is immature in *Ppt1-/-* layer II/III visual cortical neurons. (A) 281 Schematic of *in utero* electroporation procedure and timeline (bottom) (B) Left, coronal diagram from Paxino's 282 mouse brain atlas demonstrating areas of visual cortex and right, representative low-magnification (10x) confocal 283 image of a successfully transfected group of layer II/III neurons in visual cortex. Scale bar=100µm. (C) 284 Representative confocal images of GFP-transfected dendritic segments from WT and *Ppt1*^{-/-} neurons at P33. 285 Arrows mark mature, mushroom-type spines; arrowheads mark thin, filipodial spines or stubby, headless spines. 286 Scale bar=10µm. (**D**) Semi-automated quantification of dendritic spine length in WT and *Ppt1*^{-/-} visual cortical 287 neurons at P33. (E) Semi-automated quantification of dendritic spine volume and spine head volume (inset) in 288 WT and *Ppt1*^{-/-} visual cortical neurons at P33. For experiments in Figure 4, WT and *Ppt1*^{-/-} were compared (n=3-289

4 cells/animal, 3 animals/group) using t-test and the significance was indicated as follows: **p<0.01, *Ppt1^{-/-}* vs.
 WT. Error bars represent s.e.m.

Figure 5. GluN2B to GluN2A NMDAR switch and *Ppt1^{-/-}*-induced synaptic deficits are recapitulated in 292 primary cortical neurons. (A) Representative immunoblot (top) and quantification of GluN2B levels in WT and 293 294 Ppt1^{-/-} neurons at DIV7, 10, and 18. (B) Representative immunoblot (top) and quantification of GluN2A levels (bottom) in WT and *Ppt1^{-/-}* neurons at DIV7, 10, and 18. (C) Representative immunoblot (top) and guantification 295 of PSD-95 levels (bottom) in WT and *Pnt1^{-/-}* neurons at DIV7, 10, and 18, (**D**) Representative immunoblot (top) 296 297 and quantification of the GluN2A/2B ratio (bottom) in WT and *Ppt1^{-/-}* neurons at DIV7, 10, and 18. For all experiments in Figure 5, *Ppt1^{-/-}* and WT were compared (n=2 independent experiments with 2 repetitions/group) 298 at each time point using t-test and the significance was indicated as follows: *p<0.05 Ppt1^{-/-} vs. WT. Error bars 299 300 represent s.e.m.

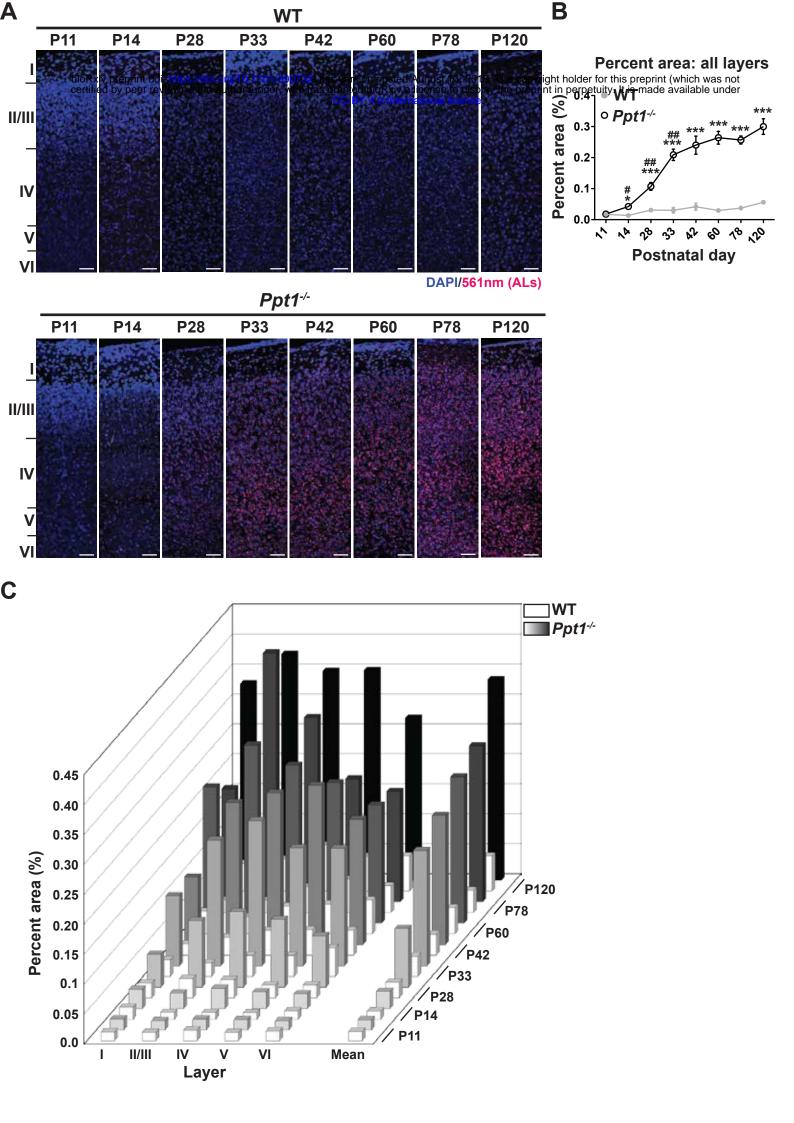
- Figure 6. Dendritic spine morphology is immature in *Ppt1^{-/-}* neurons in vitro. (A) Representative composite 301 confocal images of live DIV15 (left) and DIV20 (right) GFP-transfected, cultured WT and Ppt1^{-/-} neurons. Insets 302 represent dendrite segments within dotted line. Scale bar=10um. (B) Left, quantification of dendritic spine length 303 in WT and *Ppt1^{-/-}* neurons at DIV15 and 20. Spine length is binned into 19 discrete groups from $0 - >4\mu m$. *Right*, 304 mean length of all spines in cultured WT and Ppt1-/- neurons at DIV15 and 20. (C) Left, semi-automated 305 quantification of dendritic spine volume in WT and Ppt1-/- cultured neurons at DIV15 and 20. Spine volume is 306 binned into 27 discrete groups form 0 - >1 μ m³. *Right*, mean volume of all spines in cultured WT and *Ppt1*^{-/-} 307 neurons at DIV15 and 20. For experiments in Figure 6, Ppt1-/- and WT were compared (For DIV15: n=4-5 308 neurons/group, 3-independent experiments, WT=21,514 spines; Ppt1-/=18,013 spines. For DIV20: n=3 309 neurons/group, 2-independent experiments, WT=11,335 spines; Ppt1-/-=9,958 spines) using t-test and the 310 significance was indicated as follows: Left, *p<0.05, within bin where Ppt1^{-/-} is decreased compared to WT; 311 #p<0.05, within bin where Ppt1^{-/-} is increased compared to WT. Right, ##p<.0.01 and ###p<0.001 where Ppt1^{-/-} 312 is increased compared to WT; *p<0.05, ***p<0.001 where Ppt1^{-/-} is decreased compared to WT. Error bars 313 314 represent s.e.m.
- Video 1. Spontaneous calcium activity in DIV16-18 WT neuron. Representative video of spontaneous
 neuronal calcium activity in a WT cultured neuron at DIV16-18.
- Video 2. Spontaneous calcium activity in DIV16-18 *Ppt1^{-/-}* neuron. Representative video of spontaneous
 neuronal calcium activity in a *Ppt1^{-/-}* cultured neuron at DIV16-18.
- Figure 7. Calcium imaging reveals extrasynaptic calcium dynamics in *Ppt1-/-* neurons. DIV16-18, WT and 319 $Ppt1^{-/-}$ cortical neurons transfected with GCaMP3 and imaged in the absence of Mg²⁺ for 5 minutes. (A) Single 320 frames from Videos 1 and 2 of WT (left, note that cell is rotated 90° from Video 1) and Ppt1^{-/-} (right) cultured 321 neurons. Dendritic segments within the dotted-lines represent zoomed-in images of a single spine (left, WT) or 322 dendritic shaft segment (right, Ppt1-/-) at baseline (top) and active (bottom) states. Scale=10um. (B) 323 Representative heat maps of $\Delta F/F_0$ values at one synaptic site from WT (left) and *Ppt1*^{-/-} (right) dendrite segments 324 during a portion the imaging session (350 frames, 50 seconds). (C) Representative averaged $\Delta F/F_0$ responses at 325 one synaptic site from WT (left) and Ppt1^{-/-} (right) neurons. Area under the curve represents calcium influx and 326 is shaded in red. (D) Quantification of calcium transient area under the curve WT and $Pot1^{-/-}$ neurons. (E) 327 Quantification of calcium transient diffusion distance from WT and Ppt1-/- neurons. (F) Quantification of average 328 correlation coefficient (synaptic synchrony) across time between sites of synaptic activity in WT and Ppt1-/-329 neurons. (G) Representative heat maps of $\Delta F/F_0$ values at one synaptic site from WT (left) and Ppt1^{-/-} (right) 330 dendrite segments before (top) and after (bottom) treatment with Ro 25-6981 (130 frames, 18 seconds). (H) 331

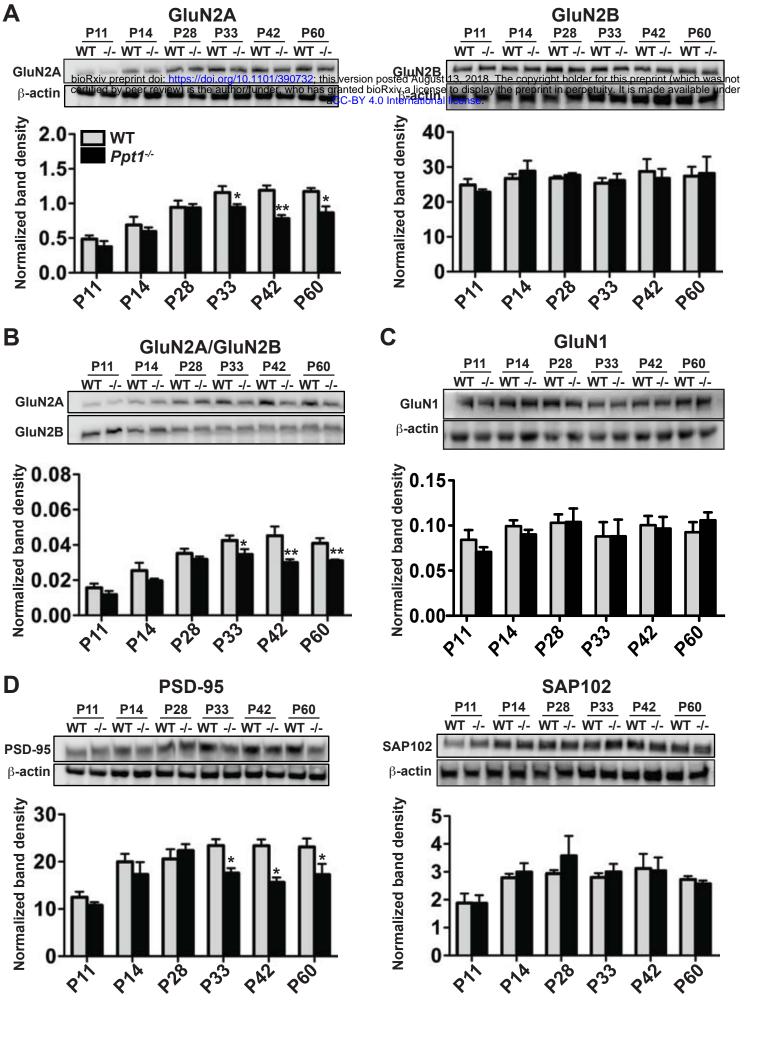
- Quantification of calcium transient area under the curve WT and Ppt1-/- neurons before and after treatment with 332 Ro 25-6981. (I) Quantification of calcium transient diffusion distance from WT and *Ppt1^{-/-}* neurons before and 333 after treatment with Ro 25-6981. For experiments in Figure 7D-E, Ppt1-/- and WT were compared (n=170 synaptic 334 sites (WT), n=131 synaptic sites (Ppt1-/-), 3-6 neurons/group, 3 individual experiments) by t-test and the 335 significance was indicated as follows: ***p<0.001 vs. WT by t-test. For experiments in Figure 7F. Ppt1^{-/-} and 336 WT were compared (n=100 synaptic sites (WT), n=100 synaptic sites (*Ppt1^{-/-}*); 3 neurons/group, 2 individual 337 experiments) by t-test and the significance was indicated as follows: ***p<0.001 vs. WT by t-test. For 338 339 experiments in Figure 7G-H, Ppt1^{-/-} and WT were compared (n=25 synaptic sites (WT), n=28 synaptic sites (Ppt1^{-/-} ^{/-}); 3 neurons/group, 2 individual experiments) by t-test and the significance was indicated as follows: ***p<0.001 340 vs. WT by t-test. 65 pixels is representative of 10µm. Error bars represent s.e.m.
- 341
- 342 Video 3. Spontaneous calcium activity in DIV16-18 WT neuron before and after treatment with Ro 25-6981. Representative video of spontaneous neuronal calcium activity in a WT cultured neuron at DIV16-18 prior 343 to, and following, bath application of Ro 25-6981 (1µM, after 30 seconds). 344
- Video 4. Spontaneous calcium activity in DIV16-18 *Ppt1*^{-/-} neuron before and after treatment with Ro 25-345 6981. Representative video of spontaneous neuronal calcium activity in a Ppt1^{-/-} cultured neuron at DIV16-18 346 prior to, and following, bath application of Ro 25-6981 (1µM, after 31 seconds). 347
- Figure 8. Ppt1-/- cultured neurons show enhanced vulnerability to NMDA-mediated excitotoxicity. (A) 348 Schematic of cellular toxicity experimental design. Briefly, neurons were grown to DIV11, treated with vehicle 349 of palmitoylation inhibitors for 7d (every 48h) and neuronal viability was measured by PrestoBlue® cellular 350 viability assay following exposure (2h exposure, 22h incubation in medium) to NMDA and glycine. (B) 351 Quantification of cellular viability in WT and Ppt1^{-/-} neurons at DIV19 treated with increasing concentrations of 352 NMDA and glycine (10/1, 100/10, and 300/30µm). Ppt1^{-/-} and WT were compared (n=4 independent experiments, 353 in duplicate) by t-test and significance was indicated as follows: *p<0.05 and ***p<0.001 where indicated; black 354 colored symbols indicate significant differences between vehicle and NMDA/glycine treatment within the same 355 genotype; green colored symbols indicate significant differences between Ppt1-/- and WT treated with the same 356 concentration of NMDA/glycine. Error bars represent s.e.m. 357
- Figure 9. Palmitovlation inhibitors rescue enhanced vulnerability to NMDA-mediated excitotoxicity in 358 **Ppt1**^{-/-} cultured neurons. (A) 3D reconstructions of a WT and Ppt1^{-/-} neuron at DIV20. Arrows point to AL 359 deposits. Scale bar=5µm (B) Representative collapsed z-stacks of WT and *Ppt1^{-/-}* DIV20 neurons, demonstrating 360 accumulations of ALs (arrows) within the soma, particularly within LAMP2-positive vesicles, of *Ppt1^{-/-}* neurons. 361 Note the enlarged lysosomes in Ppt1^{-/-}, vehicle-treated neurons. Scale bar=10µm (C) Quantification of the 362 percentage of AL-containing neurons at DIV20 with or without the palmitoylation inhibitors, 2-bromopalmitate 363 364 (2-BP, 1μ M) and cerulenin (1μ M), treatment for 6d. (D) The percentage of soma area occupied by ALs with or without the palmitovlation inhibitors. 2-BP (1uM) and cerulenin (1um), treatment for 6d. (E) Ouantification of 365 the percentage of soma area occupied by lysosomes (LAMP-2-positive vesicles) with and without palmitoylation 366 inhibitor, 2-BP (1µM) and cerulenin (1µM), treatment for 6d. Ppt1-/- and WT were compared (7-10 367 neurons/group/experiment, n=3 independent experiments) by t-test and significance was indicated as follows: 368 *p<0.05, ***p<0.001 vs. vehicle-treated $Ppt1^{-/-}$ neurons; #p<0.05 vs. vehicle-treated WT neurons. (F) 369 Quantification of cellular viability in DIV18-20 WT and Ppt1^{-/-} neurons treated with NMDA and glycine 370 (100/10µM) with or without pretreatment with vehicle (DMSO), 2-BP (1µM) or cerulenin (1µM). Ppt1^{-/-} and WT 371 were compared (n=4 independent experiments, in duplicate) by t-test and significance was indicated as follows: 372 **p<0.01, ***p<0.001 where indicated; black colored symbols indicate significant differences between treatment 373

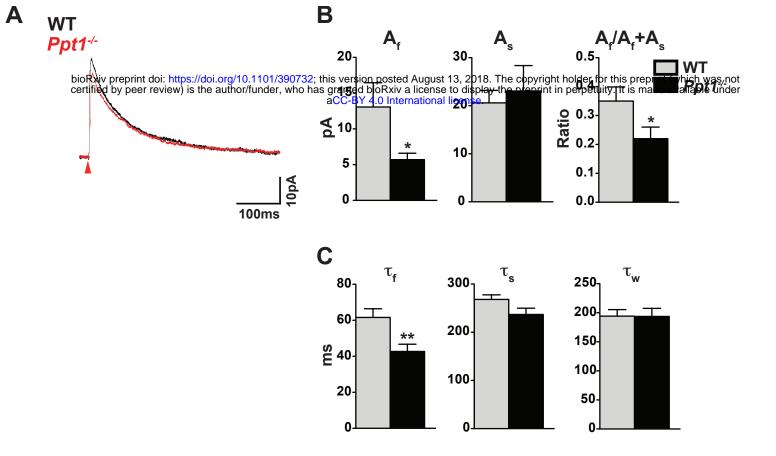
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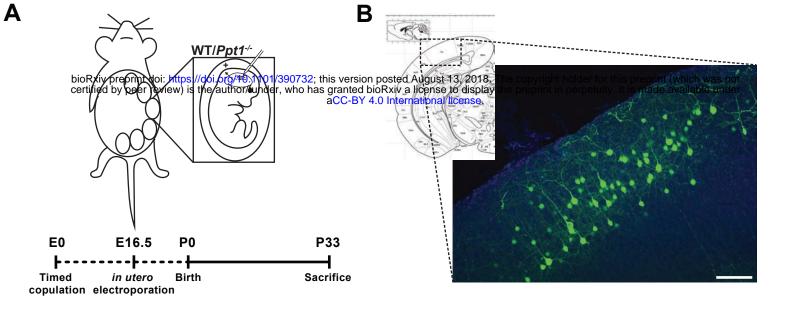
- groups within the same genotype; green colored symbols indicate significant differences between *Ppt1*^{-/-} and WT treated with the same concentration of NMDA/glycine. Error bars represent s.e.m.
- Figure 10. Hyperpalmitovlation of GluN2B and Fyn kinase is reversed in *Ppt1^{-/-}* primary cortical neurons 376 palmitovlation inhibitor treatment. (A) Representative post-APEGS immunoblot with minus 377 bv 378 hydroxylamine (-HA) control (top), and quantification of non-palmitoylated (left), palmitoylated (middle), and the ratio of (palmitoylated/non-palmitoylated, right) GluN2B levels at DIV18 (bottom). (B) Representative post-379 APEGS immunoblot with minus hydroxylamine (-HA) control (top), and quantification of palmitoylated (left), 380 381 and the ratio of (palmitoylated/non-palmitoylated, right) GluN2B levels following chronic (7d) treatment with the palmitoylation inhibitors, 2-BP (1 μ m) or cerulenin (1 μ m) or vehicle control where indicated (bottom). (C) 382 Representative post-APEGS immunoblot with minus hydroxylamine (-HA) control (top), and quantification of 383 palmitoylated (left), and the ratio of (palmitoylated/non-palmitoylated, right) Fyn levels following chronic (7d) 384 treatment with the palmitovlation inhibitors, 2-BP (1um) or cerulenin (1um) or vehicle control where indicated 385 (bottom). For experiments in Figure 10A, Ppt1^{-/-} and WT were compared (n=4 independent experiments) by t-386 test and significance was indicated as follows: **p<0.01. For experiments in Figure 10B-C, *Ppt1^{-/-}* and WT were 387 compared (n=2-4 independent experiments) at each time point using two-way ANOVA followed by Bonferroni 388 post hoc test and the significance was indicated as follows: *p<0.05, **p<0.01 ***p<0.001. Error bars represent 389 390 s.e.m.
- Supplementary Table 1. Mean values, s.e.m., and n for the bar chart in Figure 1C. Values are represented for
 each layer, at each age in WT and *Ppt1^{-/-}* mice.

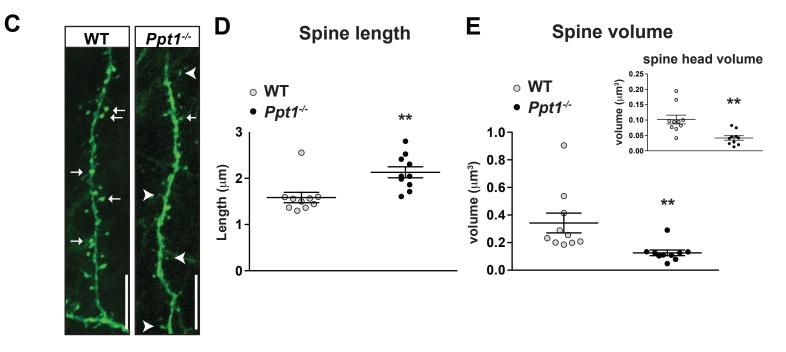
Supplementary Figure 1. (A) Representative immunoblots of the GluN2 subunits, GluN2A and GluN2B in 393 whole lysates across age and genotype as indicated (top) and quantification of band density (bottom) normalized 394 to β-actin loading control within lane. (B) Representative immunoblots of GluN2A and GluN2B (top) from whole 395 lysates across age and genotype and quantification of the ratio of GluN2A/GluN2B band density within animal 396 (bottom). (C) Representative immunoblots of GluN1 in whole lysates across age and genotype as indicated (top) 397 and quantification of band density (bottom) normalized to β-actin loading control within lane. For all experiments 398 in Supplementary figure 1, Ppt1-/- and WT were compared (n=4 independent experiments/animals with 2 399 repetitions/group) at each age using t-test and the significance was indicated as follows: *p<0.05. Error bars 400 401 represent s.e.m.

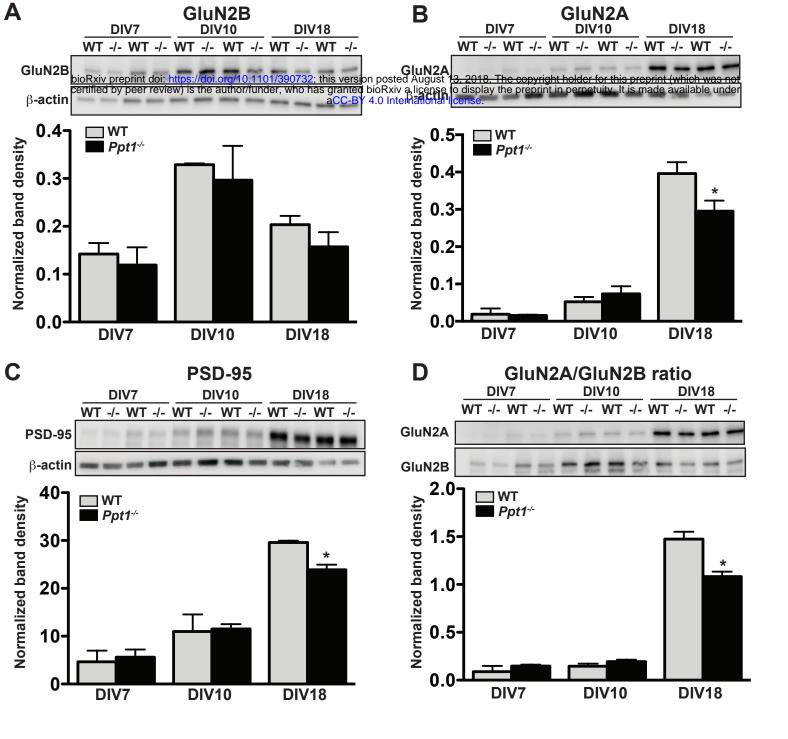


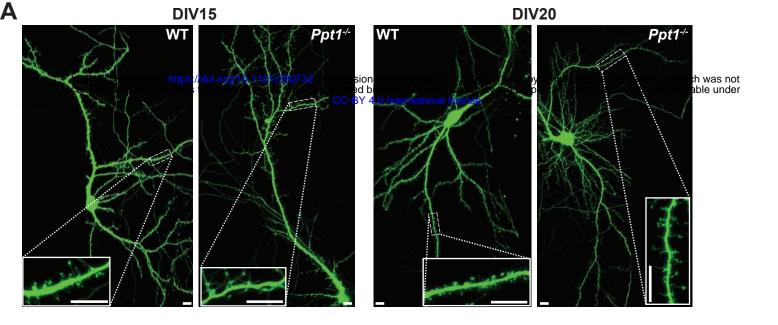


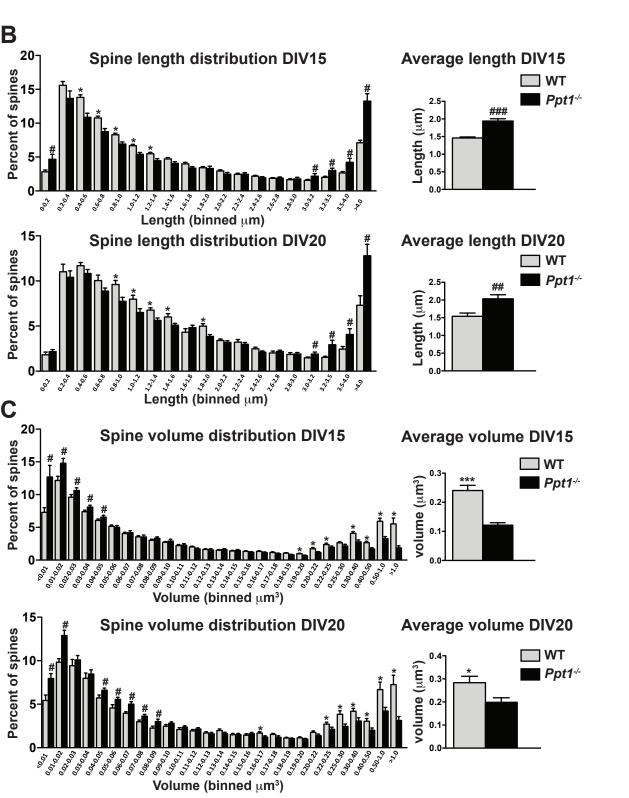


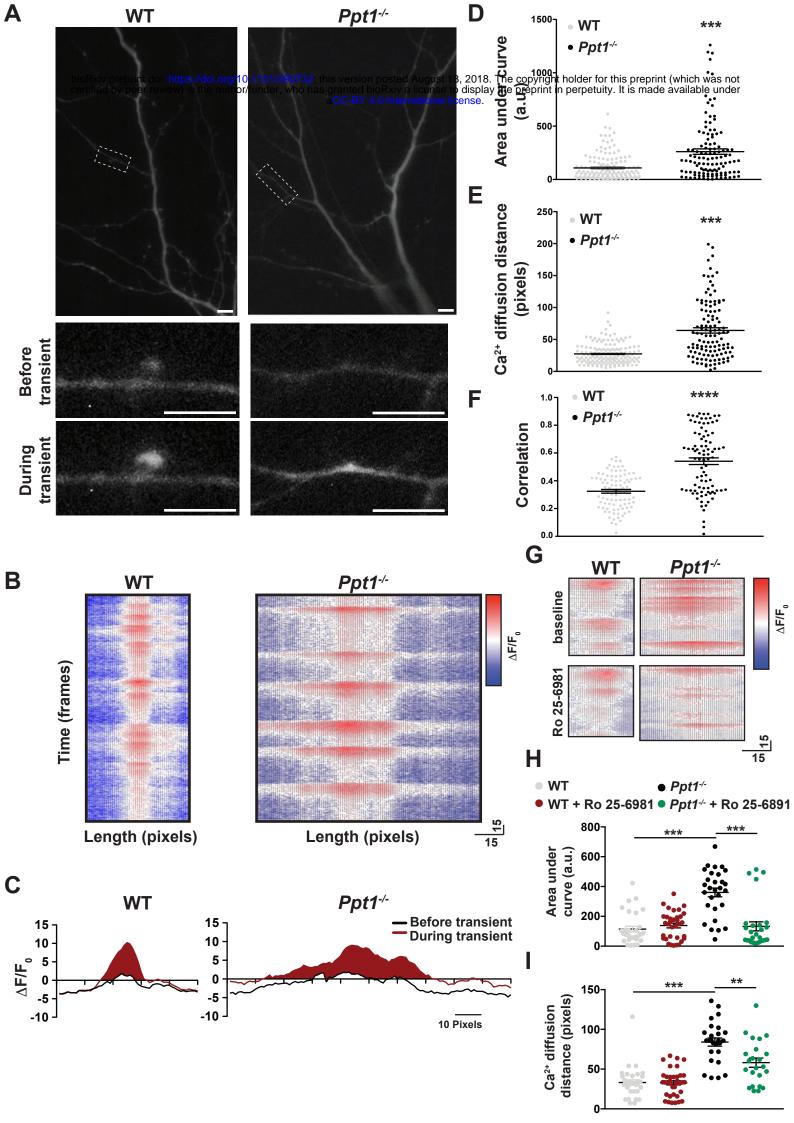












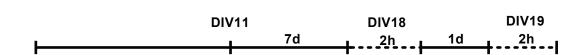
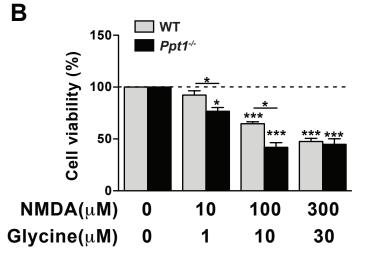
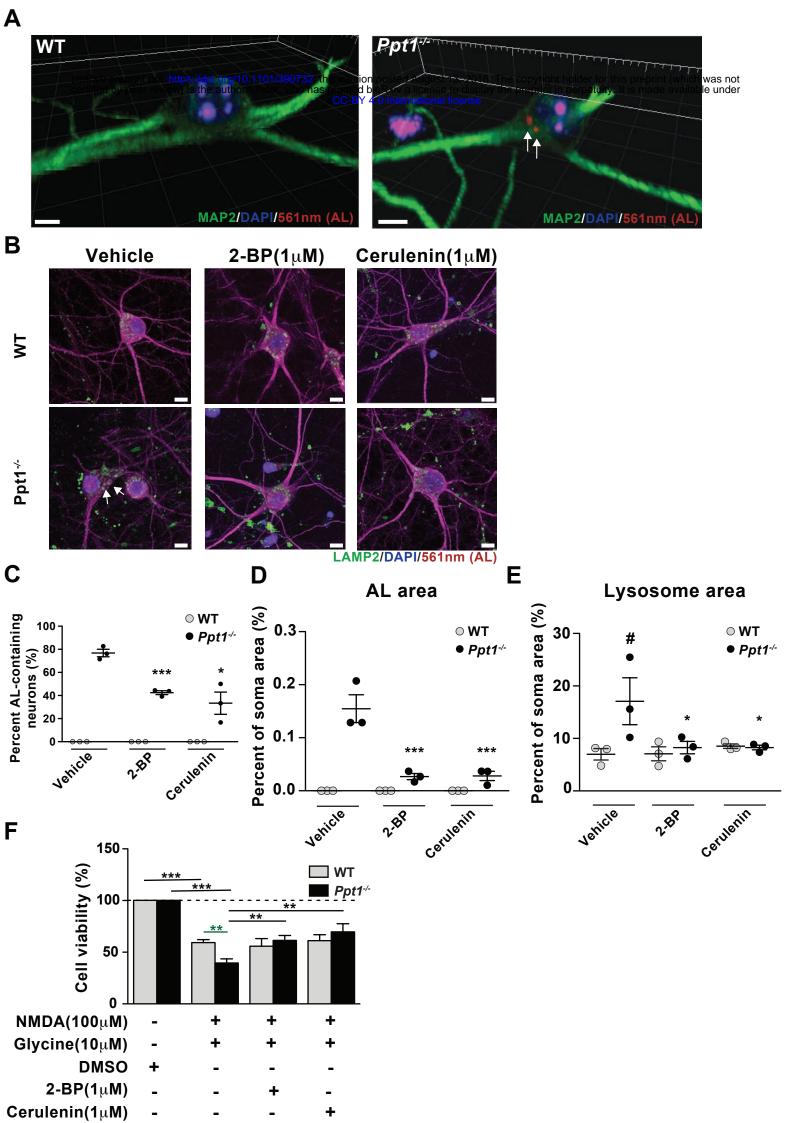
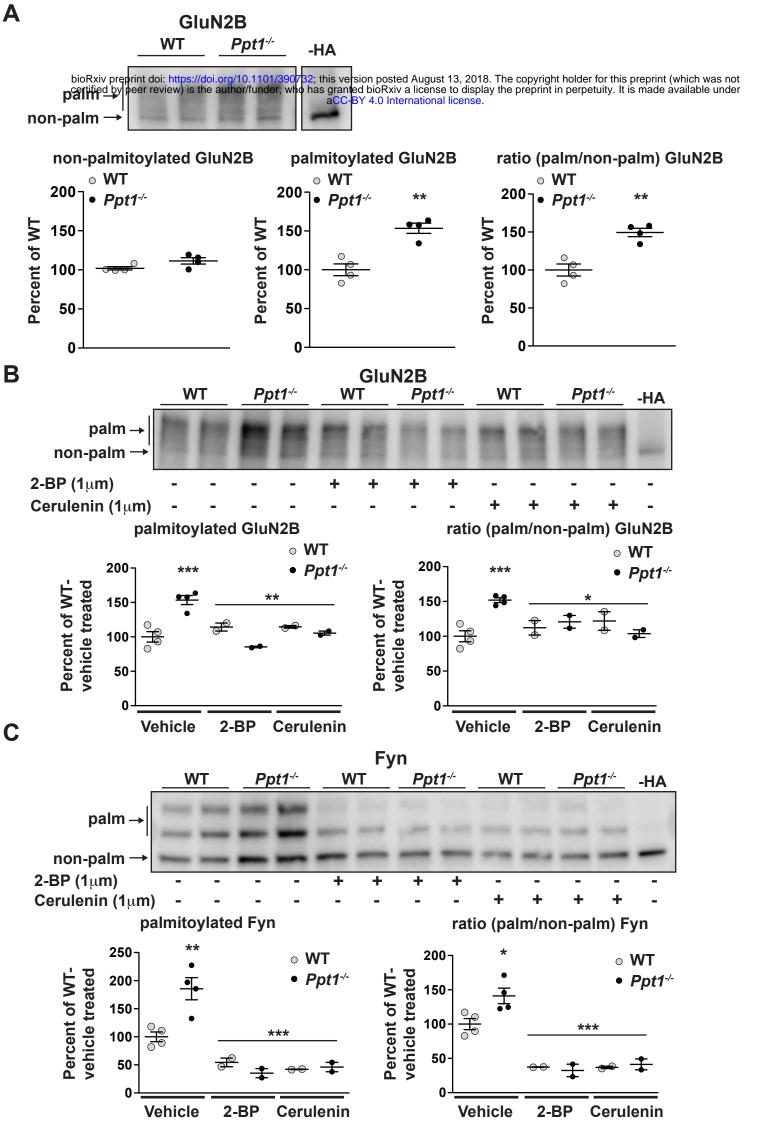


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	Layer	Mean	SEM	n	Mean	SEM	n
	1	0.014726	0.051334		0.018432	0.020171	_
	2/3	0.014029	0.002		0.015746	0.001837	
P11	4	0.017716	0.005554	4	0.018337	0.003265	5
	5	0.013956	0.003186		0.017544	0.002825	
	6	0.016376	0.004648		0.015585	0.009563	
	1	0.020027	0.003256		0.032299	0.003201	_
	2/3	0.012068	0.003681		0.026184	0.003002	
P14	4	0.011678	0.001782	3	0.03401	0.004257	6
	5	0.011427	0.003523		0.028279	0.003798	
	6	0.014201	0.004393		0.024822	0.008465	
	1	0.025066	0.030382	_	0.054899	0.050557	_
	2/3	0.032533	0.008919		0.111296	0.020856	
P28	4	0.030768	0.01448	4	0.125996	0.021164	5
	5	0.021373	0.004357		0.113626	0.017283	
	6	0.021647	0.007201		0.086127	0.013937	<u> </u>
	1	0.028305	0.073043		0.117601	0.023632	
	2/3	0.022777	0.008171		0.21026	0.013193	
P33	4	0.035548	0.011861	5	0.242556	0.034924	6
	5	0.035123	0.010396		0.197036	0.074042	
	6	0.048262	0.010111		0.19617	0.024701	
	1	0.019019	0.060801		0.113172	0.012468	
	2/3	0.030153	0.011804		0.237298	0.021055	
P42	4	0.041546	0.011364	4	0.253448	0.029969	5
	5	0.042801	0.009777		0.265477	0.041234	
	6	0.041961	0.00768		0.209104	0.035667	
	1	0.037639	0.008034		0.227769	0.053888	
	2/3	0.029154	0.009176		0.297558	0.059318	
P60	4	0.046682	0.014308	4	0.263665	0.052311	6
	5	0.049726	0.007089		0.234832	0.038626	
	6	0.056535	0.011388		0.197509	0.041092	
	1	0.020962	0.005615		0.188845	0.002442	1
	2/3	0.020522	0.001178		0.415522	0.007618	
P78	4	0.043183	0.012138	3	0.308193	0.037127	3
	5	0.055858	0.004104		0.205356	0.055491	
	6	0.045009	0.004334		0.184726	0.003858	
	1	0.046265	0.023688		0.32851	0.141037	
	2/3	0.053516	0.029019		0.378299	0.065604	
P120	4	0.077311	0.038016	3	0.349415	0.062099	3
	5	0.058412	0.038213		0.35062	0.059149	
	6	0.059228	0.040012		0.271503	0.068553	[

